



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 05:28 PM UTC

PDB ID : 9G30 / pdb_00009g30
EMDB ID : EMD-50990
Title : The structure of the *Candida albicans* ribosome with tRNA-fMet, mRNA, and compounds (GEN and MFQ) shows strong density for the A site tRNA
Authors : Kolosova, O.; Zgadzay, Y.; Jenner, L.B.; Guskov, A.; Yusupov, M.
Deposited on : 2024-07-11
Resolution : 2.35 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

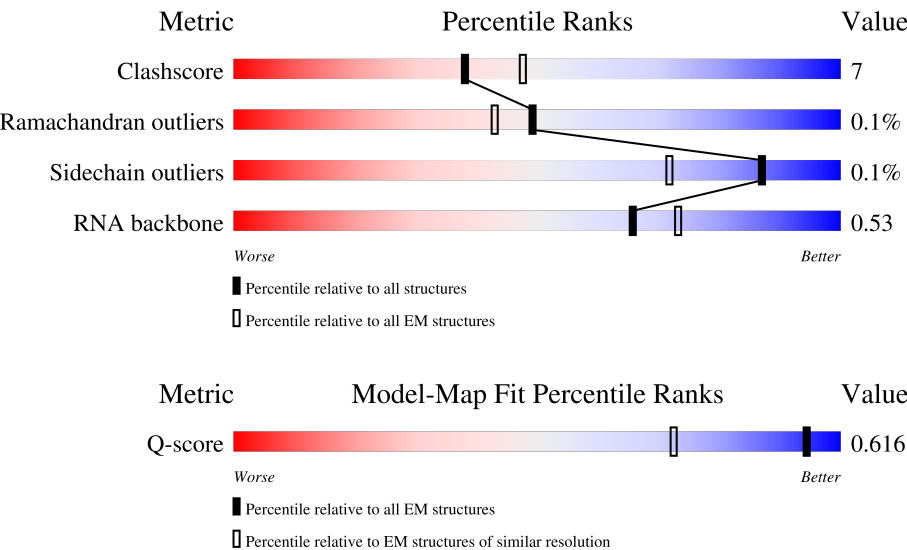
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.35 Å.

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



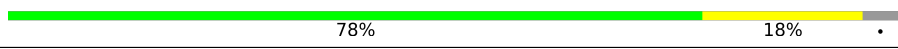
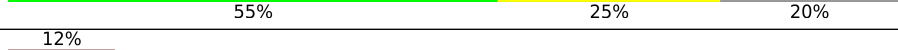
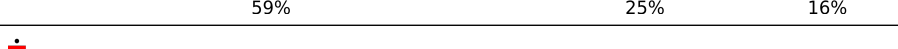
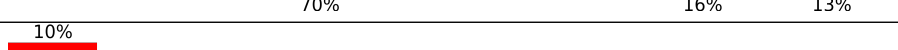
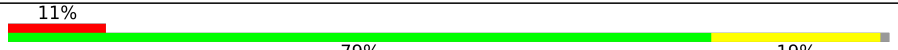
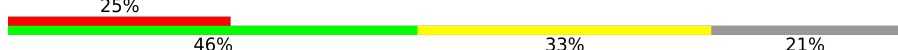
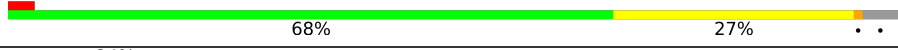
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	4607 (1.85 - 2.85)

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	0	172	
2	1	3359	
3	2	160	

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Mol	Chain	Length	Quality of chain
4	3	121	
5	4	158	
6	6	137	
7	7	155	
8	8	142	
9	9	127	
10	A	1787	
11	B	261	
12	C	256	
13	D	249	
14	E	251	
15	F	262	
16	G	225	
17	H	236	
18	I	186	
19	J	206	
20	K	189	
21	L	118	
22	M	155	
23	N	143	
24	O	151	
25	P	132	
26	Q	142	
27	T	145	
28	R	142	

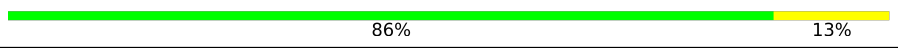
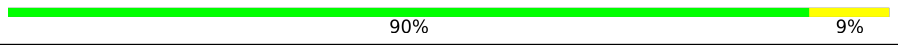
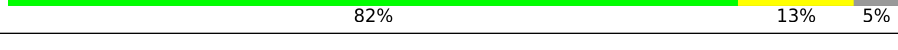
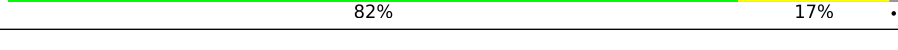
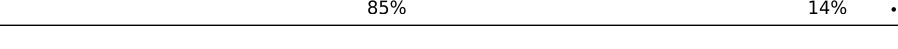
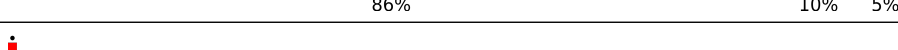
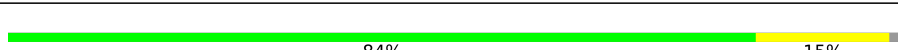
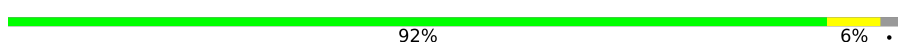
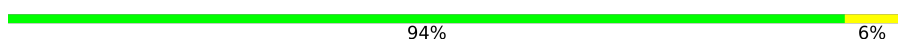
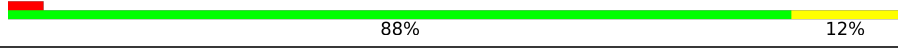
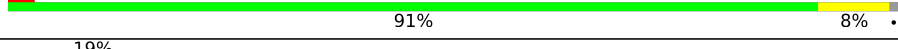
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Mol	Chain	Length	Quality of chain
29	S	137	
30	U	145	
31	V	119	
32	W	87	
33	X	130	
34	Y	145	
35	Z	135	
36	a	105	
37	b	119	
38	c	82	
39	d	67	
40	e	56	
41	f	63	
42	g	193	
43	h	317	
44	j	254	
45	k	389	
46	l	363	
47	m	298	
48	n	176	
49	o	241	
50	p	262	
51	q	191	
52	r	220	
53	s	174	

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Mol	Chain	Length	Quality of chain
54	t	202	
55	u	131	
56	v	204	
57	w	200	
58	x	185	
59	y	186	
60	z	190	
61	AA	136	
62	AB	149	
63	AC	63	
64	AD	106	
65	AE	112	
66	AF	131	
67	AG	107	
68	AH	122	
69	AI	120	
70	AJ	99	
71	AK	90	
72	AL	78	
73	AM	51	
74	AN	52	
75	AO	25	
76	AP	106	
77	AQ	92	
78	AT	77	

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Mol	Chain	Length	Quality of chain
78	PT	77	23% 56% 35% 8%
79	MR	39	18% 10% 72%

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 197420 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	171	Total	C	N	O	S	2	0
			1442	933	262	244	3		

- Molecule 2 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	3066	Total	C	N	O	P	0	0
			65536	29280	11774	21416	3066		

- Molecule 3 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	159	Total	C	N	O	S	2	0
			1276	807	244	223	2		

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	121	Total	C	N	O	P	0	0
			2579	1153	463	842	121		

- Molecule 5 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	156	Total	C	N	O	P	0	0
			3313	1482	581	1094	156		

- Molecule 6 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	131	Total	C	N	O	S	1	0
			986	621	186	171	8		

- Molecule 7 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	62	Total	C	N	O	S	0	0
			516	328	102	85	1		

- Molecule 8 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	119	Total	C	N	O	S	0	0
			960	613	172	174	1		

- Molecule 9 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	9	125	Total	C	N	O	0	0
			980	613	189	178		

- Molecule 10 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	A	1692	Total	C	N	O	P	0	0
			36083	16130	6412	11849	1692		

- Molecule 11 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	B	208	Total	C	N	O	S	0	0
			1627	1041	284	297	5		

- Molecule 12 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	C	214	Total	C	N	O	S	0	0
			1724	1094	313	313	4		

- Molecule 13 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D	216	Total	C	N	O	S	0	0
			1620	1033	287	295	5		

- Molecule 14 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	E	222	Total	C	N	O	S	0	0
			1701	1084	310	303	4		

- Molecule 15 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	F	260	Total	C	N	O	S	0	0
			2055	1306	386	358	5		

- Molecule 16 is a protein called Ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	G	199	Total	C	N	O	S	0	0
			1572	983	294	291	4		

- Molecule 17 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	H	226	Total	C	N	O	S	0	0
			1820	1133	351	330	6		

- Molecule 18 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	I	182	Total	C	N	O		0	0
			1466	939	264	263			

- Molecule 19 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	J	203	Total	C	N	O	S	0	0
			1579	973	322	283	1		

- Molecule 20 is a protein called Ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	K	178	Total	C	N	O	S	0	0
			1453	918	286	248	1		

- Molecule 21 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	L	93	Total	C	N	O	S	0	0
			783	511	129	142	1		

- Molecule 22 is a protein called 40S ribosomal protein S11A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	M	141	Total	C	N	O	S	0	0
			1129	722	212	192	3		

- Molecule 23 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	N	71	Total	C	N	O	S	0	0
			539	341	95	99	4		

- Molecule 24 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	O	150	Total	C	N	O	S	0	0
			1187	757	219	210	1		

- Molecule 25 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	P	127	Total	C	N	O	S	0	0
			942	579	186	174	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	119	IAS	ASP	conflict	UNP A0A8H6F0V4

- Molecule 26 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Q	115	Total	C	N	O	S	0	0
			906	578	164	158	6		

- Molecule 27 is a protein called 40S ribosomal protein S18-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	T	142	Total	C	N	O	S	0	0
			1169	733	228	205	3		

- Molecule 28 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	R	141	Total	C	N	O	S	0	0
			1102	706	202	193	1		

- Molecule 29 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	S	118	Total	C	N	O	S	0	0
			954	602	176	175	1		

- Molecule 30 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	U	141	Total	C	N	O	S	0	0
			1100	689	210	200	1		

- Molecule 31 is a protein called Ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	V	100	Total	C	N	O	S	0	0
			790	499	146	143	2		

- Molecule 32 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	W	87	Total	C	N	O	S	0	0
			676	415	126	133	2		

- Molecule 33 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	X	129	Total	C	N	O	S	0	0
			1032	655	191	183	3		

- Molecule 34 is a protein called Ribosomal protein S23 (S12).

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Y	143	Total	C	N	O	S	0	0
			1110	701	219	188	2		

- Molecule 35 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Z	132	Total	C	N	O		0	0
			1072	670	216	186			

- Molecule 36 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	a	72	Total	C	N	O		0	0
			578	369	103	106			

- Molecule 37 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	b	98	Total	C	N	O	S	0	0
			779	482	163	128	6		

- Molecule 38 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	c	81	Total	C	N	O	S	0	0
			614	383	110	114	7		

- Molecule 39 is a protein called 40S ribosomal protein S28-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	d	62	Total	C	N	O	S	0	0
			487	299	98	88	2		

- Molecule 40 is a protein called 40S ribosomal protein S29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	e	55	Total	C	N	O	S	0	0
			454	281	94	75	4		

- Molecule 41 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	f	58	Total	C	N	O	S	0	0
			461	289	93	77	2		

- Molecule 42 is a protein called Ubiquitin-40S ribosomal protein S31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	g	70	Total	C	N	O	S	0	0
			565	358	111	90	6		

- Molecule 43 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	h	241	Total	C	N	O	S	0	0
			1854	1176	319	355	4		

- Molecule 44 is a protein called 60S ribosomal protein L2-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	j	249	Total	C	N	O	S	1	0
			1894	1185	377	330	2		

- Molecule 45 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	k	386	Total	C	N	O	S	1	0
			3084	1955	584	538	7		

- Molecule 46 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	l	361	Total	C	N	O	S	0	0
			2751	1729	529	490	3		

- Molecule 47 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	m	292	Total	C	N	O	S	0	0
			2394	1526	416	450	2		

- Molecule 48 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	n	155	Total	C	N	O	1	0
			1237	794	226	217		

- Molecule 49 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	o	230	Total	C	N	O	S	1	0
			1860	1193	343	323	1		

- Molecule 50 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	p	231	Total	C	N	O	S	0	0
			1795	1150	319	323	3		

- Molecule 51 is a protein called 60S ribosomal protein L9-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	q	189	Total	C	N	O	S	0	0
			1510	953	275	278	4		

- Molecule 52 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	r	218	Total	C	N	O	S	0	0
			1759	1110	336	305	8		

- Molecule 53 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	s	172	Total	C	N	O	S	1	0
			1385	864	262	255	4		

- Molecule 54 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	t	195	Total	C	N	O	0	0
			1573	986	311	276		

- Molecule 55 is a protein called 60S ribosomal protein L14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	u	130	Total	C	N	O	S	0	0
			1029	660	193	175	1		

- Molecule 56 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	v	203	Total	C	N	O	S	0	0
			1713	1075	356	280	2		

- Molecule 57 is a protein called Ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	w	199	Total	C	N	O	S	0	0
			1590	1025	294	269	2		

- Molecule 58 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	x	172	Total	C	N	O		0	0
			1375	850	279	246			

- Molecule 59 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	y	185	Total	C	N	O		3	0
			1478	930	302	246			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	z	180	Total	C	N	O	S	1	0
			1471	910	313	245	3		

- Molecule 61 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AA	135	Total	C	N	O	S	0	0
			1087	705	197	183	2		

- Molecule 62 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AB	148	Total	C	N	O	S	0	0
			1170	741	231	197	1		

- Molecule 63 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AC	60	Total	C	N	O	S	1	0
			489	305	105	78	1		

- Molecule 64 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AD	96	Total	C	N	O	S	0	0
			729	469	121	137	2		

- Molecule 65 is a protein called 60S ribosomal protein L31-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AE	108	Total	C	N	O	S	0	0
			881	558	166	155	2		

- Molecule 66 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AF	125	Total	C	N	O	S	1	0
			1015	649	197	168	1		

- Molecule 67 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	AG	106	Total	C	N	O	S	3	0
			867	558	166	142	1		

- Molecule 68 is a protein called 60S ribosomal protein L34-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	AH	112	Total	C	N	O	S	4	0
			913	567	188	154	4		

- Molecule 69 is a protein called Ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
69	AI	119	Total	C	N	O	1	0
			990	629	195	166		

- Molecule 70 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	AJ	97	Total	C	N	O	S	1	0
			764	476	157	130	1		

- Molecule 71 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AK	86	Total	C	N	O	S	0	0
			677	413	148	110	6		

- Molecule 72 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
72	AL	77	Total	C	N	O	1	0
			623	398	116	109		

- Molecule 73 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
73	AM	50	Total	C	N	O	1	0
			446	280	100	66		

- Molecule 74 is a protein called 60S ribosomal protein L40-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AN	52	Total	C	N	O	S	1	0
			427	265	89	67	6		

- Molecule 75 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AO	25	Total	C	N	O	S	0	0
			236	144	63	28	1		

- Molecule 76 is a protein called 60S ribosomal protein L42-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	AP	105	Total	C	N	O	S	2	0
			863	547	171	140	5		

- Molecule 77 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	AQ	91	Total	C	N	O	S	0	0
			698	430	140	124	4		

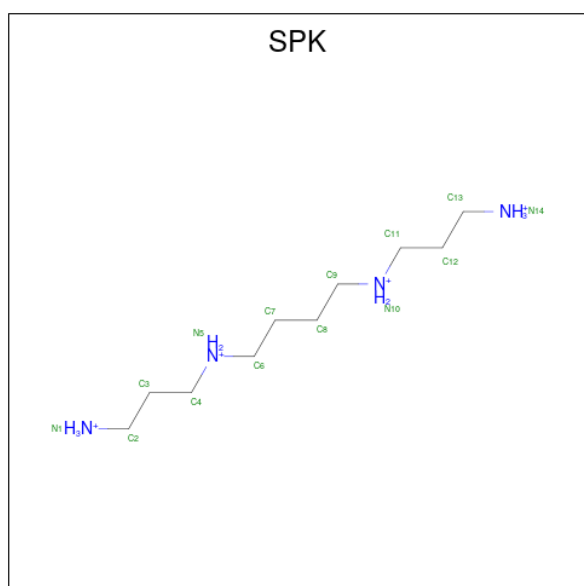
- Molecule 78 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	PT	76	Total	C	N	O	P	0	0
			1623	723	294	530	76		
78	AT	76	Total	C	N	O	P	0	0
			1623	723	294	530	76		

- Molecule 79 is a RNA chain called mRNA.

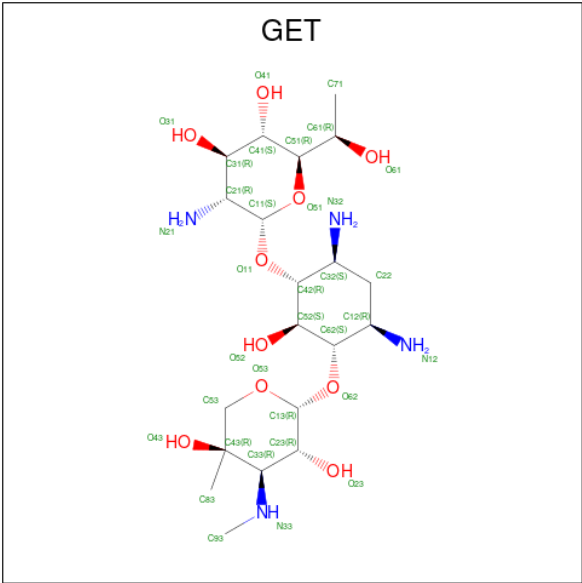
Mol	Chain	Residues	Atoms					AltConf	Trace
79	MR	11	Total	C	N	O	P	0	0
			231	104	39	77	11		

- Molecule 80 is SPERMINE (FULLY PROTONATED FORM) (CCD ID: SPK) (formula: $C_{10}H_{30}N_4$).



Mol	Chain	Residues	Atoms			AltConf
80	1	1	Total	C	N	0
			14	10	4	

- Molecule 81 is GENETICIN (CCD ID: GET) (formula: C₂₀H₄₀N₄O₁₀) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	1	1	Total	C	N	O	0
			34	20	4	10	

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Mol	Chain	Residues	Atoms				AltConf
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	A	1	Total	C	N	O	0
			34	20	4	10	
81	A	1	Total	C	N	O	0
			34	20	4	10	
81	A	1	Total	C	N	O	0
			34	20	4	10	
81	A	1	Total	C	N	O	0
			34	20	4	10	
81	AT	1	Total	C	N	O	0
			34	20	4	10	

- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
82	b	1	Total	Zn	0
			1	1	
82	e	1	Total	Zn	0
			1	1	
82	AH	1	Total	Zn	0
			1	1	
82	AK	1	Total	Zn	0
			1	1	
82	AN	1	Total	Zn	0
			1	1	
82	AP	1	Total	Zn	0
			1	1	
82	AQ	1	Total	Zn	0
			1	1	

3 Residue-property plots [i](#)

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

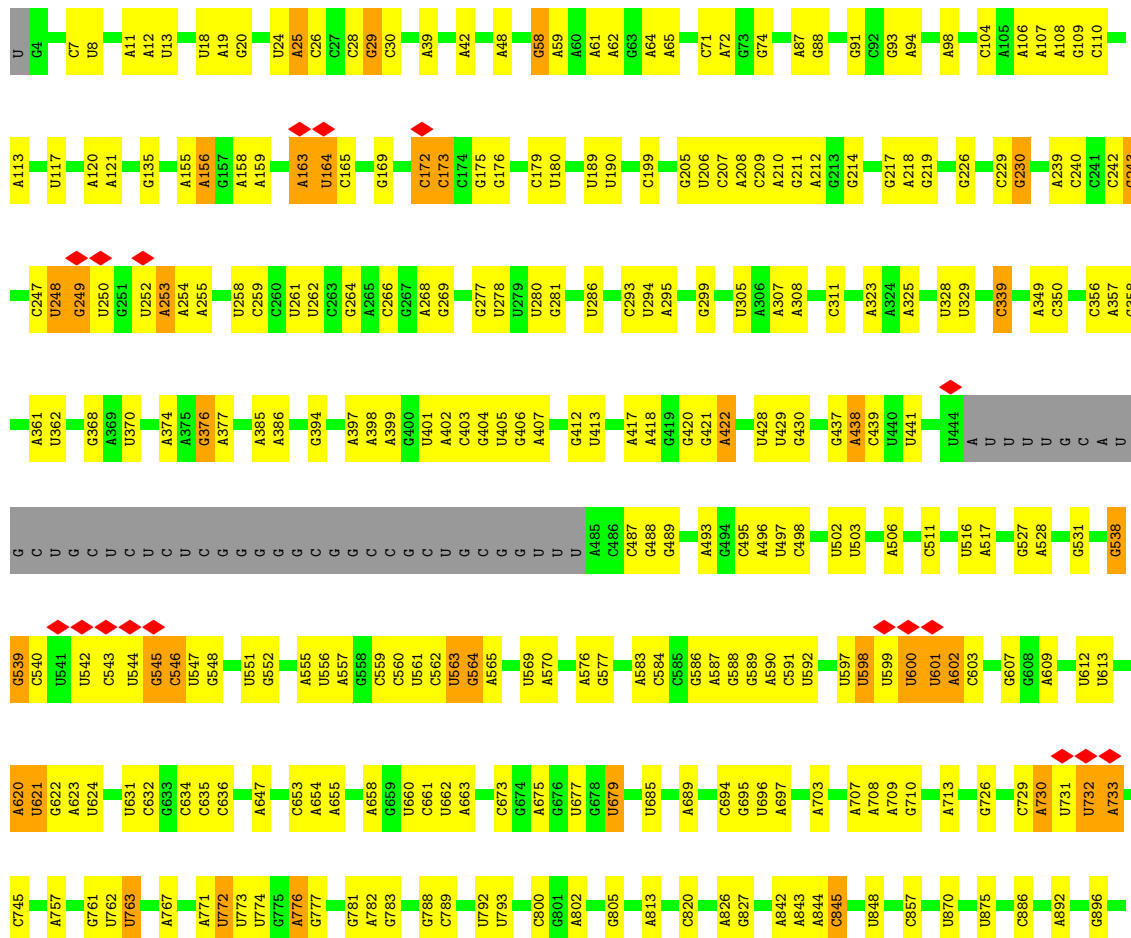
- Molecule 1: 60S ribosomal protein L20

Chain 0:  83% 16% ..

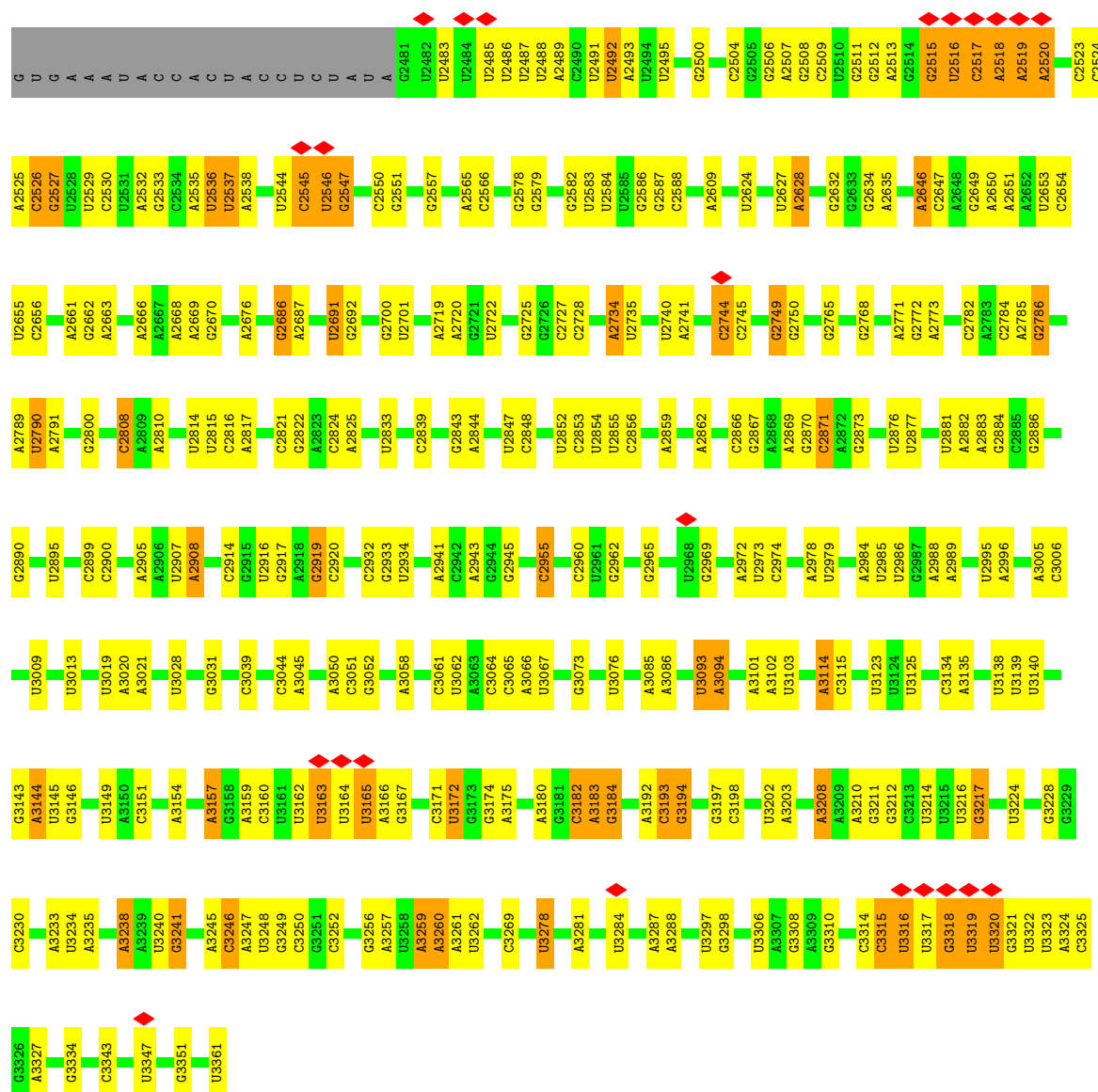


- Molecule 2: 25S rRNA

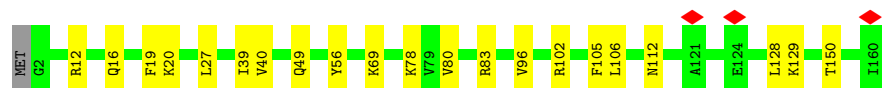
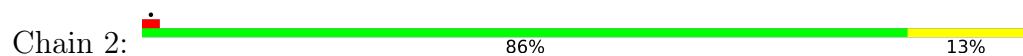
Chain 1:  61% 26% 5% 9%



C2384	G2251	A2130	G1714	A1575	U1451	A1287	G1015	G903
C2385	A2259	U2131	G1715	A1576	U1451	C1288	G1016	G904
U2386	U2260	A2136	U1720	A1585	A1464	G1303	G	C907
U2389	G2137	G2138	C1721	A1589	C1465	U1305	U	A910
A2391	G2139	U2139	G1732	A1590	U1466	U1305	G	A911
G2392	C2147	C2148	A1746	U1591	U1467	A1313	A	G912
A2397	U2148	U2149	G1747	C1592	U1468	A1314	A	A913
C2398	G2149	U2150	A1756	G1594	U1469	A1326	U	C919
U2404	U2151	A2158	A1757	A1601	C1474	U1330	A	G920
U2405	C2159	C2160	U1758	U1611	U1475	U1331	C	A921
U2406	G2163	U2163	U1759	U1612	G1476	A1339	U	A922
G2407	U2164	U2165	U1760	G1613	U1477	U1347	G	C923
A2408	U2166	U2167	G1761	G1614	U1478	U1348	U	C924
C2409	U2168	U2169	G1762	A1615	G1483	U1349	C	A925
G2413	U2171	U2172	G1763	U1616	U1491	C1352	A	A926
G2420	U2173	U2174	G1764	A1617	C1492	G1353	U	G933
A2421	U2175	U2176	G1765	U1622	C1493	U1358	U	U939
C2422	U2177	U2178	U1768	U1625	A1494	U1361	C	C941
A	U2179	U2180	G1774	U1626	U1495	C1352	G	U942
U	U2181	U2182	C1775	U1635	C1504	G1353	U	C943
G	U2183	U2184	G1776	U1636	C1523	U1358	A	C944
G	U2185	U2186	U1782	U1637	A1530	C1358	A	U951
A	U2187	U2188	A1783	A1638	A1531	A1359	U	U952
G	U2189	U2190	G1792	A1639	G1532	G1376	G	C955
G	U2191	U2192	A1793	C1640	A1535	U1380	A	U956
U	U2193	U2194	A1794	U1641	G1543	G1381	U	A963
U	U2195	U2196	A1795	C1653	U1550	A1382	G	G964
A	U2197	U2198	A1796	U1654	U1551	G1385	U	C965
A	U2199	U2200	G1803	U1655	C1552	C1387	U	U972
G	U2201	U2202	G1804	G1658	U1556	U1395	A	A976
A	U2203	U2204	U1811	U1662	U1557	U1396	U	U981
G	U2205	U2206	A1812	A1663	G1558	G1397	A	U982
G	U2207	U2208	G1813	G1664	C1559	A1415	U	U983
A	U2209	U2210	U1814	U1679	U1560	U1421	A	U984
A	U2211	U2212	U1815	U1682	G1561	U1426	C	A988
U	U2213	U2214	U1816	U1683	A1563	U1432	C	C989
U	U2215	U2216	U1817	U1684	U1564	C1433	U	G990
C	U2217	U2218	U1818	U1685	U1565	G1430	G	A998
C	U2219	U2220	U1819	U1686	U1566	U1432	C	G1006
C	U2221	U2222	U1820	U1687	U1567	U1433	A	U1011
C	U2223	U2224	U1821	U1688	U1568	G1436	C	U1012
C	U2225	U2226	U1822	U1689	U1569	A1442	G	U1013
C	U2227	U2228	U1823	U1690	C1569	G1446	U	G1014
C	U2229	U2230	U1824	U1691	U1570			
C	U2231	U2232	U1825	U1692	A1571			
C	U2233	U2234	U1826	U1693	G1572			
C	U2235	U2236	U1827	U1713	G1573			
C	U2237	U2238	U1828		C1574			
C	U2239	U2240	U1829					
C	U2241	U2242	U1830					
C	U2243	U2244	U1831					
C	U2245	U2246	U1832					
C	U2247	U2248	U1833					
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C	U2253	U2254	U1836					
C	U2255	U2256	U1837					
C	U2257	U2258	U1838					
C	U2259	U2260	U1839					
C	U2261	U2262	U1840					
C	U2263	U2264	U1841					
C	U2265	U2266	U1842					
C	U2267	U2268	U1843					
C	U2269	U2270	U1844					
C	U2271	U2272	U1845					
C	U2273	U2274	U1846					
C	U2275	U2276	U1847					
C	U2277	U2278	U1848					
C	U2279	U2280	U1849					
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C	U2313	U2314	U1866					
C	U2315	U2316	U1867					
C	U2317	U2318	U1868					
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C	U2321	U2322	U1870					
C	U2323	U2324	U1871					
C	U2325	U2326	U1872					
C	U2327	U2328	U1873					
C	U2329	U2330	U1874					
C	U2331	U2332	U1875					
C	U2333	U2334	U1876					
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C	U2369	U2370	U1894					
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C	U2499	U2500	U1959					
C	U2501	U2502	U1960					
C	U2503	U2504	U1961					
C	U2505	U2506	U1962					
C	U2507	U2508	U1963					
C	U2509	U2						



• Molecule 3: 60S ribosomal protein L21-A

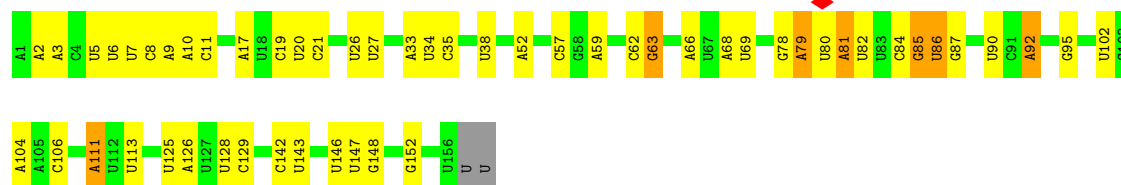


• Molecule 4: 5S rRNA



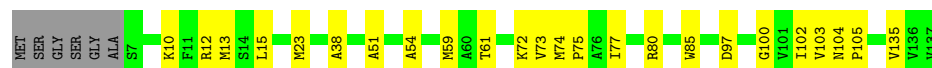
• Molecule 5: 5.8S rRNA

Chain 4:  65% 30%



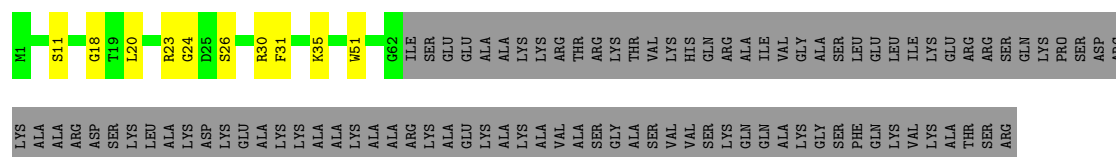
- Molecule 6: 60S ribosomal protein L23-A

Chain 6:  78% 18%



- Molecule 7: 60S ribosomal protein L24-A

Chain 7:  34% 6% 60%



- Molecule 8: 60S ribosomal protein L25

Chain 8:  73% 11% 16%



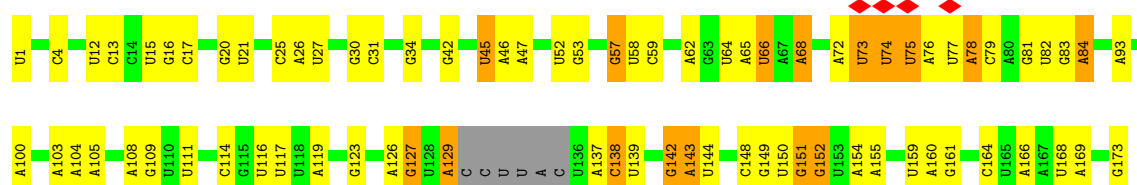
- Molecule 9: Ribosomal protein L24

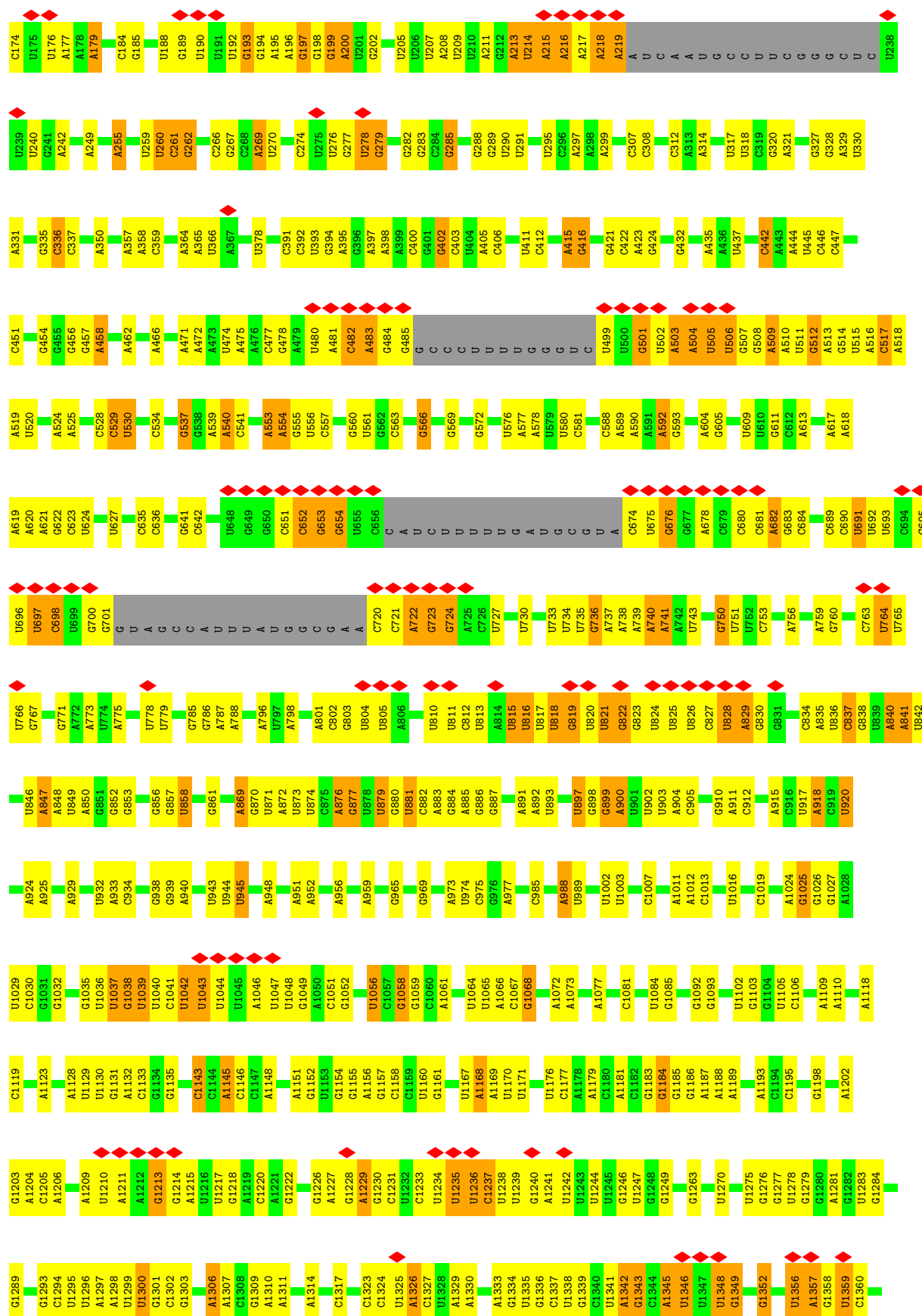
Chain 9:  88% 10%

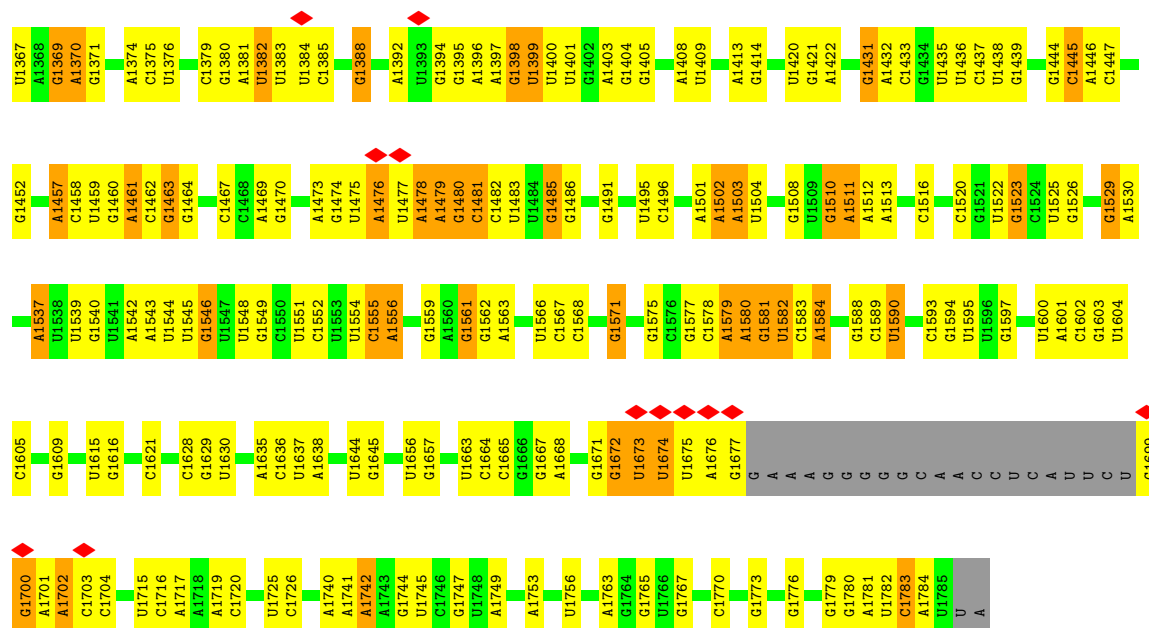


- Molecule 10: 18S rRNA

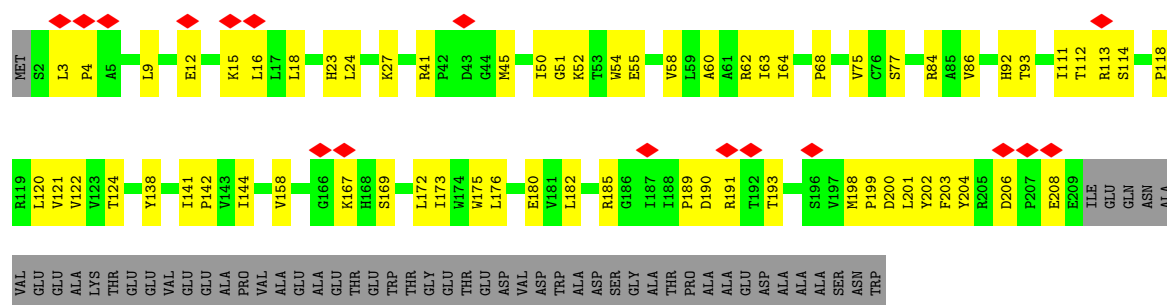
Chain A:  7% 48% 37% 10% 5%



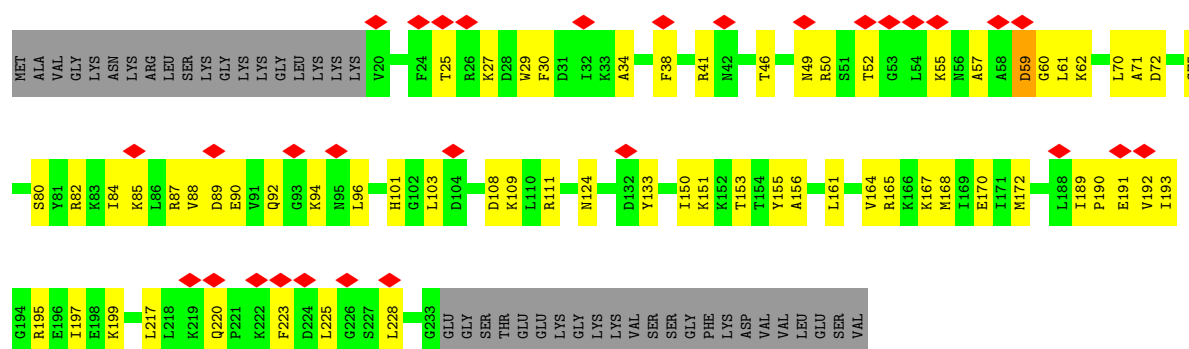




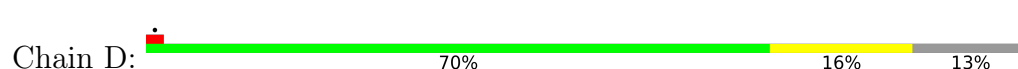
• Molecule 11: 40S ribosomal protein S0

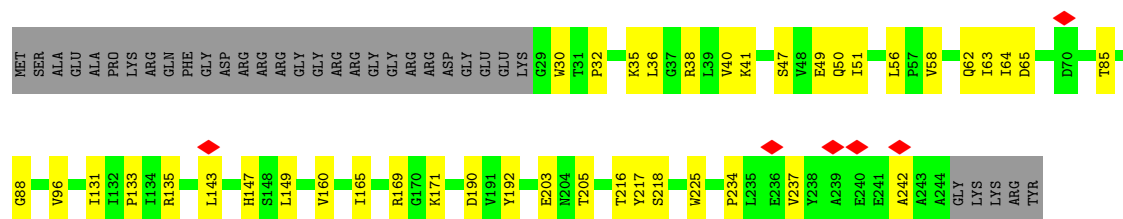


• Molecule 12: 40S ribosomal protein S1

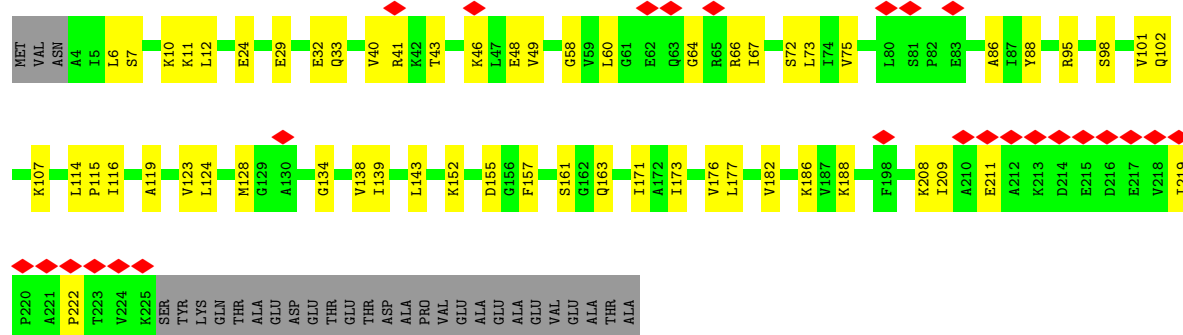


• Molecule 13: Ribosomal protein S5

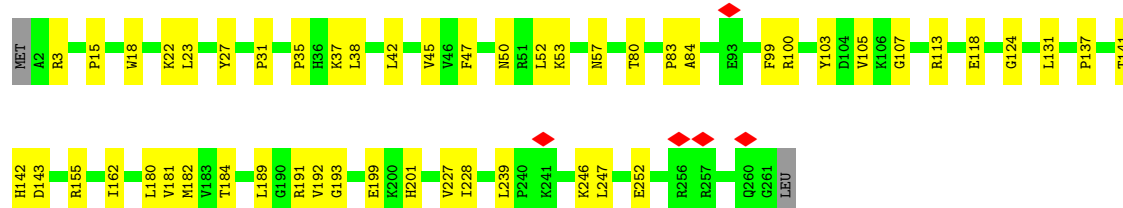
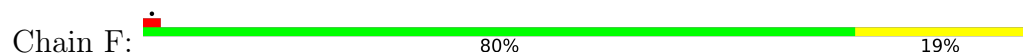




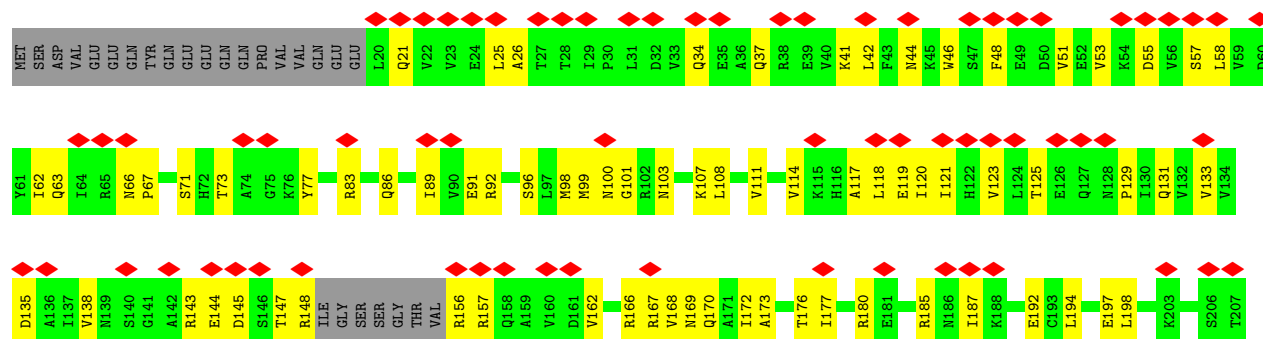
• Molecule 14: Ribosomal protein S3

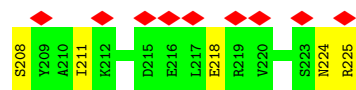


• Molecule 15: 40S ribosomal protein S4

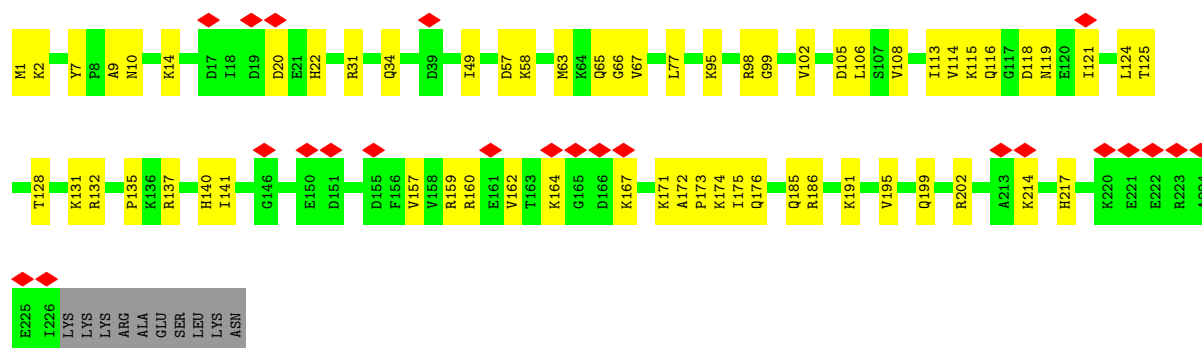


• Molecule 16: Ribosomal protein S7

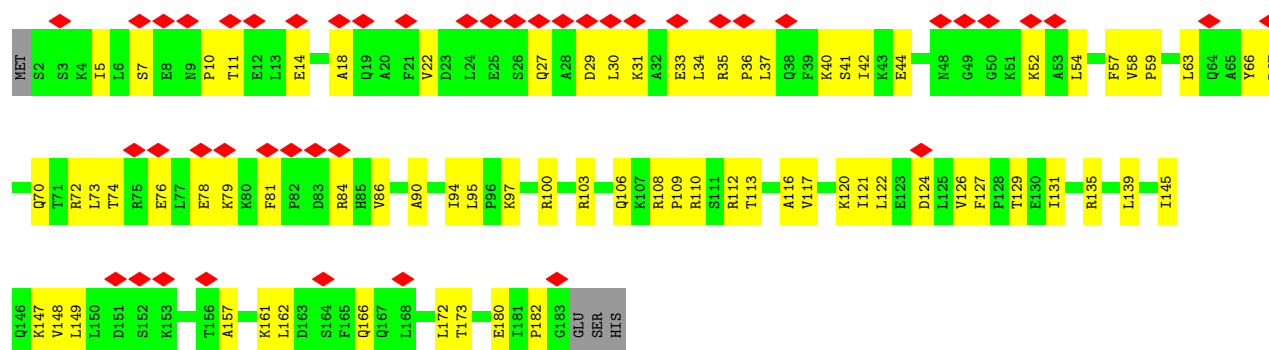




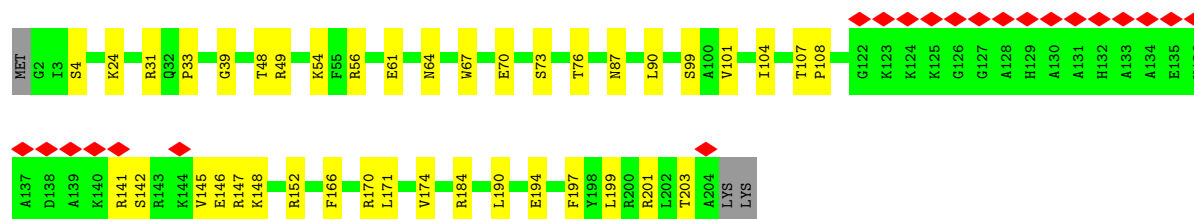
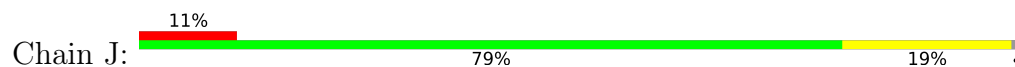
• Molecule 17: 40S ribosomal protein S6



• Molecule 18: 40S ribosomal protein S7

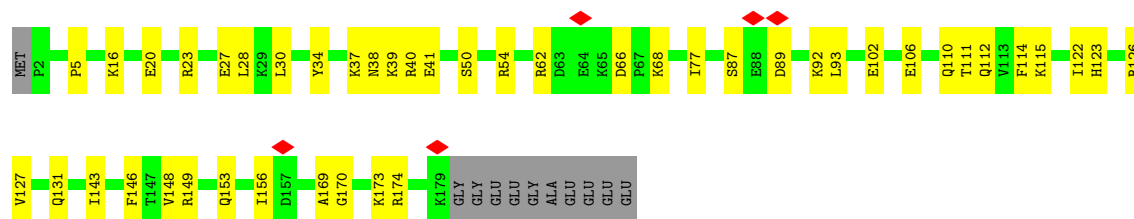


• Molecule 19: 40S ribosomal protein S8

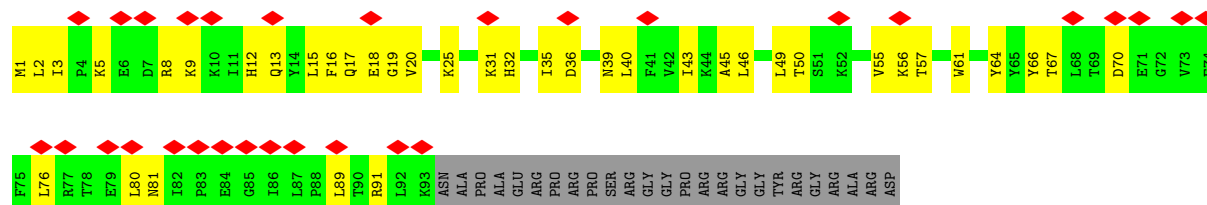


• Molecule 20: Ribosomal protein S4

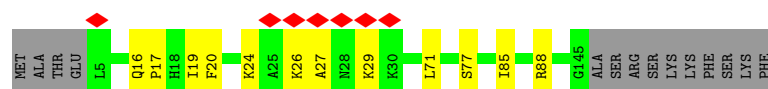
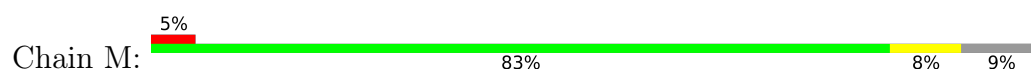




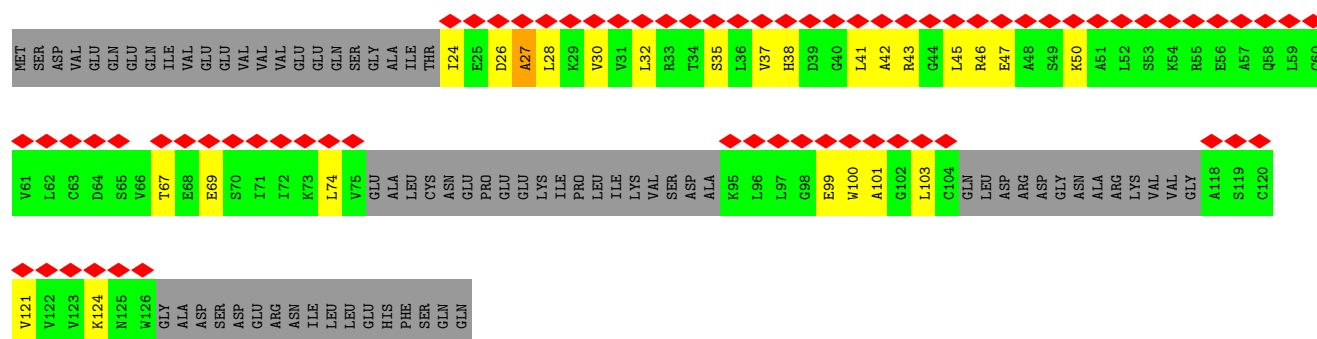
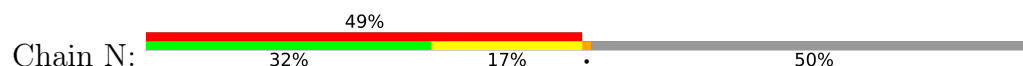
• Molecule 21: 40S ribosomal protein S10-A



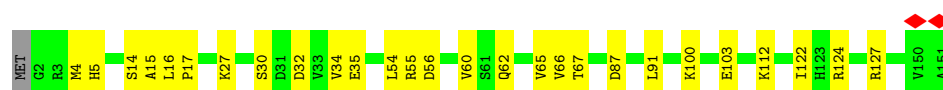
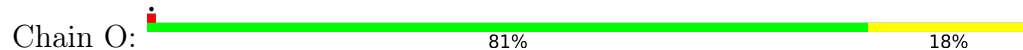
• Molecule 22: 40S ribosomal protein S11A



• Molecule 23: 40S ribosomal protein S12

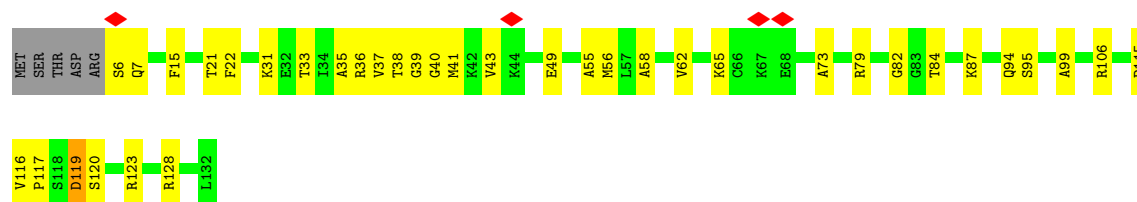


• Molecule 24: 40S ribosomal protein S13



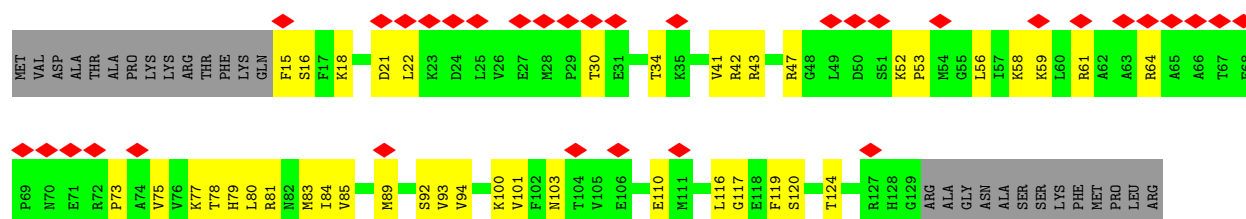
• Molecule 25: 40S ribosomal protein S14-A

Chain P: 



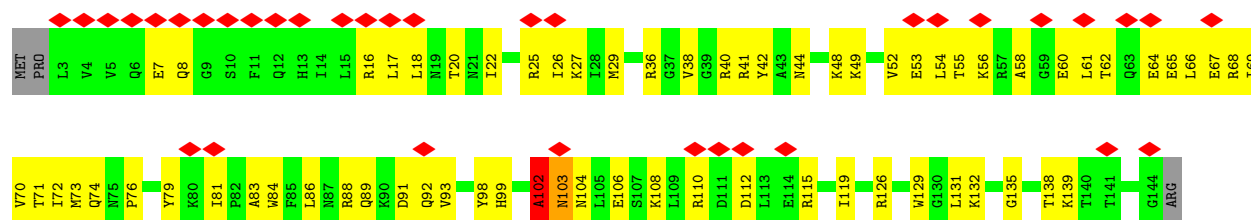
- Molecule 26: 40S ribosomal protein S15

Chain Q: 



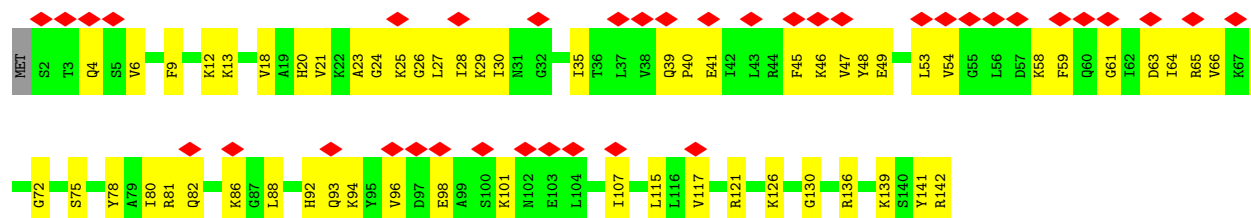
- Molecule 27: 40S ribosomal protein S18-B

Chain T: 



- Molecule 28: 40S ribosomal protein S16

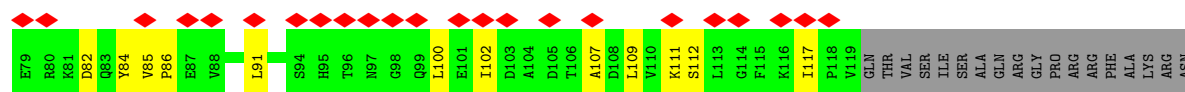
Chain R: 



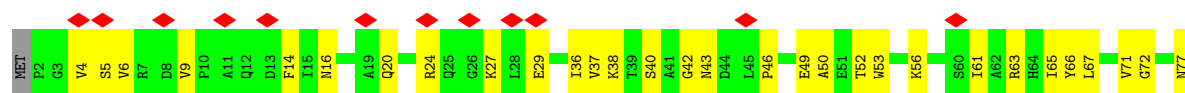
- Molecule 29: 40S ribosomal protein S17-B

Chain S: 

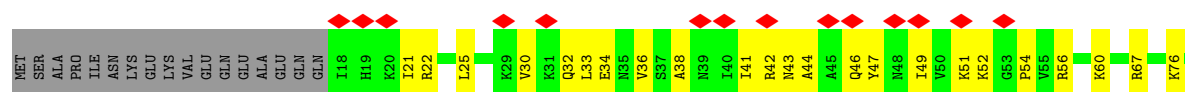




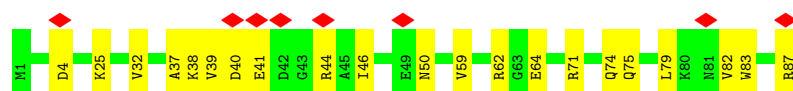
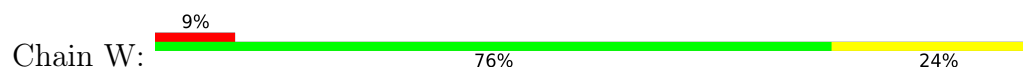
- Molecule 30: 40S ribosomal protein S19-A



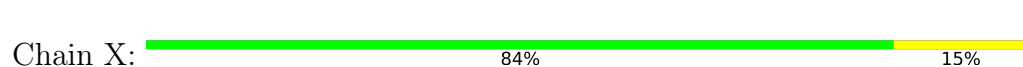
- Molecule 31: Ribosomal protein S10



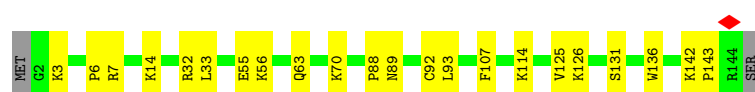
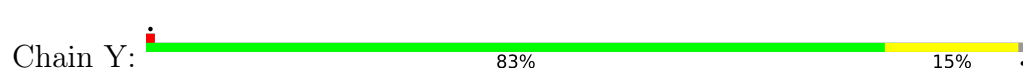
- Molecule 32: 40S ribosomal protein S21



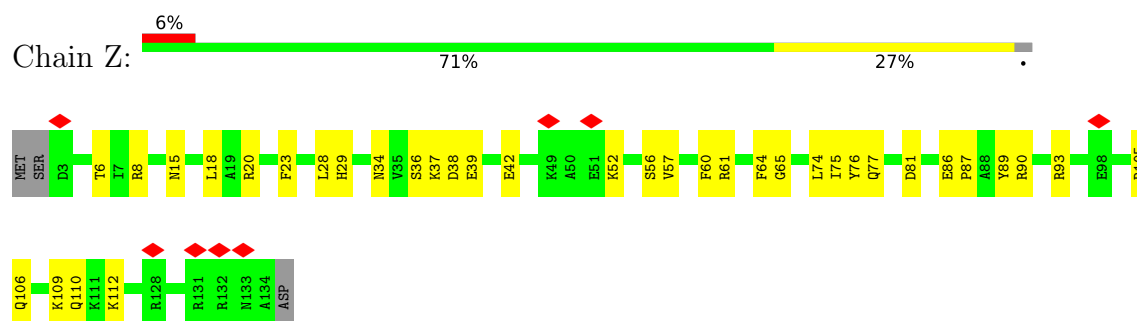
- Molecule 33: 40S ribosomal protein S22-A



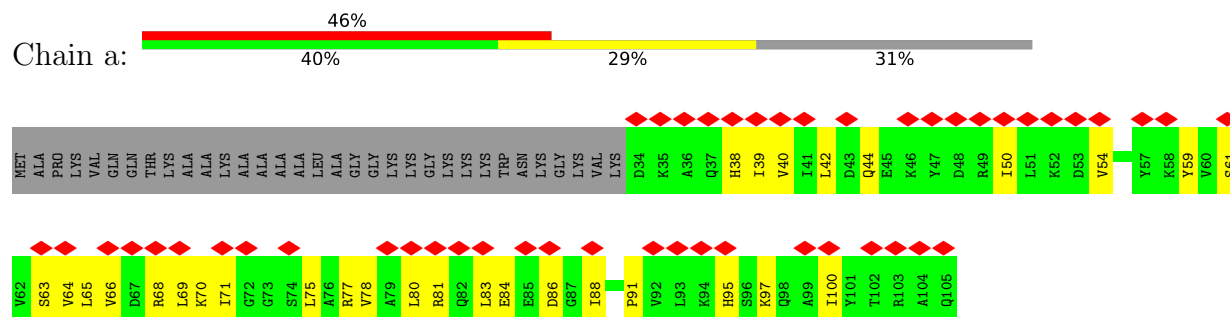
- Molecule 34: Ribosomal protein S23 (S12)



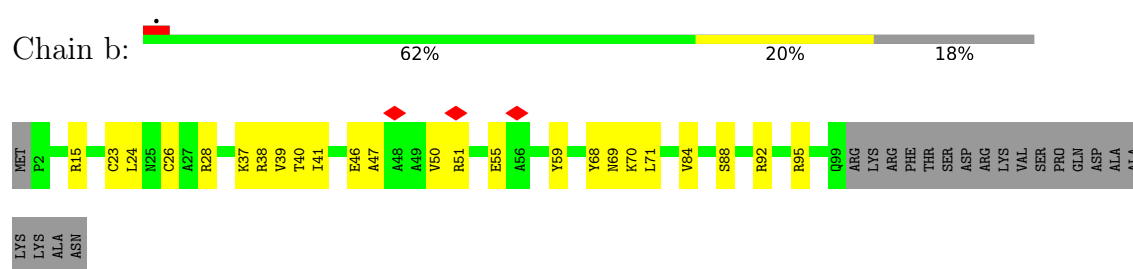
- Molecule 35: 40S ribosomal protein S24



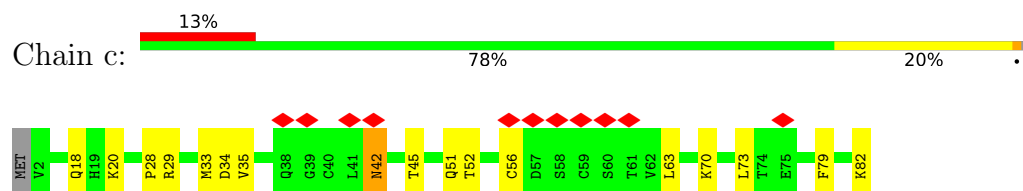
- Molecule 36: 40S ribosomal protein S25



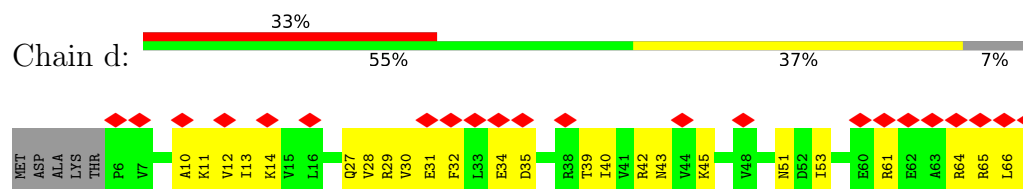
- Molecule 37: 40S ribosomal protein S26



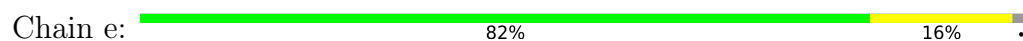
- Molecule 38: 40S ribosomal protein S27



- Molecule 39: 40S ribosomal protein S28-B

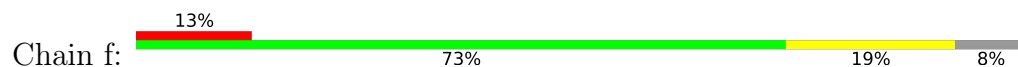


- Molecule 40: 40S ribosomal protein S29A

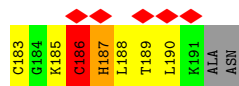
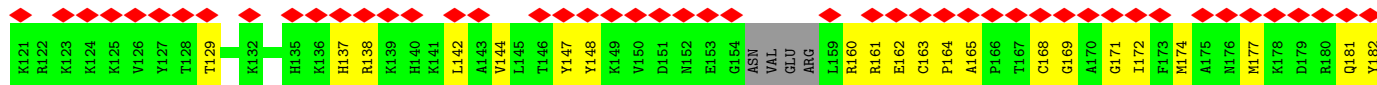
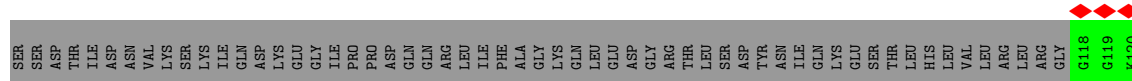
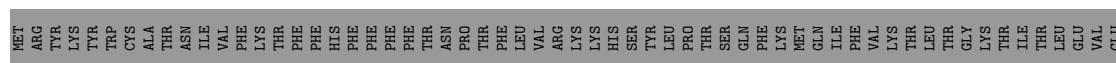




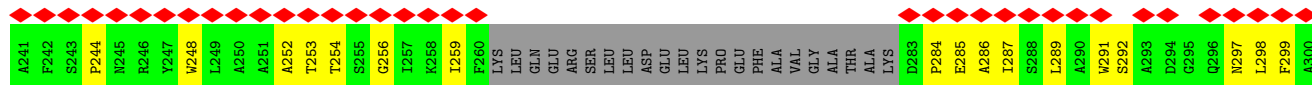
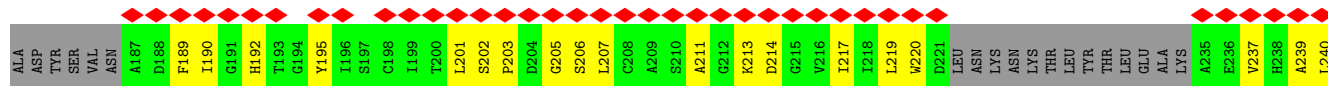
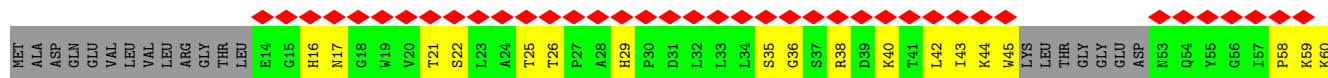
- Molecule 41: 40S ribosomal protein S30



- Molecule 42: Ubiquitin-40S ribosomal protein S31 fusion protein



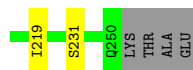
- Molecule 43: Guanine nucleotide-binding protein subunit beta-like protein





- Molecule 44: 60S ribosomal protein L2-B

Chain j: 85% 13%



- Molecule 45: 60S ribosomal protein L3

Chain k: 86% 14%



- Molecule 46: 60S ribosomal protein L4-B

Chain l: 90% 9%



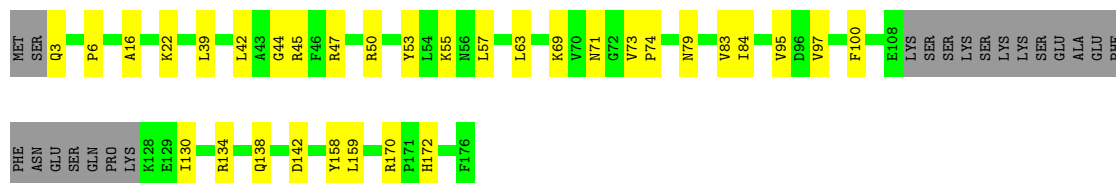
- Molecule 47: 60S ribosomal protein L5

Chain m: 84% 14%



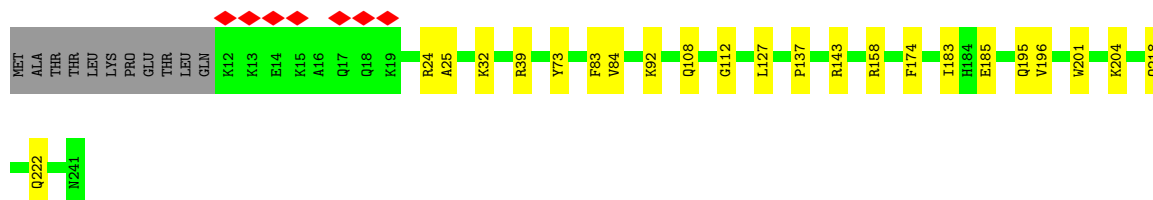
- Molecule 48: 60S ribosomal protein L6

Chain n:  70% 18% 12%



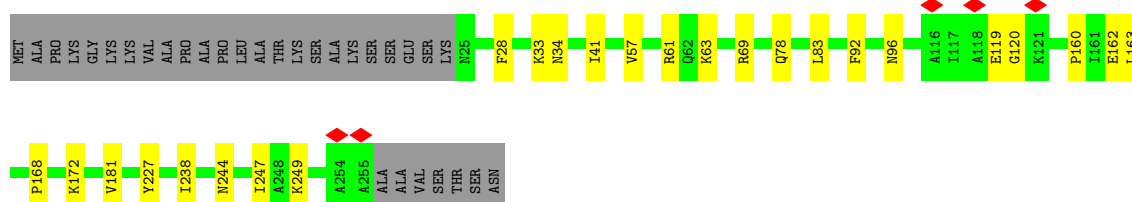
- Molecule 49: 60S ribosomal protein L7-A

Chain o:  86% 10% 5%



- Molecule 50: 60S ribosomal protein L8

Chain p:  79% 10% 12%



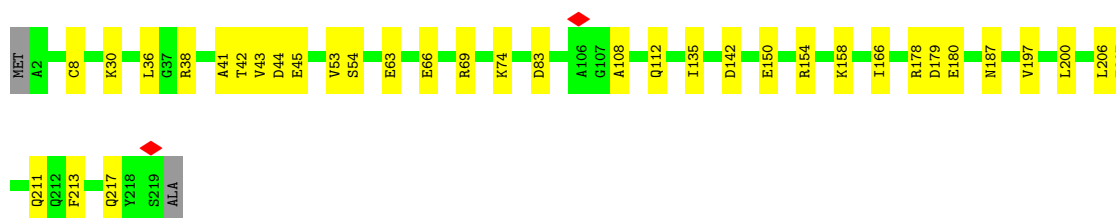
- Molecule 51: 60S ribosomal protein L9-B

Chain q:  85% 14% .

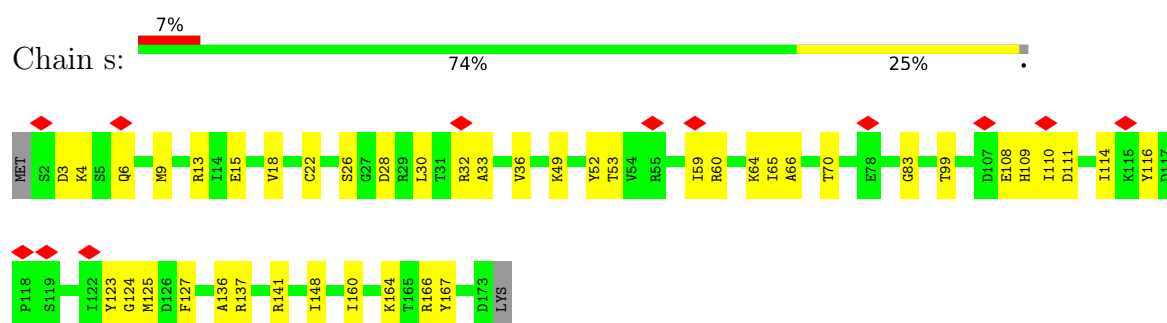


- Molecule 52: 60S ribosomal protein L10

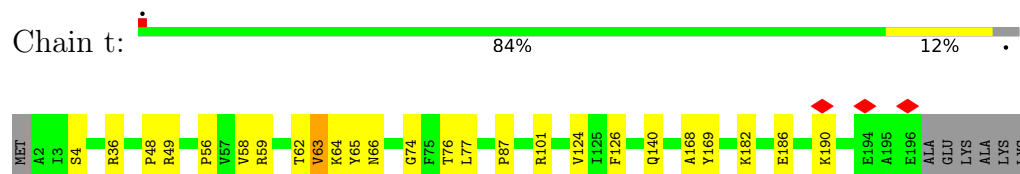
Chain r:  83% 16% .



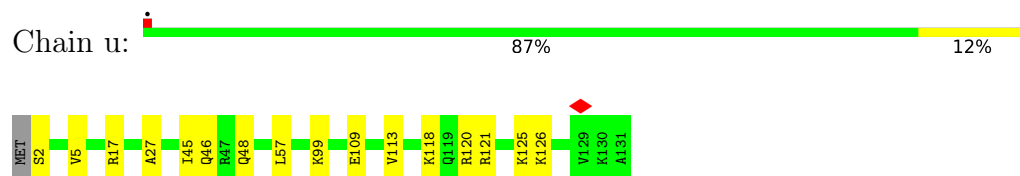
- Molecule 53: 60S ribosomal protein L11-B



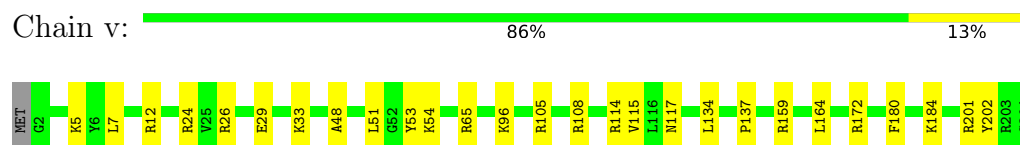
- Molecule 54: 60S ribosomal protein L13



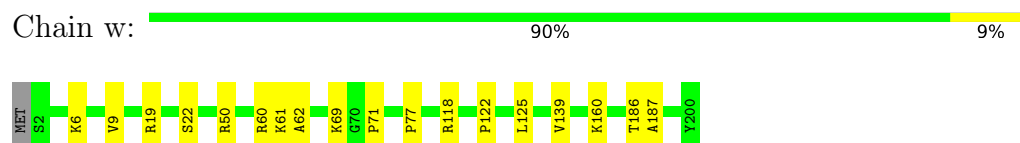
- Molecule 55: 60S ribosomal protein L14-B



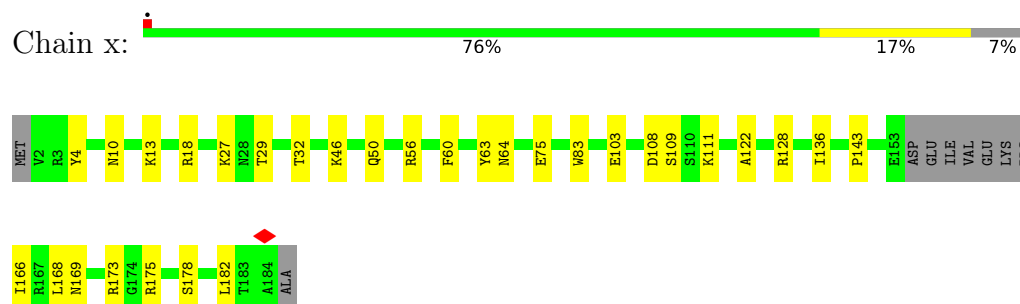
- Molecule 56: 60S ribosomal protein L15-A



- Molecule 57: Ribosomal protein L13

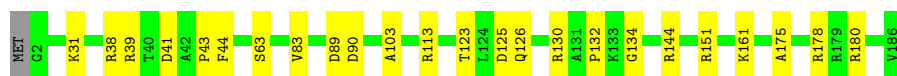


- Molecule 58: Ribosomal protein L22



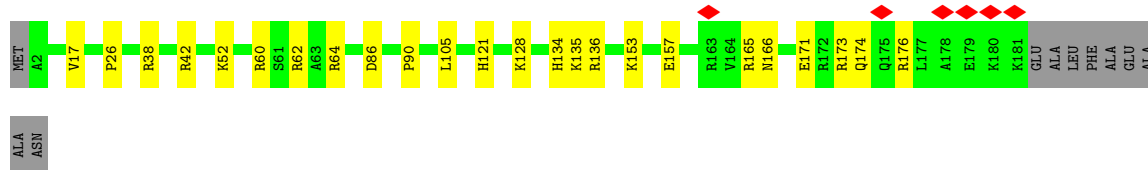
- Molecule 59: 60S ribosomal protein L18-A

Chain y:  87% 13%



- Molecule 60: 60S ribosomal protein L19-A

Chain z:  82% 13% 5%



- Molecule 61: 60S ribosomal protein L27

Chain AA:  82% 17%



- Molecule 62: 60S ribosomal protein L28

Chain AB:  85% 14%



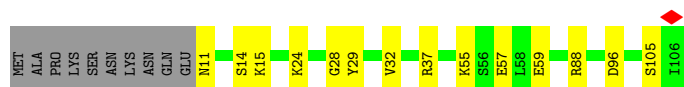
- Molecule 63: 60S ribosomal protein L29

Chain AC:  86% 10% 5%



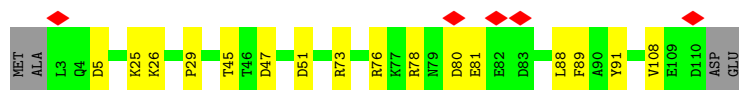
- Molecule 64: 60S ribosomal protein L30

Chain AD:  77% 13% 9%



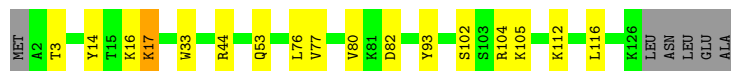
- Molecule 65: 60S ribosomal protein L31-B

Chain AE:  82% 14%



- Molecule 66: 60S ribosomal protein L32

Chain AF: 82% 12% 5%



- Molecule 67: 60S ribosomal protein L33-A

Chain AG: 86% 13%



- Molecule 68: 60S ribosomal protein L34-B

Chain AH: 80% 11% 8%



- Molecule 69: Ribosomal protein L29

Chain AI: 84% 15%



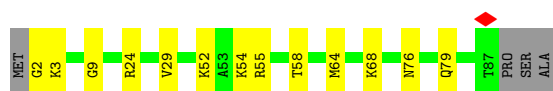
- Molecule 70: 60S ribosomal protein L36

Chain AJ: 80% 18%

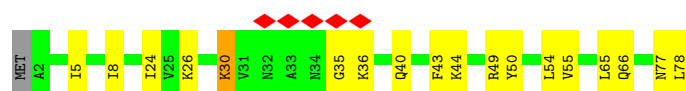
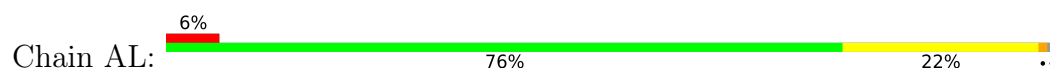


- Molecule 71: 60S ribosomal protein L37-B

Chain AK: 81% 14%



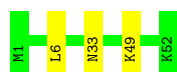
- Molecule 72: 60S ribosomal protein L38



- Molecule 73: 60S ribosomal protein L39



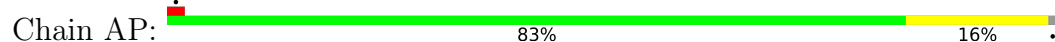
- Molecule 74: 60S ribosomal protein L40-B



- Molecule 75: 60S ribosomal protein L41



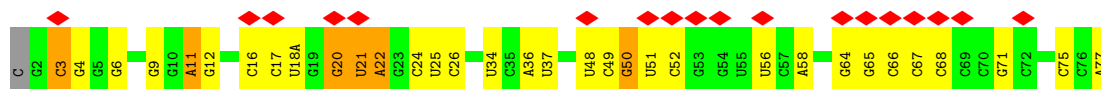
- Molecule 76: 60S ribosomal protein L42-B



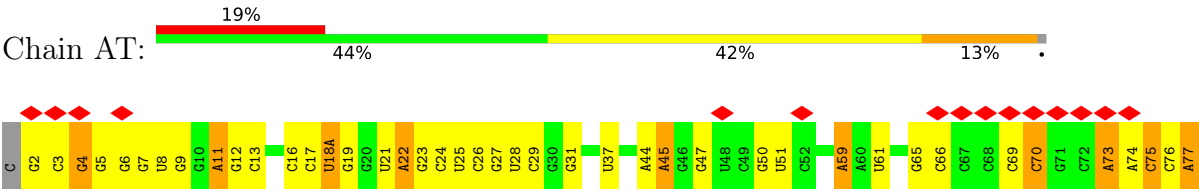
- Molecule 77: 60S ribosomal protein L43-A



- Molecule 78: tRNA



● Molecule 78: tRNA



● Molecule 79: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	44555	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	29.7	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.915	Depositor
Minimum map value	-0.740	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.055	Depositor
Recommended contour level	0.168	Depositor
Map size (Å)	510.3, 510.3, 510.3	wwPDB
Map dimensions	700, 700, 700	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.729, 0.729, 0.729	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: IAS, OMC, SPK, ZN, MLZ, GET, OMG

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	0	0.25	0/1483	0.40	0/1997
2	1	0.32	0/73296	0.36	0/114257
3	2	0.26	0/1305	0.39	0/1749
4	3	0.26	0/2884	0.29	0/4492
5	4	0.31	0/3702	0.34	0/5764
6	6	0.25	0/994	0.41	0/1339
7	7	0.25	0/528	0.41	0/701
8	8	0.25	0/976	0.39	0/1319
9	9	0.24	0/990	0.40	0/1322
10	A	0.24	0/40362	0.35	0/62888
11	B	0.20	0/1666	0.41	0/2273
12	C	0.17	0/1750	0.41	0/2354
13	D	0.20	0/1648	0.36	0/2237
14	E	0.18	0/1725	0.38	0/2316
15	F	0.20	0/2096	0.38	0/2822
16	G	0.18	0/1588	0.42	0/2139
17	H	0.18	0/1845	0.35	0/2464
18	I	0.19	0/1490	0.40	0/2004
19	J	0.21	0/1606	0.36	0/2150
20	K	0.20	0/1478	0.39	0/1978
21	L	0.19	0/801	0.41	0/1081
22	M	0.22	0/1154	0.40	0/1553
23	N	0.19	0/541	0.52	0/726
24	O	0.20	0/1210	0.32	0/1631
25	P	0.16	0/944	0.34	0/1265
26	Q	0.17	0/924	0.40	0/1243
27	T	0.18	0/1186	0.43	0/1590
28	R	0.18	0/1120	0.46	0/1500
29	S	0.17	0/966	0.40	0/1295
30	U	0.17	0/1120	0.36	0/1508
31	V	0.17	0/800	0.42	0/1082
32	W	0.19	0/683	0.38	0/918

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	X	0.23	0/1049	0.37	0/1412
34	Y	0.23	0/1128	0.41	0/1505
35	Z	0.17	0/1086	0.40	0/1447
36	a	0.19	0/585	0.49	0/789
37	b	0.20	0/791	0.39	0/1060
38	c	0.18	0/624	0.38	0/843
39	d	0.16	0/489	0.41	0/654
40	e	0.17	0/466	0.37	0/620
41	f	0.19	0/469	0.39	0/626
42	g	0.23	0/575	0.66	3/760 (0.4%)
43	h	0.15	0/1898	0.39	0/2584
44	j	0.29	0/1931	0.43	0/2592
45	k	0.27	0/3156	0.41	0/4246
46	l	0.25	0/2799	0.41	0/3777
47	m	0.21	0/2447	0.37	0/3294
48	n	0.23	0/1258	0.39	0/1696
49	o	0.25	0/1896	0.42	0/2544
50	p	0.25	0/1825	0.40	0/2458
51	q	0.23	0/1528	0.37	0/2055
52	r	0.22	0/1795	0.34	0/2411
53	s	0.19	0/1404	0.38	0/1880
54	t	0.26	0/1600	0.43	0/2147
55	u	0.25	0/1044	0.41	0/1407
56	v	0.28	0/1753	0.41	0/2347
57	w	0.26	0/1620	0.39	0/2167
58	x	0.26	0/1398	0.39	0/1879
59	y	0.26	0/1511	0.44	0/2022
60	z	0.24	0/1492	0.40	0/1983
61	AA	0.23	0/1112	0.32	0/1488
62	AB	0.26	0/1199	0.41	0/1607
63	AC	0.23	0/502	0.36	0/666
64	AD	0.21	0/738	0.31	0/994
65	AE	0.24	0/894	0.38	0/1201
66	AF	0.26	0/1039	0.41	0/1390
67	AG	0.27	0/895	0.36	0/1201
68	AH	0.25	0/934	0.42	0/1242
69	AI	0.24	0/1004	0.43	0/1337
70	AJ	0.23	0/772	0.36	0/1023
71	AK	0.30	0/690	0.48	0/916
72	AL	0.24	0/632	0.38	0/842
73	AM	0.24	0/458	0.37	0/609
74	AN	0.22	0/436	0.35	0/577
75	AO	0.14	0/237	0.43	0/304

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	AP	0.23	0/861	0.36	0/1136
77	AQ	0.25	0/705	0.36	0/940
78	AT	0.17	0/1813	0.31	0/2825
78	PT	0.15	0/1813	0.27	0/2825
79	MR	0.43	1/257 (0.4%)	0.32	0/397
All	All	0.26	1/211469 (0.0%)	0.37	3/310682 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
12	C	0	1
27	T	0	1
34	Y	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
79	MR	2	U	C1'-N1	5.83	1.57	1.48

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	g	187	HIS	N-CA-C	6.40	121.34	109.56
42	g	186	CYS	CA-C-N	-5.24	114.96	122.67
42	g	186	CYS	C-N-CA	-5.24	114.96	122.67

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	C	59	ASP	Peptide
27	T	102	ALA	Peptide
34	Y	88	PRO	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	1442	0	1500	25	0
2	1	65536	0	32944	575	0
3	2	1276	0	1333	18	0
4	3	2579	0	1304	20	0
5	4	3313	0	1674	26	0
6	6	986	0	1040	16	0
7	7	516	0	534	11	0
8	8	960	0	1014	10	0
9	9	980	0	1058	9	0
10	A	36083	0	18151	579	0
11	B	1627	0	1644	58	0
12	C	1724	0	1805	43	0
13	D	1620	0	1715	34	0
14	E	1701	0	1802	44	0
15	F	2055	0	2137	36	0
16	G	1572	0	1644	61	0
17	H	1820	0	1896	49	0
18	I	1466	0	1561	54	0
19	J	1579	0	1602	32	0
20	K	1453	0	1532	39	0
21	L	783	0	799	32	0
22	M	1129	0	1183	8	0
23	N	539	0	573	22	0
24	O	1187	0	1249	21	0
25	P	942	0	980	29	0
26	Q	906	0	940	36	0
27	T	1169	0	1216	56	0
28	R	1102	0	1168	61	0
29	S	954	0	1008	36	0
30	U	1100	0	1114	40	0
31	V	790	0	855	24	0
32	W	676	0	677	15	0
33	X	1032	0	1066	20	0
34	Y	1110	0	1182	15	0
35	Z	1072	0	1123	32	0
36	a	578	0	613	28	0
37	b	779	0	832	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	c	614	0	630	15	0
39	d	487	0	523	24	0
40	e	454	0	430	12	0
41	f	461	0	499	11	0
42	g	565	0	607	33	0
43	h	1854	0	1793	83	0
44	j	1894	0	1975	26	0
45	k	3084	0	3173	40	0
46	l	2751	0	2879	36	0
47	m	2394	0	2362	29	0
48	n	1237	0	1316	23	0
49	o	1860	0	1958	18	0
50	p	1795	0	1915	20	0
51	q	1510	0	1582	16	0
52	r	1759	0	1802	22	0
53	s	1385	0	1418	34	0
54	t	1573	0	1644	23	0
55	u	1029	0	1116	14	0
56	v	1713	0	1764	24	0
57	w	1590	0	1705	16	0
58	x	1375	0	1403	18	0
59	y	1478	0	1590	20	0
60	z	1471	0	1583	16	0
61	AA	1087	0	1154	15	0
62	AB	1170	0	1203	20	0
63	AC	489	0	522	5	0
64	AD	729	0	775	9	0
65	AE	881	0	932	11	0
66	AF	1015	0	1095	14	0
67	AG	867	0	932	11	0
68	AH	913	0	998	12	0
69	AI	990	0	1094	14	0
70	AJ	764	0	851	13	0
71	AK	677	0	697	9	0
72	AL	623	0	688	11	0
73	AM	446	0	488	2	0
74	AN	427	0	473	3	0
75	AO	236	0	285	2	0
76	AP	863	0	931	13	0
77	AQ	698	0	734	6	0
78	AT	1623	0	825	24	0
78	PT	1623	0	825	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
79	MR	231	0	118	3	0
80	1	14	0	30	1	0
81	1	408	0	480	21	0
81	A	136	0	160	7	0
81	AT	34	0	40	1	0
82	AH	1	0	0	0	0
82	AK	1	0	0	0	0
82	AN	1	0	0	0	0
82	AP	1	0	0	0	0
82	AQ	1	0	0	0	0
82	b	1	0	0	0	0
82	e	1	0	0	0	0
All	All	197420	0	146465	2539	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 2539 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:2420:G:H1	2:1:2483:U:H3	1.01	0.96
10:A:1341:U:H3	10:A:1352:G:H1	1.06	0.93
10:A:478:G:H1	10:A:506:U:H3	1.15	0.92
23:N:43:ARG:HH12	23:N:103:LEU:H	1.18	0.90
2:1:2651:A:HO2'	53:s:52:TYR:HH	1.13	0.89

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	171/172 (99%)	169 (99%)	2 (1%)	0	100	100
3	2	159/160 (99%)	157 (99%)	2 (1%)	0	100	100
6	6	129/137 (94%)	127 (98%)	2 (2%)	0	100	100
7	7	60/155 (39%)	60 (100%)	0	0	100	100
8	8	117/142 (82%)	114 (97%)	3 (3%)	0	100	100
9	9	123/127 (97%)	119 (97%)	4 (3%)	0	100	100
11	B	206/261 (79%)	191 (93%)	14 (7%)	1 (0%)	24	27
12	C	212/256 (83%)	197 (93%)	15 (7%)	0	100	100
13	D	214/249 (86%)	204 (95%)	10 (5%)	0	100	100
14	E	220/251 (88%)	204 (93%)	16 (7%)	0	100	100
15	F	258/262 (98%)	248 (96%)	10 (4%)	0	100	100
16	G	195/225 (87%)	178 (91%)	17 (9%)	0	100	100
17	H	224/236 (95%)	217 (97%)	7 (3%)	0	100	100
18	I	180/186 (97%)	166 (92%)	14 (8%)	0	100	100
19	J	201/206 (98%)	196 (98%)	5 (2%)	0	100	100
20	K	176/189 (93%)	164 (93%)	12 (7%)	0	100	100
21	L	91/118 (77%)	81 (89%)	10 (11%)	0	100	100
22	M	139/155 (90%)	134 (96%)	5 (4%)	0	100	100
23	N	65/143 (46%)	46 (71%)	18 (28%)	1 (2%)	8	7
24	O	148/151 (98%)	146 (99%)	2 (1%)	0	100	100
25	P	124/132 (94%)	116 (94%)	8 (6%)	0	100	100
26	Q	113/142 (80%)	104 (92%)	9 (8%)	0	100	100
27	T	140/145 (97%)	117 (84%)	21 (15%)	2 (1%)	9	7
28	R	139/142 (98%)	126 (91%)	13 (9%)	0	100	100
29	S	116/137 (85%)	104 (90%)	12 (10%)	0	100	100
30	U	139/145 (96%)	133 (96%)	6 (4%)	0	100	100
31	V	98/119 (82%)	95 (97%)	3 (3%)	0	100	100
32	W	85/87 (98%)	79 (93%)	6 (7%)	0	100	100
33	X	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
34	Y	141/145 (97%)	138 (98%)	3 (2%)	0	100	100
35	Z	130/135 (96%)	124 (95%)	6 (5%)	0	100	100
36	a	70/105 (67%)	64 (91%)	6 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	b	96/119 (81%)	92 (96%)	4 (4%)	0	100	100
38	c	79/82 (96%)	73 (92%)	6 (8%)	0	100	100
39	d	60/67 (90%)	51 (85%)	9 (15%)	0	100	100
40	e	53/56 (95%)	50 (94%)	3 (6%)	0	100	100
41	f	56/63 (89%)	53 (95%)	3 (5%)	0	100	100
42	g	66/193 (34%)	48 (73%)	17 (26%)	1 (2%)	8	7
43	h	229/317 (72%)	204 (89%)	25 (11%)	0	100	100
44	j	248/254 (98%)	238 (96%)	10 (4%)	0	100	100
45	k	385/389 (99%)	374 (97%)	11 (3%)	0	100	100
46	l	359/363 (99%)	347 (97%)	12 (3%)	0	100	100
47	m	290/298 (97%)	283 (98%)	7 (2%)	0	100	100
48	n	152/176 (86%)	143 (94%)	9 (6%)	0	100	100
49	o	229/241 (95%)	222 (97%)	7 (3%)	0	100	100
50	p	229/262 (87%)	223 (97%)	6 (3%)	0	100	100
51	q	187/191 (98%)	181 (97%)	6 (3%)	0	100	100
52	r	216/220 (98%)	210 (97%)	6 (3%)	0	100	100
53	s	171/174 (98%)	164 (96%)	7 (4%)	0	100	100
54	t	193/202 (96%)	184 (95%)	8 (4%)	1 (0%)	24	27
55	u	128/131 (98%)	125 (98%)	3 (2%)	0	100	100
56	v	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
57	w	197/200 (98%)	194 (98%)	3 (2%)	0	100	100
58	x	168/185 (91%)	163 (97%)	5 (3%)	0	100	100
59	y	186/186 (100%)	179 (96%)	7 (4%)	0	100	100
60	z	179/190 (94%)	178 (99%)	1 (1%)	0	100	100
61	AA	133/136 (98%)	131 (98%)	2 (2%)	0	100	100
62	AB	146/149 (98%)	141 (97%)	5 (3%)	0	100	100
63	AC	59/63 (94%)	58 (98%)	1 (2%)	0	100	100
64	AD	94/106 (89%)	93 (99%)	1 (1%)	0	100	100
65	AE	106/112 (95%)	102 (96%)	4 (4%)	0	100	100
66	AF	124/131 (95%)	123 (99%)	1 (1%)	0	100	100
67	AG	107/107 (100%)	105 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	AH	114/122 (93%)	112 (98%)	2 (2%)	0	100	100
69	AI	118/120 (98%)	113 (96%)	5 (4%)	0	100	100
70	AJ	96/99 (97%)	95 (99%)	1 (1%)	0	100	100
71	AK	84/90 (93%)	83 (99%)	1 (1%)	0	100	100
72	AL	76/78 (97%)	74 (97%)	2 (3%)	0	100	100
73	AM	49/51 (96%)	48 (98%)	1 (2%)	0	100	100
74	AN	51/52 (98%)	51 (100%)	0	0	100	100
75	AO	23/25 (92%)	21 (91%)	1 (4%)	1 (4%)	2	1
76	AP	103/106 (97%)	98 (95%)	5 (5%)	0	100	100
77	AQ	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
All	All	10639/11747 (91%)	10148 (95%)	484 (4%)	7 (0%)	49	59

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
27	T	103	ASN
42	g	186	CYS
27	T	102	ALA
54	t	63	VAL
23	N	27	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	158/157 (101%)	156 (99%)	2 (1%)	61	76
3	2	135/134 (101%)	135 (100%)	0	100	100
6	6	101/103 (98%)	101 (100%)	0	100	100
7	7	56/127 (44%)	56 (100%)	0	100	100
8	8	107/121 (88%)	107 (100%)	0	100	100
9	9	110/112 (98%)	110 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	B	176/215 (82%)	176 (100%)	0	100	100
12	C	194/229 (85%)	194 (100%)	0	100	100
13	D	174/198 (88%)	174 (100%)	0	100	100
14	E	173/196 (88%)	173 (100%)	0	100	100
15	F	218/220 (99%)	218 (100%)	0	100	100
16	G	173/197 (88%)	173 (100%)	0	100	100
17	H	195/204 (96%)	195 (100%)	0	100	100
18	I	163/167 (98%)	163 (100%)	0	100	100
19	J	157/160 (98%)	157 (100%)	0	100	100
20	K	153/160 (96%)	153 (100%)	0	100	100
21	L	87/104 (84%)	87 (100%)	0	100	100
22	M	122/134 (91%)	122 (100%)	0	100	100
23	N	60/123 (49%)	60 (100%)	0	100	100
24	O	129/130 (99%)	129 (100%)	0	100	100
25	P	96/101 (95%)	96 (100%)	0	100	100
26	Q	99/121 (82%)	99 (100%)	0	100	100
27	T	126/129 (98%)	126 (100%)	0	100	100
28	R	115/116 (99%)	115 (100%)	0	100	100
29	S	106/122 (87%)	106 (100%)	0	100	100
30	U	113/117 (97%)	113 (100%)	0	100	100
31	V	90/105 (86%)	90 (100%)	0	100	100
32	W	71/71 (100%)	71 (100%)	0	100	100
33	X	112/113 (99%)	112 (100%)	0	100	100
34	Y	116/118 (98%)	116 (100%)	0	100	100
35	Z	109/112 (97%)	109 (100%)	0	100	100
36	a	64/85 (75%)	64 (100%)	0	100	100
37	b	84/102 (82%)	84 (100%)	0	100	100
38	c	72/73 (99%)	71 (99%)	1 (1%)	59	73
39	d	54/58 (93%)	54 (100%)	0	100	100
40	e	47/48 (98%)	47 (100%)	0	100	100
41	f	50/54 (93%)	50 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	g	60/175 (34%)	60 (100%)	0	100	100
43	h	199/263 (76%)	198 (100%)	1 (0%)	81	89
44	j	191/194 (98%)	189 (99%)	2 (1%)	68	81
45	k	326/328 (99%)	326 (100%)	0	100	100
46	l	290/292 (99%)	290 (100%)	0	100	100
47	m	247/252 (98%)	247 (100%)	0	100	100
48	n	135/154 (88%)	135 (100%)	0	100	100
49	o	195/204 (96%)	195 (100%)	0	100	100
50	p	193/216 (89%)	193 (100%)	0	100	100
51	q	168/170 (99%)	168 (100%)	0	100	100
52	r	185/186 (100%)	185 (100%)	0	100	100
53	s	148/149 (99%)	148 (100%)	0	100	100
54	t	163/168 (97%)	163 (100%)	0	100	100
55	u	108/109 (99%)	108 (100%)	0	100	100
56	v	177/178 (99%)	177 (100%)	0	100	100
57	w	166/167 (99%)	166 (100%)	0	100	100
58	x	142/154 (92%)	142 (100%)	0	100	100
59	y	156/154 (101%)	154 (99%)	2 (1%)	61	76
60	z	148/153 (97%)	148 (100%)	0	100	100
61	AA	117/118 (99%)	117 (100%)	0	100	100
62	AB	120/121 (99%)	120 (100%)	0	100	100
63	AC	48/49 (98%)	46 (96%)	2 (4%)	26	35
64	AD	81/90 (90%)	81 (100%)	0	100	100
65	AE	97/100 (97%)	97 (100%)	0	100	100
66	AF	111/115 (96%)	109 (98%)	2 (2%)	51	66
67	AG	94/92 (102%)	94 (100%)	0	100	100
68	AH	99/102 (97%)	99 (100%)	0	100	100
69	AI	106/106 (100%)	106 (100%)	0	100	100
70	AJ	78/79 (99%)	78 (100%)	0	100	100
71	AK	70/73 (96%)	70 (100%)	0	100	100
72	AL	69/69 (100%)	67 (97%)	2 (3%)	37	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
73	AM	47/47 (100%)	47 (100%)	0	100	100
74	AN	48/47 (102%)	48 (100%)	0	100	100
75	AO	24/24 (100%)	24 (100%)	0	100	100
76	AP	90/89 (101%)	90 (100%)	0	100	100
77	AQ	72/73 (99%)	72 (100%)	0	100	100
All	All	9133/9896 (92%)	9119 (100%)	14 (0%)	87	94

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
59	y	31[B]	LYS
63	AC	14[A]	ARG
72	AL	30[B]	LYS
66	AF	17[B]	LYS
72	AL	30[A]	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 93 such sidechains are listed below:

Mol	Chain	Res	Type
51	q	96	HIS
59	y	58	ASN
52	r	59	GLN
56	v	32	GLN
60	z	130	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	1685/1787 (94%)	379 (22%)	25 (1%)
2	1	3060/3359 (91%)	455 (14%)	27 (0%)
4	3	120/121 (99%)	10 (8%)	0
5	4	155/158 (98%)	23 (14%)	2 (1%)
78	AT	75/77 (97%)	21 (28%)	0
78	PT	75/77 (97%)	16 (21%)	0
79	MR	10/39 (25%)	0	0
All	All	5180/5618 (92%)	904 (17%)	54 (1%)

5 of 904 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	1	13	U
2	1	24	U
2	1	25	A
2	1	29	G
2	1	39	A

5 of 54 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	4	85	G
10	A	415	A
10	A	1398	G
10	A	137	A
10	A	214	U

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

6 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	OMC	1	2808	2	19,22,23	2.89	8 (42%)	25,31,34	1.22	3 (12%)
6	MLZ	6	110	6	8,9,10	0.72	0	4,9,11	0.87	0
25	IAS	P	119	25	6,7,8	1.11	0	4,8,10	1.44	1 (25%)
2	OMG	1	2765	2	23,26,27	2.30	9 (39%)	32,38,41	1.88	9 (28%)
76	MLZ	AP	55	76	8,9,10	0.69	0	4,9,11	0.81	0
76	MLZ	AP	40	76	8,9,10	0.68	0	4,9,11	0.89	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
2	OMC	1	2808	2	-	2/9/27/28	0/2/2/2
6	MLZ	6	110	6	-	3/7/8/10	-
25	IAS	P	119	25	-	4/5/6/8	-
2	OMG	1	2765	2	-	1/9/27/28	0/3/3/3
76	MLZ	AP	55	76	-	1/7/8/10	-
76	MLZ	AP	40	76	-	0/7/8/10	-

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	1	2765	OMG	C4-N3	6.13	1.48	1.34
2	1	2808	OMC	C2-N3	6.04	1.48	1.36
2	1	2808	OMC	C6-C5	5.76	1.48	1.35
2	1	2765	OMG	C2-N3	5.27	1.46	1.33
2	1	2808	OMC	C2-N1	4.72	1.50	1.40

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	1	2765	OMG	C5-C4-N3	-4.65	120.99	128.39
2	1	2765	OMG	C2-N3-C4	4.45	119.97	112.30
2	1	2765	OMG	N9-C8-N7	-3.47	106.97	113.40
2	1	2808	OMC	O2-C2-N3	-3.40	116.97	122.33
2	1	2765	OMG	C2-N1-C6	-2.87	119.90	125.11

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	1	2808	OMC	O4'-C1'-N1-C2
2	1	2808	OMC	O4'-C1'-N1-C6
6	6	110	MLZ	CD-CE-NZ-CM
25	P	119	IAS	C-CA-CB-CG
25	P	119	IAS	N-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	1	2808	OMC	2	0
25	P	119	IAS	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 25 ligands modelled in this entry, 7 are monoatomic - leaving 18 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$
80	SPK	1	3401	-	13,13,13	0.37	0	12,12,12	0.78	0
81	GET	1	3404	-	35,36,36	0.80	1 (2%)	43,55,55	0.74	2 (4%)
81	GET	1	3412	-	35,36,36	1.49	1 (2%)	43,55,55	0.74	0
81	GET	A	1801	-	35,36,36	0.46	0	43,55,55	0.72	1 (2%)
81	GET	A	1804	-	35,36,36	1.10	1 (2%)	43,55,55	0.82	1 (2%)
81	GET	1	3407	-	35,36,36	0.46	0	43,55,55	0.88	3 (6%)
81	GET	1	3406	-	35,36,36	1.19	1 (2%)	43,55,55	0.83	2 (4%)
81	GET	1	3409	-	35,36,36	0.50	0	43,55,55	0.78	2 (4%)
81	GET	1	3410	-	35,36,36	0.94	1 (2%)	43,55,55	0.88	3 (6%)
81	GET	AT	101	-	35,36,36	0.90	1 (2%)	43,55,55	0.53	0
81	GET	1	3411	-	35,36,36	0.55	0	43,55,55	0.94	3 (6%)
81	GET	A	1803	-	35,36,36	0.63	1 (2%)	43,55,55	0.70	1 (2%)
81	GET	1	3405	-	35,36,36	0.69	1 (2%)	43,55,55	0.78	1 (2%)
81	GET	A	1802	-	35,36,36	0.98	1 (2%)	43,55,55	0.86	1 (2%)
81	GET	1	3408	-	35,36,36	0.85	1 (2%)	43,55,55	0.66	1 (2%)
81	GET	1	3413	-	35,36,36	0.79	1 (2%)	43,55,55	0.93	3 (6%)
81	GET	1	3403	-	35,36,36	0.64	1 (2%)	43,55,55	0.95	2 (4%)
81	GET	1	3402	-	35,36,36	0.87	1 (2%)	43,55,55	0.62	1 (2%)

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
80	SPK	1	3401	-	-	4/11/11/11	-
81	GET	1	3404	-	-	2/13/74/74	1/3/3/3
81	GET	1	3412	-	-	1/13/74/74	0/3/3/3
81	GET	A	1801	-	-	1/13/74/74	0/3/3/3
81	GET	A	1804	-	-	10/13/74/74	1/3/3/3
81	GET	1	3407	-	-	1/13/74/74	0/3/3/3
81	GET	1	3406	-	-	2/13/74/74	0/3/3/3
81	GET	1	3409	-	-	3/13/74/74	0/3/3/3
81	GET	1	3410	-	-	1/13/74/74	0/3/3/3
81	GET	AT	101	-	-	2/13/74/74	1/3/3/3
81	GET	1	3411	-	-	6/13/74/74	1/3/3/3
81	GET	A	1803	-	-	1/13/74/74	0/3/3/3
81	GET	1	3405	-	-	1/13/74/74	0/3/3/3
81	GET	A	1802	-	-	2/13/74/74	1/3/3/3
81	GET	1	3408	-	-	1/13/74/74	0/3/3/3
81	GET	1	3413	-	-	7/13/74/74	0/3/3/3
81	GET	1	3403	-	-	6/13/74/74	1/3/3/3
81	GET	1	3402	-	-	1/13/74/74	0/3/3/3

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
81	1	3412	GET	C33-N33	8.33	1.56	1.45
81	1	3406	GET	C33-N33	6.54	1.53	1.45
81	A	1804	GET	C33-N33	5.71	1.52	1.45
81	A	1802	GET	C33-N33	5.19	1.52	1.45
81	1	3410	GET	C33-N33	4.98	1.51	1.45

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	A	1802	GET	O11-C11-C21	4.37	115.22	108.08
81	1	3406	GET	O11-C11-C21	3.96	114.56	108.08
81	1	3410	GET	O11-C11-C21	3.89	114.44	108.08
81	1	3405	GET	O11-C11-C21	3.60	113.97	108.08
81	1	3408	GET	O11-C11-C21	3.40	113.64	108.08

There are no chirality outliers.

5 of 52 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
81	1	3402	GET	C23-C33-N33-C93
81	1	3403	GET	C21-C11-O11-C42
81	1	3403	GET	C41-C51-C61-O61
81	1	3403	GET	C41-C51-C61-C71
81	1	3403	GET	O51-C51-C61-C71

5 of 6 ring outliers are listed below:

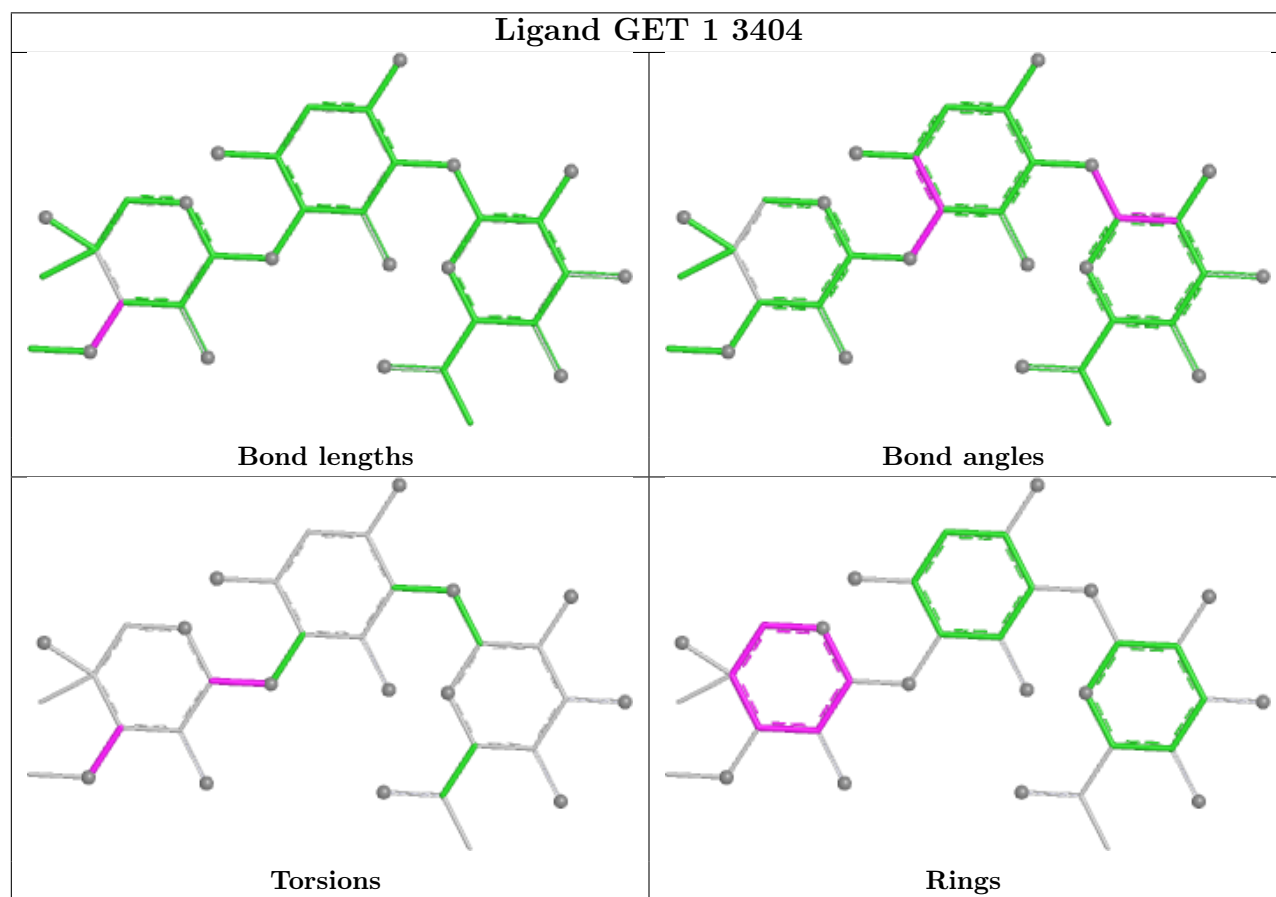
Mol	Chain	Res	Type	Atoms
81	1	3403	GET	C11-C21-C31-C41-C51-O51
81	1	3404	GET	C13-C23-C33-C43-C53-O53
81	A	1802	GET	C11-C21-C31-C41-C51-O51
81	A	1804	GET	C11-C21-C31-C41-C51-O51
81	AT	101	GET	C11-C21-C31-C41-C51-O51

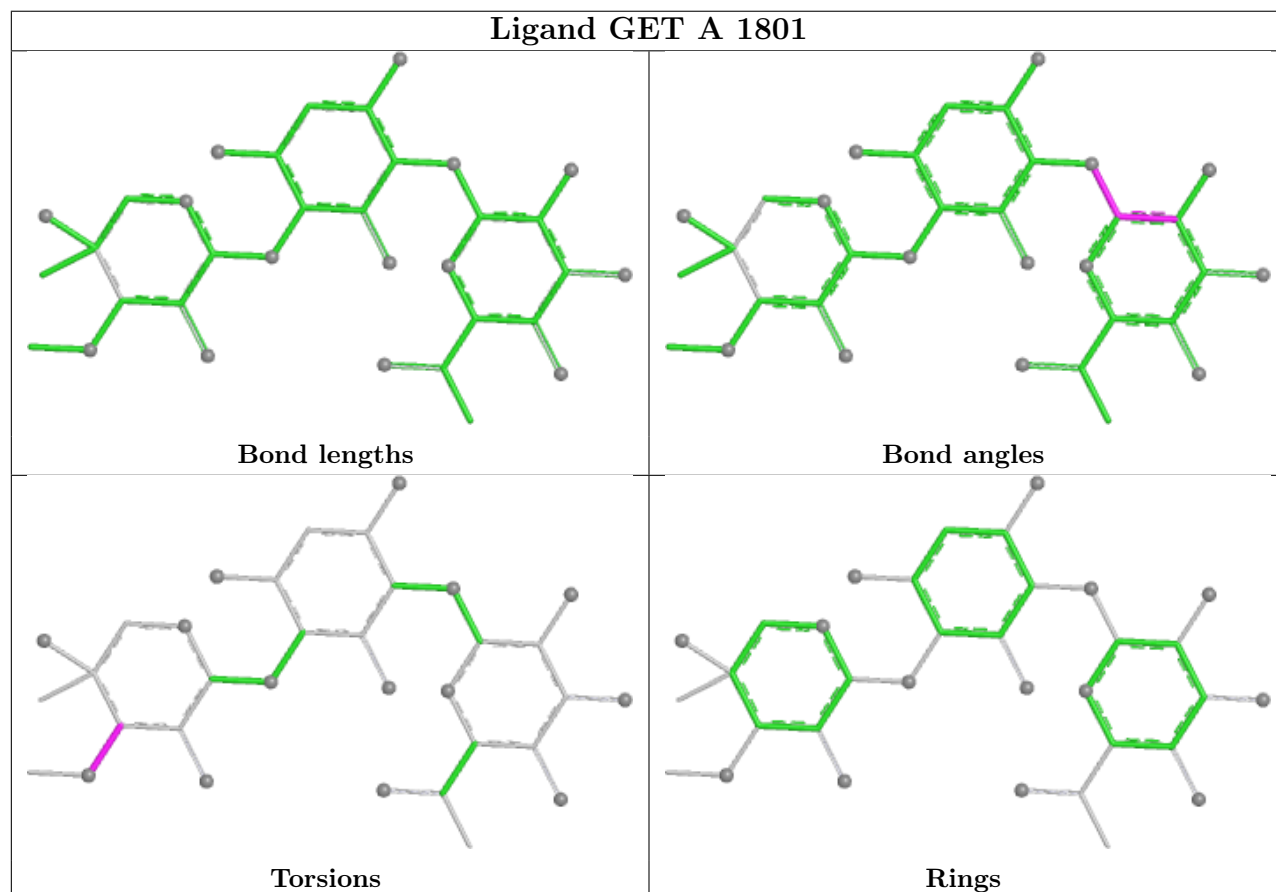
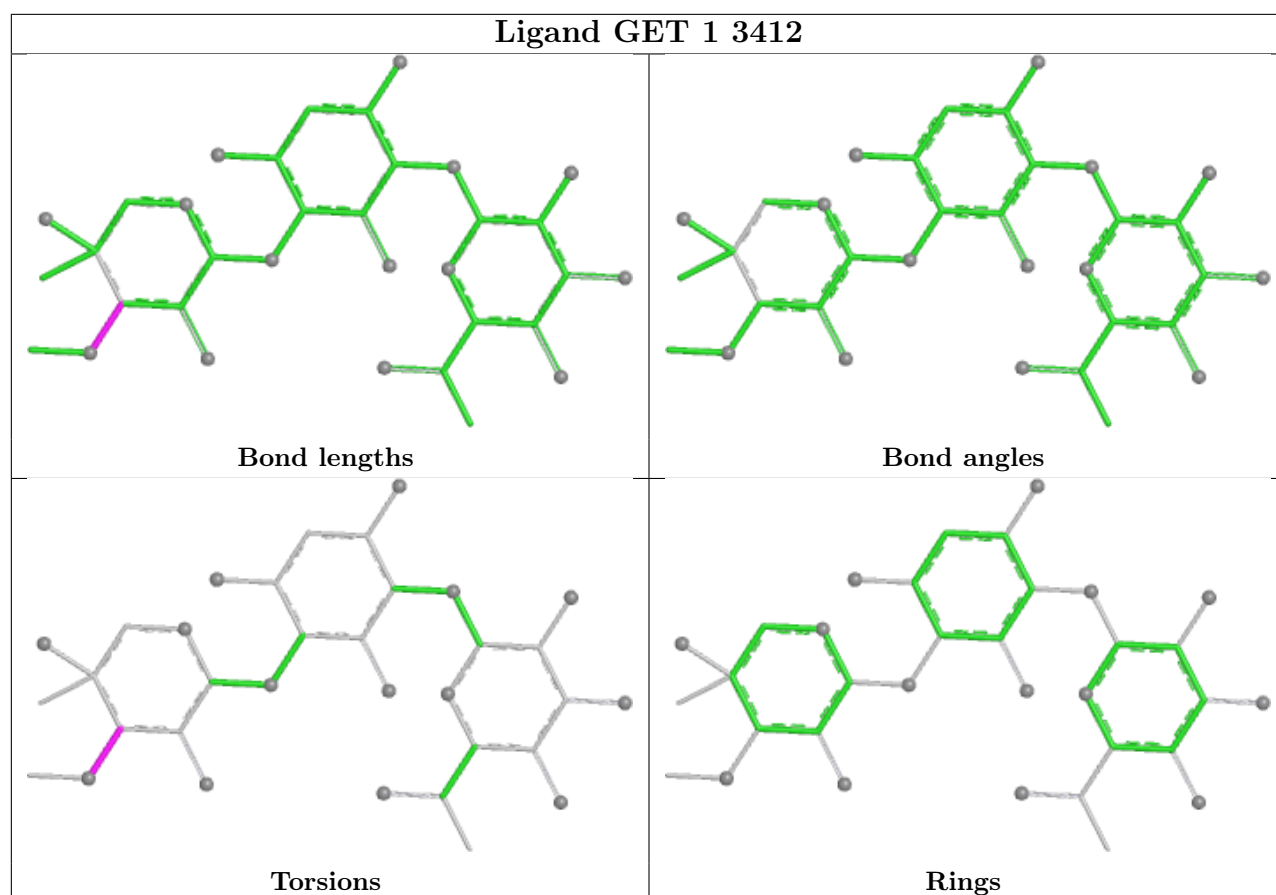
15 monomers are involved in 30 short contacts:

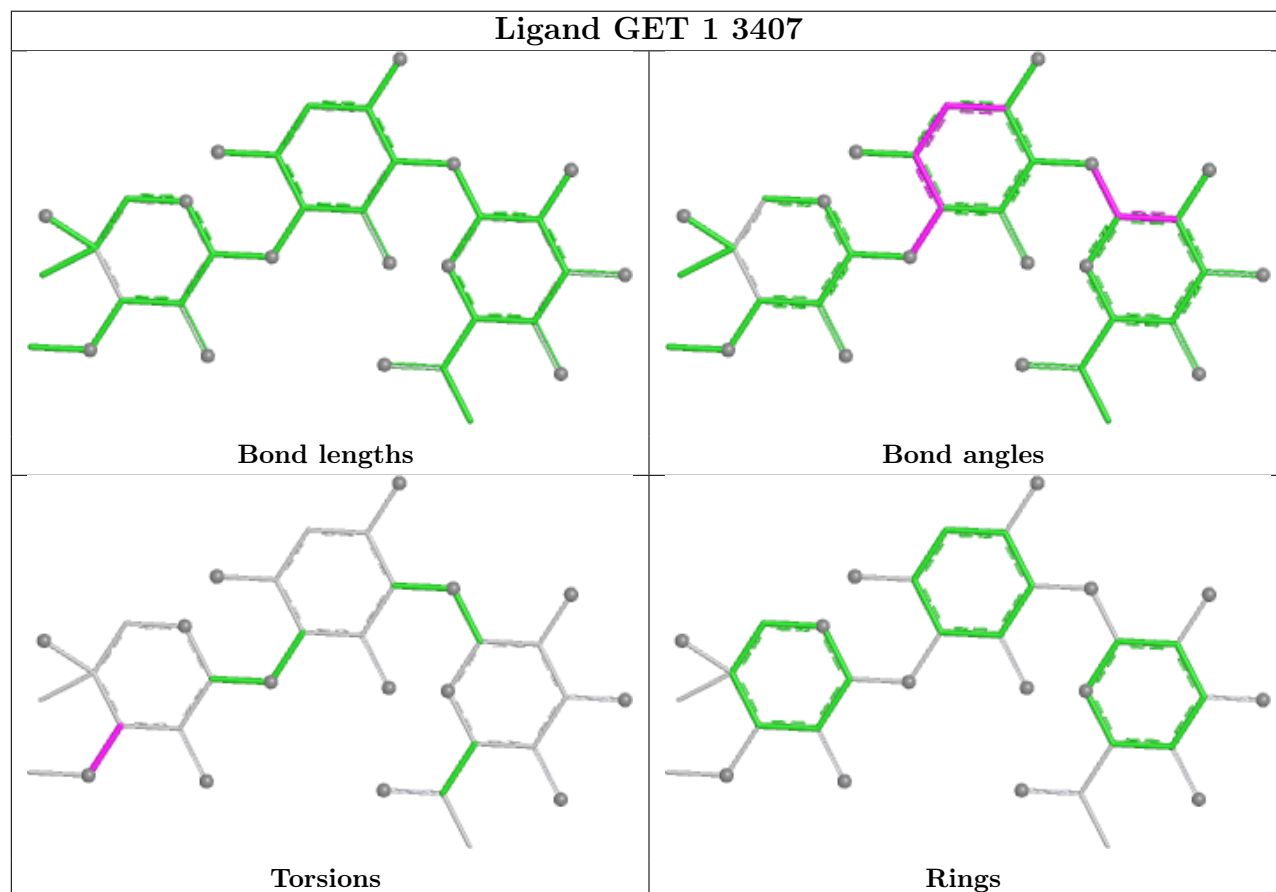
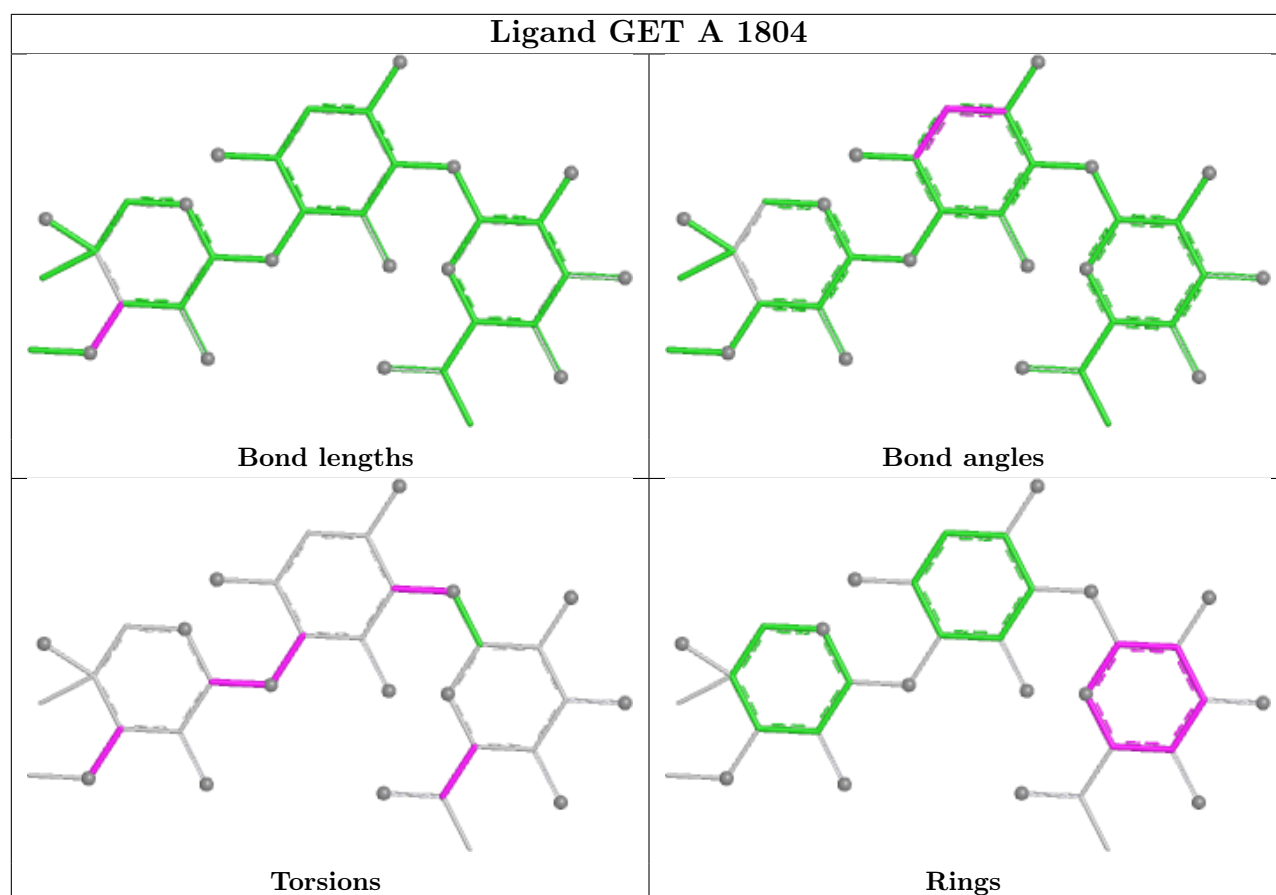
Mol	Chain	Res	Type	Clashes	Symm-Clashes
80	1	3401	SPK	1	0
81	1	3404	GET	3	0
81	1	3412	GET	3	0
81	A	1801	GET	3	0
81	A	1804	GET	3	0
81	1	3407	GET	2	0
81	1	3406	GET	2	0
81	1	3409	GET	1	0
81	1	3410	GET	1	0
81	AT	101	GET	1	0
81	1	3405	GET	1	0
81	A	1802	GET	1	0
81	1	3408	GET	2	0
81	1	3413	GET	3	0
81	1	3403	GET	3	0

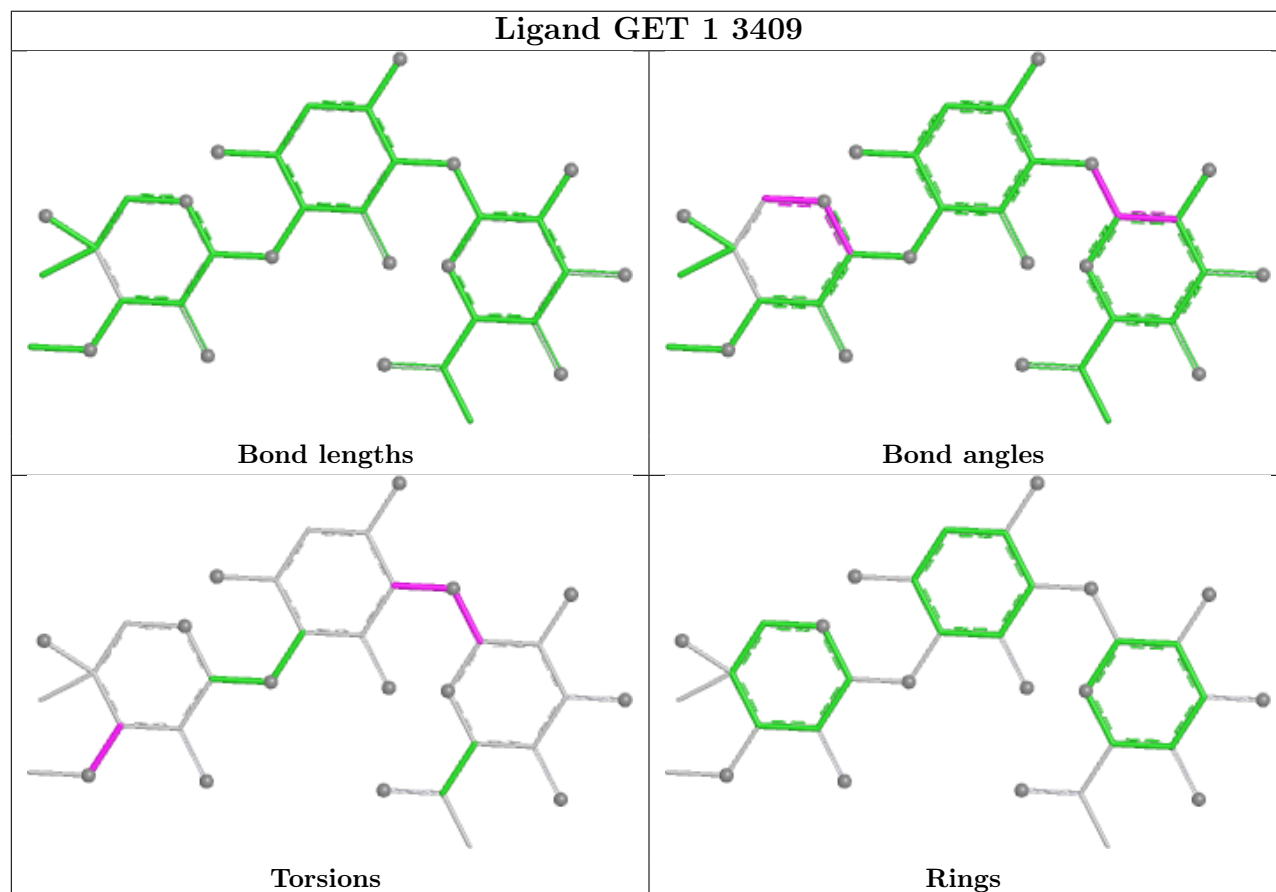
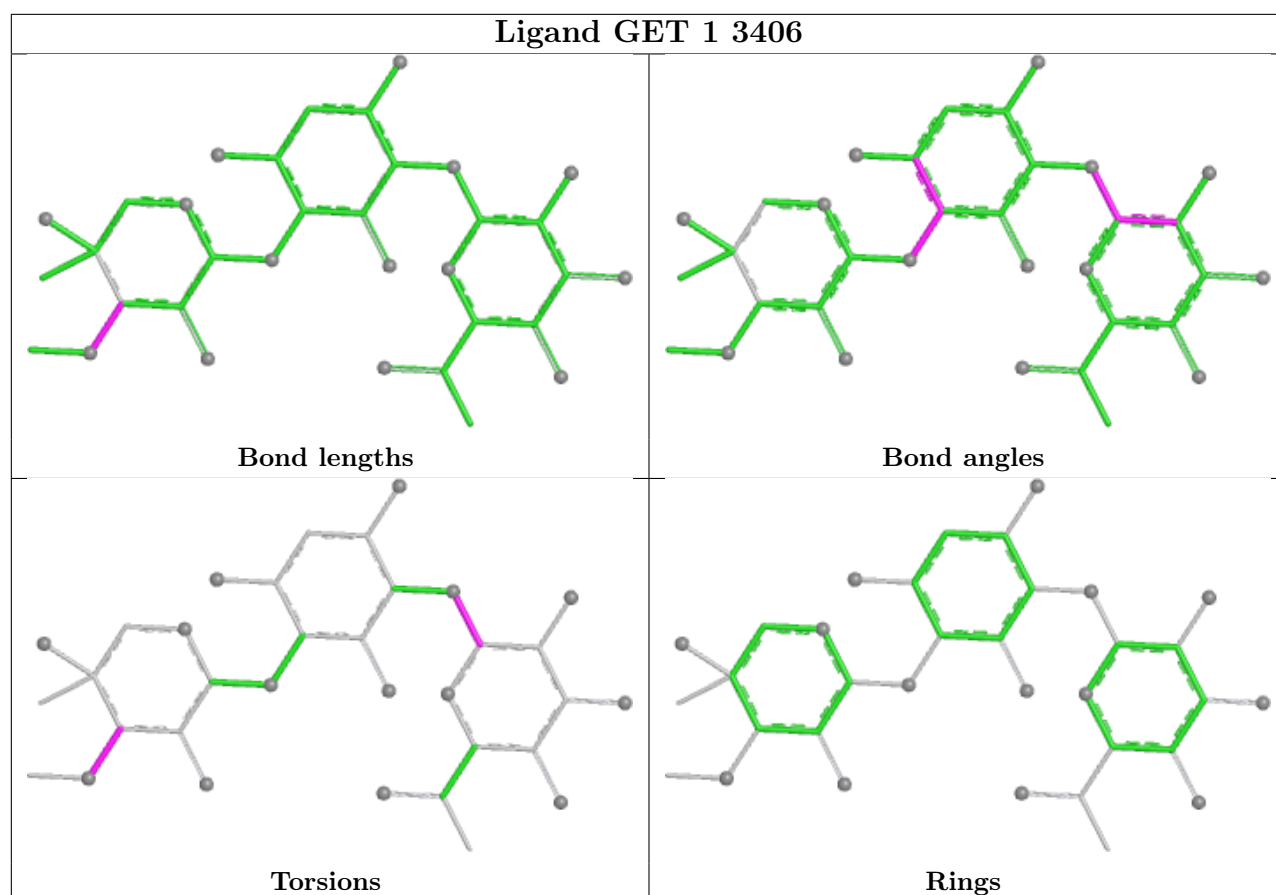
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

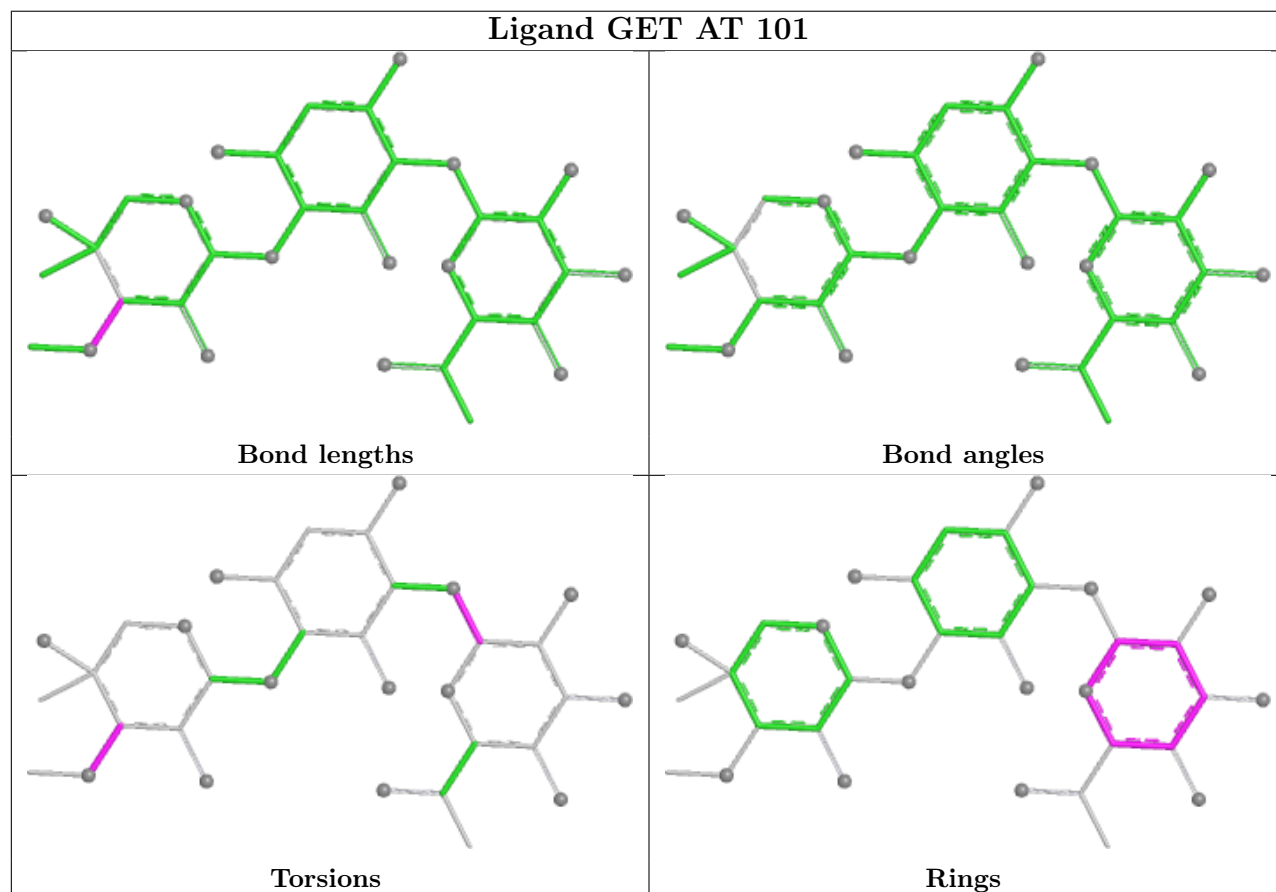
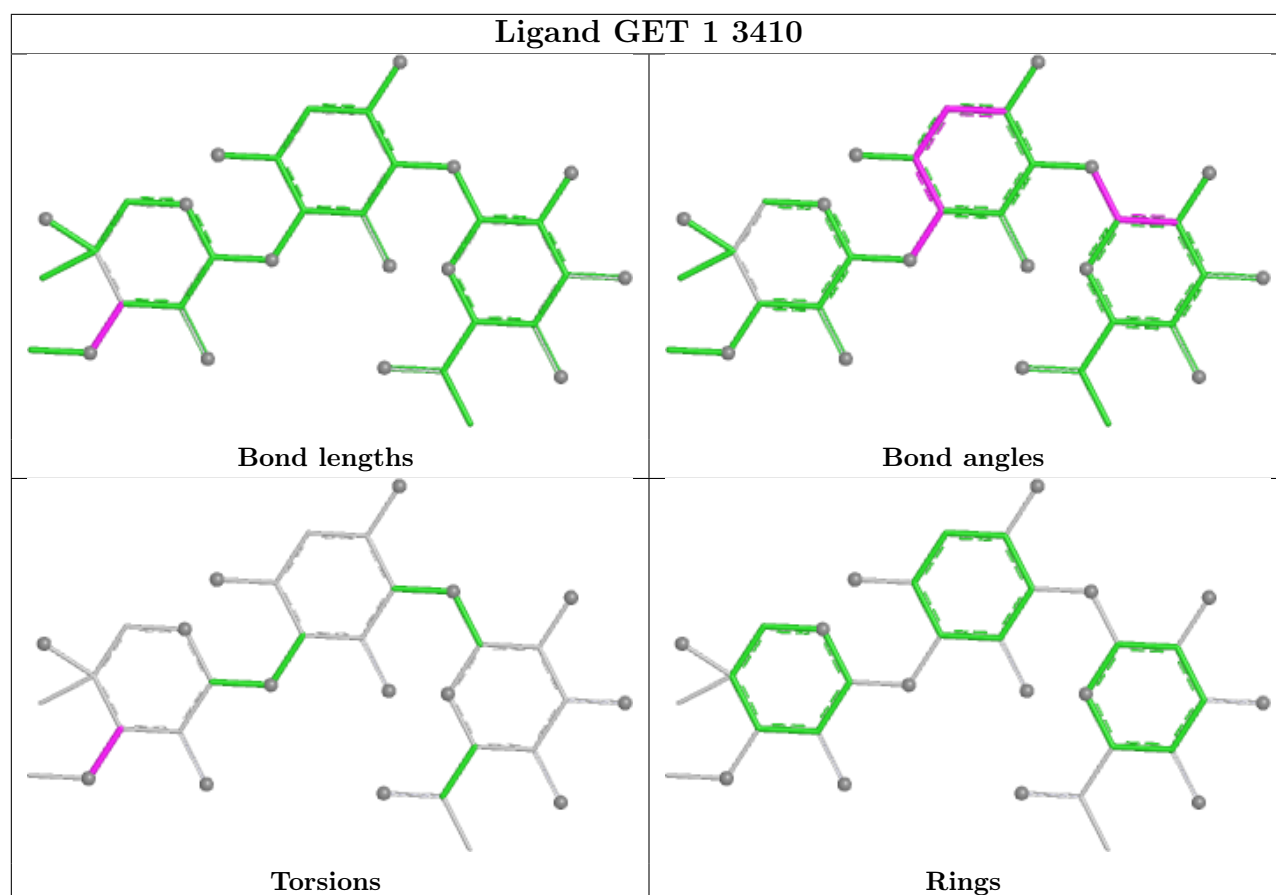
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

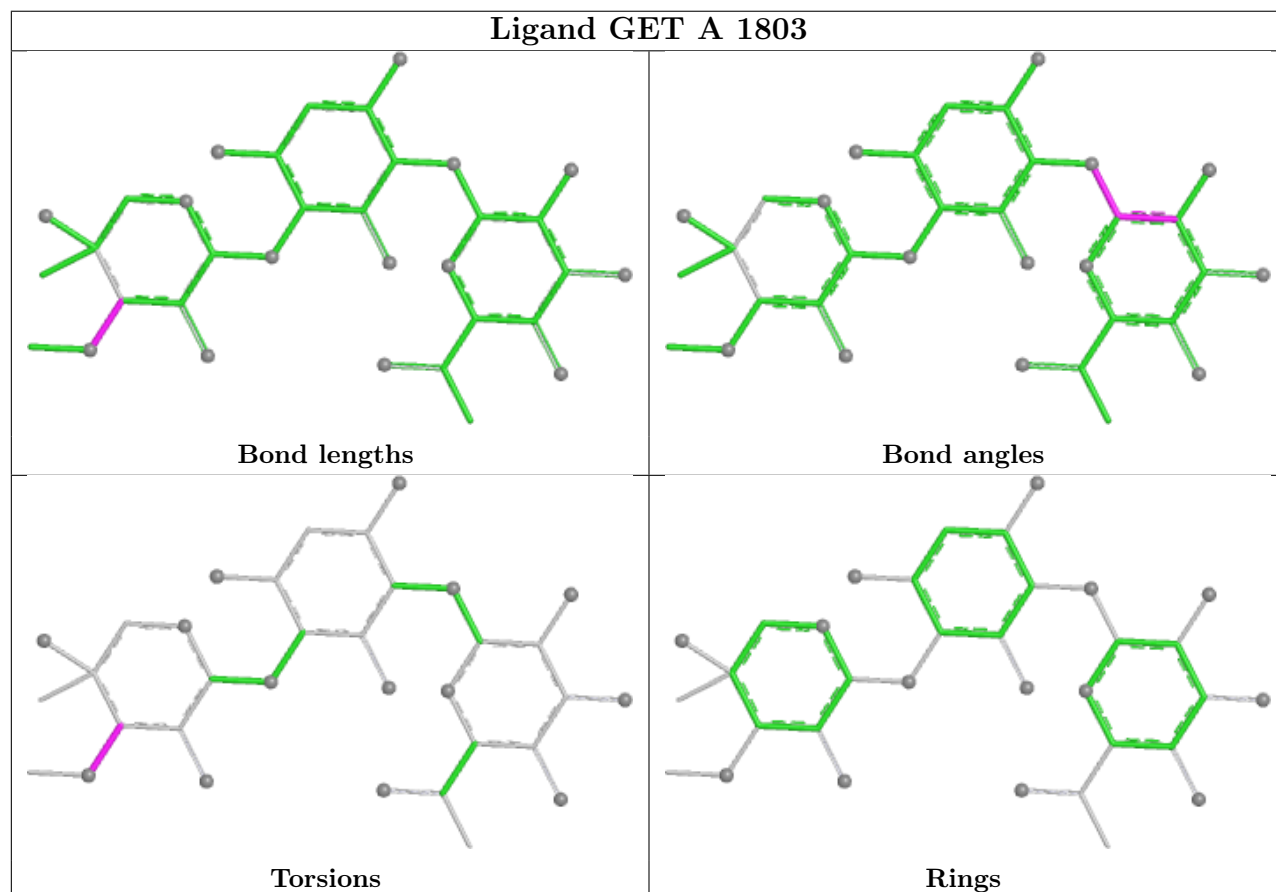
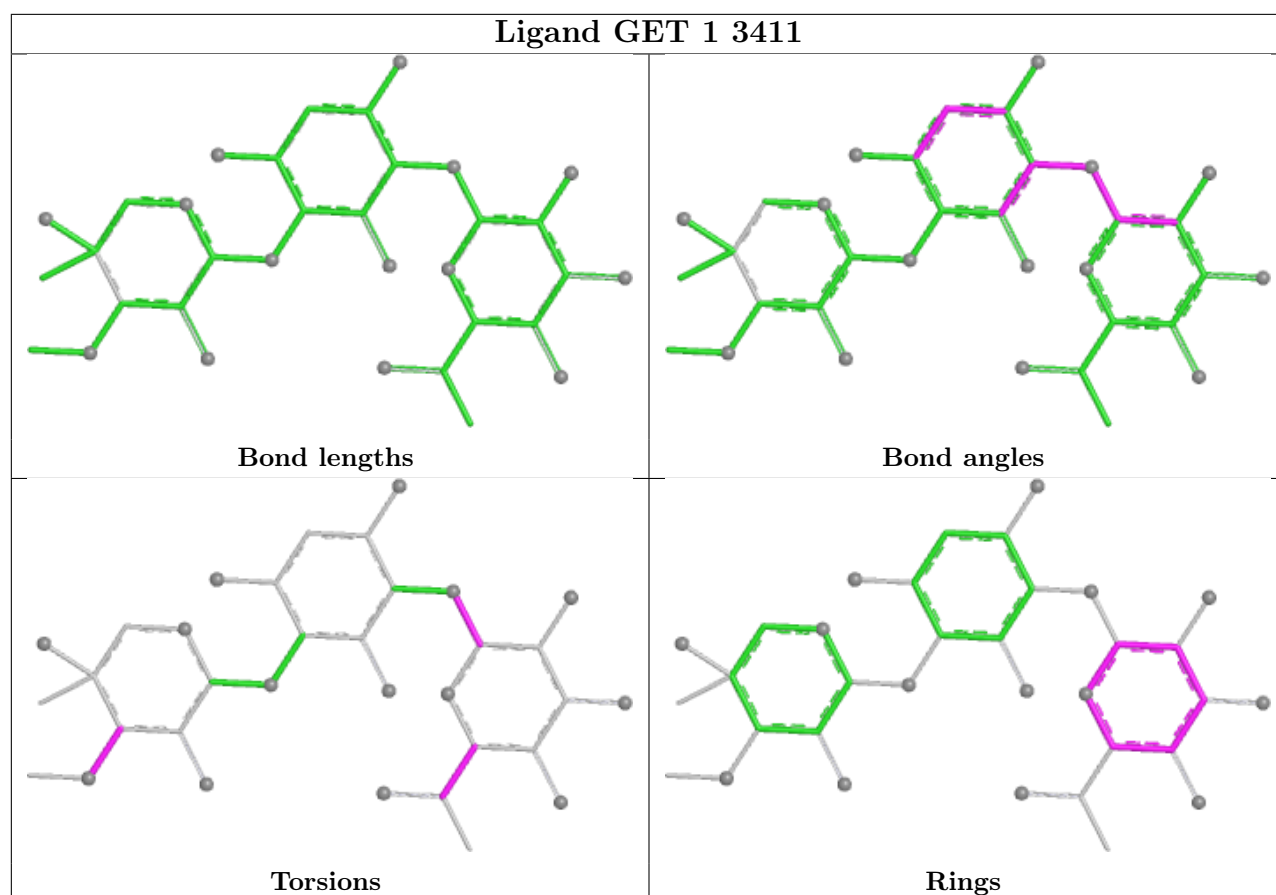


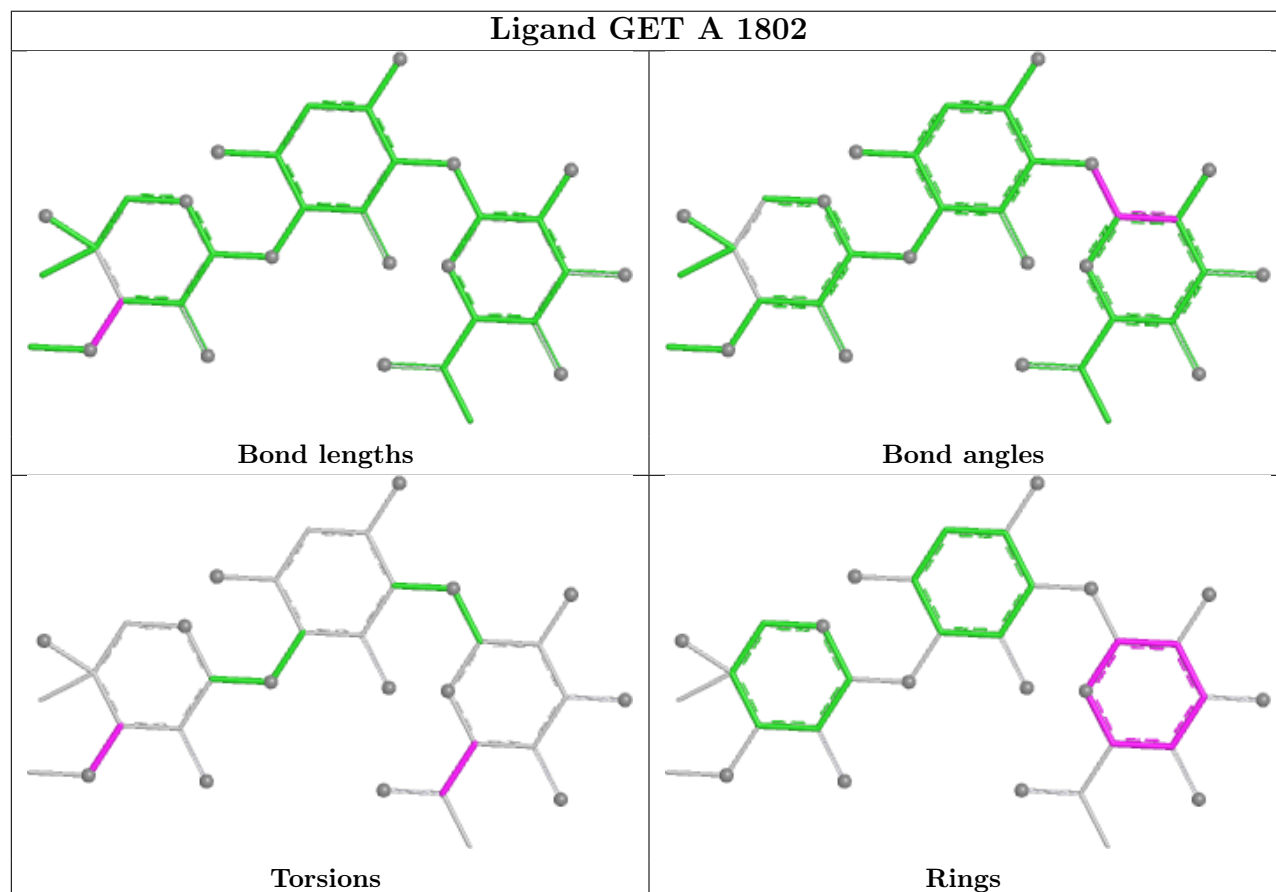
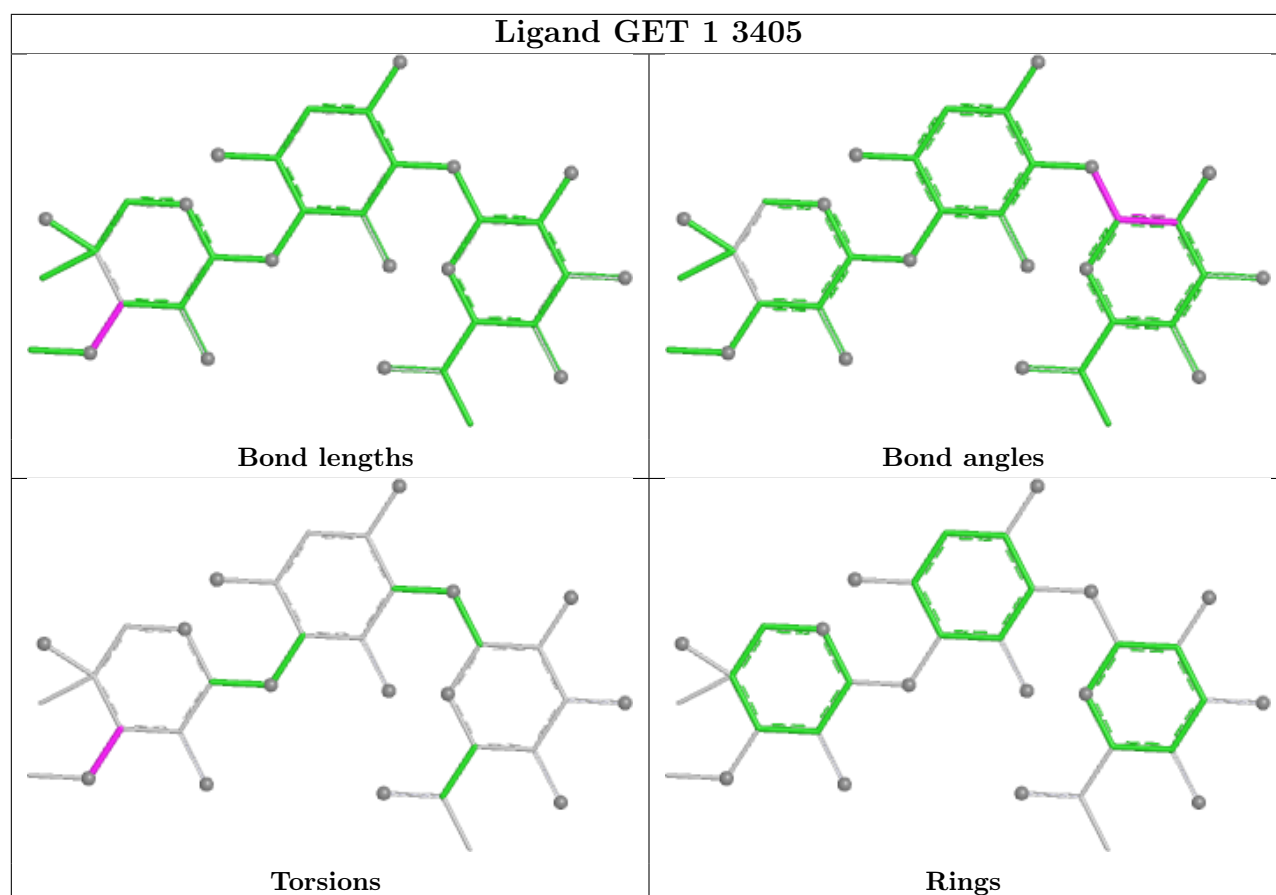


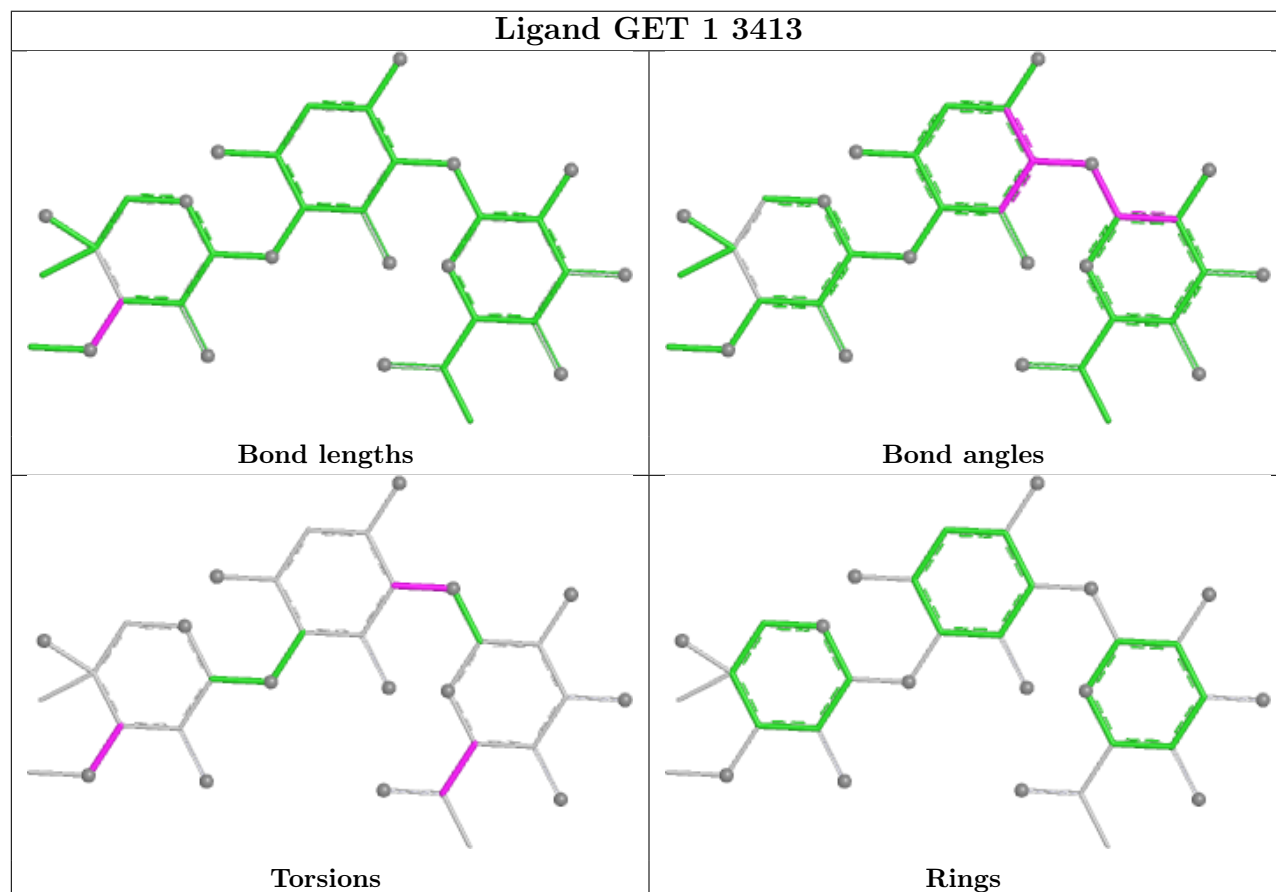
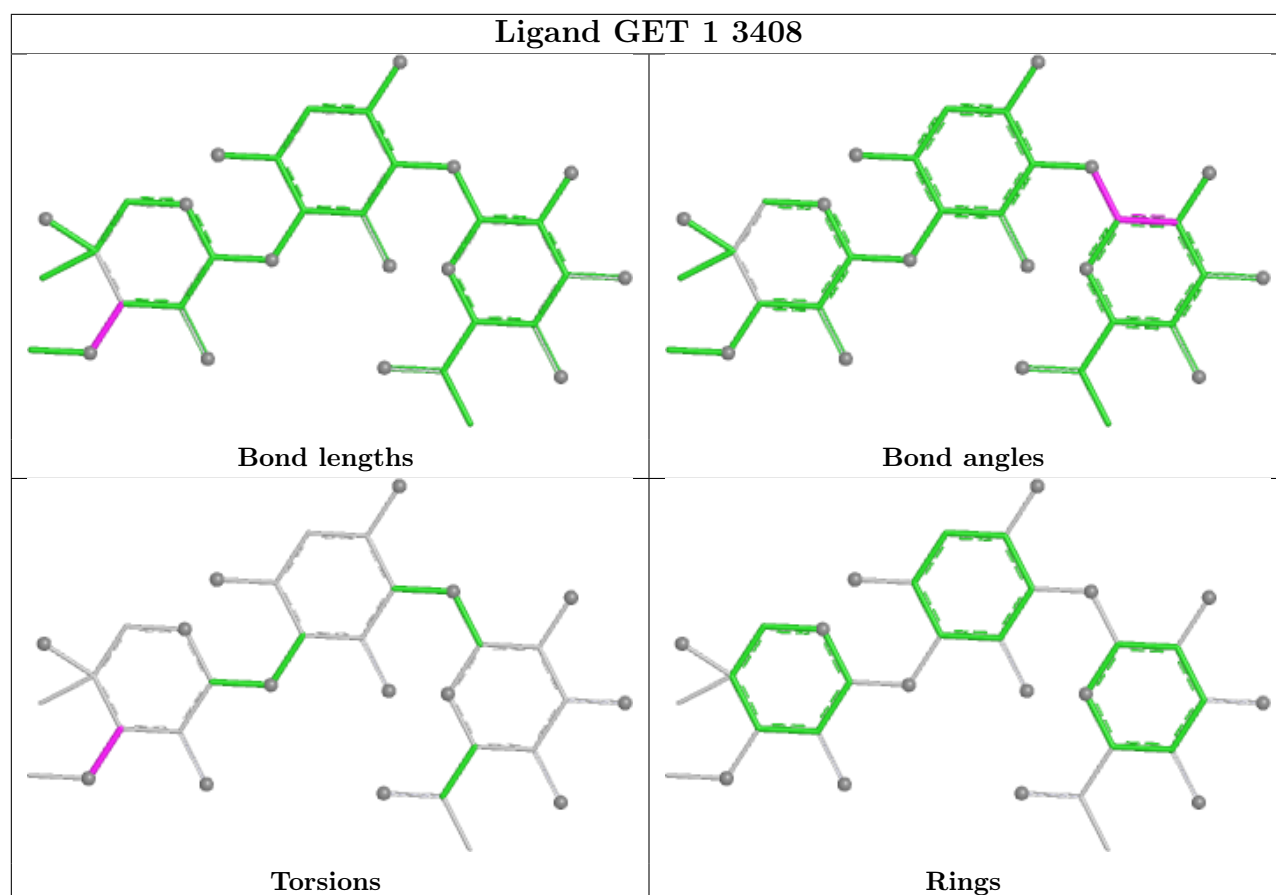


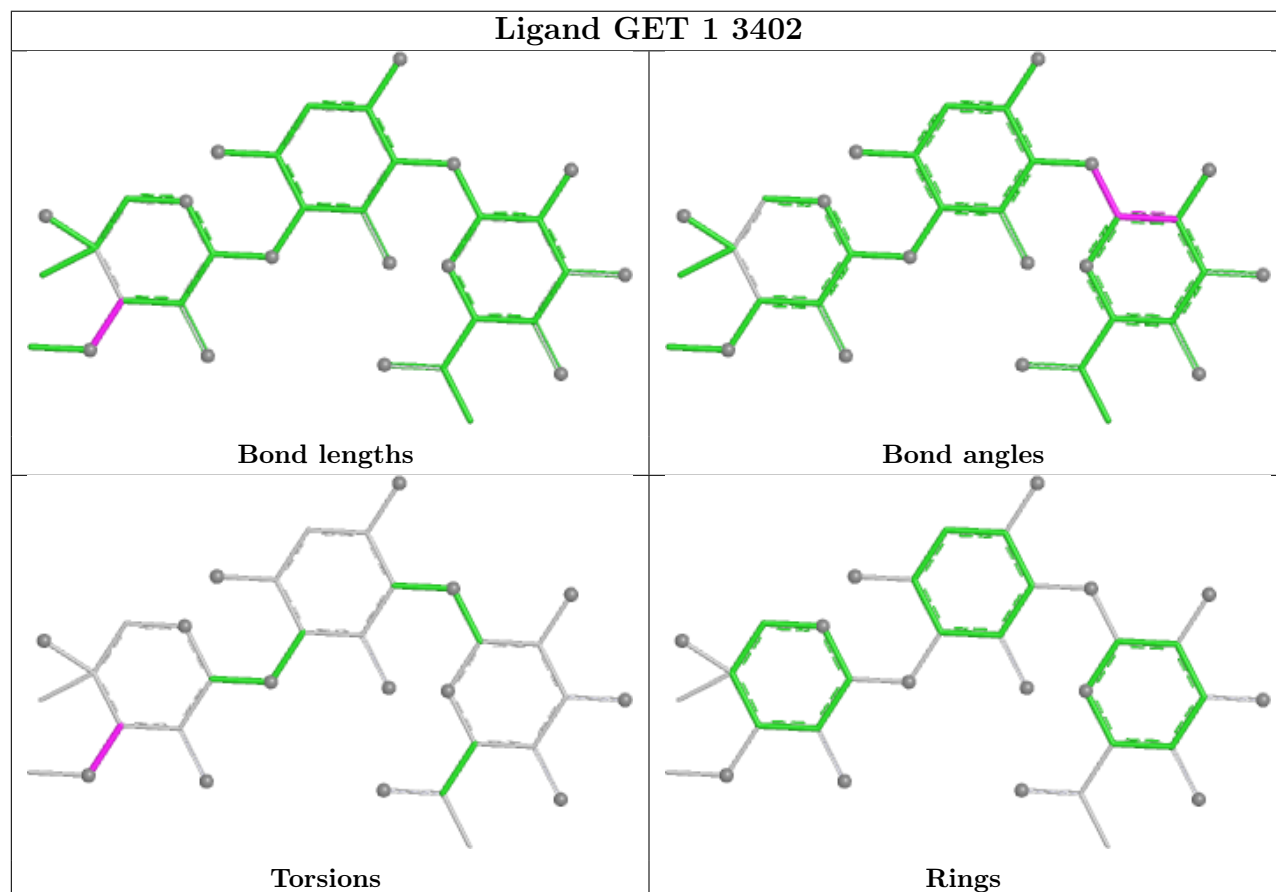
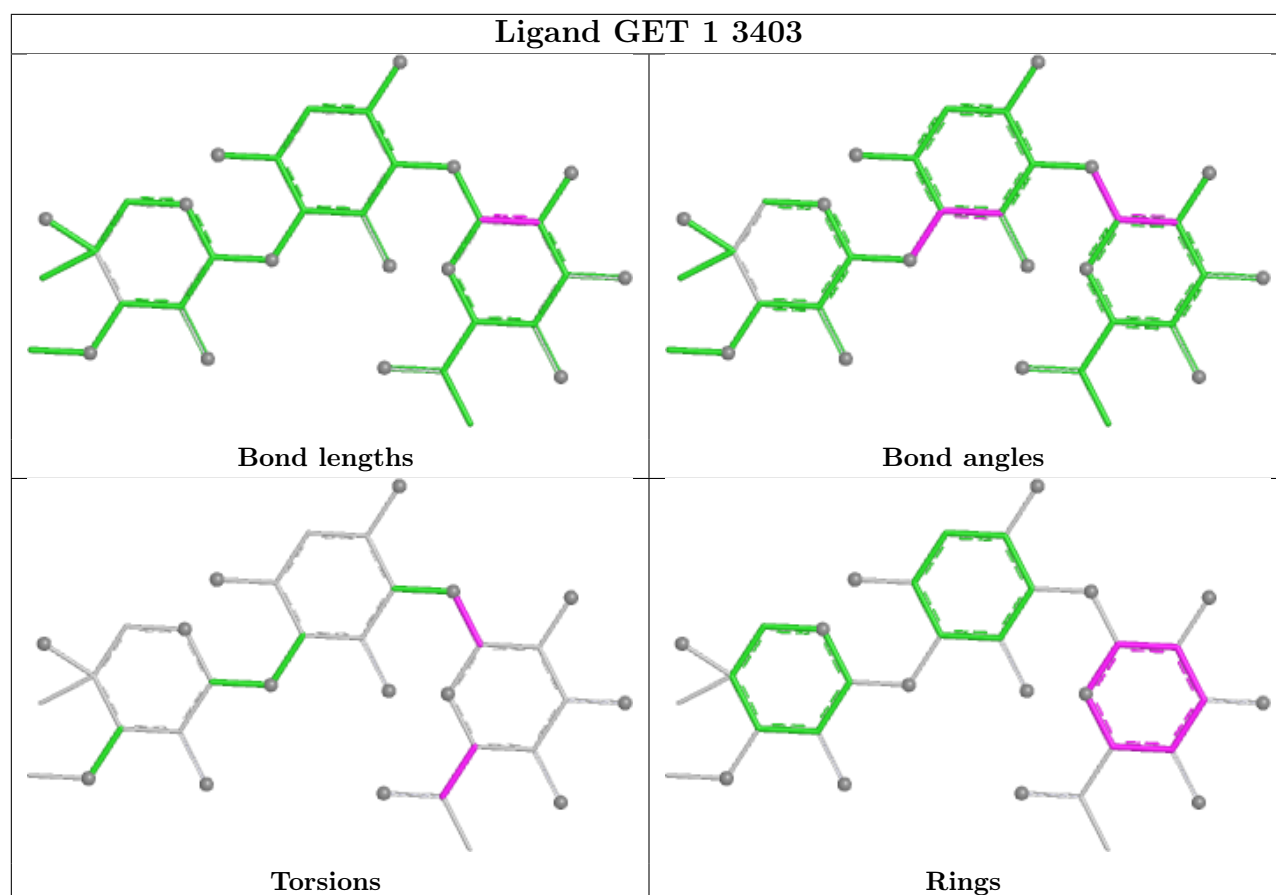












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

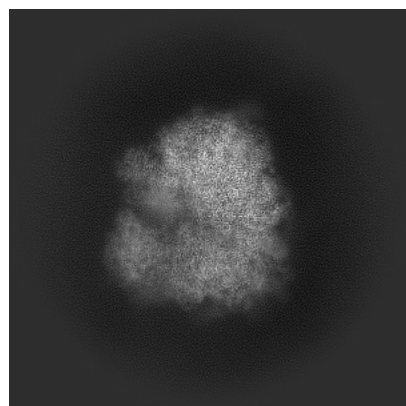
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-50990. These allow visual inspection of the internal detail of the map and identification of artifacts.

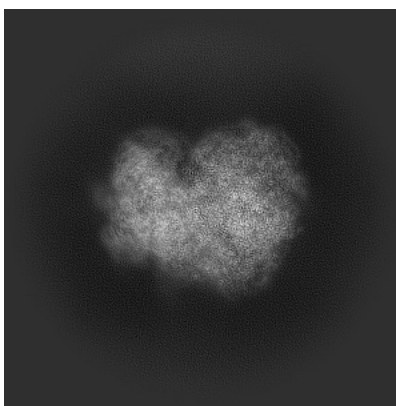
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

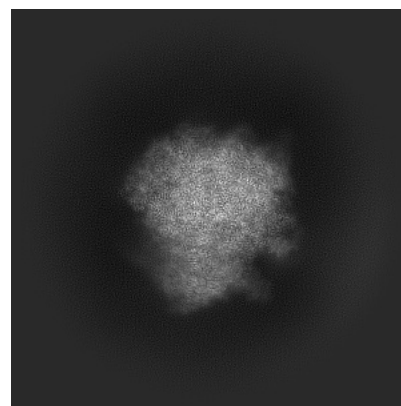
6.1.1 Primary map



X

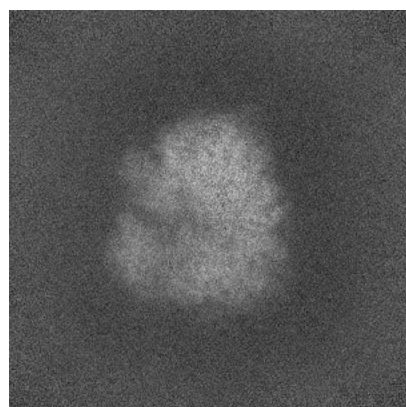


Y

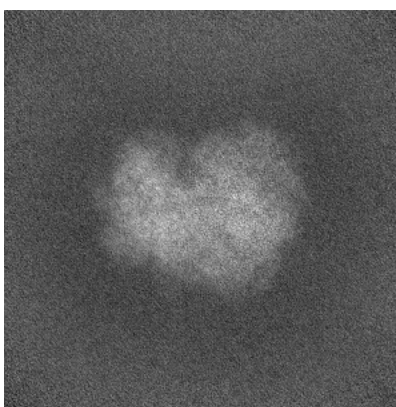


Z

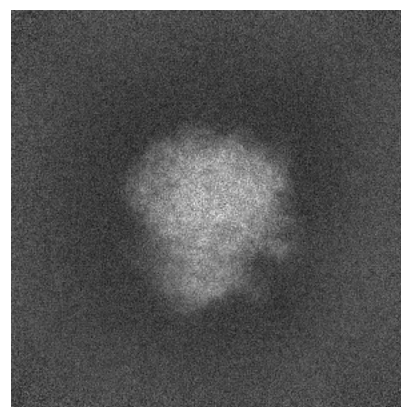
6.1.2 Raw map



X



Y

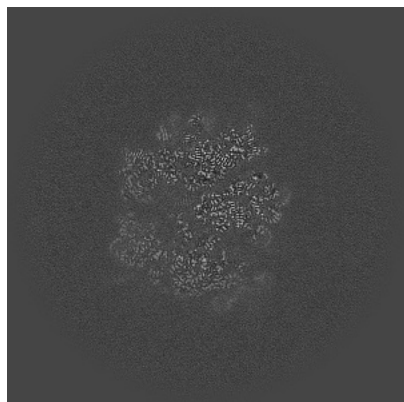


Z

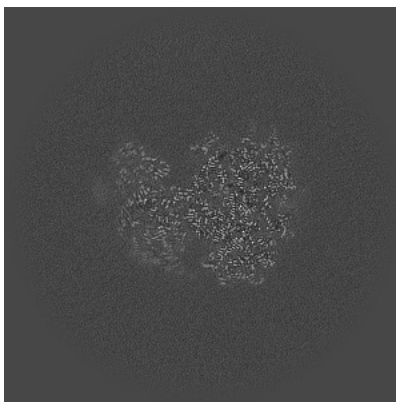
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

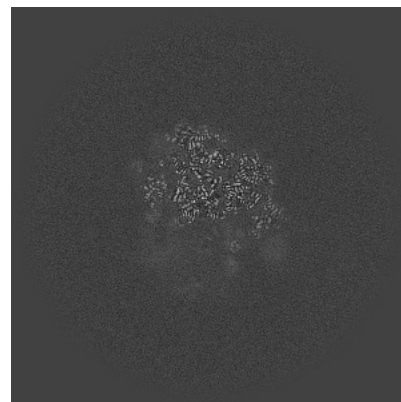
6.2.1 Primary map



X Index: 350

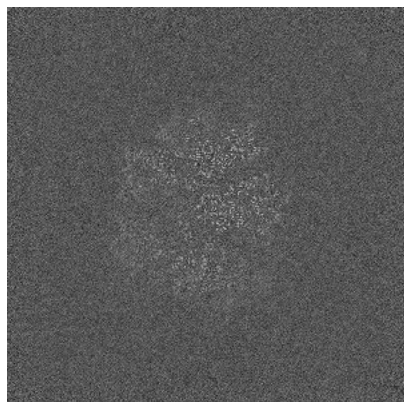


Y Index: 350

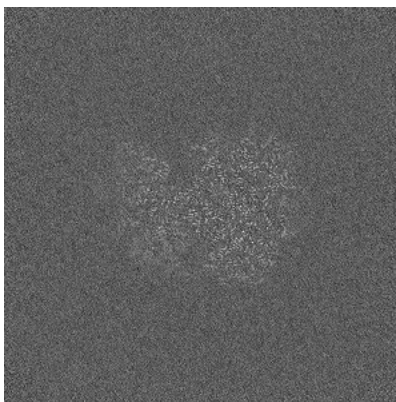


Z Index: 350

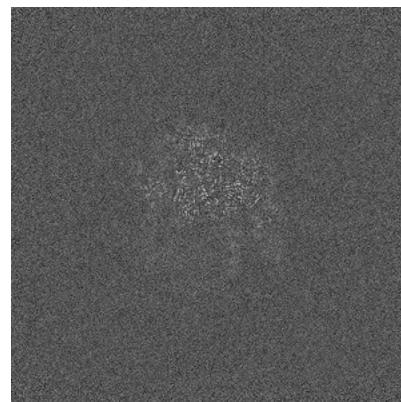
6.2.2 Raw map



X Index: 350



Y Index: 350

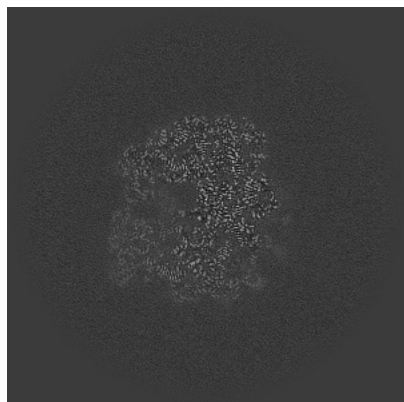


Z Index: 350

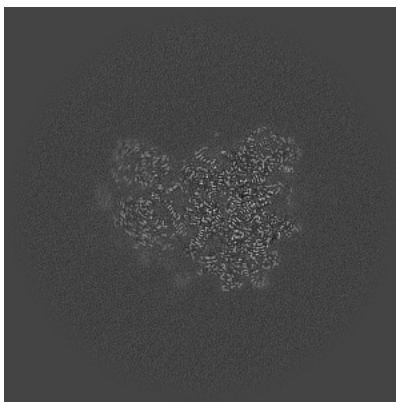
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

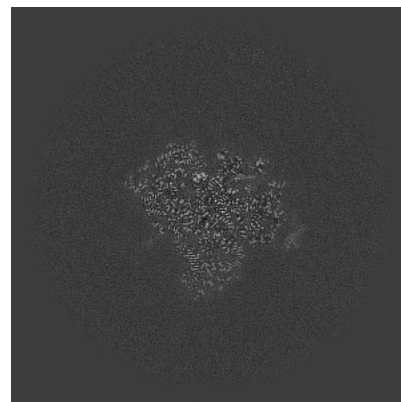
6.3.1 Primary map



X Index: 330

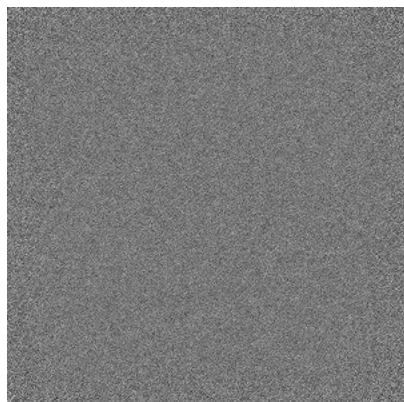


Y Index: 363

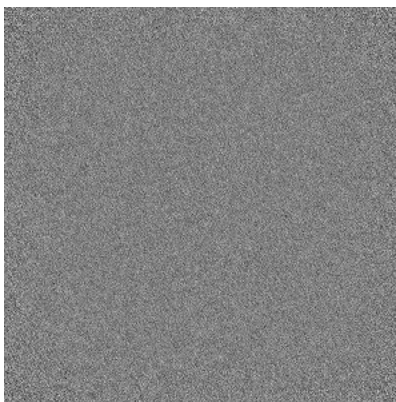


Z Index: 423

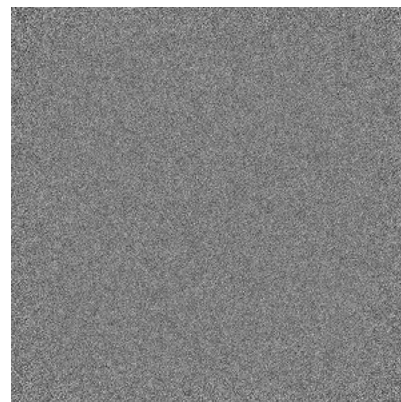
6.3.2 Raw map



X Index: 0



Y Index: 0

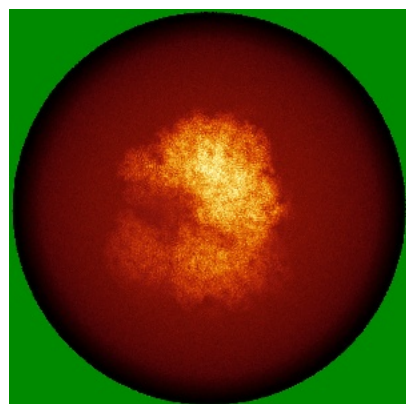


Z Index: 0

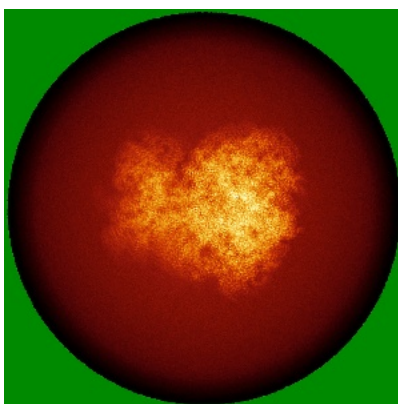
The images above show the largest variance slices of the map in three orthogonal directions.

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

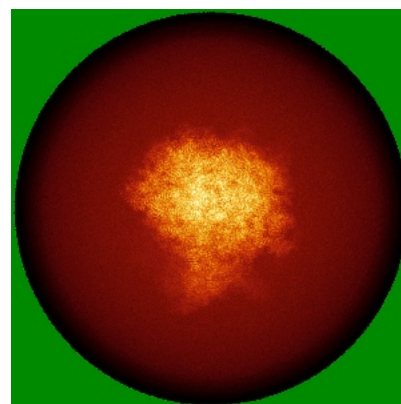
6.4.1 Primary map



X

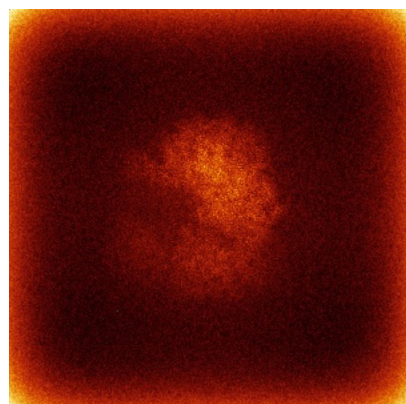


Y

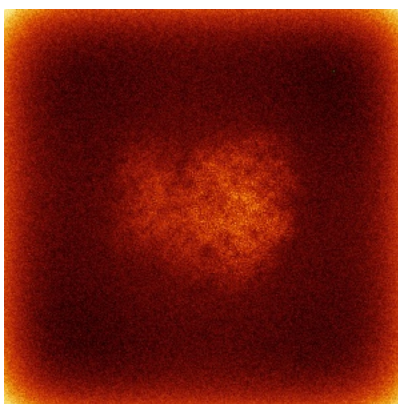


Z

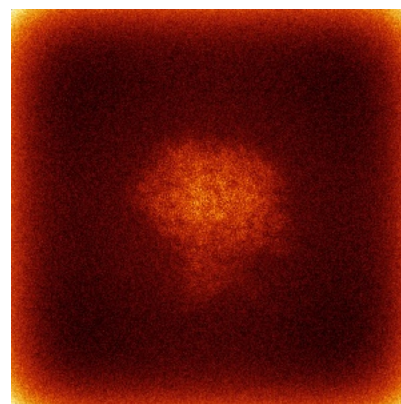
6.4.2 Raw map



X



Y

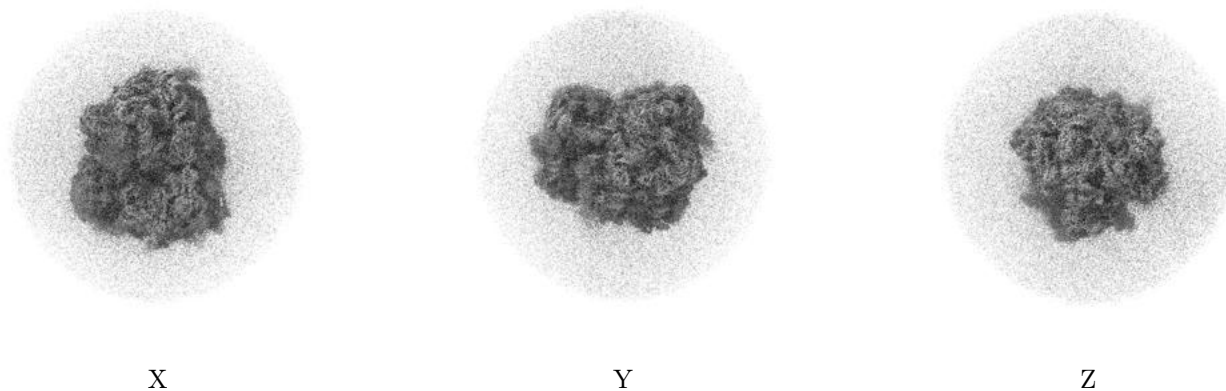


Z

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

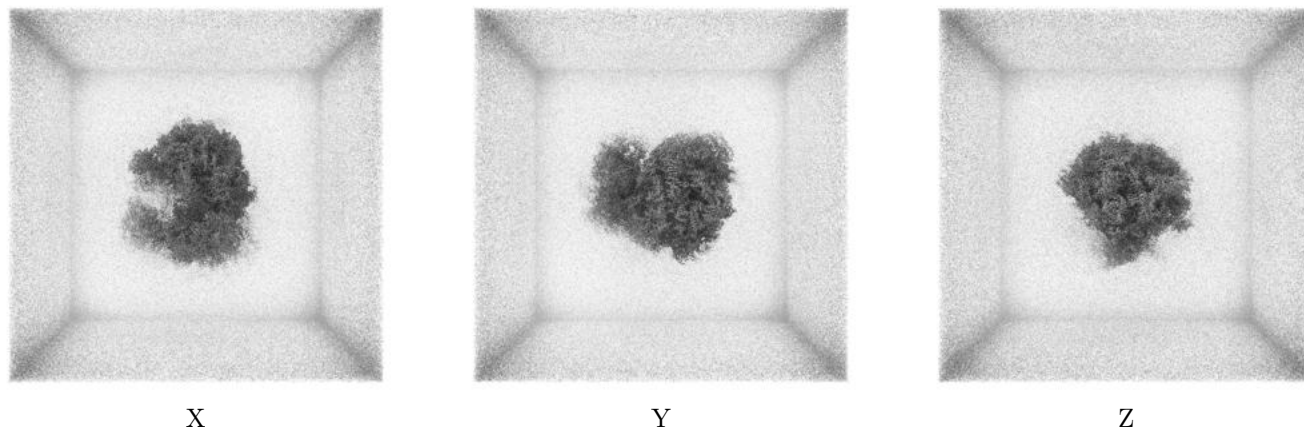
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.168. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

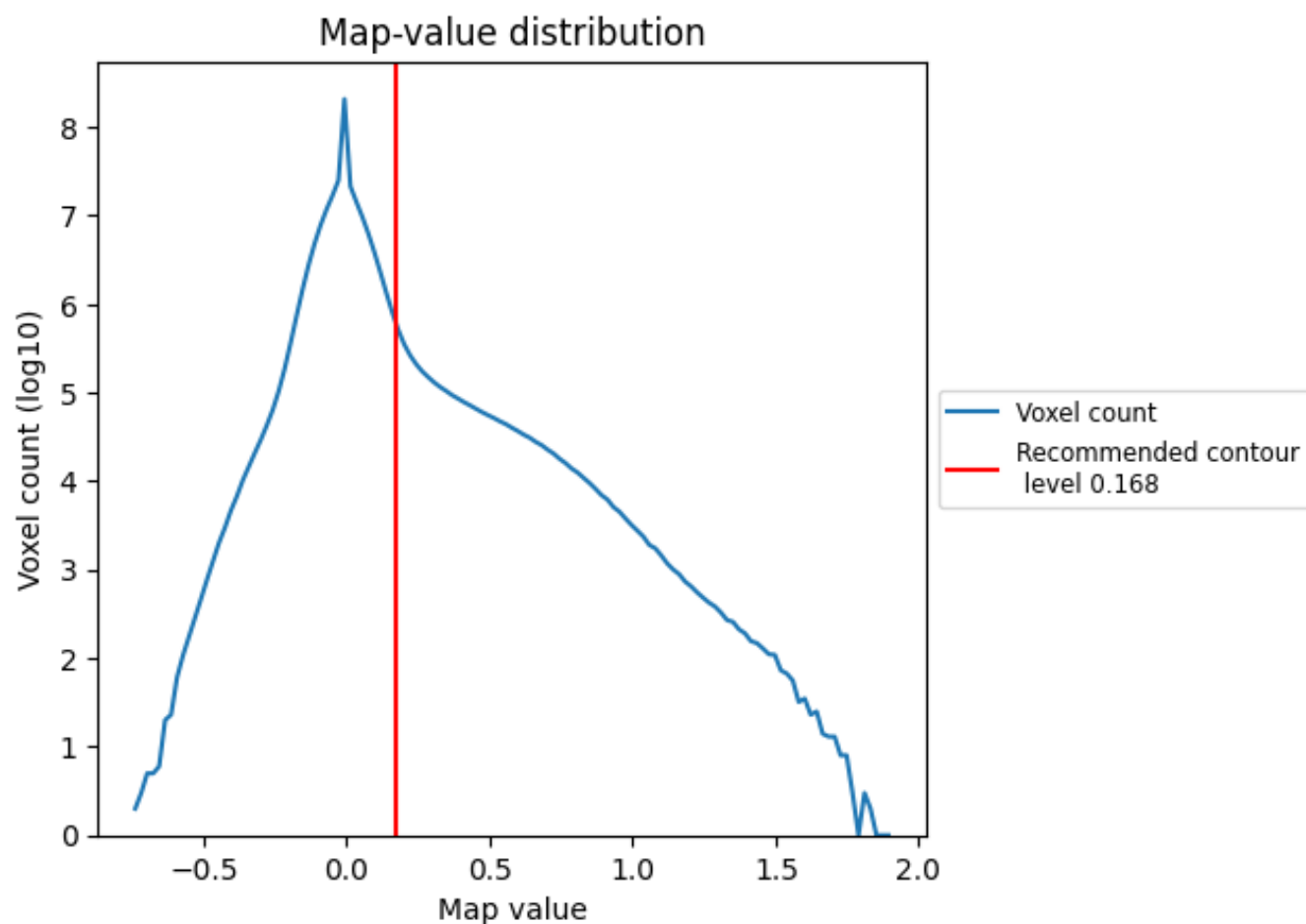
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

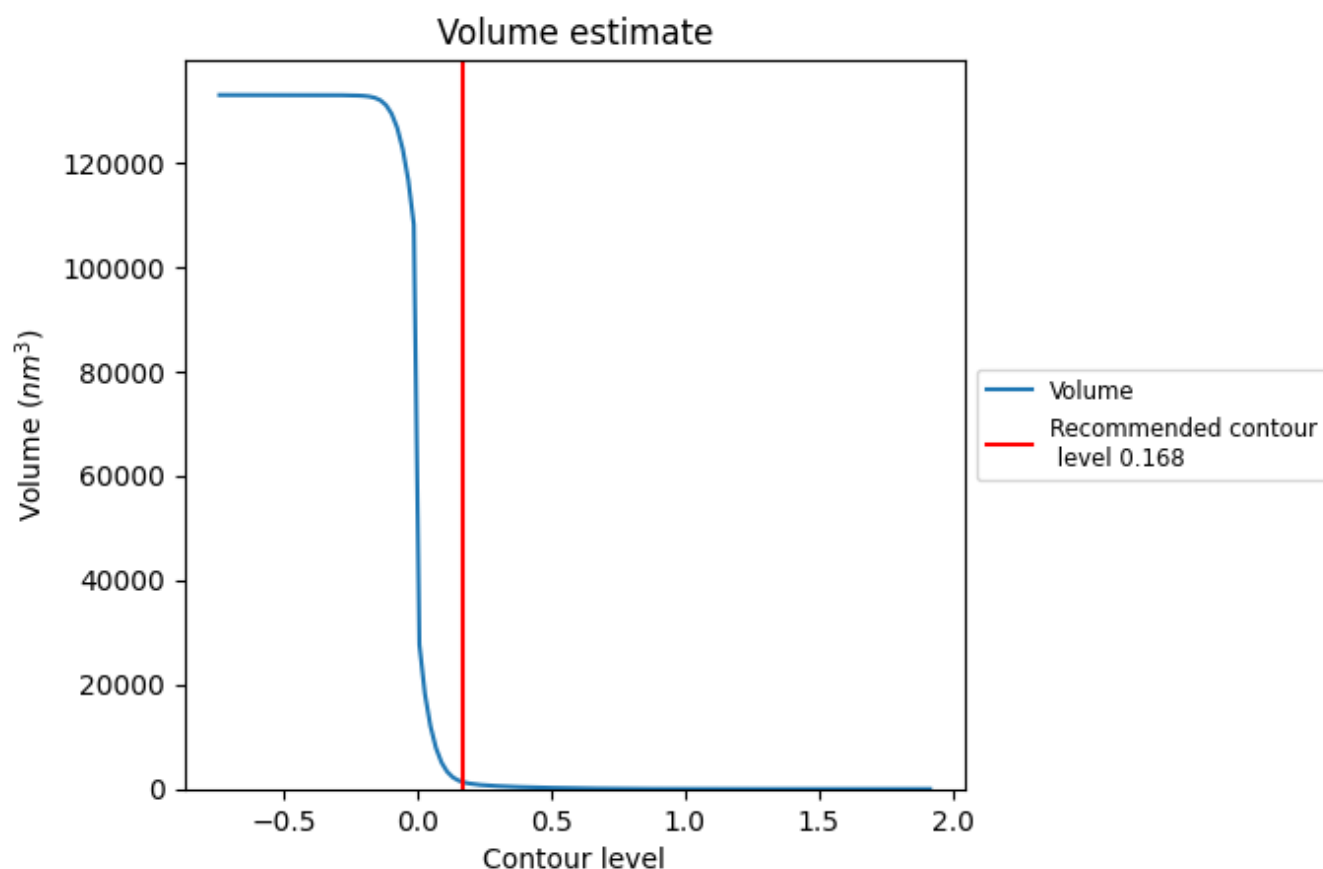
This section contains the results of statistical analysis of the map.

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.

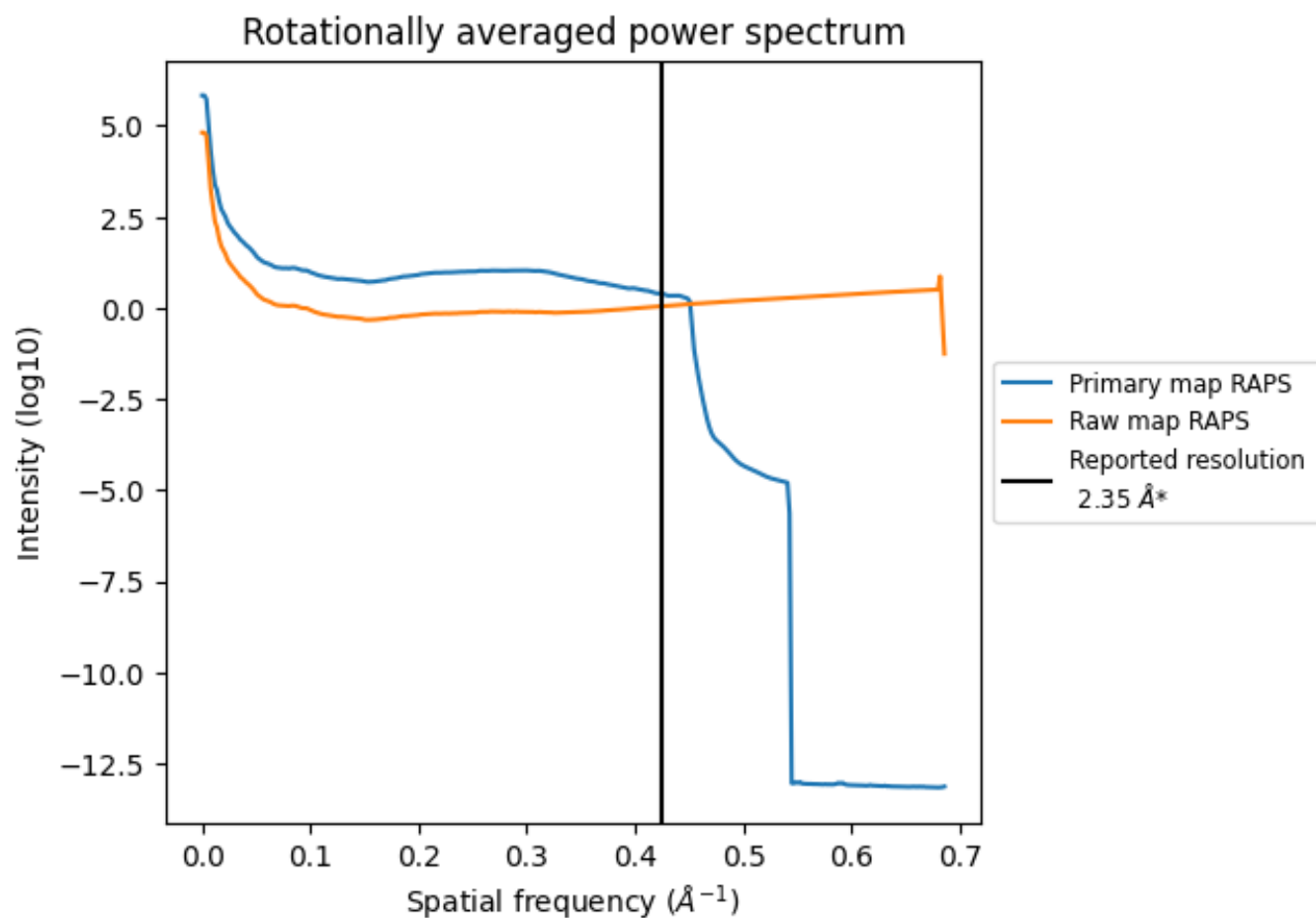
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1357 nm³; this corresponds to an approximate mass of 1225 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 ⓘ

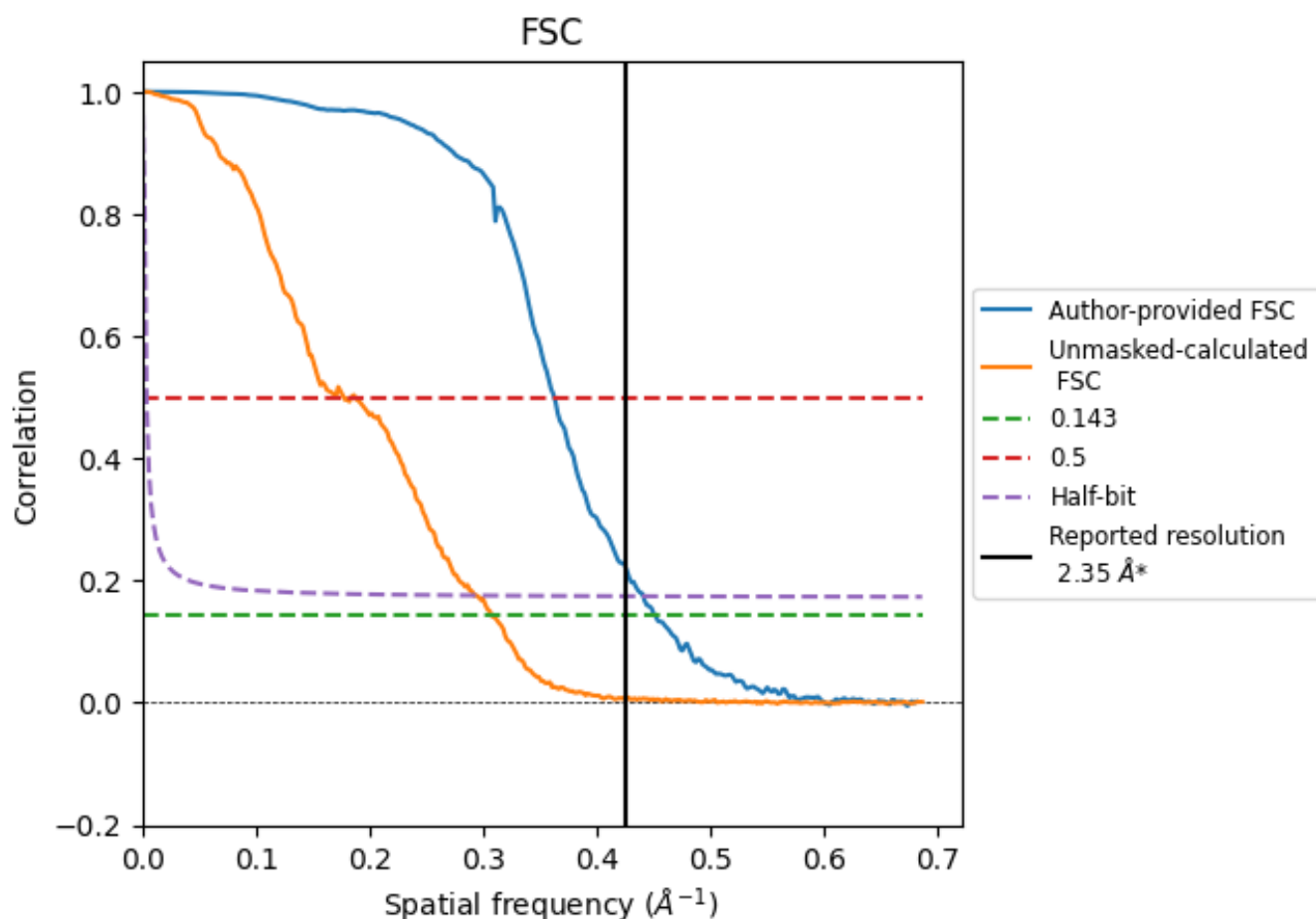


*Reported resolution corresponds to spatial frequency of 0.426 Å⁻¹

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 $0.426 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

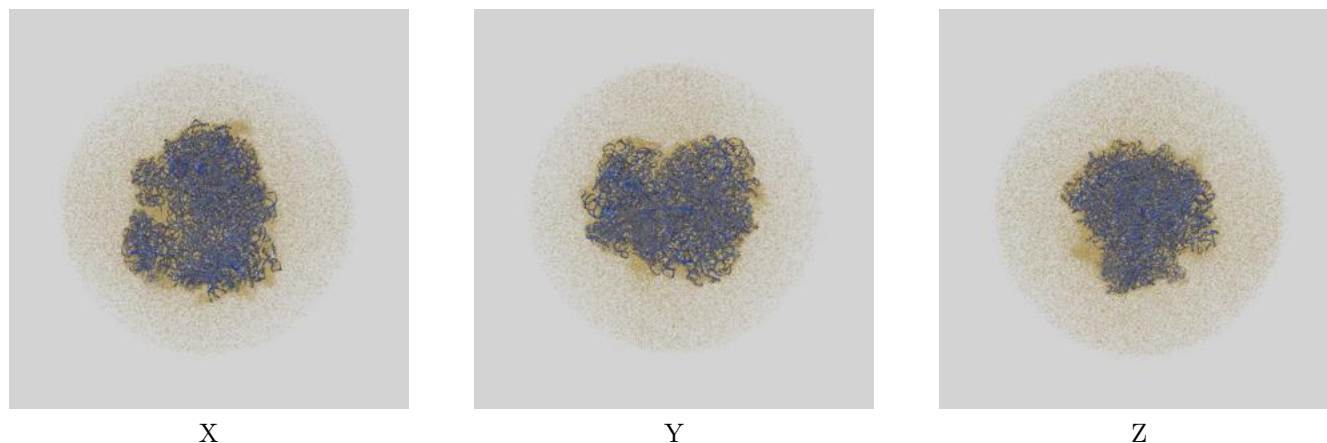
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.35	-	-
Author-provided FSC curve	2.22	2.76	2.27
Unmasked-calculated*	3.26	5.65	3.42

*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 3.26 differs from the reported value 2.35 by more than 10 %

9 Map-model fit [i](#)

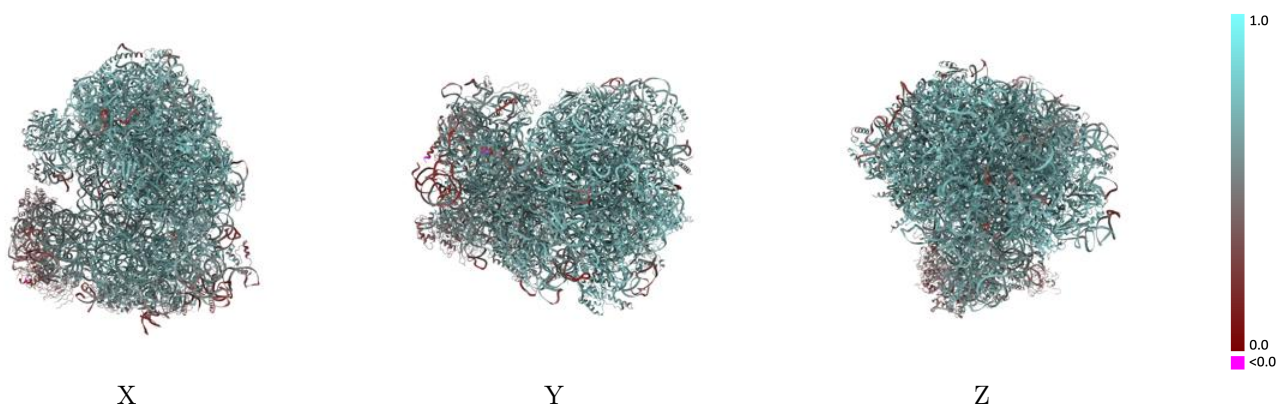
This section contains information regarding the fit between EMDB map EMD-50990 and PDB model 9G30. Per-residue inclusion information can be found in [section 3](#) on [page 21](#).

9.1 Map-model overlay [i](#)



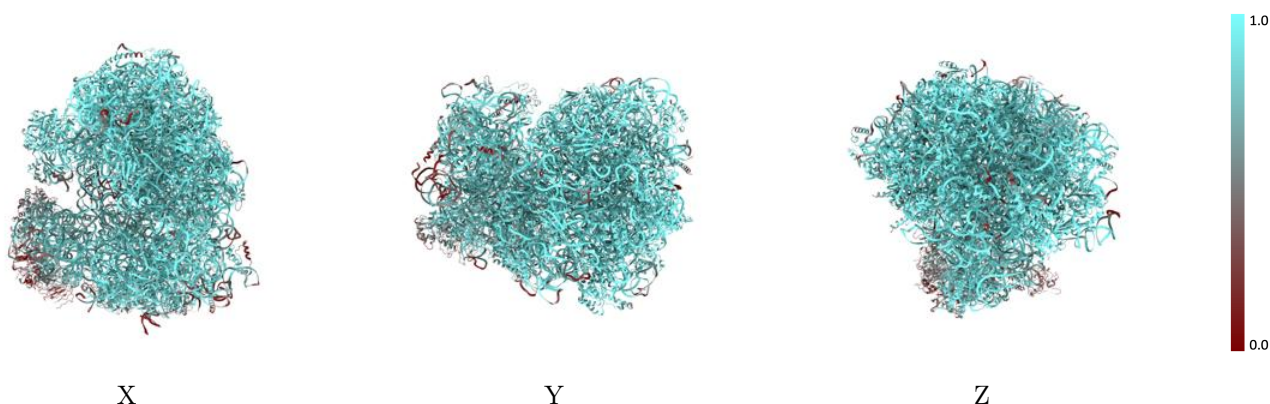
The images above show the 3D surface view of the map at the recommended contour level 0.168 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



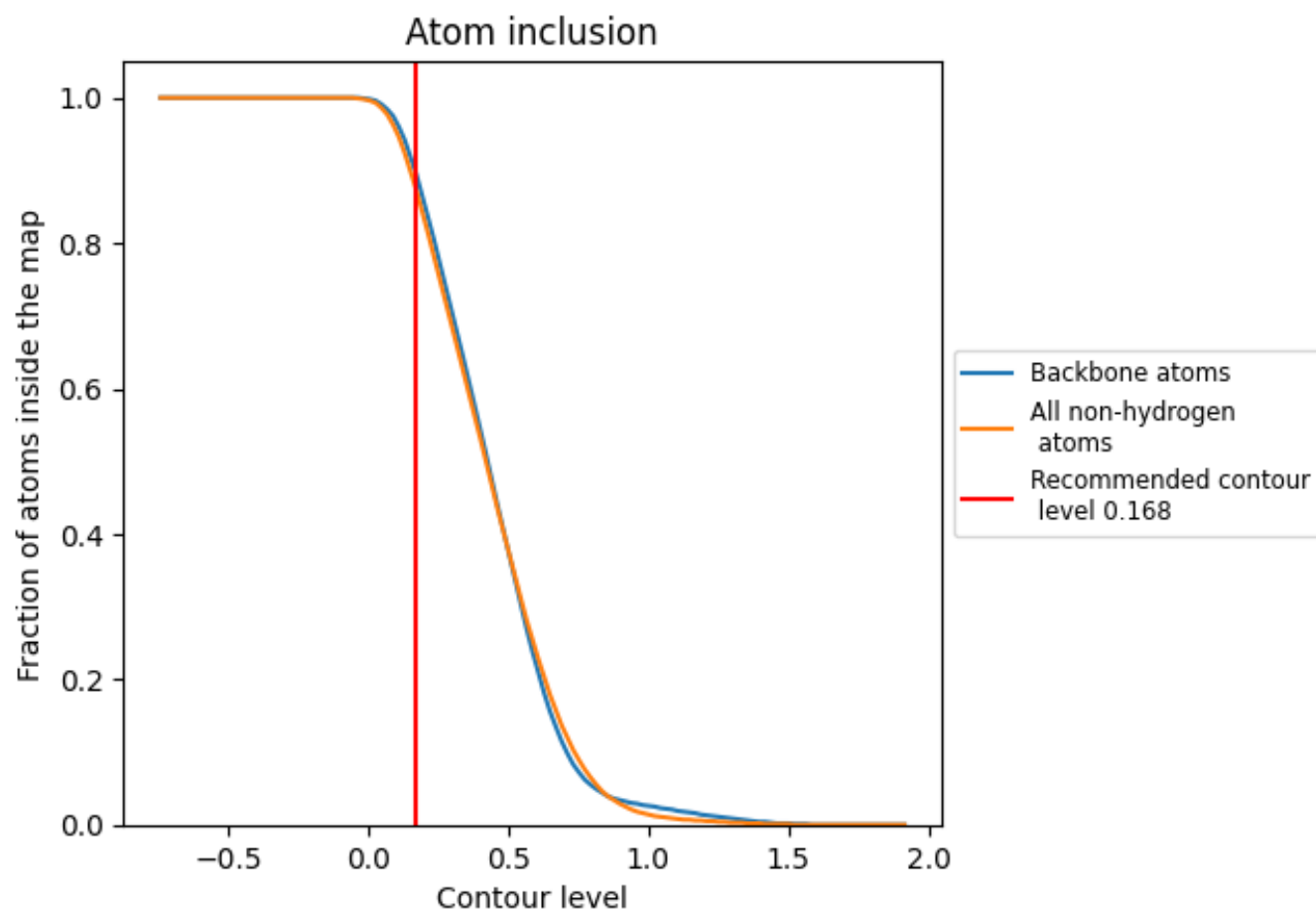
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.168).

9.4 Atom inclusion ⓘ



At the recommended contour level, 90% of all backbone atoms, 88% 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 (0.168) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8790	 0.6160
0	 0.9600	 0.6850
1	 0.9570	 0.6650
2	 0.9260	 0.6640
3	 0.9770	 0.6540
4	 0.9740	 0.6740
6	 0.9720	 0.7010
7	 0.9620	 0.6850
8	 0.9570	 0.6810
9	 0.9540	 0.6790
A	 0.8710	 0.5700
AA	 0.9130	 0.6470
AB	 0.9760	 0.7070
AC	 0.9290	 0.6550
AD	 0.9090	 0.6490
AE	 0.9140	 0.6650
AF	 0.9640	 0.6940
AG	 0.9730	 0.7010
AH	 0.9170	 0.6570
AI	 0.9330	 0.6530
AJ	 0.9050	 0.6300
AK	 0.9720	 0.7060
AL	 0.8080	 0.5710
AM	 0.9690	 0.6850
AN	 0.9210	 0.6640
AO	 0.7210	 0.5730
AP	 0.9030	 0.6540
AQ	 0.9200	 0.6700
AT	 0.6960	 0.5050
B	 0.7420	 0.5250
C	 0.6900	 0.5010
D	 0.9010	 0.6200
E	 0.7080	 0.5160
F	 0.8590	 0.5750
G	 0.4900	 0.3920



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Chain	Atom inclusion	Q-score
H	 0.7640	 0.5380
I	 0.6160	 0.4840
J	 0.8550	 0.6120
K	 0.8170	 0.5610
L	 0.5260	 0.4090
M	 0.9120	 0.6440
MR	 0.8010	 0.5640
N	 0.1660	 0.3040
O	 0.8790	 0.6090
P	 0.7570	 0.5390
PT	 0.5960	 0.5180
Q	 0.5650	 0.4570
R	 0.5670	 0.4080
S	 0.5630	 0.4390
T	 0.5750	 0.4290
U	 0.6230	 0.4500
V	 0.6050	 0.4400
W	 0.7960	 0.5530
X	 0.9310	 0.6350
Y	 0.9530	 0.6720
Z	 0.7830	 0.5290
a	 0.3350	 0.3540
b	 0.8330	 0.5690
c	 0.7430	 0.5330
d	 0.4480	 0.3740
e	 0.8970	 0.6140
f	 0.7230	 0.5350
g	 0.2610	 0.3350
h	 0.1540	 0.3000
j	 0.9720	 0.7030
k	 0.9590	 0.6940
l	 0.9400	 0.6790
m	 0.8780	 0.6160
n	 0.9090	 0.6310
o	 0.9410	 0.6830
p	 0.9130	 0.6510
q	 0.9210	 0.6500
r	 0.9210	 0.6620
s	 0.7320	 0.5150
t	 0.9280	 0.6620
u	 0.9410	 0.6620
v	 0.9900	 0.7140

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Chain	Atom inclusion	Q-score
w	 0.9550	 0.6930
x	 0.9490	 0.6910
y	 0.9700	 0.6960
z	 0.8940	 0.6410