



wwPDB EM Validation Summary Report ⓘ

Jun 8, 2026 – 05:45 PM EDT

PDB ID : 9Q2O / pdb_00009q2o
EMDB ID : EMD-72170
Title : NediV IRES in complex with Rabbit 80S ribosome with A site Ala-tRNA
Authors : De, S.; Altomare, C.G.; Abaeva, I.S.; Dadhwal, P.; Garg, P.; Acosta-Reyes, F.; Brown, Z.P.; Pestova, T.V.; Hellen, C.U.T.; Frank, J.
Deposited on : 2025-08-15
Resolution : 4.10 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

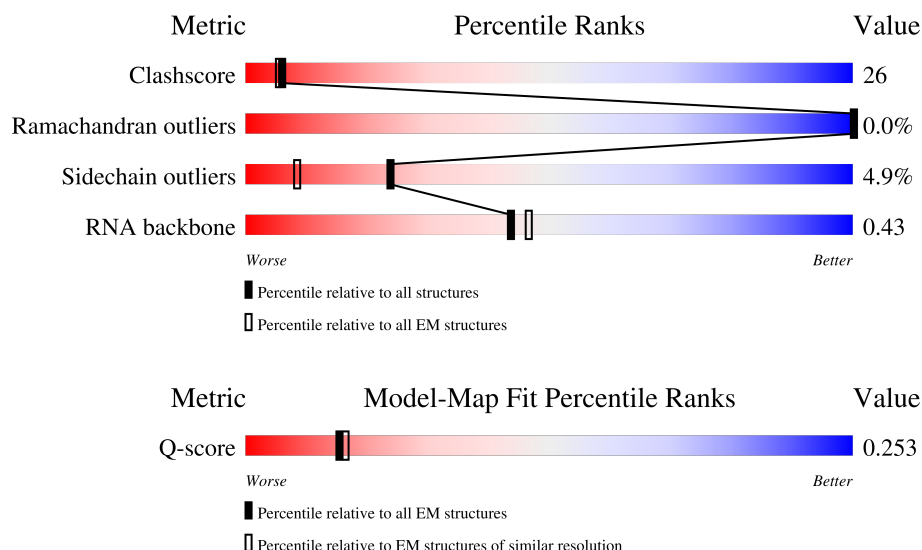
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.10 Å.

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





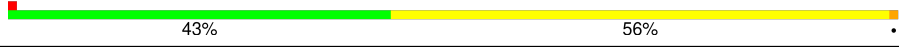
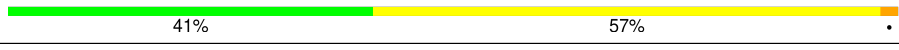
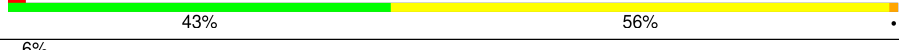


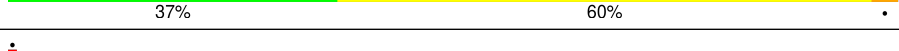
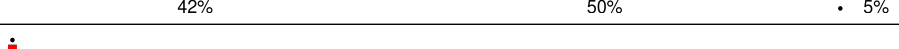
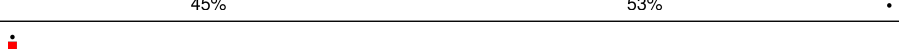
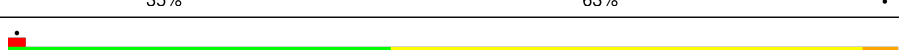
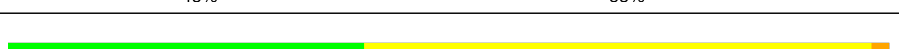
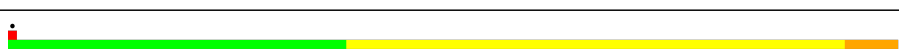
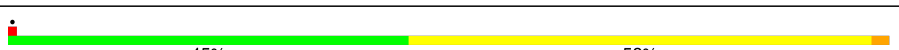
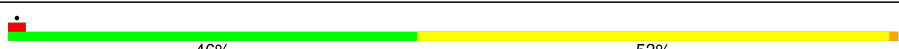





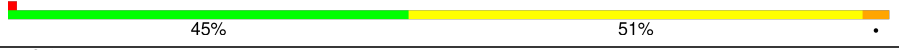

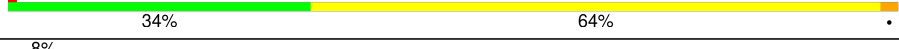


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	6458 (3.60 - 4.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	R	180	
2	W	106	
3	9	1773	

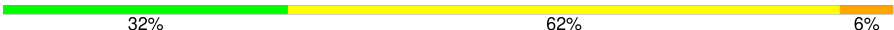


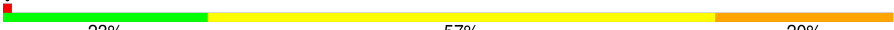
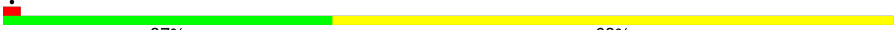





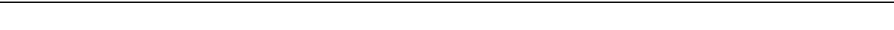

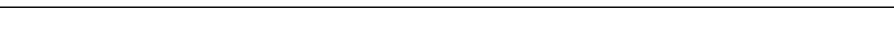
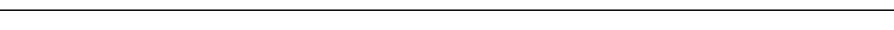










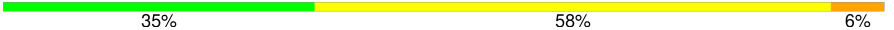
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Mol	Chain	Length	Quality of chain
4	AA	217	
5	BB	213	
6	CC	221	
7	EE	262	
8	GG	237	
9	HH	189	
10	II	206	
11	JJ	185	
12	LL	151	
13	NN	149	
14	OO	136	
15	VV	83	
16	WW	129	
17	XX	141	
18	YY	124	
19	aa	101	
20	bb	83	
21	ee	57	
22	DD	228	
23	FF	191	
24	KK	96	
25	MM	117	
26	PP	129	
27	QQ	142	
28	RR	132	



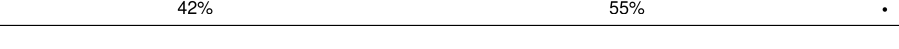
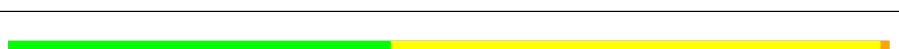



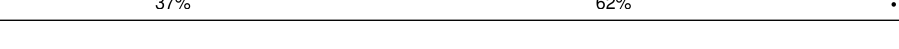


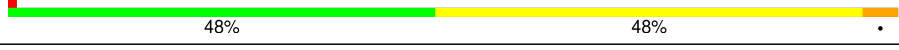
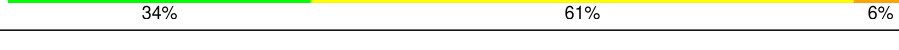

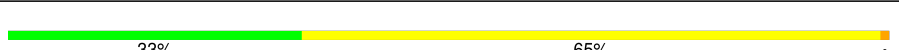


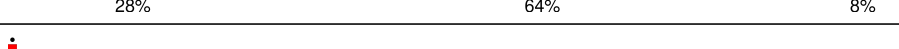
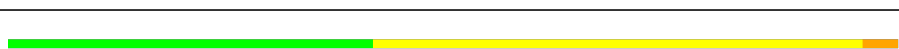






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Mol	Chain	Length	Quality of chain
29	SS	144	
30	TT	141	
31	UU	100	
32	ZZ	75	
33	cc	62	
34	dd	55	
35	ff	68	
36	gg	313	
37	A	248	
38	B	394	
39	C	362	
40	D	293	
41	E	216	
42	F	225	
43	G	240	
44	H	190	
45	I	213	
46	J	170	
47	L	210	
48	M	138	
49	N	203	
50	O	199	
51	P	153	
52	Q	187	
53	S	176	



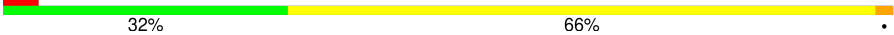
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Mol	Chain	Length	Quality of chain
54	T	159	
55	U	99	
56	V	139	
57	X	118	
58	Y	134	
59	Z	135	
60	a	147	
61	b	104	
62	c	98	
63	d	107	
64	e	128	
65	f	109	
66	g	114	
67	h	122	
68	i	102	
69	j	86	
70	k	69	
71	l	50	
72	m	52	
73	n	25	
74	o	104	
75	p	91	
76	r	124	
77	s	87	
78	t	133	

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Mol	Chain	Length	Quality of chain
79	5	3543	 27% 57% 16%
80	7	119	 30% 60% 10%
81	8	156	 15% 61% 21% •
82	AT	76	 7% 51% 46% •
83	1	166	 32% 66% •

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 219061 atoms, of which 2574 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L19.

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	38	ARG	HIS	conflict	UNP G1TYL6
R	151	ARG	HIS	conflict	UNP G1TYL6

- Molecule 2 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	W	106	Total	C	N	O	S	0	0
			860	538	174	144	4		

- Molecule 3 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	9	1697	Total	C	N	O	P	0	0
			36229	16171	6506	11856	1696		

- Molecule 4 is a protein called 40S_SA_C domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AA	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 5 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	BB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 6 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CC	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 7 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	EE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 8 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	GG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 9 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	HH	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 10 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	II	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
II	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 11 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	JJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 12 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LL	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 13 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	NN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 14 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	OO	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 15 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	VV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
VV	3	ASN	SER	conflict	UNP G1TM82
VV	4	ASP	ASN	conflict	UNP G1TM82
VV	33	GLN	PRO	conflict	UNP G1TM82
VV	50	PHE	SER	conflict	UNP G1TM82
VV	75	ALA	SER	conflict	UNP G1TM82
VV	76	ASP	HIS	conflict	UNP G1TM82
VV	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 16 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	WW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 17 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	XX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 18 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	YY	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 19 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	aa	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
aa	28	ARG	CYS	conflict	UNP G1TFE8
aa	56	ALA	VAL	conflict	UNP G1TFE8

- Molecule 20 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	bb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 21 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	ee	57	Total	C	N	O	S	0	0
			457	282	101	73	1		

- Molecule 22 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	DD	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 23 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	FF	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 24 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	KK	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 25 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	MM	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 26 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	PP	129	Total	C	N	O	S	0	0
			1058	670	201	180	7		

- Molecule 27 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	QQ	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 28 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	RR	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 29 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	SS	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 30 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	TT	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
TT	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 31 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	UU	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 32 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	ZZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 33 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	cc	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 34 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	dd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 35 is a protein called 40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	ff	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 36 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	gg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 37 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	A	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 38 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	B	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 39 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	C	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 40 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	D	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 41 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	E	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 42 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	F	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 43 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	G	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 44 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 45 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	I	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 46 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	J	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 47 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	L	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	74	ARG	HIS	conflict	UNP G1TKB3
L	190	ARG	HIS	conflict	UNP G1TKB3

- Molecule 48 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	M	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 49 is a protein called 60S ribosomal protein L15.

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

- Molecule 50 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	O	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 51 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 52 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	4	ASP	ASN	conflict	UNP G1TFE0
Q	14	ARG	TRP	conflict	UNP G1TFE0
Q	53	MET	LEU	conflict	UNP G1TFE0
Q	58	ARG	TRP	conflict	UNP G1TFE0
Q	75	ARG	GLN	conflict	UNP G1TFE0
Q	80	ALA	PRO	conflict	UNP G1TFE0
Q	86	VAL	ILE	conflict	UNP G1TFE0
Q	104	ARG	HIS	conflict	UNP G1TFE0
Q	110	ARG	CYS	conflict	UNP G1TFE0
Q	137	VAL	GLY	conflict	UNP G1TFE0
Q	157	GLY	ARG	conflict	UNP G1TFE0
Q	181	ARG	TRP	conflict	UNP G1TFE0

- Molecule 53 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	S	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 54 is a protein called 60S ribosomal protein L21.

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

- Molecule 55 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	U	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	18	LEU	VAL	conflict	UNP G1TSG1
U	32	GLY	ARG	conflict	UNP G1TSG1
U	36	ALA	GLU	conflict	UNP G1TSG1
U	39	PHE	SER	conflict	UNP G1TSG1
U	54	GLY	ARG	conflict	UNP G1TSG1
U	60	VAL	ALA	conflict	UNP G1TSG1
U	62	SER	THR	conflict	UNP G1TSG1
U	63	LEU	ILE	conflict	UNP G1TSG1
U	97	ARG	HIS	conflict	UNP G1TSG1
U	106	THR	SER	conflict	UNP G1TSG1

- Molecule 56 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	V	139	Total	C	N	O	S	0	0
			1034	648	199	182	5		

- Molecule 57 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	X	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 58 is a protein called 60S ribosomal protein L26.

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

- Molecule 59 is a protein called 60S ribosomal protein L27.

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

- Molecule 60 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	a	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 61 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	b	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 62 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	c	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 63 is a protein called 60S ribosomal protein L31.

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

- Molecule 64 is a protein called Large ribosomal subunit protein eL32.

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

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
e	3	ALA	SER	conflict	UNP G1TUN8
e	13	VAL	ILE	conflict	UNP G1TUN8
e	16	ARG	TRP	conflict	UNP G1TUN8
e	81	ASN	SER	conflict	UNP G1TUN8
e	98	GLU	LYS	conflict	UNP G1TUN8
e	108	ARG	CYS	conflict	UNP G1TUN8
e	115	ALA	VAL	conflict	UNP G1TUN8

- Molecule 65 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	f	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 66 is a protein called 60S ribosomal protein L34.

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

- Molecule 67 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	h	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 68 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 69 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	j	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 70 is a protein called Large ribosomal subunit protein eL38.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	24	LYS	ASN	conflict	UNP G1U001

- Molecule 71 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	l	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 72 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 73 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 74 is a protein called eL42.

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

- Molecule 75 is a protein called 60S ribosomal protein L37a.

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

- Molecule 76 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	r	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 77 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	s	87	Total	C	N	O	S	0	0
			695	444	128	117	6		

- Molecule 78 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	t	133	Total	C	N	O	S	0	0
			993	619	182	189	3		

- Molecule 79 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	5	3543	Total	C	N	O	P	0	0
			75955	33826	13895	24691	3543		

- Molecule 80 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	7	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

- Molecule 81 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 82 is a RNA chain called Ala-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
82	AT	76	Total	C	H	N	O	P	0	0
			2413	722	792	290	533	76		

- Molecule 83 is a RNA chain called NediV IRES.

Mol	Chain	Residues	Atoms						AltConf	Trace
83	1	166	Total	C	H	N	O	P	0	0
			5305	1577	1782	619	1161	166		

- Molecule 84 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
84	9	1	Total	Mg	0
			1	1	
84	I	1	Total	Mg	0
			1	1	
84	L	1	Total	Mg	0
			1	1	
84	P	1	Total	Mg	0
			1	1	
84	V	1	Total	Mg	0
			1	1	
84	X	1	Total	Mg	0
			1	1	
84	a	2	Total	Mg	0
			2	2	
84	e	1	Total	Mg	0
			1	1	
84	g	1	Total	Mg	0
			1	1	
84	j	1	Total	Mg	0
			1	1	
84	5	184	Total	Mg	0
			184	184	
84	7	6	Total	Mg	0
			6	6	
84	8	5	Total	Mg	0
			5	5	

- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
85	aa	1	Total	Zn	0
			1	1	
85	dd	1	Total	Zn	0
			1	1	
85	ff	1	Total	Zn	0
			1	1	
85	g	1	Total	Zn	0
			1	1	

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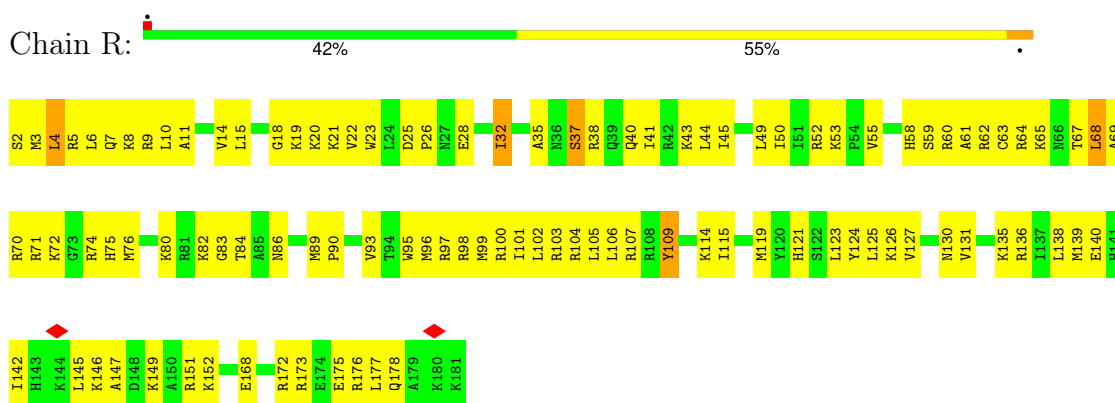
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Mol	Chain	Residues	Atoms		AltConf
85	j	1	Total 1	Zn 1	0
85	m	1	Total 1	Zn 1	0
85	o	1	Total 1	Zn 1	0
85	p	1	Total 1	Zn 1	0

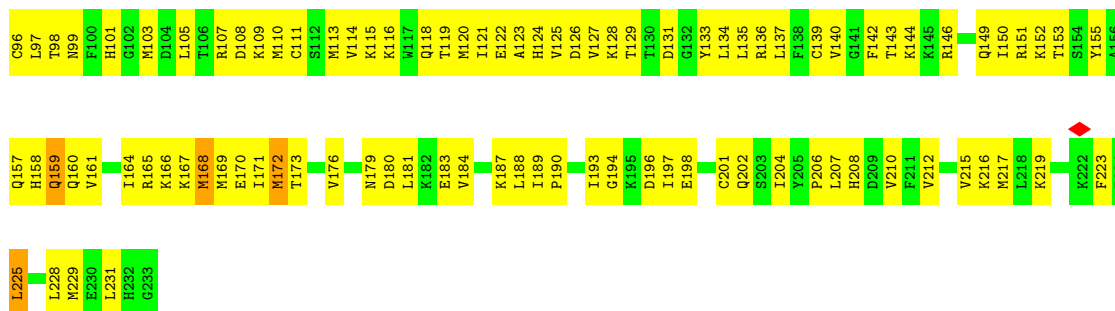
3 Residue-property plots

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

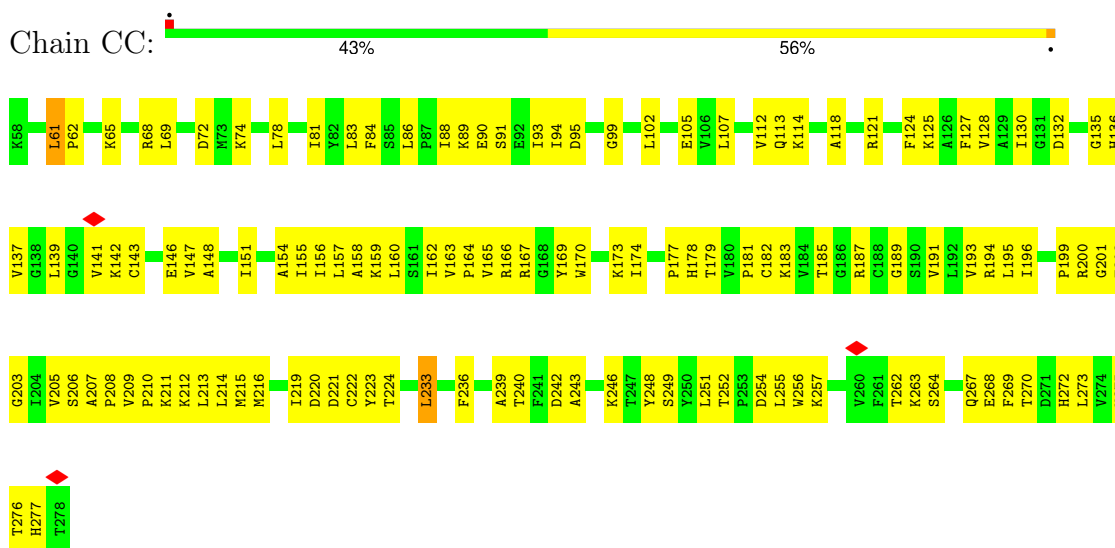
• Molecule 1: 60S ribosomal protein L19



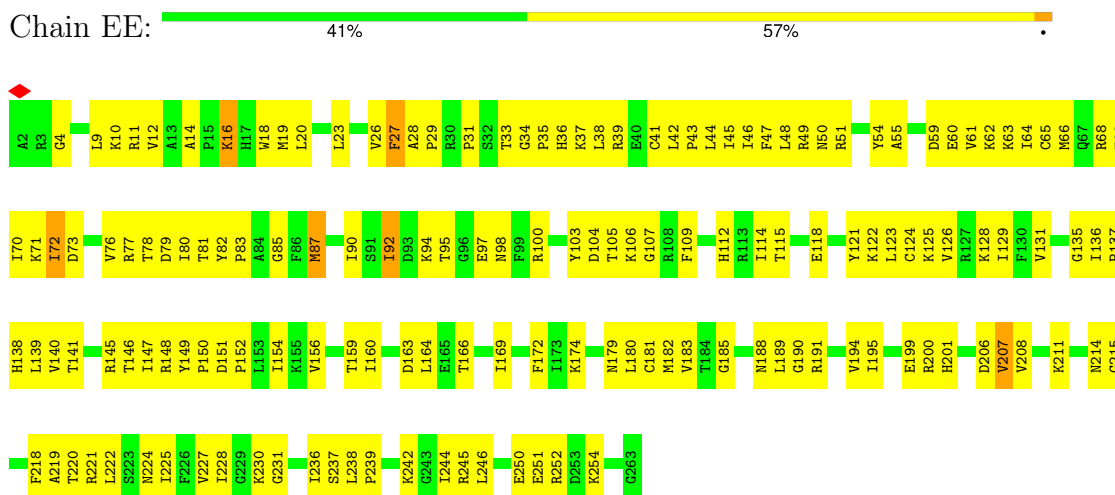
G1321	C1254	A1189	C1047	G985	G924	U844	U689	G626	U557	C491	A426	C353	U219
G1322	G1255	A1190	G1048	G986	G925	G845	G694	U627	G558	C492	U427	U354	U220
U1323	G1256	C1191	G1051	A987	A926	A987	G694	A628	G559	A493	U428	G355	A221
G1324	G1257	U1192	A1052	C988	C927	A847	G694	A629	A560	C429	C429	C356	U222
G1325	A1258	U1193	A1052	C989	G928	U848	C729	U630	A561	U495	C430	C356	C223
U1326	A1259	A1194	G1131	A990	G929	A849	C730	U631	U562	C496	C431	C356	A224
G1327	A1260	U1195	C1132	G991	C930	C850	C731	G635	G563	C497	C432	C357	G225
G1328	C1133	A1196	U1056	A992	C931	C851	U732	G636	U566	C498	A433	A363	G289
U1329	G1134	U1197	C1057	G993	G932	G852	U733	U637	C567	A500	A434	A364	U290
G1330	C1135	U1198	A1058	G993	G933	C853	C734	C638	C568	A501	G438	U367	G291
C1331	U1136	A1199	G1059	A996	G934	C853	C735	U637	C567	C501	A440	C368	A292
A1332	U1137	A1200	A996	A997	G935	U857	C736	C639	C569	C502	A449	C369	C293
U1333	A1062	A998	A998	A998	G936	A858	G752	A640	C570	G506	C441	C370	A299
C1337	C1063	G999	C1063	G999	C937	C859	G752	A641	U571	G507	C442	A371	U300
G1338	G1064	C1000	G1064	C1000	A938	C860	G754	U642	U572	A508	U443	U372	U301
U1339	G1065	A1001	G1065	A1001	U939	A643	G754	A643	U573	A509	G444	G374	A302
G1340	C1066	U1002	U1066	U1002	U940	G644	G758	C645	A574	G510	A445	U375	A303
C1341	C1067	U1003	C1067	U1003	C941	G645	G759	C646	A575	G510	A446	A376	G304
U1342	U1068	U1004	U1068	U1004	G942	G646	G790	U647	C579	G513	A447	G377	U305
C1343	U1069	G1005	U1069	G1005	U943	A869	C790	U648	C579	U514	A448	U378	U306
U1344	A1070	C1006	A1070	C1006	A944	A870	C791	A648	C579	G515	A449	C379	G307
C1345	C1075	U1007	C1075	U1007	U945	U871	C792	U649	U580	A516	A450	G380	G308
U1346	G1076	A1008	G1076	A1008	U946	A872	G793	A650	U581	C517	G451	C381	G309
A1347	C1076	U1009	G1076	U1009	G947	G874	G796	U651	U582	G518	A452	C382	G310
C1348	C1077	G1010	C1077	G1010	C948	A875	C797	A653	A584	A519	C453	G383	C311
U1349	A1080	A1011	A1080	A1011	C949	C876	G798	A654	C585	A520	U454	U384	G312
G1350	C1081	C1012	C1081	C1012	C950	C877	G799	A655	G586	A521	A455	G385	U314
U1351	G1082	U1013	G1082	U1013	C951	C878	U799	A656	G587	A522	C456	C386	U315
C1352	A1083	G1014	A1083	G1014	G952	G878	C803	U657	G588	A523	C457	C387	G316
G1353	U1084	U1015	U1084	U1015	C953	C879	C804	U658	G589	U524	A458	G394	G317
U1354	C1085	U1016	C1085	U1016	U954	A885	U804	U659	A590	A525	A459	C397	A318
C1355	U1086	U1017	U1086	U1017	A955	A886	U805	C660	C592	A526	A460	C400	G320
U1356	G1087	C1018	G1087	C1018	G956	A887	U806	U661	C592	A527	U461	A401	U399
G1357	U1088	U1019	U1088	U1019	A957	U888	A808	G662	A599	A528	C462	A402	G330
U1358	C1089	U1020	C1089	U1020	G958	U889	A809	U663	G600	A529	A465	G403	G333
C1359	A1093	U1021	A1093	U1021	U959	C891	A810	A671	G601	A530	A466	G404	C334
U1360	C1094	U1022	C1094	U1022	U960	G892	A811	A672	G602	C532	G467	G405	G335
G1361	U1095	A1023	U1095	A1023	C961	C893	A812	G673	C603	A533	A468	U406	A336
U1362	G1096	U1024	G1096	U1024	A962	G894	U813	C674	G604	C533	A469	G407	C337
C1363	U1097	C1026	U1097	C1026	U965	U895	U814	C675	A605	A534	G470	A408	G338
U1364	A1100	A1027	A1100	A1027	U966	U896	U815	U676	A606	C535	A471	C409	C340
G1365	U1101	U1028	U1101	U1028	C967	G901	G817	G677	G607	U540	C472	G410	G341
C1366	G1102	G1029	G1102	G1029	U968	G902	A818	C678	U607	U541	A473	A415	A342
U1367	C1103	A1030	C1103	A1030	U969	G907	U819	C679	C608	U542	A474	U416	A343
G1368	G1104	C1031	G1104	C1031	C970	A908	U820	U680	G611	C543	G475	C417	U344
C1369	U1105	U1032	U1105	U1032	A971	G909	U822	U681	G612	C544	A476	A418	C346
U1370	C1106	G1033	C1106	G1033	C972	G910	U823	U682	G613	A545	G477	G420	G347
G1371	U1112	A1034	U1112	A1034	C973	C911	C824	U683	C614	A546	A478	A484	A348
C1372	U1113	A1035	U1113	A1035	C974	C912	A825	U684	C615	G547	C479	G421	A349
U1373	U1114	A1036	U1114	A1036	G975	C913	A826	U685	G616	C548	A480	U422	C350
G1374	C1107	G1037	C1107	G1037	G976	A913	U827	U686	A617	C549	C481	U423	G351
C1375	U1115	U1038	U1115	U1038	C977	A914	A827	U687	C618	C550	C482	G424	C352
U1376	C1116	C1039	C1116	C1039	C978	G915	A830	G683	A619	U551	C483	A347	A348
G1377	U1117	G1040	U1117	G1040	C979	A919	A831	G684	G620	G552	A484	G421	G349
C1378	A1118	A1119	A1118	A1119	C980	A920	G832	A685	C621	U553	A485	U422	A349
U1379	U1119	C1120	U1119	C1120	A981	A921	C833	U686	C622	A554	A486	U423	C350
G1380	C1121	U1044	C1121	U1044	G982	A922	C834	U687	C623	A555	U487	G424	G351
C1381	U1122	U1045	U1122	U1045	A983	A923	C834	U688	G625	U556		G425	U352
U1382	C1123	U1046	C1123	U1046	C984	G923							



• Molecule 6: 40S ribosomal protein S2

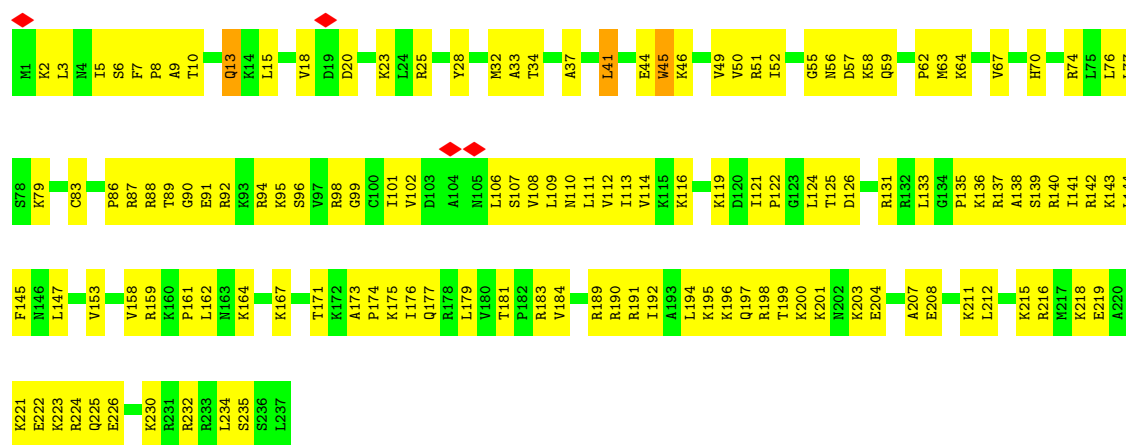


• Molecule 7: 40S ribosomal protein S4

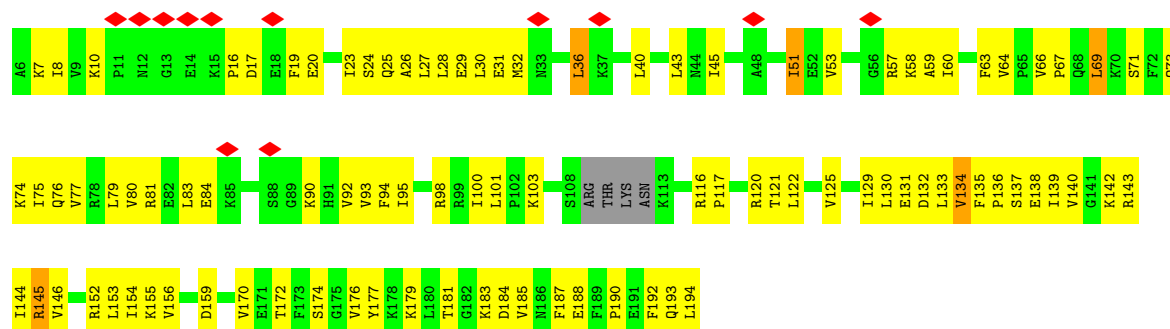


• Molecule 8: 40S ribosomal protein S6

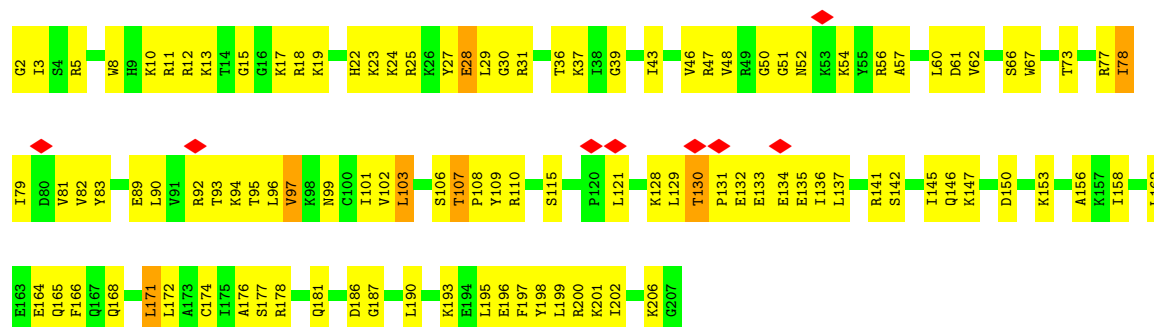




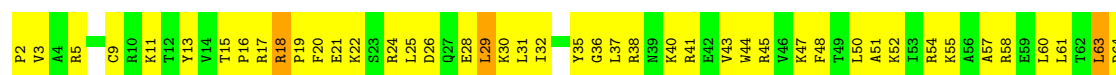
• Molecule 9: Small ribosomal subunit protein eS7

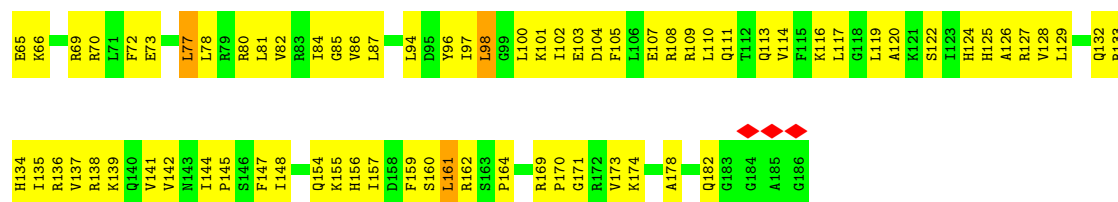


• Molecule 10: 40S ribosomal protein S8

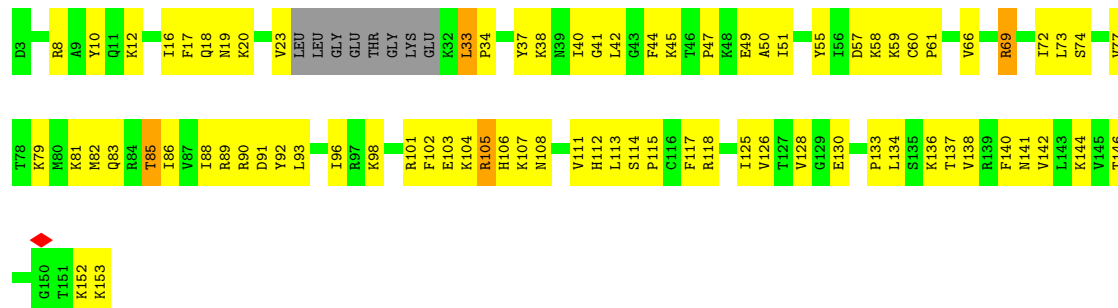


• Molecule 11: 40S ribosomal protein S9





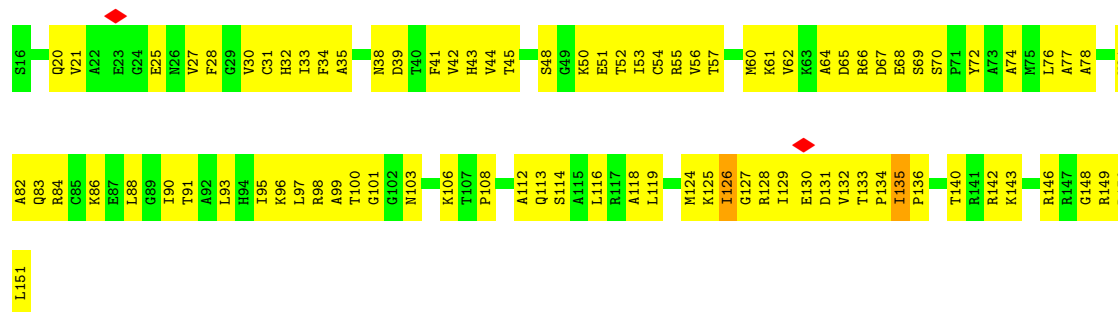
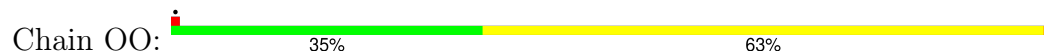
• Molecule 12: Small ribosomal subunit protein uS17



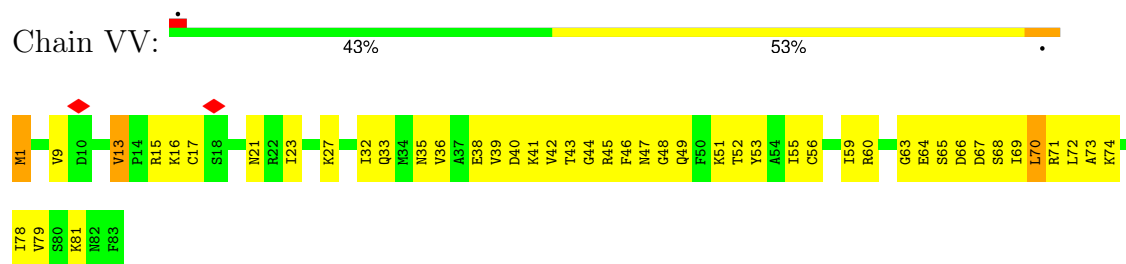
• Molecule 13: 40S ribosomal protein S13



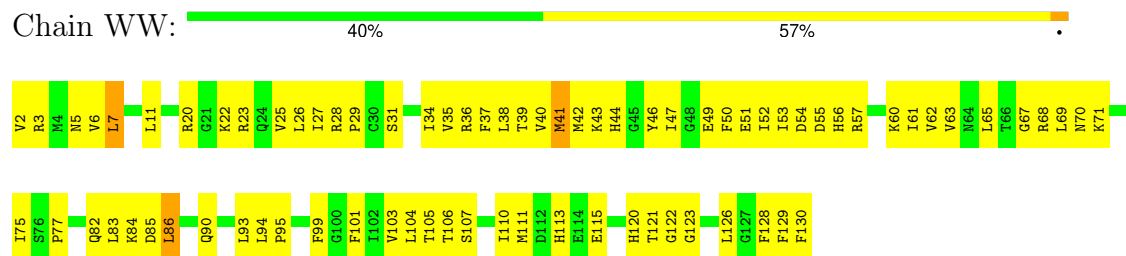
• Molecule 14: Small ribosomal subunit protein uS11



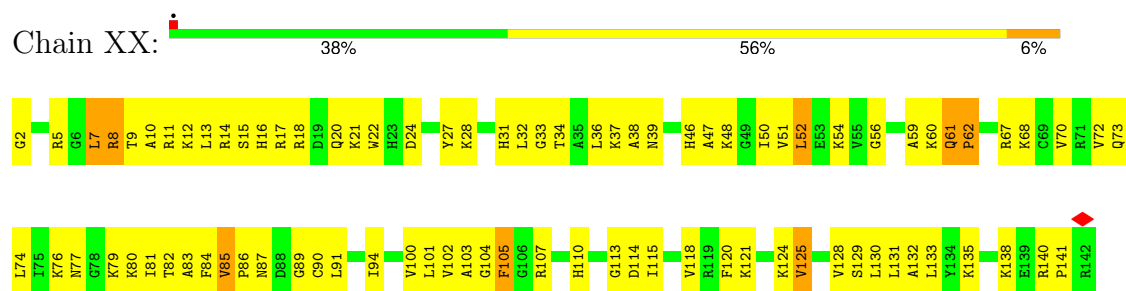
• Molecule 15: eS21



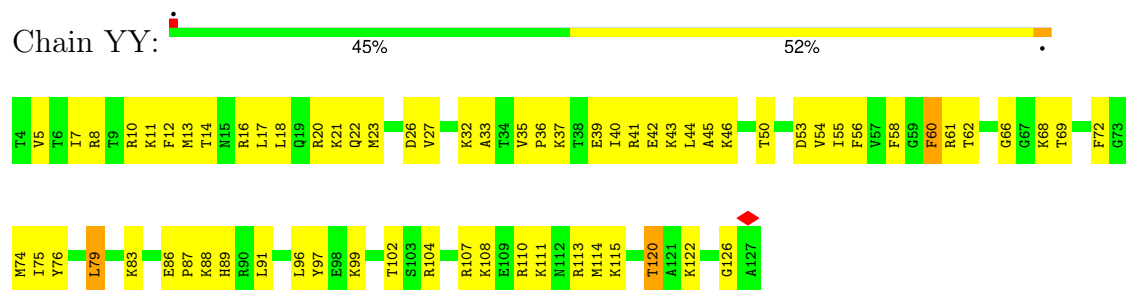
- Molecule 16: 40S ribosomal protein S15a



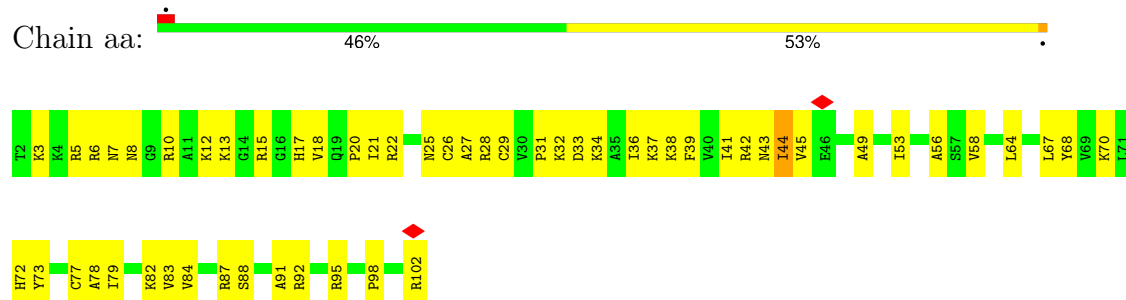
- Molecule 17: 40S ribosomal protein S23



- Molecule 18: 40S ribosomal protein S24

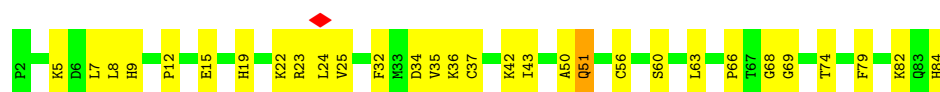


- Molecule 19: eS26



- Molecule 20: 40S ribosomal protein S27

Chain bb: 



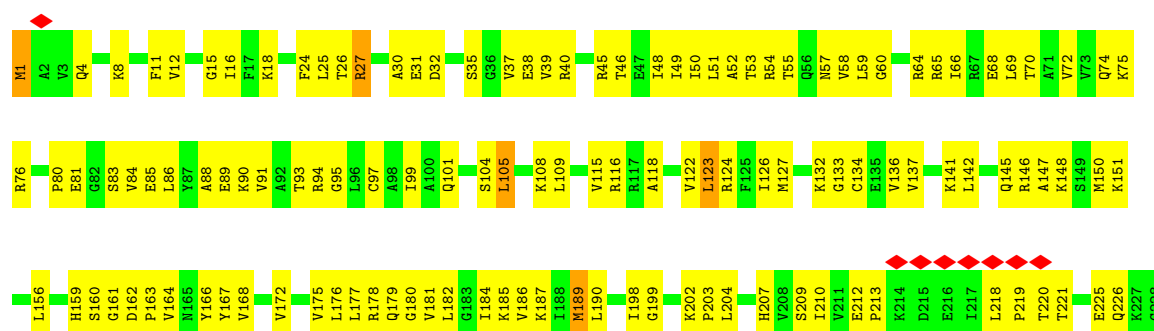
- Molecule 21: Small ribosomal subunit protein eS30

Chain ee: 



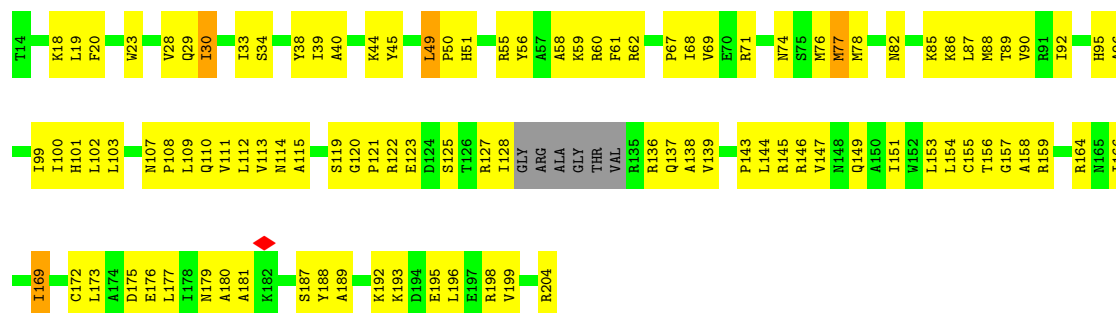
- Molecule 22: 40S ribosomal protein S3

Chain DD: 



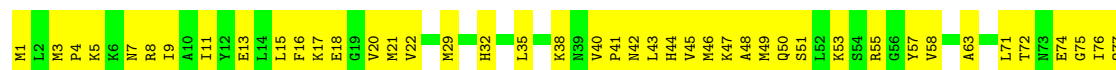
- Molecule 23: Small ribosomal subunit protein uS7

Chain FF: 



- Molecule 24: 40S ribosomal protein S10

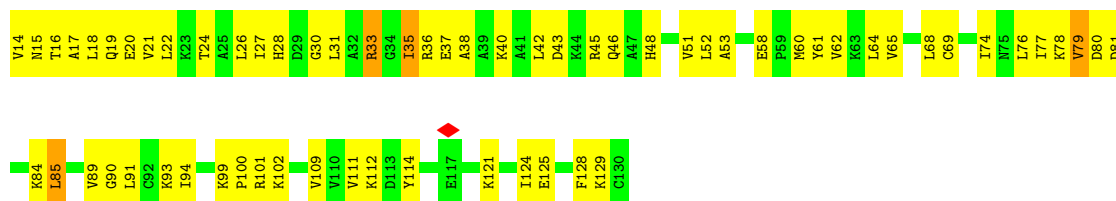
Chain KK: 





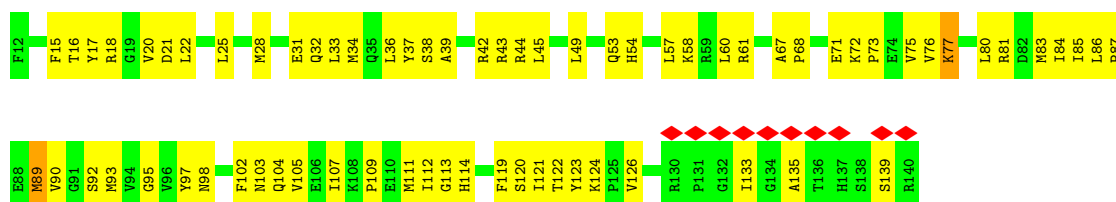
- Molecule 25: 40S ribosomal protein S12

Chain MM: 45% 51%



- Molecule 26: Small ribosomal subunit protein uS19

Chain PP: 8% 46% 53%



- Molecule 27: Small ribosomal subunit protein uS9

Chain QQ: 34% 64%

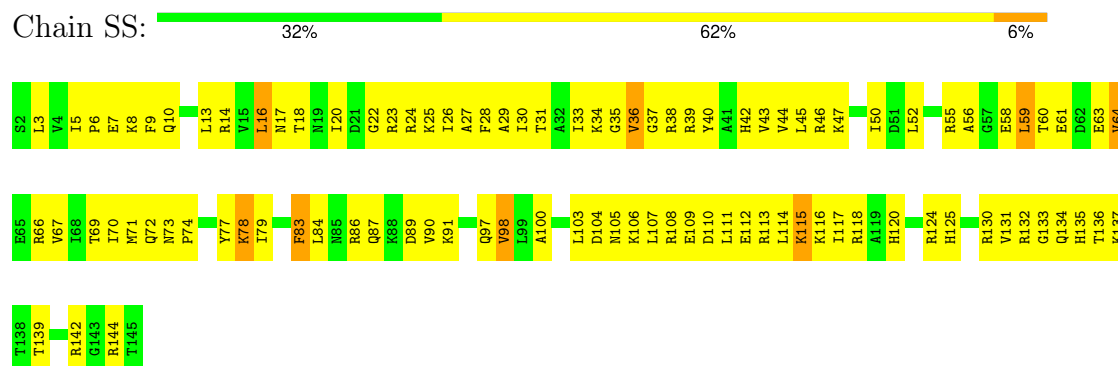


- Molecule 28: 40S ribosomal protein S17

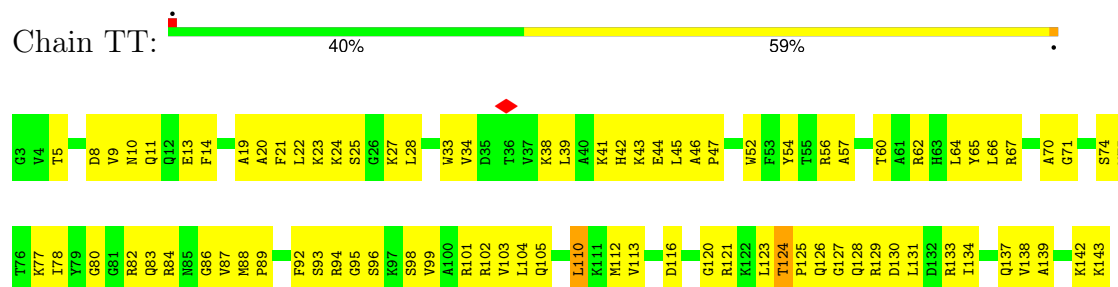
Chain RR: 8% 45% 53%



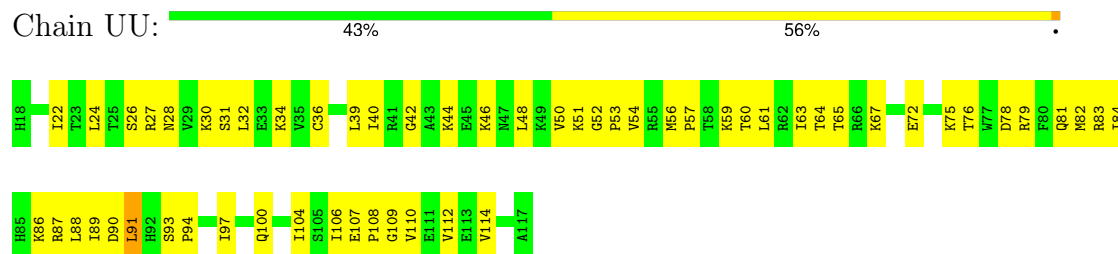
- Molecule 29: 40S ribosomal protein S18



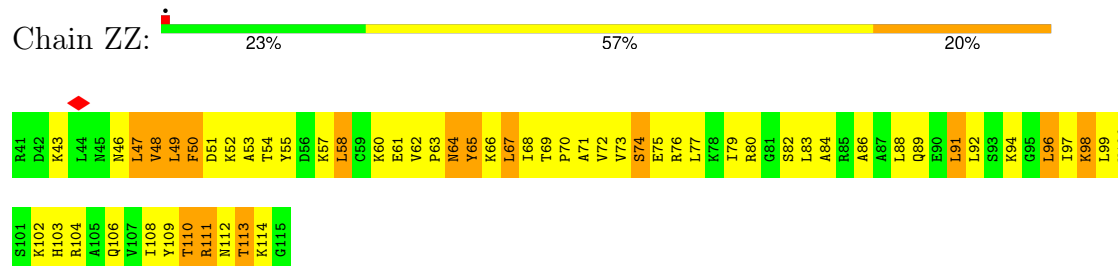
- Molecule 30: Small ribosomal subunit protein eS19



- Molecule 31: 40S ribosomal protein S20

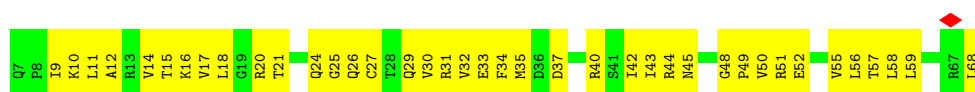


- Molecule 32: 40S ribosomal protein S25



- Molecule 33: 40S ribosomal protein S28





- Molecule 34: 40S ribosomal protein S29

Chain dd: 51% 47%



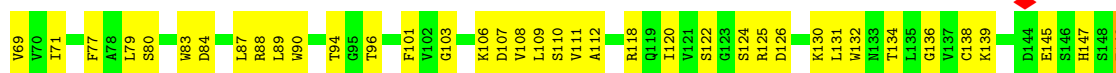
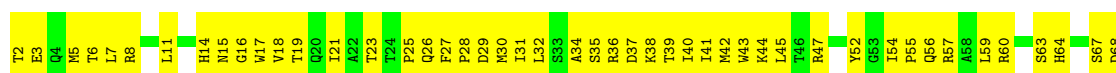
- Molecule 35: 40S ribosomal protein S27a

Chain ff: 54% 44%



- Molecule 36: Receptor of activated protein C kinase 1

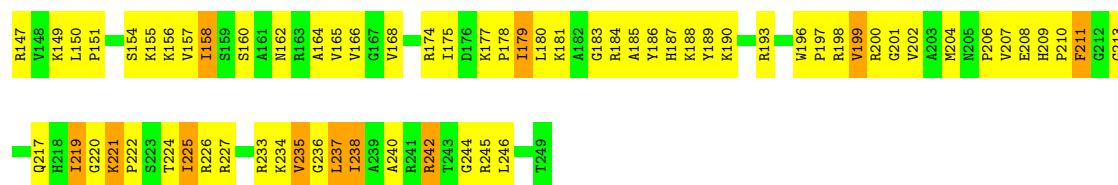
Chain gg: 46% 53%



- Molecule 37: 60S ribosomal protein L8

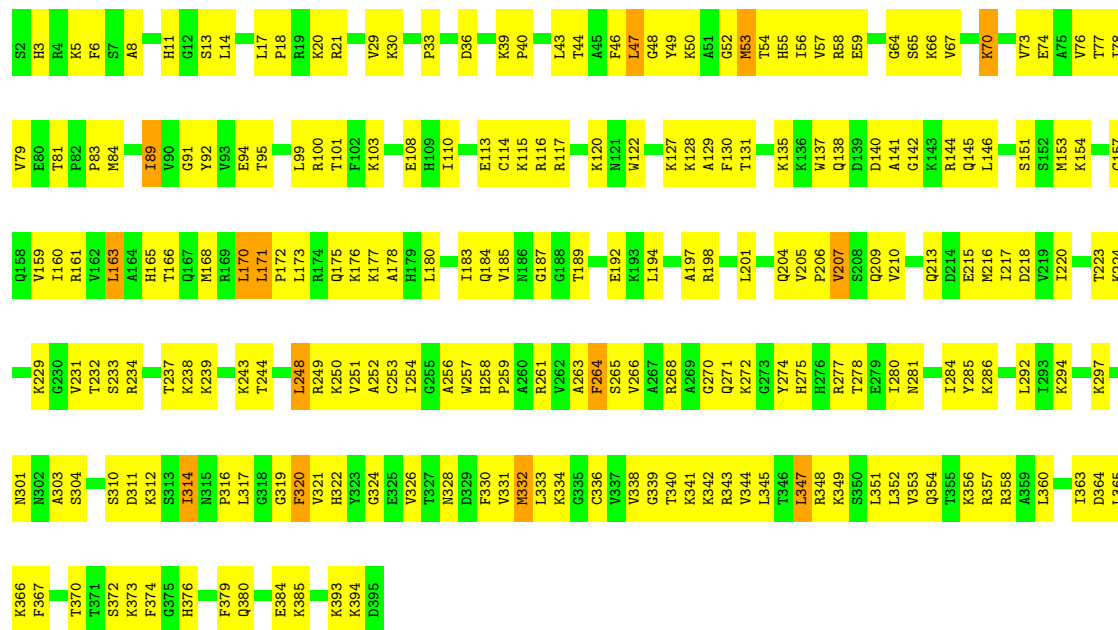
Chain A: 38% 55% 7%





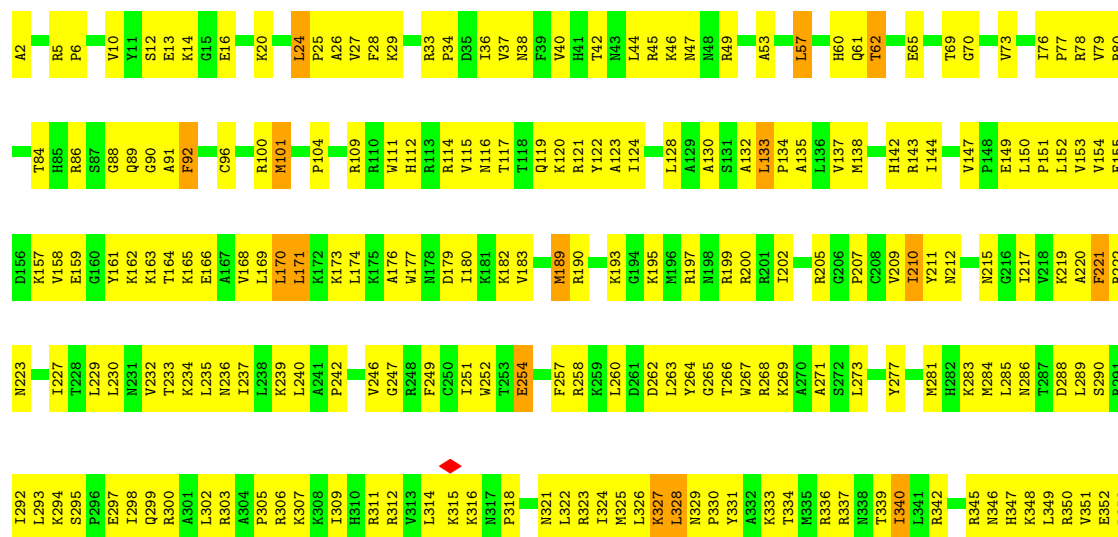
• Molecule 38: 60S ribosomal protein L3

Chain B: 44% 53%



• Molecule 39: 60S ribosomal protein L4

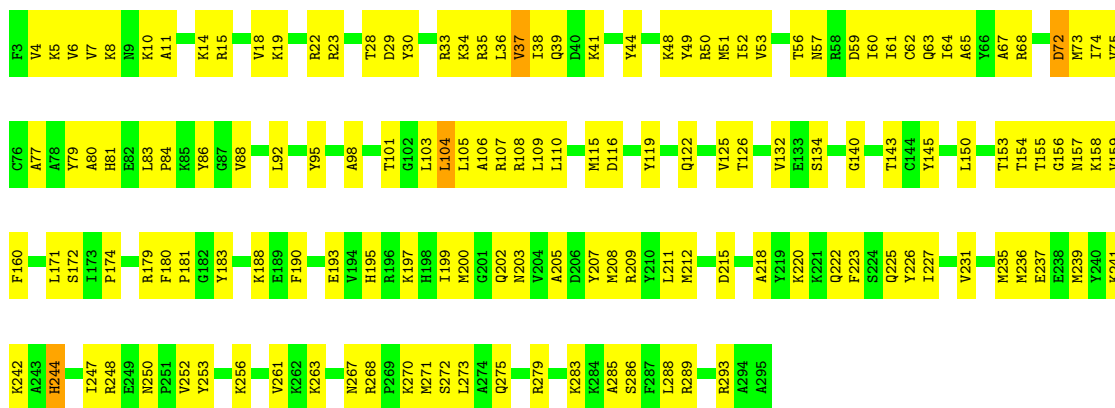
Chain C: 40% 56%





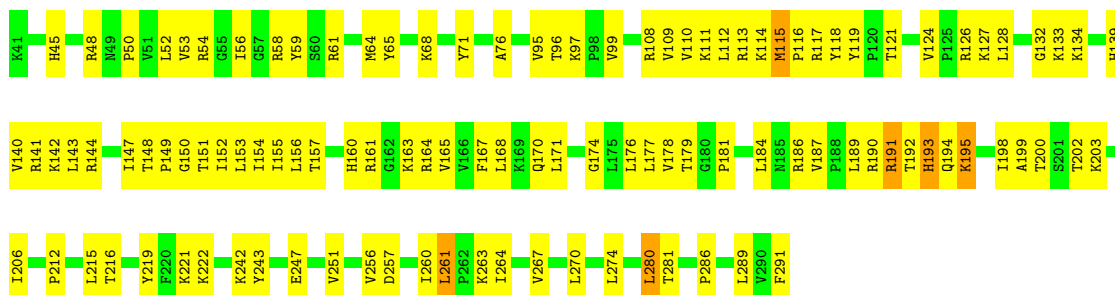
• Molecule 40: 60S ribosomal protein L5

Chain D: 50% 48%



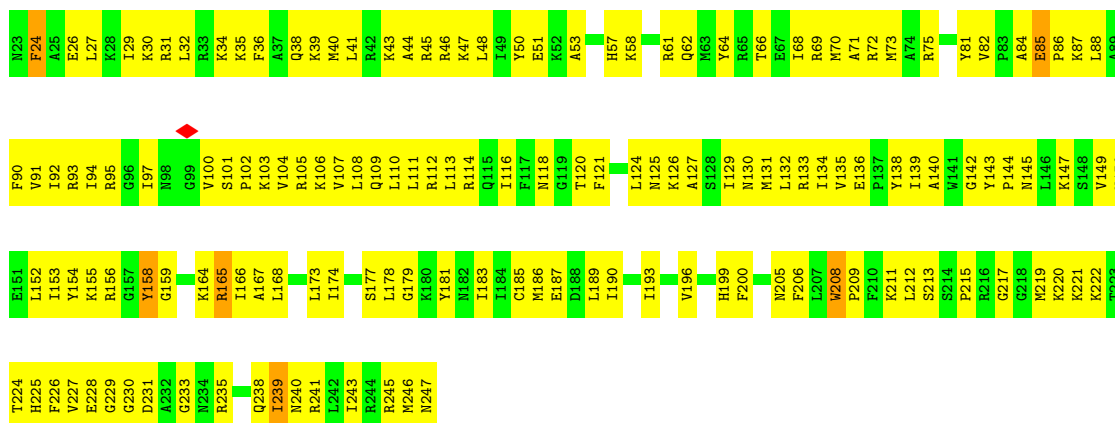
• Molecule 41: 60S ribosomal protein L6

Chain E: 49% 49%

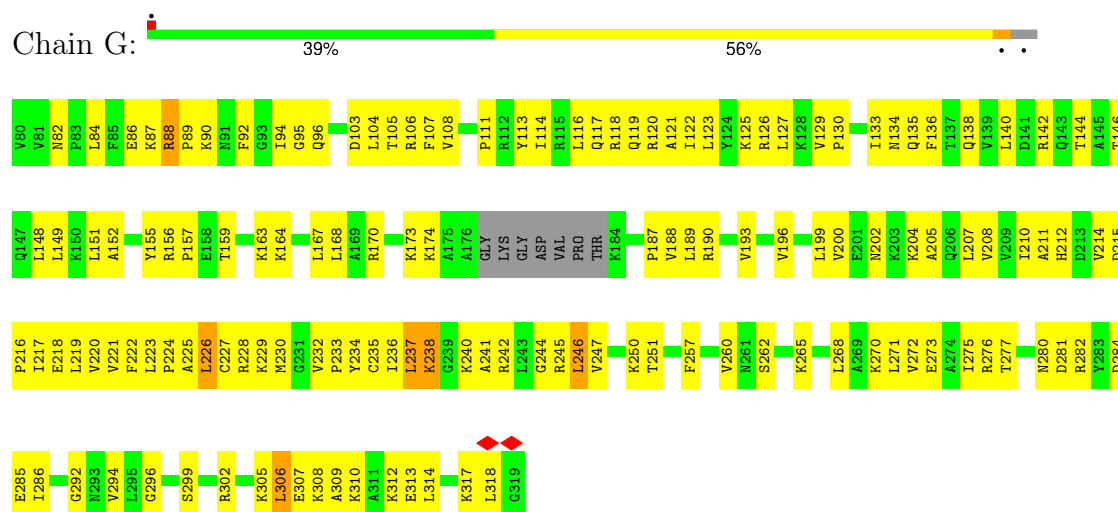


• Molecule 42: 60S ribosomal protein L7

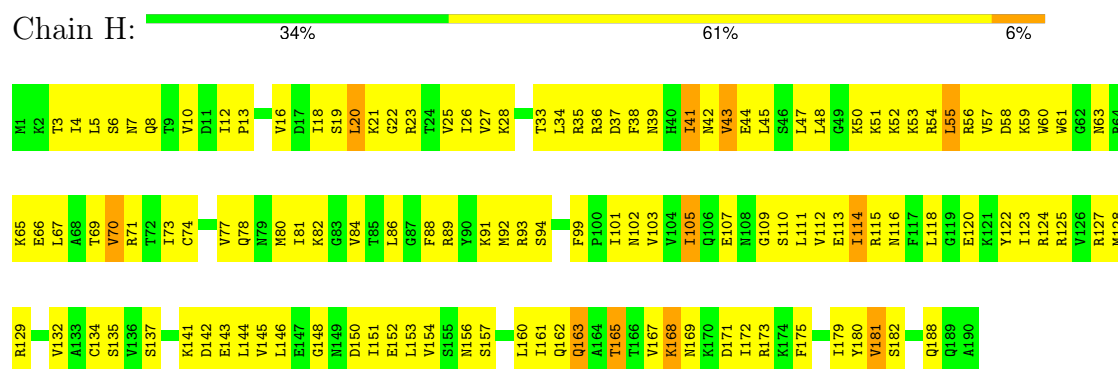
Chain F: 33% 64%



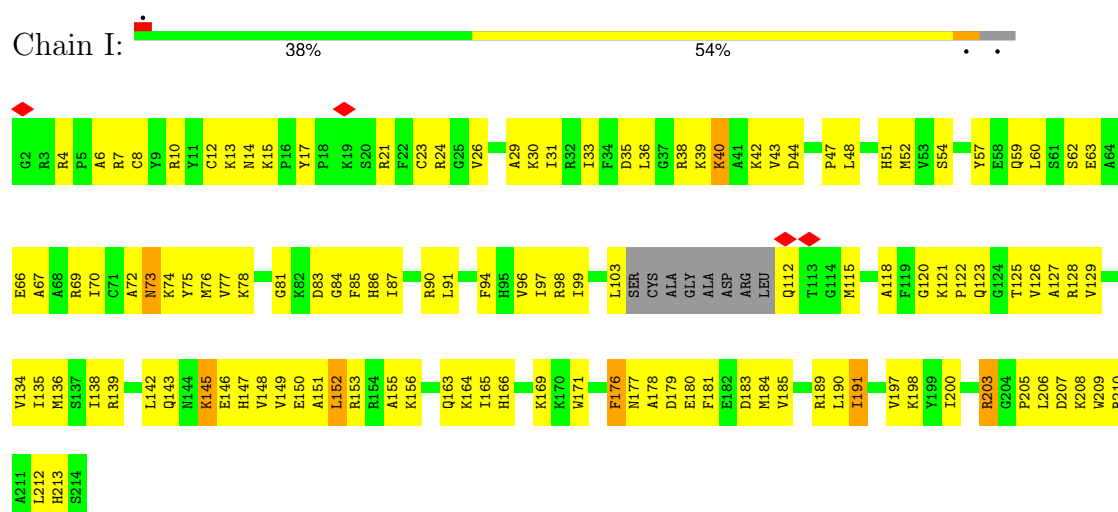
- Molecule 43: Large ribosomal subunit protein eL8



- Molecule 44: 60S ribosomal protein L9

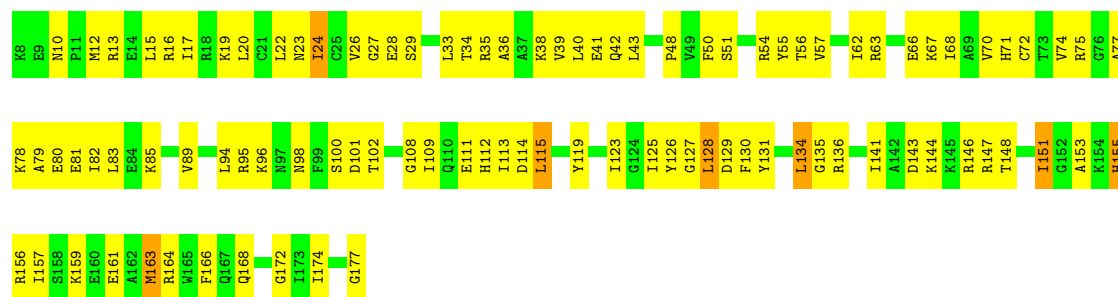


- Molecule 45: Ribosomal protein L10

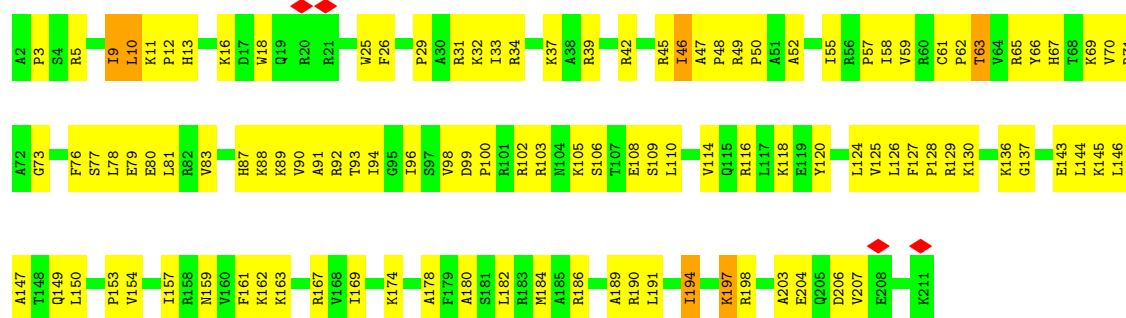


- Molecule 46: 60S ribosomal protein L11

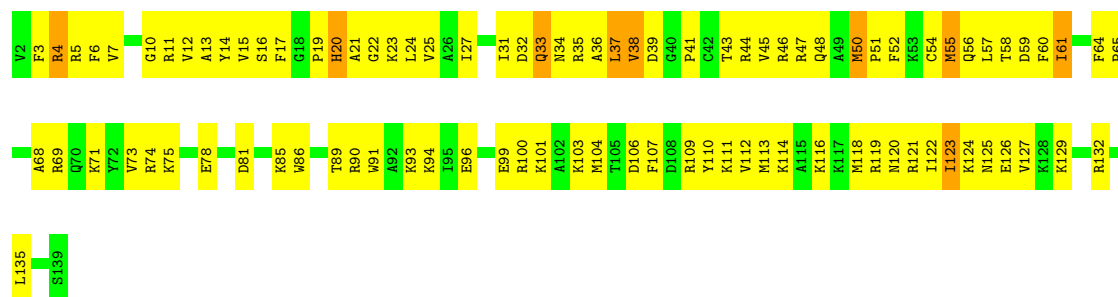




- Molecule 47: Large ribosomal subunit protein eL13



- Molecule 48: 60S ribosomal protein L14



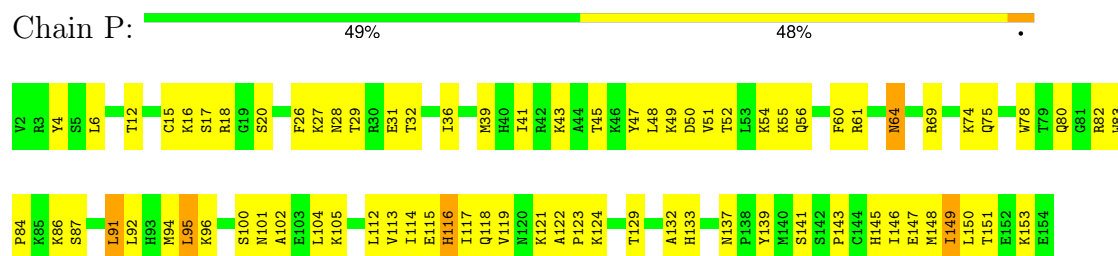
- Molecule 49: 60S ribosomal protein L15



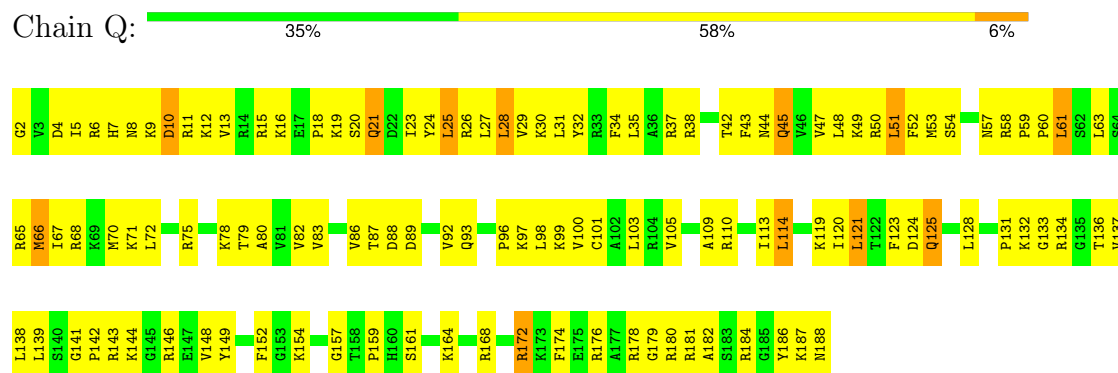
- Molecule 50: Large ribosomal subunit protein uL13



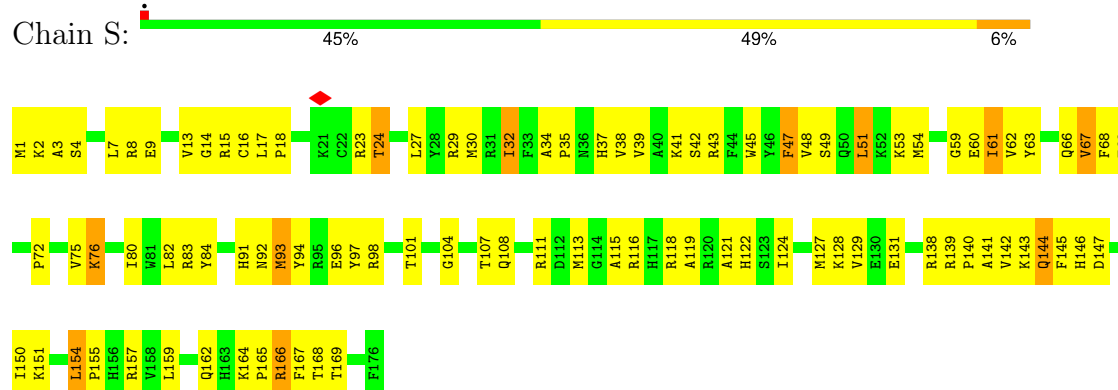
- Molecule 51: 60S ribosomal protein L17



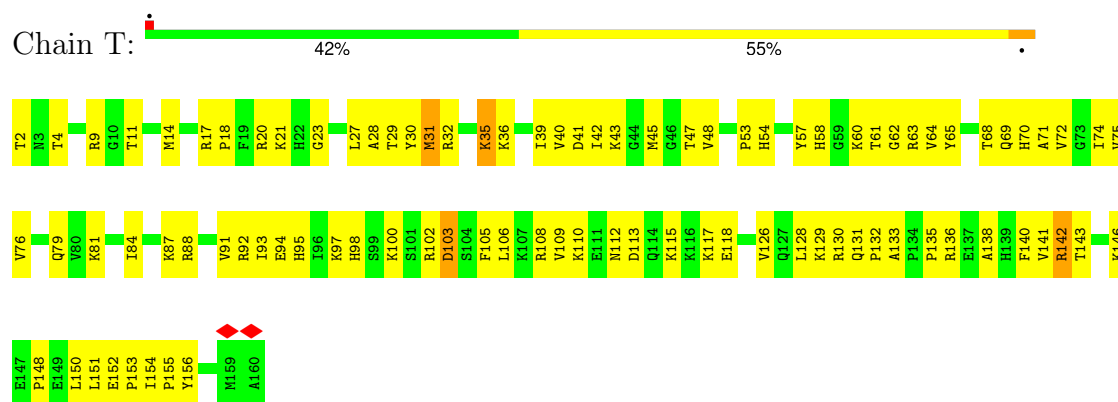
- Molecule 52: Large ribosomal subunit protein eL18



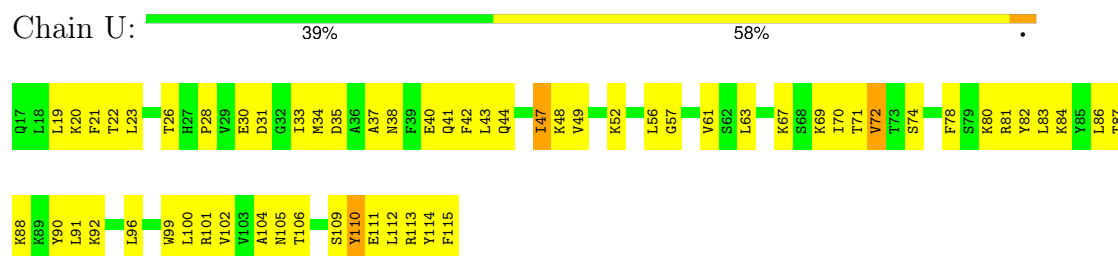
- Molecule 53: eL20



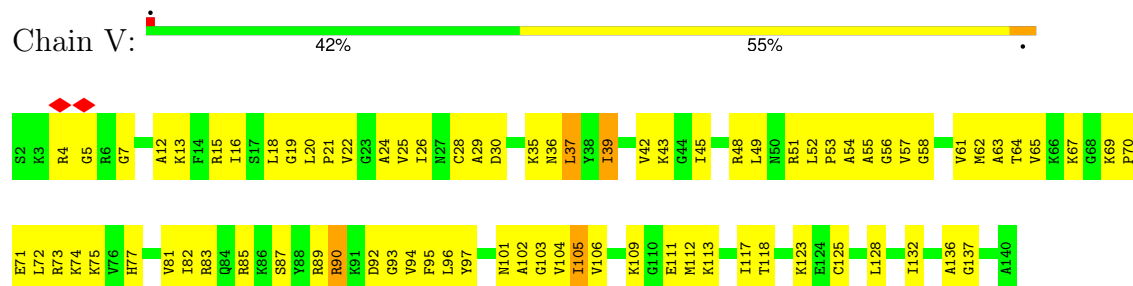
- Molecule 54: 60S ribosomal protein L21



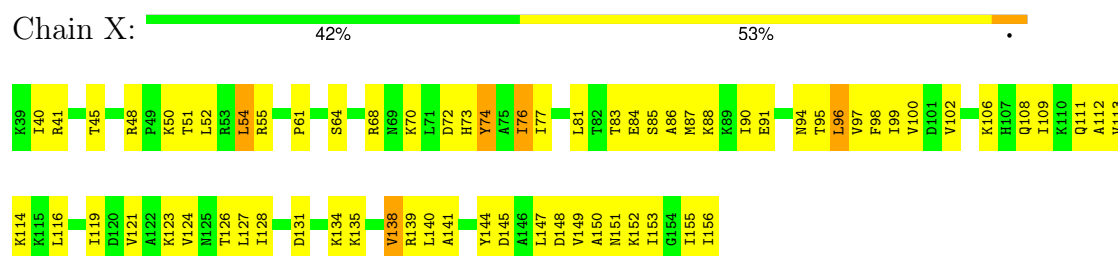
- Molecule 55: Large ribosomal subunit protein eL22



- Molecule 56: Large ribosomal subunit protein uL14

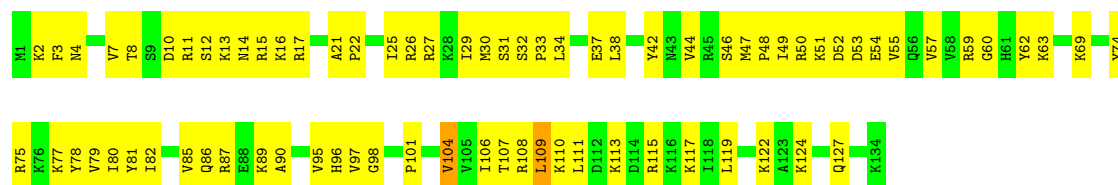


- Molecule 57: Large ribosomal subunit protein uL23



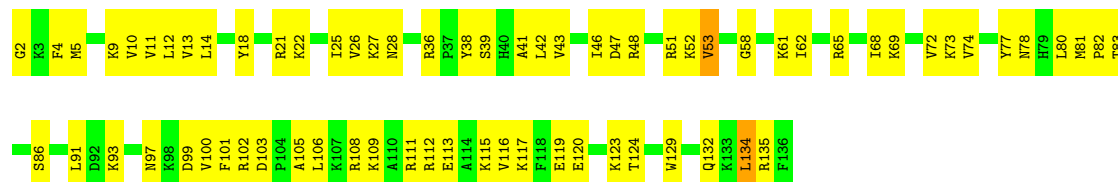
- Molecule 58: 60S ribosomal protein L26





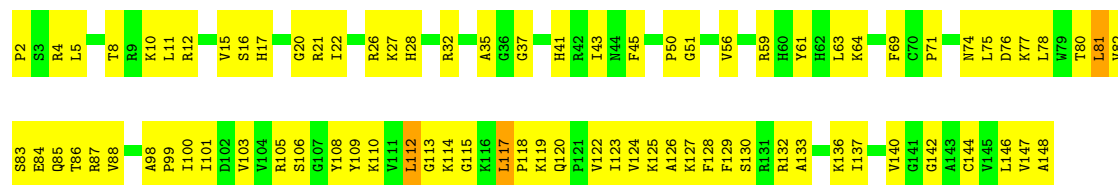
• Molecule 59: 60S ribosomal protein L27

Chain Z: 48% 50% .



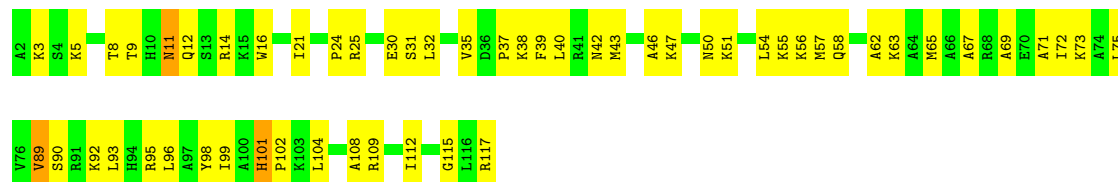
• Molecule 60: 60S ribosomal protein L27a

Chain a: 44% 54% .



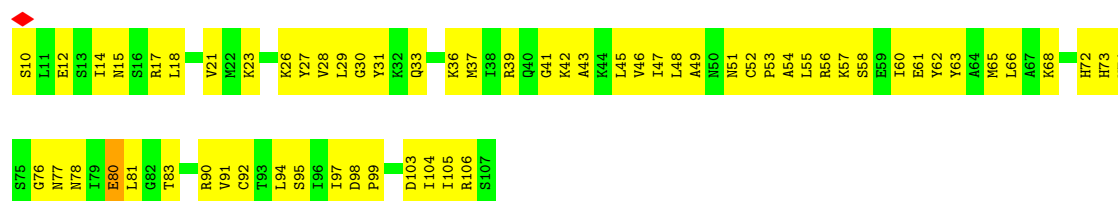
• Molecule 61: eL29

Chain b: 47% 50% .



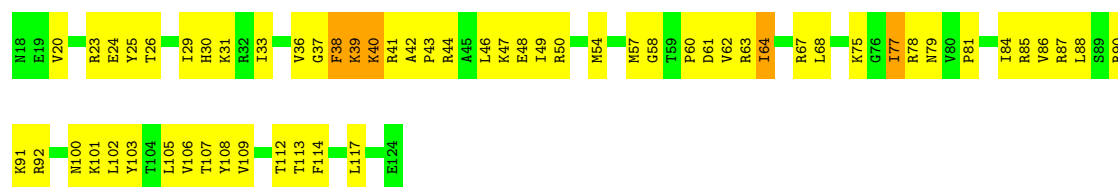
• Molecule 62: 60S ribosomal protein L30

Chain c: 37% 62% .



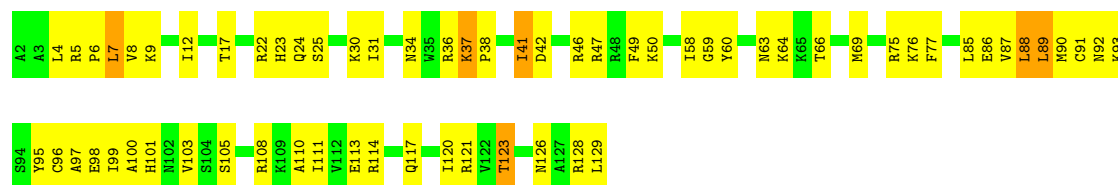
• Molecule 63: 60S ribosomal protein L31

Chain d: 



- Molecule 64: Large ribosomal subunit protein eL32

Chain e: 



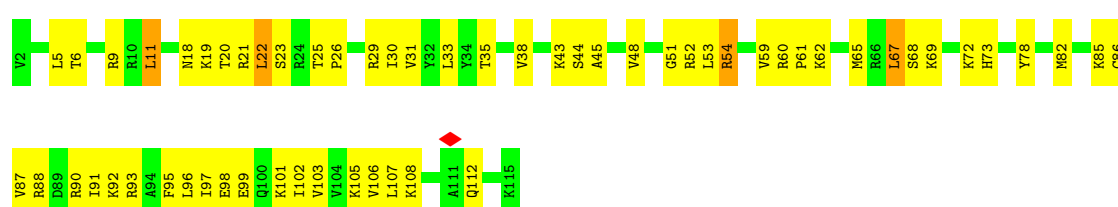
- Molecule 65: Large ribosomal subunit protein eL33

Chain f: 



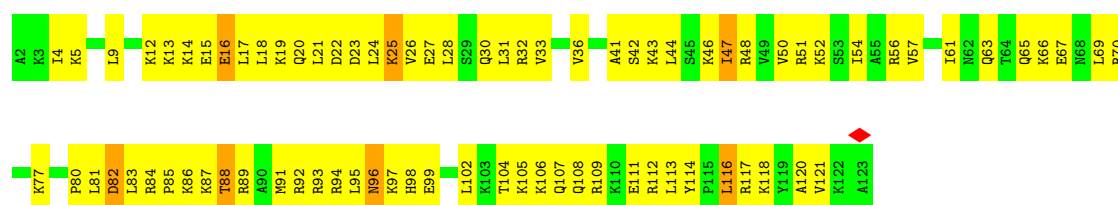
- Molecule 66: 60S ribosomal protein L34

Chain g: 

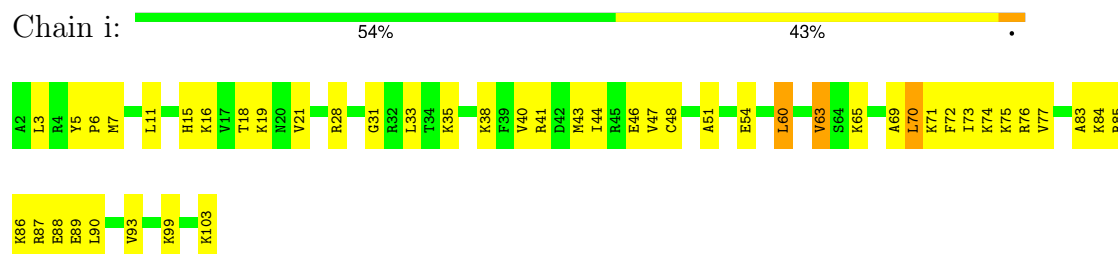


- Molecule 67: 60S ribosomal protein L35

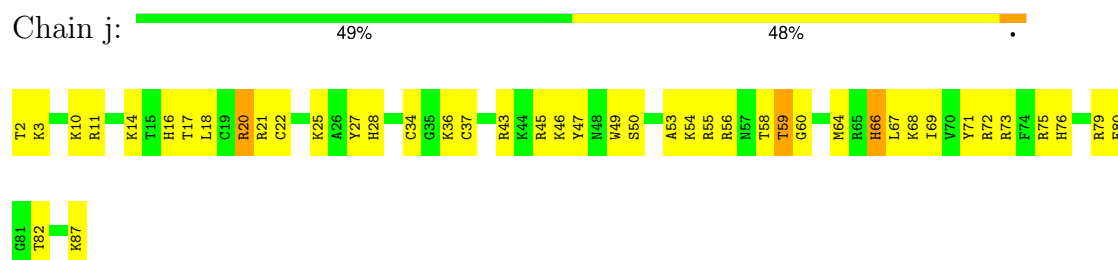
Chain h: 



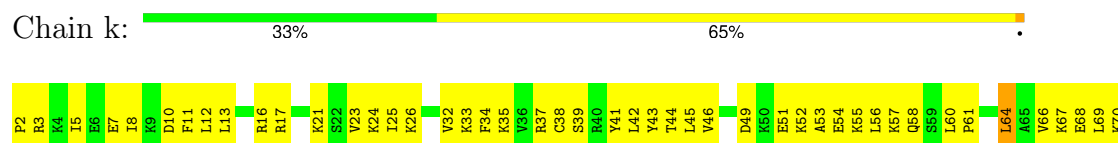
- Molecule 68: 60S ribosomal protein L36



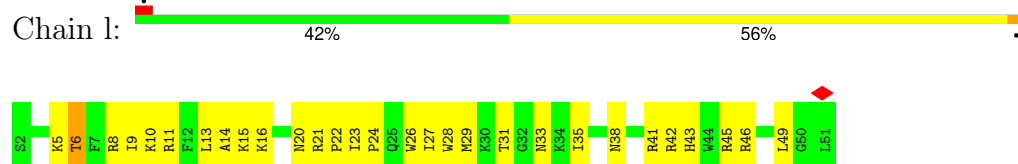
- Molecule 69: 60S ribosomal protein L37



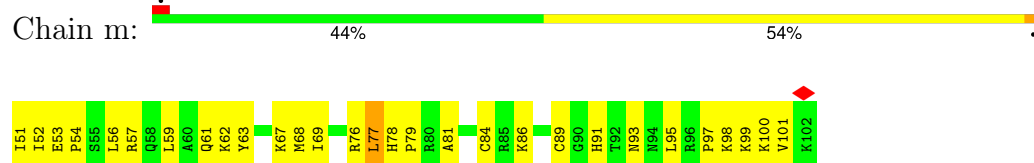
- Molecule 70: Large ribosomal subunit protein eL38



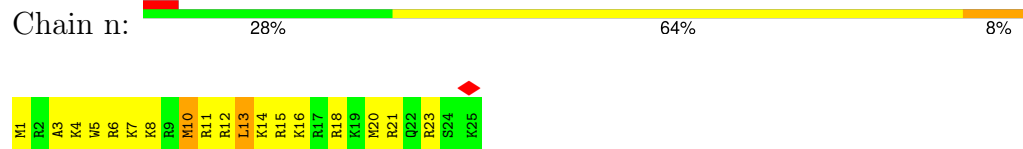
- Molecule 71: 60S ribosomal protein L39



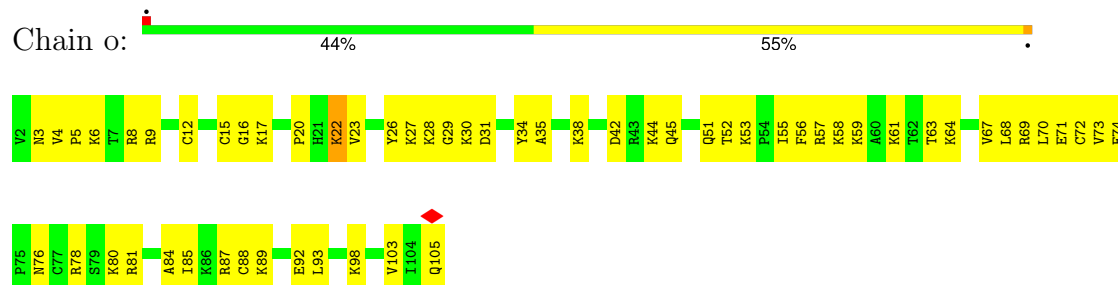
- Molecule 72: Large ribosomal subunit protein eL40



- Molecule 73: eL41



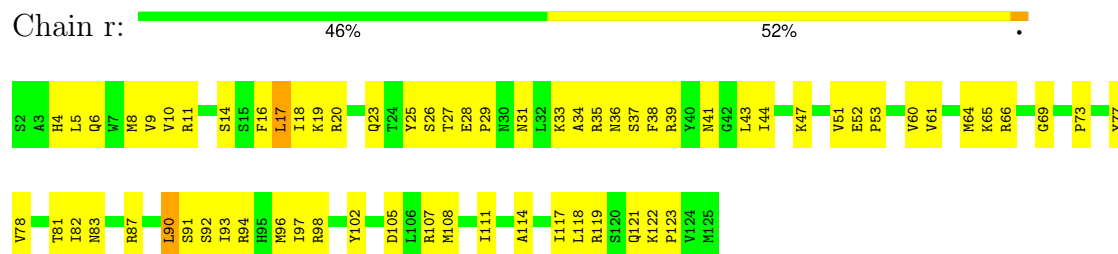
- Molecule 74: eL42



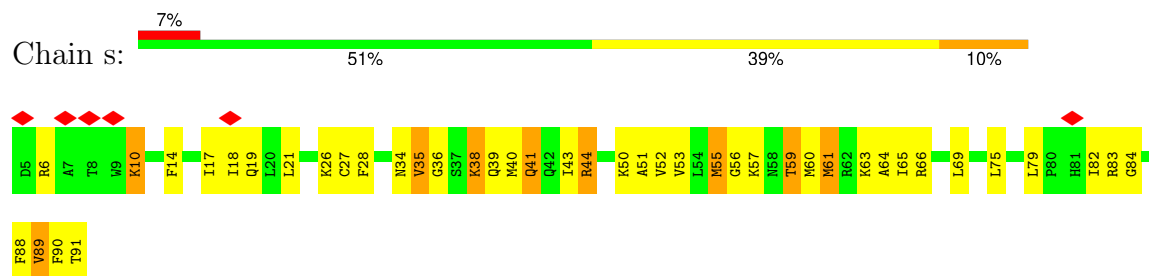
- Molecule 75: 60S ribosomal protein L37a



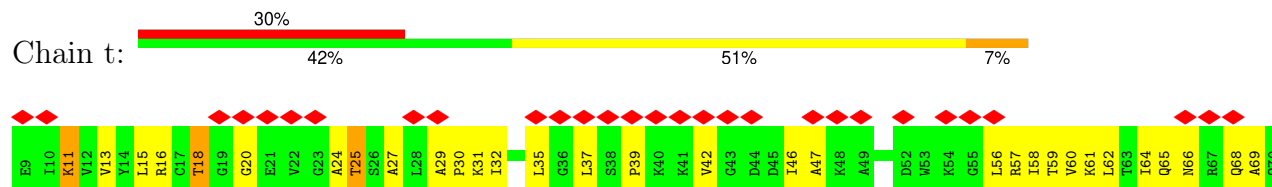
- Molecule 76: 60S ribosomal protein L28

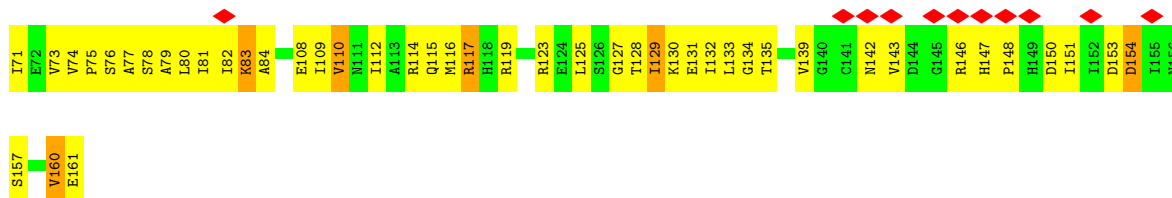


- Molecule 77: Large ribosomal subunit protein uL10



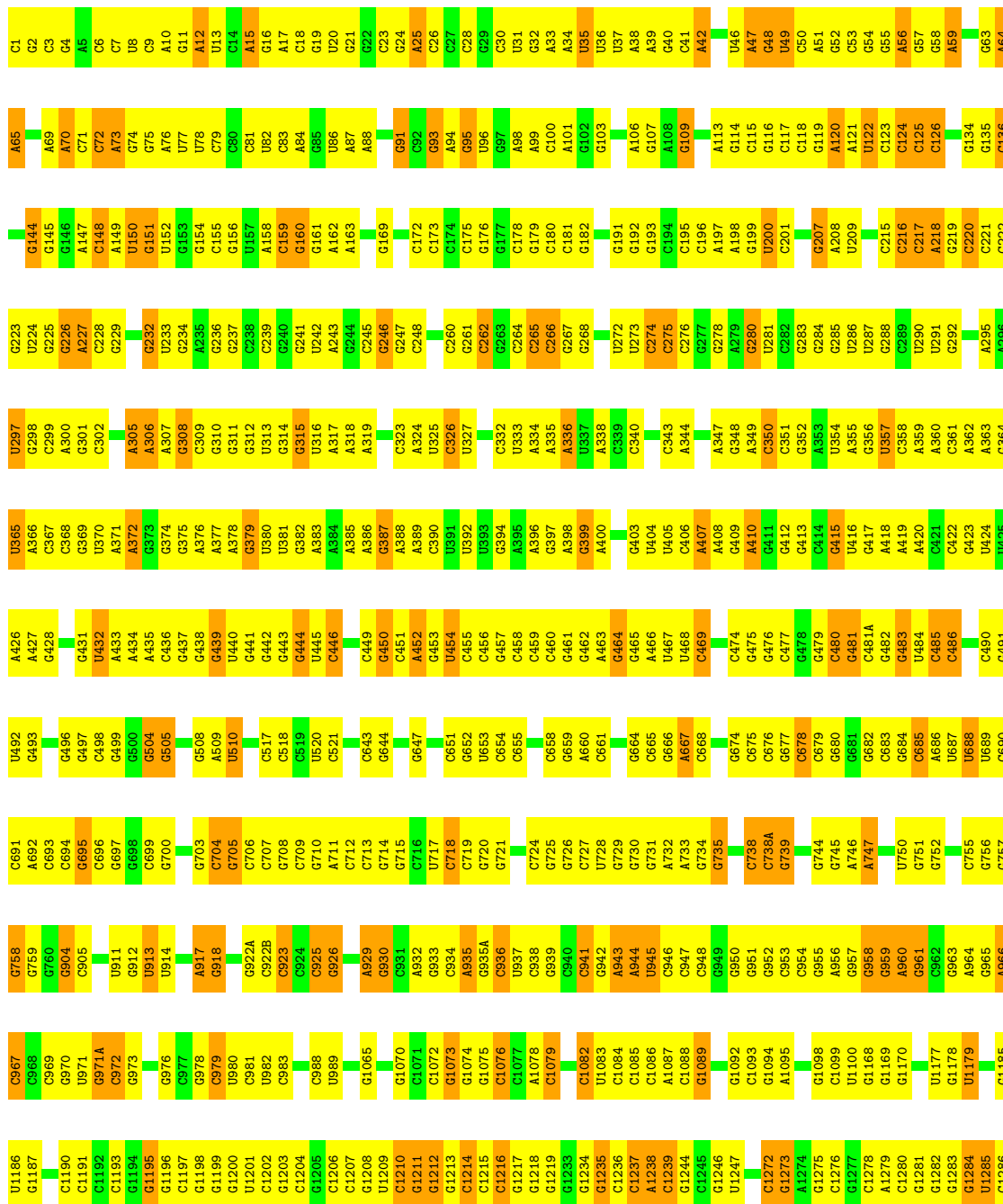
- Molecule 78: uL11





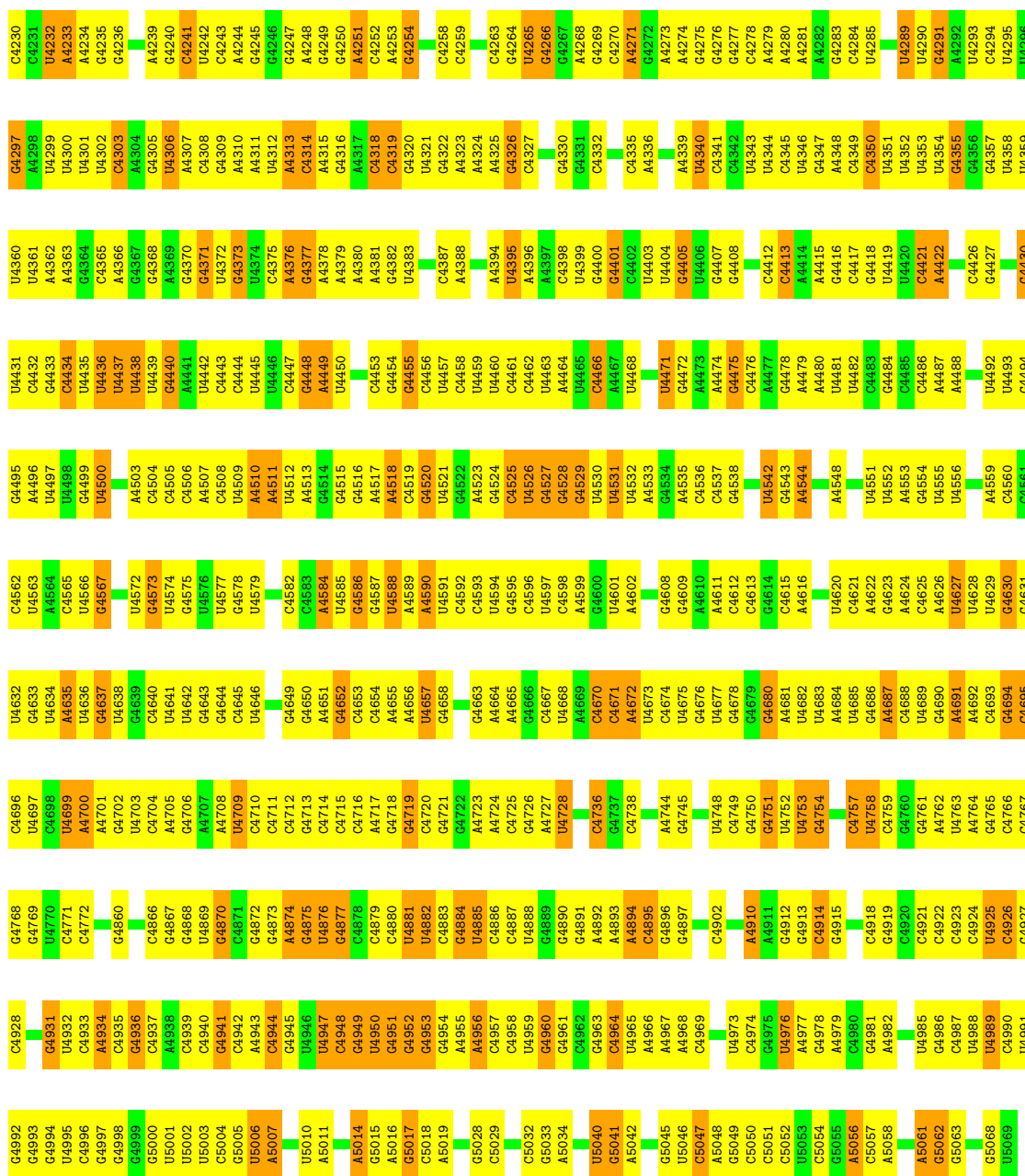
• Molecule 79: 28S rRNA

Chain 5: 27% 57% 16%

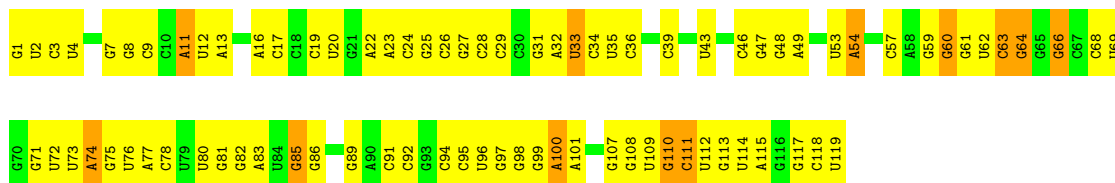


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G1347	G1415	G1418	G1419	G1420	G1421	G1422	G1423	G1424	G1427	G1435	G1437	G1438	G1439	G1440	G1441	G1442	G1443	G1444	G1445	G1446	G1447	G1448	G1449	G1450	G1451	G1452	G1453	G1454	G1455	G1456	G1457	G1458	G1459	G1460	G1461	G1462	G1463	G1464	G1465	G1466	G1467	G1468	G1469	G1470	G1471	G1472	G1473	G1474	G1475	G1476	G1477	G1478	G1479	G1480	G1481	G1482																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
C1483	G1550	G1552	G1553	G1554	G1555	G1556	G1557	G1558	G1563	G1564	G1565	G1566	G1569	G1570	G1571	G1572	G1573	G1574	G1575	G1576	G1577	G1578	G1579	G1580	G1581	G1582	G1583	G1584	G1588	G1589	G1590	G1591	G1592	G1593	G1594	G1595	G1596	G1597	G1598	G1599	G1600	G1601	G1602	G1603	G1604	G1605	G1606	G1607	G1608	G1609	G1612	G1613	G1614	G1615																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
U1616	G1620	G1621	G1622	G1623	G1624	G1625	G1626	G1627	G1628	G1631	G1632	G1633	G1634	G1635	G1636	G1637	G1638	G1641	G1642	G1643	G1644	G1645	G1646	G1647	G1651	G1652	G1653	G1654	G1655	G1661	G1662	G1663	G1664	G1665	G1666	G1667	G1668	G1669	G1670	G1671	G1672	G1673	G1674	G1675	G1676	G1677	G1678	G1679	G1680	G1683	G1684	G1685	G1686																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
U1687	G1688	G1690	G1691	G1694	G1695	G1696	G1722	G1723	U1726	U1727	U1728	U1729	U1730	U1731	U1732	U1733	U1734	U1735	U1736	U1737	U1738	U1739	U1740	U1741	U1742	U1743	U1748	U1749	G1750	U1754	U1755	U1756	U1757	G1761	G1762	G1763	G1764	G1765	G1766	G1767	G1768	G1769	U1770	U1771	G1772	U1773	U1776	U1777	U1778	U1779	U1780																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
U1781	U1782	U1783	U1784	U1785	U1786	U1787	U1788	U1789	U1790	U1791	U1792	U1793	U1794	U1795	U1796	U1797	U1798	U1799	U1800	U1801	U1802	U1803	U1804	U1805	U1806	U1807	U1810	U1811	U1812	U1813	U1814	U1815	U1816	U1817	U1818	U1819	U1820	U1821	U1822	U1823	U1824	U1825	U1826	U1827	U1828	U1829	U1830	U1833	U1834	U1835	U1836	U1837	U1838	U1839	U1840	U1841	U1842																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
A1843	A1844	A1845	A1846	A1847	A1848	A1849	A1850	A1851	A1852	A1853	A1854	A1855	A1856	A1857	A1858	U1863	U1864	U1865	U1866	U1867	U1868	U1869	U1870	U1871	U1872	U1873	U1874	U1875	U1876	U1877	U1878	U1881	U1882	U1883	U1884	U1885	U1886	U1887	U1888	U1889	U1890	U1891	U1892	U1893	U1894	U1895	U1896	U1897	U1898	U1899	U1900	U1904	U1905	U1906	U1907	U1908																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
G1909	G1910	G1911	G1912	G1913	G1914	G1915	G1916	G1917	G1918	G1919	G1920	G1921	G1922	G1923	G1924	G1925	G1926	G1927	G1928	G1929	G1930	G1931	G1932	G1933	G1934	G1935	G1936	G1937	G1938	G1939	G1940	G1941	G1942	G1943	G1944	G1945	G1946	G1947	G1948	G1949	G1950	G1951	G1952	G1953	U1957	U1958	U1959	U1960	U1961	U1962	U1963	U1964	U1965	U1966	U1967	U1968	U1969	U1970																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
C1971	G1972	G1973	G1974	G1975	G1976	G1977	G1978	A1979	U1980	G1981	G1982	G1983	A1984	G1985	U1986	G1987	G1988	G1989	A1990	G20055	G20056	U1991	U1992	G1993	G1994	G1995	G1996	U1997	U1998	A1999	G2000	G2001	A2002	G2003	U2004	G2005	G2006	G2007	G2008	G2009	G2010	G2011	G2012	G2013	G2014	G2015	G2016	G2017	G2018	G2019	U2020	G2021	G2022	G2023	G2024	A2025	G2026	U2027	G2028	A2029																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
G2034	G2035	G2036	G2037	G2038	G2039	G2040	G2041	G2042	G2043	G2044	G2045	G2046	U2047	U2048	G2049	G2050	G2051	G2052	G2053	U2054	G2055	G2056	U1992	G2057	G2058	G2059	G2060	G2061	G2062	G2063	G2064	G2067	G2068	A2069	U2070	A2071	G2072	G2073	G2074	G2075	G2076	G2077	G2078	G2079	G2080	G2081	G2082	G2083	G2084	G2085	G2086	G2087	G2088	G2089	U2090	G2091	G2092	A2093	G2094																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
A2095	U2304	G2096	U2097	G2098	G2099	G2100	G2101	G2102	G2103	G2104	G2105	G2106	G2107	G2108	G2109	G2110	G2111	G2112	G2113	G2114	G2115	G2116	G2117	G2118	G2119	G2120	G2121	G2122	G2123	G2124	G2125	G2126	G2127	G2128	G2129	G2130	G2131	G2132	G2133	G2134	G2135	G2136	G2137	G2138	G2139	G2140	G2141	G2142	G2143	G2144	G2145	G2146	G2147	G2148	G2149	G2150	G2151	G2152	G2153	G2154	G2155	G2156	G2157	G2158	G2159	G2160	G2161	G2162	G2163	G2164	G2165	G2166	G2167	G2168	G2169	G2170	G2171	G2172	G2173	G2174	G2175	G2176	G2177	G2178	G2179	G2180	G2181	G2182	G2183	G2184	G2185	G2186	G2187	G2188	G2189	G2190	G2191	G2192	G2193	G2194	G2195	G2196	G2197	G2198	G2199	G2200	G2201	G2202	G2203	G2204	G2205	G2206	G2207	G2208	G2209	G2210	G2211	G2212	G2213	G2214	G2215	G2216	G2217	G2218	G2219	G2220	G2221	G2222	G2223	G2224	G2225	G2226	G2227	G2228	G2229	G2230	G2231	G2232	G2233	G2234	G2235	G2236	G2237	G2238	G2239	G2240	G2241	G2242	G2243	G2244	G2245	G2246	G2247	G2248	G2249	G2250	G2251	G2252	G2253	G2254	G2255	G2256	G2257	G2258	G2259	G2260	G2261	G2262	G2263	G2264	G2265	G2266	G2267	G2268	G2269	G2270	G2271	G2272	G2273	G2274	G2275	G2276	G2277	G2278	G2279	G2280	G2281	G2282	G2283	G2284	G2285	G2286	G2287	G2288	G2289	G2290	G2291	G2292	G2293	G2294	G2295	G2296	G2297	G2298	G2299	G2300	G2301	G2302	G2303	G2304	G2305	G2306	G2307	G2308	G2309	G2310	G2311	G2312	G2313	G2314	G2315	G2316	G2317	G2318	G2319	G2320	G2321	G2322	G2323	G2324	G2325	G2326	G2327	G2328	G2329	G2330	G2331	G2332	G2333	G2334	G2335	G2336	G2337	G2338	G2339	G2340	G2341	G2342	G2343	G2344	G2345	G2346	G2347	G2348	G2349	G2350	G2351	G2352	G2353	G2354	G2355	G2356	G2357	G2358	G2359	G2360	G2361	G2362	G2363	G2364	G2365	G2366	G2367	G2368	G2369	G2370	G2371	G2372	G2373	G2374	G2375	G2376	G2377	G2378	G2379	G2380	G2381	G2382	G2383	G2384	G2385	G2386	G2387	G2388	G2389	G2390	G2391	G2392	G2393	G2394	G2395	G2396	G2397	G2398	G2399	G2400	G2401	G2402	G2403	G2404	G2405	G2406	G2407	G2408	G2409	G2410	G2411	G2412	G2413	G2414	G2415	G2416	G2417	G2418	G2419	G2420	G2421	G2422	G2423	G2424	G2425	G2426	G2427	G2428	G2429	G2430	G2431	G2432	G2433	G2434	G2435	G2436	G2437	G2438	G2439	G2440	G2441	G2442	G2443	G2444	G2445	G2446	G2447	G2448	G2449	G2450	G2451	G2452	G2453	G2454	G2455	G2456	G2457	G2458	G2459	G2460	G2461	G2462	G2463	G2464	G2465	G2466	G2467	G2468	G2469	G2470	G2471	G2472	G2473	G2474	G2475	G2476	G2477	G2478	G2479	G2480	G2481	G2482	G2483	G2484	G2485	G2486	G2487	G2488	G2489	G2490	G2491	G2492	G2493	G2494	G2495	G2496	G2497	G2498	G2499	G2500	G2501	G2502	G2503	G2504	G2505	G2506	G2507	G2508	G2509	G2510	G2511	G2512	G2513	G2514	G2515	G2516	G2517	G2518	G2519	G2520	G2521	G2522	G2523	G2524	G2525	G2526	G2527	G2528	G2529	G2530	G2531	G2532	G2533	G2534	G2535	G2536	G2537	G2538	G2539	G2540	G2541	G2542	G2543	G2544	G2545	G2546	G2547	G2548	G2549	G2550	G2551	G2552	G2553	G2554	G2555	G2556	G2557	G2558	G2559	G2560	G2561	G2562	G2563	G2564	G2565	G2566	G2567	G2568	G2569	G2570	G2571	G2572	G2573	G2574	G2575	G2576	G2577	G2578	G2579	G2580	G2581	G2582	G2583	G2584	G2585	G2586	G2587	G2588	G2589	G2590	G2591	G2592	G2593	G2594	G2595	G2596	G2597	G2598	G2599	G2600	G2601	G2602	G2603	G2604	G2605	G2606	G2607	G2608	G2609	G2610	G2611	G2612	G2613	G2614	G2615	G2616	G2617	G2618	G2619	G2620	G2621	G2622	G2623	G2624	G2625	G2626	G2627	G2628	G2629	G2630	G2631	G2632	G2633	G2634	G2635	G2636	G2637	G2638	G2639	G2640	G2641	G2642	G2643	G2644	G2645	G2646	G2647	G2648	G2649	G2650	G2651	G2652	G2653	G2654	G2655	G2656	G2657	G2658	G2659	G2660	G2661	G2662	G2663	G2664	G2665	G2666	G2667	G2668	G2669	G2670	G2671	G2672	G2673	G2674	G2675	G2676	G2677	G2678	G2679	G2680	G2681	G2682	G2683	G2684	G2685	G2686	G2687	G2688	G2689	G2690	G2691	G2692	G2693	G2694	G2695	G2696	G2697	G2698	G2699	G2700	G2701	G2702	G2703	G2704	G2705	G2706	G2707	G2708	G2709	G2710	G2711	G2712	G2713	G2714	G2715	G2716	G2717	G2718	G2719	G2720	G2721	G2722	G2723	G2724	G2725	G2726	G2727	G2728	G2729	G2730	G2731	G2732	G2733	G2734	G2735	G2736	G2737	G2738	G2739	G2740	G2741	G2742	G2743	G2744	G2745	G2746	G2747	G2748	G2749	G2750	G2751	G2752	G2753	G2754	G2755	G2756	G2757	G2758	G2759	G2760	G2761	G2762	G2763	G2764	G2765	G2766	G2767	G2768	G2769	G2770	G2771	G2772	G2773	G2774	G2775	G2776	G2777	G2778	G2779	G2780	G2781	G2782	G2783	G2784	G2785	G2786	G2787	G2788	G2789	G2790	G2791	G2792	G2793	G2794	G2795	G2796	G2797	G2798	G2799	G2800	G2801	G2802	G2803	G2804	G2805	G2806	G2807	G2808	G2809	G2810	G2811	G2812	G2813	G2814	G2815	G2816	G2817	G2818	G2819	G2820	G2821	G2822	G2823	G2824	G2825	G2826	G2827	G2828	G2829	G2830	G2831	G2832	G2833	G2834	G2835	G2836	G2837	G2838	G2839	G2840	G2841	G2842	G2843	G2844	G2845	G2846	G2847	G2848	G2849	G2850	G2851	G2852	G2853	G2854	G2855	G2856	G2857	G2858	G2859	G2860	G2861	G2862	G2863	G2864	G2865	G2866	G2867	G2868	G2869	G2870	G2871	G2872	G2873



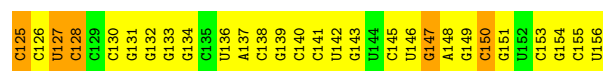
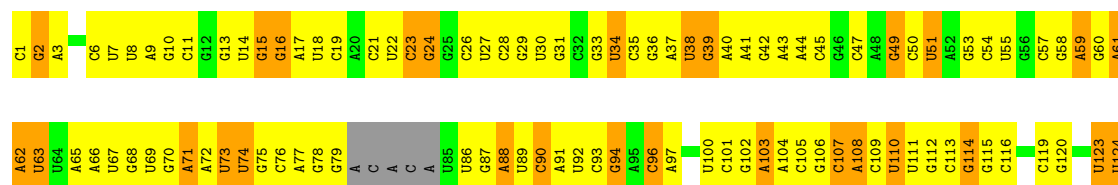


• Molecule 80: 5S rRNA

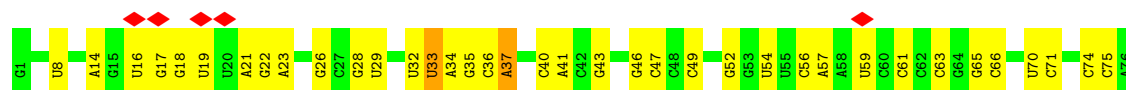


• Molecule 81: 5.8S rRNA

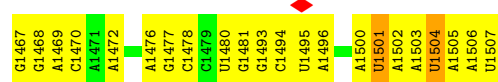
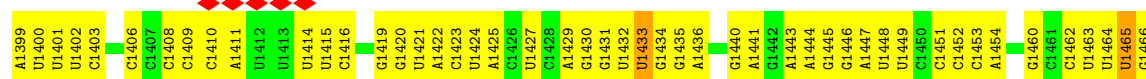
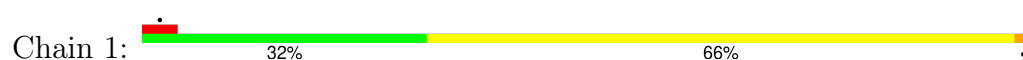




• Molecule 82: Ala-tRNA



• Molecule 83: NediV IRES



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	23922	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	64	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.293	Depositor
Minimum map value	-0.912	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.079	Depositor
Recommended contour level	0.193	Depositor
Map size (\AA)	849.92, 849.92, 849.92	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.66, 1.66, 1.66	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	R	0.10	0/1524	0.26	0/2013
2	W	0.12	0/873	0.35	0/1158
3	9	0.12	0/40500	0.26	0/63092
4	AA	0.09	0/1747	0.25	0/2374
5	BB	0.08	0/1756	0.24	0/2350
6	CC	0.09	0/1753	0.27	0/2369
7	EE	0.09	0/2118	0.28	0/2849
8	GG	0.07	0/1946	0.22	0/2590
9	HH	0.09	0/1510	0.23	0/2022
10	II	0.10	0/1715	0.28	0/2287
11	JJ	0.10	0/1550	0.27	0/2069
12	LL	0.09	0/1195	0.27	0/1597
13	NN	0.08	0/1226	0.23	0/1649
14	OO	0.09	0/1029	0.24	0/1380
15	VV	0.09	0/643	0.25	0/860
16	WW	0.09	0/1051	0.25	0/1406
17	XX	0.14	0/1116	0.38	0/1490
18	YY	0.08	0/1028	0.26	0/1366
19	aa	0.09	0/828	0.28	0/1109
20	bb	0.11	0/665	0.26	0/891
21	ee	0.09	0/462	0.25	0/607
22	DD	0.11	0/1796	0.31	0/2417
23	FF	0.11	0/1492	0.31	0/2005
24	KK	0.08	0/834	0.24	0/1125
25	MM	0.11	0/918	0.30	0/1233
26	PP	0.09	0/1079	0.25	0/1441
27	QQ	0.10	0/1146	0.26	0/1534
28	RR	0.08	0/1082	0.23	0/1452
29	SS	0.12	0/1208	0.34	0/1618
30	TT	0.09	0/1115	0.25	0/1493
31	UU	0.08	0/805	0.25	0/1081
32	ZZ	0.18	0/604	0.65	0/810

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	cc	0.08	0/490	0.24	0/656
34	dd	0.09	0/470	0.29	0/623
35	ff	0.08	0/567	0.23	0/753
36	gg	0.09	0/2493	0.27	0/3394
37	A	0.11	0/1936	0.31	0/2596
38	B	0.11	0/3240	0.31	0/4339
39	C	0.11	0/2937	0.30	0/3946
40	D	0.11	0/2437	0.29	0/3264
41	E	0.10	0/1762	0.29	0/2362
42	F	0.13	0/1911	0.35	0/2549
43	G	0.11	0/1910	0.26	0/2569
44	H	0.12	0/1535	0.32	0/2063
45	I	0.11	0/1702	0.28	0/2272
46	J	0.10	0/1385	0.29	0/1852
47	L	0.11	0/1733	0.29	0/2316
48	M	0.11	0/1158	0.29	0/1547
49	N	0.11	0/1746	0.29	0/2338
50	O	0.13	0/1662	0.32	0/2222
51	P	0.11	0/1268	0.31	0/1700
52	Q	0.10	0/1539	0.30	0/2054
53	S	0.11	0/1501	0.29	0/2012
54	T	0.11	0/1326	0.30	0/1770
55	U	0.13	0/823	0.35	0/1104
56	V	0.11	0/1048	0.28	0/1402
57	X	0.11	0/984	0.28	0/1323
58	Y	0.11	0/1132	0.27	0/1504
59	Z	0.10	0/1130	0.27	0/1507
60	a	0.10	0/1191	0.28	0/1590
61	b	0.09	0/861	0.25	0/1138
62	c	0.12	0/771	0.30	0/1034
63	d	0.12	0/903	0.30	0/1216
64	e	0.11	0/1071	0.32	0/1429
65	f	0.11	0/895	0.35	0/1198
66	g	0.10	0/916	0.26	0/1220
67	h	0.11	0/1021	0.27	0/1348
68	i	0.11	0/841	0.29	0/1112
69	j	0.11	0/720	0.32	0/952
70	k	0.12	0/575	0.30	0/761
71	l	0.10	0/459	0.30	0/608
72	m	0.12	0/435	0.34	0/575
73	n	0.14	0/240	0.28	0/305
74	o	0.10	0/864	0.26	0/1140
75	p	0.11	0/718	0.30	0/953

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	r	0.12	0/1010	0.35	0/1354
77	s	0.20	0/707	0.55	0/947
78	t	0.15	0/1003	0.41	0/1354
79	5	0.13	7/84949 (0.0%)	0.27	0/132467
80	7	0.11	0/2836	0.23	0/4421
81	8	0.11	0/3581	0.26	0/5577
82	AT	0.27	1/1810 (0.1%)	0.48	0/2820
83	1	0.27	0/3936	0.57	2/6125 (0.0%)
All	All	0.12	8/232452 (0.0%)	0.29	2/341418 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
17	XX	0	1
38	B	0	1
65	f	0	1
All	All	0	3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
79	5	904	G	C1'-N9	-6.66	1.38	1.48
82	AT	32	U	C1'-N1	6.38	1.58	1.48
79	5	2097	U	C1'-N1	6.36	1.56	1.47
79	5	4876	U	C1'-N1	5.96	1.56	1.47
79	5	2107	C	C1'-N1	5.92	1.57	1.48

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	1	1433	U	P-O3'-C3'	6.01	129.21	120.20
83	1	1433	U	C4'-C3'-O3'	5.60	117.80	109.40

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
38	B	258	HIS	Peptide

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Mol	Chain	Res	Type	Group
17	XX	61	GLN	Peptide
65	f	106	TYR	Peptide

5.2 Too-close contacts [i](#)

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	R	1508	0	1664	110	0
2	W	860	0	903	51	0
3	9	36229	0	18308	1270	0
4	AA	1710	0	1708	142	0
5	BB	1729	0	1803	160	0
6	CC	1716	0	1806	137	0
7	EE	2076	0	2177	179	0
8	GG	1923	0	2089	145	0
9	HH	1488	0	1582	108	0
10	II	1686	0	1772	115	0
11	JJ	1525	0	1640	140	0
12	LL	1175	0	1249	89	0
13	NN	1202	0	1289	82	0
14	OO	1016	0	1039	109	0
15	VV	636	0	637	58	0
16	WW	1034	0	1080	95	0
17	XX	1098	0	1167	93	0
18	YY	1011	0	1083	77	0
19	aa	814	0	863	71	0
20	bb	651	0	672	31	0
21	ee	457	0	502	41	0
22	DD	1768	0	1866	128	0
23	FF	1471	0	1522	123	0
24	KK	810	0	836	58	0
25	MM	908	0	939	78	0
26	PP	1058	0	1104	89	0
27	QQ	1128	0	1195	105	0
28	RR	1068	0	1121	91	0
29	SS	1190	0	1249	125	0
30	TT	1097	0	1132	98	0
31	UU	795	0	862	67	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	ZZ	598	0	656	79	0
33	cc	488	0	514	52	0
34	dd	459	0	448	32	0
35	ff	555	0	564	44	0
36	gg	2436	0	2393	170	0
37	A	1898	0	1993	199	0
38	B	3172	0	3310	258	0
39	C	2883	0	3053	256	0
40	D	2391	0	2424	161	0
41	E	1729	0	1887	132	0
42	F	1875	0	1995	183	0
43	G	1879	0	2027	151	0
44	H	1516	0	1597	133	0
45	I	1664	0	1712	139	0
46	J	1362	0	1399	100	0
47	L	1702	0	1820	116	0
48	M	1137	0	1211	117	0
49	N	1701	0	1749	161	0
50	O	1630	0	1778	138	0
51	P	1242	0	1274	85	0
52	Q	1515	0	1634	144	0
53	S	1462	0	1508	115	0
54	T	1298	0	1366	116	0
55	U	809	0	833	65	0
56	V	1034	0	1097	97	0
57	X	967	0	1040	75	0
58	Y	1115	0	1205	88	0
59	Z	1107	0	1182	76	0
60	a	1162	0	1209	97	0
61	b	848	0	920	61	0
62	c	761	0	794	72	0
63	d	888	0	930	74	0
64	e	1053	0	1147	79	0
65	f	876	0	912	66	0
66	g	906	0	998	69	0
67	h	1013	0	1147	96	0
68	i	830	0	916	44	0
69	j	705	0	737	52	0
70	k	569	0	637	52	0
71	l	447	0	480	28	0
72	m	429	0	465	25	0
73	n	239	0	289	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
74	o	851	0	920	67	0
75	p	708	0	756	66	0
76	r	994	0	1051	70	0
77	s	695	0	727	56	0
78	t	993	0	1034	99	0
79	5	75955	0	38377	2542	0
80	7	2538	0	1286	80	0
81	8	3208	0	1629	151	0
82	AT	1621	792	823	6	0
83	1	3523	1782	1783	5	0
84	5	184	0	0	0	0
84	7	6	0	0	0	0
84	8	5	0	0	0	0
84	9	1	0	0	0	0
84	I	1	0	0	0	0
84	L	1	0	0	0	0
84	P	1	0	0	0	0
84	V	1	0	0	0	0
84	X	1	0	0	0	0
84	a	2	0	0	0	0
84	e	1	0	0	0	0
84	g	1	0	0	0	0
84	j	1	0	0	0	0
85	aa	1	0	0	0	0
85	dd	1	0	0	0	0
85	ff	1	0	0	0	0
85	g	1	0	0	0	0
85	j	1	0	0	0	0
85	m	1	0	0	0	0
85	o	1	0	0	0	0
85	p	1	0	0	0	0
All	All	216487	2574	160495	9922	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 26.

The worst 5 of 9922 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)
79:5:759:G:O6	79:5:904:G:O6	1.66	1.13
79:5:169:G:N2	79:5:267:G:C6	2.28	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:XX:46:HIS:HB3	17:XX:101:LEU:HD11	1.43	1.00
79:5:2845:A:H61	79:5:3843:C:H42	0.99	0.98
79:5:1750:G:H1	79:5:1780:A:H61	0.98	0.97

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	R	178/180 (99%)	174 (98%)	4 (2%)	0	100	100
2	W	102/106 (96%)	98 (96%)	4 (4%)	0	100	100
4	AA	215/217 (99%)	210 (98%)	5 (2%)	0	100	100
5	BB	211/213 (99%)	201 (95%)	10 (5%)	0	100	100
6	CC	219/221 (99%)	217 (99%)	2 (1%)	0	100	100
7	EE	260/262 (99%)	252 (97%)	8 (3%)	0	100	100
8	GG	235/237 (99%)	230 (98%)	5 (2%)	0	100	100
9	HH	181/189 (96%)	178 (98%)	3 (2%)	0	100	100
10	II	204/206 (99%)	194 (95%)	10 (5%)	0	100	100
11	JJ	183/185 (99%)	182 (100%)	1 (0%)	0	100	100
12	LL	139/151 (92%)	138 (99%)	1 (1%)	0	100	100
13	NN	147/149 (99%)	146 (99%)	1 (1%)	0	100	100
14	OO	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
15	VV	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
16	WW	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
17	XX	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	18	55
18	YY	122/124 (98%)	120 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	aa	99/101 (98%)	95 (96%)	4 (4%)	0	100	100
20	bb	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
21	ee	55/57 (96%)	53 (96%)	2 (4%)	0	100	100
22	DD	226/228 (99%)	222 (98%)	4 (2%)	0	100	100
23	FF	181/191 (95%)	177 (98%)	4 (2%)	0	100	100
24	KK	94/96 (98%)	93 (99%)	1 (1%)	0	100	100
25	MM	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
26	PP	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
27	QQ	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
28	RR	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
29	SS	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
30	TT	139/141 (99%)	136 (98%)	3 (2%)	0	100	100
31	UU	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
32	ZZ	73/75 (97%)	64 (88%)	9 (12%)	0	100	100
33	cc	60/62 (97%)	60 (100%)	0	0	100	100
34	dd	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
35	ff	66/68 (97%)	64 (97%)	2 (3%)	0	100	100
36	gg	311/313 (99%)	300 (96%)	11 (4%)	0	100	100
37	A	246/248 (99%)	235 (96%)	11 (4%)	0	100	100
38	B	392/394 (100%)	381 (97%)	11 (3%)	0	100	100
39	C	360/362 (99%)	349 (97%)	11 (3%)	0	100	100
40	D	291/293 (99%)	283 (97%)	7 (2%)	1 (0%)	36	70
41	E	208/216 (96%)	201 (97%)	7 (3%)	0	100	100
42	F	223/225 (99%)	216 (97%)	7 (3%)	0	100	100
43	G	229/240 (95%)	225 (98%)	4 (2%)	0	100	100
44	H	188/190 (99%)	182 (97%)	6 (3%)	0	100	100
45	I	201/213 (94%)	194 (96%)	7 (4%)	0	100	100
46	J	168/170 (99%)	166 (99%)	2 (1%)	0	100	100
47	L	208/210 (99%)	203 (98%)	5 (2%)	0	100	100
48	M	136/138 (99%)	131 (96%)	5 (4%)	0	100	100
49	N	201/203 (99%)	197 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	O	197/199 (99%)	190 (96%)	7 (4%)	0	100	100
51	P	151/153 (99%)	148 (98%)	3 (2%)	0	100	100
52	Q	185/187 (99%)	177 (96%)	8 (4%)	0	100	100
53	S	174/176 (99%)	165 (95%)	9 (5%)	0	100	100
54	T	157/159 (99%)	151 (96%)	6 (4%)	0	100	100
55	U	97/99 (98%)	97 (100%)	0	0	100	100
56	V	137/139 (99%)	133 (97%)	4 (3%)	0	100	100
57	X	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
58	Y	132/134 (98%)	130 (98%)	2 (2%)	0	100	100
59	Z	133/135 (98%)	125 (94%)	8 (6%)	0	100	100
60	a	145/147 (99%)	142 (98%)	3 (2%)	0	100	100
61	b	100/104 (96%)	98 (98%)	2 (2%)	0	100	100
62	c	96/98 (98%)	95 (99%)	1 (1%)	0	100	100
63	d	105/107 (98%)	97 (92%)	8 (8%)	0	100	100
64	e	126/128 (98%)	120 (95%)	6 (5%)	0	100	100
65	f	107/109 (98%)	101 (94%)	6 (6%)	0	100	100
66	g	112/114 (98%)	112 (100%)	0	0	100	100
67	h	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
68	i	100/102 (98%)	97 (97%)	3 (3%)	0	100	100
69	j	84/86 (98%)	78 (93%)	6 (7%)	0	100	100
70	k	67/69 (97%)	67 (100%)	0	0	100	100
71	l	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
72	m	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
73	n	23/25 (92%)	23 (100%)	0	0	100	100
74	o	102/104 (98%)	99 (97%)	3 (3%)	0	100	100
75	p	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
76	r	122/124 (98%)	119 (98%)	3 (2%)	0	100	100
77	s	85/87 (98%)	76 (89%)	9 (11%)	0	100	100
78	t	129/133 (97%)	117 (91%)	11 (8%)	1 (1%)	16	52
All	All	11407/11616 (98%)	11055 (97%)	349 (3%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	XX	62	PRO
78	t	160	VAL
40	D	125	VAL

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	R	159/159 (100%)	153 (96%)	6 (4%)	29	51
2	W	86/86 (100%)	83 (96%)	3 (4%)	32	54
4	AA	180/181 (99%)	171 (95%)	9 (5%)	22	45
5	BB	194/194 (100%)	189 (97%)	5 (3%)	40	61
6	CC	187/187 (100%)	184 (98%)	3 (2%)	55	69
7	EE	224/224 (100%)	217 (97%)	7 (3%)	35	56
8	GG	207/207 (100%)	202 (98%)	5 (2%)	43	63
9	HH	165/169 (98%)	160 (97%)	5 (3%)	36	57
10	II	178/178 (100%)	168 (94%)	10 (6%)	19	43
11	JJ	161/161 (100%)	155 (96%)	6 (4%)	30	52
12	LL	130/136 (96%)	122 (94%)	8 (6%)	16	41
13	NN	130/130 (100%)	127 (98%)	3 (2%)	44	64
14	OO	106/106 (100%)	103 (97%)	3 (3%)	38	59
15	VV	67/67 (100%)	63 (94%)	4 (6%)	17	42
16	WW	112/112 (100%)	108 (96%)	4 (4%)	31	53
17	XX	113/113 (100%)	107 (95%)	6 (5%)	20	44
18	YY	107/107 (100%)	101 (94%)	6 (6%)	19	43
19	aa	88/88 (100%)	86 (98%)	2 (2%)	44	64
20	bb	75/75 (100%)	73 (97%)	2 (3%)	39	60
21	ee	47/47 (100%)	47 (100%)	0	100	100
22	DD	190/190 (100%)	184 (97%)	6 (3%)	34	56
23	FF	158/161 (98%)	152 (96%)	6 (4%)	29	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	KK	87/87 (100%)	86 (99%)	1 (1%)	65	74
25	MM	99/99 (100%)	94 (95%)	5 (5%)	21	45
26	PP	115/115 (100%)	113 (98%)	2 (2%)	53	68
27	QQ	117/117 (100%)	113 (97%)	4 (3%)	32	55
28	RR	119/119 (100%)	117 (98%)	2 (2%)	53	68
29	SS	125/125 (100%)	117 (94%)	8 (6%)	16	40
30	TT	111/111 (100%)	109 (98%)	2 (2%)	51	67
31	UU	92/92 (100%)	89 (97%)	3 (3%)	33	55
32	ZZ	66/66 (100%)	48 (73%)	18 (27%)	0	3
33	cc	55/55 (100%)	55 (100%)	0	100	100
34	dd	48/48 (100%)	46 (96%)	2 (4%)	26	49
35	ff	61/61 (100%)	60 (98%)	1 (2%)	55	69
36	gg	272/272 (100%)	269 (99%)	3 (1%)	65	74
37	A	190/190 (100%)	168 (88%)	22 (12%)	5	21
38	B	342/342 (100%)	327 (96%)	15 (4%)	25	48
39	C	302/302 (100%)	284 (94%)	18 (6%)	17	42
40	D	247/247 (100%)	240 (97%)	7 (3%)	38	59
41	E	190/190 (100%)	182 (96%)	8 (4%)	26	49
42	F	196/196 (100%)	186 (95%)	10 (5%)	21	45
43	G	200/205 (98%)	190 (95%)	10 (5%)	22	45
44	H	169/169 (100%)	157 (93%)	12 (7%)	13	37
45	I	175/180 (97%)	165 (94%)	10 (6%)	18	43
46	J	143/143 (100%)	135 (94%)	8 (6%)	19	43
47	L	175/175 (100%)	167 (95%)	8 (5%)	24	47
48	M	117/117 (100%)	107 (92%)	10 (8%)	10	32
49	N	171/171 (100%)	157 (92%)	14 (8%)	10	33
50	O	171/171 (100%)	159 (93%)	12 (7%)	14	38
51	P	134/134 (100%)	127 (95%)	7 (5%)	21	45
52	Q	164/164 (100%)	150 (92%)	14 (8%)	10	32
53	S	157/157 (100%)	144 (92%)	13 (8%)	10	32
54	T	139/139 (100%)	131 (94%)	8 (6%)	18	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	U	89/89 (100%)	86 (97%)	3 (3%)	32	55
56	V	106/106 (100%)	101 (95%)	5 (5%)	23	47
57	X	106/106 (100%)	98 (92%)	8 (8%)	12	35
58	Y	124/124 (100%)	121 (98%)	3 (2%)	43	63
59	Z	117/117 (100%)	114 (97%)	3 (3%)	40	61
60	a	119/119 (100%)	113 (95%)	6 (5%)	22	45
61	b	84/84 (100%)	78 (93%)	6 (7%)	13	37
62	c	84/84 (100%)	81 (96%)	3 (4%)	31	53
63	d	98/98 (100%)	93 (95%)	5 (5%)	21	45
64	e	114/114 (100%)	107 (94%)	7 (6%)	17	41
65	f	88/88 (100%)	85 (97%)	3 (3%)	32	55
66	g	98/98 (100%)	90 (92%)	8 (8%)	10	33
67	h	109/109 (100%)	100 (92%)	9 (8%)	10	32
68	i	86/86 (100%)	80 (93%)	6 (7%)	14	38
69	j	73/73 (100%)	70 (96%)	3 (4%)	27	50
70	k	64/64 (100%)	62 (97%)	2 (3%)	35	56
71	l	47/47 (100%)	45 (96%)	2 (4%)	26	49
72	m	48/48 (100%)	45 (94%)	3 (6%)	16	40
73	n	24/24 (100%)	22 (92%)	2 (8%)	10	32
74	o	92/92 (100%)	90 (98%)	2 (2%)	45	64
75	p	74/74 (100%)	68 (92%)	6 (8%)	11	33
76	r	108/108 (100%)	102 (94%)	6 (6%)	19	43
77	s	75/75 (100%)	63 (84%)	12 (16%)	2	14
78	t	107/107 (100%)	97 (91%)	10 (9%)	8	28
All	All	9947/9971 (100%)	9458 (95%)	489 (5%)	24	46

5 of 489 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	F	51	GLU
69	j	66	HIS
47	L	194	ILE
68	i	63	VAL
77	s	44	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 127 such sidechains are listed below:

Mol	Chain	Res	Type
37	A	95	GLN
65	f	78	HIS
41	E	194	GLN
65	f	56	ASN
71	l	17	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	9	1683/1773 (94%)	370 (21%)	20 (1%)
79	5	3518/3543 (99%)	852 (24%)	59 (1%)
80	7	118/119 (99%)	17 (14%)	0
81	8	149/156 (95%)	41 (27%)	1 (0%)
82	AT	75/76 (98%)	34 (45%)	1 (1%)
83	1	165/166 (99%)	111 (67%)	7 (4%)
All	All	5708/5833 (97%)	1425 (24%)	88 (1%)

5 of 1425 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	9	2	A
3	9	3	C
3	9	4	C
3	9	25	A
3	9	33	G

5 of 88 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
79	5	2089	G
79	5	4542	U
79	5	2474	G
79	5	3625	G
79	5	4925	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 214 ligands modelled in this entry, 214 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
79	5	30
3	9	20
41	E	3
2	W	1
61	b	1
83	1	1
78	t	1

The worst 5 of 57 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	42.79
1	W	63:GLN	C	79:GLN	N	40.82
1	b	76:VAL	C	89:VAL	N	37.15
1	5	1252:C	O3'	1271:G	P	36.89
1	E	77:ALA	C	92:LEU	N	29.57

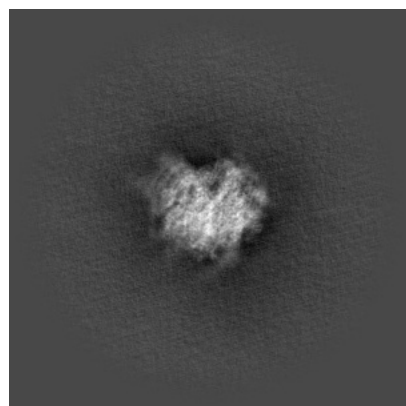
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72170. These allow visual inspection of the internal detail of the map and identification of artifacts.

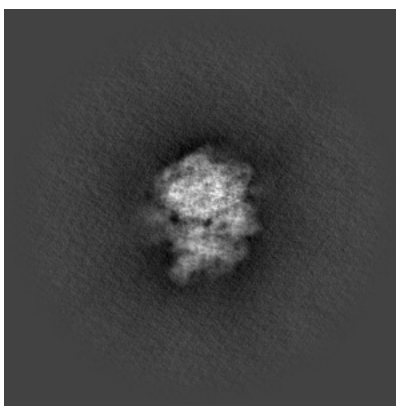
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

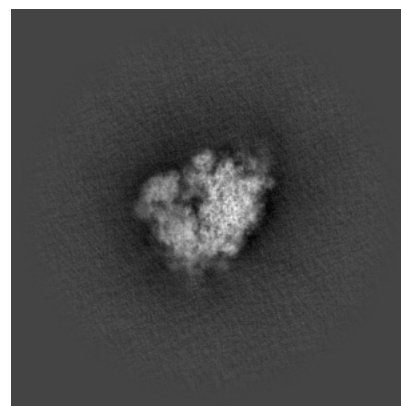
6.1.1 Primary map



X

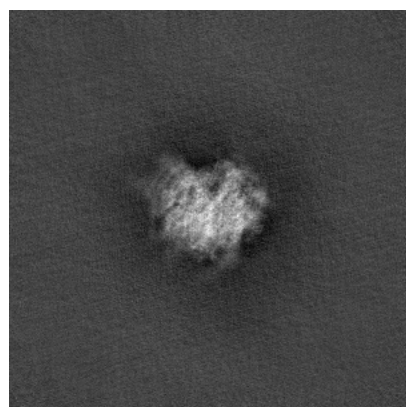


Y

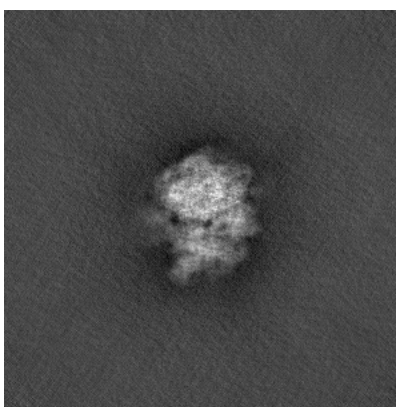


Z

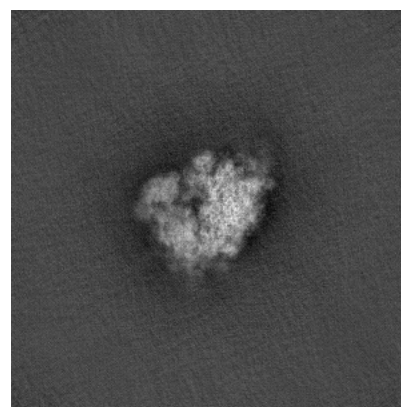
6.1.2 Raw map



X



Y

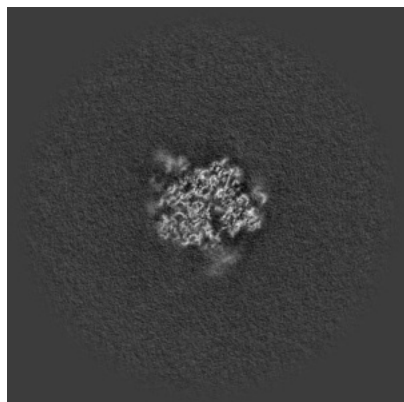


Z

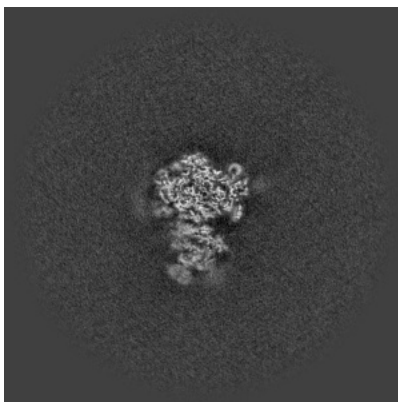
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

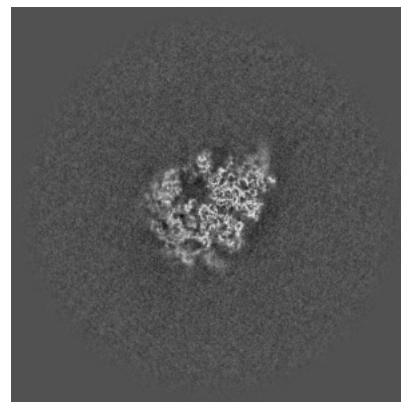
6.2.1 Primary map



X Index: 256

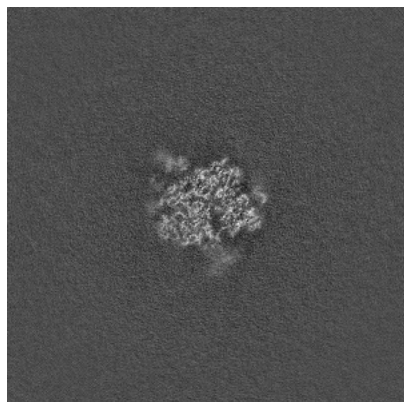


Y Index: 256

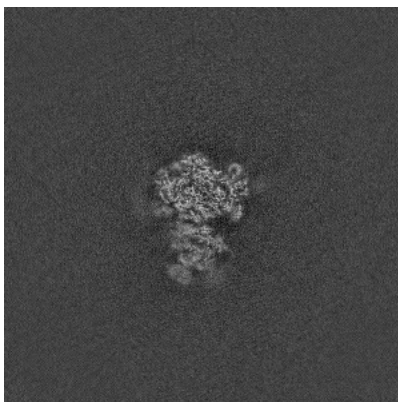


Z Index: 256

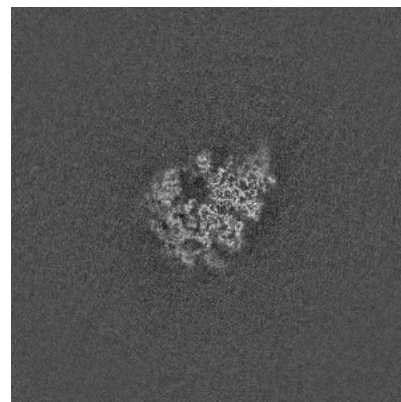
6.2.2 Raw map



X Index: 256



Y Index: 256

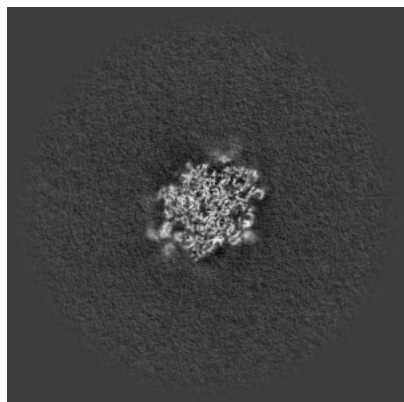


Z Index: 256

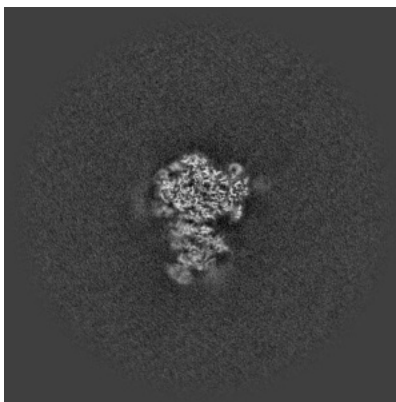
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

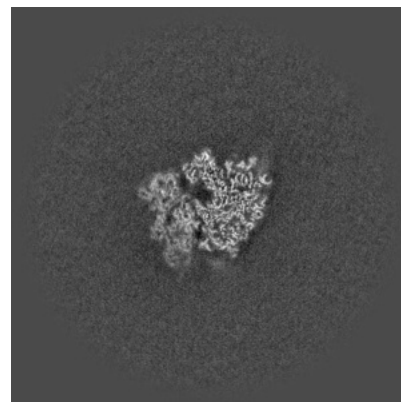
6.3.1 Primary map



X Index: 275

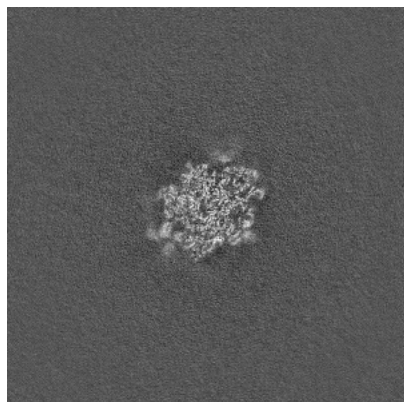


Y Index: 255

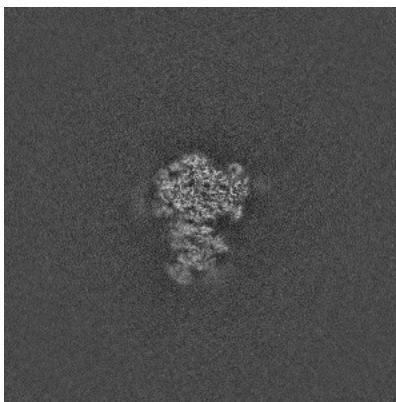


Z Index: 246

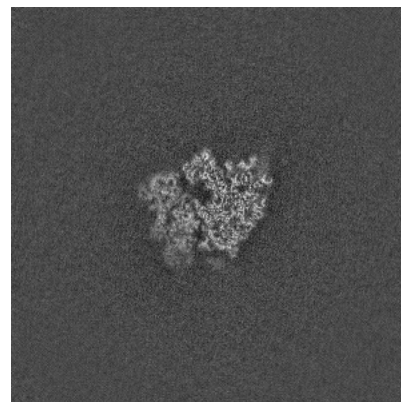
6.3.2 Raw map



X Index: 275



Y Index: 255

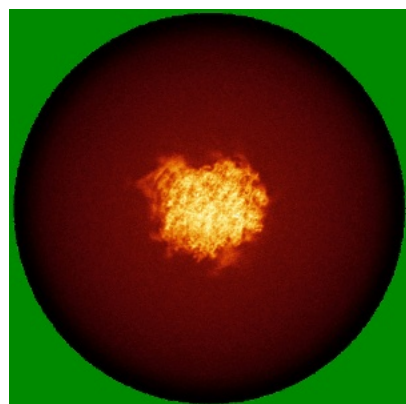


Z Index: 247

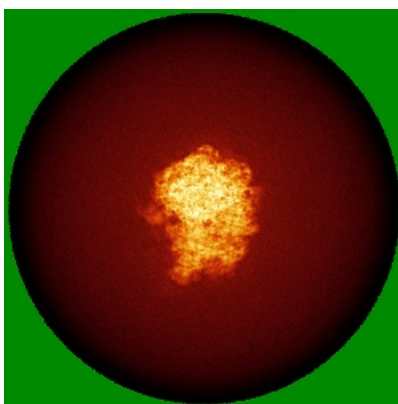
The images above show the largest variance slices of the map in three orthogonal directions.

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

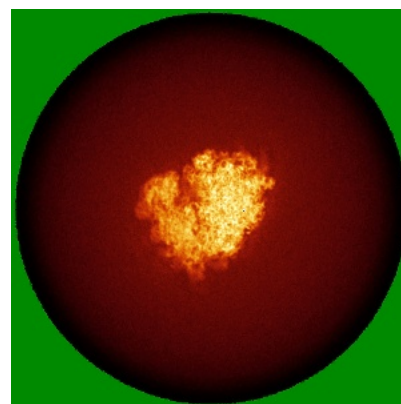
6.4.1 Primary map



X

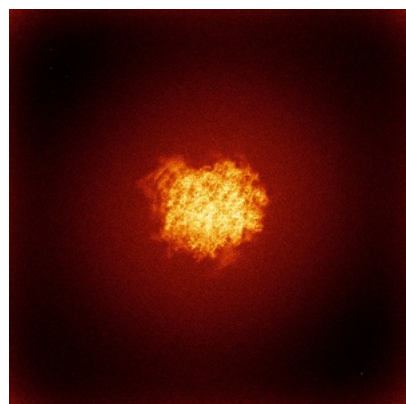


Y

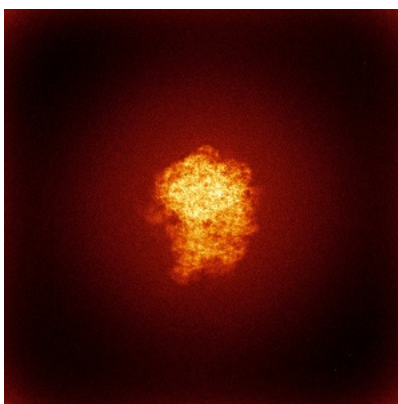


Z

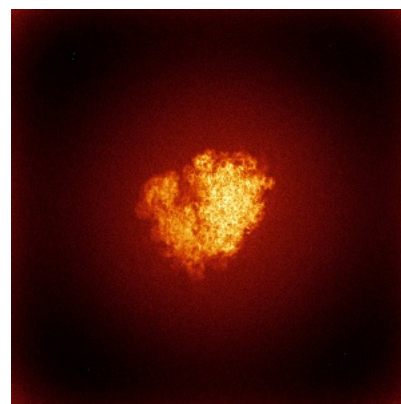
6.4.2 Raw map



X



Y

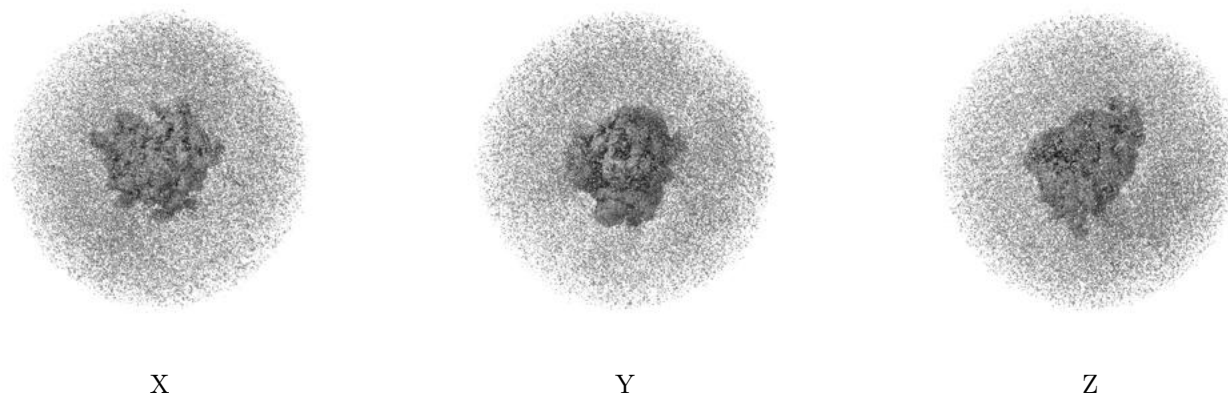


Z

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

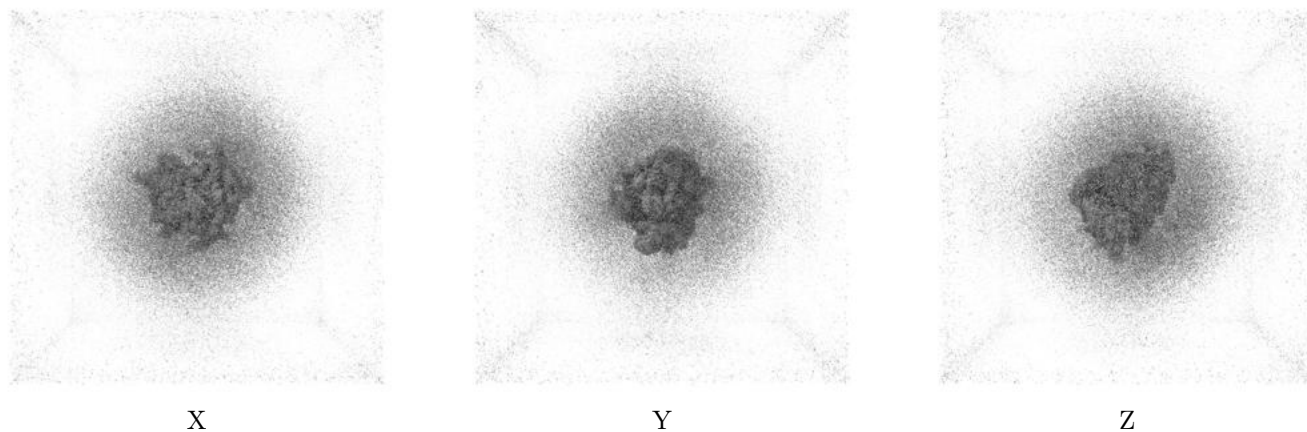
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.193. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

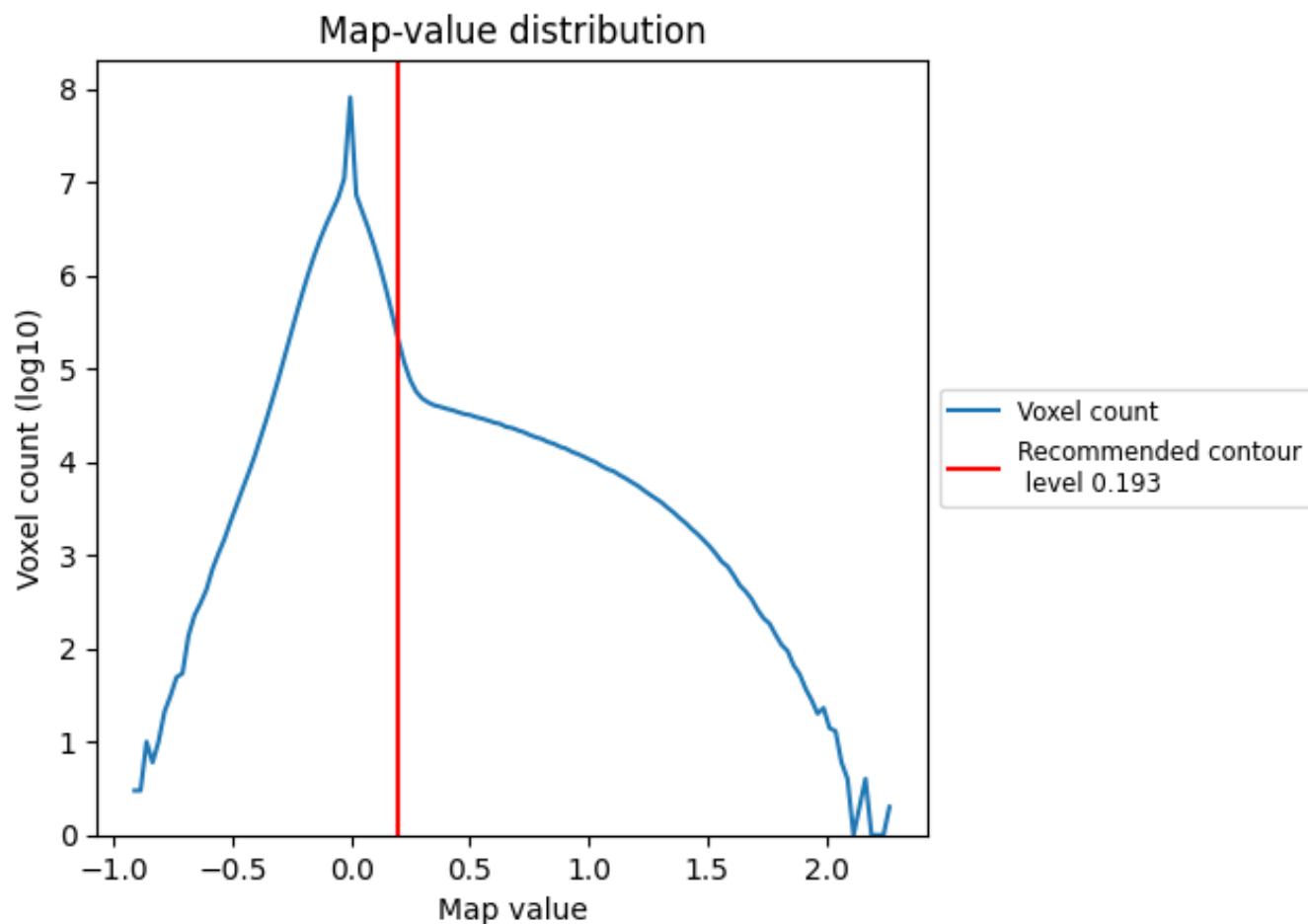
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

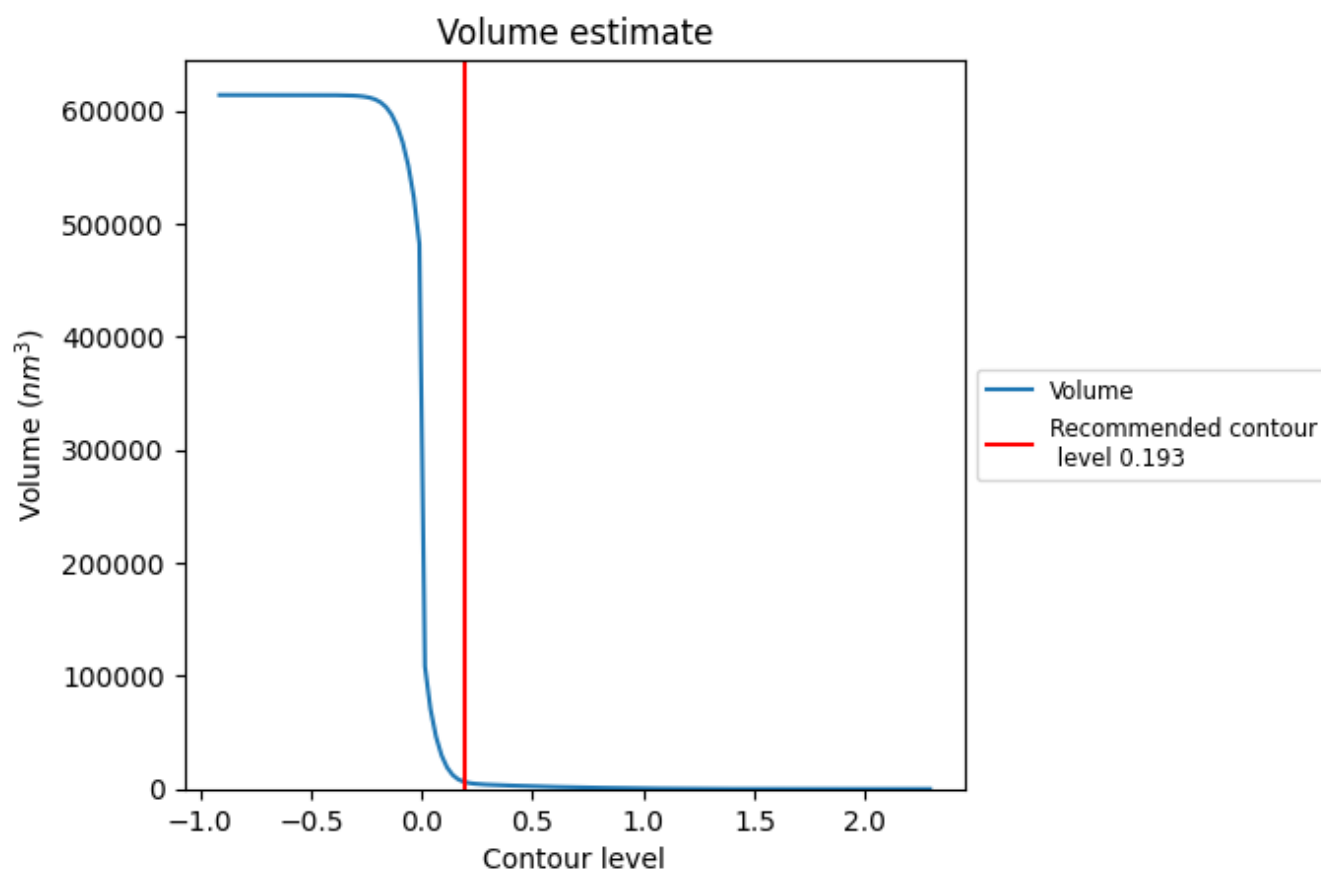
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

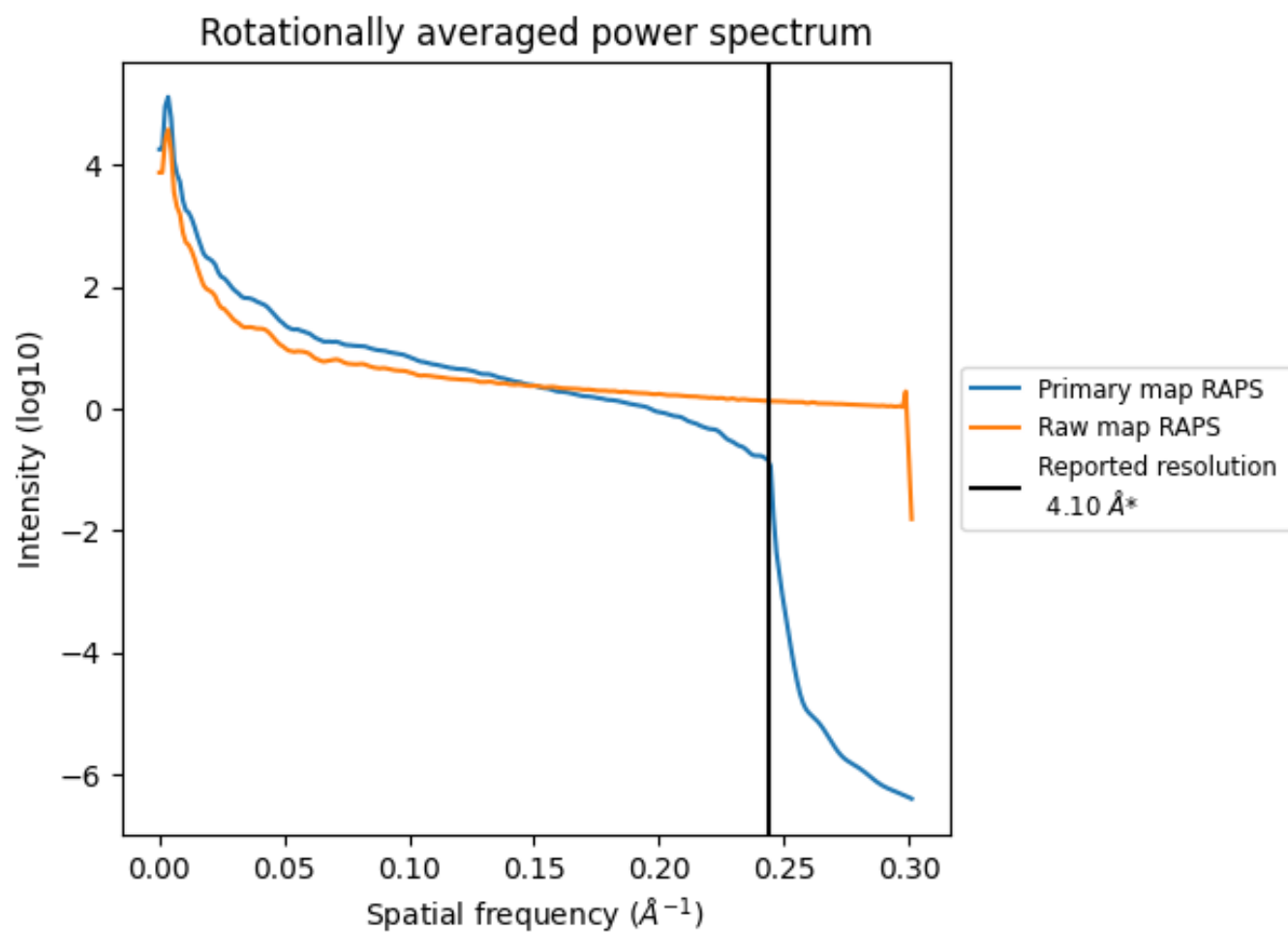
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6203 nm³; this corresponds to an approximate mass of 5603 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

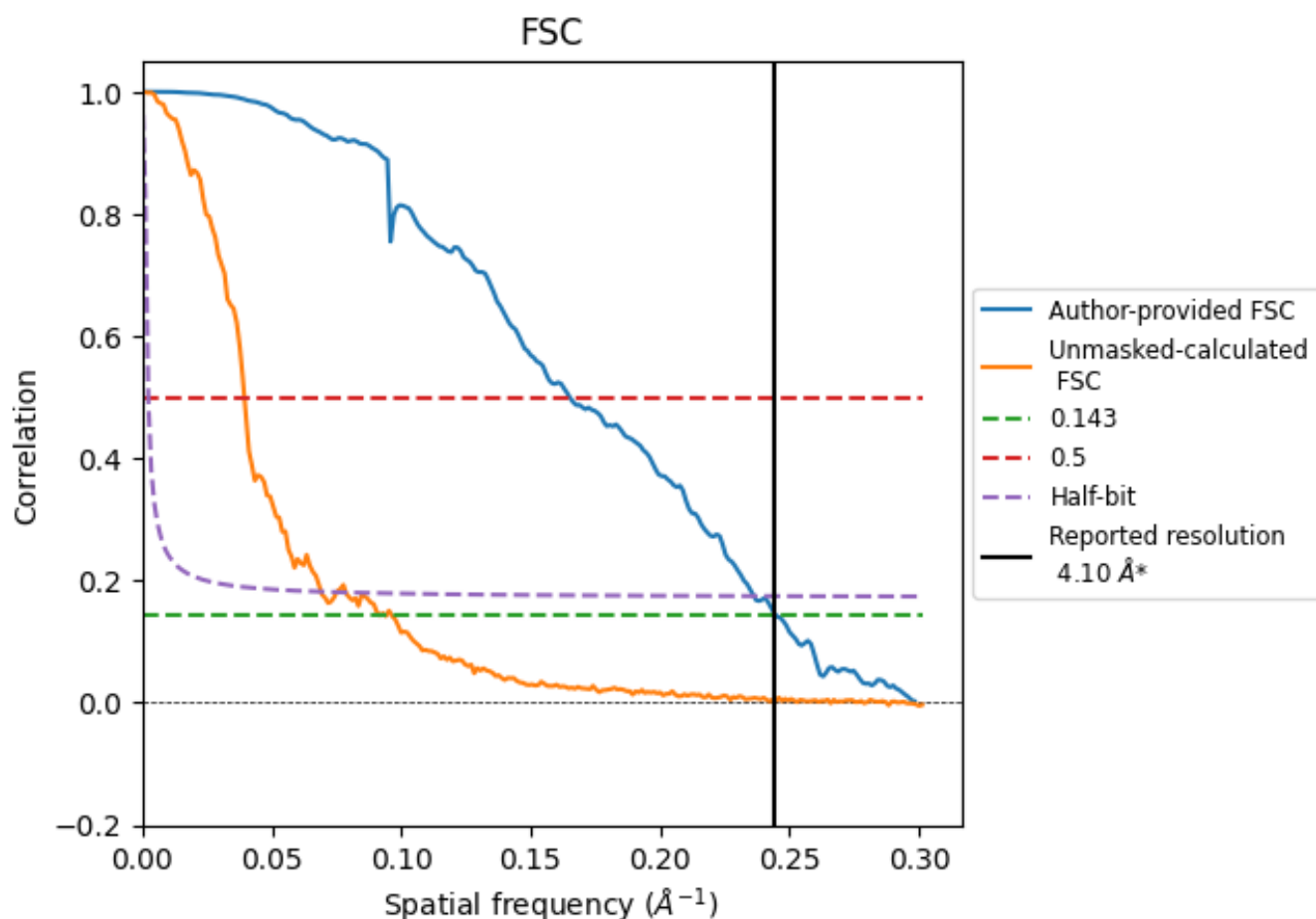


*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

8.2 Resolution estimates [i](#)

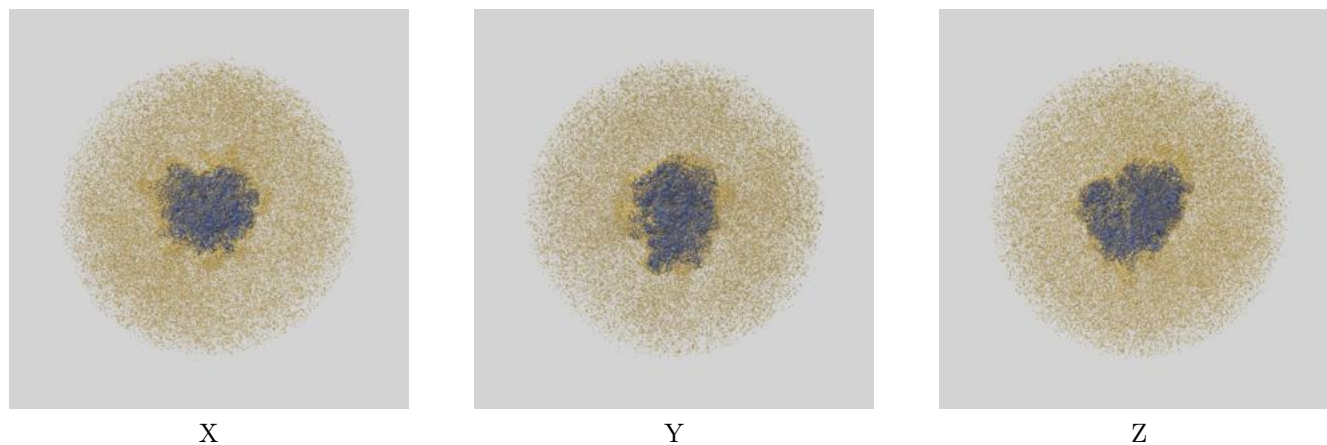
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.08	6.06	4.24
Unmasked-calculated*	10.91	25.38	14.47

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 10.91 differs from the reported value 4.1 by more than 10 %

9 Map-model fit [i](#)

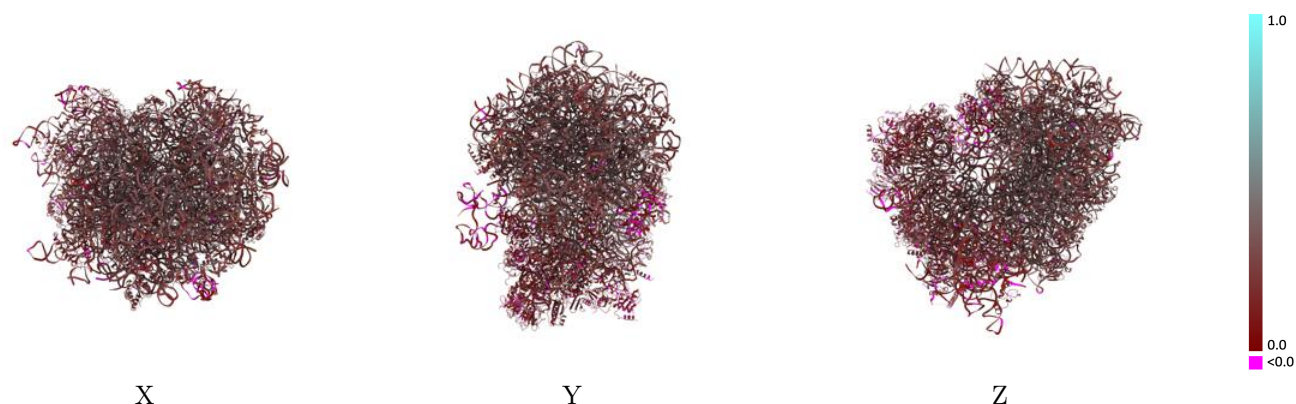
This section contains information regarding the fit between EMDB map EMD-72170 and PDB model 9Q2O. Per-residue inclusion information can be found in section [3](#) on page [23](#).

9.1 Map-model overlay [i](#)



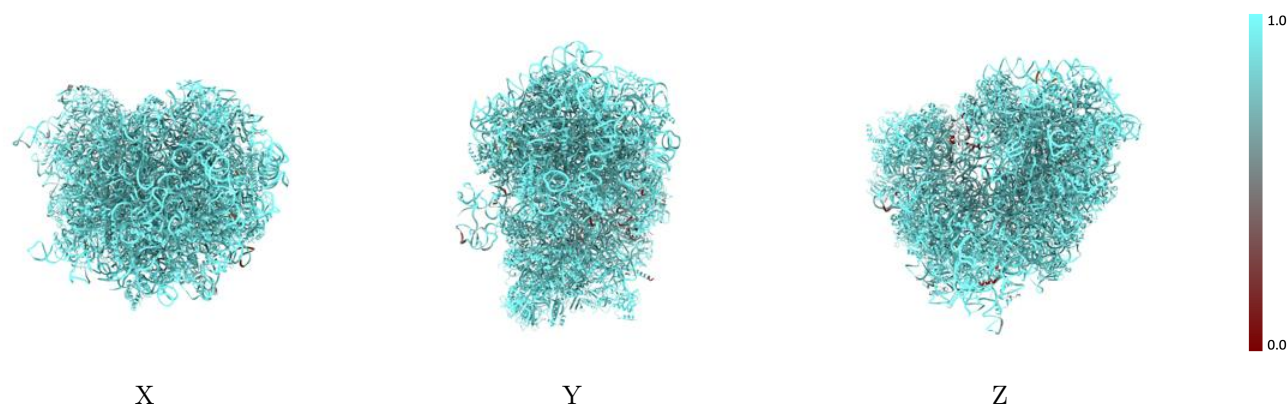
The images above show the 3D surface view of the map at the recommended contour level 0.193 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



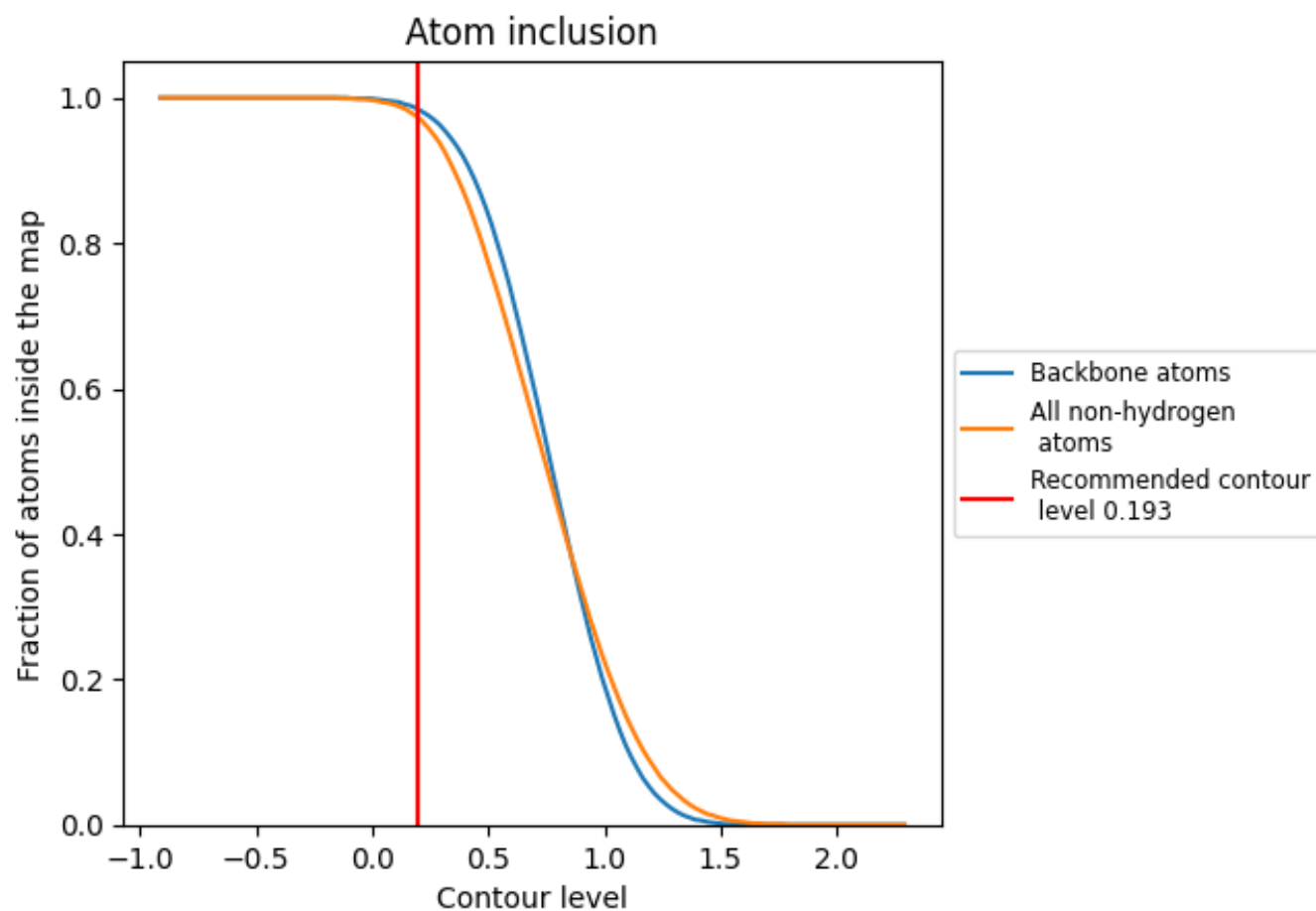
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.193).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 98% of all backbone atoms, 97% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.193) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9740	 0.2530
1	 0.8990	 0.1030
5	 0.9910	 0.2960
7	 0.9980	 0.3120
8	 0.9980	 0.2960
9	 0.9880	 0.2250
A	 0.9660	 0.2790
AA	 0.9540	 0.1940
AT	 0.8500	 0.1920
B	 0.9740	 0.3040
BB	 0.9780	 0.1610
C	 0.9680	 0.2920
CC	 0.9200	 0.2240
D	 0.9930	 0.2600
DD	 0.9330	 0.2160
E	 0.9800	 0.2900
EE	 0.9710	 0.2040
F	 0.9280	 0.2730
FF	 0.9690	 0.1620
G	 0.9690	 0.2510
GG	 0.9480	 0.1740
H	 0.9700	 0.2960
HH	 0.8890	 0.1770
I	 0.9340	 0.2930
II	 0.9320	 0.1830
J	 0.9690	 0.2490
JJ	 0.9670	 0.2000
KK	 0.9950	 0.1810
L	 0.9650	 0.2750
LL	 0.9590	 0.2250
M	 0.9780	 0.2910
MM	 0.9680	 0.1300
N	 0.9720	 0.2560
NN	 0.9580	 0.1920
O	 0.9420	 0.2880

















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Chain	Atom inclusion	Q-score
OO	 0.9710	 0.1510
P	 0.9880	 0.2900
PP	 0.9330	 0.1630
Q	 0.9630	 0.2910
QQ	 0.9890	 0.1660
R	 0.9390	 0.1900
RR	 0.8560	 0.1610
S	 0.9650	 0.3010
SS	 0.9770	 0.1830
T	 0.9530	 0.2940
TT	 0.9600	 0.1610
U	 0.9940	 0.2500
UU	 0.9860	 0.2060
V	 0.9300	 0.2850
VV	 0.9240	 0.2010
W	 0.8420	 0.1960
WW	 0.9540	 0.2230
X	 0.9830	 0.2780
XX	 0.9490	 0.2380
Y	 0.9930	 0.2730
YY	 0.9830	 0.1900
Z	 0.9910	 0.2330
ZZ	 0.9660	 0.1920
a	 0.9790	 0.2920
aa	 0.9590	 0.1850
b	 0.9760	 0.2540
bb	 0.9720	 0.1820
c	 0.9560	 0.2410
cc	 0.9400	 0.1580
d	 0.9830	 0.2840
dd	 0.9960	 0.1780
e	 0.9770	 0.3140
ee	 0.8660	 0.1750
f	 0.9370	 0.3160
ff	 0.9630	 0.1420
g	 0.9690	 0.2590
gg	 0.9720	 0.1360
h	 0.9790	 0.2470
i	 0.9770	 0.2560
j	 0.9930	 0.2620
k	 0.9770	 0.2610
l	 0.9770	 0.2730

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Chain	Atom inclusion	Q-score
m	 0.9660	 0.2860
n	 0.9310	 0.2230
o	 0.9310	 0.2690
p	 0.9390	 0.2560
r	 0.9790	 0.3080
s	 0.8620	 0.1410
t	 0.6800	 0.0940