



wwPDB EM Validation Summary Report ⓘ

Dec 17, 2022 – 11:07 pm GMT

PDB ID : 6ZQF
EMDB ID : EMD-11362
Title : Cryo-EM structure of the 90S pre-ribosome from *Saccharomyces cerevisiae*, state Dis-B (Poly-Ala)
Authors : Cheng, J.; Lau, B.; Venuta, G.L.; Berninghausen, O.; Hurt, E.; Beckmann, R.
Deposited on : 2020-07-09
Resolution : 4.90 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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

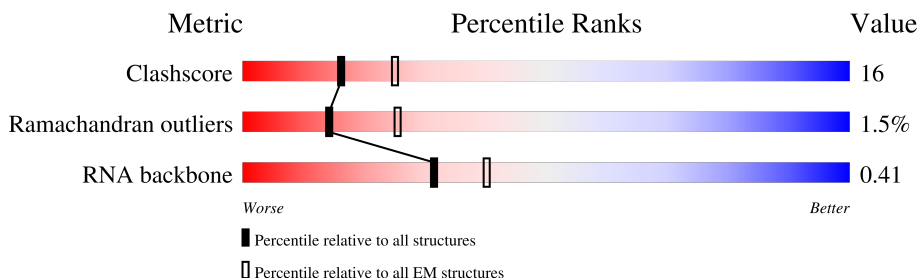
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
RNA backbone	4643	859

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	UA	923	
2	UB	810	
3	UC	610	
4	UL	943	
5	UM	817	
6	US	552	
7	UU	939	
8	UV	1237	

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Mol	Chain	Length	Quality of chain
9	CI	183	
10	CJ	290	
11	CK	593	
12	CL	1183	
13	CM	367	
14	CN	297	
15	JD	1267	
16	JF	252	
16	JG	252	
17	JH	483	
18	JL	318	
19	JJ	274	
20	DF	225	
21	DQ	143	
22	DS	146	
23	DT	144	
24	Dc	67	
25	D2	20	
26	D3	1758	
27	DA	255	
28	DE	261	
29	DG	236	
30	DH	190	
31	DI	200	
32	DJ	197	

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Mol	Chain	Length	Quality of chain
33	DL	156	
34	DN	151	
35	DO	137	
36	DZ	108	
37	DW	130	
38	DX	145	
39	DY	135	
40	Db	82	
41	D4	35	

2 Entry composition

There are 42 unique types of molecules in this entry. The entry contains 89582 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.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	UA	792	Total	C	N	O	0	0
			3916	2332	792	792		

- Molecule 2 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	UB	370	Total	C	N	O	0	0
			1845	1105	370	370		

- Molecule 3 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	UC	47	Total	C	N	O	0	0
			233	139	47	47		

- Molecule 4 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	UL	777	Total	C	N	O	0	0
			3841	2287	777	777		

- Molecule 5 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	UM	762	Total	C	N	O	0	0
			3763	2239	762	762		

- Molecule 6 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	US	499	Total	C	N	O	0	0
			2486	1488	499	499		

- Molecule 7 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	UU	878	Total	C	N	O	0	0
			4328	2572	878	878		

- Molecule 8 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	UV	1093	Total	C	N	O	0	0
			5417	3231	1093	1093		

- Molecule 9 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	CI	157	Total	C	N	O	0	0
			781	467	157	157		

- Molecule 10 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	CJ	219	Total	C	N	O	0	0
			1083	645	219	219		

- Molecule 11 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	CK	221	Total	C	N	O	0	0
			1101	659	221	221		

- Molecule 12 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	CL	695	Total	C	N	O	0	0
			3433	2044	695	694		

- Molecule 13 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	CM	360	Total	C	N	O	0	0
			1767	1047	360	360		

- Molecule 14 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	CN	184	Total	C	N	O	0	0
			916	548	184	184		

- Molecule 15 is a protein called Probable ATP-dependent RNA helicase DHR1.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	JD	807	Total	C	N	O	0	0
			3995	2381	807	807		

- Molecule 16 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	JF	216	Total	C	N	O	0	0
			1071	639	216	216		
16	JG	221	Total	C	N	O	0	0
			1096	654	221	221		

- Molecule 17 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	JH	261	Total	C	N	O	0	0
			1295	773	261	261		

- Molecule 18 is a protein called Dimethyladenosine transferase.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	JL	283	Total	C	N	O	0	0
			1401	835	283	283		

- Molecule 19 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	JJ	181	Total	C	N	O	0	0
			893	531	181	181		

- Molecule 20 is a protein called Rps5p.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	DF	213	Total	C	N	O	0	0
			1055	629	213	213		

- Molecule 21 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	DQ	125	Total	C	N	O	0	0
			616	366	125	125		

- Molecule 22 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	DS	77	Total	C	N	O	0	0
			381	227	77	77		

- Molecule 23 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	DT	143	Total	C	N	O	0	0
			700	414	143	143		

- Molecule 24 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	Dc	63	Total	C	N	O	0	0
			310	184	63	63		

- Molecule 25 is a RNA chain called 5ETS RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	D2	20	Total	C	N	O	P	0	0
			429	191	75	143	20		

- Molecule 26 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	D3	1392	Total	C	N	O	P	0	0
			29645	13257	5244	9752	1392		

- Molecule 27 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	DA	214	Total	C	N	O	0	0
			1061	633	214	214		

- Molecule 28 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	DE	260	Total	C	N	O	0	0
			1276	756	260	260		

- Molecule 29 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	DG	226	Total	C	N	O	0	0
			1113	661	226	226		

- Molecule 30 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	DH	184	Total	C	N	O	0	0
			913	545	184	184		

- Molecule 31 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	DI	188	Total	C	N	O	0	0
			924	548	188	188		

- Molecule 32 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	DJ	185	Total	C	N	O	0	0
			915	545	185	185		

- Molecule 33 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	DL	155	Total	C	N	O	0	0
			766	456	155	155		

- Molecule 34 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	DN	150	Total	C	N	O	0	0
			742	442	150	150		

- Molecule 35 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	DO	127	Total	C	N	O	0	0
			620	366	127	127		

- Molecule 36 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	DZ	67	Total	C	N	O	0	0
			332	198	67	67		

- Molecule 37 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	DW	129	Total	C	N	O	0	0
			634	376	129	129		

- Molecule 38 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	DX	140	Total	C	N	O	0	0
			684	404	140	140		

- Molecule 39 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	DY	134	Total	C	N	O	0	0
			661	393	134	134		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
40	Db	81	Total	C	N	O	0	0
			400	238	81	81		

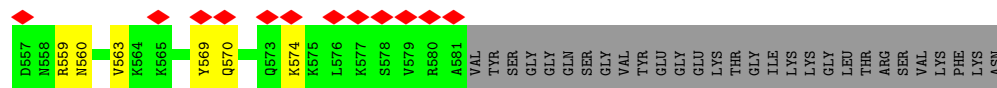
- Molecule 41 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	D4	35	Total	C	N	O	P	0	0
			743	333	134	241	35		

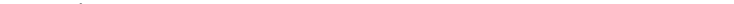
- Molecule 42 is ZINC ION (three-letter code: ZN) (formula: Zn).

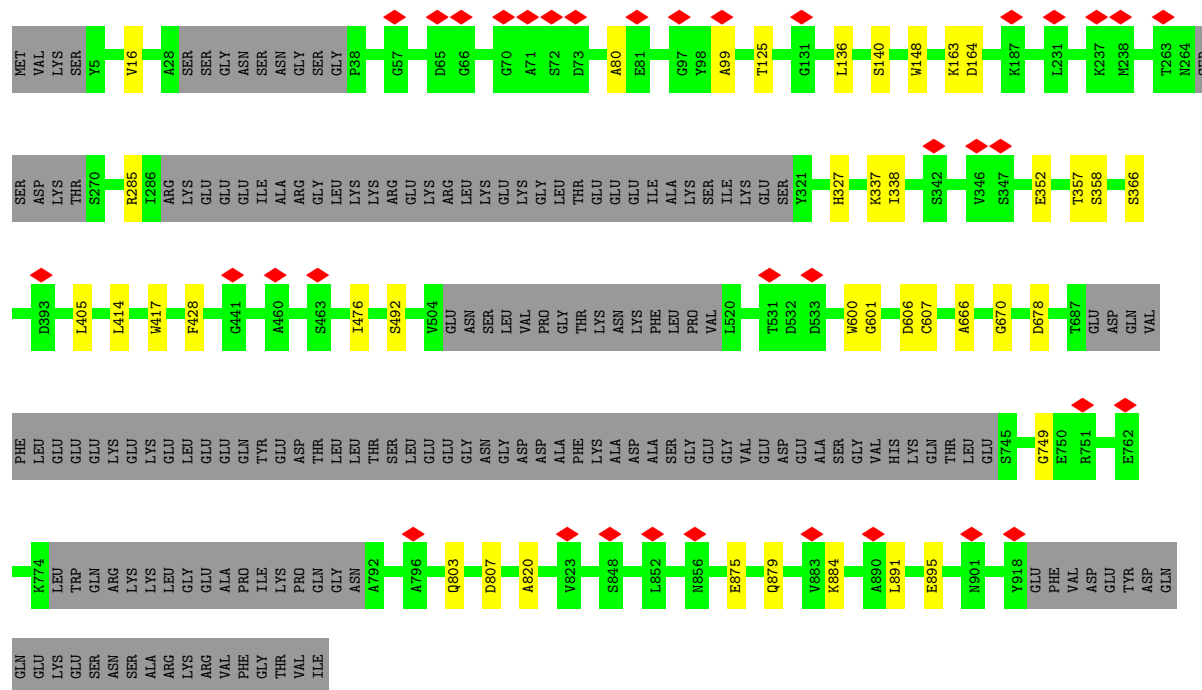
Mol	Chain	Residues	Atoms		AltConf
42	Db	1	Total	Zn	0
			1	1	






- Molecule 4: U3 small nucleolar RNA-associated protein 12

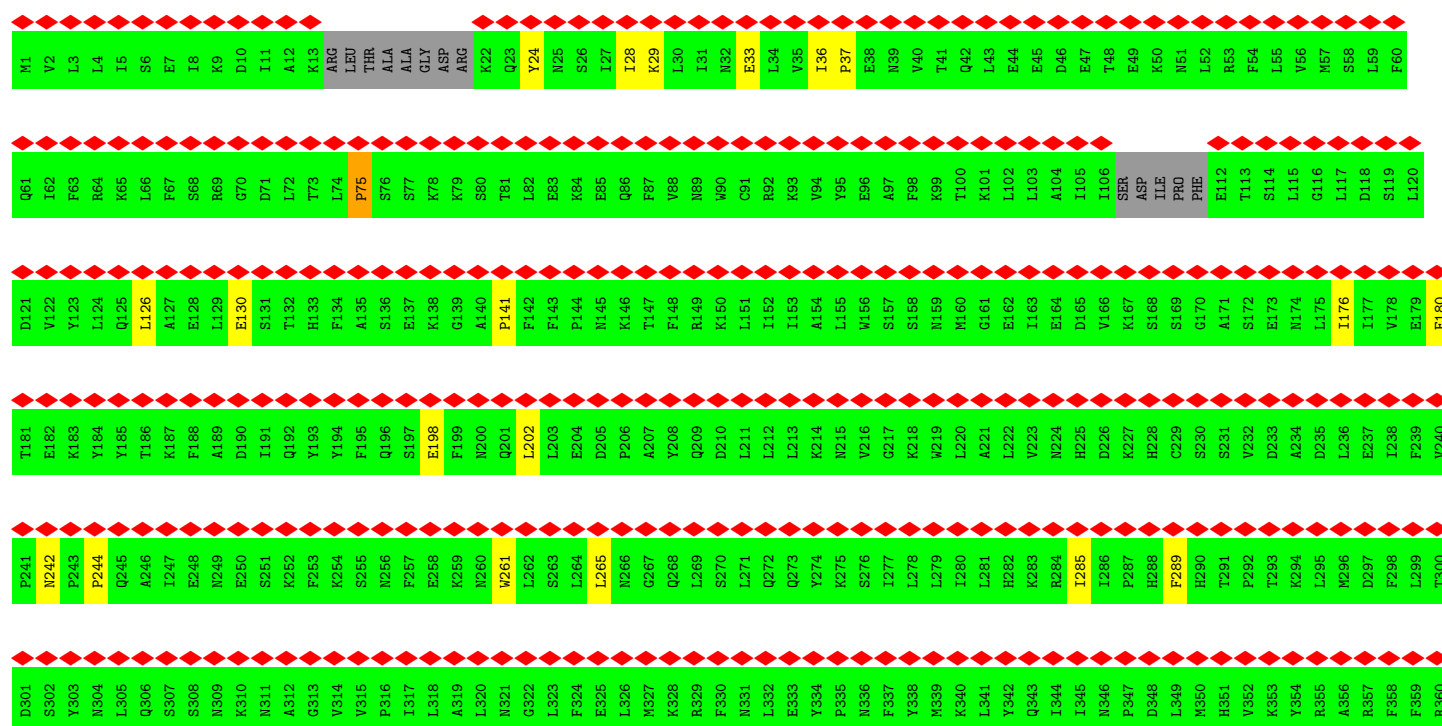
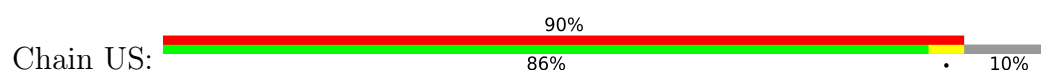
Chain UL:  78% 18%



- Molecule 5: U3 small nucleolar RNA-associated protein 13

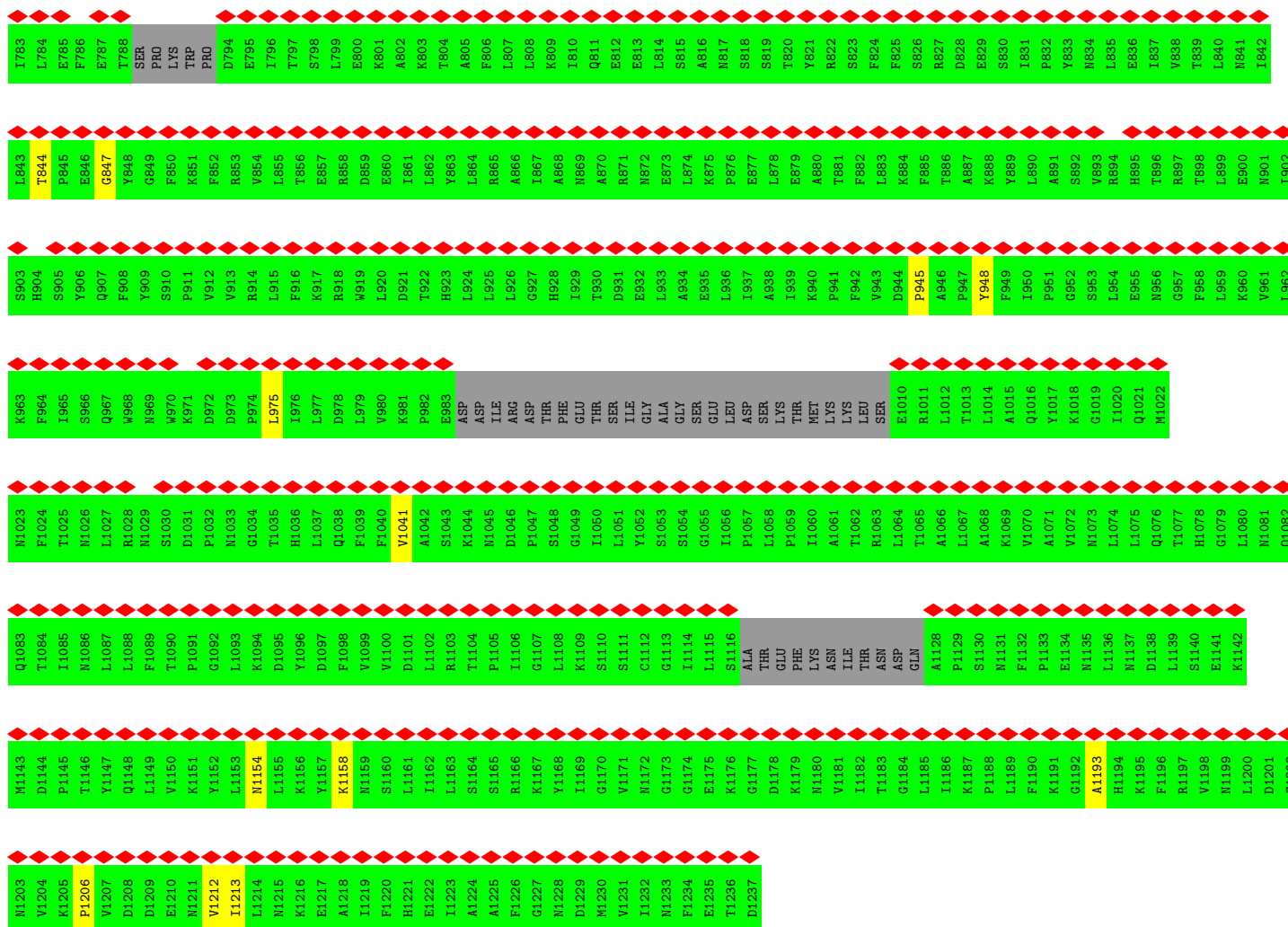
Chain UM: 

- Molecule 6: Nucleolar complex protein 4

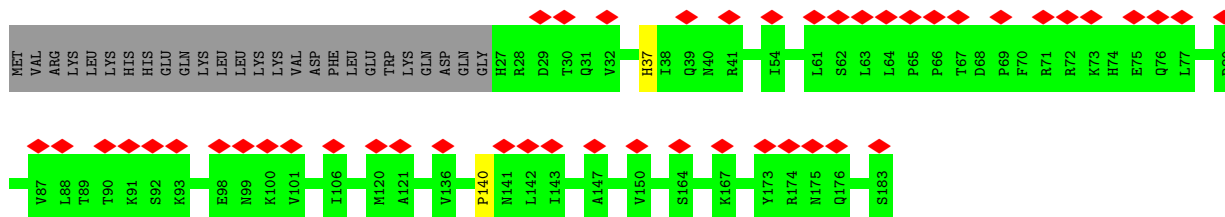
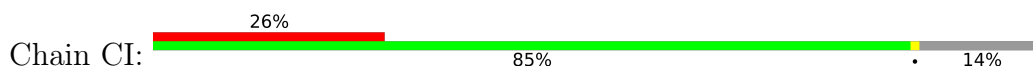


Chain UV:





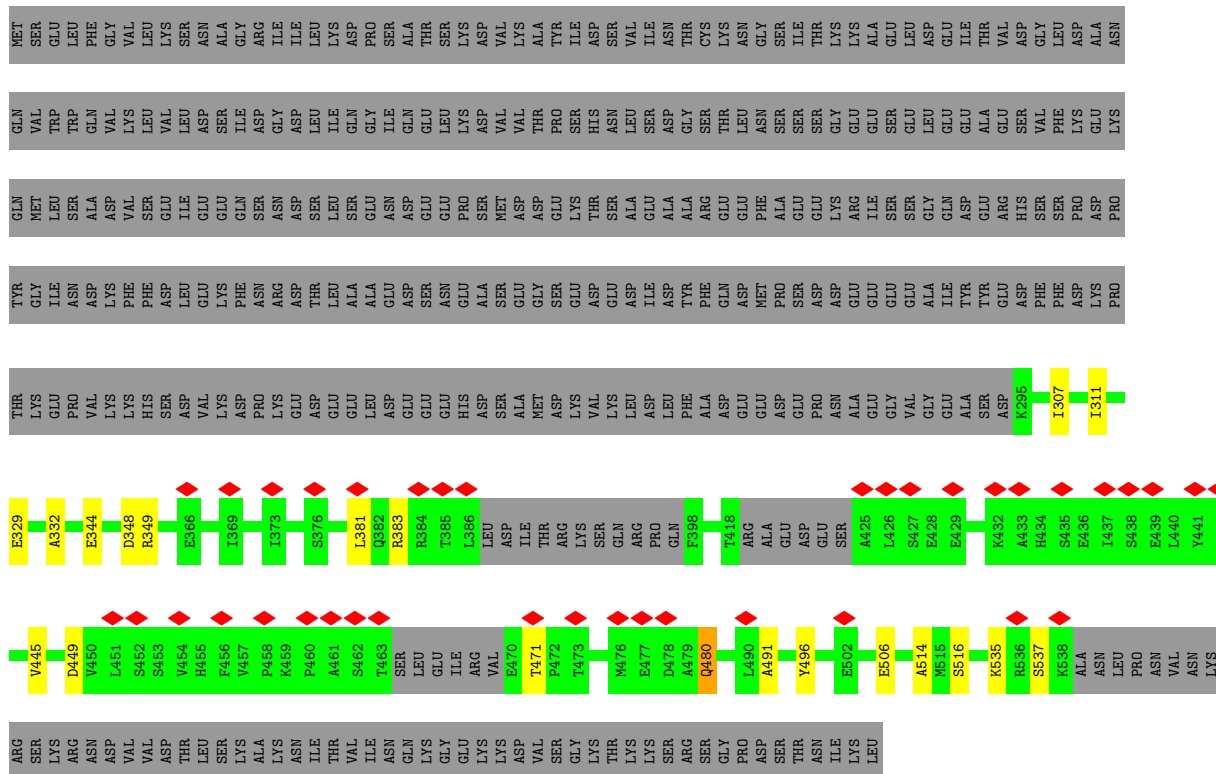
- Molecule 9: U3 small nucleolar ribonucleoprotein protein IMP3



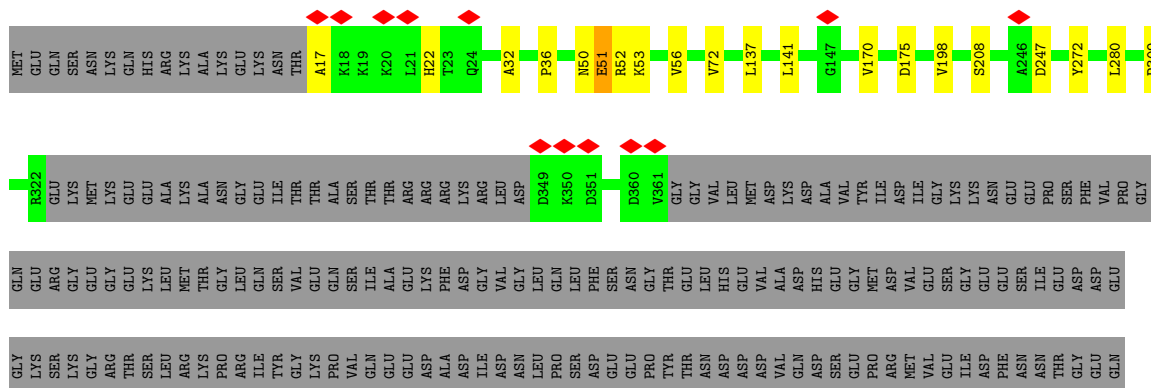
- Molecule 10: U3 small nucleolar ribonucleoprotein protein IMP4

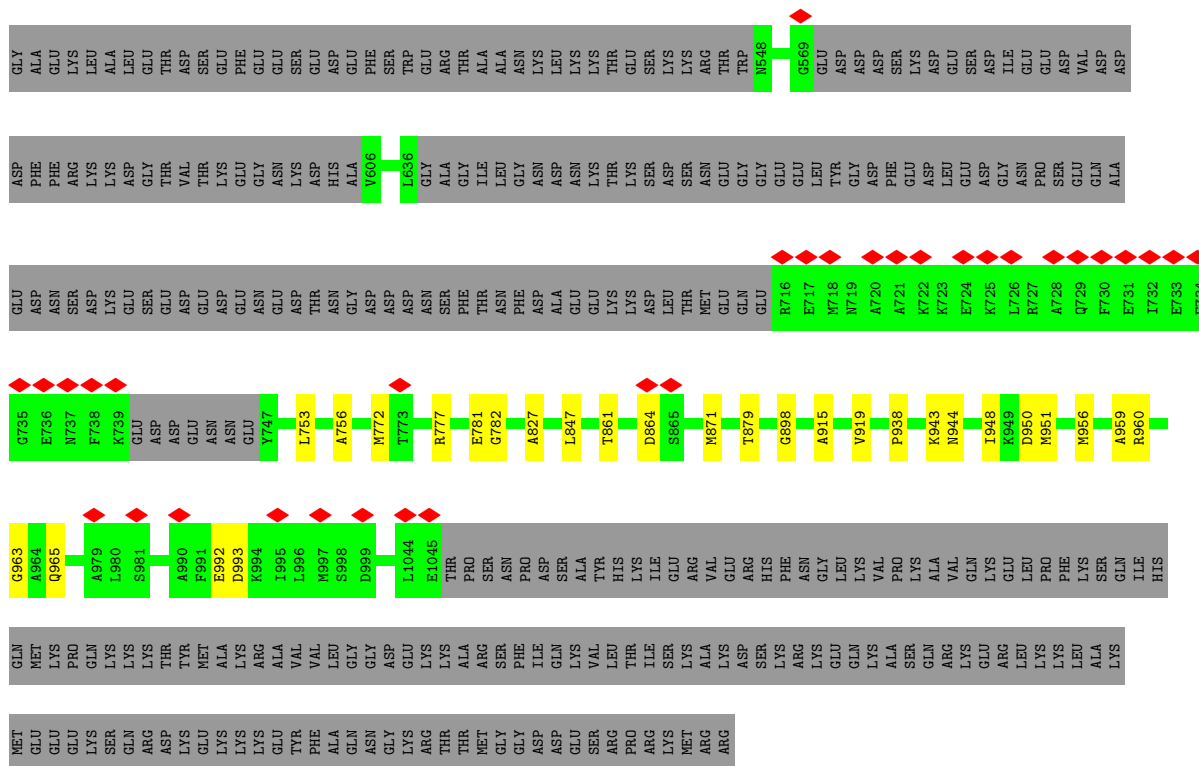


- Molecule 11: U3 small nucleolar RNA-associated protein MPP10



- Molecule 12: Ribosome biogenesis protein BMS1

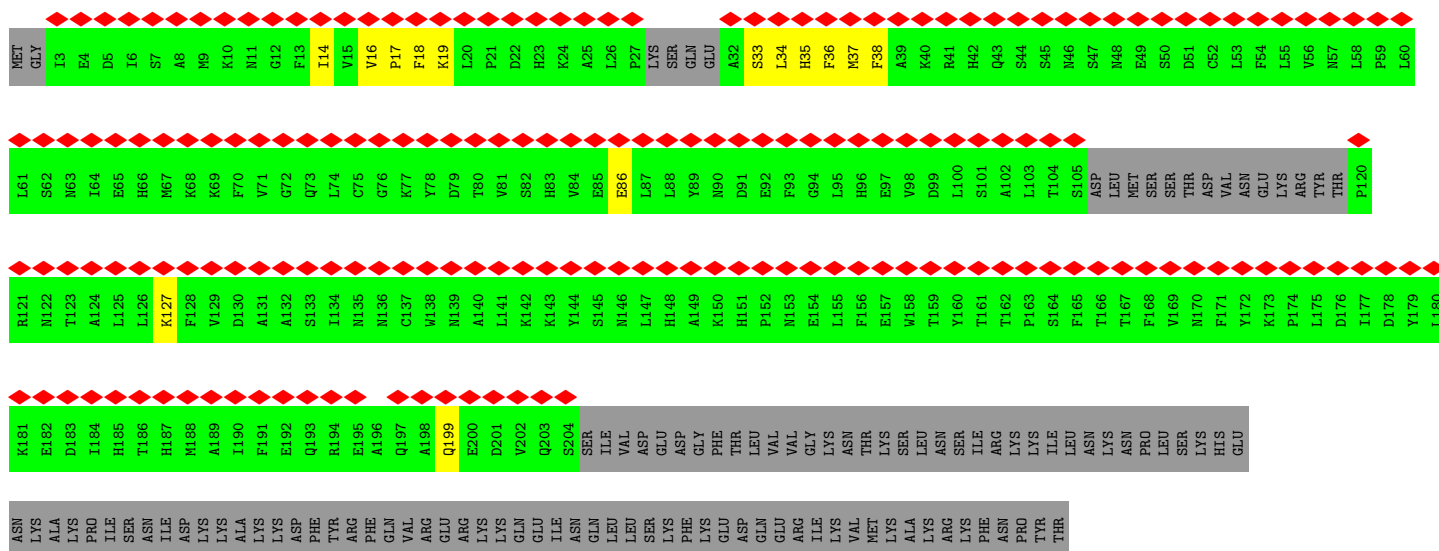




- Molecule 13: RNA 3'-terminal phosphate cyclase-like protein

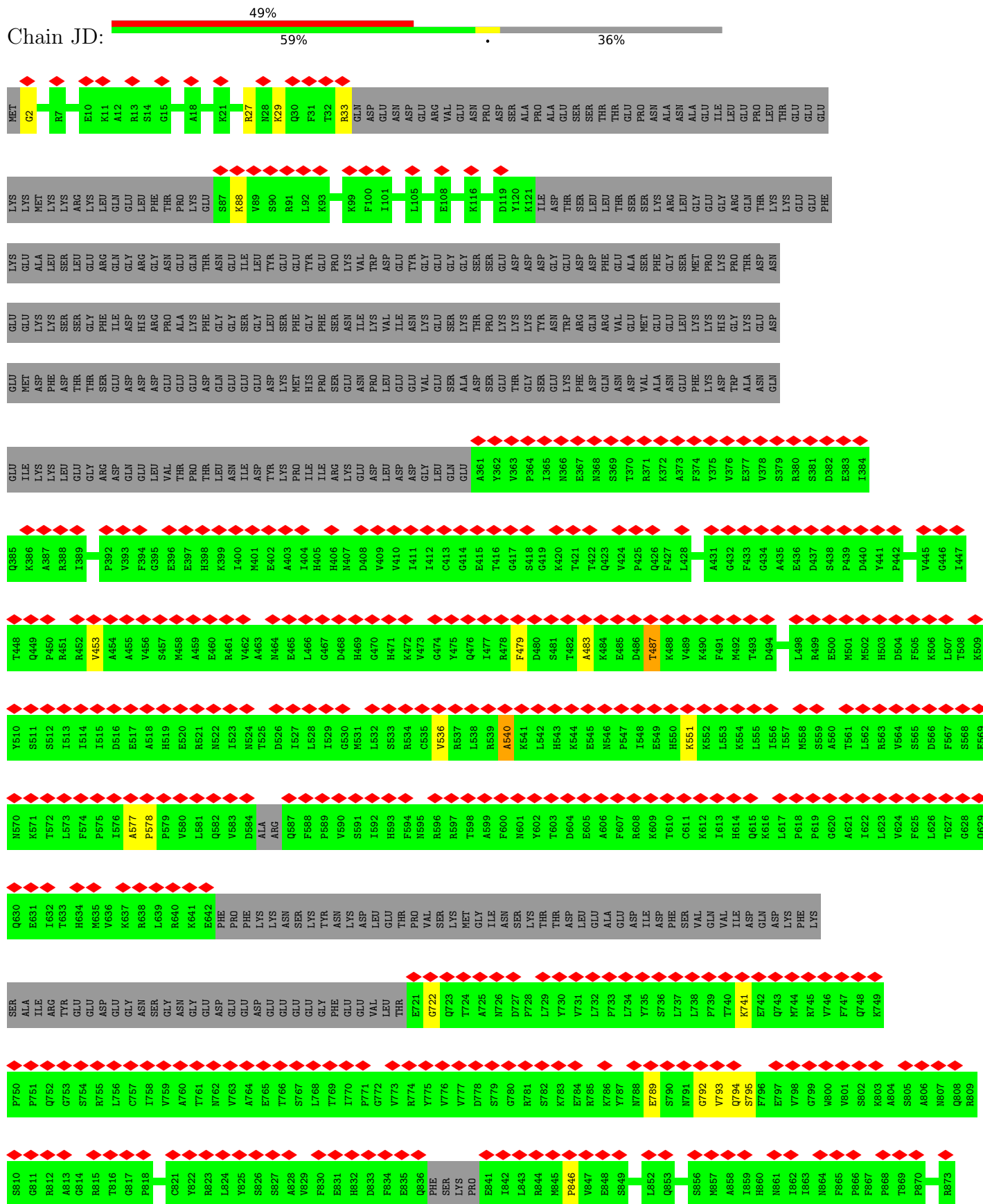


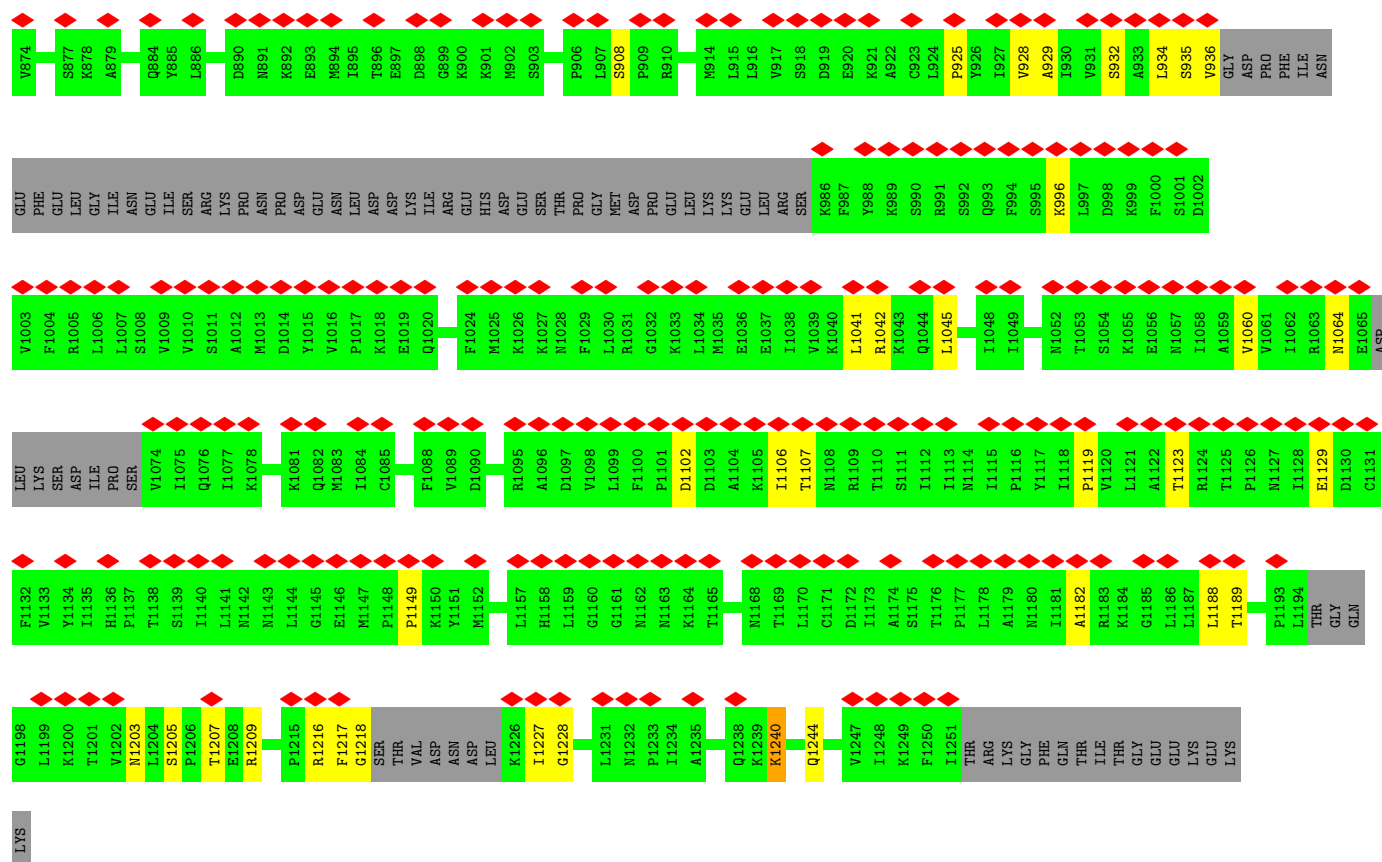
- Molecule 14: Ribosomal RNA-processing protein 7



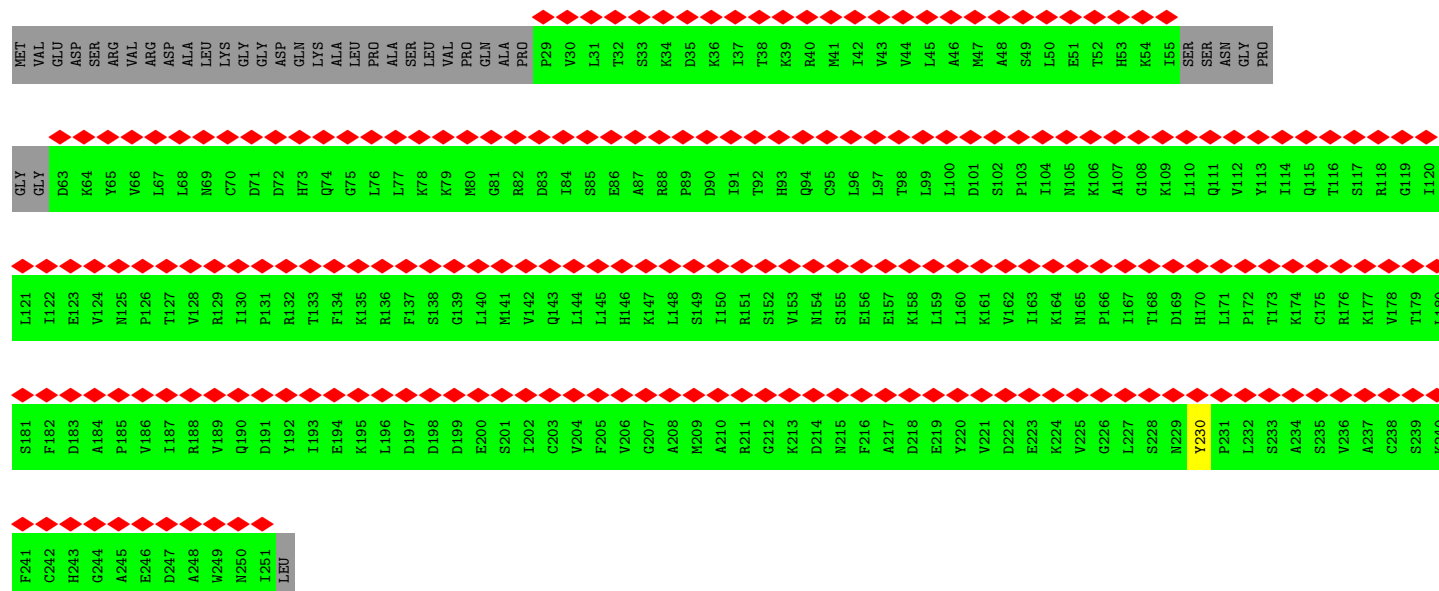
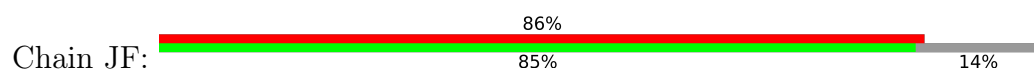
● Molecule 15: Probable ATP-dependent RNA helicase DHR1

Chain JD:

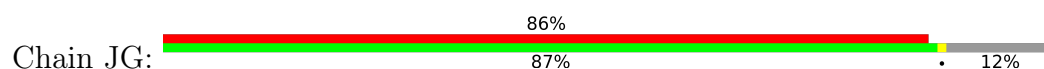




• Molecule 16: Ribosomal RNA small subunit methyltransferase NEP1

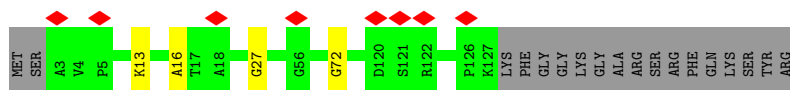


• Molecule 16: Ribosomal RNA small subunit methyltransferase NEP1

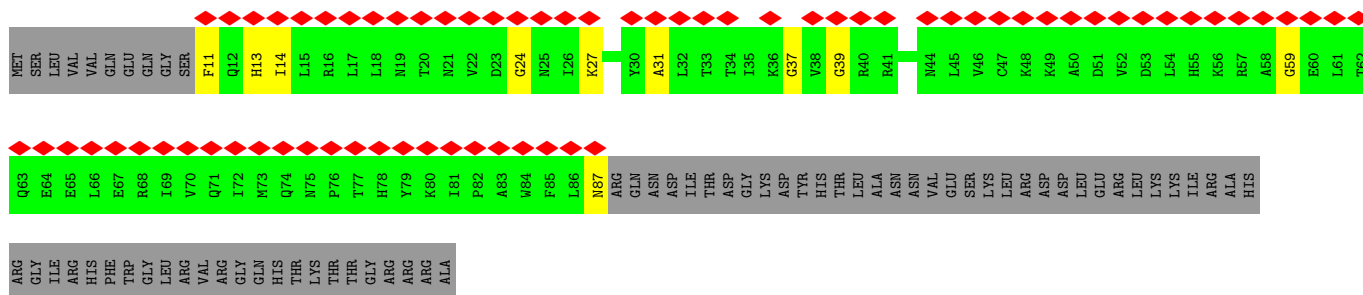




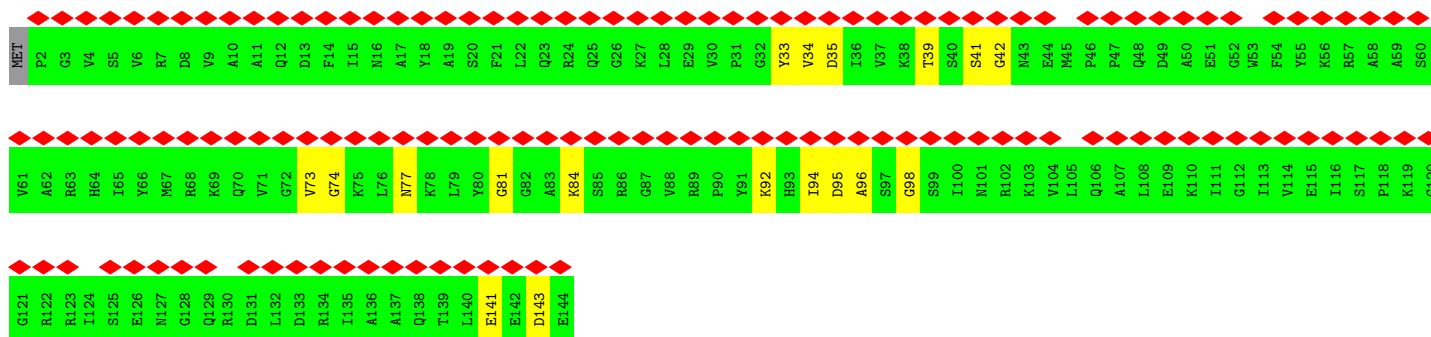
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L422	L362	H302	W242	PRO	ASP	ILE	ALA
T423	P363	I303	Q243	ALA	TTR	LEU	ARG
F424	F364	Y304	D244	ASN	GLU	LEU	SER
A425	S365	R305	R245	GLU	GLU	ALA	SER
Q426	P366	A306	I246	GLN	GLU	LYS	THR
R427	P367	V307	Y247	ASN	GLU	GLU	LYS
Y428	T368	K308	V248	THR	ILE	GLN	ALA
K429	T369	K309	T249	SER	VAL	GLN	ARG
M430	V370	S310	N250	ARG	GLU	GLU	GLN
D431	F371	L311	P251	GLY	ILE	ASP	ARG
I432	I372	Y312	E252	ASN	GLU	ILE	HIS
T433	K373	K313	E253	ILE	GLU	GLY	ASP
Q434	I374	P314	W254	SER	GLU	GLU	PRO
D435	L375	S315	P255	GLY	ALA	LEU	LEU
Q436	L376	A316	P256	LEU	ALA	LEU	LYS
R437	D377	F317	H257	LYS	ASP	ALA	ASP
D438	K378	F318	V258	GLY	GLY	ARG	ALA
F439	K379	K319	V259	VAL	PHE	ASN	ALA
L440	Y380	G320	Y260	A205	LYS	ASN	ALA
L441	A381	F321	E261	L206	LYS	GLN	GLN
E442	L382	L322	A262	L207	GLY	PHE	THR
T443	P383	F323	T263	E208	ASP	LEU	LEU
V444	Y384	P324	K264	K209	ASP	ALA	LYS
R445	Q385	L325	L265	V210	PHE	ARG	LYS
Q446	T386	V326	F266	I211	ASN	PHE	ILE
R447	F387	E327	V267	K212	LEU	THR	LYS
G448	D388	T328	S268	I213	SER	LYS	LYS
H449	D389	G329	N269	A213	GLY	SER	LYS
K450	C390	C330	L270	T215	THR	LYS	LEU
D451	V391	N331	T271	T216	TYR	TYR	LEU
I452	F392	V332	A272	V217	ASP	ASP	ALA
Q453	Y393	K333	K273	G218	ASP	ASP	ALA
P454	F394	E334	E274	S219	LYS	ASP	ALA
P455	M395	A335	S275	I220	ILE	GLU	ASN
I456	R396	T336	Q276	L221	ALA	ASP	ASP
R457	F397	I337	K277	K222	SER	ASP	ALA
R458	R398	A338	F278	T223	ILE	GLU	ASN
P459	I399	G339	I279	W224	ARG	GLU	GLU
L460	L400	S340	N280	T225	GLU	PHE	GLU
L461	D401	V341	L281	H226	SER	GLU	GLY
A462	ASP	L342	I282	G227	GLN	ASP	TYR
Q463	G403	A343	L283	K228	VAL	ILE	ILE
A464	S404	K344	L284	L229	GLU	SER	ASP
S465	N405	V345	E285	P230	MET	PHE	LYS
R466	Q406	S346	R286	K231	GLN	GLU	SER



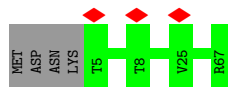
- Molecule 22: 40S ribosomal protein S18-A



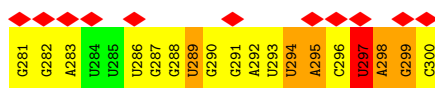
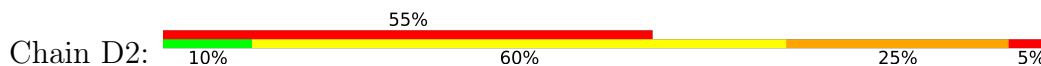
- Molecule 23: 40S ribosomal protein S19-A



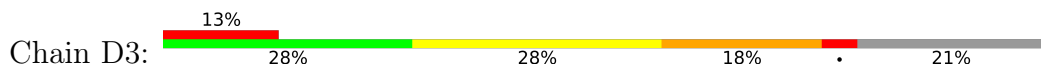
- Molecule 24: 40S ribosomal protein S28-A



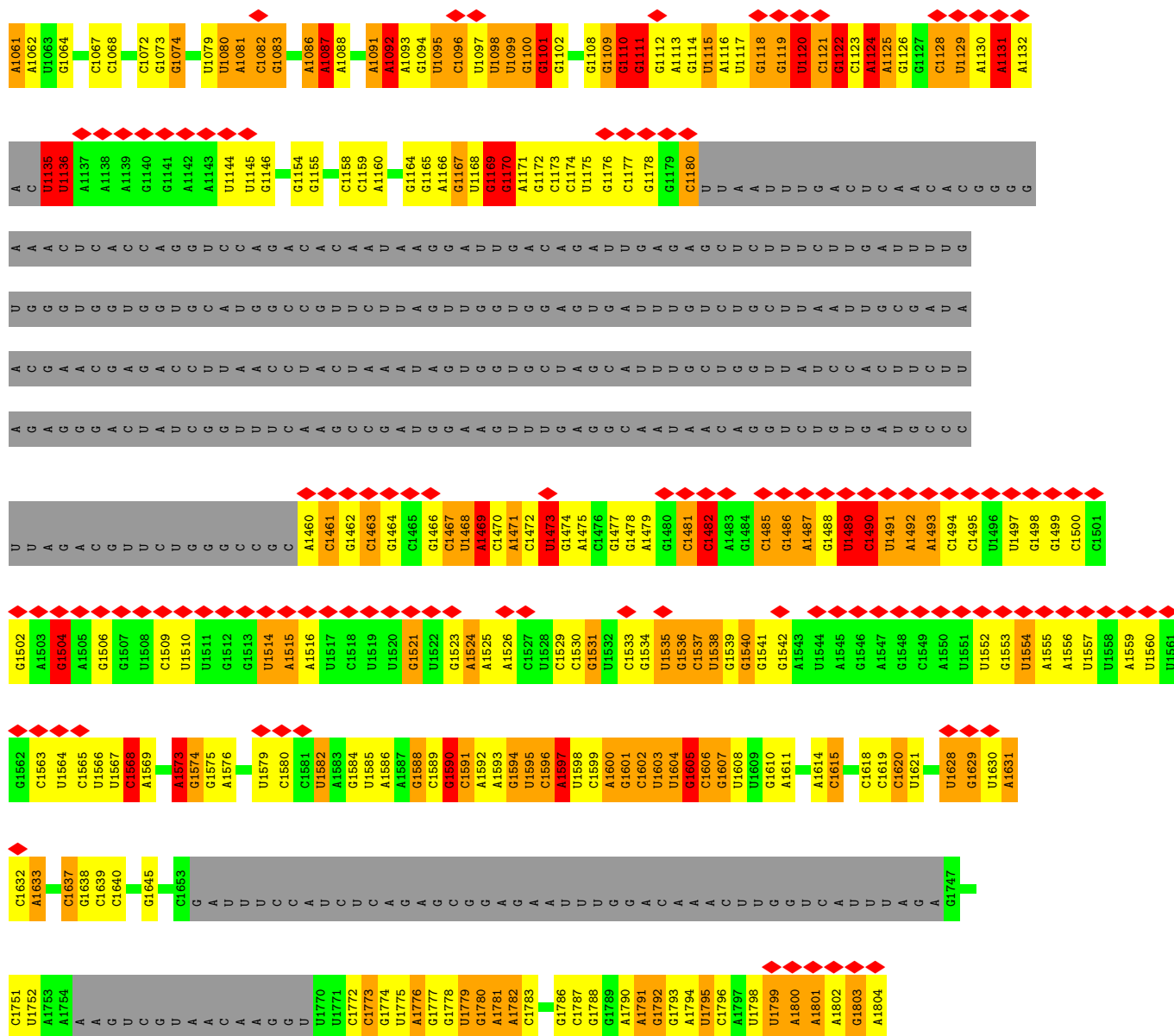
- Molecule 25: 5ETS RNA



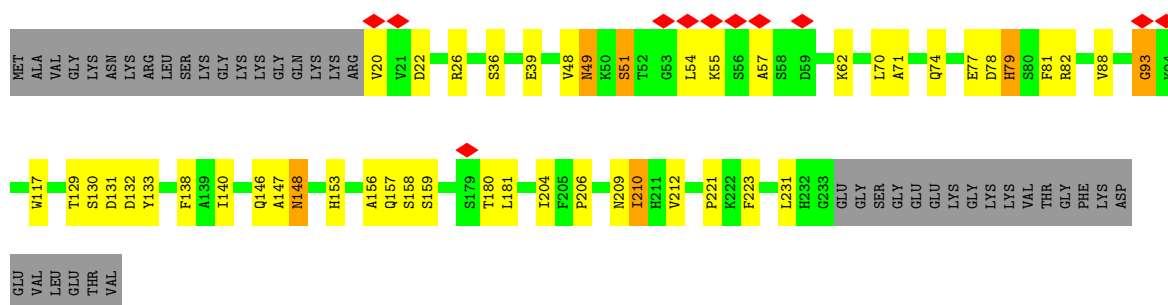
- Molecule 26: 18S rRNA







- Molecule 27: 40S ribosomal protein S1-A



- Molecule 28: 40S ribosomal protein S4-A

Chain DE:  91% 8% .




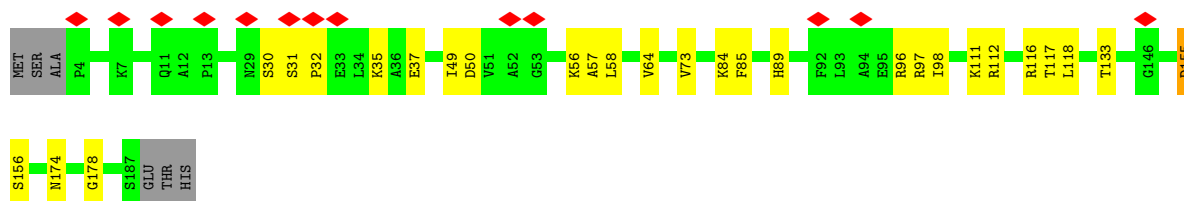
- Molecule 29: 40S ribosomal protein S6-A

Chain DG:  91% 5% .




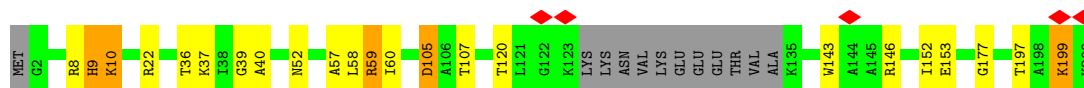
- Molecule 30: 40S ribosomal protein S7-A

Chain DH:  7% 82% 14% ..




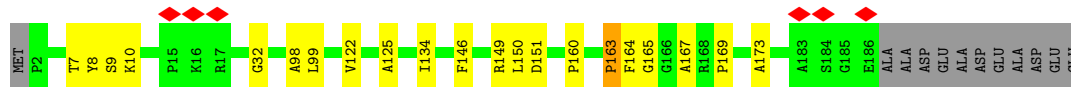
- Molecule 31: 40S ribosomal protein S8-A

Chain DI:  82% 9% 6% .




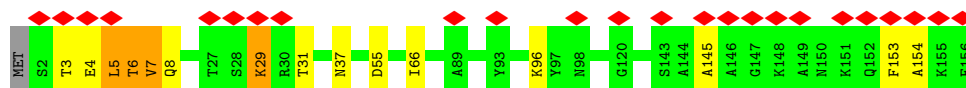
- Molecule 32: 40S ribosomal protein S9-A

Chain DJ:  83% 10% 6% .



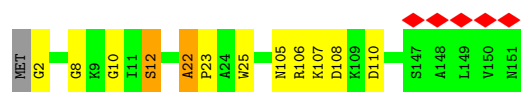
- Molecule 33: 40S ribosomal protein S11-A

Chain DL:  15% 90% 7% ..



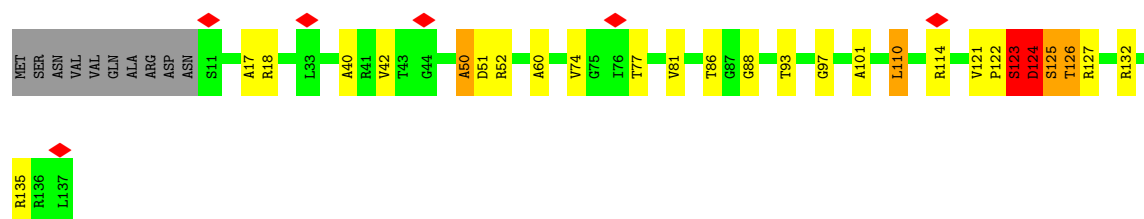
- Molecule 34: 40S ribosomal protein S13

Chain DN:  91% 7% ..



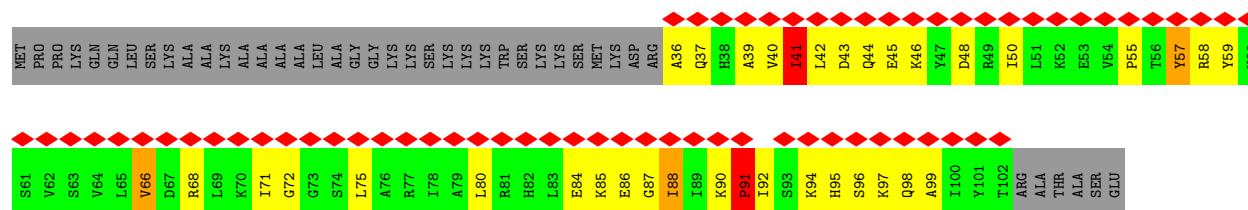
- Molecule 35: 40S ribosomal protein S14-A

Chain DO: 73% 15% 7%



- Molecule 36: 40S ribosomal protein S25-A

Chain DZ: 29% 61% 29% 38%



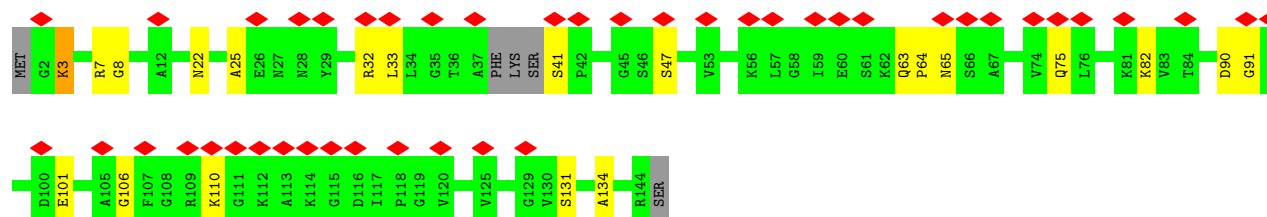
- Molecule 37: 40S ribosomal protein S22-A

Chain DW: 89% 10%



- Molecule 38: 40S ribosomal protein S23-A

Chain DX: 30% 82% 14%

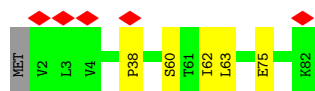


- Molecule 39: 40S ribosomal protein S24-A

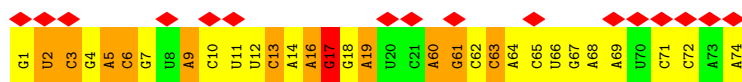
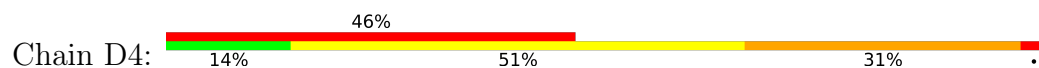
Chain DY: 81% 16%



- Molecule 40: 40S ribosomal protein S27-A



- Molecule 41: U3 snoRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	16654	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.053	Depositor
Minimum map value	-0.024	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	508.32, 508.32, 508.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	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	UA	0.66	0/3913	0.69	0/5447
2	UB	0.29	0/1841	0.49	2/2568 (0.1%)
3	UC	0.33	0/232	0.47	0/322
4	UL	0.30	0/3834	0.57	0/5330
5	UM	0.66	0/3756	0.89	3/5219 (0.1%)
6	US	0.31	0/2483	0.50	2/3466 (0.1%)
7	UU	0.44	0/4324	0.59	0/6010
8	UV	0.28	0/5410	0.47	0/7534
9	CI	0.36	0/780	0.56	0/1088
10	CJ	0.38	0/1082	0.65	0/1506
11	CK	0.55	0/1097	0.60	0/1527
12	CL	0.57	1/3427 (0.0%)	0.64	0/4764
13	CM	0.47	0/1766	0.59	0/2451
14	CN	0.27	0/913	0.47	0/1271
15	JD	0.60	1/3985 (0.0%)	1.00	3/5539 (0.1%)
16	JF	0.28	0/1069	0.49	0/1488
16	JG	0.31	0/1094	0.50	0/1523
17	JH	0.37	0/1293	0.50	0/1801
18	JL	0.71	1/1400 (0.1%)	0.91	2/1950 (0.1%)
19	JJ	0.56	0/892	0.57	0/1240
20	DF	0.34	0/1054	0.58	0/1468
21	DQ	0.38	0/615	0.62	0/854
22	DS	0.26	0/380	0.53	0/528
23	DT	0.28	0/699	0.61	0/968
24	Dc	0.33	0/309	0.56	0/428
25	D2	2.98	50/479 (10.4%)	1.85	19/745 (2.6%)
26	D3	0.69	8/33150 (0.0%)	1.27	250/51635 (0.5%)
27	DA	0.56	0/1060	0.67	0/1477
28	DE	0.48	0/1275	0.73	0/1769
29	DG	0.53	0/1112	0.66	0/1545
30	DH	0.43	0/912	0.66	0/1271
31	DI	0.53	0/922	0.73	0/1278

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	DJ	0.46	0/914	0.65	0/1272
33	DL	0.53	0/765	0.65	0/1064
34	DN	0.45	0/741	0.67	1/1031 (0.1%)
35	DO	0.51	0/619	0.67	0/856
36	DZ	0.41	0/331	0.69	2/460 (0.4%)
37	DW	0.48	0/633	0.71	0/878
38	DX	0.44	0/682	0.67	0/942
39	DY	0.41	0/660	0.61	0/917
40	Db	0.41	0/399	0.65	0/554
41	D4	1.91	37/828 (4.5%)	1.59	21/1282 (1.6%)
All	All	0.62	98/93130 (0.1%)	0.96	305/135266 (0.2%)

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
4	UL	0	2
5	UM	0	3
7	UU	0	1
10	CJ	0	3
12	CL	0	2
18	JL	0	1
21	DQ	0	1
22	DS	0	1
26	D3	0	4
35	DO	0	3
36	DZ	0	1
38	DX	0	1
All	All	0	23

The worst 5 of 98 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	D2	292	A	N9-C4	-10.81	1.31	1.37
18	JL	188	ILE	C-N	8.72	1.54	1.34
25	D2	298	A	N3-C4	-8.70	1.29	1.34
12	CL	56	VAL	C-N	8.35	1.50	1.34
25	D2	292	A	N3-C4	-8.21	1.29	1.34

The worst 5 of 305 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	D3	897	C	P-O3'-C3'	-27.03	87.27	119.70
26	D3	15	U	C4'-C3'-O3'	20.56	154.12	113.00
26	D3	1111	G	N9-C1'-C2'	-16.31	92.80	114.00
26	D3	16	G	O5'-P-OP2	-14.71	92.47	105.70
26	D3	897	C	O3'-P-O5'	-14.19	77.04	104.00

There are no chirality outliers.

5 of 23 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	UL	16	VAL	Peptide
4	UL	678	ASP	Peptide
5	UM	282	ASN	Peptide
5	UM	467	ILE	Peptide
5	UM	489	ALA	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	UA	3916	0	1763	121	0
2	UB	1845	0	787	26	0
3	UC	233	0	103	29	0
4	UL	3841	0	1710	22	0
5	UM	3763	0	1686	112	0
6	US	2486	0	1067	13	0
7	UU	4328	0	1932	17	0
8	UV	5417	0	2327	16	0
9	CI	781	0	329	0	0
10	CJ	1083	0	477	62	0
11	CK	1101	0	482	42	0
12	CL	3433	0	1517	73	0
13	CM	1767	0	795	3	0
14	CN	916	0	401	17	0
15	JD	3995	0	1737	47	0
16	JF	1071	0	467	1	0
16	JG	1096	0	478	4	0
17	JH	1295	0	570	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	JL	1401	0	604	20	0
19	JJ	893	0	397	35	0
20	DF	1055	0	496	6	0
21	DQ	616	0	285	2	0
22	DS	381	0	167	15	0
23	DT	700	0	332	22	0
24	Dc	310	0	134	0	0
25	D2	429	0	213	23	0
26	D3	29645	0	14916	1497	0
27	DA	1061	0	473	21	0
28	DE	1276	0	576	13	0
29	DG	1113	0	510	5	0
30	DH	913	0	400	12	0
31	DI	924	0	452	10	0
32	DJ	915	0	422	18	0
33	DL	766	0	340	6	0
34	DN	742	0	345	17	0
35	DO	620	0	311	49	0
36	DZ	332	0	149	22	0
37	DW	634	0	289	25	0
38	DX	684	0	315	64	0
39	DY	661	0	310	40	0
40	Db	400	0	180	0	0
41	D4	743	0	381	39	0
42	Db	1	0	0	0	0
All	All	89582	0	41625	2049	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 16.

The worst 5 of 2049 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)
15:JD:88:LYS:CB	26:D3:1118:G:H22	1.07	1.68
26:D3:904:G:H4'	26:D3:1005:A:C2	1.32	1.63
26:D3:564:G:C4	26:D3:1596:C:C6	1.88	1.61
26:D3:564:G:C4	26:D3:1596:C:H6	1.15	1.59
26:D3:473:A:H4'	26:D3:768:C:C2	1.32	1.58

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	UA	786/923 (85%)	752 (96%)	32 (4%)	2 (0%)	41	76
2	UB	362/810 (45%)	347 (96%)	14 (4%)	1 (0%)	41	76
3	UC	45/610 (7%)	45 (100%)	0	0	100	100
4	UL	763/943 (81%)	712 (93%)	51 (7%)	0	100	100
5	UM	748/817 (92%)	698 (93%)	40 (5%)	10 (1%)	12	48
6	US	493/552 (89%)	470 (95%)	21 (4%)	2 (0%)	34	72
7	UU	870/939 (93%)	823 (95%)	45 (5%)	2 (0%)	47	81
8	UV	1079/1237 (87%)	1011 (94%)	68 (6%)	0	100	100
9	CI	155/183 (85%)	145 (94%)	8 (5%)	2 (1%)	12	48
10	CJ	217/290 (75%)	193 (89%)	24 (11%)	0	100	100
11	CK	213/593 (36%)	206 (97%)	4 (2%)	3 (1%)	11	46
12	CL	683/1183 (58%)	643 (94%)	36 (5%)	4 (1%)	25	65
13	CM	358/367 (98%)	344 (96%)	14 (4%)	0	100	100
14	CN	178/297 (60%)	169 (95%)	9 (5%)	0	100	100
15	JD	787/1267 (62%)	723 (92%)	52 (7%)	12 (2%)	10	46
16	JF	212/252 (84%)	208 (98%)	4 (2%)	0	100	100
16	JG	217/252 (86%)	211 (97%)	6 (3%)	0	100	100
17	JH	257/483 (53%)	252 (98%)	5 (2%)	0	100	100
18	JL	281/318 (88%)	267 (95%)	10 (4%)	4 (1%)	11	46
19	JJ	179/274 (65%)	167 (93%)	10 (6%)	2 (1%)	14	52
20	DF	211/225 (94%)	198 (94%)	13 (6%)	0	100	100
21	DQ	123/143 (86%)	111 (90%)	12 (10%)	0	100	100
22	DS	75/146 (51%)	68 (91%)	6 (8%)	1 (1%)	12	48
23	DT	141/144 (98%)	127 (90%)	13 (9%)	1 (1%)	22	62
24	Dc	61/67 (91%)	57 (93%)	4 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	DA	212/255 (83%)	171 (81%)	18 (8%)	23 (11%)	0	8
28	DE	258/261 (99%)	223 (86%)	25 (10%)	10 (4%)	3	26
29	DG	224/236 (95%)	202 (90%)	16 (7%)	6 (3%)	5	33
30	DH	182/190 (96%)	147 (81%)	22 (12%)	13 (7%)	1	16
31	DI	184/200 (92%)	163 (89%)	10 (5%)	11 (6%)	1	19
32	DJ	183/197 (93%)	161 (88%)	15 (8%)	7 (4%)	3	26
33	DL	153/156 (98%)	126 (82%)	17 (11%)	10 (6%)	1	18
34	DN	148/151 (98%)	133 (90%)	12 (8%)	3 (2%)	7	39
35	DO	125/137 (91%)	95 (76%)	17 (14%)	13 (10%)	0	9
36	DZ	65/108 (60%)	28 (43%)	21 (32%)	16 (25%)	0	1
37	DW	127/130 (98%)	114 (90%)	12 (9%)	1 (1%)	19	60
38	DX	136/145 (94%)	120 (88%)	12 (9%)	4 (3%)	4	31
39	DY	132/135 (98%)	110 (83%)	14 (11%)	8 (6%)	1	18
40	Db	79/82 (96%)	62 (78%)	12 (15%)	5 (6%)	1	18
All	All	11702/15698 (74%)	10802 (92%)	724 (6%)	176 (2%)	14	46

5 of 176 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	UM	218	ASP
6	US	75	PRO
15	JD	1240	LYS
18	JL	232	VAL
23	DT	34	VAL

5.3.2 Protein sidechains ⓘ

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
25	D2	19/20 (95%)	4 (21%)	0
26	D3	1387/1758 (78%)	489 (35%)	148 (10%)
41	D4	34/35 (97%)	8 (23%)	4 (11%)
All	All	1440/1813 (79%)	501 (34%)	152 (10%)

5 of 501 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
25	D2	289	U
25	D2	294	U
25	D2	295	A
25	D2	297	U
26	D3	2	A

5 of 152 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	D3	1115	U
26	D3	1780	G
26	D3	1130	A
26	D3	1568	C
41	D4	13	C

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
41	D4	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D4	21:C	O3'	60:A	P	58.94
1	D4	14:A	O3'	16:A	P	3.64

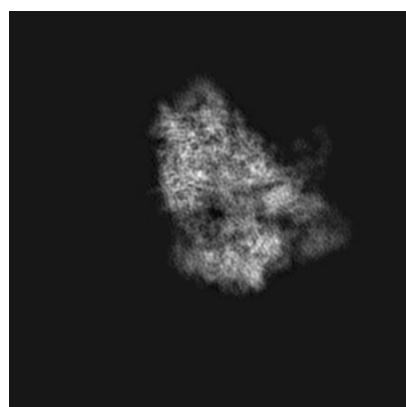
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11362. These allow visual inspection of the internal detail of the map and identification of artifacts.

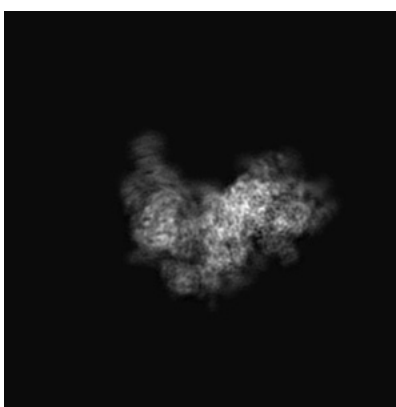
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

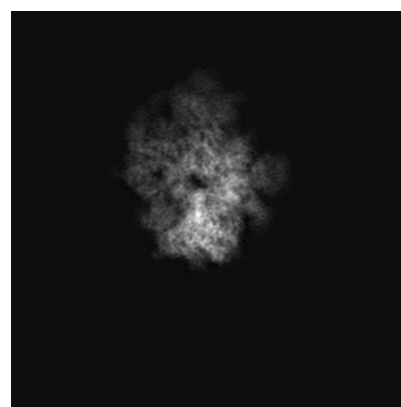
6.1.1 Primary map



X



Y

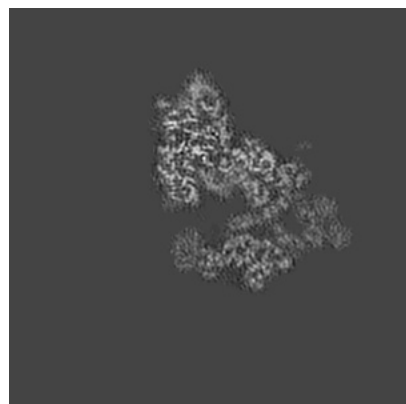


Z

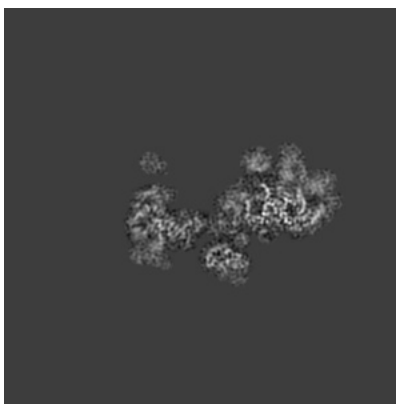
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

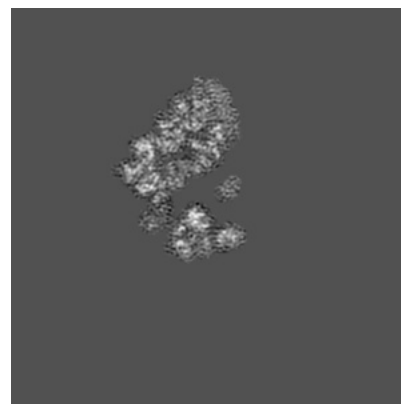
6.2.1 Primary map



X Index: 240



Y Index: 240

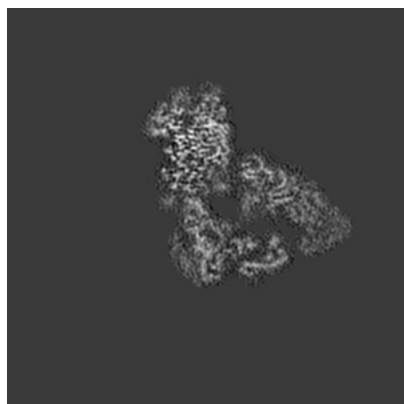


Z Index: 240

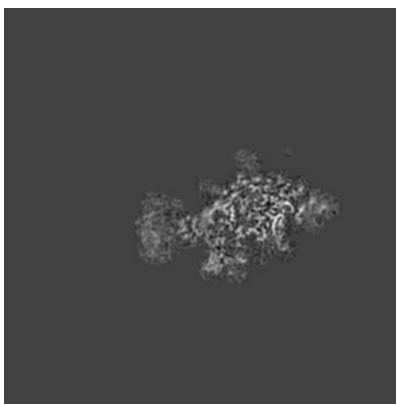
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

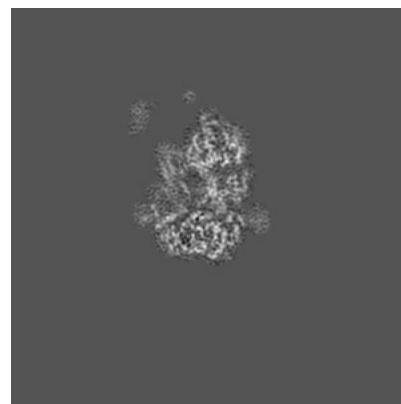
6.3.1 Primary map



X Index: 224



Y Index: 219

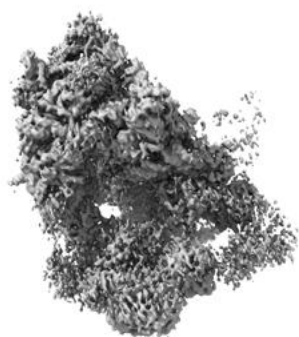


Z Index: 285

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

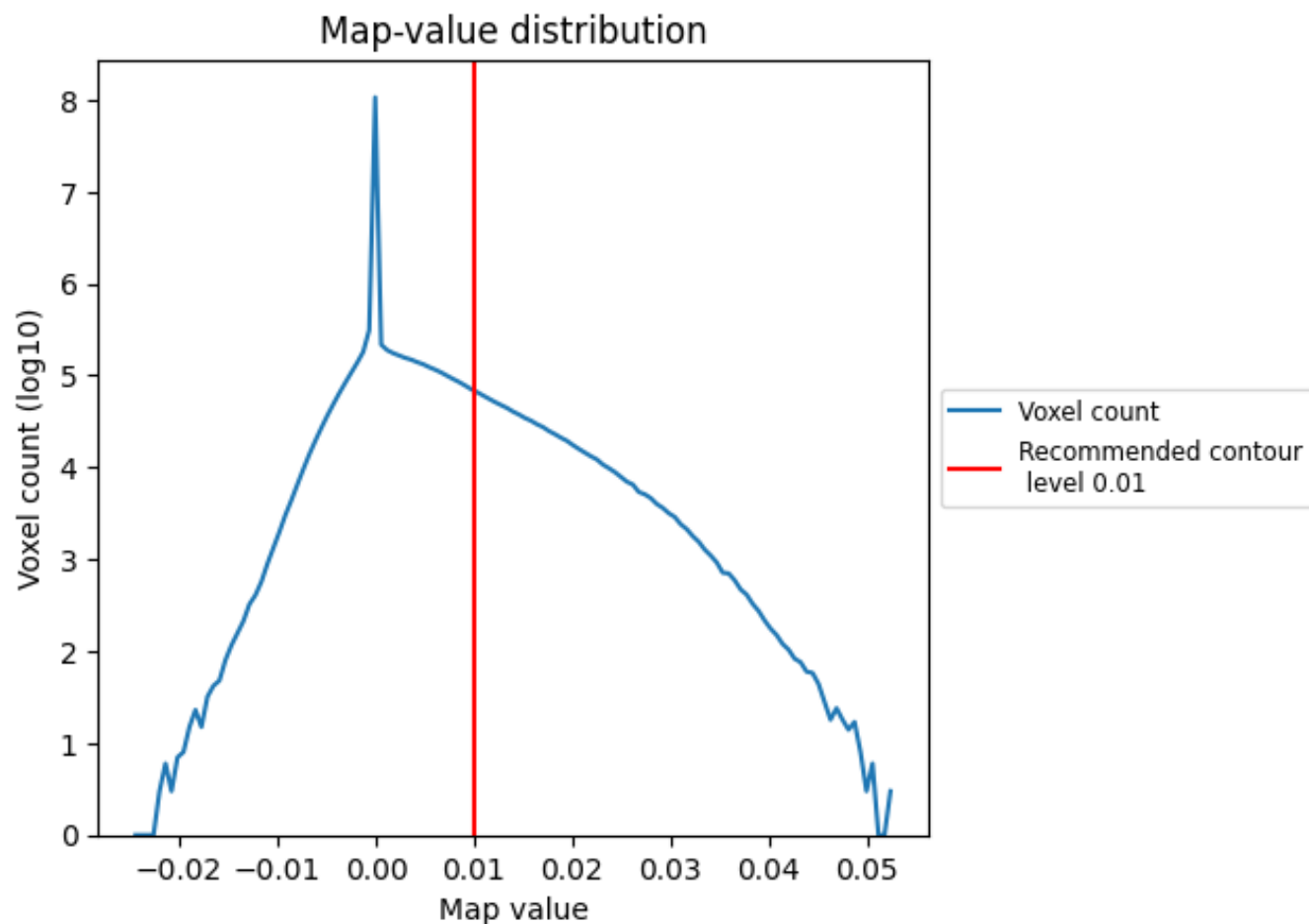
6.5 Mask visualisation

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

7 Map analysis [i](#)

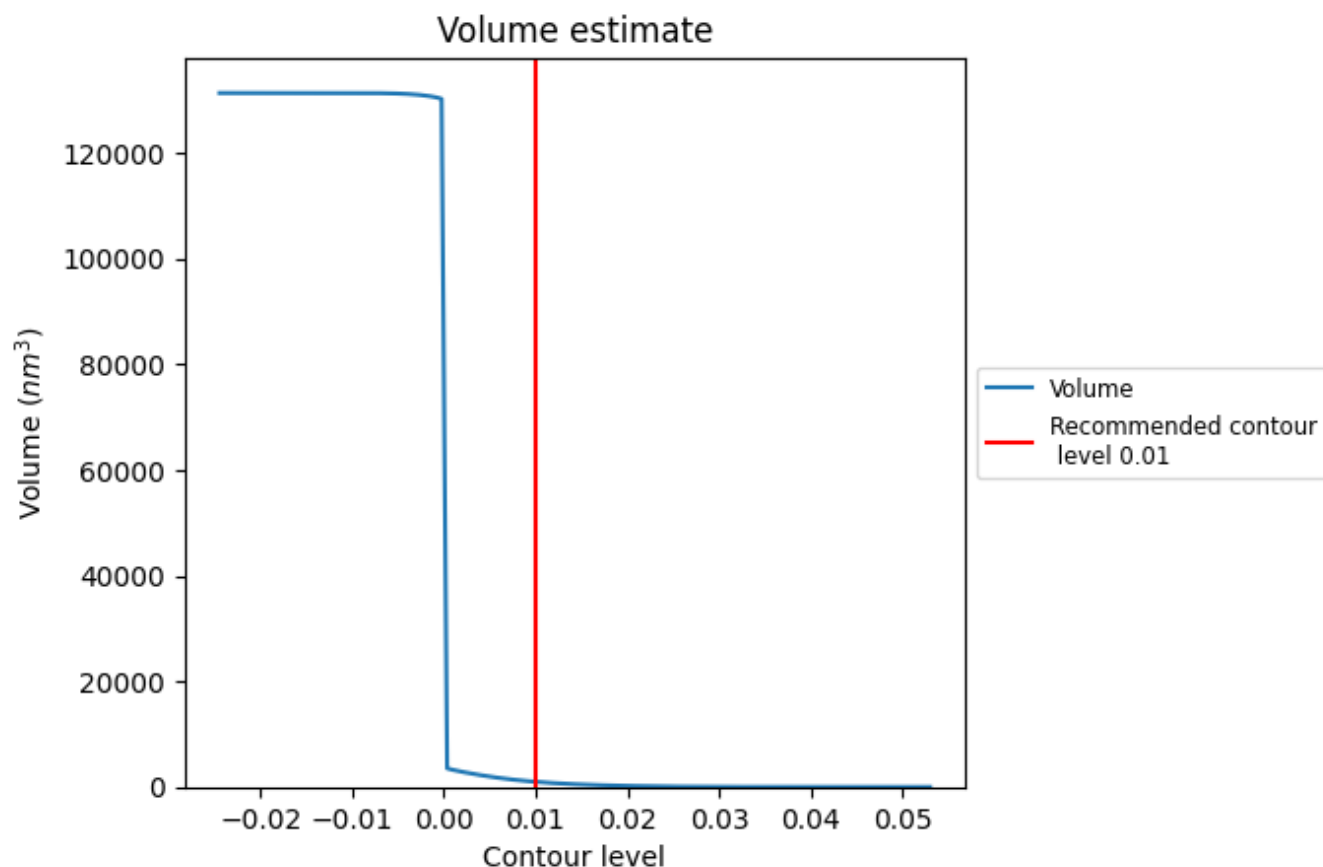
This section contains the results of statistical analysis of the map.

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.

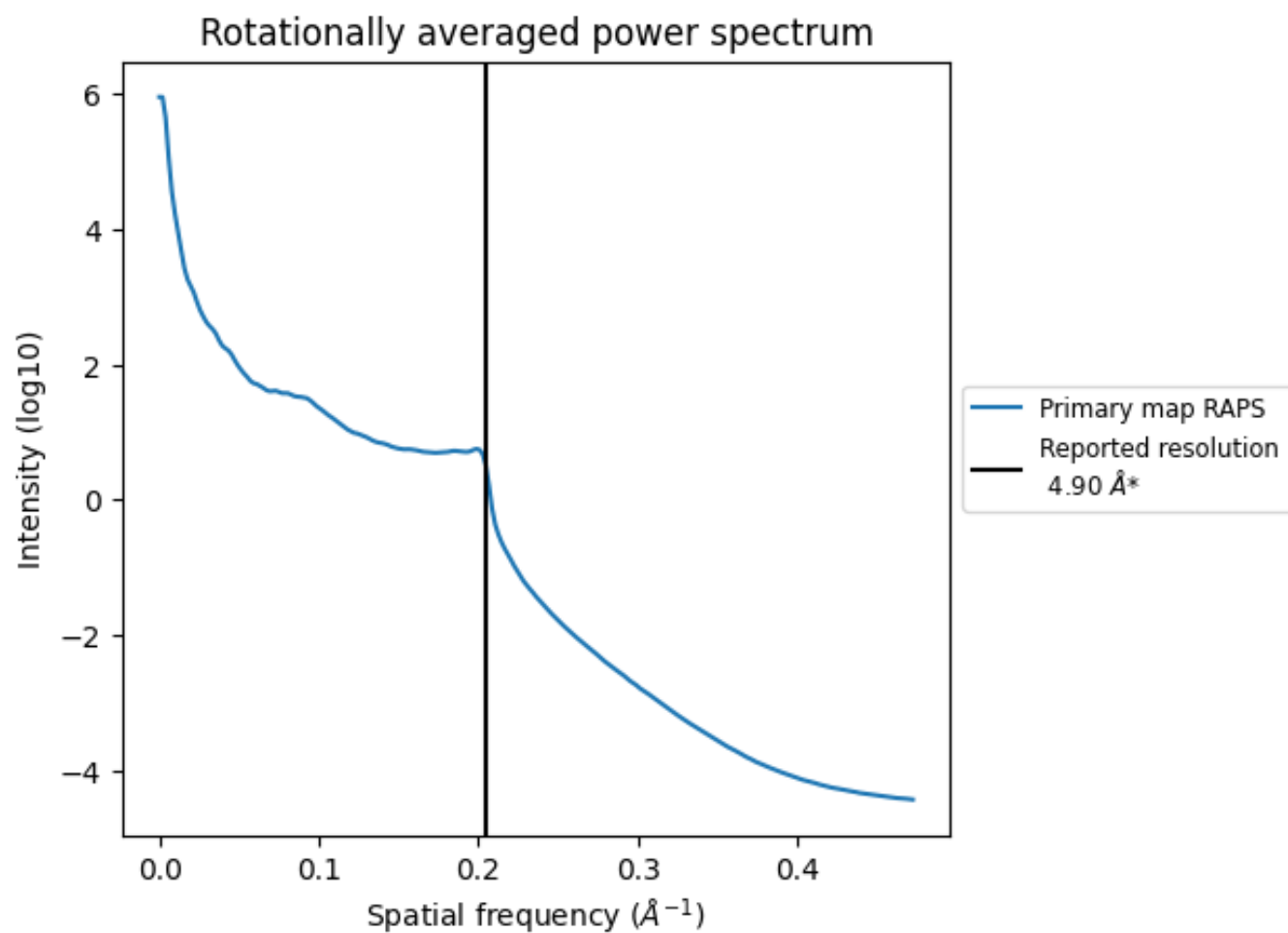
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 976 nm³; this corresponds to an approximate mass of 881 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 ⓘ

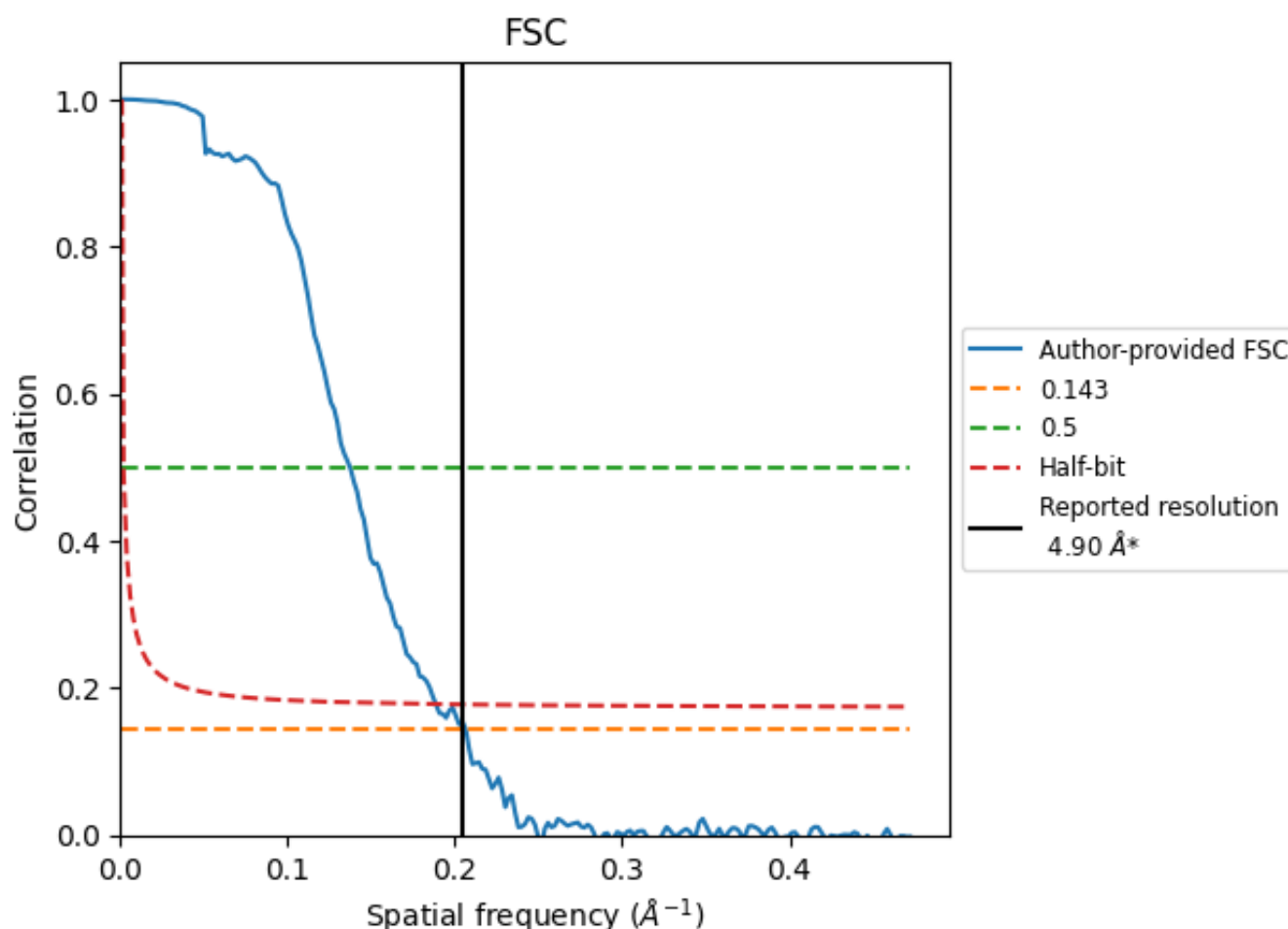


*Reported resolution corresponds to spatial frequency of 0.204 Å⁻¹

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 0.204 Å⁻¹

8.2 Resolution estimates [i](#)

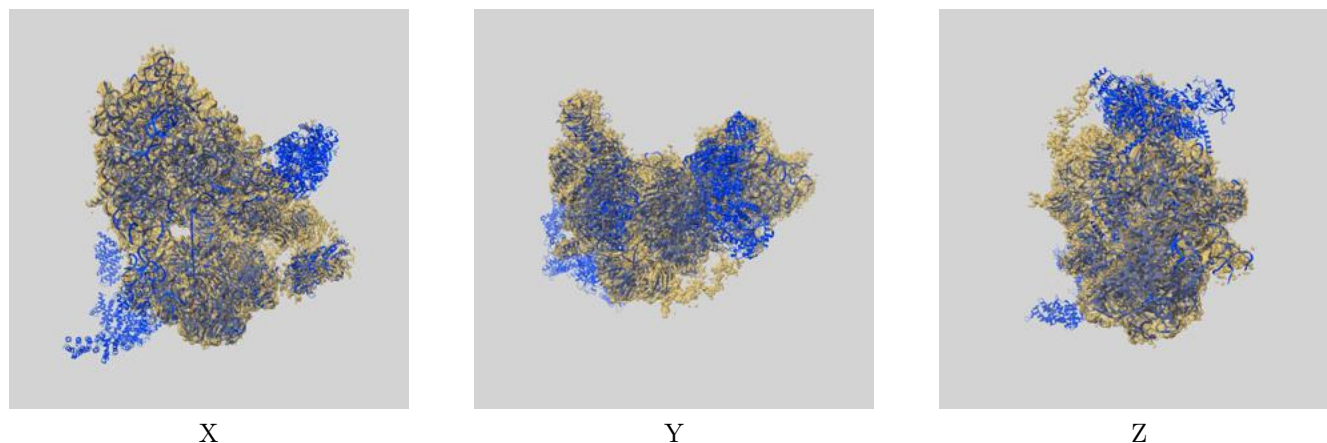
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.90	-	-
Author-provided FSC curve	4.84	7.28	5.30
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

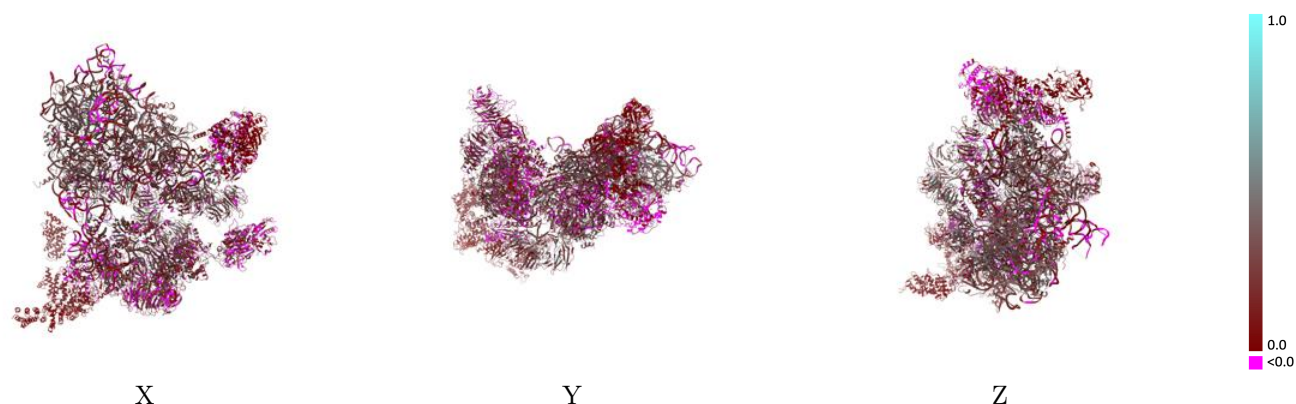
This section contains information regarding the fit between EMDB map EMD-11362 and PDB model 6ZQF. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



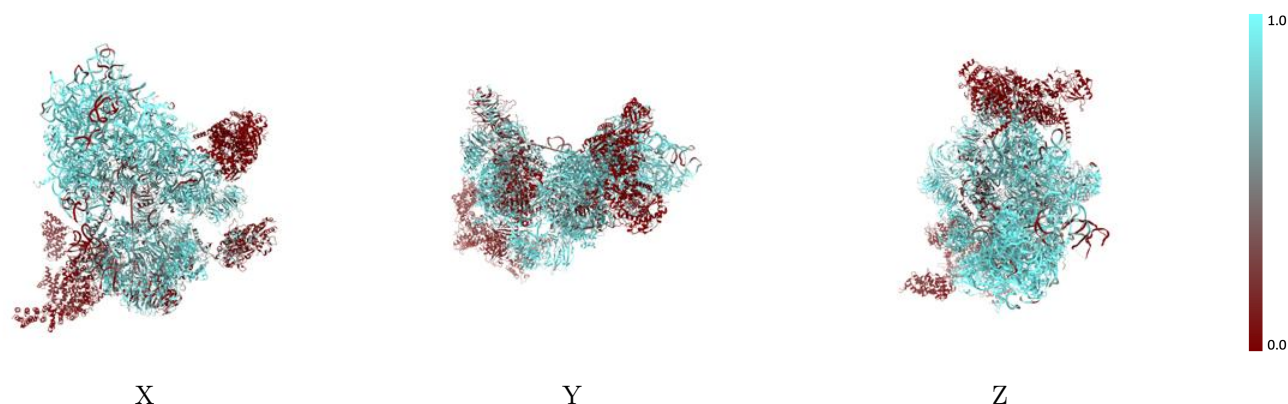
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



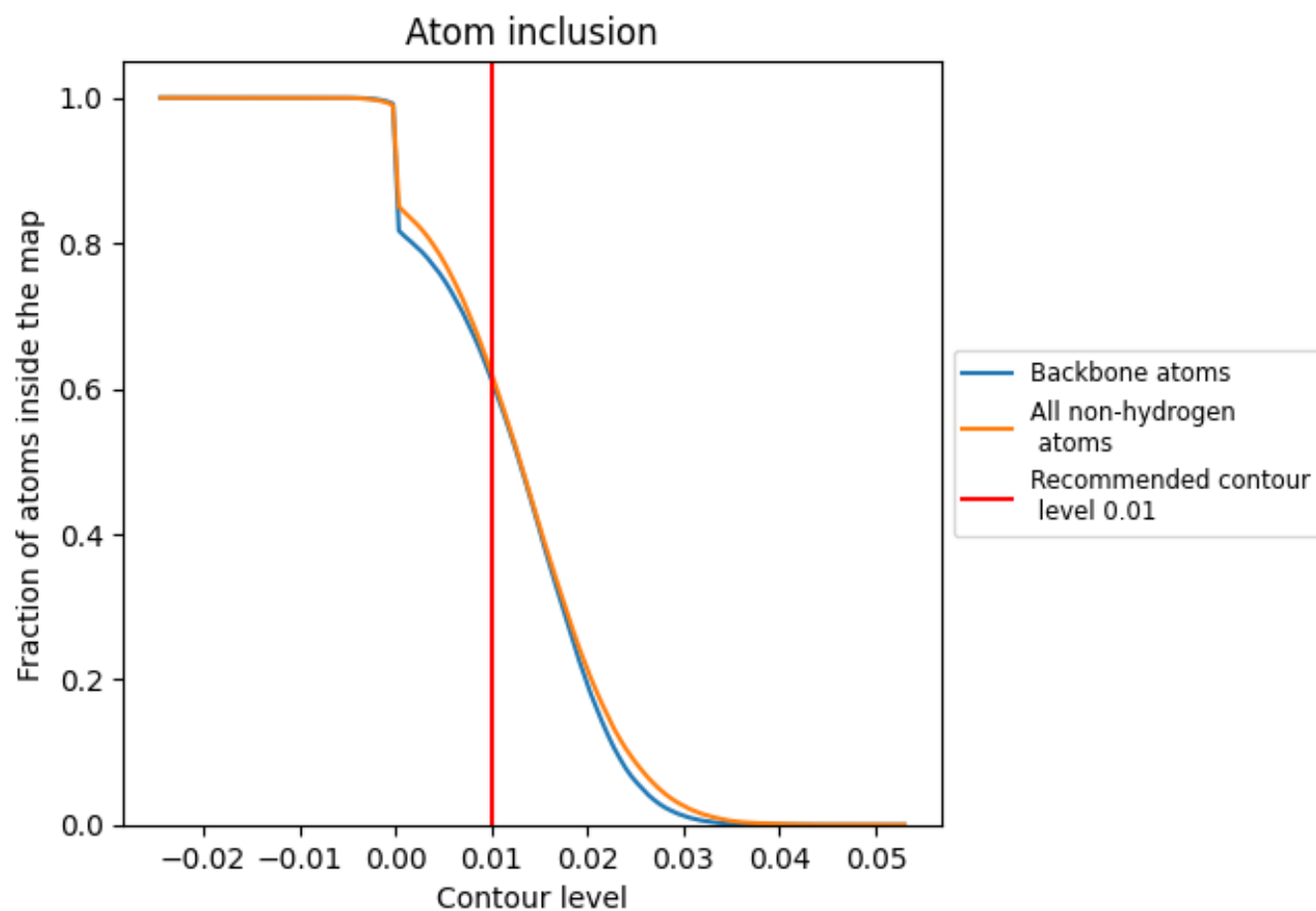
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 61% of all backbone atoms, 62% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6213	 0.1920
CI	 0.6325	 0.2070
CJ	 0.8126	 0.3020
CK	 0.7439	 0.2380
CL	 0.8806	 0.3100
CM	 0.9287	 0.3380
CN	 0.0087	 0.0120
D2	 0.4196	 0.1080
D3	 0.7557	 0.2010
D4	 0.4361	 0.1260
DA	 0.8812	 0.3130
DE	 0.9404	 0.3670
DF	 0.8123	 0.2640
DG	 0.9218	 0.2900
DH	 0.8828	 0.2930
DI	 0.9242	 0.3140
DJ	 0.9137	 0.3090
DL	 0.8055	 0.2900
DN	 0.9151	 0.3320
DO	 0.8532	 0.2910
DQ	 0.8149	 0.2670
DS	 0.0787	 0.0220
DT	 0.0900	 0.0950
DW	 0.9243	 0.3390
DX	 0.6170	 0.1520
DY	 0.9349	 0.3400
DZ	 0.0241	 0.0330
Db	 0.8579	 0.3070
Dc	 0.8968	 0.3490
JD	 0.2521	 0.1100
JF	 0.0000	 -0.0010
JG	 0.0383	 -0.0220
JH	 0.0000	 0.0000
JJ	 0.8667	 0.2910
JL	 0.4233	 0.1400



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Chain	Atom inclusion	Q-score
UA	 0.7768	 0.2520
UB	 0.0022	 0.0060
UC	 0.6910	 0.1630
UL	 0.8821	 0.2890
UM	 0.7901	 0.2440
US	 0.0000	 -0.0000
UU	 0.5984	 0.1670
UV	 0.0214	 0.0100