



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:29 PM BST

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 EM Map/Model Validation Report for a publicly released PDB/EMDB entry.  
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

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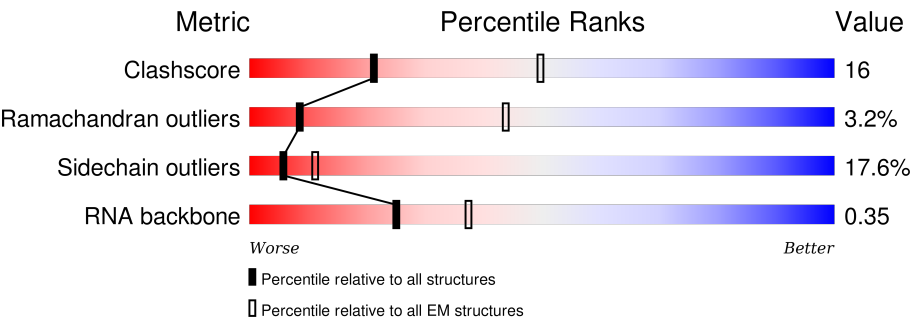
MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk27241

# 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.






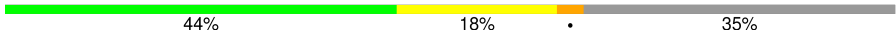







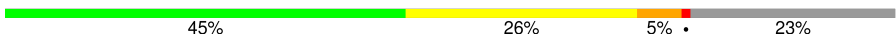













Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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  $\geq 3$ , 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	<div><div>55%</div><div>32%</div><div>8%</div><div>5%</div></div>
2	B	395	<div><div>71%</div><div>25%</div><div>.</div><div>.</div></div>
3	C	368	<div><div>62%</div><div>31%</div><div>6%</div><div>.</div></div>
4	D	297	<div><div>67%</div><div>27%</div><div>.</div><div>.</div></div>
5	E	284	<div><div>50%</div><div>26%</div><div>5%</div><div>.</div><div>17%</div></div>
6	F	250	<div><div>51%</div><div>30%</div><div>8%</div><div>.</div><div>10%</div></div>
7	G	266	<div><div>62%</div><div>24%</div><div>.</div><div>.</div><div>9%</div></div>
8	H	192	<div><div>59%</div><div>34%</div><div>5%</div><div>.</div><div>.</div></div>









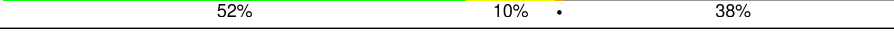


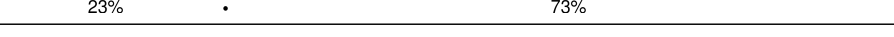
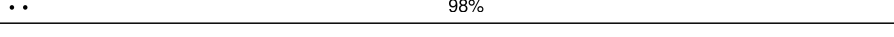
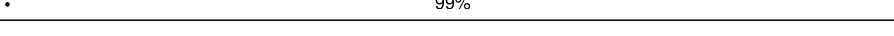
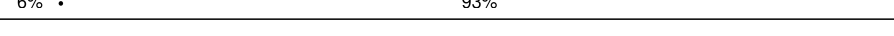
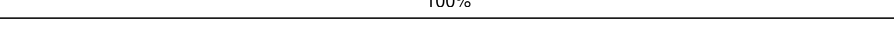
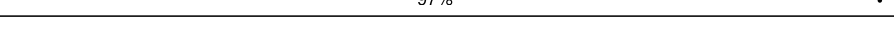

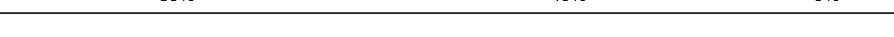



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Mol	Chain	Length	Quality of chain
9	I	214	
10	J	178	
11	L	211	
12	M	213	
13	N	204	
14	O	204	
15	P	184	
16	Q	188	
17	R	196	
18	S	224	
19	T	160	
20	U	128	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	160	
28	c	115	
29	d	125	
30	e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

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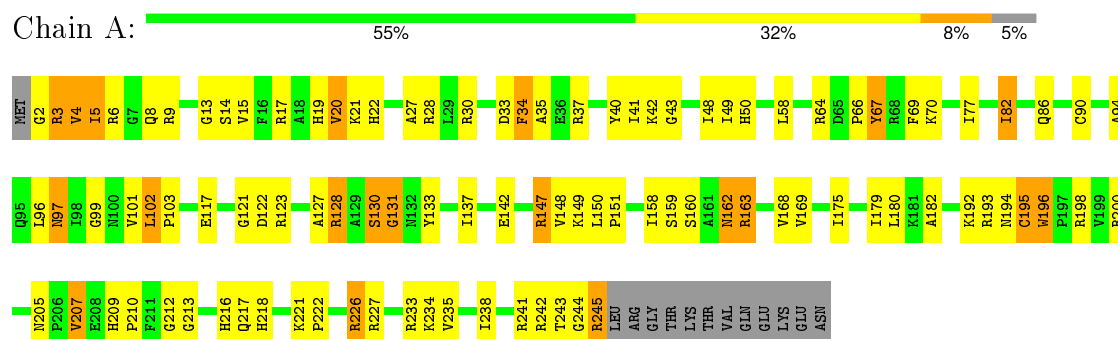
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Mol	Chain	Residues	Atoms		AltConf
53	g	1	Total 1	Zn 1	0
53	j	1	Total 1	Zn 1	0
53	p	1	Total 1	Zn 1	0
53	m	1	Total 1	Zn 1	0

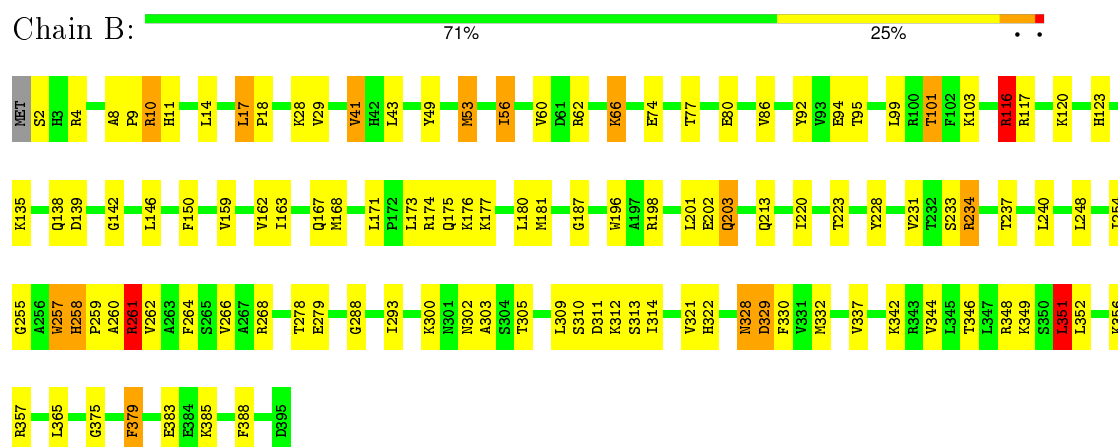
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

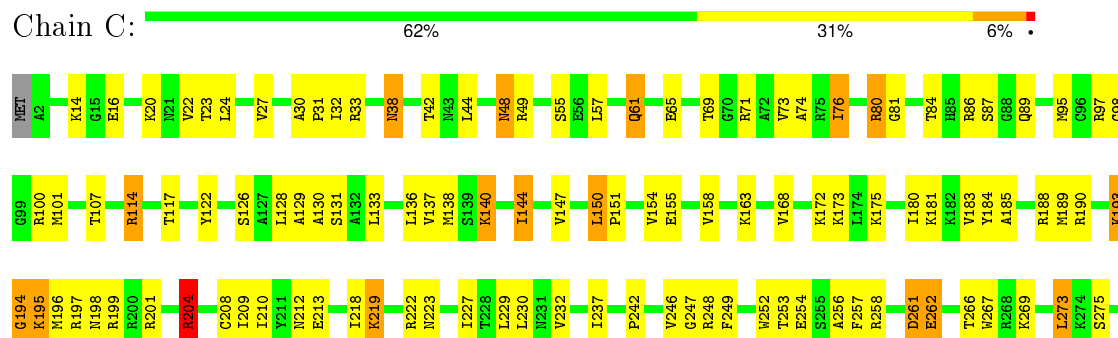
#### • Molecule 1: uL2



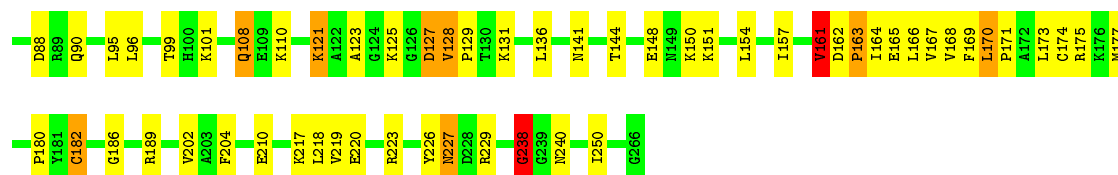
#### • Molecule 2: uL3



#### • Molecule 3: uL4

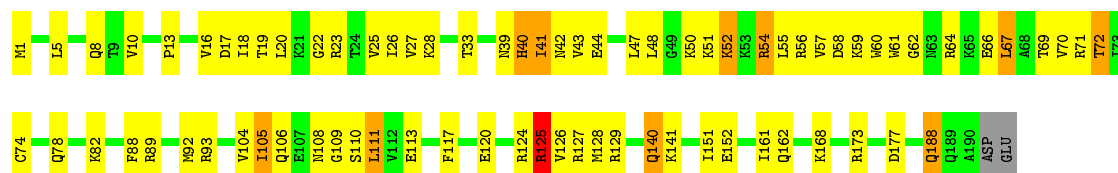






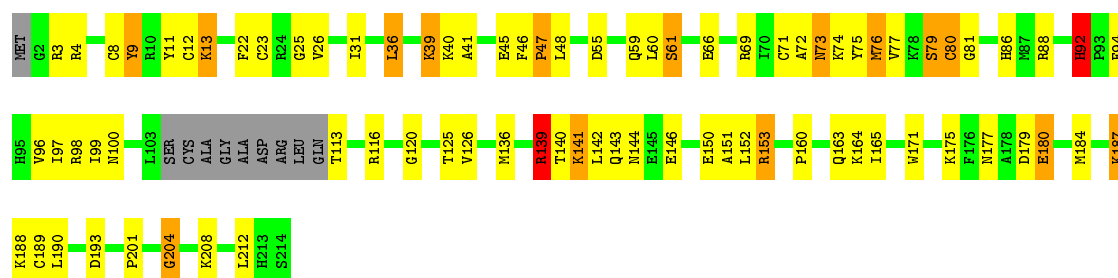
• Molecule 8: uL6

Chain H: 59% 34% 5% ..



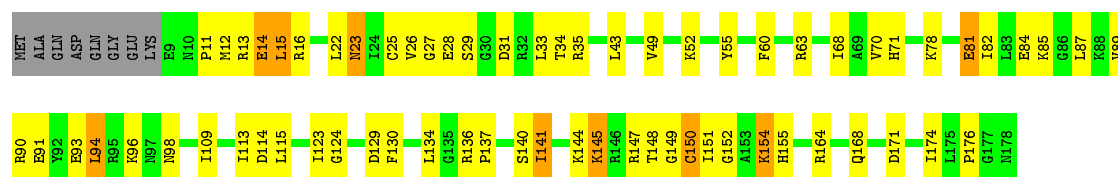
• Molecule 9: uL16

Chain I: 57% 30% 7% • 5%



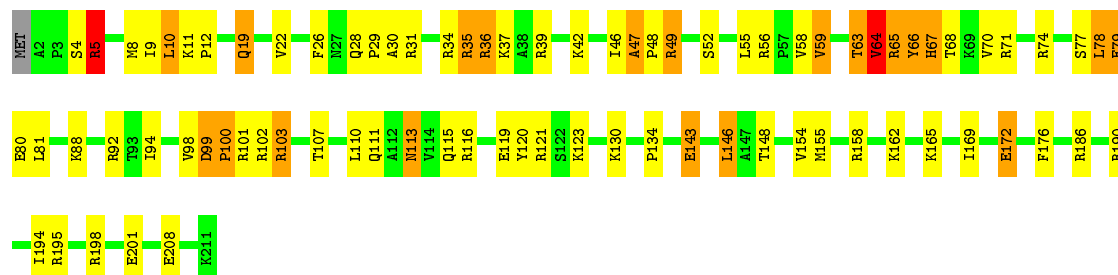
• Molecule 10: uL5

Chain J: 58% 33% 5% •



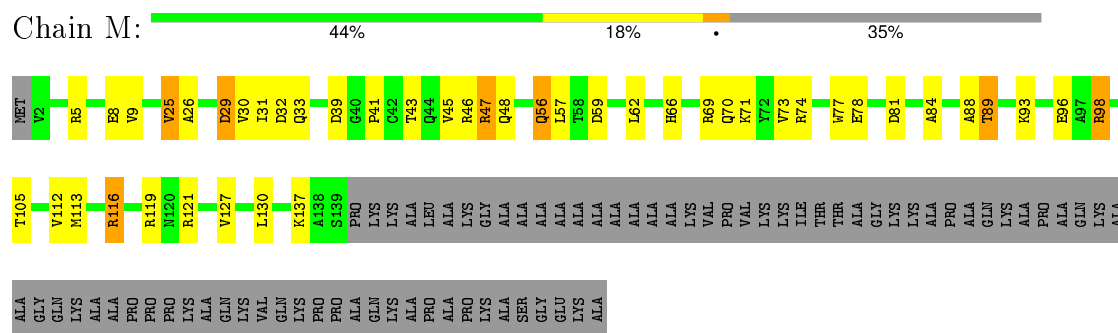
• Molecule 11: eL13

Chain L: 61% 28% 9% •

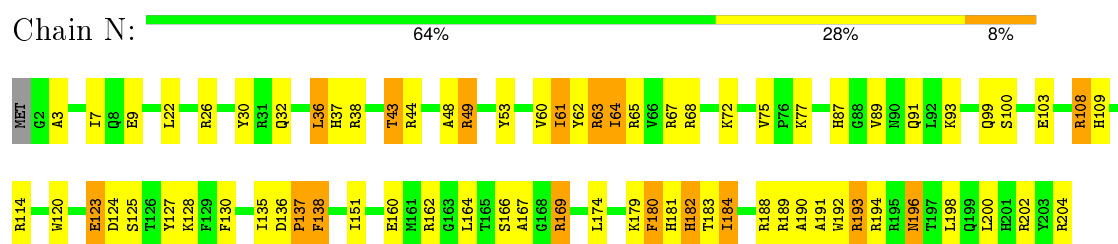




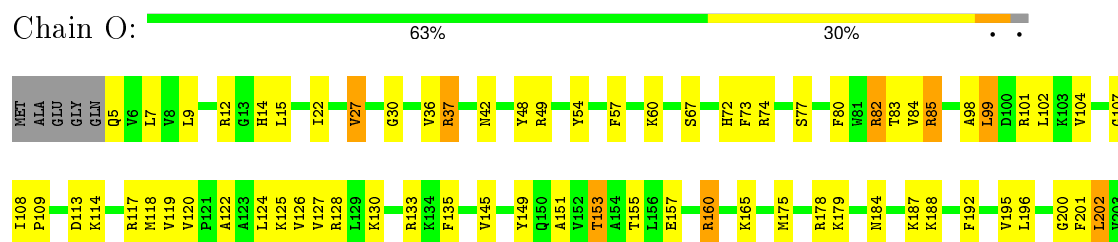
- Molecule 12: eL14



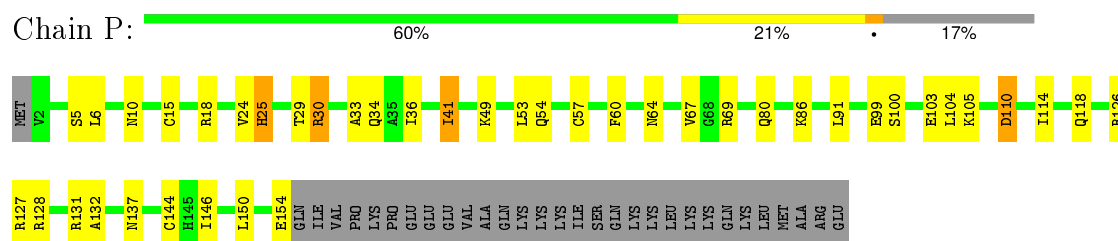
- Molecule 13: eL15



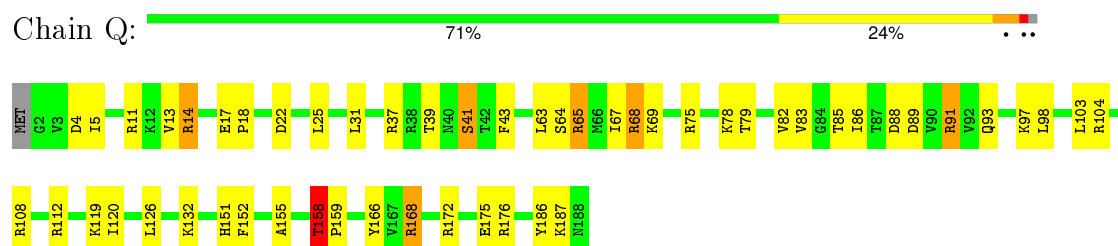
- Molecule 14: uL13



- Molecule 15: uL22

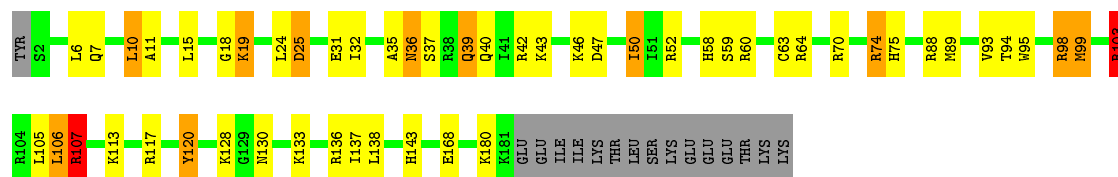


- Molecule 16: eL18



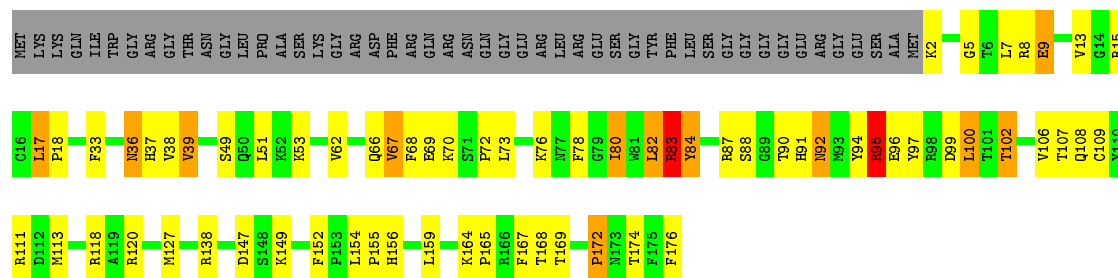
- Molecule 17: eL19

Chain R: 



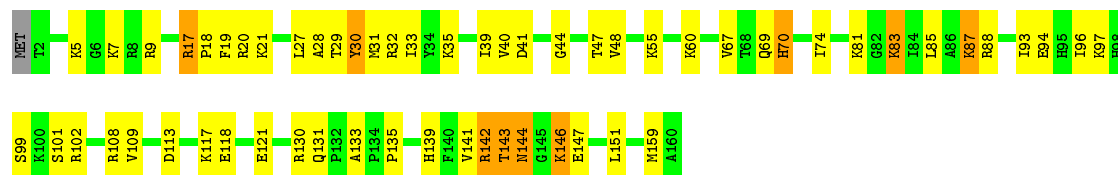
- Molecule 18: eL20

Chain S: 



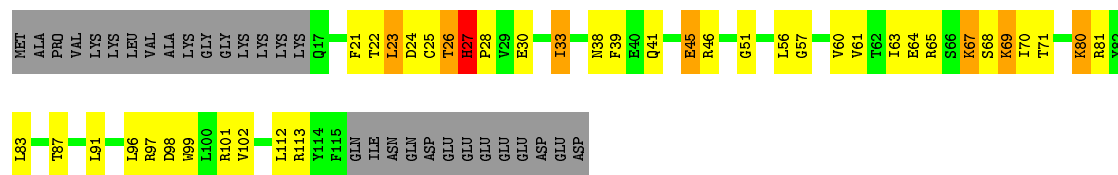
- Molecule 19: eL21

Chain T: 



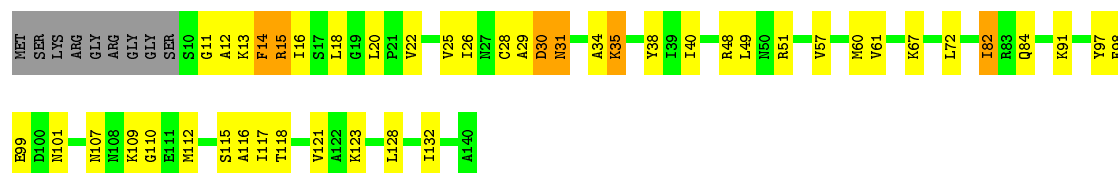
- Molecule 20: eL22

Chain U: 



- Molecule 21: uL14

Chain V: 



MET	A2	R44	M19	G20	I21	K22	R25	S26	Q27	R28	Y29	E30	D36	F39	M43	R44	K51	R68	V76	LNS	PRO	LNS	LNS	GLU	VAL	LNS	PRO	ASW	LNS	PRO	PRO	LNS	GLY	GLY	SER	ARG	LNS	LEU	LEU	TYR	ALA	ALA	ALA	ALA	HIS	PRO	LNS	LNS	GLY	GLY	LNS	PRO
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ALA
ARG
ALA
ARG
ALA
ILE
ALA
LYS
LYS
GLY
LEU
ARG
PHE
CYS
ARG
PRO
LYS
SER
SER
GLN
ALA
LYS
ALA
GLN
SER
LYS
ALA
LYS
ALA
THR
ALA
GLY
GLY
THR
ALA
ALA
PRO
VAL
PRO
PRO
ALA
SER
ALA
PRO
LYS
GLY
ALA
GLN
ALA
PRO
THR
LYS
ALA
PRO
GLN

• Molecule 28: eL30

Chain c:  72% 10% 18%

MET
VAL
ALA
ALA
LYS
LYS
THR
LYS
LYS
SER
LEU
GLU
S13
I14
M15
S16
Q19
V28
M37
Q40
M50
M51
N78
Y89
L94
R106
SER
MET
PRO
PRO
GLU
GLN
THR
GLY
GLY
LYS

• Molecule 29: eL31

Chain d:  68% 15% 14%

MET
ALA
PRO
ALA
LYS
LYS
GLY
GLY
GLU
LYS
LYS
LYS
GLY
ARG
SER
ALA
ALA
I18
E19
R23
T26
I27
N28
K31
F38
L46
K47
E48
E56
M57
G58
K75
G76
I77
R78
N79
T84
R85
E94
L102
T107
M116
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

• Molecule 31: eL33

Chain f:  77% 18% 5%


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% 4%


MET
V2
Q3
R4
L5
L11
N14
T15
N18
K19
S23
N28
E38
K43
R54
R60
L64
R65
R66
K69
H73
V74
S75
R76
A84
R88
D89
R90
R93
K105
Q112
K115
ALA
LYS

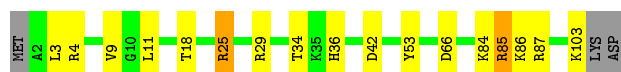
• Molecule 33: uL29

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% 5%



• Molecule 35: eL37



• Molecule 36: eL38



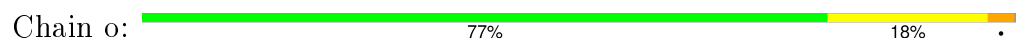
• Molecule 37: eL39



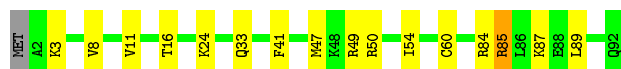
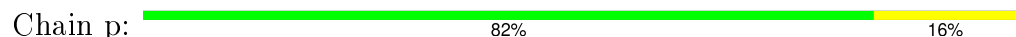
• Molecule 38: eL40



• Molecule 39: eL42

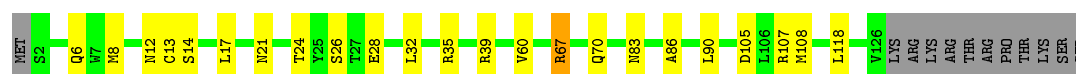


• Molecule 40: eL43

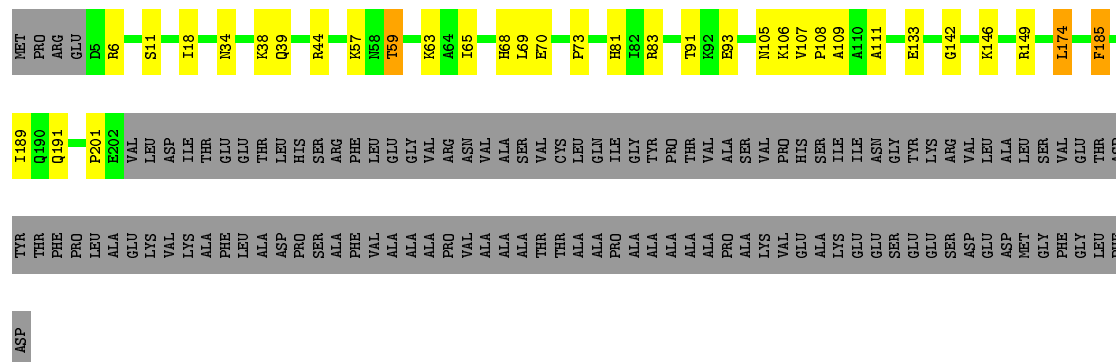


• Molecule 41: eL28

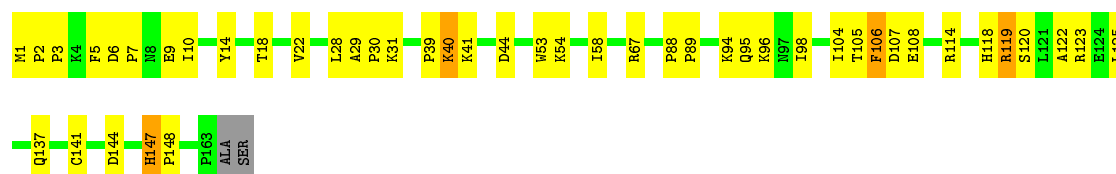




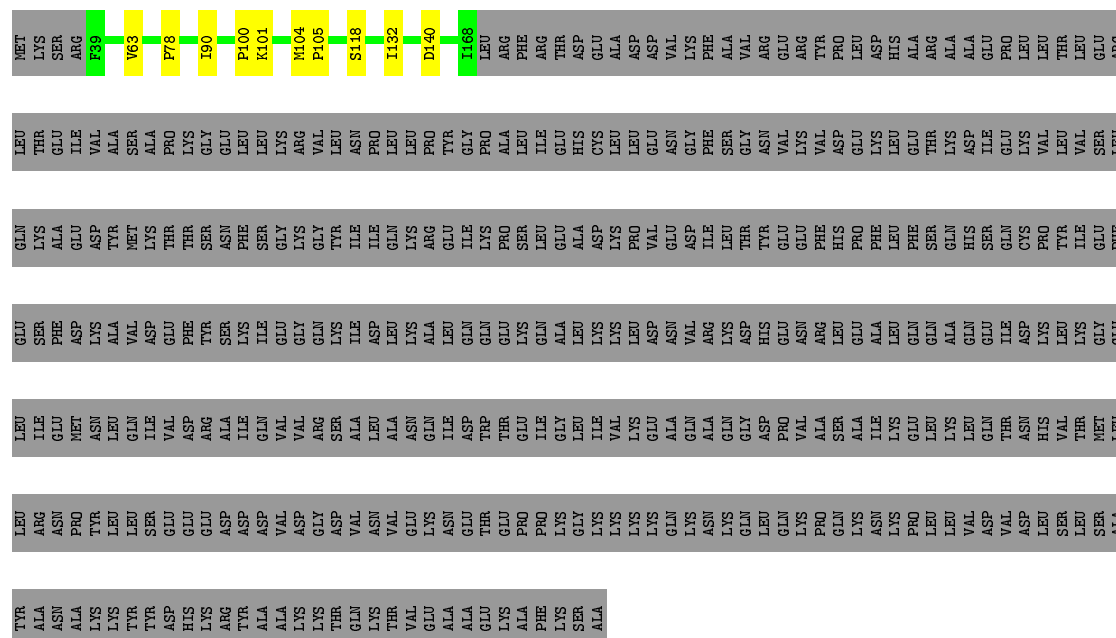
• Molecule 42: uL10



• Molecule 43: uL11

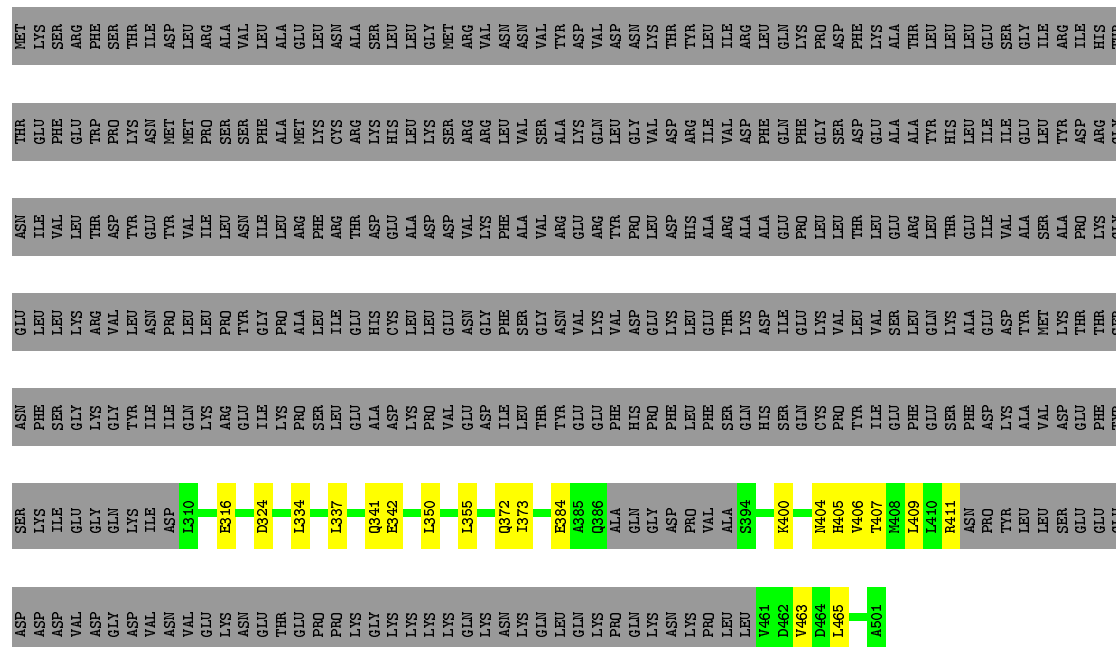


• Molecule 44: NEMF



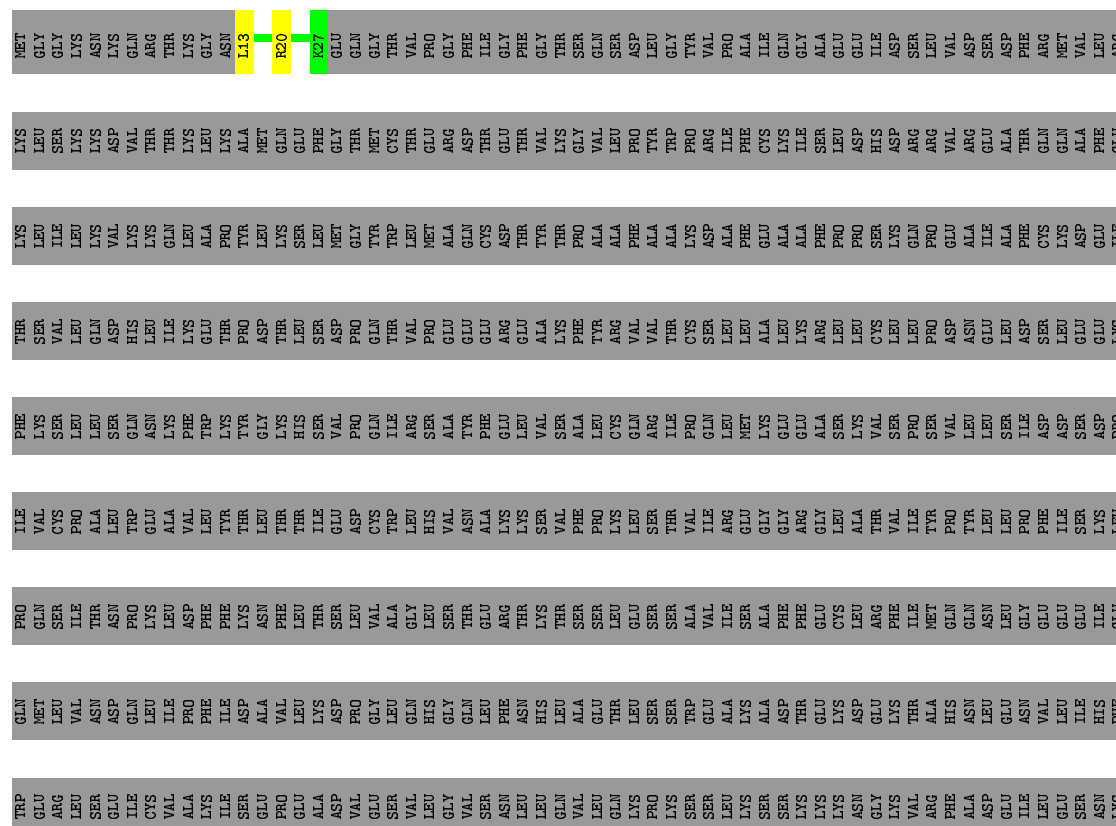
- Molecule 44: NEMF

Chain v:  23% . 73%



- Molecule 45: Listerin

Chain w:  99%








THR  
SER  
SER  
ASN  
LYS  
SER  
THR  
CYS  
PRO  
LEU  
CYS  
ARG  
GLU  
THR  
PHE  
PHE

- Molecule 45: Listerin

Chain z:  6% • 93%

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

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

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

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

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

HIS	VAL	LYS	ASN	ASP	TYR	LEU	ILE	GLY	ASP	VAL	VAL	GLU	ARG	ILE	ILE	VAL	ARG	LEU	HIS	THR	LYS	LYS	LEU	SER	GLU	ALA	GLU	SER	SER	ASP	SER	SER	VAL	PHE	CYS	ASP	VAL	ALA	TYR	ASN	PHE	SER	SER	ALA	LYS	GLY	CYS	LEU	LEU	MET
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PRO	SER	SER	SER	GLU	ASP	LEU	LEU	LEU	LEU	THR	LEU	THR	PHE	GLN	LEU	CYS	GLN	ALA	ALA	SER	SER	LYS	GLU	LYS	THR	THR	HIS	HIS	LEU	LEU	PRO	ASP	PHE	LEU	LEU	ILE	CYS	LYS	LYS	LYS	ASN	THR	THR	TRP	LEU	SER	SER	GLY	VAL	GLY	ASN	LEU	LEU	VAL	HIS	GLN	THR	THR	ASP	SER	SER	TYR	LYS	GLU	SER	THR	PHE	LEU	HIS	HIS	LEU	LEU	SER	SER	ALA
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Chain 0:  98%

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


**WORLDWIDE PDB**  
 PROTEIN DATA BANK  

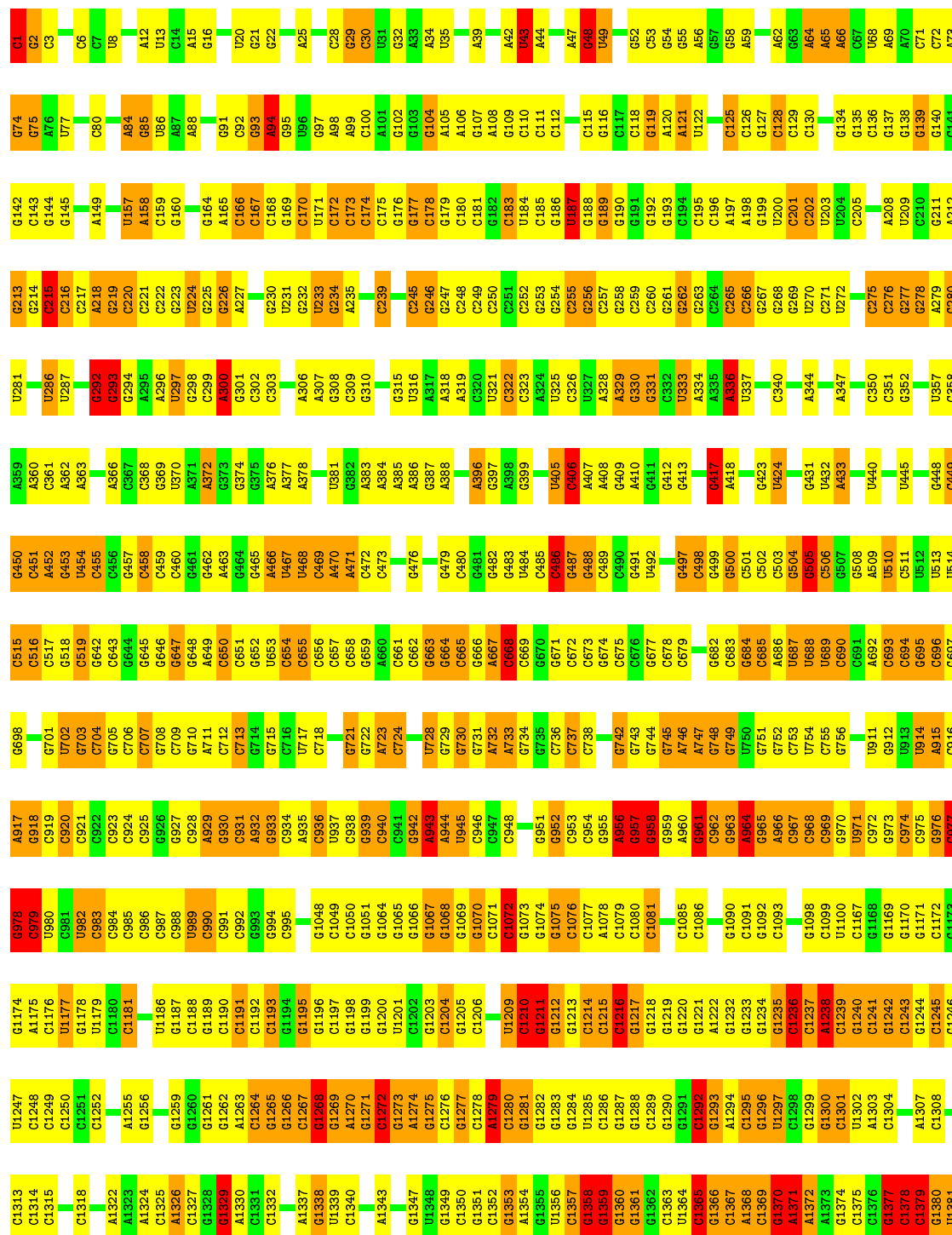
**EMDataBank**  
 Unified Data Resource for 3DEM





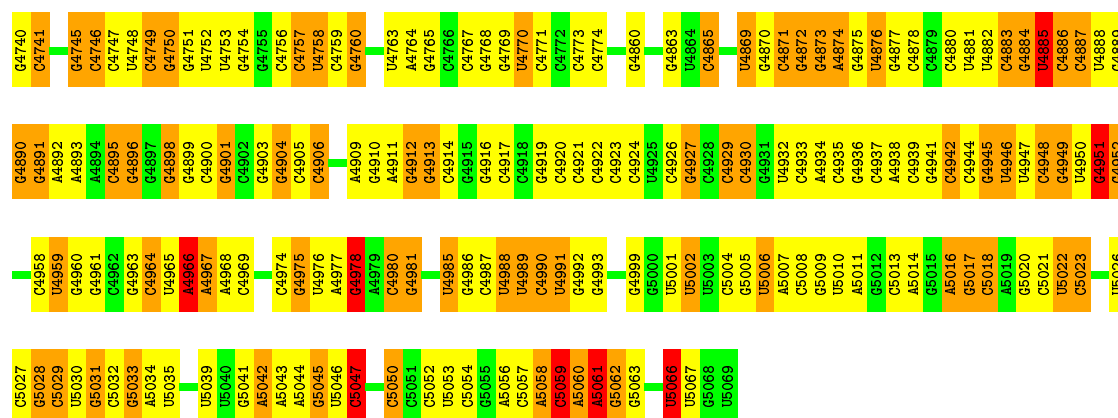
● Molecule 49: 28S rRNA

Chain 5: 36% 42% 20%



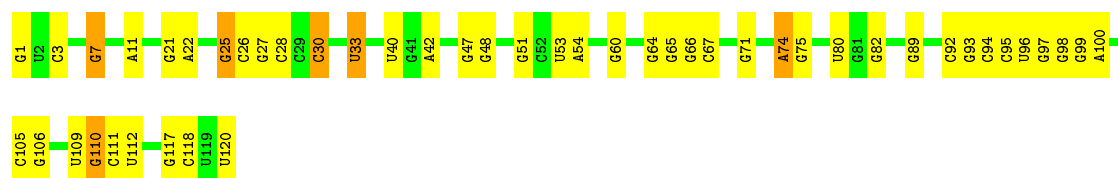
A2611	C2540	C2478	A2403	U2329	C2258	G2086	G1946	U1866	A1788	G1721	G1624	G1543	G1454	G1382
G2612	G2541	G2479	A2404	G2330	G2259	C2087	U1947	A1867	C1789	C1722	G1625	G1547	G1455	G1383
G2613	G2542	G2480		G2331	G2260	A2088	G1948	A1868	U1790	G1723	G1629	A1548	G1456	G1384
G2614	A2543	G2481	G2407	A2332	G2261	G2089	U1949	G1869	U1791			G1549	G1457	G1385
G2615	G2544	G2482	U2408	G2333	G2262	C2011	U1950	G1878	U1800	U1725	A1630	G1550		C1386
G2616	G2545	G2483	U2409	G2334	A2263	C2091	G1951	C1879		U1726	A1631	G1551	G1465	A1387
G2617	G2546	A2484		G2335	C2264	G2092	U1952		G1803	U1728	G1633	G1552	G1466	
G2618	G2547	U2485	A2412	G2336	G2265	G2093	U1953	G1880	G1804		G1634	G1553	C1467	
G2619	G2548	G2486	U2413	G2337	C2266	G2094	U1954	A1881	A1805	U1729	A1635	G1554	C1468	G1394
G2620	G2549	G2487		G2338	U2267	A2095	G1955	U1882	A1806	U1730	C1636	G1555	G1396	G1396
A2621	G2550	G2488	A2417	G2339	A2268	G2096	A1956		G1807		G1637	G1556	G1474	A1398
G2622	A2551	G2489		G2340	C2269	U2097	U1957	G1886	C1808	G1733	A1638	C1557	G1475	G1399
A2623	G2552	U2490	C2422	A2341	G2270	G2098	A1958			G1734		A1558	C1476	G1400
G2624	A2553	C2491	A2425	G2342	C2271	G2099	U1959	U1889		U1735		A1559	C1477	C1401
	U2554	C2492	G2424		C2272	C2100	A1960	A1890	G1811	A1736	G1641	A1560	C1478	
G2627	G2555	G2493	U2425	G2345	G2273	C2101	G1961	A1891	C1812	A1737	A1642	A1561	C1479	G1404
U2628	G2556	U2494	U2426	C2346	C2274	G2102	A1962	A1892	A1738		A1643	G1562	C1480	C1405
G2629	G2557	U2495	G2427	A2347	G2275	A2026	G1963	C1893			G1644	G1563	C1481	G1406
U2630	G2558	G2496	A2428	G2348		U2027	A1964	C1894	G1741		G1645	A1564	C1482	C1407
U2631	G2559	C2497	A2429		G2276	A2105	G1965		A1742		A1646		C1483	G1408
U2632	C2560		C2430	C2351	A2278			A1897	G1813			A1565	C1484	C1409
U2633		G2498	A2431	U2352	G2280	A2033		C1898	C1819	U1744	A1650	C1566	C1485	U1410
G2638	G2563		U2432	G2353	U2281	G2034	G1969	G1899	C1820	G1745		U1567	C1486	C1411
U2639		G2502	G2433	G2354	A2282	C2035	A1970	C1900	C1821	A1746	G1654	C1568	C1487	G1412
G2640	G2567	C2504	G2434	U2355	G2283		G1971		U1822		C1655	U1569	G1488	C1413
	C2568	G2505	G2435	U2356		C2046	G1972	G1904	G1823	G1750	U1656	G1570	G1489	
G2645	G2569	G2506	U2436	G2357	G2288	A2047	G1973		G	A1751		G1571		G1414
G2646	G2570	A2507	C2437	G2358	C2289	U2048	U1974	A1907	A1825	G1752	U1659		G1493	G1415
A2647	U2571	U2508	G2438	A2360	C2290	G2049	G1975		G1826	U1753	C1661	G1574		G1416
	C2572		U2439	G2361		G2051	G1976	G1910	C1827	U1754				C1417
C2664	A2573	A2362	U2440	U2362	G2294	C2052	C1977	C1911	C1828	G1755		U1578	A1497	C1418
U2665	G2574	C2363	C2441	A2363	G2295		C1978	C1912	G1829	U1756	A1669	C1579	C1498	G1419
U2666	U2575	A2511	G2442	G2364	G2296	G2055	U1979	C1913	G1830	U1757	U1670	C1580	C1499	A1420
G2667	G2576	G2512	U2443		G2297	C2056	G1980		C1831	G1758	U1671		A1500	G1421
U2668	C2577	G2513	G2444	A2367	U2298	G2057	G1981	U1918	C1832	G1759	U1672	G1584	C1501	G1425
G2669	G2578	G2514	C2445	G2368	G2299	A2058	A1982	G1919	G1833	G1760	U1673	C1585	G1502	G1426
G2670	G2579	A2515	C2446	U2369	A2300	G2059	A1983	C1920	U1834	G1761		A1503	A1503	A1427
	U2580	G2516	U2447	G2370	G2301	C2060	A1984	C1921	G1835	C1762	C1676	G1586	G1504	U1428
G2673	A2581	G2517	G2448		C2302	G2061	G1985	G1922	G1836	C1763	U1677	C1590	C1505	C1429
A2674	U2582	G2518	A2449	G2378		U2061	U1986	A1923	A1837	C1764		U1591	C1506	C1430
G2675	C2583	C2520	G2450		U2305	G2064	C1987	C1924	A1838		G1680	C1594	C1507	C1431
	G2586	G2521	G2457	A2382	G2306	G2065	G1988	G1925	U1839	A1767	G1681		A1515	G1435
G2681	A2587	G2522	C2458	U2386	A2307	C2066	G1989	U1926	C1840	G1768	U1682	G1595	A1516	C1436
G2682	C2588	U2523				C2067	A1990	U1927	G	G1769	U1683	U1596	G1517	C1437
G2683	G2589	U2524	G2463	G2389	U2312	C2068	A1991	C1928	G1842	A1770	A1684	G1597	A1518	U1438
G2684	C2590	G2525	C2464	G2390	A2313	A2069	U1992	U1930	A1843	C1772	G1685	C1598		C1439
G2685	G2591	G2526	G2465	G2391	G2314	U2070	C1993	C1931	G1846	U1773	U1687	A1601	A1523	U1440
G2686	C2594	G2527	G2466	G2392	G2315		G1994	A1932	C1847	C1774		U1602	A1524	C1441
		U2529	U2467	C2393	G2316	C2073	G1995	G1933	C1848	A1775	G1690	C1603	G1529	G1442
G2687	G2597	U2530	U2468	C2394	G2317	C2074	U1997	A1934		A1776	G1691	G1604	G1530	A1443
G2688	A2601	G2532	C2469	G2395	C2248	G2075	A1998	C1935	G1851	C1777	C1692	G1605	U1531	G1444
G2689	G2602	C2533	G2470	A2396	C2249	G2076	U1999	C1936		C1778	G1696	U1606	G1532	U1445
G2690	G2603	G2534	G2471	G2397	C2250	C2077	G2000	C1937	G1855	C1696	C1697	C1607	A1533	C1446
	G2606	G2535	A2472	U2398	G2252	G2078	G2001	C1938	C1856	A1780	C1698	C1611	A1534	C1447
G2697	C2607	A2536	A2473	G2399	A2263	G2079	A2002	A1939		U1781	A1699	G1612	C1535	G1448
G2698	G2608	U2537	G2474	G2400	G2254	C2083	G2003	G1940	U1862		C1718	A1613	C1536	C1449
G2699	G2609	U2538	G2475	A2401	C2255	C2084	U2004	A1941	G1863	C1785	C1719	G1614	U1538	
	G2610	C2539	A2477	G2402	C2257	G2085	U2006	G1945	G1865	A1787	C1720			

G4661	G4575	U4500	C4426	G4338	G4266	G4122	U3932	A3856		U3759	U3680	G3600	G2841	G2759	U2691
G4662	U4576	C4506	G4427	A4339	G4267	C4123	G3933	G3857	A3759	G3681	G3681	C3601	G2842	G2760	U2692
G4663	U4577	C4507	U4431	A4340	U4189	C4124	G3934	G3858	A3760	A3682	G3682	G3602	G2843	G2761	G2693
A4664	G4578	C4508	G4432	C4341	G4190	C4125	G3935	G3859	C3761	C3683	C3683	G3603	A2844	G2762	G2694
G4666	U4579	U4509	G4433	A4348	U4194	C4126	A3936	A3860	U3762	G3684	G3685	C3604	G2851	U2763	A2695
G4667	U4580	C4510	G4434	C4349	G4195	A4128	G3938	C3864	U3763	A3763	C3686	C3605	G2852	A2764	A2696
C4583	C4583	A4511	U4437	C4350	G4196	G4129	G3939	C3865	U3764	G3686	A3687	U3606	U2852	A2765	U2697
A4584	U4584	A4512	U4438	U4354	G4197	G4130		C3866	G3765				C2853	G2766	G2698
U4585	A4513	C4514	U4439	U4355	G4198	G4131	A3943	A3867	U3770	U3695	U3695	A3611	C2854	U2767	C2699
G4586	G4514	G4440	A4441	G4356	C4199	C4132	U4068	G3868	C3771	C3696	C3696	U3612	C2855	G2768	C2702
G4587	U4515	A4441	C4442	A4357	C4199	C4133	U4069	C3869	U3772	U3697	U3697	G3614	C2856	G2770	G2703
U4588	G4516	C4444	U4445	U4359	A4203	C4134	U4070	C3870	U3773	U3698	U3698	G3615	A2857	G2771	C2704
A4589	A4517	C4445	U4446	U4360	G4204	G4135	U4071	A3871	A3774	C3699	C3699	U3616	G2859	G2772	G2705
C4592	G4522	U4447	C4448	U4367	A4205	C4136	A4073	A3876	A3775	C3700	C3700	G3617	C2860	G2773	G2706
C4593	G4523	G4449	U4449	G4368	G4206	C4137	U4074	A3877	G3776	C2861	C2861		G2862	G2774	U2707
U4594	A4524	U4450	U4450	U4374	G4207	G4138	U4075	C3878	G3777	G3705	G3705	G3620	G2863	G2775	U2708
G4595	U4525	C4451	U4451	C4375	A4213	C4142	A4077	G3879	G3777	C3706	C3706	G3625	G2864	G2776	C2709
G4596	U4526	U4452	G4291	A4376	A4214	G4143	U4083	G3886	C3782			G3626	A2867	U2782	G2710
A4605	G4527	C4453	G4297	G4377	A4215	C4144	U4084	C3887	A3784	U3709	U3709	G3627	C2867	G2783	G2711
A4607	U4528	C4454	A4378	A4379	G4216	C4145	G4085	C3888	A3785	G3710	G3710	A3635	G2868	A2787	G2712
G4608	U4529	U4455	A4379	A4380	G4217	C4146	G4086	C3889	G3787	A3712	A3712	G3636	U2869	U2788	G2713
C4609	U4530	C4456	U4456	A4387	G4218	C4147	G4087	A3890	U3790	G3713	G3713	U3637	A2870	A2789	G2714
C4614	U4531	U4461	C4461	C4387	A4219	C4148	G4088	A3891	C3791	G3714	G3714	U3641	C2872	U2790	G2715
G4615	U4532	C4462	U4462	A4388	A4220	C4149	G4089	U3892	G3792	U2873	U2873	A3642			C2720
A4616	G4533	U4463	C4463	A4389	G4221	C4150	G4090	C3896	C3793	G2794	G2794	A3643			G2721
G4617	U4534	A4464	U4464	A4390	G4222	G4151	G4091	C3897	U3795	A2795	A2795	G3644			G2722
G4618	U4535	U4465	U4465	A4391	G4223	G4152	G4092	C3898	A3799	G3724	G3724	A3645			U2723
U4619	C4537	C4466	U4466	A4392	G4224	C4153	G4093	C3899	A3800	A3725	A3725	A3646			G2724
U4708	G4543	A4467	U4467	U4393	G4225	C4154	G4094	G3900	U3801	G3726	G3726	A3647			A2725
U4709	U4544	G4470	U4470	A4394	G4226	C4155	G4095	A3901	U3802	A3727	A3727	A3648			G2726
C4714	A4548	U4471	U4471	U4395	G4227	C4156	G4096	A3904	C3803	G3728	G3728	A3651			C2727
C4715	G4549	G4472	U4472	U4396	G4228	C4157	G4097	A3905	C3804	U3729	U3729	A3652			U2730
U4627	U4550	A4473	U4473	A4397	G4229	C4158	G4098	A3906	C3810	U3730	U3730	A3653			C2731
U4628	U4551	G4474	U4474	U4398	G4230	C4159	G4099	A3907	G3811	C3731	C3731	A3656			G2736
G4719	U4552	C4475	U4475	C4401	G4231	C4160	C4100	A3908	U3814	G3735	G3735	C3658			C2737
C4720	A4553	G4476	U4476	U4403	G4232	C4161	C4101	A3909	A3736	A2905	A2905	G3659			G2738
A4635	U4554	U4477	U4477	U4404	G4233	C4162	C4102	C3910	A3737	G2906	G2906	G3660			U2740
U4636	G4555	C4478	U4478	U4405	G4234	C4163	C4103	C3911	A3816	G3738	G3738	G3661			A2743
G4637	U4556	U4480	U4480	U4406	G4235	C4164	C4104	U3912	U3817	C3739	C3739	G3662			A2744
A4724	A4559	U4481	U4481	C4408	G4236	C4165	C4105	U3913	U3818			A3663			A2745
C4725	C4560	U4482	U4482	C4409	G4237	C4166	G4106	U3914	G3819	G3742	G3742	A3664			U2746
G4726	U4561	C4483	G4411	G4411	G4238	C4167	G4107	U3915	U3822	G3743	G3743	G3665			C2747
A4727	C4562	A4484	A4412	A4412	G4239	C4168	C4108	U3916	U3823	G3744	G3744	G3666			G2748
U4728	G4563	C4485	C4413	C4413	G4240	C4169	C4109	U3917	G3824	U3745	U3745	G3667			C2749
U4646	U4564	C4486	A4414	A4414	G4241	C4170	C4110	U3918	U3825	A2825	A2825	G3668			G2750
G4647	A4565	U4487	U4415	U4415	G4242	C4171	G4111	U3919	U3831	U2826	U2826	G3669			C2751
A4648	C4566	U4488	G4416	G4416	G4243	C4172	G4112	U3920	U3832	G2827	G2827	G3670			G2752
G4732	U4567	C4489	C4417	C4417	G4244	C4173	C4113	U3921	U3833	U2828	U2828	G3671			C2753
A4651	G4568	U4490	G4418	G4418	G4245	C4174	G4114	U3922	U3834	U2829	U2829	G3672			G2754
G4734	C4569	G4491	U4419	U4419	G4246	C4175	C4115	U3923	U3835	G3587	G3587	G3673			A2755
G4735	C4653	U4492	C4332	C4332	G4247	C4176	C4116	U3924	U3840	A2835	A2835	G3674			G2756
C4736	U4570	U4421	U4421	U4421	G4248	C4177	U4117	U3925	U3851	G2838	G2838	G3675			U2757
A4656	U4573	C4496	C4335	C4335	G4249	C4178	U4118	U3926	U3855	A2840	A2840	G3679			G2758
G4738	U4657	U4497	A4336	A4336	G4250	C4179	C4119	U3927	C3855			U3679			
C4739			C4337	C4337	G4251	C4180	G4121								



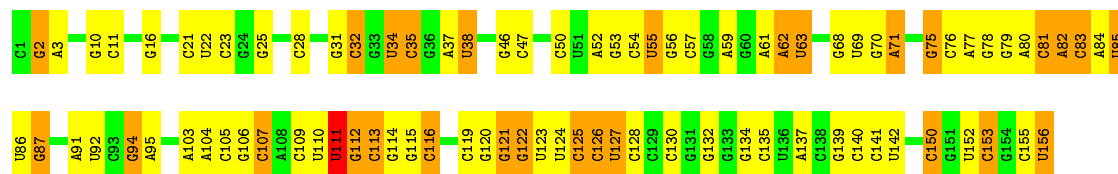
• Molecule 50: 5S rRNA

Chain 7: 60% 35% 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 images	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	59000, 59000	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	31
2	B	392/395 (99%)	342 (87%)	44 (11%)	6 (2%)	13	57
3	C	365/368 (99%)	315 (86%)	43 (12%)	7 (2%)	10	53
4	D	290/297 (98%)	266 (92%)	18 (6%)	6 (2%)	9	52
5	E	232/284 (82%)	176 (76%)	39 (17%)	17 (7%)	1	18
6	F	223/250 (89%)	203 (91%)	16 (7%)	4 (2%)	11	54
7	G	239/266 (90%)	196 (82%)	36 (15%)	7 (3%)	6	44
8	H	188/192 (98%)	164 (87%)	17 (9%)	7 (4%)	4	38
9	I	200/214 (94%)	171 (86%)	22 (11%)	7 (4%)	4	40
10	J	168/178 (94%)	143 (85%)	17 (10%)	8 (5%)	3	30
11	L	208/211 (99%)	174 (84%)	22 (11%)	12 (6%)	2	25
12	M	136/213 (64%)	118 (87%)	16 (12%)	2 (2%)	13	57
13	N	201/204 (98%)	172 (86%)	28 (14%)	1 (0%)	34	77
14	O	197/204 (97%)	173 (88%)	23 (12%)	1 (0%)	34	77
15	P	151/184 (82%)	133 (88%)	17 (11%)	1 (1%)	26	72
16	Q	185/188 (98%)	161 (87%)	22 (12%)	2 (1%)	17	64

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	R	178/196 (91%)	160 (90%)	14 (8%)	4 (2%)	8	51
18	S	173/224 (77%)	153 (88%)	16 (9%)	4 (2%)	8	50
19	T	157/160 (98%)	136 (87%)	19 (12%)	2 (1%)	15	60
20	U	97/128 (76%)	84 (87%)	9 (9%)	4 (4%)	3	34
21	V	129/140 (92%)	112 (87%)	16 (12%)	1 (1%)	24	69
22	W	61/157 (39%)	55 (90%)	5 (8%)	1 (2%)	12	56
23	X	117/156 (75%)	105 (90%)	11 (9%)	1 (1%)	21	67
24	Y	132/145 (91%)	121 (92%)	9 (7%)	2 (2%)	13	57
25	Z	133/136 (98%)	115 (86%)	13 (10%)	5 (4%)	4	37
26	a	145/148 (98%)	118 (81%)	20 (14%)	7 (5%)	3	30
27	b	73/160 (46%)	68 (93%)	4 (6%)	1 (1%)	14	59
28	c	92/115 (80%)	86 (94%)	5 (5%)	1 (1%)	17	64
29	d	105/125 (84%)	93 (89%)	9 (9%)	3 (3%)	6	44
30	e	126/135 (93%)	113 (90%)	11 (9%)	2 (2%)	12	56
31	f	107/110 (97%)	93 (87%)	10 (9%)	4 (4%)	4	38
32	g	112/117 (96%)	98 (88%)	12 (11%)	2 (2%)	11	54
33	h	120/123 (98%)	103 (86%)	16 (13%)	1 (1%)	24	69
34	i	100/105 (95%)	92 (92%)	5 (5%)	3 (3%)	5	44
35	j	84/97 (87%)	70 (83%)	12 (14%)	2 (2%)	7	49
36	k	67/70 (96%)	56 (84%)	8 (12%)	3 (4%)	3	31
37	l	48/51 (94%)	38 (79%)	8 (17%)	2 (4%)	3	33
38	m	50/128 (39%)	45 (90%)	3 (6%)	2 (4%)	4	35
39	o	102/106 (96%)	88 (86%)	11 (11%)	3 (3%)	6	44
40	p	89/92 (97%)	74 (83%)	13 (15%)	2 (2%)	8	51
41	r	123/137 (90%)	102 (83%)	18 (15%)	3 (2%)	7	49
42	s	196/317 (62%)	159 (81%)	22 (11%)	15 (8%)	1	16
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	16
44	v	130/501 (26%)	125 (96%)	3 (2%)	2 (2%)	13	57
45	0	34/1766 (2%)	29 (85%)	3 (9%)	2 (6%)	2	24
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%)	5	41
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	42

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	18
2	B	335/336 (100%)	285 (85%)	50 (15%)	4	25
3	C	305/306 (100%)	243 (80%)	62 (20%)	1	11
4	D	247/250 (99%)	207 (84%)	40 (16%)	3	20
5	E	209/246 (85%)	172 (82%)	37 (18%)	2	16
6	F	194/217 (89%)	156 (80%)	38 (20%)	1	12
7	G	208/226 (92%)	170 (82%)	38 (18%)	2	14
8	H	169/171 (99%)	135 (80%)	34 (20%)	1	11
9	I	174/181 (96%)	137 (79%)	37 (21%)	1	10
10	J	143/149 (96%)	124 (87%)	19 (13%)	5	30
11	L	176/177 (99%)	137 (78%)	39 (22%)	1	8
12	M	116/160 (72%)	95 (82%)	21 (18%)	2	15
13	N	171/172 (99%)	142 (83%)	29 (17%)	2	18
14	O	171/174 (98%)	149 (87%)	22 (13%)	5	31

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	w	11/1611 (1%)	9 (82%)	2 (18%)	2	14
45	z	119/1611 (7%)	103 (87%)	16 (13%)	5	29
47	1	13/79 (16%)	11 (85%)	2 (15%)	3	23
All	All	6105/11841 (52%)	5029 (82%)	1076 (18%)	6	16

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%)	2 (2%)
49	5	3646/3664 (99%)	1364 (37%)	373 (10%)
50	7	119/120 (99%)	27 (22%)	1 (0%)
51	8	155/156 (99%)	50 (32%)	9 (5%)
All	All	3993/4017 (99%)	1472 (36%)	385 (9%)

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

5 of 385 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	5	2002	A
49	5	2361	G
49	5	4912	G
49	5	2075	G
49	5	2256	C

## 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	13,22,23	0.81	1 (7%)	16,32,35	3.01	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'	2.05	1.44	1.41

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
48	2	54	5MU	C5-C4-N3	-8.02	118.62	125.35
48	2	54	5MU	O4'-C1'-N1	2.21	112.31	108.10
48	2	54	5MU	C4-N3-C2	8.07	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.