



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Mar 2, 2017 – 12:01 pm GMT

PDB ID : 3J92
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 PDB ID : 4W20, 4W1Z

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

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

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

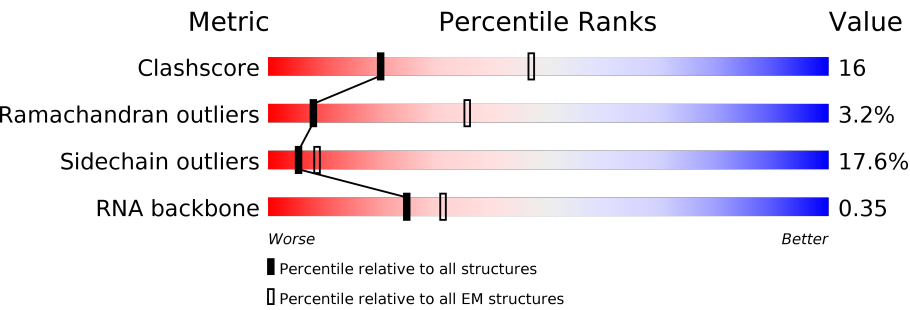
MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : recalc29047

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 3.60 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.






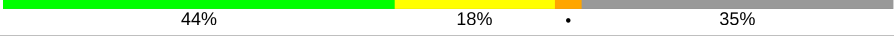




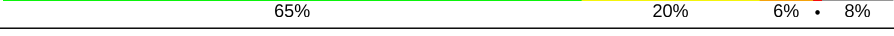


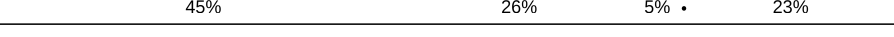

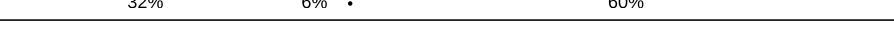


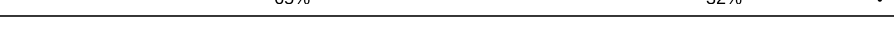

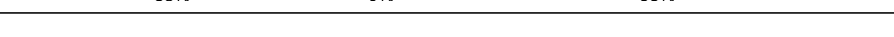
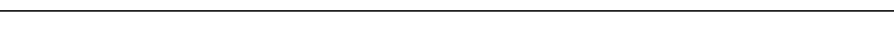

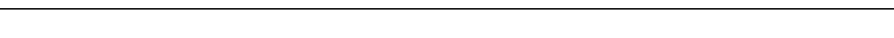
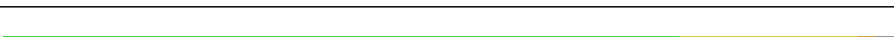


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	257	
2	B	395	
3	C	368	
4	D	297	
5	E	284	
6	F	250	
7	G	266	
8	H	192	













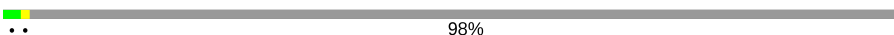
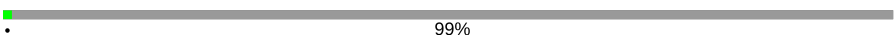
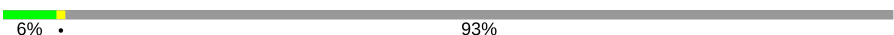

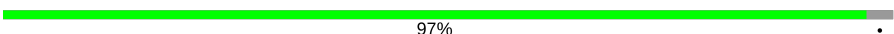





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Mol	Chain	Length	Quality of chain
9	I	214	
10	J	178	
11	L	211	
12	M	213	
13	N	204	
14	O	204	
15	P	184	
16	Q	188	
17	R	196	
18	S	224	
19	T	160	
20	U	128	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	160	
28	c	115	
29	d	125	
30	e	135	
31	f	110	
32	g	117	
33	h	123	

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

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 (three-letter code: MG) (formula: Mg).

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

- Molecule 53 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

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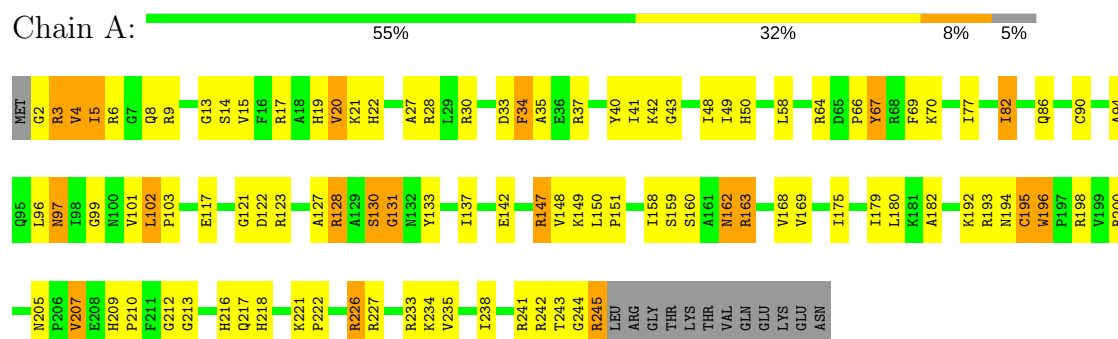
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Mol	Chain	Residues	Atoms		AltConf
53	g	1	Total 1	Zn 1	0
53	j	1	Total 1	Zn 1	0
53	p	1	Total 1	Zn 1	0
53	m	1	Total 1	Zn 1	0

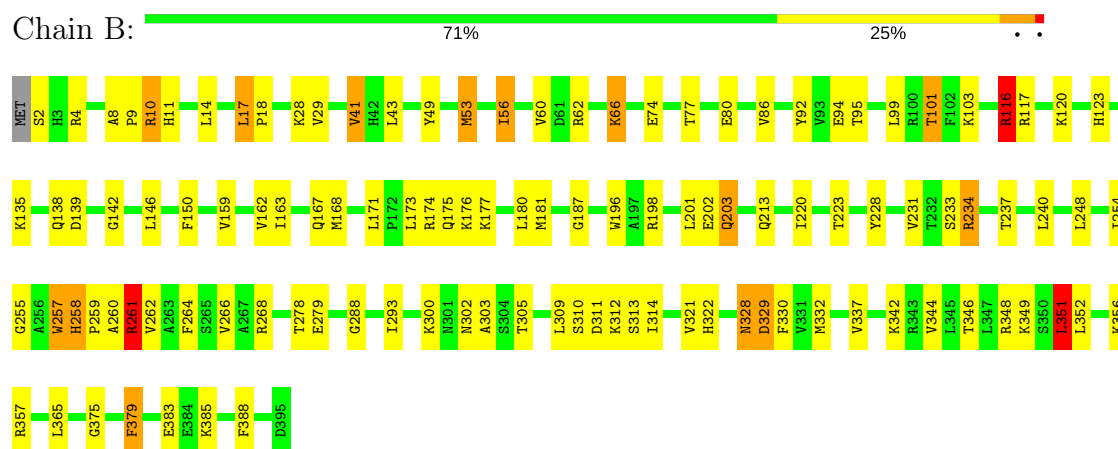
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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. 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. 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.

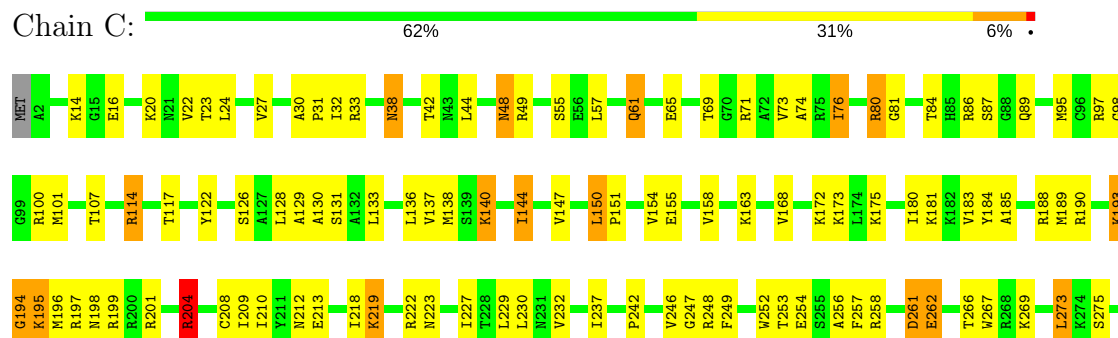
• Molecule 1: uL2



• Molecule 2: uL3

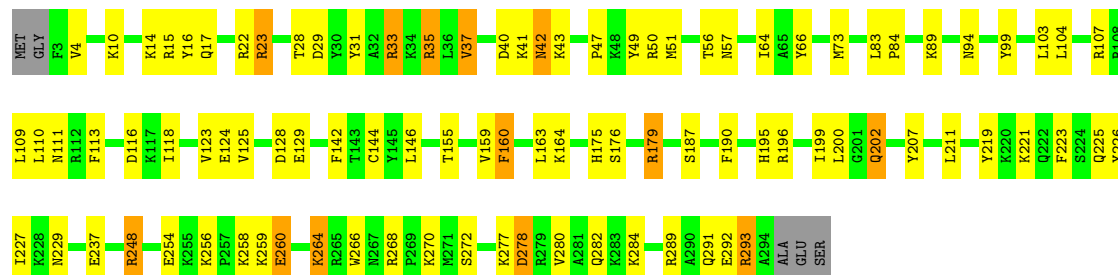


• Molecule 3: uL4

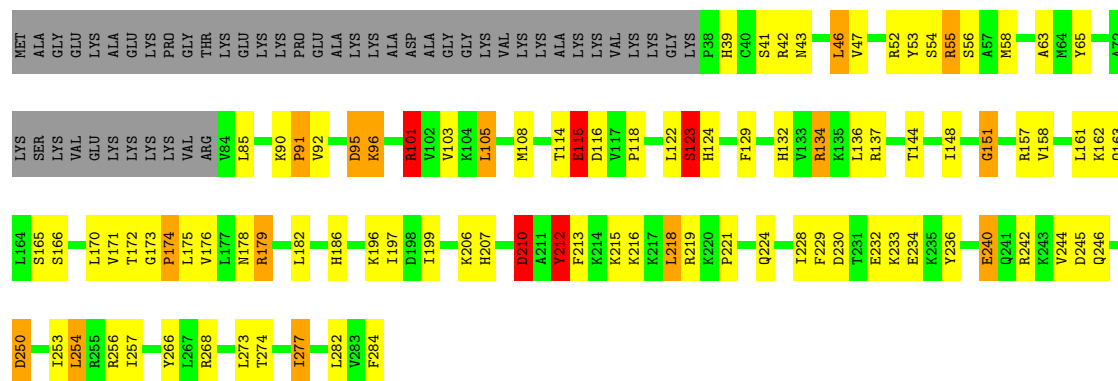




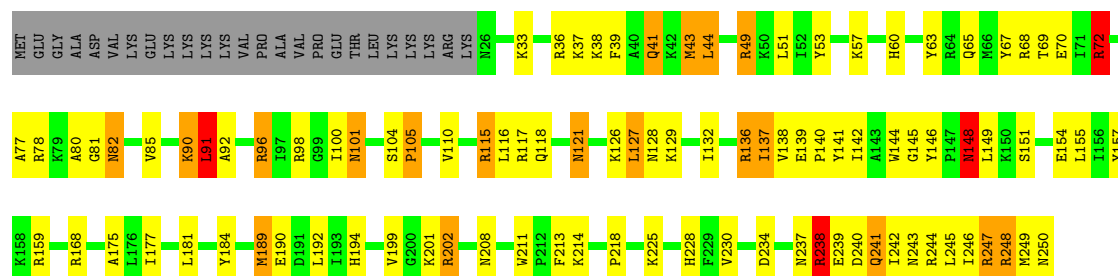
• Molecule 4: uL18



• Molecule 5: eL6

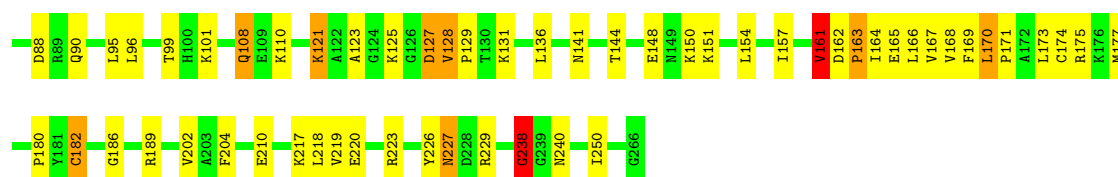


• Molecule 6: eL30



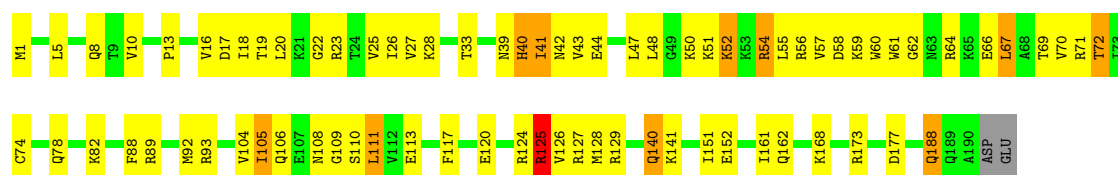
• Molecule 7: eL8





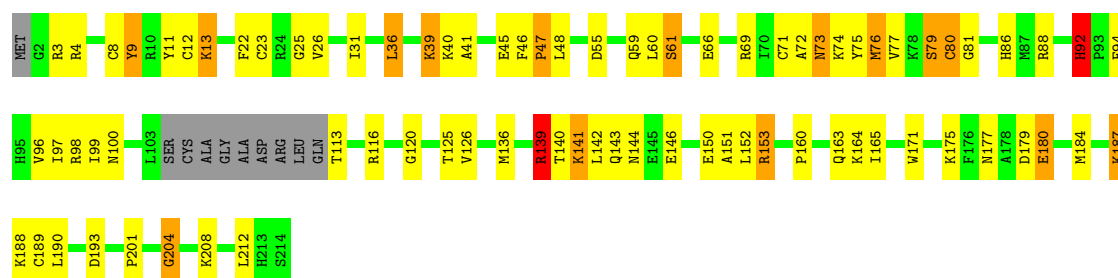
• Molecule 8: uL6

Chain H: 59% 34% 5% ..



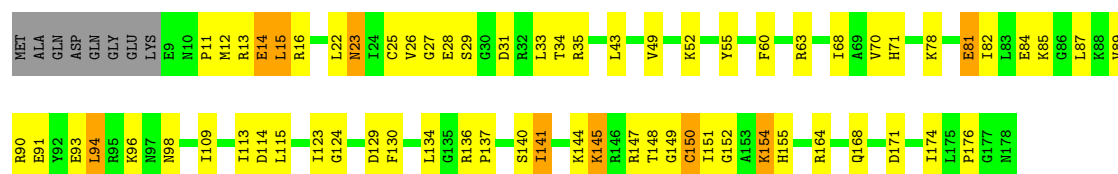
• Molecule 9: uL16

Chain I: 57% 30% 7% • 5%



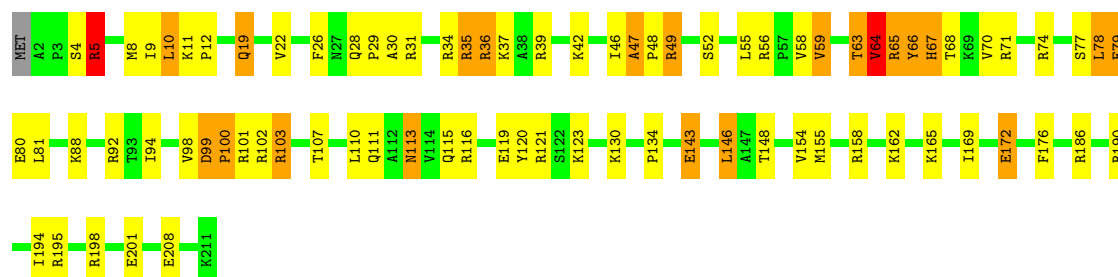
• Molecule 10: uL5

Chain J: 58% 33% 5% •

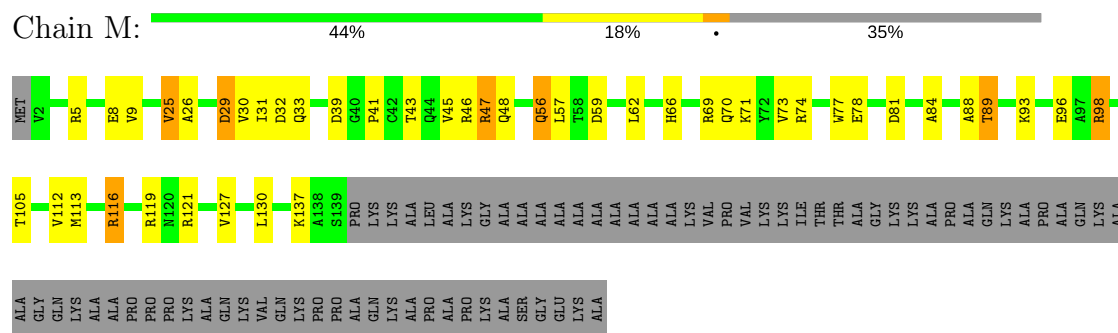


• Molecule 11: eL13

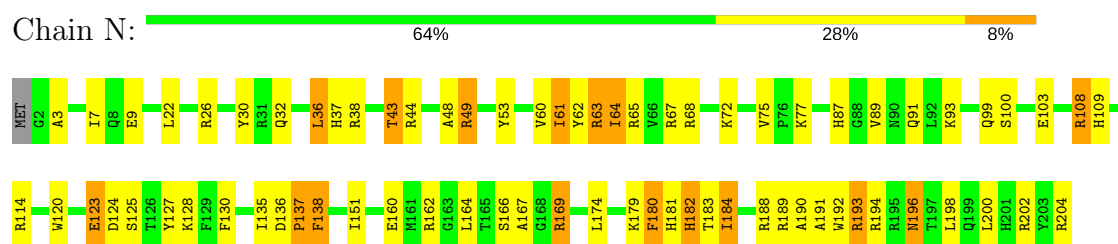
Chain L: 61% 28% 9% •



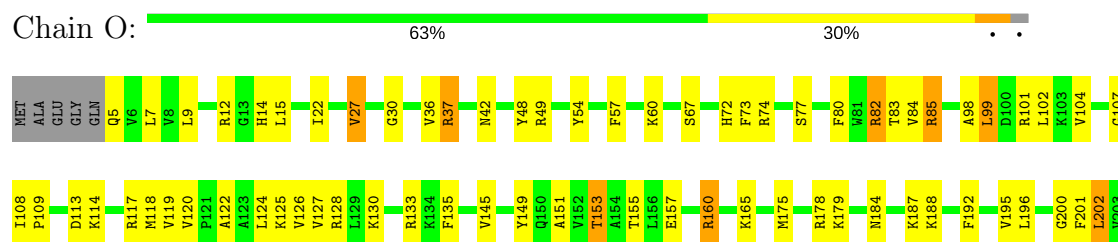
- Molecule 12: eL14



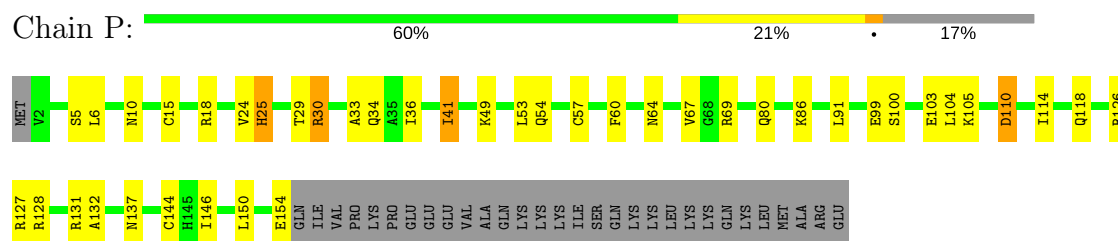
- Molecule 13: eL15



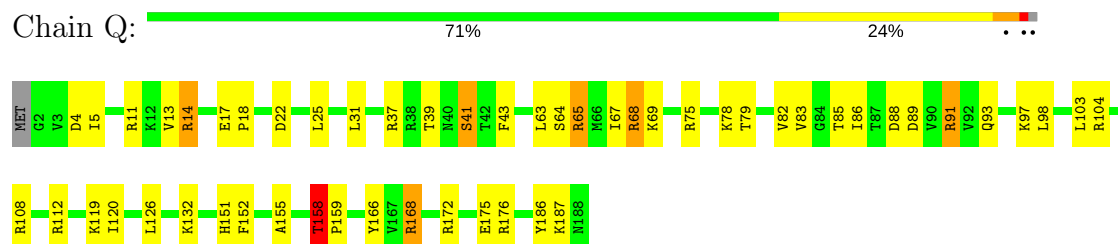
- Molecule 14: uL13



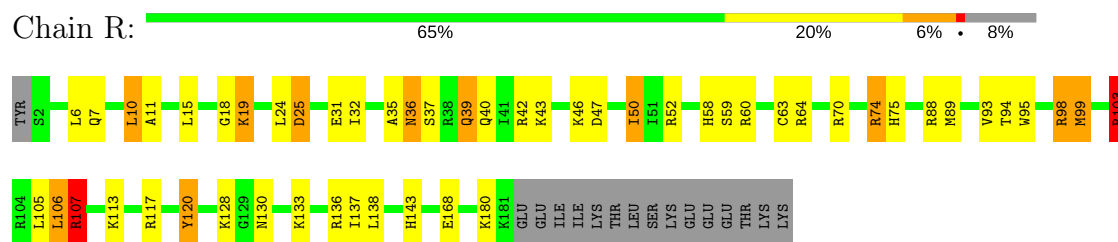
- Molecule 15: uL22



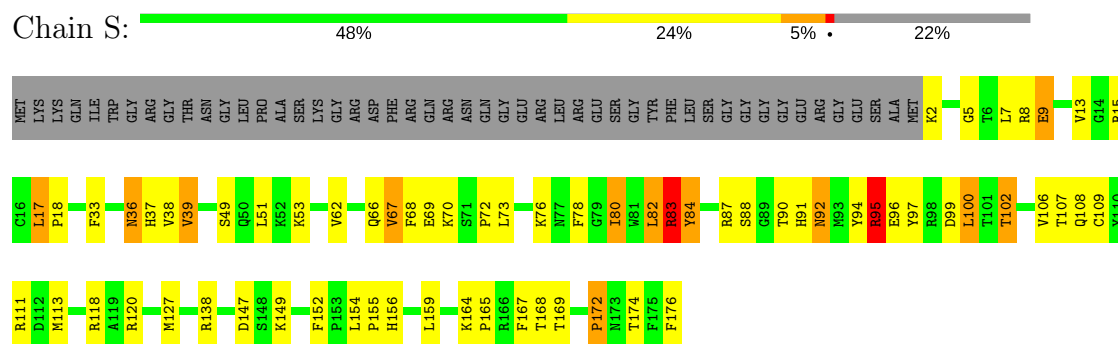
- Molecule 16: eL18



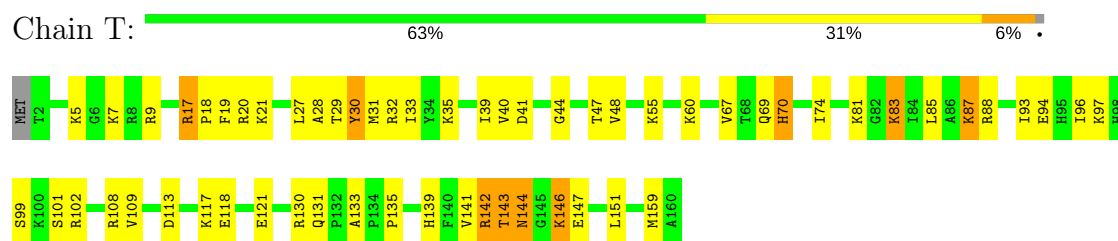
- Molecule 17: eL19



- Molecule 18: eL20

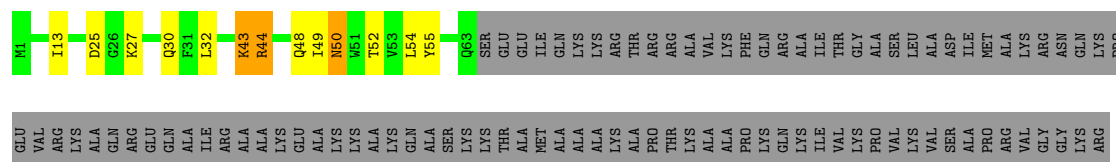


- Molecule 19: eL21



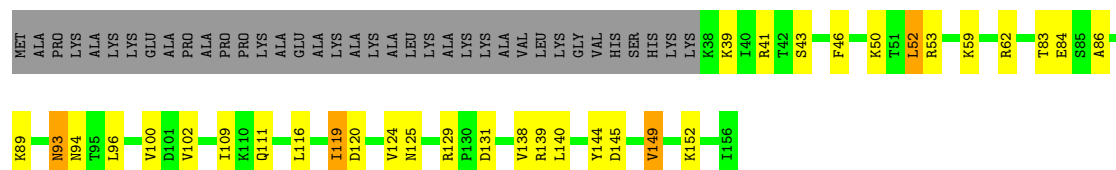
- Molecule 22: eL24

Chain W:  32% 6% 60%



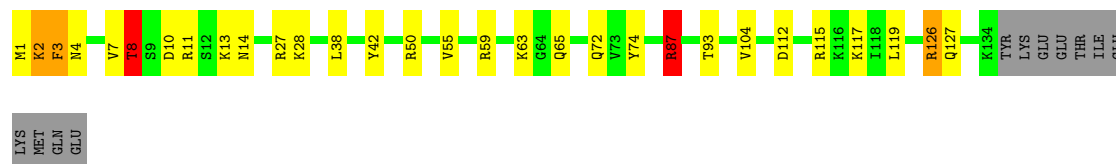
- Molecule 23: uL23

Chain X: 54% 19% . 24%



- Molecule 24: uL24

Chain Y:  72% 17% .. 8%

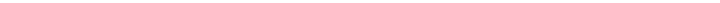


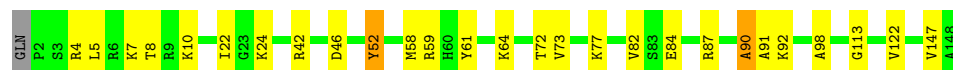
- Molecule 25: eL27

Chain Z:  65% 32% .



- Molecule 26: uL15

Chain a:  81% 17% ..



- Molecule 27: eL29

Chain b: 38% 9% 53%



ALA ARG ALA ARG ALA ARG ILE ALA LYS LYS LEU ARG PHE CYS ARG PRO LYS SER GLN ALA LYS ALA GLN LYS SER LYS ALA LYS ALA THR ALA GLY GLY THR ALA ALA ALA PRO VAL PRO PRO ALA SER ALA PRO LYS GLY LYS ALA ALA GLN

• Molecule 28: eL30

Chain c:  72% 10% 18%

MET VAL ALA ALA LYS LYS THR LYS LYS LEU SER LEU GLU S13 S14 S15 S16 Q19 V28 M37 Q40 N50 N51 N78 Y89 L94 R106 SER MET PRO PRO GLN GLN THR GLY LYS

• Molecule 29: eL31

Chain d:  68% 15% 14%

MET ALA PRO ALA LYS LYS GLY GLY LYS LYS LYS LYS ARG SER SER ILE N18 E19 R23 T26 T27 N28 K31 F38 L46 L47 E48 E56 E57 Q58 K75 G76 I77 R78 N79 T84 R85 E94 L102 T107 M16 L117 E124 ASN

• Molecule 30: eL32

Chain e:  70% 24% 5%

MET A2 A3 L4 V13 R16 K19 F20 I21 R22 K32 R46 R47 R48 F49 K50 M55 I58 K64 K76 F77 L78 N81 V82 K83 E84 L85 E86 N92 K93 M102 V103 S104 S105 K106 M107 Q117 L118 V122 T123 A127 R128 L129 ARG SER


GLU
GLU
ASN
GLU

• Molecule 31: eL33

Chain f:  77% 18% 2%


MET S2 S7 Y14 K15 R16 R19 N20 Q21 K29 R36 D37 E38 T39 E40 R46 K52 P60 K63 P64 V69 G79 N80 V84 R100 I101 R102 V103 Y106 P107 I110

• Molecule 32: eL34

Chain g:  76% 20% 2%

MET V2 Q3 R4 L5 L11 N14 T15 N18 K19 S23 N28 N29 K43 R54 R60 L64 M65 R66 K69 H73 V74 S75 R76 A94 R88 D89 R90 R93 K105 Q112 K115 ALA LYS

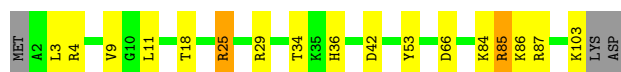
• Molecule 33: uL29

Chain h:  83% 15% 2%

MET A2 R7 R10 K14 K19 L28 K46 R51 T59 N62 Q65 K71 T88 R89 L95 N96 K97 H98 R117 K118 V121 K122 A123

• Molecule 34: eL36

Chain i:  81% 14% 2%



• Molecule 35: eL37



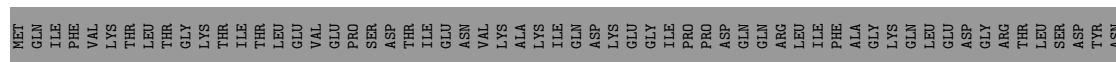
• Molecule 36: eL38



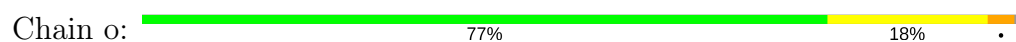
• Molecule 37: eL39



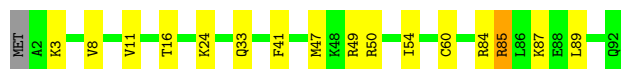
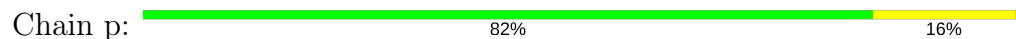
• Molecule 38: eL40



• Molecule 39: eL42

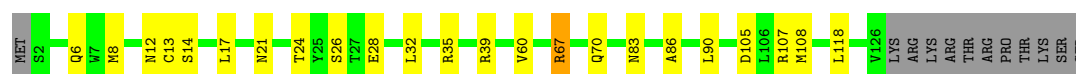


• Molecule 40: eL43

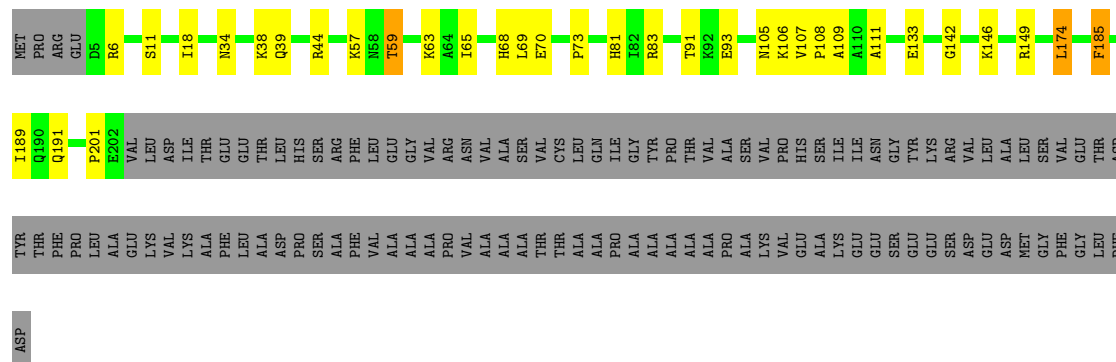


• Molecule 41: eL28

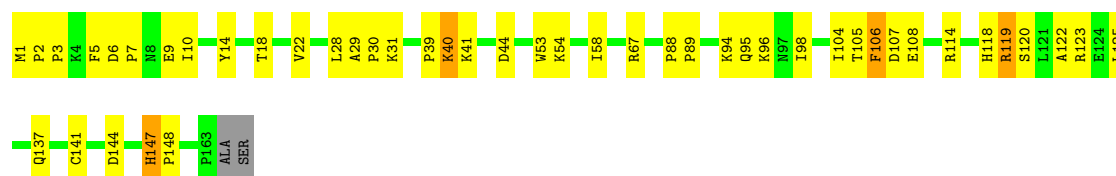




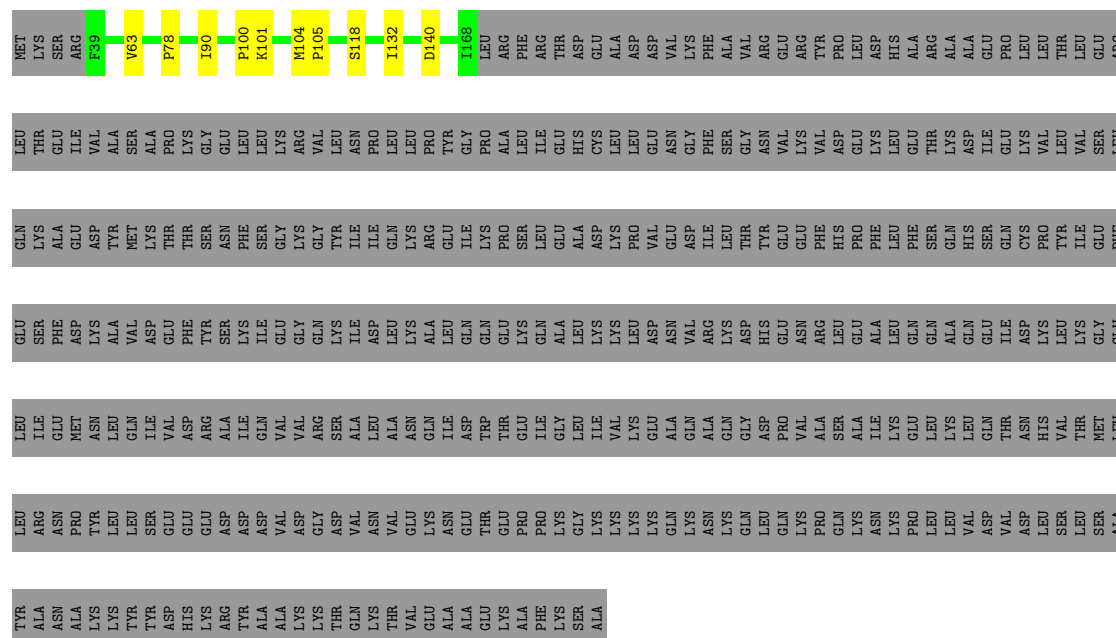
• Molecule 42: uL10



• Molecule 43: uL11

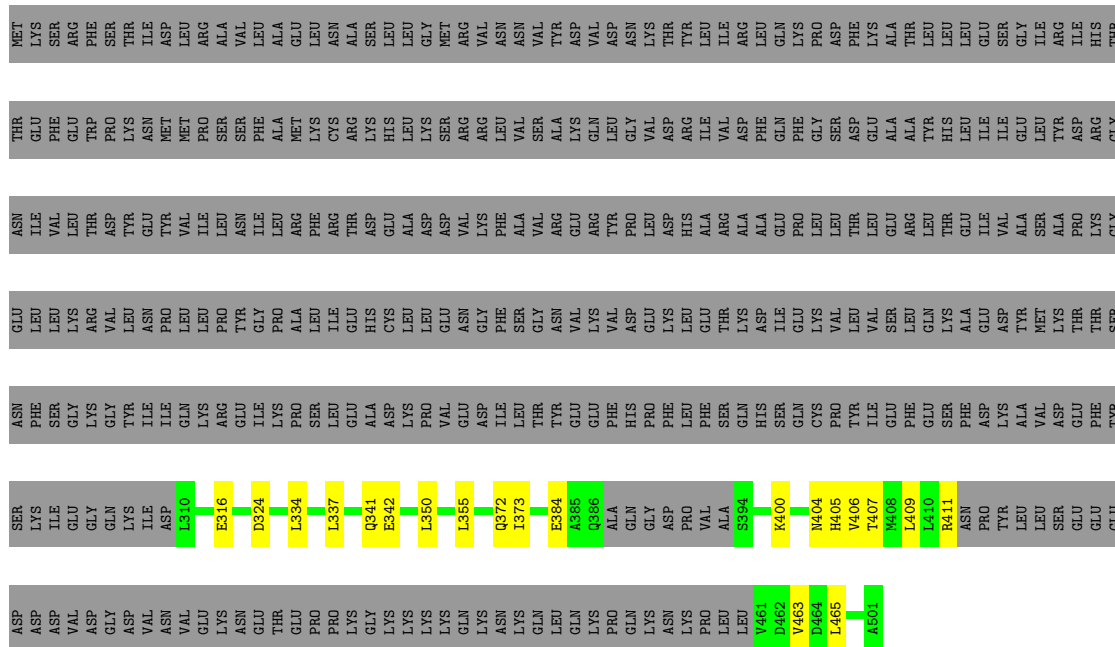


• Molecule 44: NEMF



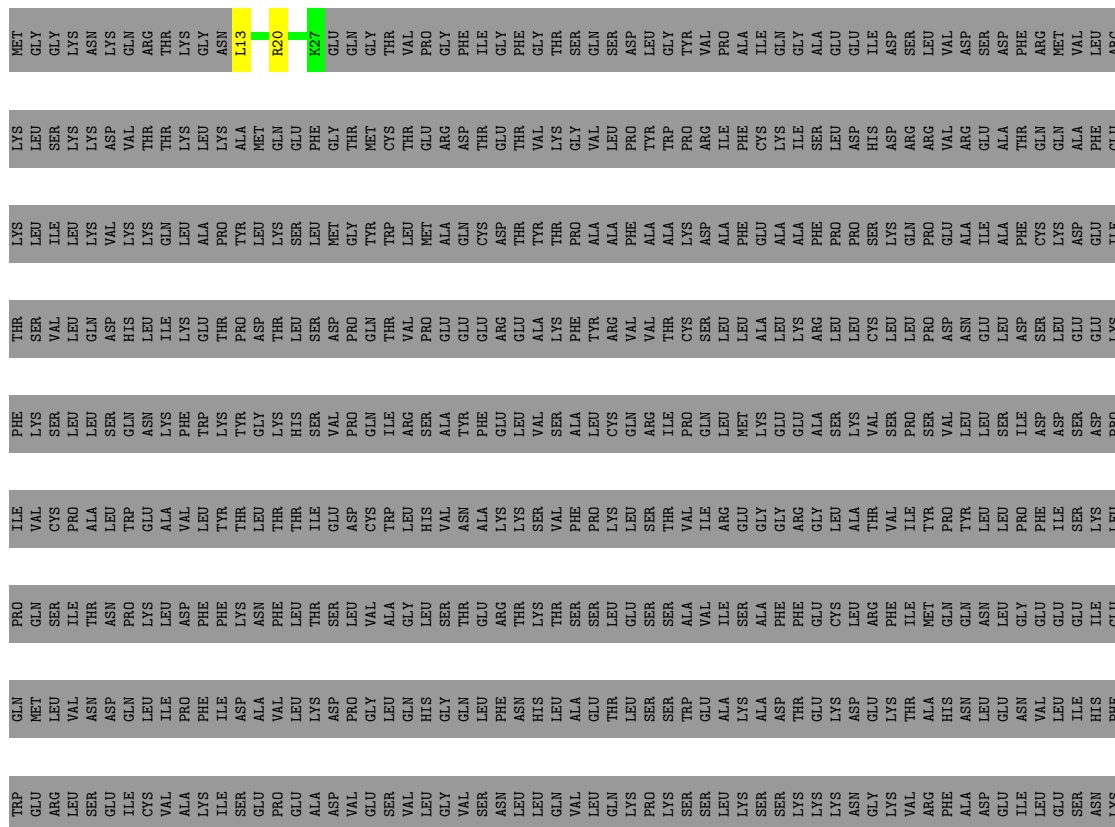
- Molecule 44: NEMF

Chain v:  23% 1% 73%



- Molecule 45: Listerin

Chain w: 99%






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

- Molecule 45: Listerin

Chain z: 6% 93%

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

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

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

SER ILE ASN TYR VAL ASN GLU ARG LYS SER GLU GLN HIS LEU ARG PHE ASP SER PHE SER SER SER ARG VAL PHE LYS MET LEU LEU LEU GLY ASP GLU GLN LYS SER SER SER PRO LEU LEU LEU TLE VAL GLN ALA LYS PRO LEU VAL GLN LYS ASN PRO ALA VAL

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

lys ala ala pro pro ser ser asp lys his ala ala val thr pro trp trp lys lys gly asp gly ile leu leu gly glu glu leu leu val asn ala ala asp cys leu leu cys asn asn glu glu asp leu leu glu ser ser arg arg val ser ser glu glu his his phe phe ser ser glu glu trp trp thr thr leu leu ser ser val val leu leu ser ser tin

HIS
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LEU
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GLY
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VAL
GLU
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ARG
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HIS
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GLU
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CYS
ASP
VAL
ALA
TYR
ASN
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SER
ALA
LYS
GLY
CYS
LEU
LEU
MET

[illegible]

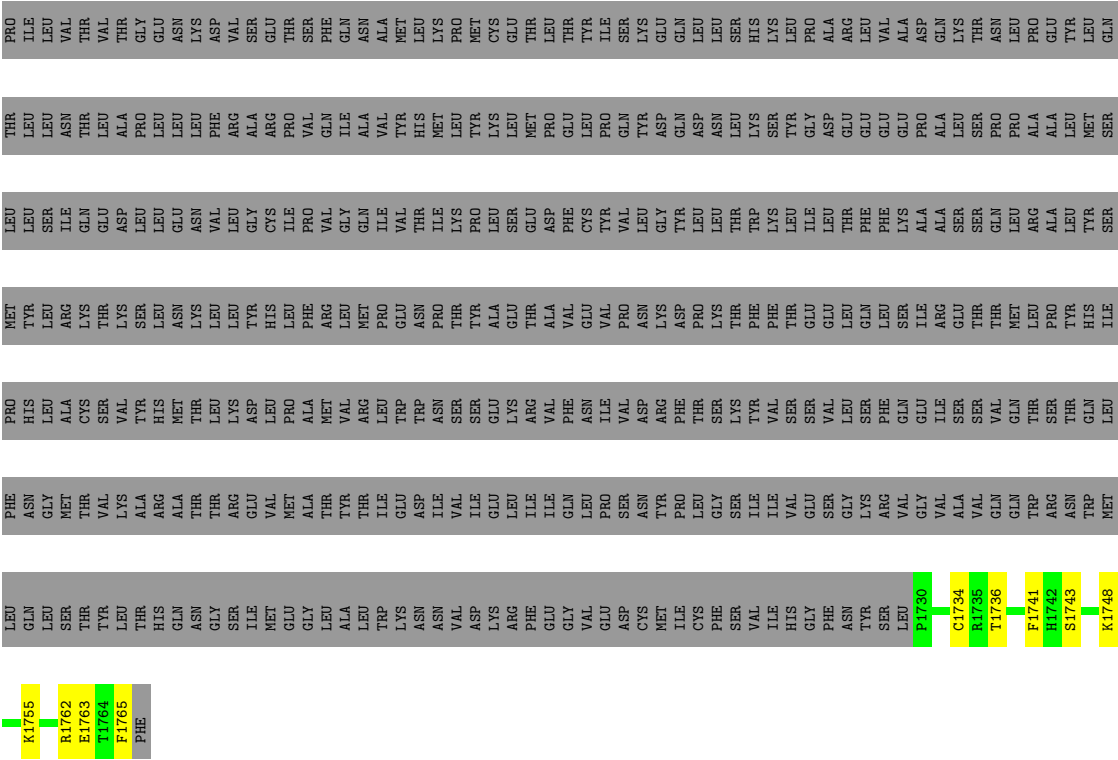
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			L1694	LEU	LEU	ILE	GLN	ALA	GLU	ARG	GLU	GLU	MET	LEU	
PHE	PHE	PHE	M1695	L1563	ILE	ASN	VAL	TYR	LEU	PHE	GLY	GLY	GLY	GLY	GLY
			D1706	GLN	THR	THR	TYR	LEU	SER	PHE	CYS	THR	ILE	ILE	ILE
F1709	GLU	GLY	VAL	W1582	ASP	ALA	THR	ILE	PRO	SER	ILE	TRP	ALA	ARG	GLN
				D1595	LEU	GLY	GLY	LEU	ASN	VAL	ASN	ALA	SER	GLU	PRO
ASP	ASP	CYS	F1597	GLU	GLU	LEU	LYS	GLN	LEU	SER	LEU	LEU	LEU	LEU	SER
			Q1615	VAL	PHE	VAL	LEU	ASN	VAL	PHE	GLY	GLY	ILE	ILE	ILE
MET	ILE	PHE	THR	LEU	ARG	ARG	VAL	ASN	ALA	TRP	ALA	ALA	ALA	GLY	ASP
			THR	GLY	ALA	SER	ALA	SER	THR	SER	THR	LYS	LEU	LEU	ILE
ILE	HIS	PHE	THR	THR	ARG	GLU	THR	CYS	PRO	GLY	PRO	GLN	GLN	GLN	ASN
			GLN	PRO	VAL	SER	VAL	VAL	VAL	SER	VAL	ASP	ASP	LEU	LEU
VAL	SER	PHE	LEU	VAL	VAL	GLN	PHE	CYS	LEU	GLY	CYS	GLY	CYS	GLY	TTR
			PHE	GLY	ILE	GLN	ASP	GLY	VAL	SER	GLY	VAL	GLY	GLY	GLY
ILE	HIS	GLY	ASN	ASN	GLN	ALA	ASN	ASP	VAL	VAL	ILE	ASN	GLU	GLU	GLU
			ASN	VAL	ALA	ALA	ALA	ILE	ASN	ASN	ASN	ASN	ASN	ASN	ASN
THR	SER	PRO	G1623	THR	LYS	LEU	PRO	LEU	ILE	GLY	GLY	GLY	GLY	GLY	GLY
			R1629	LYS	HIS	LEU	ASP	ILE	GLY	ASP	PRO	PRO	ILE	ILE	ILE
LYS	ALA	CYS	T1632	PRO	PRO	TYR	MET	ALA	ARG	GLY	VAL	VAL	VAL	VAL	VAL
			R1633	THR	THR	THR	THR	CYS	PHE	PHE	GLY	GLY	GLY	GLY	GLY
THR	GLY	LYS	T1638	LEU	GLU	GLU	GLU	ASP	SER	ALA	HIS	GLY	GLN	GLN	GLN
			E1642	ASP	PRO	LEU	SER	LEU	SER	LEU	ILE	TYR	TYR	PHE	ASP
ALA	CYS	ARG	D1643	VAL	PHE	GLU	THR	THR	THR	PHE	PHE	CYS	ILE	ILE	ILE
			I1649	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
LYS	LYS	PHE	P1653	ASN	GLY	TYR	LYS	ILE	GLY	CYS	LEU	GLN	GLN	PRO	GLU
			Y1656	THR	ASP	GLN	GLN	GLY	ILE	GLY	SER	SER	THR	THR	HIS
HIS	SER	ALA	G1659	THR	LEU	ASN	SER	ASN	ASN	PRO	PRO	ASN	ASN	CYS	GLY
			S1660	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
CYS	CYS	CYS	I1661	LYS	LYS	SER	LYS	ASN	ASN	GLU	ASP	ASP	ASP	ALA	VAL
			R1668	GLU	GLY	PRO	ILE	ILE	GLY	PRO	ILE	GLY	GLY	ASN	ASN
THR	TRP	PHE	V1669	LEU	THR	GLU	ARG	GLU	GLU	ASP	HIS	ARG	GLY	GLY	ILE
			G1670	VAL	GLN	VAL	LEU	GLU	GLU	PHE	ILE	HIS	GLY	GLY	VAL
SER	SER	SER	W1676	LEU	PHE	GLU	VAL	TRP	LYS	MET	ILE	GLN	GLY	VAL	MET
			L1681	VAL	GLU	GLU	VAL	GLY	LYS	GLY	CYS	ILE	GLY	ASN	ASN
THR	PRO	CYS	T1688	THR	THR	THR	ASN	ILE	LEU	TRP	ILE	GLN	GLY	LEU	TRP
			HIS	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	CYS	CYS	HIS	THR	THR	THR	PRO	HIS	GLU	GLU	LYS	CYS	GLY	GLY	GLY
			ASN	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
CYS	CYS	CYS	ASN	THR	THR	THR	GLN	GLY	LEU	TRP	ILE	GLN	GLY	LEU	GLY
			THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR

- Molecule 45: Listerin

Chain 0: 98%

[illegible]



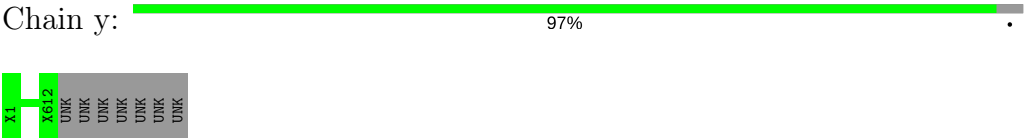



• Molecule 46: Listerin

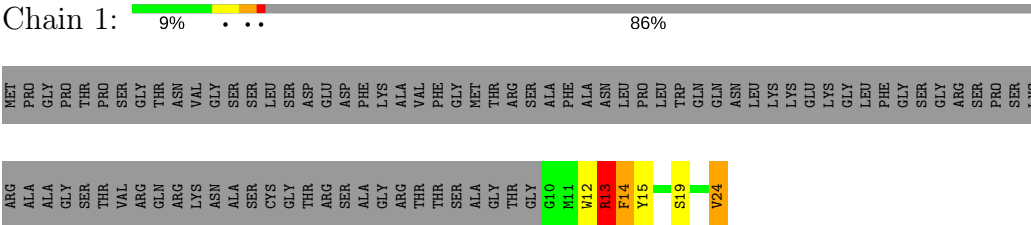
Chain x: 100%

There are no outlier residues recorded for this chain.

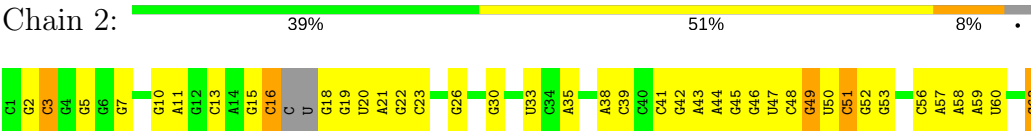
• Molecule 46: Listerin



• Molecule 47: nascent chain



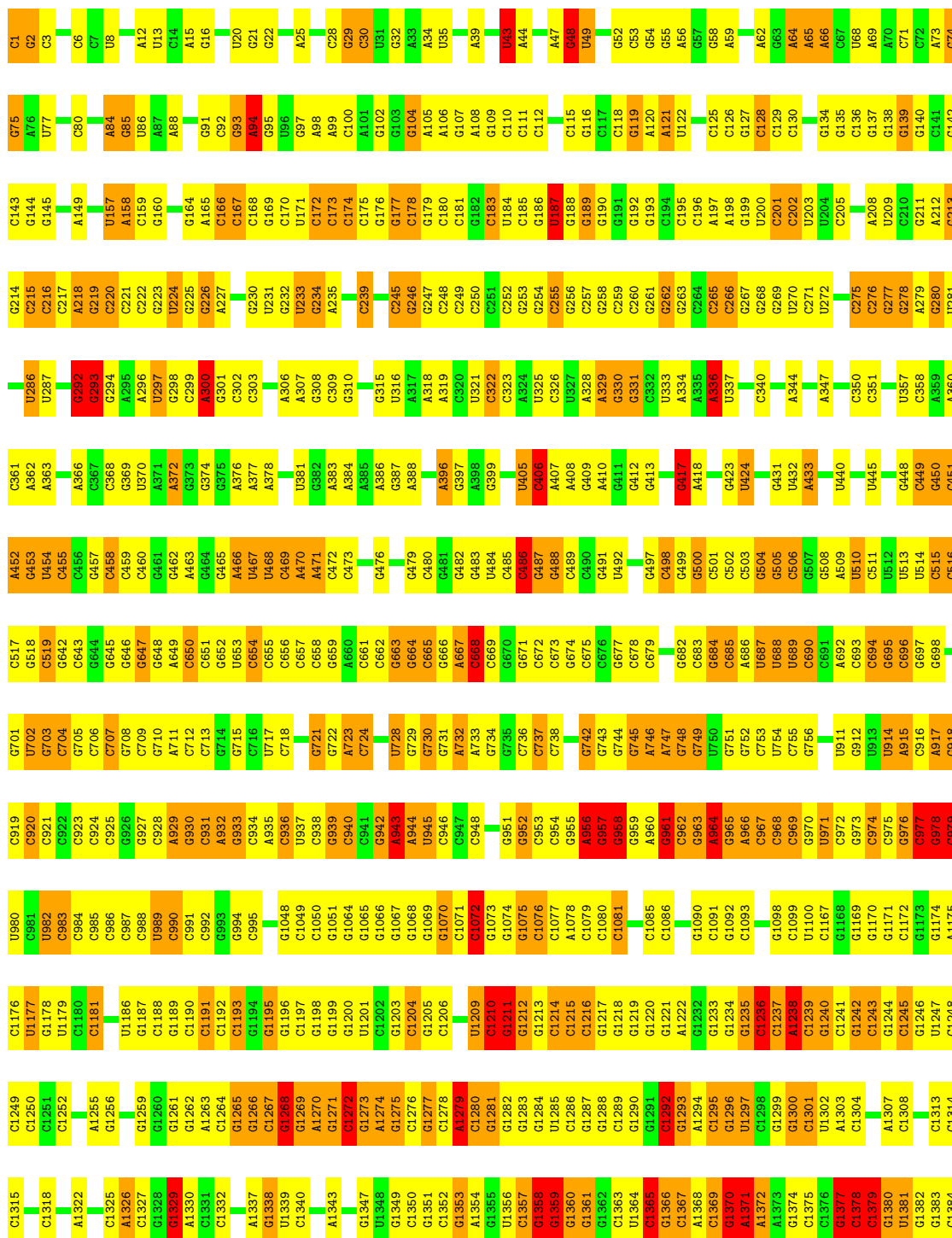
• Molecule 48: tRNA





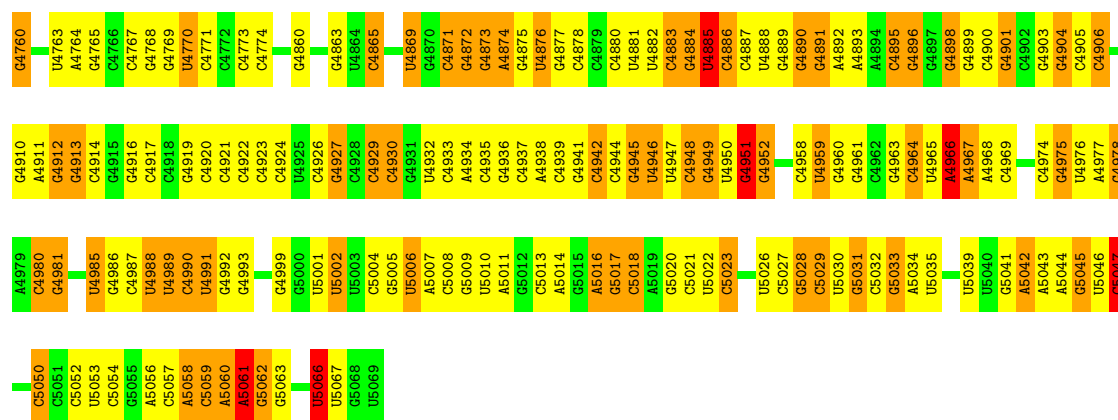
● Molecule 49: 28S rRNA

Chain 5: 36% 42% 19%



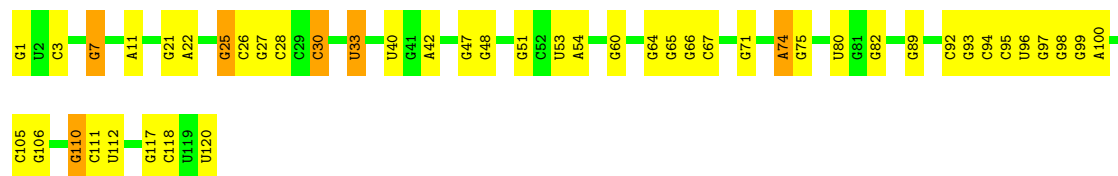



G4690	U4594	G4522	G4448	G4368	G4287	C4207	G4136		A3876	A3774	C3699	U3616	G2859	G2771	C2704
G4595	G4595	A4523	A4449	U4374	G4288	U4206	C4137	A4073	A3877	A3775	C3700	G3617	C2860	G2772	G2705
G4596	G4596	G4525	U4450	C4375	U4289	G4209	G4138	C4074	C3878	G3777	C3701	G3620	G2862	G2773	G2706
A4605	A4605	G4528	U4453	G4376	G4291	U4210	G4139	A4075	G3879	G3778	G3705	G3625	G2863	G2774	U2707
G4606	G4606	U4529	G4454	A4377	G4297	A4213	G4141	A4077	G3886	C3782	C3706	G3626	A2864	C2708	U2709
A4607	A4607	U4530	G4455	A4378		A4214	G4142	C4078	G3887	A3783		G3627		G2710	G2711
G4608	G4608	U4531	G4456	A4379	U4301	G4215	G4143		G3888	A3784	U3709	G3627	G2867	G2712	G2711
		A4532	C4387		U4302	G4216	G4144	U4083	G3889	A3785	G3710		G2868	G2713	G2712
G4614	G4614	U4533	A4388	C4387	G4302	G4217	G4145	G4084	G3890	A3786	A3711	A3635	U2869	U2788	C2713
A4700	A4700	G4534	C4389	A4376	A4304	U4219	G4146	A4085	A3890	G3787	A3712	G3637	A2870	U2789	G2714
G4702	G4702	G4534	A4462	G4377	G4305	A4219	G4147	G4086	A3891	G3788	U3713	U3637	A2871	G2715	G2715
U4703	U4703		A4463	A4377	G4306		G4148	G4087	U3892	U3790	G3714		C2872	G2716	
A4707	A4707	C4537	G4464	A4378	U4307	G4225	C4149	A4088	G3896	C3791	U3715	U3641	U2873		
			U4465	A4379	C4308	U4226	G4150	G4089	G3897	G3792	U3716	A3642	U2874	G2720	
G4708	G4708	G4543	A4466	A4379	G4309	G4227	G4151	G4090	G3898	A3795	C3717	A3643	C2875	G2721	G2721
U4709	U4709	A4544	A4467	U4395	A4310	U4228	G4152	G4091	G3899	A3796	A3717	U3644	C2876	G2722	G2722
				A4396	A4311	G4229	C4153	G4092	G3900	A3799	A3723	U3645	G2889	U2723	U2723
G4714	G4714	A4548	G4470	A4397	U4312	G4230	G4154	G4093	A3901	A3800	A3724	A3646	C2890	G2724	G2724
G4715	G4715	G4549	U4471	C4398	U4313	G4231	C4155	G4094		U3801	G3725	A3647	U2891	A2725	
G4716	G4716	U4550	A4472	A4399	C4314	G4232	C4156	G4095	G3904	U3802	A3726	A3648	G2897	A2726	G2726
G4717	G4717	U4551	A4473	G4400	G4315	U4233	C4157	G4096	A3905	U3803	A3727	A3649	G2898	C2727	
G4718	G4718	U4552	A4474	G4401	G4316	G4234	C4158	G4097	A3906	C3810	U3728	A3651	C2899	U2730	U2730
G4719	G4719	A4553	A4475	G4402	U4317	G4235	G4159	G4098	G3907	U3811	U3729	A3652	U2900	G2731	
G4720	G4720	G4554	C4476	U4403	C4318	G4236	G4161	G4099	A3908	G3812	C3731	A3653	U2901	A2807	
					C4319	G4237	C4162	G4099	A3909	A3814				G2808	
A4723	A4723	U4555	G4480	G4408	G4320	G4238	U4163	G4101	A3910	U3815	G3735	A3656	U2904	G2736	
A4724	A4724	A4559	U4481	C4409	U4321	G4239	C4164	G4102	C3911	G3816	G3736	C3658	C2905	C2737	
G4725	G4725	C4560	U4482	G4410	G4322	G4240	C4165	G4103	C3912	A3817	A3737	G3659	G2906	G2738	
G4726	G4726	A4561	C4483	G4411	A4323	G4241	C4166	G4104	U3913	U3818	G3738	C3660	G2907	C2739	
G4727	G4727	U4562	G4484	C4412	A4324	C4241	C4167	G4105	G3914	G3819	C3739	G3661	G2908	U2740	
U4728	U4728	G4563	C4485	C4413	G4325		C4171	G4106	U3915				C2909		
U4646	U4646	A4564	C4486	C4414	A4326	G4249	A4172	G4107	G3916	U3822	G3742	A3662	G2910	A2743	
A4648	A4648	U4565	U4487	G4415	G4327	G4250	C4173	G4108	G3917	U3823	G3743	A3663		A2744	
		A4566	A4488	G4416	G4328	A4251	U4174	G4109	A3918	A3824	G3744	G3664	G3586	A2745	
A4651	A4651	U4567	G4489	C4417	G4329	G4254	C4175	G4110	G3919	U3825	U3745	G3667	C3587	A2746	
G4732	G4732	A4568	C4490	G4418	G4330	G4255	C4176	C4111	C3920	U3831	A3746	C3668	G3590	U2747	
A4733	A4733	G4569	U4491	U4419	G4331	A4256	C4177	U4113	U3921			G3669	G3591	G2748	
G4734	G4734	U4570	G4426	G4427	C4332	G4257	A4178	G4114	U3922	U3838	A3747	G3670	C3592	C2749	
G4735	G4735	G4571	U4421	C4421	G4333	C4258	G4179	C4115	G3923	U3839	A3748	G3671	C3593	G2750	
				U4422	A4336	G4259	U4181	G4116	C3924	U3840	C3749	G3672	C3594	G2751	
G4736	G4736	U4572	G4423	U4423	G4337	U4260	G4182	U4117	C3925	U3841	G3750	C3673	C3595	G2752	
					C4338	G4261	G4183	C4118	C3926	U3851	G3753	G3674	A3596	G2753	
G4737	G4737	A4573	C4426	G4427	G4339	G4267	G4184	U4120	U3927		G3754	G3675	G3597	G2754	
					U4340	A4268	G4185	G4121	U3932	C3855	G3755		G3598	A2755	
G4738	G4738	U4574	U4431	U4431	C4341	G4269	U4189	G4122	U3933	A3856	A3756	U3679	C3599	G2756	
C4739	C4739	G4575	C4432	C4432	G4342	G4270	U4190	C4123	G3933	G3857	U3680	U3680	G3600	A2757	
					A4348	G4271	G4191	G4124	G3934	C3858	G3681	G3681	C3601	G2758	
G4740	G4740	U4576	G4433	G4433	C4349	G4272	G4195	C4125	C3935	A3859	A3759	A3760	C3602	G2759	
					U4350	A4273	G4196	C4126	A3936	A3860	C3761	G3683	G3603	U2761	
G4741	G4741	U4577	U4437	U4437	C4350	G4274	G4197	A4127	C3937		C3762	G3684	A3604	G2762	
					U4354	A4275	G4198	G4128	G3938	C3864	U3763	G3685	C3605	U2763	
G4745	G4745	A4584	U4438	U4438	U4355	G4280	G4199	G4129	G3939	A3865	U3764	G3686	U3606	A2764	
G4746	G4746	U4585	G4439	G4439	G4356	A4281	C4199	C4130	C3940	C3866	G3765	A3687	G3607	G2765	
G4747	G4747	A4586	A4441	A4441	C4356	A4282	C4199	C4131	A3943	A3867				A2766	
U4748	U4748	G4587	U4442	U4442	U4357	A4283	A4203	C4132		C3868	U3770	U3695	A3611	U2767	
					U4358	G4284	C4204	C4133	U4068	C3869	C3771	C3696	U3612	G2768	
G4749	G4749	U4588	U4443	U4443	U4360	G4285	A4205	C4134	U4069	C3870	U3772	U3697	C3613	U2769	
G4750	G4750	A4589	U4444	U4444	U4361	G4286	C4206	G4135	U4070	A3871	U3773	G3698	G3615	A2858	
G4751	G4751	G4590	C4445	C4445	G4367										
G4752	G4752	U4591	U4446	U4446											
U4753	U4753	A4592	U4447	U4447											
G4754	G4754	G4593	U4448	U4448											
G4755	G4755	U4594	U4449	U4449											
G4756	G4756	A4595	U4450	U4450											
G4757	G4757	G4596	U4451	U4451											
U4758	U4758	U4597	U4452	U4452											
G4759	G4759	A4598	U4453	U4453											



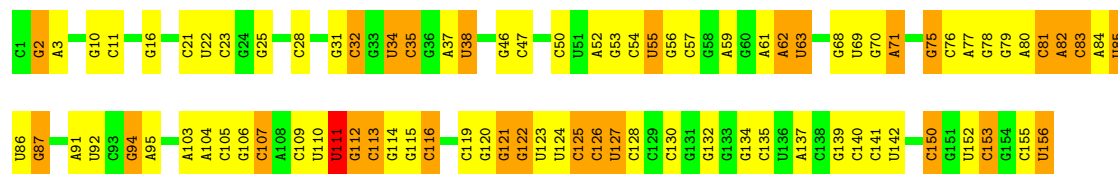
• Molecule 50: 5S rRNA

Chain 7: 61% 34% 5%



• Molecule 51: 5.8S rRNA

Chain 8: 44% 37% 18%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	63826	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS, FEI TITAN KRIOS	Depositor
Voltage (kV)	300, 300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30, 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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, 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 >2	RMSZ	# Z >2
1	A	0.59	0/1906	0.90	2/2556 (0.1%)
10	J	0.47	0/1382	0.83	1/1849 (0.1%)
11	L	0.59	0/1734	0.98	2/2318 (0.1%)
12	M	0.59	0/1152	0.89	0/1539
13	N	0.62	0/1746	0.97	0/2338
14	O	0.68	0/1671	1.01	1/2234 (0.0%)
15	P	0.62	0/1268	0.89	0/1701
16	Q	0.59	0/1530	0.99	1/2041 (0.0%)
17	R	0.51	0/1524	1.02	3/2013 (0.1%)
18	S	0.62	0/1493	0.97	3/2002 (0.1%)
19	T	0.60	0/1326	0.88	1/1770 (0.1%)
2	B	0.57	0/3214	0.88	1/4308 (0.0%)
20	U	0.46	0/822	0.83	0/1103
21	V	0.59	0/993	0.86	0/1332
22	W	0.53	0/541	0.90	1/720 (0.1%)
23	X	0.50	0/993	0.85	0/1334
24	Y	0.53	0/1132	0.98	4/1504 (0.3%)
25	Z	0.51	0/1130	0.82	0/1507
26	a	0.68	0/1192	0.95	3/1591 (0.2%)
27	b	0.57	0/620	0.97	1/819 (0.1%)
28	c	0.51	0/742	0.78	0/996
29	d	0.58	0/903	1.03	3/1216 (0.2%)
3	C	0.61	0/2973	0.95	5/3990 (0.1%)
30	e	0.62	0/1071	0.97	4/1429 (0.3%)
31	f	0.68	0/895	1.00	1/1198 (0.1%)
32	g	0.51	0/916	0.96	3/1220 (0.2%)
33	h	0.51	0/1023	0.96	3/1350 (0.2%)
34	i	0.50	0/843	1.05	4/1115 (0.4%)
35	j	0.69	0/721	1.00	1/953 (0.1%)
36	k	0.41	0/575	0.83	0/761
37	l	0.57	0/454	0.98	1/599 (0.2%)
38	m	0.56	0/435	0.96	1/575 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	o	0.53	0/864	0.90	1/1140 (0.1%)
4	D	0.51	0/2430	0.85	3/3256 (0.1%)
40	p	0.54	0/718	0.89	1/953 (0.1%)
41	r	0.60	0/1017	0.96	0/1365
42	s	0.50	0/1546	0.77	2/2087 (0.1%)
43	t	0.52	0/1257	0.87	1/1697 (0.1%)
44	u	0.46	0/644	0.61	0/897
44	v	0.44	0/1099	0.82	1/1470 (0.1%)
45	0	0.53	0/301	0.69	0/400
45	w	0.47	0/110	0.78	0/146
45	z	0.45	0/1076	0.80	0/1451
47	1	0.59	0/129	0.83	0/173
48	2	0.26	0/1765	0.73	0/2749
49	5	0.49	11/87791 (0.0%)	0.88	177/136941 (0.1%)
5	E	0.52	0/1941	0.95	3/2601 (0.1%)
50	7	0.42	0/2858	0.72	1/4455 (0.0%)
51	8	0.45	1/3701 (0.0%)	0.77	1/5766 (0.0%)
6	F	0.66	0/1905	1.00	4/2539 (0.2%)
7	G	0.51	0/1971	0.90	2/2652 (0.1%)
8	H	0.52	0/1537	0.91	1/2066 (0.0%)
9	I	0.56	0/1690	0.89	2/2257 (0.1%)
All	All	0.52	12/155270 (0.0%)	0.88	250/229042 (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
1	A	0	1
11	L	0	2
13	N	0	1
14	O	0	1
17	R	0	2
18	S	0	3
19	T	0	3
2	B	0	4
21	V	0	1
24	Y	0	1
25	Z	0	1
26	a	0	2
27	b	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	C	0	2
31	f	0	2
33	h	0	1
34	i	0	1
36	k	0	1
4	D	0	1
42	s	0	2
43	t	0	4
47	l	0	1
49	5	0	3
5	E	0	4
6	F	0	1
7	G	0	2
8	H	0	1
9	I	0	3
All	All	0	52

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	5	957	G	O3'-P	8.72	1.71	1.61
49	5	1358	G	O3'-P	7.41	1.70	1.61
49	5	956	A	O3'-P	7.15	1.69	1.61
49	5	1370	G	O3'-P	6.23	1.68	1.61
49	5	4375	C	O3'-P	-5.70	1.54	1.61

The worst 5 of 250 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	5	1358	G	C4'-C3'-O3'	11.60	136.20	113.00
24	Y	87	ARG	NE-CZ-NH2	10.23	125.41	120.30
34	i	25	ARG	NE-CZ-NH1	10.20	125.40	120.30
18	S	83	ARG	NE-CZ-NH2	9.56	125.08	120.30
49	5	336	A	O4'-C1'-N9	9.31	115.65	108.20

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	68	0
2	B	3147	0	3280	84	0
3	C	2919	0	3100	127	0
4	D	2384	0	2423	54	0
5	E	1904	0	2055	68	0
6	F	1870	0	1994	136	0
7	G	1939	0	2095	60	0
8	H	1518	0	1601	53	0
9	I	1651	0	1692	43	0
10	J	1359	0	1390	63	0
11	L	1703	0	1818	60	0
12	M	1131	0	1209	41	0
13	N	1701	0	1749	59	0
14	O	1638	0	1777	58	0
15	P	1242	0	1269	16	0
16	Q	1506	0	1623	26	0
17	R	1508	0	1664	22	0
18	S	1454	0	1496	55	0
19	T	1298	0	1366	54	0
20	U	808	0	831	42	0
21	V	979	0	1039	43	0
22	W	528	0	541	7	0
23	X	976	0	1053	19	0
24	Y	1115	0	1205	19	0
25	Z	1107	0	1182	26	0
26	a	1163	0	1209	0	0
27	b	610	0	650	0	0
28	c	732	0	769	0	0
29	d	888	0	930	0	0
30	e	1053	0	1147	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	f	876	0	912	0	0
32	g	906	0	1000	0	0
33	h	1015	0	1150	0	0
34	i	832	0	917	0	0
35	j	706	0	742	0	0
36	k	569	0	637	0	0
37	l	444	0	483	0	0
38	m	429	0	465	0	0
39	o	851	0	921	0	0
40	p	708	0	755	0	0
41	r	1001	0	1062	0	0
42	s	1522	0	1575	0	0
43	t	1238	0	1293	0	0
44	u	645	0	285	0	0
44	v	1092	0	1143	0	0
45	0	293	0	299	3	0
45	w	110	0	118	0	0
45	z	1057	0	1074	0	0
46	x	1090	0	248	0	0
46	y	1055	0	237	0	0
47	1	125	0	117	6	0
48	2	1601	0	818	28	0
49	5	78486	0	39661	2237	0
50	7	2558	0	1296	23	0
51	8	3314	0	1683	73	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	0	0
53	j	1	0	0	0	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	3319	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 3319 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)
11:L:80:GLU:OE1	11:L:102:ARG:NH1	1.63	1.31
6:F:110:VAL:HG21	6:F:137:ILE:CD1	1.58	1.30
2:B:150:PHE:CE2	2:B:198:ARG:NH1	1.99	1.30
49:5:1983:A:N1	49:5:2008:U:O4	1.65	1.27
6:F:39:PHE:CE1	49:5:2123:C:H3'	1.70	1.26

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%)	3	29
2	B	392/395 (99%)	342 (87%)	44 (11%)	6 (2%)	12	55
3	C	365/368 (99%)	315 (86%)	43 (12%)	7 (2%)	9	50
4	D	290/297 (98%)	266 (92%)	18 (6%)	6 (2%)	8	48
5	E	232/284 (82%)	176 (76%)	39 (17%)	17 (7%)	1	17
6	F	223/250 (89%)	203 (91%)	16 (7%)	4 (2%)	10	51
7	G	239/266 (90%)	196 (82%)	36 (15%)	7 (3%)	5	41
8	H	188/192 (98%)	164 (87%)	17 (9%)	7 (4%)	4	35
9	I	200/214 (94%)	171 (86%)	22 (11%)	7 (4%)	4	37
10	J	168/178 (94%)	143 (85%)	17 (10%)	8 (5%)	2	27
11	L	208/211 (99%)	174 (84%)	22 (11%)	12 (6%)	2	23
12	M	136/213 (64%)	118 (87%)	16 (12%)	2 (2%)	12	55
13	N	201/204 (98%)	172 (86%)	28 (14%)	1 (0%)	32	73
14	O	197/204 (97%)	173 (88%)	23 (12%)	1 (0%)	32	73
15	P	151/184 (82%)	133 (88%)	17 (11%)	1 (1%)	25	68
16	Q	185/188 (98%)	161 (87%)	22 (12%)	2 (1%)	17	61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	R	178/196 (91%)	160 (90%)	14 (8%)	4 (2%)	8	47
18	S	173/224 (77%)	153 (88%)	16 (9%)	4 (2%)	7	46
19	T	157/160 (98%)	136 (87%)	19 (12%)	2 (1%)	14	57
20	U	97/128 (76%)	84 (87%)	9 (9%)	4 (4%)	3	32
21	V	129/140 (92%)	112 (87%)	16 (12%)	1 (1%)	22	65
22	W	61/157 (39%)	55 (90%)	5 (8%)	1 (2%)	11	53
23	X	117/156 (75%)	105 (90%)	11 (9%)	1 (1%)	20	64
24	Y	132/145 (91%)	121 (92%)	9 (7%)	2 (2%)	12	55
25	Z	133/136 (98%)	115 (86%)	13 (10%)	5 (4%)	4	34
26	a	145/148 (98%)	118 (81%)	20 (14%)	7 (5%)	2	27
27	b	73/160 (46%)	68 (93%)	4 (6%)	1 (1%)	13	56
28	c	92/115 (80%)	86 (94%)	5 (5%)	1 (1%)	17	61
29	d	105/125 (84%)	93 (89%)	9 (9%)	3 (3%)	5	41
30	e	126/135 (93%)	113 (90%)	11 (9%)	2 (2%)	11	53
31	f	107/110 (97%)	93 (87%)	10 (9%)	4 (4%)	4	35
32	g	112/117 (96%)	98 (88%)	12 (11%)	2 (2%)	10	51
33	h	120/123 (98%)	103 (86%)	16 (13%)	1 (1%)	22	65
34	i	100/105 (95%)	92 (92%)	5 (5%)	3 (3%)	5	40
35	j	84/97 (87%)	70 (83%)	12 (14%)	2 (2%)	7	45
36	k	67/70 (96%)	56 (84%)	8 (12%)	3 (4%)	3	29
37	l	48/51 (94%)	38 (79%)	8 (17%)	2 (4%)	3	31
38	m	50/128 (39%)	45 (90%)	3 (6%)	2 (4%)	3	32
39	o	102/106 (96%)	88 (86%)	11 (11%)	3 (3%)	5	41
40	p	89/92 (97%)	74 (83%)	13 (15%)	2 (2%)	8	47
41	r	123/137 (90%)	102 (83%)	18 (15%)	3 (2%)	7	45
42	s	196/317 (62%)	159 (81%)	22 (11%)	15 (8%)	1	15
43	t	161/165 (98%)	93 (58%)	39 (24%)	29 (18%)	0	3
44	u	128/501 (26%)	88 (69%)	30 (23%)	10 (8%)	1	15
44	v	130/501 (26%)	125 (96%)	3 (2%)	2 (2%)	12	55
45	0	34/1766 (2%)	29 (85%)	3 (9%)	2 (6%)	2	23
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%)	4	38
47	1	13/104 (12%)	9 (69%)	1 (8%)	3 (23%)	0	1
All	All	7132/14052 (51%)	6110 (86%)	793 (11%)	229 (3%)	8	38

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%)	155 (83%)	32 (17%)	2	16
2	B	335/336 (100%)	285 (85%)	50 (15%)	3	23
3	C	305/306 (100%)	243 (80%)	62 (20%)	1	10
4	D	247/250 (99%)	207 (84%)	40 (16%)	3	19
5	E	209/246 (85%)	172 (82%)	37 (18%)	2	14
6	F	194/217 (89%)	156 (80%)	38 (20%)	1	11
7	G	208/226 (92%)	170 (82%)	38 (18%)	2	12
8	H	169/171 (99%)	135 (80%)	34 (20%)	1	10
9	I	174/181 (96%)	137 (79%)	37 (21%)	1	8
10	J	143/149 (96%)	124 (87%)	19 (13%)	4	28
11	L	176/177 (99%)	137 (78%)	39 (22%)	1	7
12	M	116/160 (72%)	95 (82%)	21 (18%)	2	13
13	N	171/172 (99%)	142 (83%)	29 (17%)	2	17
14	O	171/174 (98%)	149 (87%)	22 (13%)	5	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	P	134/163 (82%)	110 (82%)	24 (18%)	2	13
16	Q	163/164 (99%)	137 (84%)	26 (16%)	3	20
17	R	159/175 (91%)	126 (79%)	33 (21%)	1	9
18	S	156/192 (81%)	125 (80%)	31 (20%)	1	10
19	T	139/140 (99%)	111 (80%)	28 (20%)	1	10
20	U	89/114 (78%)	72 (81%)	17 (19%)	2	11
21	V	101/107 (94%)	86 (85%)	15 (15%)	3	23
22	W	55/126 (44%)	49 (89%)	6 (11%)	7	37
23	X	107/133 (80%)	91 (85%)	16 (15%)	3	23
24	Y	124/135 (92%)	104 (84%)	20 (16%)	3	19
25	Z	117/118 (99%)	101 (86%)	16 (14%)	4	27
26	a	119/120 (99%)	102 (86%)	17 (14%)	4	26
27	b	63/123 (51%)	52 (82%)	11 (18%)	2	15
28	c	79/97 (81%)	69 (87%)	10 (13%)	5	30
29	d	98/110 (89%)	78 (80%)	20 (20%)	1	10
30	e	114/121 (94%)	83 (73%)	31 (27%)	0	4
31	f	88/89 (99%)	67 (76%)	21 (24%)	1	6
32	g	98/100 (98%)	75 (76%)	23 (24%)	1	6
33	h	109/110 (99%)	90 (83%)	19 (17%)	2	15
34	i	86/89 (97%)	73 (85%)	13 (15%)	3	23
35	j	73/80 (91%)	57 (78%)	16 (22%)	1	7
36	k	64/65 (98%)	51 (80%)	13 (20%)	1	10
37	l	47/48 (98%)	37 (79%)	10 (21%)	1	8
38	m	48/116 (41%)	37 (77%)	11 (23%)	1	7
39	o	92/94 (98%)	71 (77%)	21 (23%)	1	7
40	p	74/75 (99%)	60 (81%)	14 (19%)	2	11
41	r	109/121 (90%)	88 (81%)	21 (19%)	1	11
42	s	166/258 (64%)	148 (89%)	18 (11%)	7	38
43	t	136/137 (99%)	120 (88%)	16 (12%)	6	33
44	v	116/445 (26%)	99 (85%)	17 (15%)	3	24
45	0	34/1611 (2%)	30 (88%)	4 (12%)	6	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	w	11/1611 (1%)	9 (82%)	2 (18%)	2	13
45	z	119/1611 (7%)	103 (87%)	16 (13%)	4	28
47	1	13/79 (16%)	11 (85%)	2 (15%)	3	22
All	All	6105/11841 (52%)	5029 (82%)	1076 (18%)	5	14

5 of 1076 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	O	99	LEU
18	S	100	LEU
41	r	67	ARG
15	P	25	HIS
16	Q	172	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 64 such sidechains are listed below:

Mol	Chain	Res	Type
13	N	182	HIS
15	P	40	HIS
39	o	90	HIS
14	O	5	GLN
14	O	96	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
48	2	73/77 (94%)	31 (42%)	0
49	5	3644/3664 (99%)	1364 (37%)	0
50	7	119/120 (99%)	27 (22%)	0
51	8	155/156 (99%)	50 (32%)	0
All	All	3991/4017 (99%)	1472 (36%)	0

5 of 1472 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

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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	14,22,23	0.85	1 (7%)	16,32,35	2.62	3 (18%)

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	-	0/3/25/26	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	2	54	5MU	O4'-C1'	2.10	1.44	1.41

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	2	54	5MU	C5-C4-N3	-6.00	118.62	125.24
48	2	54	5MU	O4'-C1'-N1	2.11	112.31	108.08
48	2	54	5MU	C4-N3-C2	7.69	121.89	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates 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 [i](#)

There are no chain breaks in this entry.