



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:03 PM UTC

PDB ID : 3J92 / pdb_00003j92
EMDB ID : EMD-2832
Title : Structure and assembly pathway of the ribosome quality control complex
Authors : Shao, S.; Brown, A.; Santhanam, B.; Hegde, R.S.
Deposited on : 2014-12-02
Resolution : 3.60 Å(reported)
Based on initial models : 4W1Z, 4W20

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
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

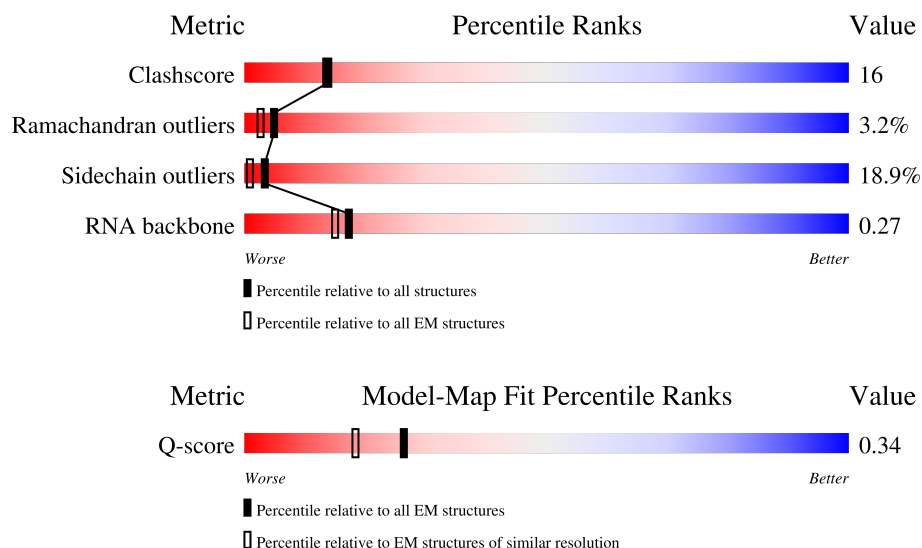
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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	12797 (3.10 - 4.10)

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	257	 53% 31% 11% 5%
2	B	395	 68% 25% 5%
3	C	368	 10% 59% 32% 7%

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Mol	Chain	Length	Quality of chain
4	D	297	
5	E	284	
6	F	250	
7	G	266	
8	H	192	
9	I	214	
10	J	178	
11	L	211	
12	M	213	
13	N	204	
14	O	204	
15	P	184	
16	Q	188	
17	R	196	
18	S	224	
19	T	160	
20	U	128	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	160	
28	c	115	

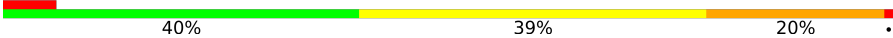
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Mol	Chain	Length	Quality of chain
29	d	125	
30	e	135	
31	f	110	
32	g	117	
33	h	123	
34	i	105	
35	j	97	
36	k	70	
37	l	51	
38	m	128	
39	o	106	
40	p	92	
41	r	137	
42	s	317	
43	t	165	
44	u	501	
44	v	501	
45	0	1766	
45	w	1766	
45	z	1766	
46	x	218	
46	y	218	
47	1	104	
48	2	77	
49	5	3664	

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Mol	Chain	Length	Quality of chain
50	7	120	
51	8	156	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
53	ZN	j	101	-	-	X	-

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 146386 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 uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	244	Total	C	N	O	S	0	0
			1868	1171	382	309	6		

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	394	Total	C	N	O	S	0	0
			3147	2005	591	538	13		

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	367	Total	C	N	O	S	0	0
			2919	1836	582	486	15		

- Molecule 4 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	292	Total	C	N	O	S	0	0
			2384	1511	435	426	12		

- Molecule 5 is a protein called eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	236	Total	C	N	O	S	0	0
			1904	1219	364	316	5		

- Molecule 6 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 7 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	241	Total	C	N	O	S	0	0
			1939	1235	372	328	4		

- Molecule 8 is a protein called uL6.

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

- Molecule 9 is a protein called uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	204	Total	C	N	O	S	0	0
			1651	1048	318	271	14		

- Molecule 10 is a protein called uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	170	Total	C	N	O	S	0	0
			1359	856	256	241	6		

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	210	Total	C	N	O	S	0	0
			1703	1064	354	280	5		

- Molecule 12 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	138	Total	C	N	O	S	0	0
			1131	727	216	181	7		

- Molecule 13 is a protein called eL15.

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

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	199	Total	C	N	O	S	0	0
			1638	1056	321	256	5		

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 16 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- Molecule 19 is a protein called eL21.

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

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 21 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 22 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 24 is a protein called uL24.

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

- Molecule 25 is a protein called eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	147	Total	C	N	O	S	0	0
			1163	735	239	185	4		

- Molecule 27 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 29 is a protein called eL31.

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

- Molecule 30 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 32 is a protein called eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 33 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	122	Total	C	N	O	S	0	0
			1015	642	205	167	1		

- Molecule 34 is a protein called eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 35 is a protein called eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	86	Total	C	N	O	S	0	0
			706	436	155	110	5		

- Molecule 36 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 39 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 40 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 41 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	r	125	Total	C	N	O	S	0	0
			1001	622	206	168	5		

- Molecule 42 is a protein called uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	s	198	Total	C	N	O	S	0	0
			1522	968	265	280	9		

- Molecule 43 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	t	163	Total	C	N	O	S	0	0
			1238	773	230	230	5		

- Molecule 44 is a protein called NEMF.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	u	130	Total	C	N	O		0	0
			645	385	130	130			
44	v	136	Total	C	N	O	S	0	0
			1092	687	197	206	2		

- Molecule 45 is a protein called Listerin.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	w	15	Total	C	N	O		0	0
			110	67	23	20			
45	z	130	Total	C	N	O	S	0	0
			1057	681	180	189	7		
45	0	36	Total	C	N	O	S	0	0
			293	187	53	48	5		

- Molecule 46 is a protein called Listerin.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	x	218	Total	C	N	O		0	0
			1090	654	218	218			
46	y	211	Total	C	N	O		0	0
			1055	633	211	211			

- Molecule 47 is a protein called nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	1	15	Total	C	N	O	S	0	0
			125	82	20	22	1		

- Molecule 48 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	2	75	Total	C	N	O	P	0	0
			1601	715	292	520	74		

- Molecule 49 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	5	3662	Total	C	N	O	P	0	0
			78486	34947	14363	25515	3661		

- Molecule 50 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 51 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 52 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
52	P	1	Total	Mg	0
			1	1	
52	V	1	Total	Mg	0
			1	1	
52	g	1	Total	Mg	0
			1	1	
52	5	150	Total	Mg	0
			150	150	
52	7	5	Total	Mg	0
			5	5	
52	8	1	Total	Mg	0
			1	1	

- Molecule 53 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
53	g	1	Total	Zn	0
			1	1	

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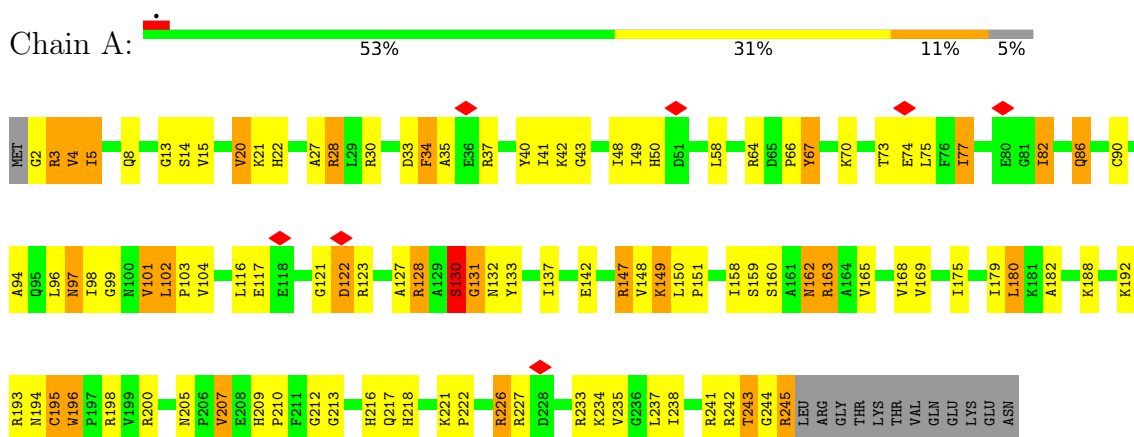
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Mol	Chain	Residues	Atoms		AltConf
53	j	1	Total 1	Zn 1	0
53	m	1	Total 1	Zn 1	0
53	o	1	Total 1	Zn 1	0
53	p	1	Total 1	Zn 1	0

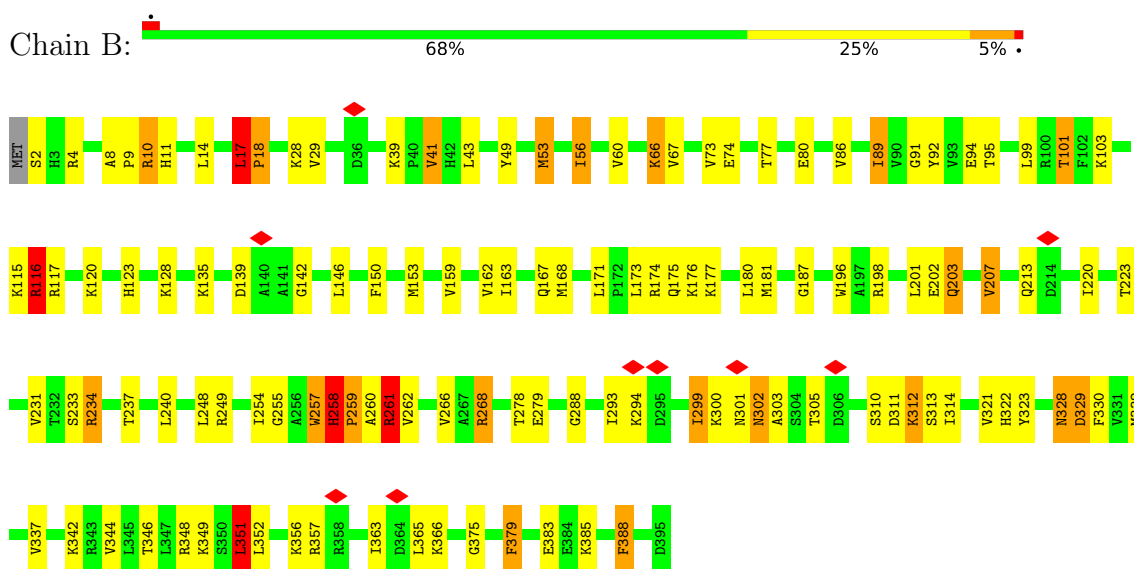
3 Residue-property plots

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

• Molecule 1: uL2

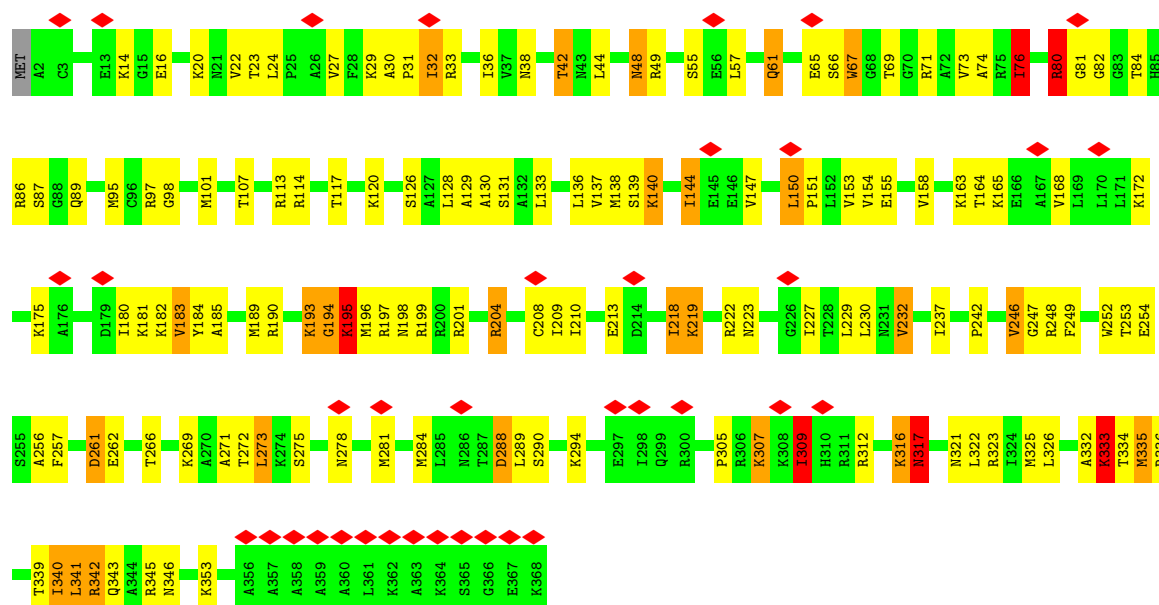


• Molecule 2: uL3

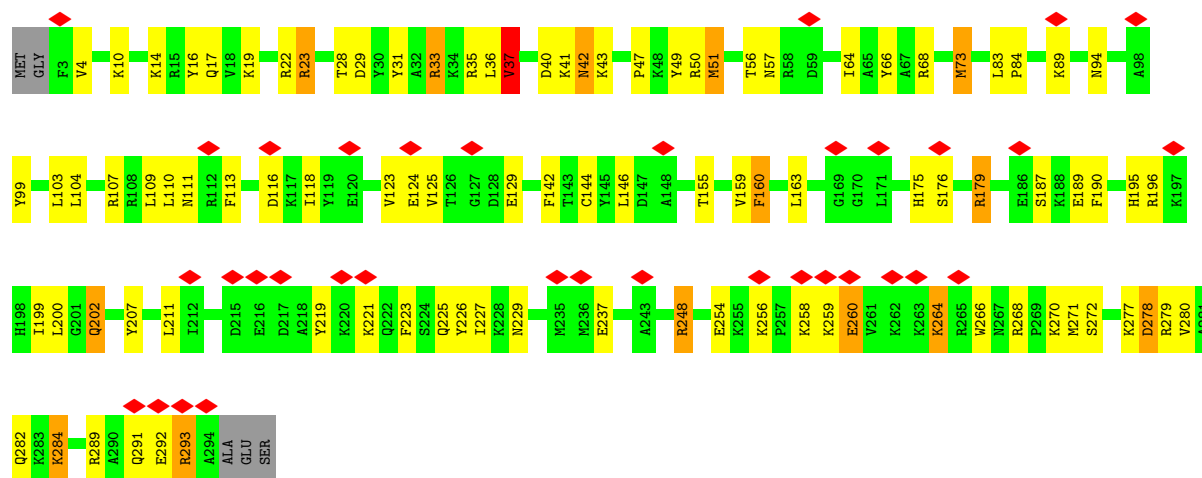


• Molecule 3: uL4

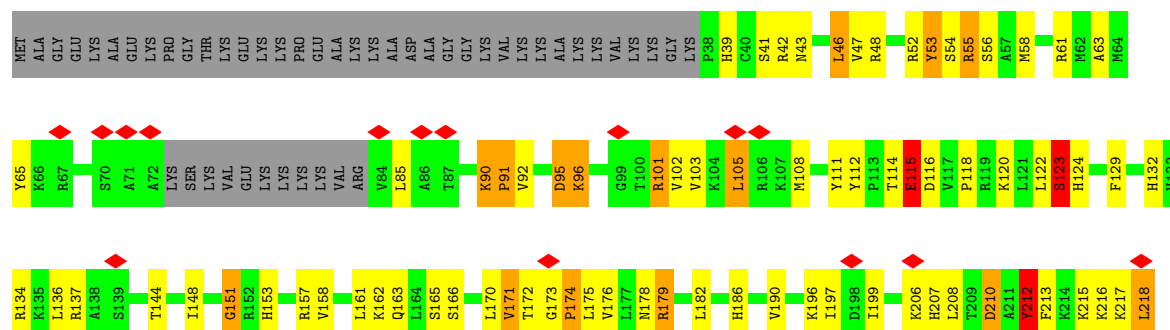


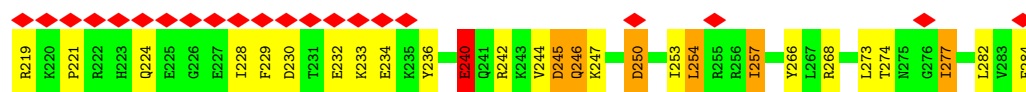


• Molecule 4: uL18

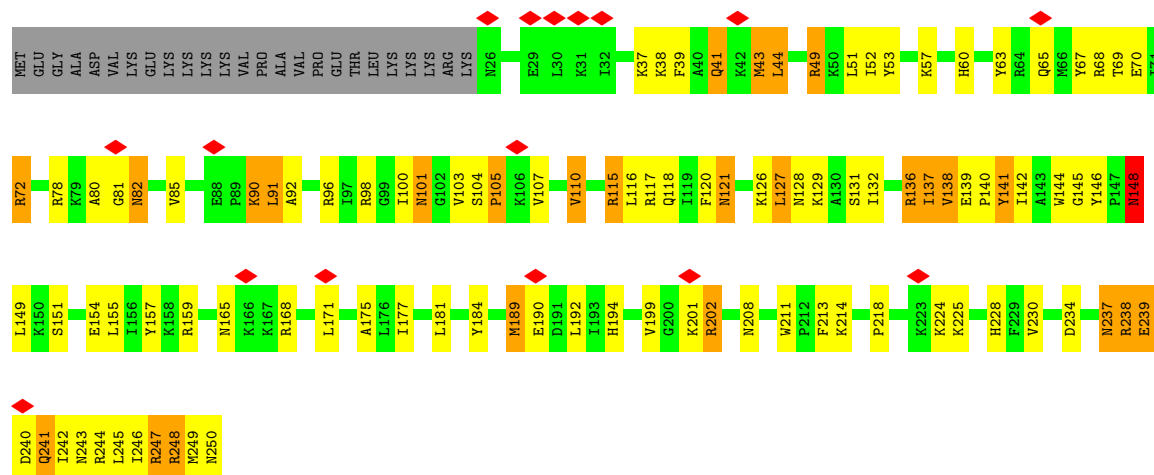


• Molecule 5: eL6

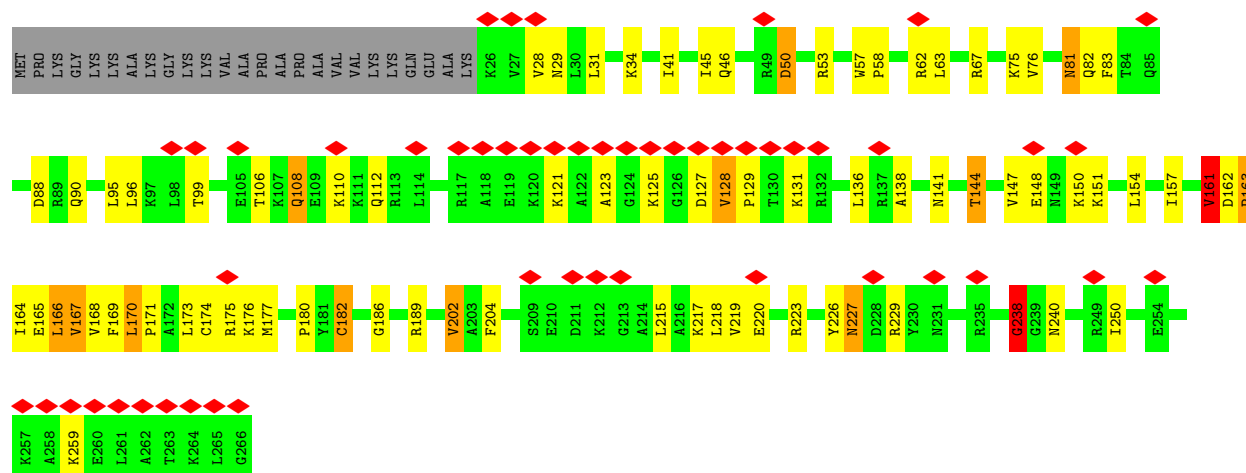




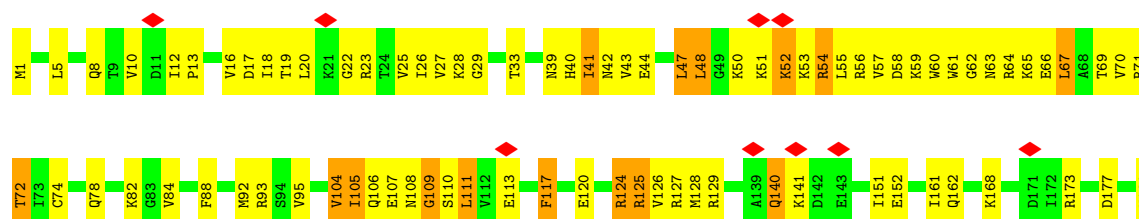
• Molecule 6: eL30

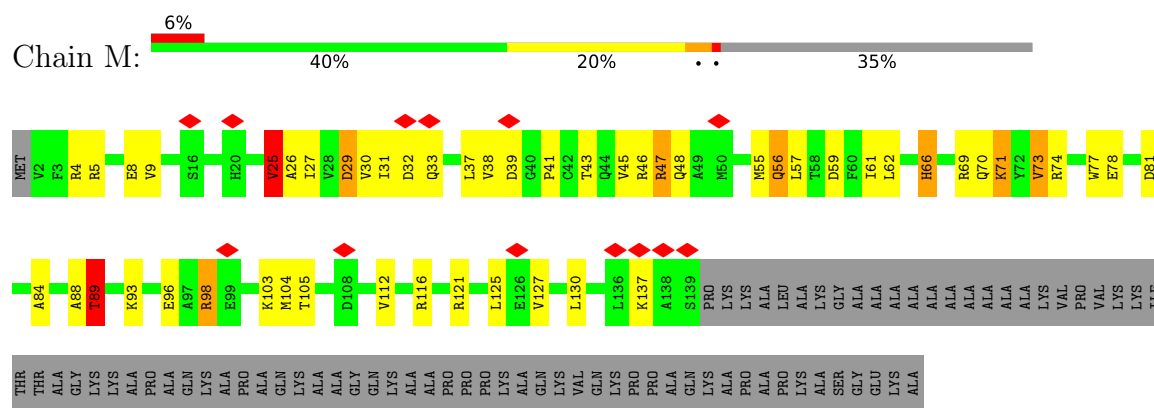


• Molecule 7: eL8

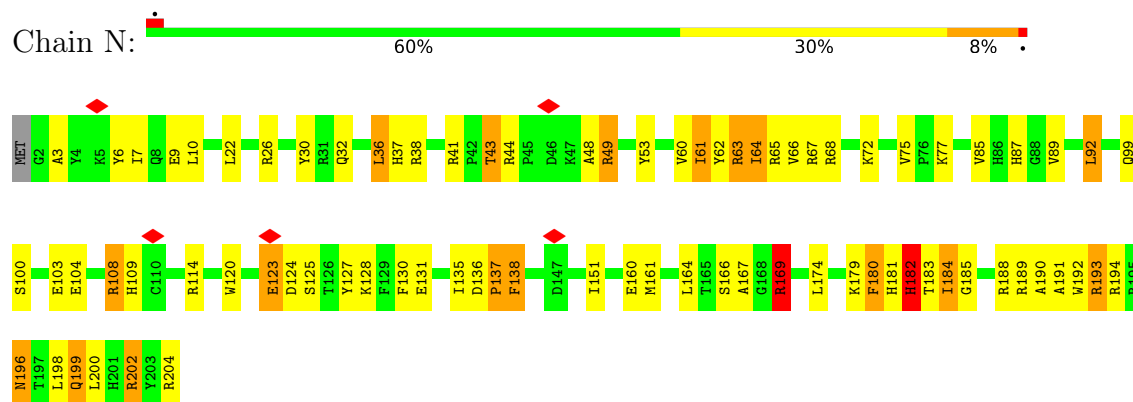


• Molecule 8: uL6

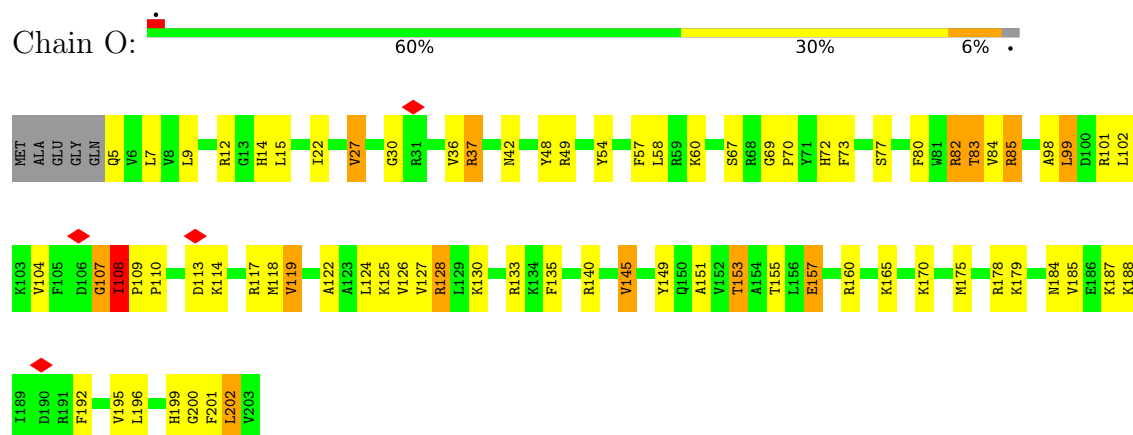




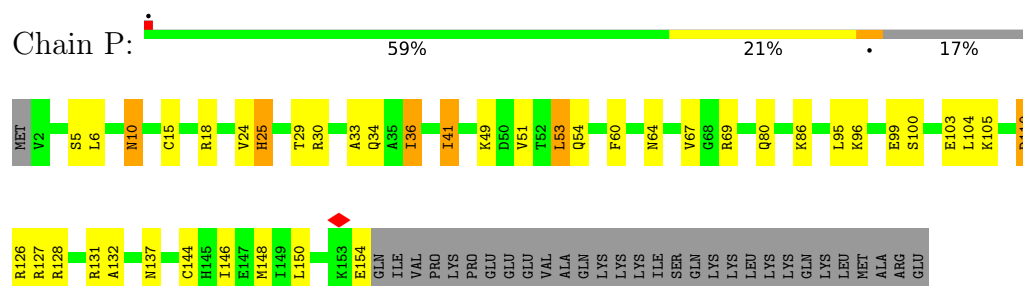
• Molecule 13: eL15

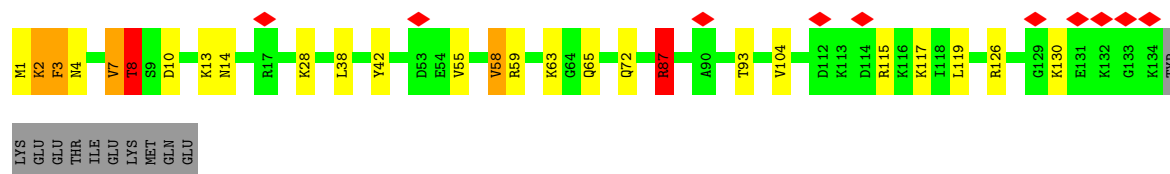
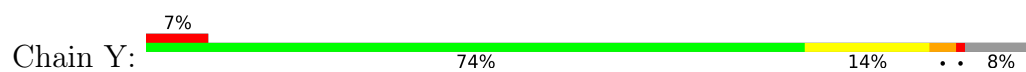


• Molecule 14: uL13

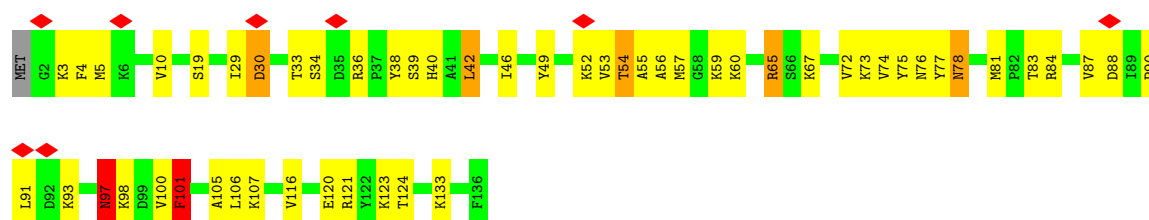


• Molecule 15: uL22

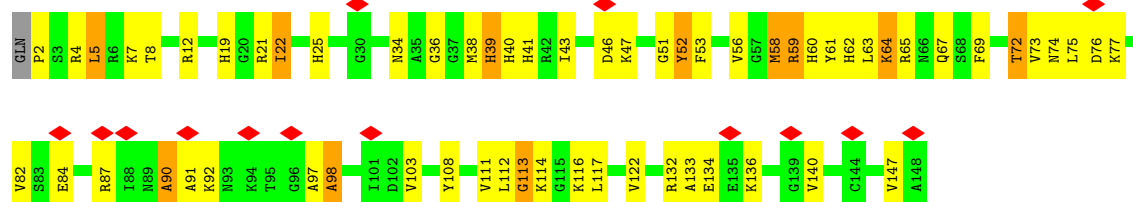




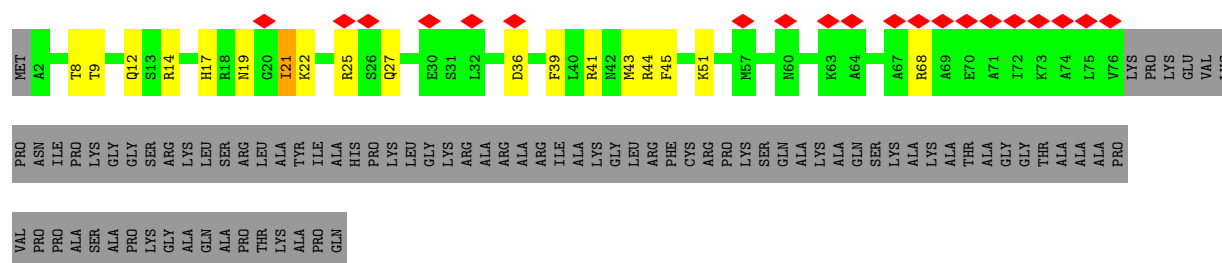
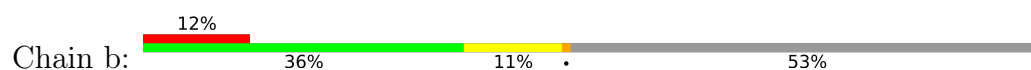
• Molecule 25: eL27



• Molecule 26: uL15

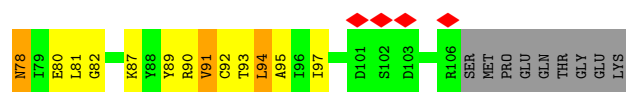


• Molecule 27: eL29

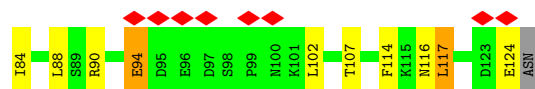
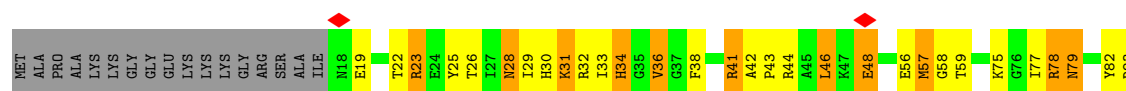


• Molecule 28: eL30

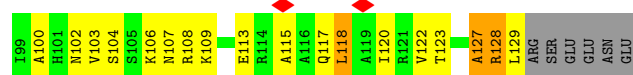
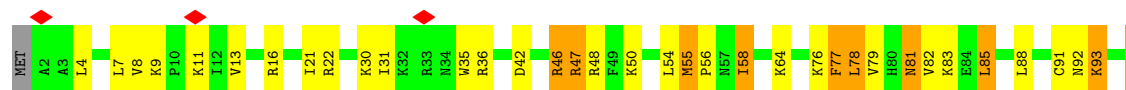




• Molecule 29: eL31



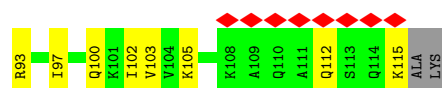
• Molecule 30: eL32



• Molecule 31: eL33

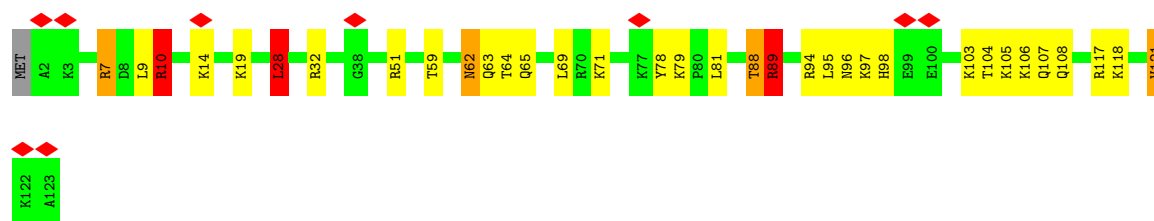


• Molecule 32: eL34

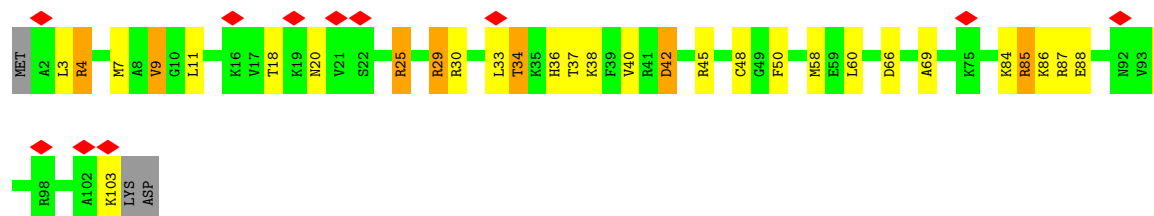


• Molecule 33: uL29





• Molecule 34: eL36



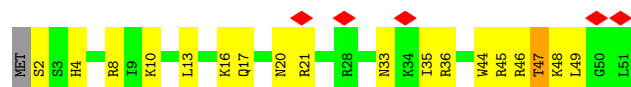
• Molecule 35: eL37



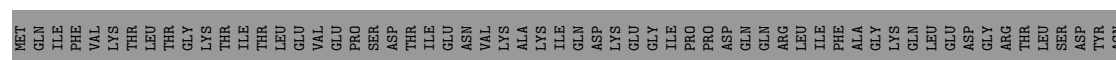
• Molecule 36: eL38

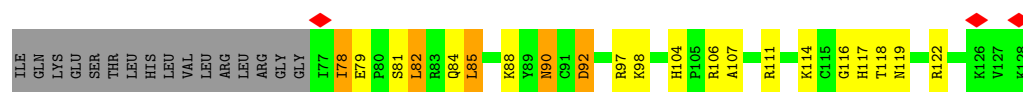


• Molecule 37: eL39

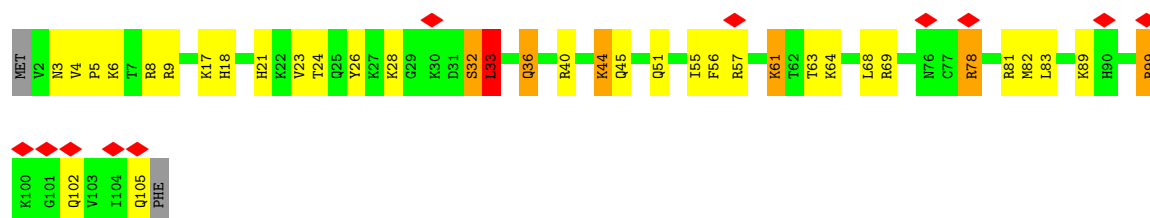


• Molecule 38: eL40

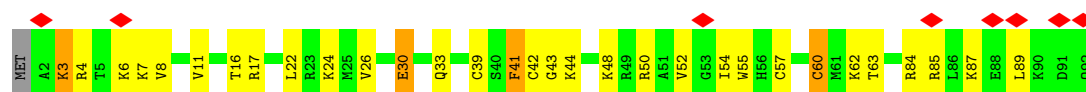




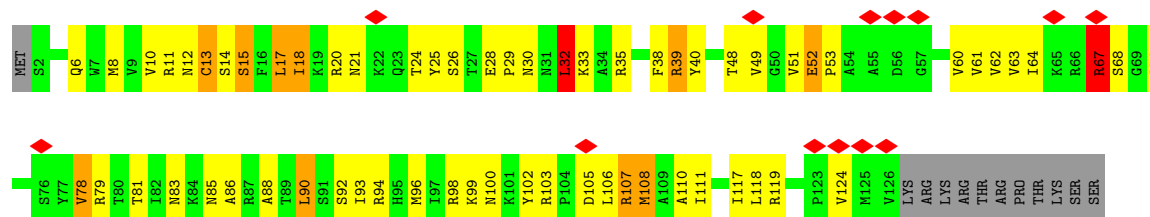
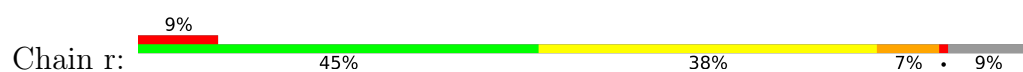
• Molecule 39: eL42



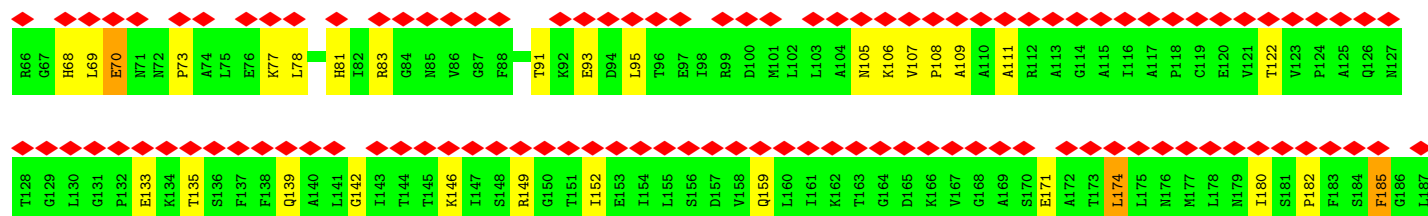
• Molecule 40: eL43

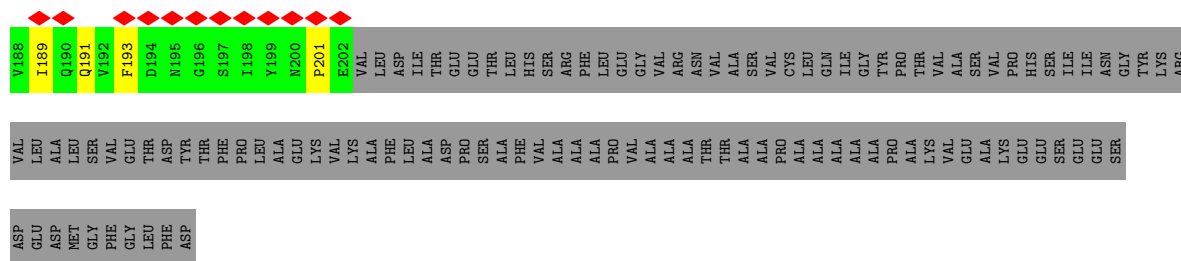


• Molecule 41: eL28

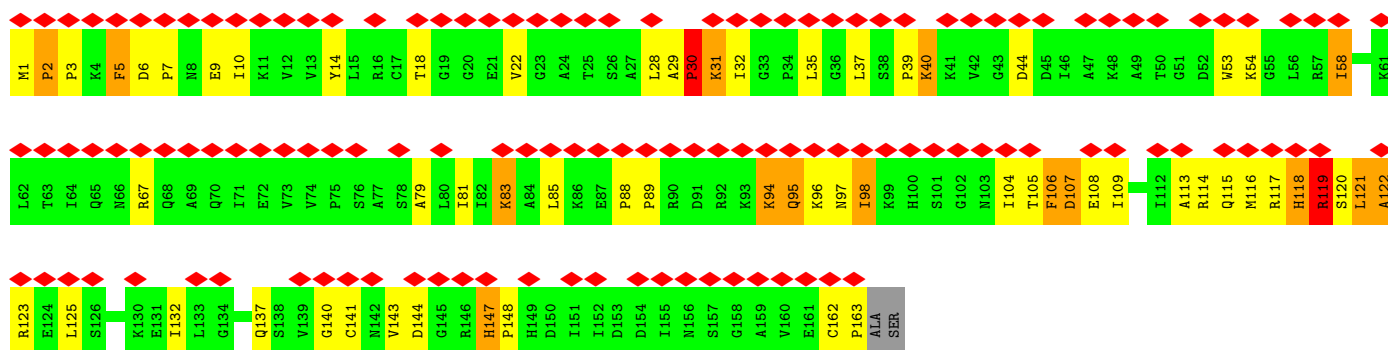
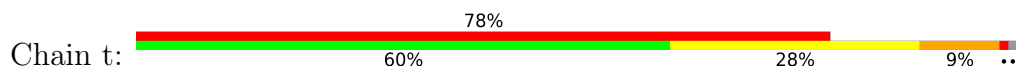


• Molecule 42: uL10

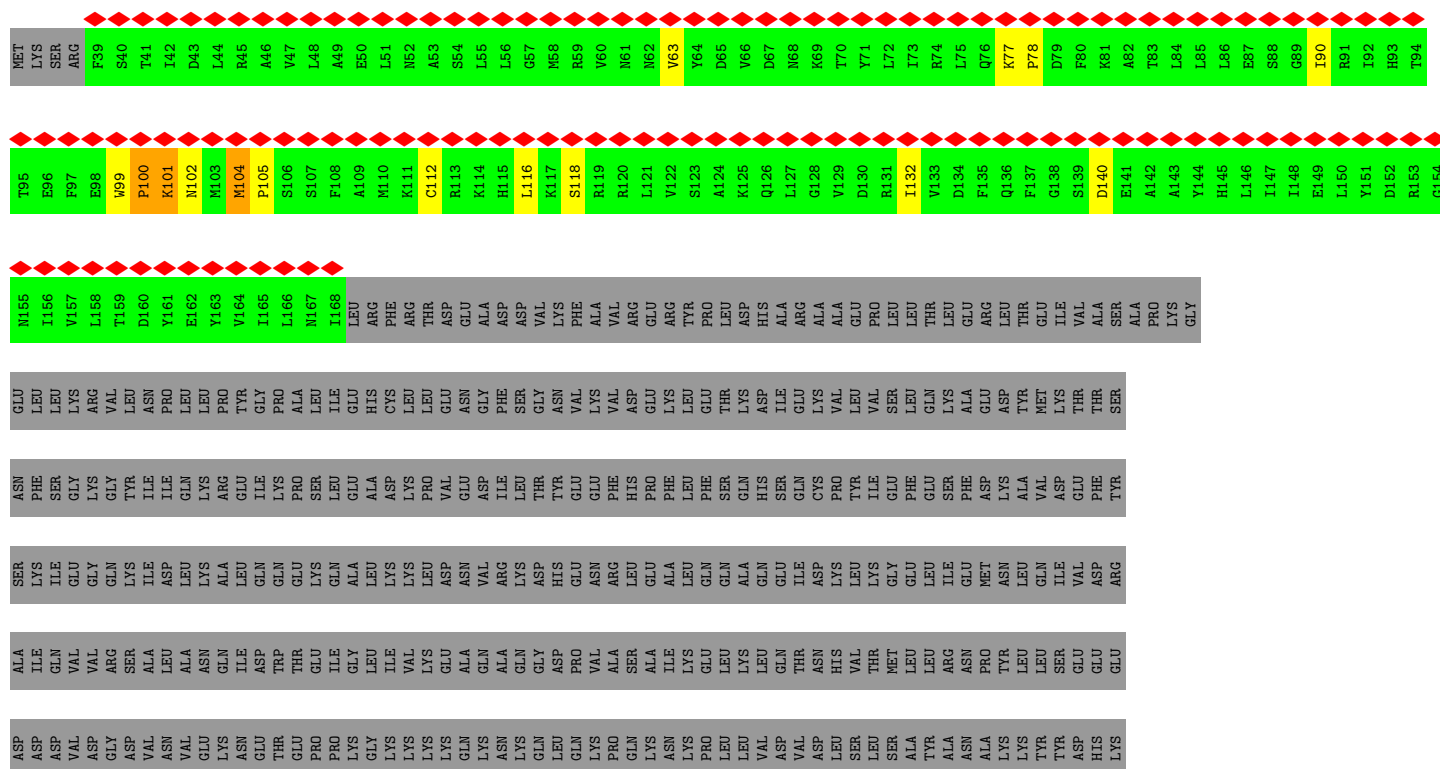




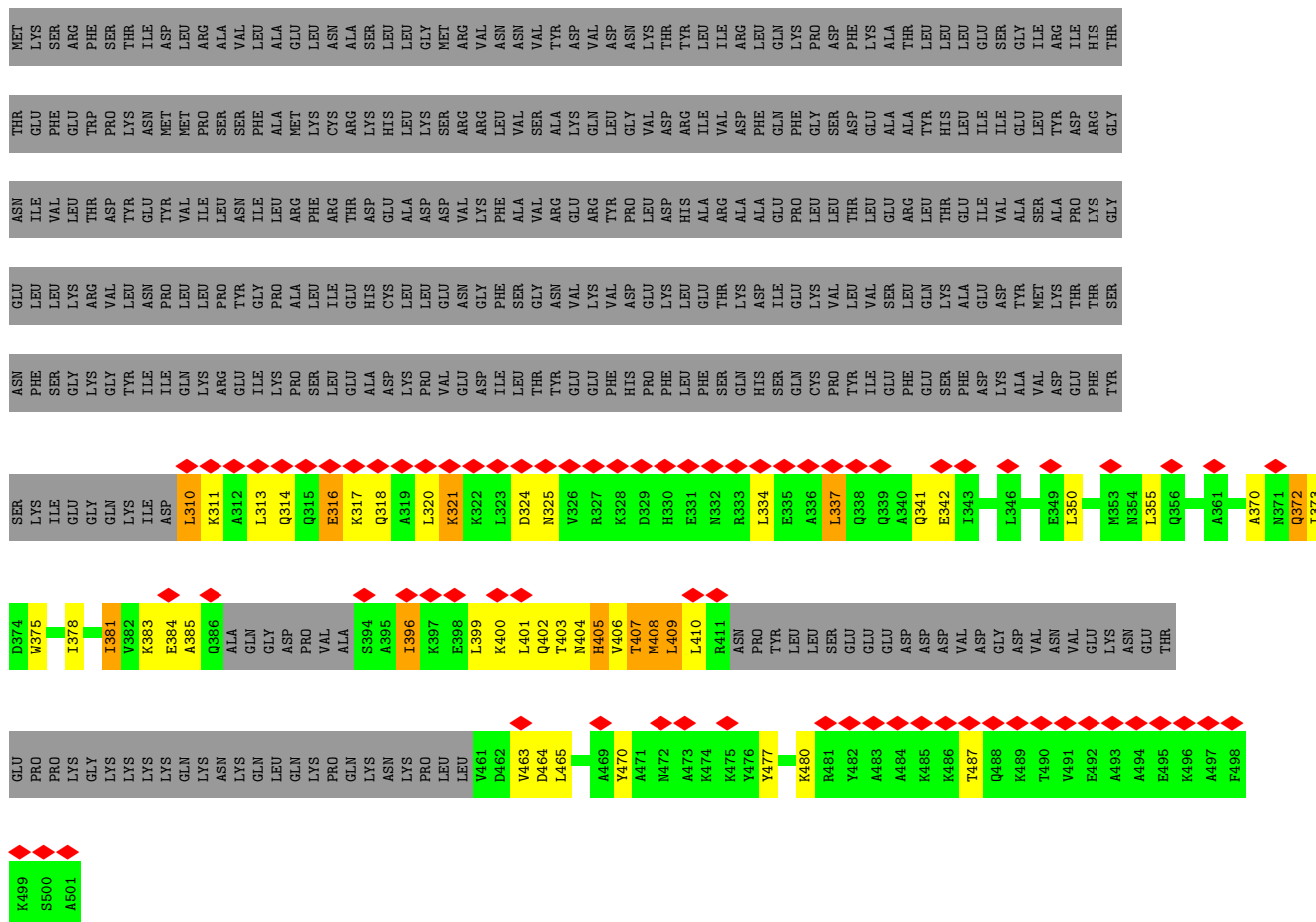
• Molecule 43: uL11



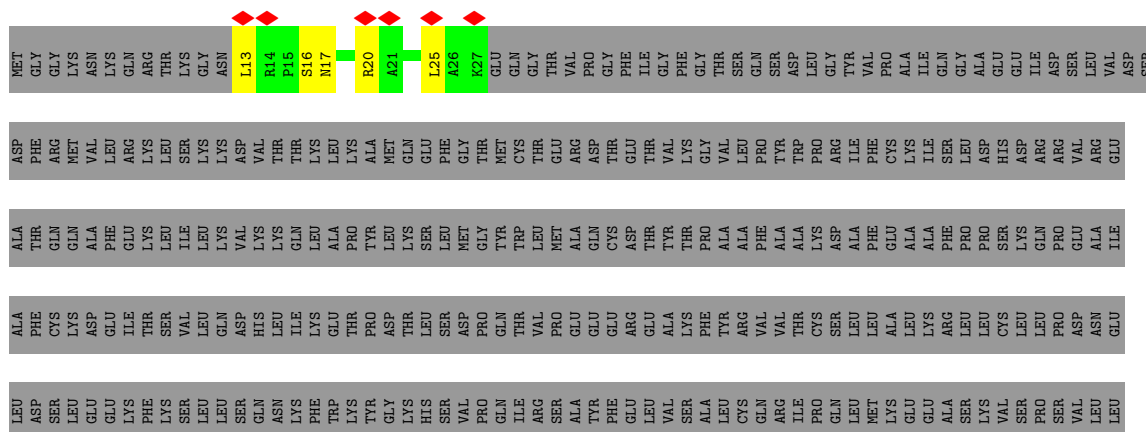
• Molecule 44: NEMF



Chain v:



Chain w: 99%



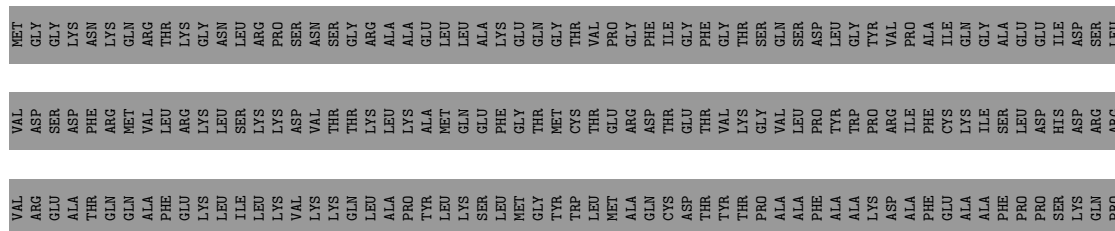


[illegible]

- Molecule 45: Listerin

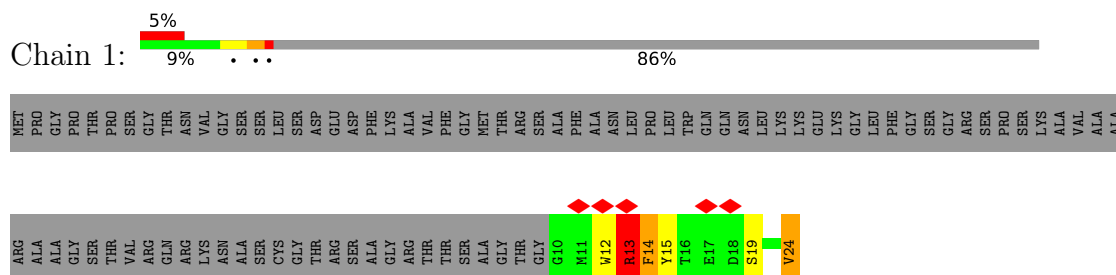
Chain z: 6% 93%

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ASN	ASP	PRO	GLN	VAL	GLY	ASN	GLU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	GLU	ASN	GLY	ASP
TYR	SER	SER	LEU	ASN	ILE	VAL	VAL	GLY	PRO	ILE	ASP	PHE	ASP	SER	CYS	GLN	GLN	ASP
LEU	ASP	ILE	ILE	GLY	GLY	ASN	LEU	GLY	ILE	ASP	LEU	GLU	ASP	LEU	LYS	GLN	GLN	ARG
ILE	LYS	HIS	TRP	ASN	ASN	HIS	ILE	GLY	SER	SER	ASP	GLU	GLU	GLU	ASP	ALA	ALA	THR
GLY	ALA	ASP	LEU	SER	PHE	LYS	PHE	GLY	LEU	ASP	GLU	GLU	GLU	GLU	ILE	PRO	LYS	LEU
VAL	VAL	LEU	ASN	GLN	GLY	TRP	GLY	GLN	PRO	ILE	PHE	THR	THR	THR	LYS	LYS	GLY	ALA
TYR	VAL	THR	ASP	HIS	GLY	ARG	GLY	LEU	GLN	VAL	GLN	ASP	VAL	GLN	SER	LEU	LEU	ASN
VAL	GLU	PRO	GLN	ARG	GLY	LEU	LEU	VAL	ILE	CYS	ASP	VAL	CYS	SER	VAL	LEU	LEU	PRO
GLU	TRP	ARG	GLN	LEU	CYS	SER	SER	ASN	THR	ALA	PHE	THR	LEU	GLN	ASP	GLN	GLN	ARG
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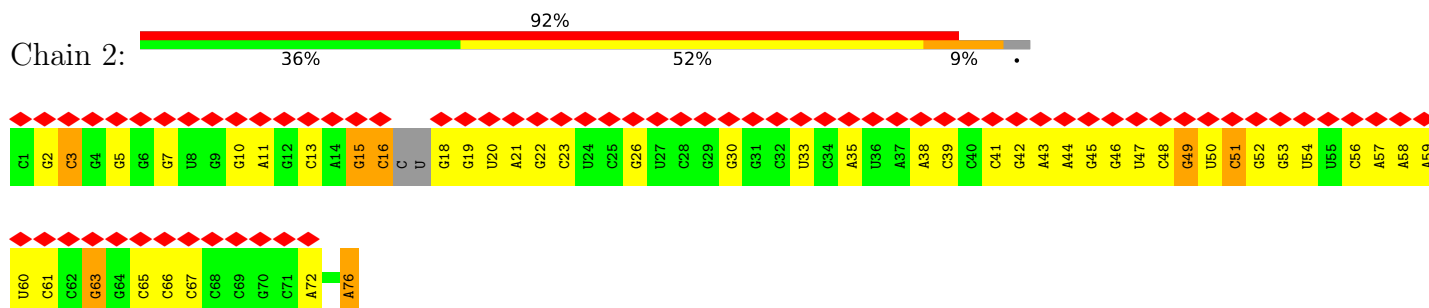




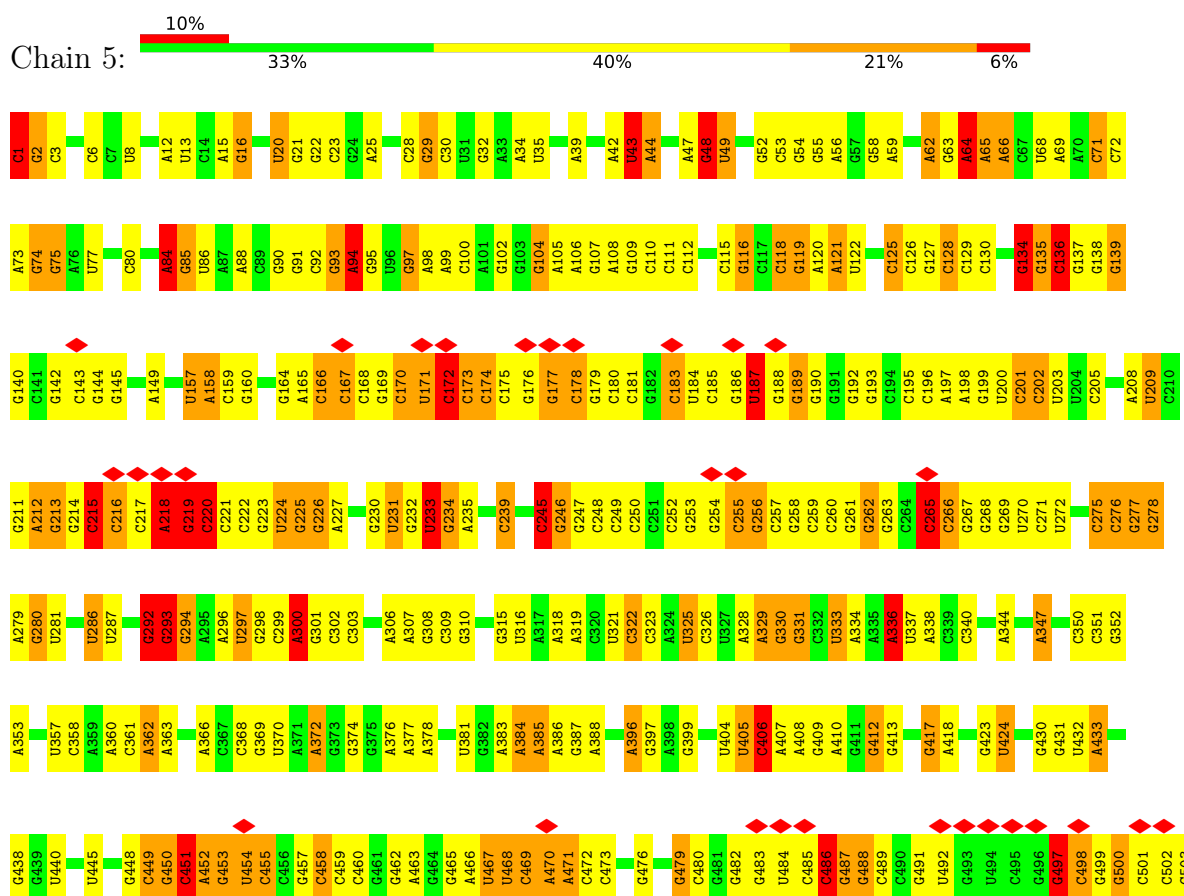
- Molecule 47: nascent chain

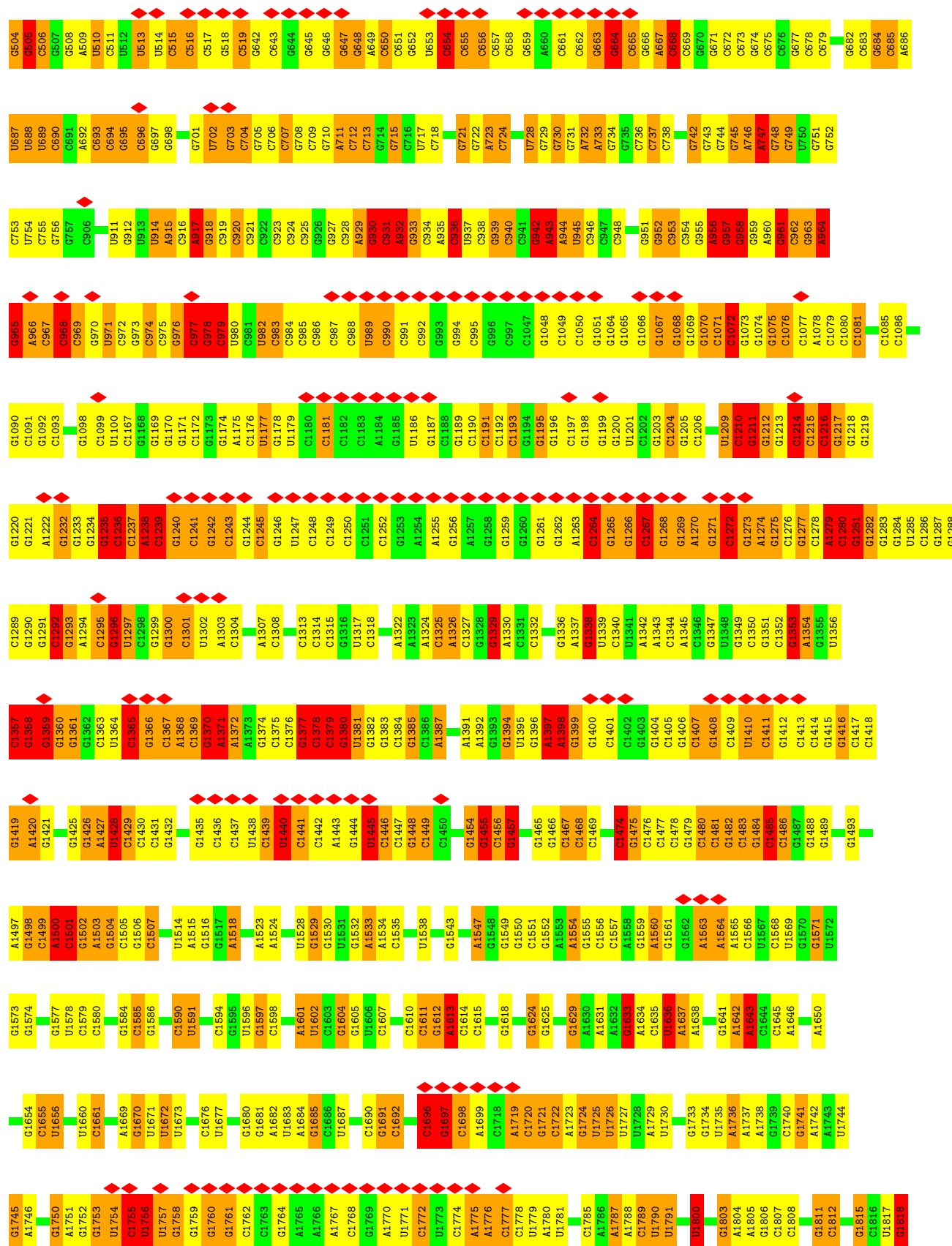


- Molecule 48: tRNA



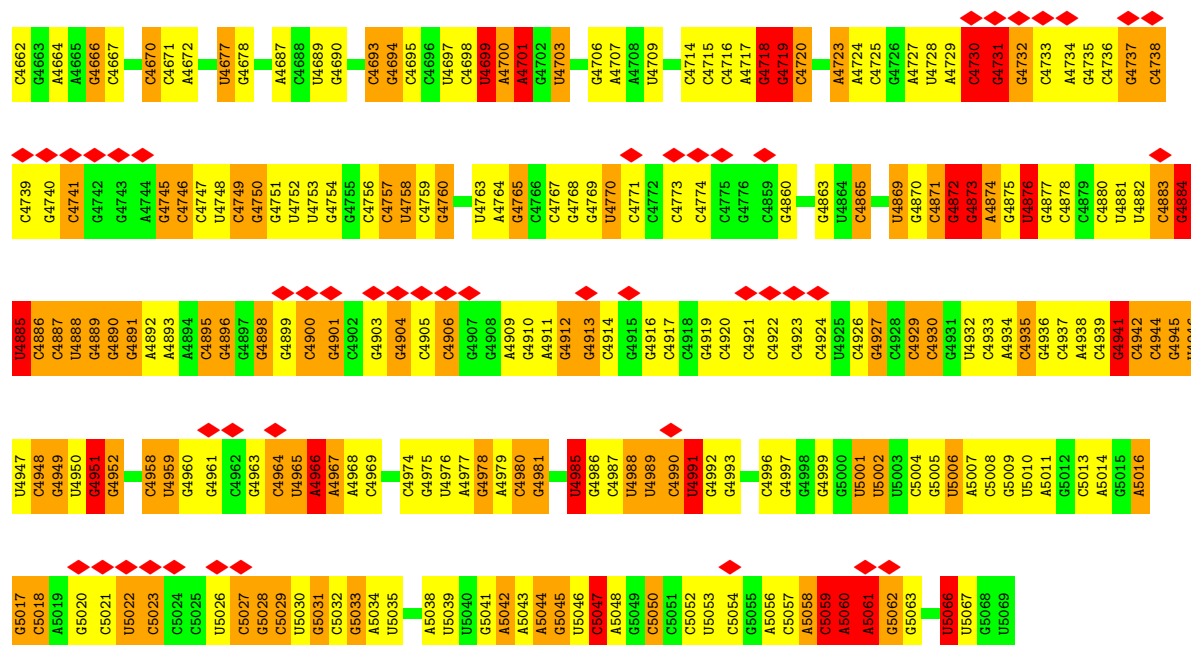
- Molecule 49: 28S rRNA



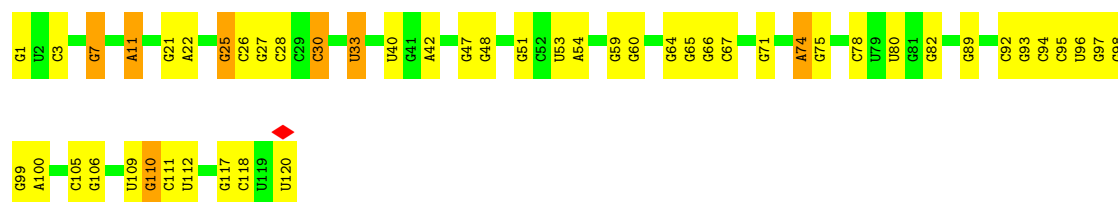


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G2756	C2689	C2614	G2544	C2482	C2340	C2271	G2100	G2024	C1820
A2757	C2690	C2615	U2545	G2483	G2341	C2272	C2101	A2025	C1893
G2758	C2691	C2616	G2546	A2484	G2342	G2273	G2102	A2026	U1821
G2759	U2692	G2617	G2547	U2485	G2343	G2274	G2103	U2027	U1822
G2760	G2693	G2618	G2548	G2486	G2344	G2275	G2104	G2028	G1823
G2761	C2694	G2619	C2549	G2487	A2345	G2276	A2105	A2029	G
A2695	A2621	G2620	G2550	G2488	A2346	G2277	G2106	A1825	A1825
A2696	G2621	A2622	A2551	C2489	G2347	A2278	G2107	G2034	G1826
A2697	A2623	G2622	G2552	U2490	U2350	U2281	G2108	G1904	C1827
G2698	A2624	G2623	A2553	U2491	G2351	A2282	G2109	G1907	G1828
A2766	G2624	G2624	U2554	C2492	G2352	G2283	G2110	A1907	G1829
U2767	G2625	G2625	G2555	C2493	U2353	G2284	G2111	G1910	G1830
U2767	G2626	G2626	G2556	G2494	G2354	G2285	G2112	G1911	G1831
U2769	G2627	G2627	G2557	U2495	G2355	G2286	G2113	G1912	G1832
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U2770	G2629	G2629	C2559	U2497	G2357	C2290	G2115	G1914	U1834
G2771	G2630	G2630	G2560	C2498	A2360	G2291	G2116	G1915	G1835
G2772	U2631	U2631	C2561	G2499	G2361	G2292	G2117	U1918	G1836
G2773	G2632	U2632	G2562	G2500	U2362	G2293	G2118	G1919	A1837
G2774	U2633	U2633	G2563	G2501	A2363	G2294	G2119	G1920	U1838
G2775	G2634	G2634	G2564	G2502	G2364	G2295	G2120	G1921	U1839
G2776	G2635	G2635	G2565	G2503	A2365	G2296	G2121	G1922	G
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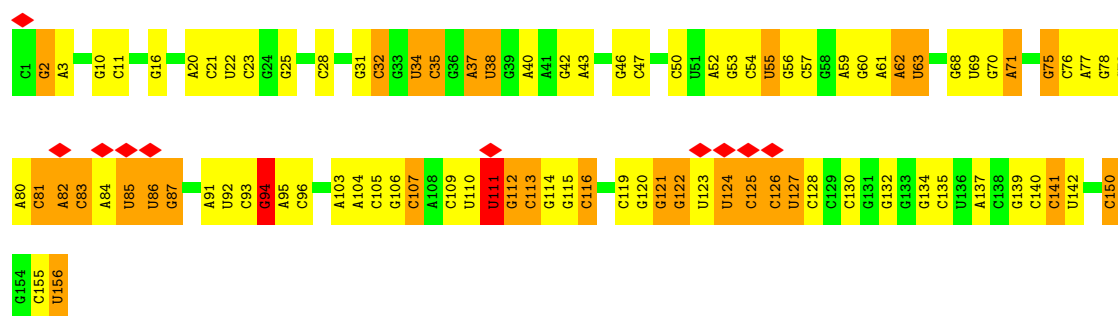
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U4594	A4594	U4517	U4447	U4372	G4301	U4223	C4163	C3981	C3817	C3817	C3740	C3661	U2933
U4595	A4595	U4518	U4448	U4373	G4302	U4224	C4164	C3982	C3818	C3818	C3741	C3662	U2934
C4596	A4596	U4519	U4449	U4374	G4303	U4225	C4165	C3983	C3819	C3819	C3742	C3663	U2935
A4605	A4605	U4520	U4450	U4375	G4304	U4226	C4166	C3984	C3820	C3820	C3743	C3664	U2936
U4606	A4606	U4521	U4451	U4376	G4305	U4227	C4167	C3985	C3821	C3821	C3744	C3665	U2937
U4607	A4607	U4522	U4452	U4377	G4306	U4228	C4168	C3986	C3822	C3822	C3745	C3666	U2938
U4608	A4608	U4523	U4453	U4378	G4307	U4229	C4169	C3987	C3823	C3823	C3746	C3667	U2939
U4609	A4609	U4524	U4454	U4379	G4308	U4230	C4170	C3988	C3824	C3824	C3747	C3668	U2940
U4610	A4610	U4525	U4455	U4380	G4309	U4231	C4171	C3989	C3825	C3825	C3748	C3669	U2941
U4611	A4611	U4526	U4456	U4381	G4310	U4232	C4172	C3990	C3826	C3826	C3749	C3670	U2942
U4612	A4612	U4527	U4457	U4382	G4311	U4233	C4173	C3991	C3827	C3827	C3750	C3671	U2943
U4613	A4613	U4528	U4458	U4383	G4312	U4234	C4174	C3992	C3828	C3828	C3751	C3672	U2944
U4614	A4614	U4529	U4459										



- Molecule 50: 5S rRNA



- Molecule 51: 5.8S rRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	63826	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS, FEI TITAN KRIOS	Depositor
Voltage (kV)	300, 300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	2000, 2000	Depositor
Maximum defocus (nm)	3500, 3500	Depositor
Magnification	104478, 104478	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.494	Depositor
Minimum map value	-0.237	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.08	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: ZN, MG, 5MU

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	0.79	0/1906	1.08	5/2556 (0.2%)
2	B	0.78	1/3214 (0.0%)	1.07	12/4308 (0.3%)
3	C	0.80	1/2973 (0.0%)	1.19	16/3990 (0.4%)
4	D	0.67	0/2430	1.09	1/3256 (0.0%)
5	E	0.74	0/1941	1.17	13/2601 (0.5%)
6	F	0.90	0/1905	1.21	8/2539 (0.3%)
7	G	0.69	1/1971 (0.1%)	1.17	5/2652 (0.2%)
8	H	0.71	0/1537	1.12	6/2066 (0.3%)
9	I	0.75	0/1690	1.13	6/2257 (0.3%)
10	J	0.63	0/1382	1.08	6/1849 (0.3%)
11	L	0.79	0/1734	1.24	7/2318 (0.3%)
12	M	0.79	0/1152	1.16	2/1539 (0.1%)
13	N	0.81	0/1746	1.22	8/2338 (0.3%)
14	O	0.93	1/1671 (0.1%)	1.32	8/2234 (0.4%)
15	P	0.79	0/1268	1.09	3/1701 (0.2%)
16	Q	0.79	0/1530	1.17	2/2041 (0.1%)
17	R	0.68	0/1524	1.25	2/2013 (0.1%)
18	S	0.84	0/1493	1.11	2/2002 (0.1%)
19	T	0.83	0/1326	1.10	7/1770 (0.4%)
20	U	0.57	0/822	1.06	3/1103 (0.3%)
21	V	0.83	0/993	1.10	4/1332 (0.3%)
22	W	0.66	0/541	0.96	0/720
23	X	0.67	0/993	1.04	3/1334 (0.2%)
24	Y	0.68	0/1132	1.21	3/1504 (0.2%)
25	Z	0.67	0/1130	1.05	6/1507 (0.4%)
26	a	0.86	0/1192	1.19	4/1591 (0.3%)
27	b	0.74	0/620	1.26	2/819 (0.2%)
28	c	0.72	0/742	1.13	2/996 (0.2%)
29	d	0.77	0/903	1.16	1/1216 (0.1%)
30	e	0.80	0/1071	1.11	4/1429 (0.3%)
31	f	0.92	0/895	1.23	10/1198 (0.8%)
32	g	0.67	0/916	1.12	2/1220 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.67	0/1023	1.22	5/1350 (0.4%)
34	i	0.63	0/843	1.26	1/1115 (0.1%)
35	j	0.92	0/721	1.23	1/953 (0.1%)
36	k	0.58	0/575	1.21	4/761 (0.5%)
37	l	0.71	0/454	1.10	1/599 (0.2%)
38	m	0.77	0/435	1.15	1/575 (0.2%)
39	o	0.70	0/864	1.04	1/1140 (0.1%)
40	p	0.71	0/718	1.10	1/953 (0.1%)
41	r	0.85	1/1017 (0.1%)	1.27	7/1365 (0.5%)
42	s	0.75	1/1546 (0.1%)	1.04	2/2087 (0.1%)
43	t	0.85	1/1257 (0.1%)	1.17	5/1697 (0.3%)
44	u	0.80	0/644	1.32	6/897 (0.7%)
44	v	0.60	0/1099	1.29	4/1470 (0.3%)
45	0	0.71	0/301	0.99	0/400
45	w	0.59	0/110	1.18	0/146
45	z	0.58	0/1076	1.12	0/1451
47	1	0.77	0/129	1.06	0/173
48	2	0.41	0/1765	0.76	0/2749
49	5	0.48	3/87791 (0.0%)	1.02	540/136941 (0.4%)
50	7	0.44	0/2858	0.85	3/4455 (0.1%)
51	8	0.45	0/3701	0.90	9/5766 (0.2%)
All	All	0.60	10/155270 (0.0%)	1.06	754/229042 (0.3%)

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
1	A	0	1
2	B	0	4
3	C	0	2
4	D	0	1
5	E	0	4
6	F	0	1
7	G	0	2
8	H	0	1
9	I	0	3
11	L	0	2
13	N	0	1
14	O	0	1
17	R	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
18	S	0	3
19	T	0	3
21	V	0	1
24	Y	0	1
25	Z	0	1
26	a	0	2
27	b	0	1
31	f	0	2
33	h	0	1
34	i	0	1
36	k	0	1
42	s	0	2
43	t	0	4
47	l	0	1
49	5	0	3
All	All	0	52

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	5	957	G	O3'-P	6.98	1.71	1.61
41	r	52	GLU	C-N	6.45	1.41	1.33
49	5	1358	G	O3'-P	5.93	1.70	1.61
7	G	138	ALA	CA-C	5.77	1.55	1.52
49	5	956	A	O3'-P	5.72	1.69	1.61

The worst 5 of 754 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	a	61	TYR	N-CA-C	19.46	131.89	111.07
49	5	1358	G	C4'-C3'-O3'	15.46	136.20	113.00
24	Y	8	THR	N-CA-C	14.91	127.03	111.07
44	u	77	LYS	CA-C-N	13.13	136.25	119.84
44	u	77	LYS	C-N-CA	13.13	136.25	119.84

There are no chirality outliers.

5 of 52 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	131	GLY	Peptide
2	B	17	LEU	Peptide

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Mol	Chain	Res	Type	Group
2	B	257	TRP	Peptide
2	B	332	MET	Peptide
2	B	351	LEU	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	1868	0	1959	69	0
2	B	3147	0	3280	91	0
3	C	2919	0	3100	133	0
4	D	2384	0	2423	58	0
5	E	1904	0	2055	76	0
6	F	1870	0	1994	140	0
7	G	1939	0	2095	61	0
8	H	1518	0	1601	57	0
9	I	1651	0	1692	40	0
10	J	1359	0	1390	53	0
11	L	1703	0	1818	69	0
12	M	1131	0	1209	45	0
13	N	1701	0	1749	63	0
14	O	1638	0	1777	61	0
15	P	1242	0	1269	16	0
16	Q	1506	0	1623	28	0
17	R	1508	0	1664	21	0
18	S	1454	0	1496	59	0
19	T	1298	0	1366	59	0
20	U	808	0	831	42	0
21	V	979	0	1039	42	0
22	W	528	0	541	7	0
23	X	976	0	1053	22	0
24	Y	1115	0	1205	19	0
25	Z	1107	0	1182	28	0
26	a	1163	0	1209	53	0
27	b	610	0	650	12	0
28	c	732	0	769	57	0
29	d	888	0	930	31	0
30	e	1053	0	1147	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	f	876	0	912	23	0
32	g	906	0	1000	18	0
33	h	1015	0	1150	17	0
34	i	832	0	917	28	0
35	j	706	0	742	43	0
36	k	569	0	637	22	0
37	l	444	0	483	6	0
38	m	429	0	465	11	0
39	o	851	0	921	15	0
40	p	708	0	755	17	0
41	r	1001	0	1062	46	0
42	s	1522	0	1575	64	0
43	t	1238	0	1293	20	0
44	u	645	0	285	22	0
44	v	1092	0	1143	55	0
45	0	293	0	299	3	0
45	w	110	0	118	3	0
45	z	1057	0	1074	25	0
46	x	1090	0	248	0	0
46	y	1055	0	237	2	0
47	1	125	0	117	7	0
48	2	1601	0	818	27	0
49	5	78486	0	39661	2358	0
50	7	2558	0	1296	24	0
51	8	3314	0	1683	86	0
52	5	150	0	0	0	0
52	7	5	0	0	0	0
52	8	1	0	0	0	0
52	P	1	0	0	0	0
52	V	1	0	0	0	0
52	g	1	0	0	0	0
53	g	1	0	0	1	0
53	j	1	0	0	2	0
53	m	1	0	0	0	0
53	o	1	0	0	0	0
53	p	1	0	0	0	0
All	All	146386	0	105007	3948	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 16.

The worst 5 of 3948 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)
36:k:8:ILE:CD1	36:k:56:LEU:HD12	1.37	1.54
36:k:8:ILE:CD1	36:k:56:LEU:CD1	1.86	1.49
26:a:116:LYS:NZ	49:5:1419:G:C4	1.72	1.41
36:k:8:ILE:CG1	36:k:56:LEU:HD11	1.52	1.40
26:a:116:LYS:NZ	49:5:1419:G:C5	1.91	1.36

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	A	242/257 (94%)	203 (84%)	28 (12%)	11 (4%)	2	17
2	B	392/395 (99%)	342 (87%)	44 (11%)	6 (2%)	8	37
3	C	365/368 (99%)	315 (86%)	43 (12%)	7 (2%)	6	33
4	D	290/297 (98%)	266 (92%)	18 (6%)	6 (2%)	5	31
5	E	232/284 (82%)	176 (76%)	39 (17%)	17 (7%)	1	10
6	F	223/250 (89%)	203 (91%)	16 (7%)	4 (2%)	6	34
7	G	239/266 (90%)	196 (82%)	36 (15%)	7 (3%)	3	26
8	H	188/192 (98%)	164 (87%)	17 (9%)	7 (4%)	2	21
9	I	200/214 (94%)	171 (86%)	22 (11%)	7 (4%)	3	23
10	J	168/178 (94%)	143 (85%)	17 (10%)	8 (5%)	2	16
11	L	208/211 (99%)	174 (84%)	22 (11%)	12 (6%)	1	13
12	M	136/213 (64%)	118 (87%)	16 (12%)	2 (2%)	8	37
13	N	201/204 (98%)	172 (86%)	28 (14%)	1 (0%)	24	57
14	O	197/204 (97%)	173 (88%)	23 (12%)	1 (0%)	24	57
15	P	151/184 (82%)	133 (88%)	17 (11%)	1 (1%)	18	51
16	Q	185/188 (98%)	161 (87%)	22 (12%)	2 (1%)	11	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	R	178/196 (91%)	160 (90%)	14 (8%)	4 (2%)	5	30
18	S	173/224 (77%)	153 (88%)	16 (9%)	4 (2%)	5	30
19	T	157/160 (98%)	136 (87%)	19 (12%)	2 (1%)	9	39
20	U	97/128 (76%)	84 (87%)	9 (9%)	4 (4%)	2	19
21	V	129/140 (92%)	112 (87%)	16 (12%)	1 (1%)	16	49
22	W	61/157 (39%)	55 (90%)	5 (8%)	1 (2%)	7	36
23	X	117/156 (75%)	105 (90%)	11 (9%)	1 (1%)	14	46
24	Y	132/145 (91%)	121 (92%)	9 (7%)	2 (2%)	8	37
25	Z	133/136 (98%)	115 (86%)	13 (10%)	5 (4%)	2	21
26	a	145/148 (98%)	118 (81%)	20 (14%)	7 (5%)	2	16
27	b	73/160 (46%)	68 (93%)	4 (6%)	1 (1%)	9	38
28	c	92/115 (80%)	86 (94%)	5 (5%)	1 (1%)	11	43
29	d	105/125 (84%)	93 (89%)	9 (9%)	3 (3%)	3	26
30	e	126/135 (93%)	113 (90%)	11 (9%)	2 (2%)	7	36
31	f	107/110 (97%)	93 (87%)	10 (9%)	4 (4%)	2	21
32	g	112/117 (96%)	98 (88%)	12 (11%)	2 (2%)	6	34
33	h	120/123 (98%)	103 (86%)	16 (13%)	1 (1%)	16	49
34	i	100/105 (95%)	92 (92%)	5 (5%)	3 (3%)	3	25
35	j	84/97 (87%)	70 (83%)	12 (14%)	2 (2%)	4	29
36	k	67/70 (96%)	56 (84%)	8 (12%)	3 (4%)	2	17
37	l	48/51 (94%)	38 (79%)	8 (17%)	2 (4%)	2	19
38	m	50/128 (39%)	45 (90%)	3 (6%)	2 (4%)	2	20
39	o	102/106 (96%)	88 (86%)	11 (11%)	3 (3%)	3	26
40	p	89/92 (97%)	74 (83%)	13 (15%)	2 (2%)	5	30
41	r	123/137 (90%)	102 (83%)	18 (15%)	3 (2%)	4	29
42	s	196/317 (62%)	159 (81%)	22 (11%)	15 (8%)	1	9
43	t	161/165 (98%)	93 (58%)	39 (24%)	29 (18%)	0	1
44	u	128/501 (26%)	88 (69%)	30 (23%)	10 (8%)	1	8
44	v	130/501 (26%)	125 (96%)	3 (2%)	2 (2%)	8	37
45	0	34/1766 (2%)	29 (85%)	3 (9%)	2 (6%)	1	13
45	w	13/1766 (1%)	13 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	z	120/1766 (7%)	106 (88%)	10 (8%)	4 (3%)	3	24
47	1	13/104 (12%)	9 (69%)	1 (8%)	3 (23%)	0	0
All	All	7132/14052 (51%)	6110 (86%)	793 (11%)	229 (3%)	5	24

5 of 229 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	34	PHE
1	A	195	CYS
2	B	18	PRO
3	C	273	LEU
5	E	91	PRO

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	A	187/199 (94%)	145 (78%)	42 (22%)	1	6
2	B	335/336 (100%)	277 (83%)	58 (17%)	2	12
3	C	305/306 (100%)	244 (80%)	61 (20%)	1	8
4	D	247/250 (99%)	205 (83%)	42 (17%)	2	13
5	E	209/246 (85%)	170 (81%)	39 (19%)	1	10
6	F	194/217 (89%)	154 (79%)	40 (21%)	1	8
7	G	208/226 (92%)	167 (80%)	41 (20%)	1	8
8	H	169/171 (99%)	129 (76%)	40 (24%)	1	5
9	I	174/181 (96%)	141 (81%)	33 (19%)	1	9
10	J	143/149 (96%)	125 (87%)	18 (13%)	4	22
11	L	176/177 (99%)	136 (77%)	40 (23%)	1	6
12	M	116/160 (72%)	89 (77%)	27 (23%)	1	5
13	N	171/172 (99%)	138 (81%)	33 (19%)	1	9
14	O	171/174 (98%)	144 (84%)	27 (16%)	2	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	P	134/163 (82%)	109 (81%)	25 (19%)	1	10
16	Q	163/164 (99%)	135 (83%)	28 (17%)	2	12
17	R	159/175 (91%)	122 (77%)	37 (23%)	1	5
18	S	156/192 (81%)	127 (81%)	29 (19%)	1	10
19	T	139/140 (99%)	110 (79%)	29 (21%)	1	7
20	U	89/114 (78%)	74 (83%)	15 (17%)	2	13
21	V	101/107 (94%)	79 (78%)	22 (22%)	1	7
22	W	55/126 (44%)	45 (82%)	10 (18%)	2	11
23	X	107/133 (80%)	91 (85%)	16 (15%)	3	17
24	Y	124/135 (92%)	107 (86%)	17 (14%)	3	20
25	Z	117/118 (99%)	98 (84%)	19 (16%)	2	15
26	a	119/120 (99%)	101 (85%)	18 (15%)	3	17
27	b	63/123 (51%)	54 (86%)	9 (14%)	3	19
28	c	79/97 (81%)	67 (85%)	12 (15%)	3	17
29	d	98/110 (89%)	75 (76%)	23 (24%)	1	5
30	e	114/121 (94%)	79 (69%)	35 (31%)	0	2
31	f	88/89 (99%)	68 (77%)	20 (23%)	1	6
32	g	98/100 (98%)	74 (76%)	24 (24%)	1	4
33	h	109/110 (99%)	91 (84%)	18 (16%)	2	14
34	i	86/89 (97%)	74 (86%)	12 (14%)	3	19
35	j	73/80 (91%)	57 (78%)	16 (22%)	1	6
36	k	64/65 (98%)	53 (83%)	11 (17%)	2	12
37	l	47/48 (98%)	39 (83%)	8 (17%)	2	13
38	m	48/116 (41%)	37 (77%)	11 (23%)	1	6
39	o	92/94 (98%)	70 (76%)	22 (24%)	1	5
40	p	74/75 (99%)	57 (77%)	17 (23%)	1	6
41	r	109/121 (90%)	83 (76%)	26 (24%)	1	5
42	s	166/258 (64%)	147 (89%)	19 (11%)	5	26
43	t	136/137 (99%)	117 (86%)	19 (14%)	3	19
44	v	116/445 (26%)	96 (83%)	20 (17%)	2	12
45	0	34/1611 (2%)	31 (91%)	3 (9%)	9	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	w	11/1611 (1%)	9 (82%)	2 (18%)	2	11
45	z	119/1611 (7%)	102 (86%)	17 (14%)	3	19
47	1	13/79 (16%)	11 (85%)	2 (15%)	2	16
All	All	6105/11841 (52%)	4953 (81%)	1152 (19%)	3	9

5 of 1152 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	g	105	LYS
45	z	1709	PHE
34	i	66	ASP
32	g	103	VAL
40	p	84	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 94 such sidechains are listed below:

Mol	Chain	Res	Type
27	b	11	ASN
31	f	56	ASN
27	b	17	HIS
29	d	18	ASN
33	h	108	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
48	2	73/77 (94%)	32 (43%)	2 (2%)
49	5	3650/3664 (99%)	1403 (38%)	373 (10%)
50	7	119/120 (99%)	28 (23%)	1 (0%)
51	8	155/156 (99%)	50 (32%)	9 (5%)
All	All	3997/4017 (99%)	1513 (37%)	385 (9%)

5 of 1513 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
48	2	3	C
48	2	5	G
48	2	7	G
48	2	11	A

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Mol	Chain	Res	Type
48	2	13	C

5 of 385 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	5	2513	A
49	5	3888	G
49	5	2588	C
49	5	2857	A
49	5	4124	G

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
48	5MU	2	54	48	19,22,23	1.50	4 (21%)	27,32,35	2.02	8 (29%)

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
48	5MU	2	54	48	-	2/7/25/26	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	2	54	5MU	C6-C5	3.36	1.40	1.34
48	2	54	5MU	C2-N1	3.20	1.43	1.38
48	2	54	5MU	C4-C5	2.72	1.49	1.44
48	2	54	5MU	C4-N3	-2.12	1.34	1.38

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	2	54	5MU	N3-C2-N1	4.91	121.28	114.89
48	2	54	5MU	C4-N3-C2	-4.16	121.89	127.34
48	2	54	5MU	C5-C4-N3	3.79	118.62	115.32
48	2	54	5MU	O4-C4-C5	-3.39	121.04	124.92
48	2	54	5MU	C5M-C5-C4	2.90	121.88	118.78

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
48	2	54	5MU	O4'-C4'-C5'-O5'
48	2	54	5MU	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 164 ligands modelled in this entry, 164 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
46	x	14
49	5	13
46	y	12

The worst 5 of 39 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	x	1211:UNK	C	1300:UNK	N	25.67
1	x	608:UNK	C	700:UNK	N	22.35
1	x	1014:UNK	C	1100:UNK	N	19.48
1	x	817:UNK	C	900:UNK	N	18.97
1	y	223:UNK	C	250:UNK	N	18.15

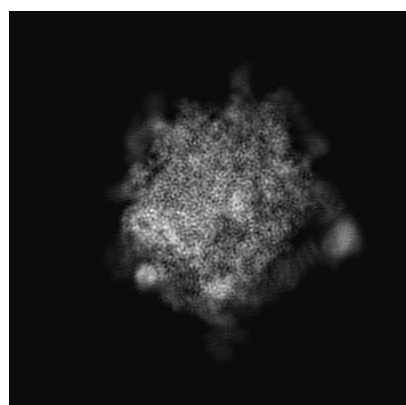
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2832. These allow visual inspection of the internal detail of the map and identification of artifacts.

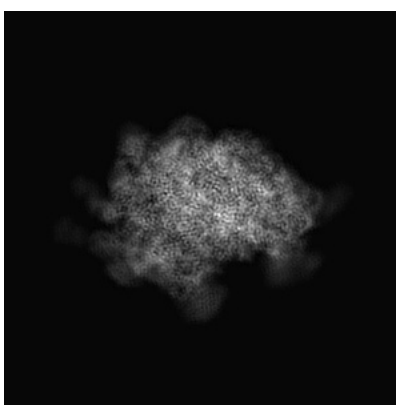
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

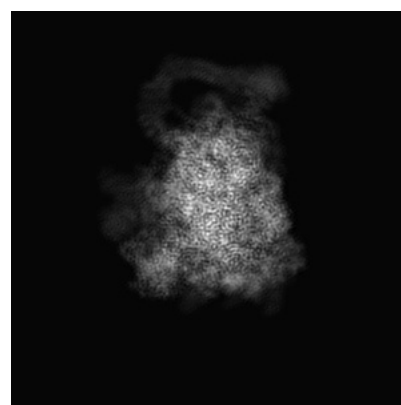
6.1.1 Primary map



X



Y

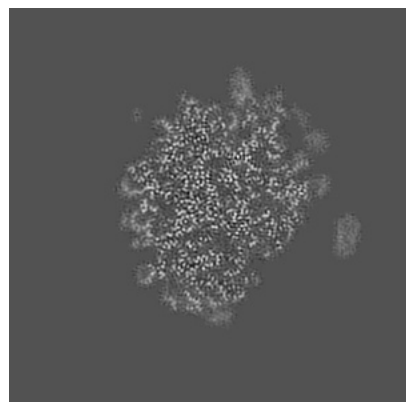


Z

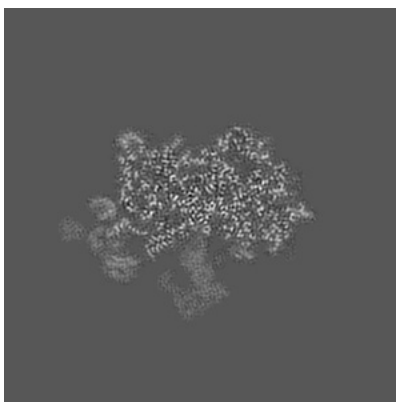
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

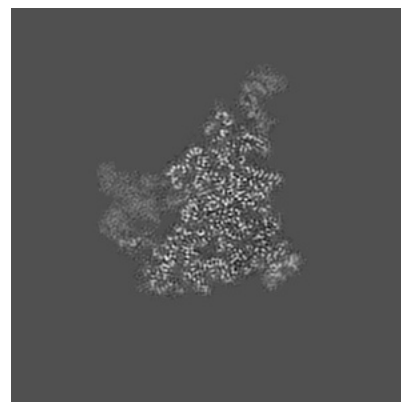
6.2.1 Primary map



X Index: 160



Y Index: 160

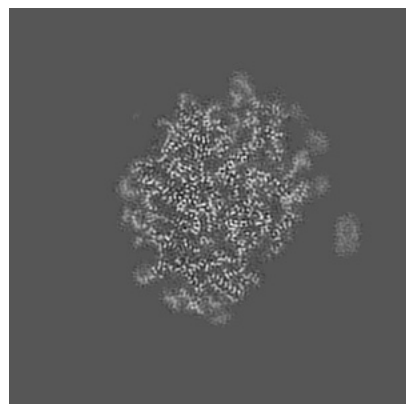


Z Index: 160

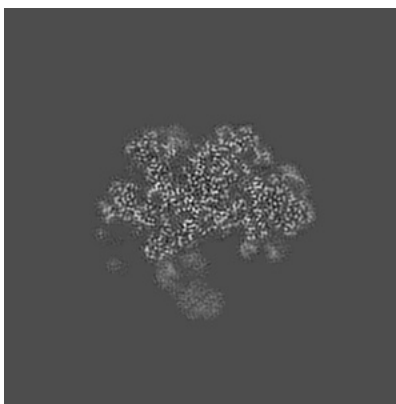
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

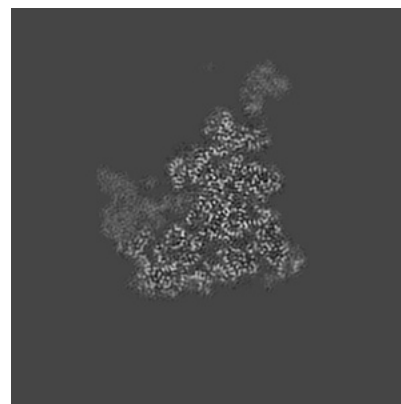
6.3.1 Primary map



X Index: 158



Y Index: 149

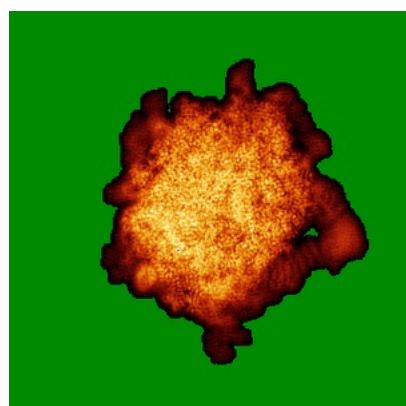


Z Index: 156

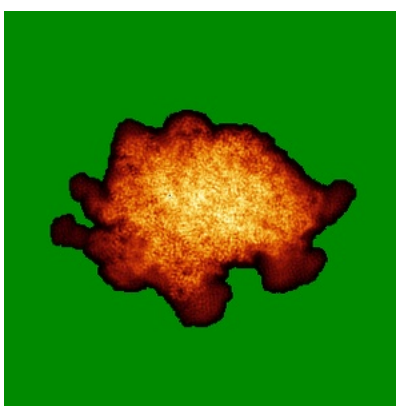
The images above show the largest variance slices of the map in three orthogonal directions.

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

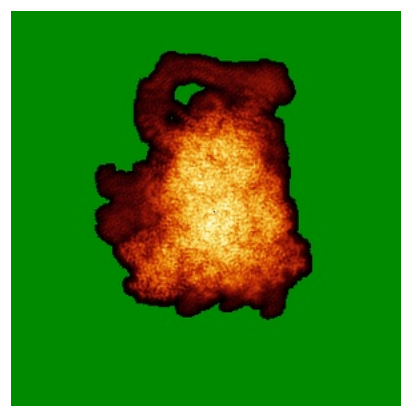
6.4.1 Primary map



X



Y

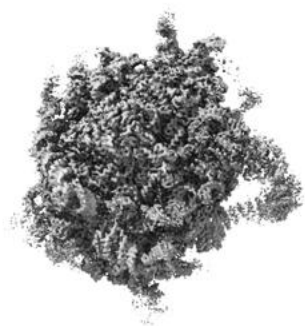


Z

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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

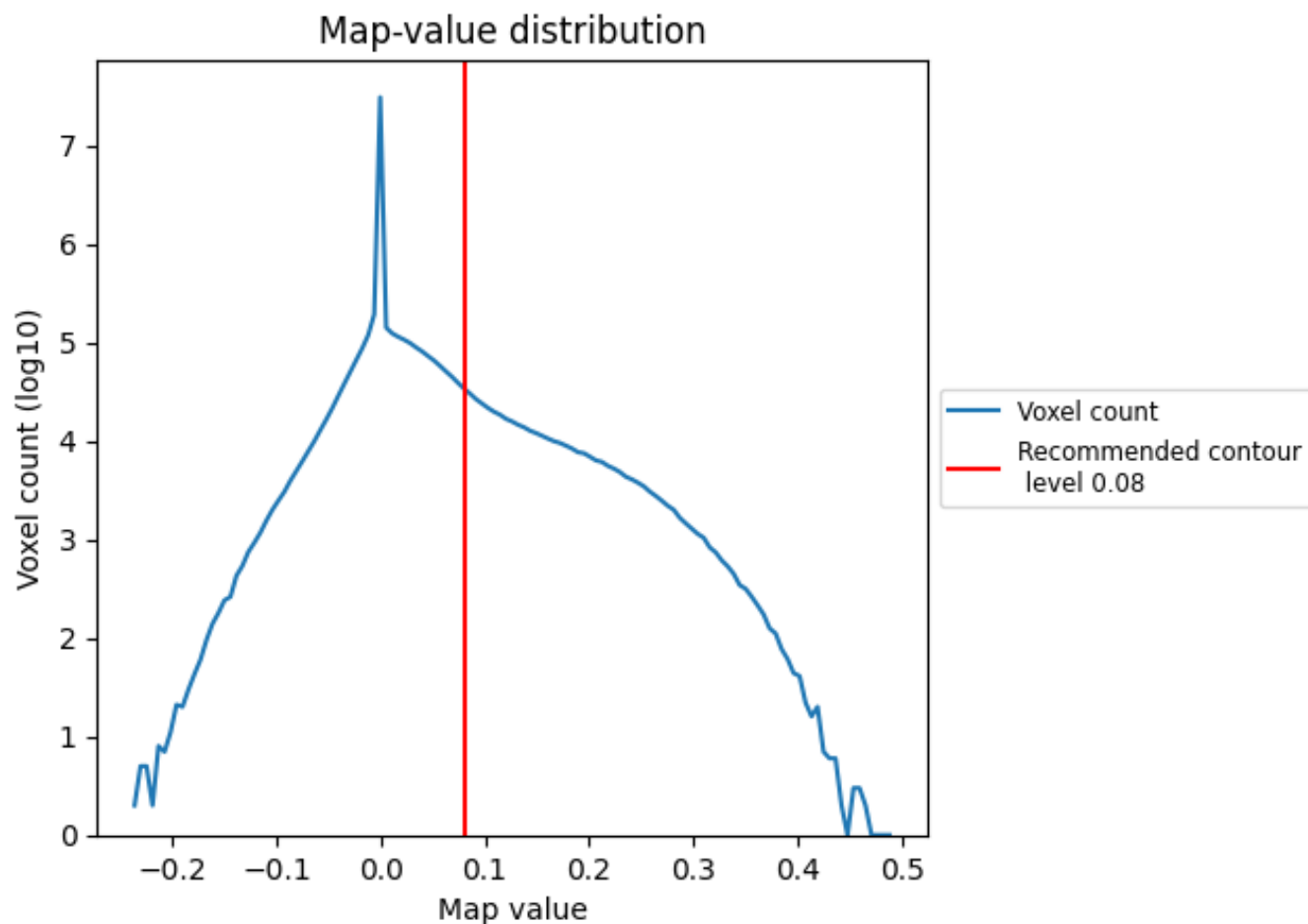
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

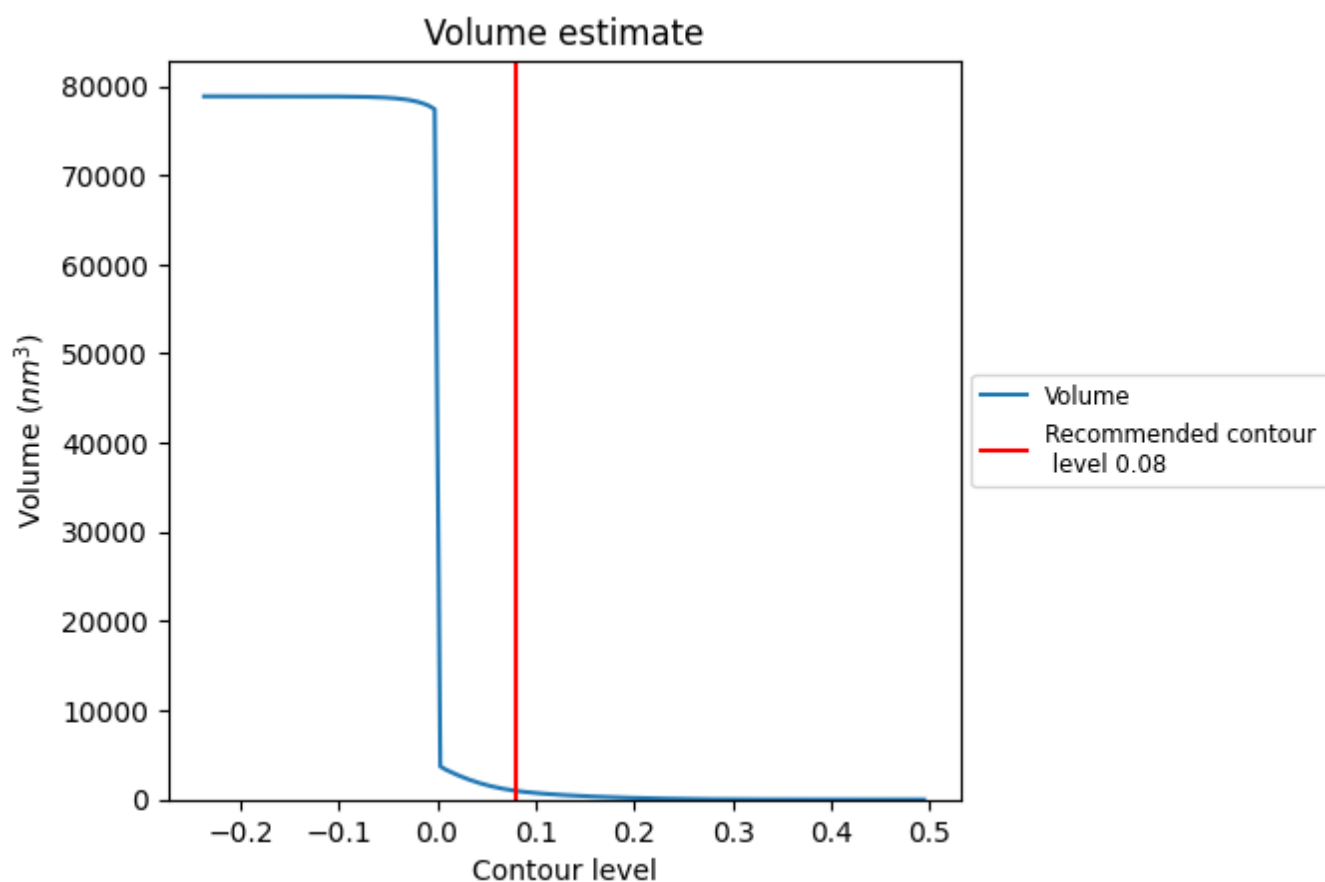
This section contains the results of statistical analysis of the map.

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.

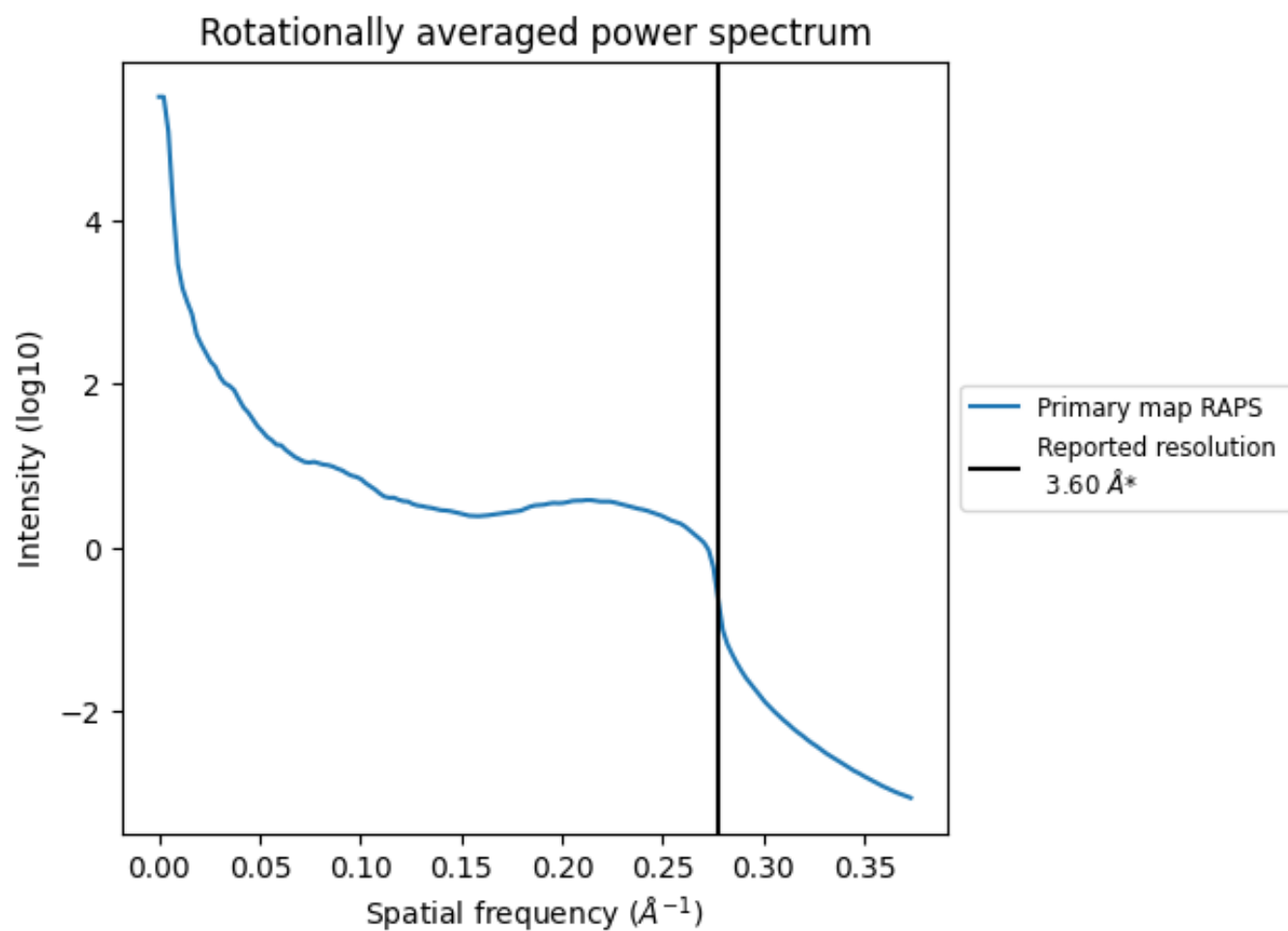
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 982 nm³; this corresponds to an approximate mass of 887 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 0.278 Å⁻¹

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

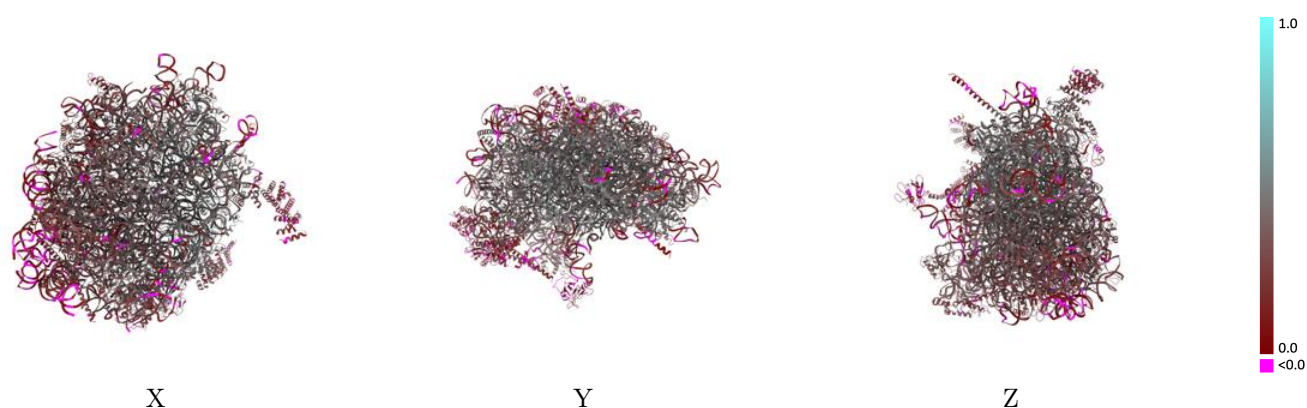
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2832 and PDB model 3J92. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)

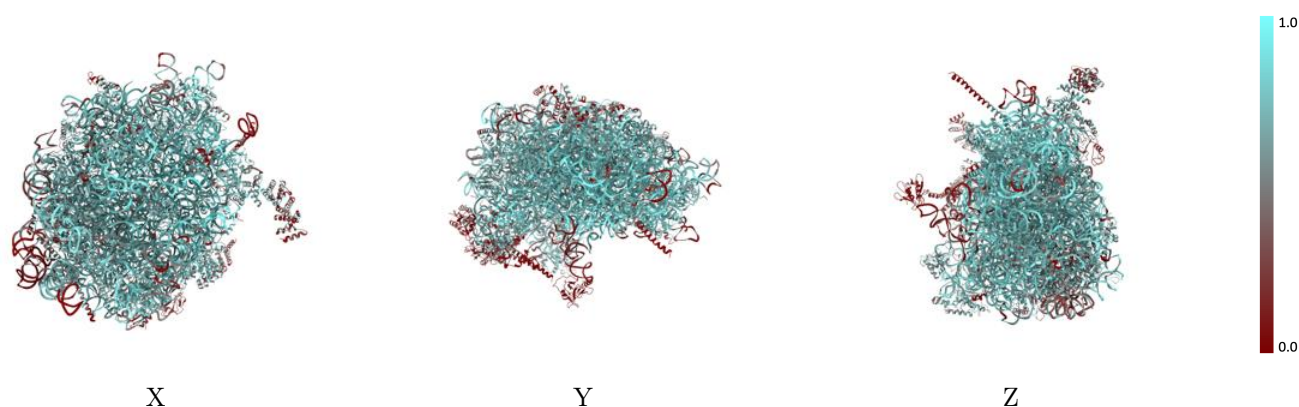
This section was not generated.

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



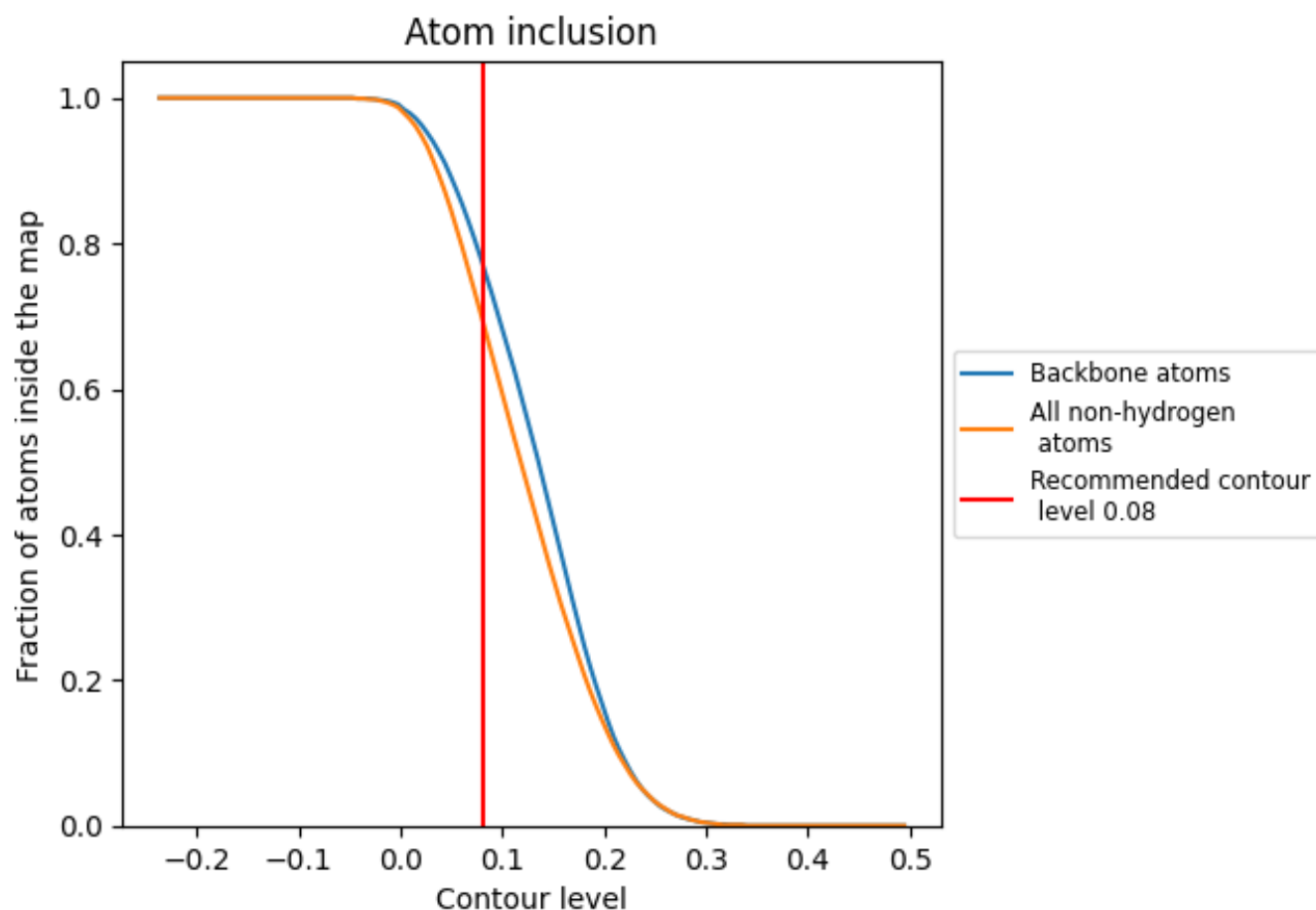
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6970	 0.3400
0	 0.1040	 0.1200
1	 0.4960	 0.3720
2	 0.1420	 0.1480
5	 0.7510	 0.3290
7	 0.7880	 0.3270
8	 0.7770	 0.3580
A	 0.7640	 0.4550
B	 0.7690	 0.4700
C	 0.6620	 0.3490
D	 0.6230	 0.2770
E	 0.6090	 0.3340
F	 0.6590	 0.3210
G	 0.5920	 0.3360
H	 0.6800	 0.3990
I	 0.6840	 0.3810
J	 0.6240	 0.3070
L	 0.6220	 0.3110
M	 0.6950	 0.3750
N	 0.7330	 0.3860
O	 0.7360	 0.4310
P	 0.7530	 0.4430
Q	 0.6540	 0.3320
R	 0.6340	 0.3880
S	 0.6960	 0.3580
T	 0.6470	 0.3510
U	 0.6780	 0.4340
V	 0.7530	 0.4820
W	 0.7110	 0.4620
X	 0.6830	 0.4060
Y	 0.6810	 0.3670
Z	 0.6890	 0.4210
a	 0.6950	 0.3540
b	 0.5500	 0.2830
c	 0.7260	 0.4490



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Chain	Atom inclusion	Q-score
d	 0.7000	 0.4590
e	 0.7050	 0.3930
f	 0.7390	 0.4080
g	 0.7080	 0.4350
h	 0.6490	 0.3590
i	 0.6390	 0.3470
j	 0.7490	 0.4210
k	 0.5800	 0.3760
l	 0.7020	 0.4410
m	 0.7090	 0.4040
o	 0.6480	 0.3570
p	 0.7180	 0.4660
r	 0.6770	 0.3480
s	 0.2370	 0.1680
t	 0.2130	 0.1390
u	 0.0110	 0.0690
v	 0.3540	 0.2610
w	 0.4910	 0.3660
x	 0.4690	 0.2410
y	 0.4040	 0.2100
z	 0.4930	 0.3510