



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 11:33 PM UTC

PDB ID : 3J9M / pdb_00003j9m
EMDB ID : EMD-2876
Title : Structure of the human mitochondrial ribosome (class 1)
Authors : Amunts, A.; Brown, A.; Toots, J.; Scheres, S.H.; Ramakrishnan, V.
Deposited on : 2015-02-08
Resolution : 3.50 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

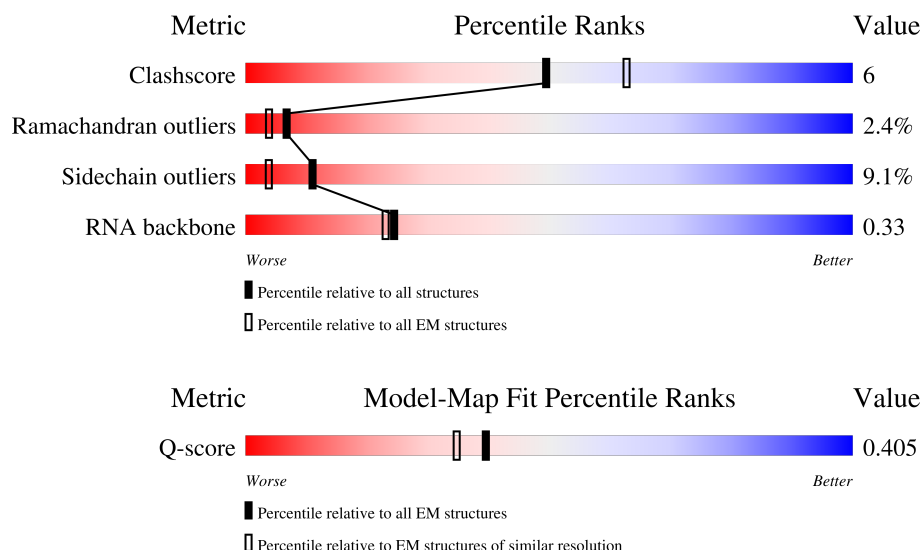
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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.



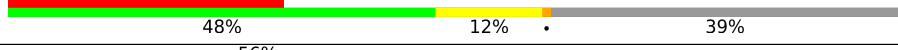
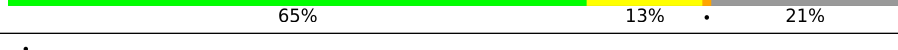
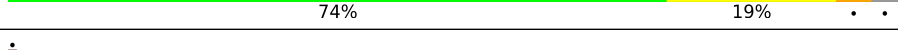
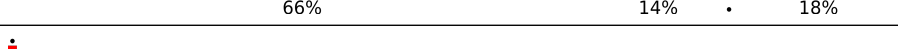
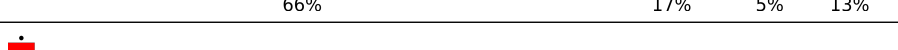
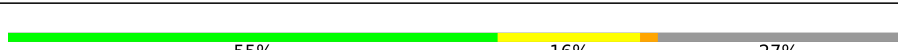
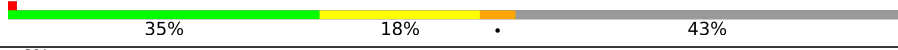
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	A	1559	
2	B	73	
3	D	305	

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Mol	Chain	Length	Quality of chain
4	E	348	
5	F	311	
6	H	267	
7	I	261	
8	J	192	
9	K	178	
10	L	145	
11	M	296	
12	N	251	
13	O	175	
14	P	179	
15	Q	292	
16	R	149	
17	S	205	
18	T	212	
19	U	153	
20	V	216	
21	W	148	
22	X	256	
23	Y	250	
24	Z	161	
25	0	188	
26	1	65	
27	2	92	
28	3	188	

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Mol	Chain	Length	Quality of chain
29	4	103	
30	5	423	
31	6	380	
32	7	338	
33	8	206	
34	9	137	
35	a	142	
36	b	155	
37	c	332	
38	d	306	
39	e	279	
40	f	194	
41	g	166	
42	h	158	
43	i	128	
44	j	123	
45	k	112	
46	l	138	
47	m	128	
48	o	102	
49	p	206	
50	q	222	
51	r	196	
52	s	439	
53	t	28	

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Mol	Chain	Length	Quality of chain
54	u	2	
55	AA	954	
56	AB	296	
57	AC	167	
58	AD	430	
59	AE	125	
60	AF	242	
61	AG	396	
62	AH	201	
63	AI	194	
64	AJ	138	
65	AK	128	
66	AL	257	
67	AM	137	
68	AN	130	
69	AO	258	
70	AP	142	
71	AQ	87	
72	AR	360	
73	AS	190	
74	AT	173	
75	AU	205	
76	AV	414	
77	AW	187	
78	AX	398	

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Mol	Chain	Length	Quality of chain
79	AY	395	
80	AZ	106	
81	A0	218	
82	A1	323	
83	A2	118	
84	A3	199	
85	A4	579	

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 158384 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1472	Total	C	N	O	P	0	0
			31261	14025	5642	10122	1472		

- Molecule 2 is a RNA chain called mt-tRNAVal.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	56	Total	C	N	O	P	0	0
			1191	534	214	387	56		

- Molecule 3 is a protein called uL2m.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	236	Total	C	N	O	S	0	0
			1842	1145	373	315	9		

- Molecule 4 is a protein called uL3m.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	300	Total	C	N	O	S	0	0
			2365	1523	410	422	10		

- Molecule 5 is a protein called uL4m.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	250	Total	C	N	O	S	0	0
			2013	1294	365	348	6		

- Molecule 6 is a protein called bL9m.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	H	95	Total	C	N	O	0	0
			784	498	152	134		

- Molecule 7 is a protein called uL10m.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	158	Total	C	N	O	S	0	0
			1283	828	235	210	10		

- Molecule 8 is a protein called uL11m.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	140	Total	C	N	O	S	0	0
			1061	680	192	187	2		

- Molecule 9 is a protein called uL13m.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	177	Total	C	N	O	S	0	0
			1451	934	259	251	7		

- Molecule 10 is a protein called uL14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	115	Total	C	N	O	S	0	0
			889	559	171	154	5		

- Molecule 11 is a protein called uL15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	287	Total	C	N	O	S	0	0
			2305	1472	425	402	6		

- Molecule 12 is a protein called uL16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	205	Total	C	N	O	S	0	0
			1654	1056	308	280	10		

- Molecule 13 is a protein called bL17m.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O	152	Total	C	N	O	S	0	0
			1245	784	239	215	7		

- Molecule 14 is a protein called uL18m.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P	133	Total	C	N	O	S	0	0
			1080	677	209	189	5		

- Molecule 15 is a protein called bL19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q	219	Total	C	N	O	S	0	0
			1822	1168	322	323	9		

- Molecule 16 is a protein called bL20m.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	R	140	Total	C	N	O	S	0	0
			1153	732	231	186	4		

- Molecule 17 is a protein called bL21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	S	156	Total	C	N	O	S	0	0
			1251	806	222	219	4		

- Molecule 18 is a protein called uL22m.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	166	Total	C	N	O	S	0	0
			1368	875	254	232	7		

- Molecule 19 is a protein called uL23m.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	U	111	Total	C	N	O	S	0	0
			922	591	176	153	2		

- Molecule 20 is a protein called uL24m.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	189	Total	C	N	O	S	0	0
			1551	987	278	278	8		

- Molecule 21 is a protein called bL27m.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	111	Total	C	N	O	S	0	0
			871	558	164	146	3		

- Molecule 22 is a protein called bL28m.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	243	Total	C	N	O	S	0	0
			2027	1310	350	362	5		

- Molecule 23 is a protein called uL29m.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	176	Total	C	N	O	S	0	0
			1517	970	291	252	4		

- Molecule 24 is a protein called uL30m.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	120	Total	C	N	O	S	0	0
			978	626	183	166	3		

- Molecule 25 is a protein called bL32m.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	0	108	Total	C	N	O	S	0	0
			880	545	172	157	6		

- Molecule 26 is a protein called bL33m.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	1	52	Total	C	N	O	S	0	0
			433	278	83	70	2		

- Molecule 27 is a protein called bL34m.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	2	46	Total	C	N	O	S	0	0
			376	233	83	59	1		

- Molecule 28 is a protein called bL35m.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	3	95	Total	C	N	O	S	0	0
			831	539	162	127	3		

- Molecule 29 is a protein called bL36m.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	4	36	Total	C	N	O	S	0	0
			322	203	70	46	3		

- Molecule 30 is a protein called mL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	5	376	Total	C	N	O	S	0	0
			3064	1987	529	538	10		

- Molecule 31 is a protein called mL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	6	325	Total	C	N	O	S	0	0
			2636	1692	465	470	9		

- Molecule 32 is a protein called mL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	7	266	Total	C	N	O	S	0	0
			2158	1383	371	388	16		

- Molecule 33 is a protein called mL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	8	99	Total	C	N	O	S	0	0
			836	535	144	155	2		

- Molecule 34 is a protein called mL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	9	109	Total	C	N	O	S	0	0
			873	565	152	154	2		

- Molecule 35 is a protein called mL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	a	82	Total	C	N	O	S	0	0
			686	434	124	123	5		

- Molecule 36 is a protein called mL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	b	148	Total	C	N	O	S	0	0
			1178	733	229	213	3		

- Molecule 37 is a protein called mL44.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	c	275	Total	C	N	O	S	0	0
			2217	1415	383	410	9		

- Molecule 38 is a protein called mL45.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	d	162	Total	C	N	O	S	0	0
			1347	870	234	235	8		

- Molecule 39 is a protein called mL46.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	e	217	Total	C	N	O	S	0	0
			1762	1124	310	323	5		

- Molecule 40 is a protein called mL48.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	f	131	Total	C	N	O	S	0	0
			1039	663	169	203	4		

- Molecule 41 is a protein called mL49.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	g	129	Total	C	N	O	S	0	0
			1067	690	185	190	2		

- Molecule 42 is a protein called mL50.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	h	100	Total	C	N	O	S	0	0
			827	524	146	155	2		

- Molecule 43 is a protein called mL51.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	i	97	Total	C	N	O	S	0	0
			827	532	165	126	4		

- Molecule 44 is a protein called mL52.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	j	85	Total	C	N	O	S	0	0
			684	423	133	126	2		

- Molecule 45 is a protein called mL53.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	k	84	Total	C	N	O	S	0	0
			655	407	122	121	5		

- Molecule 46 is a protein called mL54.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	l	23	Total	C	N	O	0	0
			221	137	52	32		

- Molecule 47 is a protein called bL31m.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	m	45	Total	C	N	O	S	0	0
			372	232	76	62	2		

- Molecule 48 is a protein called mL63.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	o	94	Total	C	N	O	S	0	0
			797	501	165	128	3		

- Molecule 49 is a protein called mL62 (ICT1).

Mol	Chain	Residues	Atoms					AltConf	Trace
49	p	127	Total	C	N	O	S	0	0
			1058	661	201	192	4		

- Molecule 50 is a protein called mL64 (CRIF1).

Mol	Chain	Residues	Atoms					AltConf	Trace
50	q	128	Total	C	N	O	S	0	0
			1076	671	208	192	5		

- Molecule 51 is a protein called mL66 (bS18a).

Mol	Chain	Residues	Atoms					AltConf	Trace
51	r	146	Total	C	N	O	S	0	0
			1203	764	232	199	8		

- Molecule 52 is a protein called mL65 (mS30).

Mol	Chain	Residues	Atoms					AltConf	Trace
52	s	370	Total	C	N	O	S	0	0
			3036	1946	542	534	14		

- Molecule 53 is a protein called Unknown protein/protein extension.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	t	28	Total	C	N	O	0	0
			140	84	28	28		

- Molecule 54 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	u	2	Total	C	N	O	P	0	0
			42	19	8	13	2		

- Molecule 55 is a RNA chain called 12S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AA	923	Total	C	N	O	P	0	0
			19606	8790	3535	6358	923		

- Molecule 56 is a protein called uS2m.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AB	217	Total	C	N	O	S	0	0
			1768	1131	321	306	10		

- Molecule 57 is a protein called uS3m.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AC	132	Total	C	N	O	S	0	0
			1082	699	195	184	4		

- Molecule 58 is a protein called uS5m.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AD	322	Total	C	N	O	S	0	0
			2557	1611	476	457	13		

- Molecule 59 is a protein called bS6m.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AE	122	Total	C	N	O	S	0	0
			972	614	177	177	4		

- Molecule 60 is a protein called uS7m.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AF	201	Total	C	N	O	S	0	0
			1668	1069	305	283	11		

- Molecule 61 is a protein called uS9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AG	305	Total	C	N	O	S	0	0
			2516	1599	448	455	14		

- Molecule 62 is a protein called uS10m.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AH	122	Total	C	N	O	S	0	0
			999	643	168	185	3		

- Molecule 63 is a protein called uS11m.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AI	136	Total	C	N	O	S	0	0
			1011	637	192	178	4		

- Molecule 64 is a protein called uS12m.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AJ	108	Total	C	N	O	S	0	0
			838	521	169	142	6		

- Molecule 65 is a protein called uS14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AK	101	Total	C	N	O	S	0	0
			861	537	179	140	5		

- Molecule 66 is a protein called uS15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AL	164	Total	C	N	O	S	0	0
			1382	883	257	235	7		

- Molecule 67 is a protein called bS16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	AM	116	Total	C	N	O	S	0	0
			920	582	182	150	6		

- Molecule 68 is a protein called uS17m.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	AN	107	Total	C	N	O	S	0	0
			846	549	153	141	3		

- Molecule 69 is a protein called mS40 (bS18b).

Mol	Chain	Residues	Atoms					AltConf	Trace
69	AO	185	Total	C	N	O	S	0	0
			1528	970	285	267	6		

- Molecule 70 is a protein called bS18m (bS18c).

Mol	Chain	Residues	Atoms					AltConf	Trace
70	AP	96	Total	C	N	O	S	0	0
			774	498	133	135	8		

- Molecule 71 is a protein called bS21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AQ	86	Total	C	N	O	S	0	0
			740	458	150	124	8		

- Molecule 72 is a protein called mS22.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AR	242	Total	C	N	O	S	0	0
			2008	1285	343	372	8		

- Molecule 73 is a protein called mS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	AS	126	Total	C	N	O	S	0	0
			1042	673	183	185	1		

- Molecule 74 is a protein called mS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AT	162	Total	C	N	O	S	0	0
			1330	850	231	238	11		

- Molecule 75 is a protein called mS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AU	173	Total	C	N	O	S	0	0
			1461	900	294	263	4		

- Molecule 76 is a protein called mS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	AV	328	Total	C	N	O	S	0	0
			2702	1737	452	502	11		

- Molecule 77 is a protein called bS1m.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	AW	97	Total	C	N	O	S	0	0
			766	486	137	139	4		

- Molecule 78 is a protein called mS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	AX	316	Total	C	N	O	S	0	0
			2531	1625	440	455	11		

- Molecule 79 is a protein called mS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	AY	108	Total	C	N	O	S	0	0
			914	593	150	169	2		

- Molecule 80 is a protein called mS33.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	AZ	87	Total	C	N	O	S	0	0
			740	473	133	130	4		

- Molecule 81 is a protein called mS34.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	A0	201	Total	C	N	O	S	0	0
			1684	1065	322	292	5		

- Molecule 82 is a protein called mS35.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	A1	256	Total	C	N	O	S	0	0
			2076	1321	350	395	10		

- Molecule 83 is a protein called mS37.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	A2	116	Total	C	N	O	S	0	0
			925	574	181	162	8		

- Molecule 84 is a protein called mS38.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	A3	69	Total	C	N	O	S	0	0
			610	393	130	86	1		

- Molecule 85 is a protein called mS39.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	A4	414	Total	C	N	O	S	0	0
			2838	1805	490	529	14		

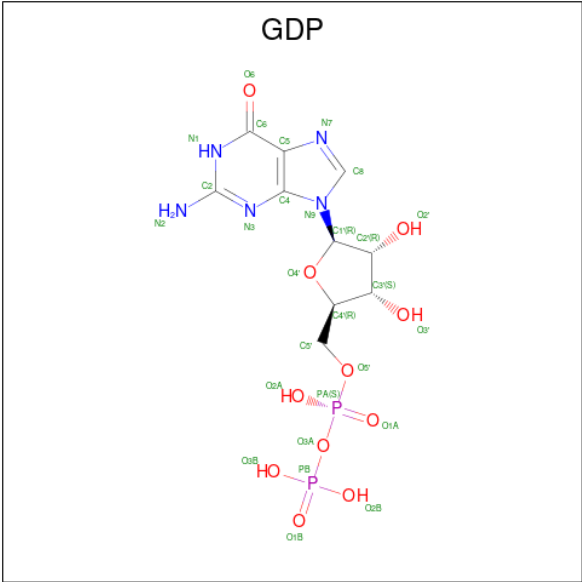
- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	A	97	Total	Mg	0
			97	97	
86	M	1	Total	Mg	0
			1	1	
86	g	1	Total	Mg	0
			1	1	
86	AA	28	Total	Mg	0
			28	28	

- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
87	0	1	Total	Zn	0
			1	1	
87	4	1	Total	Zn	0
			1	1	
87	r	1	Total	Zn	0
			1	1	
87	AB	1	Total	Zn	0
			1	1	
87	AO	1	Total	Zn	0
			1	1	
87	AP	1	Total	Zn	0
			1	1	
87	AT	1	Total	Zn	0
			1	1	

- Molecule 88 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).

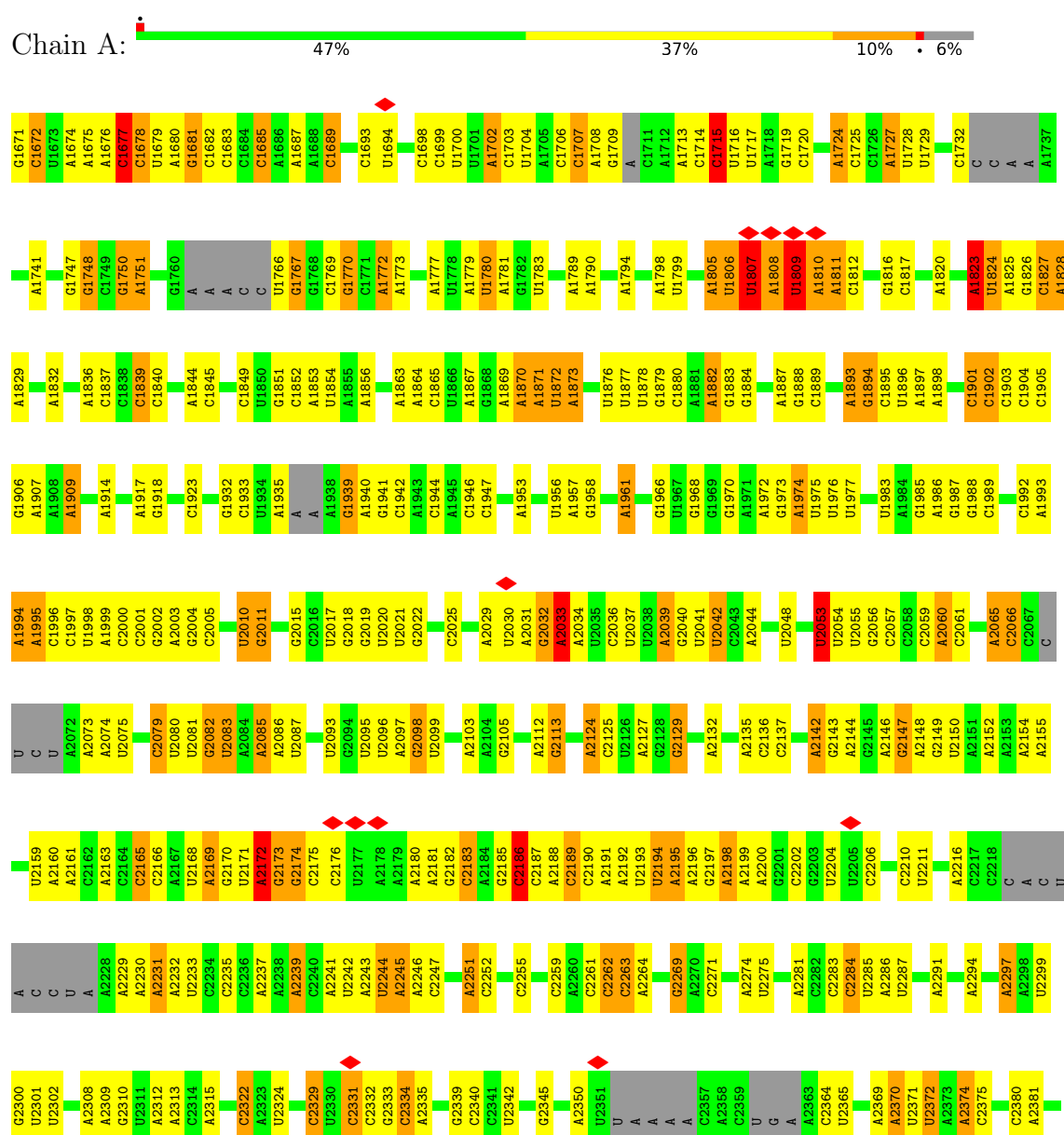


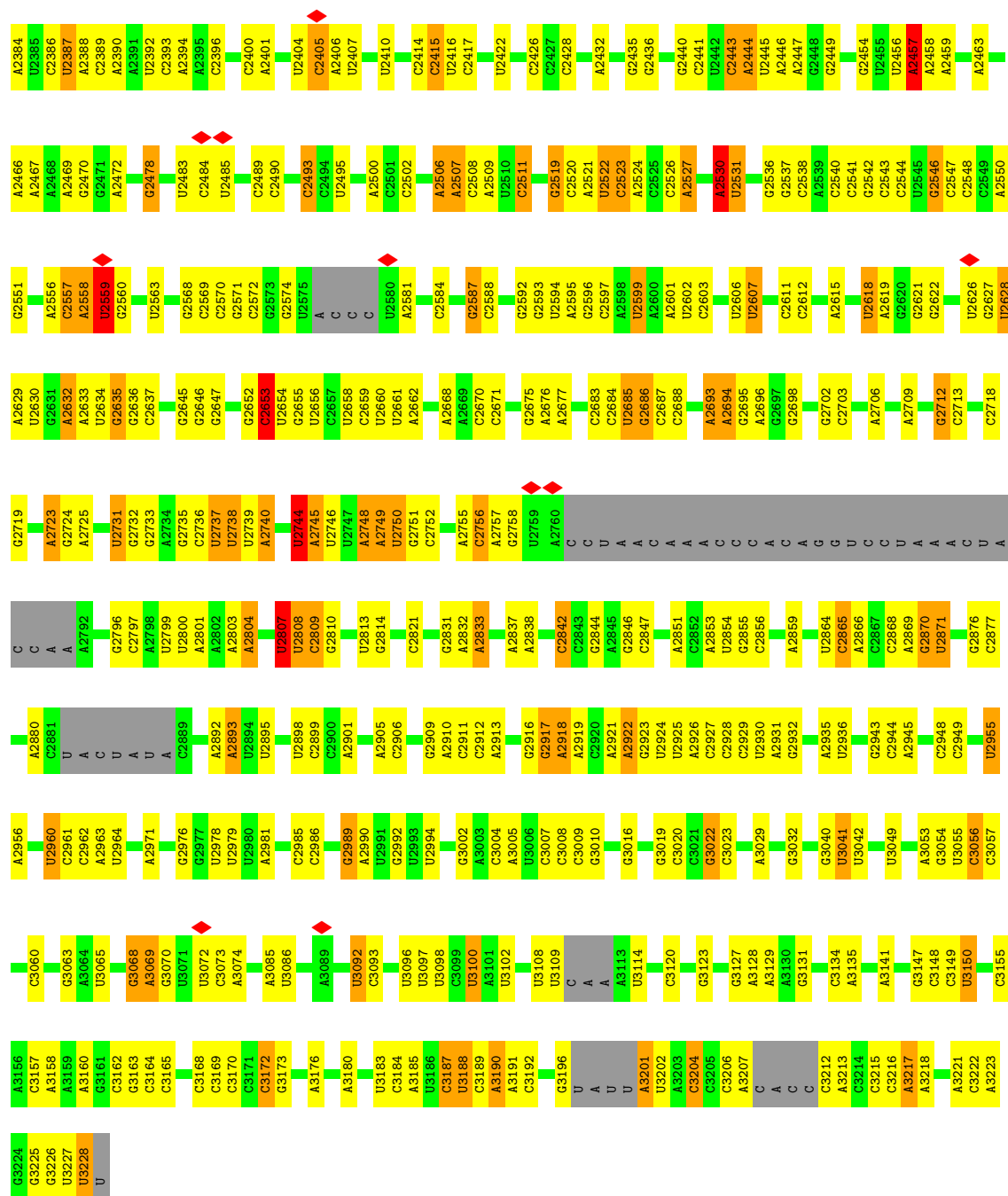
Mol	Chain	Residues	Atoms					AltConf
88	AX	1	Total	C	N	O	P	0
			28	10	5	11	2	

3 Residue-property plots

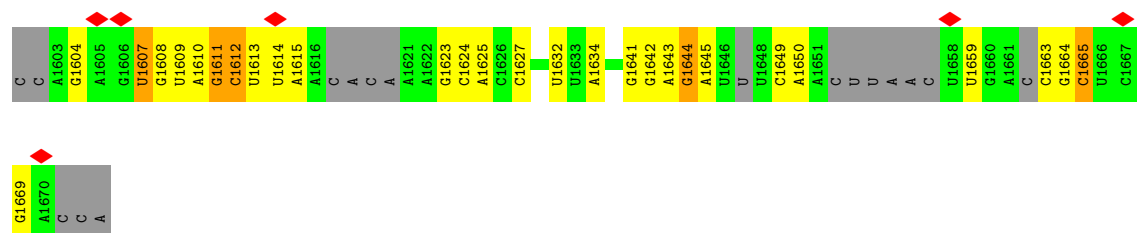
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S rRNA

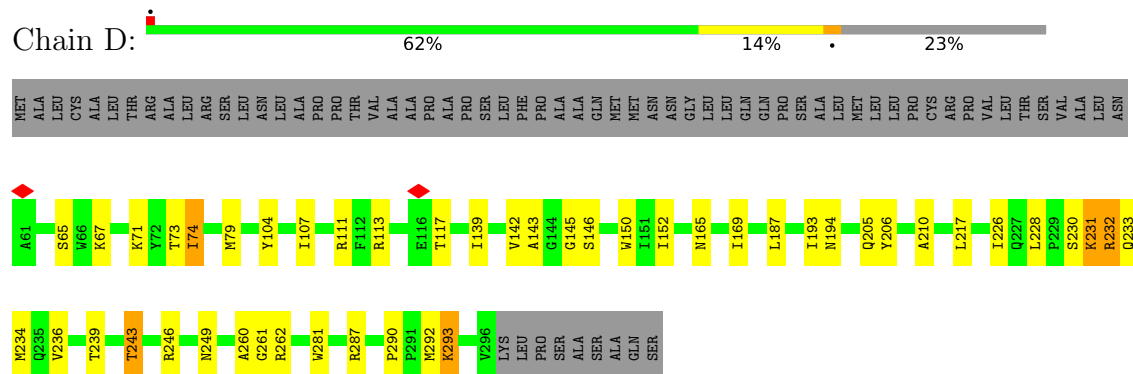




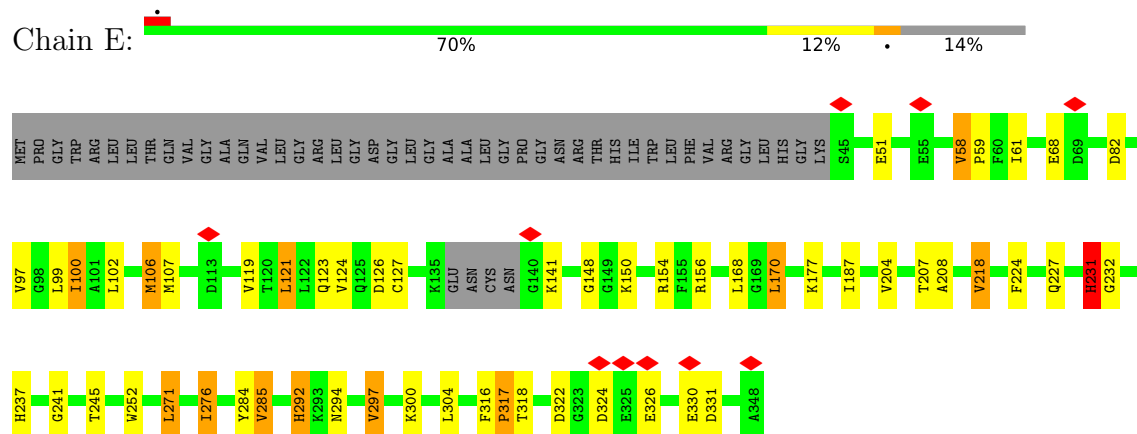
• Molecule 2: mt-tRNAVal



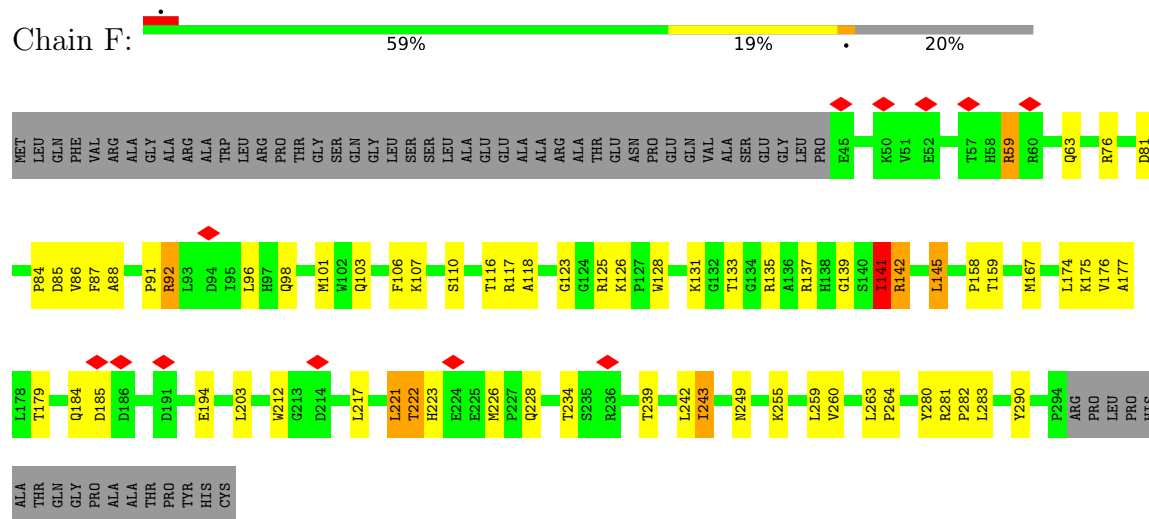
- Molecule 3: uL2m



- Molecule 4: uL3m

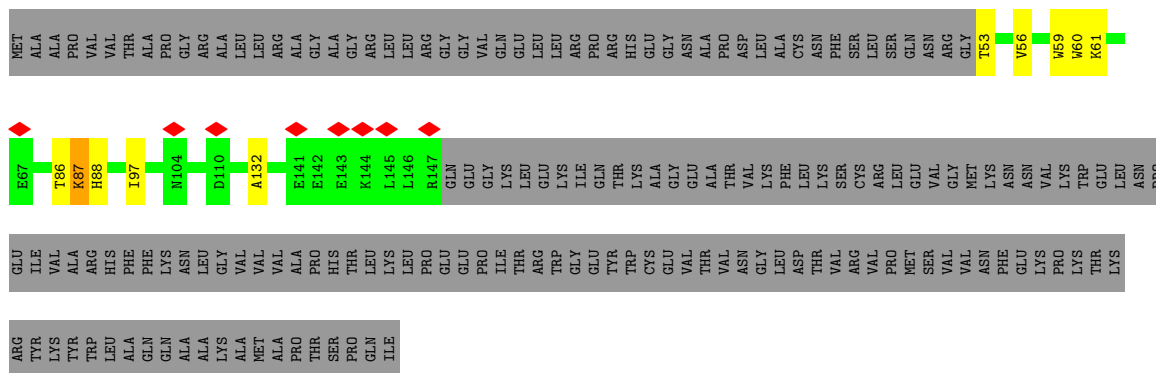


- Molecule 5: uL4m

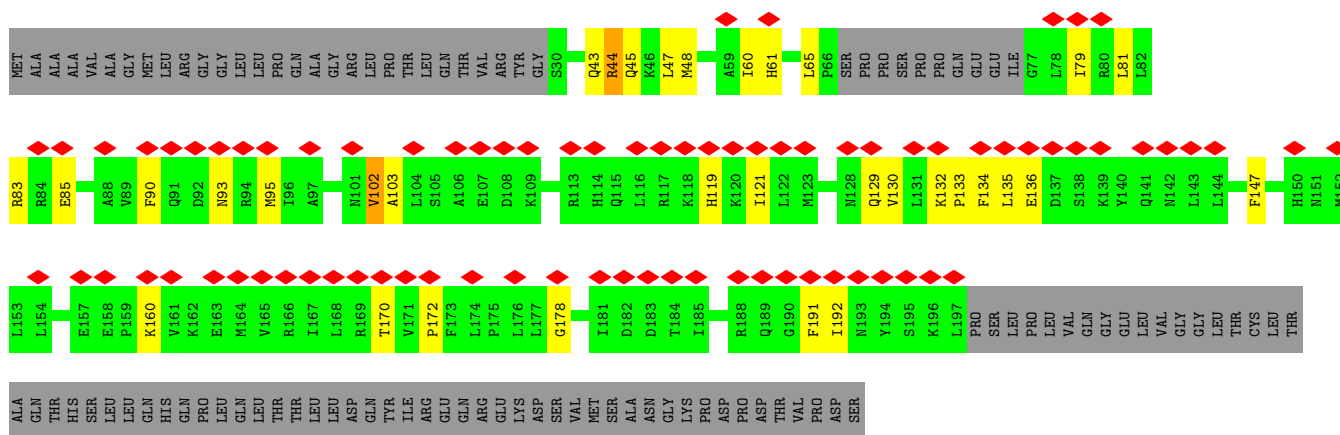


- Molecule 6: bL9m

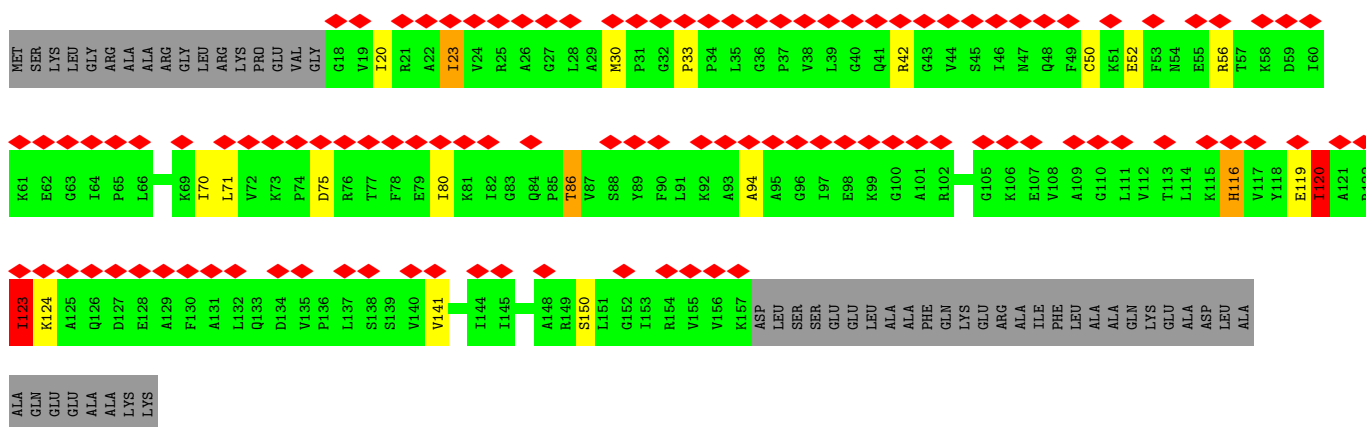




- Molecule 7: uL10m

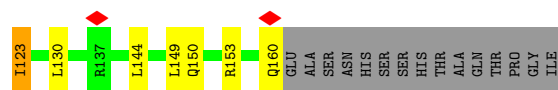


- Molecule 8: uL11m

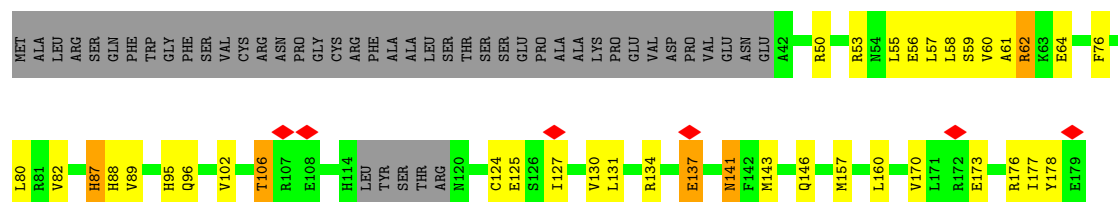


- Molecule 9: uL13m

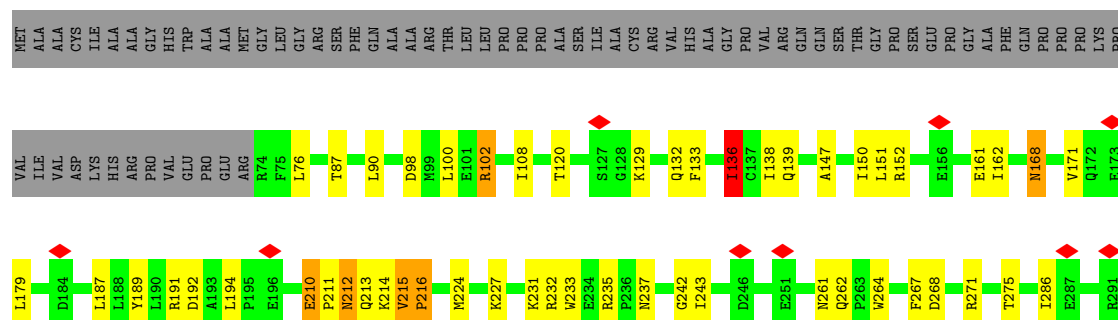




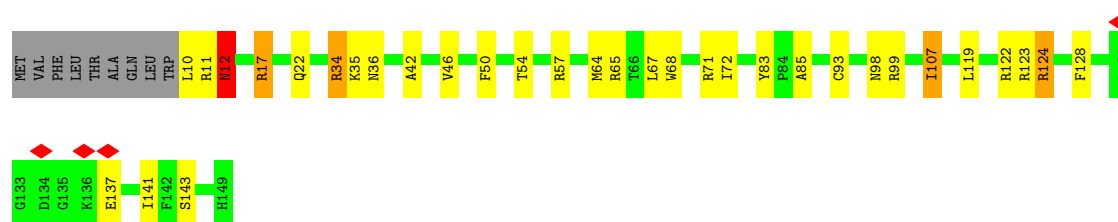
• Molecule 14: uL18m



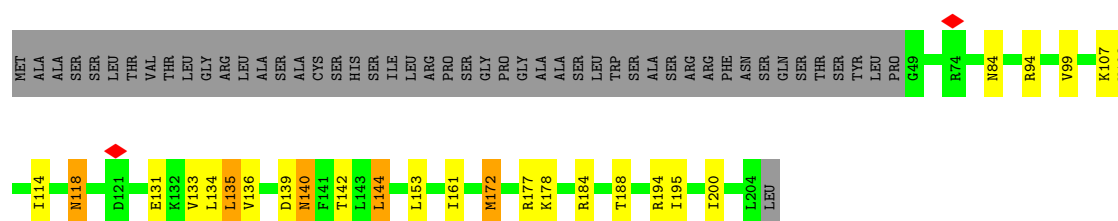
• Molecule 15: bL19m



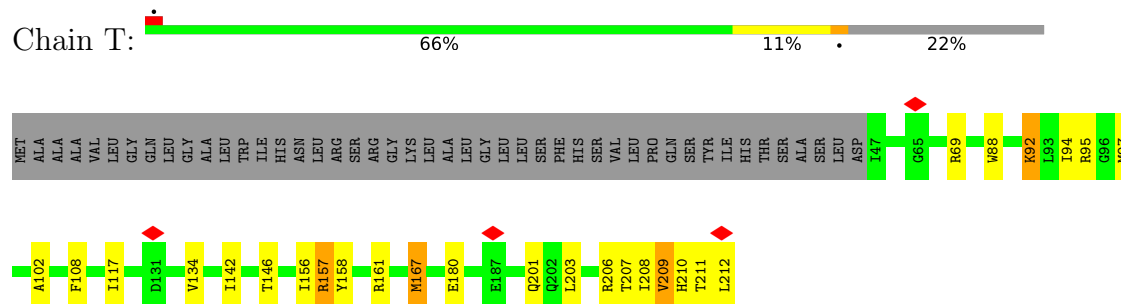
• Molecule 16: bL20m



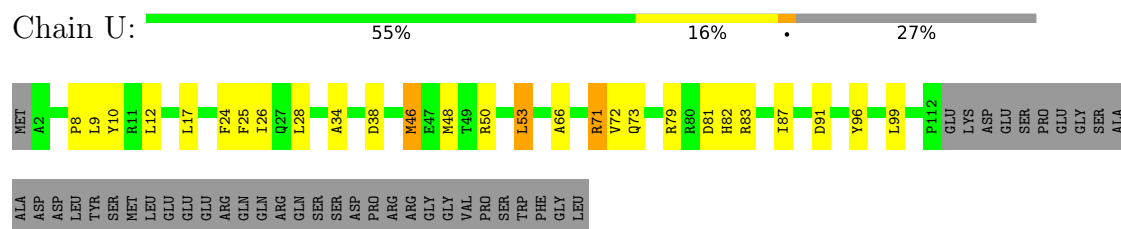
• Molecule 17: bL21m



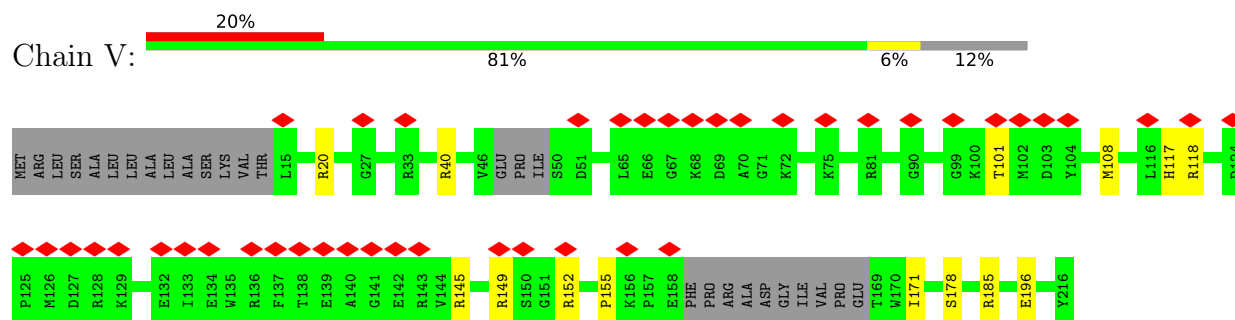
- Molecule 18: uL22m



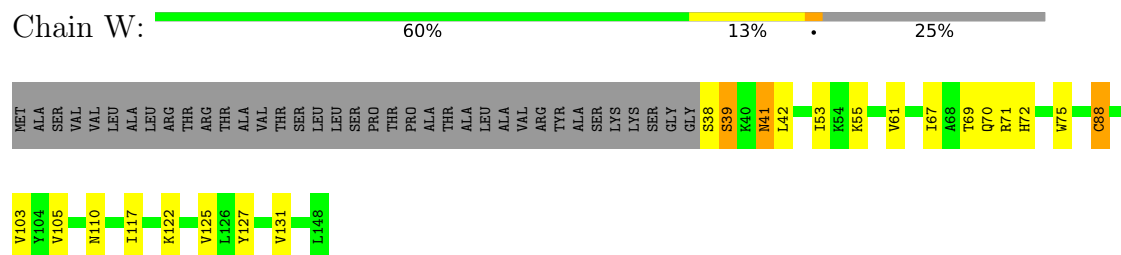
- Molecule 19: uL23m



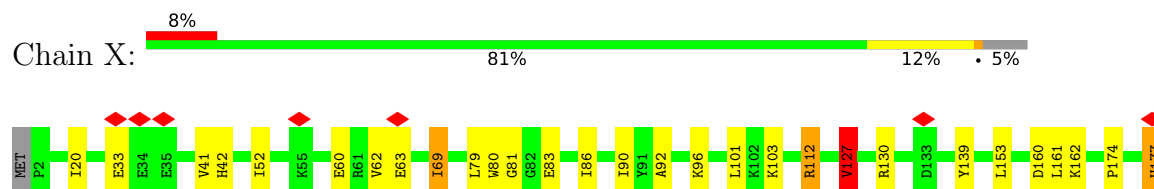
- Molecule 20: uL24m

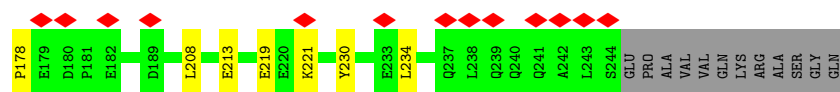


- Molecule 21: bL27m

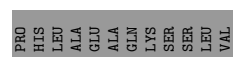
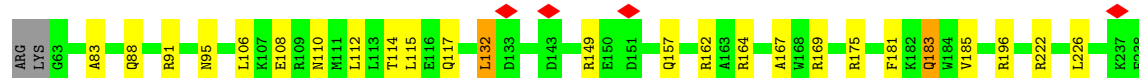
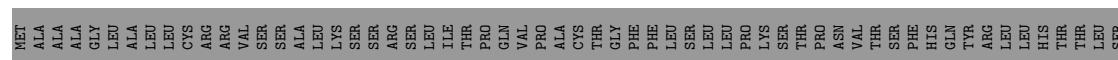


- Molecule 22: bL28m

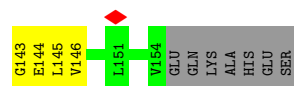
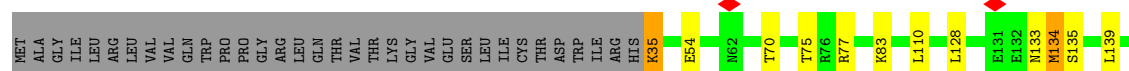




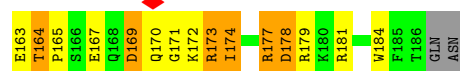
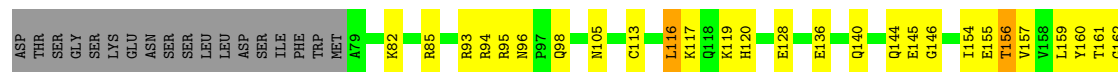
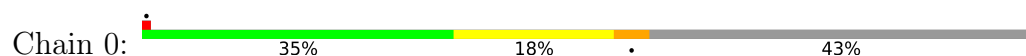
• Molecule 23: uL29m



• Molecule 24: uL30m



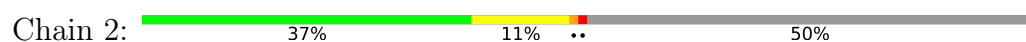
• Molecule 25: bL32m

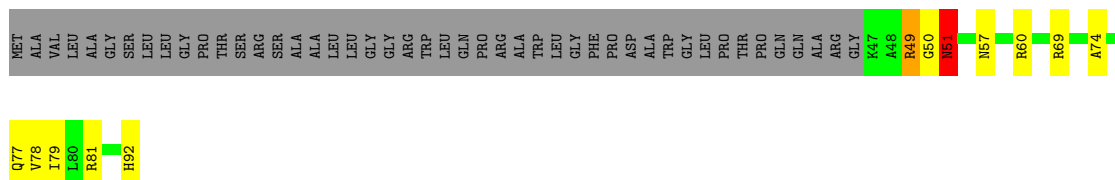


• Molecule 26: bL33m

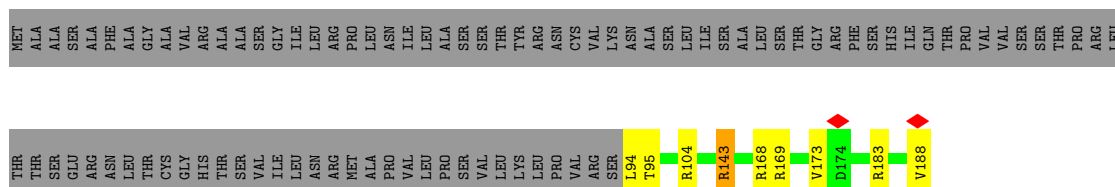


• Molecule 27: bL34m

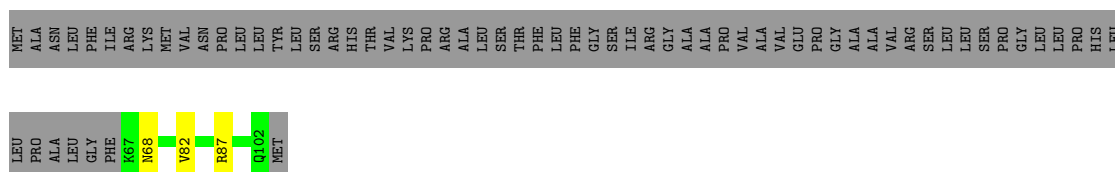




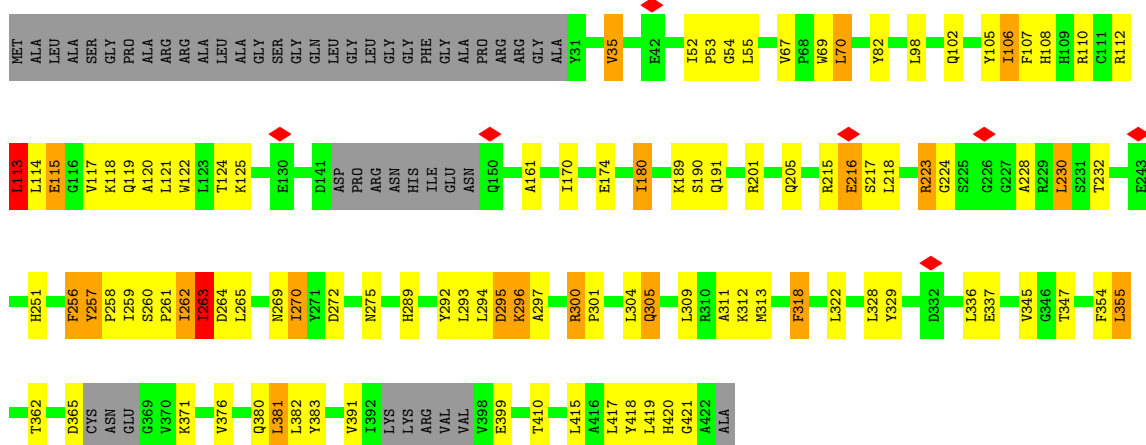
• Molecule 28: bL35m



• Molecule 29: bL36m



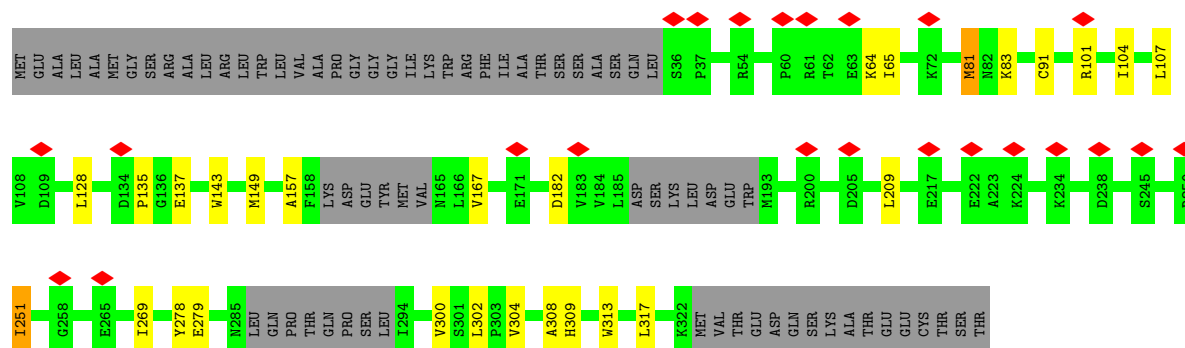
• Molecule 30: mL37



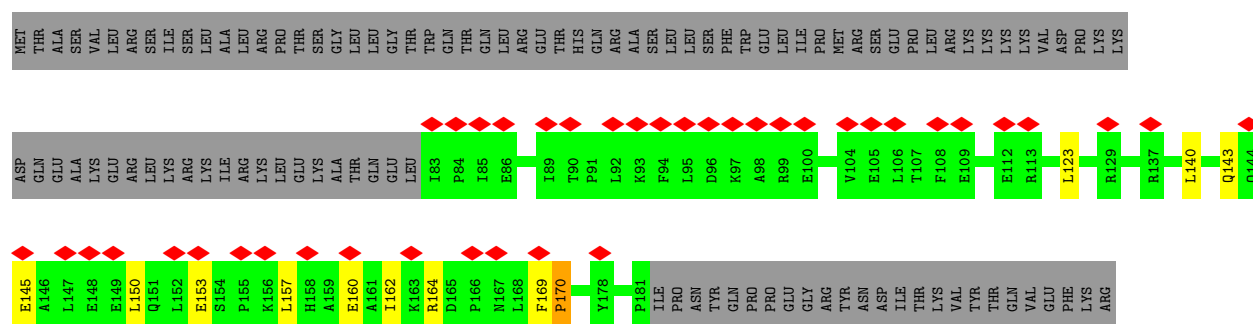
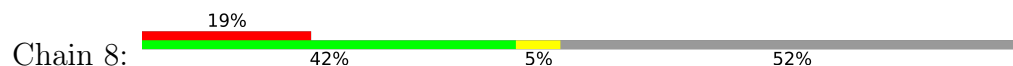
• Molecule 31: mL38



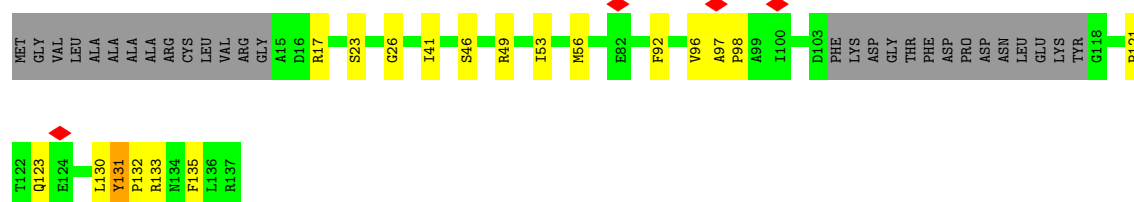
- Molecule 32: mL39



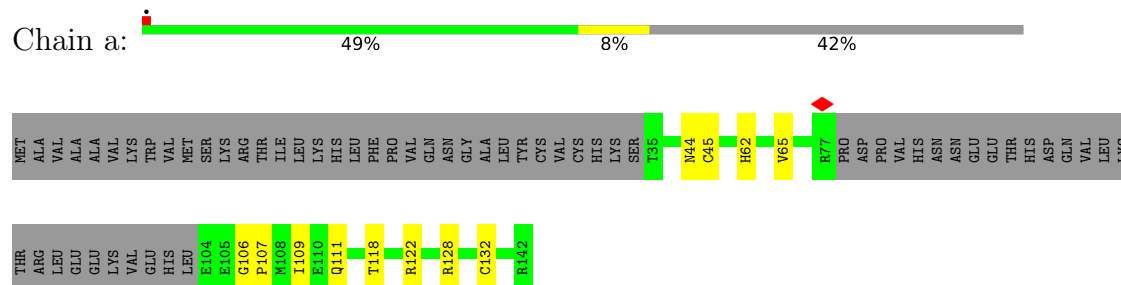
- Molecule 33: mL40



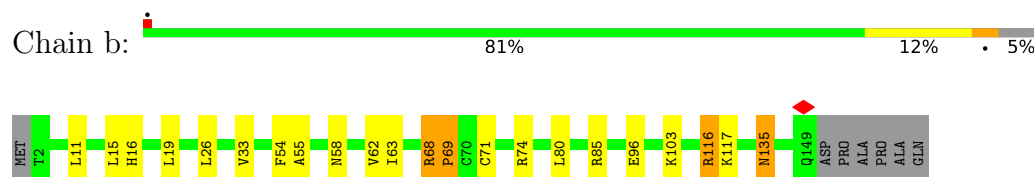
- Molecule 34: mL41



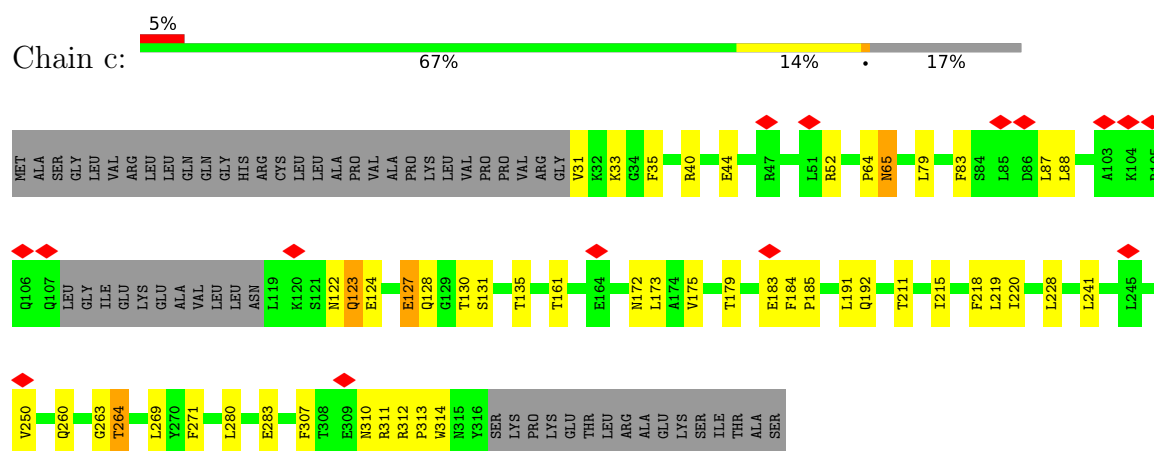
- Molecule 35: mL42



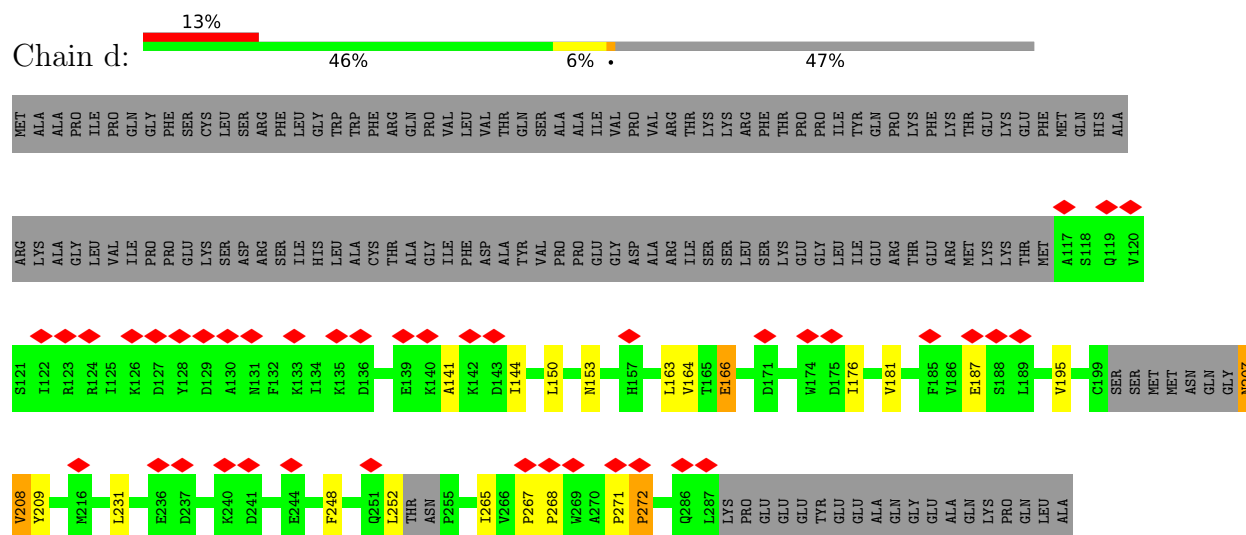
- Molecule 36: mL43



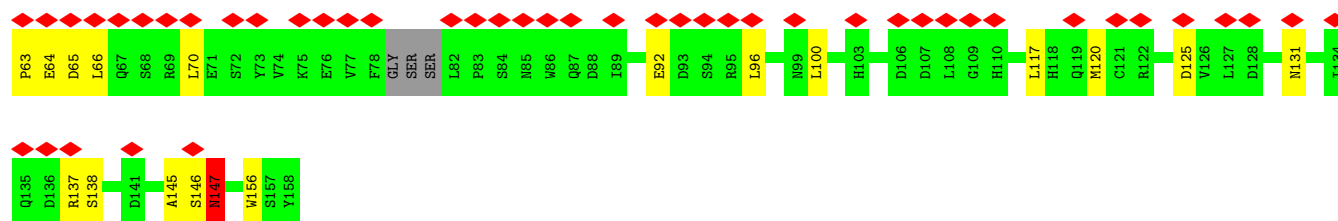
- Molecule 37: mL44



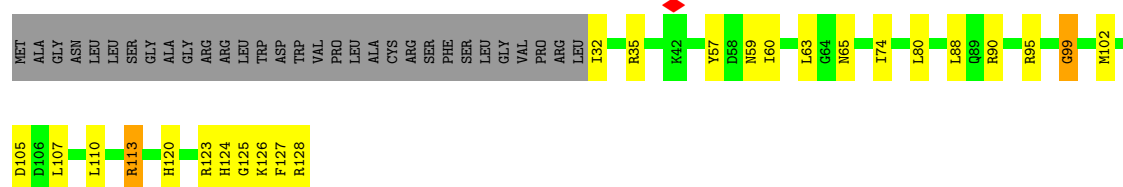
- Molecule 38: mL45



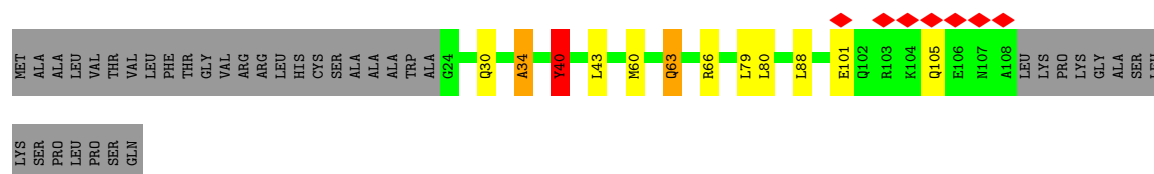
- Molecule 39: mL46



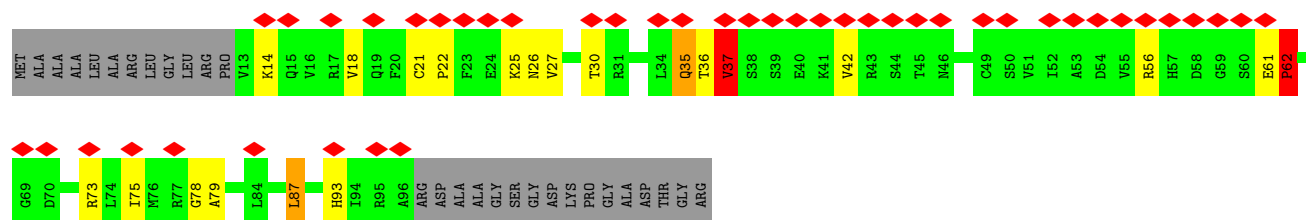
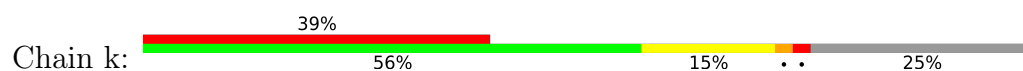
• Molecule 43: mL51



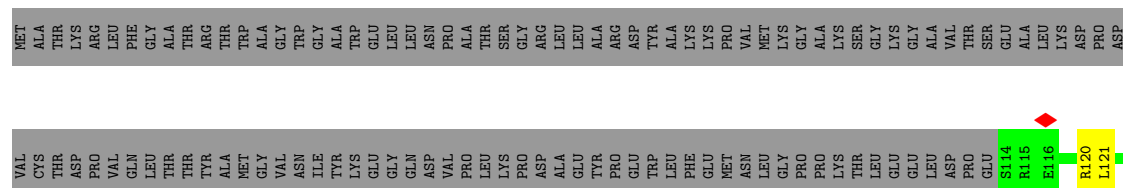
• Molecule 44: mL52

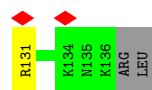


• Molecule 45: mL53

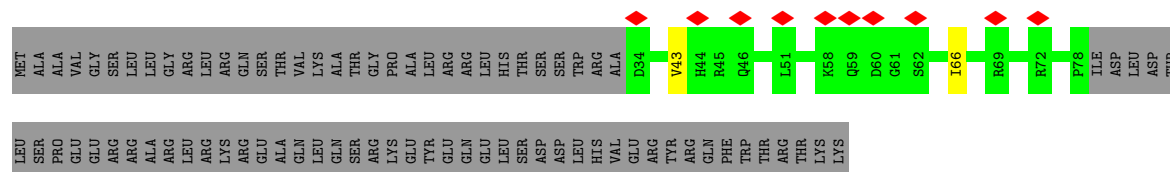


• Molecule 46: mL54

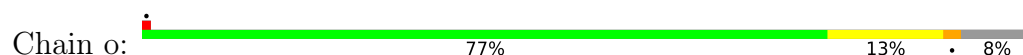




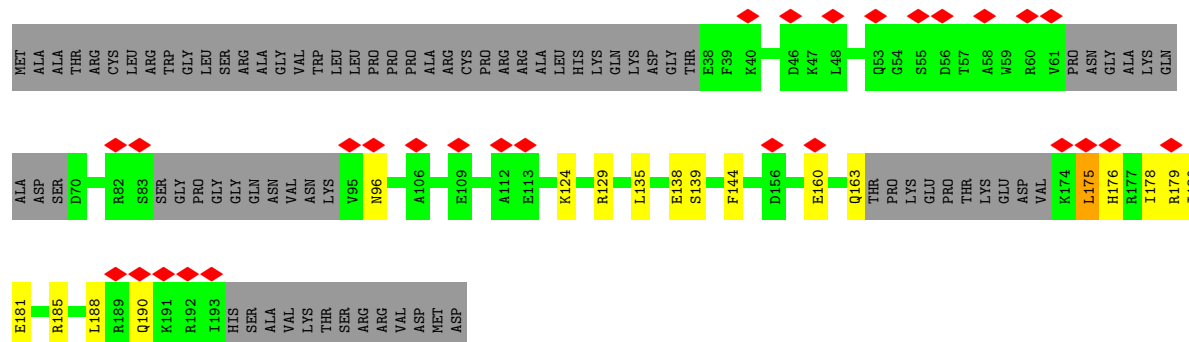
• Molecule 47: bL31m



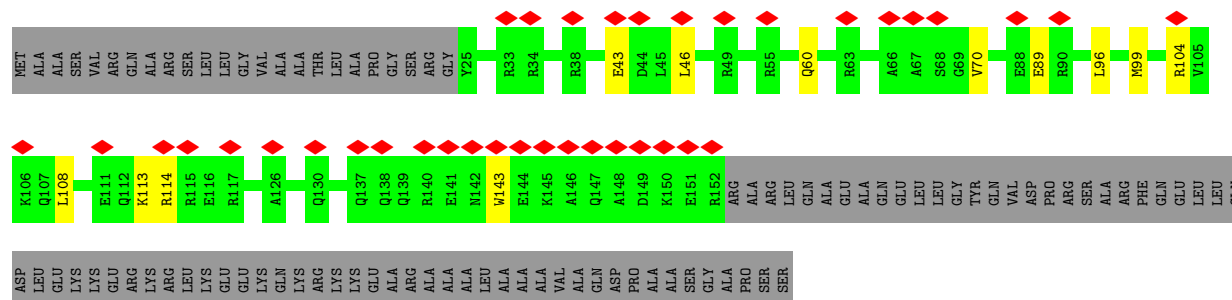
• Molecule 48: mL63



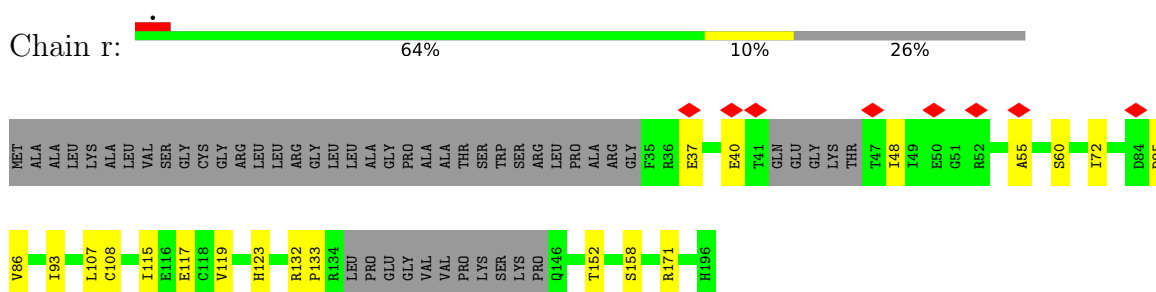
• Molecule 49: mL62 (ICT1)



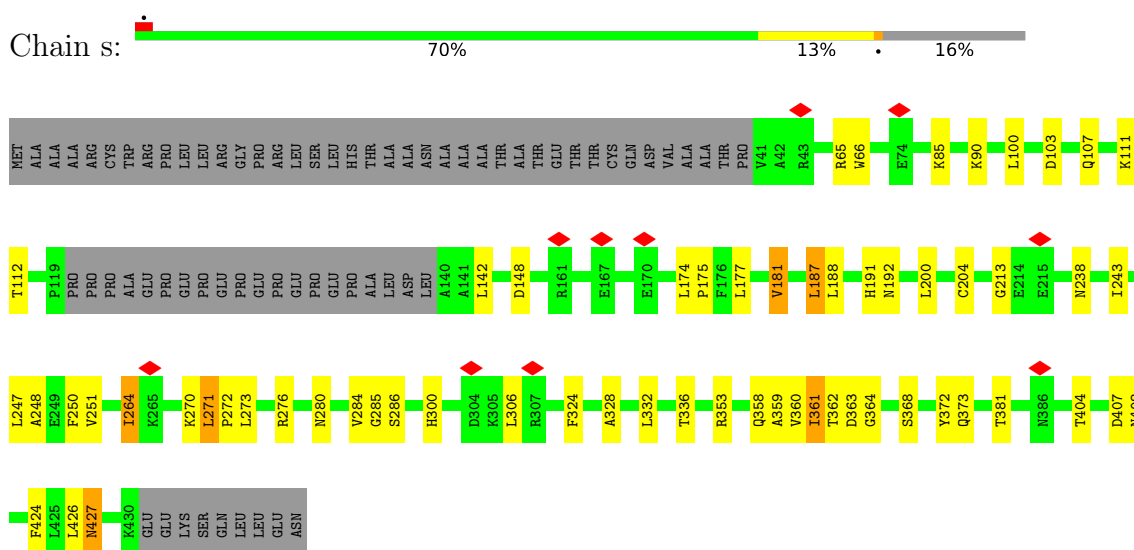
• Molecule 50: mL64 (CRIF1)



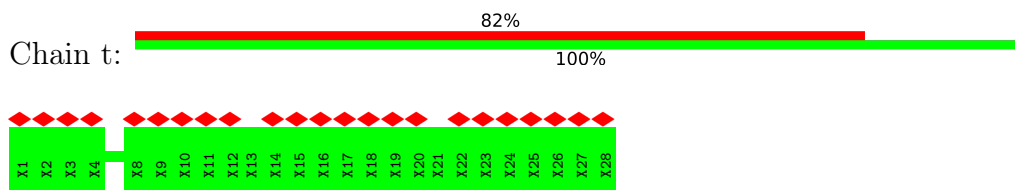
- Molecule 51: mL66 (bS18a)



- Molecule 52: mL65 (mS30)



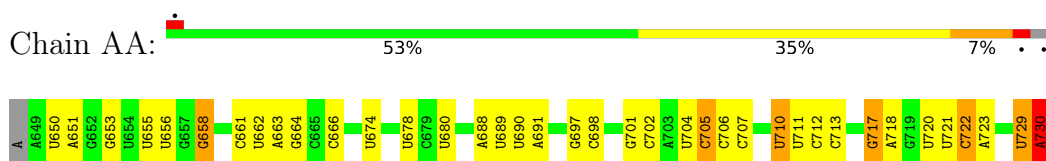
- Molecule 53: Unknown protein/protein extension

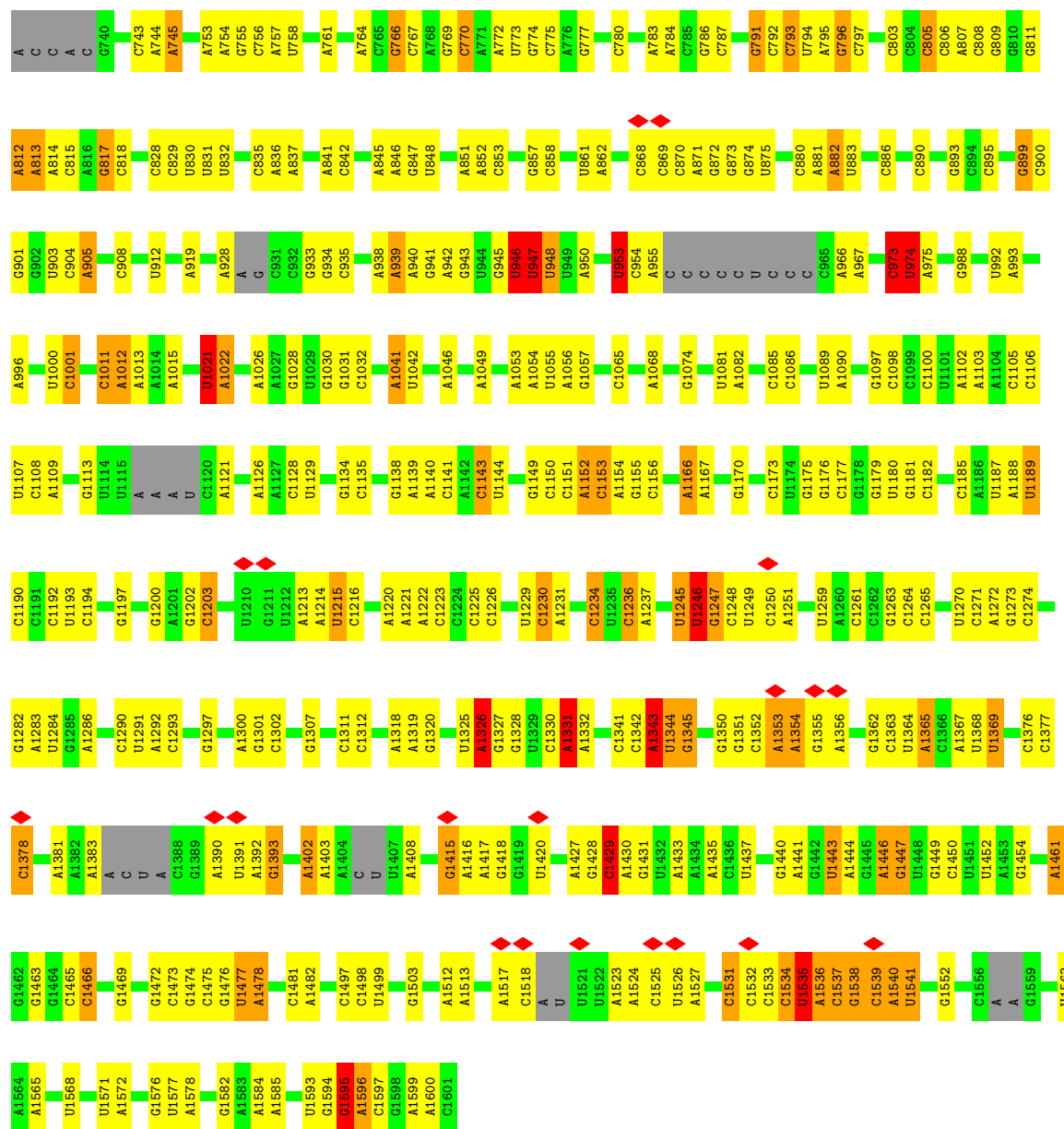


- Molecule 54: E-site tRNA



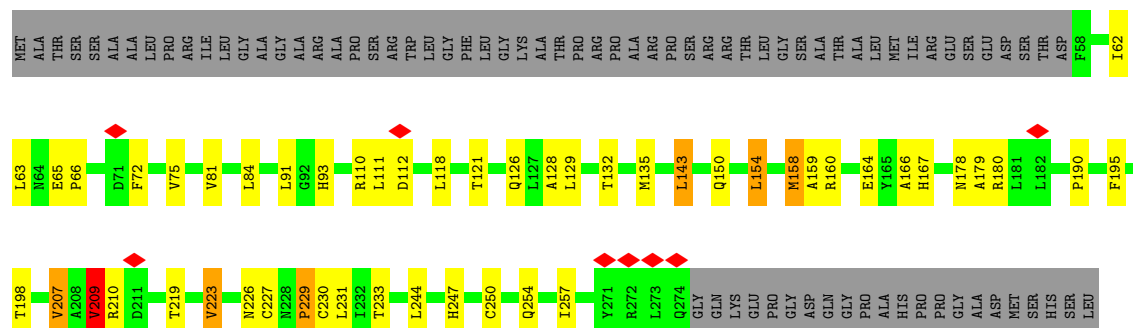
- Molecule 55: 12S rRNA



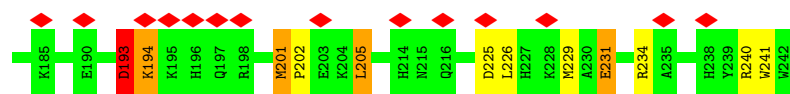


• Molecule 56: uS2m

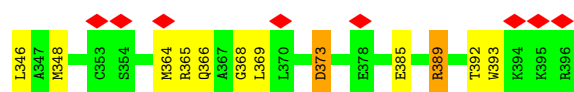
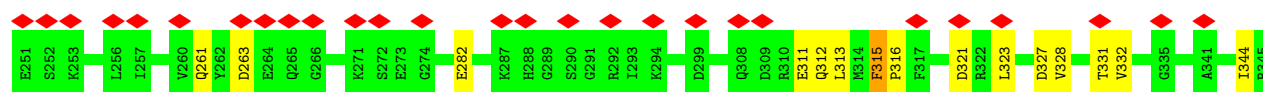
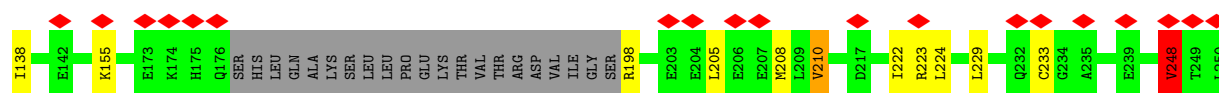
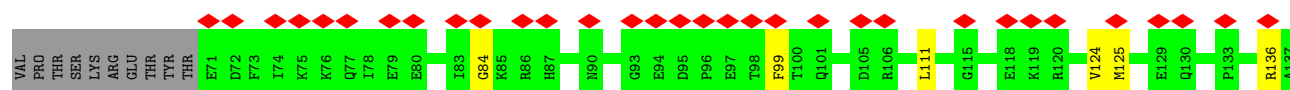
Chain AB: 56% 15% 27%



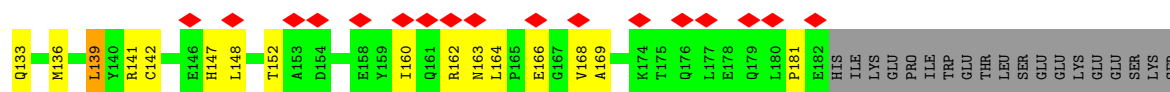
• Molecule 57: uS3m



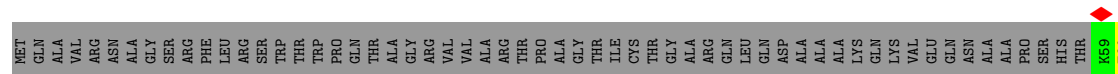
• Molecule 61: uS9m



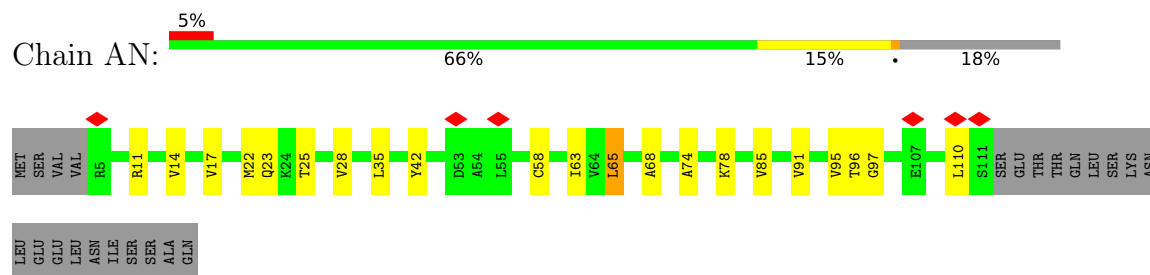
• Molecule 62: uS10m



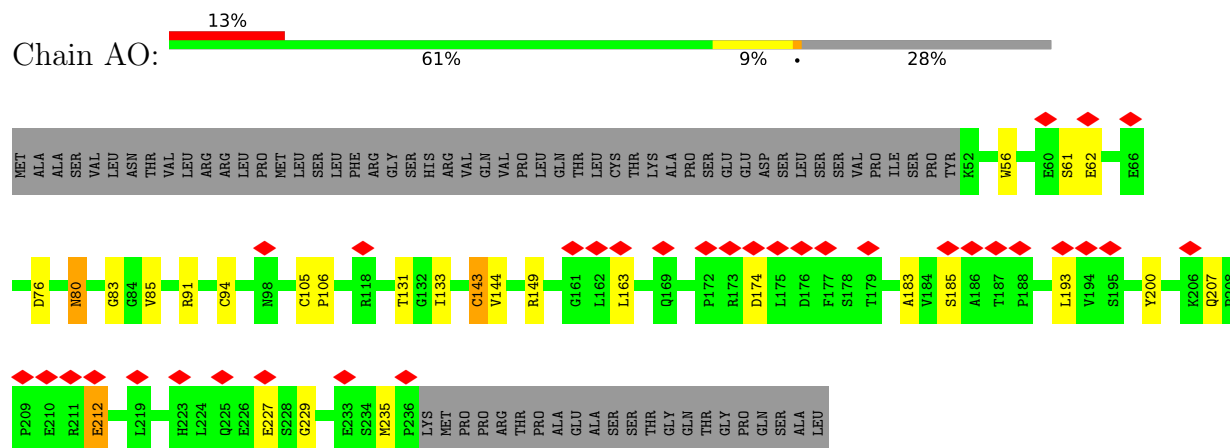
• Molecule 63: uS11m



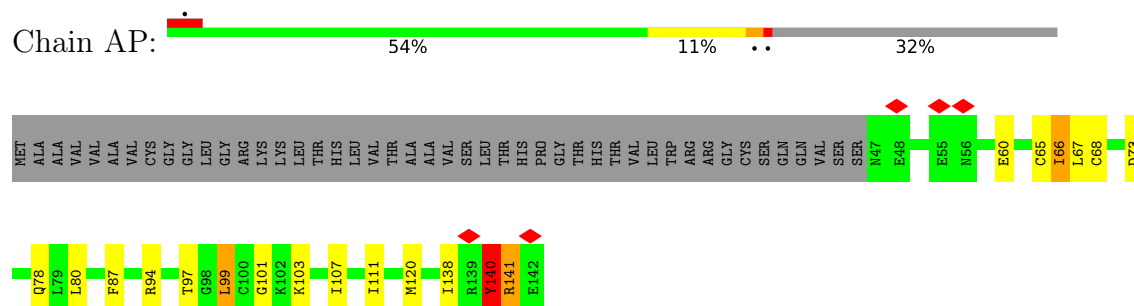
- Molecule 68: uS17m



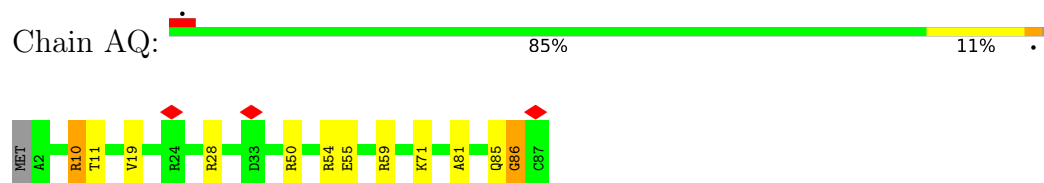
- Molecule 69: mS40 (bS18b)



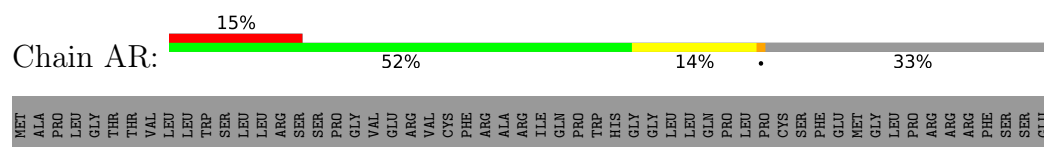
- Molecule 70: bS18m (bS18c)

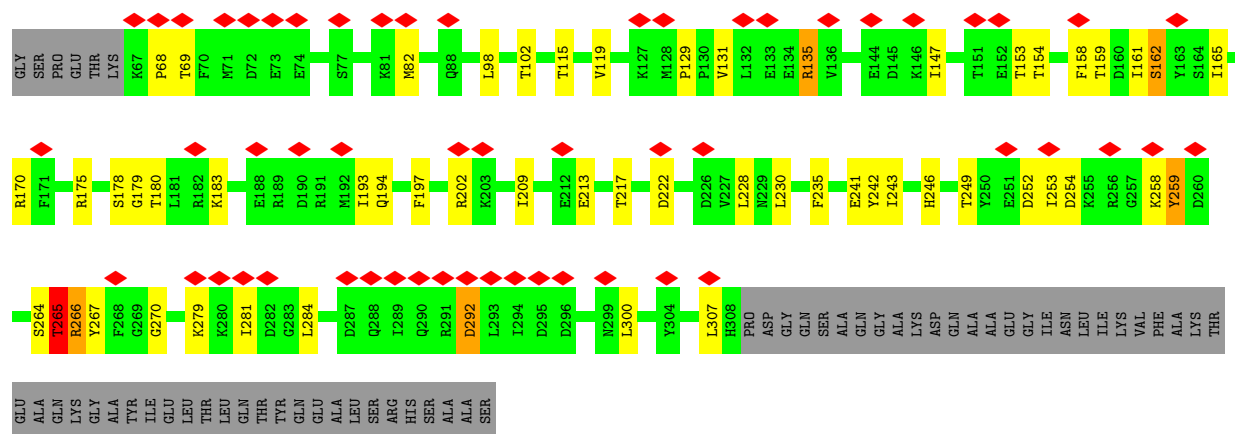


- Molecule 71: bS21m

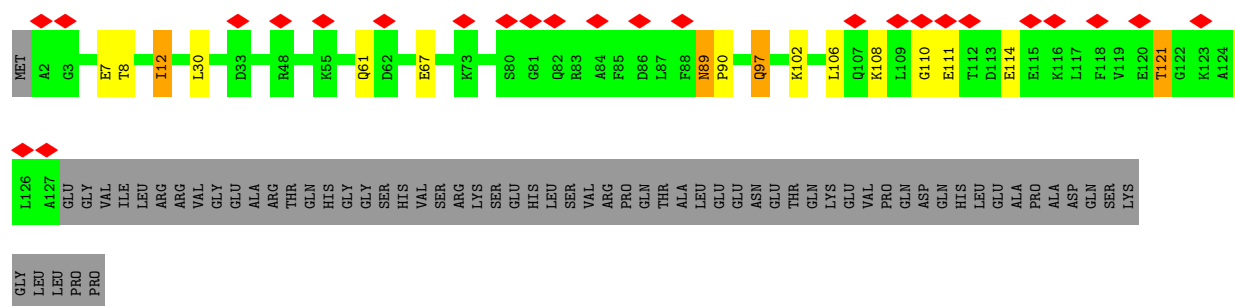


- Molecule 72: mS22

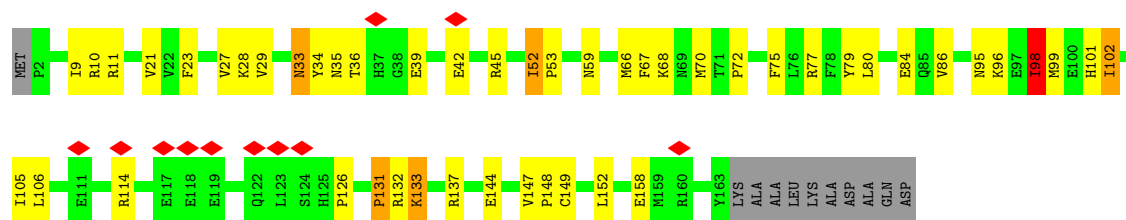




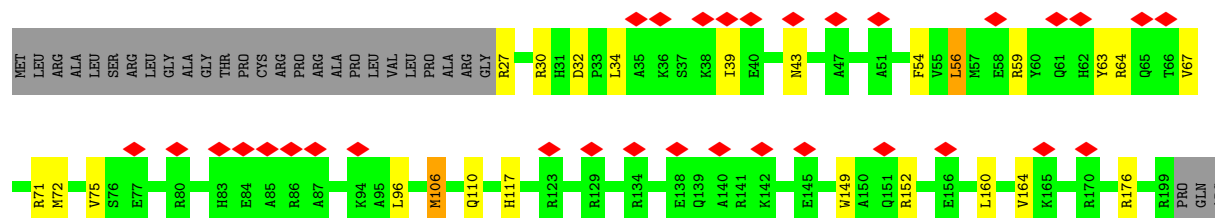
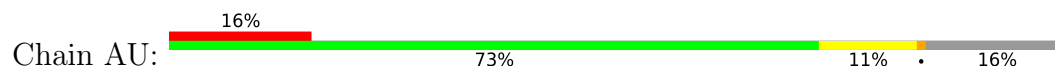
• Molecule 73: mS23



• Molecule 74: mS25



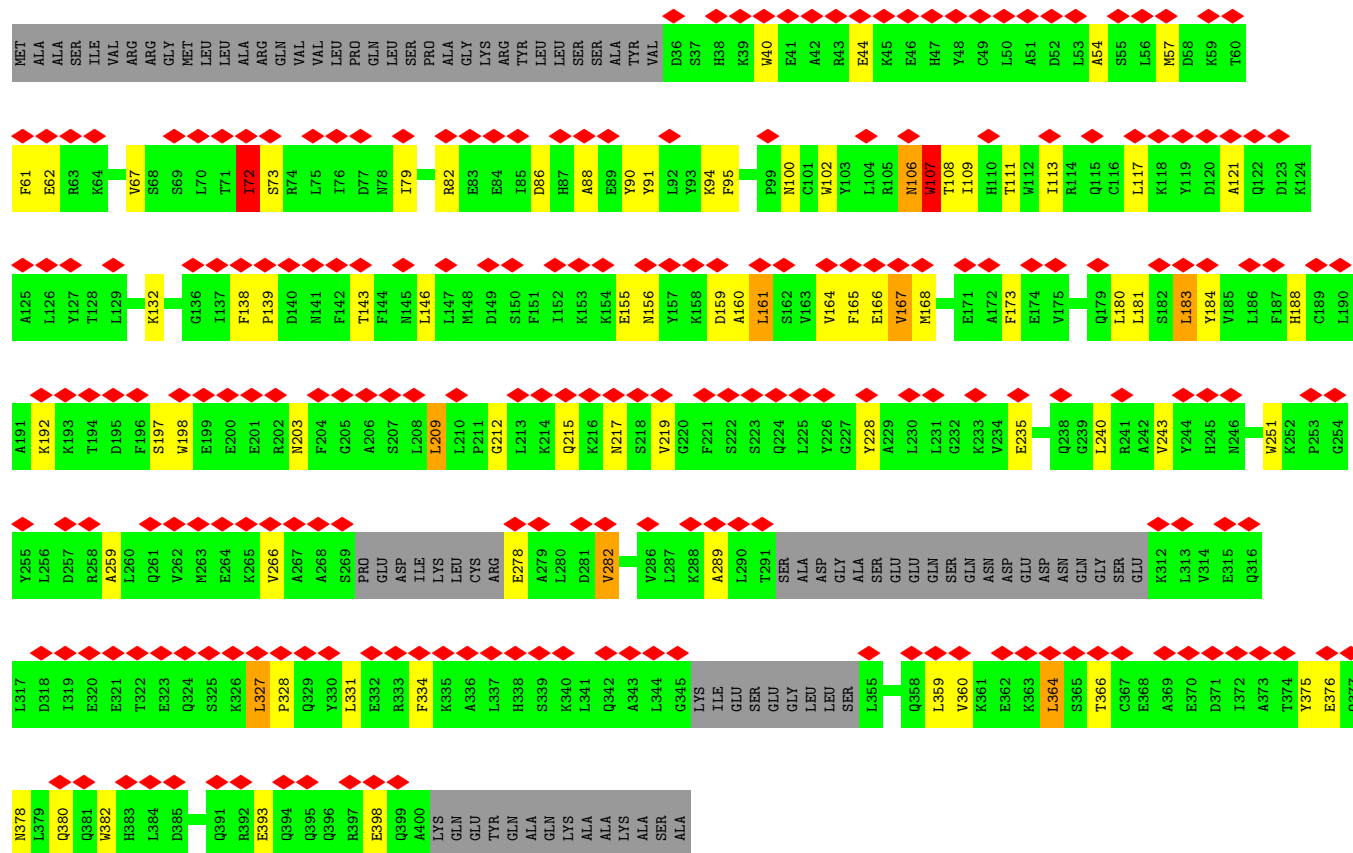
• Molecule 75: mS26



ARG
ASP
SER

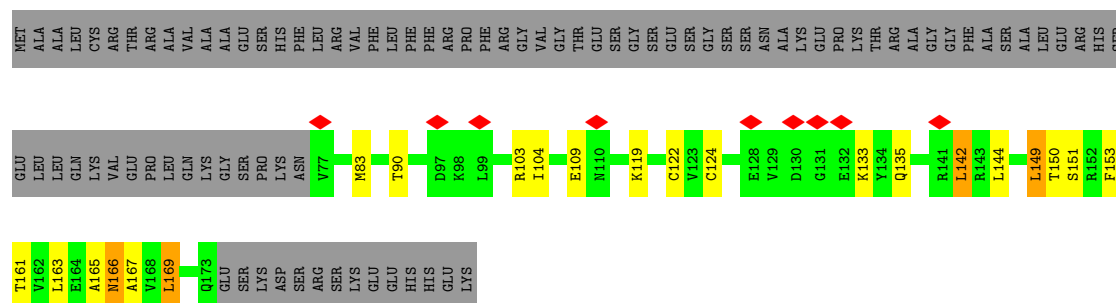
• Molecule 76: mS27

Chain AV: 



• Molecule 77: bS1m

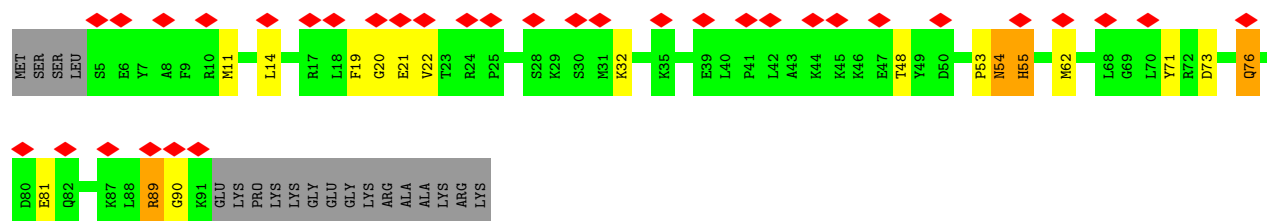
Chain AW: 



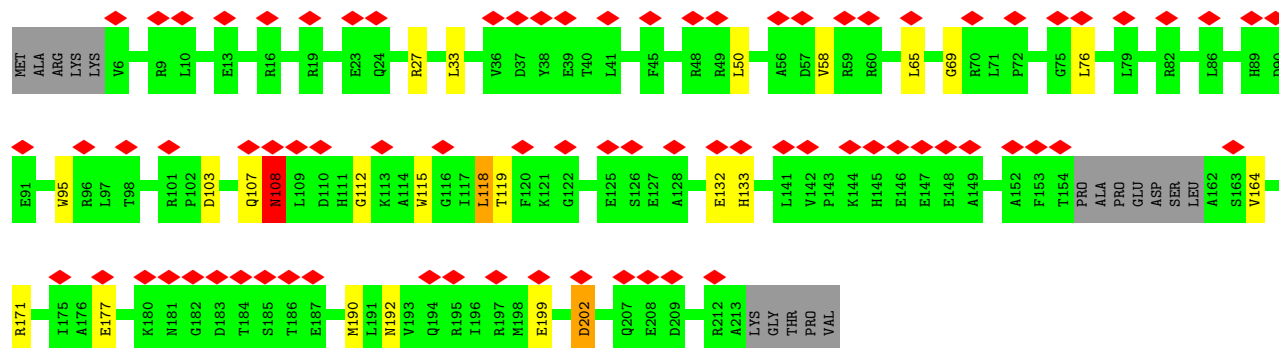
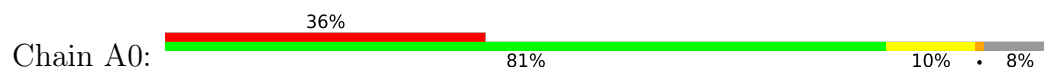
• Molecule 78: mS29

Chain AX: 

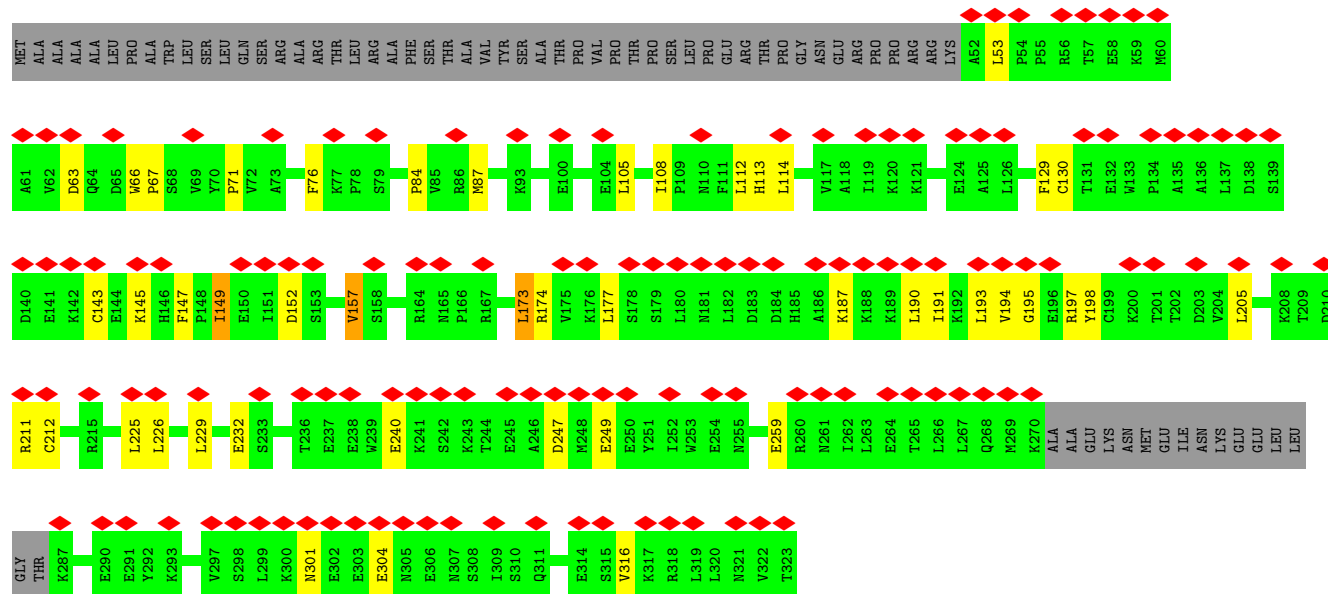
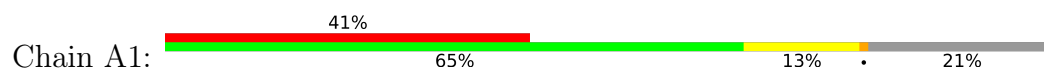




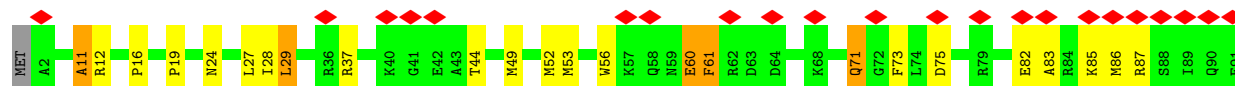
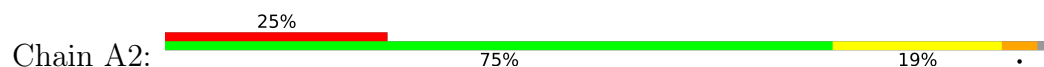
• Molecule 81: mS34



• Molecule 82: mS35



• Molecule 83: mS37





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	884122	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS, FEI TITAN KRIOS, FEI TITAN KRIOS, FEI TITAN KRIOS	Depositor
Voltage (kV)	300, 300, 300, 300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1500, 1500, 1500, 1500	Depositor
Maximum defocus (nm)	3500, 3500, 3500, 3500	Depositor
Magnification	104478, 104478, 104478, 104478	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.973	Depositor
Minimum map value	-0.588	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.029	Depositor
Recommended contour level	0.1	Depositor
Map size ($\text{\AA}$)	428.80002, 428.80002, 428.80002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.34, 1.34, 1.34	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	A	0.38	0/34967	0.80	44/54407 (0.1%)
2	B	0.38	0/1328	0.74	1/2056 (0.0%)
3	D	0.52	0/1879	0.83	0/2527
4	E	0.53	1/2433 (0.0%)	0.91	3/3299 (0.1%)
5	F	0.54	0/2071	0.99	2/2817 (0.1%)
6	H	0.56	0/798	0.89	0/1073
7	I	0.60	0/1308	1.05	0/1761
8	J	0.64	0/1077	1.06	3/1452 (0.2%)
9	K	0.62	1/1495 (0.1%)	1.06	6/2029 (0.3%)
10	L	0.53	0/904	0.84	0/1218
11	M	0.62	0/2359	1.06	7/3185 (0.2%)
12	N	0.53	0/1697	0.99	4/2281 (0.2%)
13	O	0.59	0/1269	1.14	1/1708 (0.1%)
14	P	0.54	0/1103	1.03	1/1491 (0.1%)
15	Q	0.56	0/1863	0.95	6/2509 (0.2%)
16	R	0.58	0/1174	1.20	3/1572 (0.2%)
17	S	0.52	0/1276	0.84	0/1729
18	T	0.52	0/1402	0.99	1/1886 (0.1%)
19	U	0.54	0/946	0.89	0/1283
20	V	0.57	0/1590	0.81	0/2151
21	W	0.50	0/893	0.86	0/1204
22	X	0.54	0/2081	1.00	3/2812 (0.1%)
23	Y	0.56	0/1552	1.09	0/2079
24	Z	0.51	0/1003	0.93	0/1354
25	0	0.60	0/895	1.06	4/1201 (0.3%)
26	1	0.52	0/438	0.83	0/583
27	2	0.54	0/382	1.25	2/507 (0.4%)
28	3	0.49	0/852	0.92	1/1136 (0.1%)
29	4	0.47	0/329	0.63	0/435
30	5	0.57	0/3154	1.00	11/4295 (0.3%)
31	6	0.57	0/2722	0.94	1/3709 (0.0%)
32	7	0.53	0/2207	1.01	2/2978 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	8	0.56	0/855	1.07	1/1152 (0.1%)
34	9	0.54	0/896	0.95	0/1205
35	a	0.55	0/709	0.84	0/963
36	b	0.53	0/1202	0.91	0/1626
37	c	0.55	0/2264	1.10	3/3059 (0.1%)
38	d	0.61	0/1385	0.90	2/1877 (0.1%)
39	e	0.56	0/1797	0.95	2/2422 (0.1%)
40	f	0.53	0/1055	0.86	0/1427
41	g	0.55	0/1102	0.90	0/1503
42	h	0.59	0/847	1.01	0/1150
43	i	0.55	0/849	1.08	0/1135
44	j	0.56	0/698	1.15	0/940
45	k	0.68	0/665	1.02	1/897 (0.1%)
46	l	0.53	0/226	1.21	0/299
47	m	0.57	0/379	0.67	0/510
48	o	0.61	0/818	1.21	4/1097 (0.4%)
49	p	0.52	0/1071	0.91	0/1433
50	q	0.59	0/1107	1.11	0/1498
51	r	0.55	0/1238	0.91	2/1676 (0.1%)
52	s	0.54	0/3114	0.99	1/4225 (0.0%)
54	u	0.38	0/46	1.14	0/69
55	AA	0.38	0/21926	0.79	38/34121 (0.1%)
56	AB	0.57	0/1811	1.05	1/2451 (0.0%)
57	AC	0.55	0/1112	0.90	0/1505
58	AD	0.57	0/2607	0.97	2/3498 (0.1%)
59	AE	0.54	0/989	1.06	1/1335 (0.1%)
60	AF	0.58	0/1708	1.14	2/2291 (0.1%)
61	AG	0.55	0/2570	1.05	1/3443 (0.0%)
62	AH	0.57	0/1019	0.95	0/1379
63	AI	0.51	0/1031	0.97	2/1390 (0.1%)
64	AJ	0.56	0/854	0.83	0/1148
65	AK	0.54	0/879	1.11	0/1182
66	AL	0.59	0/1406	1.17	0/1878
67	AM	0.53	0/941	1.07	0/1265
68	AN	0.50	0/864	0.78	0/1169
69	AO	0.57	0/1580	0.99	2/2150 (0.1%)
70	AP	0.61	0/791	0.99	0/1062
71	AQ	0.52	0/752	1.16	1/1001 (0.1%)
72	AR	0.59	0/2050	1.11	6/2770 (0.2%)
73	AS	0.56	0/1069	1.04	1/1441 (0.1%)
74	AT	0.58	0/1361	1.03	2/1829 (0.1%)
75	AU	0.56	0/1482	1.21	1/1987 (0.1%)
76	AV	0.59	0/2758	1.22	7/3724 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
77	AW	0.57	0/778	0.81	0/1048
78	AX	0.60	0/2596	1.09	6/3519 (0.2%)
79	AY	0.59	1/943 (0.1%)	1.12	0/1274
80	AZ	0.57	0/757	1.15	1/1011 (0.1%)
81	A0	0.56	0/1727	0.97	1/2338 (0.0%)
82	A1	0.58	0/2121	1.01	0/2873
83	A2	0.57	0/939	1.09	1/1256 (0.1%)
84	A3	0.53	0/621	1.19	0/820
85	A4	0.50	0/2137	1.17	0/2872
All	All	0.50	3/165949 (0.0%)	0.94	198/235920 (0.1%)

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
8	J	0	1
15	Q	0	1
58	AD	0	1
72	AR	0	1
74	AT	0	1
78	AX	0	2
80	AZ	0	1
All	All	0	8

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	58	VAL	CA-CB	5.48	1.56	1.54
9	K	26	GLN	C-N	5.15	1.39	1.33
79	AY	371	GLU	CD-OE1	5.06	1.34	1.25

The worst 5 of 198 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	AA	953	U	C2'-C3'-O3'	10.35	125.02	109.50
12	N	225	GLY	N-CA-C	-9.61	101.46	115.30
55	AA	722	C	C2'-C3'-O3'	9.48	123.71	109.50
30	5	117	VAL	N-CA-C	9.43	120.24	110.62
1	A	2457	A	C2'-C3'-O3'	9.28	123.42	109.50

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
58	AD	287	ASP	Peptide
72	AR	265	THR	Peptide
74	AT	147	VAL	Peptide
8	J	30	MET	Peptide
15	Q	215	VAL	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	A	31261	0	15877	413	0
2	B	1191	0	607	11	0
3	D	1842	0	1896	29	0
4	E	2365	0	2378	22	0
5	F	2013	0	2044	39	0
6	H	784	0	832	4	0
7	I	1283	0	1369	14	0
8	J	1061	0	1141	7	0
9	K	1451	0	1448	38	0
10	L	889	0	941	8	0
11	M	2305	0	2378	49	0
12	N	1654	0	1681	28	0
13	O	1245	0	1283	21	0
14	P	1080	0	1081	34	0
15	Q	1822	0	1859	32	0
16	R	1153	0	1214	22	0
17	S	1251	0	1322	12	0
18	T	1368	0	1410	24	0
19	U	922	0	935	12	0
20	V	1551	0	1558	0	0
21	W	871	0	898	21	0
22	X	2027	0	2040	11	0
23	Y	1517	0	1561	8	0
24	Z	978	0	1030	3	0
25	0	880	0	903	71	0
26	1	433	0	475	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	2	376	0	406	15	0
28	3	831	0	883	8	0
29	4	322	0	344	0	0
30	5	3064	0	3059	71	0
31	6	2636	0	2450	40	0
32	7	2158	0	2173	8	0
33	8	836	0	844	7	0
34	9	873	0	878	8	0
35	a	686	0	658	4	0
36	b	1178	0	1180	7	0
37	c	2217	0	2220	21	0
38	d	1347	0	1343	8	0
39	e	1762	0	1767	29	0
40	f	1039	0	1044	8	0
41	g	1067	0	1056	8	0
42	h	827	0	806	3	0
43	i	827	0	857	18	0
44	j	684	0	673	3	0
45	k	655	0	656	8	0
46	l	221	0	227	0	0
47	m	372	0	387	1	0
48	o	797	0	804	8	0
49	p	1058	0	1083	15	0
50	q	1076	0	1049	5	0
51	r	1203	0	1221	7	0
52	s	3036	0	3022	26	0
53	t	140	0	30	0	0
54	u	42	0	23	2	0
55	AA	19606	0	9962	221	0
56	AB	1768	0	1765	21	0
57	AC	1082	0	1088	6	0
58	AD	2557	0	2596	16	0
59	AE	972	0	1000	16	0
60	AF	1668	0	1716	17	0
61	AG	2516	0	2503	14	0
62	AH	999	0	1024	20	0
63	AI	1011	0	1052	11	0
64	AJ	838	0	887	4	0
65	AK	861	0	885	9	0
66	AL	1382	0	1472	9	0
67	AM	920	0	951	13	0
68	AN	846	0	908	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
69	AO	1528	0	1488	6	0
70	AP	774	0	801	6	0
71	AQ	740	0	754	5	0
72	AR	2008	0	2031	17	0
73	AS	1042	0	1037	8	0
74	AT	1330	0	1344	21	0
75	AU	1461	0	1471	8	0
76	AV	2702	0	2690	35	0
77	AW	766	0	785	10	0
78	AX	2531	0	2520	39	0
79	AY	914	0	859	7	0
80	AZ	740	0	747	5	0
81	A0	1684	0	1685	6	0
82	A1	2076	0	2097	23	0
83	A2	925	0	962	11	0
84	A3	610	0	682	6	0
85	A4	2838	0	2263	21	0
86	A	97	0	0	0	0
86	AA	28	0	0	0	0
86	M	1	0	0	0	0
86	g	1	0	0	0	0
87	0	1	0	0	0	0
87	4	1	0	0	0	0
87	AB	1	0	0	0	0
87	AO	1	0	0	0	0
87	AP	1	0	0	0	0
87	AT	1	0	0	0	0
87	r	1	0	0	0	0
88	AX	28	0	12	0	0
All	All	158384	0	133341	1647	0

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

The worst 5 of 1647 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)
1:A:2807:U:N3	1:A:2922:A:N6	1.61	1.47
25:0:156:THR:CG2	25:0:173:ARG:HH11	1.31	1.44
25:0:156:THR:HG21	25:0:173:ARG:NH1	1.38	1.35
1:A:2731:U:O4	1:A:2918:A:N1	1.60	1.34

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:0:154:ILE:HG21	25:0:171:GLY:O	1.27	1.34

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	
3	D	234/305 (77%)	214 (92%)	18 (8%)	2 (1%)	14	47
4	E	296/348 (85%)	266 (90%)	20 (7%)	10 (3%)	3	23
5	F	248/311 (80%)	228 (92%)	13 (5%)	7 (3%)	4	26
6	H	93/267 (35%)	84 (90%)	8 (9%)	1 (1%)	11	43
7	I	154/261 (59%)	139 (90%)	11 (7%)	4 (3%)	4	27
8	J	138/192 (72%)	126 (91%)	11 (8%)	1 (1%)	18	51
9	K	175/178 (98%)	156 (89%)	11 (6%)	8 (5%)	2	17
10	L	113/145 (78%)	100 (88%)	11 (10%)	2 (2%)	6	34
11	M	285/296 (96%)	247 (87%)	34 (12%)	4 (1%)	9	38
12	N	203/251 (81%)	186 (92%)	16 (8%)	1 (0%)	24	57
13	O	150/175 (86%)	130 (87%)	16 (11%)	4 (3%)	4	27
14	P	129/179 (72%)	117 (91%)	9 (7%)	3 (2%)	5	30
15	Q	217/292 (74%)	186 (86%)	22 (10%)	9 (4%)	2	19
16	R	138/149 (93%)	126 (91%)	9 (6%)	3 (2%)	5	30
17	S	154/205 (75%)	141 (92%)	11 (7%)	2 (1%)	9	39
18	T	164/212 (77%)	154 (94%)	7 (4%)	3 (2%)	6	34
19	U	109/153 (71%)	95 (87%)	10 (9%)	4 (4%)	2	21
20	V	183/216 (85%)	159 (87%)	20 (11%)	4 (2%)	5	30
21	W	109/148 (74%)	100 (92%)	6 (6%)	3 (3%)	4	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	X	241/256 (94%)	211 (88%)	22 (9%)	8 (3%)	3	23
23	Y	174/250 (70%)	162 (93%)	9 (5%)	3 (2%)	7	35
24	Z	118/161 (73%)	110 (93%)	5 (4%)	3 (2%)	4	28
25	0	106/188 (56%)	93 (88%)	8 (8%)	5 (5%)	2	17
26	1	50/65 (77%)	44 (88%)	5 (10%)	1 (2%)	6	32
27	2	44/92 (48%)	43 (98%)	1 (2%)	0	100	100
28	3	93/188 (50%)	88 (95%)	4 (4%)	1 (1%)	11	43
29	4	34/103 (33%)	34 (100%)	0	0	100	100
30	5	368/423 (87%)	326 (89%)	32 (9%)	10 (3%)	4	27
31	6	313/380 (82%)	281 (90%)	25 (8%)	7 (2%)	5	30
32	7	258/338 (76%)	226 (88%)	28 (11%)	4 (2%)	7	36
33	8	97/206 (47%)	90 (93%)	6 (6%)	1 (1%)	12	44
34	9	105/137 (77%)	92 (88%)	10 (10%)	3 (3%)	3	26
35	a	78/142 (55%)	74 (95%)	3 (4%)	1 (1%)	9	39
36	b	146/155 (94%)	127 (87%)	16 (11%)	3 (2%)	5	31
37	c	271/332 (82%)	236 (87%)	28 (10%)	7 (3%)	4	27
38	d	156/306 (51%)	137 (88%)	12 (8%)	7 (4%)	2	17
39	e	211/279 (76%)	193 (92%)	14 (7%)	4 (2%)	6	33
40	f	125/194 (64%)	115 (92%)	6 (5%)	4 (3%)	3	24
41	g	127/166 (76%)	114 (90%)	8 (6%)	5 (4%)	2	20
42	h	96/158 (61%)	82 (85%)	9 (9%)	5 (5%)	1	14
43	i	95/128 (74%)	76 (80%)	16 (17%)	3 (3%)	3	24
44	j	83/123 (68%)	77 (93%)	4 (5%)	2 (2%)	4	29
45	k	82/112 (73%)	64 (78%)	12 (15%)	6 (7%)	1	9
46	l	21/138 (15%)	20 (95%)	1 (5%)	0	100	100
47	m	43/128 (34%)	39 (91%)	4 (9%)	0	100	100
48	o	92/102 (90%)	77 (84%)	12 (13%)	3 (3%)	3	23
49	p	119/206 (58%)	113 (95%)	4 (3%)	2 (2%)	7	35
50	q	126/222 (57%)	118 (94%)	8 (6%)	0	100	100
51	r	140/196 (71%)	124 (89%)	13 (9%)	3 (2%)	5	31
52	s	366/439 (83%)	332 (91%)	28 (8%)	6 (2%)	7	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
56	AB	215/296 (73%)	193 (90%)	18 (8%)	4 (2%)	6	33
57	AC	130/167 (78%)	117 (90%)	12 (9%)	1 (1%)	16	49
58	AD	316/430 (74%)	284 (90%)	28 (9%)	4 (1%)	9	39
59	AE	120/125 (96%)	114 (95%)	5 (4%)	1 (1%)	16	49
60	AF	197/242 (81%)	183 (93%)	12 (6%)	2 (1%)	12	44
61	AG	301/396 (76%)	265 (88%)	30 (10%)	6 (2%)	6	32
62	AH	120/201 (60%)	105 (88%)	11 (9%)	4 (3%)	3	23
63	AI	134/194 (69%)	116 (87%)	11 (8%)	7 (5%)	1	14
64	AJ	106/138 (77%)	91 (86%)	14 (13%)	1 (1%)	14	47
65	AK	99/128 (77%)	96 (97%)	2 (2%)	1 (1%)	12	44
66	AL	162/257 (63%)	148 (91%)	13 (8%)	1 (1%)	21	54
67	AM	114/137 (83%)	105 (92%)	9 (8%)	0	100	100
68	AN	105/130 (81%)	94 (90%)	8 (8%)	3 (3%)	3	26
69	AO	183/258 (71%)	157 (86%)	21 (12%)	5 (3%)	4	27
70	AP	94/142 (66%)	85 (90%)	6 (6%)	3 (3%)	3	24
71	AQ	84/87 (97%)	75 (89%)	6 (7%)	3 (4%)	2	22
72	AR	240/360 (67%)	202 (84%)	28 (12%)	10 (4%)	2	19
73	AS	124/190 (65%)	110 (89%)	14 (11%)	0	100	100
74	AT	160/173 (92%)	144 (90%)	8 (5%)	8 (5%)	1	15
75	AU	171/205 (83%)	163 (95%)	8 (5%)	0	100	100
76	AV	320/414 (77%)	283 (88%)	29 (9%)	8 (2%)	4	28
77	AW	95/187 (51%)	82 (86%)	9 (10%)	4 (4%)	2	19
78	AX	310/398 (78%)	263 (85%)	30 (10%)	17 (6%)	1	13
79	AY	106/395 (27%)	95 (90%)	8 (8%)	3 (3%)	4	26
80	AZ	85/106 (80%)	72 (85%)	8 (9%)	5 (6%)	1	12
81	A0	197/218 (90%)	175 (89%)	19 (10%)	3 (2%)	8	37
82	A1	252/323 (78%)	212 (84%)	34 (14%)	6 (2%)	4	29
83	A2	114/118 (97%)	97 (85%)	13 (11%)	4 (4%)	3	23
84	A3	67/199 (34%)	62 (92%)	4 (6%)	1 (2%)	8	37
85	A4	237/579 (41%)	230 (97%)	5 (2%)	2 (1%)	16	49
All	All	12628/17789 (71%)	11290 (89%)	1039 (8%)	299 (2%)	7	29

5 of 299 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	E	170	LEU
4	E	245	THR
5	F	223	HIS
7	I	102	VAL
8	J	70	ILE

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	
3	D	190/245 (78%)	172 (90%)	18 (10%)	8	31
4	E	255/290 (88%)	228 (89%)	27 (11%)	6	27
5	F	217/262 (83%)	195 (90%)	22 (10%)	7	28
6	H	86/228 (38%)	84 (98%)	2 (2%)	44	64
7	I	145/232 (62%)	131 (90%)	14 (10%)	8	30
8	J	113/150 (75%)	102 (90%)	11 (10%)	8	30
9	K	155/156 (99%)	142 (92%)	13 (8%)	10	34
10	L	98/124 (79%)	89 (91%)	9 (9%)	8	32
11	M	245/249 (98%)	221 (90%)	24 (10%)	7	30
12	N	172/211 (82%)	154 (90%)	18 (10%)	6	27
13	O	133/150 (89%)	114 (86%)	19 (14%)	3	18
14	P	115/154 (75%)	105 (91%)	10 (9%)	9	33
15	Q	201/256 (78%)	190 (94%)	11 (6%)	19	46
16	R	118/126 (94%)	102 (86%)	16 (14%)	3	19
17	S	141/180 (78%)	129 (92%)	12 (8%)	10	34
18	T	146/182 (80%)	140 (96%)	6 (4%)	27	53
19	U	99/135 (73%)	89 (90%)	10 (10%)	7	28
20	V	169/191 (88%)	159 (94%)	10 (6%)	18	44
21	W	91/119 (76%)	83 (91%)	8 (9%)	9	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	X	217/227 (96%)	202 (93%)	15 (7%)	14	39
23	Y	159/223 (71%)	147 (92%)	12 (8%)	12	37
24	Z	111/147 (76%)	101 (91%)	10 (9%)	9	32
25	0	97/164 (59%)	83 (86%)	14 (14%)	3	18
26	1	49/60 (82%)	43 (88%)	6 (12%)	5	22
27	2	40/72 (56%)	35 (88%)	5 (12%)	4	22
28	3	88/166 (53%)	84 (96%)	4 (4%)	24	50
29	4	35/89 (39%)	32 (91%)	3 (9%)	10	33
30	5	337/368 (92%)	303 (90%)	34 (10%)	7	28
31	6	266/332 (80%)	243 (91%)	23 (9%)	10	33
32	7	242/303 (80%)	231 (96%)	11 (4%)	24	50
33	8	91/190 (48%)	87 (96%)	4 (4%)	25	51
34	9	91/112 (81%)	84 (92%)	7 (8%)	12	37
35	a	78/133 (59%)	74 (95%)	4 (5%)	21	48
36	b	130/135 (96%)	118 (91%)	12 (9%)	8	32
37	c	241/288 (84%)	220 (91%)	21 (9%)	9	33
38	d	151/274 (55%)	147 (97%)	4 (3%)	40	62
39	e	188/236 (80%)	179 (95%)	9 (5%)	23	49
40	f	117/173 (68%)	115 (98%)	2 (2%)	53	70
41	g	119/148 (80%)	109 (92%)	10 (8%)	10	34
42	h	95/148 (64%)	84 (88%)	11 (12%)	5	24
43	i	86/110 (78%)	76 (88%)	10 (12%)	5	24
44	j	68/97 (70%)	60 (88%)	8 (12%)	5	23
45	k	74/90 (82%)	65 (88%)	9 (12%)	5	22
46	l	23/116 (20%)	20 (87%)	3 (13%)	4	21
47	m	40/113 (35%)	39 (98%)	1 (2%)	42	63
48	o	80/87 (92%)	74 (92%)	6 (8%)	12	37
49	p	117/181 (65%)	107 (92%)	10 (8%)	10	34
50	q	110/178 (62%)	100 (91%)	10 (9%)	9	32
51	r	133/169 (79%)	124 (93%)	9 (7%)	14	40
52	s	326/381 (86%)	298 (91%)	28 (9%)	10	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	AB	191/249 (77%)	171 (90%)	20 (10%)	6	27
57	AC	115/143 (80%)	111 (96%)	4 (4%)	32	57
58	AD	269/357 (75%)	242 (90%)	27 (10%)	7	28
59	AE	104/107 (97%)	98 (94%)	6 (6%)	18	44
60	AF	178/209 (85%)	164 (92%)	14 (8%)	11	36
61	AG	265/342 (78%)	240 (91%)	25 (9%)	8	31
62	AH	112/180 (62%)	96 (86%)	16 (14%)	3	18
63	AI	104/147 (71%)	89 (86%)	15 (14%)	3	18
64	AJ	93/118 (79%)	86 (92%)	7 (8%)	12	37
65	AK	91/113 (80%)	81 (89%)	10 (11%)	6	26
66	AL	152/226 (67%)	131 (86%)	21 (14%)	3	19
67	AM	95/113 (84%)	83 (87%)	12 (13%)	4	21
68	AN	93/115 (81%)	85 (91%)	8 (9%)	10	33
69	AO	166/230 (72%)	152 (92%)	14 (8%)	10	34
70	AP	87/123 (71%)	76 (87%)	11 (13%)	4	21
71	AQ	78/79 (99%)	73 (94%)	5 (6%)	16	42
72	AR	224/318 (70%)	198 (88%)	26 (12%)	5	24
73	AS	109/164 (66%)	100 (92%)	9 (8%)	10	34
74	AT	150/157 (96%)	129 (86%)	21 (14%)	3	19
75	AU	149/174 (86%)	133 (89%)	16 (11%)	6	27
76	AV	295/364 (81%)	267 (90%)	28 (10%)	8	31
77	AW	84/158 (53%)	74 (88%)	10 (12%)	5	23
78	AX	275/351 (78%)	232 (84%)	43 (16%)	2	15
79	AY	99/357 (28%)	93 (94%)	6 (6%)	17	43
80	AZ	80/95 (84%)	72 (90%)	8 (10%)	7	28
81	A0	176/190 (93%)	160 (91%)	16 (9%)	9	32
82	A1	237/291 (81%)	221 (93%)	16 (7%)	14	40
83	A2	99/101 (98%)	85 (86%)	14 (14%)	3	18
84	A3	63/166 (38%)	54 (86%)	9 (14%)	3	18
85	A4	226/379 (60%)	211 (93%)	15 (7%)	15	41
All	All	11347/15266 (74%)	10320 (91%)	1027 (9%)	11	32

5 of 1027 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
78	AX	243	VAL
80	AZ	55	HIS
78	AX	242	ILE
32	7	81	MET
31	6	298	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 191 such sidechains are listed below:

Mol	Chain	Res	Type
49	p	96	ASN
61	AG	384	GLN
50	q	137	GLN
57	AC	115	ASN
66	AL	152	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1459/1559 (93%)	486 (33%)	99 (6%)
2	B	52/73 (71%)	21 (40%)	3 (5%)
54	u	1/2 (50%)	1 (100%)	0
55	AA	914/954 (95%)	285 (31%)	57 (6%)
All	All	2426/2588 (93%)	793 (32%)	159 (6%)

5 of 793 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	1672	C
1	A	1674	A
1	A	1675	A
1	A	1676	A
1	A	1678	C

5 of 159 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
55	AA	882	A
55	AA	1353	A
55	AA	953	U

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Mol	Chain	Res	Type
55	AA	1189	U
55	AA	1465	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 135 ligands modelled in this entry, 134 are monoatomic - leaving 1 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
88	GDP	AX	500	-	29,30,30	1.21	4 (13%)	45,47,47	1.90	8 (17%)

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
88	GDP	AX	500	-	-	6/16/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
88	AX	500	GDP	C5-C4	3.39	1.48	1.38
88	AX	500	GDP	C5-N7	-2.19	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
88	AX	500	GDP	C6-N1	-2.14	1.34	1.38
88	AX	500	GDP	PA-O3A	2.07	1.61	1.59

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
88	AX	500	GDP	C5-C4-N3	-6.55	117.97	128.39
88	AX	500	GDP	C2-N3-C4	5.33	121.47	112.30
88	AX	500	GDP	N9-C4-N3	5.17	136.29	125.95
88	AX	500	GDP	C6-C5-N7	2.93	135.62	130.29
88	AX	500	GDP	C3'-C2'-C1'	2.79	106.74	101.46

There are no chirality outliers.

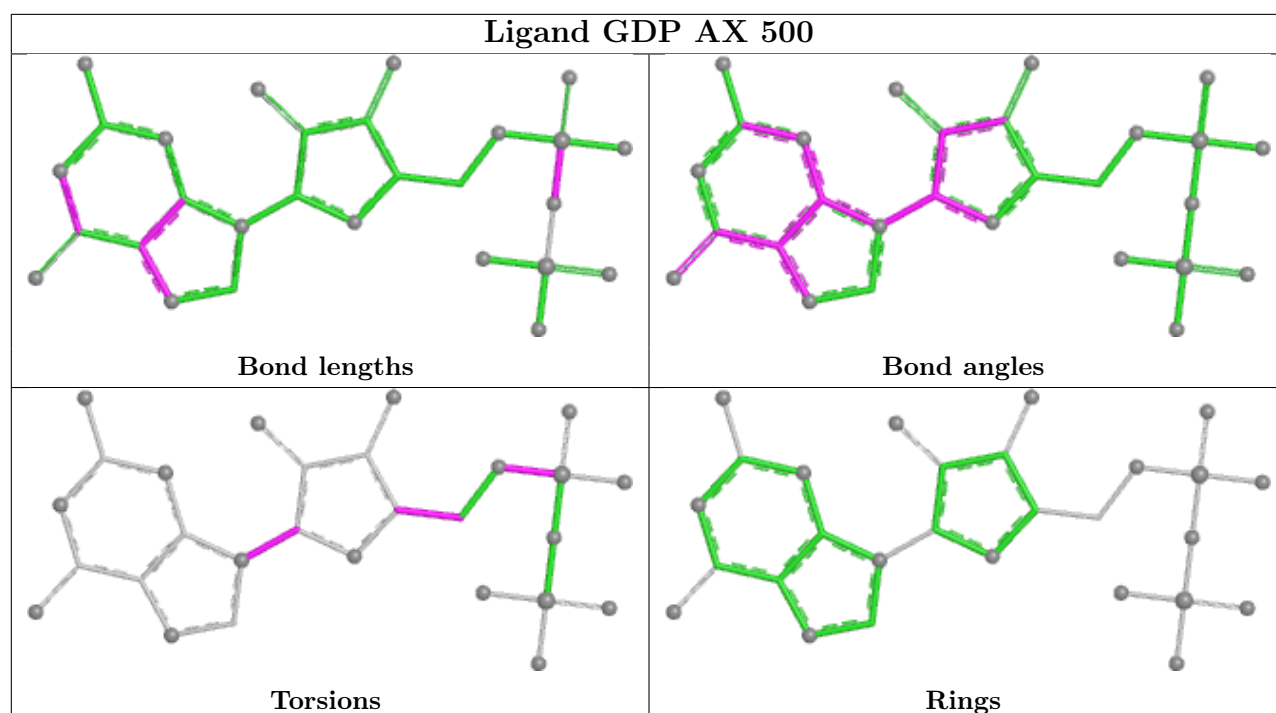
5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
88	AX	500	GDP	C5'-O5'-PA-O3A
88	AX	500	GDP	C3'-C4'-C5'-O5'
88	AX	500	GDP	O4'-C1'-N9-C8
88	AX	500	GDP	O4'-C1'-N9-C4
88	AX	500	GDP	O4'-C4'-C5'-O5'

There are no ring outliers.

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
85	A4	13

The worst 5 of 13 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A4	380:ASP	C	386:UNK	N	26.68
1	A4	143:GLU	C	145:UNK	N	21.71
1	A4	399:UNK	C	414:LYS	N	20.81
1	A4	173:UNK	C	220:UNK	N	13.65
1	A4	300:UNK	C	311:UNK	N	13.15

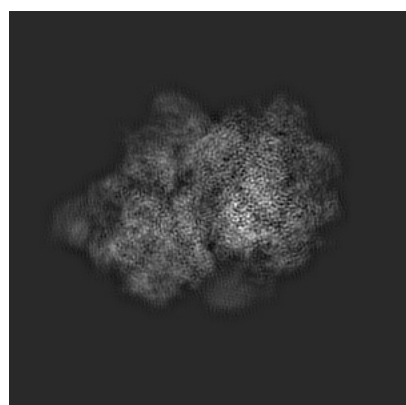
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2876. These allow visual inspection of the internal detail of the map and identification of artifacts.

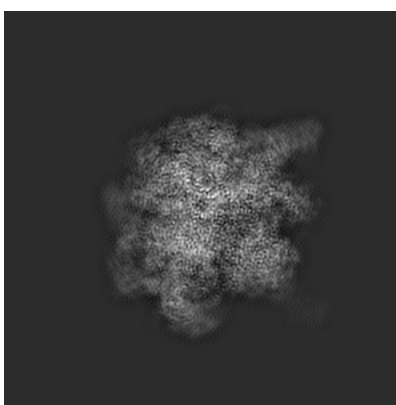
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

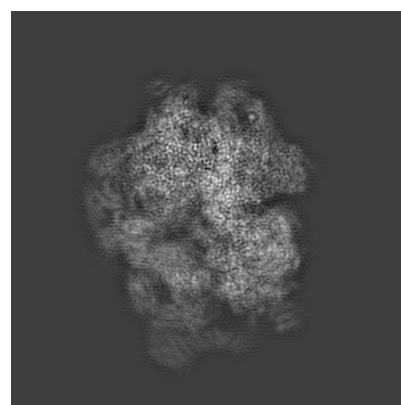
6.1.1 Primary map



X



Y

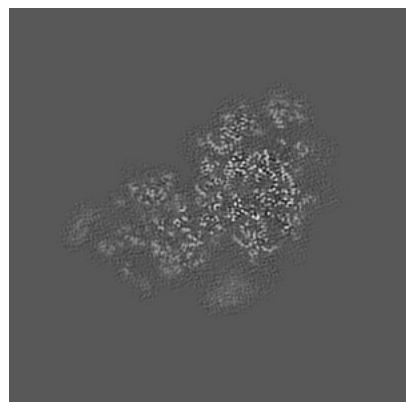


Z

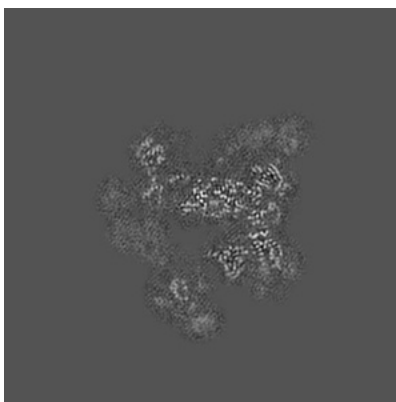
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

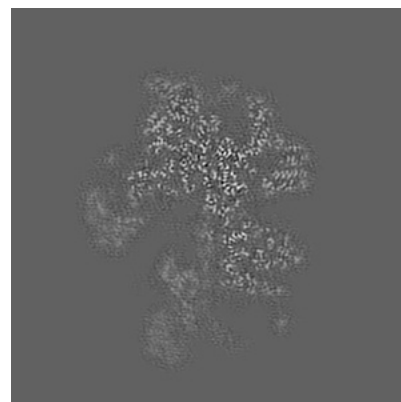
6.2.1 Primary map



X Index: 160



Y Index: 160

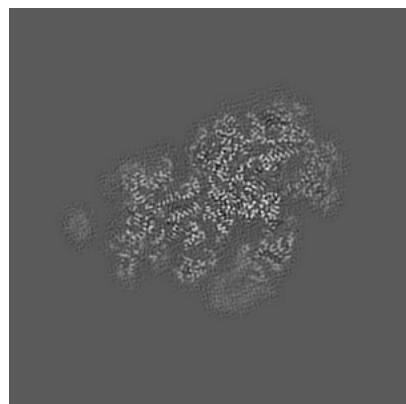


Z Index: 160

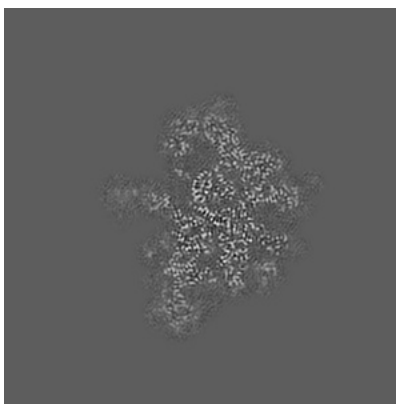
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

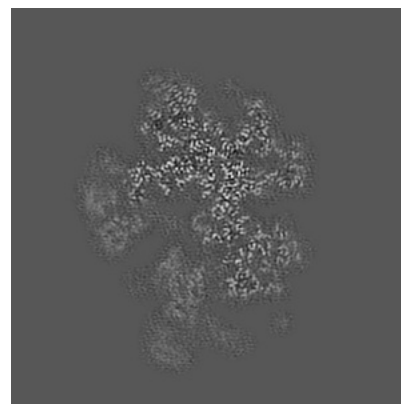
6.3.1 Primary map



X Index: 173



Y Index: 194

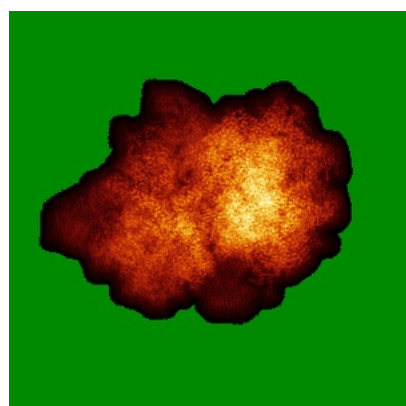


Z Index: 155

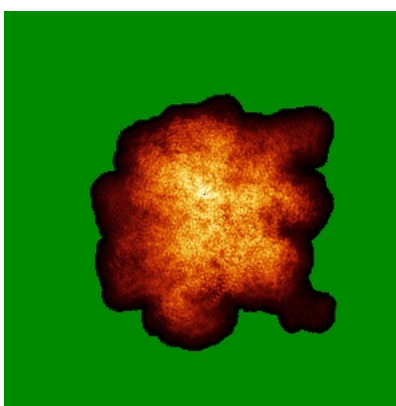
The images above show the largest variance slices of the map in three orthogonal directions.

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

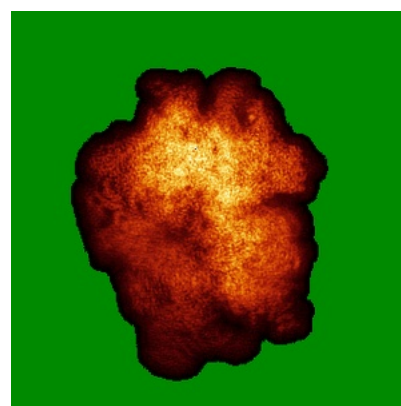
6.4.1 Primary map



X



Y

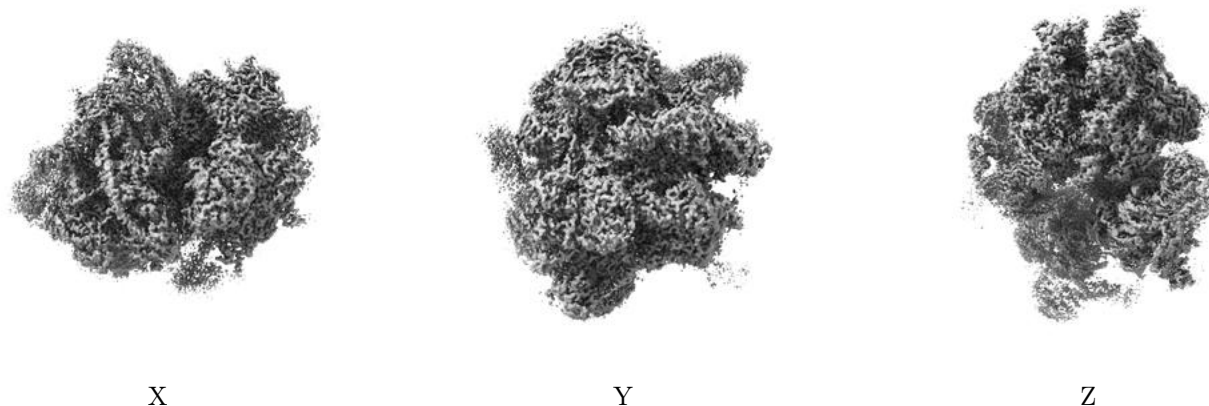


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

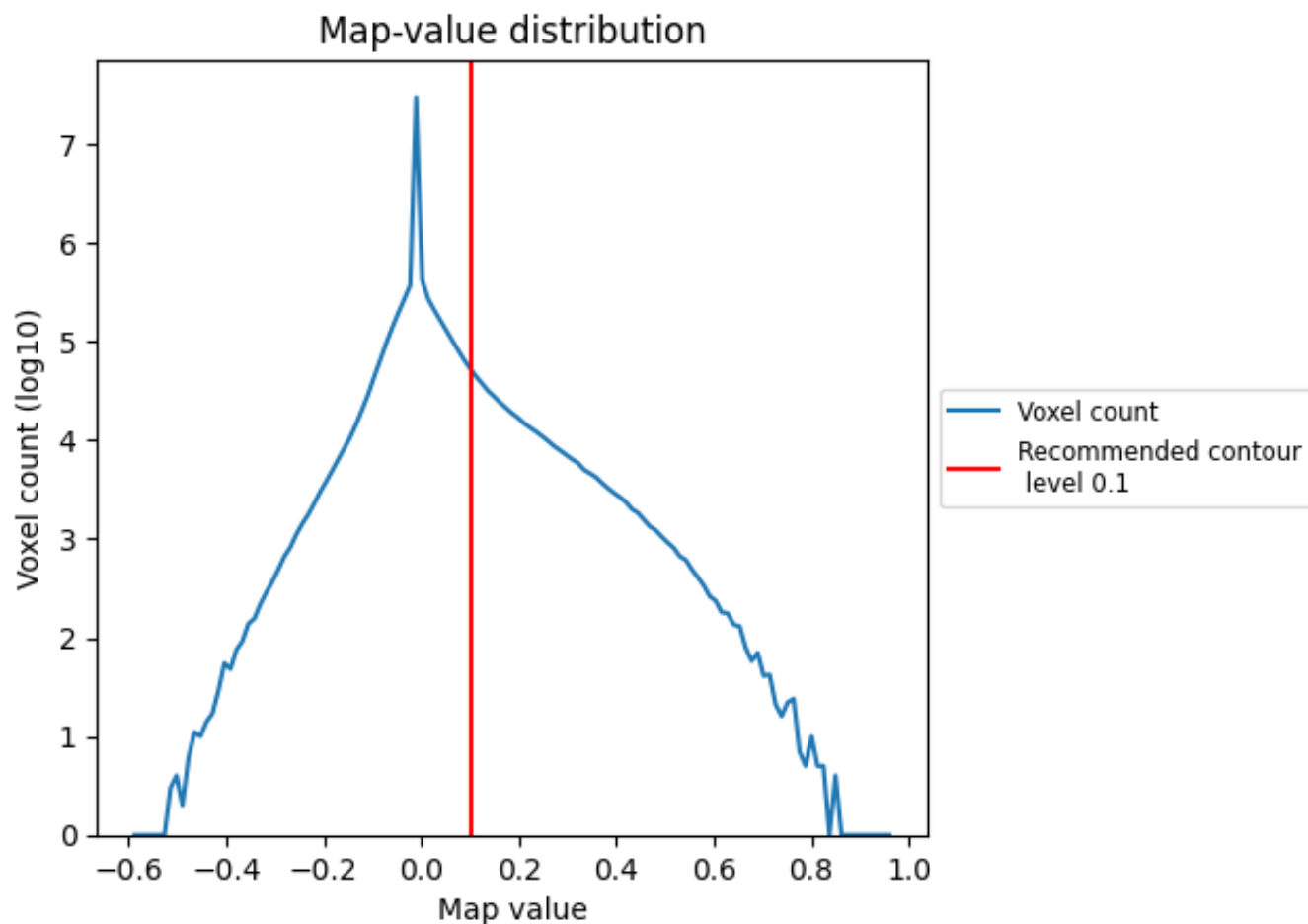
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

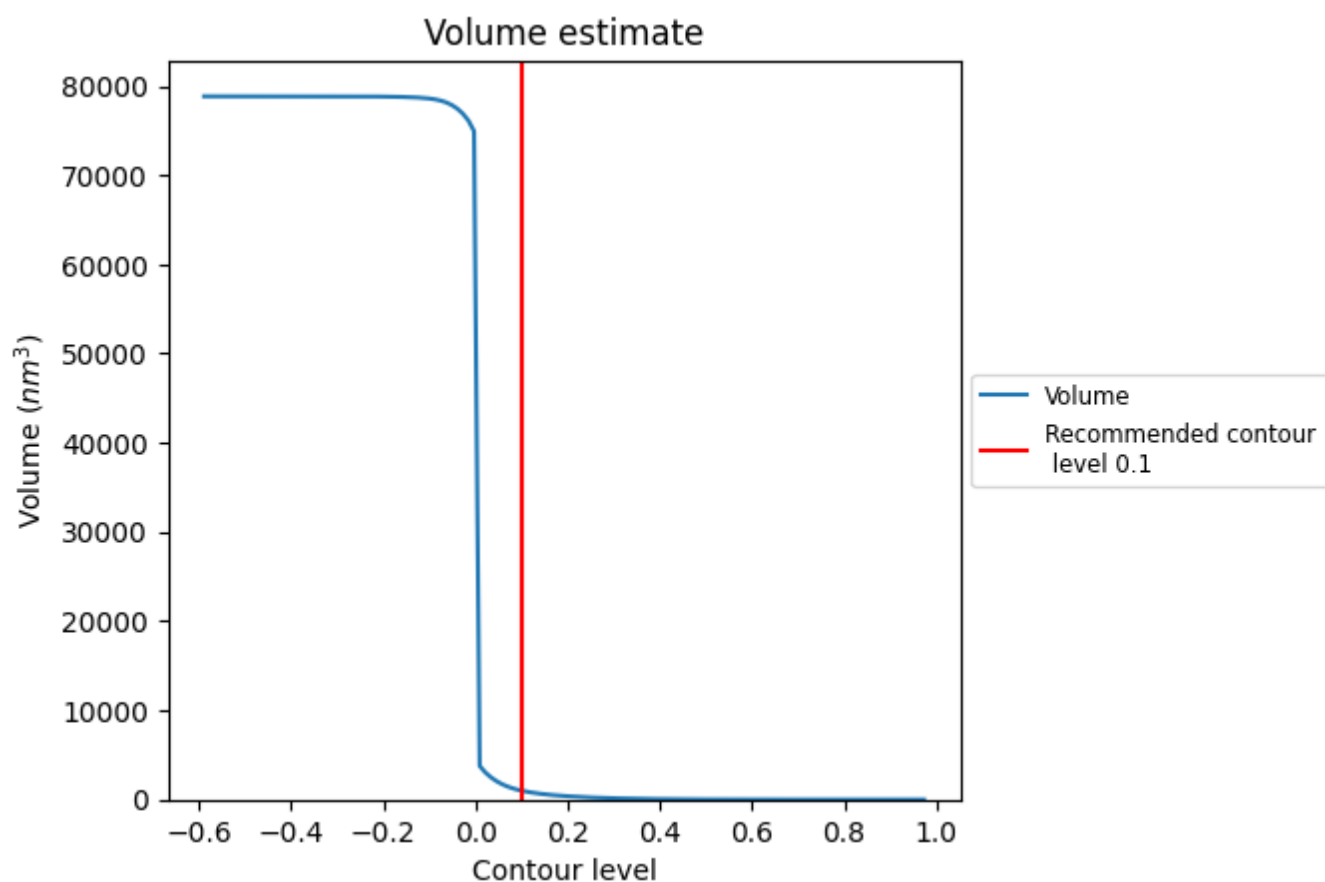
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

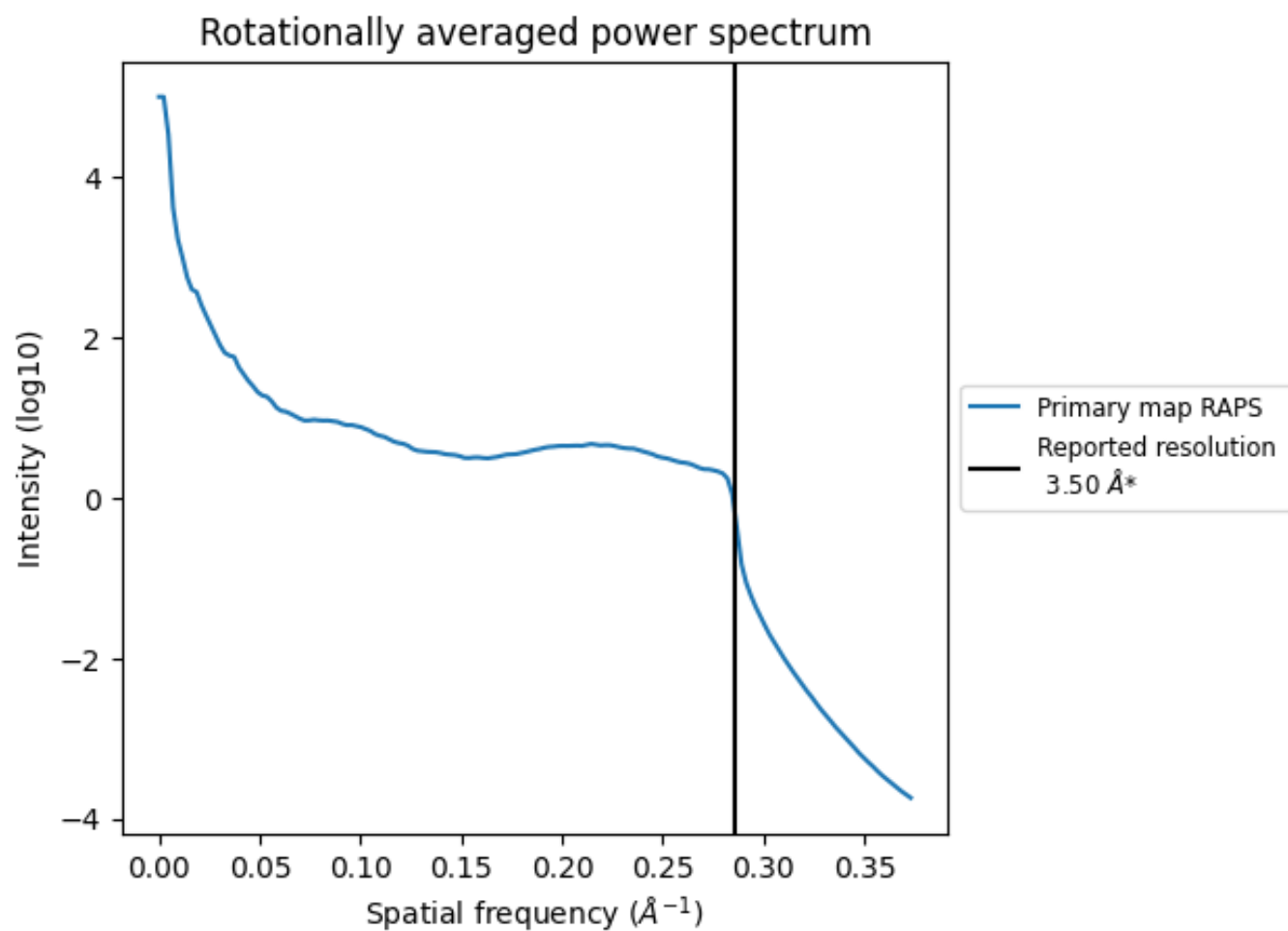
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1002 nm³; this corresponds to an approximate mass of 905 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 ⓘ

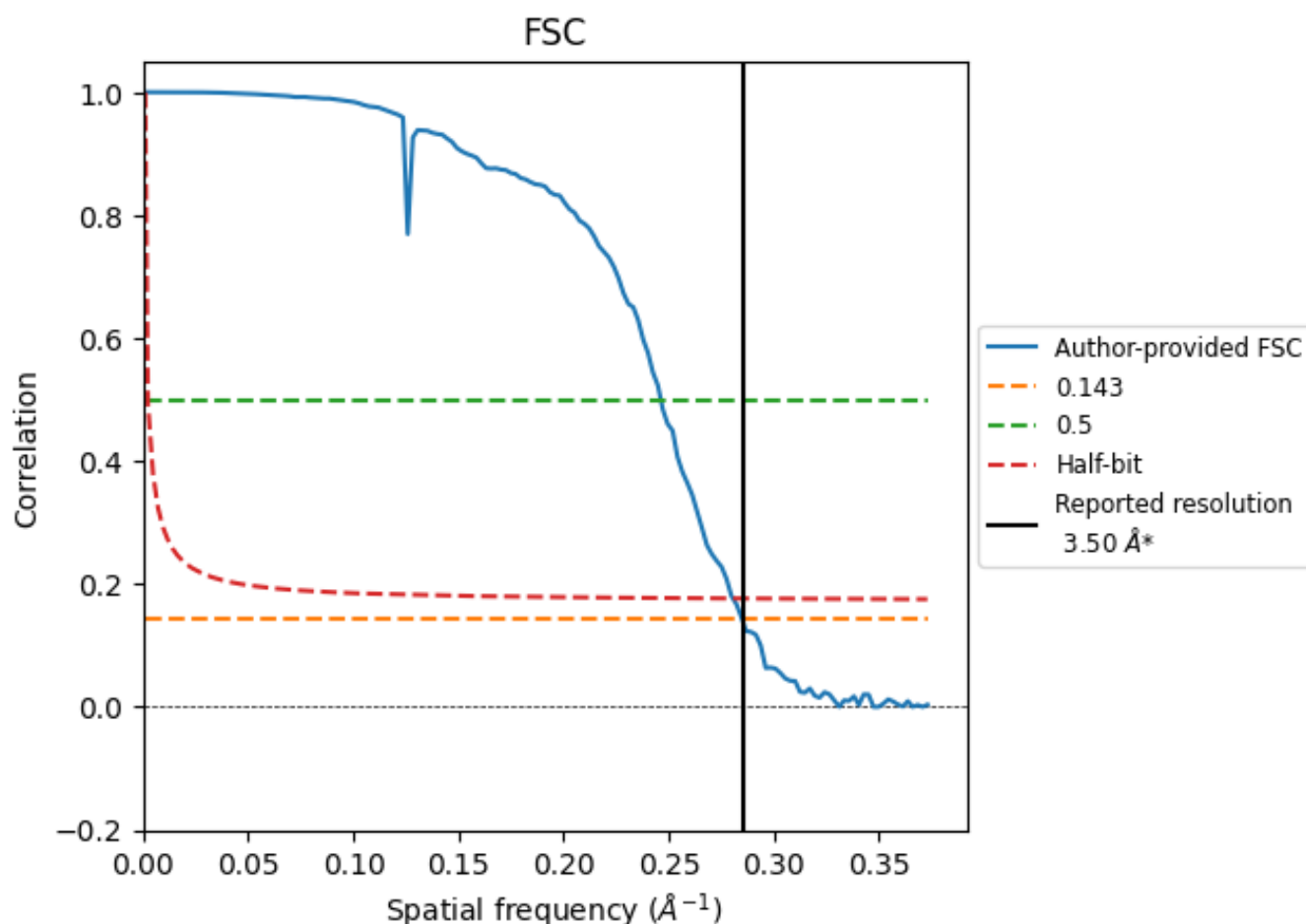


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

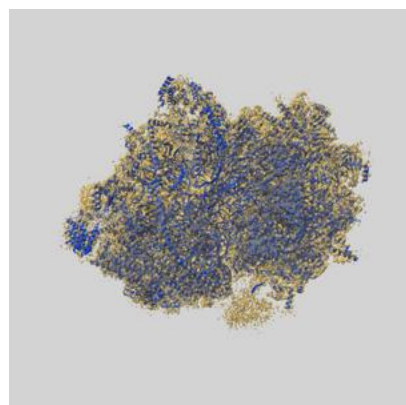
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.51	4.06	3.57
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

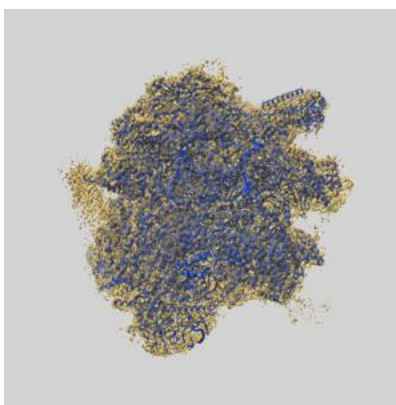
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2876 and PDB model 3J9M. Per-residue inclusion information can be found in section [3](#) on page [21](#).

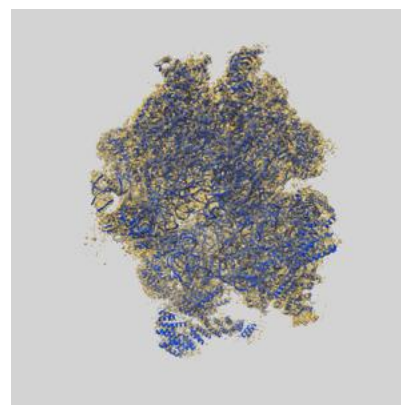
9.1 Map-model overlay [i](#)



X



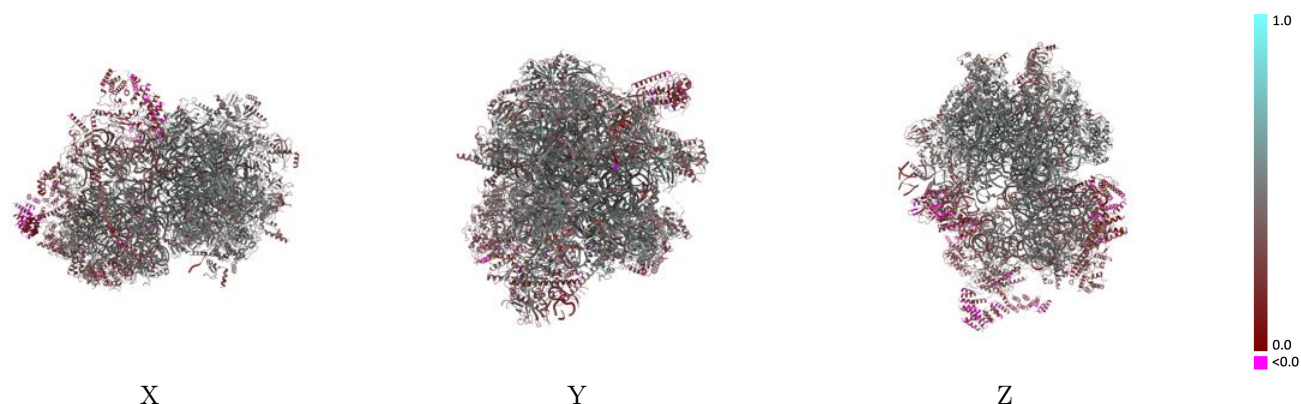
Y



Z

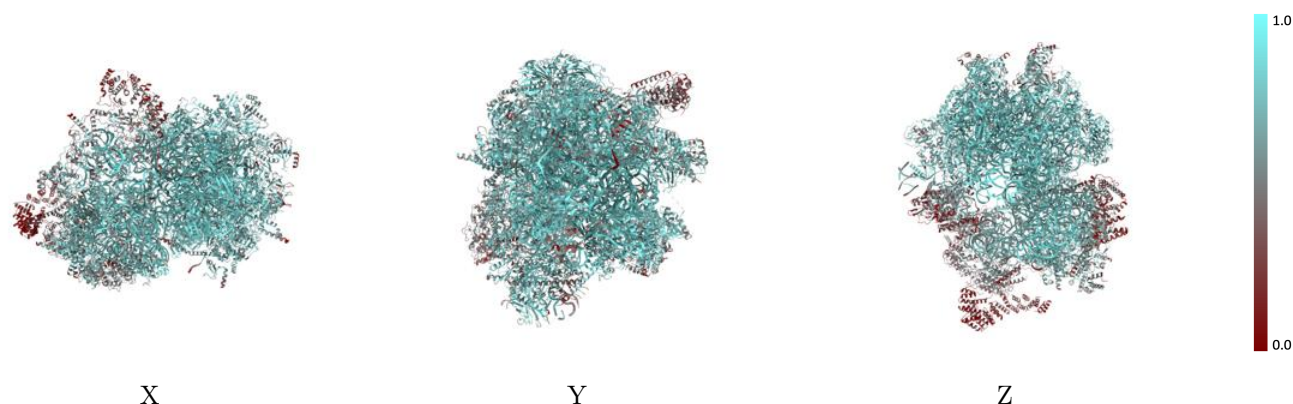
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



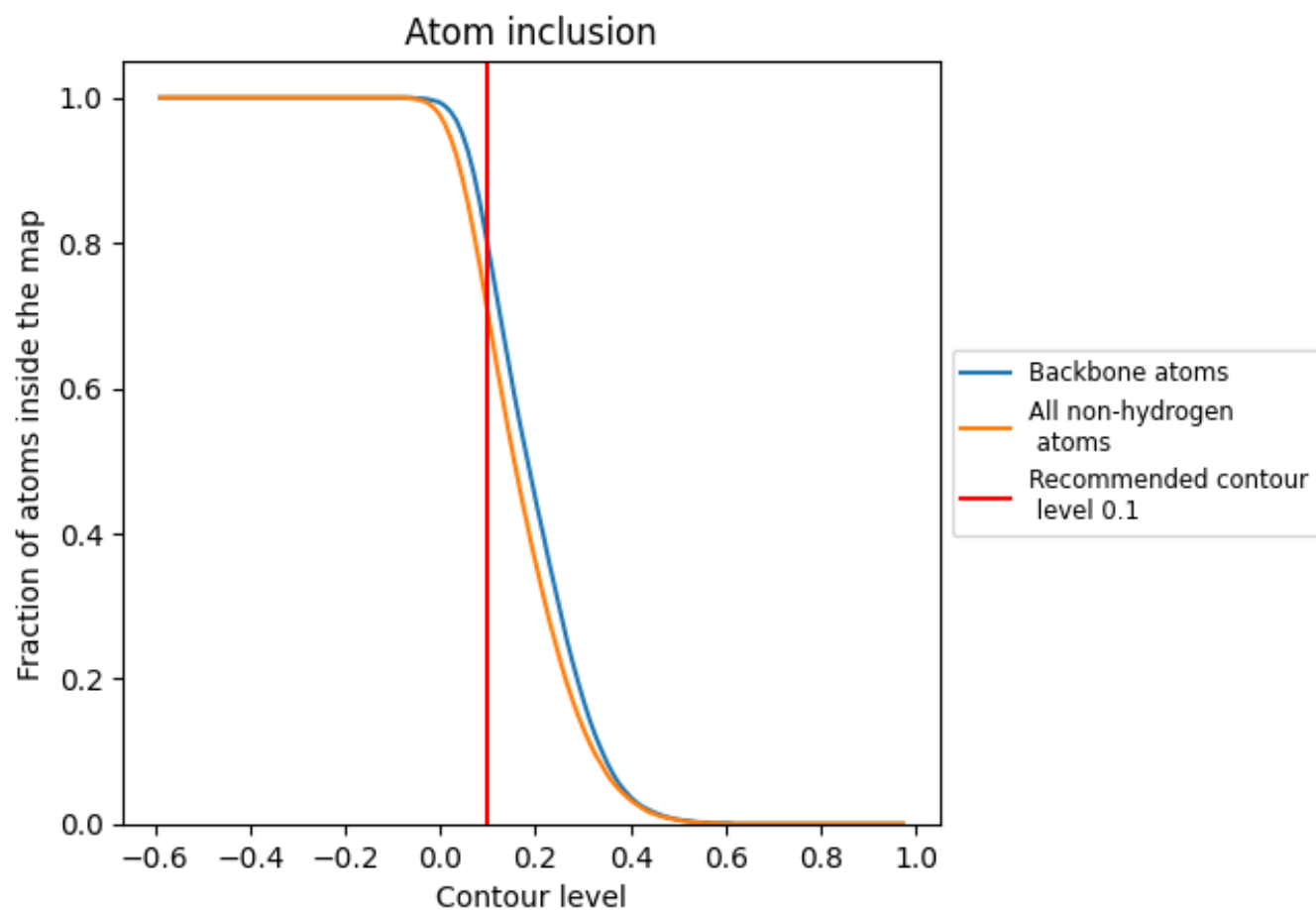
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 70% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7030	 0.4050
0	 0.7460	 0.4550
1	 0.6710	 0.4370
2	 0.8250	 0.5220
3	 0.8160	 0.5040
4	 0.8080	 0.4930
5	 0.7690	 0.4560
6	 0.7080	 0.3820
7	 0.6680	 0.4070
8	 0.4420	 0.2020
9	 0.7450	 0.4570
A	 0.8660	 0.4680
A0	 0.5020	 0.2750
A1	 0.3950	 0.2390
A2	 0.5770	 0.3860
A3	 0.7010	 0.4310
A4	 0.1710	 0.1280
AA	 0.8200	 0.4200
AB	 0.7210	 0.4360
AC	 0.5250	 0.3760
AD	 0.6000	 0.4020
AE	 0.6980	 0.4360
AF	 0.5410	 0.3390
AG	 0.5490	 0.3410
AH	 0.4980	 0.3420
AI	 0.7360	 0.4550
AJ	 0.6430	 0.4200
AK	 0.5330	 0.3260
AL	 0.6620	 0.4080
AM	 0.5820	 0.3600
AN	 0.6990	 0.4370
AO	 0.6080	 0.3590
AP	 0.7240	 0.4430
AQ	 0.7260	 0.4560
AR	 0.5370	 0.3140



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Chain	Atom inclusion	Q-score
AS	 0.6070	 0.3750
AT	 0.6780	 0.4070
AU	 0.5750	 0.3010
AV	 0.3260	 0.1820
AW	 0.6510	 0.3990
AX	 0.4510	 0.2580
AY	 0.3310	 0.2180
AZ	 0.4690	 0.2710
B	 0.7150	 0.2990
D	 0.8120	 0.4920
E	 0.7750	 0.4780
F	 0.7680	 0.4770
H	 0.6610	 0.4060
I	 0.4380	 0.2580
J	 0.2530	 0.1600
K	 0.7810	 0.4720
L	 0.7360	 0.4580
M	 0.7540	 0.4650
N	 0.7730	 0.4660
O	 0.7640	 0.4680
P	 0.7390	 0.4210
Q	 0.7280	 0.4520
R	 0.7910	 0.4880
S	 0.7570	 0.4760
T	 0.7630	 0.4830
U	 0.8240	 0.4840
V	 0.5870	 0.3990
W	 0.7950	 0.5060
X	 0.7000	 0.4390
Y	 0.7560	 0.4630
Z	 0.7760	 0.4870
a	 0.7680	 0.4620
b	 0.7780	 0.4770
c	 0.7210	 0.4310
d	 0.5690	 0.3720
e	 0.3650	 0.1630
f	 0.5500	 0.3300
g	 0.7550	 0.4650
h	 0.4410	 0.3230
i	 0.8150	 0.4900
j	 0.7280	 0.4430
k	 0.3740	 0.2260

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Chain	Atom inclusion	Q-score
l	 0.6020	 0.3260
m	 0.5210	 0.2970
o	 0.7990	 0.4790
p	 0.6080	 0.3690
q	 0.5370	 0.3600
r	 0.7600	 0.4520
s	 0.7640	 0.4570
t	 0.2790	 0.1140
u	 0.5480	 0.4340