



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 06:42 PM UTC

PDB ID : 5OQL / pdb_00005oql
EMDB ID : EMD-3847
Title : Cryo-EM structure of the 90S pre-ribosome from *Chaetomium thermophilum*
Authors : Cheng, J.; Kellner, N.; Berninghausen, O.; Hurt, E.; Beckmann, R.
Deposited on : 2017-08-12
Resolution : 3.20 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

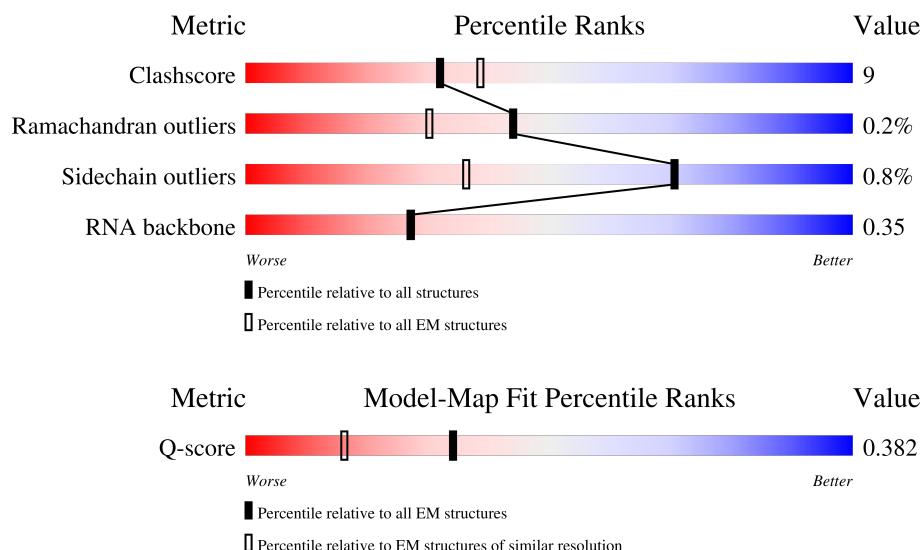
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	A	904	
2	B	907	
3	C	648	

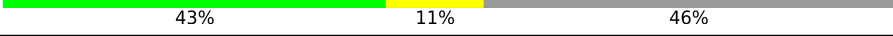
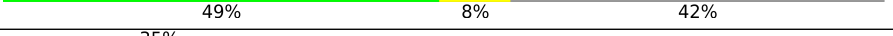
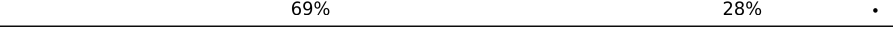
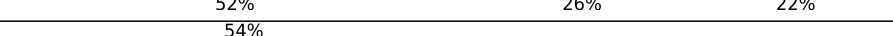
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	D	884	
5	E	414	
6	F	558	
7	G	1802	
8	H	270	
9	I	962	
10	J	912	
11	K	938	
12	L	557	
13	M	960	
14	N	618	
15	O	1049	
16	P	194	
17	Q	391	
18	R	313	
18	S	313	
19	T	523	
20	U	582	
21	V	127	
21	W	127	
22	X	630	
23	Y	411	
24	Z	1163	
25	a	183	
26	b	297	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
27	c	785	
28	d	446	
29	e	252	
29	f	252	
30	g	322	
31	h	259	
32	i	1073	
32	j	1073	
33	k	203	
34	l	255	
35	m	264	
36	n	212	
37	o	239	
38	p	203	
39	q	202	
40	r	190	
41	s	151	
42	t	150	
43	u	143	
44	v	161	
45	w	130	
46	x	145	
47	y	136	
48	z	68	
49	0	311	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
50	1	2568	7%26%21%6%47%
51	2	274	18%45%30%9%16%

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 135120 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Periodic tryptophan protein 2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	827	Total	C	N	O	S	0	0
			6242	4029	1114	1077	22		

- Molecule 2 is a protein called Utp2.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	69	Total	C	N	O	0	0
			537	338	121	78		

- Molecule 3 is a protein called Utp3.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	74	Total	C	N	O	0	0
			588	371	120	97		

- Molecule 4 is a protein called Utp4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	292	Total	C	N	O	S	0	0
			2170	1383	403	373	11		

- Molecule 5 is a protein called Utp6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	331	Total	C	N	O	S	0	0
			2591	1674	504	399	14		

- Molecule 6 is a protein called Utp7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	429	Total	C	N	O	S	0	0
			3282	2103	611	557	11		

- Molecule 7 is a protein called Utp10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	363	Total	C	N	O	S	0	0
			2772	1784	501	473	14		

- Molecule 8 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	190	Total	C	N	O	S	0	0
			1456	915	306	230	5		

- Molecule 9 is a protein called Utp12.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	155	Total	C	N	O	S	0	0
			1230	788	222	214	6		

- Molecule 10 is a protein called Utp13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	151	Total	C	N	O	S	0	0
			1201	765	214	222			

- Molecule 11 is a protein called Utp14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	147	Total	C	N	O	S	0	0
			1139	725	215	194	5		

- Molecule 12 is a protein called Utp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	280	Total	C	N	O	S	0	0
			2070	1320	379	363	8		

- Molecule 13 is a protein called Utp17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	284	Total	C	N	O	S	0	0
			2134	1386	364	378	6		

- Molecule 14 is a protein called Utp18.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	443	Total	C	N	O	S	0	0
			3435	2181	646	598	10		

- Molecule 15 is a protein called Putative U3 snoRNP protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	864	Total	C	N	O	S	0	0
			6446	4152	1189	1079	26		

- Molecule 16 is a protein called Utp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	190	Total	C	N	O	S	0	0
			1460	928	281	241	10		

- Molecule 17 is a protein called Utp30.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	182	Total	C	N	O		0	0
			905	541	182	182			

- Molecule 18 is a protein called Nop1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	242	Total	C	N	O	S	0	0
			1778	1149	327	293	9		
18	S	237	Total	C	N	O	S	0	0
			1816	1154	318	335	9		

- Molecule 19 is a protein called Putative nucleolar protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	387	Total	C	N	O	S	0	0
			2866	1836	527	492	11		

- Molecule 20 is a protein called Nop58.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	405	Total	C	N	O	S	0	0
			3035	1954	539	532	10		

- Molecule 21 is a protein called Snu13.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	121	Total	C	N	O	S	0	0
			879	557	165	154	3		
21	W	120	Total	C	N	O	S	0	0
			864	550	161	150	3		

- Molecule 22 is a protein called Rrp9.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	347	Total	C	N	O	S	0	0
			2686	1707	486	481	12		

- Molecule 23 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	345	Total	C	N	O	S	0	0
			2594	1648	465	472	9		

- Molecule 24 is a protein called Bms1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	639	Total	C	N	O	S	0	0
			4848	3145	903	782	18		

- Molecule 25 is a protein called Imp3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a	179	Total	C	N	O	S	0	0
			1434	918	283	226	7		

- Molecule 26 is a protein called Putative U3 small nucleolar ribonucleoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b	291	Total	C	N	O	S	0	0
			2279	1445	437	389	8		

- Molecule 27 is a protein called Putative U3 small nucleolar ribonucleoprotein protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c	175	Total	C	N	O	S	0	0
			1387	869	269	244	5		

- Molecule 28 is a protein called Sof1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	439	Total	C	N	O	S	0	0
			3436	2158	663	600	15		

- Molecule 29 is a protein called Emg1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	e	215	Total	C	N	O	S	0	0
			1683	1067	293	313	10		
29	f	215	Total	C	N	O	S	0	0
			1683	1067	293	313	10		

- Molecule 30 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	g	174	Total	C	N	O	S	0	0
			1393	890	250	244	9		

- Molecule 31 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	h	167	Total	C	N	O	S	0	0
			1288	817	234	231	6		

- Molecule 32 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	i	659	Total	C	N	O		0	0
			3254	1936	659	659			
32	j	677	Total	C	N	O		0	0
			3342	1988	677	677			

- Molecule 33 is a protein called Fcf2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	k	117	Total	C	N	O	S	0	0
			930	589	179	158	4		

- Molecule 34 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	l	214	Total	C	N	O	S	0	0
			1735	1105	322	303	5		

- Molecule 35 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	m	258	Total	C	N	O	S	0	0
			2057	1305	386	359	7		

- Molecule 36 is a protein called 40S ribosomal protein s5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	n	192	Total	C	N	O	S	0	0
			1447	918	277	245	7		

- Molecule 37 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	o	237	Total	C	N	O	S	0	0
			1911	1192	384	330	5		

- Molecule 38 is a protein called 40S ribosomal protein S7-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	p	159	Total	C	N	O	S	0	0
			1279	810	237	232			

- Molecule 39 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	q	201	Total	C	N	O	S	0	0
			1622	1009	330	282	1		

- Molecule 40 is a protein called 40S ribosomal protein s9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	r	159	Total	C	N	O	S	0	0
			1242	801	255	184	2		

- Molecule 41 is a protein called 40S ribosomal protein S13-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	s	49	Total	C	N	O	S	0	0
			416	270	82	64			

- Molecule 42 is a protein called 40S ribosomal protein S14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	t	115	Total	C	N	O	S	0	0
			791	492	154	141	4		

- Molecule 43 is a protein called 40S ribosomal protein S16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	u	126	Total	C	N	O	S	0	0
			943	613	177	151	2		

- Molecule 44 is a protein called 40S ribosomal protein S11-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	v	157	Total	C	N	O	S	0	0
			1286	825	248	208	5		

- Molecule 45 is a protein called 40S ribosomal protein S22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	w	126	Total	C	N	O	S	0	0
			985	632	184	164	5		

- Molecule 46 is a protein called 40S ribosomal protein s23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	x	94	Total	C	N	O	S	0	0
			684	445	129	108	2		

- Molecule 47 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	y	93	Total	C	N	O	S	0	0
			752	481	140	129	2		

- Molecule 48 is a protein called 40S ribosomal protein S28-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	z	61	Total	C	N	O	0	0
			455	284	97	74		

- Molecule 49 is a protein called Faf1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	0	92	Total	C	N	O	S	0	0
			694	426	144	120	4		

- Molecule 50 is a RNA chain called 35S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	1	1350	Total	C	N	O	P	0	0
			28796	12851	5157	9440	1348		

- Molecule 51 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	2	230	Total	C	N	O	P	0	0
			4891	2182	856	1623	230		

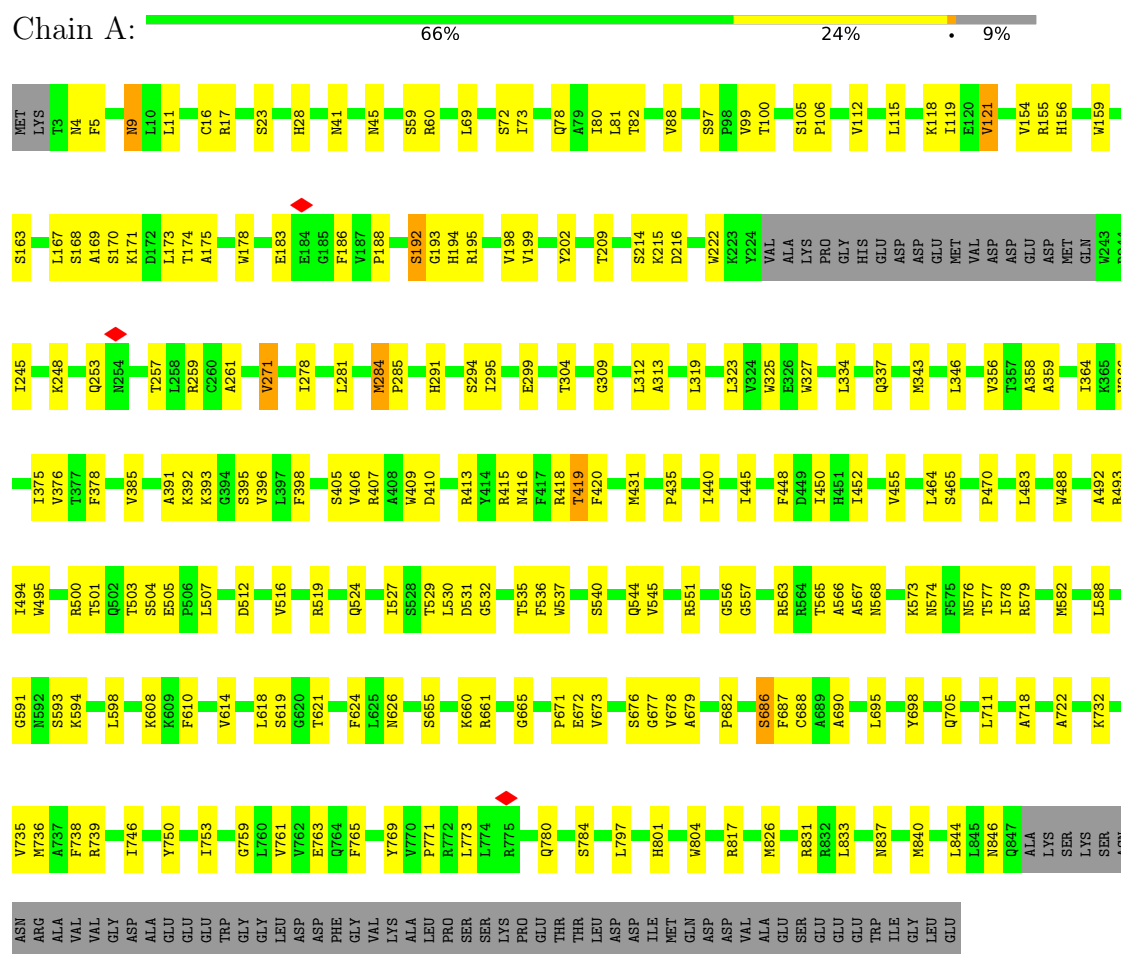
- Molecule 52 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
52	P	1	Total	Zn	0
			1	1	

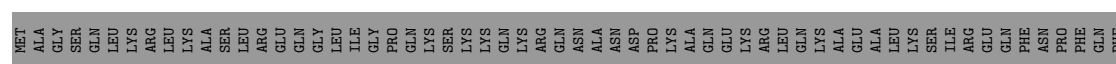
3 Residue-property plots

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: Periodic tryptophan protein 2-like protein

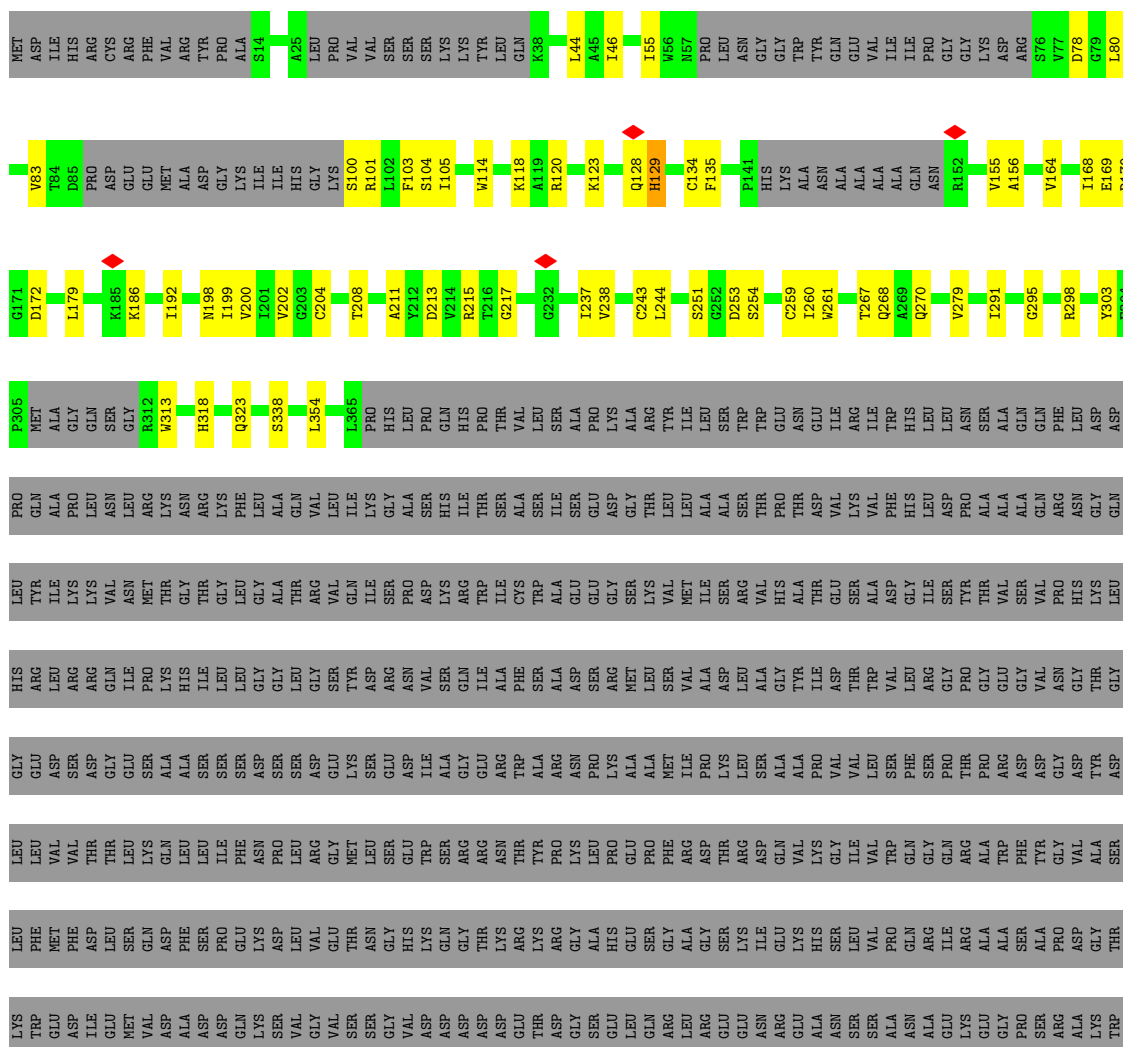


- Molecule 2: Utp2





- Molecule 4: Utp4



TRP
HIS
THR
TYR
PHE
ARG
PRO
ILE
MET
GLY
ILE
VAL
PRO
ILE
GLY
GLY
MET
MET
GLY
LYS
LYS
LEU
GLY
ALA
VAL
GLY
GLY
ASP
ASP
LEU
PRO
GLY
ARG
TYR
PHE
ALA
GLY
GLY
THR
GLY
GLY
ARG

• Molecule 5: Utp6

Chain E:  9% 68% 12% 20%

MET
A2
V4
K7
A8
R9
R40
L274
L48
P54
V61
W62
W63
A87
R91
T92
I95
F96
P104
L109
A122
W126
M130
L136
A147
R150
D156
R161
R169
R173
K196
GLN
GLY
GLY
GLY
VAL
ASP
ALA
GLY
GLN

VAL
ASN
ALA
LEU
GLU
ILE
LYS
ALA
THR
GLY
GLN
GLY
ASP
ILE
PRO
ILE
ILE
GLY
GLY
THR
ASP
GLY
ASP
PRO
ASP
ALA
GLY
THR
LYS
LYS
ALA
LYS
PRO
VAL
PHE
ASP
ALA
GLY
GLN

THR
LYS
LYS
LEU
GLU
GLN
SER
P272
A273
L275
S276
I278
V282
F283
D284
V285
A286
R287
F301
A305
G308
C312
R313
E314
R315
S318
H319
V320
M324
L327
N330
P332
C333
T334
V337
H338
Q341
D347
VAL
LEU
T350
P351
A352
P353
K355

A356
L357
R358
E359
S360
L361
A362
R363
L364
K365
A366
A367
L368
Q369
S370
T371
T372
D373
R374
L377
V382
L389
A390
I391
E392
K393
L394
D395
A396
A397
I398
R399
H404
T405
K406
R407
S408
L409
GLU
GLU
SER
PRO
SER

• Molecule 6: Utp7

Chain F:  58% 18% 23%

MET
ASP
THR
SER
GLU
ALA
VAL
ASP
LEU
ALA
PRO
PRO
ALA
LYS
GLN
GLY
ARG
GLN
ALA
ALA
GLY
ALA
HIS
SER
ILE
ALA
ASN
ALA
ALA
ARG
THR
GLU
PHE
ARG
SER
K36
Y45
K51
P56
R57
I60
LYS
SER
VAL
ARG
ASP
K66
R70
K80
T81
A82
L100

Q114
I117
V121
L137
G138
P139
Y140
A154
H159
D164
K169
L176
V200
H205
E209
L213
R214
K215
V219
M222
L225
F229
L230
L231
A232
T233
L234
S235
K241
Y242
Q243
D244
T245
S246
I250
L264
T265
Q266
M267
N270

A271
I272
H273
I275
Q278
V282
L284
L293
V294
K295
L297
R300
G301
P302
V303
R304
V308
R313
Y314
M315
T318
G319
Q320
D321
K323
L326
I329
R330
N331
F332
N337
S338
Y339
F340
T341
R342
A345
T346
S351
D352
L355
T356
A357

V358
G359
W360
L370
F371
N372
K373
Q378
V379
K380
M386
V394
V395
V398
F403
I406
I409
M412
L418
I419
V420
P421
A423
D429
R442
L450
K453
P456
L461
M468
L469
ASP
LEU
ARG
SER
GLU
LYS
D352
L355
T356
A357

ARG
ASP
LEU
ASP
GLN
PRO
ALA
GLN
ASP
ILE
VAL
GLU
ALA
GLY
LEU
ARG
LYS
ALA
ARG
GLY
ARG
ASN
THR
ALA
LEU
LYS
TYR
LEU
ARG
LYS
GLN
ARG
L109
R123
R124
F125
R126
I127
M131
L136
F139
L140
L155
A181
N188
A195
R198
R205
I214

LYS
GLU
LYS
GLN
ALA
GLU
VAL
GLY
PRO
ALA
ALA
ALA
ARG
PHE
VAL
ARG
LYS
GLU

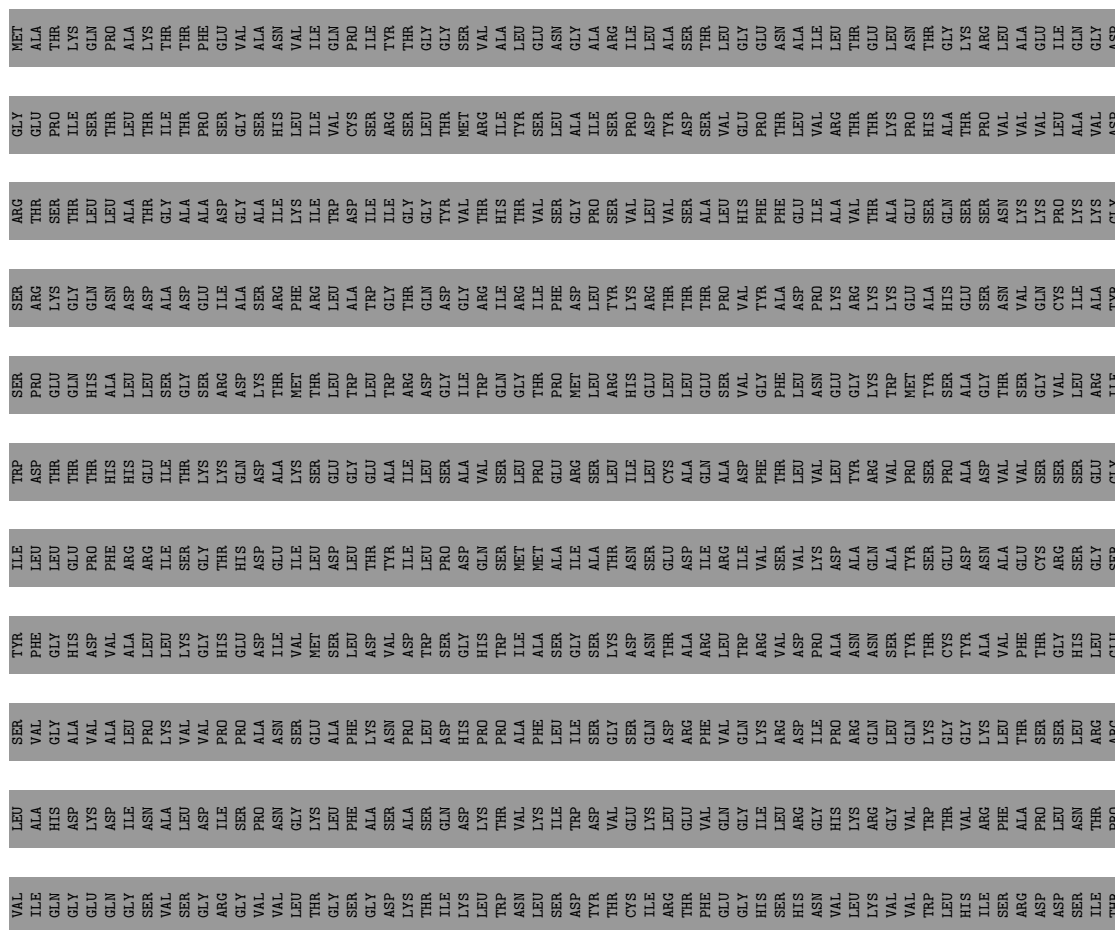
• Molecule 7: Utp10

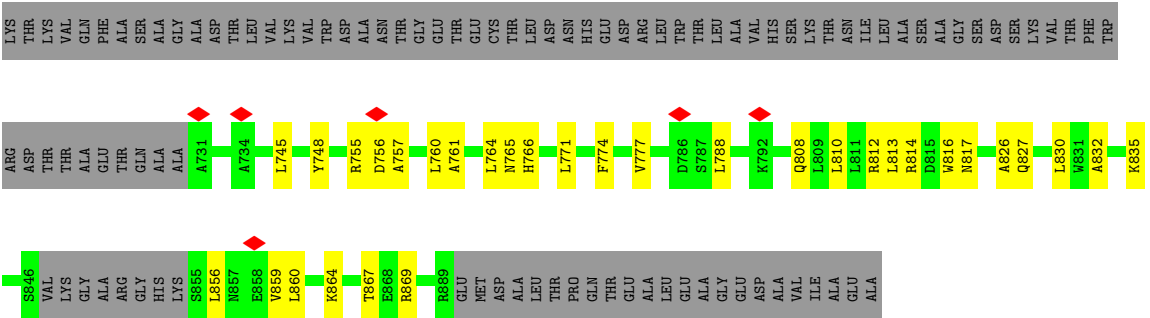
Chain G:  17% 80%

MET
ALA
S3
A6
S18
S19
A24
S28
S32
F45
I48
C52
G55
T72
R83
M86
E90
L109
R123
R124
F125
R126
I127
M131
L136
F139
L140
L155
A181
N188
A195
R198
R205
I214

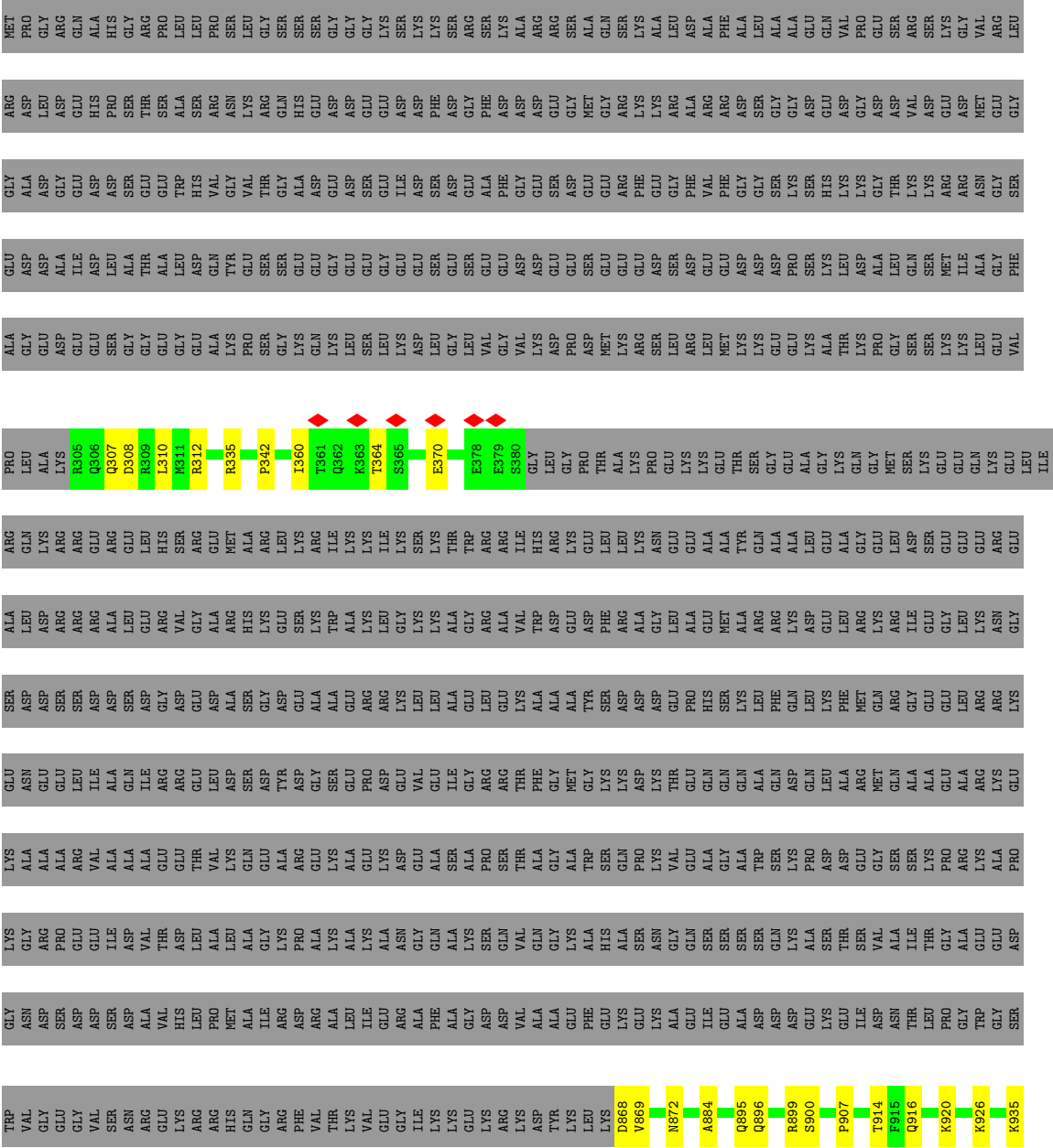


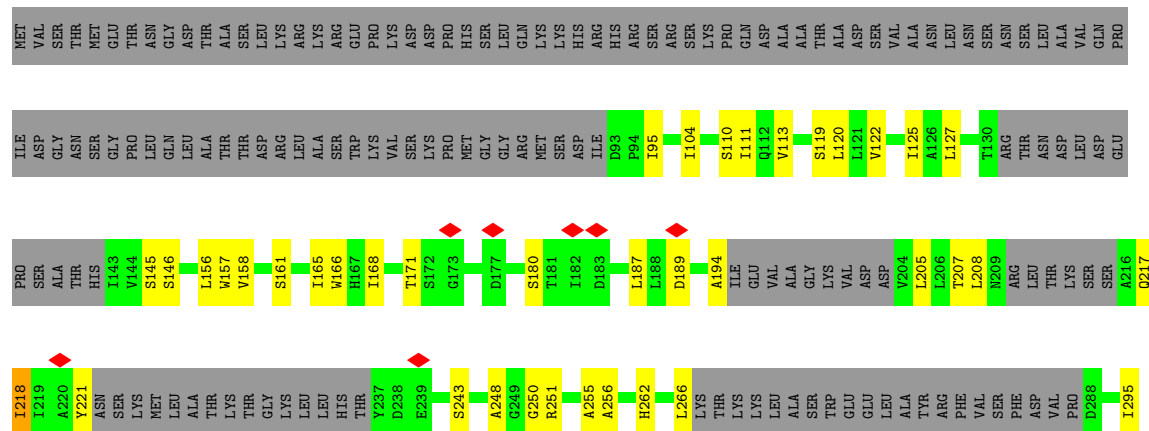
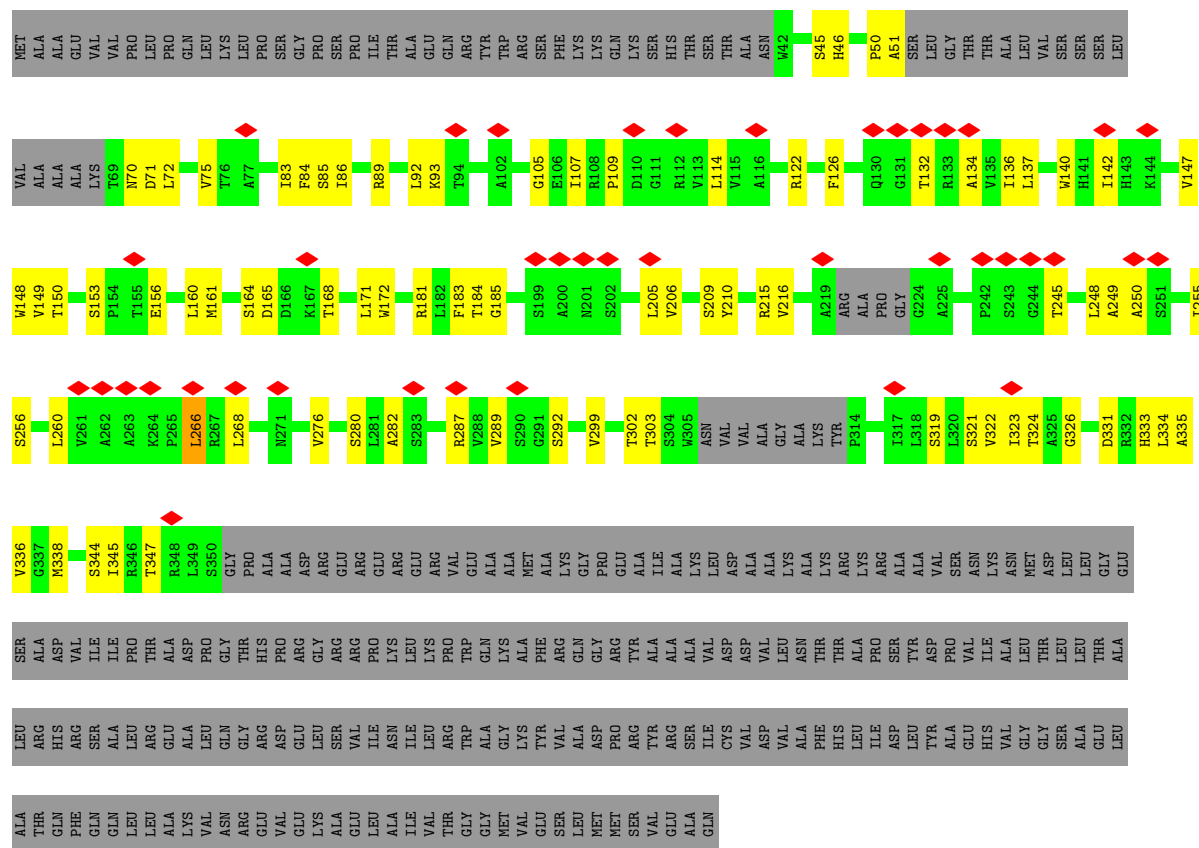
- Molecule 10: Utp13



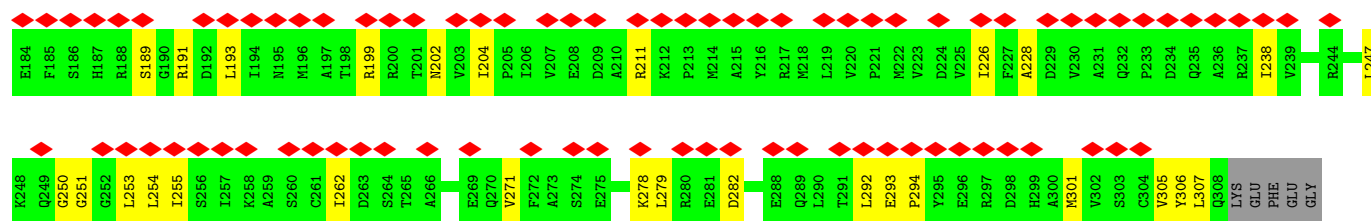


● Molecule 11: Utp14

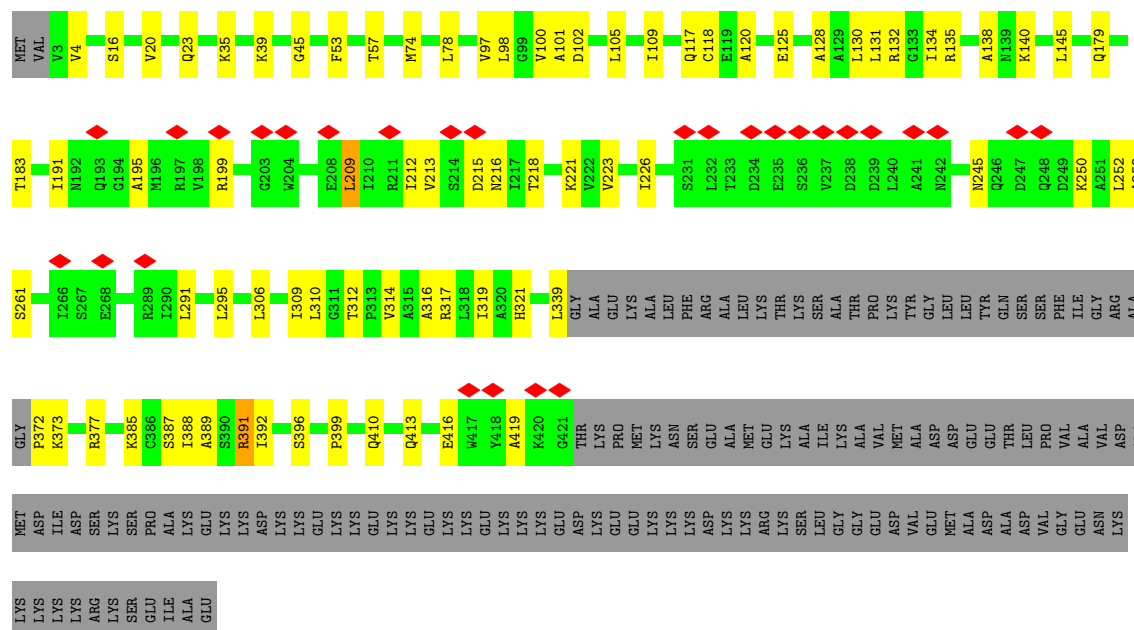




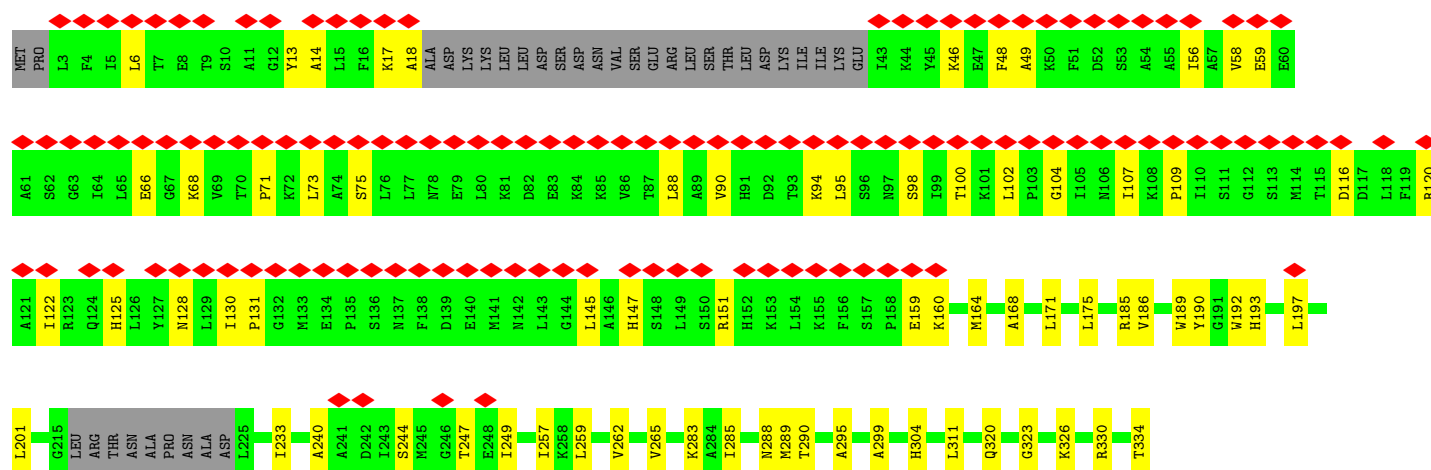


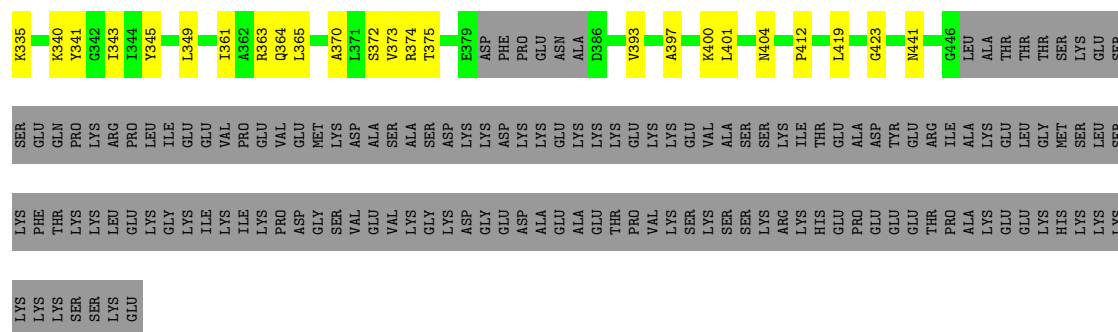


• Molecule 19: Putative nucleolar protein

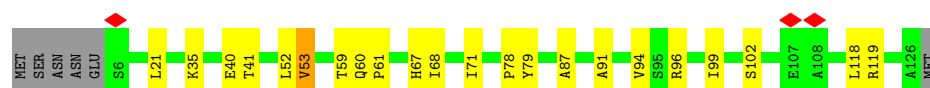
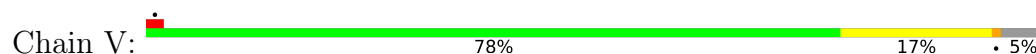


• Molecule 20: Nop58

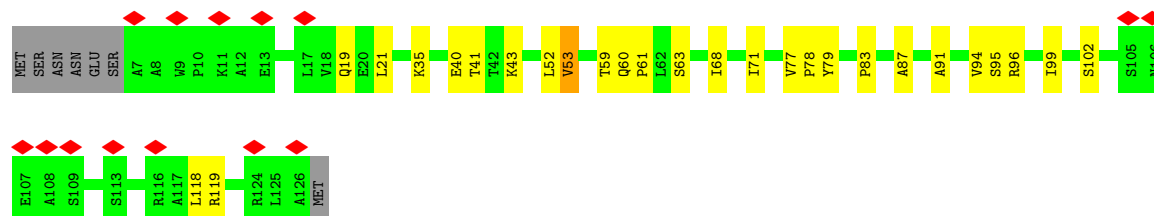
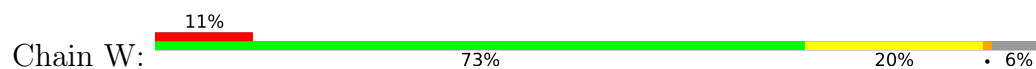




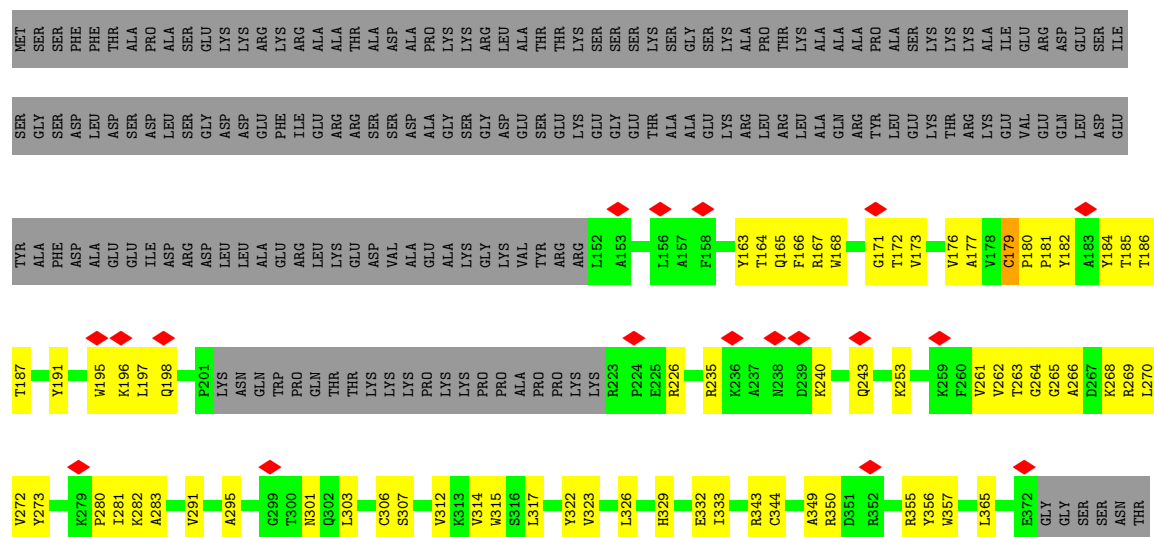
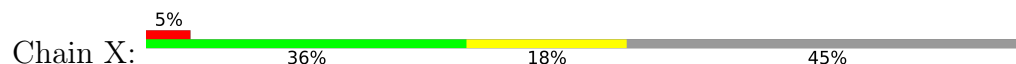
• Molecule 21: Snu13



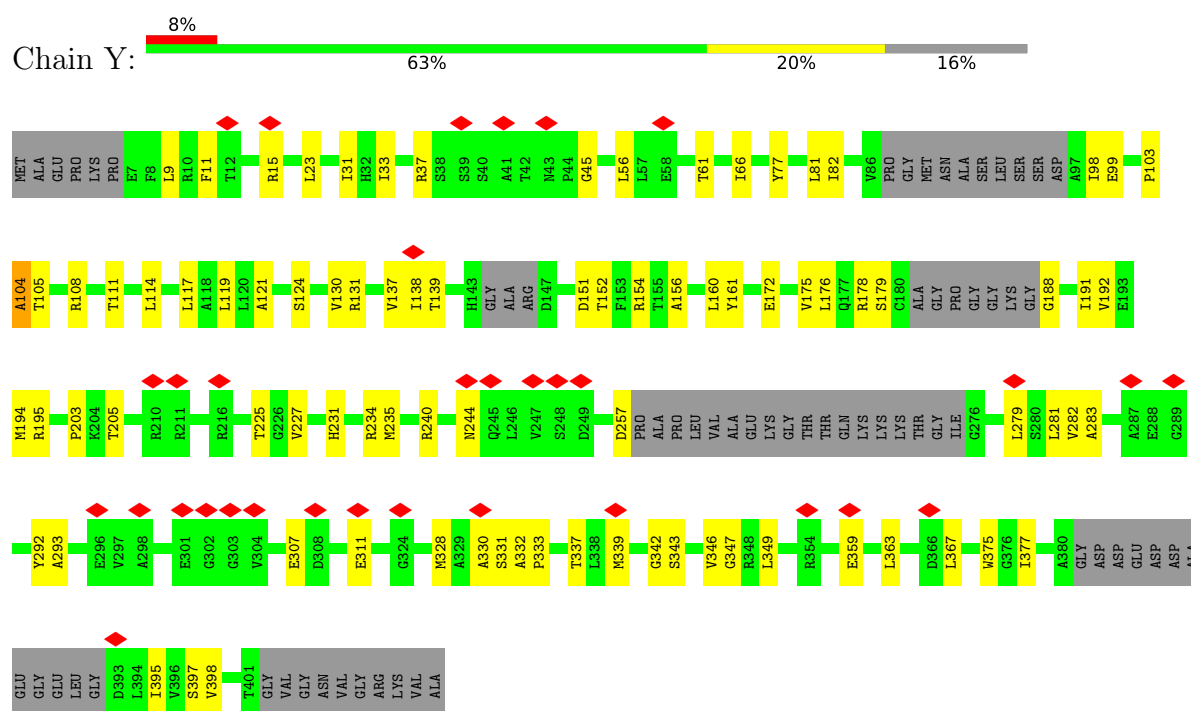
• Molecule 21: Snu13



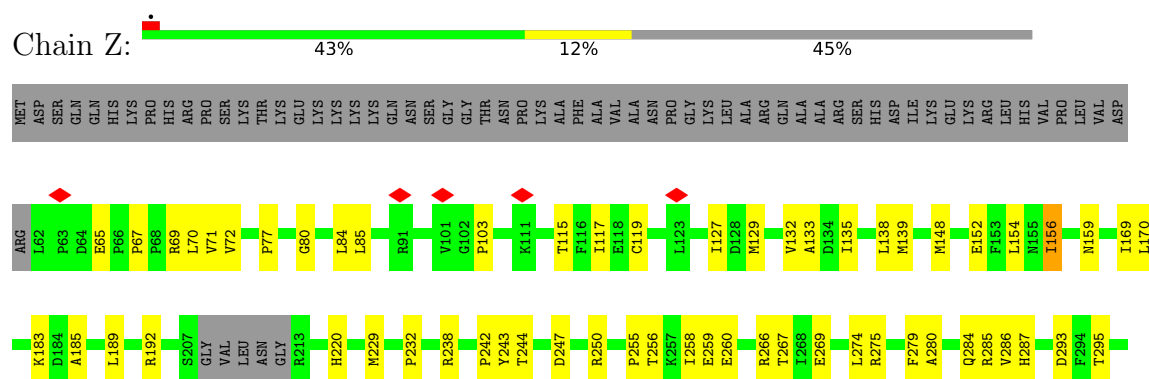
• Molecule 22: Rrp9



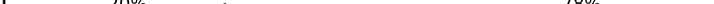
- Molecule 23: RNA 3'-terminal phosphate cyclase-like protein.

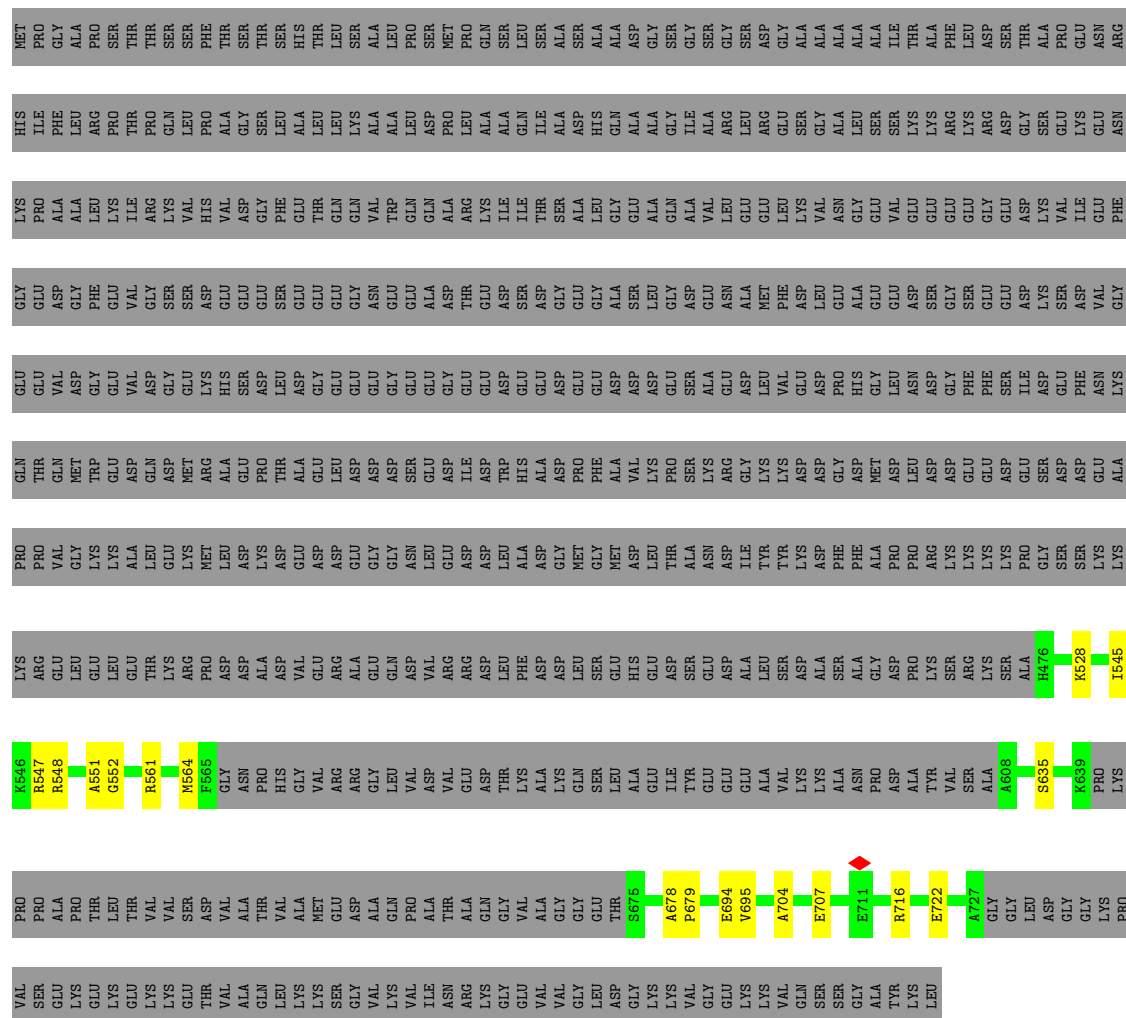


- Molecule 24: Bms1



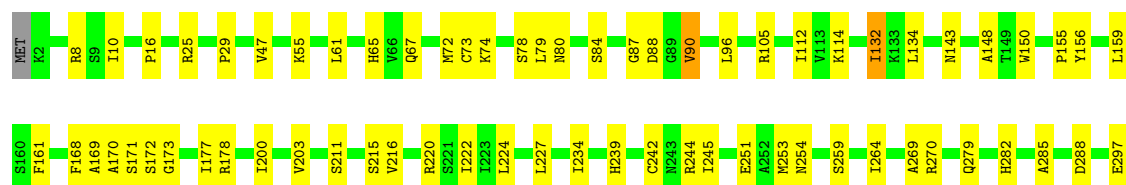
- Molecule 27: Putative U3 small nucleolar ribonucleoprotein protein

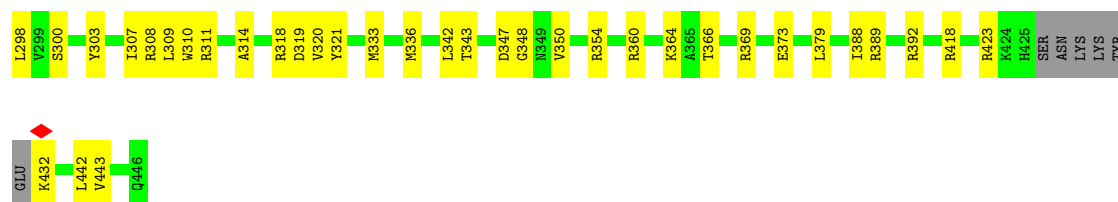
Chain c:  20% 78%



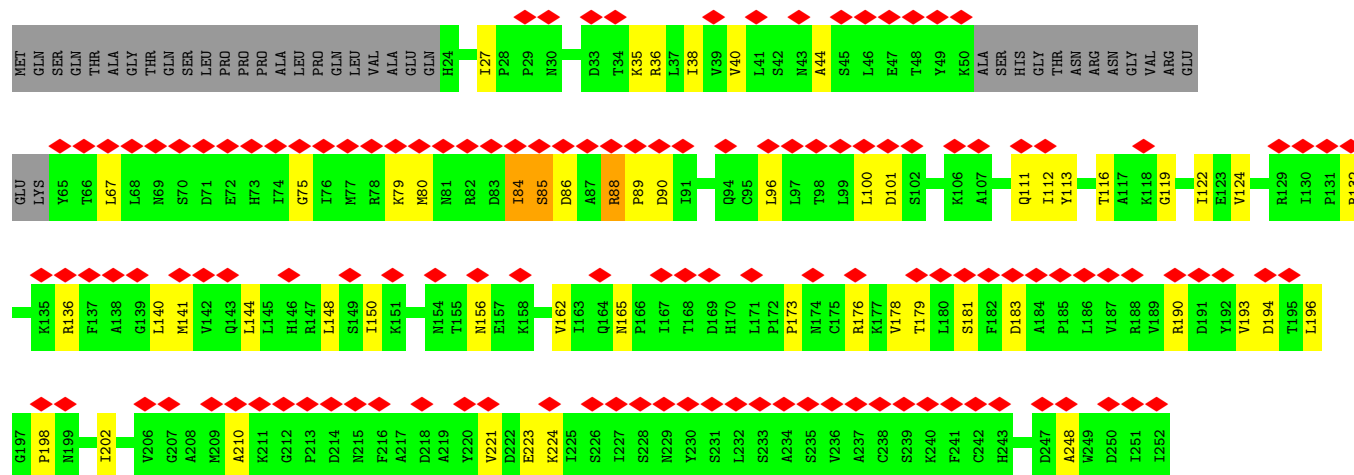
- Molecule 28: Sof1

Chain d: 76% 22%

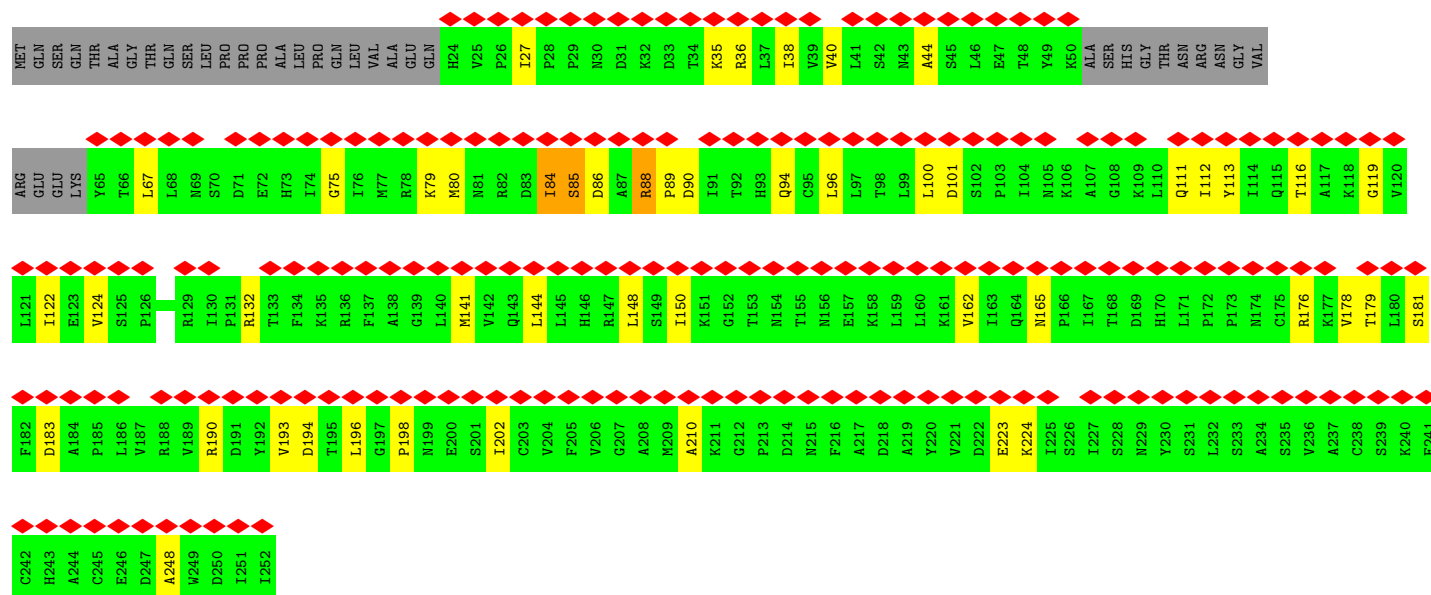
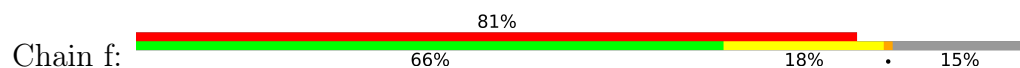




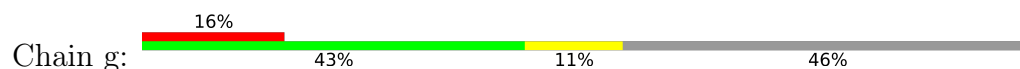
• Molecule 29: Emg1

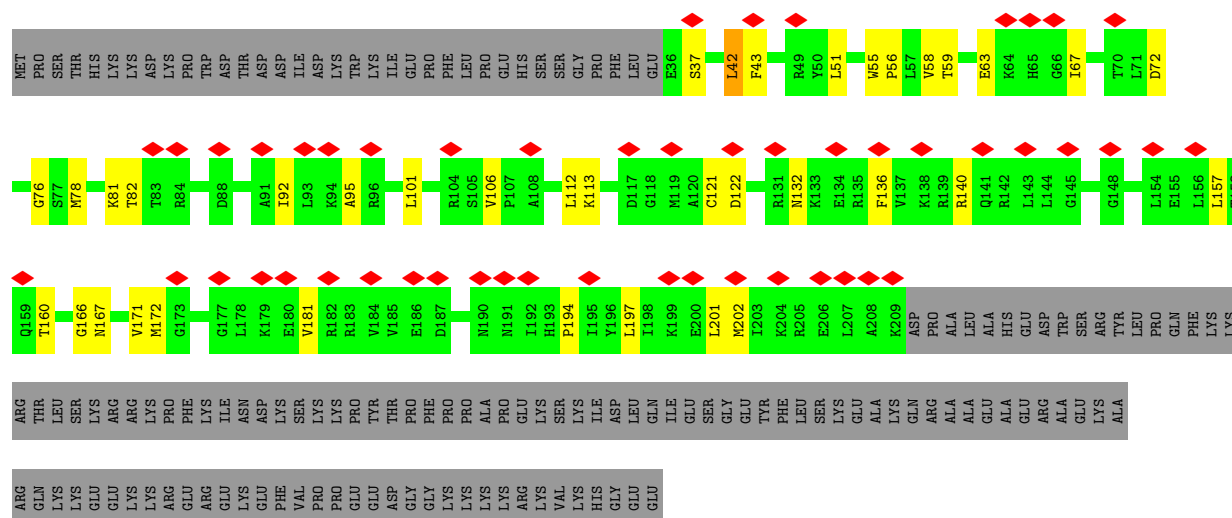


• Molecule 29: Emg1

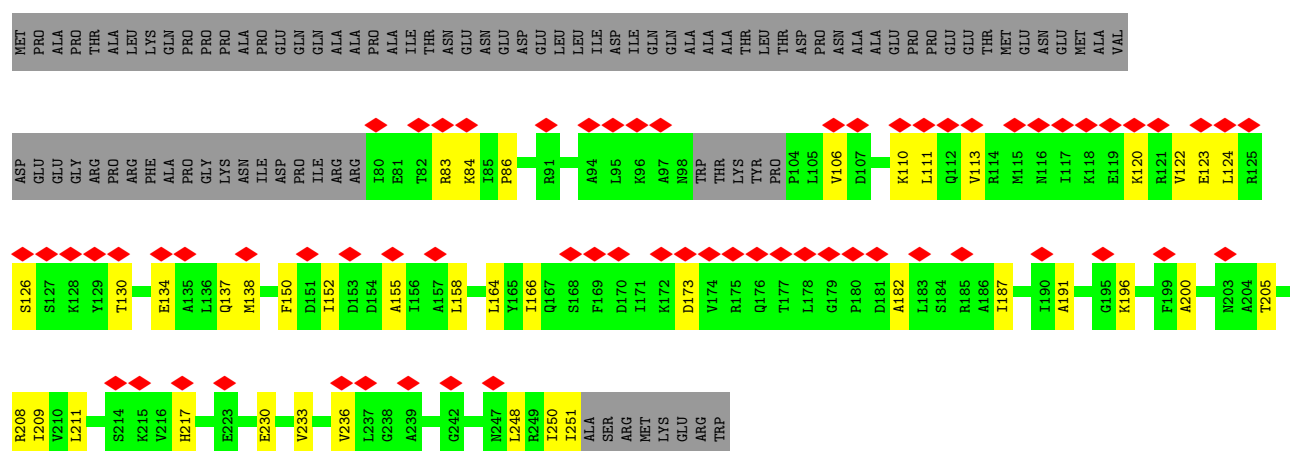


• Molecule 30: KRR1 small subunit processome component

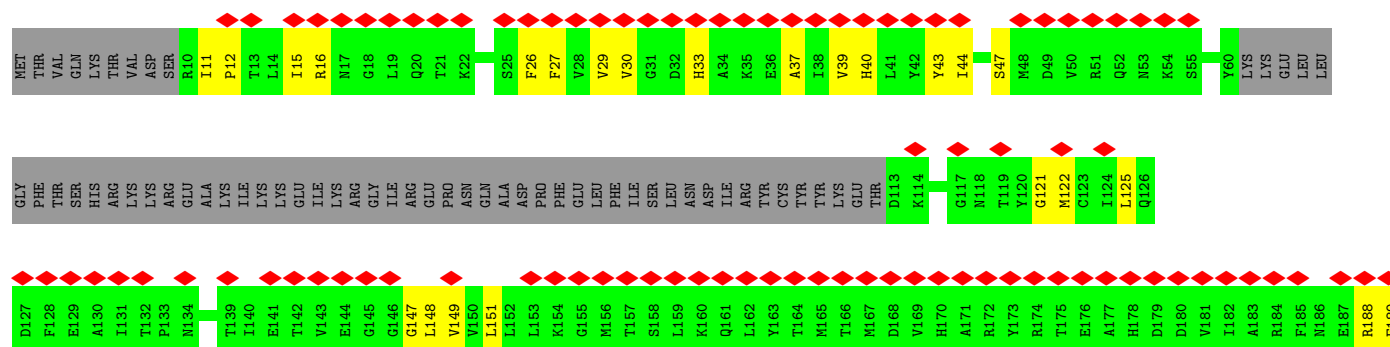




• Molecule 31: Pre-rRNA-processing protein PNO1



• Molecule 32: RNA cytidine acetyltransferase





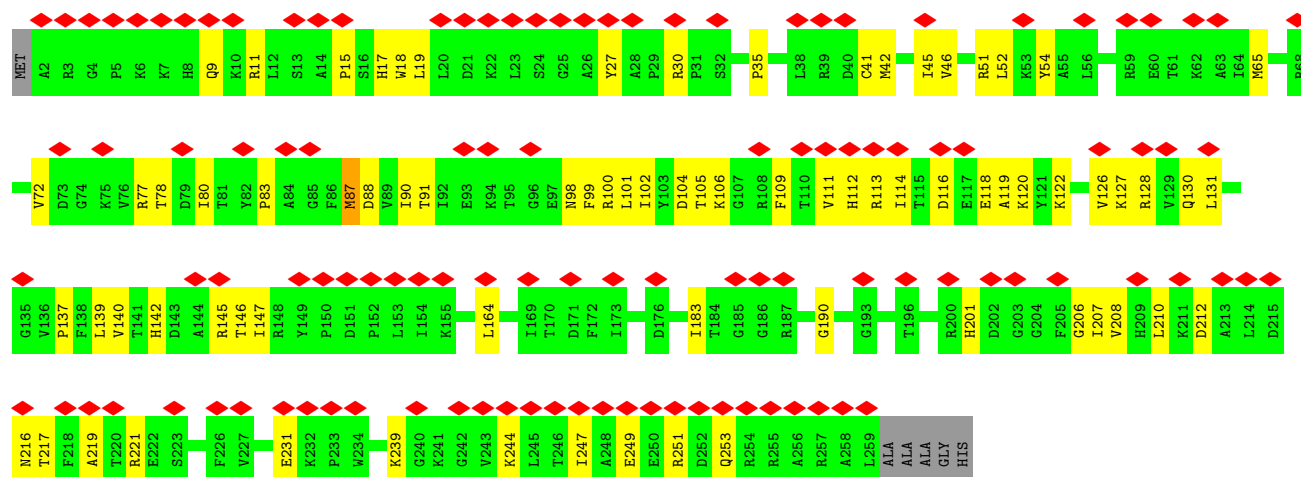
ALA
LEU
ARG
ASP
GLN
GLY
LEU
VAL
GLU
LYS
MET
SER
HIS
GLY
LYS
GLY
LYS
GLY
GLU
ARG
GLY
SER
LYS
LYS
ALA
LYS
LYS
GLY
LYS
ARG
ARG

● Molecule 32: RNA cytidine acetyltransferase

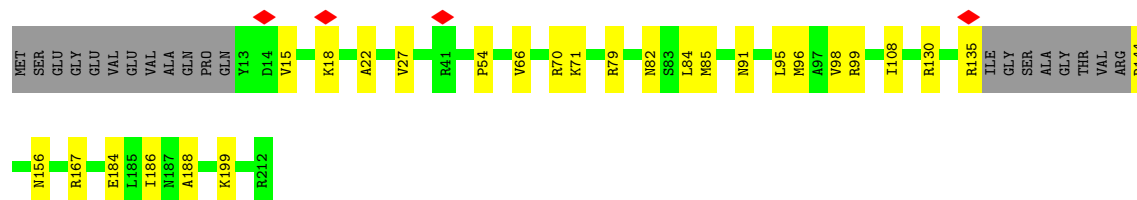
Chain j: 

TYR	K601	V541	A481	G421	ILE	A301	ASP	V181	G121	LYS	LYS	MET
GLU	S602	A542	Q482	R422	HIS	A302	GLU	I182	M122	LYS	THR	
LYS	L603	L543	G483	S423	ARG	A303	LEU	T182		GLU	VAL	
PHE	S604	Y544	D484	L424	ASN	V303	GLU	A183	C123	LEU	GLN	
ALA	R605	V545	N485	S425	HIS	A304	ASP	R184	I124	LEU	LYS	
ASP	G606	A546	V486	L426	ARG	Y305	THR	F185	L125	GLY	THR	
LEU	Q607	S547	E487	K427	T368	G306	GLN	N186	Q126	PHE	VAL	
SER	W608	H548	K488	L428	I369	Y307	PRO	E187	D127	THR	ASP	
ASP	Y609	Y549	W489	I429	Q370	N309	ILE	R188	F128	SER	SER	
ALA	A610	K550	L490	K430	Y371	I310	GLY	F189	E129	HIS	THR	
ALA	G611	N551	N491	Q431	I372	F311	LEU	A130	A130	ARG	ASP	
GLU	D612	S552	T492	L432	R373	I312	ALA	I131	T132	LYS	ASP	
VAL	L613	P553	L493	ARG	P374	T313	ARG	S192	T132	GLU	THR	
PRO	T614	L494	L494	GLU	Q375	S314	THR	L193	P133	LYS	VAL	
ARG	P615	N554	L494	GLN	D376	P315	V259	G194	N134	ILE	R16	
SER	W616	D555	C495	SER	A377	S316	D260	S195	I135	LYS	N17	
ILE	L617	L556	L496	ARG	H378	P317	Q261	C196	L136	LYS	G18	
ARG	V618	Q557	D497	ALA	V379	E318	A262	E197	A137	GLU	L19	
VAL	S619	L558	A498	GLY	L380	N319	K263	S198	R138	LYS	Q20	
THR	W620	M559	T499	ALA	G381	I319	A264	C199	T139	ARG	T21	
ASP	Q620	S560	L500	PRO	Q382	L320	L200	L201	I140	GLY	K22	
ALA	D621	D561	P501	ASN	A383	K321	L265	V201	E141	ILE	Z22	
GLU	F622	A562	R502	GLY	E384	T322	L266	T202	T142	ARG	K23	
LYS	L624	P563	S503	ASN	L385	L323	T267	D203	V143	GLU	R24	
GLY	D625	A564	K504	VAL	V386	F324	F268	D204	E144	ASN	S25	
SER	E626	H565	I505	GLU	V387	E325	V269	E205	G145	GLN	F26	
LEU	F627	E566	S506	VAL	I388	F326	D270	L206	G146	ALA	F27	
PHE	A628	L567	T507	ASP	D389	V327	A271	N207	G147	ASP	V28	
ASP	S629	F568	T508	ARG	E390	PHE	T272	M207	L148	PRO	V29	
SER	L630	V569	G509	THR	A391	LYS	A273	V208	L149	GLU	V30	
ILE	S631	L570	C510	LEU	A392	PHE	E274	L209	V149	LEU	G31	
VAL	G632	T571	P511	LYS	A393	ASP	K275	P210	V150	ILE	D32	
ARG	A633	G572	D512	ALA	I394	LEU	T276	I211	L151	SER	H33	
ASP	R634	P573	P513	THR	P395	ASP	L277	S212	L152	LEU	A34	
HIS	L635	I574	S514	GLU	L396	LYS	R278	G213	L153	ASN	K35	
GLU	V636	T575	Q515	THR	P397	THR	N279	G214	K154	ASP	E36	
LEU	R637	Q575	Q516	THR	L398	ASP	T280	K215	M156	ARG	A37	
PRO	S638	E576	C516	SER	V399	HIS	V281	G216	T157	TYR	I38	
PRO	T638	G577	E517	VAL	V399	ALA	T282	V217	T157	CYS	V39	
PHE	A639	R578	L518	GLY	K400	ASP	T283	K218	S158	TYR	H40	
SER	L640	L579	L519	ARG	K401	THR	L284	P219	L159	LYS	L41	
LYS	N641	P580	H520	SER	L402	ILE	T284	L220	K160	GLU	Y42	
LEU	P642	E581	V521	L469	M403	ILE	A285	P221	Q161	THR	Y43	
SER	W643	P582	N522	K470	G404	GLN	A286	P222	L162	D113	Y43	
GLU	D643	E471	R523	E471	P405	SER	R287	P223	L162	K114	I44	
ARG	Y644	L583	D524	I472	Y406	THR	G288	T223	T164	I115	M45	
ARG	M645	C584	L525	T473	L407	PRO	R289	D224	M165	L116	S46	
PRO	S646	V585	T525	L474	L407	GLU	G290	E225	T166	G117	S47	
LYS	W647	I586	L526	L474	V408	PHE	Q290	D226	T166	N118	M48	
GLU	G648	Q587	F527	S475	F409	ASN	K291	E227	M167	T119	D49	
LEU	Y649	V588	S528	E476	M410	LYS	S292	GLU	D168	Y120	V50	
ASP	G650	S589	F529	P477	ALA	ALA	A293	LEU	V169	R51	V50	
GLU	S651	L590	H530	I478	ILE	VAL	A294	SER	H170	Q52	R51	
LEU	K652	E591	P531	R479	S412	ARG	M295	PRO	A171	N53	K54	
ARG	A653	G592	V532	Y480	T413	VAL	Q296	ALA	R172	LYS	S65	
GLU	L654	K593	S533	E471	I414	ASN	V297	ALA	Y173	GLY	V56	
ARG	Q655	I594	E534	E471	S415	VAL	A298	GLU	R174	LYS	L57	
PRO	L656	S595	K535	L474	G416	VAL	I299	LEU	T175	LYS	W58	
GLU	L657	K596	F536	L474	E418	VAL	I299	LYS	E176	ILE	A59	
LEU	V658	Q597	L537	R479	G419	ASN	A300	LYS	A177	LYS	Y60	
ASP	D659	S598	Q538	Y480	T420	ASN			H178			
GLU	Y660	I599	Q539						D180			

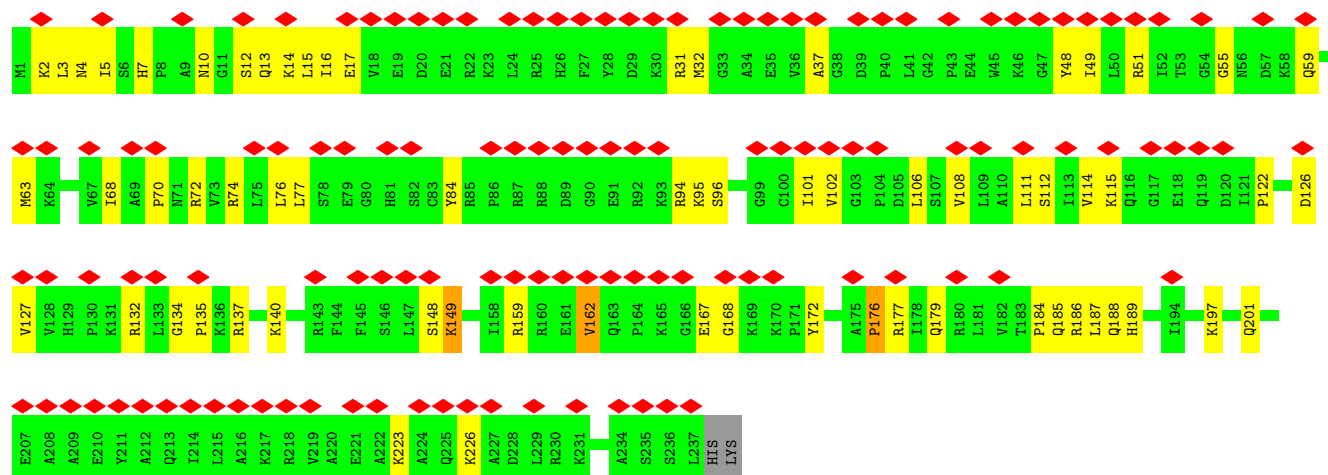
Chain m: 43% 69% 28%



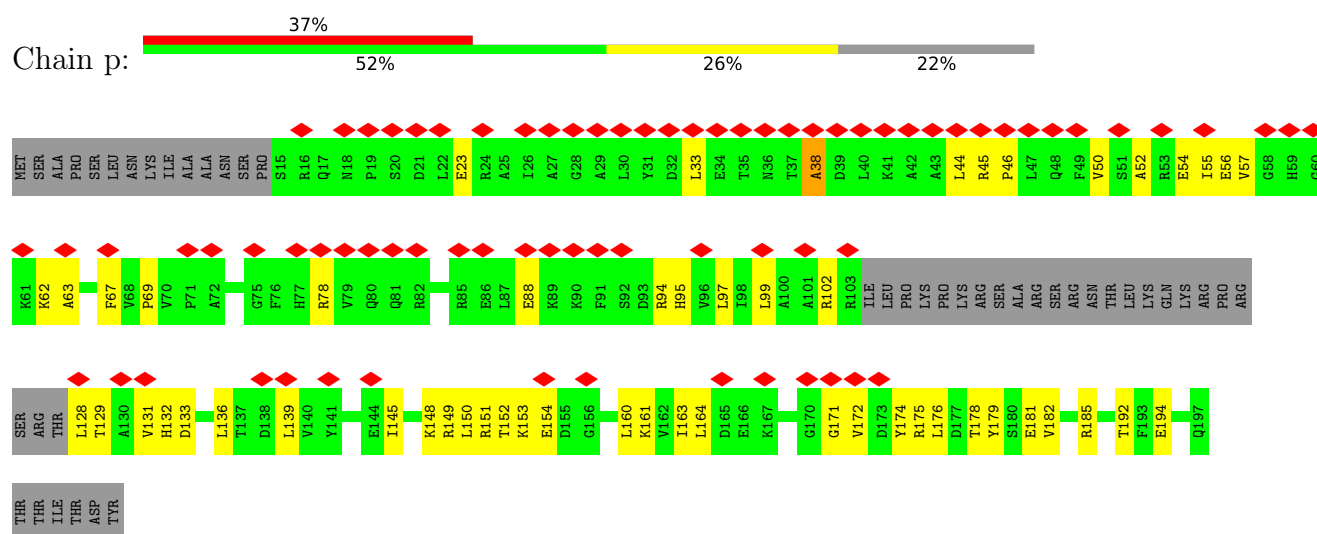
Chain n: 78% 13% 9%



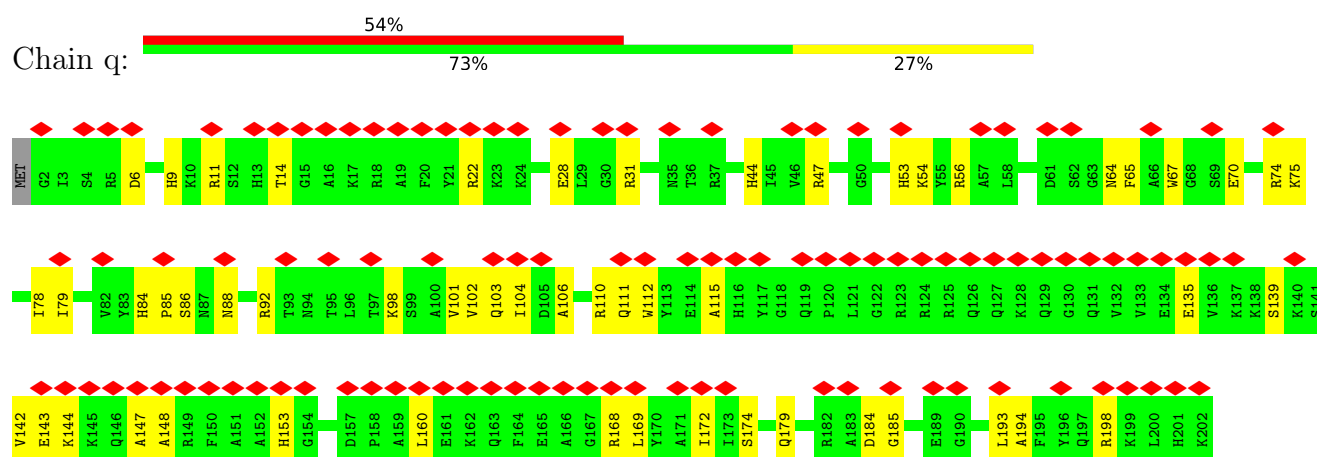
Chain o: 53% 71% 27%



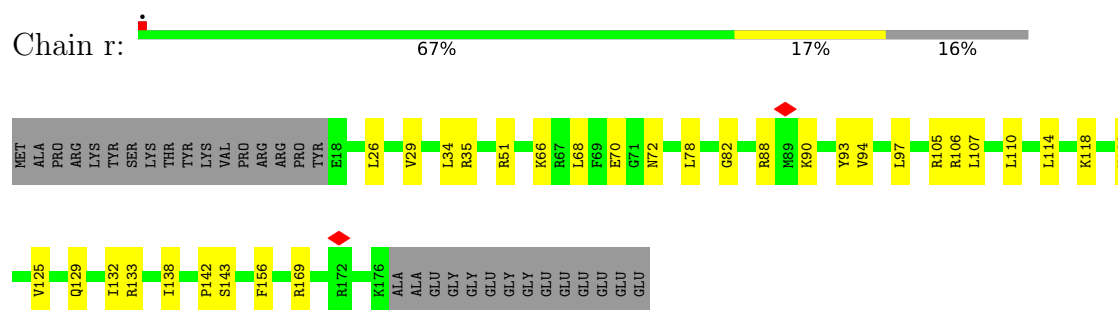
WORLDWIDE
PDB
PROTEIN DATA BANK



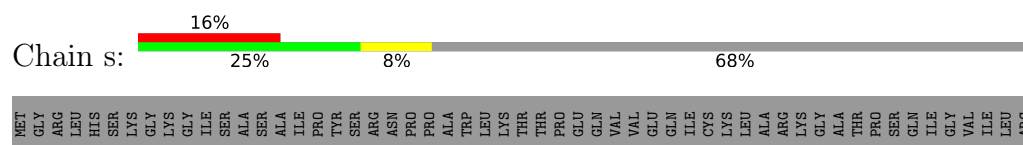
- Molecule 39: 40S ribosomal protein S8

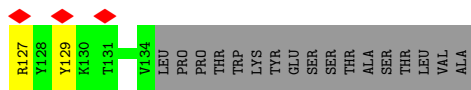


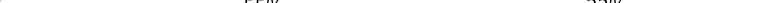
- Molecule 40: 40S ribosomal protein s9-like protein

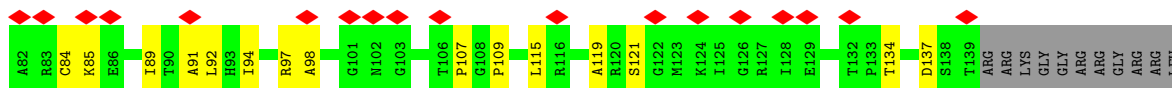


- Molecule 41: 40S ribosomal protein S13-like protein

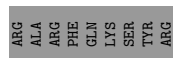


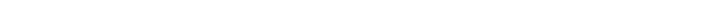


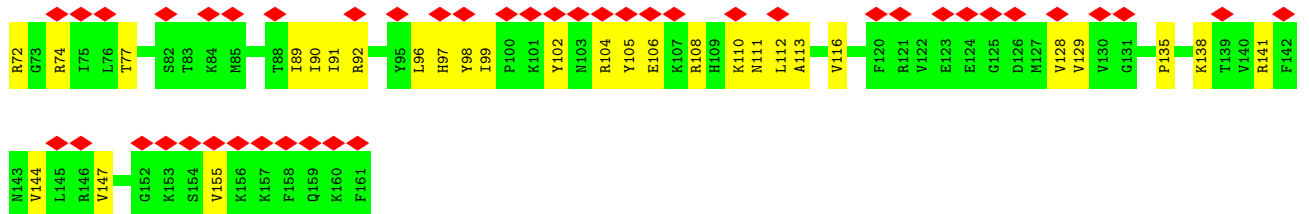
- Chain t: 



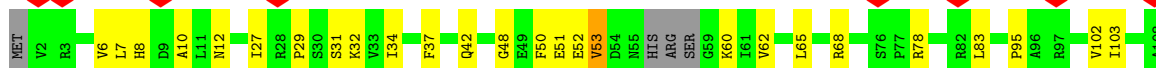
- Chain u: 67% 20% • 12%



- Chain v:  50% 72% 25%

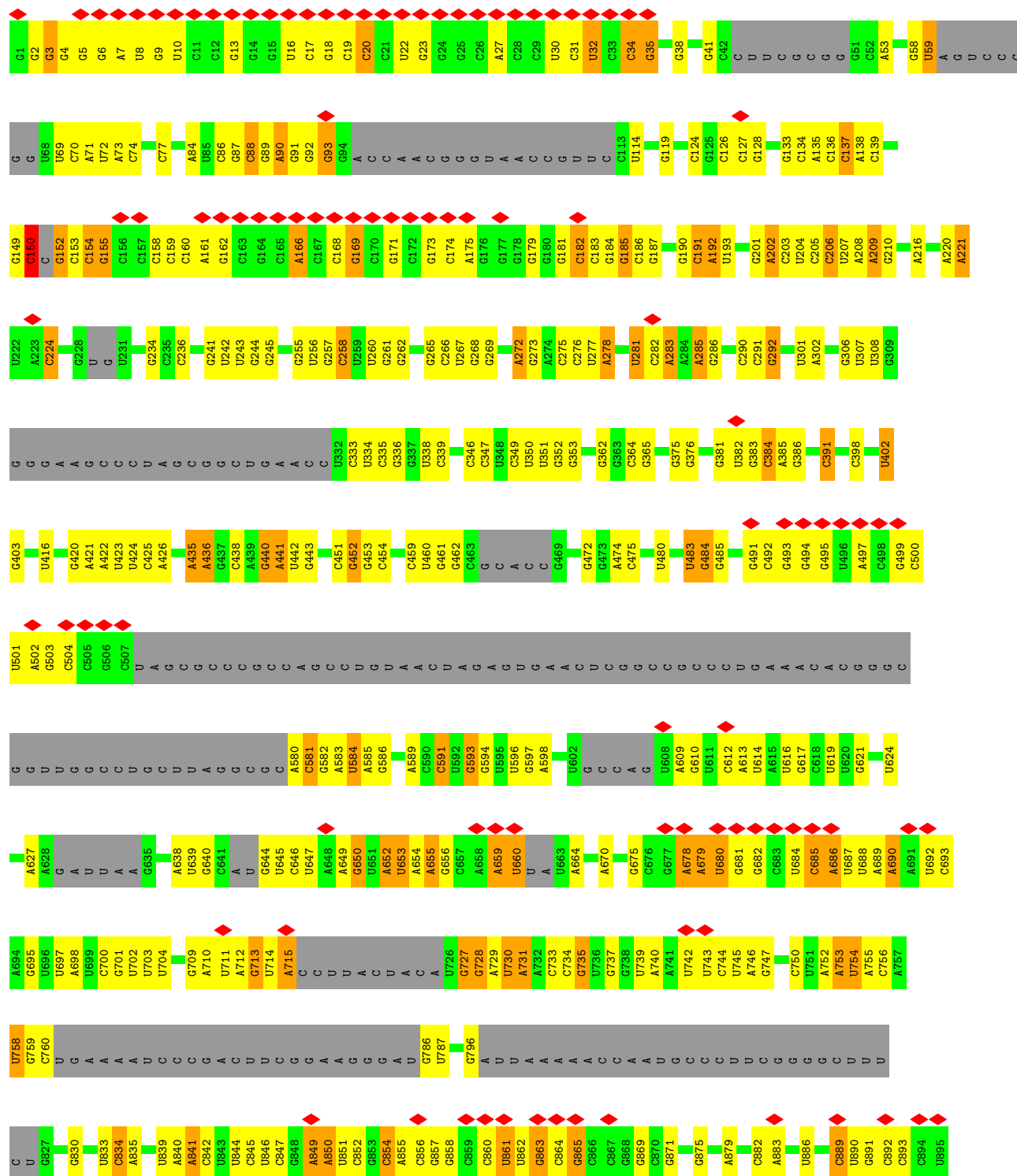
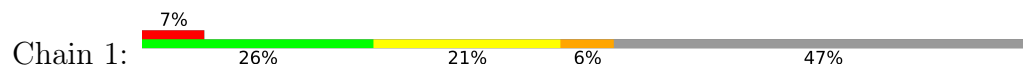


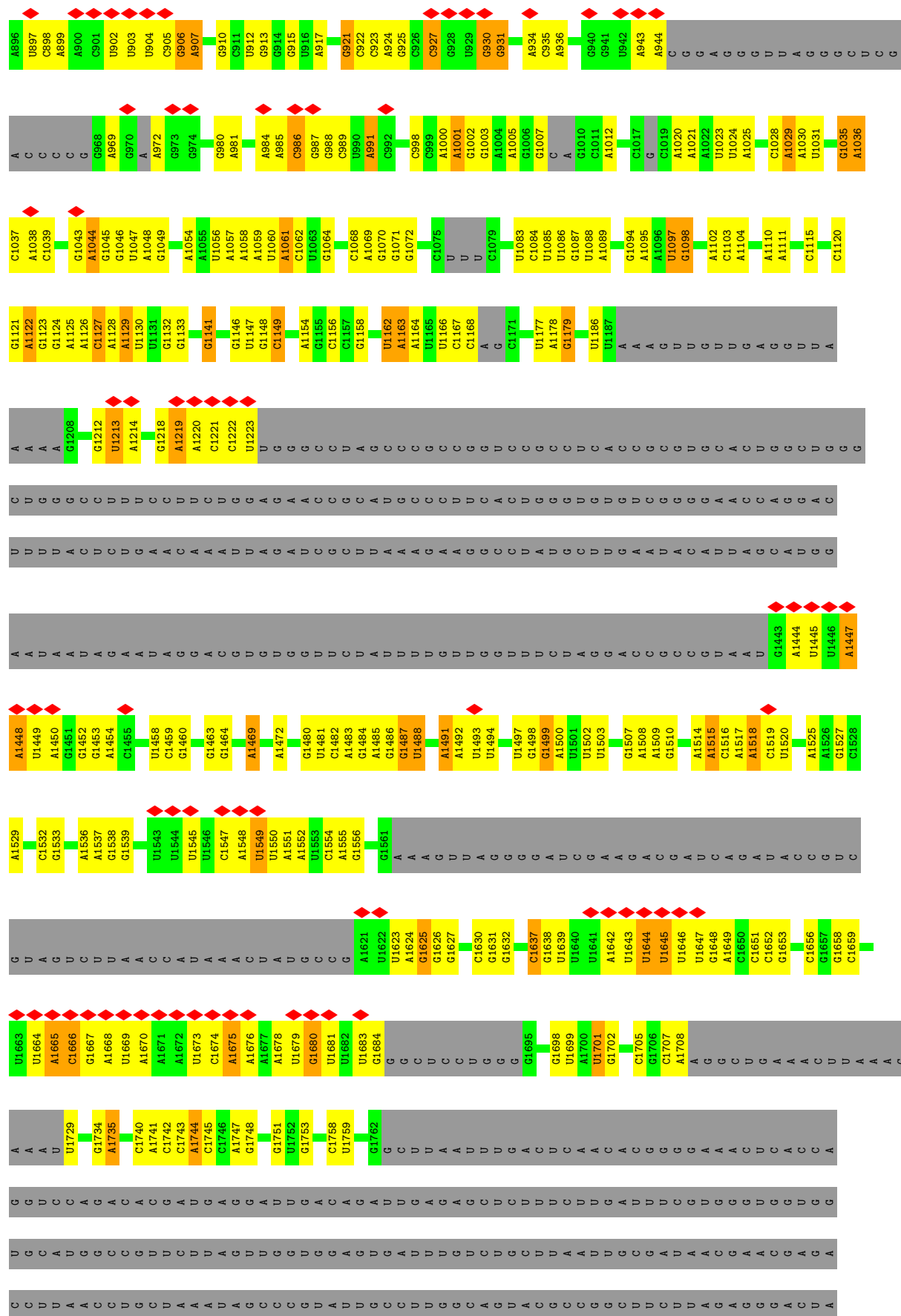
- Chain w: 7% 75% 22% 6%

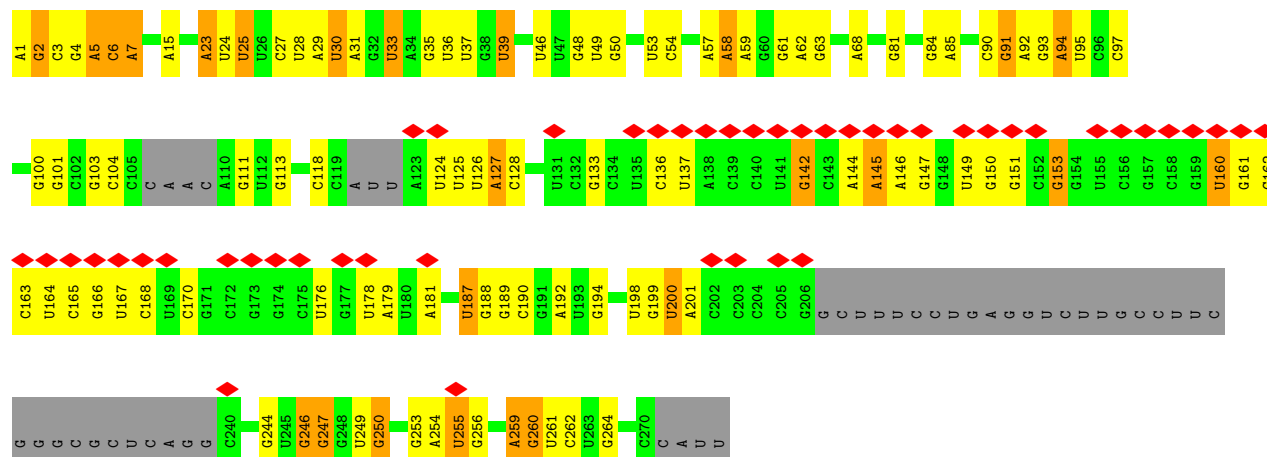
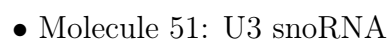


GLU
VAL
ARG
GLY
PRO
GLN
GLY
ARG
GLY
LYS
ARG
ARG
ARG

● Molecule 50: 35S rRNA







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	231121	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.4	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.596	Depositor
Minimum map value	-0.325	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.04	Depositor
Map size ($\text{\AA}$)	520.32, 520.32, 520.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.45	0/6395	0.80	4/8703 (0.0%)
2	B	0.26	0/541	0.54	0/713
3	C	0.35	0/595	0.61	0/786
4	D	0.33	0/2209	0.70	1/2986 (0.0%)
5	E	0.33	0/2657	0.61	0/3596
6	F	0.47	0/3353	0.80	3/4544 (0.1%)
7	G	0.38	0/2828	0.69	3/3841 (0.1%)
8	H	0.38	0/1468	0.63	0/1946
9	I	0.31	0/1251	0.68	0/1696
10	J	0.34	0/1221	0.71	0/1662
11	K	0.37	0/1161	0.65	0/1570
12	L	0.29	0/2117	0.70	0/2887
13	M	0.33	0/2179	0.82	4/2972 (0.1%)
14	N	0.38	0/3508	0.65	0/4742
15	O	0.42	0/6604	0.83	7/8981 (0.1%)
16	P	0.38	0/1483	0.73	0/1998
17	Q	0.18	0/900	0.56	0/1249
18	R	0.32	0/1814	0.63	0/2456
18	S	0.33	0/1853	0.62	0/2511
19	T	0.33	0/2911	0.69	0/3937
20	U	0.31	0/3085	0.68	1/4169 (0.0%)
21	V	0.35	0/891	0.71	0/1214
21	W	0.35	0/876	0.71	0/1195
22	X	0.32	0/2739	0.75	4/3699 (0.1%)
23	Y	0.29	0/2638	0.61	0/3580
24	Z	0.35	0/4960	0.69	2/6710 (0.0%)
25	a	0.46	0/1462	0.78	0/1967
26	b	0.42	0/2324	0.77	1/3144 (0.0%)
27	c	0.32	0/1405	0.61	0/1879
28	d	0.44	0/3506	0.76	2/4739 (0.0%)
29	e	0.21	0/1714	0.54	1/2325 (0.0%)
29	f	0.21	0/1714	0.54	1/2325 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	g	0.33	1/1412 (0.1%)	0.64	0/1897
31	h	0.23	0/1304	0.63	0/1751
32	i	0.15	0/3246	0.44	0/4507
32	j	0.15	0/3335	0.44	0/4632
33	k	0.34	0/945	0.62	0/1264
34	l	0.30	0/1764	0.84	0/2377
35	m	0.25	0/2097	0.69	0/2821
36	n	0.35	0/1468	0.69	0/1987
37	o	0.31	0/1942	0.74	2/2595 (0.1%)
38	p	0.34	1/1298 (0.1%)	0.80	4/1750 (0.2%)
39	q	0.24	0/1655	0.64	0/2213
40	r	0.34	0/1259	0.67	0/1687
41	s	0.20	0/422	0.50	0/561
42	t	0.28	0/801	0.65	0/1087
43	u	0.42	0/958	0.80	0/1293
44	v	0.24	0/1315	0.64	0/1760
45	w	0.29	0/1001	0.63	0/1345
46	x	0.35	0/693	0.58	0/928
47	y	0.24	0/766	0.65	0/1027
48	z	0.33	0/458	0.71	0/617
49	0	0.29	0/702	0.60	0/939
50	1	0.28	0/32166	0.51	11/50073 (0.0%)
51	2	0.32	0/5459	0.59	8/8498 (0.1%)
All	All	0.33	2/140828 (0.0%)	0.65	59/198331 (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
1	A	0	4
4	D	0	1
6	F	0	3
12	L	0	1
13	M	0	4
14	N	0	1
15	O	0	5
17	Q	0	3
18	R	0	1
18	S	0	1
21	V	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
21	W	0	1
22	X	0	4
23	Y	0	2
24	Z	0	3
26	b	0	1
28	d	0	1
29	e	0	3
29	f	0	3
31	h	0	2
32	i	0	1
32	j	0	1
34	l	0	5
35	m	0	2
37	o	0	2
38	p	0	1
39	q	0	1
42	t	0	1
43	u	0	1
44	v	0	2
46	x	0	1
47	y	0	1
All	All	0	64

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	g	42	LEU	C-N	6.37	1.44	1.33
38	p	45	ARG	C-N	5.12	1.39	1.34

The worst 5 of 59 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	O	222	LEU	CA-C-N	17.52	145.38	120.49
15	O	222	LEU	C-N-CA	17.52	145.38	120.49
51	2	2	G	OP1-P-OP2	-13.34	79.59	119.60
51	2	2	G	O5'-P-OP1	-12.24	71.28	108.00
51	2	1	A	OP2-P-O3'	-9.42	79.73	108.00

There are no chirality outliers.

5 of 64 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	192	SER	Peptide
1	A	284	MET	Peptide
1	A	556	GLY	Peptide
1	A	686	SER	Peptide
4	D	169	GLU	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6242	0	6135	148	0
2	B	537	0	569	3	0
3	C	588	0	647	10	0
4	D	2170	0	2191	34	0
5	E	2591	0	2642	33	0
6	F	3282	0	3289	72	0
7	G	2772	0	2847	30	0
8	H	1456	0	1571	31	0
9	I	1230	0	1297	30	0
10	J	1201	0	1218	35	0
11	K	1139	0	1151	21	0
12	L	2070	0	2073	53	0
13	M	2134	0	2117	48	0
14	N	3435	0	3455	46	0
15	O	6446	0	6453	128	0
16	P	1460	0	1522	31	0
17	Q	905	0	400	10	0
18	R	1778	0	1830	38	0
18	S	1816	0	1847	34	0
19	T	2866	0	2960	56	0
20	U	3035	0	3159	71	0
21	V	879	0	918	14	0
21	W	864	0	900	20	0
22	X	2686	0	2676	78	0
23	Y	2594	0	2660	51	0
24	Z	4848	0	4850	89	0
25	a	1434	0	1482	26	0
26	b	2279	0	2314	57	0
27	c	1387	0	1424	17	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	d	3436	0	3437	67	0
29	e	1683	0	1726	32	0
29	f	1683	0	1726	28	0
30	g	1393	0	1499	28	0
31	h	1288	0	1357	25	0
32	i	3254	0	1481	57	0
32	j	3342	0	1522	59	0
33	k	930	0	957	16	0
34	l	1735	0	1825	58	0
35	m	2057	0	2140	50	0
36	n	1447	0	1483	18	0
37	o	1911	0	2022	51	0
38	p	1279	0	1322	34	0
39	q	1622	0	1645	43	0
40	r	1242	0	1354	21	0
41	s	416	0	451	9	0
42	t	791	0	795	24	0
43	u	943	0	1002	18	0
44	v	1286	0	1366	27	0
45	w	985	0	1021	18	0
46	x	684	0	730	3	0
47	y	752	0	797	24	0
48	z	455	0	482	10	0
49	0	694	0	717	12	0
50	1	28796	0	14588	317	0
51	2	4891	0	2476	58	0
52	P	1	0	0	0	0
All	All	135120	0	116518	2140	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 9.

The worst 5 of 2140 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)
50:1:152:G:O2'	50:1:153:C:H6	1.28	1.17
4:D:83:VAL:O	4:D:100:SER:HA	1.57	1.03
10:J:748:TYR:CD2	10:J:757:ALA:HB2	1.93	1.03
50:1:2237:G:H1	50:1:2329:A:N6	1.56	1.02
50:1:149:G:O2'	50:1:150:C:H5'	1.65	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	A	823/904 (91%)	739 (90%)	83 (10%)	1 (0%)	48	79
2	B	67/907 (7%)	66 (98%)	1 (2%)	0	100	100
3	C	72/648 (11%)	64 (89%)	8 (11%)	0	100	100
4	D	280/884 (32%)	256 (91%)	23 (8%)	1 (0%)	30	62
5	E	325/414 (78%)	312 (96%)	13 (4%)	0	100	100
6	F	425/558 (76%)	390 (92%)	34 (8%)	1 (0%)	43	73
7	G	361/1802 (20%)	340 (94%)	21 (6%)	0	100	100
8	H	186/270 (69%)	178 (96%)	8 (4%)	0	100	100
9	I	153/962 (16%)	141 (92%)	12 (8%)	0	100	100
10	J	147/912 (16%)	139 (95%)	8 (5%)	0	100	100
11	K	9/938 (1%)	8 (89%)	1 (11%)	0	100	100
14	N	210/618 (34%)	197 (94%)	13 (6%)	0	100	100
15	O	850/1049 (81%)	768 (90%)	82 (10%)	0	100	100
16	P	188/194 (97%)	173 (92%)	15 (8%)	0	100	100
17	Q	172/391 (44%)	146 (85%)	23 (13%)	3 (2%)	7	35
18	R	238/313 (76%)	222 (93%)	15 (6%)	1 (0%)	30	62
18	S	235/313 (75%)	221 (94%)	13 (6%)	1 (0%)	30	62
19	T	383/523 (73%)	352 (92%)	31 (8%)	0	100	100
20	U	397/582 (68%)	375 (94%)	22 (6%)	0	100	100
21	V	119/127 (94%)	105 (88%)	13 (11%)	1 (1%)	16	50
21	W	118/127 (93%)	104 (88%)	13 (11%)	1 (1%)	16	50
22	X	337/630 (54%)	294 (87%)	42 (12%)	1 (0%)	36	68

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	Y	333/411 (81%)	300 (90%)	30 (9%)	3 (1%)	14	47
24	Z	627/1163 (54%)	582 (93%)	44 (7%)	1 (0%)	43	73
25	a	177/183 (97%)	162 (92%)	15 (8%)	0	100	100
26	b	287/297 (97%)	263 (92%)	24 (8%)	0	100	100
27	c	169/785 (22%)	160 (95%)	9 (5%)	0	100	100
28	d	435/446 (98%)	390 (90%)	45 (10%)	0	100	100
29	e	211/252 (84%)	199 (94%)	10 (5%)	2 (1%)	14	47
29	f	211/252 (84%)	199 (94%)	10 (5%)	2 (1%)	14	47
30	g	172/322 (53%)	164 (95%)	8 (5%)	0	100	100
31	h	163/259 (63%)	154 (94%)	9 (6%)	0	100	100
32	i	643/1073 (60%)	569 (88%)	74 (12%)	0	100	100
32	j	663/1073 (62%)	588 (89%)	75 (11%)	0	100	100
33	k	115/203 (57%)	101 (88%)	14 (12%)	0	100	100
34	l	212/255 (83%)	184 (87%)	27 (13%)	1 (0%)	24	59
35	m	256/264 (97%)	219 (86%)	37 (14%)	0	100	100
36	n	188/212 (89%)	170 (90%)	17 (9%)	1 (0%)	24	59
37	o	235/239 (98%)	202 (86%)	31 (13%)	2 (1%)	14	47
38	p	155/203 (76%)	137 (88%)	18 (12%)	0	100	100
39	q	199/202 (98%)	187 (94%)	12 (6%)	0	100	100
40	r	157/190 (83%)	152 (97%)	5 (3%)	0	100	100
41	s	47/151 (31%)	45 (96%)	2 (4%)	0	100	100
42	t	113/150 (75%)	95 (84%)	16 (14%)	2 (2%)	6	34
43	u	124/143 (87%)	113 (91%)	11 (9%)	0	100	100
44	v	155/161 (96%)	134 (86%)	21 (14%)	0	100	100
45	w	122/130 (94%)	113 (93%)	9 (7%)	0	100	100
46	x	90/145 (62%)	79 (88%)	11 (12%)	0	100	100
47	y	91/136 (67%)	82 (90%)	9 (10%)	0	100	100
48	z	59/68 (87%)	51 (86%)	8 (14%)	0	100	100
49	0	90/311 (29%)	82 (91%)	8 (9%)	0	100	100
All	All	12594/23745 (53%)	11466 (91%)	1103 (9%)	25 (0%)	44	73

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
29	e	85	SER
29	f	85	SER
34	l	62	LYS
23	Y	105	THR
36	n	91	ASN

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	633/775 (82%)	627 (99%)	6 (1%)	70	81
2	B	43/788 (6%)	43 (100%)	0	100	100
3	C	61/536 (11%)	60 (98%)	1 (2%)	55	75
4	D	222/738 (30%)	220 (99%)	2 (1%)	70	81
5	E	248/341 (73%)	248 (100%)	0	100	100
6	F	326/474 (69%)	314 (96%)	12 (4%)	30	63
7	G	289/1526 (19%)	287 (99%)	2 (1%)	76	83
8	H	135/227 (60%)	135 (100%)	0	100	100
9	I	134/821 (16%)	134 (100%)	0	100	100
10	J	129/770 (17%)	128 (99%)	1 (1%)	73	82
11	K	115/765 (15%)	115 (100%)	0	100	100
12	L	218/456 (48%)	218 (100%)	0	100	100
13	M	219/817 (27%)	218 (100%)	1 (0%)	81	85
14	N	351/524 (67%)	349 (99%)	2 (1%)	78	84
15	O	638/863 (74%)	626 (98%)	12 (2%)	50	73
16	P	147/168 (88%)	145 (99%)	2 (1%)	59	77
18	R	175/228 (77%)	172 (98%)	3 (2%)	53	75
18	S	195/228 (86%)	193 (99%)	2 (1%)	68	80
19	T	287/435 (66%)	284 (99%)	3 (1%)	68	80
20	U	307/489 (63%)	307 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	V	91/108 (84%)	90 (99%)	1 (1%)	65	79
21	W	88/108 (82%)	87 (99%)	1 (1%)	65	79
22	X	273/525 (52%)	272 (100%)	1 (0%)	84	86
23	Y	275/320 (86%)	274 (100%)	1 (0%)	84	86
24	Z	466/1009 (46%)	462 (99%)	4 (1%)	70	81
25	a	147/169 (87%)	144 (98%)	3 (2%)	48	72
26	b	238/266 (90%)	236 (99%)	2 (1%)	73	82
27	c	138/642 (22%)	138 (100%)	0	100	100
28	d	354/383 (92%)	350 (99%)	4 (1%)	65	79
29	e	193/223 (86%)	193 (100%)	0	100	100
29	f	193/223 (86%)	193 (100%)	0	100	100
30	g	153/287 (53%)	153 (100%)	0	100	100
31	h	138/215 (64%)	138 (100%)	0	100	100
33	k	95/167 (57%)	95 (100%)	0	100	100
34	l	189/223 (85%)	187 (99%)	2 (1%)	65	79
35	m	219/221 (99%)	219 (100%)	0	100	100
36	n	144/178 (81%)	143 (99%)	1 (1%)	76	83
37	o	202/204 (99%)	201 (100%)	1 (0%)	81	85
38	p	137/177 (77%)	136 (99%)	1 (1%)	76	83
39	q	163/164 (99%)	162 (99%)	1 (1%)	78	84
40	r	122/162 (75%)	121 (99%)	1 (1%)	73	82
41	s	43/130 (33%)	43 (100%)	0	100	100
42	t	74/117 (63%)	74 (100%)	0	100	100
43	u	92/115 (80%)	90 (98%)	2 (2%)	45	71
44	v	140/143 (98%)	140 (100%)	0	100	100
45	w	103/113 (91%)	102 (99%)	1 (1%)	68	80
46	x	68/116 (59%)	68 (100%)	0	100	100
47	y	81/115 (70%)	81 (100%)	0	100	100
48	z	46/61 (75%)	45 (98%)	1 (2%)	45	71
49	0	68/260 (26%)	67 (98%)	1 (2%)	57	76
All	All	9605/19113 (50%)	9527 (99%)	78 (1%)	70	82

5 of 78 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
25	a	82	LEU
39	q	101	VAL
25	a	158	VAL
28	d	342	LEU
45	w	53	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 164 such sidechains are listed below:

Mol	Chain	Res	Type
29	f	93	HIS
37	o	201	GLN
30	g	165	HIS
35	m	17	HIS
39	q	163	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	1	1319/2568 (51%)	479 (36%)	27 (2%)
51	2	226/274 (82%)	76 (33%)	5 (2%)
All	All	1545/2842 (54%)	555 (35%)	32 (2%)

5 of 555 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	1	3	G
50	1	5	G
50	1	6	G
50	1	7	A
50	1	8	U

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	2	23	A
51	2	35	G
50	1	612	C
50	1	593	G
51	2	246	G

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

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 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

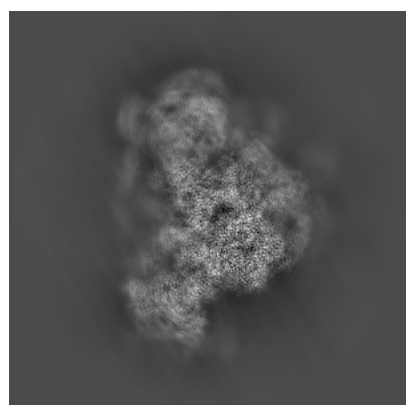
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3847. These allow visual inspection of the internal detail of the map and identification of artifacts.

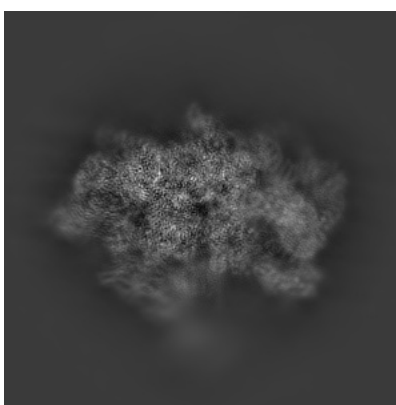
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

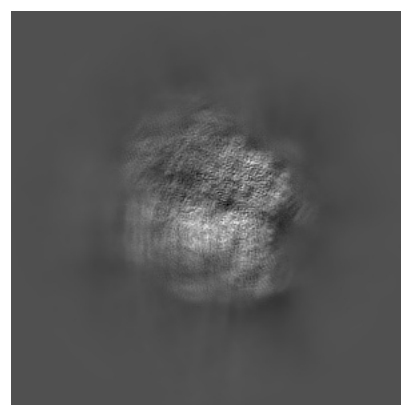
6.1.1 Primary map



X



Y

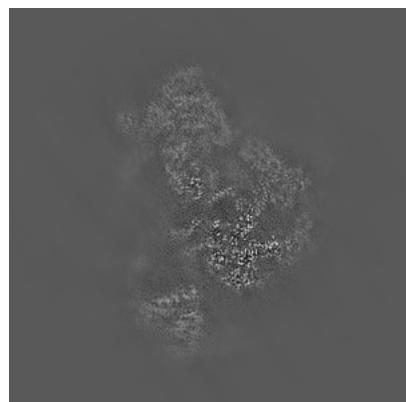


Z

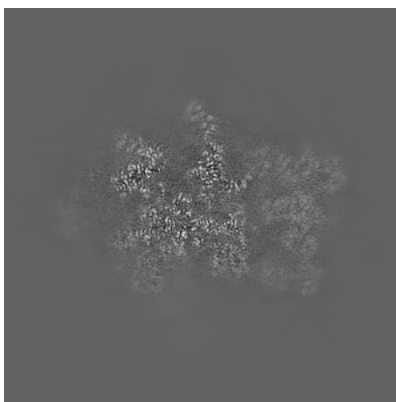
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

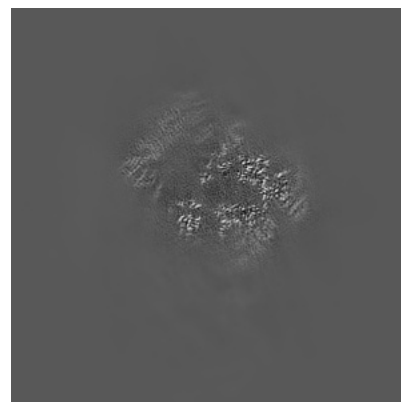
6.2.1 Primary map



X Index: 240



Y Index: 240

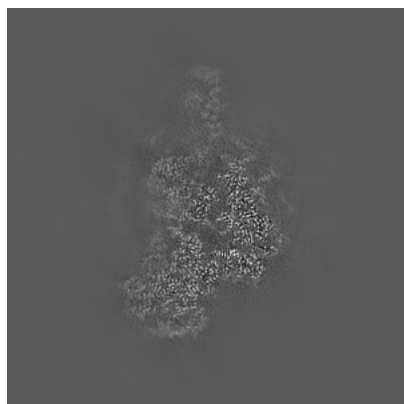


Z Index: 240

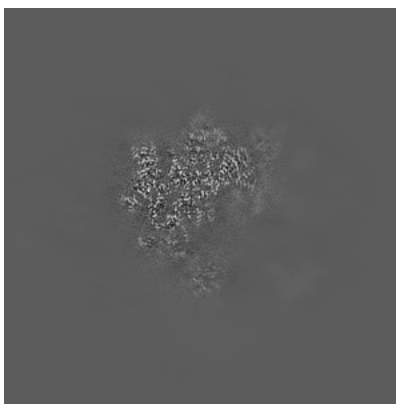
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

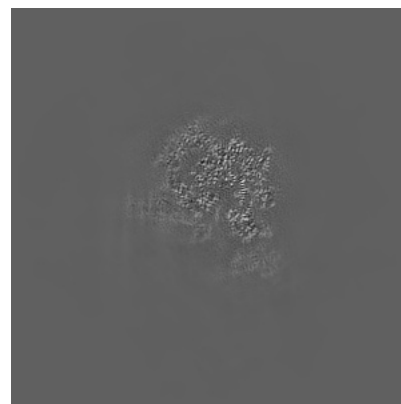
6.3.1 Primary map



X Index: 279



Y Index: 281

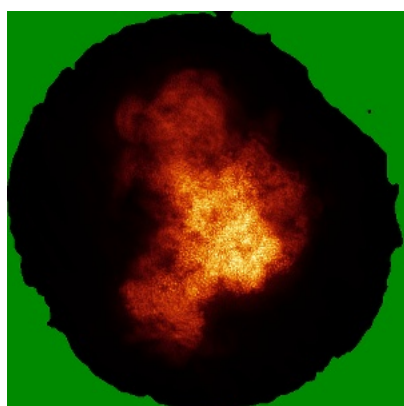


Z Index: 183

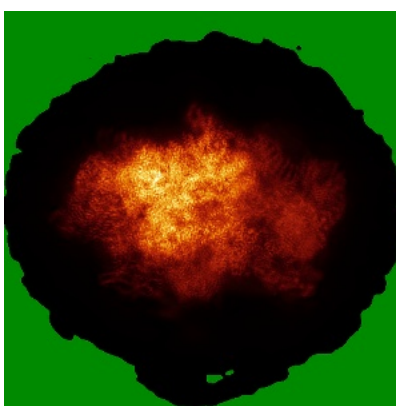
The images above show the largest variance slices of the map in three orthogonal directions.

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

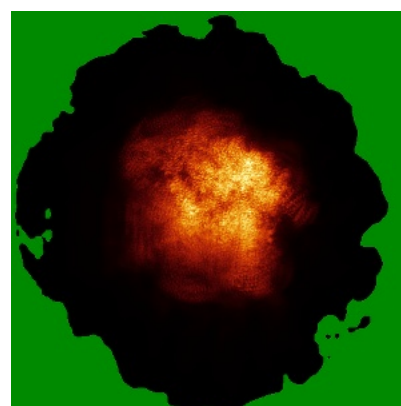
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

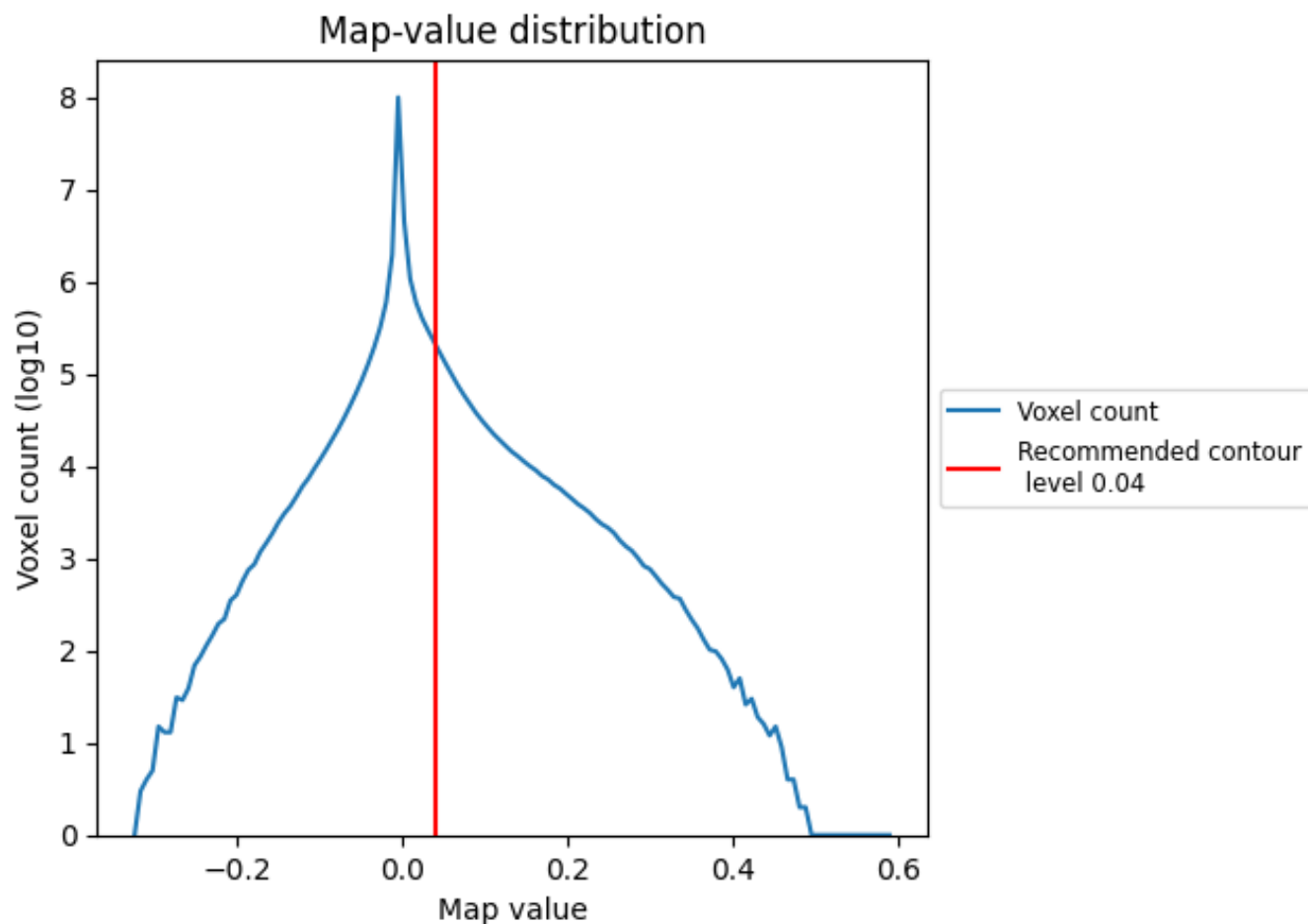
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

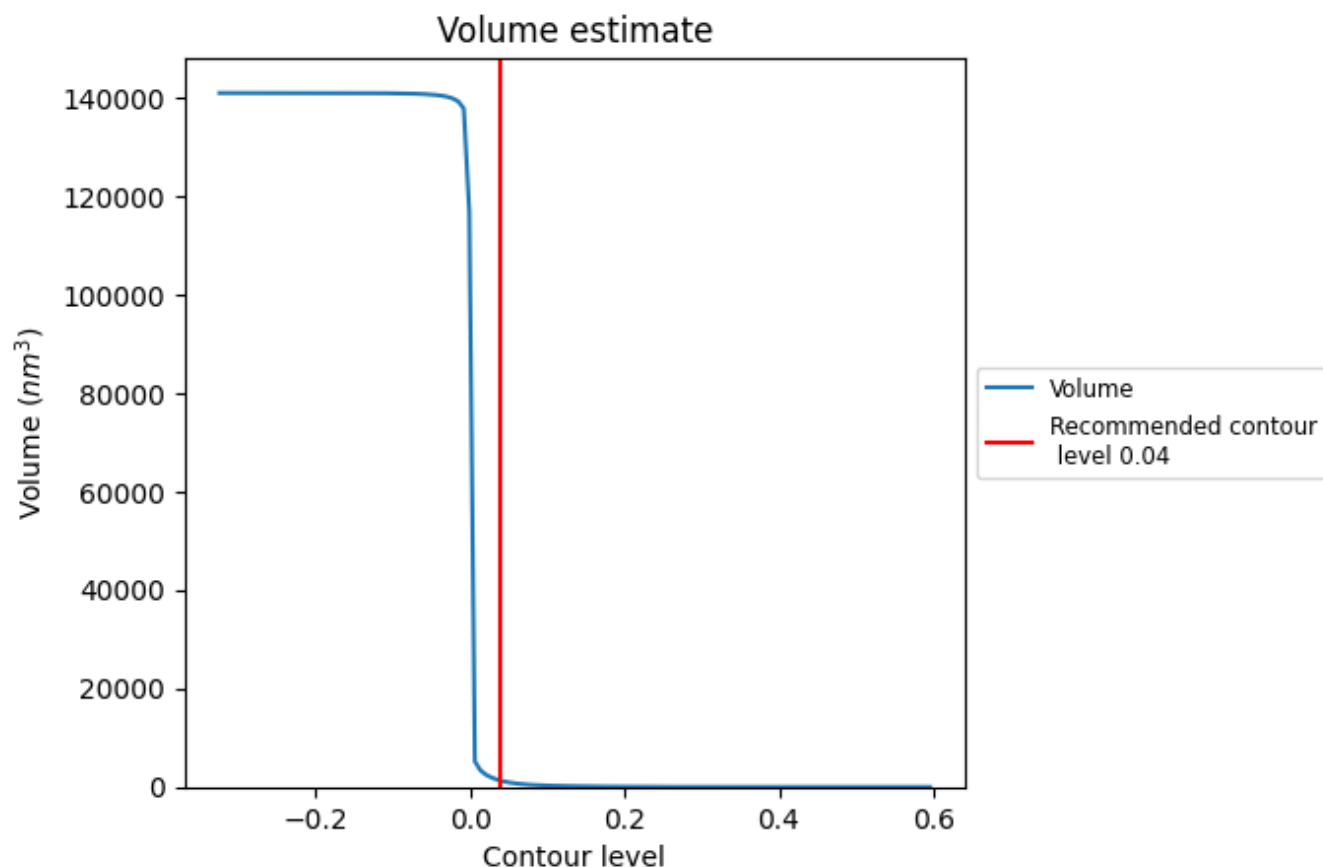
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

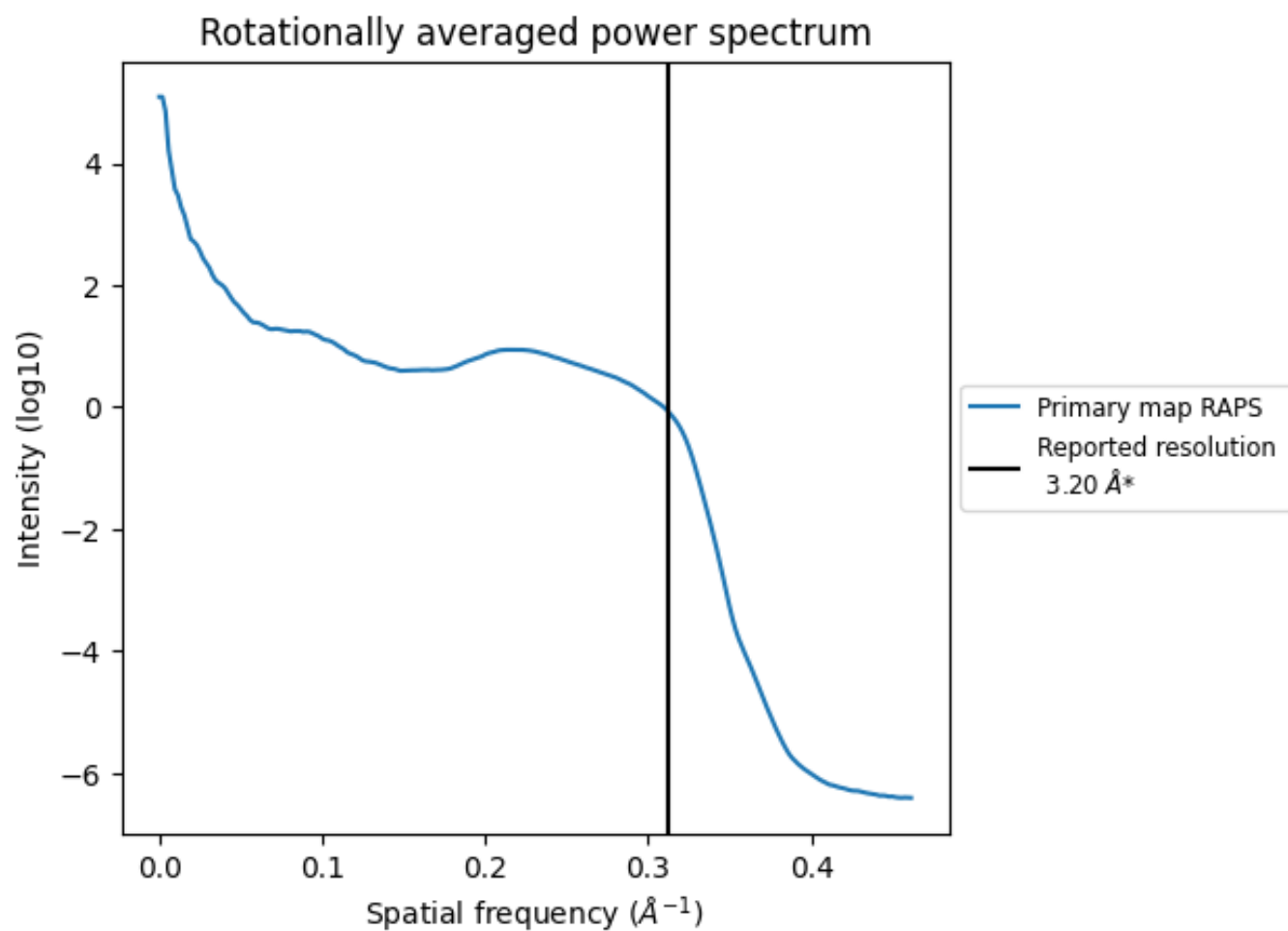
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1269 nm³; this corresponds to an approximate mass of 1146 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 ⓘ

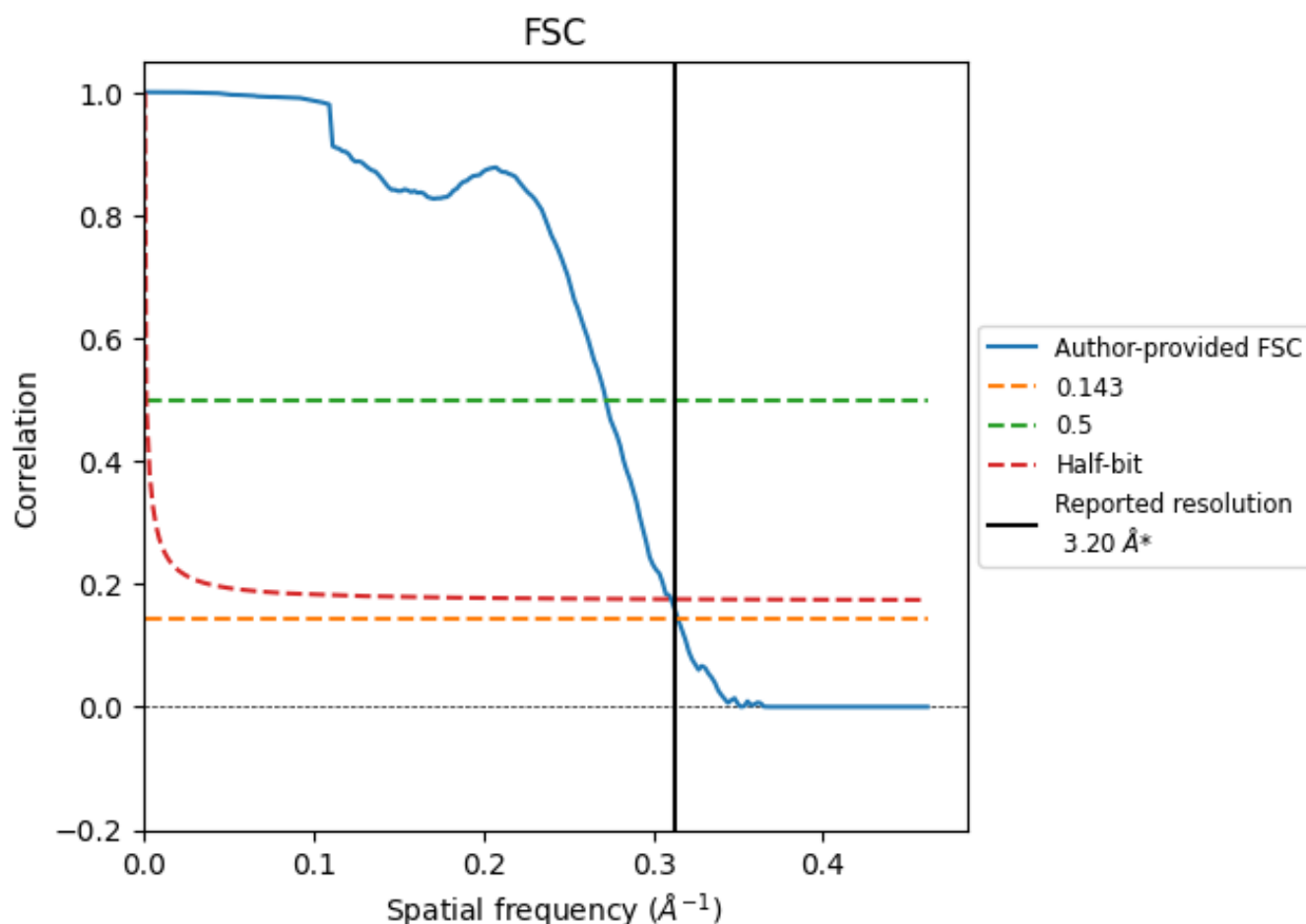


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

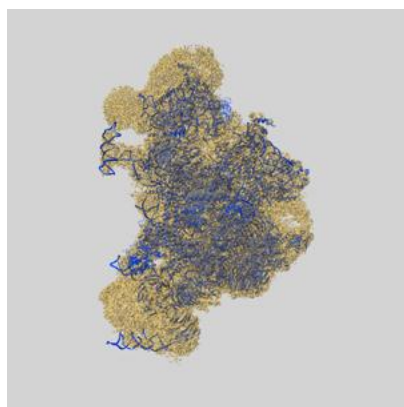
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.18	3.68	3.22
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

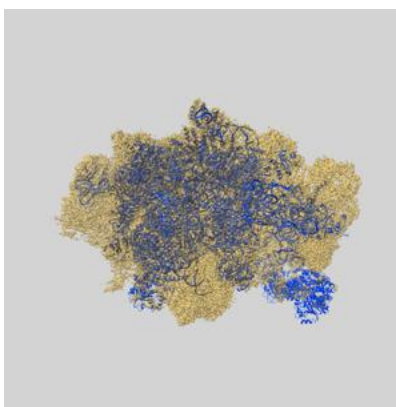
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3847 and PDB model 5OQL. Per-residue inclusion information can be found in section 3 on page 14.

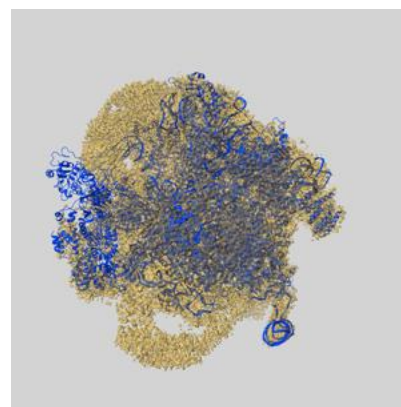
9.1 Map-model overlay [i](#)



X



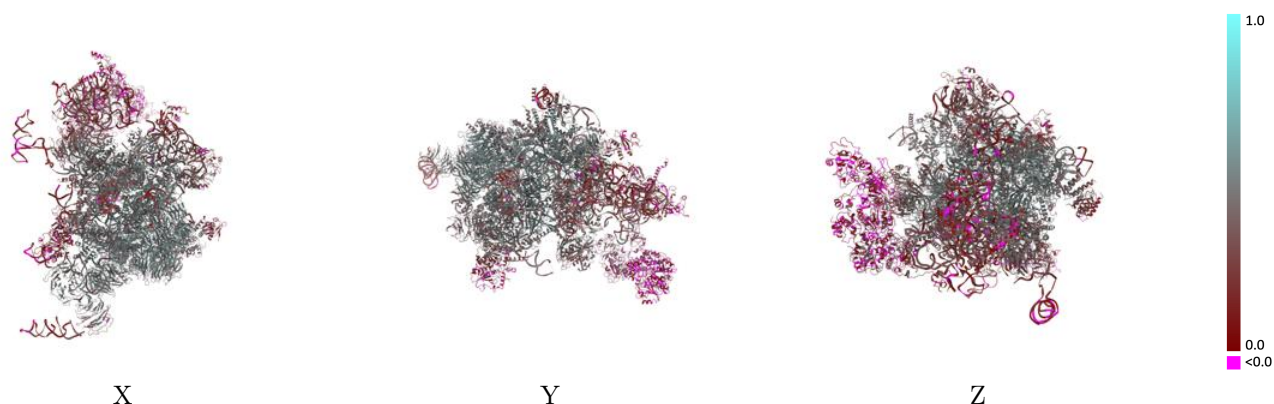
Y



Z

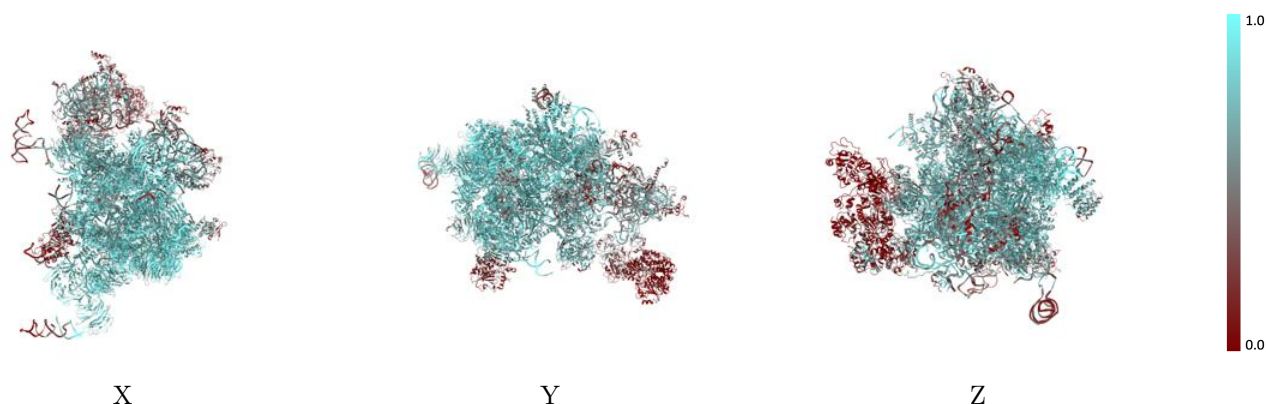
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



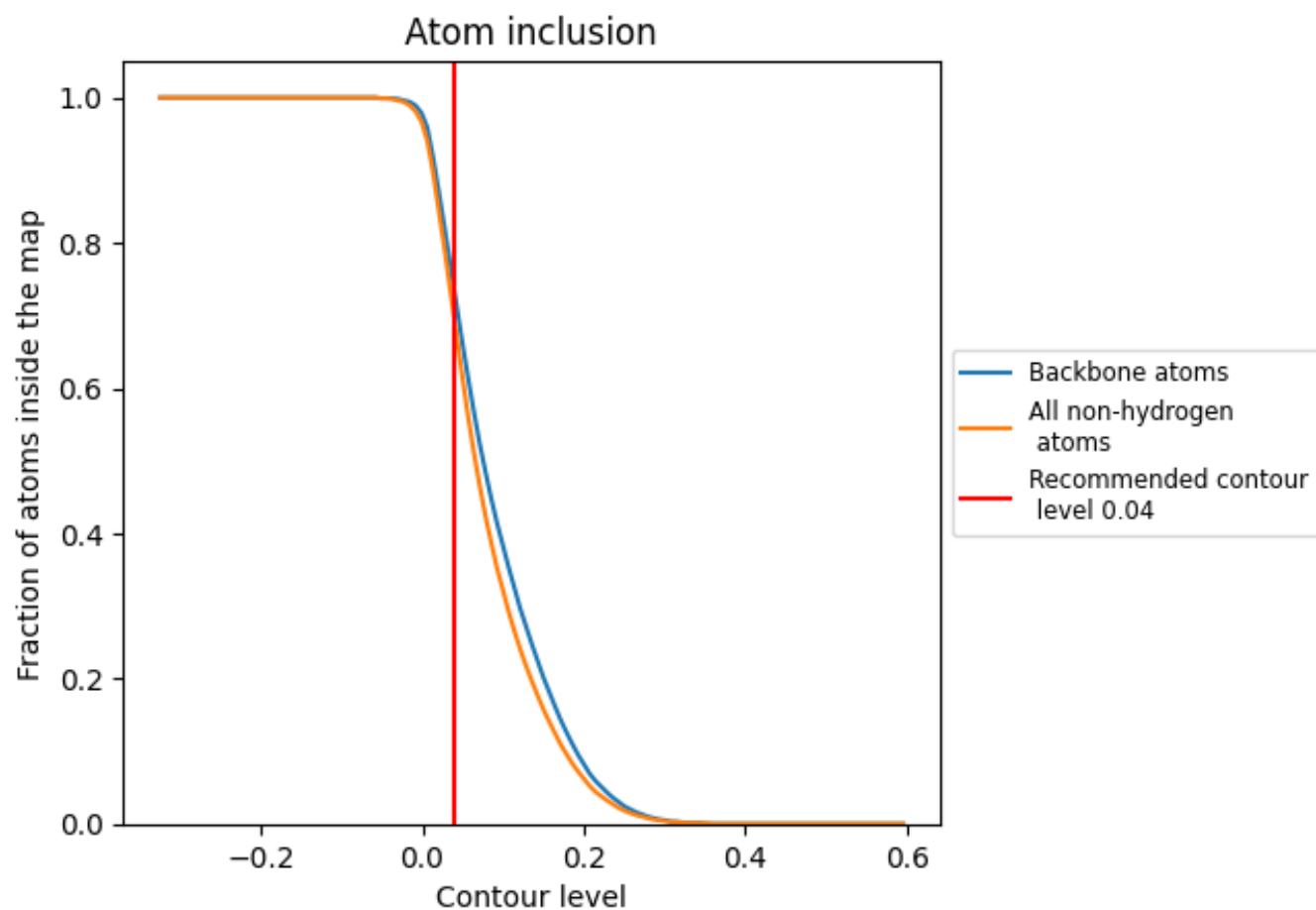
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 69% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6910	 0.3820
0	 0.7120	 0.4640
1	 0.7330	 0.3550
2	 0.7240	 0.3600
A	 0.8650	 0.4950
B	 0.7520	 0.4400
C	 0.8250	 0.4940
D	 0.8140	 0.4580
E	 0.7670	 0.3920
F	 0.8920	 0.5210
G	 0.8690	 0.4970
H	 0.8380	 0.4990
I	 0.6940	 0.3900
J	 0.7810	 0.4010
K	 0.8400	 0.4800
L	 0.6570	 0.3730
M	 0.8070	 0.4230
N	 0.8740	 0.5100
O	 0.8820	 0.5000
P	 0.8120	 0.4790
Q	 0.6090	 0.3400
R	 0.8710	 0.5060
S	 0.2730	 0.2150
T	 0.7630	 0.4080
U	 0.5740	 0.3530
V	 0.8010	 0.4560
W	 0.6850	 0.3740
X	 0.6950	 0.3800
Y	 0.6760	 0.3870
Z	 0.8120	 0.4610
a	 0.8960	 0.5260
b	 0.8090	 0.4820
c	 0.7780	 0.4460
d	 0.8740	 0.5080
e	 0.3280	 0.2480



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
f	 0.0890	 0.0800
g	 0.5350	 0.3700
h	 0.4820	 0.2610
i	 0.2140	 0.1550
j	 0.0390	 0.0820
k	 0.8280	 0.4800
l	 0.4560	 0.2900
m	 0.4330	 0.2260
n	 0.8200	 0.4630
o	 0.4030	 0.1770
p	 0.4310	 0.2430
q	 0.3830	 0.1720
r	 0.8210	 0.4630
s	 0.4440	 0.2070
t	 0.5710	 0.3280
u	 0.8700	 0.5000
v	 0.3860	 0.1660
w	 0.7540	 0.4290
x	 0.8430	 0.4850
y	 0.4620	 0.2300
z	 0.7820	 0.4430