



wwPDB EM Validation Summary Report ⓘ

Jun 8, 2026 – 05:46 PM EDT

PDB ID : 9Q2T / pdb_00009q2t
EMDB ID : EMD-72175
Title : NediV IRES in complex with Rabbit 80S ribosome with eEF2 and P 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:

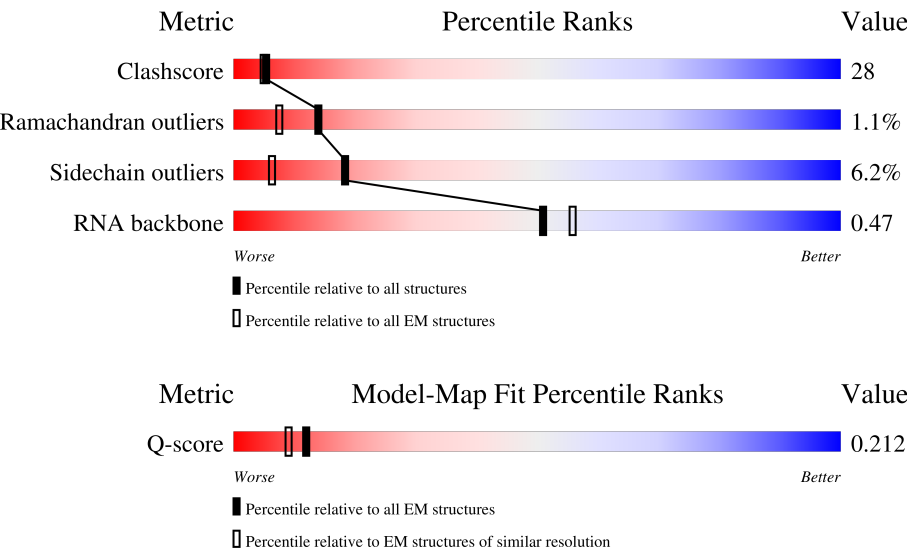
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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	DD	228	<div><div>6%</div><div>60%</div><div>38%</div><div>.</div></div>
2	FF	191	<div><div>49%</div><div>47%</div><div>..</div></div>
3	KK	96	<div><div>51%</div><div>46%</div><div>.</div></div>





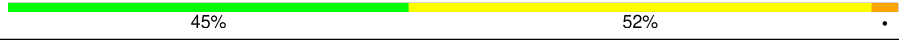

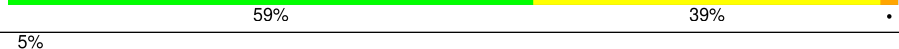
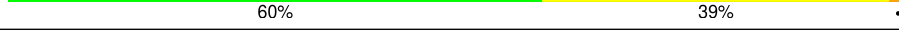
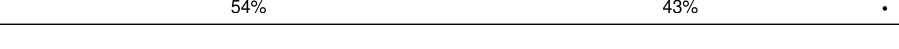
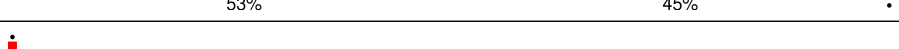
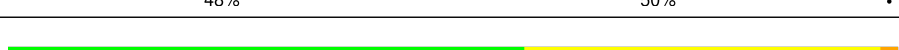
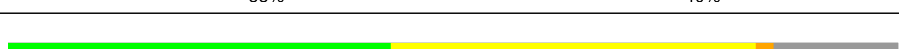
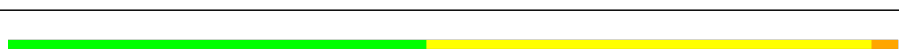
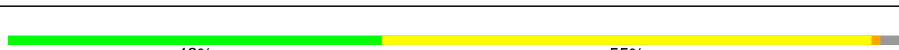
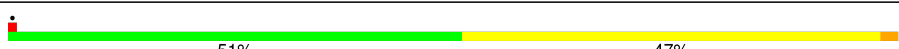





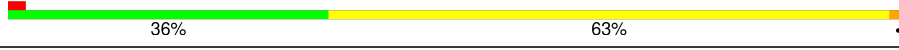
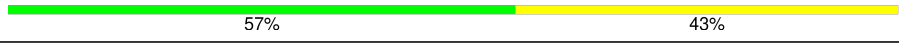



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Mol	Chain	Length	Quality of chain
4	MM	117	
5	PP	111	
6	QQ	142	
7	RR	132	
8	SS	144	
9	TT	141	
10	UU	100	
11	ZZ	75	
12	cc	62	
13	dd	55	
14	ff	68	
15	gg	313	
16	R	180	
17	W	121	
18	9	1697	
19	AA	217	
20	BB	213	
21	CC	221	
22	EE	262	
23	GG	237	
24	HH	189	
25	II	206	
26	JJ	185	
27	LL	151	
28	NN	149	



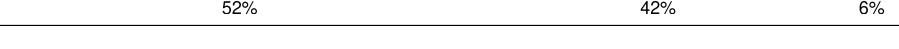

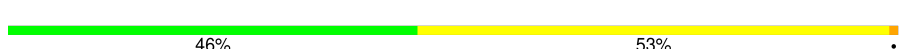


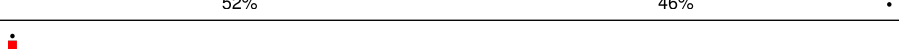
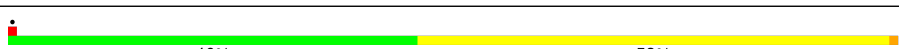

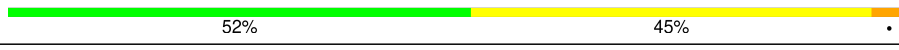
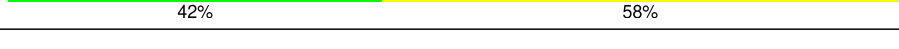

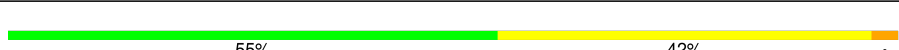


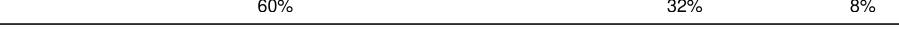







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Mol	Chain	Length	Quality of chain
29	OO	136	
30	VV	83	
31	WW	129	
32	XX	141	
33	YY	124	
34	aa	101	
35	bb	83	
36	ee	57	
37	A	248	
38	B	394	
39	C	362	
40	D	293	
41	E	251	
42	F	225	
43	G	240	
44	H	190	
45	I	213	
46	J	170	
47	L	210	
48	M	138	
49	N	203	
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	116	
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	196	
78	t	153	

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Mol	Chain	Length	Quality of chain
79	5	3543	<div><div></div><div>31%55%14%</div></div>
80	7	119	<div><div></div><div>30%64%6%</div></div>
81	8	156	<div><div></div><div>29%53%14%</div></div>
82	1	154	<div><div></div><div>36%62%</div></div>
83	PT	76	<div><div></div><div>5%51%42%</div></div>
84	EF	853	<div><div></div><div>12%55%30%</div></div>

2 Entry composition [i](#)

There are 86 unique types of molecules in this entry. The entry contains 231165 atoms, of which 7569 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 40S ribosomal protein S3.

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

- Molecule 2 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 3 is a protein called 40S ribosomal protein S10.

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

- Molecule 4 is a protein called 40S ribosomal protein S12.

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

- Molecule 5 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	PP	111	Total	C	N	O	S	0	0
			921	585	171	158	7		

- Molecule 6 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 7 is a protein called 40S ribosomal protein S17.

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

- Molecule 8 is a protein called 40S ribosomal protein S18.

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

- Molecule 9 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	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 10 is a protein called 40S ribosomal protein S20.

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

- Molecule 11 is a protein called 40S ribosomal protein S25.

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

- Molecule 12 is a protein called 40S ribosomal protein S28.

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

- Molecule 13 is a protein called 40S ribosomal protein S29.

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

- Molecule 14 is a protein called 40S ribosomal protein S27a.

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

- Molecule 15 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 16 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	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 17 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	W	91	Total	C	N	O	S	0	0
			732	463	144	121	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	9	1697	Total	C	N	O	P	0	0
			36229	16171	6507	11855	1696		

- Molecule 19 is a protein called 40S_SA_C domain-containing protein.

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

- Molecule 20 is a protein called 40S ribosomal protein S3a.

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

- Molecule 21 is a protein called 40S ribosomal protein S2.

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

- Molecule 22 is a protein called 40S ribosomal protein S4.

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

- Molecule 23 is a protein called 40S ribosomal protein S6.

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

- Molecule 24 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 25 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	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 26 is a protein called 40S ribosomal protein S9.

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

- Molecule 27 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 28 is a protein called 40S ribosomal protein S13.

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

- Molecule 29 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 30 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	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 31 is a protein called 40S ribosomal protein S15a.

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

- Molecule 32 is a protein called 40S ribosomal protein S23.

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

- Molecule 33 is a protein called 40S ribosomal protein S24.

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

- Molecule 34 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	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 35 is a protein called 40S ribosomal protein S27.

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

- Molecule 36 is a protein called Small ribosomal subunit protein eS30.

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

- 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 Large ribosomal subunit protein eL6.

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 Large ribosomal subunit protein 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

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Chain	Residue	Modelled	Actual	Comment	Reference
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 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	s	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 78 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	t	153	Total	C	N	O	S	0	0
			1160	722	218	217	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
			75952	33825	13893	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 NediV IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	1	154	Total	C	N	O	P	0	0
			3261	1459	566	1082	154		

- Molecule 83 is a RNA chain called ala-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
83	PT	76	Total	C	H	N	O	P	0	0
			2445	722	823	290	534	76		

- Molecule 84 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
84	EF	853	Total	C	H	N	O	S	0	0
			13405	4226	6746	1146	1243	44		

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

Mol	Chain	Residues	Atoms		AltConf
85	dd	1	Total	Zn	0
			1	1	
85	ff	1	Total	Zn	0
			1	1	
85	aa	1	Total	Zn	0
			1	1	
85	g	1	Total	Zn	0
			1	1	
85	j	1	Total	Zn	0
			1	1	
85	m	1	Total	Zn	0
			1	1	
85	o	1	Total	Zn	0
			1	1	
85	p	1	Total	Zn	0
			1	1	

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

Mol	Chain	Residues	Atoms		AltConf
86	aa	1	Total	Mg	0
			1	1	
86	B	1	Total	Mg	0
			1	1	
86	I	1	Total	Mg	0
			1	1	
86	P	1	Total	Mg	0
			1	1	
86	Q	1	Total	Mg	0
			1	1	
86	V	1	Total	Mg	0
			1	1	
86	a	2	Total	Mg	0
			2	2	
86	g	1	Total	Mg	0
			1	1	
86	j	1	Total	Mg	0
			1	1	

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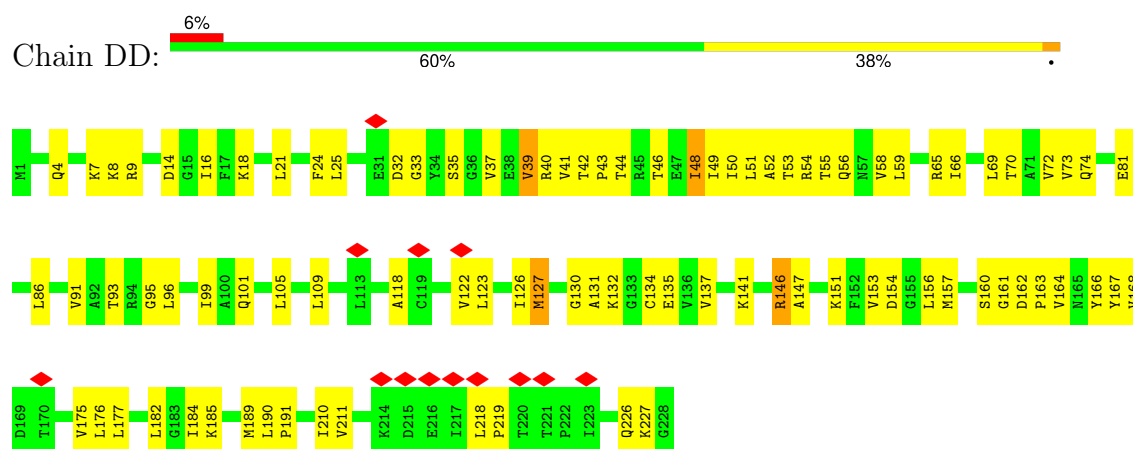
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Mol	Chain	Residues	Atoms		AltConf
86	5	185	Total 185	Mg 185	0
86	7	6	Total 6	Mg 6	0
86	8	5	Total 5	Mg 5	0

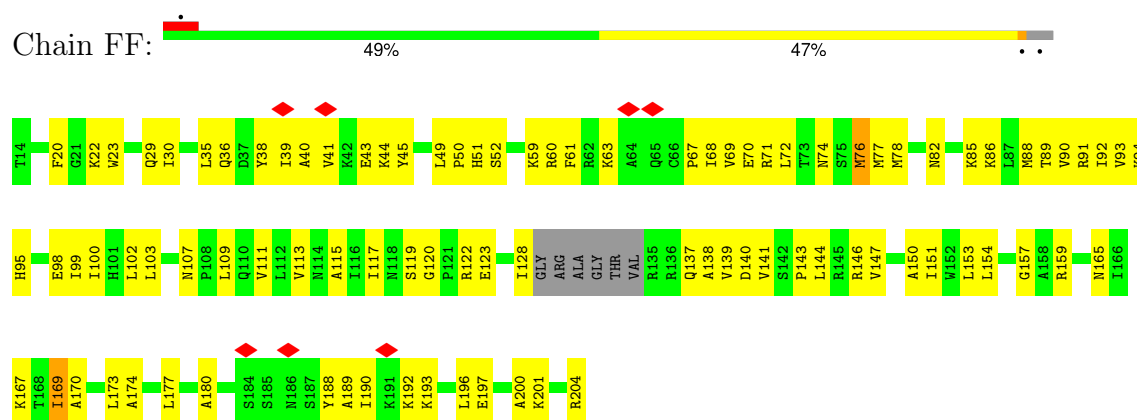
3 Residue-property plots

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.

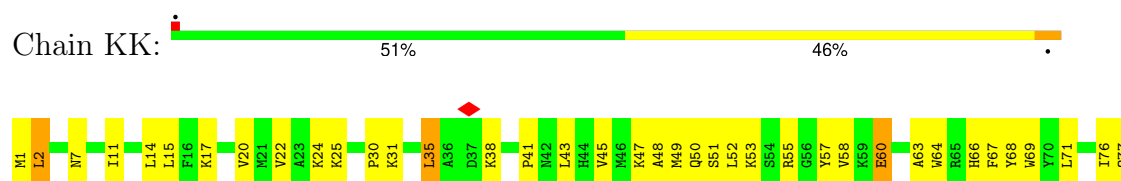
• Molecule 1: 40S ribosomal protein S3



• Molecule 2: Small ribosomal subunit protein uS7



• Molecule 3: 40S ribosomal protein S10





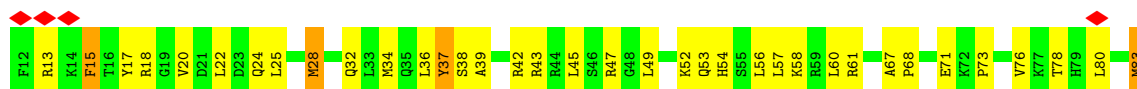
- Molecule 4: 40S ribosomal protein S12

Chain MM: 50% 47%



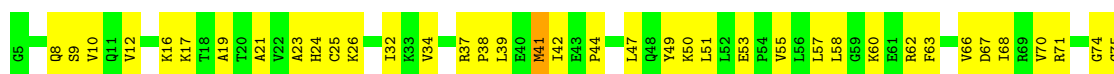
- Molecule 5: Small ribosomal subunit protein uS19

Chain PP: 6% 53% 41% 5%



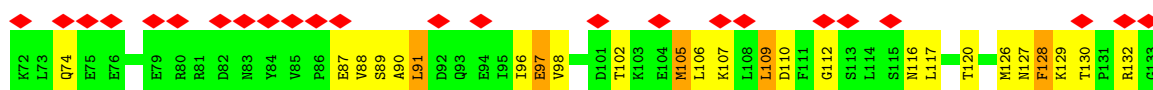
- Molecule 6: Small ribosomal subunit protein uS9

Chain QQ: 45% 54%



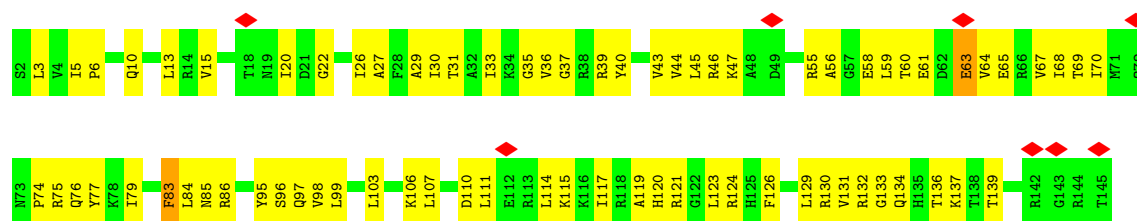
- Molecule 7: 40S ribosomal protein S17

Chain RR: 23% 52% 43% 5%

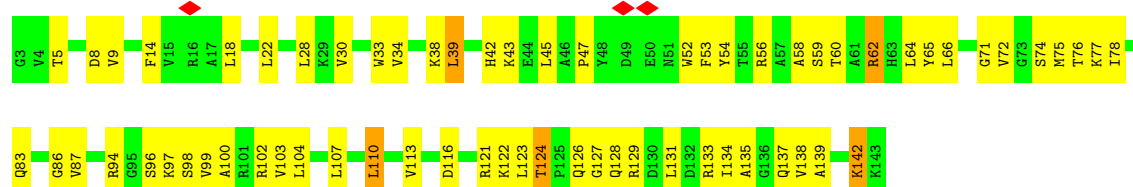


- Molecule 8: 40S ribosomal protein S18

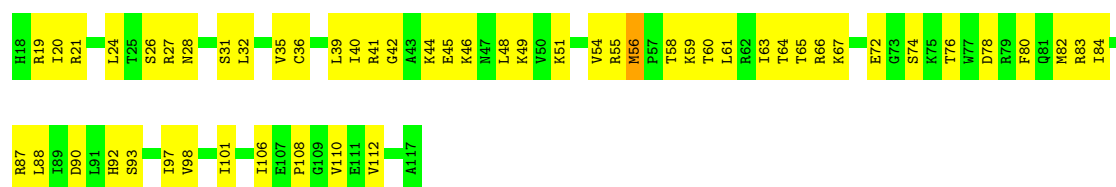
Chain SS: 6% 49% 50%



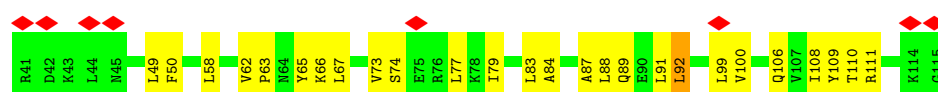
- Molecule 9: Small ribosomal subunit protein eS19



- Molecule 10: 40S ribosomal protein S20



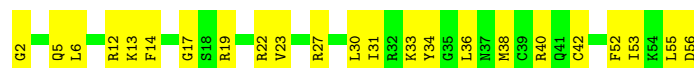
- Molecule 11: 40S ribosomal protein S25



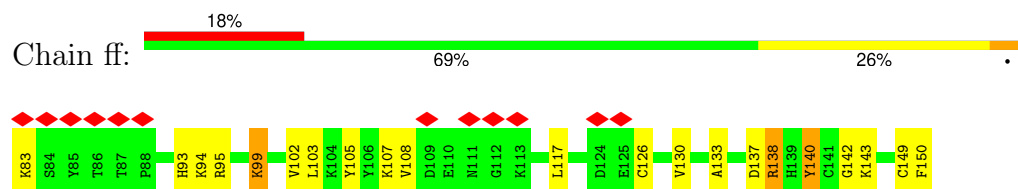
- Molecule 12: 40S ribosomal protein S28



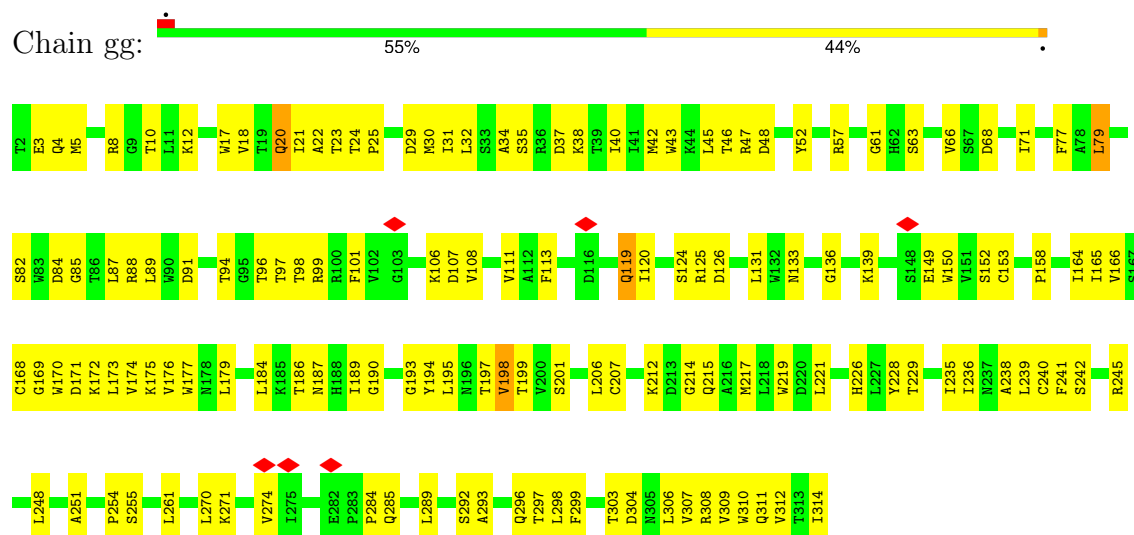
- Molecule 13: 40S ribosomal protein S29



- Molecule 14: 40S ribosomal protein S27a



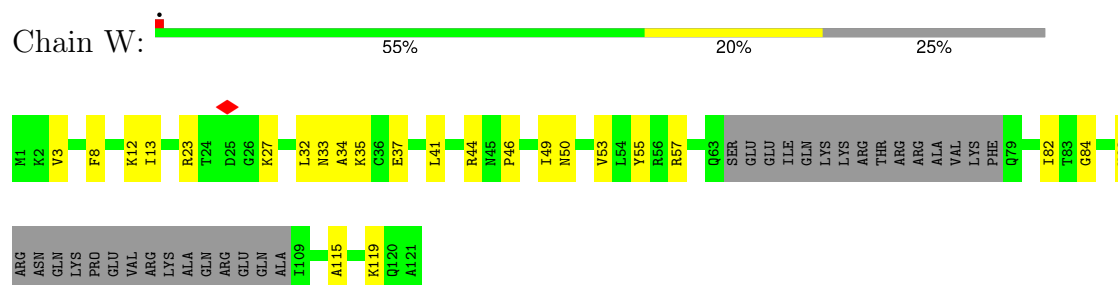
- Molecule 15: Receptor of activated protein C kinase 1



- Molecule 16: 60S ribosomal protein L19



- Molecule 17: Large ribosomal subunit protein eL24



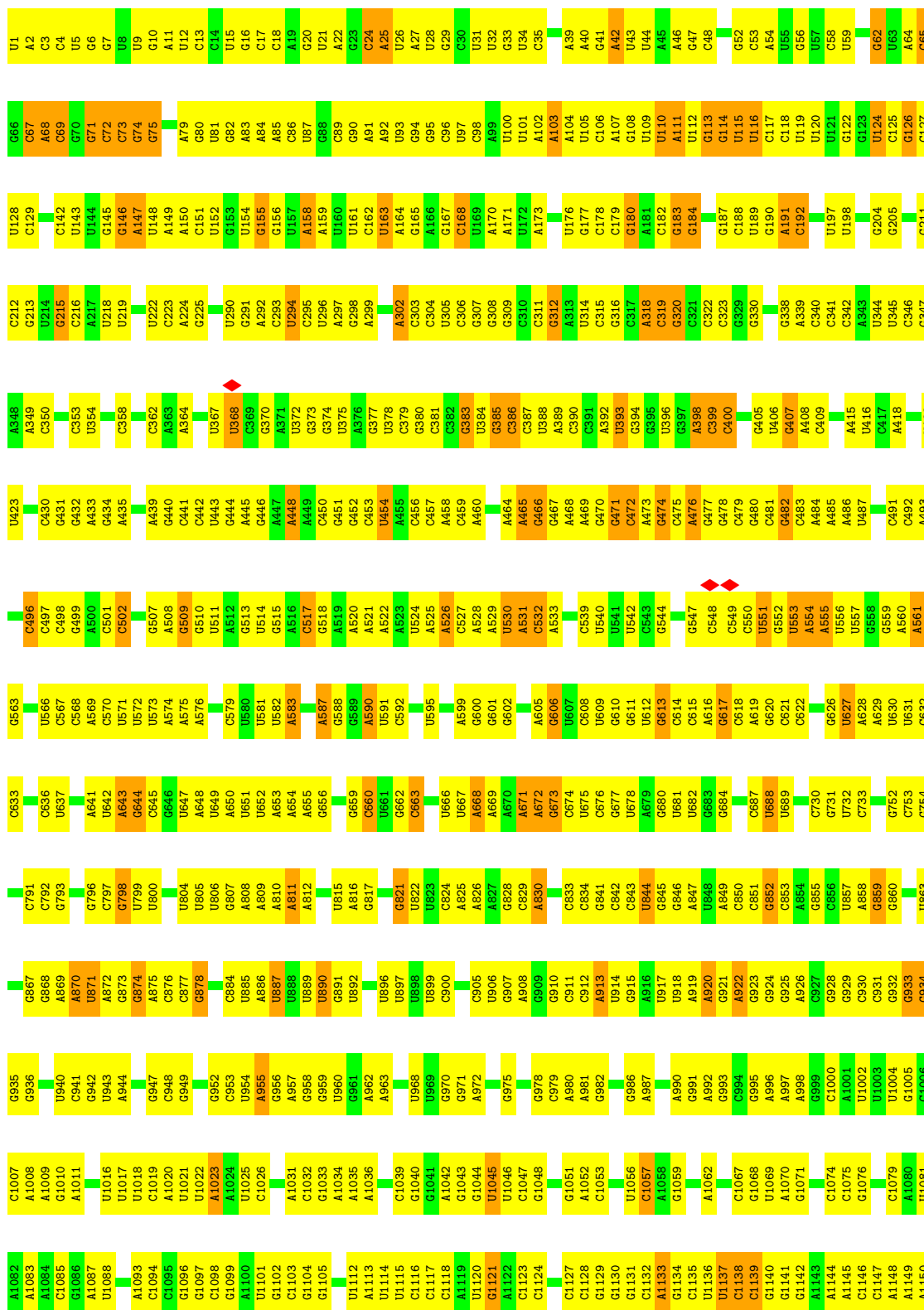
- Molecule 18: 18S rRNA

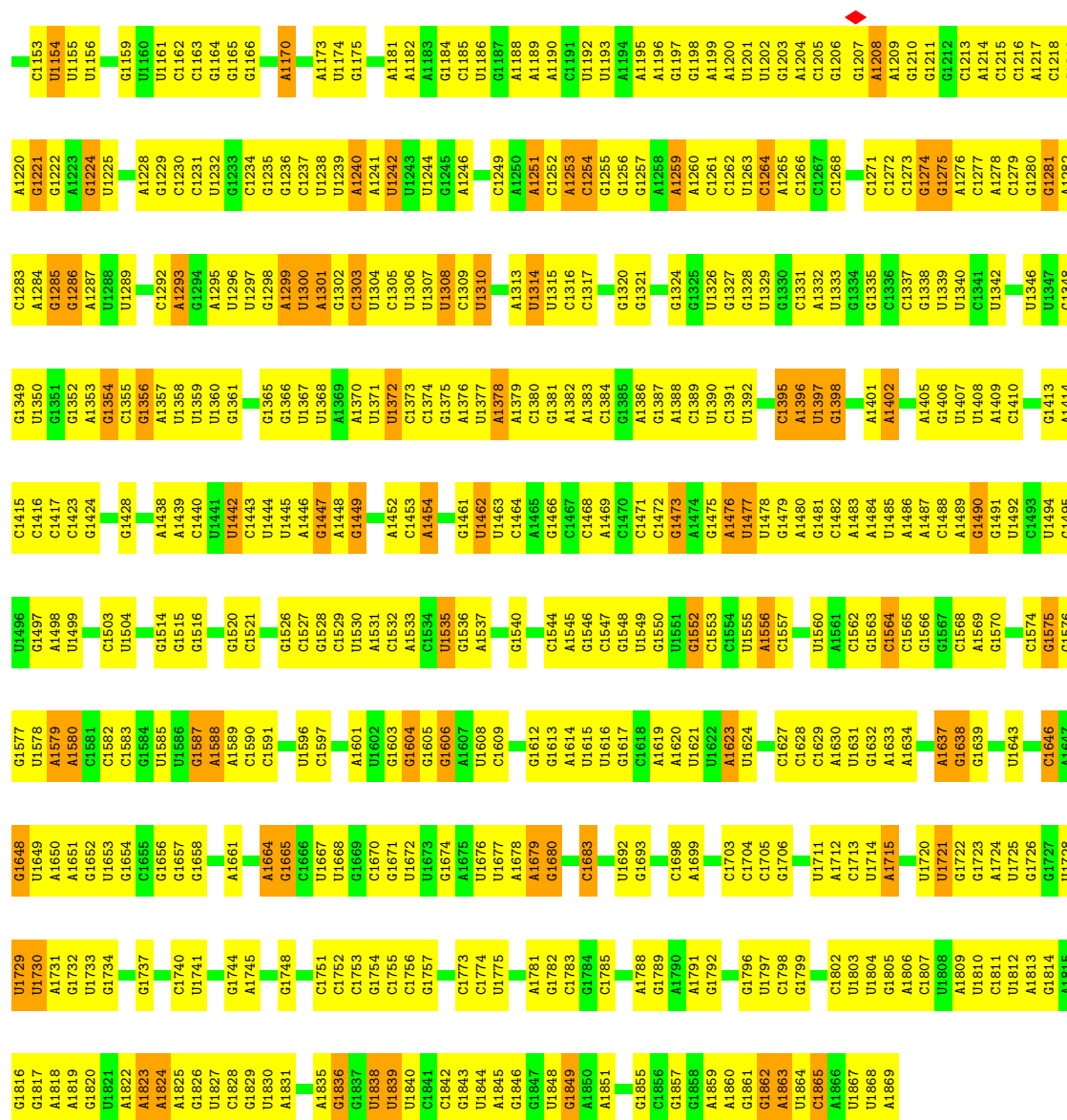
Chain 9:

32%

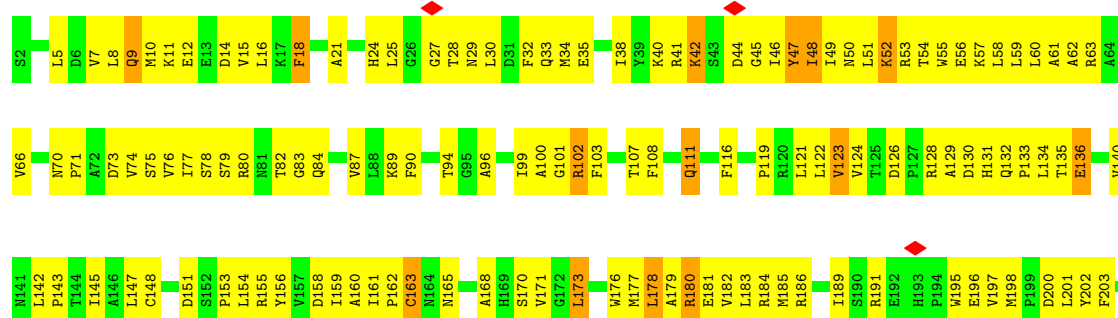
56%

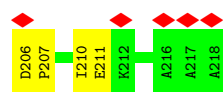
11%



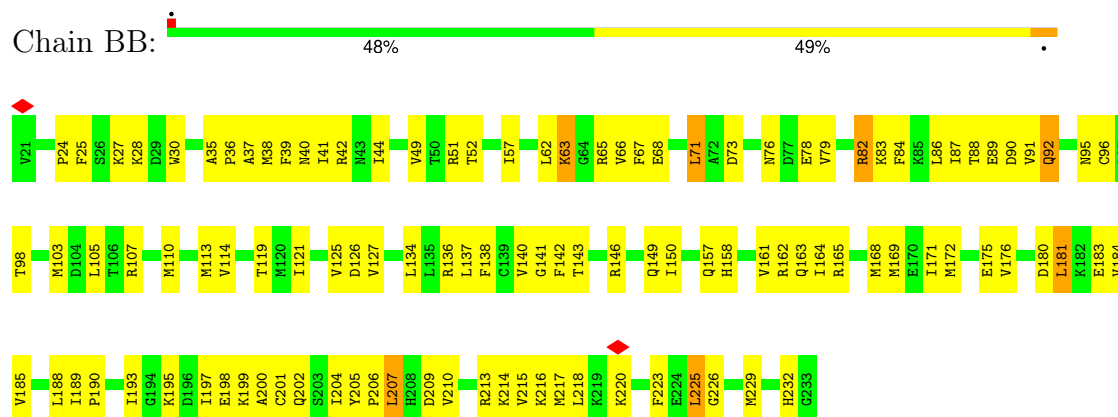


• Molecule 19: 40S_SA_C domain-containing protein





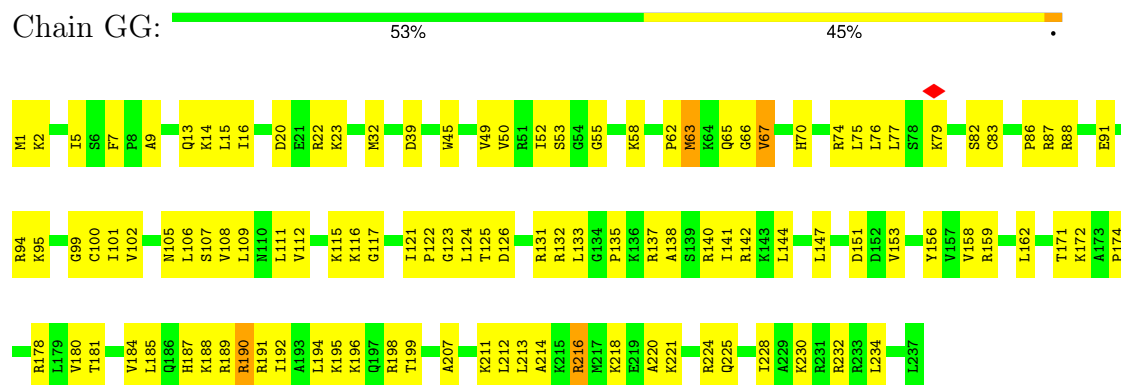
• Molecule 20: 40S ribosomal protein S3a



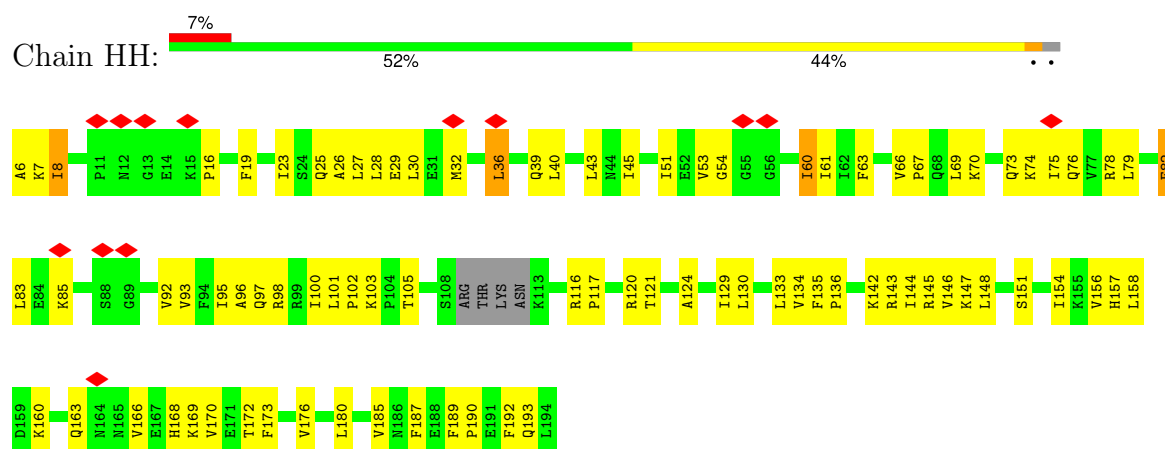
• Molecule 21: 40S ribosomal protein S2



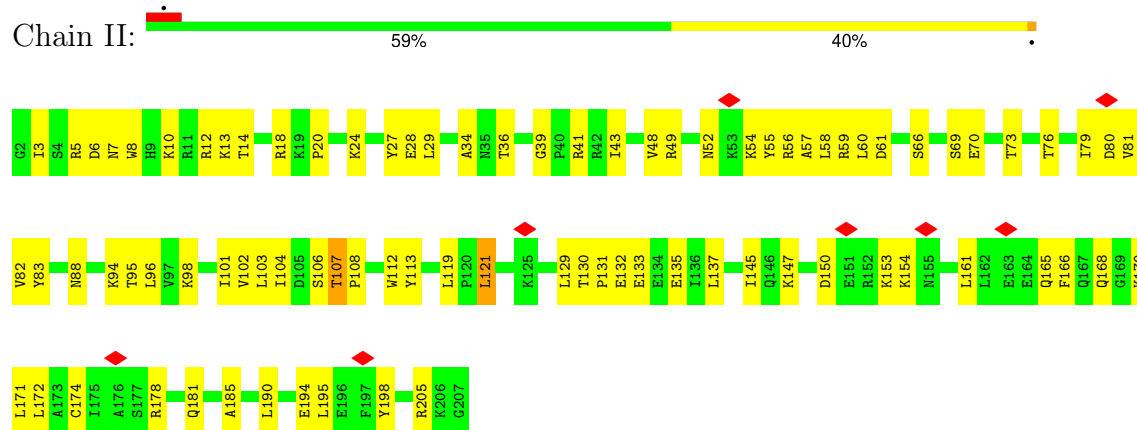
- Molecule 23: 40S ribosomal protein S6



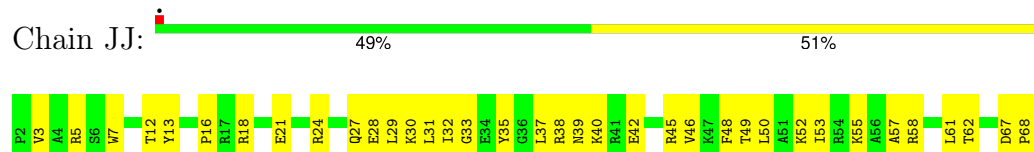
- Molecule 24: Small ribosomal subunit protein eS7

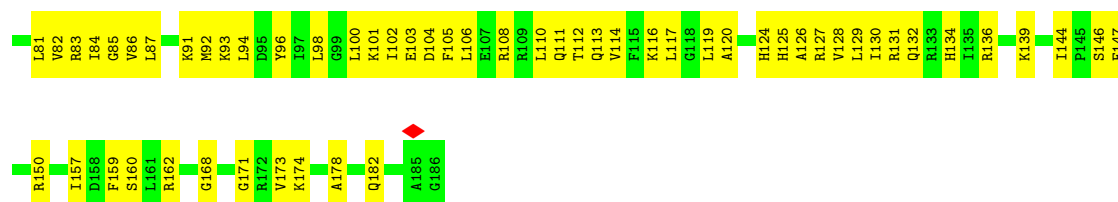


- Molecule 25: 40S ribosomal protein S8

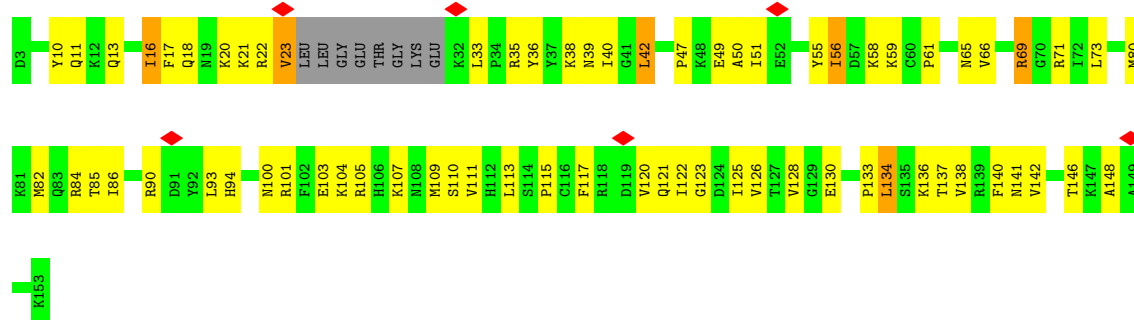


- Molecule 26: 40S ribosomal protein S9

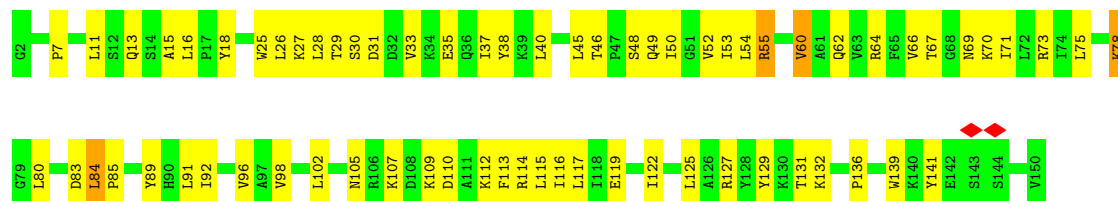




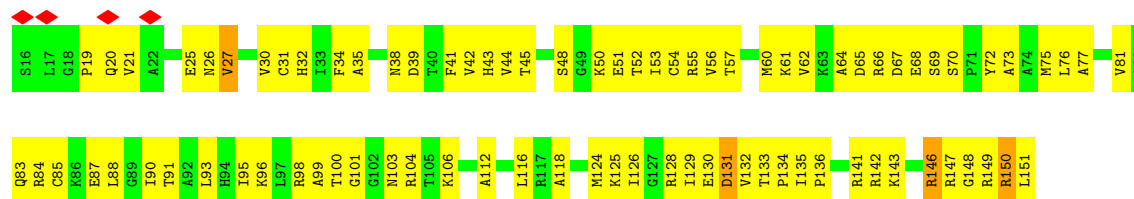
• Molecule 27: Small ribosomal subunit protein uS17



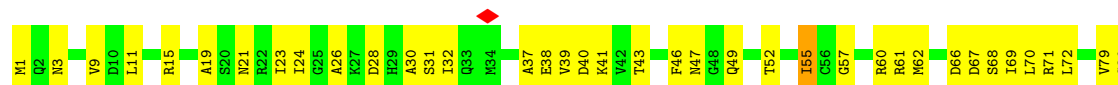
• Molecule 28: 40S ribosomal protein S13



• Molecule 29: Small ribosomal subunit protein uS11



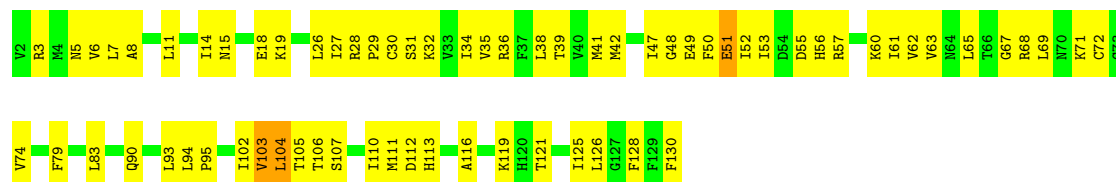
• Molecule 30: eS21





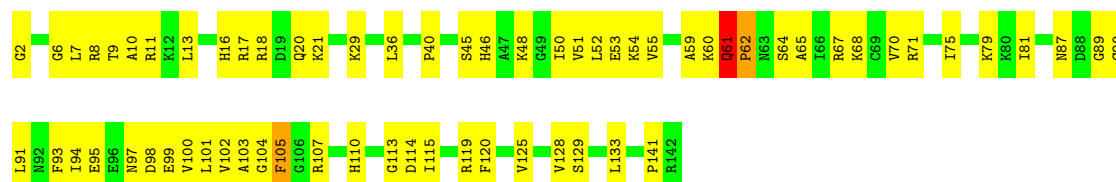
- Molecule 31: 40S ribosomal protein S15a

Chain WW: 47% 50%



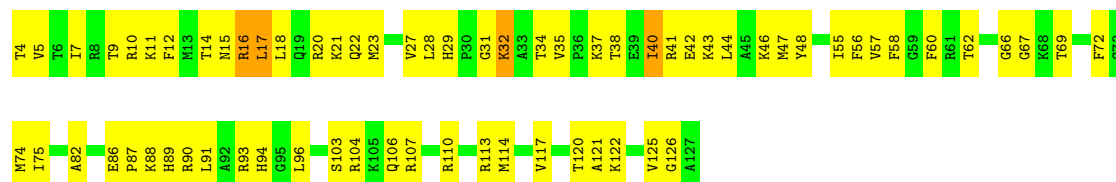
- Molecule 32: 40S ribosomal protein S23

Chain XX: 53% 45%



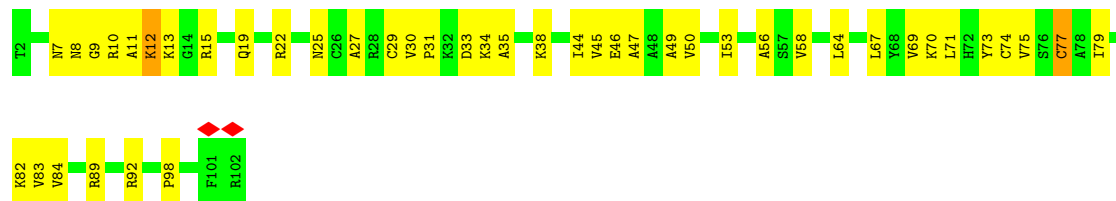
- Molecule 33: 40S ribosomal protein S24

Chain YY: 45% 52%



- Molecule 34: eS26

Chain aa: 56% 42%

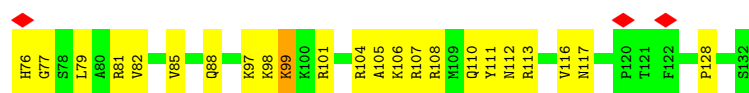


- Molecule 35: 40S ribosomal protein S27

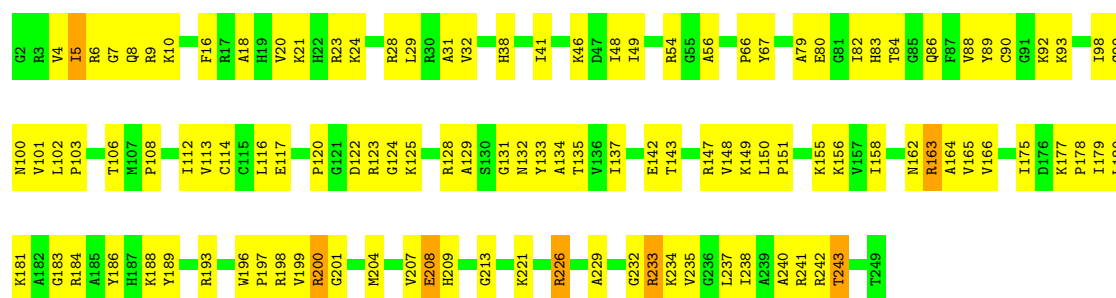
Chain bb: 59% 39%



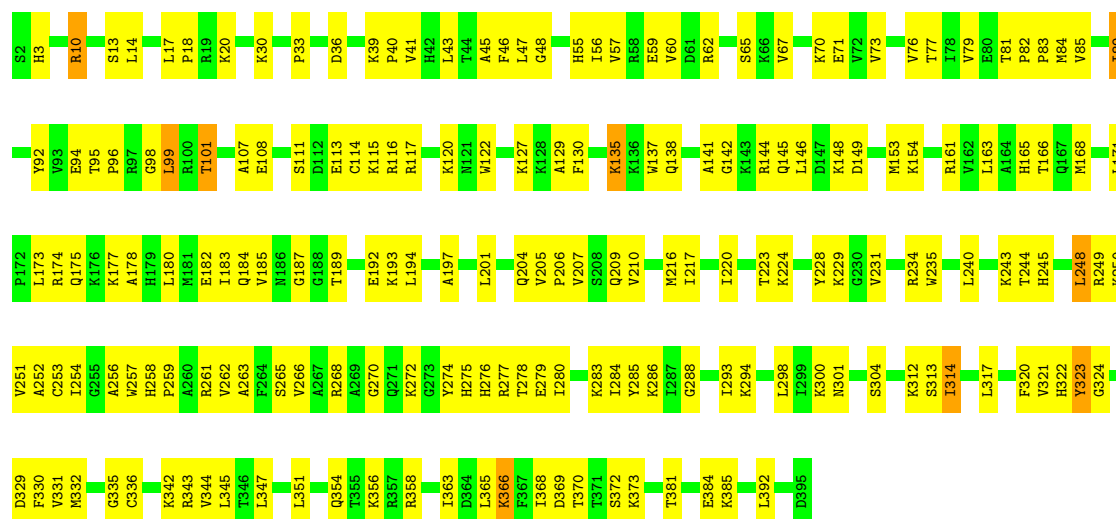
- Molecule 36: Small ribosomal subunit protein eS30



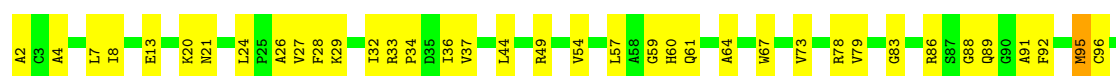
- Molecule 37: 60S ribosomal protein L8

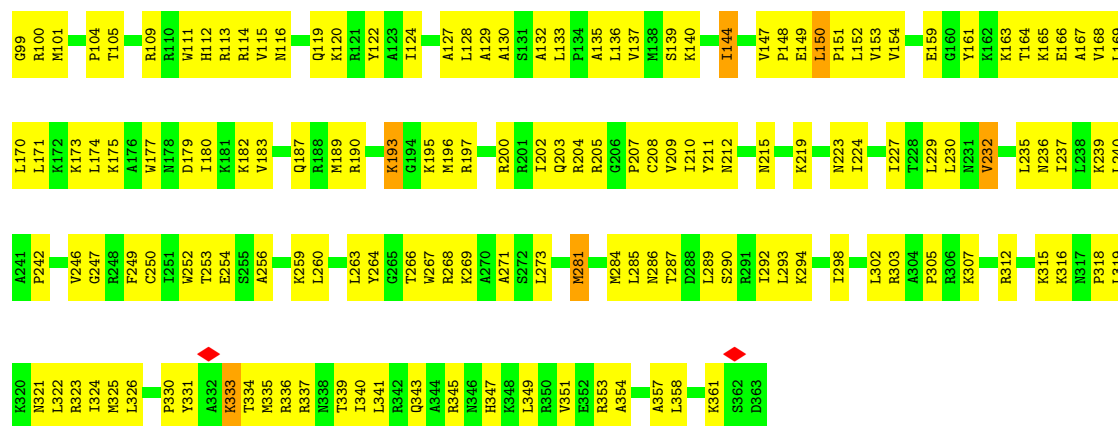


- Molecule 38: 60S ribosomal protein L3



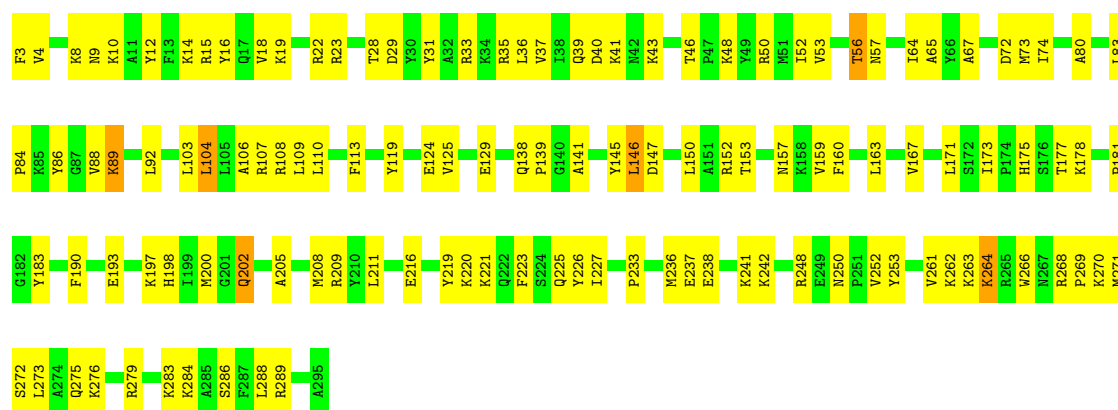
- Molecule 39: 60S ribosomal protein L4





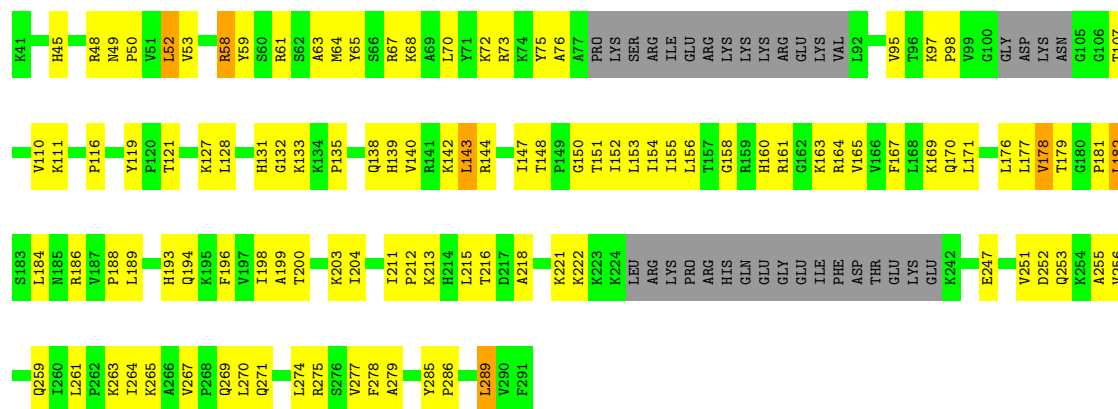
• Molecule 40: 60S ribosomal protein L5

Chain D: 58% 40%



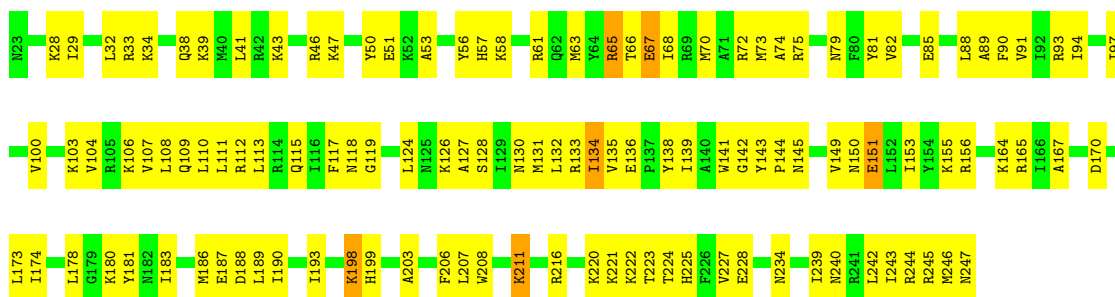
• Molecule 41: Large ribosomal subunit protein eL6

Chain E: 43% 41% 14%



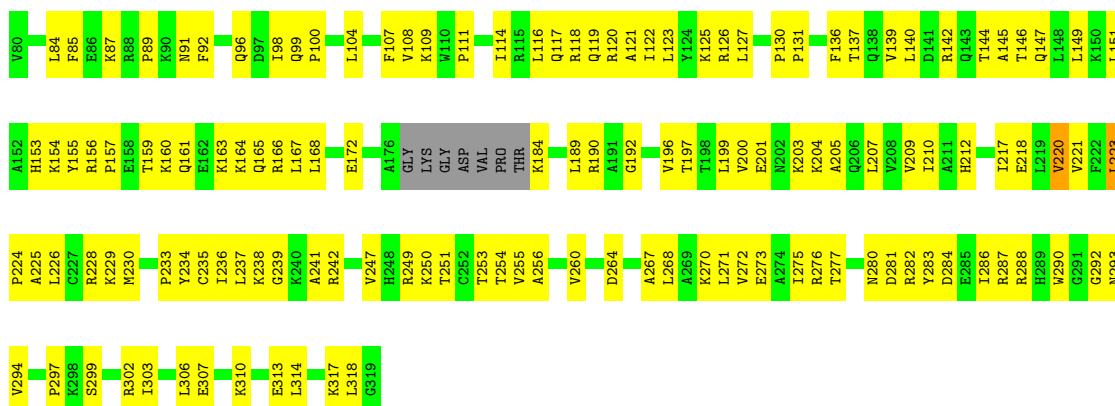
• Molecule 42: 60S ribosomal protein L7

Chain F: 47% 50%



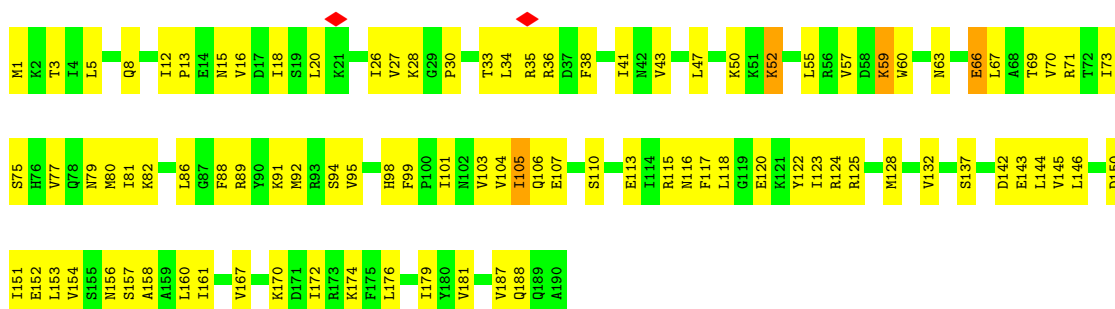
- Molecule 43: Large ribosomal subunit protein eL8

Chain G: 42% 55%



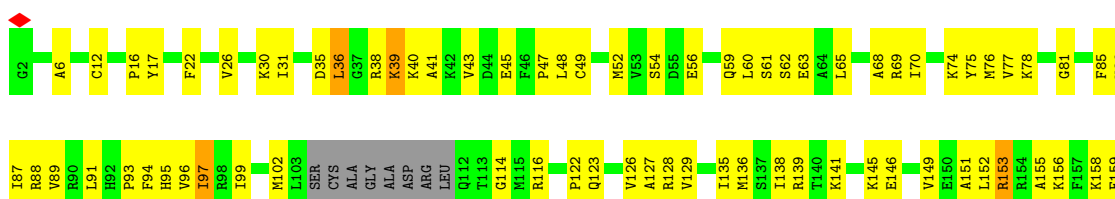
- Molecule 44: 60S ribosomal protein L9

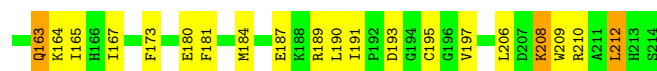
Chain H: 51% 47%



- Molecule 45: Ribosomal protein L10

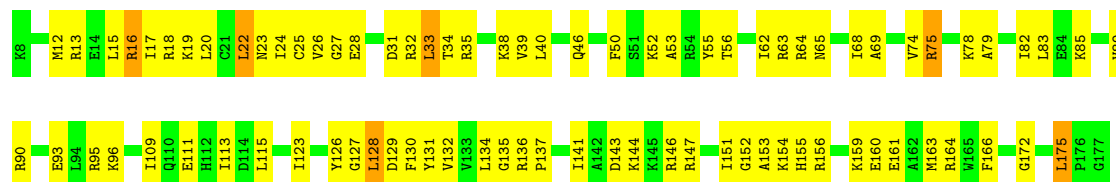
Chain I: 53% 40%





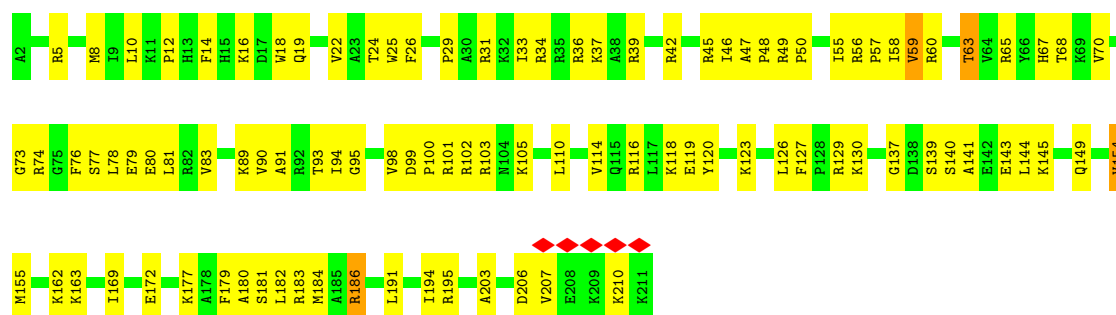
• Molecule 46: 60S ribosomal protein L11

Chain J: 52% 45%



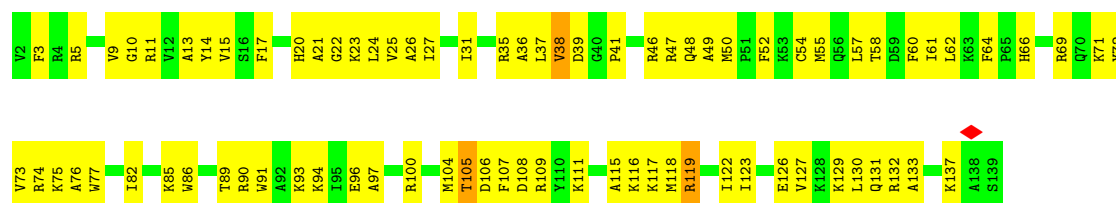
• Molecule 47: Large ribosomal subunit protein eL13

Chain L: 53% 45%



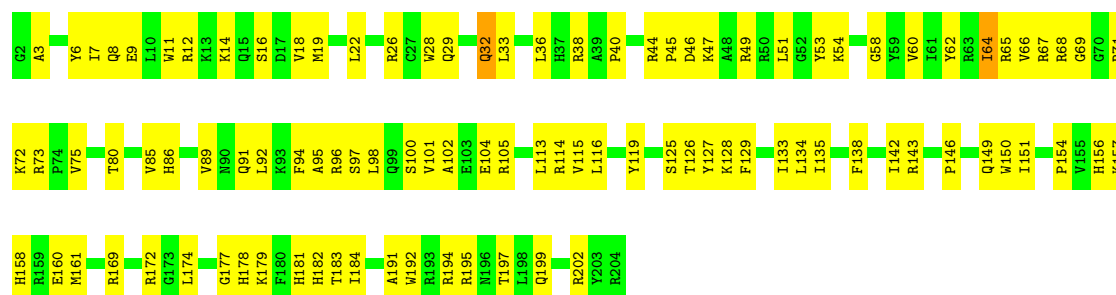
• Molecule 48: 60S ribosomal protein L14

Chain M: 42% 56%

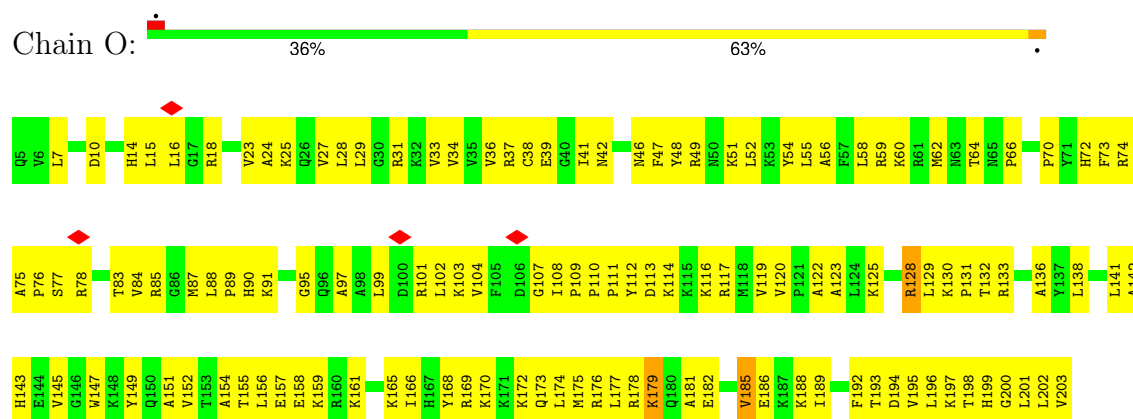


• Molecule 49: 60S ribosomal protein L15

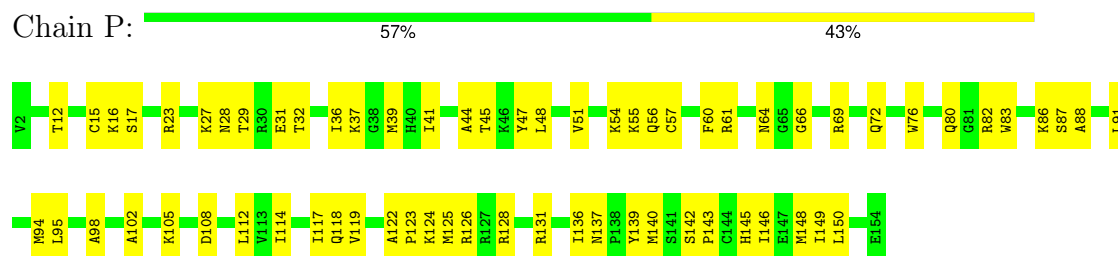
Chain N: 51% 48%



- Molecule 50: Large ribosomal subunit protein uL13



- Molecule 51: 60S ribosomal protein L17



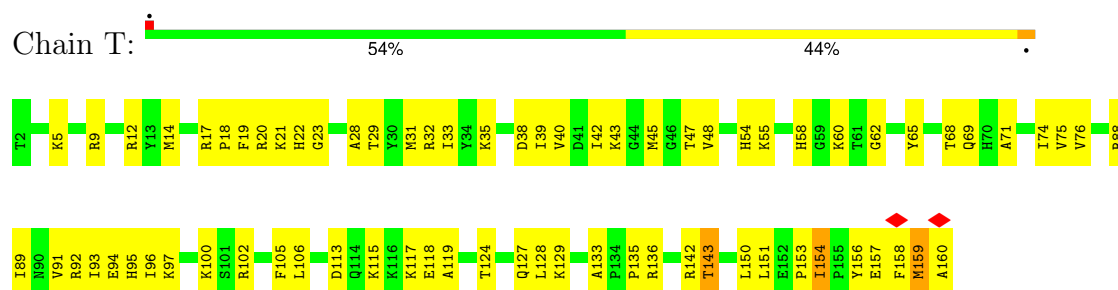
- Molecule 52: Large ribosomal subunit protein eL18



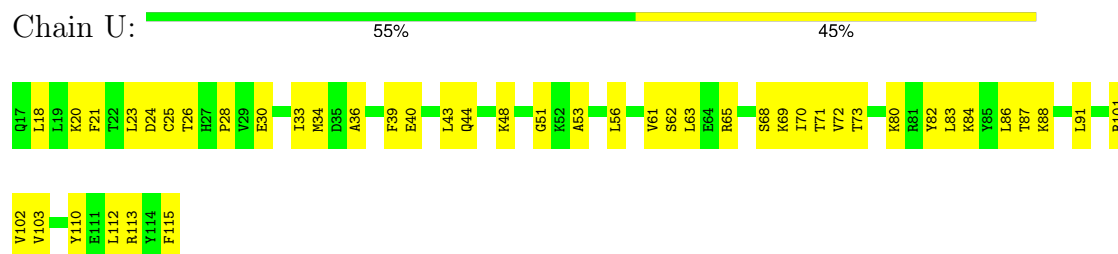
- Molecule 53: eL20



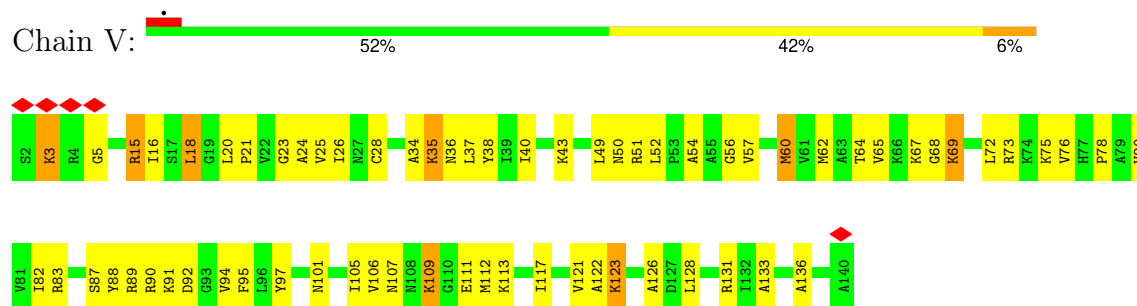
- Molecule 54: 60S ribosomal protein L21



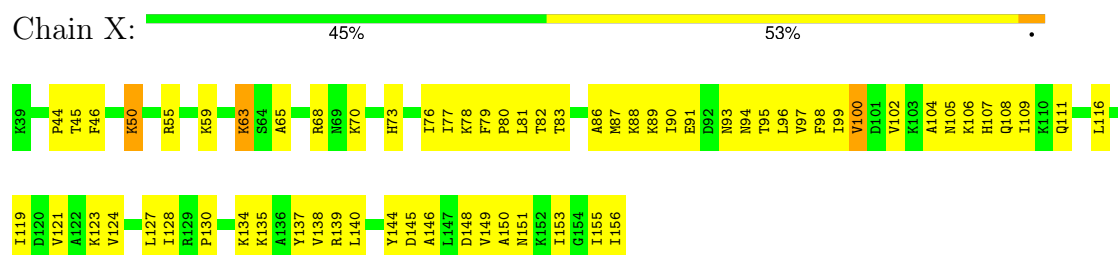
- Molecule 55: Large ribosomal subunit protein eL22



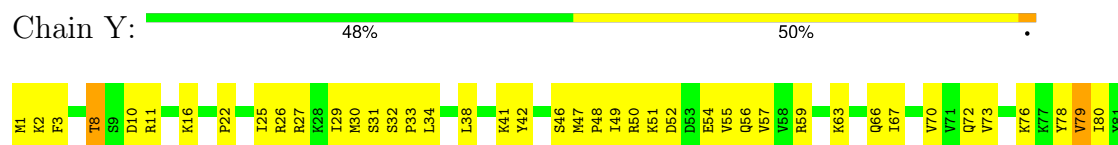
- Molecule 56: Large ribosomal subunit protein uL14



- Molecule 57: Large ribosomal subunit protein uL23



- Molecule 58: 60S ribosomal protein L26





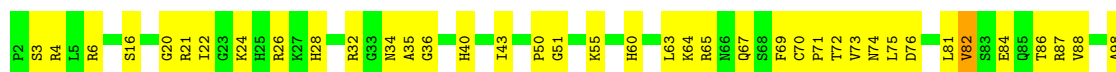
- Molecule 59: 60S ribosomal protein L27

Chain Z: 46% 53%



- Molecule 60: 60S ribosomal protein L27a

Chain a: 51% 48%



- Molecule 61: Large ribosomal subunit protein eL29

Chain b: 53% 37% 10%



- Molecule 62: 60S ribosomal protein L30

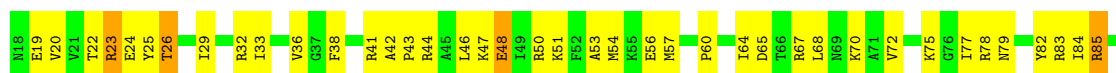
Chain c: 52% 46%



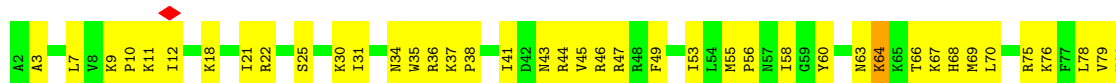
- Molecule 63: 60S ribosomal protein L31


Chain d: 50% 46%





- Molecule 64: Large ribosomal subunit protein eL32

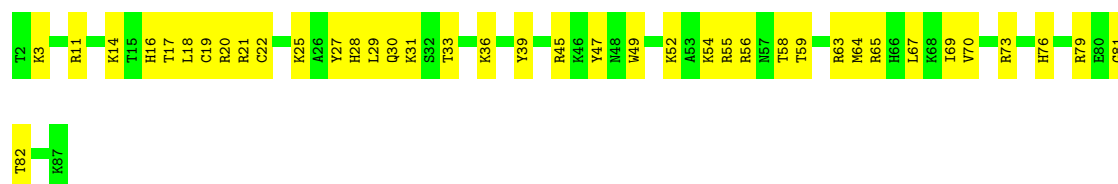


Chain i: 



- Molecule 69: 60S ribosomal protein L37

Chain j: 



- Molecule 70: Large ribosomal subunit protein eL38

Chain k: 



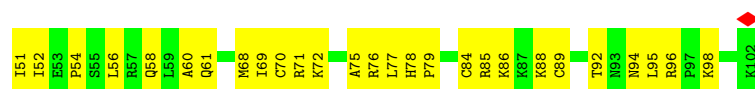
- Molecule 71: 60S ribosomal protein L39

Chain l: 



- Molecule 72: Large ribosomal subunit protein eL40

Chain m: 



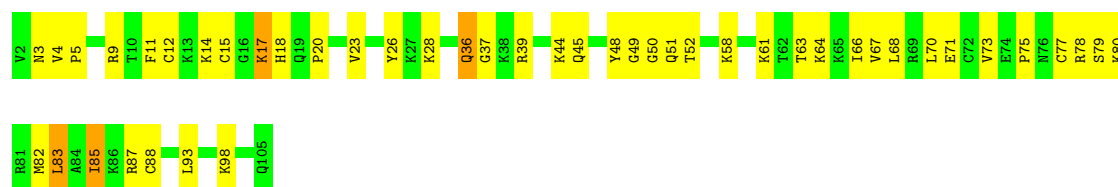
- Molecule 73: eL41

Chain n: 



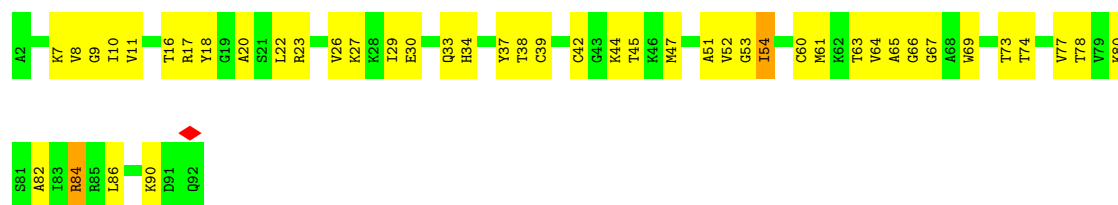
- Molecule 74: eL42

Chain o:  56% 40%



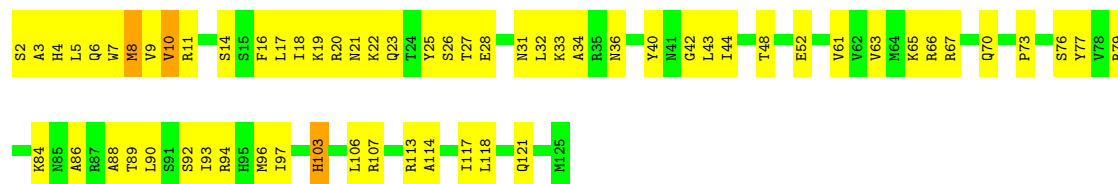
- Molecule 75: 60S ribosomal protein L37a

Chain p:  51% 47%




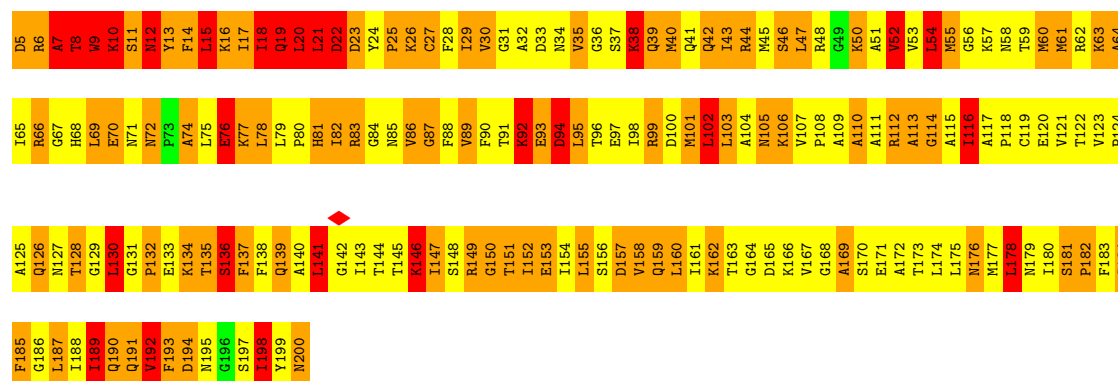
- Molecule 76: 60S ribosomal protein L28

Chain r:  50% 48%



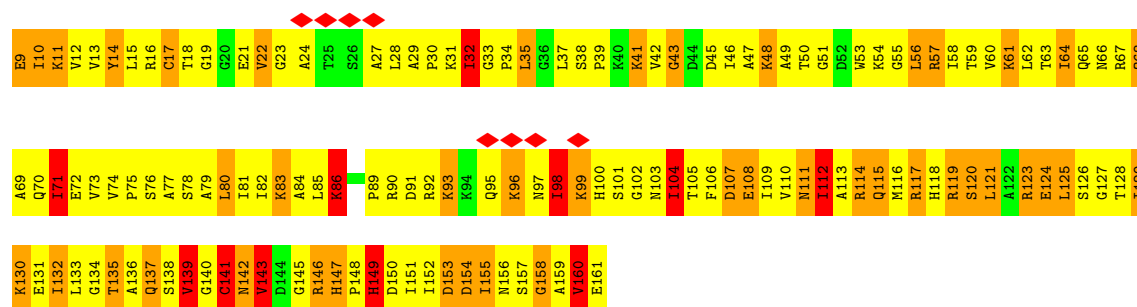
- Molecule 77: 60S acidic ribosomal protein P0

Chain s:  43% 42% 14%



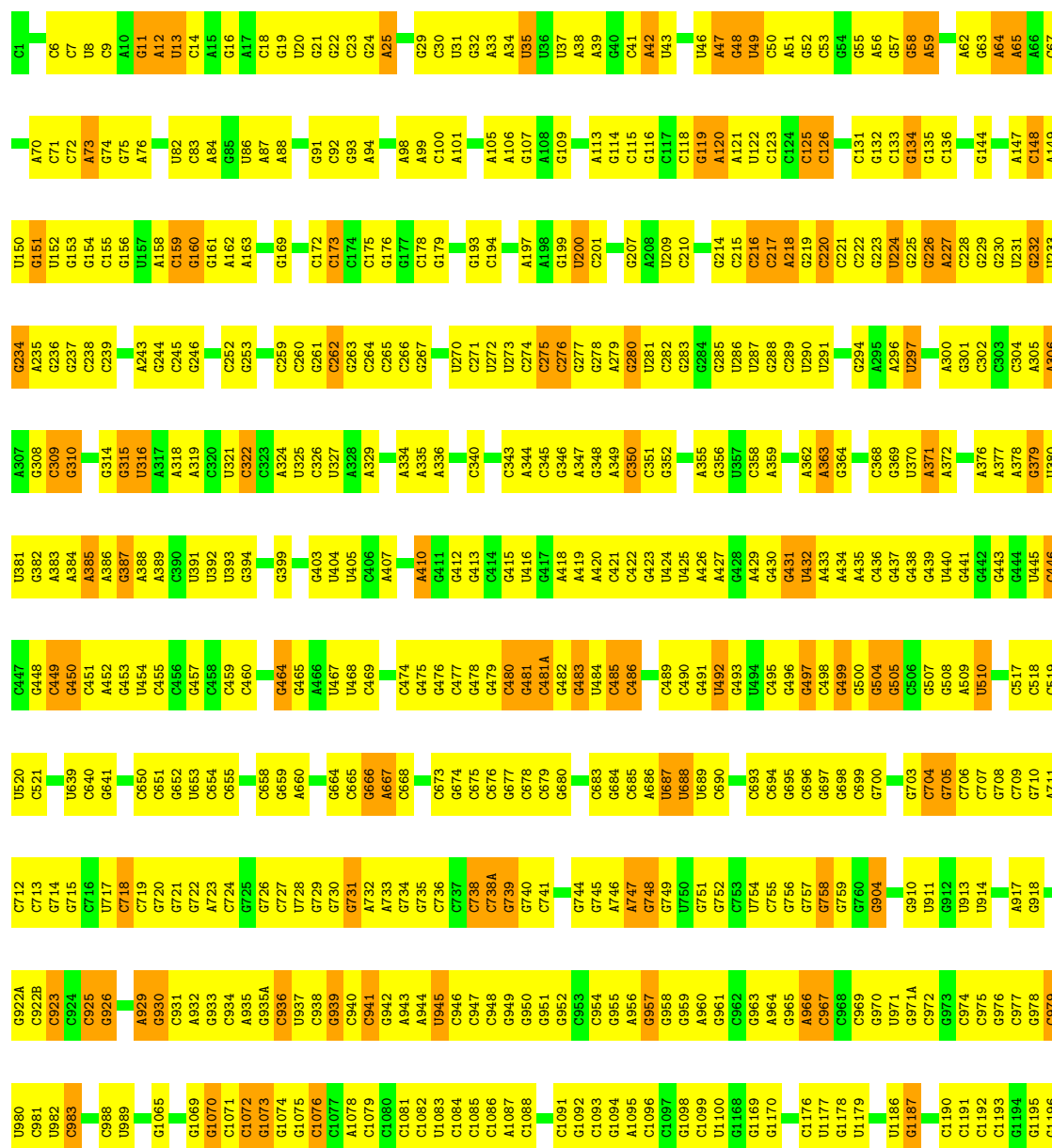
- Molecule 78: uL11

Chain t:  5% 8% 56% 29% 7%



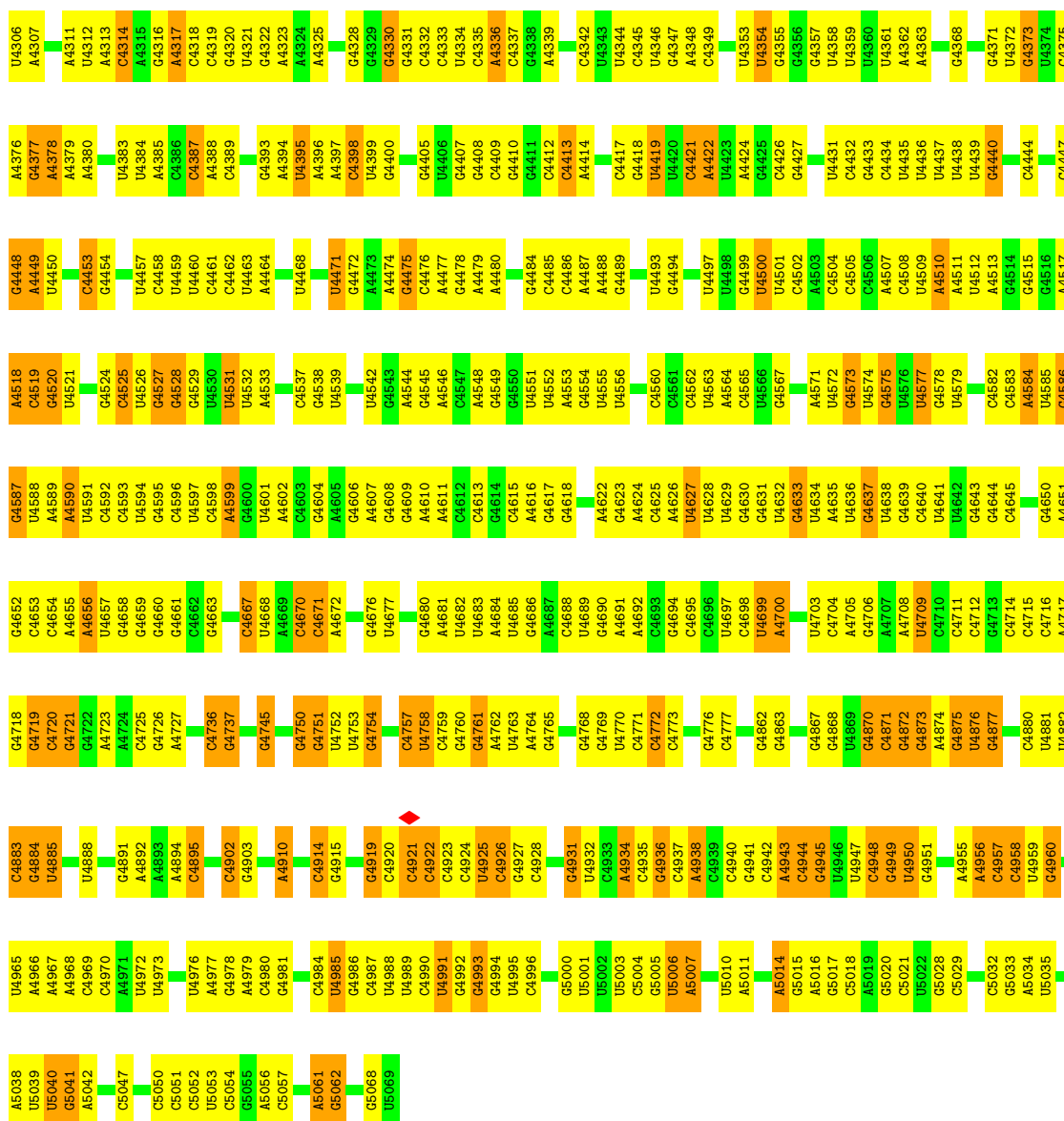
Molecule 79: 28S rRNA

Chain 5: 31% 55% 14%



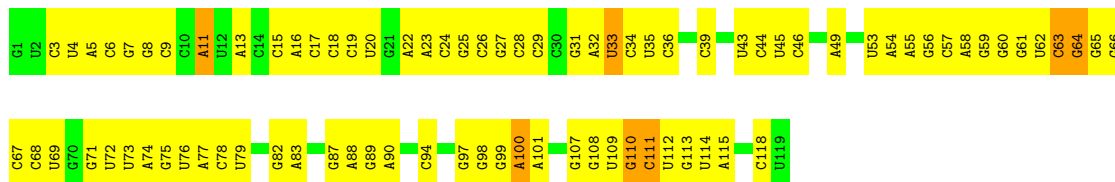






• Molecule 80: 5S rRNA

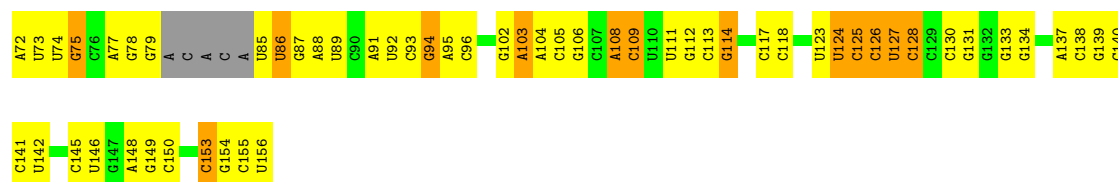
Chain 7: 30% 64% 6%



• Molecule 81: 5.8S rRNA

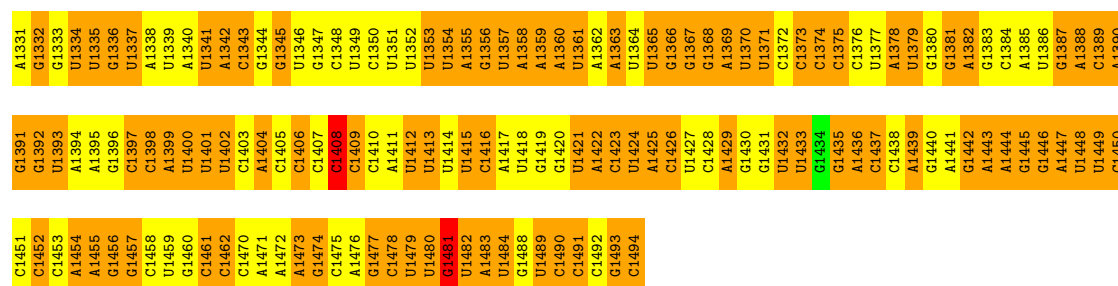
Chain 8: 29% 53% 14%





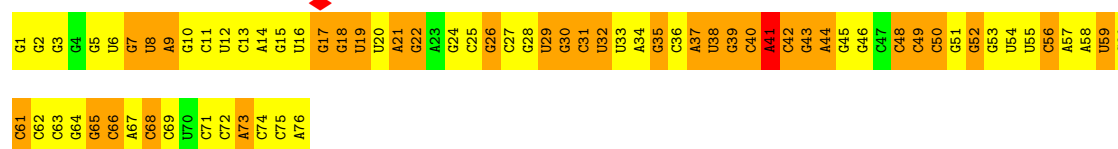
• Molecule 82: NediV IRES

Chain 1: 36% 62%



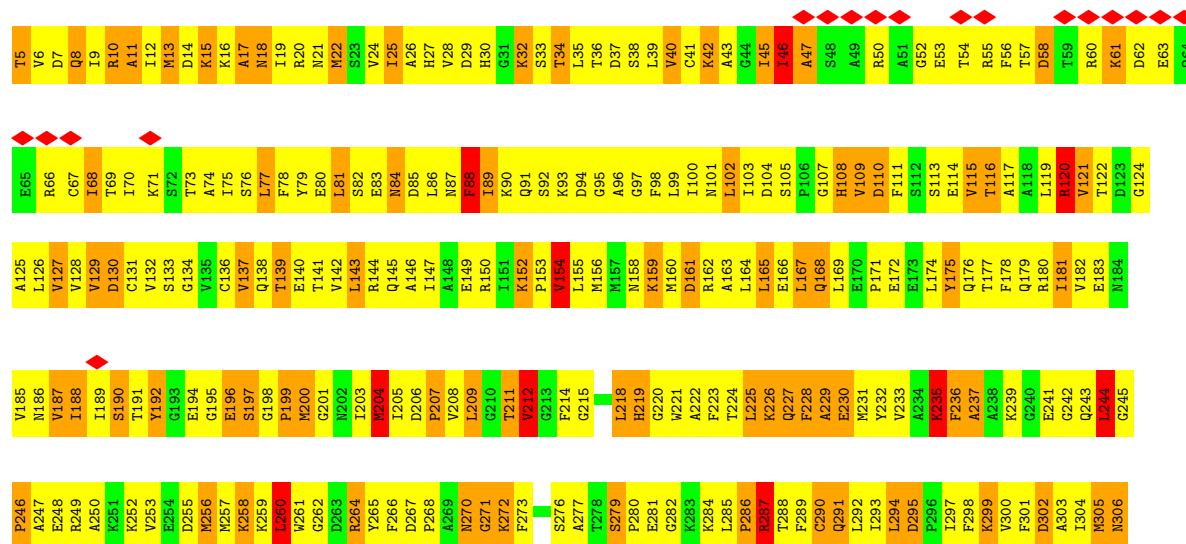
• Molecule 83: ala-tRNA

Chain PT: 5% 51% 42%



• Molecule 84: Elongation factor 2

Chain EF: 12% 55% 30%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	17367	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	1.926	Depositor
Minimum map value	-0.872	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.105	Depositor
Recommended contour level	0.15	Depositor
Map size (\AA)	597.6, 597.6, 597.6	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.66, 1.66, 1.66	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, DDE, 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	DD	0.12	0/1796	0.31	0/2417
2	FF	0.10	0/1492	0.29	0/2005
3	KK	0.10	0/834	0.29	0/1125
4	MM	0.12	0/918	0.35	0/1233
5	PP	0.13	0/937	0.33	0/1250
6	QQ	0.10	0/1146	0.28	0/1534
7	RR	0.15	0/1082	0.42	0/1452
8	SS	0.11	0/1208	0.31	0/1618
9	TT	0.10	0/1115	0.33	0/1493
10	UU	0.11	0/805	0.31	0/1081
11	ZZ	0.10	0/604	0.27	0/810
12	cc	0.09	0/490	0.30	0/656
13	dd	0.12	0/470	0.36	0/623
14	ff	0.09	0/567	0.31	0/753
15	gg	0.10	0/2493	0.29	0/3394
16	R	0.09	0/1524	0.25	0/2013
17	W	0.10	0/743	0.26	0/984
18	9	0.10	0/40500	0.25	0/63092
19	AA	0.13	0/1747	0.38	1/2374 (0.0%)
20	BB	0.10	0/1756	0.27	0/2350
21	CC	0.11	0/1753	0.30	0/2369
22	EE	0.10	0/2118	0.30	0/2849
23	GG	0.10	0/1946	0.28	1/2590 (0.0%)
24	HH	0.10	0/1510	0.32	0/2022
25	II	0.10	0/1715	0.27	0/2287
26	JJ	0.10	0/1550	0.30	2/2069 (0.1%)
27	LL	0.10	0/1195	0.29	0/1597
28	NN	0.10	0/1226	0.27	0/1649
29	OO	0.10	0/1029	0.31	0/1380
30	VV	0.10	0/643	0.28	0/860
31	WW	0.12	0/1051	0.31	0/1406
32	XX	0.12	0/1116	0.34	0/1490

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	YY	0.09	0/1028	0.27	0/1366
34	aa	0.10	0/828	0.30	0/1109
35	bb	0.11	0/665	0.27	0/891
36	ee	0.09	0/462	0.27	0/607
37	A	0.13	0/1936	0.33	0/2596
38	B	0.10	0/3240	0.29	0/4339
39	C	0.10	0/2937	0.28	0/3946
40	D	0.11	0/2437	0.28	0/3264
41	E	0.11	0/1762	0.28	0/2362
42	F	0.10	0/1911	0.28	0/2549
43	G	0.10	0/1910	0.26	0/2569
44	H	0.12	0/1535	0.32	0/2063
45	I	0.12	0/1702	0.27	0/2272
46	J	0.10	0/1385	0.31	0/1852
47	L	0.10	0/1733	0.29	0/2316
48	M	0.12	0/1158	0.28	0/1547
49	N	0.10	0/1746	0.28	0/2338
50	O	0.12	0/1662	0.29	0/2222
51	P	0.09	0/1268	0.28	0/1700
52	Q	0.11	0/1539	0.29	0/2054
53	S	0.11	0/1501	0.31	0/2012
54	T	0.11	0/1326	0.29	0/1770
55	U	0.10	0/823	0.30	0/1104
56	V	0.11	0/1048	0.29	0/1402
57	X	0.09	0/984	0.24	0/1323
58	Y	0.09	0/1132	0.27	0/1504
59	Z	0.11	0/1130	0.28	0/1507
60	a	0.10	0/1191	0.28	0/1590
61	b	0.09	0/861	0.26	0/1138
62	c	0.10	0/771	0.26	0/1034
63	d	0.12	0/903	0.28	0/1216
64	e	0.09	0/1071	0.27	0/1429
65	f	0.12	0/895	0.29	0/1198
66	g	0.10	0/916	0.31	0/1220
67	h	0.09	0/1021	0.23	0/1348
68	i	0.11	0/841	0.30	0/1112
69	j	0.10	0/720	0.32	0/952
70	k	0.09	0/575	0.25	0/761
71	l	0.10	0/459	0.25	0/608
72	m	0.11	0/435	0.29	0/575
73	n	0.08	0/240	0.19	0/305
74	o	0.10	0/864	0.27	0/1140
75	p	0.08	0/718	0.26	0/953

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	r	0.10	0/1010	0.31	0/1354
77	s	0.69	0/1530	1.06	20/2064 (1.0%)
78	t	0.58	0/1174	0.99	8/1582 (0.5%)
79	5	0.12	8/84945 (0.0%)	0.26	0/132460
80	7	0.08	0/2836	0.19	0/4421
81	8	0.09	0/3581	0.23	0/5577
82	1	0.38	0/3639	0.76	2/5659 (0.0%)
83	PT	0.36	0/1811	0.72	2/2820 (0.1%)
84	EF	1.17	14/6767 (0.2%)	1.32	116/9139 (1.3%)
All	All	0.24	22/239641 (0.0%)	0.37	152/351064 (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
32	XX	0	1

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	EF	709	LEU	CA-C	-7.22	1.44	1.53
84	EF	708	THR	CA-C	-7.07	1.44	1.53
84	EF	595	SER	CA-C	-6.72	1.45	1.53
79	5	904	G	C1'-N9	-6.59	1.38	1.48
84	EF	836	ALA	C-O	-6.39	1.16	1.24

The worst 5 of 152 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	EF	841	ARG	N-CA-C	-13.82	94.53	111.11
84	EF	617	ILE	N-CA-C	-13.04	97.32	110.62
84	EF	552	LEU	N-CA-C	-12.65	97.49	111.28
84	EF	371	LEU	N-CA-C	-11.42	98.60	112.54
84	EF	456	ARG	N-CA-C	-10.94	97.98	111.11

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
32	XX	61	GLN	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	DD	1768	0	1866	93	0
2	FF	1471	0	1522	91	0
3	KK	810	0	836	36	0
4	MM	908	0	939	64	0
5	PP	921	0	964	61	0
6	QQ	1128	0	1195	71	0
7	RR	1068	0	1121	92	0
8	SS	1190	0	1249	71	0
9	TT	1097	0	1132	64	0
10	UU	795	0	862	62	0
11	ZZ	598	0	656	25	0
12	cc	488	0	514	34	0
13	dd	459	0	448	24	0
14	ff	555	0	563	27	0
15	gg	2436	0	2393	121	0
16	R	1508	0	1664	101	0
17	W	732	0	769	19	0
18	9	36229	0	18309	1043	0
19	AA	1710	0	1708	183	0
20	BB	1729	0	1803	110	0
21	CC	1716	0	1806	121	0
22	EE	2076	0	2177	108	0
23	GG	1923	0	2089	108	0
24	HH	1488	0	1582	82	0
25	II	1686	0	1772	76	0
26	JJ	1525	0	1640	95	0
27	LL	1175	0	1249	75	0
28	NN	1202	0	1289	66	0
29	OO	1016	0	1039	84	0
30	VV	636	0	637	41	0
31	WW	1034	0	1080	79	0
32	XX	1098	0	1167	70	0
33	YY	1011	0	1083	66	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	aa	814	0	863	52	0
35	bb	651	0	672	30	0
36	ee	457	0	502	30	0
37	A	1898	0	1993	133	0
38	B	3172	0	3310	171	0
39	C	2883	0	3053	181	0
40	D	2391	0	2424	124	0
41	E	1729	0	1887	102	0
42	F	1875	0	1995	134	0
43	G	1879	0	2027	122	0
44	H	1516	0	1597	100	0
45	I	1664	0	1712	90	0
46	J	1362	0	1399	68	0
47	L	1702	0	1820	93	0
48	M	1137	0	1211	83	0
49	N	1701	0	1749	115	0
50	O	1630	0	1778	126	0
51	P	1242	0	1274	61	0
52	Q	1515	0	1634	110	0
53	S	1462	0	1508	89	0
54	T	1298	0	1366	66	0
55	U	809	0	833	40	0
56	V	1034	0	1097	60	0
57	X	967	0	1040	63	0
58	Y	1115	0	1205	65	0
59	Z	1107	0	1182	69	0
60	a	1162	0	1209	73	0
61	b	848	0	920	45	0
62	c	761	0	794	45	0
63	d	888	0	930	46	0
64	e	1053	0	1147	66	0
65	f	876	0	912	57	0
66	g	906	0	998	52	0
67	h	1013	0	1147	69	0
68	i	830	0	916	51	0
69	j	705	0	737	44	0
70	k	569	0	637	25	0
71	l	447	0	480	29	0
72	m	429	0	465	21	0
73	n	239	0	289	8	0
74	o	851	0	920	39	0
75	p	708	0	756	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
76	r	994	0	1051	58	0
77	s	1507	0	1549	945	0
78	t	1160	0	1216	593	0
79	5	75952	0	38383	2251	0
80	7	2538	0	1286	75	0
81	8	3208	0	1629	108	0
82	1	3261	0	1653	455	0
83	PT	1622	823	823	131	0
84	EF	6659	6746	6745	1218	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
86	5	185	0	0	0	0
86	7	6	0	0	0	0
86	8	5	0	0	0	0
86	B	1	0	0	0	0
86	I	1	0	0	0	0
86	P	1	0	0	0	0
86	Q	1	0	0	0	0
86	V	1	0	0	0	0
86	a	2	0	0	0	0
86	aa	1	0	0	0	0
86	g	1	0	0	0	0
86	j	1	0	0	0	0
All	All	223596	7569	167846	11022	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 28.

The worst 5 of 11022 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)
77:s:130:LEU:HD21	77:s:132:PRO:CG	1.18	1.63
77:s:101:MET:CE	77:s:102:LEU:HD22	1.36	1.52
77:s:130:LEU:CD2	77:s:132:PRO:HG3	1.07	1.51
77:s:18:ILE:C	77:s:21:LEU:HB2	1.10	1.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:s:18:ILE:CA	77:s:21:LEU:HG	1.35	1.49

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	DD	226/228 (99%)	221 (98%)	4 (2%)	1 (0%)	30	65
2	FF	181/191 (95%)	178 (98%)	3 (2%)	0	100	100
3	KK	94/96 (98%)	91 (97%)	3 (3%)	0	100	100
4	MM	115/117 (98%)	106 (92%)	9 (8%)	0	100	100
5	PP	109/111 (98%)	103 (94%)	6 (6%)	0	100	100
6	QQ	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
7	RR	130/132 (98%)	124 (95%)	6 (5%)	0	100	100
8	SS	142/144 (99%)	140 (99%)	2 (1%)	0	100	100
9	TT	139/141 (99%)	137 (99%)	2 (1%)	0	100	100
10	UU	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
11	ZZ	73/75 (97%)	72 (99%)	1 (1%)	0	100	100
12	cc	60/62 (97%)	60 (100%)	0	0	100	100
13	dd	53/55 (96%)	53 (100%)	0	0	100	100
14	ff	66/68 (97%)	64 (97%)	2 (3%)	0	100	100
15	gg	311/313 (99%)	302 (97%)	9 (3%)	0	100	100
16	R	178/180 (99%)	175 (98%)	3 (2%)	0	100	100
17	W	85/121 (70%)	84 (99%)	1 (1%)	0	100	100
19	AA	215/217 (99%)	202 (94%)	13 (6%)	0	100	100
20	BB	211/213 (99%)	201 (95%)	10 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	CC	219/221 (99%)	213 (97%)	6 (3%)	0	100	100
22	EE	260/262 (99%)	252 (97%)	8 (3%)	0	100	100
23	GG	235/237 (99%)	232 (99%)	3 (1%)	0	100	100
24	HH	181/189 (96%)	178 (98%)	3 (2%)	0	100	100
25	II	204/206 (99%)	193 (95%)	11 (5%)	0	100	100
26	JJ	183/185 (99%)	180 (98%)	3 (2%)	0	100	100
27	LL	139/151 (92%)	132 (95%)	7 (5%)	0	100	100
28	NN	147/149 (99%)	144 (98%)	3 (2%)	0	100	100
29	OO	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
30	VV	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
31	WW	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
32	XX	139/141 (99%)	133 (96%)	5 (4%)	1 (1%)	18	55
33	YY	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
34	aa	99/101 (98%)	95 (96%)	4 (4%)	0	100	100
35	bb	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
36	ee	55/57 (96%)	53 (96%)	2 (4%)	0	100	100
37	A	246/248 (99%)	239 (97%)	7 (3%)	0	100	100
38	B	392/394 (100%)	383 (98%)	8 (2%)	1 (0%)	36	70
39	C	360/362 (99%)	353 (98%)	7 (2%)	0	100	100
40	D	291/293 (99%)	282 (97%)	8 (3%)	1 (0%)	36	70
41	E	208/251 (83%)	205 (99%)	3 (1%)	0	100	100
42	F	223/225 (99%)	218 (98%)	5 (2%)	0	100	100
43	G	229/240 (95%)	226 (99%)	3 (1%)	0	100	100
44	H	188/190 (99%)	185 (98%)	3 (2%)	0	100	100
45	I	201/213 (94%)	197 (98%)	4 (2%)	0	100	100
46	J	168/170 (99%)	167 (99%)	1 (1%)	0	100	100
47	L	208/210 (99%)	204 (98%)	4 (2%)	0	100	100
48	M	136/138 (99%)	130 (96%)	6 (4%)	0	100	100
49	N	201/203 (99%)	198 (98%)	3 (2%)	0	100	100
50	O	197/199 (99%)	192 (98%)	5 (2%)	0	100	100
51	P	151/153 (99%)	146 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	Q	185/187 (99%)	177 (96%)	8 (4%)	0	100	100
53	S	174/176 (99%)	169 (97%)	5 (3%)	0	100	100
54	T	157/159 (99%)	153 (98%)	4 (2%)	0	100	100
55	U	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
56	V	137/139 (99%)	132 (96%)	5 (4%)	0	100	100
57	X	116/118 (98%)	115 (99%)	1 (1%)	0	100	100
58	Y	132/134 (98%)	132 (100%)	0	0	100	100
59	Z	133/135 (98%)	128 (96%)	5 (4%)	0	100	100
60	a	145/147 (99%)	142 (98%)	3 (2%)	0	100	100
61	b	100/116 (86%)	98 (98%)	2 (2%)	0	100	100
62	c	96/98 (98%)	94 (98%)	2 (2%)	0	100	100
63	d	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
64	e	126/128 (98%)	125 (99%)	1 (1%)	0	100	100
65	f	107/109 (98%)	103 (96%)	4 (4%)	0	100	100
66	g	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
67	h	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
68	i	100/102 (98%)	98 (98%)	2 (2%)	0	100	100
69	j	84/86 (98%)	82 (98%)	2 (2%)	0	100	100
70	k	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
71	l	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
72	m	50/52 (96%)	50 (100%)	0	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%)	86 (97%)	3 (3%)	0	100	100
76	r	122/124 (98%)	117 (96%)	5 (4%)	0	100	100
77	s	194/196 (99%)	101 (52%)	50 (26%)	43 (22%)	0	1
78	t	151/153 (99%)	93 (62%)	44 (29%)	14 (9%)	0	9
84	EF	850/853 (100%)	550 (65%)	225 (26%)	75 (9%)	0	10
All	All	12353/12642 (98%)	11614 (94%)	603 (5%)	136 (1%)	14	44

5 of 136 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
32	XX	62	PRO
77	s	6	ARG
77	s	7	ALA
77	s	8	THR
77	s	10	LYS

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	DD	190/190 (100%)	185 (97%)	5 (3%)	40	61
2	FF	158/161 (98%)	153 (97%)	5 (3%)	34	56
3	KK	87/87 (100%)	82 (94%)	5 (6%)	18	43
4	MM	99/99 (100%)	93 (94%)	6 (6%)	17	41
5	PP	101/101 (100%)	95 (94%)	6 (6%)	18	42
6	QQ	117/117 (100%)	113 (97%)	4 (3%)	32	55
7	RR	119/119 (100%)	111 (93%)	8 (7%)	15	39
8	SS	125/125 (100%)	122 (98%)	3 (2%)	43	63
9	TT	111/111 (100%)	106 (96%)	5 (4%)	24	48
10	UU	92/92 (100%)	90 (98%)	2 (2%)	45	64
11	ZZ	66/66 (100%)	64 (97%)	2 (3%)	36	57
12	cc	55/55 (100%)	55 (100%)	0	100	100
13	dd	48/48 (100%)	48 (100%)	0	100	100
14	ff	61/61 (100%)	56 (92%)	5 (8%)	10	33
15	gg	272/272 (100%)	266 (98%)	6 (2%)	45	64
16	R	159/159 (100%)	150 (94%)	9 (6%)	18	43
17	W	73/100 (73%)	73 (100%)	0	100	100
19	AA	180/181 (99%)	164 (91%)	16 (9%)	9	30
20	BB	194/194 (100%)	185 (95%)	9 (5%)	24	47
21	CC	187/187 (100%)	181 (97%)	6 (3%)	34	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	EE	224/224 (100%)	216 (96%)	8 (4%)	31	53
23	GG	207/207 (100%)	203 (98%)	4 (2%)	50	67
24	HH	165/169 (98%)	159 (96%)	6 (4%)	31	53
25	II	178/178 (100%)	171 (96%)	7 (4%)	28	51
26	JJ	161/161 (100%)	159 (99%)	2 (1%)	63	73
27	LL	130/136 (96%)	121 (93%)	9 (7%)	14	38
28	NN	130/130 (100%)	125 (96%)	5 (4%)	29	51
29	OO	106/106 (100%)	100 (94%)	6 (6%)	18	43
30	VV	67/67 (100%)	66 (98%)	1 (2%)	57	70
31	WW	112/112 (100%)	109 (97%)	3 (3%)	39	60
32	XX	113/113 (100%)	108 (96%)	5 (4%)	25	48
33	YY	107/107 (100%)	101 (94%)	6 (6%)	19	43
34	aa	88/88 (100%)	85 (97%)	3 (3%)	32	55
35	bb	75/75 (100%)	73 (97%)	2 (3%)	39	60
36	ee	47/47 (100%)	46 (98%)	1 (2%)	47	65
37	A	190/190 (100%)	180 (95%)	10 (5%)	20	44
38	B	342/342 (100%)	327 (96%)	15 (4%)	25	48
39	C	302/302 (100%)	289 (96%)	13 (4%)	26	49
40	D	247/247 (100%)	239 (97%)	8 (3%)	34	56
41	E	190/223 (85%)	180 (95%)	10 (5%)	20	44
42	F	196/196 (100%)	186 (95%)	10 (5%)	21	45
43	G	200/205 (98%)	193 (96%)	7 (4%)	32	54
44	H	169/169 (100%)	162 (96%)	7 (4%)	27	50
45	I	175/180 (97%)	166 (95%)	9 (5%)	21	45
46	J	143/143 (100%)	133 (93%)	10 (7%)	14	38
47	L	175/175 (100%)	169 (97%)	6 (3%)	32	55
48	M	117/117 (100%)	112 (96%)	5 (4%)	26	49
49	N	171/171 (100%)	166 (97%)	5 (3%)	37	58
50	O	171/171 (100%)	166 (97%)	5 (3%)	37	58
51	P	134/134 (100%)	134 (100%)	0	100	100
52	Q	164/164 (100%)	156 (95%)	8 (5%)	22	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	S	157/157 (100%)	149 (95%)	8 (5%)	21	45
54	T	139/139 (100%)	133 (96%)	6 (4%)	26	49
55	U	89/89 (100%)	86 (97%)	3 (3%)	32	55
56	V	106/106 (100%)	96 (91%)	10 (9%)	8	28
57	X	106/106 (100%)	101 (95%)	5 (5%)	23	47
58	Y	124/124 (100%)	119 (96%)	5 (4%)	28	50
59	Z	117/117 (100%)	115 (98%)	2 (2%)	53	68
60	a	119/119 (100%)	118 (99%)	1 (1%)	73	77
61	b	84/95 (88%)	82 (98%)	2 (2%)	43	63
62	c	84/84 (100%)	82 (98%)	2 (2%)	43	63
63	d	98/98 (100%)	92 (94%)	6 (6%)	17	41
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%)	91 (93%)	7 (7%)	13	37
67	h	109/109 (100%)	108 (99%)	1 (1%)	70	76
68	i	86/86 (100%)	84 (98%)	2 (2%)	44	64
69	j	73/73 (100%)	71 (97%)	2 (3%)	39	60
70	k	64/64 (100%)	60 (94%)	4 (6%)	16	40
71	l	47/47 (100%)	46 (98%)	1 (2%)	47	65
72	m	48/48 (100%)	48 (100%)	0	100	100
73	n	24/24 (100%)	22 (92%)	2 (8%)	10	32
74	o	92/92 (100%)	87 (95%)	5 (5%)	20	44
75	p	74/74 (100%)	72 (97%)	2 (3%)	39	60
76	r	108/108 (100%)	105 (97%)	3 (3%)	38	59
77	s	164/164 (100%)	87 (53%)	77 (47%)	0	0
78	t	126/126 (100%)	79 (63%)	47 (37%)	0	1
84	EF	725/725 (100%)	564 (78%)	161 (22%)	1	6
All	All	10753/10848 (99%)	10081 (94%)	672 (6%)	18	41

5 of 672 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
77	s	200	ASN

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Mol	Chain	Res	Type
84	EF	333	LYS
78	t	61	LYS
77	s	198	ILE
84	EF	46	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 177 such sidechains are listed below:

Mol	Chain	Res	Type
53	S	125	GLN
74	o	25	GLN
54	T	22	HIS
60	a	67	GLN
77	s	127	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
18	9	1679/1697 (98%)	322 (19%)	20 (1%)
79	5	3519/3543 (99%)	748 (21%)	71 (2%)
80	7	118/119 (99%)	12 (10%)	0
81	8	149/156 (95%)	32 (21%)	2 (1%)
82	1	151/154 (98%)	101 (66%)	22 (14%)
83	PT	75/76 (98%)	39 (52%)	2 (2%)
All	All	5691/5745 (99%)	1254 (22%)	117 (2%)

5 of 1254 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
18	9	3	C
18	9	4	C
18	9	25	A
18	9	33	G
18	9	41	G

5 of 117 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
79	5	1835	G
82	1	1473	A
79	5	2468	U

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Mol	Chain	Res	Type
82	1	1461	C
82	1	1390	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
84	DDE	EF	715	-	18,20,21	7.02	4 (22%)	17,28,30	21.12	9 (52%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
84	DDE	EF	715	-	-	5/20/21/23	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	EF	715	DDE	CD2-NE2	-21.42	0.93	1.36
84	EF	715	DDE	CG-ND1	-19.73	1.01	1.38
84	EF	715	DDE	CD2-CG	-4.03	1.27	1.36
84	EF	715	DDE	CBW-NCB	-2.39	1.49	1.54

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	EF	715	DDE	CD2-NE2-CE1	79.94	174.42	107.55
84	EF	715	DDE	CB-CG-ND1	18.19	176.63	121.68
84	EF	715	DDE	CG-CD2-NE2	-17.51	79.76	106.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	EF	715	DDE	CD2-CG-ND1	-16.05	76.53	108.87
84	EF	715	DDE	CB-CG-CD2	-11.02	106.81	129.33

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
84	EF	715	DDE	CA-CB-CG-CD2
84	EF	715	DDE	CA-CB-CG-ND1
84	EF	715	DDE	CE1-CAT-CAU-CBW
84	EF	715	DDE	NAD-CBI-CBW-NCB
84	EF	715	DDE	NAD-CBI-CBW-CAU

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
84	EF	715	DDE	7	0

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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
79	5	30
18	9	20
82	1	2

The worst 5 of 52 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	41.91
1	5	1252:C	O3'	1271:G	P	36.16
1	1	1484:U	O3'	1488:G	P	22.09
1	5	1219:G	O3'	1233:G	P	21.55
1	5	3948:C	O3'	4065:G	P	19.77

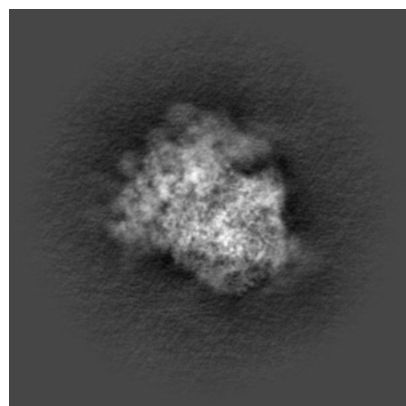
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72175. These allow visual inspection of the internal detail of the map and identification of artifacts.

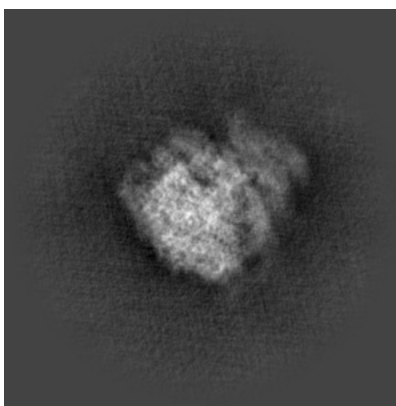
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

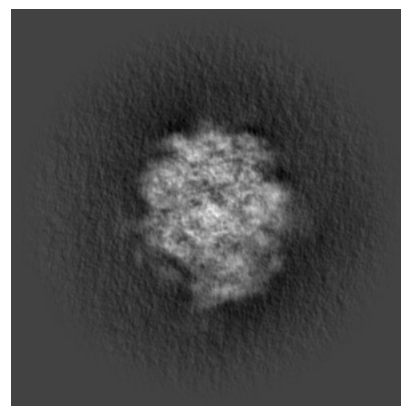
6.1.1 Primary map



X

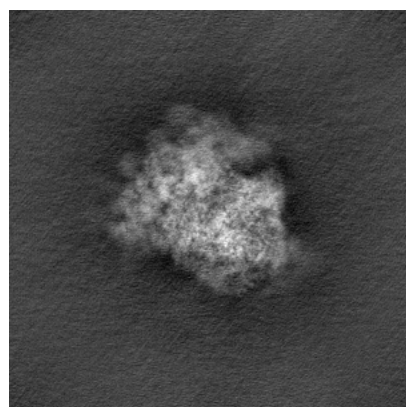


Y

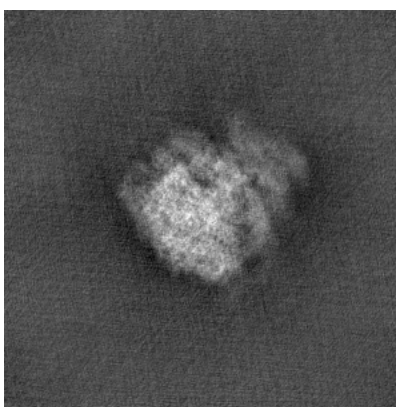


Z

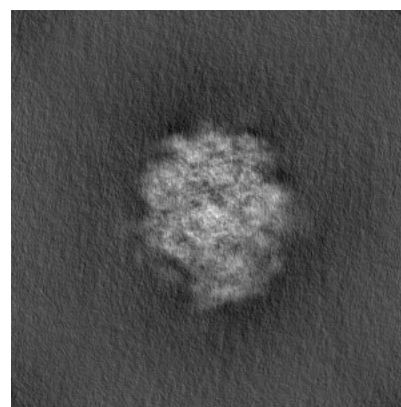
6.1.2 Raw map



X



Y

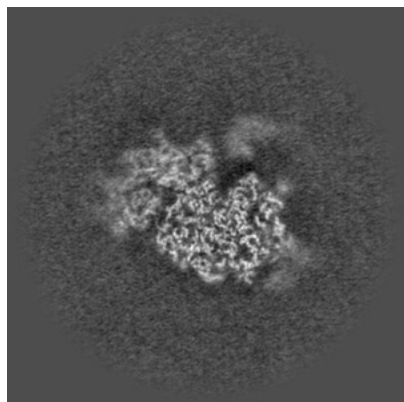


Z

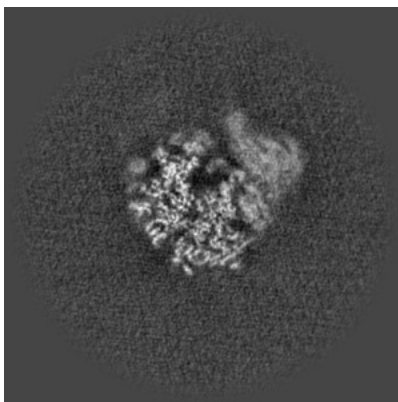
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

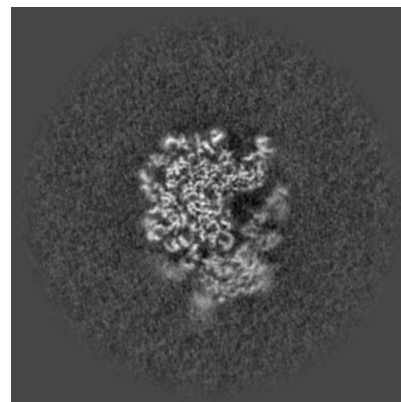
6.2.1 Primary map



X Index: 180

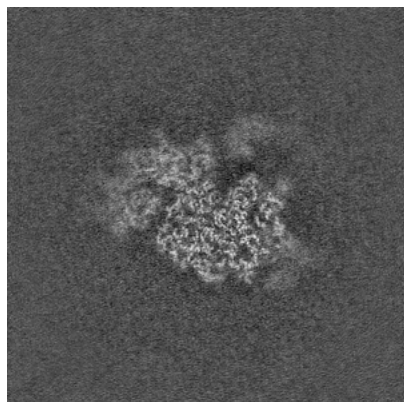


Y Index: 180

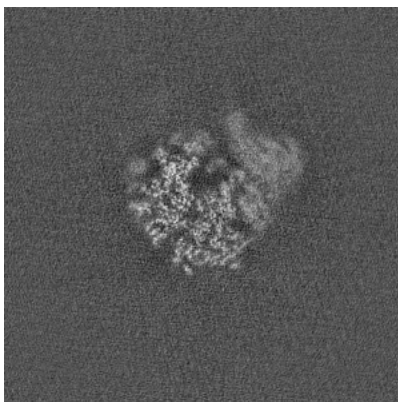


Z Index: 180

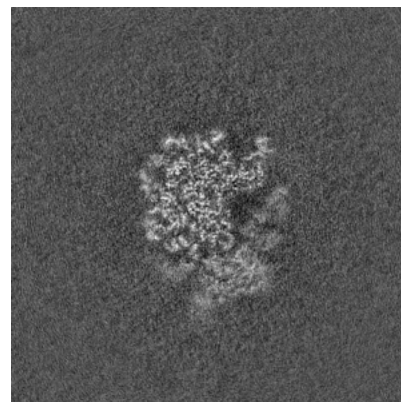
6.2.2 Raw map



X Index: 180



Y Index: 180

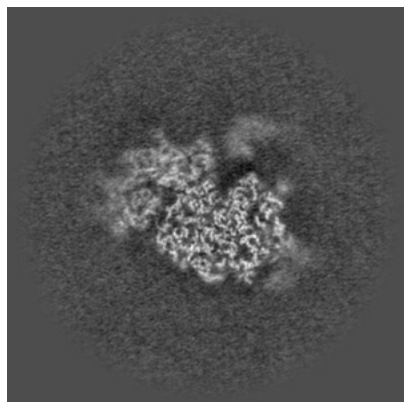


Z Index: 180

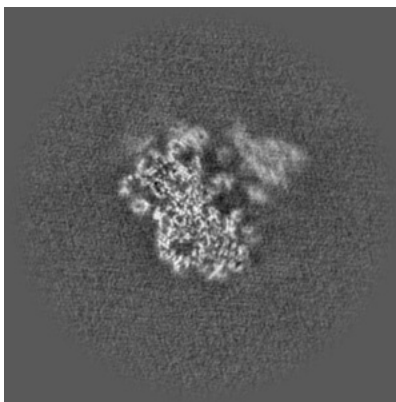
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

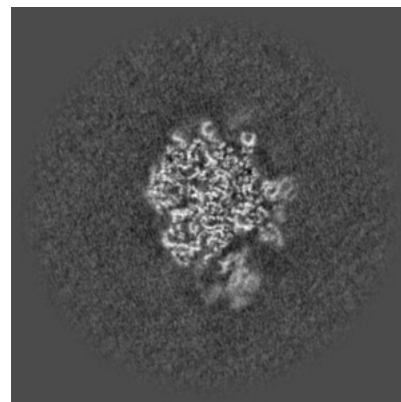
6.3.1 Primary map



X Index: 180

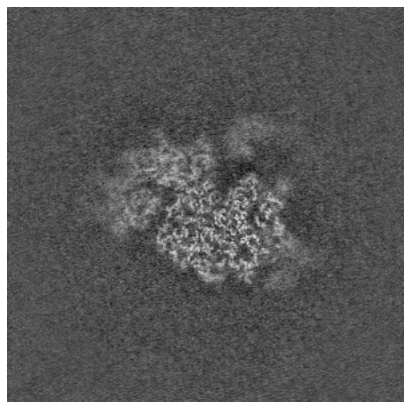


Y Index: 193

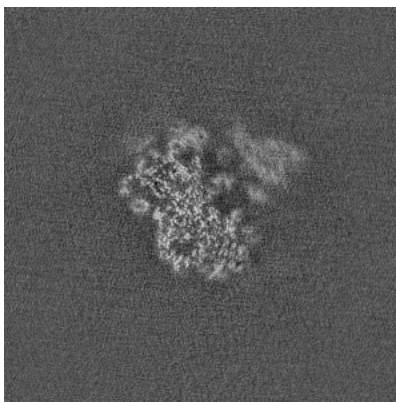


Z Index: 154

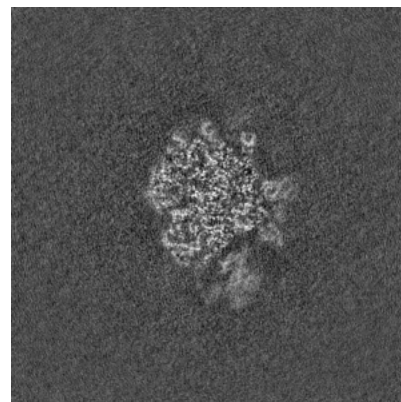
6.3.2 Raw map



X Index: 180



Y Index: 193

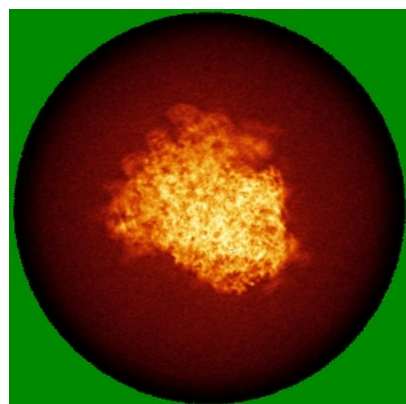


Z Index: 154

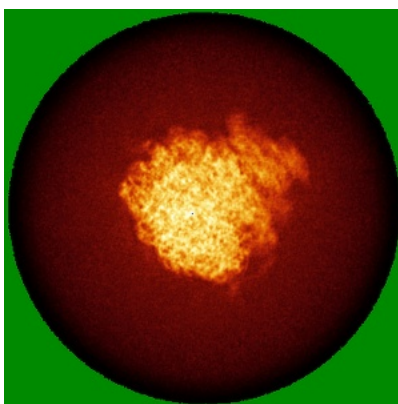
The images above show the largest variance slices of the map in three orthogonal directions.

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

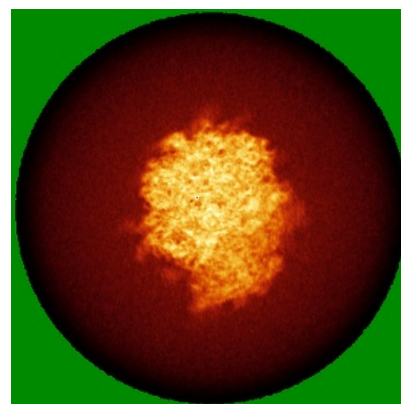
6.4.1 Primary map



X

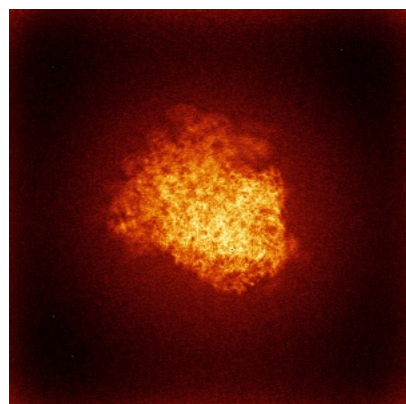


Y

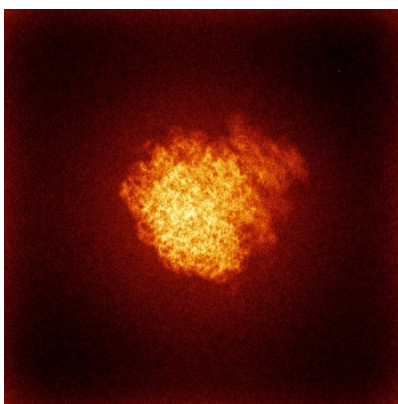


Z

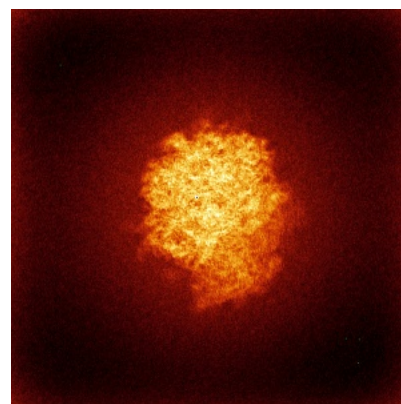
6.4.2 Raw map



X



Y

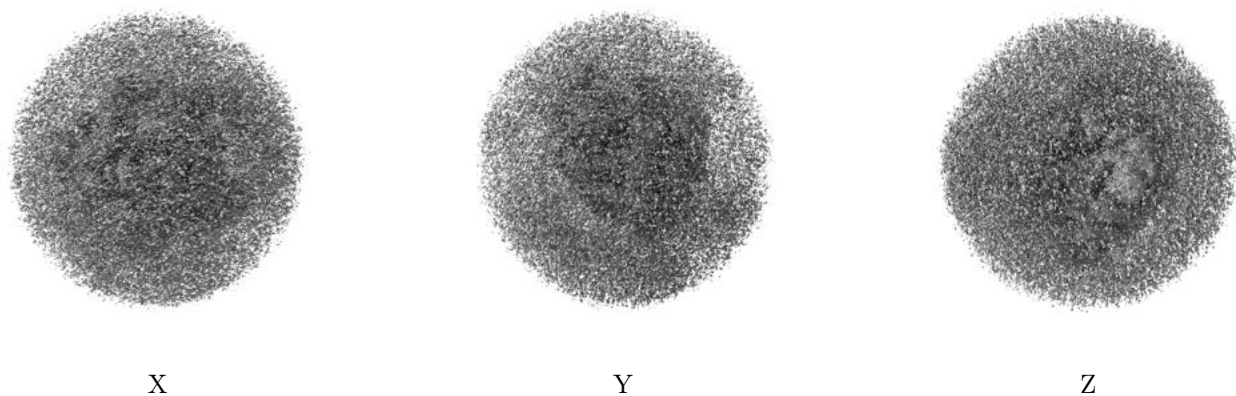


Z

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.

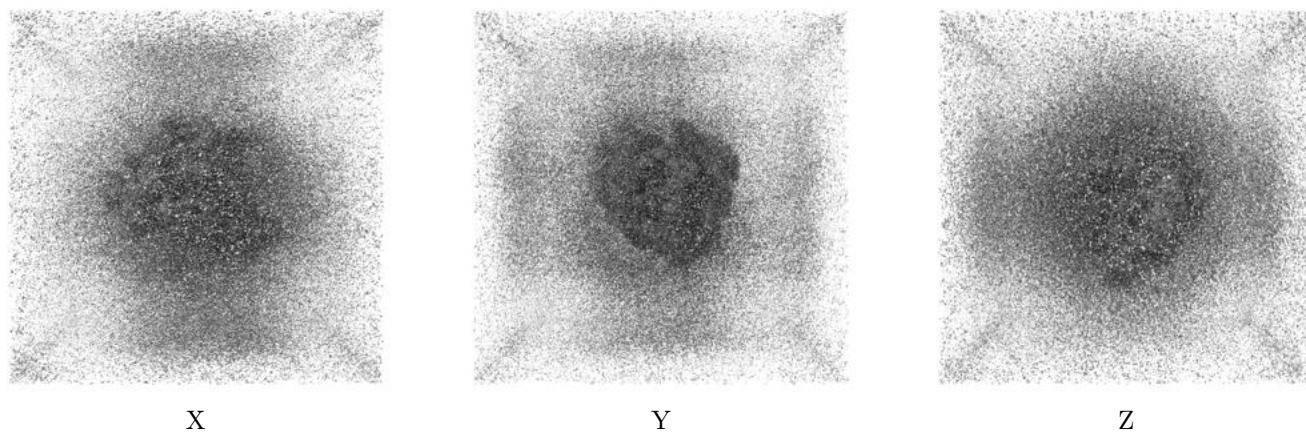
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. 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.

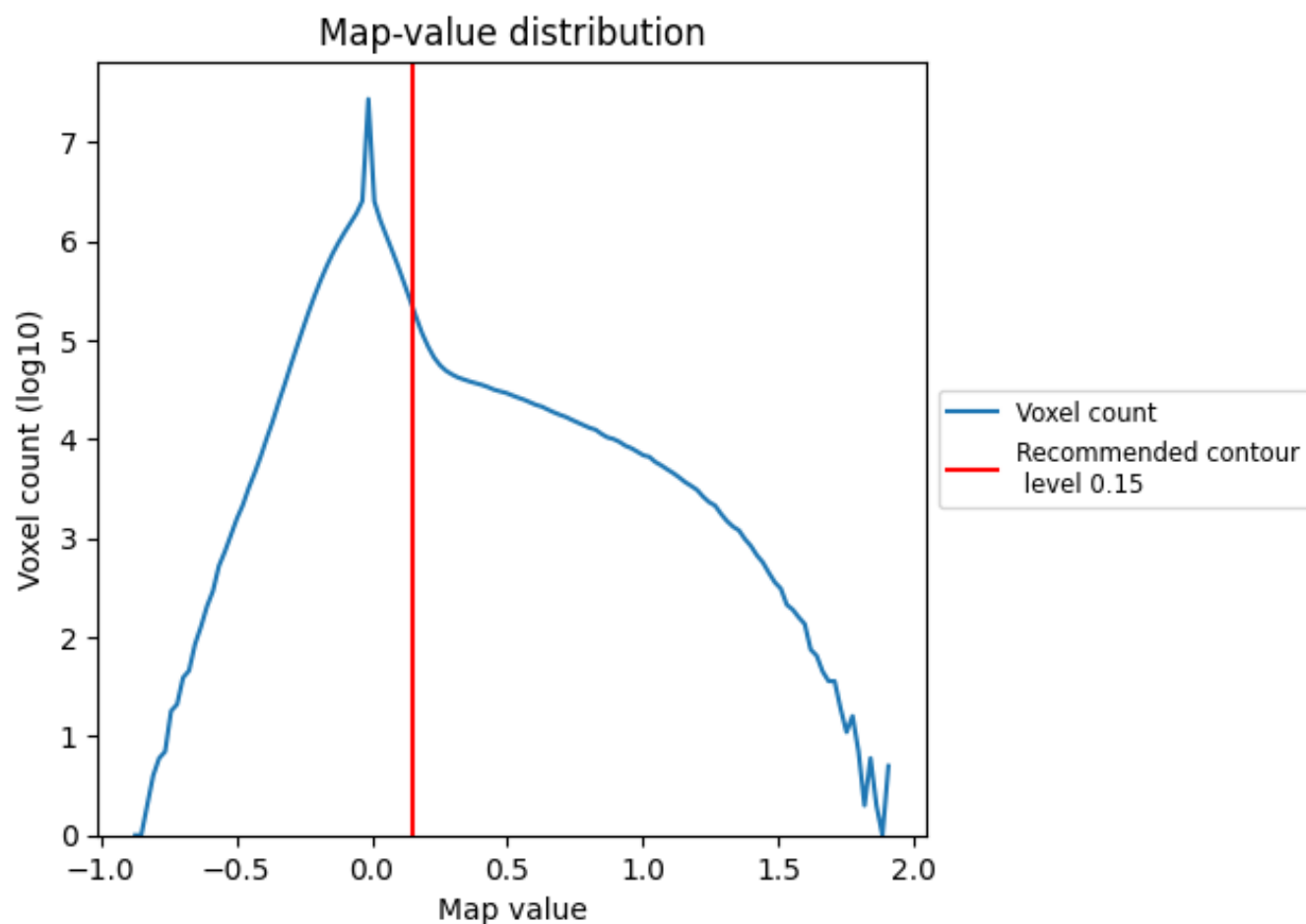
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

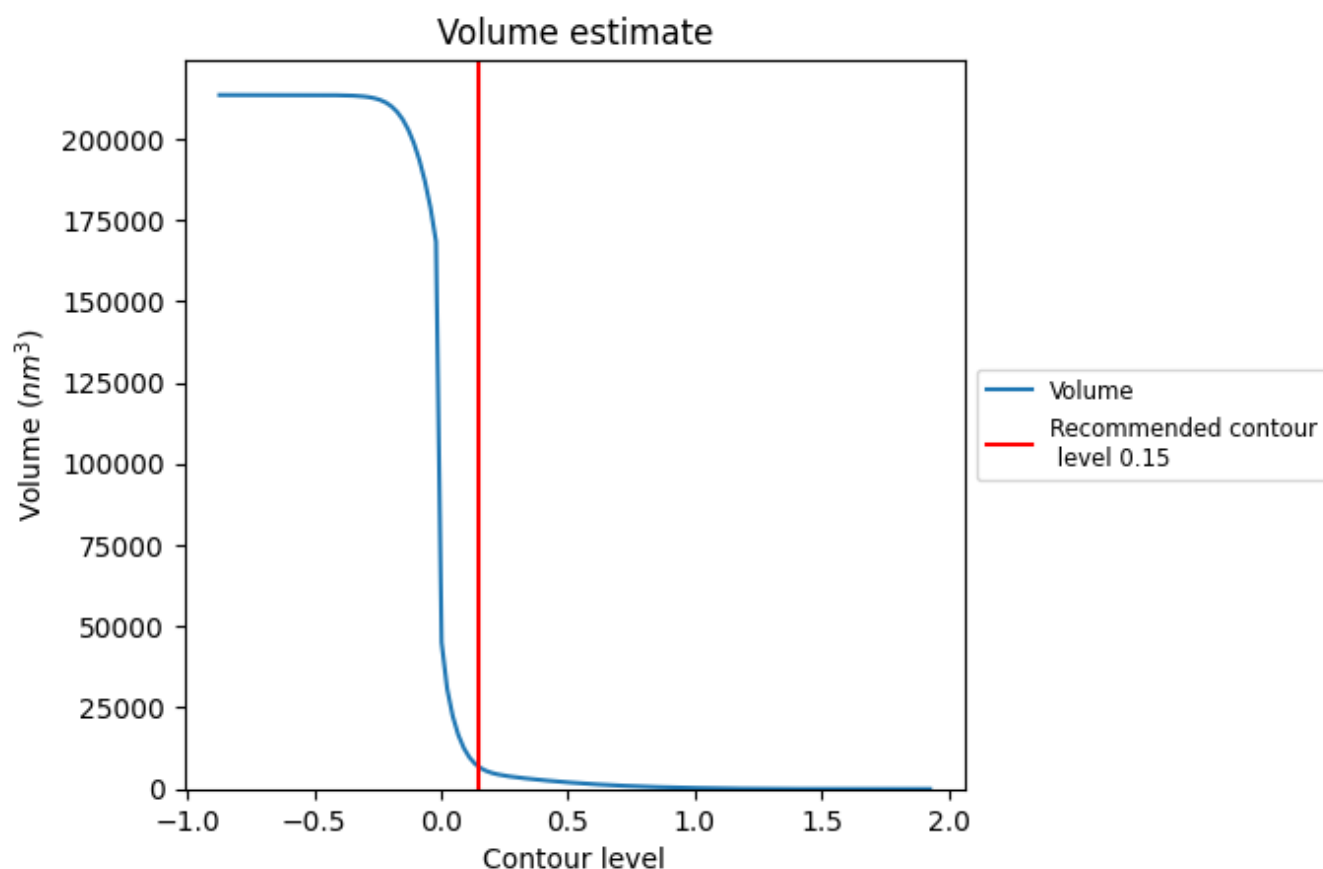
This section contains the results of statistical analysis of the map.

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.

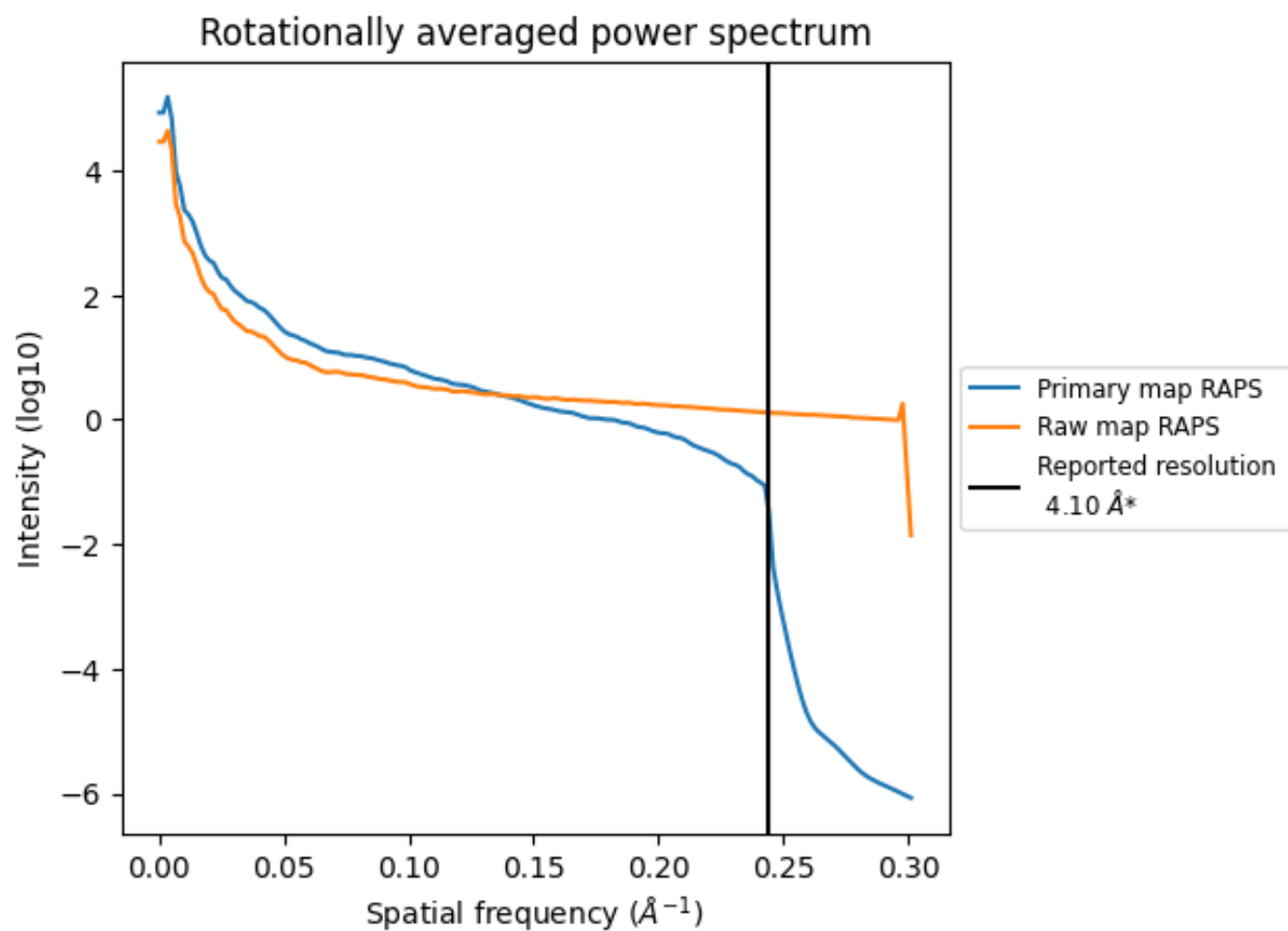
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6774 nm^3 ; this corresponds to an approximate mass of 6119 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 ⓘ

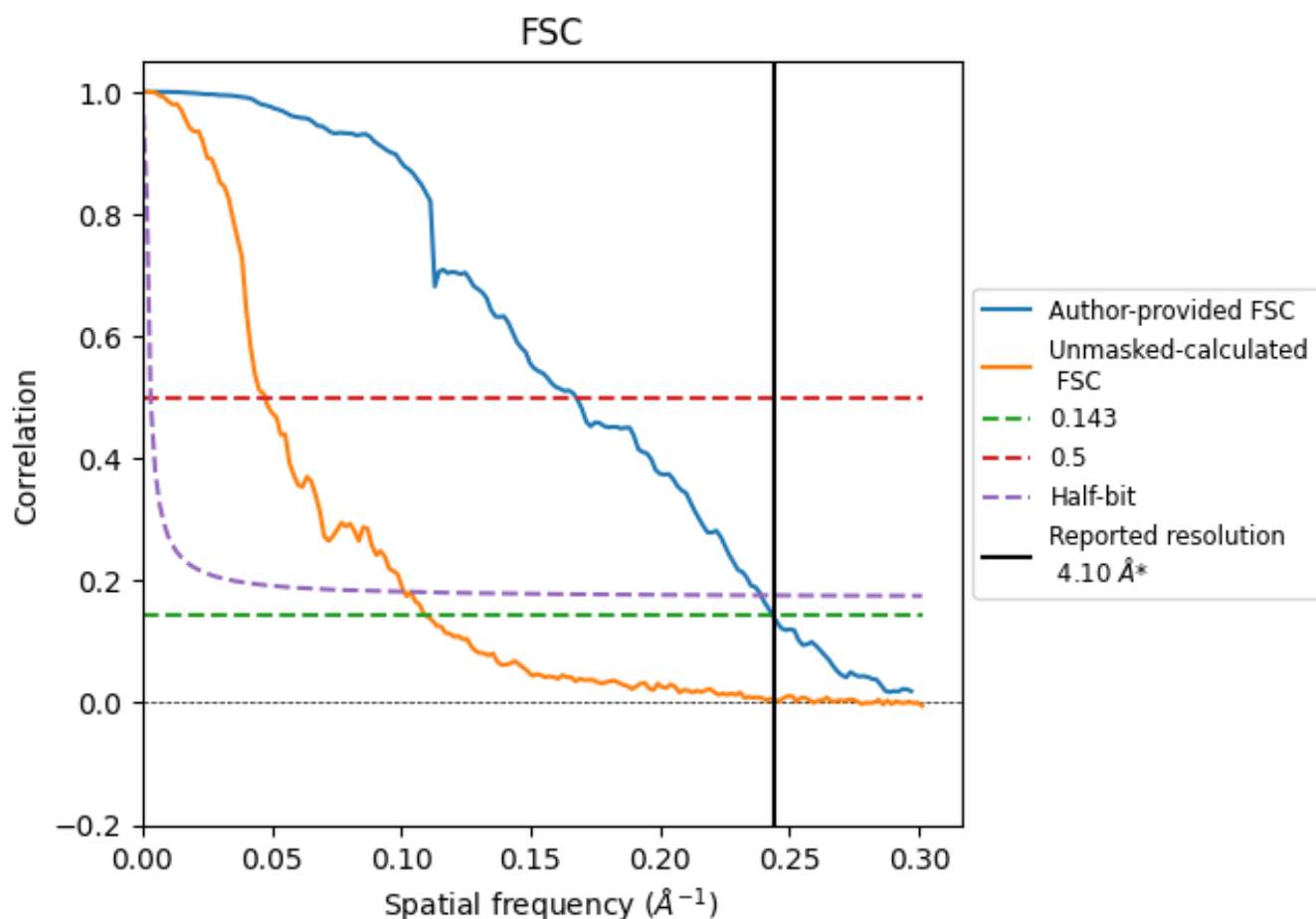


*Reported resolution corresponds to spatial frequency of 0.244 \AA^{-1}

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 \AA^{-1}

8.2 Resolution estimates [i](#)

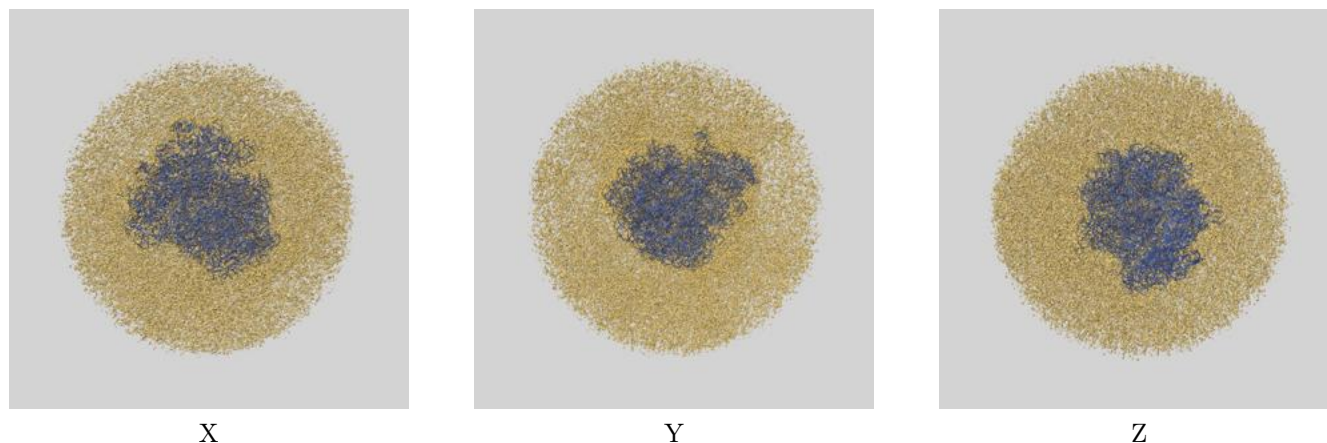
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.11	5.97	4.18
Unmasked-calculated*	9.13	21.14	9.88

*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 9.13 differs from the reported value 4.1 by more than 10 %

9 Map-model fit [i](#)

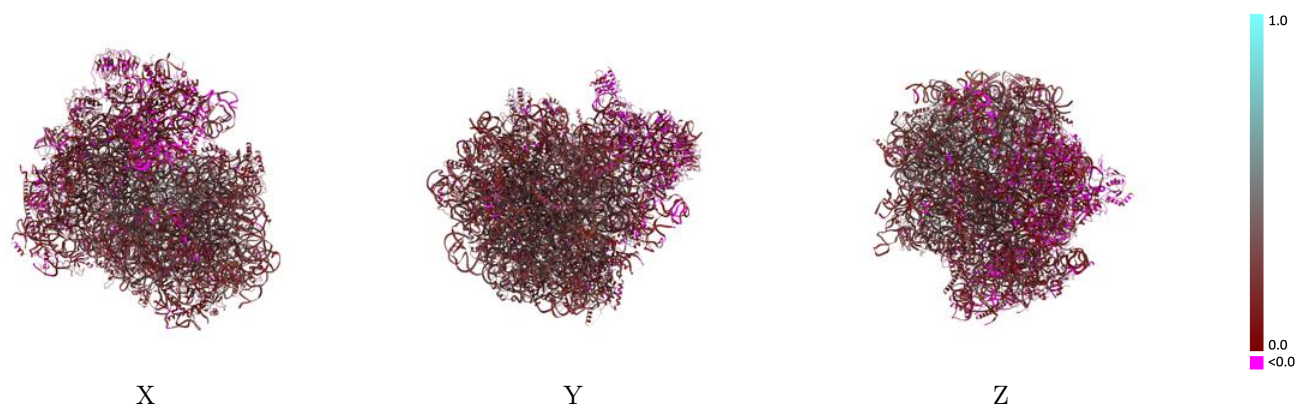
This section contains information regarding the fit between EMDB map EMD-72175 and PDB model 9Q2T. Per-residue inclusion information can be found in [section 3](#) on [page 23](#).

9.1 Map-model overlay [i](#)



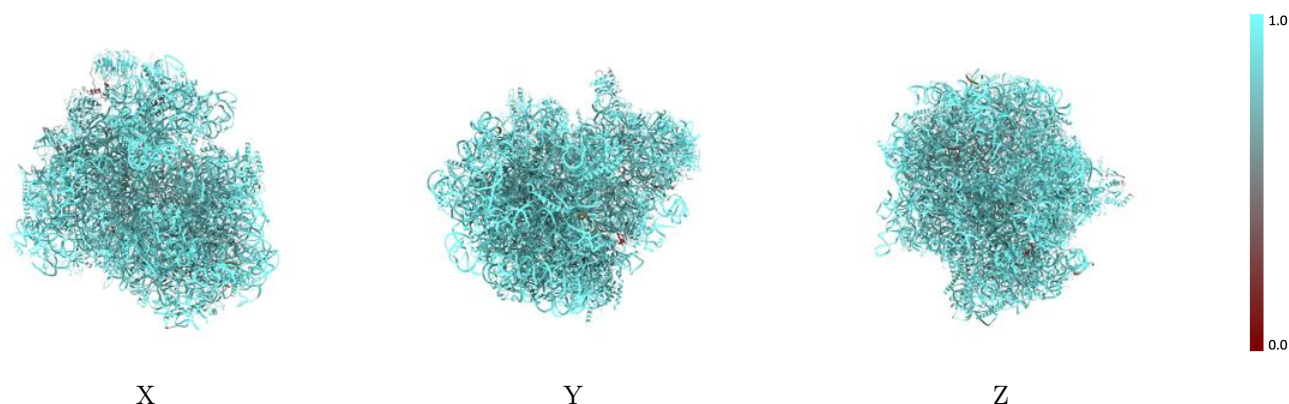
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



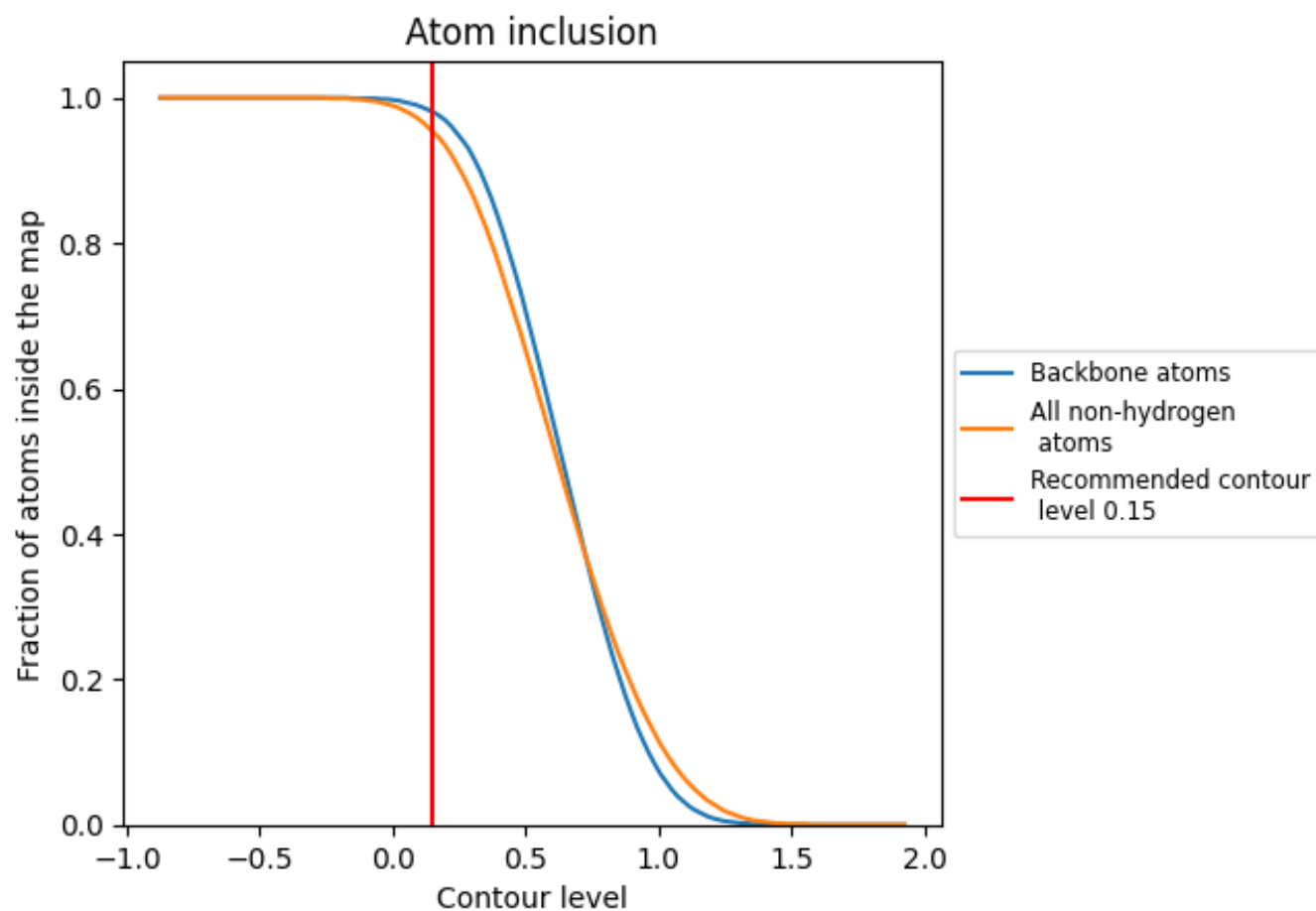
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 95% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9540	 0.2120
1	 0.9810	 0.1220
5	 0.9910	 0.2690
7	 0.9940	 0.2490
8	 0.9950	 0.2980
9	 0.9800	 0.1870
A	 0.9190	 0.2520
AA	 0.8970	 0.1470
B	 0.9220	 0.2240
BB	 0.9420	 0.1410
C	 0.9160	 0.2470
CC	 0.8670	 0.1660
D	 0.9650	 0.1740
DD	 0.8830	 0.1100
E	 0.9260	 0.1950
EE	 0.9230	 0.1390
EF	 0.8850	 0.1900
F	 0.8740	 0.2080
FF	 0.9140	 0.0870
G	 0.9270	 0.2080
GG	 0.9320	 0.1390
H	 0.8770	 0.1830
HH	 0.8620	 0.1490
I	 0.8870	 0.2120
II	 0.8870	 0.1360
J	 0.9430	 0.1670
JJ	 0.9240	 0.1500
KK	 0.9670	 0.0590
L	 0.9150	 0.2380
LL	 0.8550	 0.1600
M	 0.9250	 0.1700
MM	 0.9150	 0.0040
N	 0.9300	 0.2360
NN	 0.8940	 0.1800
O	 0.8600	 0.2050



















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Chain	Atom inclusion	Q-score
OO	 0.9350	 0.1660
P	 0.9620	 0.2480
PP	 0.8860	 0.0700
PT	 0.9750	 0.2310
Q	 0.9060	 0.2260
QQ	 0.9800	 0.0950
R	 0.9350	 0.1910
RR	 0.6860	 0.0740
S	 0.8880	 0.1970
SS	 0.8630	 0.0590
T	 0.8880	 0.2100
TT	 0.9570	 0.0680
U	 0.9550	 0.2100
UU	 0.9300	 0.0930
V	 0.8540	 0.2270
VV	 0.8840	 0.1620
W	 0.9010	 0.1340
WW	 0.9180	 0.1640
X	 0.9610	 0.2610
XX	 0.9070	 0.1700
Y	 0.9600	 0.2790
YY	 0.9690	 0.1280
Z	 0.9630	 0.1960
ZZ	 0.8200	 0.0790
a	 0.9250	 0.2370
aa	 0.9300	 0.1870
b	 0.9260	 0.1940
bb	 0.9250	 0.1690
c	 0.9340	 0.2190
cc	 0.8720	 0.0800
d	 0.9490	 0.2480
dd	 0.9840	 0.0850
e	 0.9330	 0.2600
ee	 0.8710	 0.1400
f	 0.8840	 0.2180
ff	 0.7890	 0.0360
g	 0.9520	 0.2340
gg	 0.9300	 0.0890
h	 0.9540	 0.2470
i	 0.9150	 0.2250
j	 0.9530	 0.2550
k	 0.9210	 0.2280

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Chain	Atom inclusion	Q-score
l	 0.9440	 0.2480
m	 0.9110	 0.1810
n	 0.8670	 0.1870
o	 0.9080	 0.2270
p	 0.8910	 0.2320
r	 0.9350	 0.2570
s	 0.9540	 0.1780
t	 0.9170	 0.1350