wwPDB EM Validation Summary Report (i)

Jun 18, 2026 – 10:13 am BST

PDB ID	:	6ZMW / pdb_00006zmw
EMDB ID	:	EMD-11302
Title	:	Structure of a human 48S translational initiation complex
Authors	:	Brito Querido, J.; Sokabe, M.; Kraatz, S.; Gordiyenko, Y.; Skehel, M.; Fraser, C.; Ramakrishnan, V.
Deposited on	:	2020-07-04
Resolution	:	3.70 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 (i) 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 (1)) were used in the production of this report:

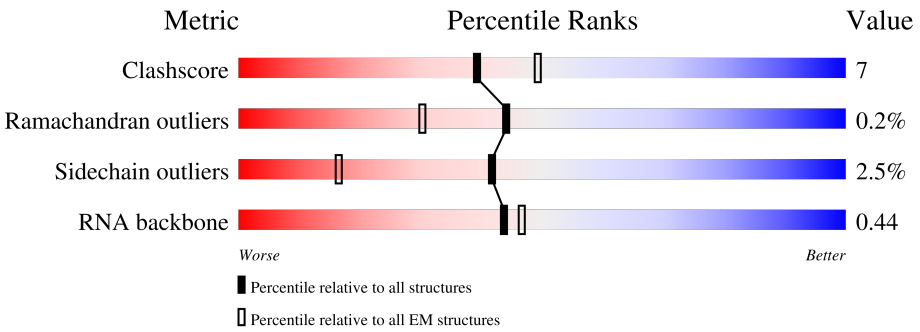
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

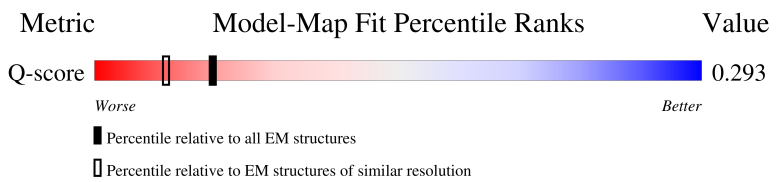
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.70 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	11569 (3.20 - 4.20)

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 <=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	2	325	82% 91% • 6%
2	1	814	30% 65% 7% 28%
3	6	374	17% 80% 13% 6%

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Mol	Chain	Length	Quality of chain
4	4	357	18% 69% • 28%
5	u	1382	7% 40% 10% 49%
6	v	445	7% 71% 14% • 14%
7	S	249	71% 21% • 8%
8	y	913	15% 65% 12% 24%
9	8	352	26% 86% • 10%
10	G	194	71% 21% 9%
11	H	84	• 79% 18% •
12	K	83	78% 19% •
13	L	293	• 62% 13% 25%
14	O	264	65% 15% 20%
15	N	295	62% 8% 30%
16	Q	115	58% 27% • 14%
17	P	151	• 65% 23% 12%
18	I	151	• 84% 15% •
19	x	548	52% 64% 12% 23%
20	3	218	32% 89% 8% •
21	5	564	18% 55% • 43%
22	7	28	75% 25% 71% •
23	9	25	8% 76% 20% •
24	A	1869	54% 30% 8% 8%
25	B	158	77% 13% 10%
26	C	263	87% 10% •
27	D	194	76% 14% • 9%
28	E	143	86% 12% •

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Mol	Chain	Length	Quality of chain
29	F	59	71% 7% 20%
30	r	315	83% 67% 19% 13%
31	J	130	87% 10%
32	R	208	78% 16% 5%
33	T	133	78% 15% 6%
34	V	204	11% 70% 20% 10%
35	Y	146	76% 21%
36	Z	243	6% 80% 13% 7%
37	a	165	5% 46% 14% 40%
38	b	145	19% 58% 18% 24%
39	c	317	12% 75% 23%
40	d	145	10% 82% 15%
41	e	125	6% 39% 12% 47%
42	f	152	20% 64% 29% 7%
43	i	56	70% 20% 11%
44	k	156	21% 13% 66%
45	m	132	20% 63% 28% 8%
46	n	69	23% 62% 28% 9%
47	o	320	8% 17% 7% 76%
48	p	113	55% 20% 25%
49	q	144	25% 36% 22% 39%
50	z	258	62% 62% 38%
51	M	135	79% 19%
52	h	119	81% 6% 13%
53	s	333	40% 33% 8% 59%

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Mol	Chain	Length	Quality of chain
54	w	75	97% 41% 53% 5%
55	t	472	71% 72% 25%
56	j	406	55% 71% 23% 5%
57	g	1310	11% 12% 5% 83%

2 Entry composition (i)

There are 59 unique types of molecules in this entry. The entry contains 118155 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 Eukaryotic translation initiation factor 3 subunit I.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	2	304	1493	885	304	304	0	0

- Molecule 2 is a protein called Eukaryotic translation initiation factor 3 subunit B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	588	3258	1986	633	634	5	0	0

- Molecule 3 is a protein called Eukaryotic translation initiation factor 3 subunit M.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	6	350	1917	1159	376	380	2	0	0

- Molecule 4 is a protein called Eukaryotic translation initiation factor 3 subunit F.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	4	257	1272	757	257	258	0	0

- Molecule 5 is a protein called Eukaryotic translation initiation factor 3 subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	u	706	5383	3379	982	999	23	1	0

- Molecule 6 is a protein called Eukaryotic translation initiation factor 3 subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	v	384	2635	1657	477	489	12	0	0

- Molecule 7 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	S	230	1862	1164	371	320	7	0	0

- Molecule 8 is a protein called Eukaryotic translation initiation factor 3 subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	y	697	5470	3437	980	1018	35	0	0

- Molecule 9 is a protein called Eukaryotic translation initiation factor 3 subunit H.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	8	317	1571	936	317	318	0	0

- Molecule 10 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	G	177	1430	917	260	252	1	0	0

- Molecule 11 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	H	81	631	397	116	111	7	0	0

- Molecule 12 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	K	81	617	380	114	118	5	0	0

- Molecule 13 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	L	220	1707	1104	292	301	10	0	0

- Molecule 14 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	O	211	1715	1088	307	306	14	0	0

- Molecule 15 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	N	207	1633	1040	288	297	8	0	0

- Molecule 16 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	Q	99	792	492	165	130	5	0	0

- Molecule 17 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	P	133	997	610	196	185	6	0	0

- Molecule 18 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	I	150	1208	773	229	205	1	0	0

- Molecule 19 is a protein called Eukaryotic translation initiation factor 3 subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	x	421	2831	1746	521	555	9	0	0

- Molecule 20 is a protein called Eukaryotic translation initiation factor 3 subunit K.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
20	3	213	1057	631	213	213	0	0

- Molecule 21 is a protein called Eukaryotic translation initiation factor 3 subunit L.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
21	5	319	1581	943	319	319	0	0

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	O	P		
22	7	28	336	140	168	28	0	0

- Molecule 23 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	9	24	230	139	62	26	3	0	0

- Molecule 24 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
24	A	1719	36670	16380	6574	11998	1718	0	0

- Molecule 25 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	B	142	1166	743	218	199	6	0	0

- Molecule 26 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	C	256	2035	1302	378	347	8	0	0

- Molecule 27 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	D	177	1477	941	295	239	2	0	0

- Molecule 28 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	E	140	1087	687	215	182	3	0	0

- Molecule 29 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	F	47	378	231	85	61	1	0	0

- Molecule 30 is a protein called Eukaryotic translation initiation factor 2 subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	r	275	2215	1398	387	418	12	0	0

- Molecule 31 is a protein called 40S ribosomal protein S15a.

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

- Molecule 32 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	R	198	1627	1021	322	279	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	T	125	1015	642	199	169	5	0	0

- Molecule 34 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	V	184	1461	914	276	264	7	0	0

- Molecule 35 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	Y	141	1124	715	212	194	3	0	0

- Molecule 36 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	Z	227	1765	1125	317	315	8	0	0

- Molecule 37 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	a	99	834	544	149	135	6	0	0

- Molecule 38 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	b	110	913	580	168	158	7	0	0

- Molecule 39 is a protein called Receptor of activated protein C kinase 1.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	d	142	1105	692	213	197	3	0	0

- Molecule 41 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	e	66	523	338	93	91	1	0	0

- Molecule 42 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	f	142	1176	737	239	199	1	0	0

- Molecule 43 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	i	50	419	262	85	67	5	0	0

- Molecule 44 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	k	53	435	276	82	70	7	0	0

- Molecule 45 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	m	122	950	596	168	177	9	0	0

- Molecule 46 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	n	63	498	302	101	93	2	0	0

- Molecule 47 is a protein called Eukaryotic translation initiation factor 3 subunit G.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
47	o	77	616	389	111	116	0	0

- Molecule 48 is a protein called Eukaryotic translation initiation factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	p	85	691	438	125	126	2	0	0

- Molecule 49 is a protein called Eukaryotic translation initiation factor 1A, X-chromosomal.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	q	88	714	451	129	130	4	0	0

- Molecule 50 is a protein called Eukaryotic translation initiation factor 3 subunit J.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
50	z	160	795	475	160	160	0	0

- Molecule 51 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	M	131	1064	668	198	194	4	0	0

- Molecule 52 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	h	103	817	511	155	147	4	0	0

- Molecule 53 is a protein called Eukaryotic translation initiation factor 2 subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	s	138	1123	709	206	199	9	0	0

- Molecule 54 is a RNA chain called Initiator Met-tRNA-i.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
54	w	75	1604	717	298	515	74	0	0

- Molecule 55 is a protein called Eukaryotic translation initiation factor 2 subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
55	t	356	1750	1038	356	356	0	0

- Molecule 56 is a protein called Eukaryotic initiation factor 4A-I.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	j	384	3073	1940	533	581	19	0	0

- Molecule 57 is a protein called Eukaryotic translation initiation factor 4 gamma 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	g	224	1848	1168	324	341	15	0	0

- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
58	Q	1	1	1	0
58	k	1	1	1	0

- Molecule 59 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

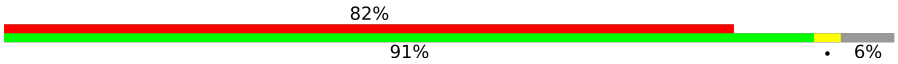
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
59	A	87	87	87	0
59	d	1	1	1	0
59	f	1	1	1	0

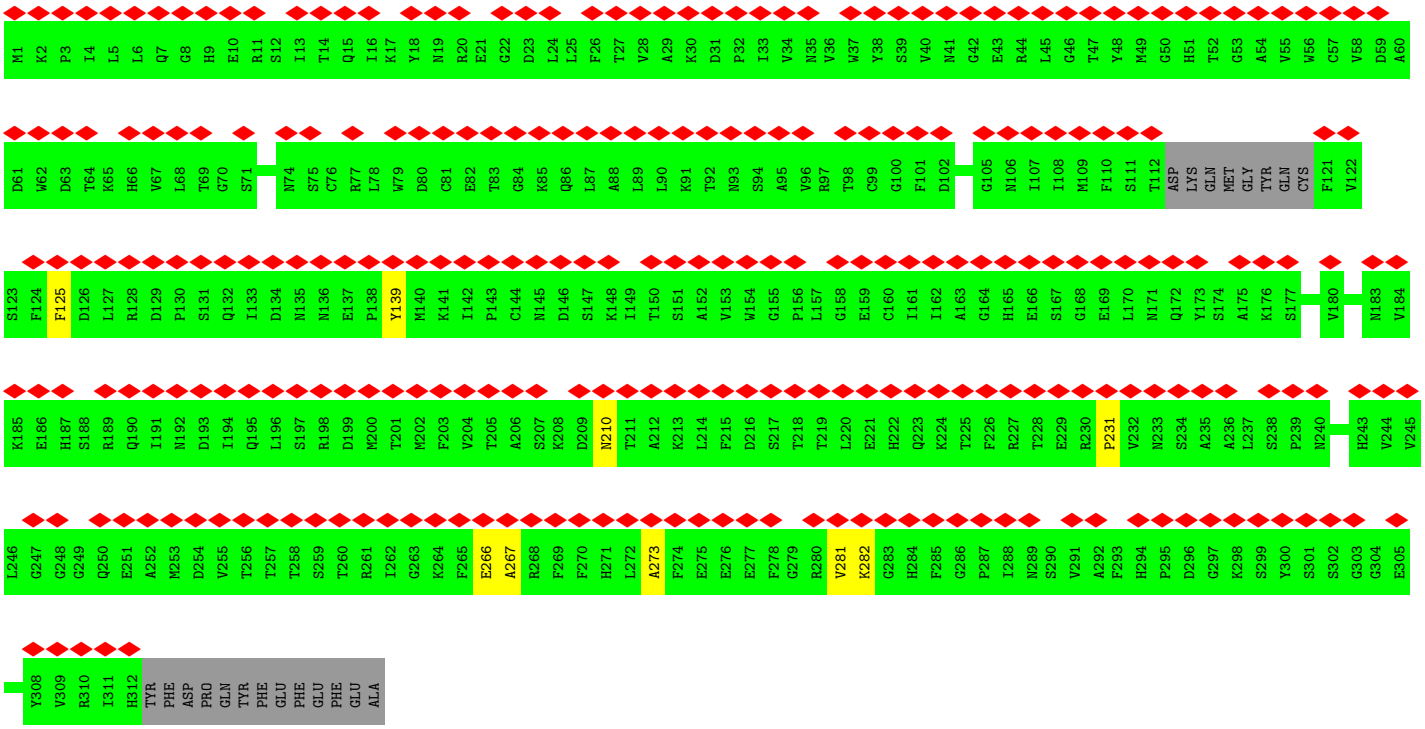
3 Residue-property plots (i)

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: Eukaryotic translation initiation factor 3 subunit I

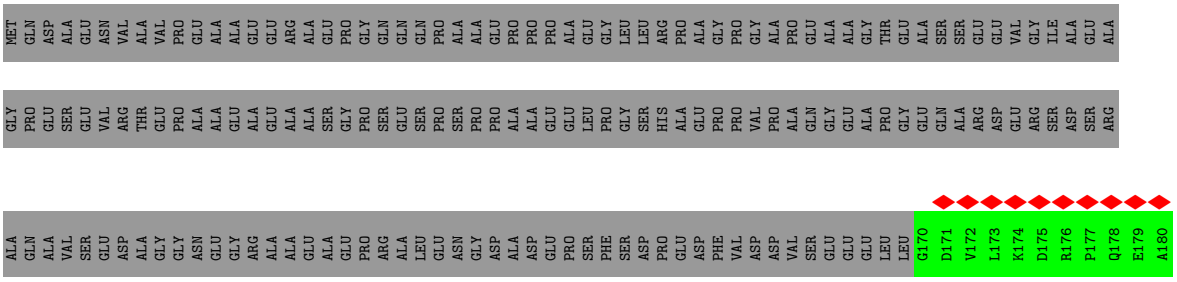
Chain 2:

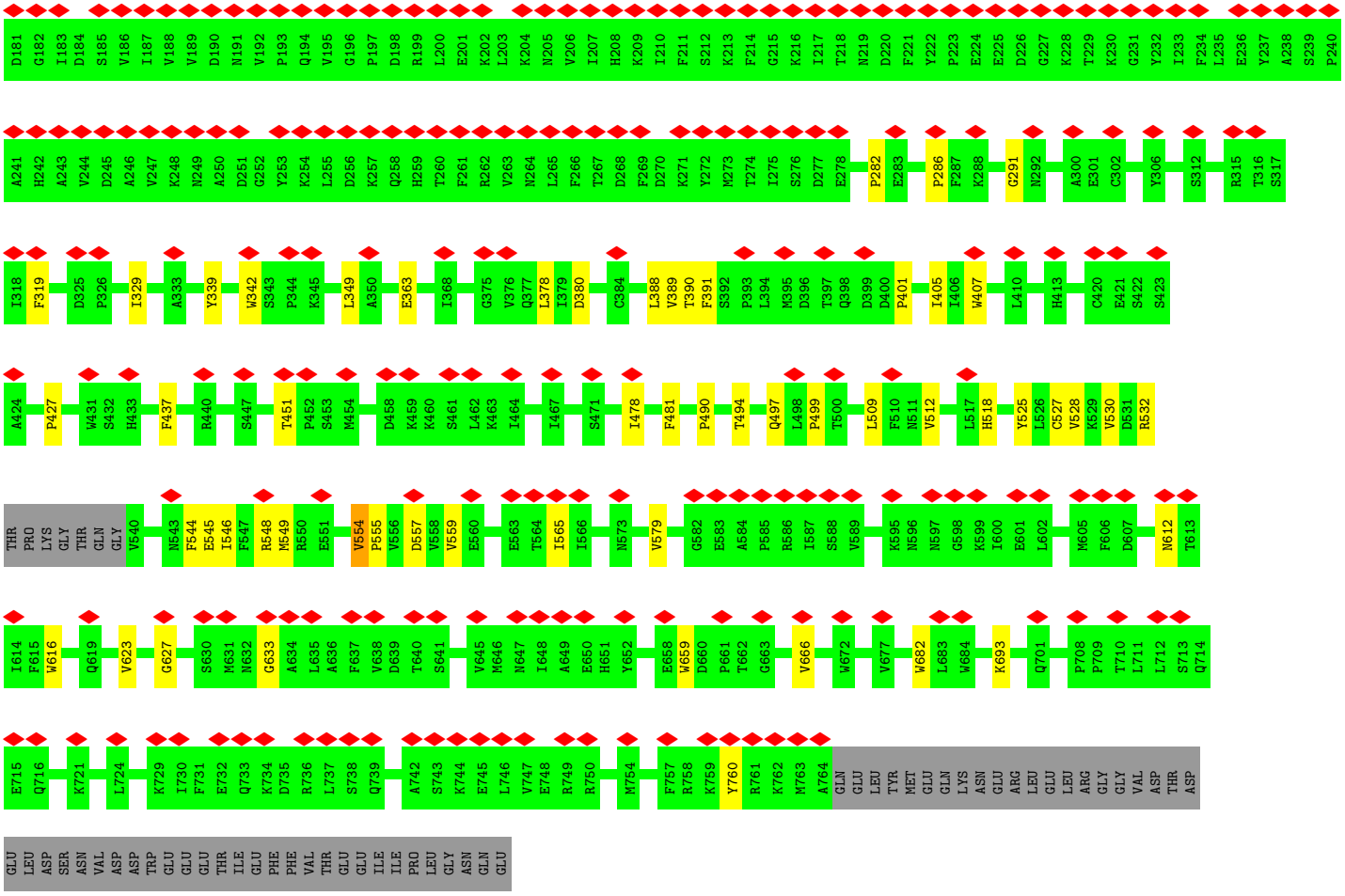




- Molecule 2: Eukaryotic translation initiation factor 3 subunit B

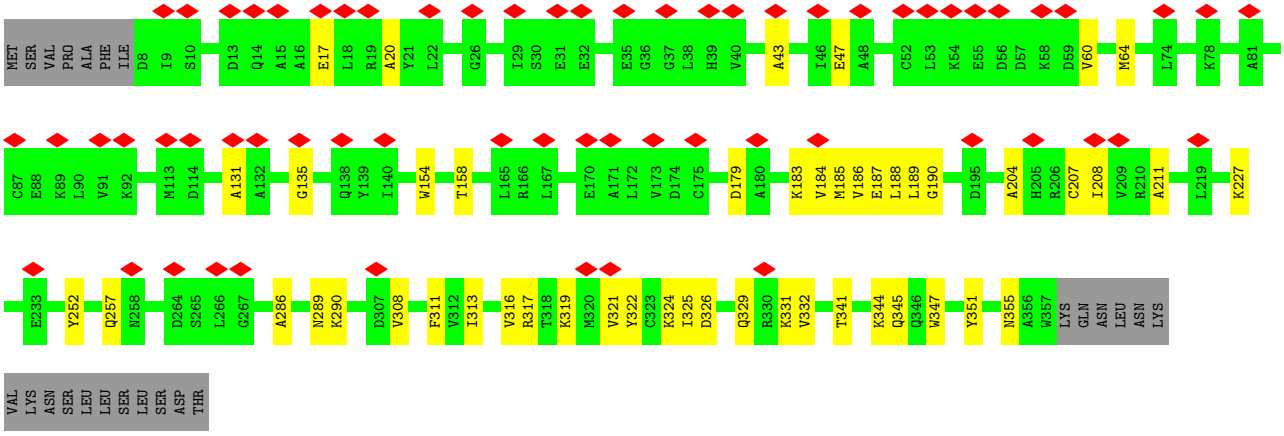
Chain 1:





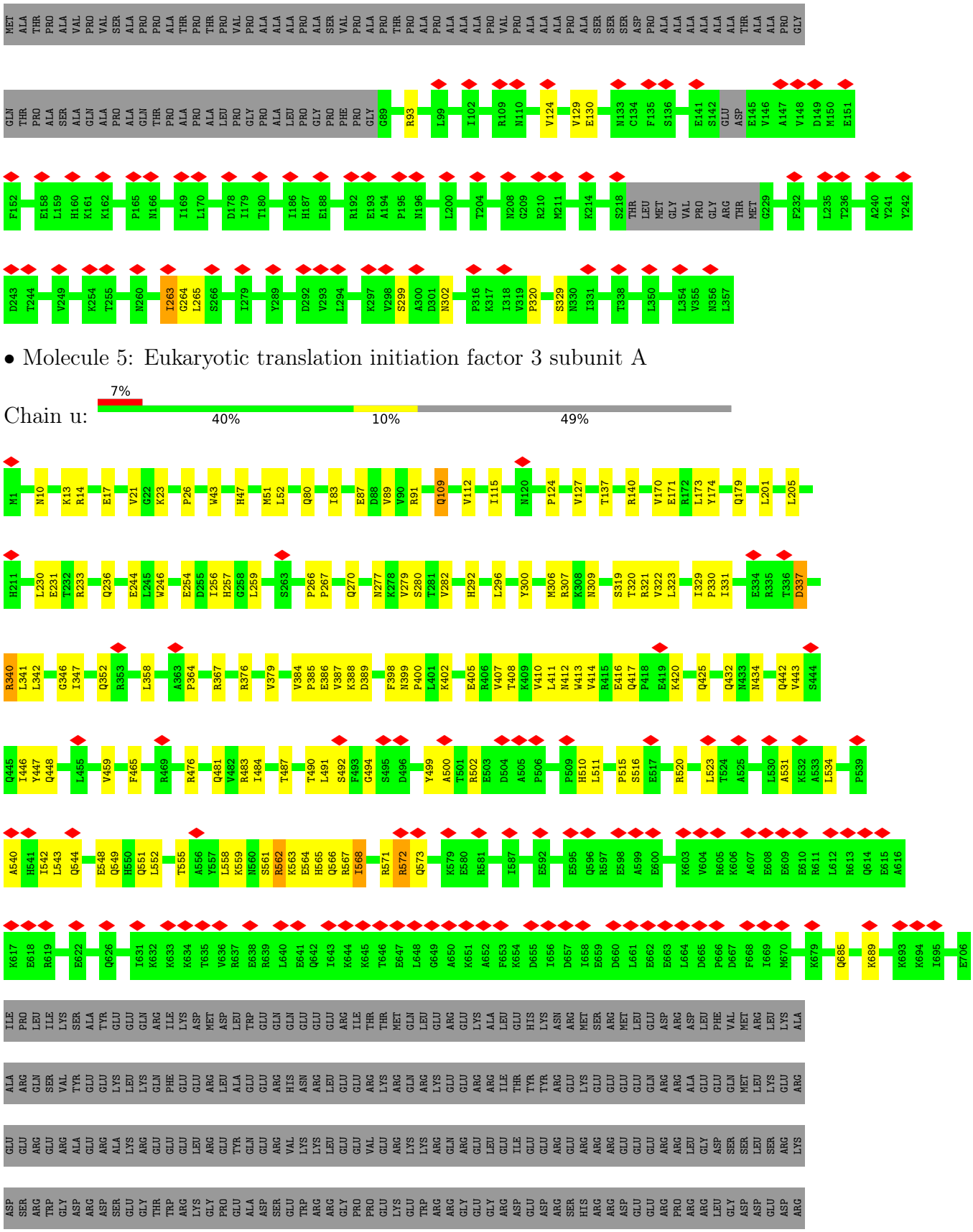
- Molecule 3: Eukaryotic translation initiation factor 3 subunit M

Chain 6:



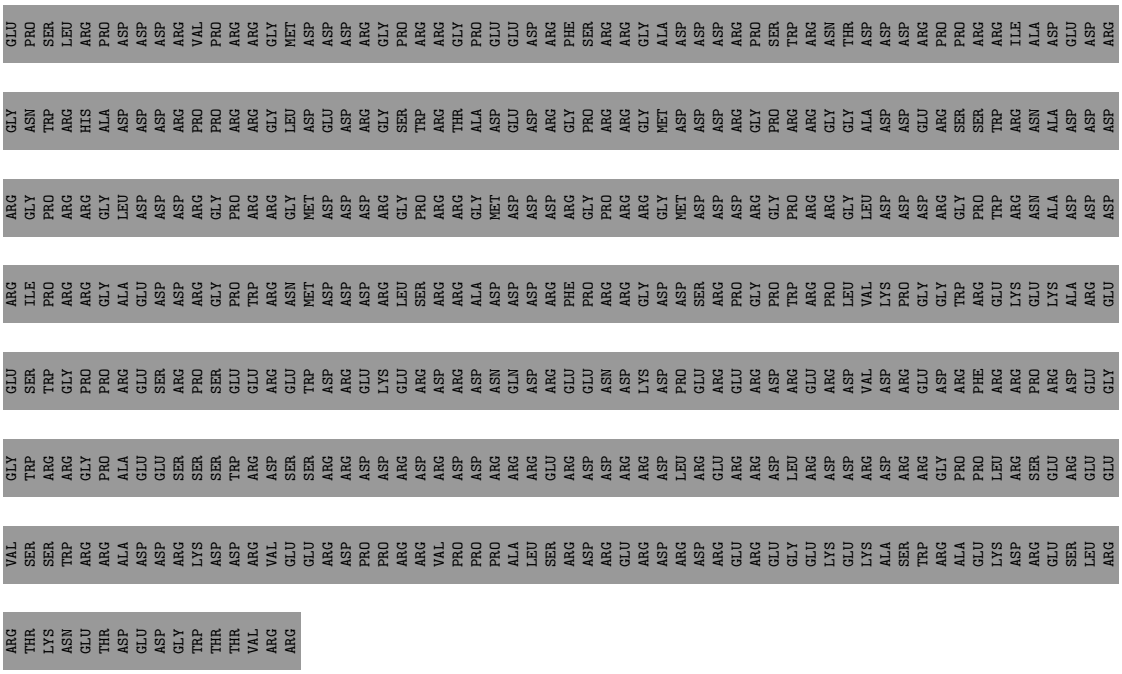
- Molecule 4: Eukaryotic translation initiation factor 3 subunit F

Chain 4:

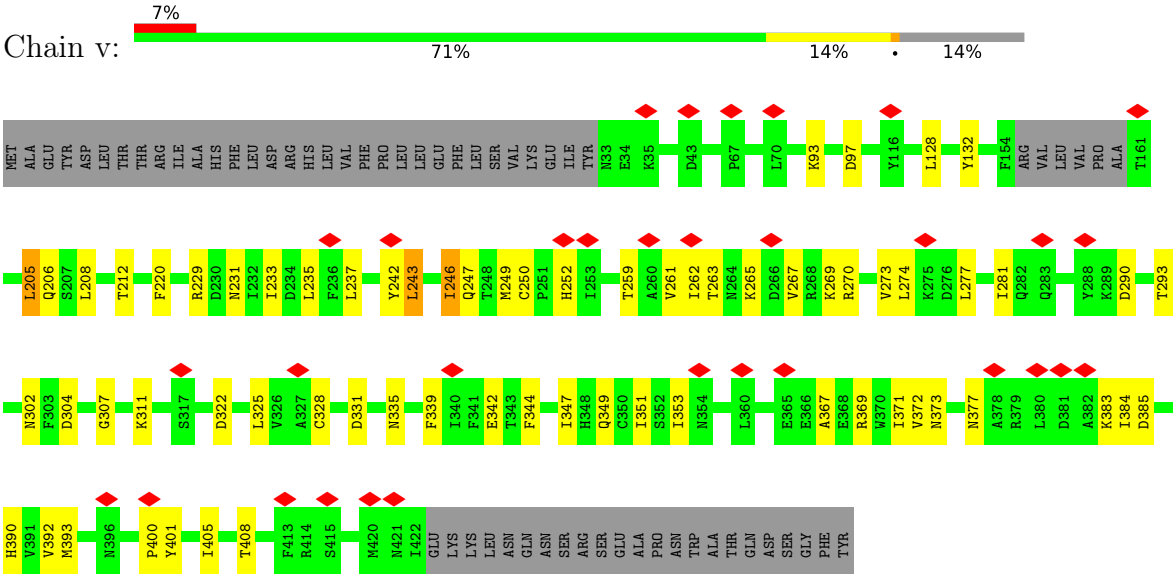


• Molecule 5: Eukaryotic translation initiation factor 3 subunit A

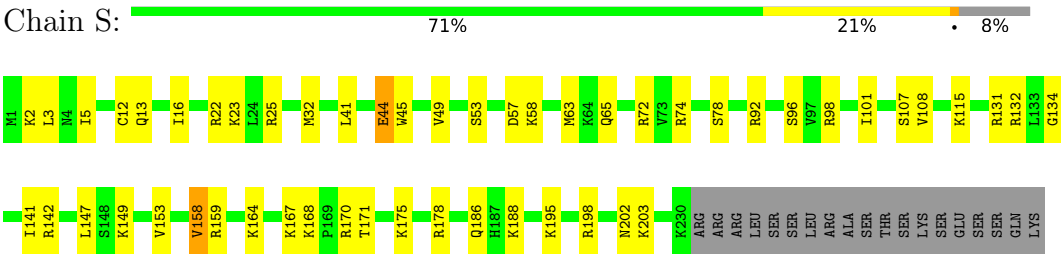
Chain u: 7% 40% 10% 49%



• Molecule 6: Eukaryotic translation initiation factor 3 subunit E

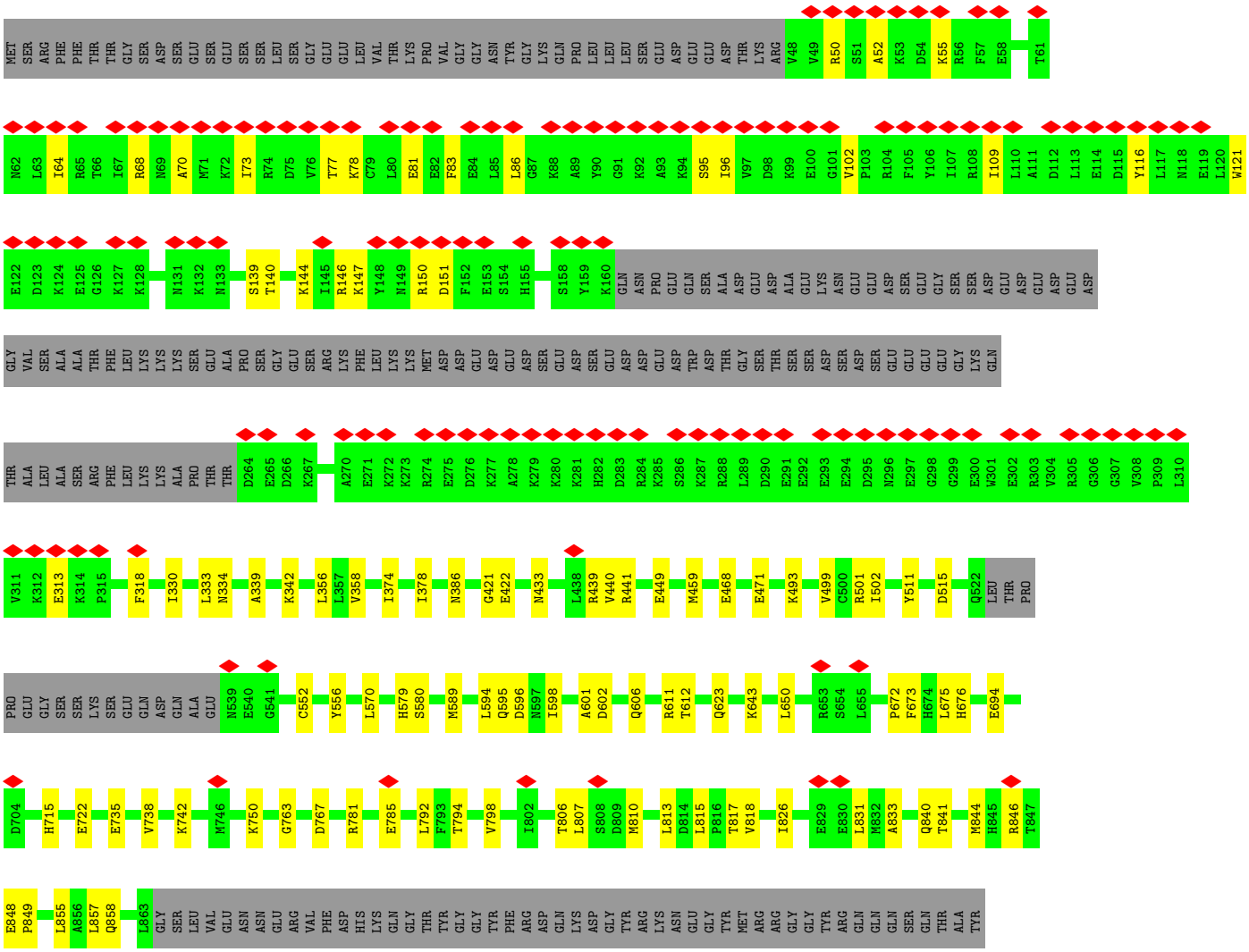


• Molecule 7: 40S ribosomal protein S6



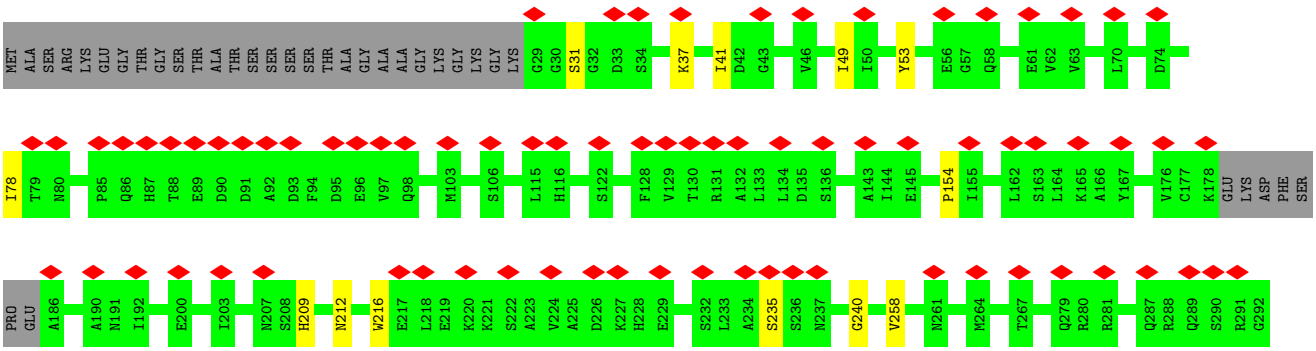
• Molecule 8: Eukaryotic translation initiation factor 3 subunit C

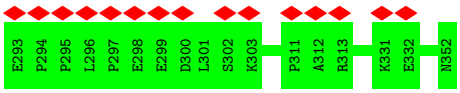
Chain y:



- Molecule 9: Eukaryotic translation initiation factor 3 subunit H

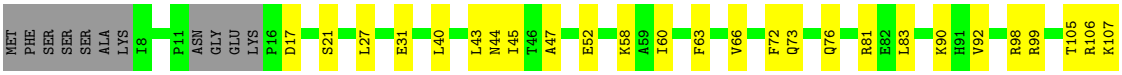
Chain 8:

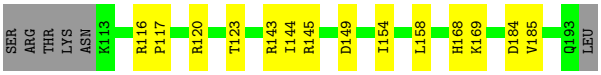




• Molecule 10: 40S ribosomal protein S7

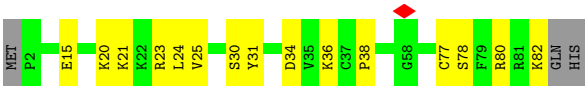
Chain G:





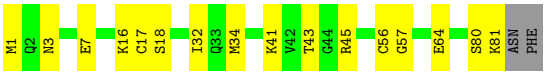
• Molecule 11: 40S ribosomal protein S27

Chain H:



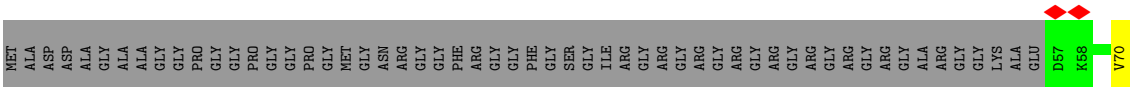
• Molecule 12: 40S ribosomal protein S21

Chain K:



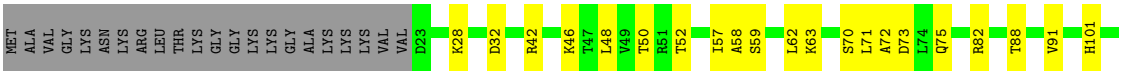
• Molecule 13: 40S ribosomal protein S2

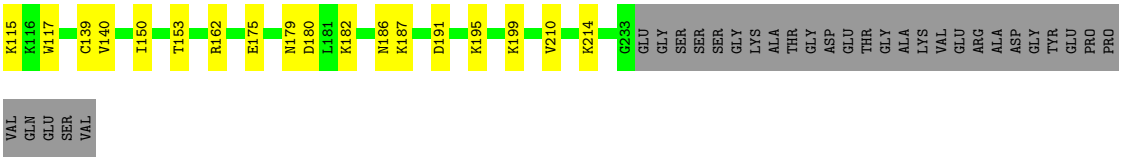
Chain L:



• Molecule 14: 40S ribosomal protein S3a

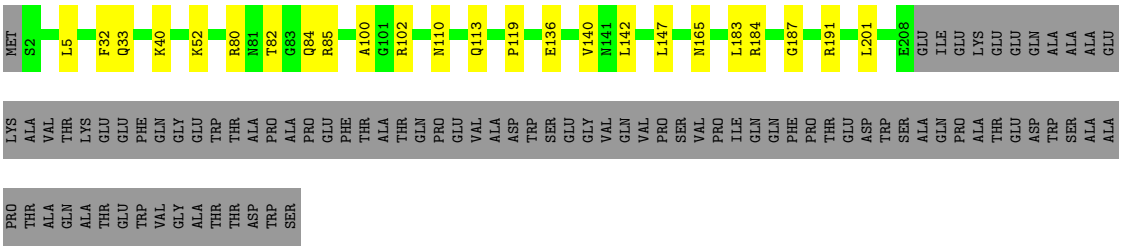
Chain O:





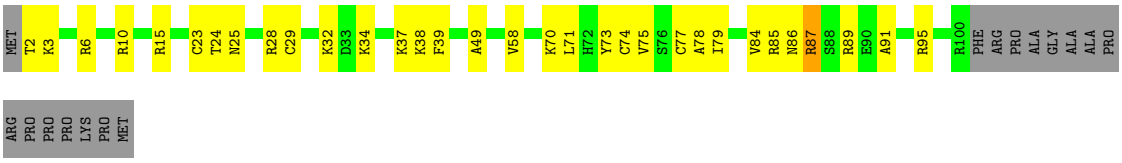
• Molecule 15: 40S ribosomal protein SA

Chain N:



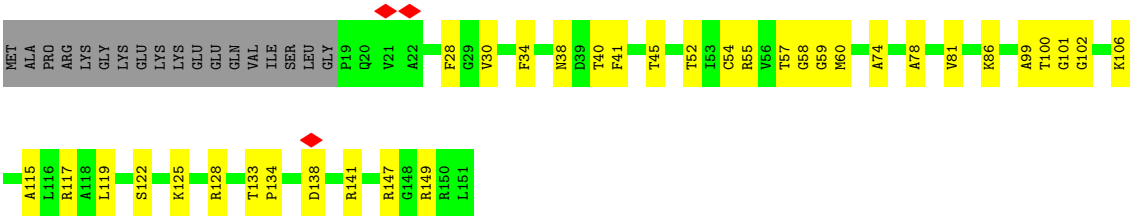
• Molecule 16: 40S ribosomal protein S26

Chain Q:



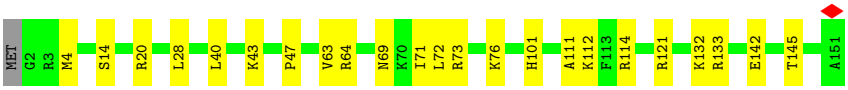
• Molecule 17: 40S ribosomal protein S14

Chain P:



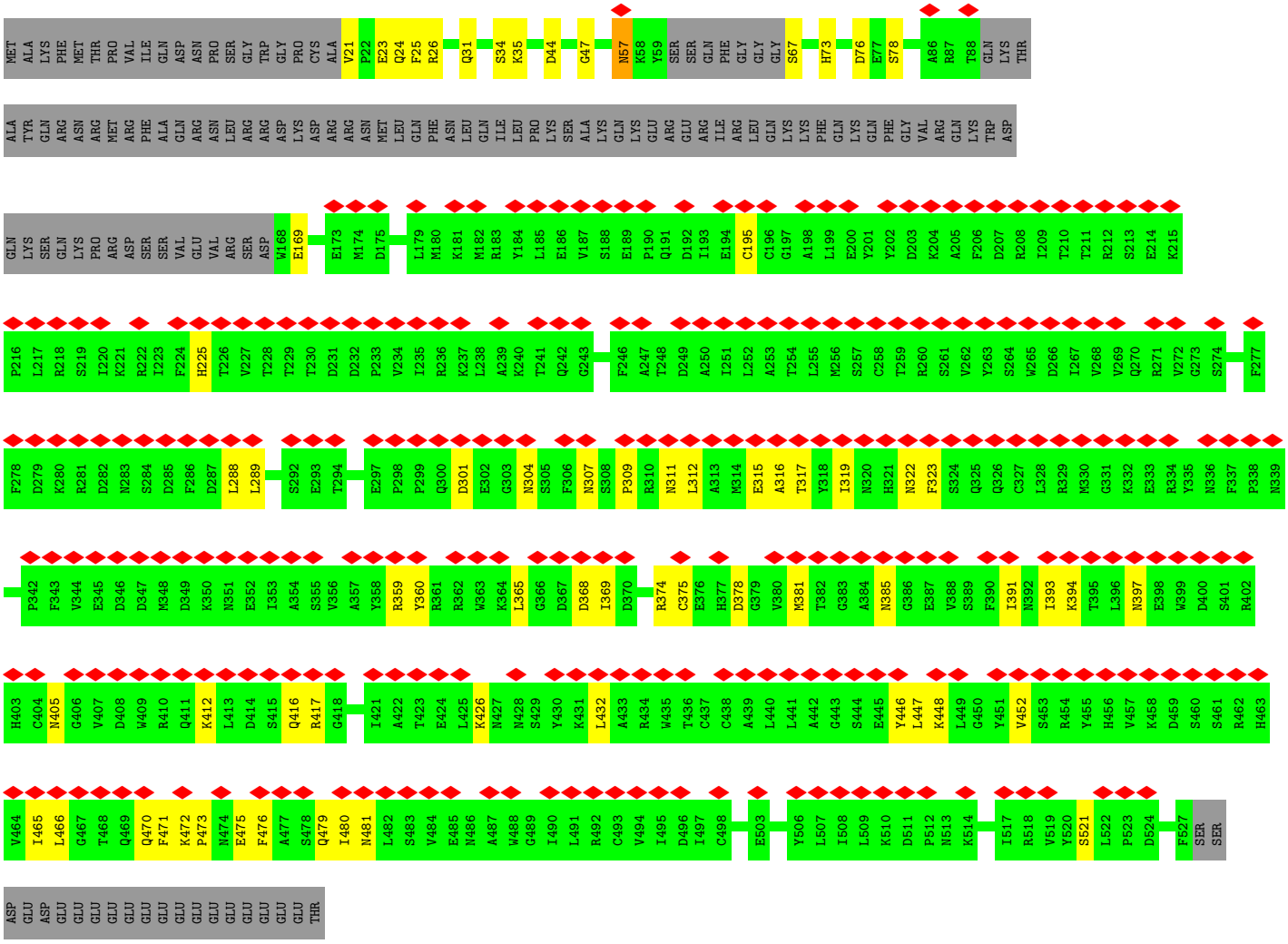
• Molecule 18: 40S ribosomal protein S13

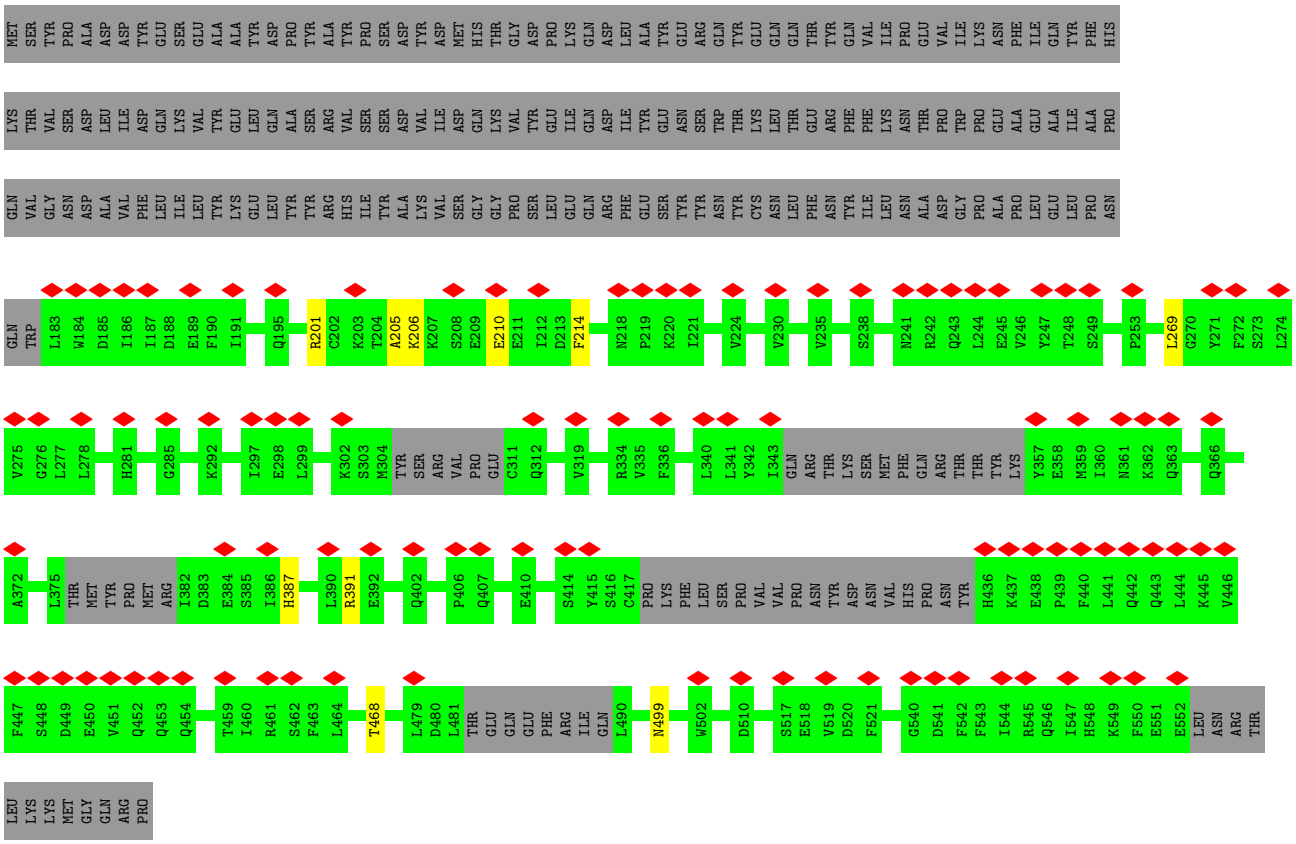
Chain I:



• Molecule 19: Eukaryotic translation initiation factor 3 subunit D

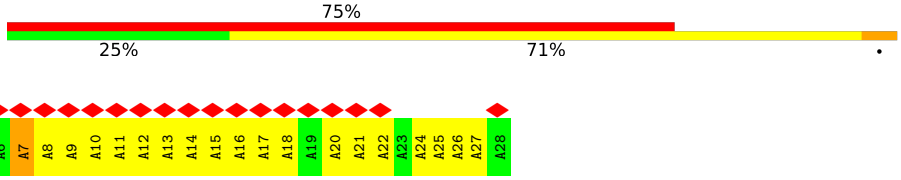
Chain x:


MET ALA LYS PHE MET THR PRO VAL ILE GLN ASP ASN PRO SER GLY TRP GLY PRO CYS ALA V21 P22 E23 Q24 F25 R26 Q31 S34 K35 D44 G47 N57 K58 Y59 SER SER GLN PHE GLY GLY GLY S67 H73 D76 E77 S78 A86 R87 T88 GLN LYS THR
ALA TYR GLN ARG ASN ARG MET ARG PHE ALA GLN ARG ASN LEU ARG ARG ASP LYS ASP ARG ARG ASN MET LEU GLN PHE ASN LEU GLN ILE LEU PRO LYS SER ALA LYS GLN LYS GLU ARG GLU ARG ILE ARG LEU GLN LYS LYS PHE GLN LYS GLN PHE GLY VAL ARG GLN LYS TRP ASP
GLN LYS SER GLN LYS PRO ARG ASP SER SER VAL GLU VAL ARG SER ASP W168 E169 E173 M174 D175 L179 M180 K181 M182 R183 Y184 L185 E186 V187 S188 E189 P190 Q191 D192 I193 E194 C195 C196 G197 A198 L199 E200 Y201 Y202 D203 K204 A205 F206 D207 R208 I209 T210 T211 R212 S213 E214 K215
P216 L217 R218 S219 I220 K221 R222 I223 F224 H225 T226 V227 T228 T229 T230 D231 D232 P233 V234 I235 R236 K237 L238 A239 K240 T241 Q242 G243 F246 A247 T248 D249 A250 I251 L252 A253 T254 L255 M256 S257 C258 T259 R260 S261 V262 Y263 S264 W265 D266 I267 V268 V269 Q270 R271 V272 G273 S274 F277
F278 D279 K280 R281 D282 N283 S284 D285 F286 D287 L288 L289 S292 E293 T294 E297 P298 P299 Q300 D301 E302 G303 N304 S305 F306 N307 S308 P309 R310 N311 L312 A313 M314 E315 A316 T317 Y318 I319 N320 H321 N322 F323 S324 Q325 Q326 C327 L328 R329 M330 G331 K332 E333 R334 Y335 N336 F337 P338 N339
P342 F343 V344 E345 D346 D347 M348 D349 K350 N351 E352 I353 A354 S355 V356 A357 Y358 R359 Y360 R361 R362 W363 K364 L365 G366 D367 D368 I369 D370 R374 C375 E376 H377 D378 G379 V380 M381 T382 G383 A384 N385 G386 E387 V388 S389 F390 I391 N392 I393 K394 T395 L396 N397 E398 W399 D400 S401 R402
H403 C404 N405 G406 V407 D408 W409 R410 Q411 K412 L413 D414 S415 Q416 R417 G418 T421 A422 T423 E424 L425 K426 N427 N428 S429 Y430 K431 L432 A433 R434 W435 T436 C437 C438 A439 L440 L441 A442 G443 S444 E445 Y446 L447 K448 L449 G450 Y451 V452 S453 R454 Y455 H456 V457 K458 D459 S460 S461 R462 H463
V464 I465 L466 G467 T468 Q469 Q470 F471 K472 P473 N474 E475 F476 A477 S478 Q479 I480 N481 L482 S483 V484 E485 N486 A487 W488 G489 I490 L491 R492 C493 V494 I495 D496 I497 C498 E503 Y506 L507 I508 L509 K510 D511 P512 N513 K514 I517 R518 V519 Y520 S521 L522 P523 D524 F527 SER SER
ASP GLU ASP GLU GLU GLU



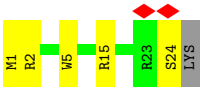
• Molecule 22: mRNA

Chain 7:



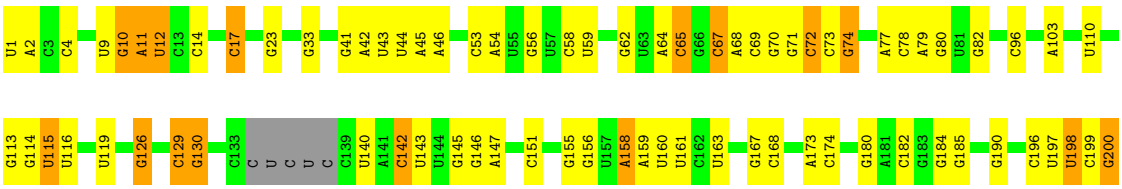
• Molecule 23: 60S ribosomal protein L41

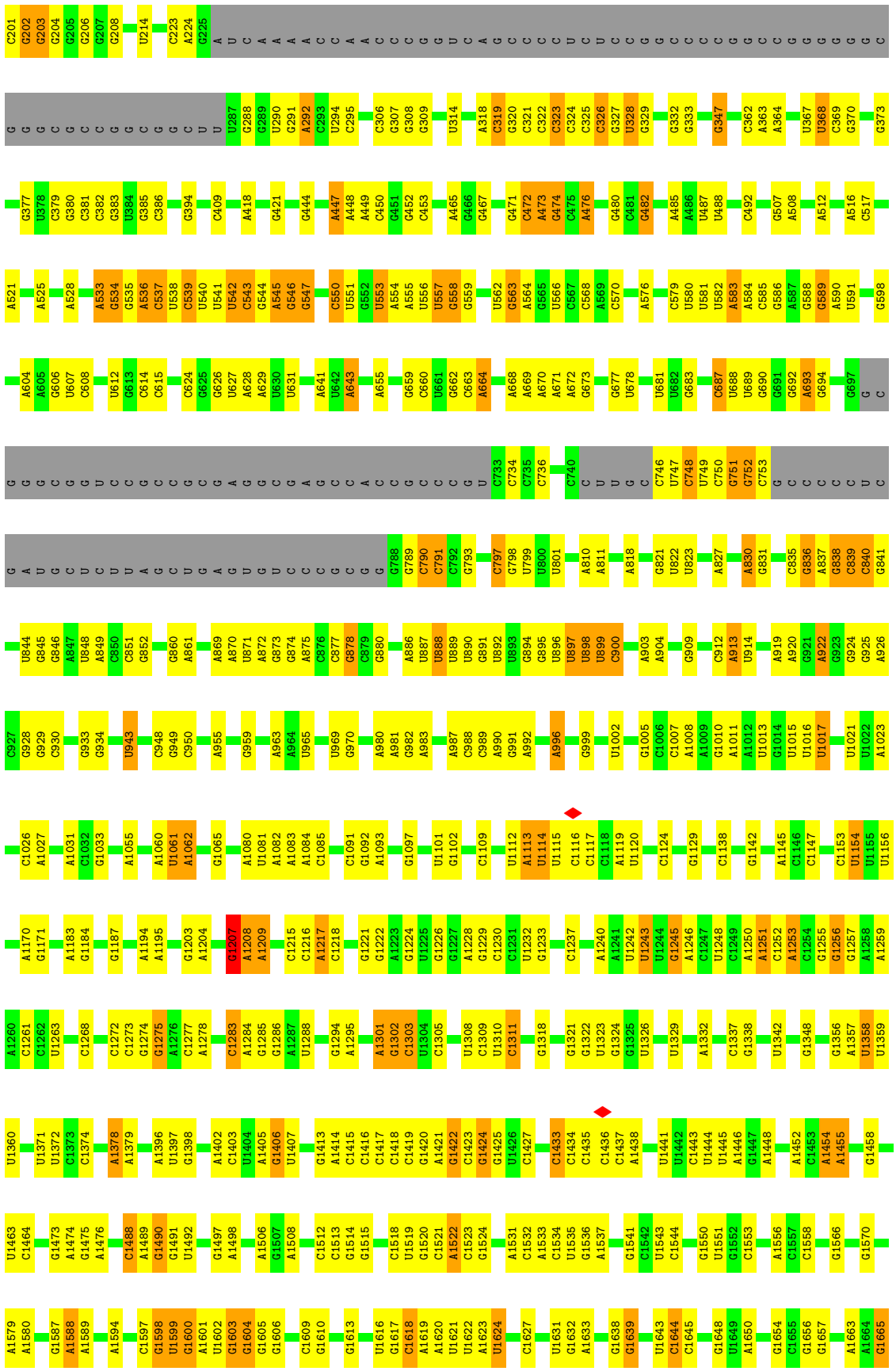
Chain 9:



• Molecule 24: 18S rRNA

Chain A:

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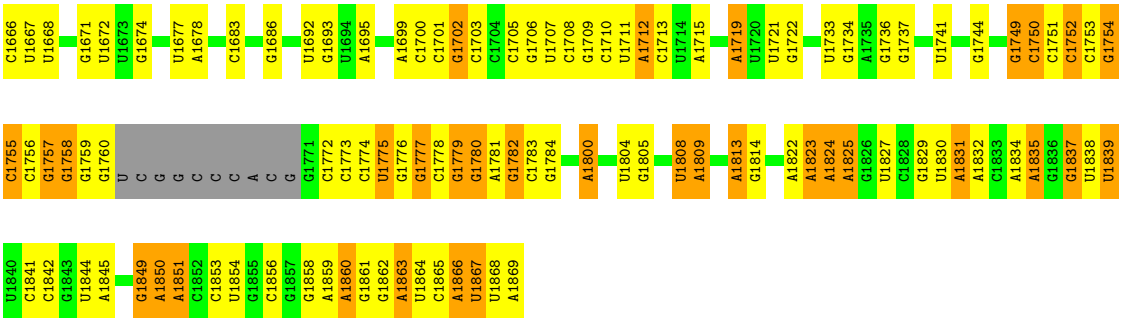
U1463 C1464 G1473 A1474 G1475 A1476 C1488 A1489 G1490 G1491 U1492 G1497 A1498 A1506 G1507 A1508 C1512 C1513 G1514 G1515 C1518 U1519 G1520 C1521 A1522 C1523 G1524 A1531 C1532 A1533 C1534 U1535 G1536 A1537 G1541 C1542 U1543 C1544 G1550 U1551 G1552 C1553 A1556 C1557 C1558 G1566 G1570
U1360 U1371 U1372 C1373 C1374 A1378 A1379 A1396 U1397 G1398 A1402 C1403 U1404 A1405 G1406 U1407 G1413 A1414 C1415 C1416 C1417 C1418 C1419 G1420 A1421 G1422 C1423 G1424 G1425 U1426 C1427 C1433 C1434 C1435 C1436 C1437 A1438 U1441 U1442 C1443 C1444 U1445 A1446 G1447 A1448 A1452 C1453 A1454 A1455 G1458
A1260 C1261 C1262 U1263 C1268 C1272 C1273 G1274 G1275 A1276 C1277 A1278 C1283 A1284 G1285 G1286 A1287 U1288 G1294 A1295 A1301 G1302 C1303 U1304 C1305 U1308 C1309 U1310 C1311 G1318 G1321 G1322 U1323 G1324 G1325 U1326 U1329 A1332 C1337 G1338 U1342 G1348 G1356 A1357 U1358 U1359
A1170 G1171 A1183 G1184 G1187 A1194 A1195 G1203 A1204 G1207 A1208 A1209 C1215 C1216 A1217 C1218 G1221 G1222 A1223 G1224 U1225 G1226 G1227 A1228 G1229 C1230 C1231 U1232 G1233 C1237 A1240 A1241 U1242 U1243 U1244 G1245 A1246 C1247 U1248 C1249 A1250 A1251 C1252 A1253 C1254 G1255 G1256 G1257 A1258 A1259
C1026 A1027 A1031 C1032 G1033 A1055 A1060 U1061 A1062 G1065 A1080 U1081 A1082 A1083 A1084 C1085 C1091 G1092 A1093 G1097 U1101 G1102 C1109 U1112 A1113 U1114 U1115 C1116 C1117 C1118 A1119 U1120 C1124 G1129 C1138 G1142 A1145 C1146 C1147 C1153 U1154 U1155 U1156
C927 G928 G929 C930 G933 G934 U943 C948 G949 C950 A955 G959 A963 A964 U965 U969 G970 A980 A981 G982 A983 A987 C988 C989 A990 G991 A992 A996 G999 U1002 G1005 C1006 C1007 A1008 A1009 G1010 A1011 A1012 U1013 G1014 U1015 U1016 U1017 U1021 U1022 A1023
U844 G845 G846 A847 U848 A849 C850 C851 G852 G860 A861 A869 A870 U871 A872 G873 G874 A875 C876 C877 G878 C879 G880 A886 U887 U888 U889 U890 G891 U892 U893 G894 G895 U896 U897 U898 U899 C900 A903 A904 G909 C912 A913 U914 A919 A920 G921 A922 G923 G924 G925 A926
G A U G C C U C U U A G C U G A G U G U C C A C C G G G G A U G C C C C C C G G G G C C C C C C

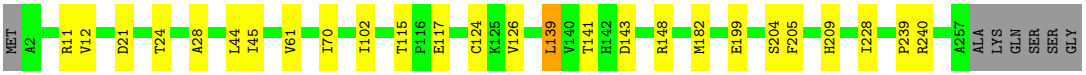


- Molecule 25: 40S ribosomal protein S11

Chain B:

- Molecule 26: 40S ribosomal protein S4, X isoform

Chain C:

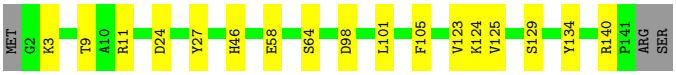


- Molecule 27: 40S ribosomal protein S9

Chain D:

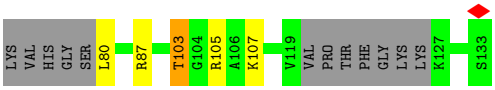
- Molecule 28: 40S ribosomal protein S23

Chain E:



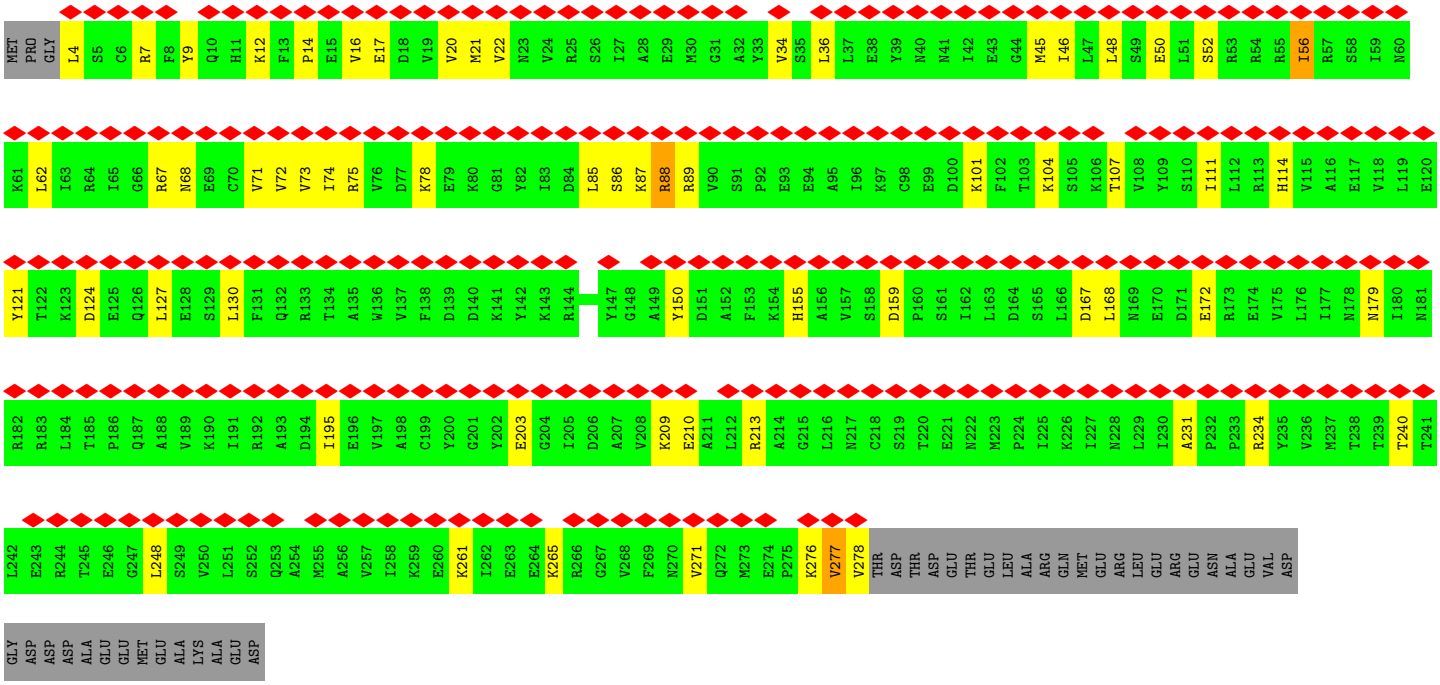
- Molecule 29: 40S ribosomal protein S30

Chain F:



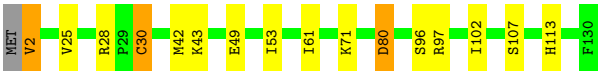
- Molecule 30: Eukaryotic translation initiation factor 2 subunit 1

Chain r:



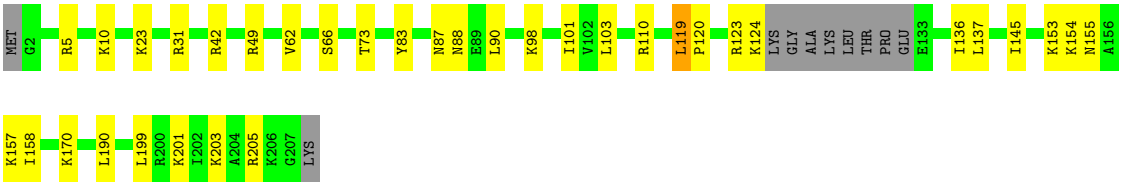
- Molecule 31: 40S ribosomal protein S15a

Chain J:



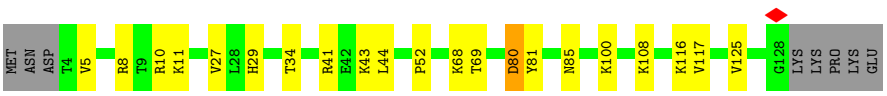
- Molecule 32: 40S ribosomal protein S8

Chain R:



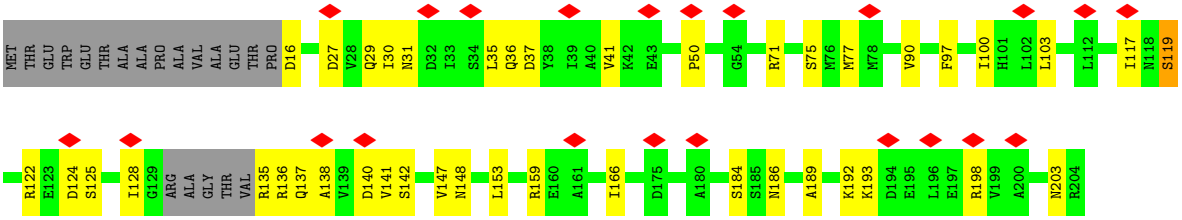
- Molecule 33: 40S ribosomal protein S24

Chain T:



- Molecule 34: 40S ribosomal protein S5

Chain V:

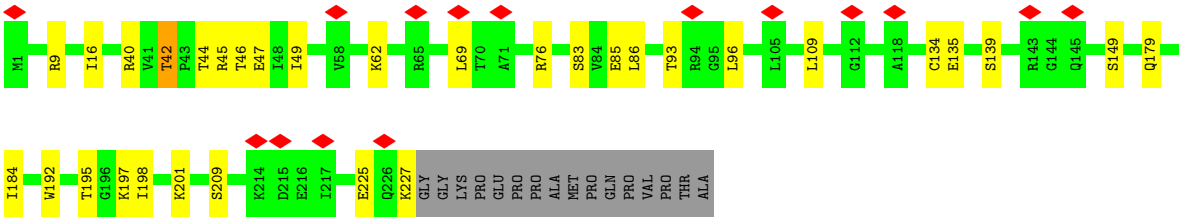


- Molecule 35: 40S ribosomal protein S16

Chain Y:

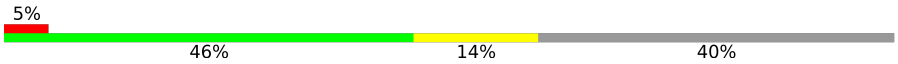
- Molecule 36: 40S ribosomal protein S3

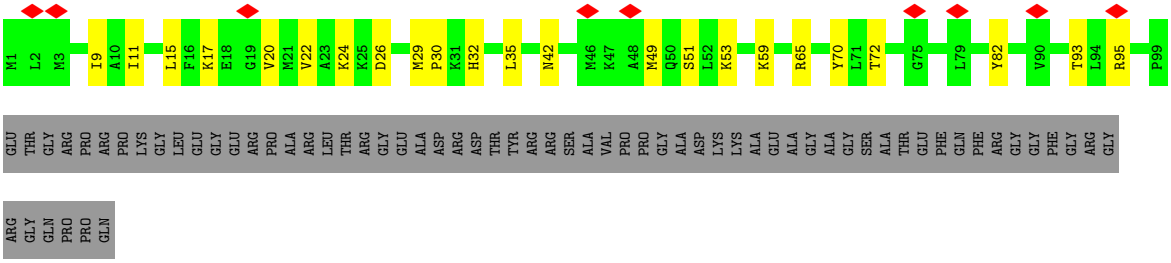
Chain Z:



- Molecule 37: 40S ribosomal protein S10

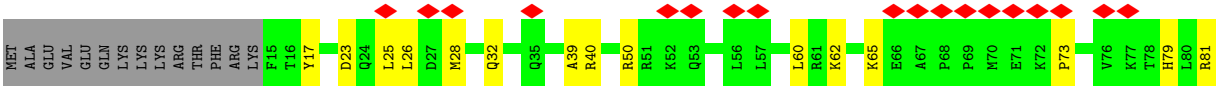
Chain a:

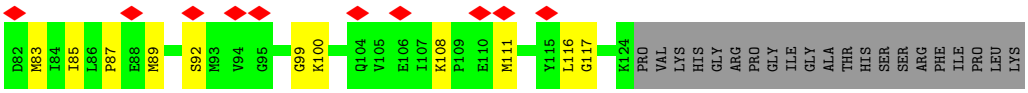




- Molecule 38: 40S ribosomal protein S15

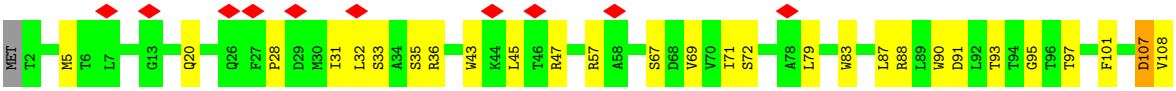
Chain b:

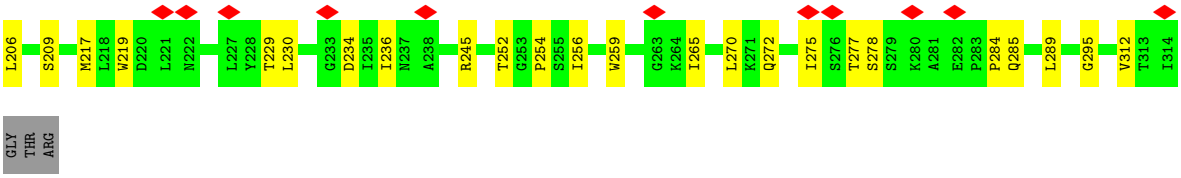




• Molecule 39: Receptor of activated protein C kinase 1

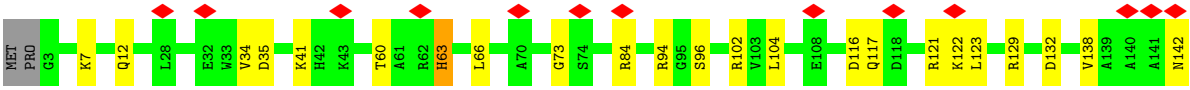
Chain c:





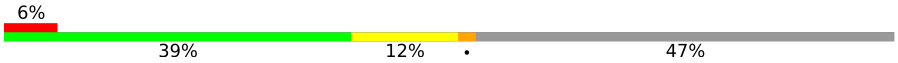
• Molecule 40: 40S ribosomal protein S19

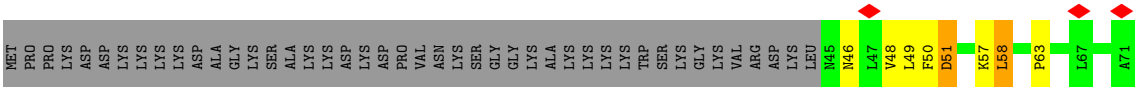
Chain d:

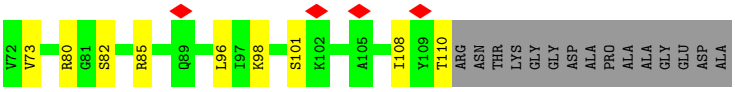


• Molecule 41: 40S ribosomal protein S25

Chain e:

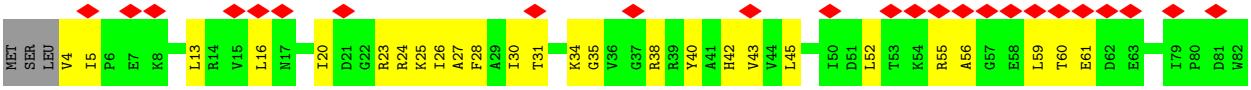


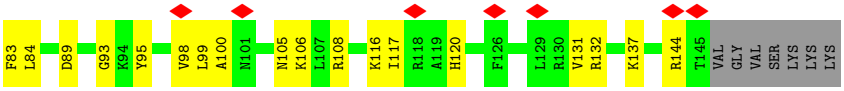




• Molecule 42: 40S ribosomal protein S18

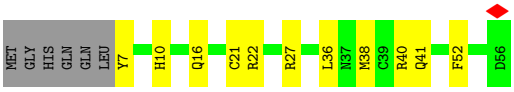
Chain f:





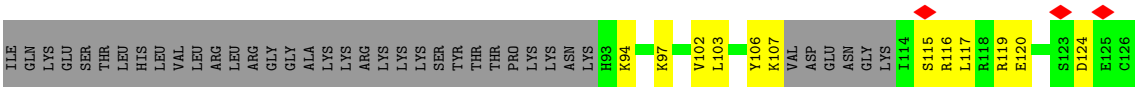
• Molecule 43: 40S ribosomal protein S29

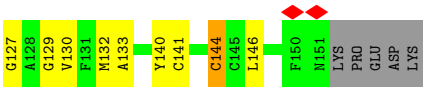
Chain i:



• Molecule 44: Ubiquitin-40S ribosomal protein S27a

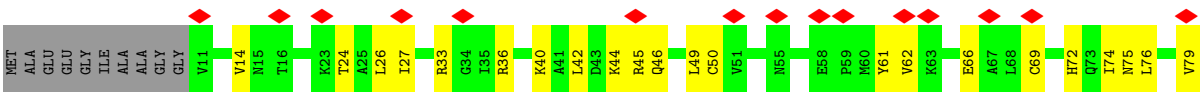
Chain k:

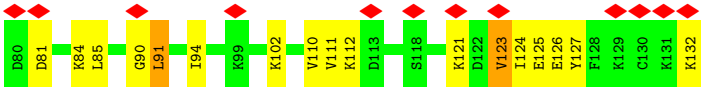




• Molecule 45: 40S ribosomal protein S12

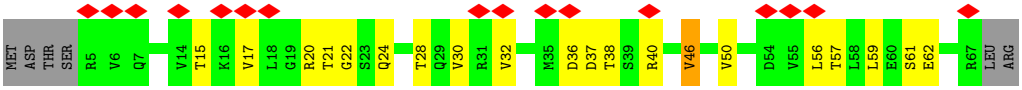
Chain m:





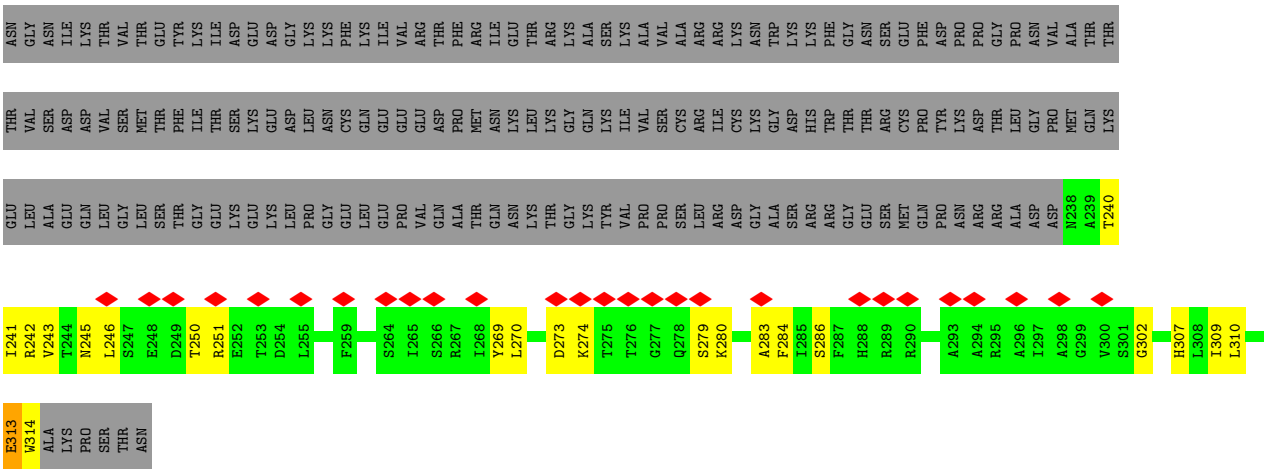
• Molecule 46: 40S ribosomal protein S28

Chain n:



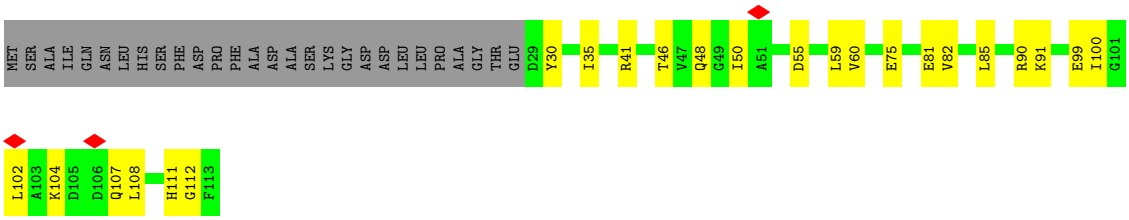
• Molecule 47: Eukaryotic translation initiation factor 3 subunit G

Chain o:



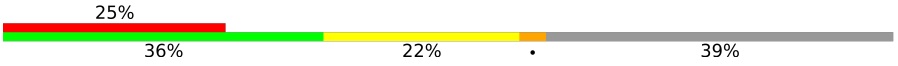
- Molecule 48: Eukaryotic translation initiation factor 1

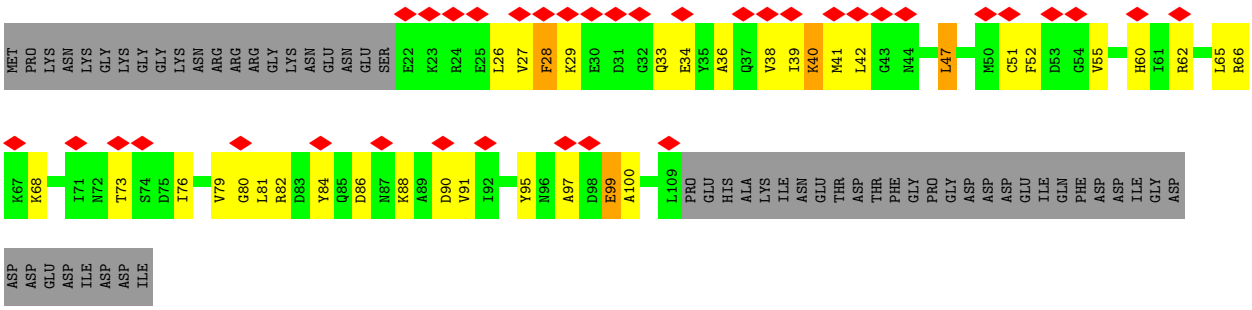
Chain p:



- Molecule 49: Eukaryotic translation initiation factor 1A, X-chromosomal

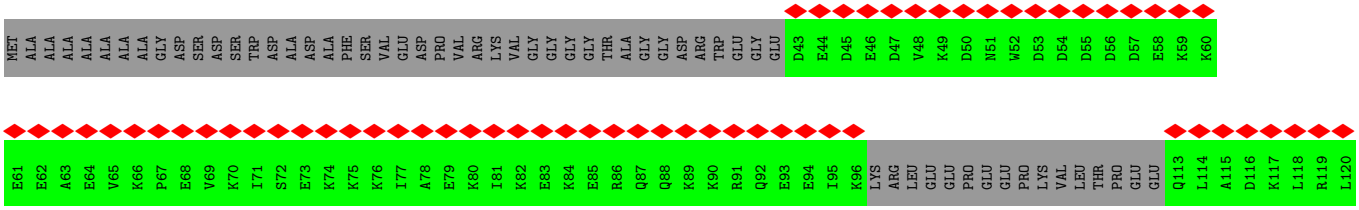
Chain q:

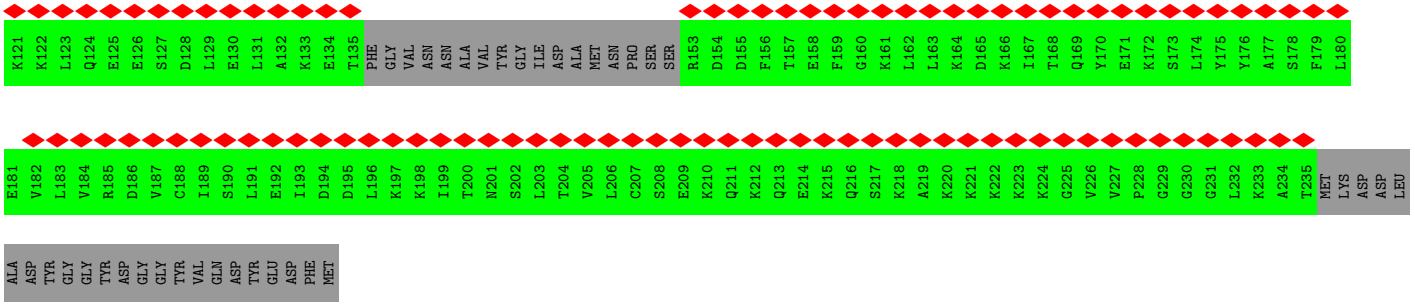




- Molecule 50: Eukaryotic translation initiation factor 3 subunit J

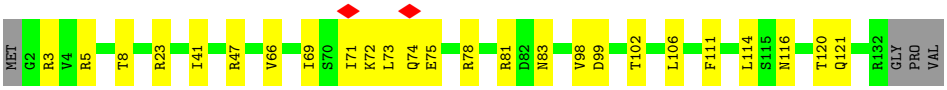
Chain z:





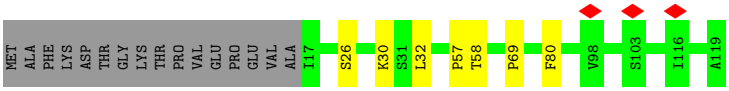
- Molecule 51: 40S ribosomal protein S17

Chain M:



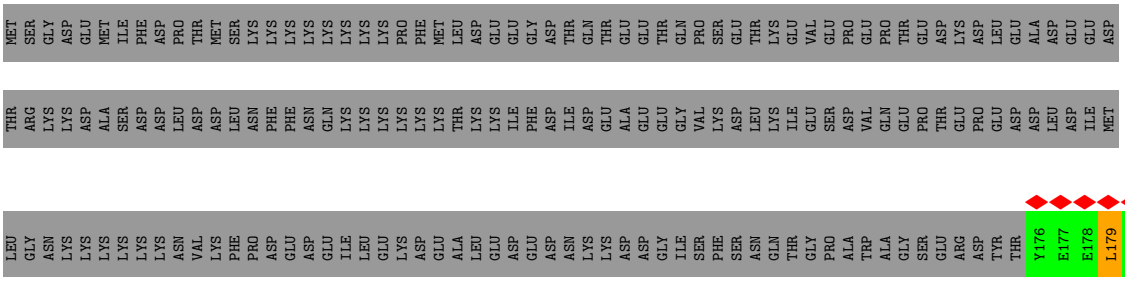
- Molecule 52: 40S ribosomal protein S20

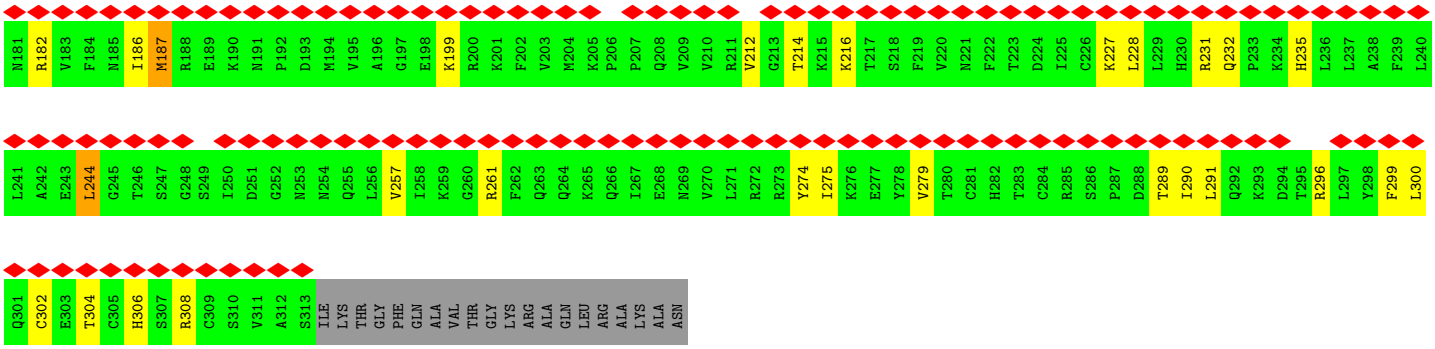
Chain h:



- Molecule 53: Eukaryotic translation initiation factor 2 subunit 2

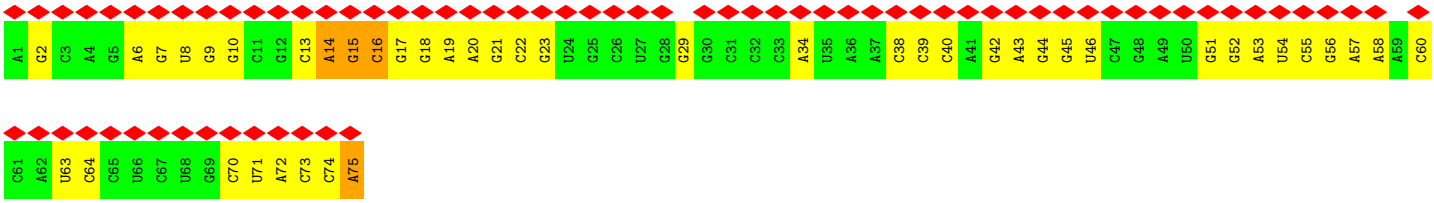
Chain s:





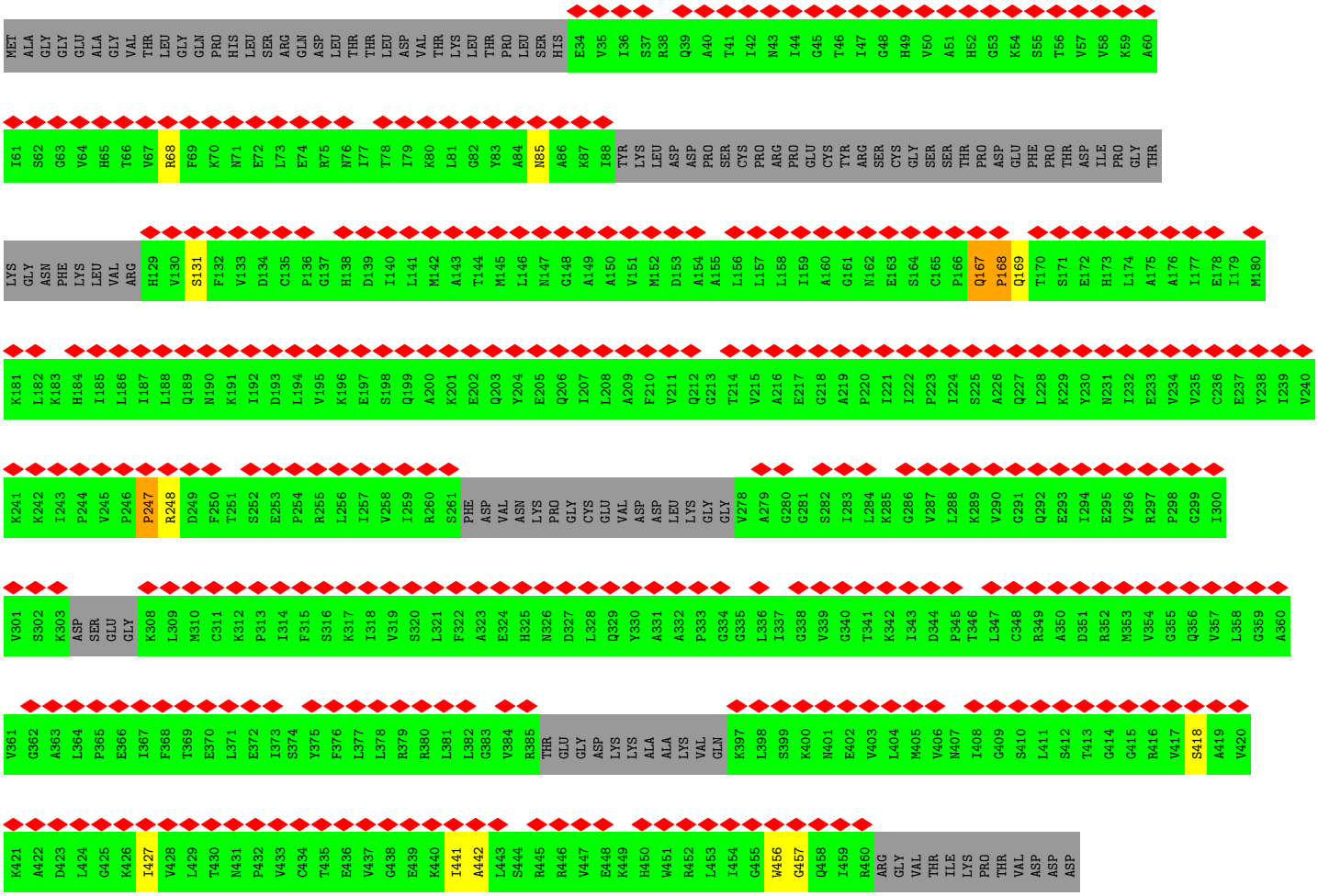
- Molecule 54: Initiator Met-tRNA-i

Chain w: 97% 41% 53% 5%



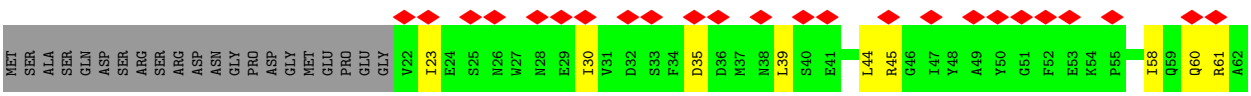
- Molecule 55: Eukaryotic translation initiation factor 2 subunit 3

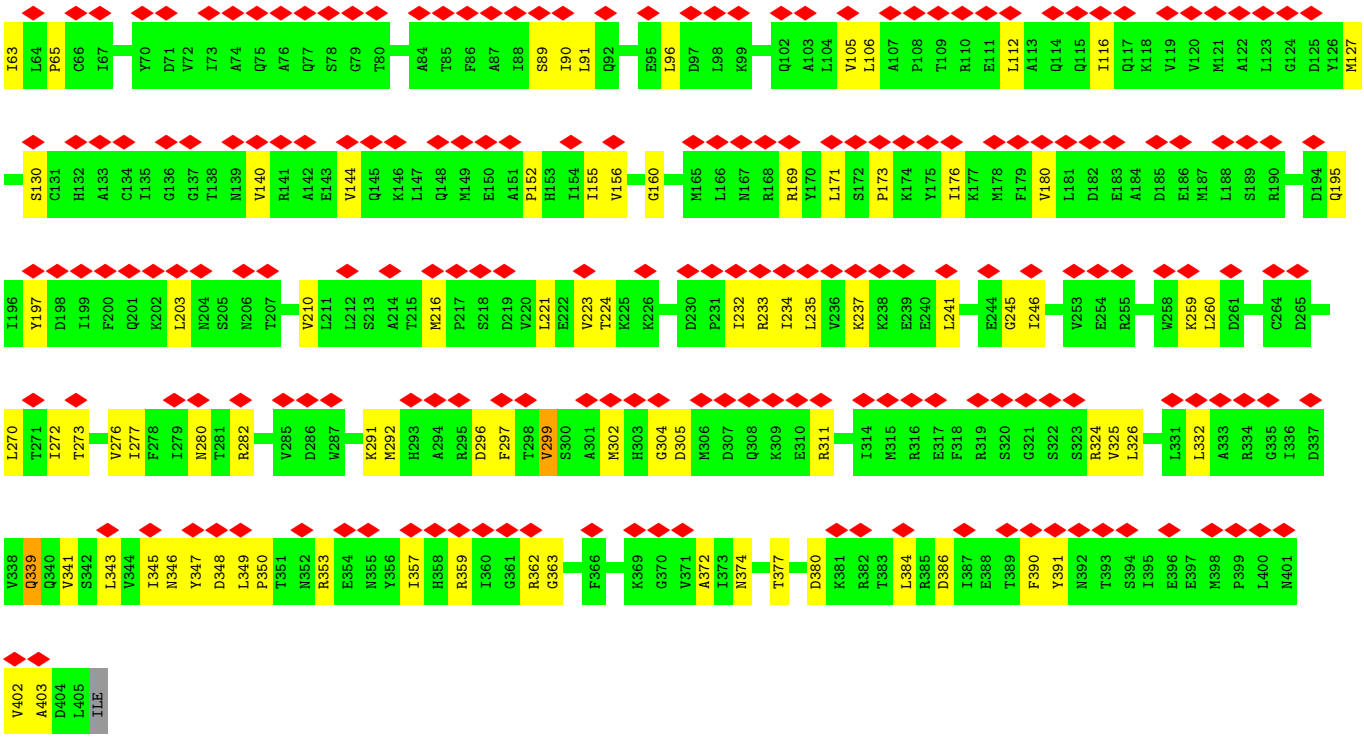
Chain t: 71% 72% 25%



- Molecule 56: Eukaryotic initiation factor 4A-I

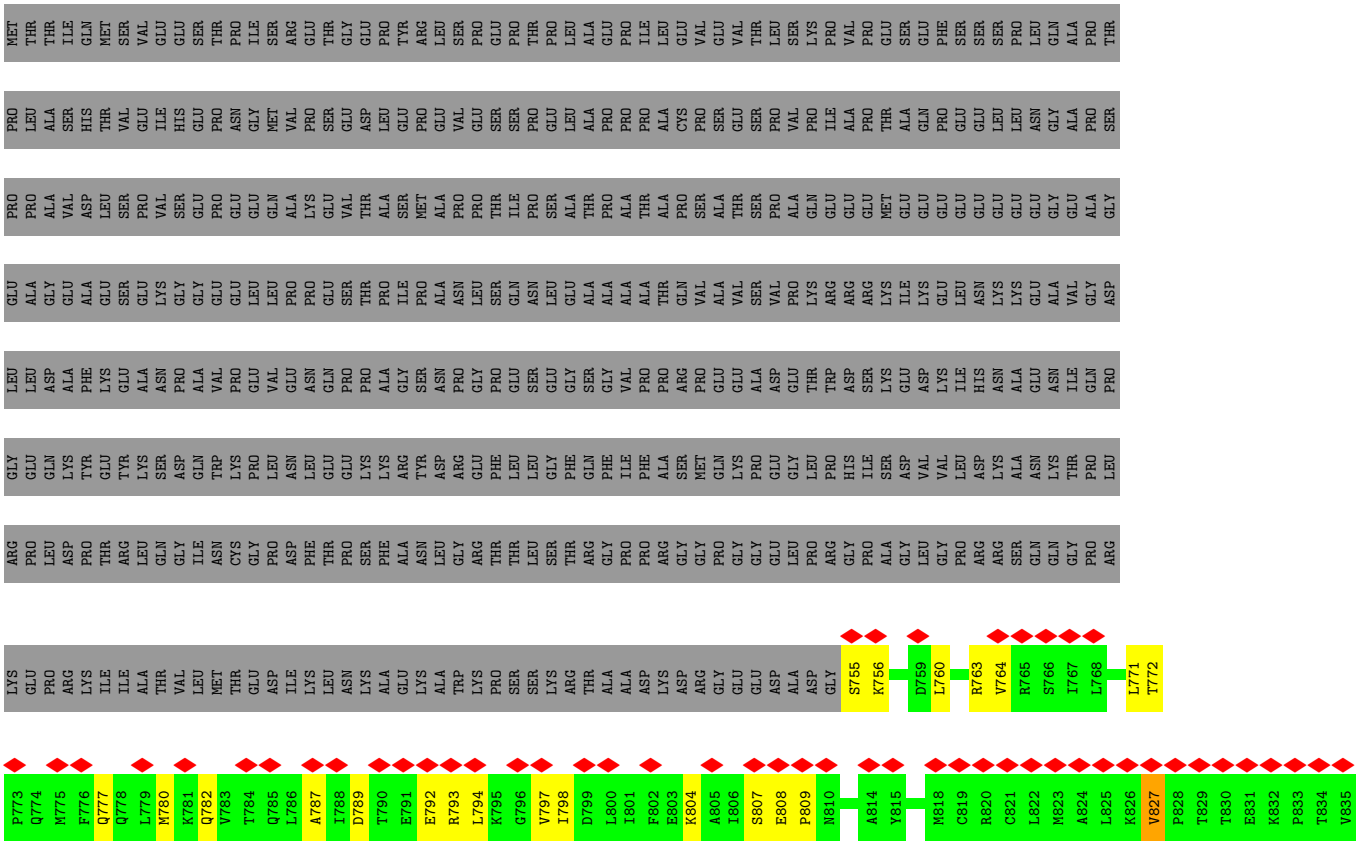
Chain j: 55% 71% 23% 5%

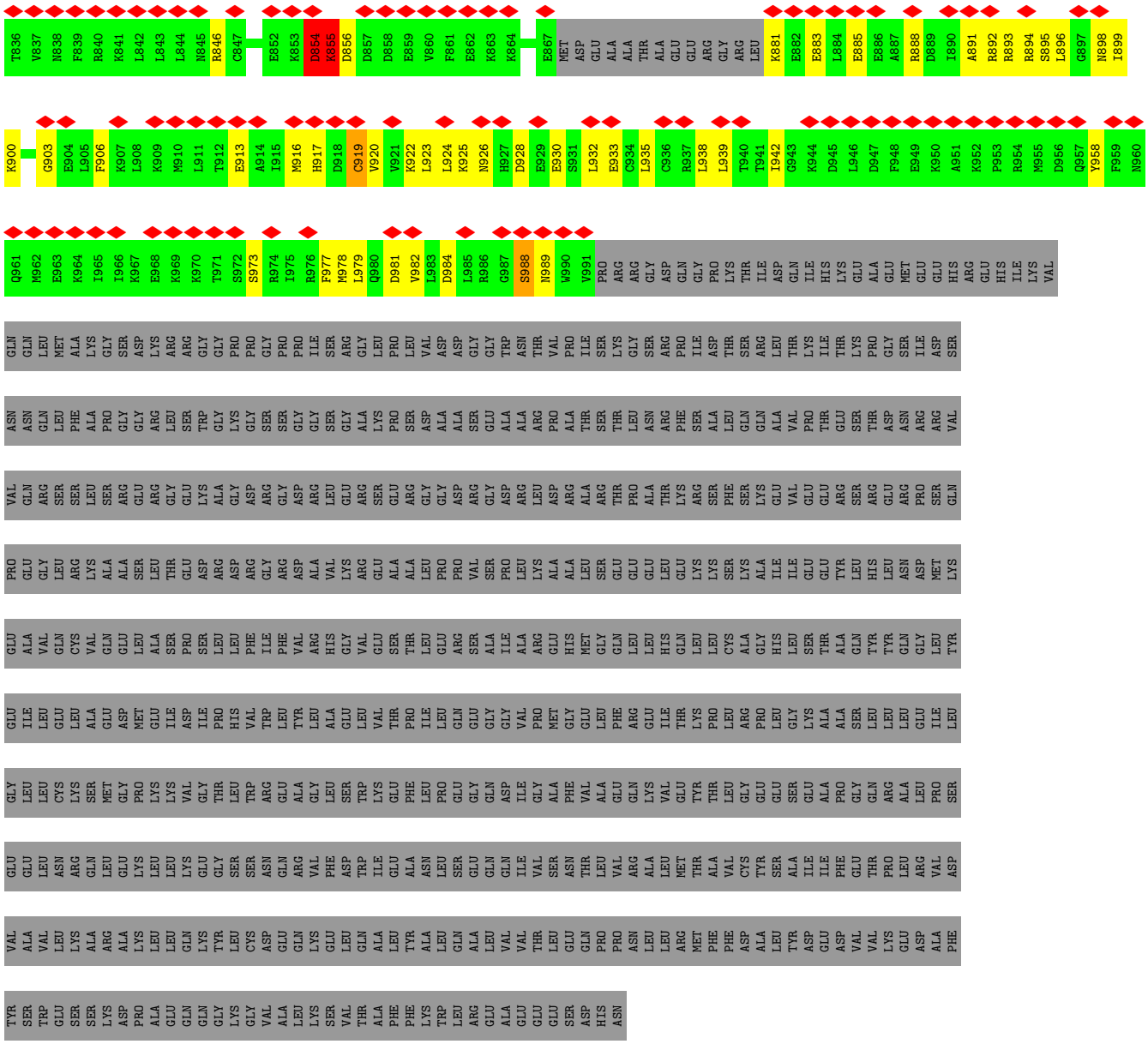




- Molecule 57: Eukaryotic translation initiation factor 4 gamma 1

Chain g:




T836 V837 N838 F839 R840 K841 L842 L843 L844 N845 R846 C847 E852 K853 D854 K855 D856 D857 D858 E859 V860 F861 E862 K863 K864 E867 MET ASP GLU ALA ALA THR ALA GLU GLU ARG GLY ARG LEU K881 E882 E883 L884 E885 E886 A887 R888 D889 I890 A891 R892 R893 R894 S895 L896 G897 N898 I899
K900 G903 E904 L905 F906 K907 L908 K909 M910 L911 T912 E913 A914 I915 M916 H917 D918 C919 V920 V921 K922 L923 L924 K925 N926 H927 D928 E929 E930 S931 L932 E933 C934 L935 C936 R937 L938 L939 T940 T941 I942 G943 K944 D945 L946 D947 F948 E949 K950 A951 K952 P953 R954 M955 D956 Q957 Y958 F959 N960
Q961 M962 E963 K964 I965 I966 K967 E968 K969 K970 T971 S972 S973 R974 I975 R976 F977 M978 L979 Q980 D981 V982 L983 D984 L985 R986 G987 S988 N989 W990 V991 PRO ARG ARG GLY ASP GLN GLY PRO LYS THR ILE ASP GLN ILE HIS LYS GLU ALA GLU MET GLU GLU HIS ARG GLU HIS ILE LYS VAL
GLN GLN LEU MET ALA LYS GLY SER ASP LYS ARG ARG GLY GLY PRO PRO GLY PRO PRO ILE SER ARG GLY LEU PRO LEU VAL ASP ASP GLY GLY TRP ASN THR VAL PRO ILE SER LYS GLY SER ARG PRO ILE ASP THR SER ARG LEU THR LYS ILE THR LYS PRO GLY SER ILE ASP SER
ASN ASN GLN LEU PHE ALA PRO GLY GLY ARG LEU SER TRP GLY LYS GLY SER SER GLY GLY SER GLY ALA LYS PRO SER ASP ALA ALA SER GLU ALA ALA ARG PRO ALA THR SER THR LEU ASN ARG PHE SER ALA LEU GLN GLN ALA VAL PRO THR GLU SER THR ASP ASN ARG ARG VAL
VAL GLN ARG SER SER LEU SER ARG GLU ARG GLY GLU LYS ALA GLY ASP ARG GLY ASP ARG LEU GLU ARG SER GLU ARG GLY GLY ASP ARG GLY ASP ARG ALA ARG THR PRO ALA THR LYS ARG SER PHE SER LYS GLU VAL GLU GLU ARG SER ARG GLU ARG PRO SER GLN
PRO GLU GLY LEU ARG LYS ALA ALA SER LEU THR GLU ASP ARG ASP ARG GLY ARG ASP ARG ALA VAL LYS ARG GLU ALA ALA LEU PRO PRO VAL SER PRO LEU LYS ALA ALA LEU SER GLU GLU GLU LEU GLU LYS LYS SER LYS ALA ILE ILE GLU GLU TYR LEU HIS LEU ASN ASP MET LYS
GLU ALA VAL GLN CYS VAL GLN GLU LEU ALA SER PRO SER LEU LEU PHE ILE PHE VAL ARG HIS GLY VAL GLU SER THR LEU GLU ARG SER ALA ILE ALA ARG GLU HIS MET GLY GLN LEU LEU HIS GLN LEU LEU CYS ALA GLY HIS LEU SER THR ALA GLN TYR TYR GLN GLY LEU TYR
GLU ILE LEU GLU LEU ALA GLU ASP MET GLU ILE ASP ILE PRO HIS VAL TRP LEU TYR LEU ALA GLU LEU VAL THR PRO ILE LEU GLN GLU GLY GLY VAL PRO MET GLY GLU LEU PHE ARG GLU ILE THR LYS PRO LEU ARG PRO LEU GLY LYS ALA ALA SER LEU LEU LEU GLU ILE LEU
GLY LEU LEU CYS LYS SER MET GLY PRO LYS LYS VAL GLY THR LEU TRP ARG GLU ALA GLY LEU SER TRP LYS GLU PHE LEU PRO GLU GLN GLY GLN ASP ILE GLY ALA PHE VAL ALA GLU GLN LYS VAL GLU TYR THR LEU GLY GLU GLU SER GLU ALA PRO GLY GLN ARG ALA LEU PRO SER
GLU GLU LEU ASN ARG GLN LEU GLU LYS LEU LEU LEU LYS GLU GLY SER SER ASN GLN ARG VAL PHE ASP TRP ILE GLU ALA ASN LEU SER GLU GLN GLN ILE VAL SER ASN THR LEU VAL ARG ALA LEU MET THR ALA VAL CYS TYR SER ALA ILE ILE PHE GLU THR PRO LEU ARG VAL ASP
VAL ALA VAL LEU LYS ALA ARG ALA LYS LEU LEU GLN LYS TYR LEU CYS ASP GLU GLN LYS GLU LEU GLN ALA LEU TYR ALA LEU GLN ALA LEU VAL VAL THR LEU GLU GLN PRO PRO ASN LEU LEU ARG MET PHE PHE ASP ALA LEU TYR ASP GLU ASP VAL VAL LYS GLU ASP ALA PHE
TYR SER TRP GLU SER SER LYS ASP PRO ALA GLU GLN GLN GLY LYS GLY VAL ALA LEU LYS SER VAL THR ALA PHE PHE LYS TRP LEU ARG GLU ALA GLU GLU GLU SER ASP HIS ASN

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	37870	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 ($e^-/Å^2$)	107	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.339	Depositor
Minimum map value	-0.216	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	537.0, 537.0, 537.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.074, 1.074, 1.074	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, OMC, MA6, UR3, 6MZ, 5MU, OMG, PSU, 5MC, MG, OMU, JMH, A2M

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	2	0.22	0/1491	0.90	0/2068
2	1	0.29	0/3279	0.94	0/4534
3	6	0.25	0/1926	0.82	1/2669 (0.0%)
4	4	0.24	0/1269	0.82	0/1762
5	u	0.31	0/5475	0.77	0/7432
6	v	0.29	0/2672	0.81	0/3647
7	S	0.30	0/1885	0.69	0/2510
8	y	0.28	0/5557	0.70	0/7503
9	8	0.26	0/1569	0.93	0/2183
10	G	0.35	0/1451	0.79	0/1942
11	H	0.37	0/644	0.68	0/864
12	K	0.38	0/623	0.64	0/833
13	L	0.45	0/1743	0.82	1/2354 (0.0%)
14	O	0.34	0/1742	0.64	0/2330
15	N	0.39	0/1670	0.60	1/2271 (0.0%)
16	Q	0.43	0/805	0.78	0/1079
17	P	0.37	0/1010	0.82	1/1353 (0.1%)
18	I	0.43	0/1232	0.70	0/1656
19	x	0.29	0/2874	0.82	1/3925 (0.0%)
20	3	0.27	0/1055	0.92	0/1469
21	5	0.27	0/1575	0.88	2/2187 (0.1%)
22	7	0.36	0/363	1.03	0/556
23	9	0.29	0/231	0.64	0/294
24	A	0.41	0/40313	0.61	6/62824 (0.0%)
25	B	0.38	0/1186	0.52	0/1585
26	C	0.35	0/2077	0.56	0/2796
27	D	0.38	0/1502	0.63	0/2008
28	E	0.38	0/1105	0.58	0/1476
29	F	0.32	0/380	0.52	0/496
30	r	0.25	0/2247	0.72	0/3029
31	J	0.41	0/1051	0.64	0/1406
32	R	0.33	0/1654	0.63	0/2203

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	T	0.31	0/1032	0.55	0/1371
34	V	0.26	0/1481	0.76	1/1988 (0.1%)
35	Y	0.30	0/1142	0.78	0/1528
36	Z	0.28	0/1793	0.67	0/2414
37	a	0.28	0/859	0.76	0/1159
38	b	0.28	0/929	0.76	0/1241
39	c	0.30	0/2493	0.75	0/3394
40	d	0.29	0/1123	0.79	0/1504
41	e	0.30	0/529	0.80	0/712
42	f	0.29	0/1194	0.80	0/1599
43	i	0.27	0/429	0.66	0/568
44	k	0.40	0/444	1.05	0/588
45	m	0.36	0/960	0.89	0/1286
46	n	0.32	0/500	0.80	0/669
47	o	0.31	0/628	0.87	0/846
48	p	0.29	0/701	0.76	0/936
49	q	0.24	0/722	0.74	0/963
50	z	0.23	0/792	0.87	0/1101
51	M	0.32	0/1078	0.71	0/1447
52	h	0.30	0/827	0.78	0/1110
53	s	0.26	0/1142	0.79	0/1534
54	w	0.24	0/1795	0.68	0/2798
55	t	0.23	0/1745	0.89	3/2417 (0.1%)
56	j	0.35	0/3119	0.90	0/4210
57	g	0.40	0/1869	0.99	5/2494 (0.2%)
All	All	0.35	0/122982	0.72	22/175121 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
24	A	1631	U	C5'-C4'-C3'	-6.79	105.81	116.00
57	g	855	LYS	N-CA-CB	6.75	121.90	110.49
17	P	138	ASP	N-CA-CB	-5.62	102.50	110.58
15	N	102	ARG	CA-CB-CG	-5.53	103.03	114.10
24	A	1311	C	C5'-C4'-C3'	-5.52	107.72	116.00

There are no chirality outliers.

There are no planarity outliers.

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	2	1493	0	677	5	0
2	1	3258	0	1917	28	0
3	6	1917	0	1096	30	0
4	4	1272	0	564	6	0
5	u	5383	0	5085	101	0
6	v	2635	0	2207	49	0
7	S	1862	0	2018	43	0
8	y	5470	0	5329	72	0
9	8	1571	0	683	7	0
10	G	1430	0	1520	30	0
11	H	631	0	657	10	0
12	K	617	0	622	11	0
13	L	1707	0	1794	26	0
14	O	1715	0	1785	29	0
15	N	1633	0	1640	16	0
16	Q	792	0	844	23	0
17	P	997	0	1021	24	0
18	I	1208	0	1294	22	0
19	x	2831	0	2199	44	0
20	3	1057	0	475	9	0
21	5	1581	0	689	5	0
22	7	336	0	169	1	0
23	9	230	0	276	4	0
24	A	36670	0	18540	357	0
25	B	1166	0	1233	14	0
26	C	2035	0	2138	15	0
27	D	1477	0	1589	19	0
28	E	1087	0	1154	11	0
29	F	378	0	417	4	0
30	r	2215	0	2266	36	0
31	J	1034	0	1080	13	0
32	R	1627	0	1706	23	0
33	T	1015	0	1086	15	0
34	V	1461	0	1511	30	0
35	Y	1124	0	1193	22	0
36	Z	1765	0	1865	20	0
37	a	834	0	861	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	b	913	0	952	21	0
39	c	2436	0	2393	42	0
40	d	1105	0	1138	15	0
41	e	523	0	573	13	0
42	f	1176	0	1233	31	0
43	i	419	0	415	10	0
44	k	435	0	435	15	0
45	m	950	0	987	23	0
46	n	498	0	525	14	0
47	o	616	0	600	14	0
48	p	691	0	706	11	0
49	q	714	0	735	22	0
50	z	795	0	341	0	0
51	M	1064	0	1118	11	0
52	h	817	0	882	7	0
53	s	1123	0	1157	19	0
54	w	1604	0	816	13	0
55	t	1750	0	806	6	0
56	j	3073	0	3114	57	0
57	g	1848	0	1924	50	0
58	Q	1	0	0	0	0
58	k	1	0	0	0	0
59	A	87	0	0	0	0
59	d	1	0	0	0	0
59	f	1	0	0	0	0
All	All	118155	0	92050	1339	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 7.

The worst 5 of 1339 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)
24:A:1091:C:HO2'	31:J:2:VAL:N	1.81	0.79
24:A:925:G:H1	24:A:1017:U:H3	1.29	0.79
13:L:202:THR:HG22	27:D:54:ARG:HH12	1.48	0.76
19:x:359:ARG:H	19:x:375:CYS:HB2	1.52	0.73
39:c:87:LEU:HB2	39:c:101:PHE:HB2	1.67	0.73

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	2	300/325 (92%)	277 (92%)	23 (8%)	0	100	100
2	1	584/814 (72%)	541 (93%)	36 (6%)	7 (1%)	10	40
3	6	348/374 (93%)	296 (85%)	52 (15%)	0	100	100
4	4	251/357 (70%)	217 (86%)	31 (12%)	3 (1%)	10	40
5	u	705/1382 (51%)	656 (93%)	47 (7%)	2 (0%)	36	65
6	v	380/445 (85%)	331 (87%)	49 (13%)	0	100	100
7	S	228/249 (92%)	222 (97%)	6 (3%)	0	100	100
8	y	691/913 (76%)	645 (93%)	44 (6%)	2 (0%)	36	65
9	8	313/352 (89%)	264 (84%)	48 (15%)	1 (0%)	36	65
10	G	171/194 (88%)	158 (92%)	13 (8%)	0	100	100
11	H	79/84 (94%)	73 (92%)	6 (8%)	0	100	100
12	K	79/83 (95%)	75 (95%)	4 (5%)	0	100	100
13	L	218/293 (74%)	205 (94%)	13 (6%)	0	100	100
14	O	209/264 (79%)	193 (92%)	16 (8%)	0	100	100
15	N	205/295 (70%)	189 (92%)	16 (8%)	0	100	100
16	Q	97/115 (84%)	92 (95%)	5 (5%)	0	100	100
17	P	131/151 (87%)	116 (88%)	15 (12%)	0	100	100
18	I	148/151 (98%)	141 (95%)	7 (5%)	0	100	100
19	x	415/548 (76%)	373 (90%)	42 (10%)	0	100	100
20	3	209/218 (96%)	203 (97%)	5 (2%)	1 (0%)	24	56
21	5	307/564 (54%)	299 (97%)	8 (3%)	0	100	100
23	9	22/25 (88%)	22 (100%)	0	0	100	100
25	B	138/158 (87%)	135 (98%)	3 (2%)	0	100	100
26	C	254/263 (97%)	250 (98%)	4 (2%)	0	100	100
27	D	175/194 (90%)	174 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	E	138/143 (96%)	133 (96%)	5 (4%)	0	100	100
29	F	43/59 (73%)	42 (98%)	1 (2%)	0	100	100
30	r	273/315 (87%)	250 (92%)	23 (8%)	0	100	100
31	J	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
32	R	194/208 (93%)	186 (96%)	8 (4%)	0	100	100
33	T	123/133 (92%)	122 (99%)	1 (1%)	0	100	100
34	V	180/204 (88%)	170 (94%)	10 (6%)	0	100	100
35	Y	139/146 (95%)	131 (94%)	8 (6%)	0	100	100
36	Z	225/243 (93%)	218 (97%)	7 (3%)	0	100	100
37	a	97/165 (59%)	93 (96%)	4 (4%)	0	100	100
38	b	108/145 (74%)	105 (97%)	3 (3%)	0	100	100
39	c	311/317 (98%)	295 (95%)	16 (5%)	0	100	100
40	d	140/145 (97%)	133 (95%)	7 (5%)	0	100	100
41	e	64/125 (51%)	59 (92%)	5 (8%)	0	100	100
42	f	140/152 (92%)	136 (97%)	4 (3%)	0	100	100
43	i	48/56 (86%)	45 (94%)	3 (6%)	0	100	100
44	k	49/156 (31%)	43 (88%)	6 (12%)	0	100	100
45	m	120/132 (91%)	117 (98%)	3 (2%)	0	100	100
46	n	61/69 (88%)	58 (95%)	3 (5%)	0	100	100
47	o	75/320 (23%)	72 (96%)	3 (4%)	0	100	100
48	p	83/113 (74%)	80 (96%)	3 (4%)	0	100	100
49	q	86/144 (60%)	76 (88%)	10 (12%)	0	100	100
50	z	154/258 (60%)	140 (91%)	14 (9%)	0	100	100
51	M	129/135 (96%)	121 (94%)	7 (5%)	1 (1%)	16	48
52	h	101/119 (85%)	94 (93%)	7 (7%)	0	100	100
53	s	136/333 (41%)	119 (88%)	17 (12%)	0	100	100
55	t	346/472 (73%)	334 (96%)	8 (2%)	4 (1%)	10	40
56	j	382/406 (94%)	365 (96%)	15 (4%)	2 (0%)	24	56
57	g	220/1310 (17%)	207 (94%)	9 (4%)	4 (2%)	6	34
All	All	10949/15464 (71%)	10216 (93%)	706 (6%)	27 (0%)	44	72

5 of 27 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	1	282	PRO
4	4	264	GLY
9	8	154	PRO
55	t	167	GLN
55	t	168	PRO

5.3.2 Protein sidechains (i)

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	
2	1	97/702 (14%)	96 (99%)	1 (1%)	68	74
3	6	49/335 (15%)	49 (100%)	0	100	100
5	u	528/1259 (42%)	518 (98%)	10 (2%)	50	65
6	v	206/406 (51%)	200 (97%)	6 (3%)	37	57
7	S	200/218 (92%)	197 (98%)	3 (2%)	57	68
8	y	564/811 (70%)	559 (99%)	5 (1%)	70	75
10	G	159/174 (91%)	159 (100%)	0	100	100
11	H	73/76 (96%)	72 (99%)	1 (1%)	59	70
12	K	65/67 (97%)	65 (100%)	0	100	100
13	L	186/225 (83%)	181 (97%)	5 (3%)	39	59
14	O	192/231 (83%)	191 (100%)	1 (0%)	81	80
15	N	173/243 (71%)	173 (100%)	0	100	100
16	Q	86/98 (88%)	83 (96%)	3 (4%)	32	54
17	P	104/119 (87%)	103 (99%)	1 (1%)	68	74
18	I	130/131 (99%)	129 (99%)	1 (1%)	73	76
19	x	206/494 (42%)	199 (97%)	7 (3%)	32	55
23	9	23/24 (96%)	23 (100%)	0	100	100
25	B	129/142 (91%)	128 (99%)	1 (1%)	73	76
26	C	220/225 (98%)	218 (99%)	2 (1%)	70	75
27	D	158/168 (94%)	155 (98%)	3 (2%)	50	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	E	112/115 (97%)	110 (98%)	2 (2%)	51	67
29	F	38/48 (79%)	37 (97%)	1 (3%)	40	60
30	r	247/280 (88%)	232 (94%)	15 (6%)	17	44
31	J	112/113 (99%)	108 (96%)	4 (4%)	31	54
32	R	172/180 (96%)	167 (97%)	5 (3%)	37	57
33	T	107/115 (93%)	104 (97%)	3 (3%)	38	58
34	V	156/170 (92%)	153 (98%)	3 (2%)	50	65
35	Y	117/121 (97%)	115 (98%)	2 (2%)	53	67
36	Z	190/202 (94%)	185 (97%)	5 (3%)	40	60
37	a	90/136 (66%)	89 (99%)	1 (1%)	65	73
38	b	100/130 (77%)	100 (100%)	0	100	100
39	c	272/275 (99%)	263 (97%)	9 (3%)	33	55
40	d	112/115 (97%)	107 (96%)	5 (4%)	24	49
41	e	58/103 (56%)	56 (97%)	2 (3%)	32	55
42	f	123/132 (93%)	121 (98%)	2 (2%)	55	68
43	i	44/49 (90%)	44 (100%)	0	100	100
44	k	47/140 (34%)	43 (92%)	4 (8%)	10	35
45	m	104/108 (96%)	96 (92%)	8 (8%)	12	38
46	n	56/62 (90%)	55 (98%)	1 (2%)	51	67
47	o	64/277 (23%)	61 (95%)	3 (5%)	23	48
48	p	74/96 (77%)	67 (90%)	7 (10%)	8	31
49	q	75/123 (61%)	65 (87%)	10 (13%)	4	20
51	M	119/122 (98%)	111 (93%)	8 (7%)	15	42
52	h	94/107 (88%)	94 (100%)	0	100	100
53	s	128/304 (42%)	119 (93%)	9 (7%)	14	41
56	j	339/357 (95%)	332 (98%)	7 (2%)	47	64
57	g	210/1121 (19%)	206 (98%)	4 (2%)	50	65
All	All	6908/11249 (61%)	6738 (98%)	170 (2%)	42	61

5 of 170 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	m	74	ILE

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Mol	Chain	Res	Type
51	M	66	VAL
45	m	124	ILE
48	p	102	LEU
53	s	179	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
19	x	470	GLN
57	g	980	GLN
28	E	61	GLN
57	g	898	ASN
52	h	81	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
22	7	27/28 (96%)	20 (74%)	0
24	A	1710/1869 (91%)	415 (24%)	42 (2%)
54	w	74/75 (98%)	33 (44%)	0
All	All	1811/1972 (91%)	468 (25%)	42 (2%)

5 of 468 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
22	7	4	A
22	7	5	A
22	7	7	A
22	7	9	A
22	7	10	A

5 of 42 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
24	A	1701	C
24	A	1861	G
24	A	1753	C
24	A	1781	A
24	A	1863	A

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

28 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
24	PSU	A	119	24	18,21,22	0.97	1 (5%)	22,30,33	0.69	0
24	OMG	A	683	24	23,26,27	0.37	0	33,38,41	0.58	0
24	OMG	A	644	24	23,26,27	0.44	0	33,38,41	0.45	0
24	OMC	A	1703	24	19,22,23	0.44	0	26,31,34	0.49	0
24	OMC	A	517	24	19,22,23	0.46	0	26,31,34	0.41	0
24	MA6	A	1850	24	23,26,27	0.43	0	34,38,41	0.78	1 (2%)
24	A2M	A	484	24	22,25,26	0.22	0	31,36,39	0.42	0
24	OMC	A	174	59,24	19,22,23	0.43	0	26,31,34	0.44	0
24	OMU	A	116	24	19,22,23	0.39	0	26,31,34	0.51	0
24	PSU	A	612	24	18,21,22	1.10	2 (11%)	22,30,33	0.75	1 (4%)
24	A2M	A	668	59,24	22,25,26	0.27	0	31,36,39	0.54	0
24	JMH	A	1219	59,24	18,22,23	0.64	0	21,32,35	0.65	0
24	OMG	A	509	59,24	23,26,27	0.43	0	33,38,41	0.50	0
24	A2M	A	166	24	22,25,26	0.17	0	31,36,39	0.63	0
24	PSU	A	1243	24	18,21,22	1.00	1 (5%)	22,30,33	0.70	0
24	MA6	A	1851	24	23,26,27	0.45	0	34,38,41	0.84	1 (2%)
24	6MZ	A	1832	59,24	22,25,26	0.50	0	30,36,39	0.55	0
24	A2M	A	1678	24	22,25,26	0.18	0	31,36,39	0.43	0
24	A2M	A	1031	24	22,25,26	0.20	0	31,36,39	0.51	0
24	OMU	A	121	24	19,22,23	0.44	0	26,31,34	0.51	0
24	PSU	A	1081	24	18,21,22	1.04	2 (11%)	22,30,33	0.82	0
24	A2M	A	159	24	22,25,26	0.20	0	31,36,39	0.43	0
24	5MC	A	1374	24	18,22,23	0.44	0	26,32,35	0.61	0
24	UR3	A	1830	24	19,22,23	0.41	0	26,32,35	1.00	2 (7%)
24	PSU	A	822	24	18,21,22	1.04	2 (11%)	22,30,33	0.84	1 (4%)
24	PSU	A	823	24	18,21,22	1.05	1 (5%)	22,30,33	0.68	0
24	A2M	A	27	59,24	22,25,26	0.22	0	31,36,39	0.46	0
24	5MU	A	814	24	19,22,23	0.45	0	28,32,35	0.50	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	PSU	A	119	24	-	0/7/25/26	0/2/2/2
24	OMG	A	683	24	-	0/9/27/28	0/3/3/3
24	OMG	A	644	24	-	1/9/27/28	0/3/3/3
24	OMC	A	1703	24	-	0/9/27/28	0/2/2/2
24	OMC	A	517	24	-	0/9/27/28	0/2/2/2
24	MA6	A	1850	24	-	3/11/29/30	0/3/3/3
24	A2M	A	484	24	-	0/9/27/28	0/3/3/3
24	OMC	A	174	59,24	-	0/9/27/28	0/2/2/2
24	OMU	A	116	24	-	0/9/27/28	0/2/2/2
24	PSU	A	612	24	-	0/7/25/26	0/2/2/2
24	A2M	A	668	59,24	-	2/9/27/28	0/3/3/3
24	JMH	A	1219	59,24	-	0/7/25/26	0/2/2/2
24	OMG	A	509	59,24	-	0/9/27/28	0/3/3/3
24	A2M	A	166	24	-	0/9/27/28	0/3/3/3
24	PSU	A	1243	24	-	0/7/25/26	0/2/2/2
24	MA6	A	1851	24	-	5/11/29/30	0/3/3/3
24	6MZ	A	1832	59,24	-	2/9/27/28	0/3/3/3
24	A2M	A	1678	24	-	0/9/27/28	0/3/3/3
24	A2M	A	1031	24	-	0/9/27/28	0/3/3/3
24	OMU	A	121	24	-	0/9/27/28	0/2/2/2
24	PSU	A	1081	24	-	1/7/25/26	0/2/2/2
24	A2M	A	159	24	-	2/9/27/28	0/3/3/3
24	5MC	A	1374	24	-	0/7/25/26	0/2/2/2
24	UR3	A	1830	24	-	2/7/25/26	0/2/2/2
24	PSU	A	822	24	-	0/7/25/26	0/2/2/2
24	PSU	A	823	24	-	0/7/25/26	0/2/2/2
24	A2M	A	27	59,24	-	0/9/27/28	0/3/3/3
24	5MU	A	814	24	-	0/7/25/26	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	A	1243	PSU	C6-C5	3.37	1.39	1.35
24	A	823	PSU	C6-C5	3.35	1.39	1.35
24	A	119	PSU	C6-C5	3.23	1.39	1.35
24	A	612	PSU	C6-C5	3.22	1.39	1.35
24	A	1081	PSU	C6-C5	3.20	1.39	1.35

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
24	A	1850	MA6	C2-N1-C6	3.06	118.98	111.75
24	A	1851	MA6	C2-N1-C6	3.05	118.95	111.75
24	A	822	PSU	O4'-C1'-C2'	2.28	108.36	105.14
24	A	1830	UR3	C6-N1-C2	-2.25	119.77	121.79
24	A	612	PSU	O4'-C1'-C2'	2.23	108.29	105.14

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	A	1832	6MZ	N1-C6-N6-C9
24	A	1850	MA6	C5-C6-N6-C10
24	A	1850	MA6	N1-C6-N6-C10
24	A	1851	MA6	O4'-C4'-C5'-O5'
24	A	1851	MA6	C5-C6-N6-C10

There are no ring outliers.

11 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	A	683	OMG	1	0
24	A	1703	OMC	2	0
24	A	517	OMC	1	0
24	A	1850	MA6	2	0
24	A	174	OMC	1	0
24	A	116	OMU	3	0
24	A	1832	6MZ	2	0
24	A	1678	A2M	2	0
24	A	1031	A2M	1	0
24	A	159	A2M	1	0
24	A	1374	5MC	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 91 ligands modelled in this entry, 91 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

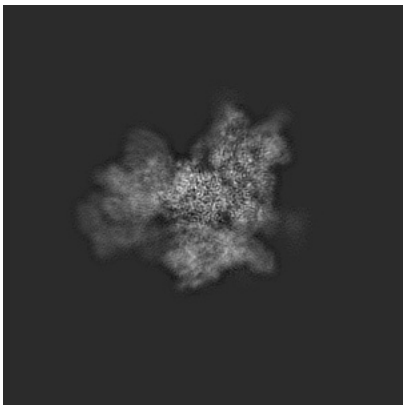
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-11302. These allow visual inspection of the internal detail of the map and identification of artifacts.

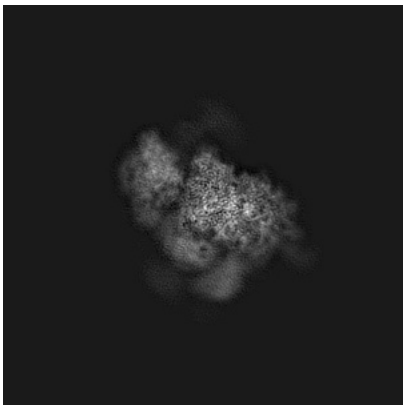
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

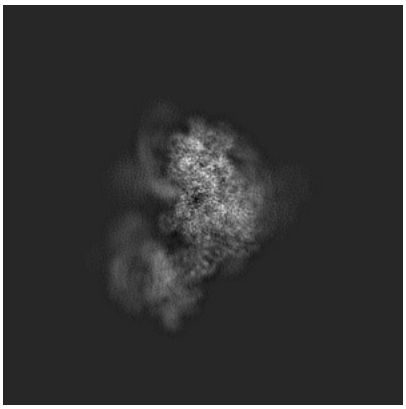
6.1.1 Primary map



X

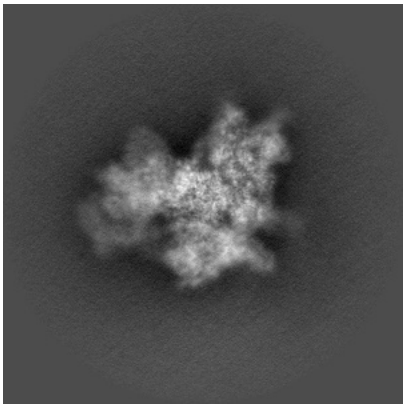


Y

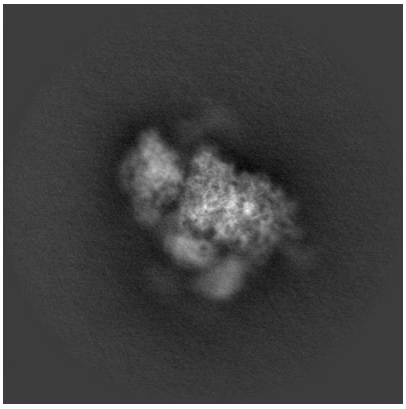


Z

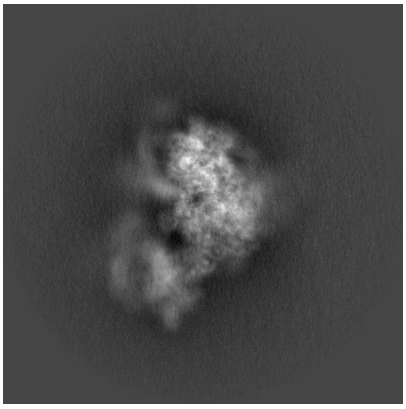
6.1.2 Raw map



X



Y



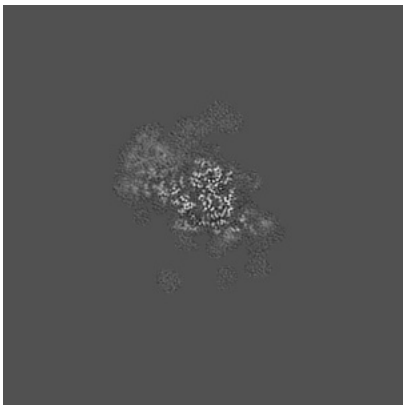
Z

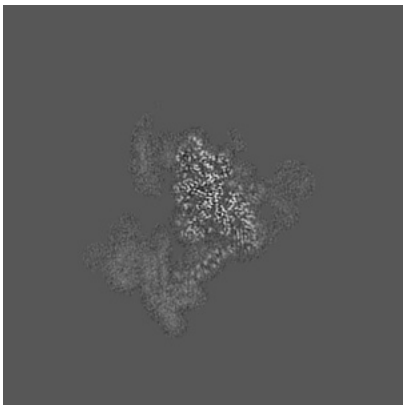
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

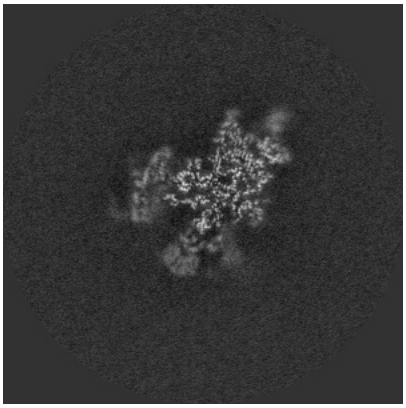
6.2.1 Primary map

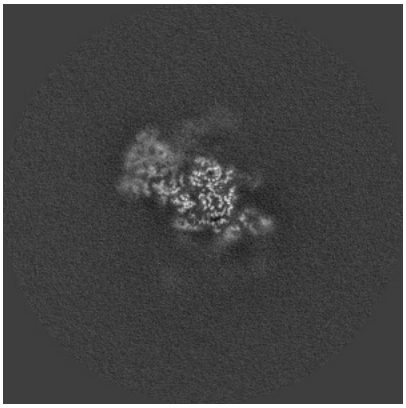
X Index: 250

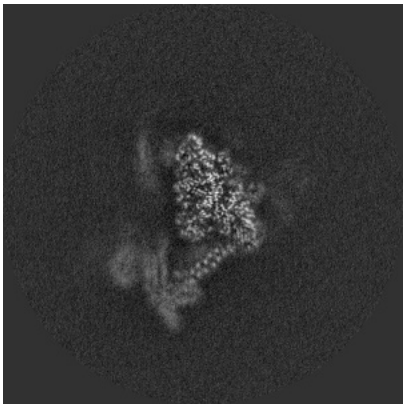

Y Index: 250


Z Index: 250

6.2.2 Raw map


X Index: 250

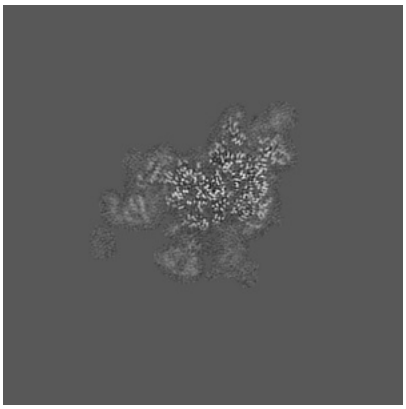

Y Index: 250


Z Index: 250

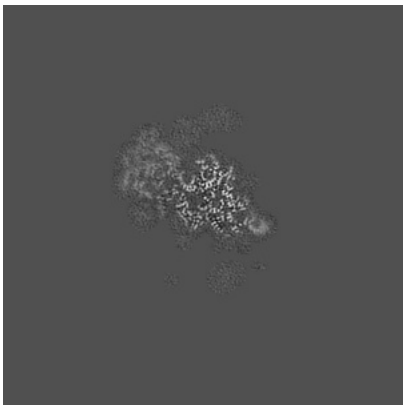
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

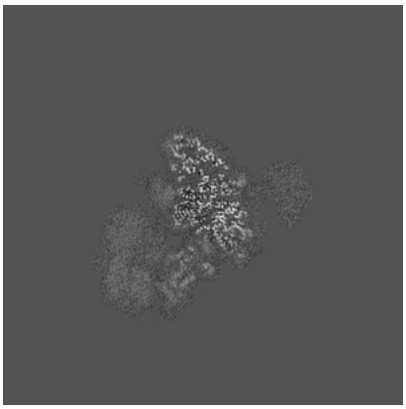
6.3.1 Primary map



X Index: 244

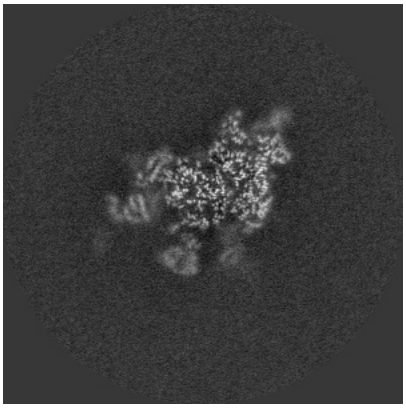


Y Index: 244

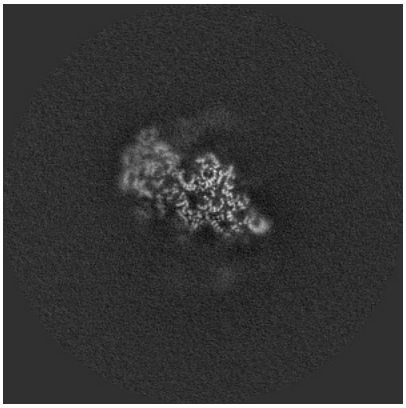


Z Index: 271

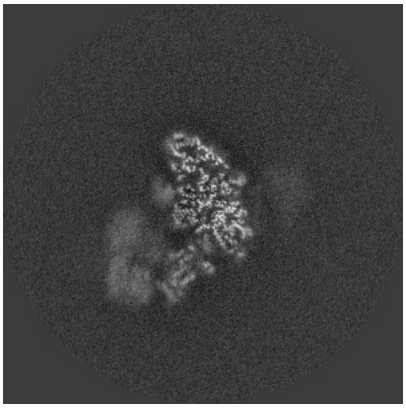
6.3.2 Raw map



X Index: 244



Y Index: 244

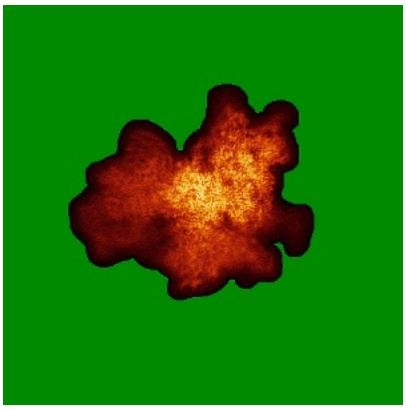


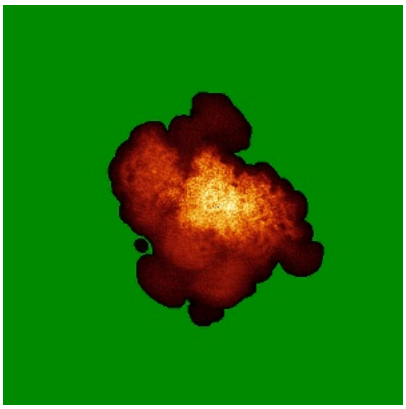
Z Index: 271

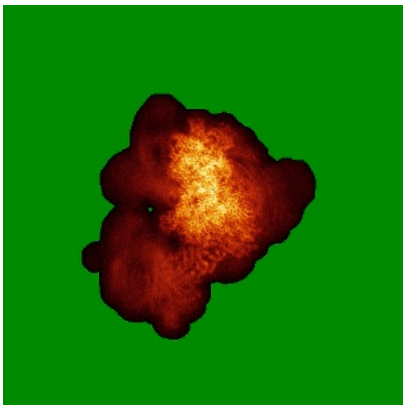
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

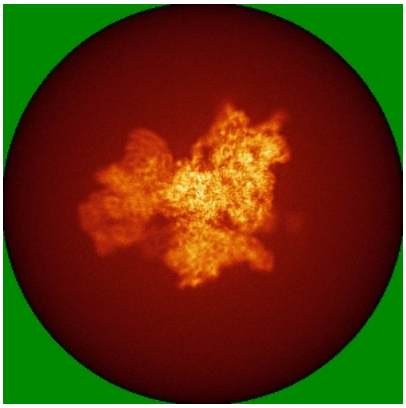
6.4.1 Primary map

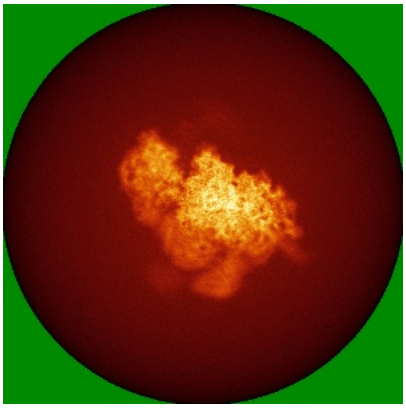

X

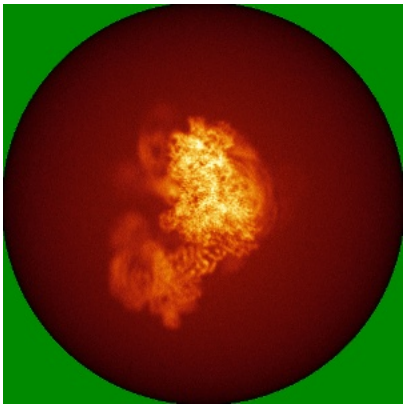

Y


Z

6.4.2 Raw map


X

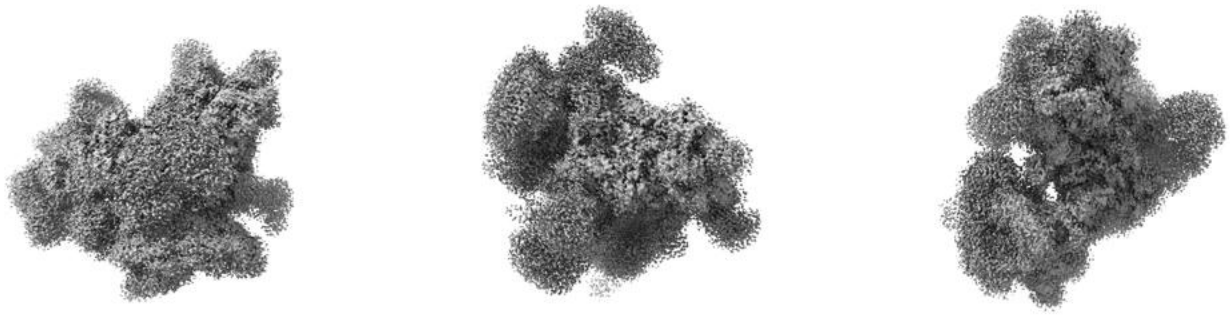

Y


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map

X Y Z

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

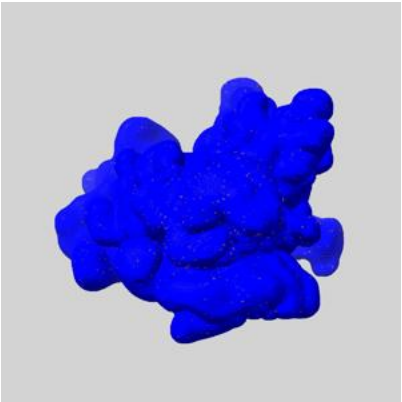
6.6 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

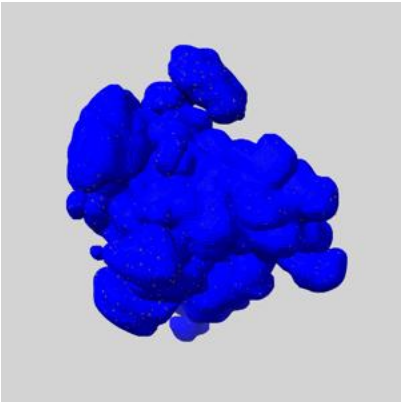
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

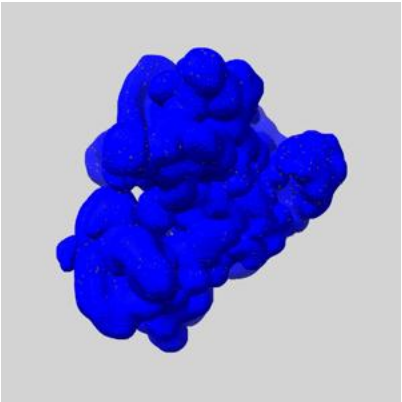
6.6.1 emd_11302_msk_1.map (i)



X



Y

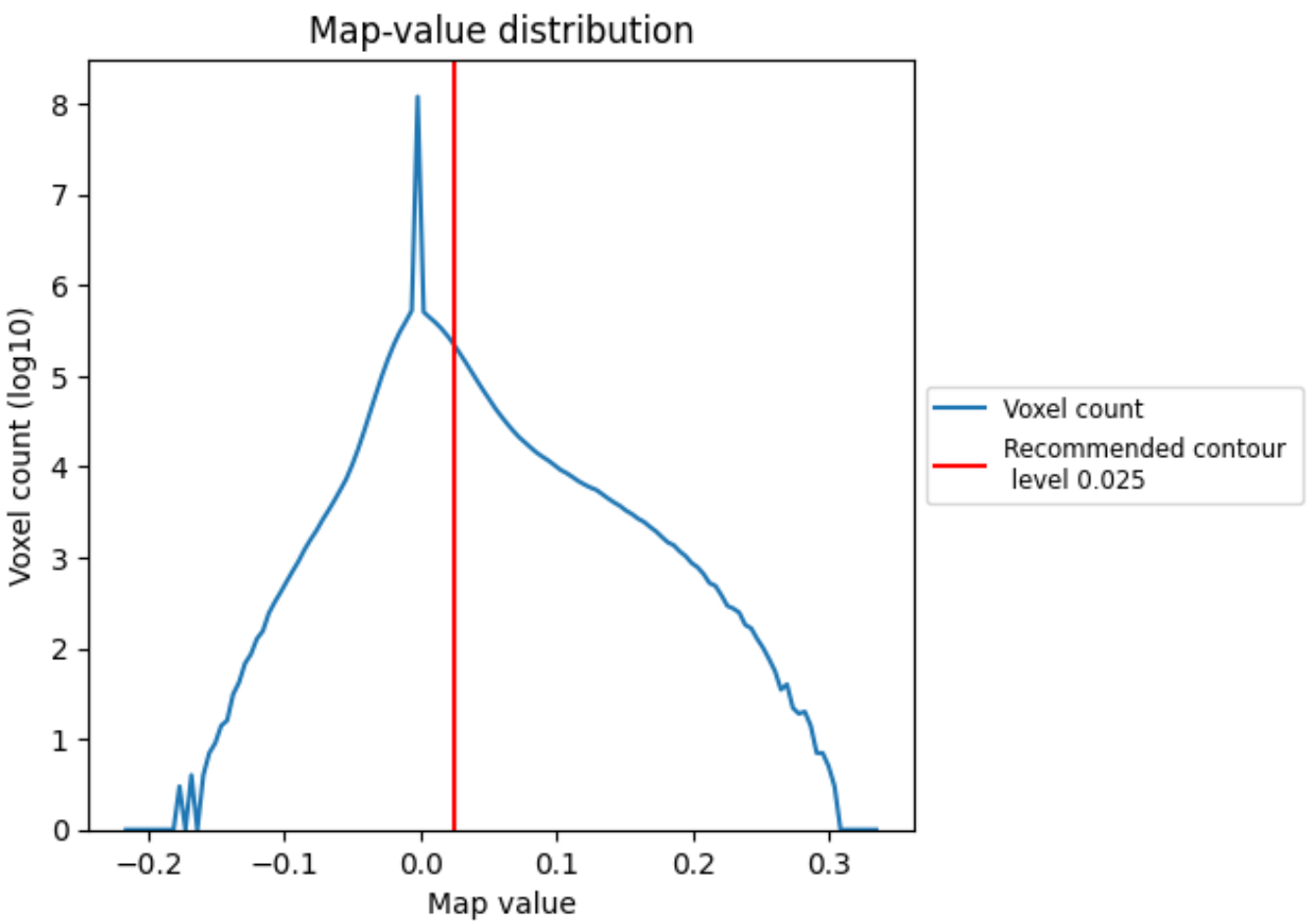


Z

7 Map analysis (i)

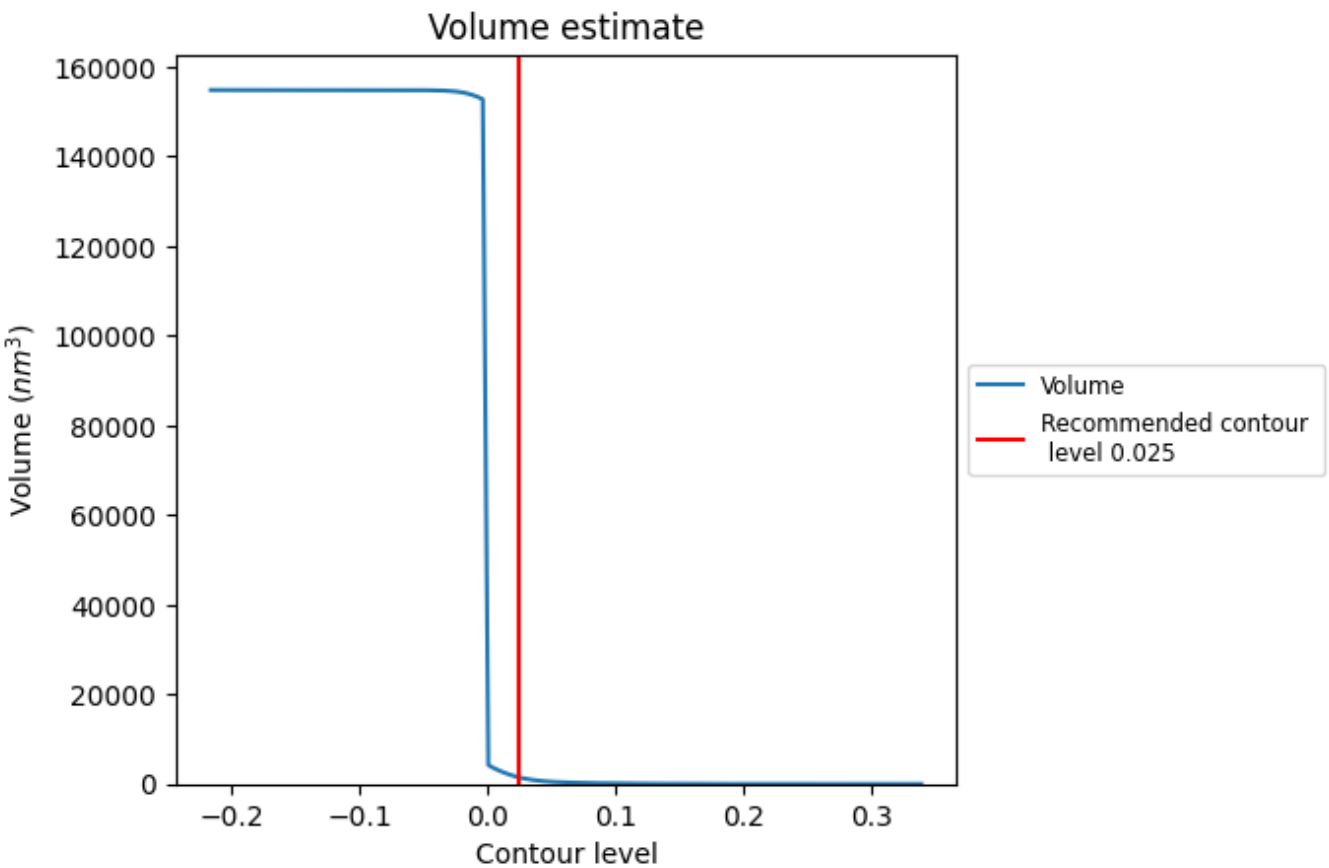
This section contains the results of statistical analysis of the map.

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.

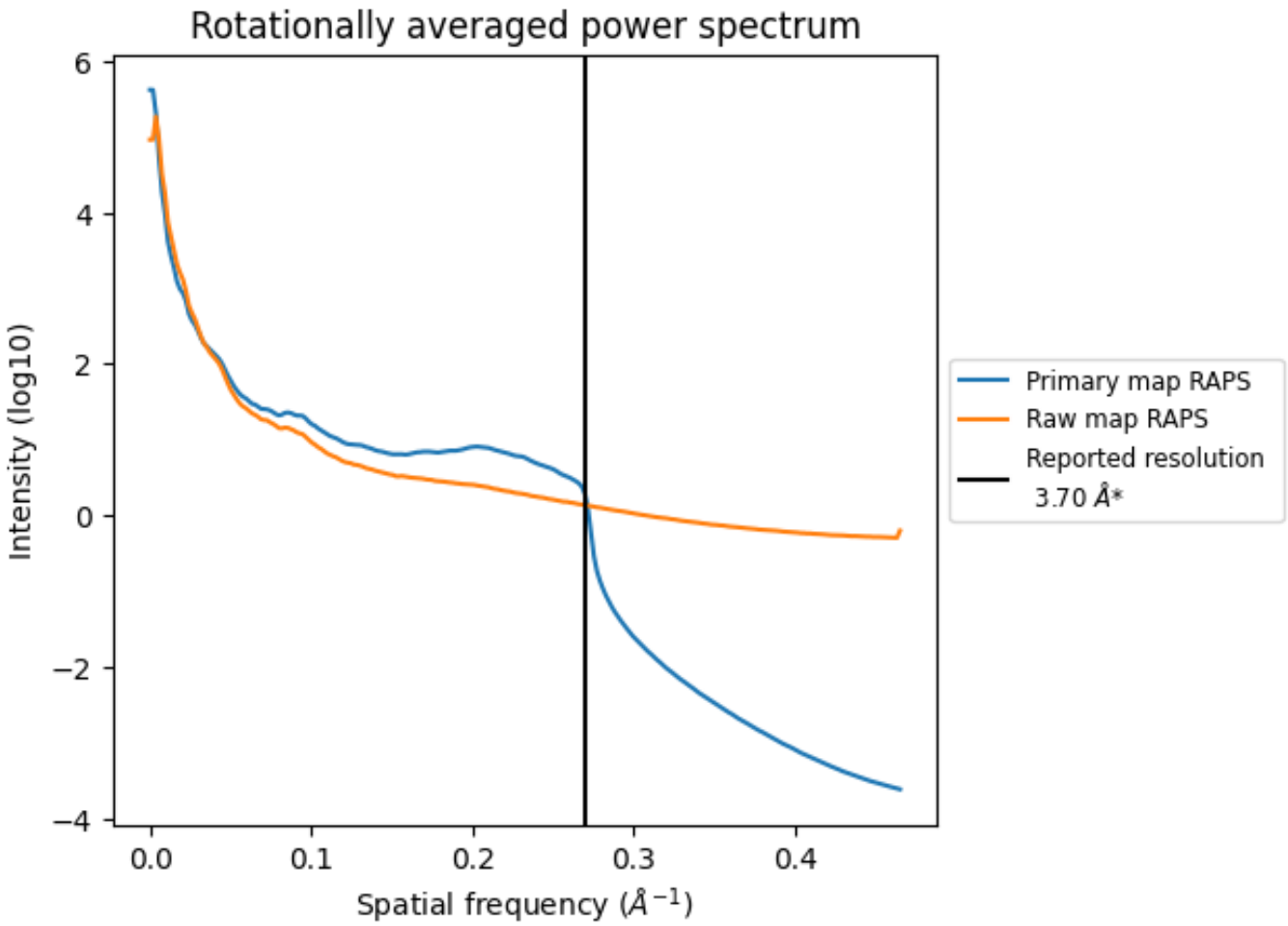
7.2 Volume estimate (i)



The volume at the recommended contour level is 1449 nm^3; this corresponds to an approximate mass of 1309 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 (i)

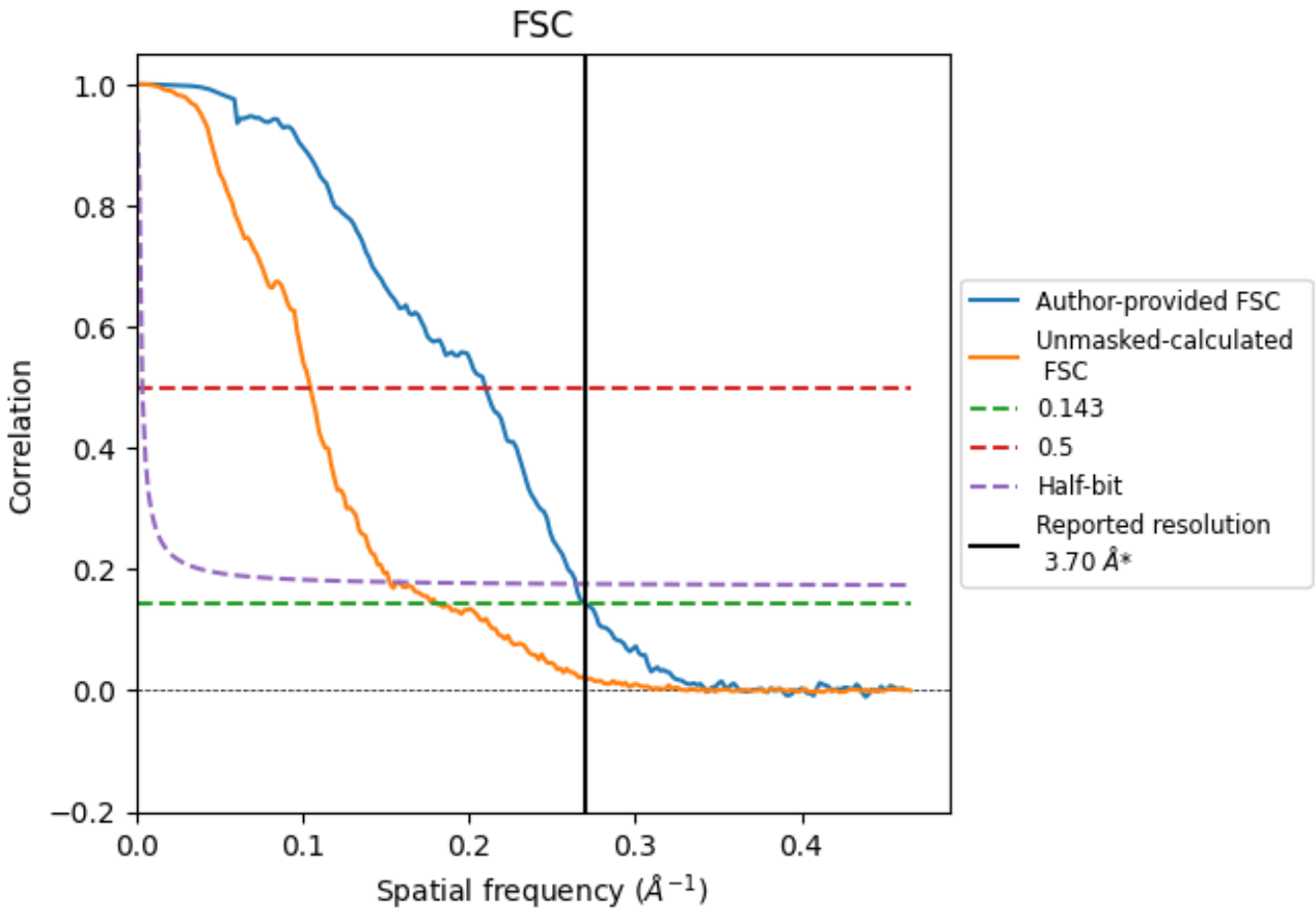


*Reported resolution corresponds to spatial frequency of 0.270 Å^{-1}

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 0.270 Å^{-1}

8.2 Resolution estimates (i)

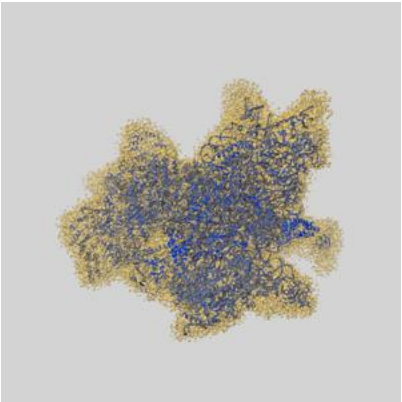
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.70	4.76	3.78
Unmasked-calculated*	5.54	9.55	6.56

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.54 differs from the reported value 3.7 by more than 10 %

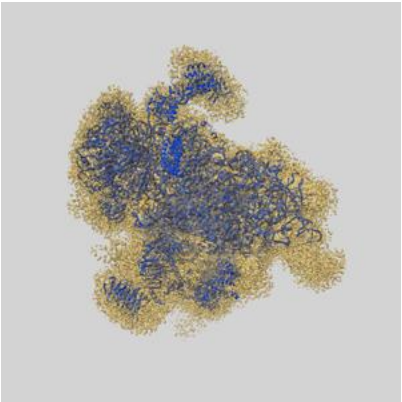
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-11302 and PDB model 6ZMW. Per-residue inclusion information can be found in section 3 on page 15.

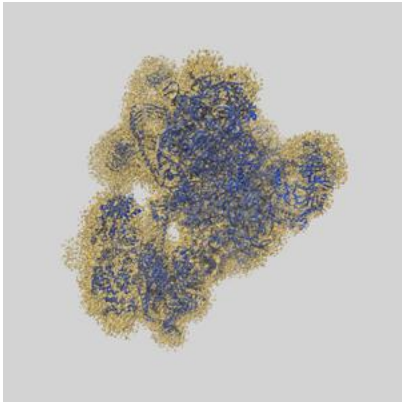
9.1 Map-model overlay (i)



X



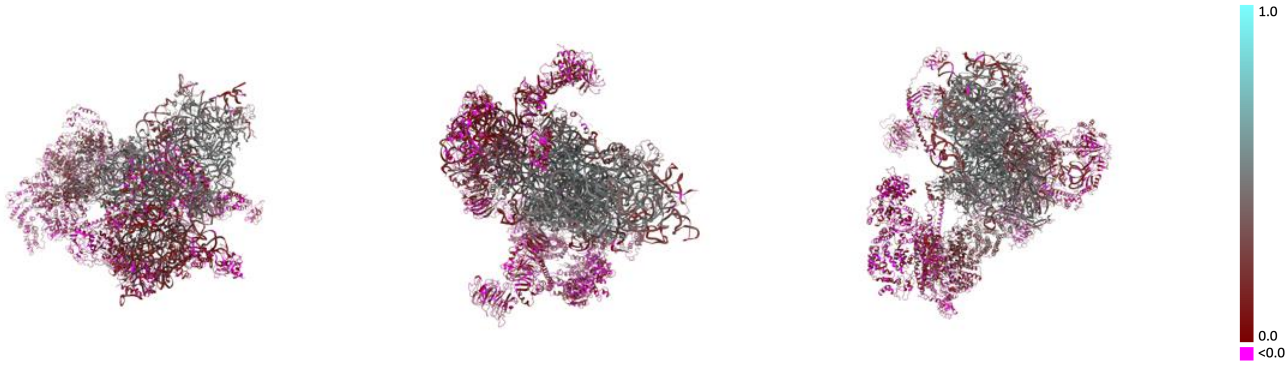
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.025 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.

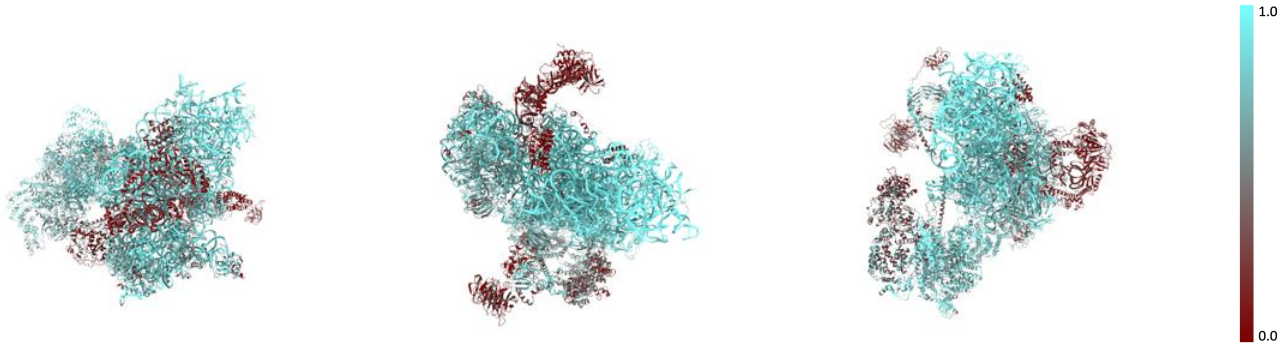
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

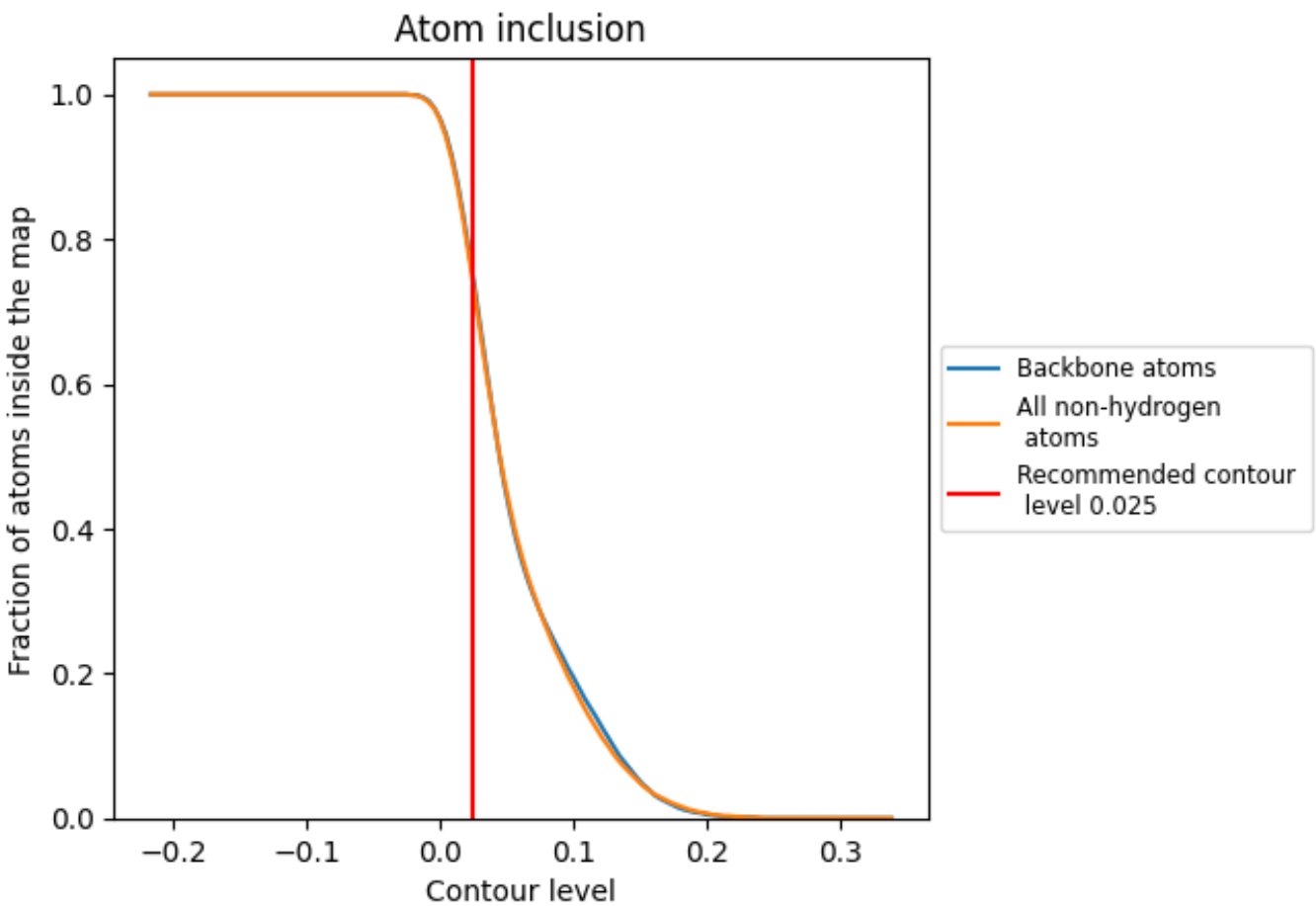
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.025).

9.4 Atom inclusion (i)



At the recommended contour level, 75% of all backbone atoms, 74% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7430	0.2930
1	0.5380	0.1670
2	0.1960	0.1120
3	0.6320	0.1030
4	0.6660	0.1060
5	0.6180	0.1130
6	0.7170	0.1180
7	0.2230	0.1670
8	0.6360	0.1240
9	0.8180	0.4460
A	0.9520	0.3820
B	0.9230	0.4960
C	0.9230	0.5070
D	0.9080	0.4880
E	0.9250	0.5170
F	0.9120	0.4880
G	0.8600	0.4030
H	0.8970	0.4780
I	0.9040	0.4790
J	0.9110	0.5190
K	0.8870	0.4740
L	0.8660	0.4630
M	0.8020	0.3830
N	0.9090	0.4780
O	0.8840	0.4420
P	0.8680	0.4280
Q	0.9070	0.4850
R	0.9180	0.4460
S	0.9230	0.4040
T	0.9260	0.4690
V	0.6710	0.1900
Y	0.7280	0.2530
Z	0.7390	0.3100
a	0.7030	0.1760
b	0.5820	0.0970

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
c	0.7180	0.1900
d	0.6890	0.1350
e	0.6250	0.1070
f	0.6540	0.1310
g	0.3190	0.0700
h	0.7650	0.3260
i	0.8130	0.2940
j	0.3680	0.0680
k	0.6610	0.0570
m	0.5900	0.0640
n	0.5540	0.1890
o	0.5360	0.1060
p	0.7190	0.3500
q	0.4400	0.2350
r	0.1020	0.1310
s	0.0940	0.1190
t	0.1420	0.1150
u	0.7290	0.2270
v	0.7640	0.1550
w	0.1860	0.1340
x	0.3490	0.1270
y	0.6920	0.2760
z	0.0810	0.1120