



wwPDB EM Validation Summary Report ⓘ

Feb 5, 2024 – 06:23 PM JST

PDB ID : 8IFE
EMDB ID : EMD-35414
Title : Arbekacin-added human 80S ribosome
Authors : Tomono, J.; Asano, K.; Chiashi, T.; Tanaka, Y.; Yokoyama, T.
Deposited on : 2023-02-17
Resolution : 2.57 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

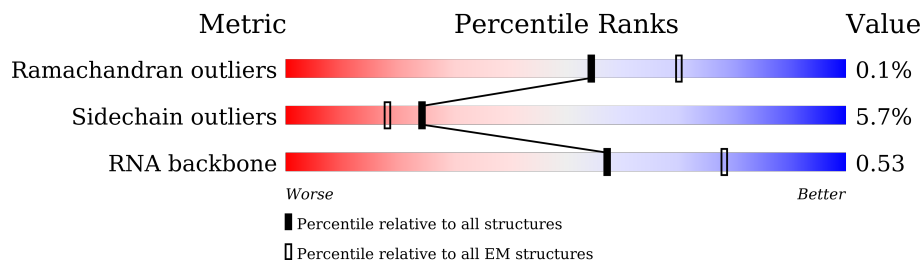
EMDB validation analysis : 0.0.1.dev70
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance

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

The reported resolution of this entry is 2.57 Å.

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





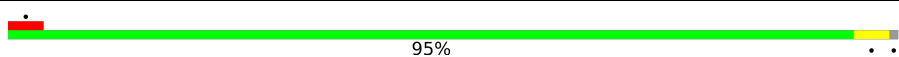
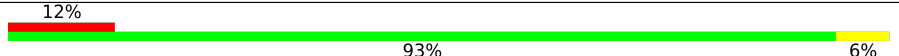
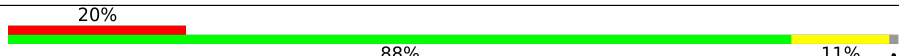
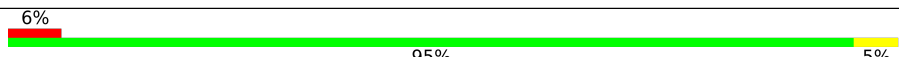
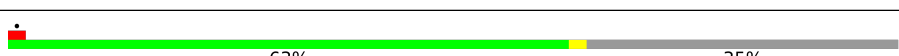
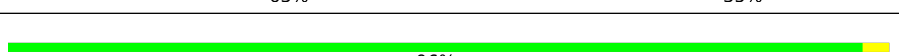
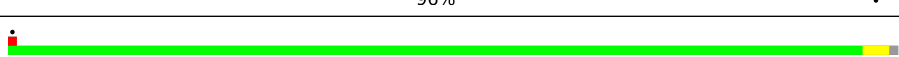
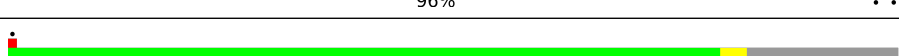
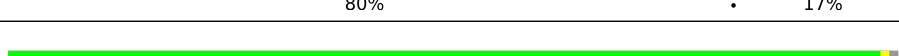
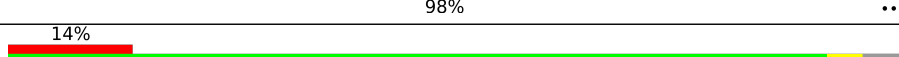
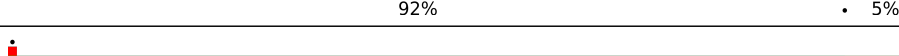
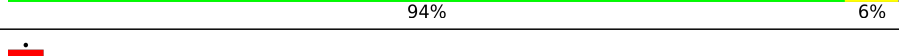
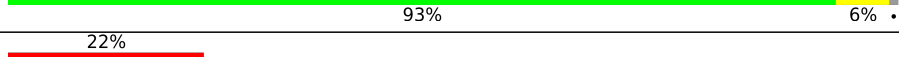

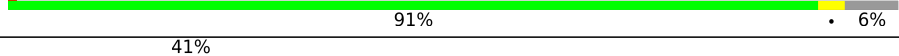


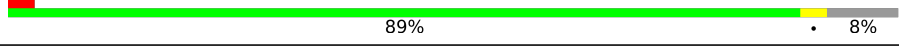
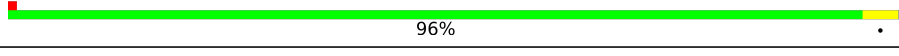
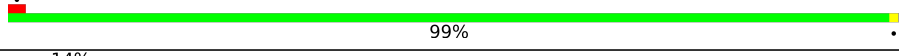



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	1A	5070	
2	1B	121	
3	1C	157	
4	1D	257	
5	1E	403	
6	1F	427	
7	1G	297	
8	1H	288	

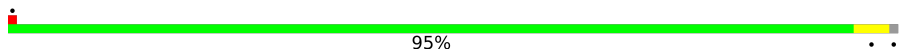
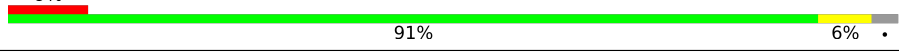
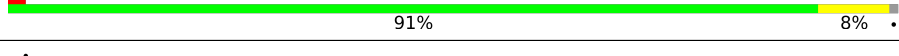
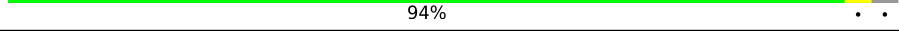
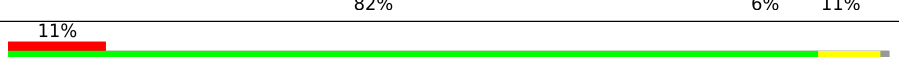
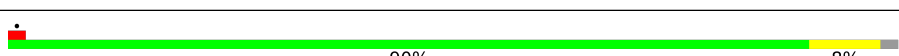


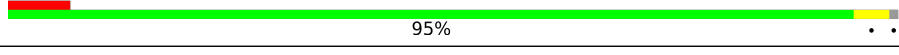
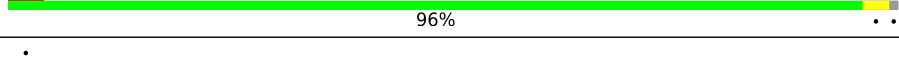
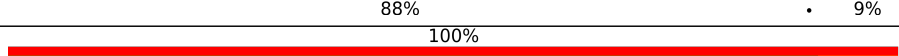
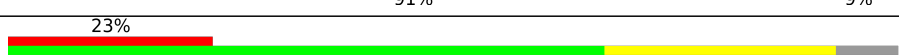


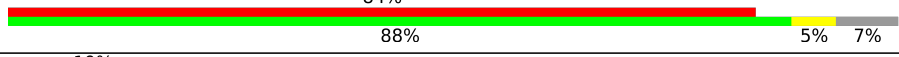
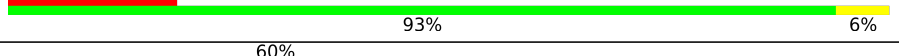



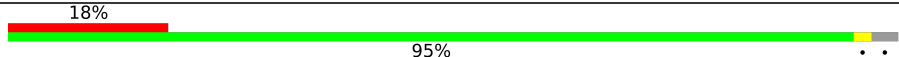

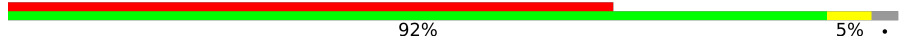



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Mol	Chain	Length	Quality of chain
9	2A	248	
10	2B	266	
11	2C	192	
12	2D	214	
13	2E	178	
14	2F	211	
15	2G	215	
16	2H	204	
17	2I	203	
18	2J	184	
19	2K	188	
20	2L	196	
21	2M	176	
22	2N	160	
23	2O	128	
24	2P	140	
25	2Q	157	
26	2R	156	
27	2S	145	
28	2T	136	
29	2U	148	
30	2V	159	
31	2W	115	
32	2X	125	
33	2Y	135	

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Mol	Chain	Length	Quality of chain
34	2Z	110	 95%
35	2a	117	 91% 6%
36	2b	123	 91% 8%
37	2c	105	 94%
38	2d	97	 82% 6% 11%
39	2e	70	 91% 7%
40	2f	51	 90% 8%
41	2g	128	 38% 59%
42	2h	25	 88% 8%
43	2i	106	 95%
44	2j	92	 96%
45	2k	137	 88% 9%
46	2l	217	 100% 91% 9%
47	2m	1869	 23% 67% 26% 7%
48	2n	295	 44% 71% 25%
49	2o	264	 13% 78% 19%
50	2p	243	 84% 88% 5% 7%
51	2q	263	 19% 93% 6%
52	2r	204	 60% 85% 8% 7%
53	2s	194	 60% 89% 7%
54	2t	208	 22% 92% 7%
55	2u	165	 59% 56% 41%
56	2v	158	 18% 95%
57	2w	145	 85% 81% 6% 12%
58	2x	146	 68% 92% 5%

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Mol	Chain	Length	Quality of chain
59	2y	135	87% 90% 10%
60	2z	152	77% 87% 9% 5%
61	20	145	64% 91% 8%
62	21	119	72% 81% 6% 13%
63	3A	83	60% 93% 7%
64	3B	143	15% 93% 6%
65	3C	115	16% 84% 11%
66	3D	69	59% 87% 6% 7%
67	3E	56	73% 86% 12%
68	3F	317	98% 95%
69	3G	293	15% 72% 24%
70	3H	249	52% 90% 6% 5%
71	3I	194	27% 90% 6% 5%
72	3J	132	92% 89% 8%
73	3K	151	13% 94% 5%
74	3L	151	13% 89% 7%
75	3M	130	7% 95%
76	3N	133	39% 94% 5%
77	3O	125	50% 58% 40%
78	3P	84	63% 94% 5%
79	3Q	59	53% 92% 7%
80	3R	156	43% 41% 57%

2 Entry composition

There are 83 unique types of molecules in this entry. The entry contains 219097 atoms, of which 1012 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 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1A	3717	79676	35480	14585	25895	3716	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1A	2113	C	G	conflict	GB 86475748

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	1B	120	2558	1141	456	842	119	0	0

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	1C	156	3314	1480	585	1094	155	0	0

- Molecule 4 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	1D	248	1898	1189	389	314	6	0	0

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	1E	402	3238	2060	608	556	14	0	0

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	1F	368	2927	1840	583	489	15	0	0

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	1G	293	2382	1507	434	427	14	0	0

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	1H	236	1904	1222	361	317	4	0	0

- Molecule 9 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	2A	225	1878	1207	361	301	9	1	0

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	2B	241	1935	1233	374	324	4	1	0

- Molecule 11 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	2C	190	1518	956	284	272	6	0	0

- Molecule 12 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	2D	213	1711	1082	329	285	15	0	0

- Molecule 13 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	2E	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	2F	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	2G	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	2H	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 17 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	2I	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 18 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	2J	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	2K	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	2L	187	1566	971	336	250	9	0	0

- Molecule 21 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	2M	175	1453	925	283	235	10	0	0

- Molecule 22 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	2N	159	1298	823	252	217	6	0	0

- Molecule 23 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	2O	101	825	529	144	150	2	0	0

- Molecule 24 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	2P	131	979	618	184	172	5	0	0

- Molecule 25 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	2Q	124	1015	634	207	170	4	0	0

- Molecule 26 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	2R	120	985	630	185	169	1	0	0

- Molecule 27 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	2S	134	1115	700	226	186	3	0	0

- Molecule 28 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	2T	135	1107	714	208	182	3	0	0

- Molecule 29 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	2U	147	1162	736	237	186	3	0	0

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	2V	109	882	549	192	137	4	0	0

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	2W	98	764	485	135	138	6	0	0

- Molecule 32 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	2X	107	888	560	171	155	2	0	0

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	2Y	128	1053	667	216	165	5	0	0

- Molecule 34 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	2Z	109	876	555	174	144	3	0	0

- Molecule 35 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	2a	114	906	566	187	147	6	0	0

- Molecule 36 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	2b	122	1015	641	205	168	1	0	0

- Molecule 37 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	2c	102	832	521	177	129	5	0	0

- Molecule 38 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	2d	86	713	439	158	111	5	1	0

- Molecule 39 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	2e	69	569	366	103	99	1	0	0

- Molecule 40 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	2f	50	444	281	98	64	1	0	0

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	2g	52	Total	C	N	O	S	0	0
			430	267	90	67	6		

- Molecule 42 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	2h	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 43 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	2i	105	Total	C	N	O	S	1	0
			870	547	178	139	6		

- Molecule 44 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	2j	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 45 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	2k	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 46 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	2l	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 47 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	2m	1742	Total	C	N	O	P	0	0
			36900	16458	6595	12106	1741		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2m	582	C	U	conflict	GB 36162
2m	583	C	A	conflict	GB 36162
2m	584	G	A	conflict	GB 36162
2m	798	A	G	conflict	GB 36162
2m	1095	U	C	conflict	GB 36162

- Molecule 48 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	2n	221	1741	1106	305	322	8	0	0

- Molecule 49 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	2o	214	1738	1103	310	311	14	0	0

- Molecule 50 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	2p	227	1765	1125	317	315	8	0	0

- Molecule 51 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	2q	262	2076	1324	386	358	8	0	0

- Molecule 52 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	2r	189	1495	934	284	270	7	0	0

- Molecule 53 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	2s	186	1497	956	274	266	1	0	0

- Molecule 54 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	2t	206	1686	1058	332	291	5	0	0

- Molecule 55 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	2u	98	827	539	148	134	6	0	0

- Molecule 56 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	2v	153	1247	793	234	214	6	0	0

- Molecule 57 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	2w	127	1045	663	198	177	7	0	0

- Molecule 58 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	2x	141	1124	715	212	194	3	0	0

- Molecule 59 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	2y	135	1090	685	202	198	5	0	0

- Molecule 60 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	2z	145	1198	751	242	203	2	0	0

- Molecule 61 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	20	143	1112	697	214	198	3	0	0

- Molecule 62 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	21	103	817	511	155	147	4	0	0

- Molecule 63 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	3A	83	636	393	117	121	5	0	0

- Molecule 64 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	3B	141	1098	693	219	183	3	0	0

- Molecule 65 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	3C	102	829	517	174	133	5	1	0

- Molecule 66 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	3D	64	506	308	102	94	2	0	0

- Molecule 67 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	3E	55	459	286	94	74	5	0	0

- Molecule 68 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	3F	313	2436	1535	424	465	12	0	0

- Molecule 69 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	3G	222	1733	1120	301	302	10	1	0

- Molecule 70 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
70	3H	237	1923	1200	387	329	7	0	0

- Molecule 71 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	3I	185	1533	974	309	248	2	1	0

- Molecule 72 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	3J	122	942	590	165	179	8	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3J	52	GLN	LEU	conflict	UNP P25398
3J	69	LEU	CYS	conflict	UNP P25398
3J	99	ASN	LYS	conflict	UNP P25398

- Molecule 73 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	3K	150	1208	773	229	205	1	0	0

- Molecule 74 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	3L	140	1049	642	204	197	6	0	0

- Molecule 75 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	3M	129	1034	659	193	176	6	0	0

- Molecule 76 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	3N	131	1073	678	212	178	5	1	0

- Molecule 77 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
77	3O	75	598	382	111	104	1	0	0

- Molecule 78 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
78	3P	83	651	408	121	115	7	0	0

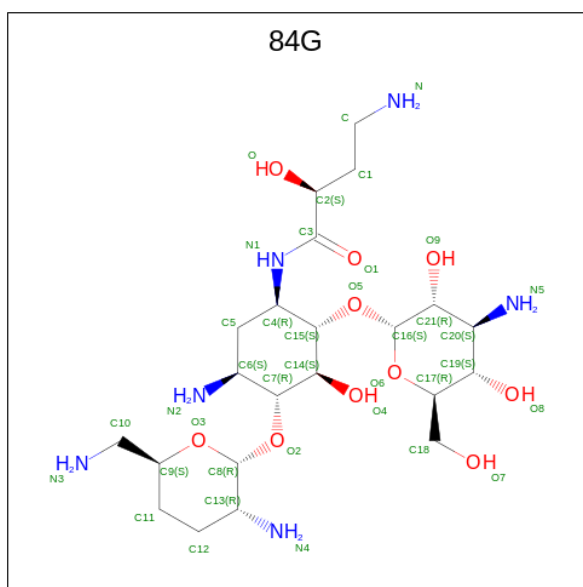
- Molecule 79 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
79	3Q	58	459	284	100	74	1	0	0

- Molecule 80 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
80	3R	67	548	346	102	93	7	0	0

- Molecule 81 is Arbekacin (three-letter code: 84G) (formula: C₂₂H₄₄N₆O₁₀) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf	
			Total	C	H	N		O
81	1A	1	Total	C	H	N	O	0
			82	22	44	6	10	
81	1A	1	Total	C	H	N	O	0
			82	22	44	6	10	
81	1A	1	Total	C	H	N	O	0
			82	22	44	6	10	
81	1A	1	Total	C	H	N	O	0
			82	22	44	6	10	
81	1A	1	Total	C	H	N	O	0
			82	22	44	6	10	
81	1A	1	Total	C	H	N	O	0
			82	22	44	6	10	
81	1A	1	Total	C	H	N	O	0
			82	22	44	6	10	
81	1A	1	Total	C	H	N	O	0
			82	22	44	6	10	
81	1A	1	Total	C	H	N	O	0
			82	22	44	6	10	
81	1A	1	Total	C	H	N	O	0
			82	22	44	6	10	
81	1A	1	Total	C	H	N	O	0
			82	22	44	6	10	

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Mol	Chain	Residues	Atoms					AltConf
81	1A	1	Total	C	H	N	O	0
			82	22	44	6	10	
81	1A	1	Total	C	H	N	O	0
			82	22	44	6	10	
81	1A	1	Total	C	H	N	O	0
			82	22	44	6	10	
81	1A	1	Total	C	H	N	O	0
			82	22	44	6	10	
81	1A	1	Total	C	H	N	O	0
			82	22	44	6	10	
81	2D	1	Total	C	H	N	O	0
			82	22	44	6	10	
81	2i	1	Total	C	H	N	O	0
			82	22	44	6	10	
81	2m	1	Total	C	H	N	O	0
			82	22	44	6	10	
81	2m	1	Total	C	H	N	O	0
			82	22	44	6	10	

- Molecule 82 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
82	1A	268	Total	Mg	0
			268	268	
82	1B	3	Total	Mg	0
			3	3	
82	1C	5	Total	Mg	0
			5	5	
82	1D	1	Total	Mg	0
			1	1	
82	1E	1	Total	Mg	0
			1	1	
82	2H	1	Total	Mg	0
			1	1	
82	2J	1	Total	Mg	0
			1	1	
82	2L	1	Total	Mg	0
			1	1	
82	2M	2	Total	Mg	0
			2	2	
82	2P	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
82	2Y	1	Total 1	Mg 1	0
82	2Z	1	Total 1	Mg 1	0
82	2a	1	Total 1	Mg 1	0
82	2d	1	Total 1	Mg 1	0
82	2m	120	Total 120	Mg 120	0
82	2o	1	Total 1	Mg 1	0
82	3H	1	Total 1	Mg 1	0

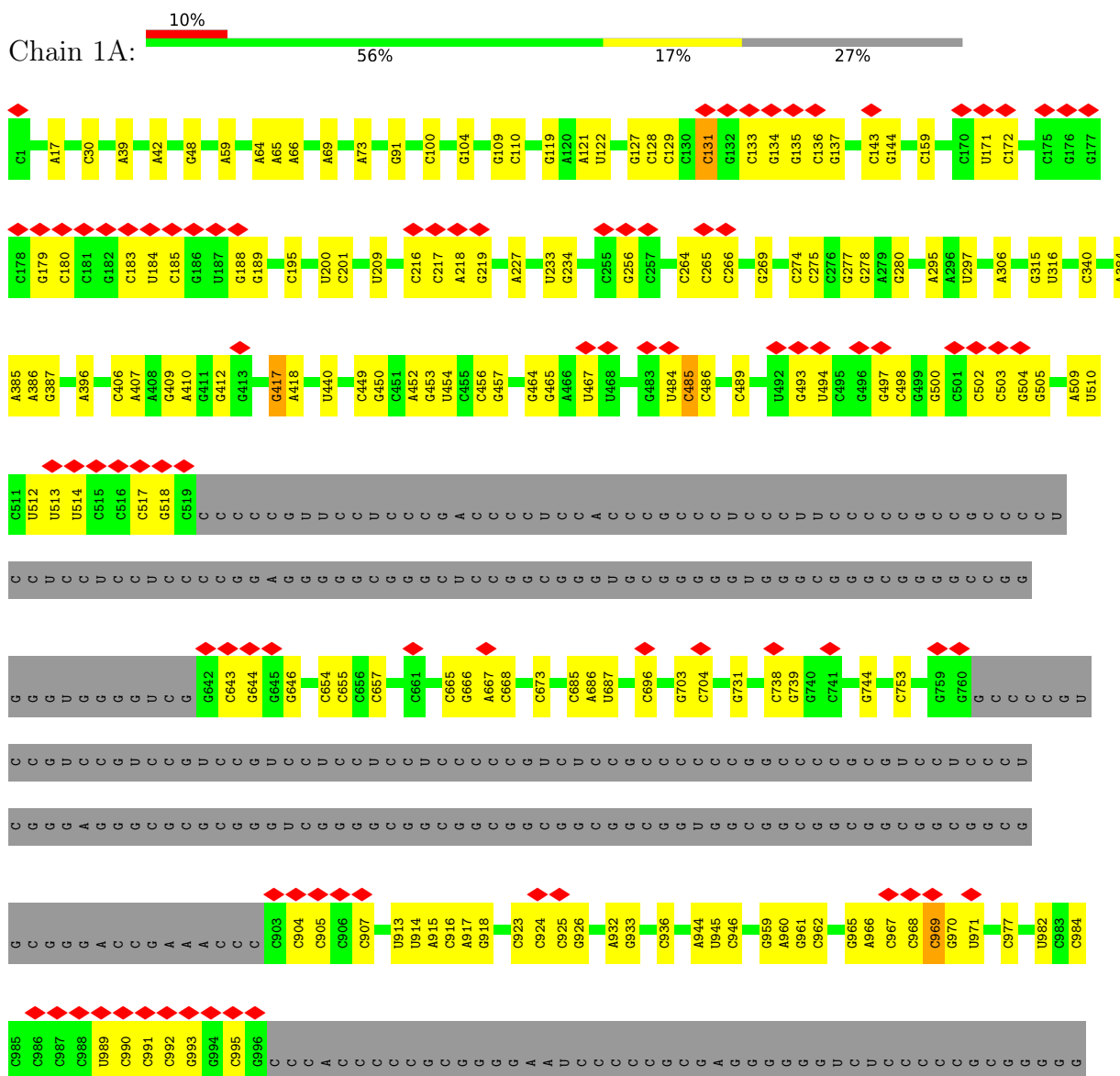
- Molecule 83 is ZINC ION (three-letter code: ZN) (formula: Zn).

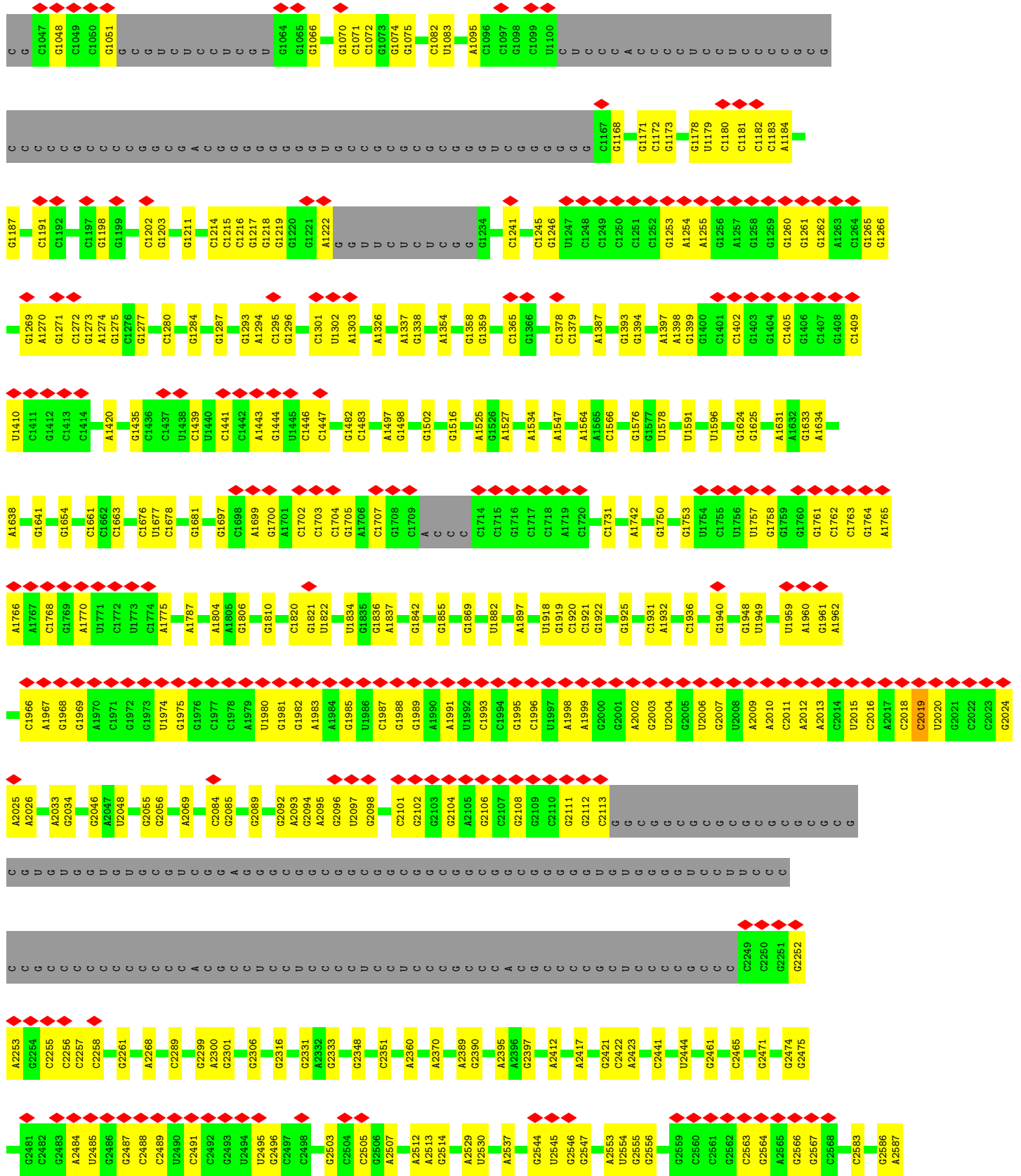
Mol	Chain	Residues	Atoms		AltConf
83	2d	1	Total 1	Zn 1	0
83	2g	1	Total 1	Zn 1	0
83	2i	1	Total 1	Zn 1	0
83	2j	1	Total 1	Zn 1	0
83	3C	1	Total 1	Zn 1	0
83	3E	1	Total 1	Zn 1	0

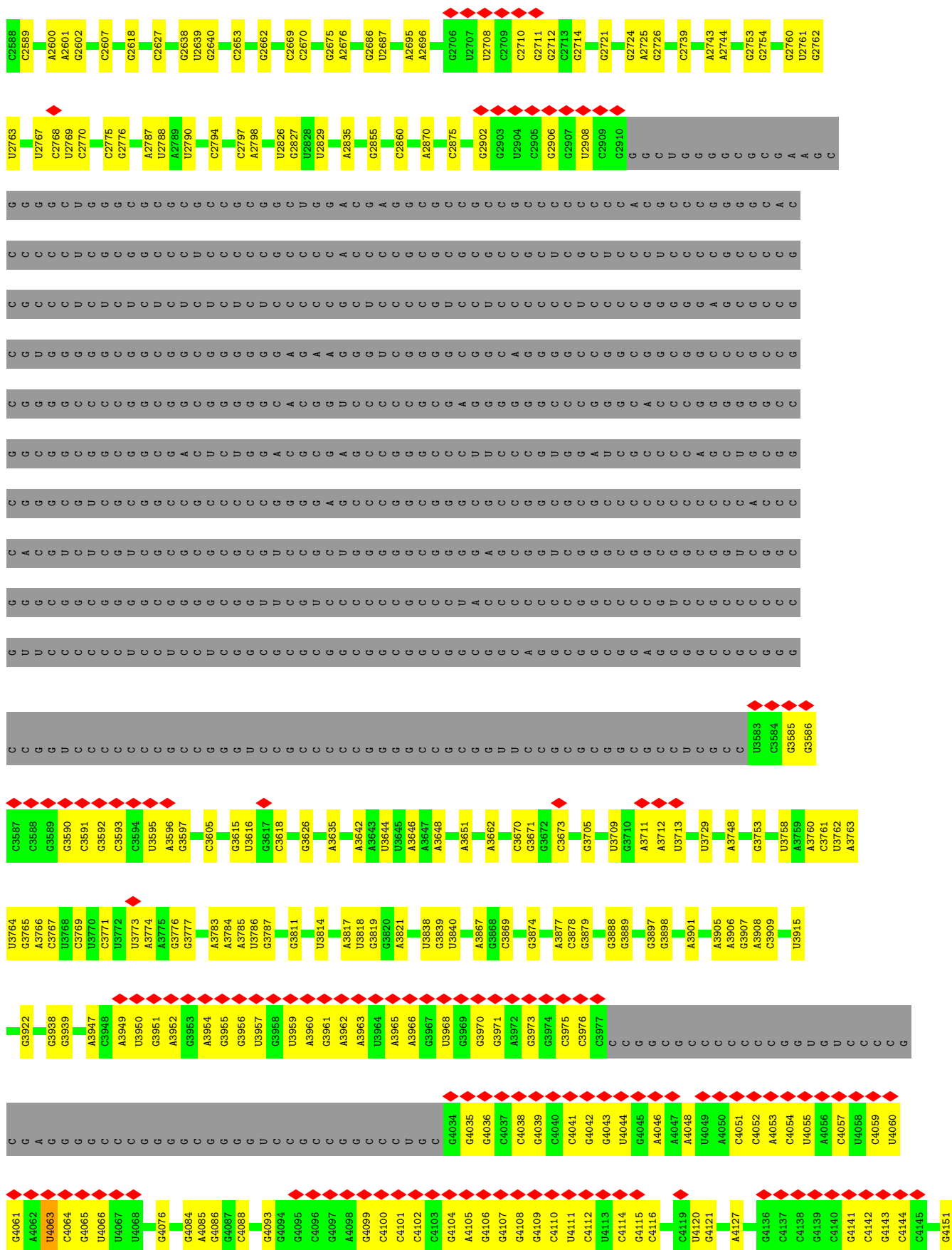
3 Residue-property plots

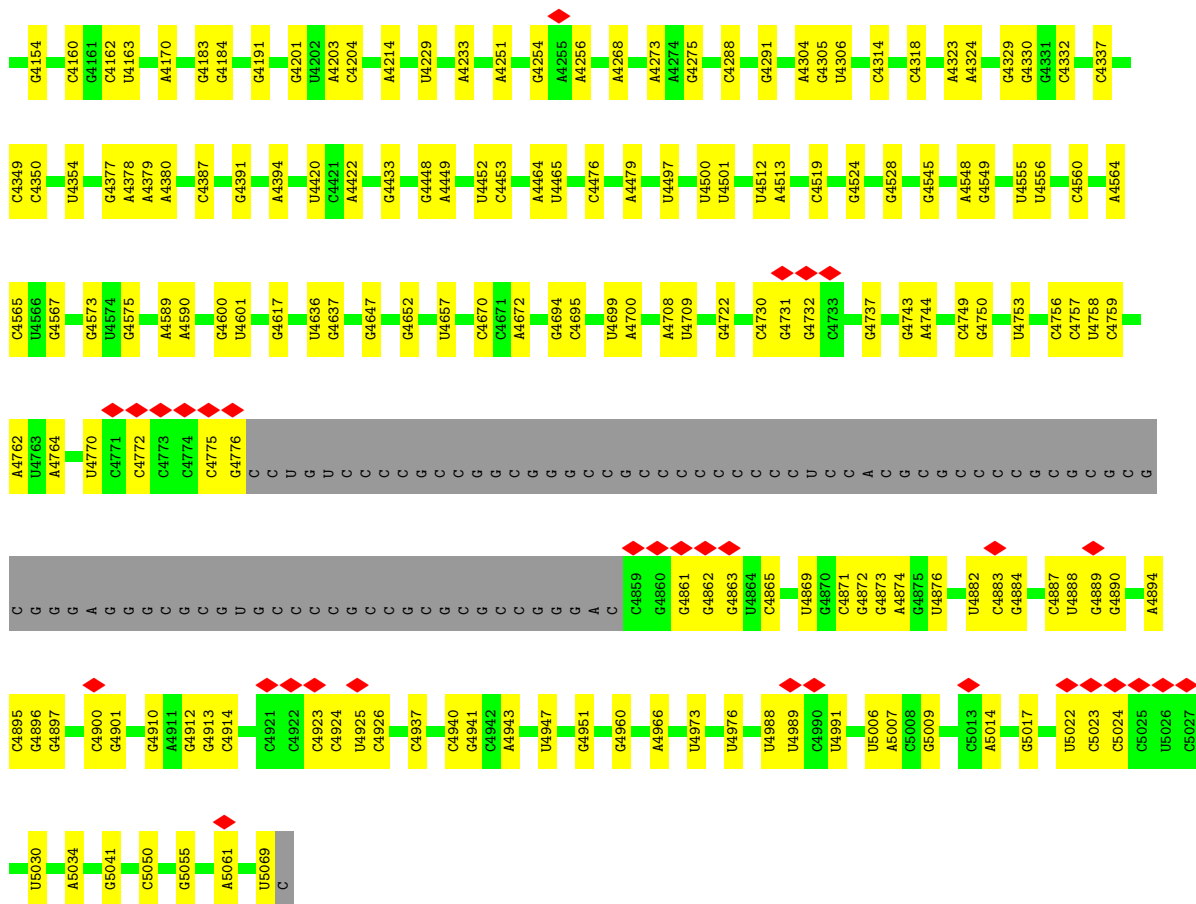
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 28S ribosomal RNA

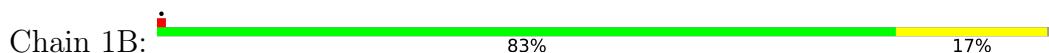




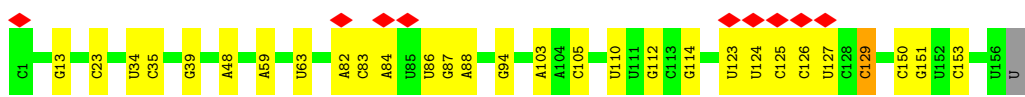
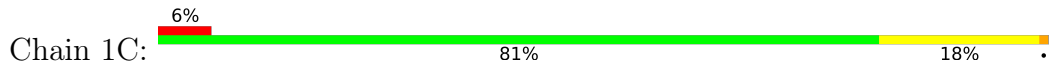




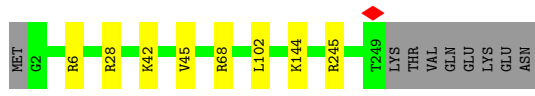
• Molecule 2: 5S ribosomal RNA



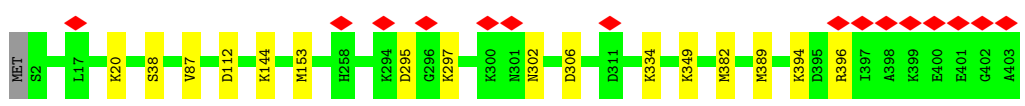
• Molecule 3: 5.8S ribosomal RNA



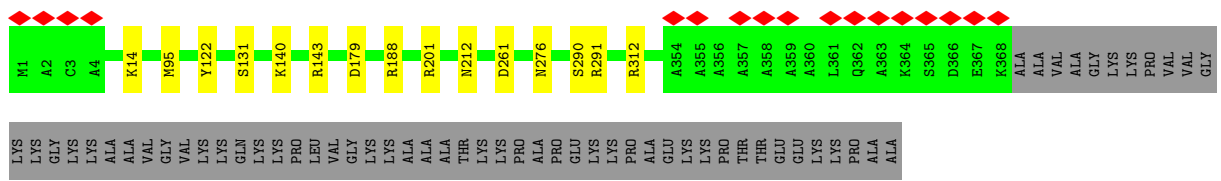
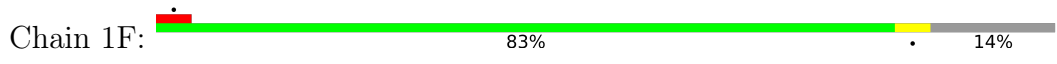
• Molecule 4: 60S ribosomal protein L8



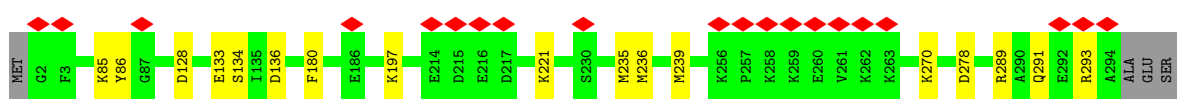
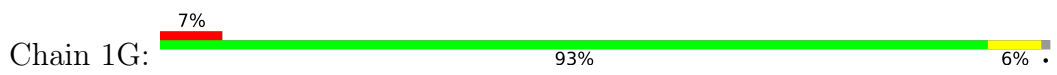
• Molecule 5: 60S ribosomal protein L3



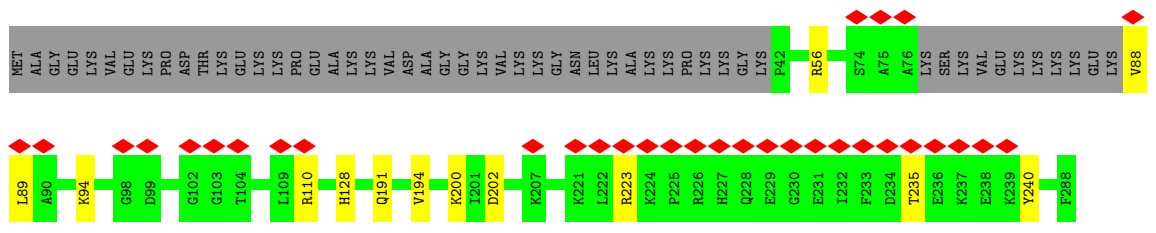
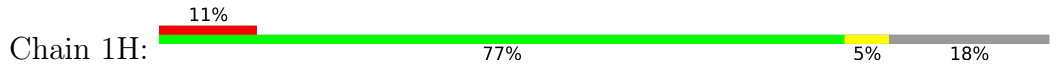
• Molecule 6: 60S ribosomal protein L4



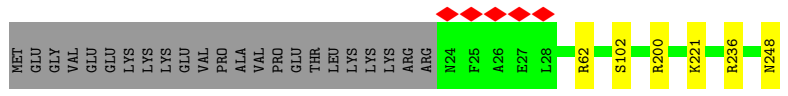
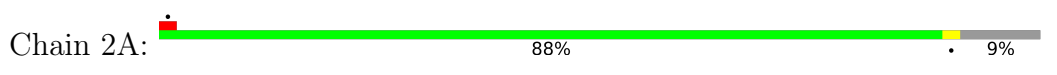
• Molecule 7: 60S ribosomal protein L5



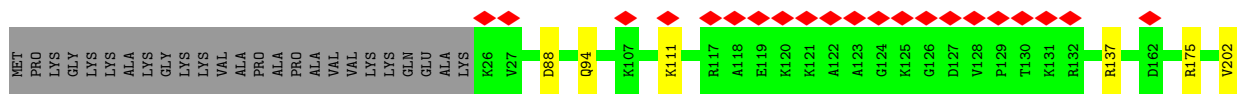
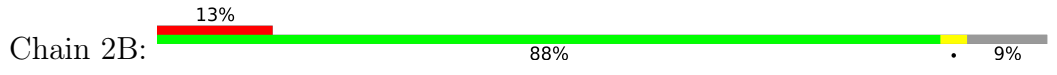
• Molecule 8: 60S ribosomal protein L6

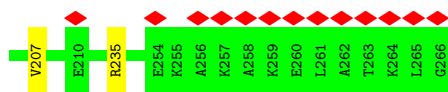


• Molecule 9: 60S ribosomal protein L7

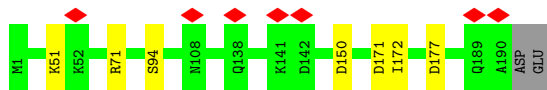


• Molecule 10: 60S ribosomal protein L7a

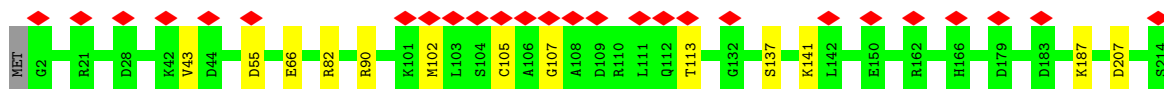




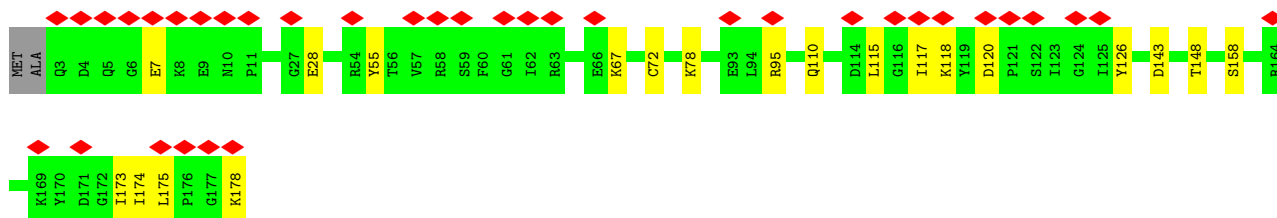
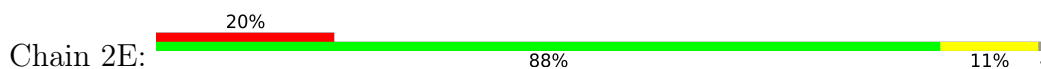
- Molecule 11: 60S ribosomal protein L9



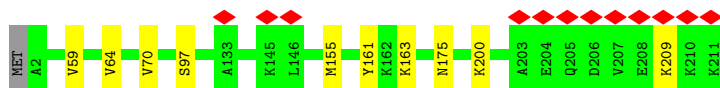
- Molecule 12: 60S ribosomal protein L10-like



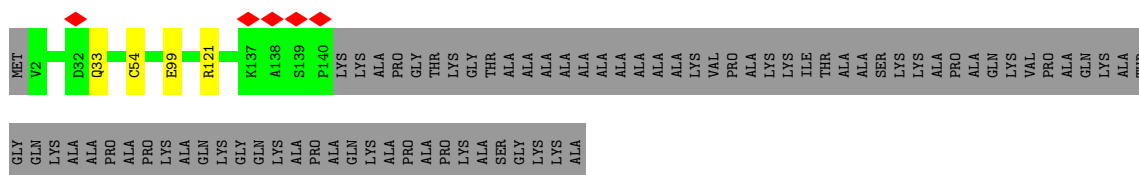
- Molecule 13: 60S ribosomal protein L11



- Molecule 14: 60S ribosomal protein L13



- Molecule 15: 60S ribosomal protein L14



- Molecule 16: 60S ribosomal protein L15

Chain 2H:  96%




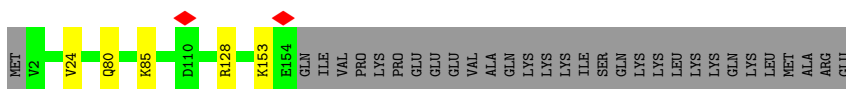
- Molecule 17: 60S ribosomal protein L13a

Chain 2I:  96%



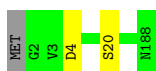
- Molecule 18: 60S ribosomal protein L17

Chain 2J:  80%

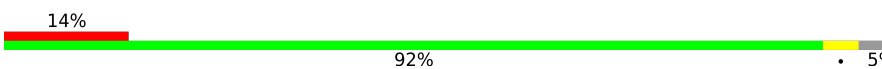


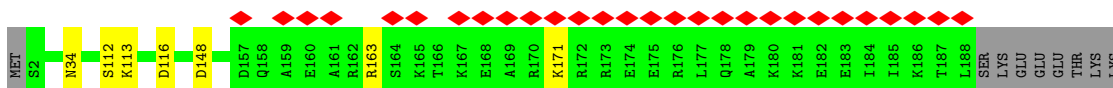
- Molecule 19: 60S ribosomal protein L18

Chain 2K:  98%



- Molecule 20: 60S ribosomal protein L19

Chain 2L:  14% 92% 5%



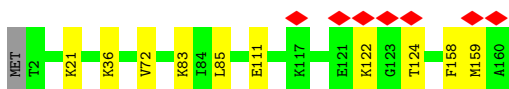
- Molecule 21: 60S ribosomal protein L18a

Chain 2M:  94%

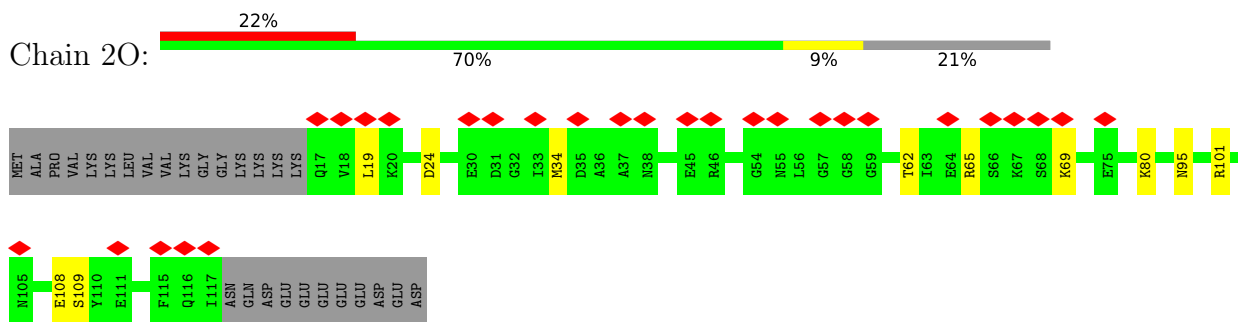


- Molecule 22: 60S ribosomal protein L21

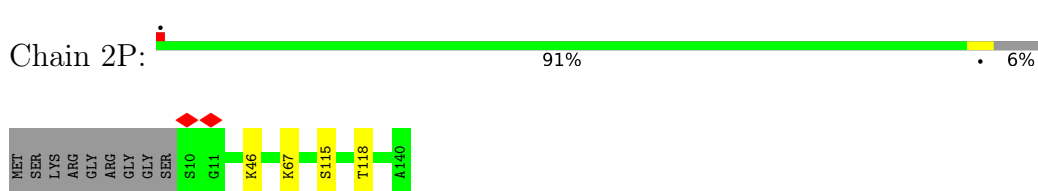
Chain 2N:  93%



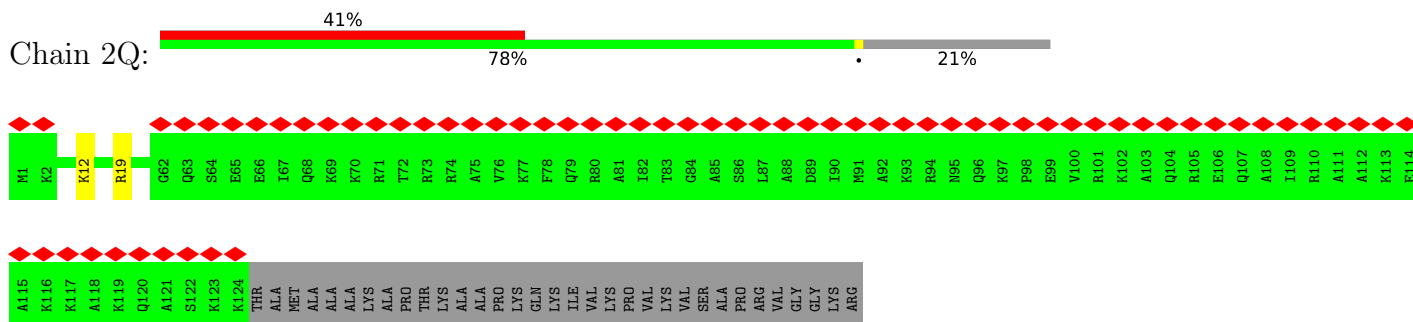
• Molecule 23: 60S ribosomal protein L22



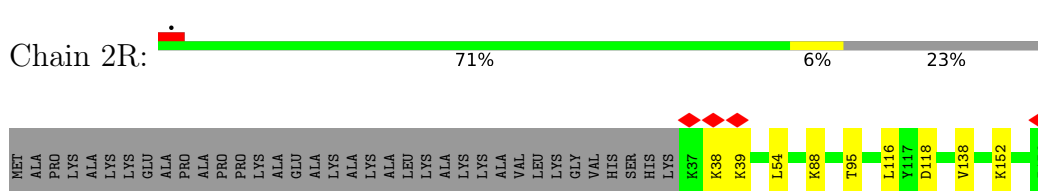
• Molecule 24: 60S ribosomal protein L23



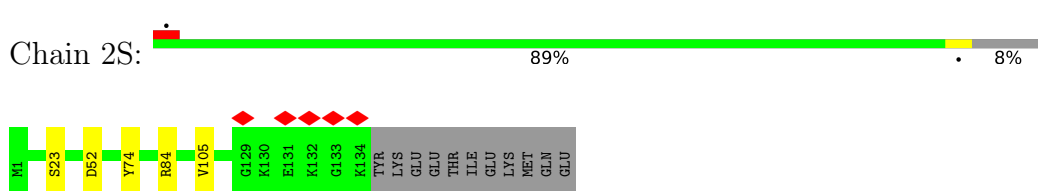
• Molecule 25: 60S ribosomal protein L24



• Molecule 26: 60S ribosomal protein L23a

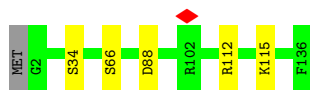


• Molecule 27: 60S ribosomal protein L26

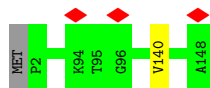


• Molecule 28: 60S ribosomal protein L27

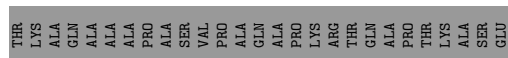




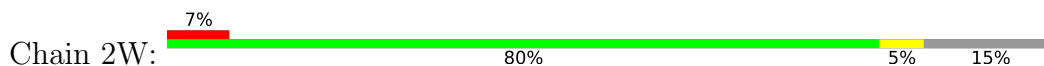
- Molecule 29: 60S ribosomal protein L27a



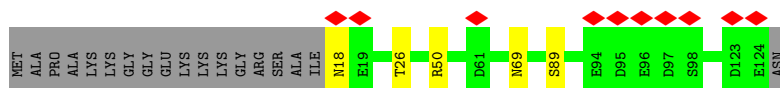
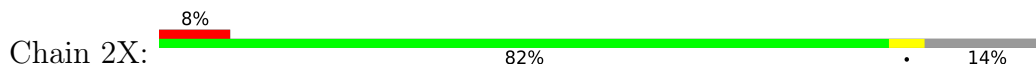
- Molecule 30: 60S ribosomal protein L29



- Molecule 31: 60S ribosomal protein L30



- Molecule 32: 60S ribosomal protein L31



- Molecule 33: 60S ribosomal protein L32

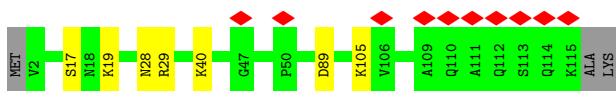
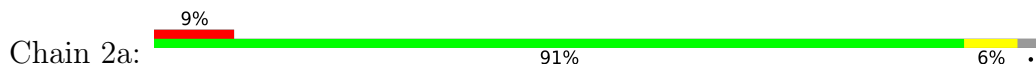


- Molecule 34: 60S ribosomal protein L35a

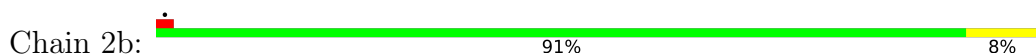




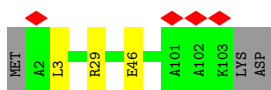
- Molecule 35: 60S ribosomal protein L34



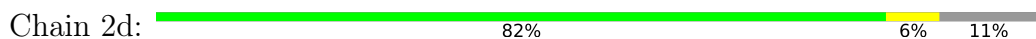
- Molecule 36: 60S ribosomal protein L35



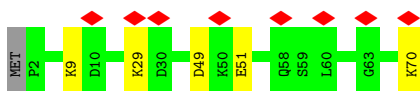
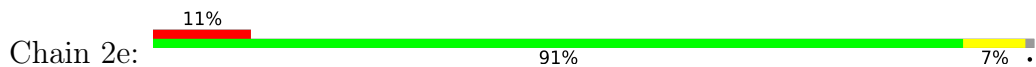
- Molecule 37: 60S ribosomal protein L36



- Molecule 38: 60S ribosomal protein L37



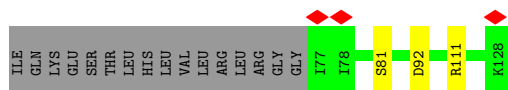
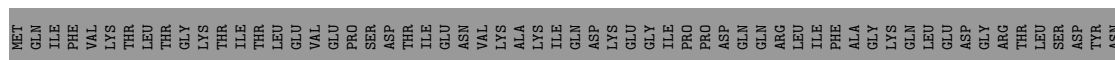
- Molecule 39: 60S ribosomal protein L38



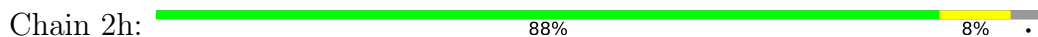
- Molecule 40: 60S ribosomal protein L39



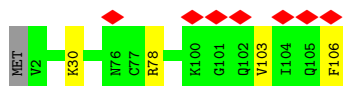
- Molecule 41: Ubiquitin-60S ribosomal protein L40



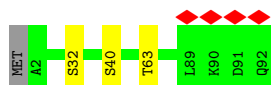
- Molecule 42: 60S ribosomal protein L41



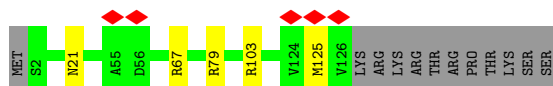
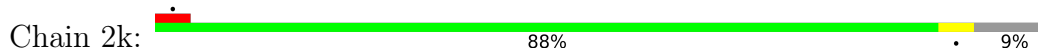
- Molecule 43: 60S ribosomal protein L36a



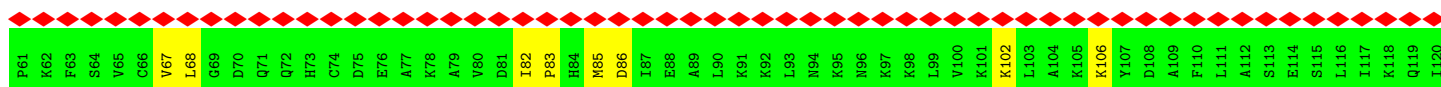
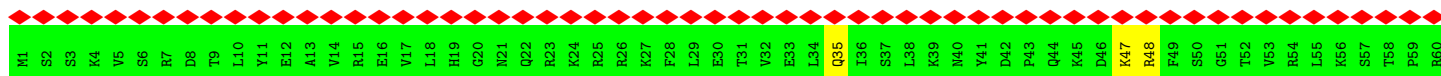
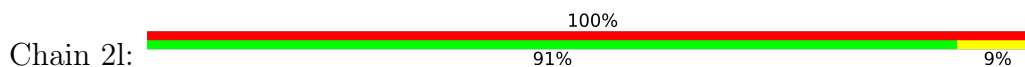
- Molecule 44: 60S ribosomal protein L37a

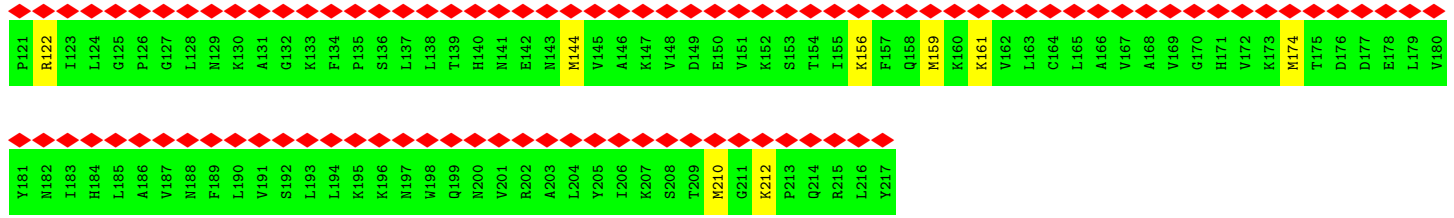


- Molecule 45: 60S ribosomal protein L28

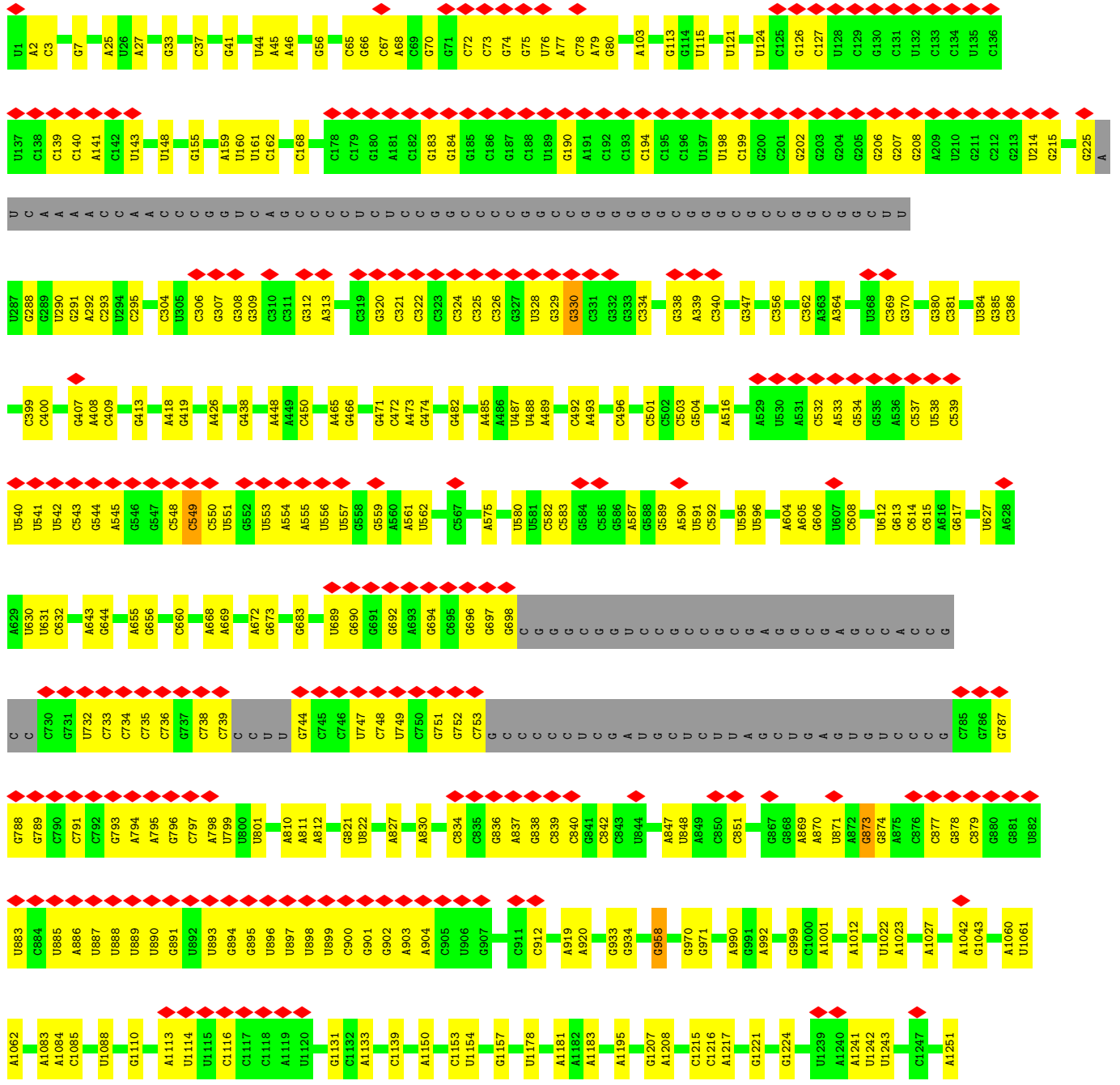


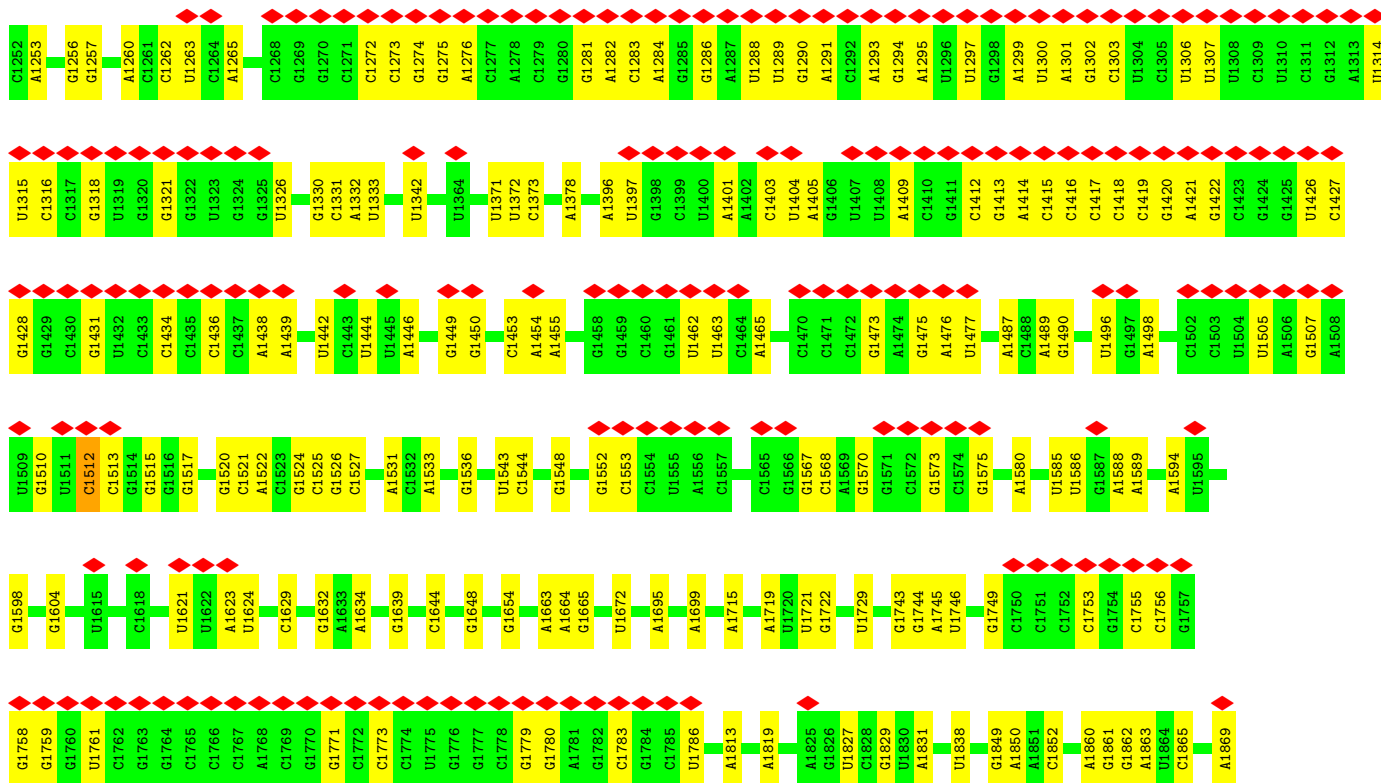
- Molecule 46: 60S ribosomal protein L10a



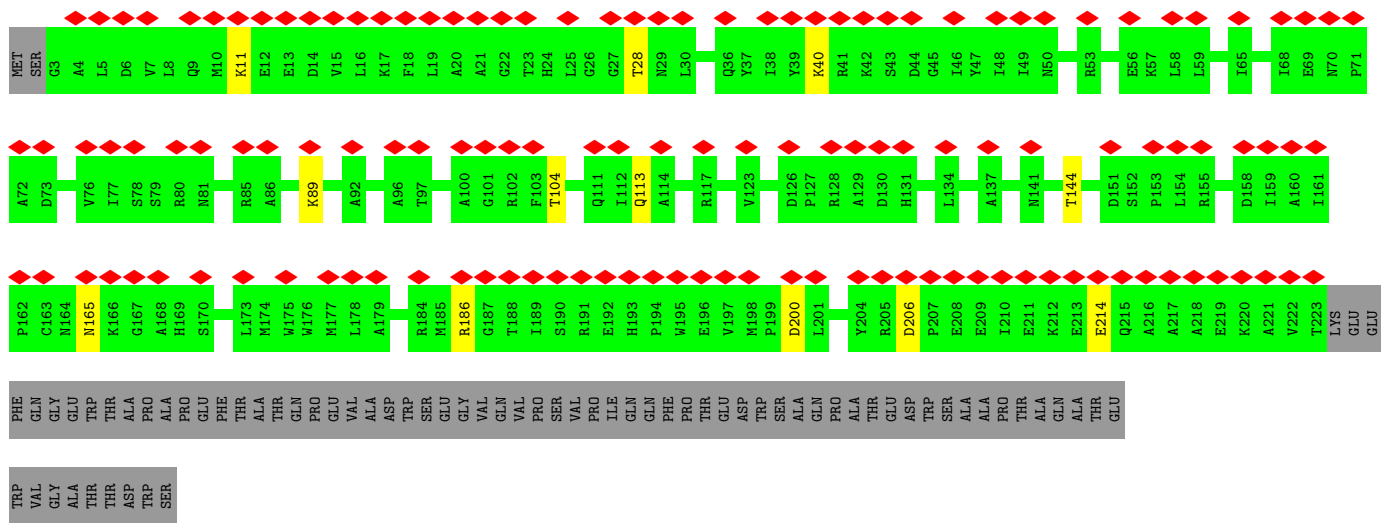
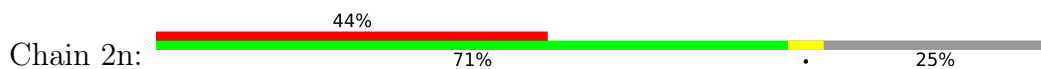


• Molecule 47: 18S ribosomal RNA

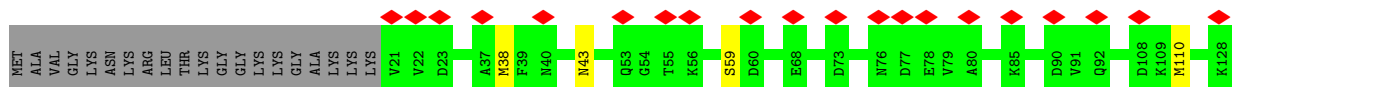
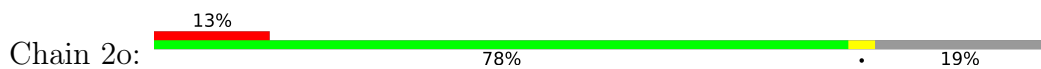


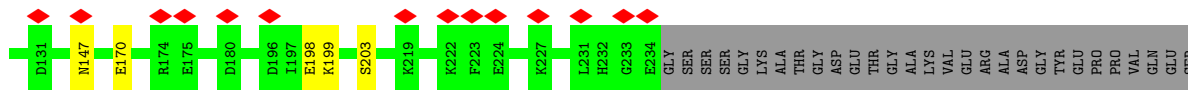


• Molecule 48: 40S ribosomal protein SA



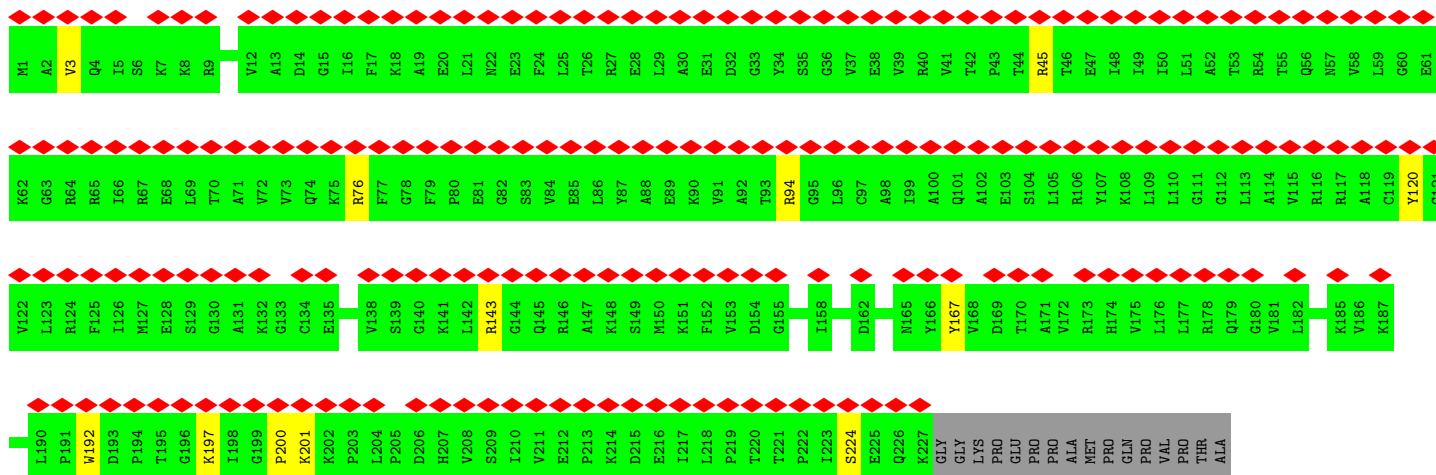
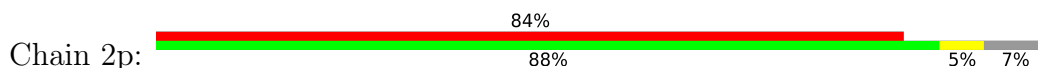
• Molecule 49: 40S ribosomal protein S3a



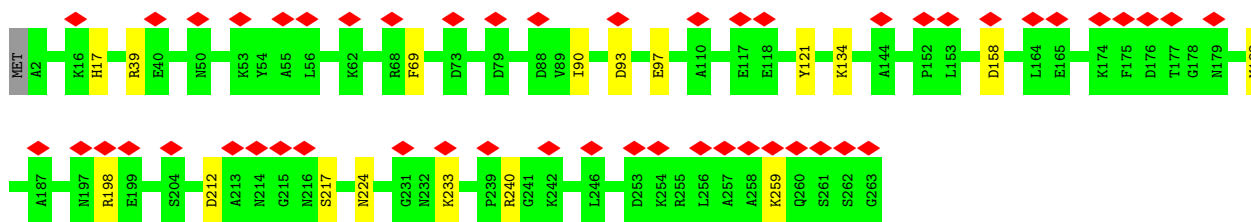


VAL

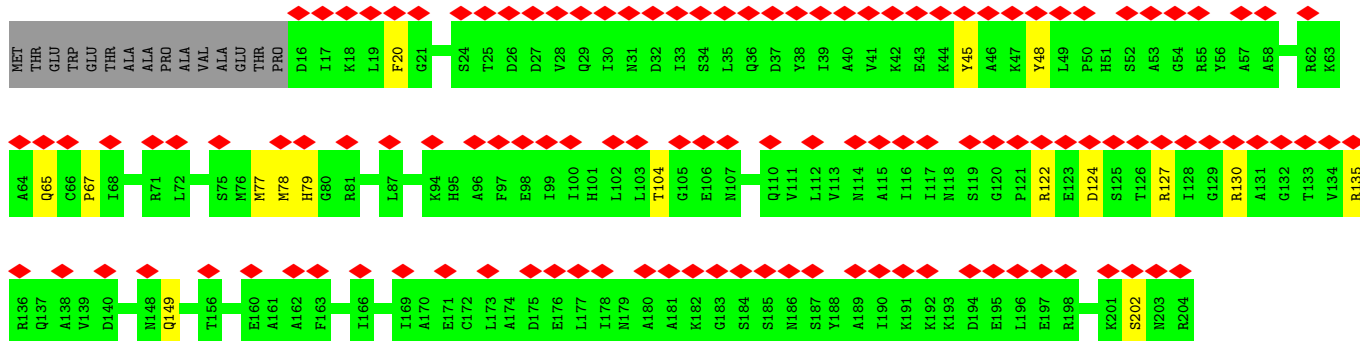
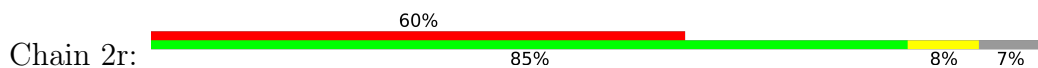
• Molecule 50: 40S ribosomal protein S3



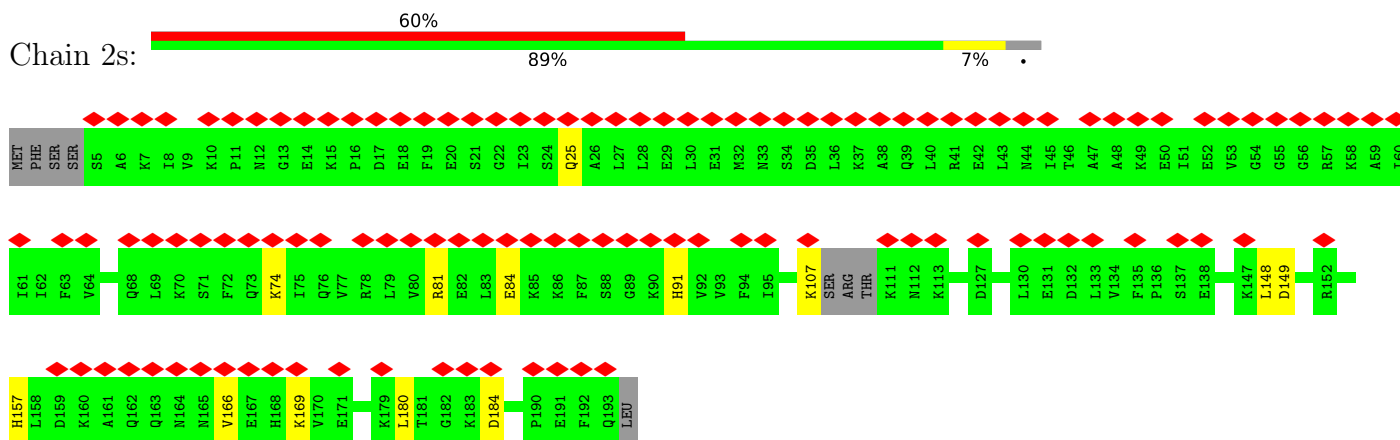
• Molecule 51: 40S ribosomal protein S4, X isoform



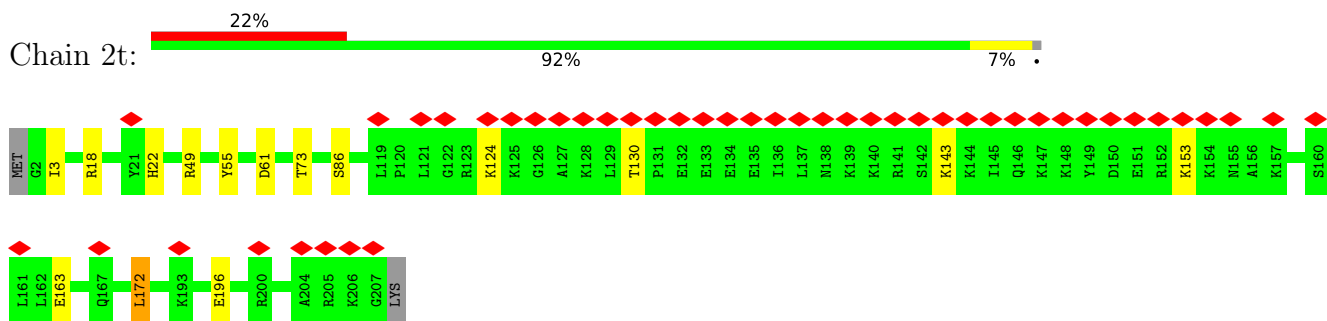
• Molecule 52: 40S ribosomal protein S5



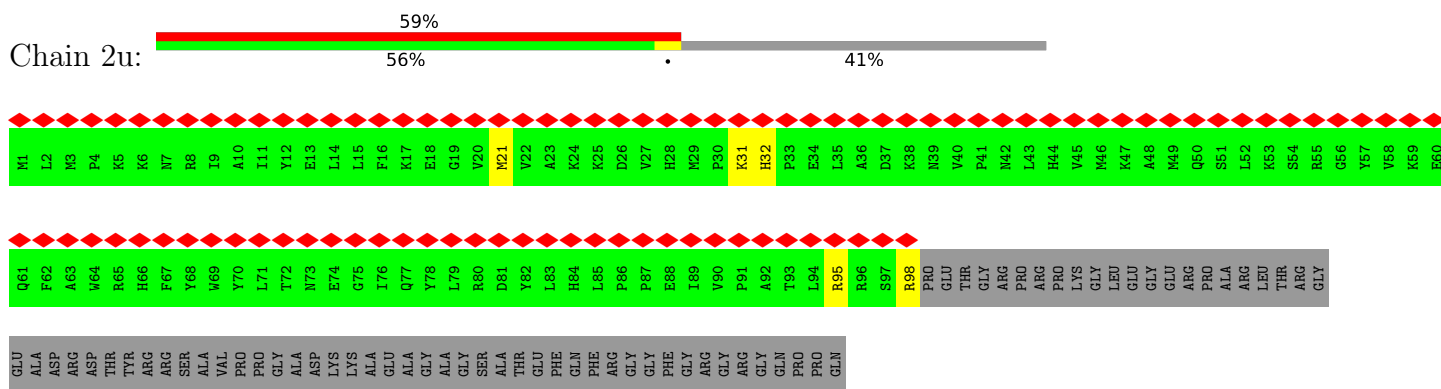
• Molecule 53: 40S ribosomal protein S7



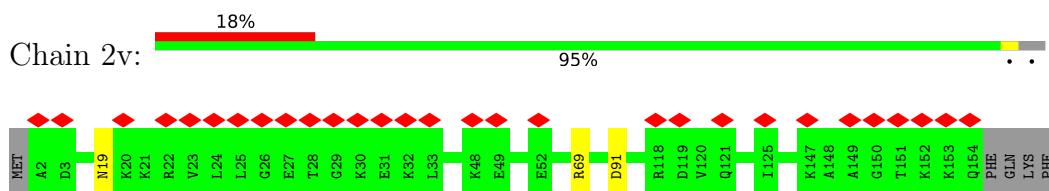
• Molecule 54: 40S ribosomal protein S8



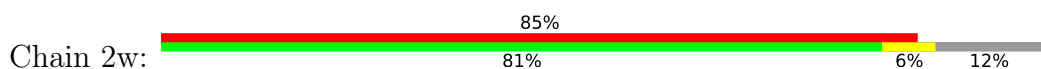
• Molecule 55: 40S ribosomal protein S10

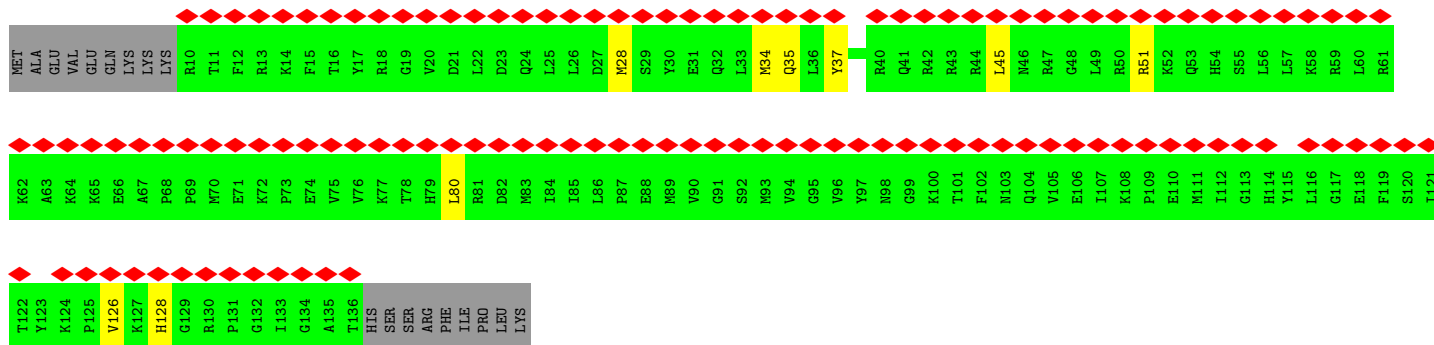


• Molecule 56: 40S ribosomal protein S11

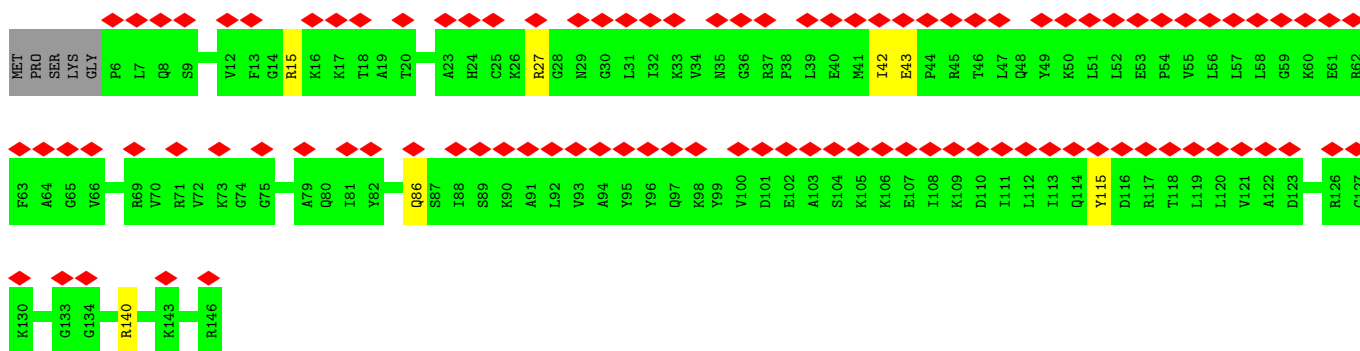
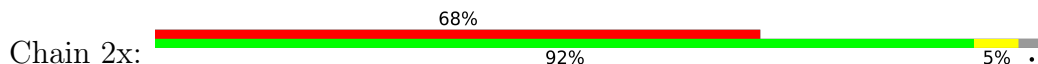


• Molecule 57: 40S ribosomal protein S15

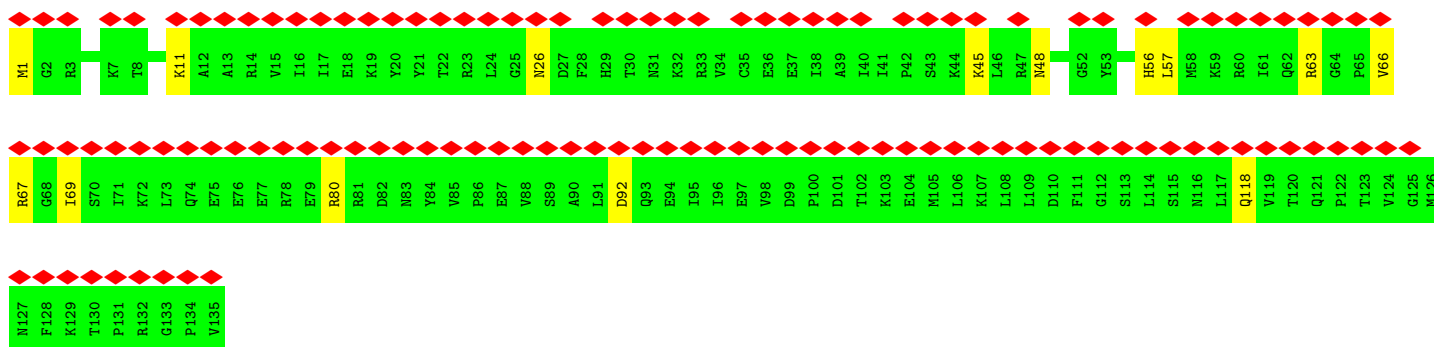
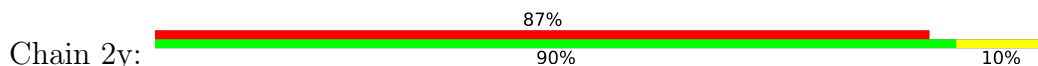




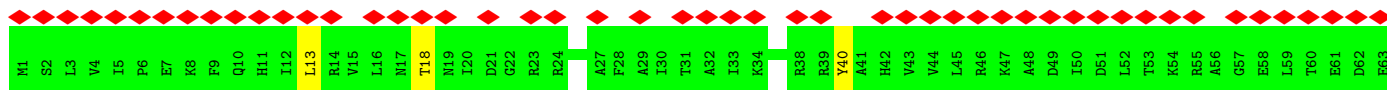
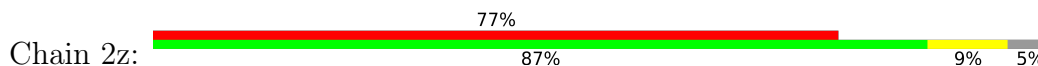
• Molecule 58: 40S ribosomal protein S16

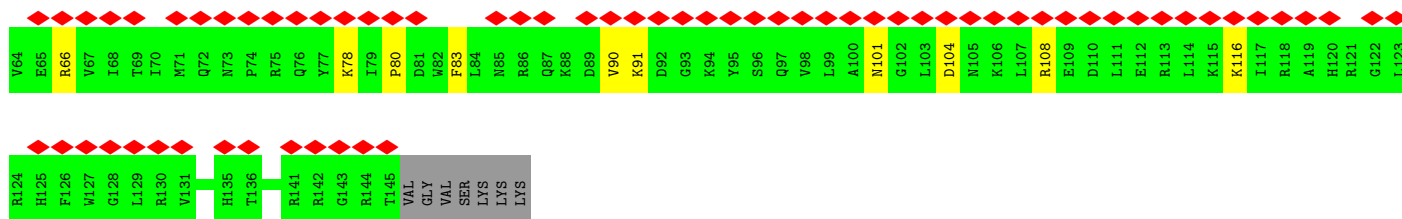


• Molecule 59: 40S ribosomal protein S17

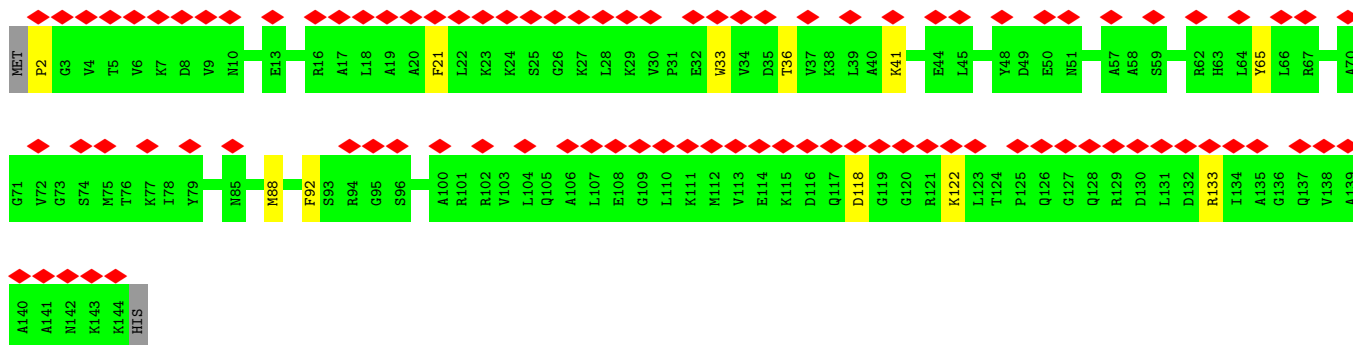
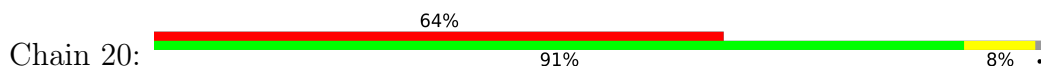


• Molecule 60: 40S ribosomal protein S18

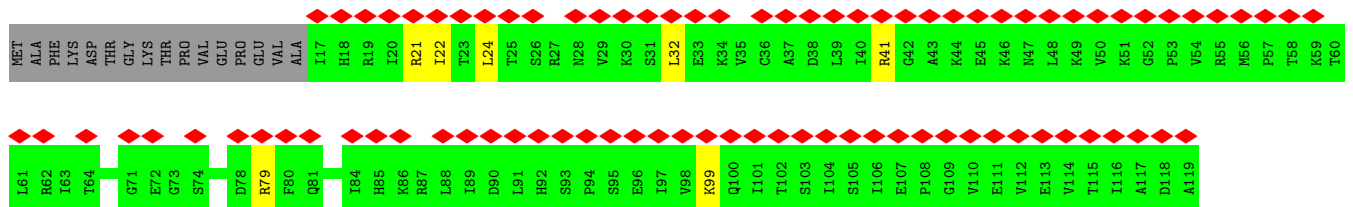
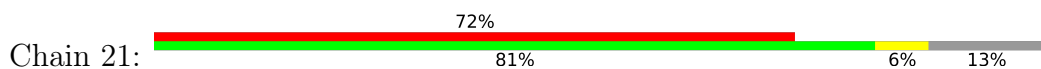




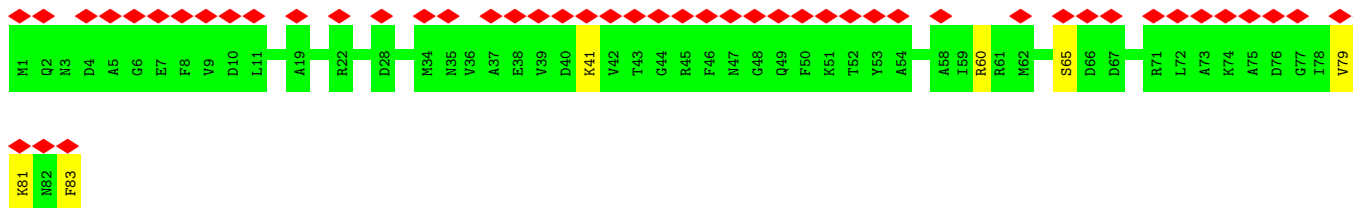
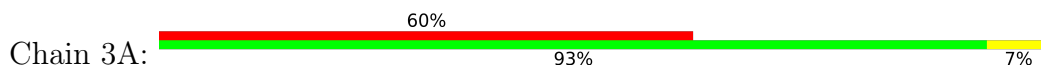
• Molecule 61: 40S ribosomal protein S19



• Molecule 62: 40S ribosomal protein S20

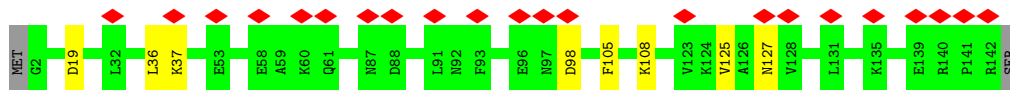


• Molecule 63: 40S ribosomal protein S21

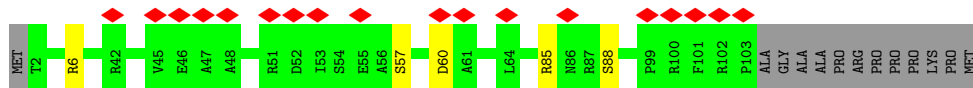
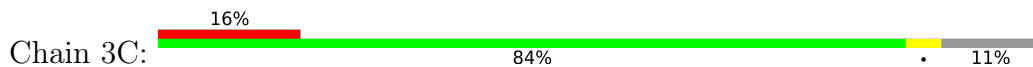


• Molecule 64: 40S ribosomal protein S23

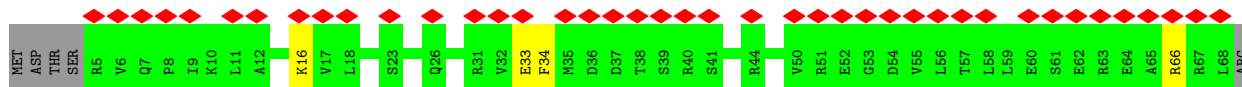
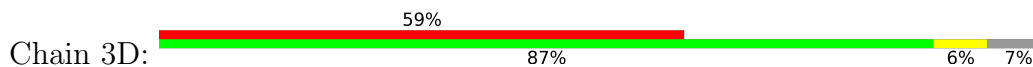




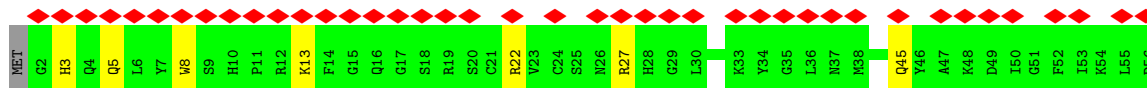
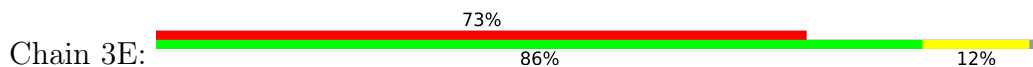
• Molecule 65: 40S ribosomal protein S26



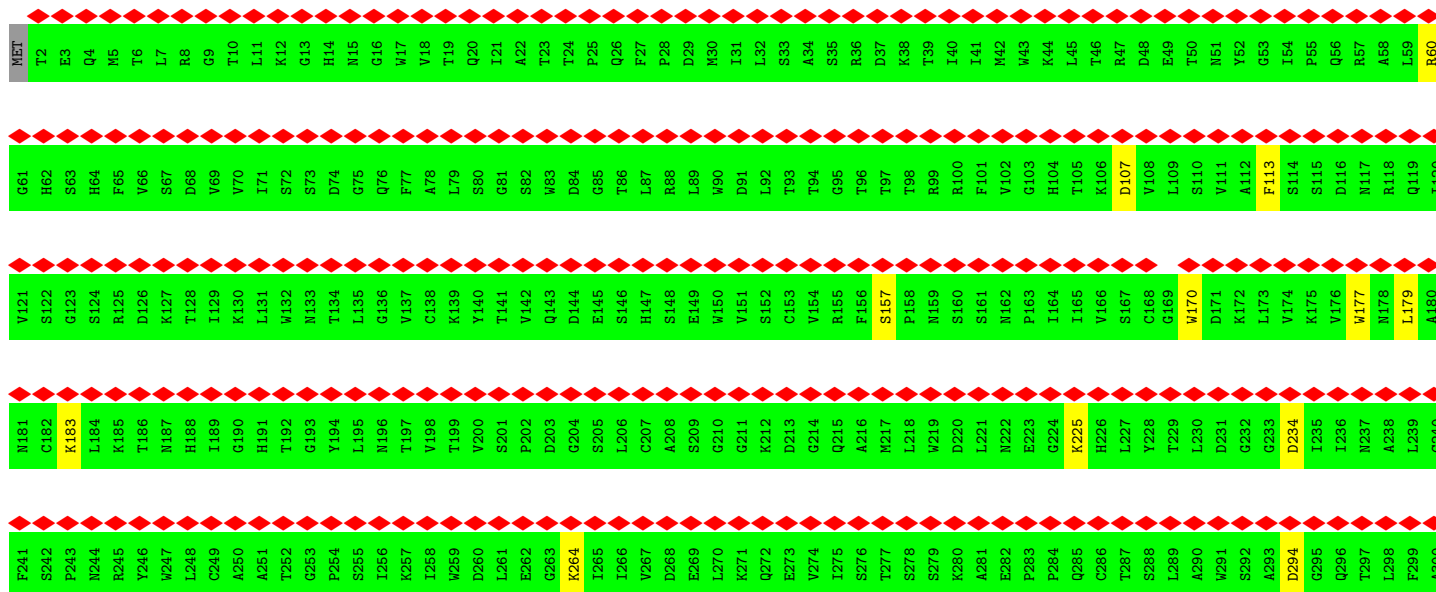
• Molecule 66: 40S ribosomal protein S28

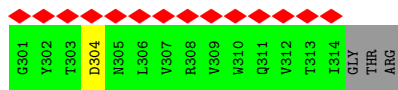


• Molecule 67: 40S ribosomal protein S29

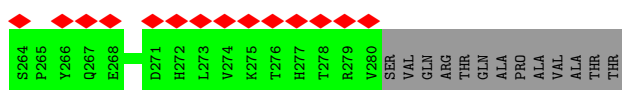
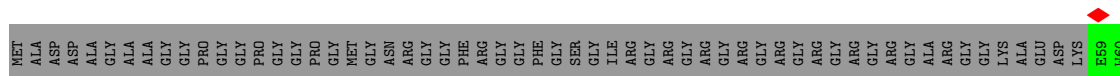
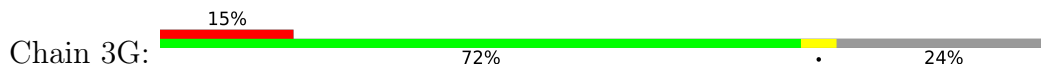


• Molecule 68: Receptor of activated protein C kinase 1

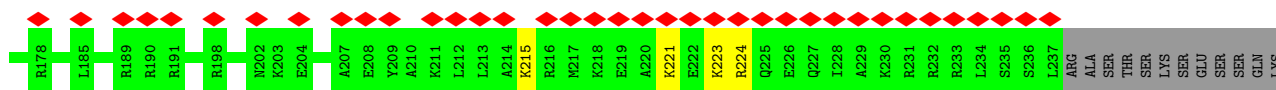
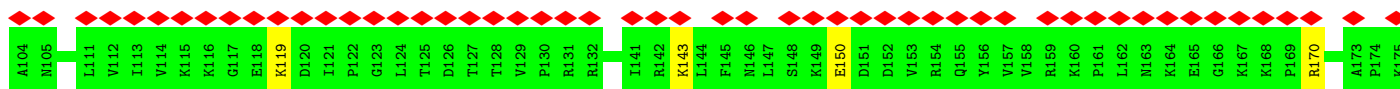
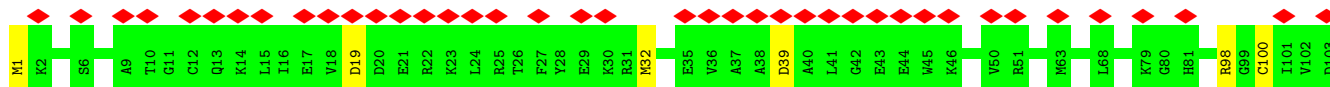
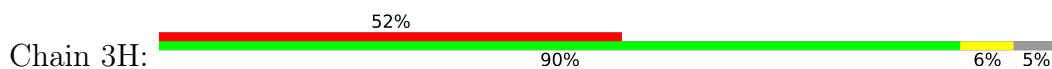




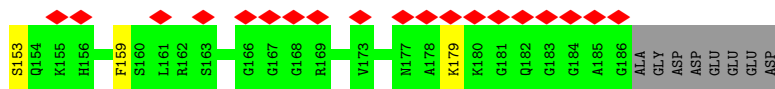
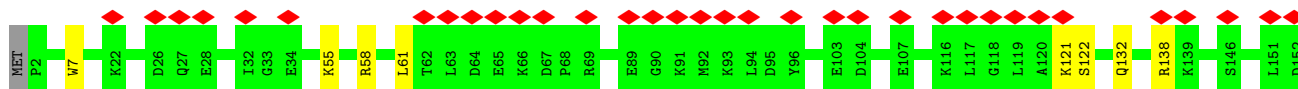
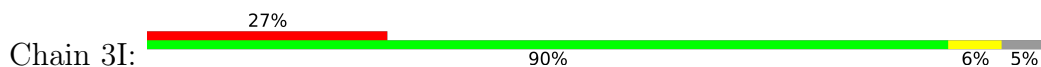
- Molecule 69: 40S ribosomal protein S2



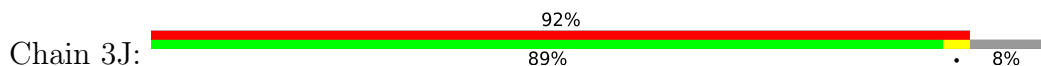
- Molecule 70: 40S ribosomal protein S6

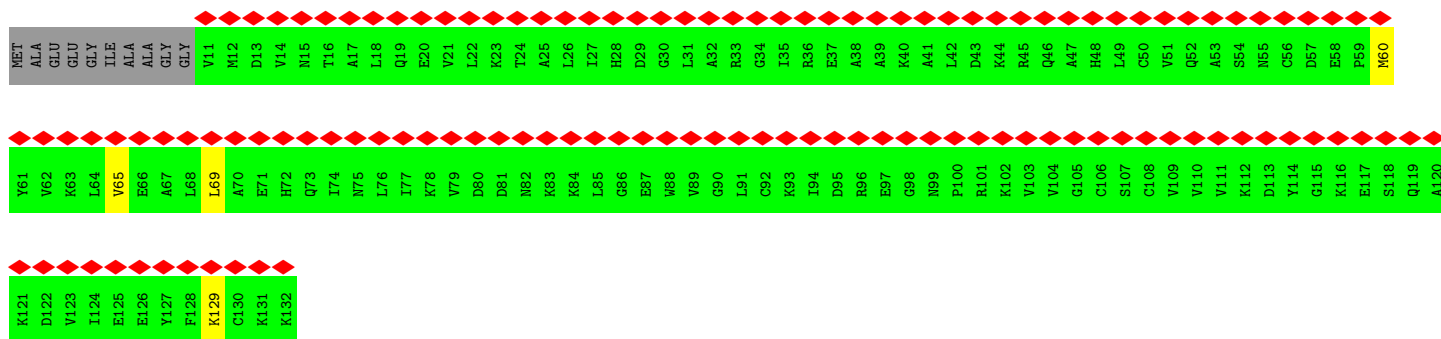


- Molecule 71: 40S ribosomal protein S9

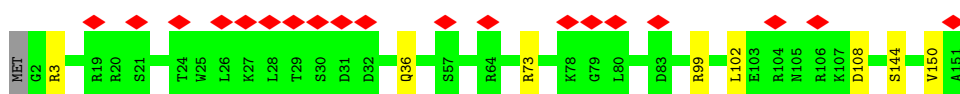


- Molecule 72: 40S ribosomal protein S12

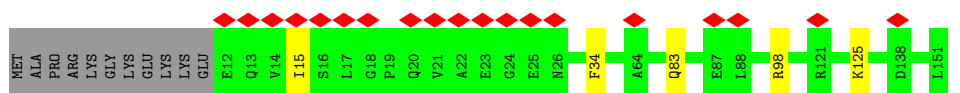
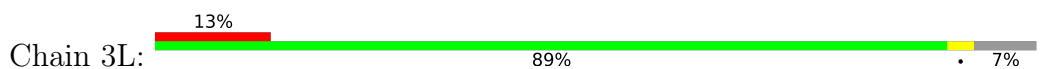




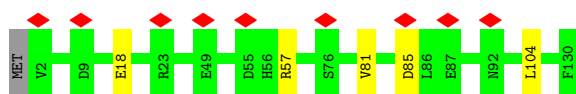
• Molecule 73: 40S ribosomal protein S13



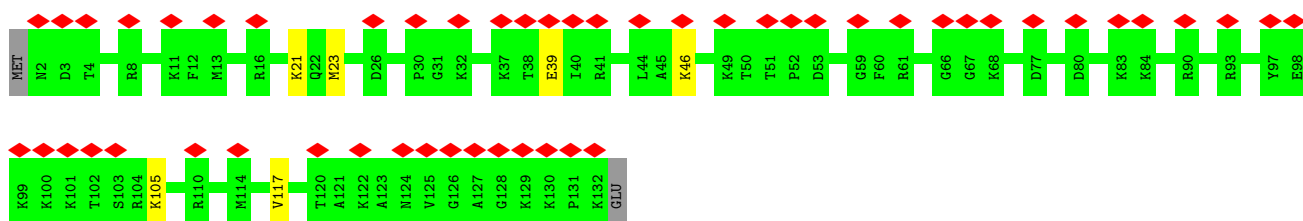
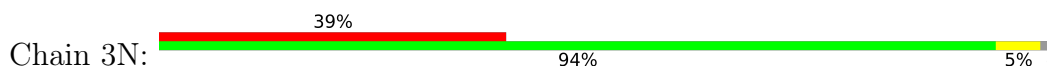
• Molecule 74: 40S ribosomal protein S14



• Molecule 75: 40S ribosomal protein S15a

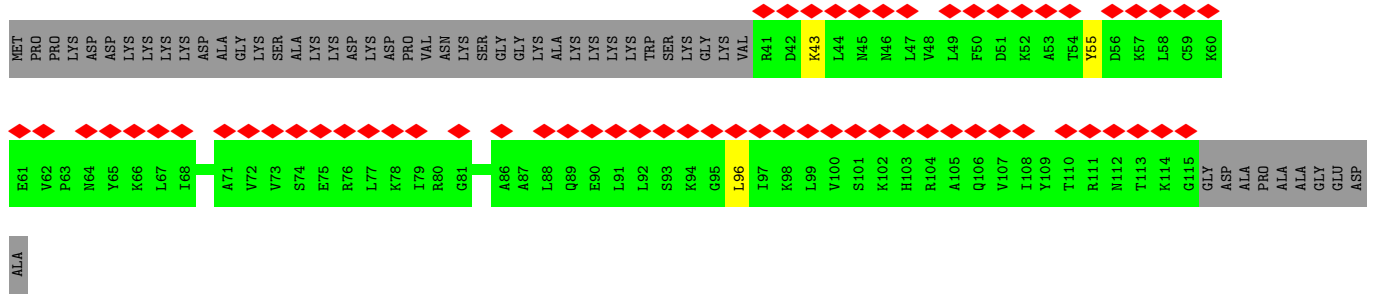


• Molecule 76: 40S ribosomal protein S24

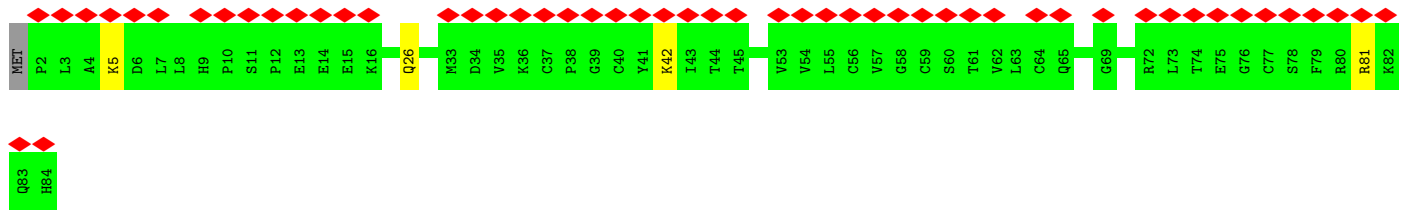


• Molecule 77: 40S ribosomal protein S25

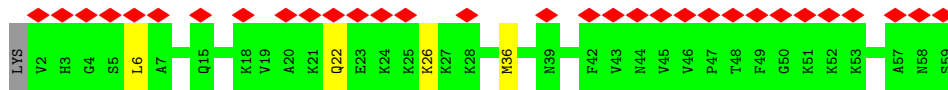
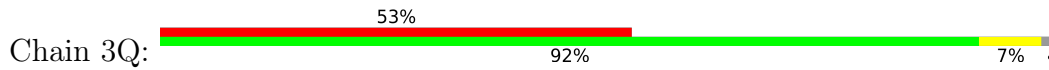




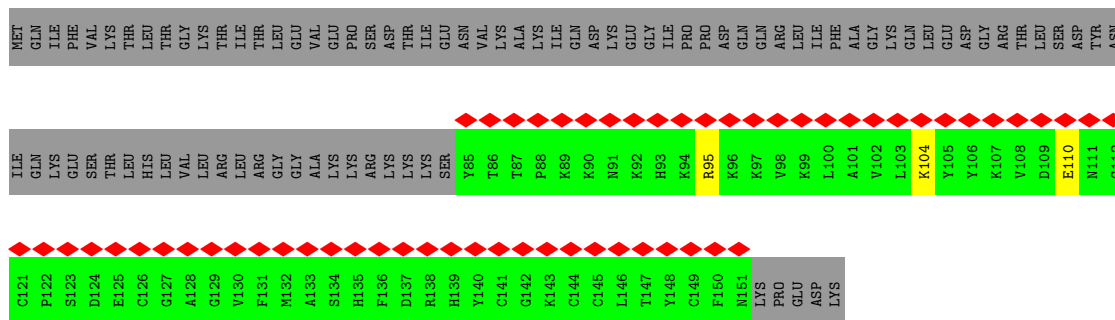
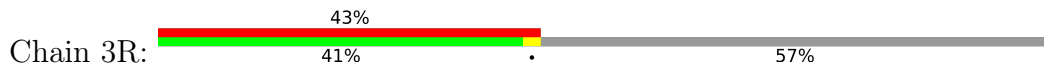
• Molecule 78: 40S ribosomal protein S27



• Molecule 79: 40S ribosomal protein S30



• Molecule 80: Ubiquitin-40S ribosomal protein S27a



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	29424	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	60000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.099	Depositor
Minimum map value	-0.030	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.013	Depositor
Map size (Å)	504.32, 504.32, 504.32	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.788, 0.788, 0.788	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MLZ, 84G, MG, 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	1A	0.45	0/89129	0.80	27/139038 (0.0%)
2	1B	0.44	0/2858	0.77	0/4455
3	1C	0.45	0/3701	0.77	1/5766 (0.0%)
4	1D	0.30	0/1936	0.57	0/2596
5	1E	0.29	0/3306	0.54	1/4424 (0.0%)
6	1F	0.27	0/2981	0.55	0/4002
7	1G	0.29	0/2428	0.54	0/3252
8	1H	0.28	0/1942	0.55	0/2606
9	2A	0.29	0/1916	0.54	0/2553
10	2B	0.29	0/1971	0.55	0/2651
11	2C	0.27	0/1537	0.55	0/2066
12	2D	0.27	0/1751	0.55	0/2340
13	2E	0.29	0/1433	0.59	0/1915
14	2F	0.27	0/1732	0.57	0/2315
15	2G	0.28	0/1161	0.53	0/1554
16	2H	0.29	0/1746	0.58	1/2338 (0.0%)
17	2I	0.28	0/1682	0.53	0/2250
18	2J	0.28	0/1268	0.52	0/1701
19	2K	0.29	0/1537	0.59	0/2052
20	2L	0.25	0/1582	0.56	0/2091
21	2M	0.29	0/1493	0.54	0/2003
22	2N	0.28	0/1326	0.52	0/1770
23	2O	0.27	0/839	0.55	0/1126
24	2P	0.28	0/993	0.52	0/1332
25	2Q	0.26	0/1030	0.55	0/1364
26	2R	0.27	0/1002	0.54	1/1345 (0.1%)
27	2S	0.29	0/1132	0.56	0/1504
28	2T	0.30	0/1130	0.55	0/1507
29	2U	0.28	0/1191	0.51	0/1591
30	2V	0.28	0/895	0.56	0/1182
31	2W	0.29	0/774	0.51	0/1038
32	2X	0.28	0/903	0.56	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	2Y	0.27	0/1071	0.55	0/1429
34	2Z	0.32	0/895	0.58	0/1198
35	2a	0.28	0/916	0.57	0/1220
36	2b	0.26	0/1023	0.54	0/1351
37	2c	0.26	0/843	0.56	0/1115
38	2d	0.30	0/731	0.62	0/966
39	2e	0.29	0/575	0.53	0/761
40	2f	0.25	0/454	0.57	0/599
41	2g	0.27	0/425	0.54	0/561
42	2h	0.25	0/231	0.71	0/294
43	2i	0.34	0/887	0.59	0/1170
44	2j	0.28	0/718	0.51	0/953
45	2k	0.27	0/1017	0.58	0/1364
46	2l	0.42	1/1769 (0.1%)	0.57	1/2371 (0.0%)
47	2m	0.44	6/41243 (0.0%)	0.80	36/64257 (0.1%)
48	2n	0.25	0/1778	0.51	0/2416
49	2o	0.26	0/1765	0.51	0/2362
50	2p	0.31	1/1793 (0.1%)	0.66	2/2414 (0.1%)
51	2q	0.26	0/2118	0.55	0/2849
52	2r	0.26	0/1516	0.55	0/2037
53	2s	1.50	1/1519 (0.1%)	0.60	3/2033 (0.1%)
54	2t	0.26	0/1715	0.58	1/2287 (0.0%)
55	2u	0.25	0/851	0.55	0/1147
56	2v	0.28	0/1268	0.55	0/1696
57	2w	0.25	0/1065	0.54	0/1423
58	2x	0.25	0/1142	0.54	0/1528
59	2y	0.26	0/1105	0.57	0/1484
60	2z	0.26	0/1216	0.60	2/1628 (0.1%)
61	20	0.36	1/1131 (0.1%)	0.55	0/1515
62	21	0.27	0/827	0.58	0/1110
63	3A	0.26	0/643	0.54	0/860
64	3B	0.27	0/1116	0.53	0/1490
65	3C	0.27	0/847	0.59	0/1135
66	3D	0.24	0/508	0.63	0/680
67	3E	0.28	0/470	0.54	0/623
68	3F	0.24	0/2493	0.53	0/3394
69	3G	0.26	0/1773	0.52	0/2395
70	3H	0.25	0/1946	0.58	0/2590
71	3I	0.26	0/1561	0.59	1/2083 (0.0%)
72	3J	0.36	1/952 (0.1%)	0.47	0/1279
73	3K	0.26	0/1232	0.51	0/1656
74	3L	0.26	0/1062	0.58	0/1425
75	3M	0.28	0/1051	0.57	0/1406

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	3N	0.29	0/1094	0.60	0/1452
77	3O	0.26	0/604	0.62	0/810
78	3P	0.24	0/665	0.51	0/891
79	3Q	0.25	0/465	0.56	0/612
80	3R	0.25	0/560	0.56	0/745
All	All	0.40	11/232954 (0.0%)	0.72	77/342007 (0.0%)

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	2s	107	LYS	CD-CE	57.64	2.95	1.51
47	2m	744	G	C6-N1	35.66	1.64	1.39
47	2m	744	G	N1-C2	30.77	1.62	1.37
47	2m	744	G	N3-C4	27.48	1.54	1.35
47	2m	744	G	C2-N3	24.65	1.52	1.32

The worst 5 of 77 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	2m	744	G	C2-N3-C4	20.01	121.91	111.90
47	2m	744	G	N1-C2-N3	-14.37	115.28	123.90
50	2p	200	PRO	N-CD-CG	-13.47	83.00	103.20
50	2p	200	PRO	CA-CB-CG	-11.00	83.10	104.00
47	2m	744	G	C4-C5-N7	-9.46	107.01	110.80

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	
4	1D	246/257 (96%)	223 (91%)	23 (9%)	0	100	100
5	1E	400/403 (99%)	384 (96%)	16 (4%)	0	100	100
6	1F	366/427 (86%)	342 (93%)	24 (7%)	0	100	100
7	1G	291/297 (98%)	279 (96%)	12 (4%)	0	100	100
8	1H	232/288 (81%)	209 (90%)	23 (10%)	0	100	100
9	2A	224/248 (90%)	215 (96%)	9 (4%)	0	100	100
10	2B	240/266 (90%)	227 (95%)	13 (5%)	0	100	100
11	2C	188/192 (98%)	178 (95%)	10 (5%)	0	100	100
12	2D	211/214 (99%)	192 (91%)	18 (8%)	1 (0%)	29	50
13	2E	174/178 (98%)	163 (94%)	9 (5%)	2 (1%)	14	28
14	2F	208/211 (99%)	190 (91%)	18 (9%)	0	100	100
15	2G	137/215 (64%)	132 (96%)	5 (4%)	0	100	100
16	2H	201/204 (98%)	191 (95%)	9 (4%)	1 (0%)	29	50
17	2I	199/203 (98%)	193 (97%)	6 (3%)	0	100	100
18	2J	151/184 (82%)	143 (95%)	8 (5%)	0	100	100
19	2K	185/188 (98%)	179 (97%)	6 (3%)	0	100	100
20	2L	185/196 (94%)	178 (96%)	7 (4%)	0	100	100
21	2M	173/176 (98%)	160 (92%)	12 (7%)	1 (1%)	25	45
22	2N	157/160 (98%)	150 (96%)	7 (4%)	0	100	100
23	2O	99/128 (77%)	87 (88%)	12 (12%)	0	100	100
24	2P	129/140 (92%)	123 (95%)	6 (5%)	0	100	100
25	2Q	122/157 (78%)	110 (90%)	12 (10%)	0	100	100
26	2R	118/156 (76%)	113 (96%)	4 (3%)	1 (1%)	19	37
27	2S	132/145 (91%)	129 (98%)	3 (2%)	0	100	100
28	2T	133/136 (98%)	124 (93%)	9 (7%)	0	100	100
29	2U	145/148 (98%)	134 (92%)	11 (8%)	0	100	100
30	2V	105/159 (66%)	95 (90%)	10 (10%)	0	100	100
31	2W	96/115 (84%)	92 (96%)	4 (4%)	0	100	100
32	2X	105/125 (84%)	100 (95%)	5 (5%)	0	100	100
33	2Y	126/135 (93%)	118 (94%)	7 (6%)	1 (1%)	19	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	2Z	107/110 (97%)	102 (95%)	4 (4%)	1 (1%)	17	34
35	2a	112/117 (96%)	111 (99%)	1 (1%)	0	100	100
36	2b	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
37	2c	100/105 (95%)	96 (96%)	4 (4%)	0	100	100
38	2d	85/97 (88%)	83 (98%)	2 (2%)	0	100	100
39	2e	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
40	2f	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
41	2g	49/128 (38%)	47 (96%)	2 (4%)	0	100	100
42	2h	22/25 (88%)	22 (100%)	0	0	100	100
43	2i	104/106 (98%)	96 (92%)	8 (8%)	0	100	100
44	2j	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
45	2k	123/137 (90%)	115 (94%)	8 (6%)	0	100	100
46	2l	215/217 (99%)	171 (80%)	42 (20%)	2 (1%)	17	34
48	2n	219/295 (74%)	205 (94%)	13 (6%)	1 (0%)	29	50
49	2o	212/264 (80%)	205 (97%)	7 (3%)	0	100	100
50	2p	225/243 (93%)	199 (88%)	26 (12%)	0	100	100
51	2q	260/263 (99%)	245 (94%)	15 (6%)	0	100	100
52	2r	187/204 (92%)	164 (88%)	23 (12%)	0	100	100
53	2s	182/194 (94%)	162 (89%)	20 (11%)	0	100	100
54	2t	204/208 (98%)	199 (98%)	5 (2%)	0	100	100
55	2u	96/165 (58%)	87 (91%)	9 (9%)	0	100	100
56	2v	151/158 (96%)	137 (91%)	14 (9%)	0	100	100
57	2w	125/145 (86%)	118 (94%)	7 (6%)	0	100	100
58	2x	139/146 (95%)	127 (91%)	10 (7%)	2 (1%)	11	21
59	2y	133/135 (98%)	120 (90%)	11 (8%)	2 (2%)	10	20
60	2z	143/152 (94%)	126 (88%)	17 (12%)	0	100	100
61	20	141/145 (97%)	127 (90%)	14 (10%)	0	100	100
62	21	101/119 (85%)	94 (93%)	7 (7%)	0	100	100
63	3A	81/83 (98%)	73 (90%)	8 (10%)	0	100	100
64	3B	139/143 (97%)	129 (93%)	10 (7%)	0	100	100
65	3C	101/115 (88%)	92 (91%)	9 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	3D	62/69 (90%)	50 (81%)	12 (19%)	0	100	100
67	3E	53/56 (95%)	49 (92%)	3 (6%)	1 (2%)	8	14
68	3F	311/317 (98%)	284 (91%)	27 (9%)	0	100	100
69	3G	221/293 (75%)	209 (95%)	12 (5%)	0	100	100
70	3H	235/249 (94%)	221 (94%)	14 (6%)	0	100	100
71	3I	184/194 (95%)	164 (89%)	20 (11%)	0	100	100
72	3J	120/132 (91%)	113 (94%)	7 (6%)	0	100	100
73	3K	148/151 (98%)	145 (98%)	3 (2%)	0	100	100
74	3L	138/151 (91%)	122 (88%)	15 (11%)	1 (1%)	22	41
75	3M	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
76	3N	130/133 (98%)	122 (94%)	8 (6%)	0	100	100
77	3O	73/125 (58%)	62 (85%)	11 (15%)	0	100	100
78	3P	81/84 (96%)	70 (86%)	11 (14%)	0	100	100
79	3Q	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
80	3R	65/156 (42%)	55 (85%)	10 (15%)	0	100	100
All	All	11562/12905 (90%)	10759 (93%)	786 (7%)	17 (0%)	54	73

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	2Y	92	ASN
34	2Z	107	PRO
48	2n	28	THR
58	2x	42	ILE
58	2x	43	GLU

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	
4	1D	190/199 (96%)	182 (96%)	8 (4%)	30	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	1E	348/349 (100%)	333 (96%)	15 (4%)	29	52
6	1F	306/348 (88%)	291 (95%)	15 (5%)	25	46
7	1G	246/250 (98%)	229 (93%)	17 (7%)	15	30
8	1H	209/252 (83%)	196 (94%)	13 (6%)	18	35
9	2A	195/215 (91%)	189 (97%)	6 (3%)	40	64
10	2B	204/223 (92%)	195 (96%)	9 (4%)	28	51
11	2C	169/171 (99%)	162 (96%)	7 (4%)	30	54
12	2D	180/181 (99%)	168 (93%)	12 (7%)	16	31
13	2E	148/149 (99%)	130 (88%)	18 (12%)	5	8
14	2F	176/177 (99%)	166 (94%)	10 (6%)	20	39
15	2G	118/161 (73%)	114 (97%)	4 (3%)	37	60
16	2H	171/172 (99%)	166 (97%)	5 (3%)	42	66
17	2I	173/174 (99%)	167 (96%)	6 (4%)	36	59
18	2J	134/163 (82%)	129 (96%)	5 (4%)	34	57
19	2K	164/165 (99%)	162 (99%)	2 (1%)	71	86
20	2L	166/175 (95%)	159 (96%)	7 (4%)	30	53
21	2M	156/157 (99%)	147 (94%)	9 (6%)	20	38
22	2N	139/140 (99%)	129 (93%)	10 (7%)	14	27
23	2O	91/115 (79%)	80 (88%)	11 (12%)	5	8
24	2P	101/107 (94%)	97 (96%)	4 (4%)	31	55
25	2Q	103/126 (82%)	101 (98%)	2 (2%)	57	77
26	2R	108/133 (81%)	101 (94%)	7 (6%)	17	33
27	2S	124/135 (92%)	119 (96%)	5 (4%)	31	55
28	2T	117/118 (99%)	112 (96%)	5 (4%)	29	52
29	2U	120/121 (99%)	119 (99%)	1 (1%)	81	92
30	2V	89/126 (71%)	83 (93%)	6 (7%)	16	31
31	2W	83/97 (86%)	77 (93%)	6 (7%)	14	27
32	2X	98/110 (89%)	93 (95%)	5 (5%)	24	44
33	2Y	114/121 (94%)	110 (96%)	4 (4%)	36	59
34	2Z	88/89 (99%)	85 (97%)	3 (3%)	37	60
35	2a	98/100 (98%)	91 (93%)	7 (7%)	14	28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	2b	109/110 (99%)	99 (91%)	10 (9%)	9	16
37	2c	86/89 (97%)	83 (96%)	3 (4%)	36	59
38	2d	74/80 (92%)	68 (92%)	6 (8%)	11	22
39	2e	64/65 (98%)	59 (92%)	5 (8%)	12	23
40	2f	47/48 (98%)	43 (92%)	4 (8%)	10	20
41	2g	47/115 (41%)	44 (94%)	3 (6%)	17	34
42	2h	23/24 (96%)	21 (91%)	2 (9%)	10	19
43	2i	94/94 (100%)	90 (96%)	4 (4%)	29	52
44	2j	74/75 (99%)	71 (96%)	3 (4%)	30	54
45	2k	109/121 (90%)	104 (95%)	5 (5%)	27	49
46	2l	195/196 (100%)	179 (92%)	16 (8%)	11	21
48	2n	183/243 (75%)	172 (94%)	11 (6%)	19	37
49	2o	195/231 (84%)	186 (95%)	9 (5%)	27	49
50	2p	190/202 (94%)	179 (94%)	11 (6%)	20	38
51	2q	224/225 (100%)	207 (92%)	17 (8%)	13	25
52	2r	159/170 (94%)	143 (90%)	16 (10%)	7	13
53	2s	166/174 (95%)	155 (93%)	11 (7%)	16	32
54	2t	178/180 (99%)	163 (92%)	15 (8%)	11	20
55	2u	89/136 (65%)	84 (94%)	5 (6%)	21	40
56	2v	137/142 (96%)	134 (98%)	3 (2%)	52	74
57	2w	113/130 (87%)	104 (92%)	9 (8%)	12	22
58	2x	117/121 (97%)	112 (96%)	5 (4%)	29	52
59	2y	122/122 (100%)	110 (90%)	12 (10%)	8	14
60	2z	126/132 (96%)	114 (90%)	12 (10%)	8	15
61	20	113/115 (98%)	103 (91%)	10 (9%)	10	18
62	21	94/107 (88%)	87 (93%)	7 (7%)	13	26
63	3A	67/67 (100%)	61 (91%)	6 (9%)	9	17
64	3B	113/115 (98%)	105 (93%)	8 (7%)	14	28
65	3C	90/98 (92%)	84 (93%)	6 (7%)	16	31
66	3D	57/62 (92%)	53 (93%)	4 (7%)	15	29
67	3E	48/49 (98%)	42 (88%)	6 (12%)	4	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	3F	272/275 (99%)	259 (95%)	13 (5%)	25	47
69	3G	189/225 (84%)	177 (94%)	12 (6%)	18	35
70	3H	207/218 (95%)	193 (93%)	14 (7%)	16	30
71	3I	162/168 (96%)	151 (93%)	11 (7%)	16	30
72	3J	102/108 (94%)	99 (97%)	3 (3%)	42	66
73	3K	130/131 (99%)	122 (94%)	8 (6%)	18	35
74	3L	110/119 (92%)	106 (96%)	4 (4%)	35	59
75	3M	112/113 (99%)	107 (96%)	5 (4%)	27	50
76	3N	114/115 (99%)	108 (95%)	6 (5%)	22	43
77	3O	66/103 (64%)	63 (96%)	3 (4%)	27	50
78	3P	75/76 (99%)	71 (95%)	4 (5%)	22	43
79	3Q	47/48 (98%)	43 (92%)	4 (8%)	10	20
80	3R	60/140 (43%)	57 (95%)	3 (5%)	24	45
All	All	10075/10996 (92%)	9497 (94%)	578 (6%)	24	39

5 of 578 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
63	3A	83	PHE
79	3Q	26	LYS
65	3C	85[B]	ARG
63	3A	81	LYS
70	3H	143	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
52	2r	148	ASN
59	2y	31	ASN
77	3O	106	GLN
57	2w	128	HIS
61	20	63	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	3704/5070 (73%)	833 (22%)	30 (0%)
2	1B	119/121 (98%)	18 (15%)	2 (1%)
3	1C	155/157 (98%)	29 (18%)	2 (1%)
47	2m	1716/1869 (91%)	480 (27%)	0
All	All	5694/7217 (78%)	1360 (23%)	34 (0%)

5 of 1360 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	17	A
1	1A	30	C
1	1A	39	A
1	1A	42	A
1	1A	48	G

5 of 34 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	4896	G
1	1A	4913	G
3	1C	86	U
1	1A	2389	A
1	1A	2299	G

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
41	MLZ	2g	98	41	8,9,10	0.78	0	4,9,11	0.59	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.

'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
41	MLZ	2g	98	41	-	1/7/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
41	2g	98	MLZ	CD-CE-NZ-CM

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 439 ligands modelled in this entry, 416 are monoatomic - leaving 23 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
81	84G	1A	5112	-	39,40,40	1.82	6 (15%)	47,57,57	1.24	3 (6%)
81	84G	2m	1901	-	39,40,40	1.78	7 (17%)	47,57,57	2.03	12 (25%)
81	84G	1A	5108	-	39,40,40	1.83	7 (17%)	47,57,57	1.13	3 (6%)
81	84G	2i	201	-	39,40,40	1.94	9 (23%)	47,57,57	1.29	5 (10%)
81	84G	1A	5106	-	39,40,40	1.84	9 (23%)	47,57,57	1.07	5 (10%)
81	84G	1A	5104	82	39,40,40	1.85	8 (20%)	47,57,57	1.22	3 (6%)
81	84G	1A	5105	-	39,40,40	1.83	6 (15%)	47,57,57	1.16	5 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
81	84G	1A	5102	-	39,40,40	1.87	7 (17%)	47,57,57	1.25	5 (10%)
81	84G	1A	5107	-	39,40,40	1.83	8 (20%)	47,57,57	1.12	2 (4%)
81	84G	1A	5111	-	39,40,40	1.82	7 (17%)	47,57,57	1.31	4 (8%)
81	84G	1A	5115	-	39,40,40	1.84	7 (17%)	47,57,57	1.18	6 (12%)
81	84G	2D	301	-	39,40,40	1.82	7 (17%)	47,57,57	1.25	5 (10%)
81	84G	1A	5118	-	39,40,40	1.81	7 (17%)	47,57,57	1.13	3 (6%)
81	84G	1A	5101	-	39,40,40	1.84	6 (15%)	47,57,57	1.49	8 (17%)
81	84G	1A	5117	-	39,40,40	1.82	7 (17%)	47,57,57	1.20	4 (8%)
81	84G	1A	5113	-	39,40,40	1.83	7 (17%)	47,57,57	1.13	3 (6%)
81	84G	1A	5110	-	39,40,40	1.87	7 (17%)	47,57,57	1.07	4 (8%)
81	84G	1A	5116	-	39,40,40	1.82	8 (20%)	47,57,57	1.21	4 (8%)
81	84G	1A	5119	-	39,40,40	1.84	8 (20%)	47,57,57	1.11	4 (8%)
81	84G	1A	5103	-	39,40,40	1.81	6 (15%)	47,57,57	1.05	3 (6%)
81	84G	2m	1902	-	39,40,40	1.83	7 (17%)	47,57,57	1.25	5 (10%)
81	84G	1A	5114	-	39,40,40	1.83	7 (17%)	47,57,57	1.19	4 (8%)
81	84G	1A	5109	-	39,40,40	1.84	6 (15%)	47,57,57	1.18	3 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
81	84G	1A	5112	-	-	8/23/76/76	0/3/3/3
81	84G	2m	1901	-	-	3/23/76/76	0/3/3/3
81	84G	1A	5108	-	-	8/23/76/76	0/3/3/3
81	84G	2i	201	-	-	9/23/76/76	0/3/3/3
81	84G	1A	5106	-	-	11/23/76/76	0/3/3/3
81	84G	1A	5104	82	-	7/23/76/76	0/3/3/3
81	84G	1A	5105	-	-	6/23/76/76	0/3/3/3
81	84G	1A	5102	-	-	8/23/76/76	0/3/3/3
81	84G	1A	5107	-	-	10/23/76/76	0/3/3/3
81	84G	1A	5111	-	-	13/23/76/76	1/3/3/3
81	84G	1A	5115	-	-	6/23/76/76	0/3/3/3
81	84G	2D	301	-	-	7/23/76/76	0/3/3/3
81	84G	1A	5118	-	-	5/23/76/76	1/3/3/3

Continued on next page...

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
81	84G	1A	5101	-	-	8/23/76/76	1/3/3/3
81	84G	1A	5117	-	-	6/23/76/76	0/3/3/3
81	84G	1A	5113	-	-	5/23/76/76	0/3/3/3
81	84G	1A	5110	-	-	10/23/76/76	0/3/3/3
81	84G	1A	5116	-	-	4/23/76/76	0/3/3/3
81	84G	1A	5119	-	-	7/23/76/76	0/3/3/3
81	84G	1A	5103	-	-	7/23/76/76	0/3/3/3
81	84G	2m	1902	-	-	7/23/76/76	0/3/3/3
81	84G	1A	5114	-	-	9/23/76/76	0/3/3/3
81	84G	1A	5109	-	-	5/23/76/76	0/3/3/3

The worst 5 of 164 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
81	1A	5111	84G	C3-N1	6.58	1.48	1.34
81	1A	5109	84G	C3-N1	6.51	1.48	1.34
81	1A	5119	84G	C3-N1	6.48	1.48	1.34
81	1A	5112	84G	C3-N1	6.48	1.48	1.34
81	1A	5102	84G	C3-N1	6.47	1.48	1.34

The worst 5 of 103 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	2m	1901	84G	C16-C21-C20	6.30	118.86	110.40
81	2m	1901	84G	O6-C17-C19	4.48	117.84	109.69
81	1A	5111	84G	C16-O5-C15	-4.43	107.00	117.96
81	2m	1901	84G	C16-O6-C17	4.39	122.30	113.69
81	1A	5101	84G	C5-C4-C15	4.25	117.38	109.47

There are no chirality outliers.

5 of 169 torsion outliers are listed below:

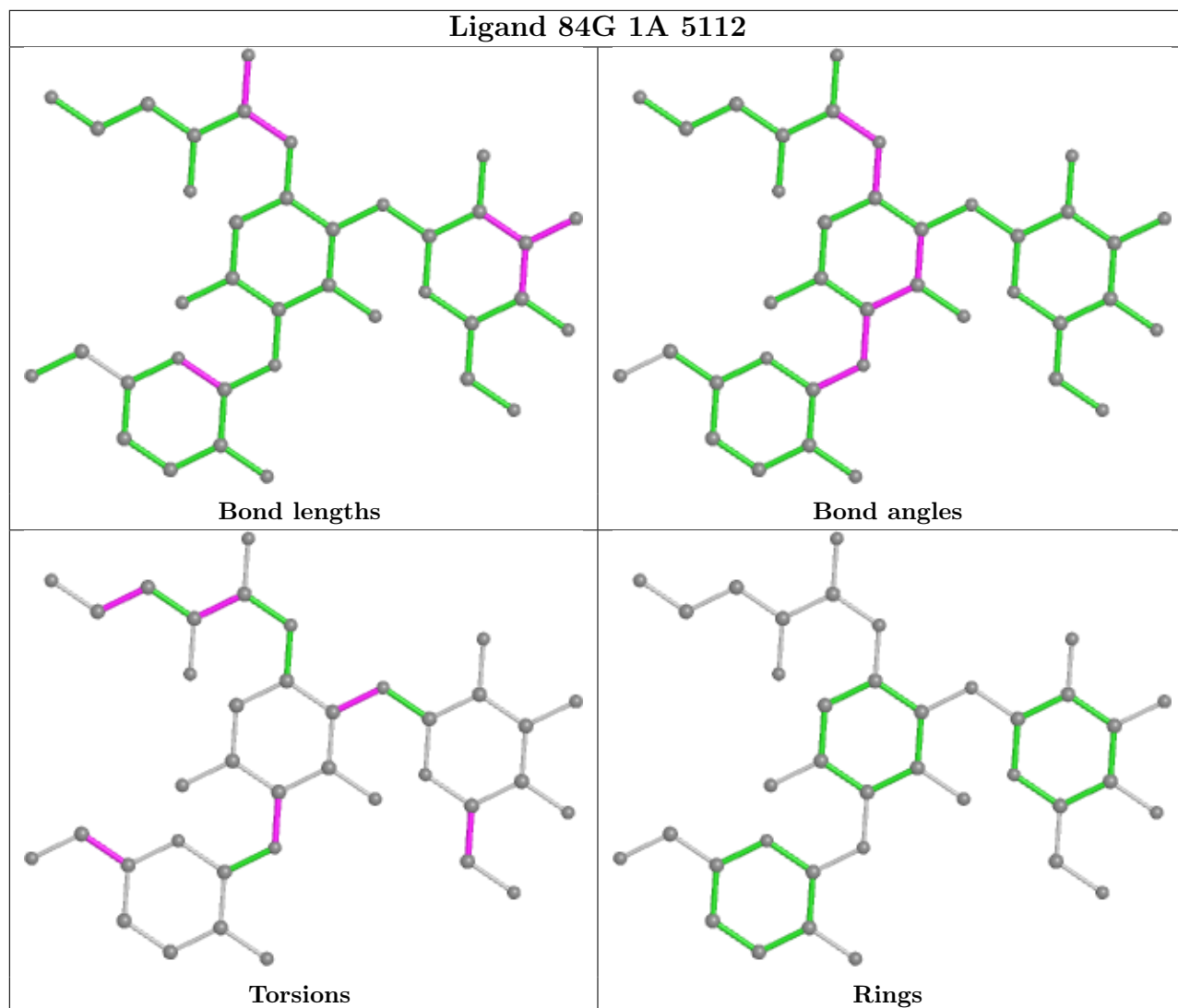
Mol	Chain	Res	Type	Atoms
81	1A	5102	84G	C-C1-C2-O
81	1A	5102	84G	N-C-C1-C2
81	1A	5102	84G	C1-C2-C3-O1
81	1A	5102	84G	C1-C2-C3-N1
81	1A	5102	84G	O-C2-C3-N1

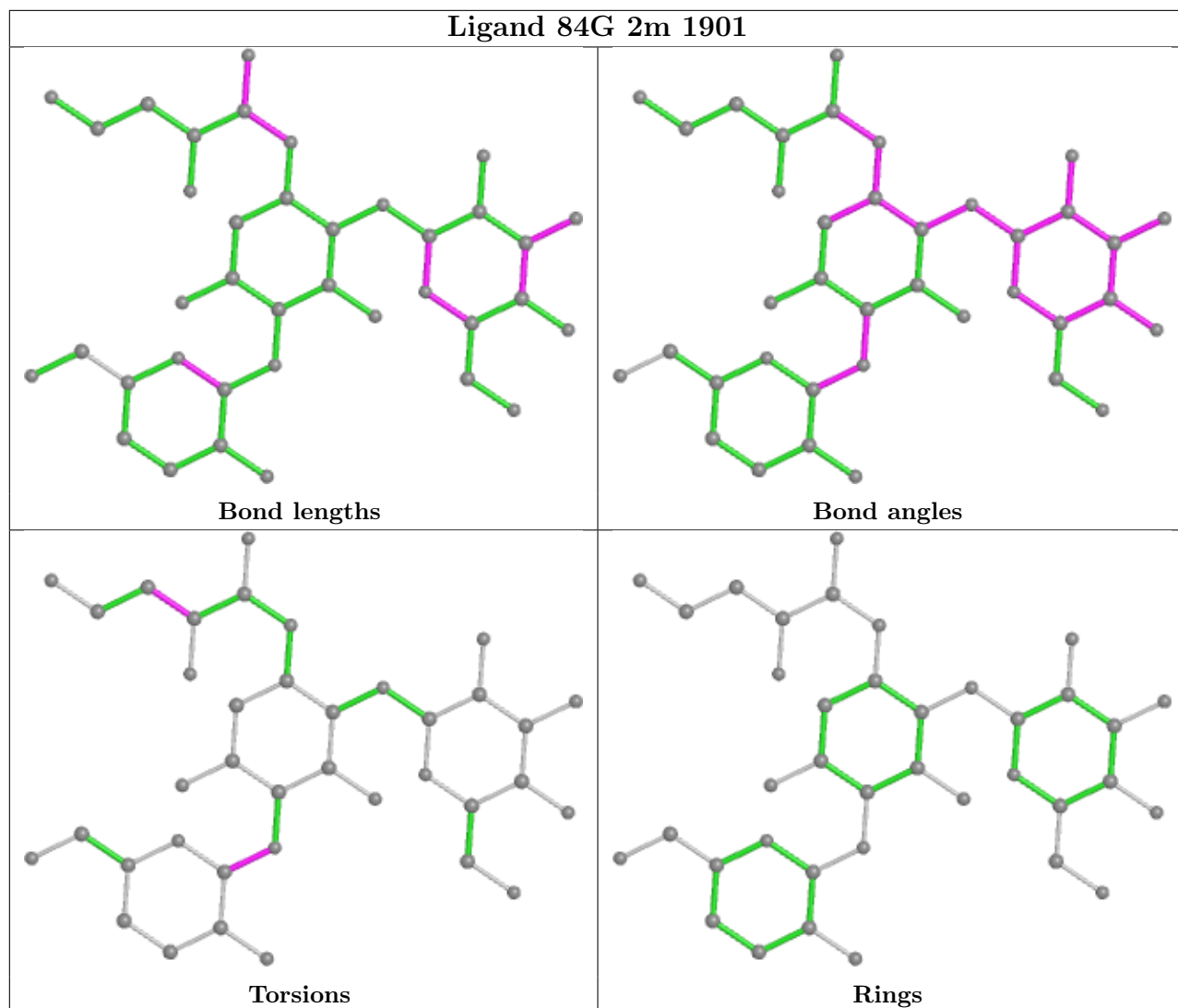
All (3) ring outliers are listed below:

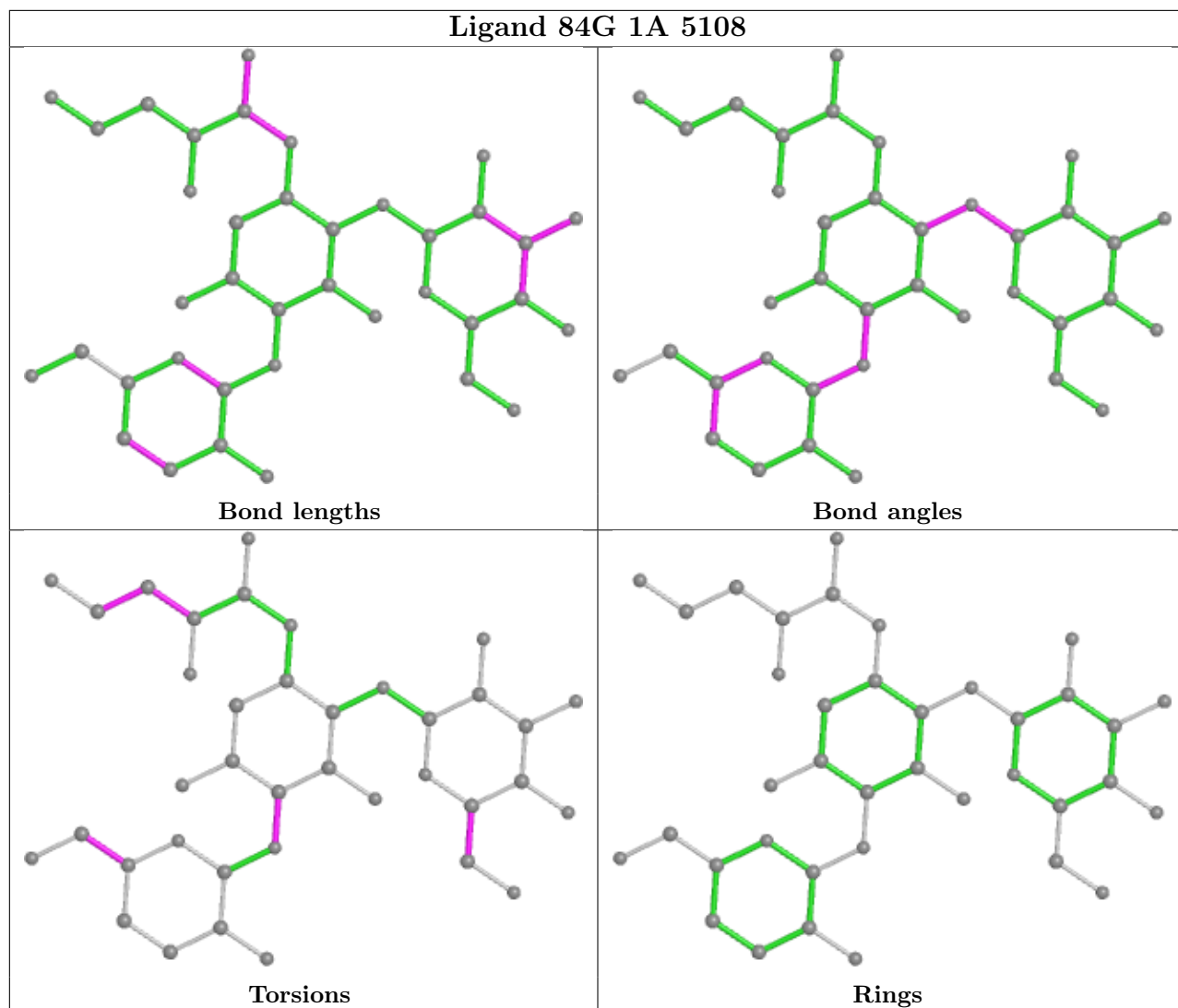
Mol	Chain	Res	Type	Atoms
81	1A	5118	84G	C11-C12-C13-C8-C9-O3
81	1A	5111	84G	C11-C12-C13-C8-C9-O3
81	1A	5101	84G	C11-C12-C13-C8-C9-O3

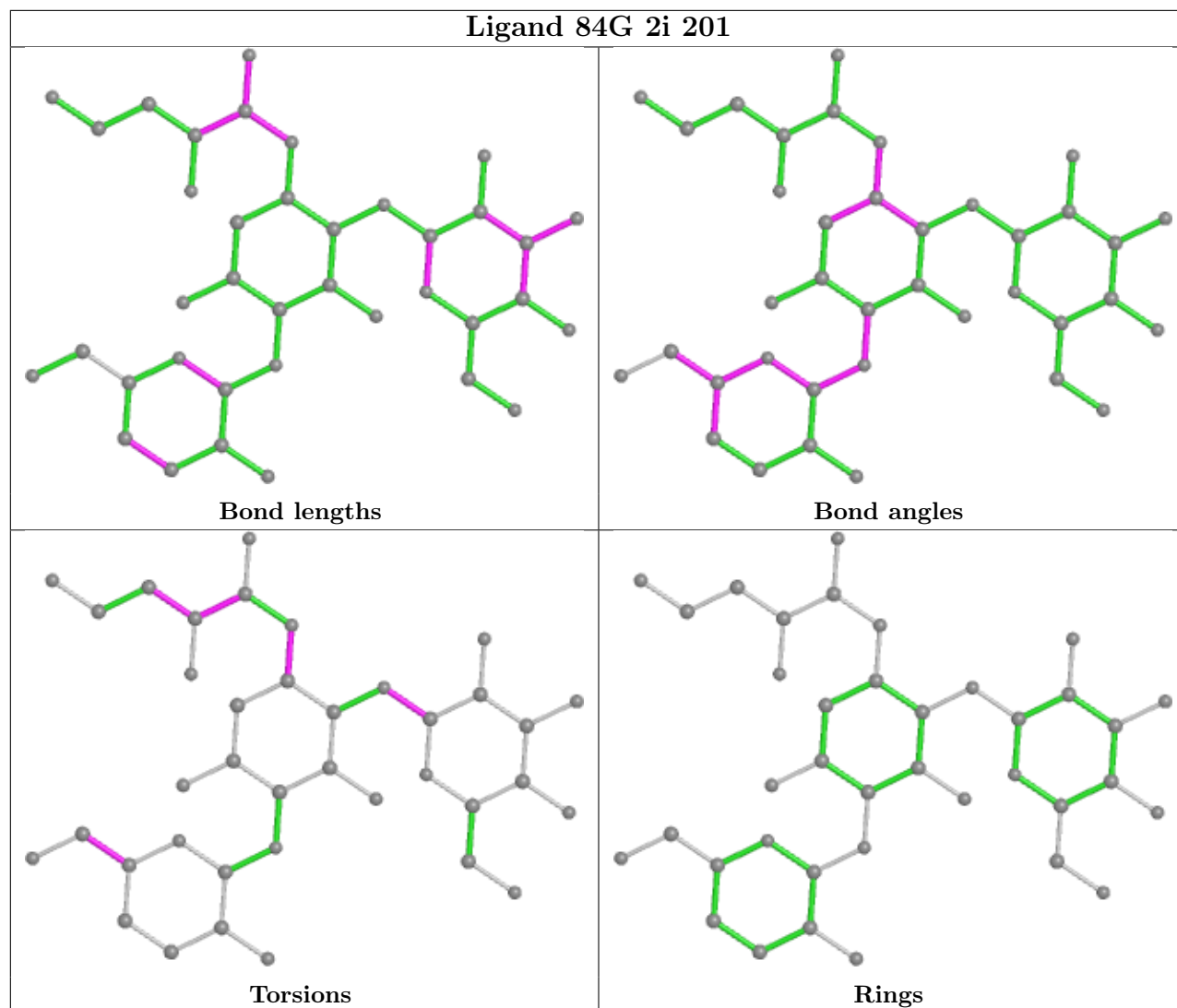
No monomer is involved in short contacts.

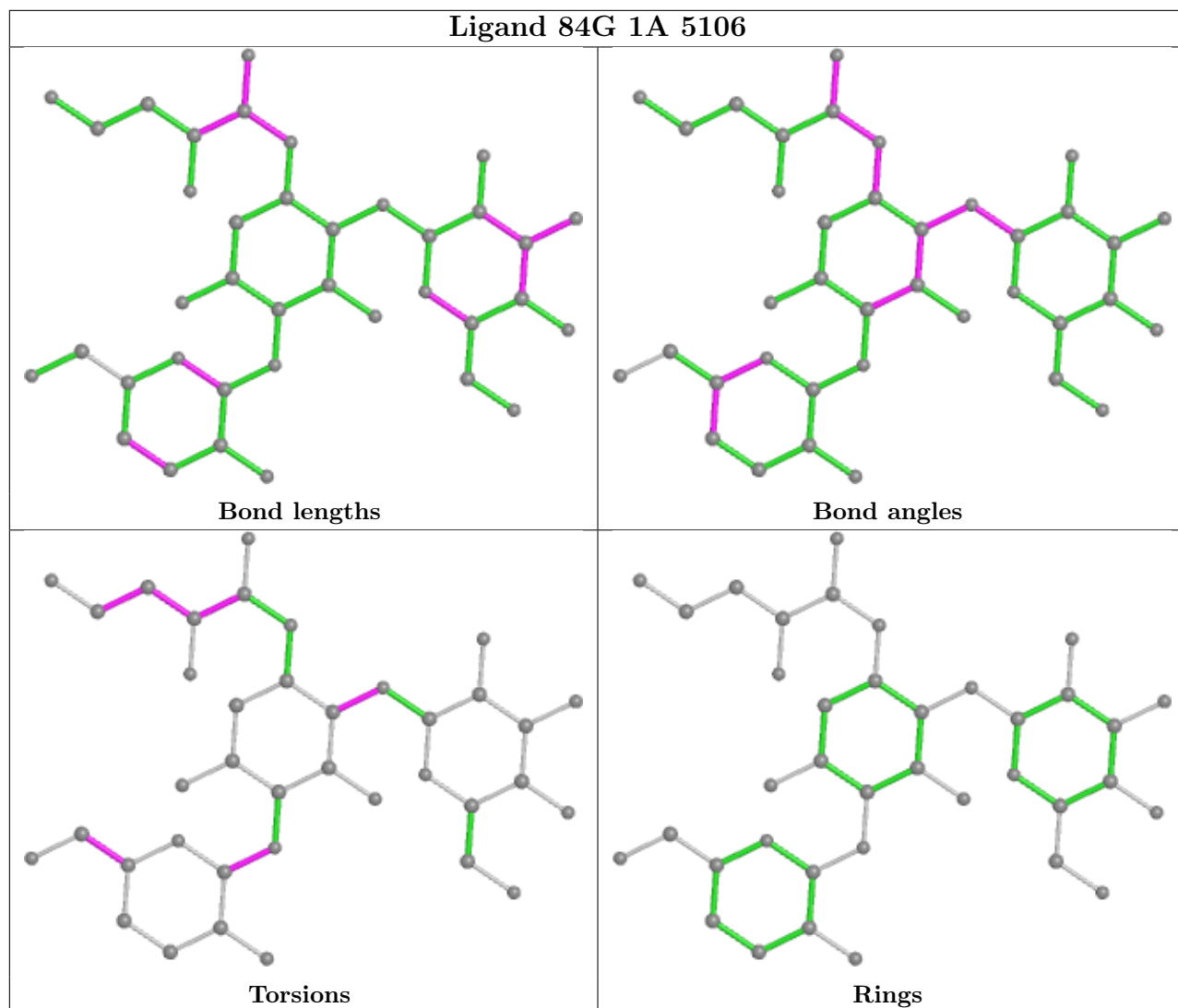
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

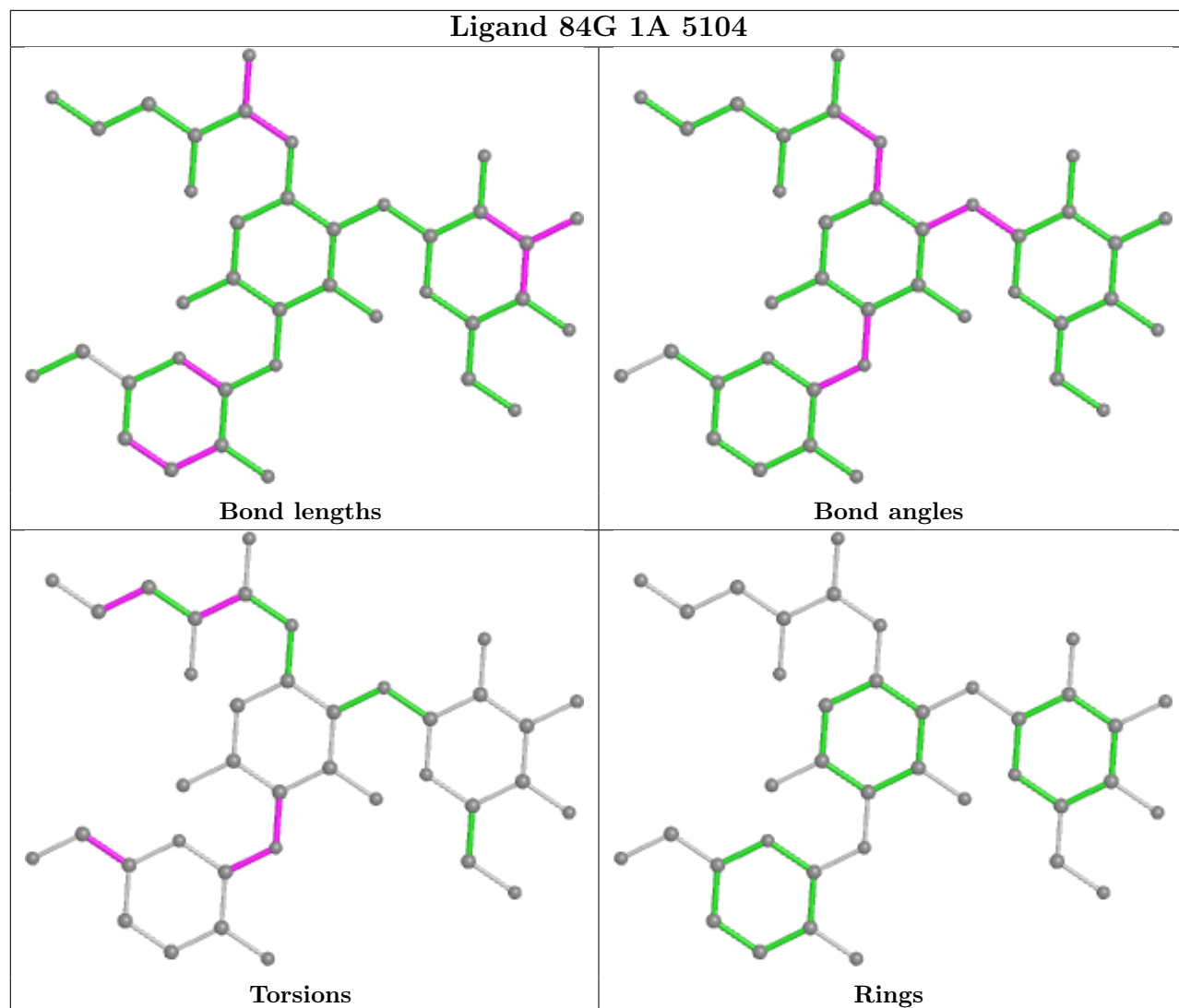


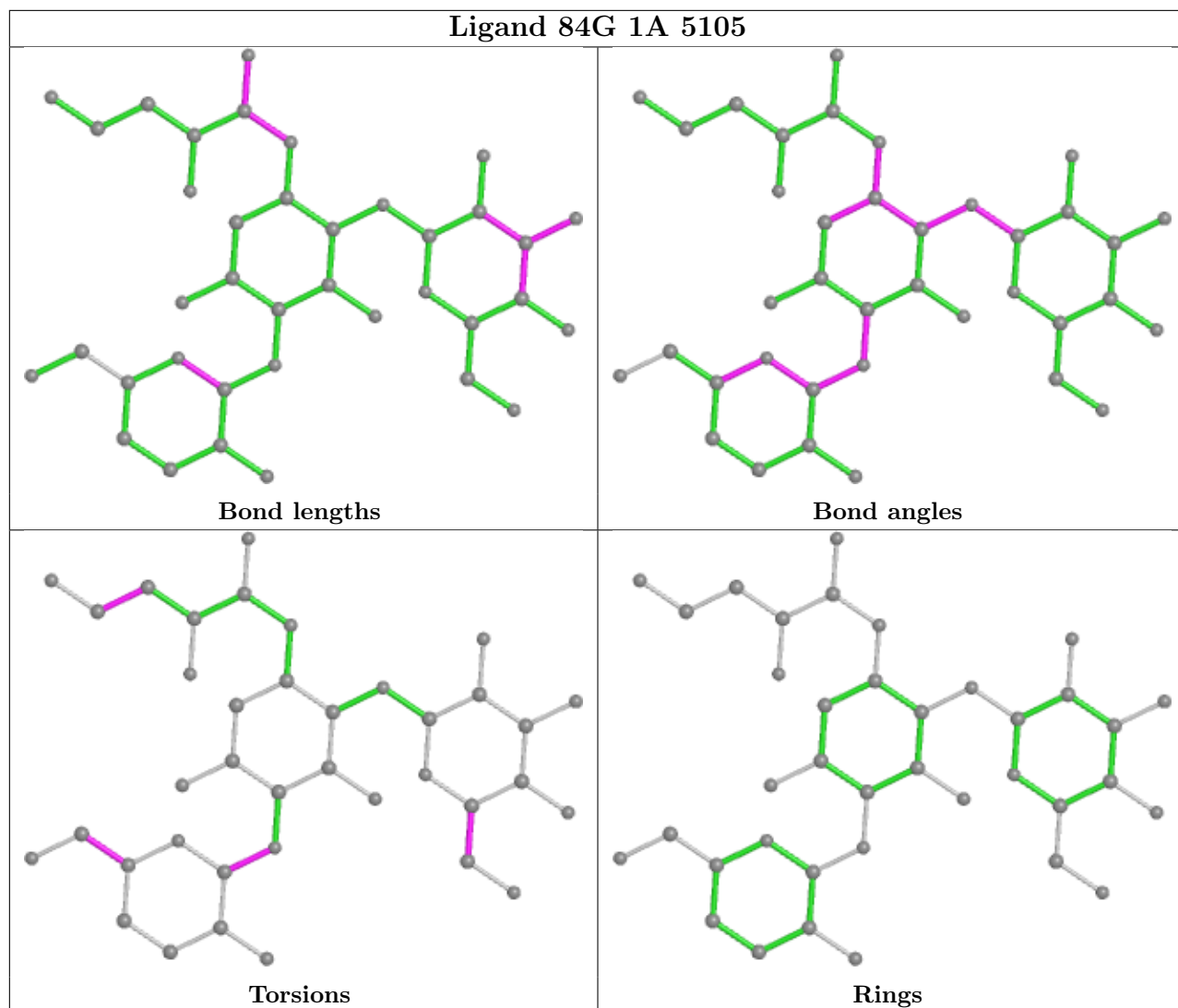


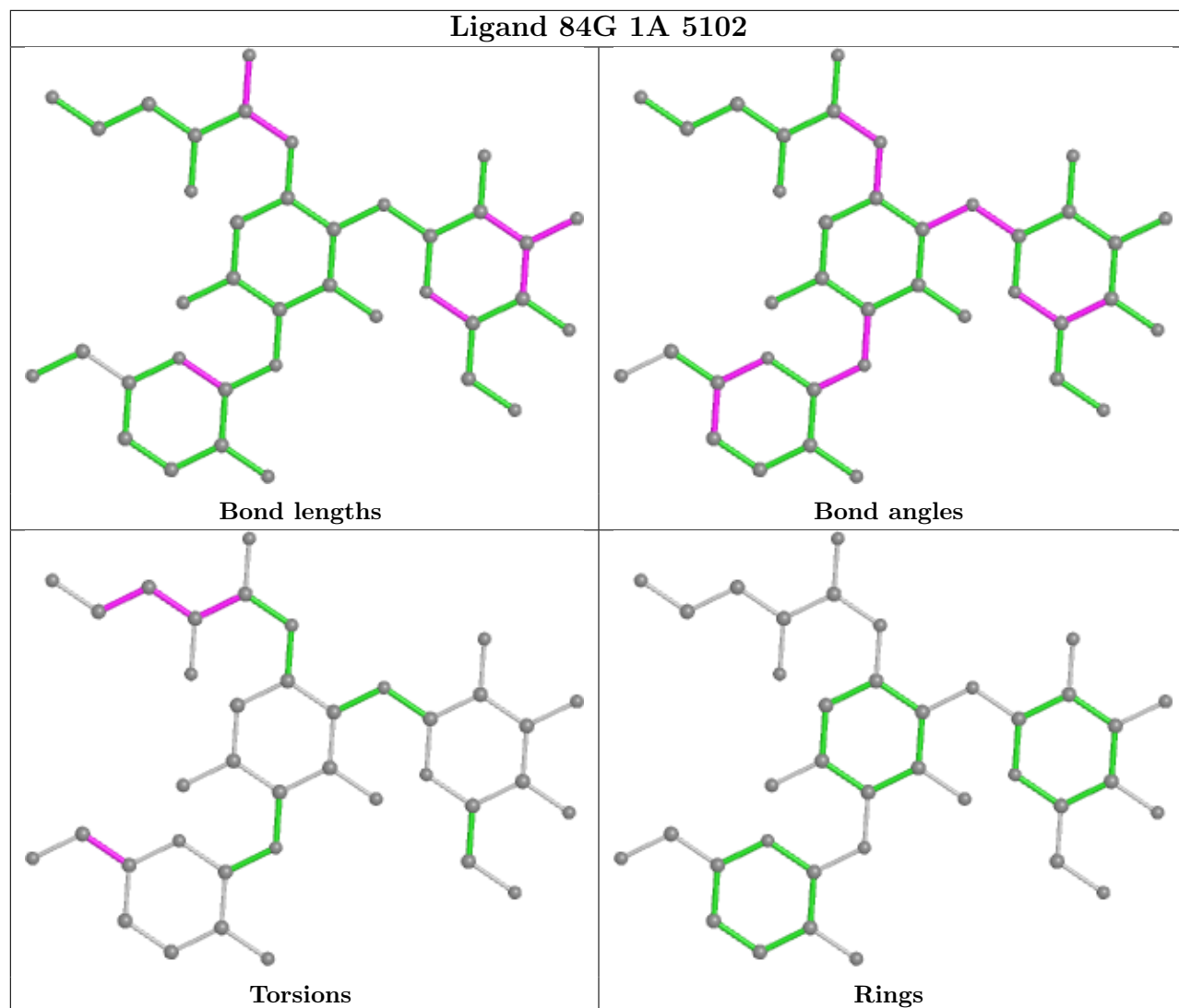


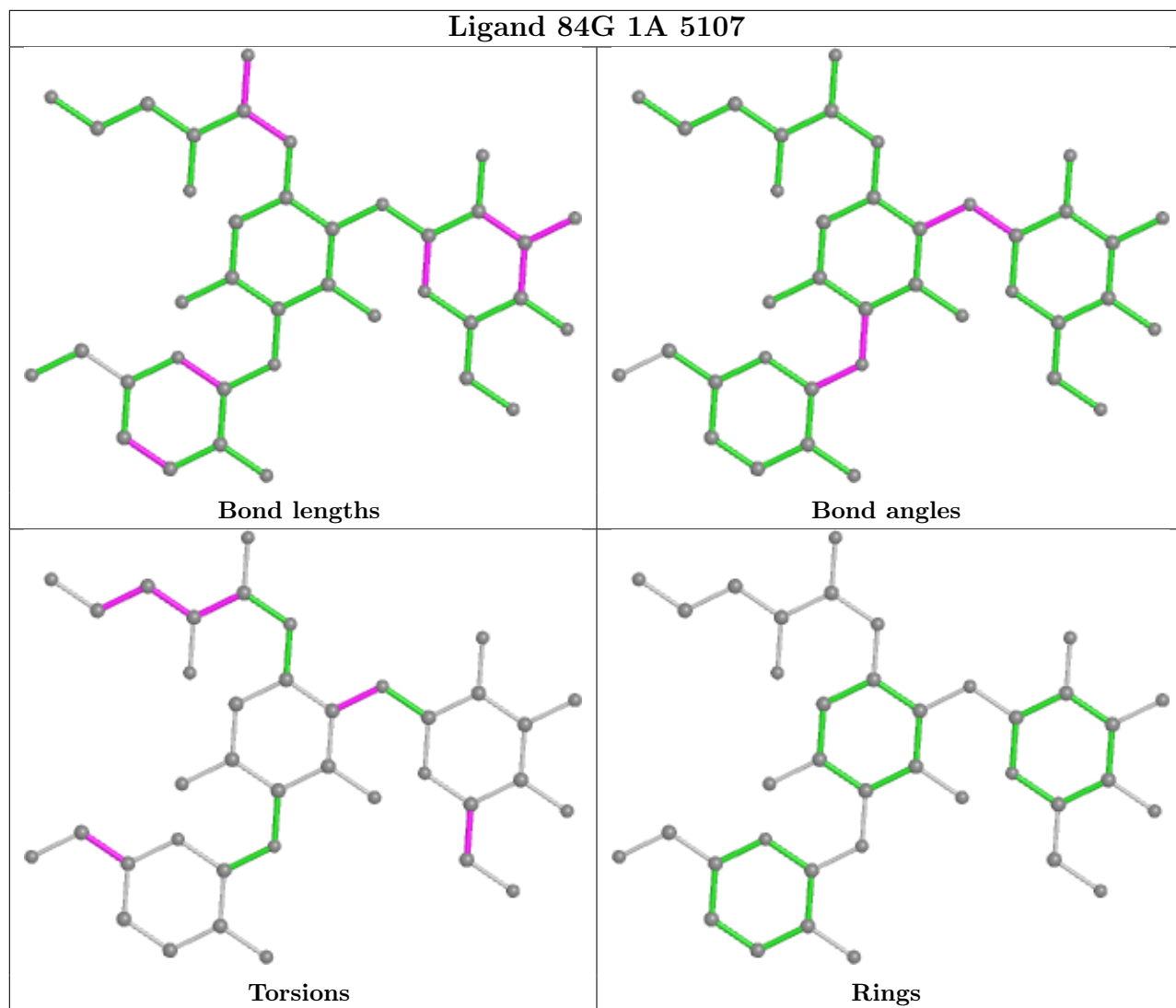


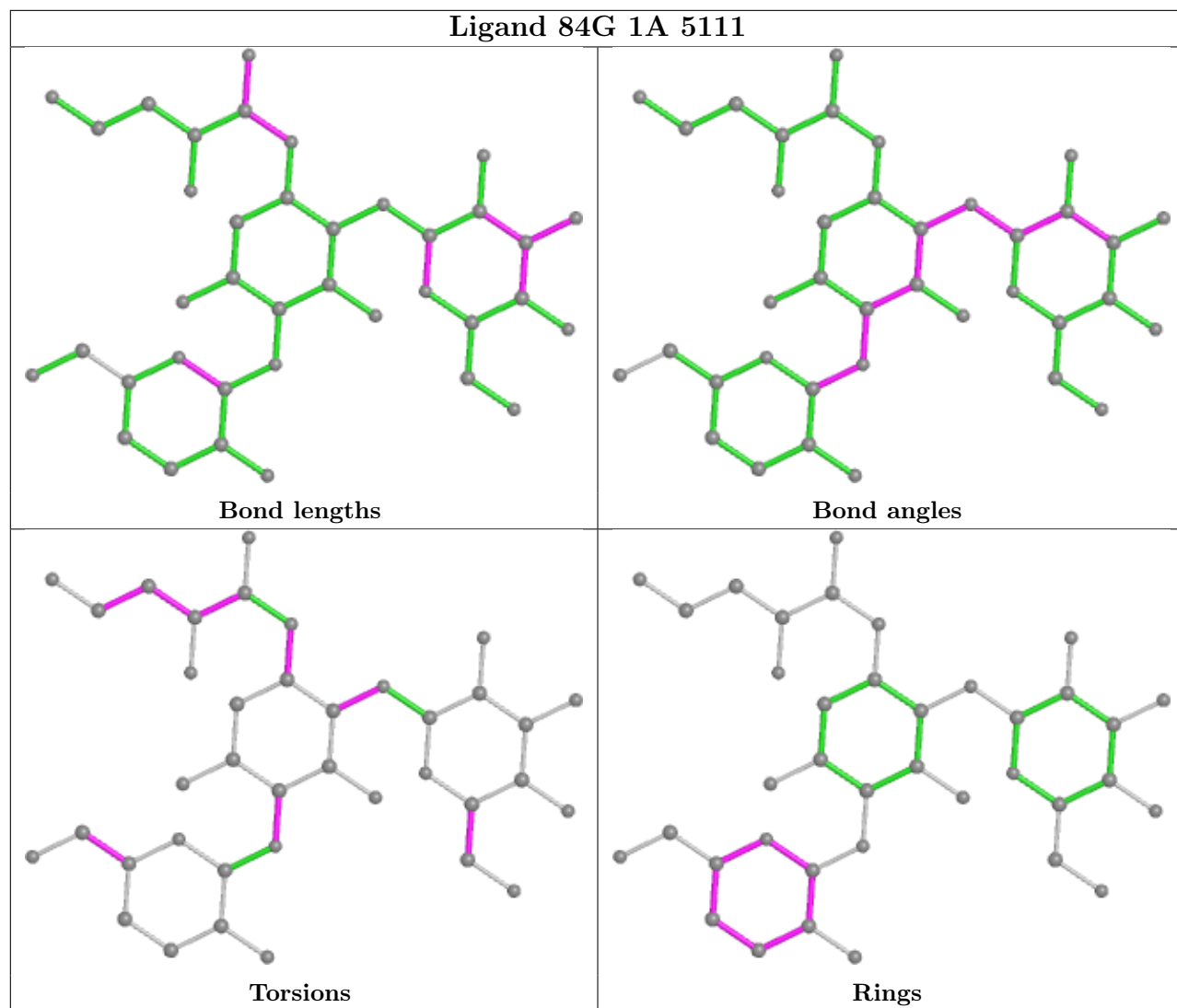


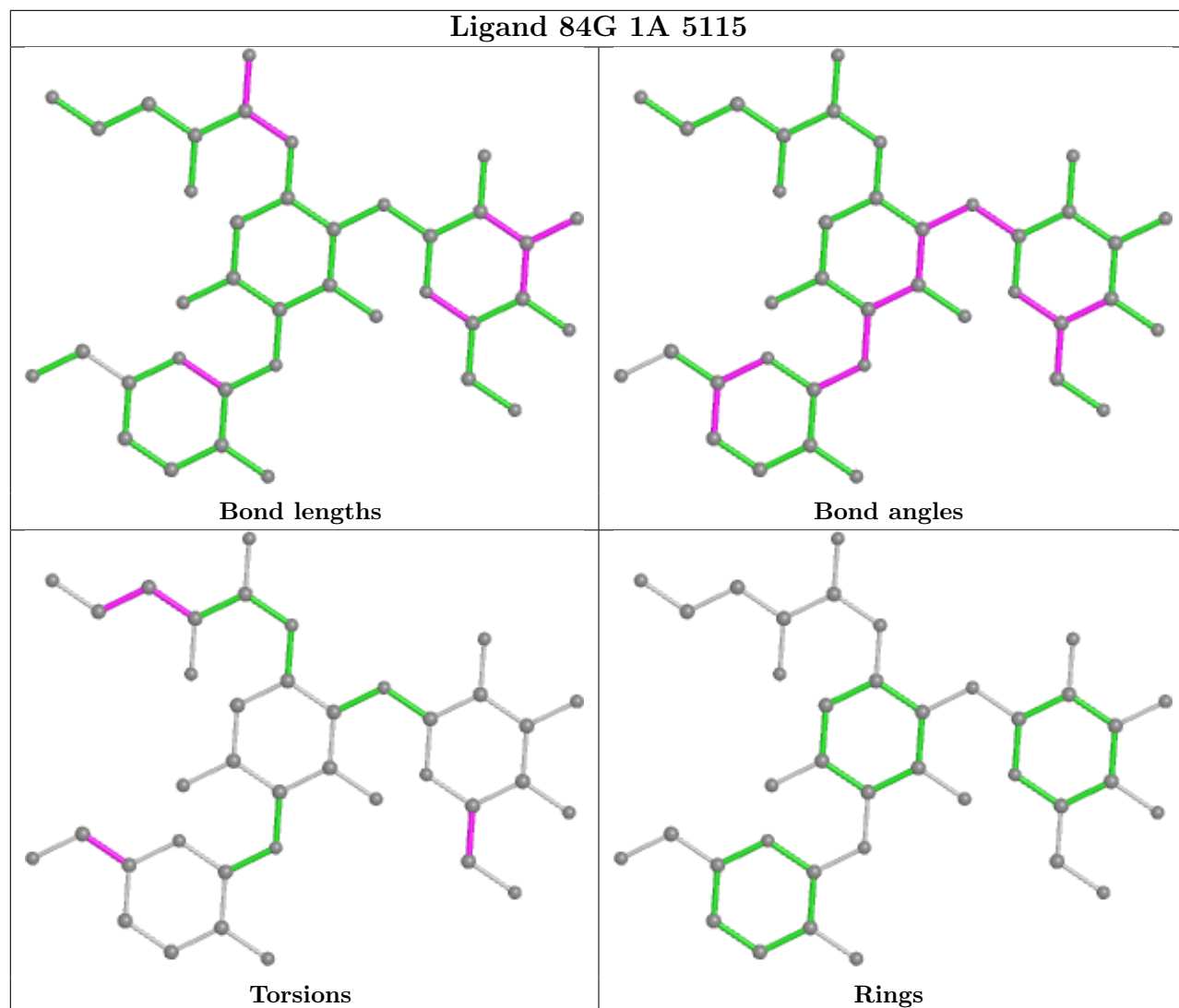


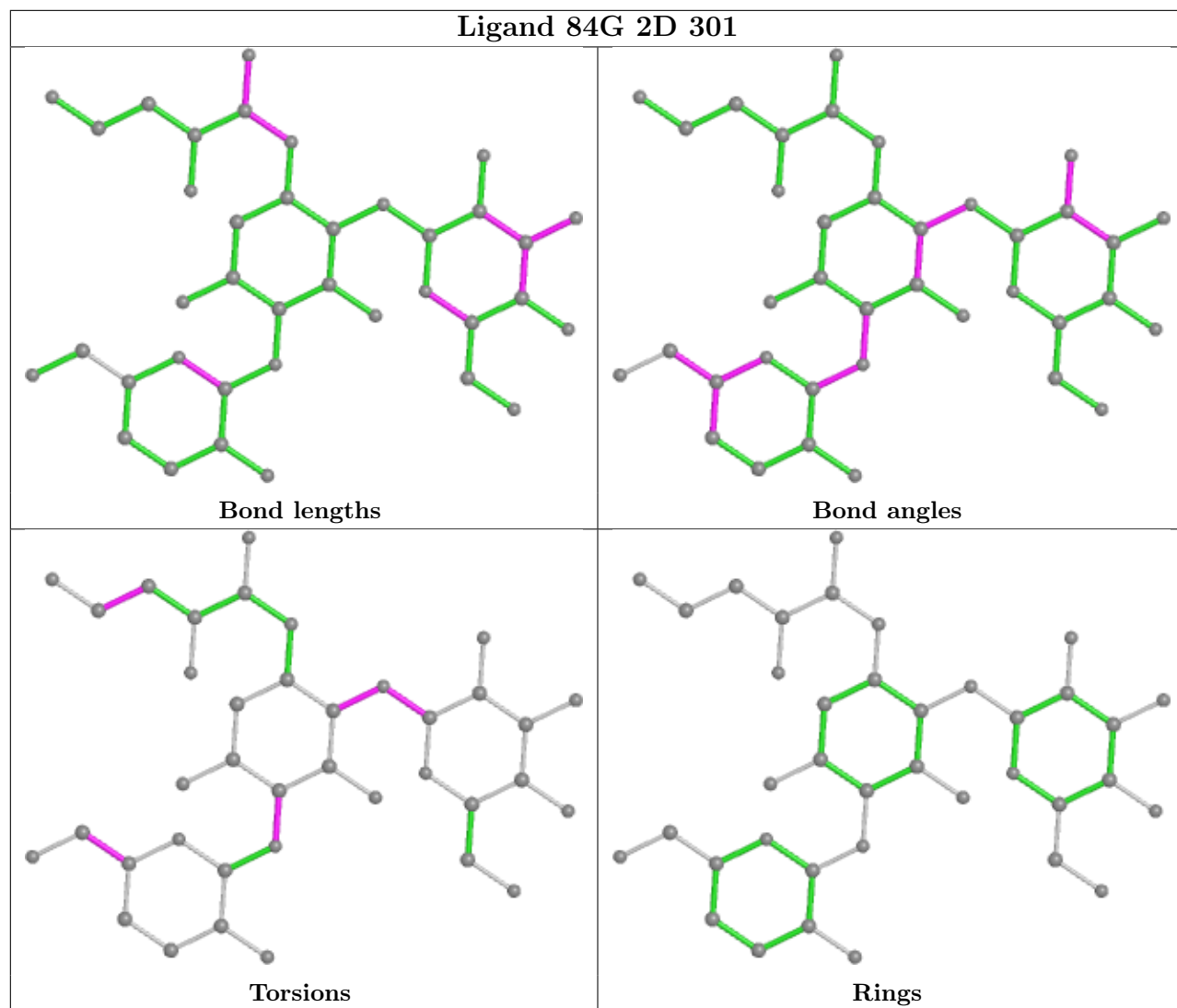


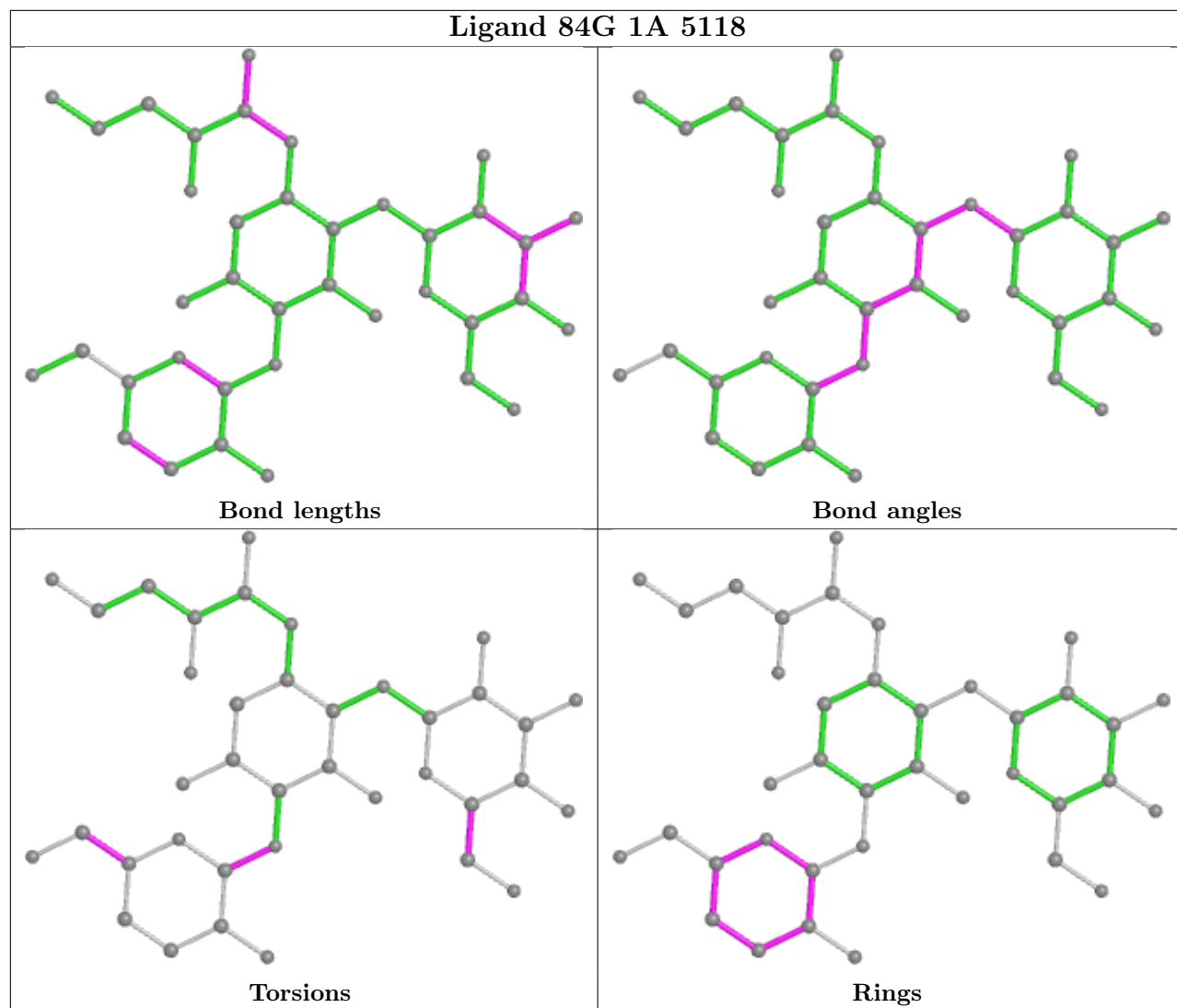


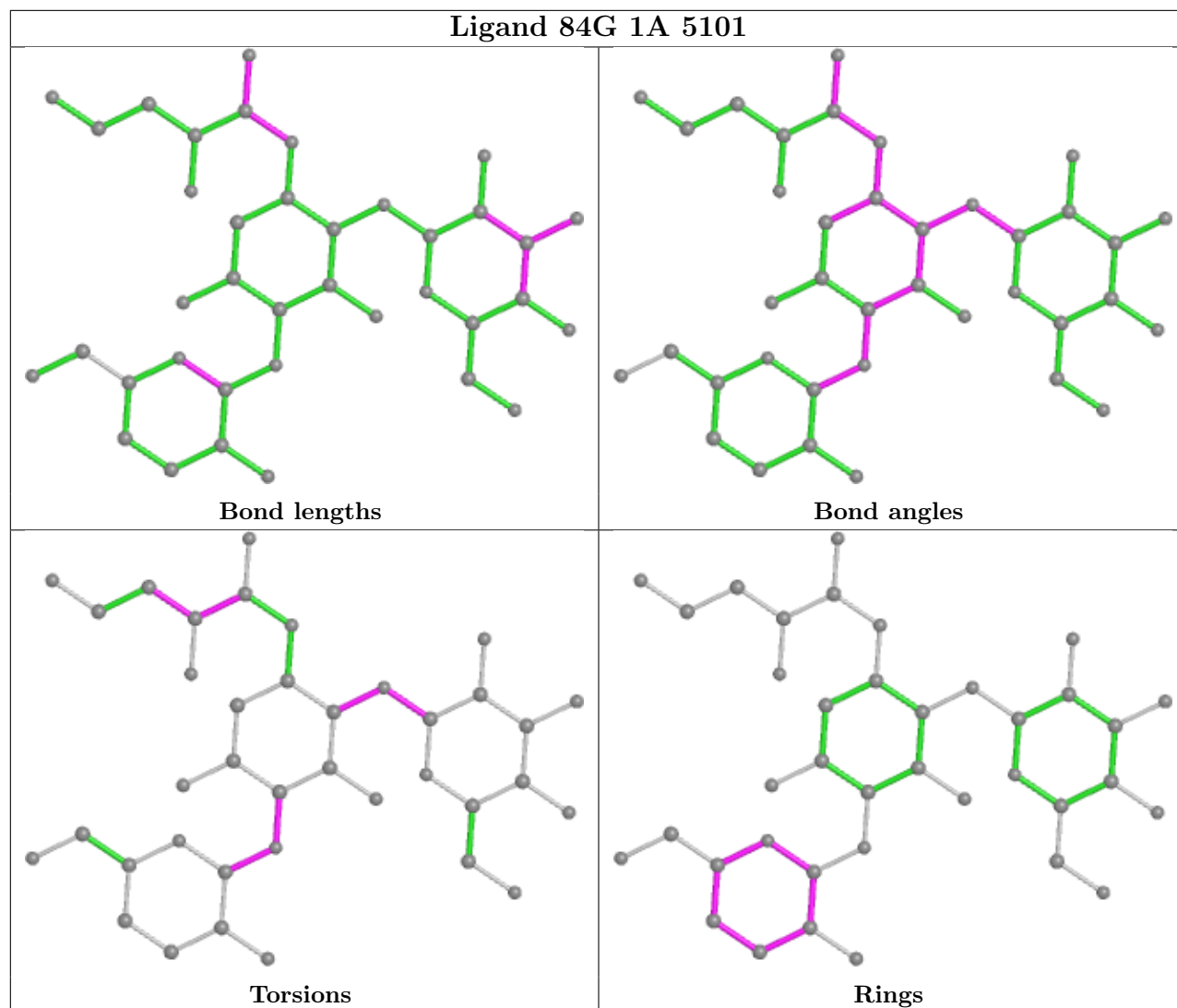


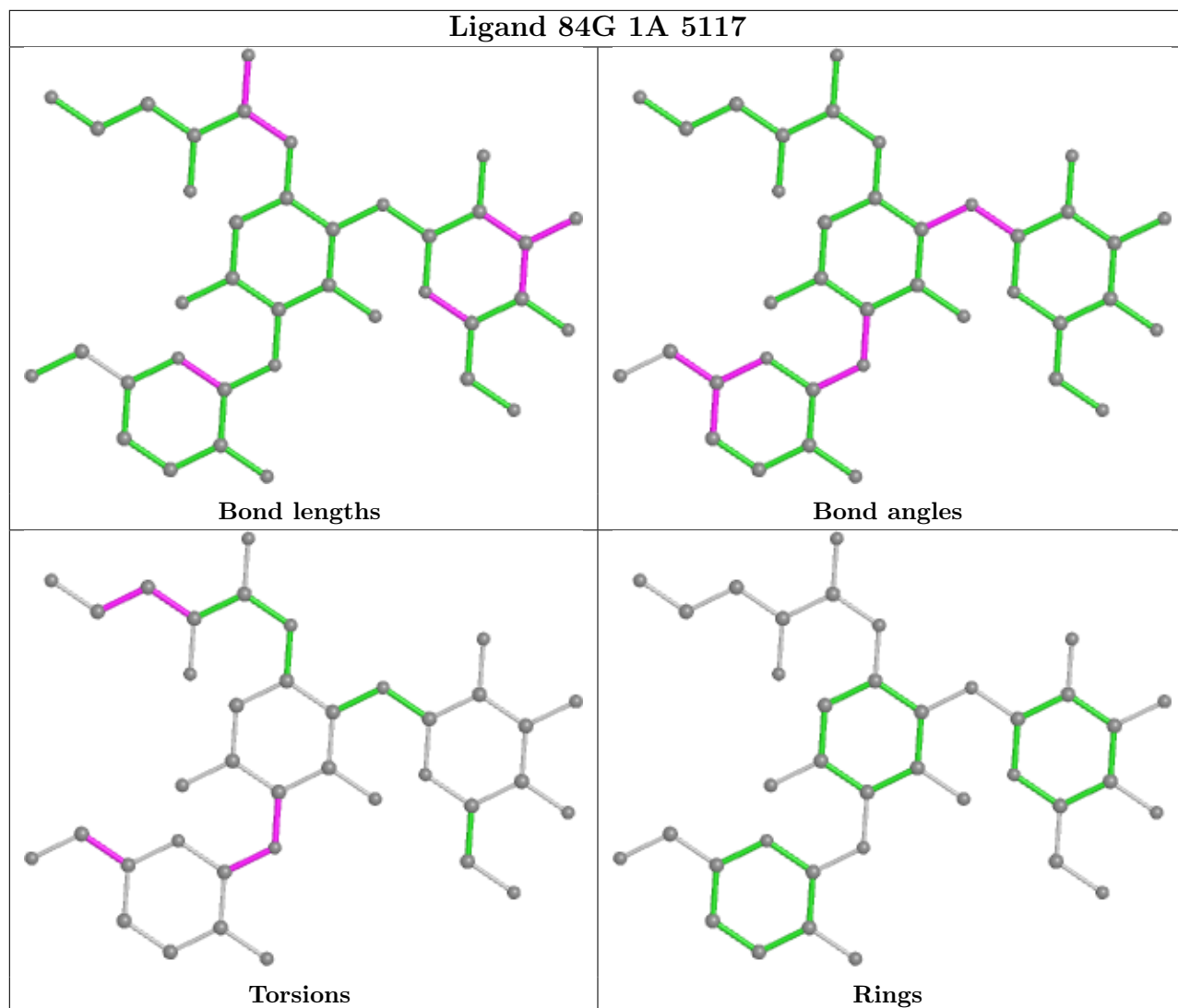


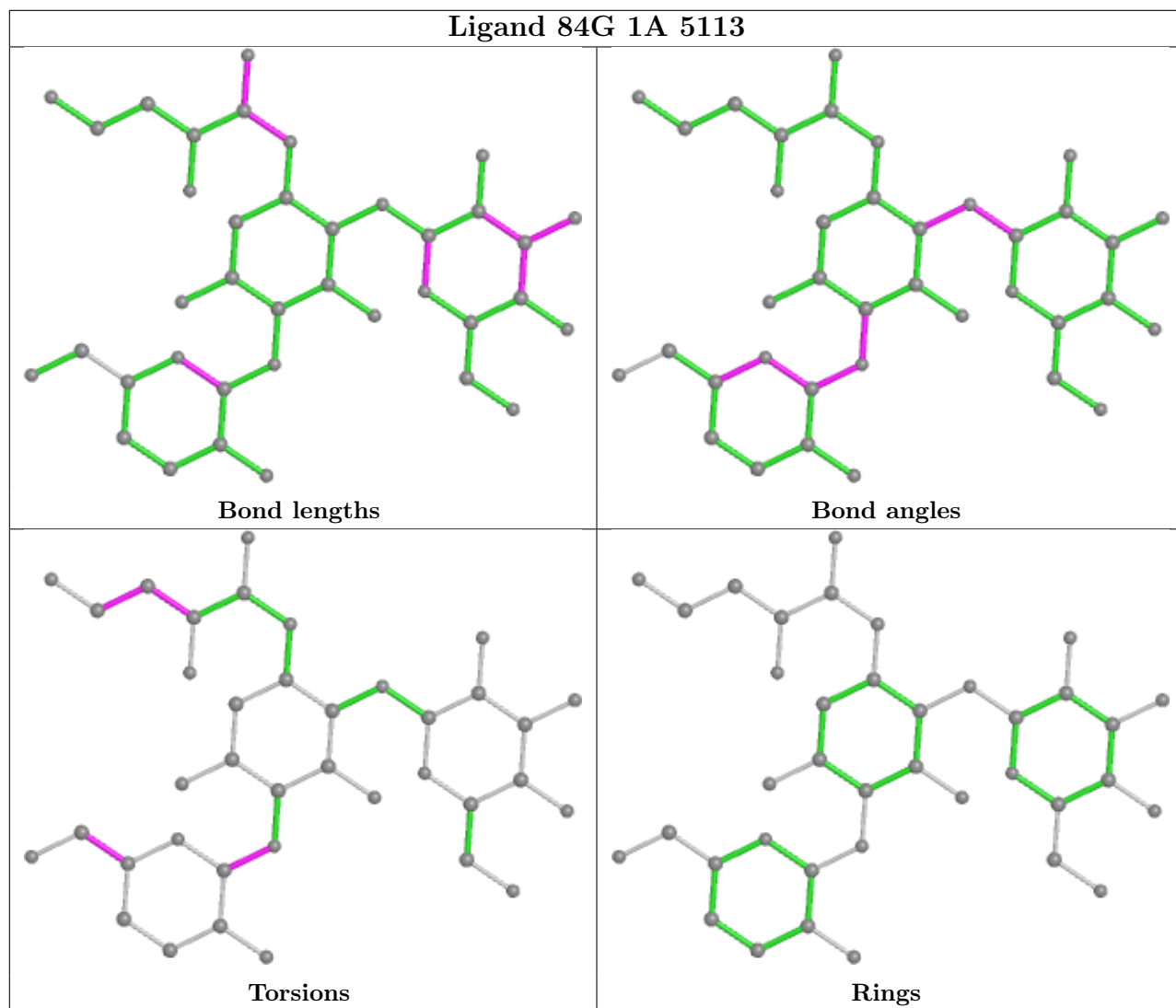


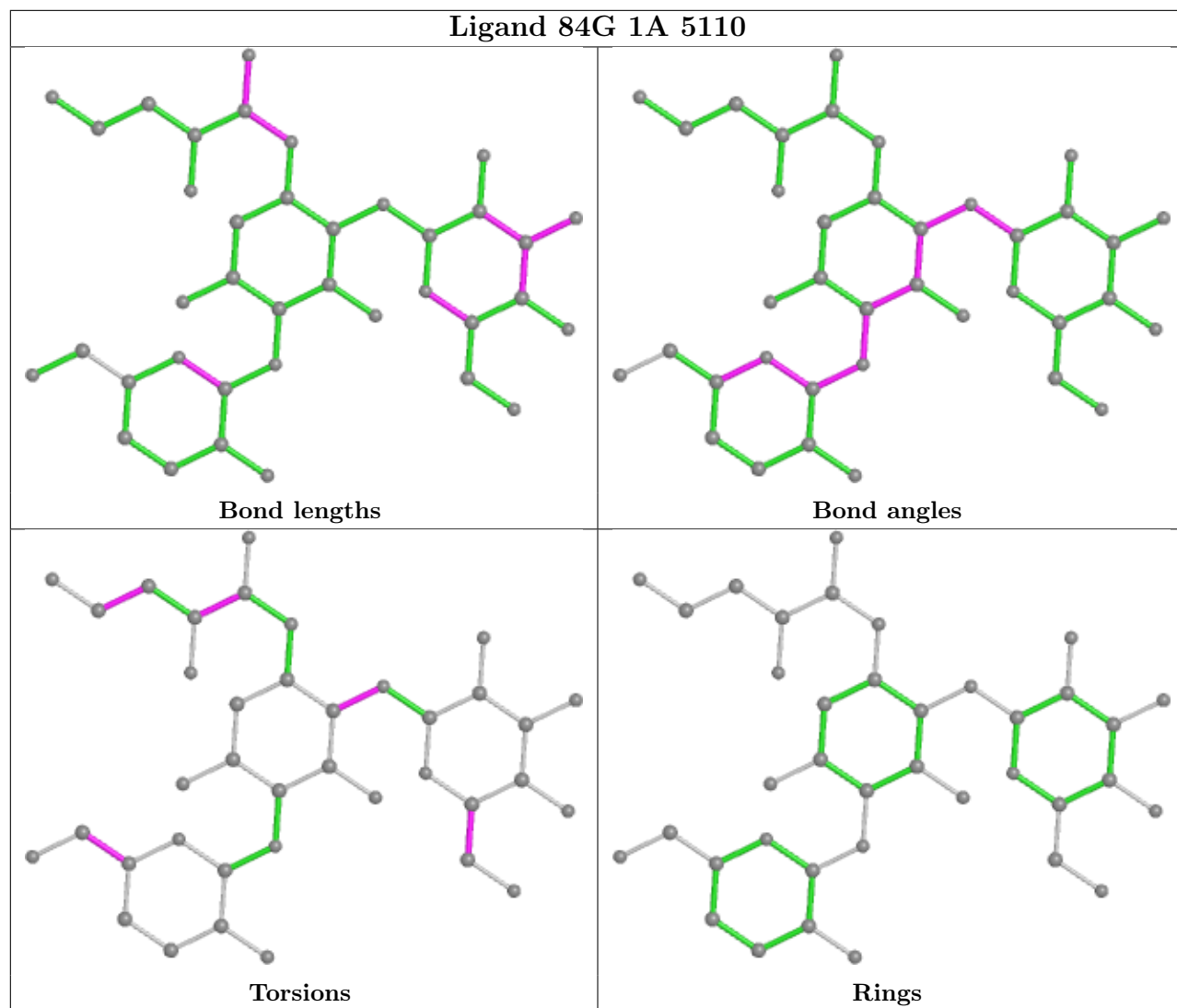


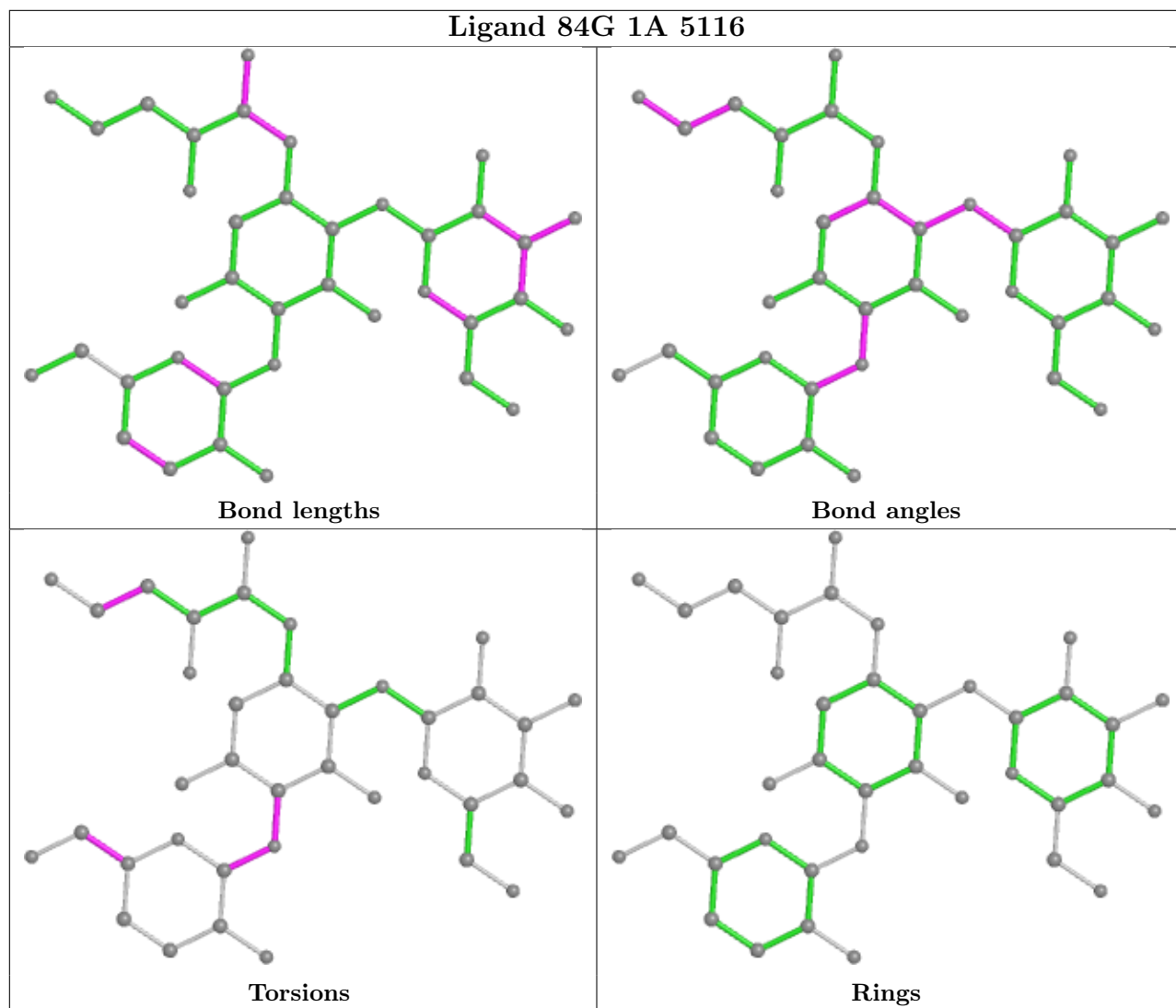


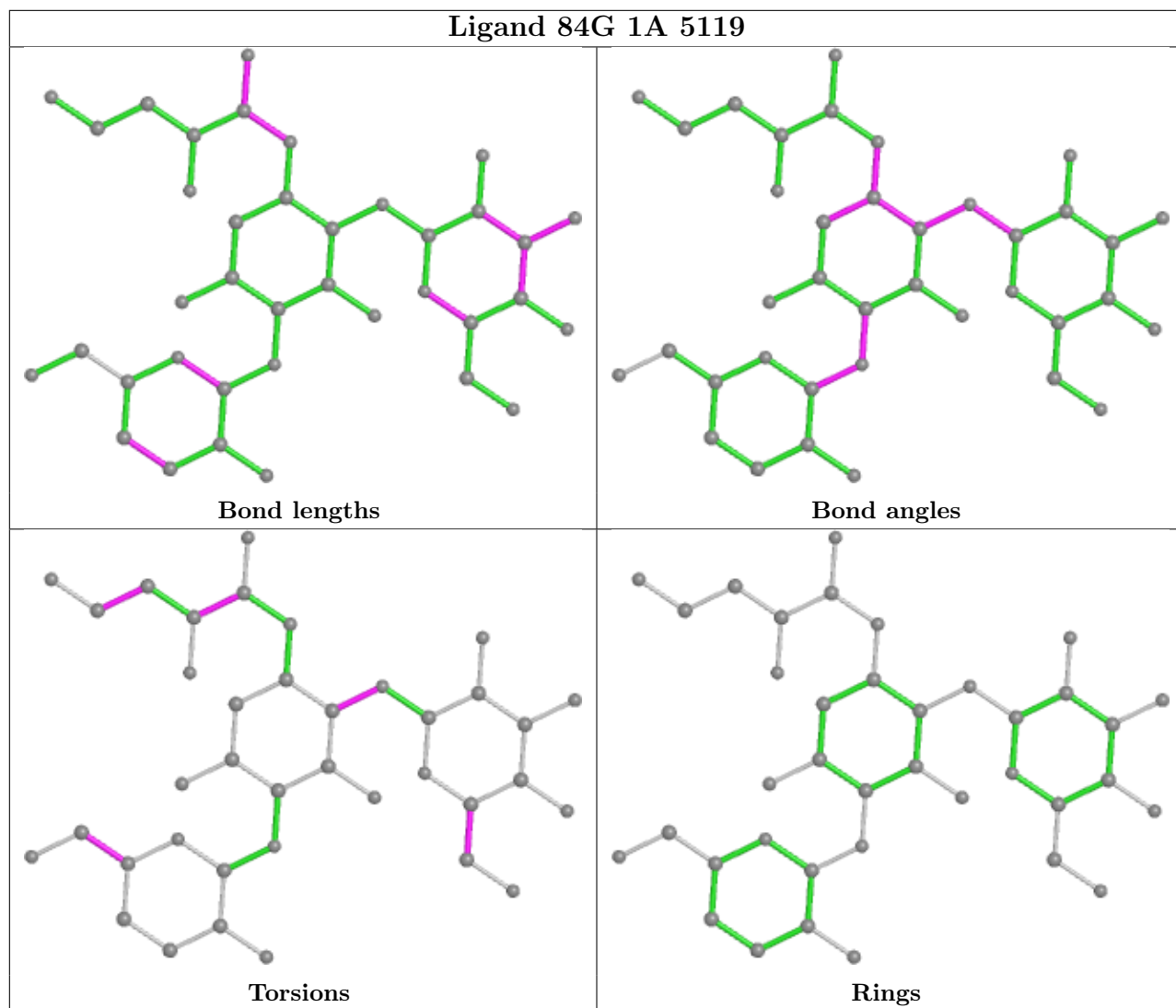


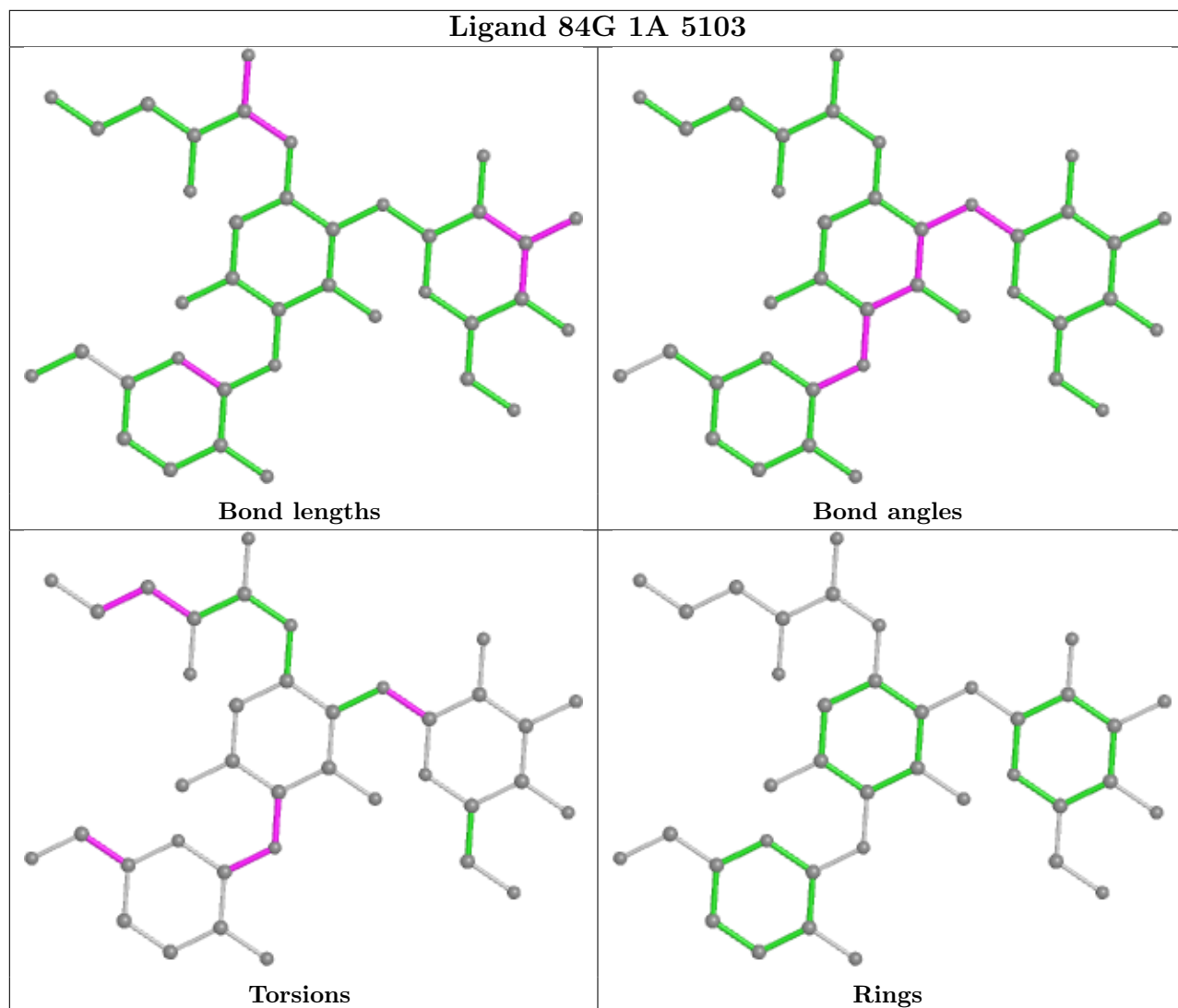


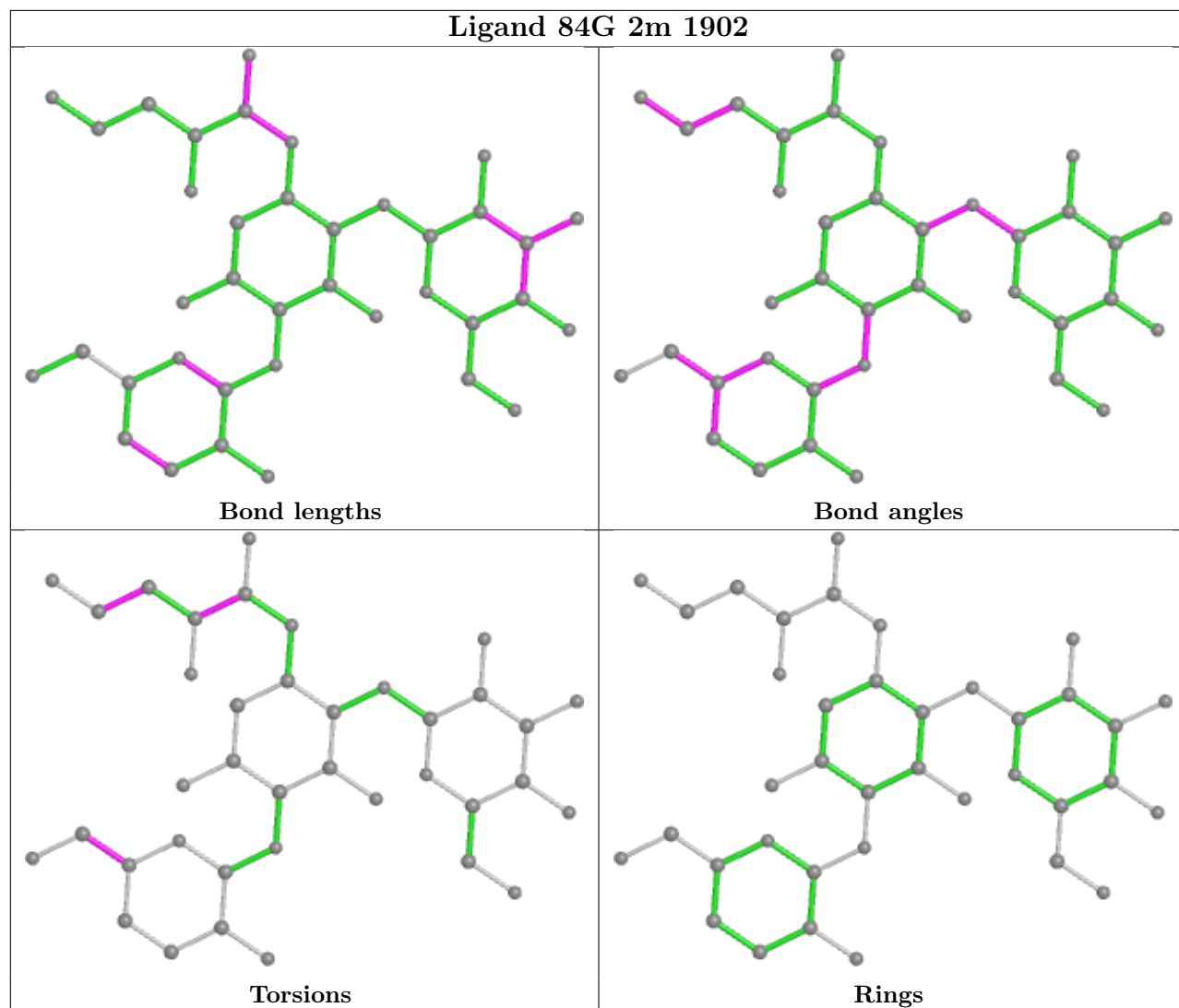


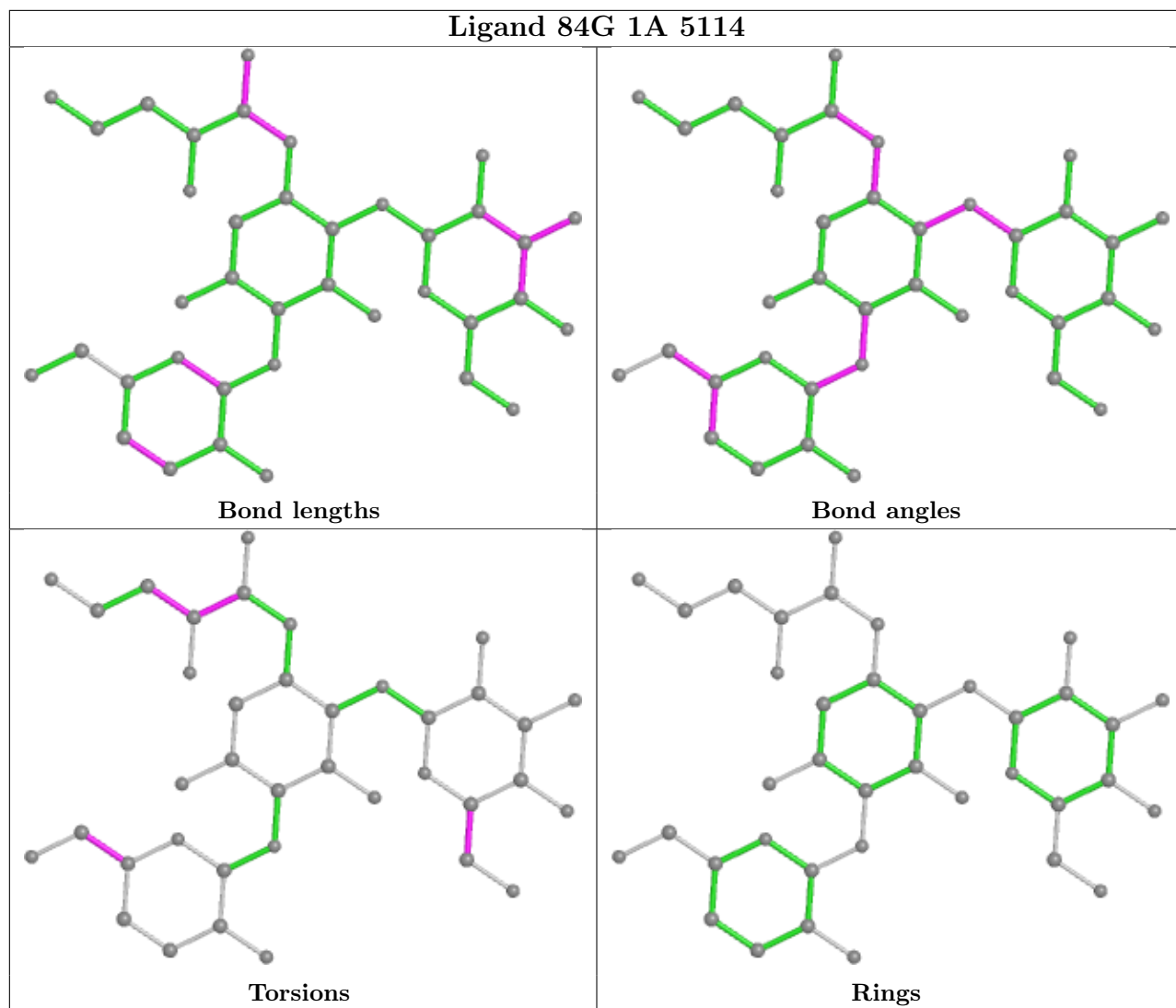


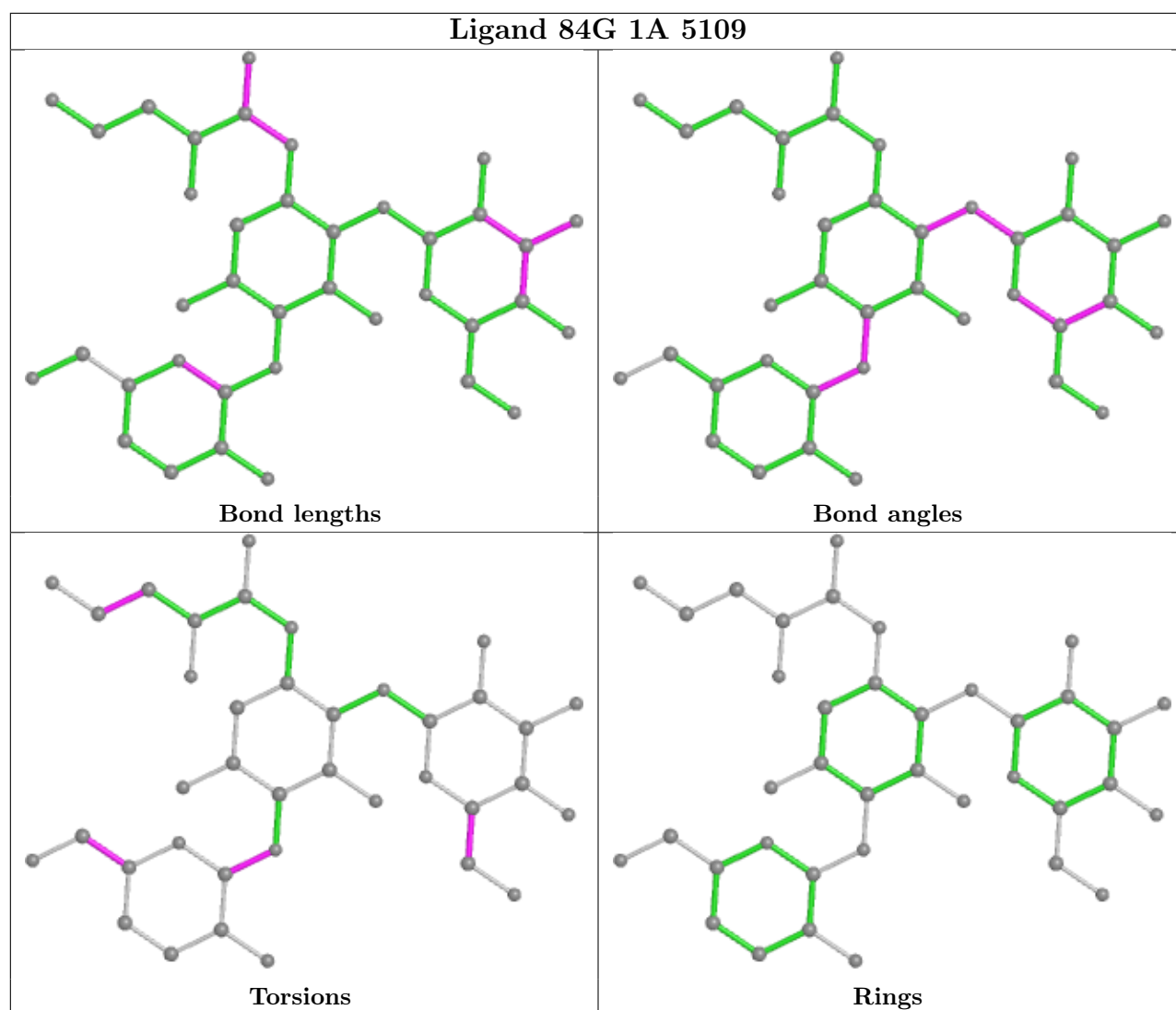












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

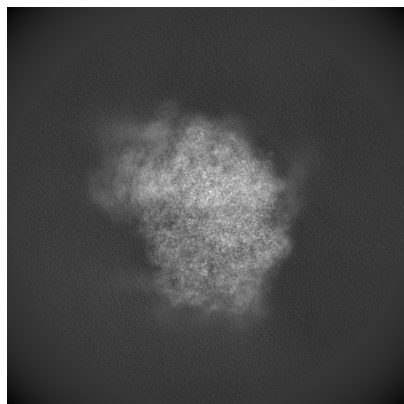
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35414. These allow visual inspection of the internal detail of the map and identification of artifacts.

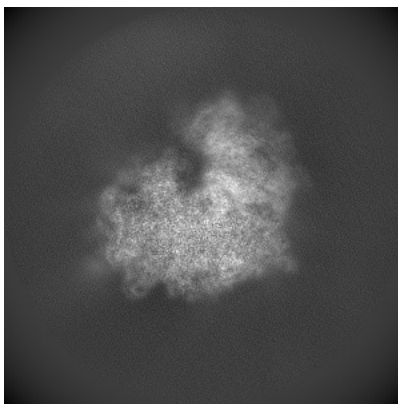
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

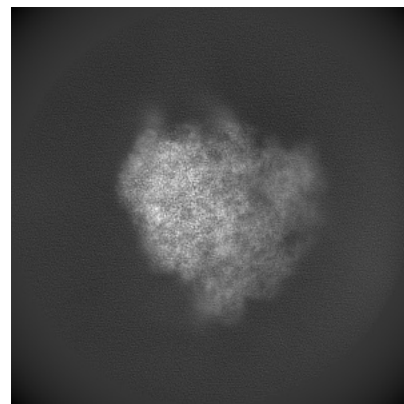
6.1.1 Primary map



X

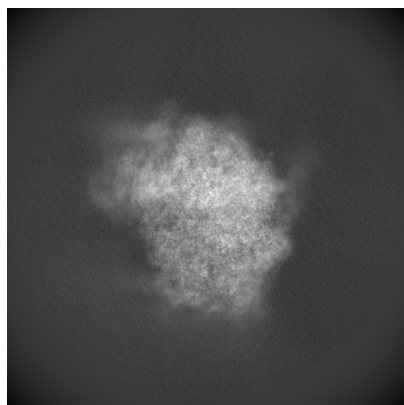


Y

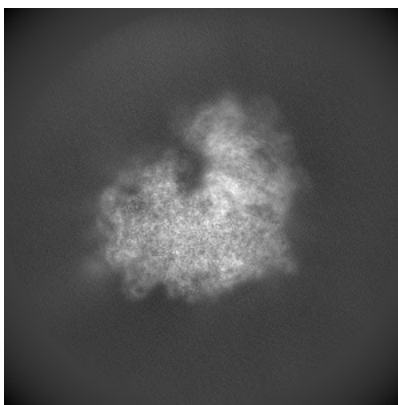


Z

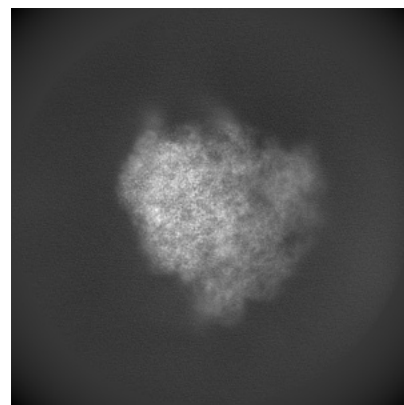
6.1.2 Raw map



X



Y

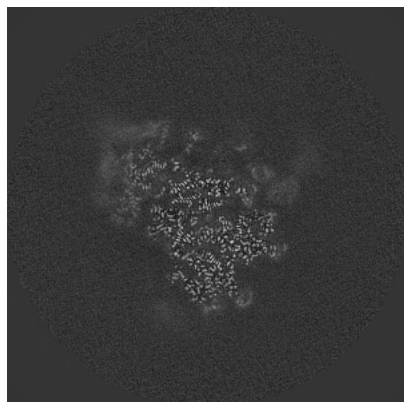


Z

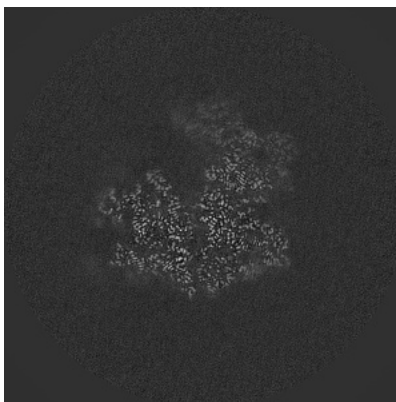
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

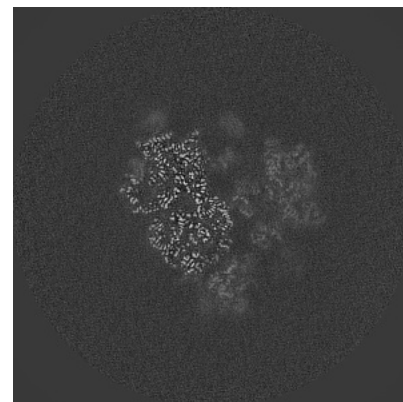
6.2.1 Primary map



X Index: 320

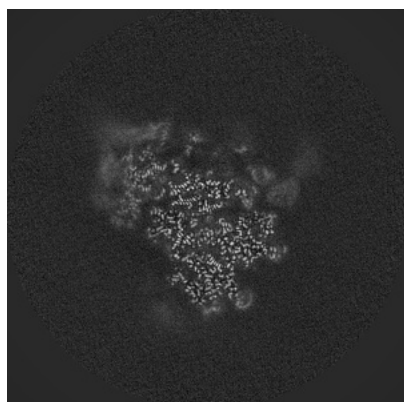


Y Index: 320

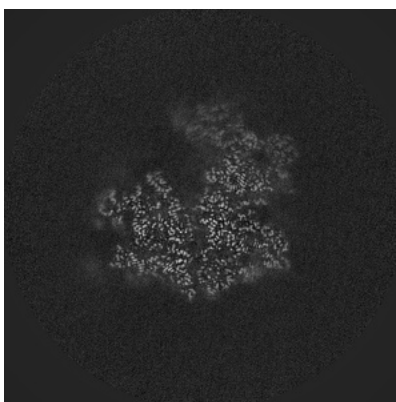


Z Index: 320

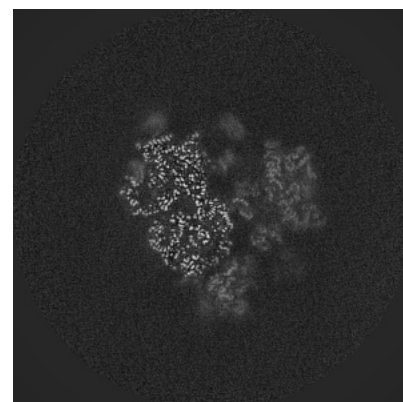
6.2.2 Raw map



X Index: 320



Y Index: 320

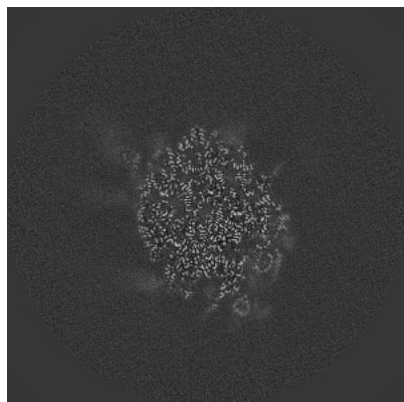


Z Index: 320

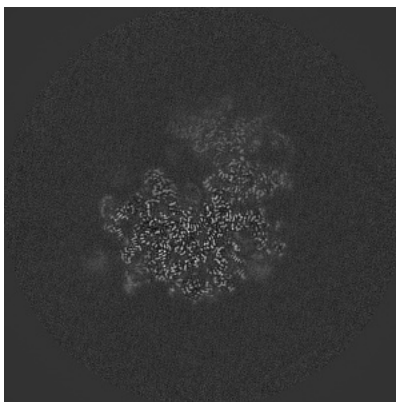
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

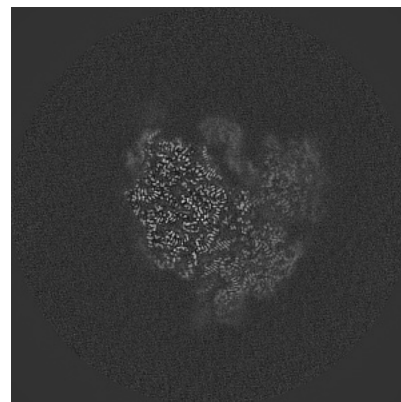
6.3.1 Primary map



X Index: 290

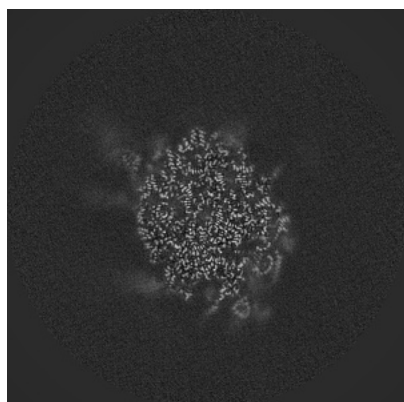


Y Index: 336

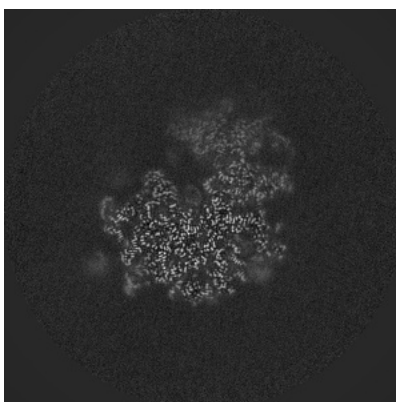


Z Index: 348

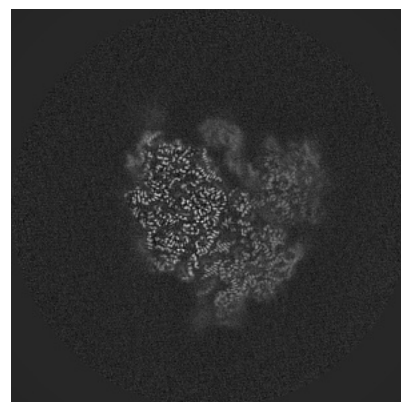
6.3.2 Raw map



X Index: 290



Y Index: 336

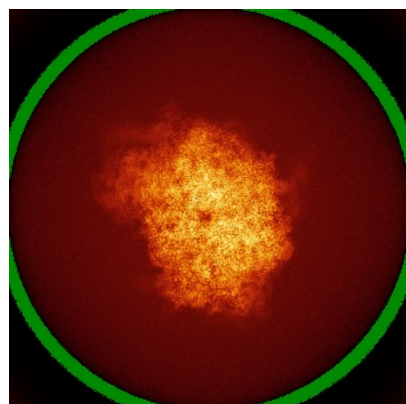


Z Index: 349

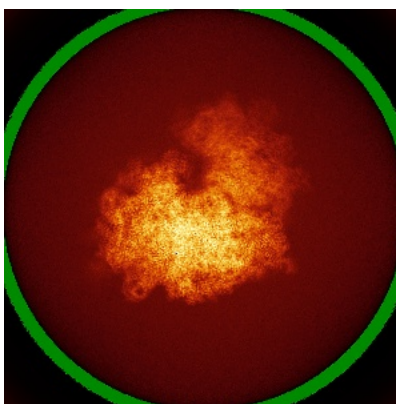
The images above show the largest variance slices of the map in three orthogonal directions.

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

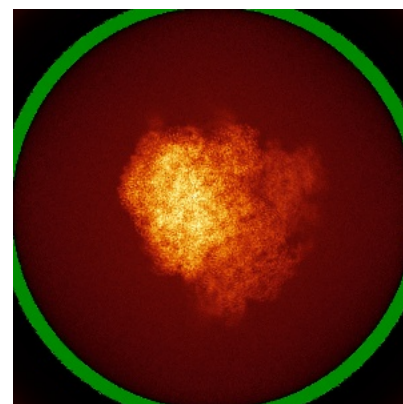
6.4.1 Primary map



X

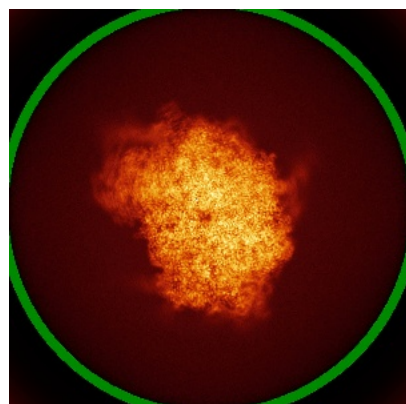


Y

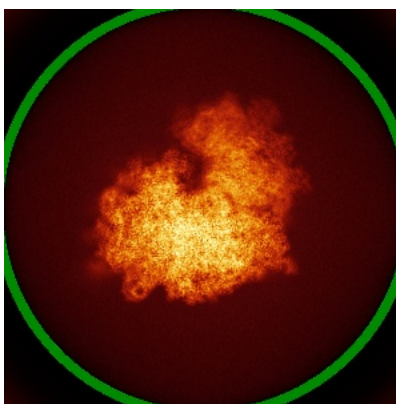


Z

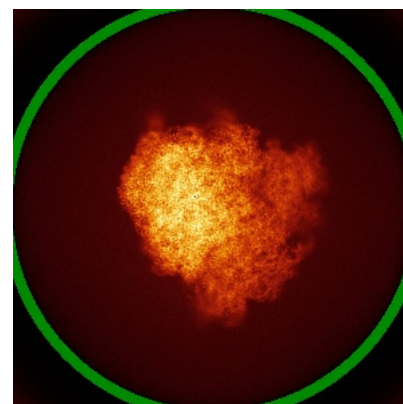
6.4.2 Raw map



X



Y



Z

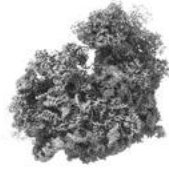
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



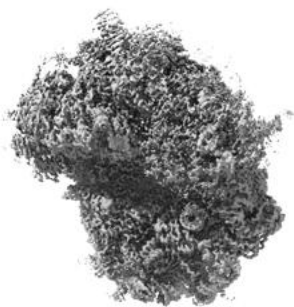
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.013. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

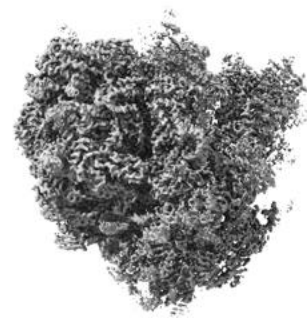
6.5.2 Raw map



X



Y



Z

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

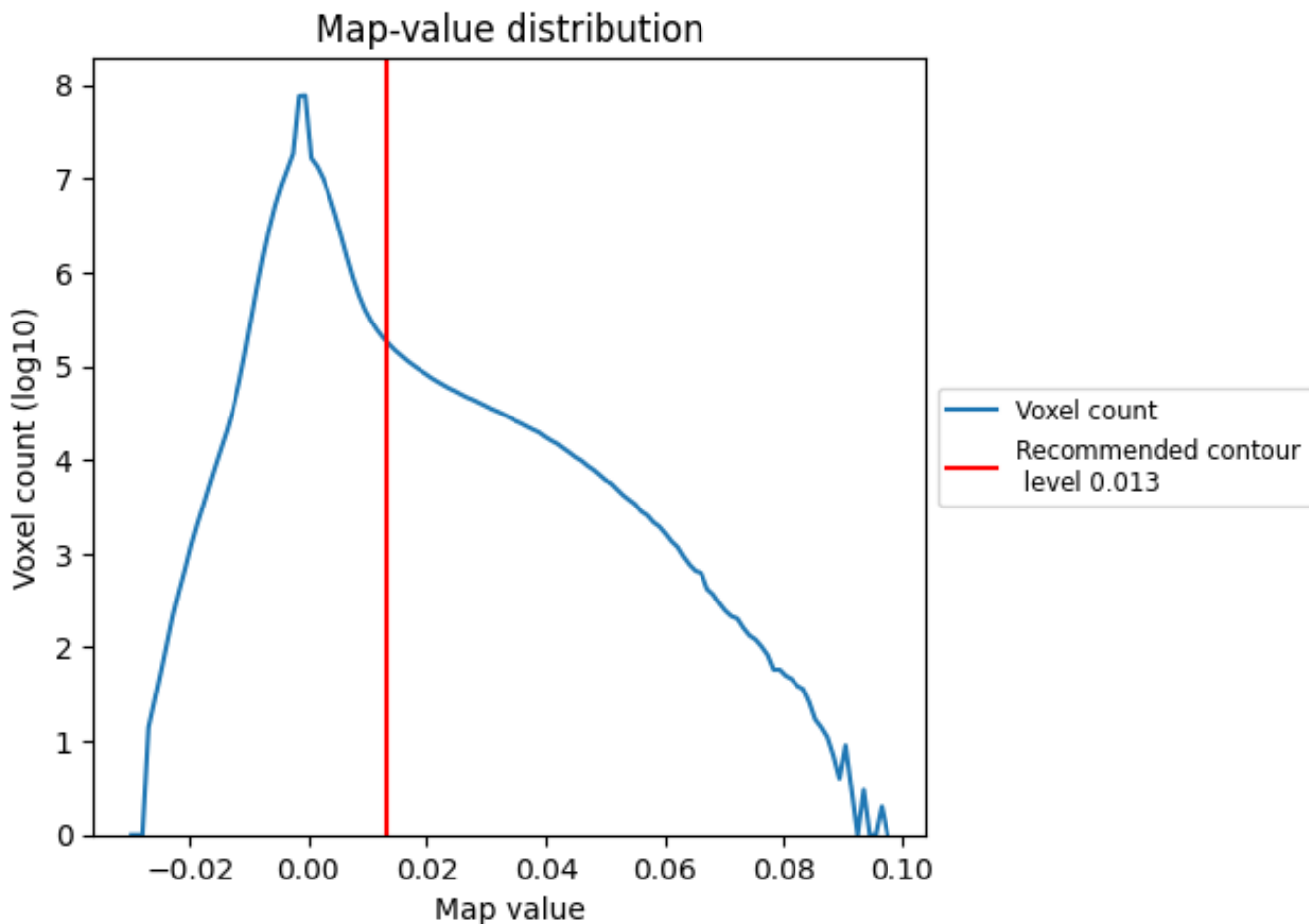
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

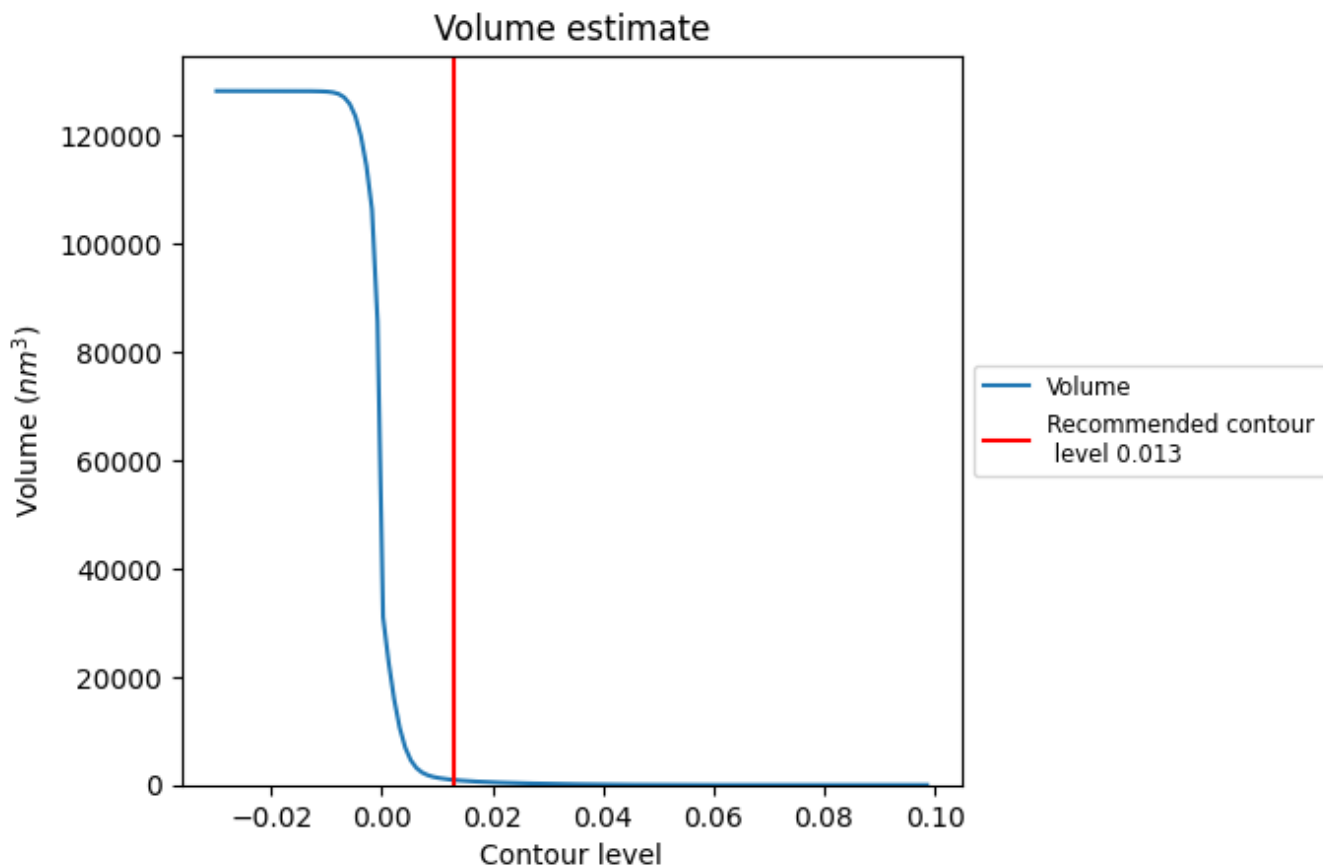
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

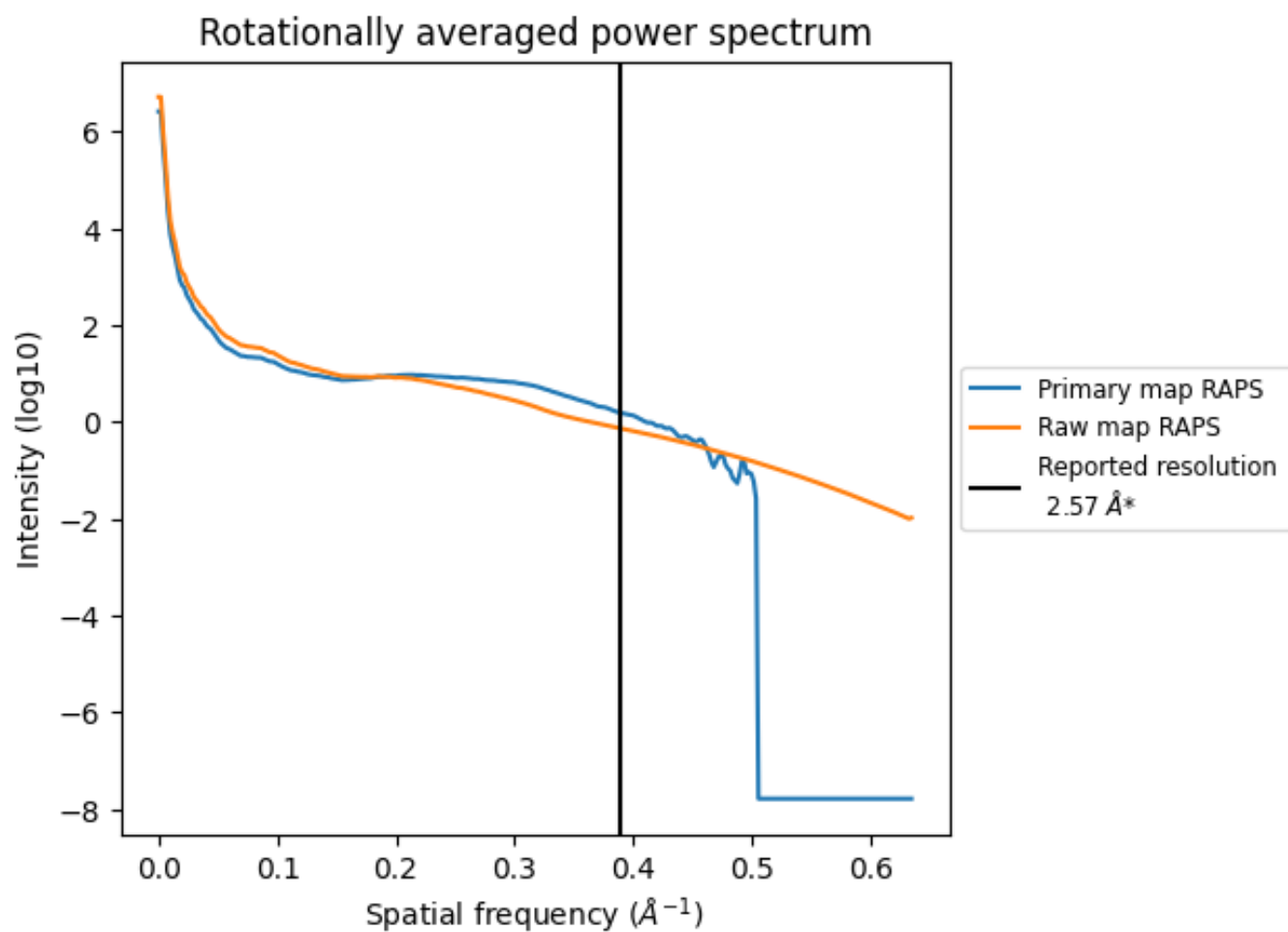
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 931 nm^3 ; this corresponds to an approximate mass of 841 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

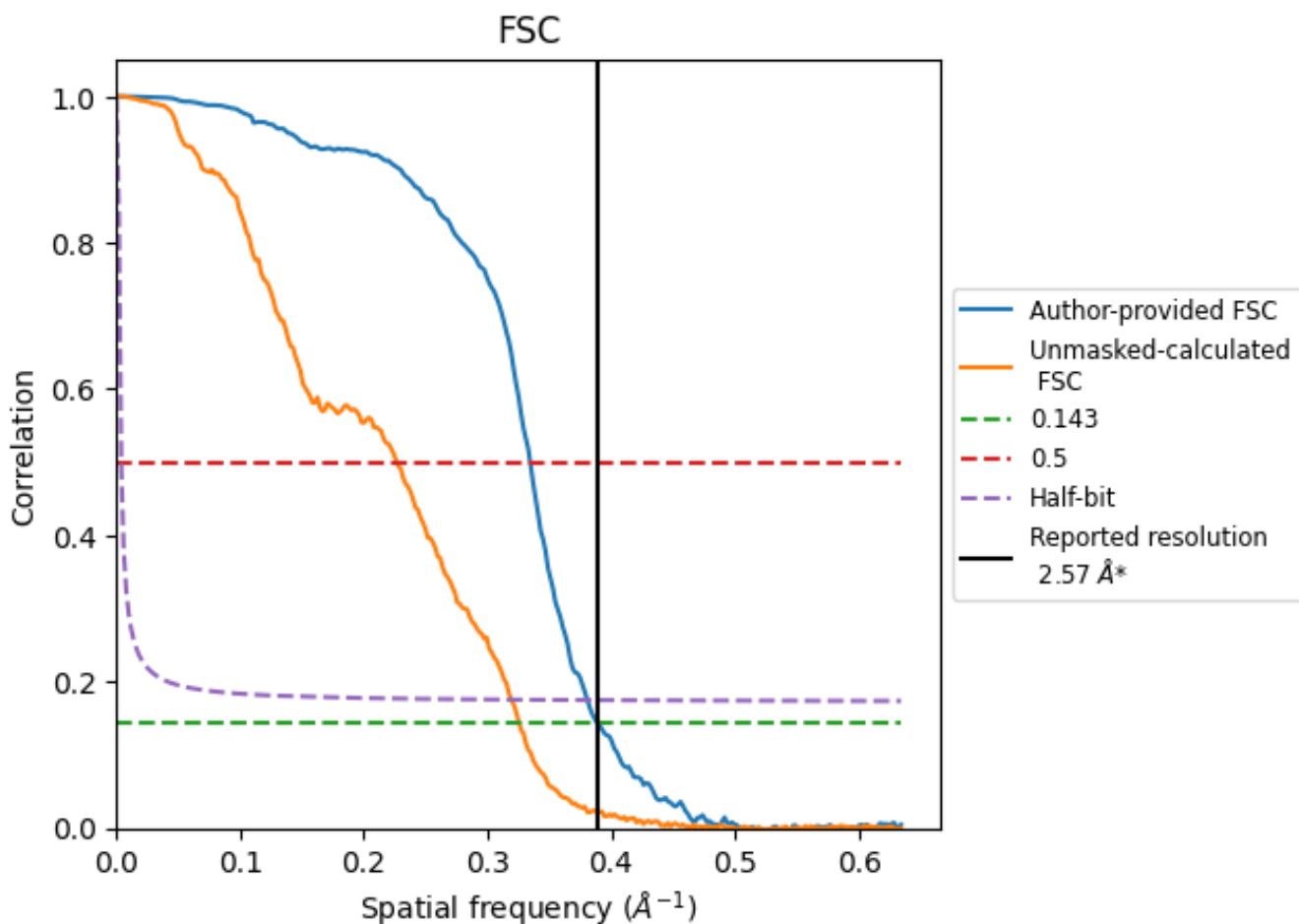


*Reported resolution corresponds to spatial frequency of 0.389 Å⁻¹

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 0.389 \AA^{-1}

8.2 Resolution estimates [i](#)

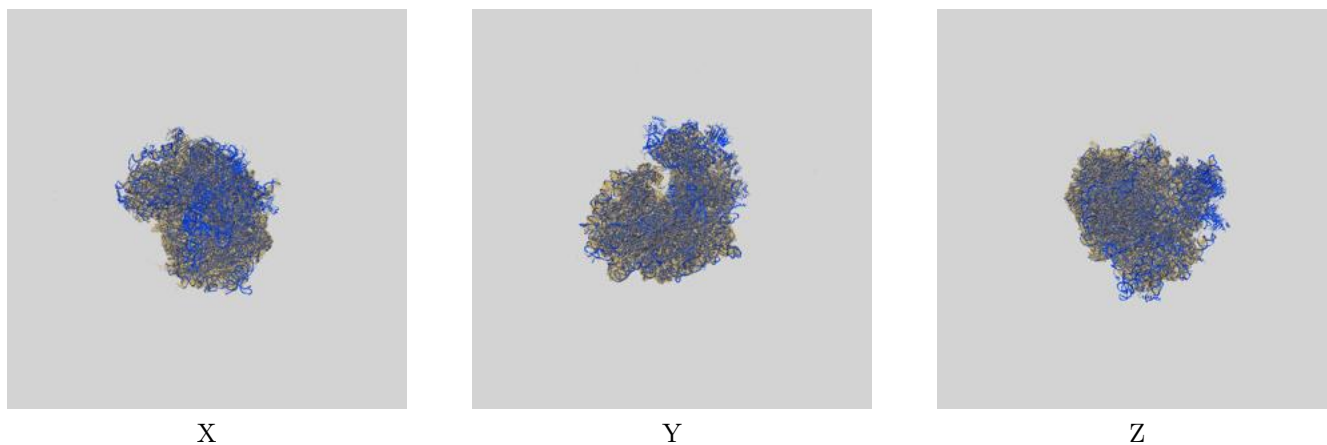
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.57	-	-
Author-provided FSC curve	2.57	2.99	2.63
Unmasked-calculated*	3.07	4.41	3.13

*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 3.07 differs from the reported value 2.57 by more than 10 %

9 Map-model fit [i](#)

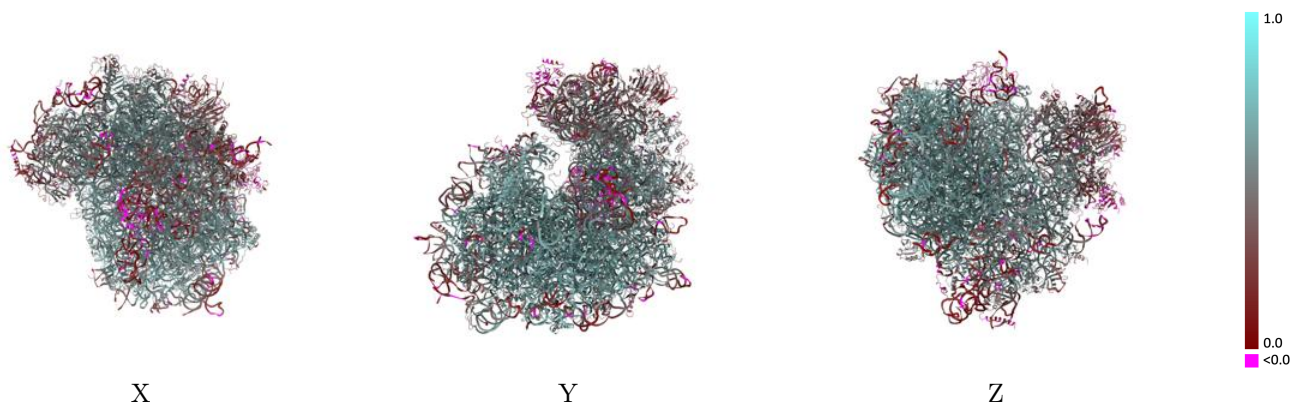
This section contains information regarding the fit between EMDB map EMD-35414 and PDB model 8IFE. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



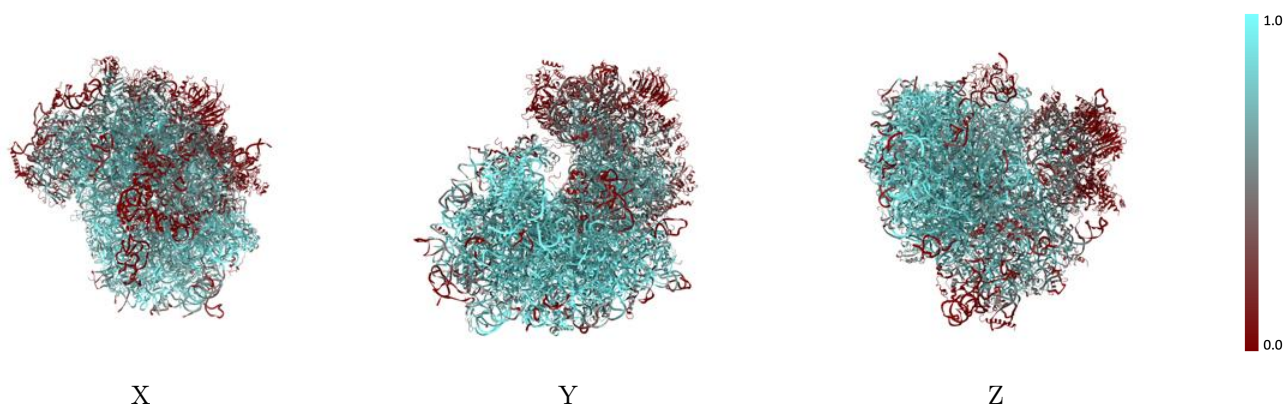
The images above show the 3D surface view of the map at the recommended contour level 0.013 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



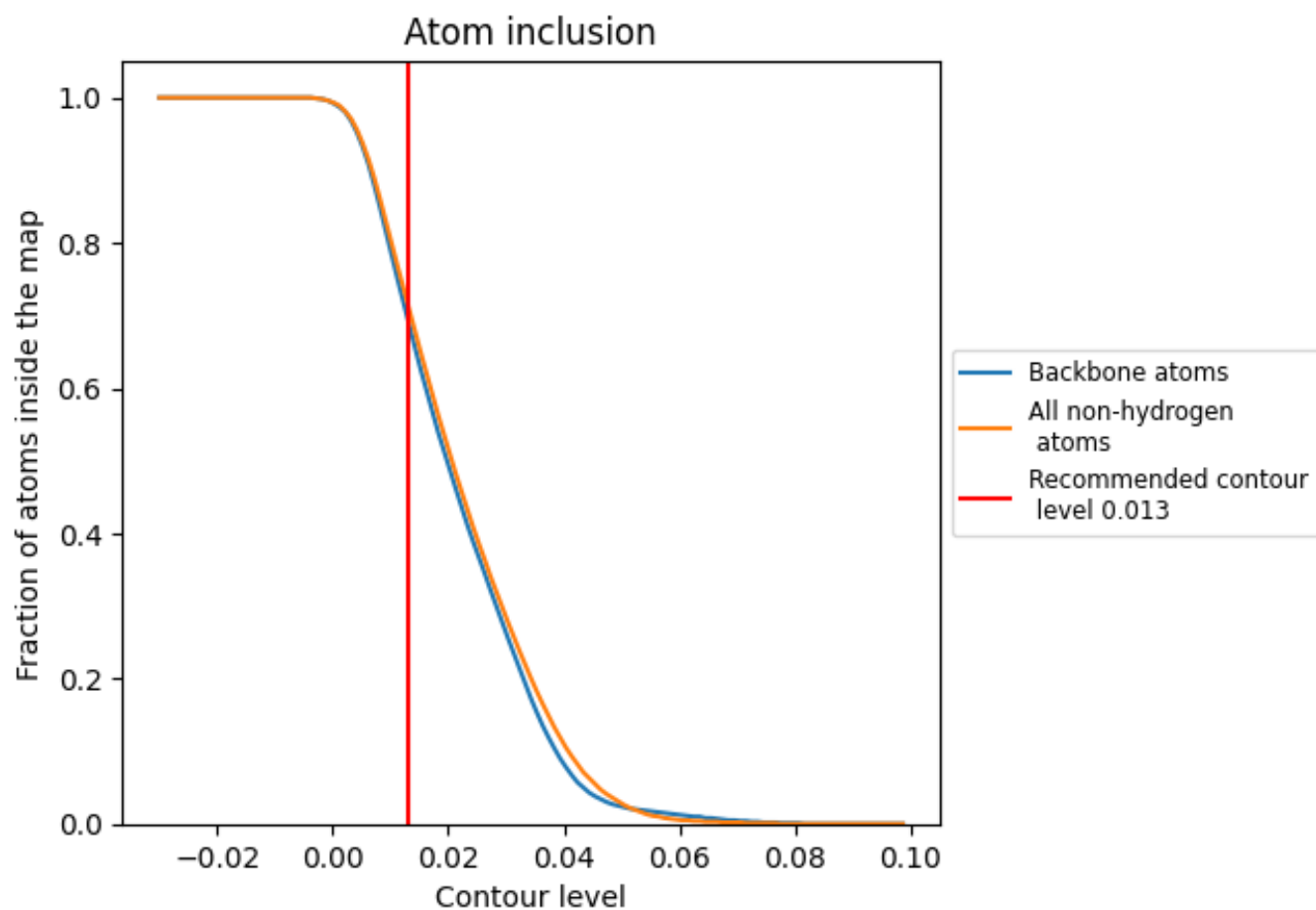
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.013).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 72% 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 (0.013) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7160	 0.5300
1A	 0.8280	 0.5530
1B	 0.9500	 0.6200
1C	 0.9060	 0.6010
1D	 0.9320	 0.6580
1E	 0.8720	 0.6290
1F	 0.8930	 0.6350
1G	 0.8160	 0.5770
1H	 0.7630	 0.5590
20	 0.3210	 0.4190
21	 0.1650	 0.3550
2A	 0.9030	 0.6440
2B	 0.7550	 0.5620
2C	 0.8110	 0.6030
2D	 0.7030	 0.5700
2E	 0.6140	 0.5010
2F	 0.8340	 0.5990
2G	 0.8650	 0.6150
2H	 0.9540	 0.6680
2I	 0.9080	 0.6460
2J	 0.9150	 0.6550
2K	 0.9450	 0.6650
2L	 0.7650	 0.5820
2M	 0.9170	 0.6470
2N	 0.8520	 0.6210
2O	 0.5500	 0.4620
2P	 0.8770	 0.6410
2Q	 0.4250	 0.3940
2R	 0.8600	 0.6270
2S	 0.8660	 0.6270
2T	 0.8310	 0.6070
2U	 0.9320	 0.6590
2V	 0.6920	 0.5440
2W	 0.8110	 0.5930
2X	 0.8340	 0.6150











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Chain	Atom inclusion	Q-score
2Y	 0.9210	 0.6570
2Z	 0.9360	 0.6540
2a	 0.8510	 0.6190
2b	 0.8620	 0.6160
2c	 0.8350	 0.6110
2d	 0.9350	 0.6560
2e	 0.6820	 0.5600
2f	 0.8770	 0.6350
2g	 0.8420	 0.6170
2h	 0.8570	 0.6510
2i	 0.8190	 0.6130
2j	 0.8550	 0.6350
2k	 0.9150	 0.6320
2l	 0.0210	 0.1270
2m	 0.6600	 0.4670
2n	 0.3450	 0.5060
2o	 0.6210	 0.5470
2p	 0.1420	 0.3750
2q	 0.5870	 0.5320
2r	 0.3420	 0.4270
2s	 0.3190	 0.4360
2t	 0.6140	 0.5280
2u	 0.0460	 0.2860
2v	 0.6770	 0.5640
2w	 0.0910	 0.3310
2x	 0.2890	 0.4220
2y	 0.1740	 0.3950
2z	 0.2380	 0.3770
3A	 0.3680	 0.5110
3B	 0.6490	 0.5610
3C	 0.6680	 0.5500
3D	 0.2920	 0.4060
3E	 0.2600	 0.4020
3F	 0.0340	 0.2940
3G	 0.6120	 0.5400
3H	 0.3580	 0.4010
3I	 0.5520	 0.5010
3J	 0.0000	 0.0340
3K	 0.6470	 0.5820
3L	 0.6790	 0.5550
3M	 0.7190	 0.5810
3N	 0.4720	 0.4480

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Chain	Atom inclusion	Q-score
3O	 0.1820	 0.2990
3P	 0.3470	 0.4800
3Q	 0.3690	 0.4350
3R	 0.0000	 0.0470