wwPDB EM Validation Summary Report (i)

Dec 31, 2024 – 08:44 PM EST

PDB ID	:	8PJ1
EMDB ID	:	EMD-17696
Title	:	Structure of human 48S translation initiation complex in open codon scanning state (48S-1)
Authors	:	Petrychenko, V.; Yi, S.-H.; Liedtke, D.; Peng, B.Z.; Rodnina, M.V.; Fischer, N.
Deposited on	:	2023-06-22
Resolution	:	3.40 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 (i)) were used in the production of this report:

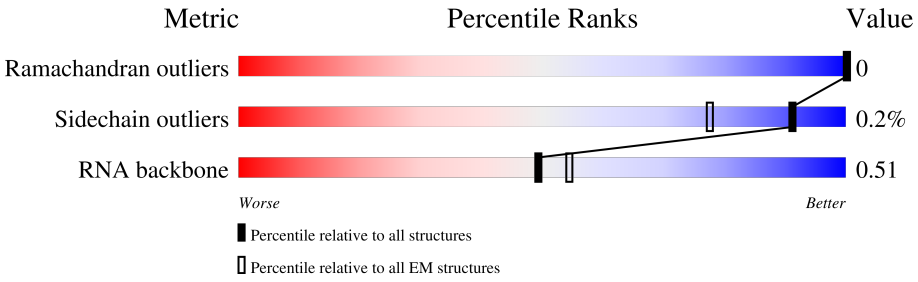
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

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 3.40 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.



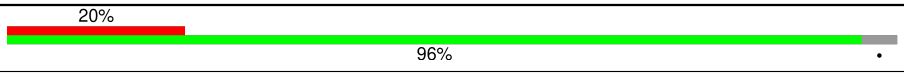
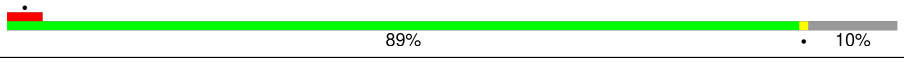
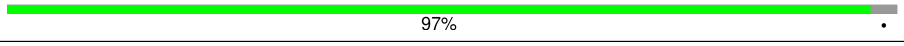
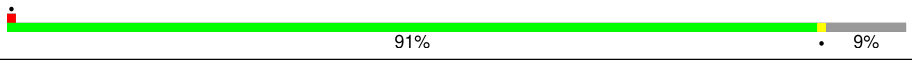
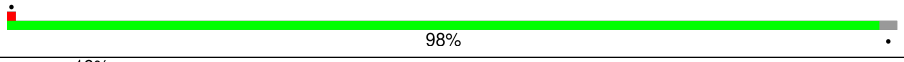
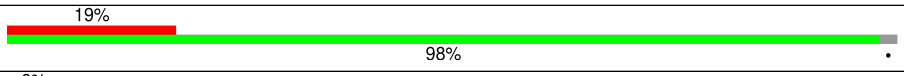
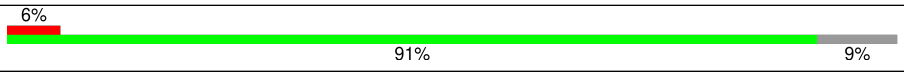
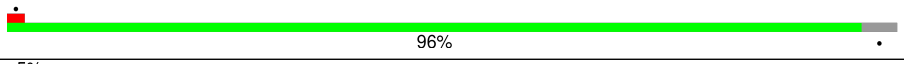
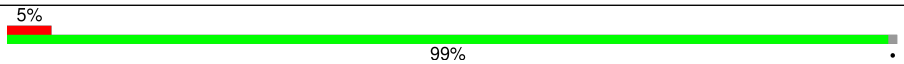
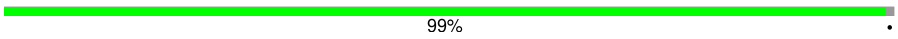
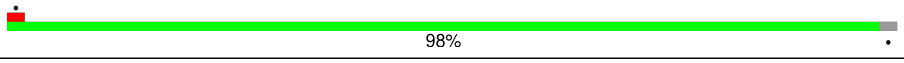
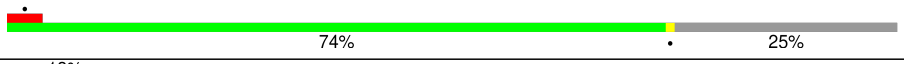
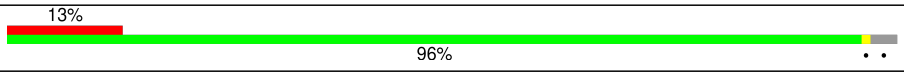
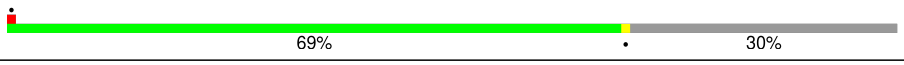
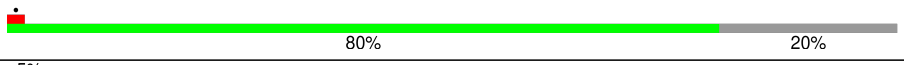
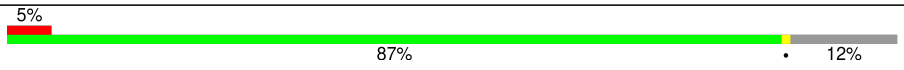
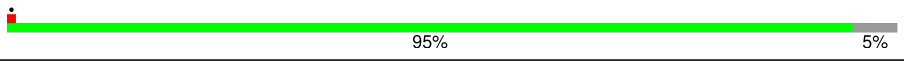
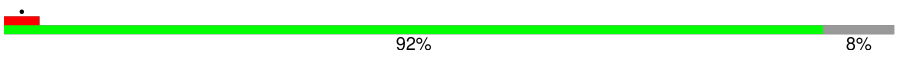
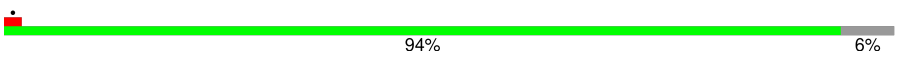
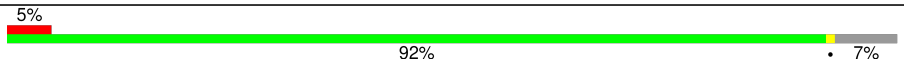
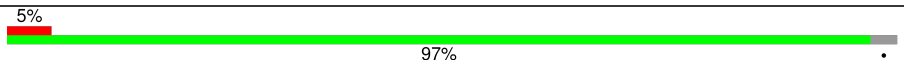
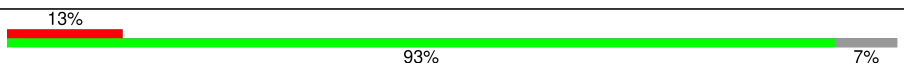
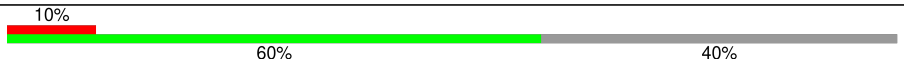
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	1	814	72% 72% 28%
2	2	325	94% 94% 6%
3	3	218	96% 98% .
4	4	357	62% 72% 28%
5	5	564	89% 92% 8%
6	6	374	84% 97% .
7	7	255	13% 5% 13% 82%
8	8	352	75% 90% 10%

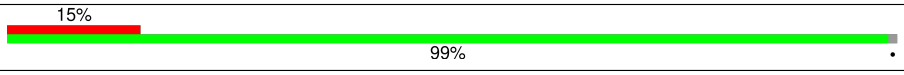
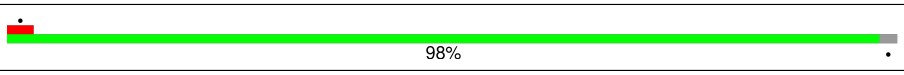
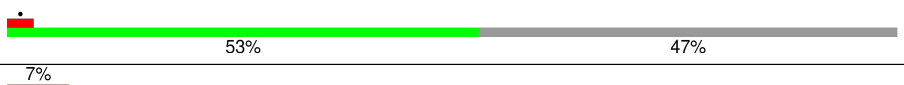
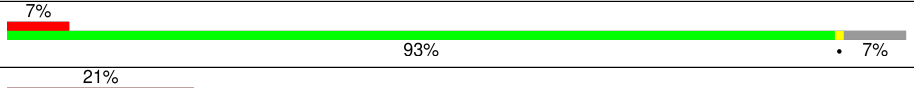
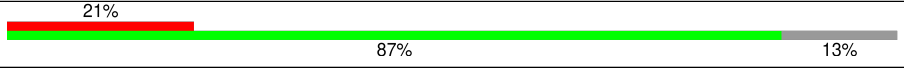
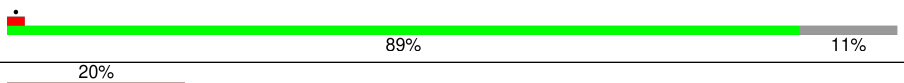
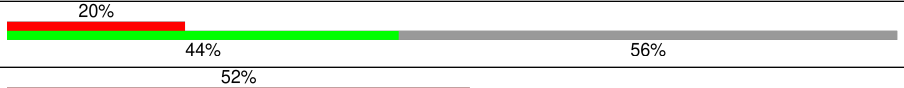
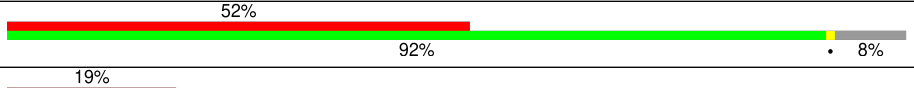
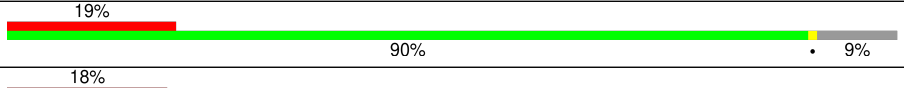
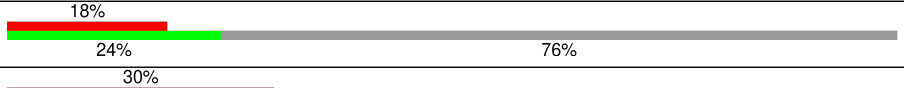
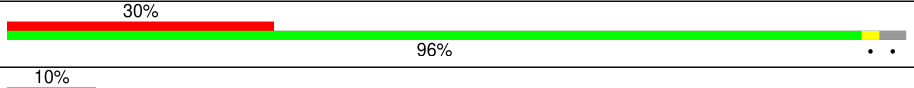
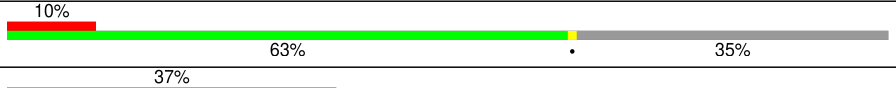
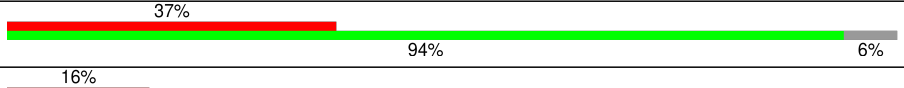
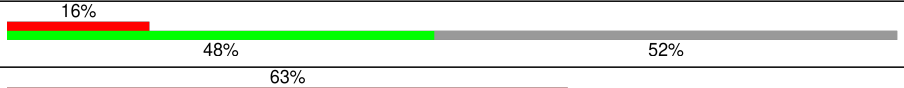
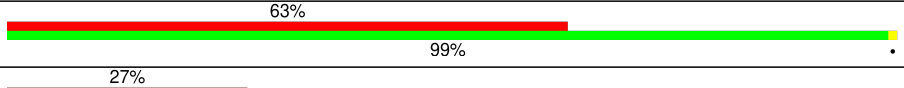
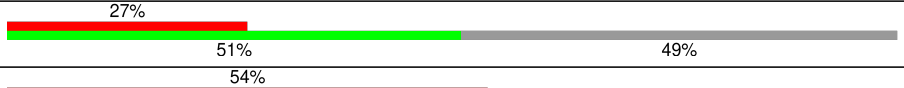
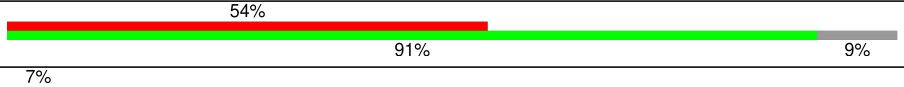
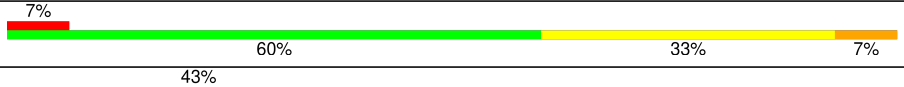
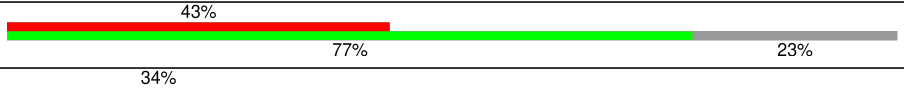
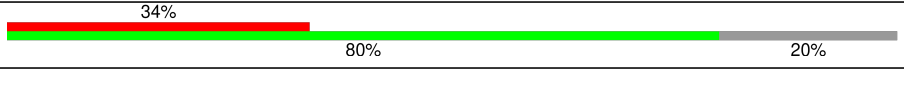
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	9	25	
10	A	1869	
11	B	158	
12	C	263	
13	D	194	
14	E	143	
15	F	59	
16	G	194	
17	H	84	
18	I	151	
19	J	130	
20	K	83	
21	L	293	
22	M	135	
23	N	295	
24	O	264	
25	P	151	
26	Q	115	
27	R	208	
28	S	249	
29	T	133	
30	V	204	
31	Y	146	
32	Z	243	
33	a	165	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	b	145	
35	c	317	
36	d	145	
37	e	125	
38	f	152	
39	h	119	
40	i	56	
41	k	157	
42	m	132	
43	n	69	
44	o	320	
45	p	113	
46	q	144	
47	r	315	
48	s	333	
49	t	472	
50	u	1382	
51	v	445	
52	w	75	
53	x	548	
54	y	913	

2 Entry composition (i)

There are 58 unique types of molecules in this entry. The entry contains 119663 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 B.

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

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	3	213	1057	631	213	213	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 L.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	5	520	4347	2814	721	793	19	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	6	362	2196	1348	414	427	7	0	0

- Molecule 7 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	47	Total	C	N	O	P	0	0
			1003	453	199	304	47		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
8	8	317	Total	C	N	O	0	0
			1574	937	318	319		

- Molecule 9 is a protein called 60S ribosomal protein L41.

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

- Molecule 10 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	A	1754	Total	C	N	O	P	0	0
			37429	16718	6714	12244	1753		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1248	B8N	U	conflict	GB NR_046235.3

- Molecule 11 is a protein called 40S ribosomal protein S11.

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

- Molecule 12 is a protein called 40S ribosomal protein S4, X isoform.

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

- Molecule 13 is a protein called 40S ribosomal protein S9.

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

- Molecule 14 is a protein called 40S ribosomal protein S23.

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

- Molecule 15 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	F	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 16 is a protein called 40S ribosomal protein S7.

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

- Molecule 17 is a protein called 40S ribosomal protein S27.

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

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

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

- Molecule 19 is a protein called 40S ribosomal protein S15a.

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

- Molecule 20 is a protein called 40S ribosomal protein S21.

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

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

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

- Molecule 22 is a protein called 40S ribosomal protein S17.

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

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

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

- Molecule 24 is a protein called 40S ribosomal protein S3a.

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

- Molecule 25 is a protein called 40S ribosomal protein S14.

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

- Molecule 26 is a protein called 40S ribosomal protein S26.

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

- Molecule 27 is a protein called 40S ribosomal protein S8.

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

- Molecule 28 is a protein called 40S ribosomal protein S6.

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

- Molecule 29 is a protein called 40S ribosomal protein S24.

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

- Molecule 30 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	V	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 31 is a protein called 40S ribosomal protein S16.

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

- Molecule 32 is a protein called 40S ribosomal protein S3.

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

- Molecule 33 is a protein called 40S ribosomal protein S10.

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

- Molecule 34 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	121	Total	C	N	O	S	0	0
			989	628	185	169	7		

- Molecule 35 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 36 is a protein called 40S ribosomal protein S19.

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

- Molecule 37 is a protein called 40S ribosomal protein S25.

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

- Molecule 38 is a protein called 40S ribosomal protein S18.

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

- Molecule 39 is a protein called 40S ribosomal protein S20.

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

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

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

- Molecule 41 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	69	Total	C	N	O	S	0	0
			559	352	104	96	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	87	ALA	-	insertion	UNP P62979

- Molecule 42 is a protein called 40S ribosomal protein S12.

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

- Molecule 43 is a protein called 40S ribosomal protein S28.

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

- Molecule 44 is a protein called Eukaryotic translation initiation factor 3 subunit G.

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

- Molecule 45 is a protein called Eukaryotic translation initiation factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	p	110	Total	C	N	O	S	0	0
			830	524	150	154	2		

- Molecule 46 is a protein called Eukaryotic translation initiation factor 1A, X-chromosomal.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	93	Total	C	N	O	S	0	0
			754	476	137	137	4		

- Molecule 47 is a protein called Eukaryotic translation initiation factor 2 subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	296	Total	C	N	O	S	0	0
			2138	1342	384	404	8		

- Molecule 48 is a protein called Eukaryotic translation initiation factor 2 subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	s	159	Total	C	N	O	S	0	0
			1275	804	236	226	9		

- Molecule 49 is a protein called Eukaryotic translation initiation factor 2 subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	t	472	Total	C	N	O	S	0	0
			3586	2272	628	668	18		

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

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

- Molecule 51 is a protein called Eukaryotic translation initiation factor 3 subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	v	405	Total	C	N	O	S	0	0
			2740	1720	498	510	12		

- Molecule 52 is a RNA chain called Initiator Met-tRNA-i.

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

- Molecule 53 is a protein called Eukaryotic translation initiation factor 3 subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	x	423	Total	C	N	O	S	0	0
			2842	1752	523	557	10		

- Molecule 54 is a protein called Eukaryotic translation initiation factor 3 subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	y	731	Total	C	N	O	S	0	0
			5657	3547	1018	1057	35		

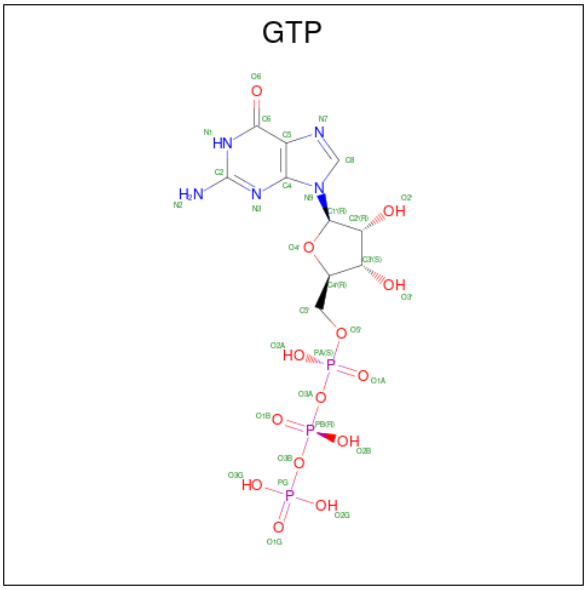
- Molecule 55 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
55	A	88	Total	Mg	0
			88	88	
55	f	1	Total	Mg	0
			1	1	
55	t	1	Total	Mg	0
			1	1	

- Molecule 56 is ZINC ION (three-letter code: ZN) (formula: Zn).

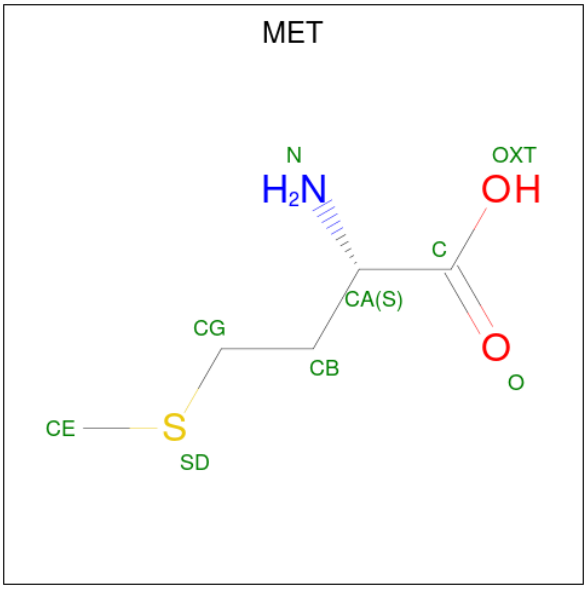
Mol	Chain	Residues	Atoms		AltConf
56	Q	1	Total	Zn	0
			1	1	
56	k	1	Total	Zn	0
			1	1	
56	s	1	Total	Zn	0
			1	1	

- Molecule 57 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
57	t	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 58 is METHIONINE (three-letter code: MET) (formula: $C_5H_{11}NO_2S$).



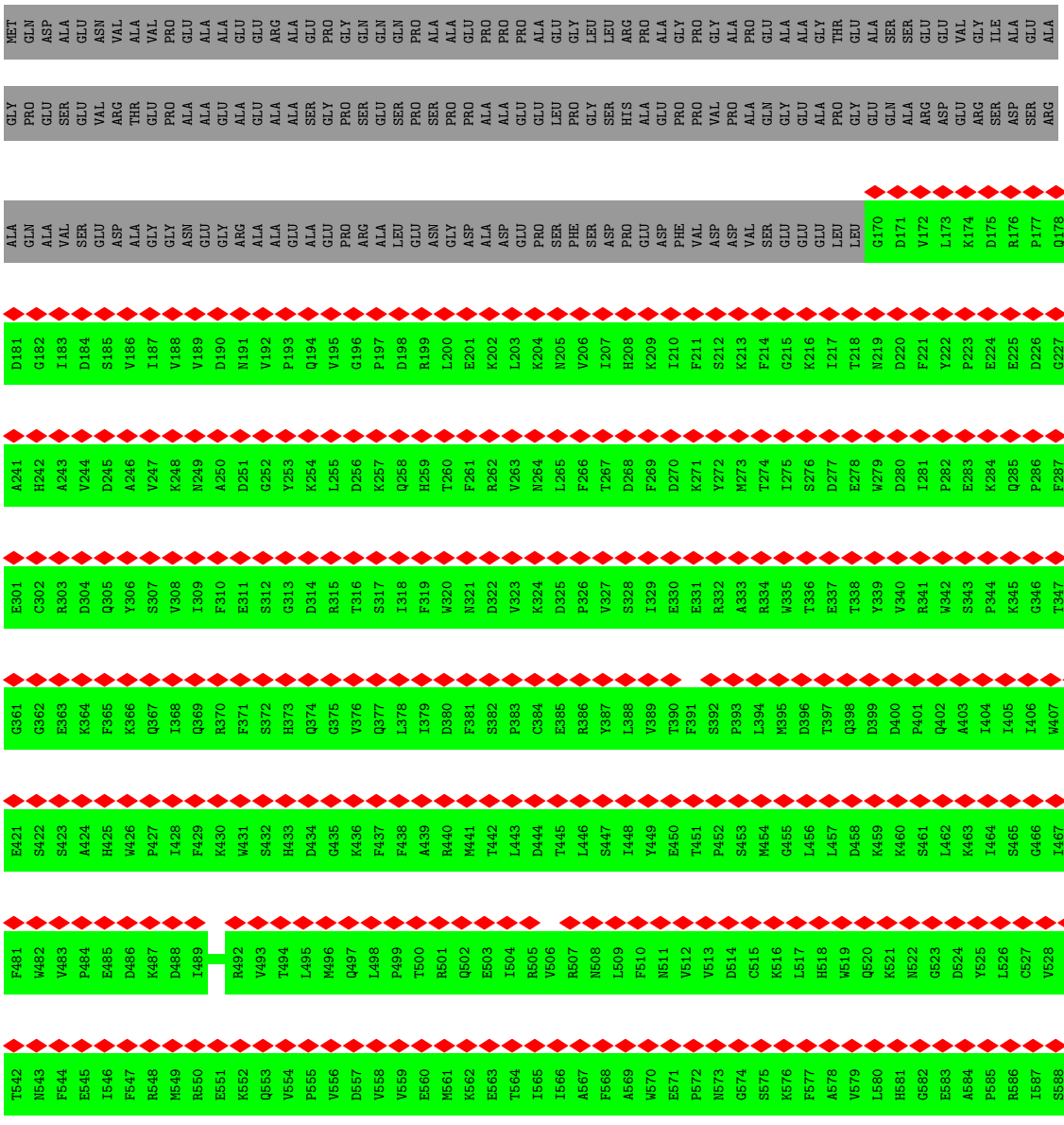
Mol	Chain	Residues	Atoms					AltConf
58	w	1	Total	C	N	O	S	0
			8	5	1	1	1	

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 B

Chain 1:



L602 I603 K604 M605 F606 D607 K608 Q609 Q610 A611 N612 T613 I614 F615 W616 S617 P618 Q619 G620 Q621 F622 V623 V624 L625 A626 G627 L628 R629 S630 M631 N632 G633 A634 L635 A636 F637 V638 D639 T640 S641 D642 C643 T644 V645 M646 N647 I648 A649 E650 H651 Y652 M653 A654 S655 D656 V657 E658 W659 D660 P661

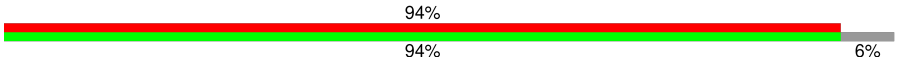
T662 G663 R664 Y665 V666 V667 T668 S669 V670 S671 W672 W673 S674 H675 K676 V677 D678 N679 A680 Y681 W682 L683 W684 T685 F686 Q687 G688 R689 L690 L691 Q692 K693 N694 N695 K696 D697 R698 F699 C700 Q701 L702 L703 W704 R705 P706 R707 P708 P709 T710 L711 L712 S713 Q714 E715 Q716 I717 K718 Q719 I720 K721

K722 D723 L724 K725 K726 Y727 S728 K729 I730 F731 E732 Q733 K734 D735 R736 L737 S738 Q739 S740 K741 A742 S743 K744 E745 L746 V747 E748 R749 R750 R751 T752 M753 M754 E755 D756 F757 R758 K759 Y760 R761 K762 M763 A764 GLN GLU LEU TYR MET GLU GLN LYS ASN GLU ARG LEU GLU LEU ARG GLY GLY

VAL ASP THR ASP GLU LEU ASP SER ASN VAL ASP ASP TRP GLU GLU GLU THR ILE GLU PHE PHE VAL THR GLU GLU ILE ILE PRO LEU GLY ASN GLN GLU

• Molecule 2: Eukaryotic translation initiation factor 3 subunit I

Chain 2:



M1 K2 P3 I4 L5 L6 Q7 G8 H9 E10 R11 S12 I13 T14 Q15 I16 K17 Y18 N19 R20 E21 G22 D23 L24 L25 F26 T27 V28 A29 K30 D31 P32 I33 V34 N35 V36 W37 Y38 S39 V40 N41 G42 E43 R44 L45 G46 T47 Y48 M49 G50 H51 T52 G53 A54 V55 W56 C57 V58 D59 A60

D61 W62 D63 T64 K65 H66 V67 L68 T69 G70 S71 A72 D73 N74 S75 C76 R77 L78 W79 D80 C81 E82 T83 G84 K85 Q86 L87 A88 L89 L90 K91 T92 N93 S94 A95 V96 R97 T98 C99 G100 F101 D102 F103 G104 G105 N106 I107 I108 M109 F110 S111 T112 ASP LYS GLN MET GLY TYR GLN CYS

F121 V122 S123 F124 F125 D126 L127 R128 D129 P130 S131 Q132 I133 D134 N135 N136 E137 P138 Y139 M140 K141 I142 P143 C144 N145 D146 S147 K148 I149 T150 S151 A152 V153 W154 G155 P156 L157 G158 E159 C160 I161 I162 A163 G164 H165 E166 S167 G168 E169 L170 N171 Q172 Y173 S174 A175 K176 S177 G178 E179 V180

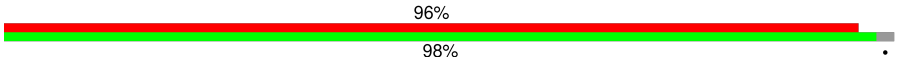
L181 V182 N183 V184 K185 E186 H187 S188 R189 Q190 I191 N192 D193 I194 Q195 L196 S197 R198 D199 M200 T201 M202 F203 V204 T205 A206 S207 K208 D209 N210 T211 A212 K213 L214 F215 D216 S217 T218 T219 L220 E221 H222 Q223 K224 T225 F226 R227 T228 E229 R230 P231 V232 N233 S234 A235 A236 L237 S238 P239 N240

Y241 D242 H243 V244 V245 L246 G247 G248 G249 Q250 E251 A252 M253 D254 V255 T256 T257 T258 S259 T260 R261 I262 G263 K264 F265 E266 A267 R268 F269 F270 H271 L272 A273 F274 E275 E276 E277 F278 G279 R280 V281 K282 G283 H284 F285 G286 P287 I288 N289 S290 V291 A292 F293 H294 P295 D296 G297 K298 S299 Y300

S301 S302 G303 G304 E305 D306 G307 Y308 V309 R310 I311 H312 TYR PHE ASP PRO GLN TYR PHE GLU PHE GLU PHE GLU ALA

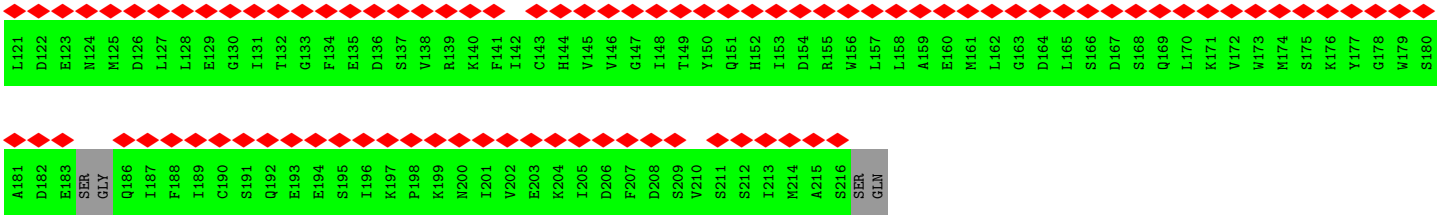
• Molecule 3: Eukaryotic translation initiation factor 3 subunit K

Chain 3:



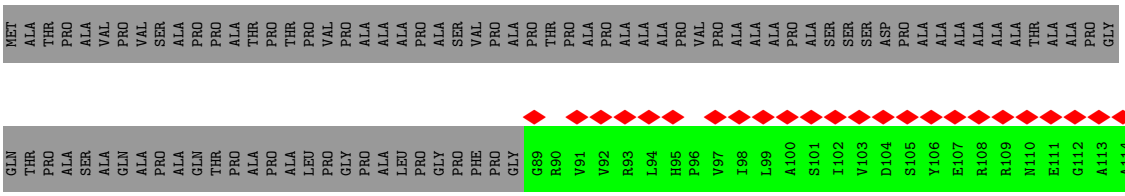
MET A2 M3 F4 E5 Q6 M7 R8 A9 N10 V11 G12 K13 L14 L15 K16 G17 I18 D19 R20 Y21 N22 P23 E24 N25 L26 A27 T28 L29 E30 R31 Y32 V33 E34 T35 Q36 A37 K38 E39 N40 A41 Y42 D43 L44 E45 A46 N47 L48 A49 V50 L51 K52 L53 Y54 Q55 F56 N57 P58 A59 F60

F61 Q62 T63 T64 V65 T66 A67 Q68 I69 L70 L71 K72 A73 L74 T75 N76 L77 P78 H79 T80 D81 F82 T83 L84 C85 K86 C87 M88 I89 D90 Q91 A92 H93 Q94 E95 E96 R97 P98 I99 R100 Q101 I102 L103 Y104 L105 G106 D107 L108 L109 E110 T111 C112 H113 F114 Q115 A116 F117 W118 Q119 A120



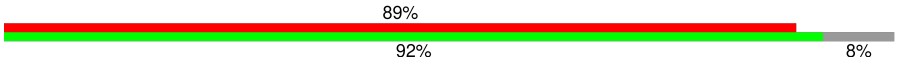
• Molecule 4: Eukaryotic translation initiation factor 3 subunit F

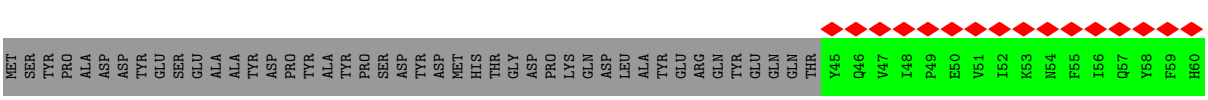
Chain 4:

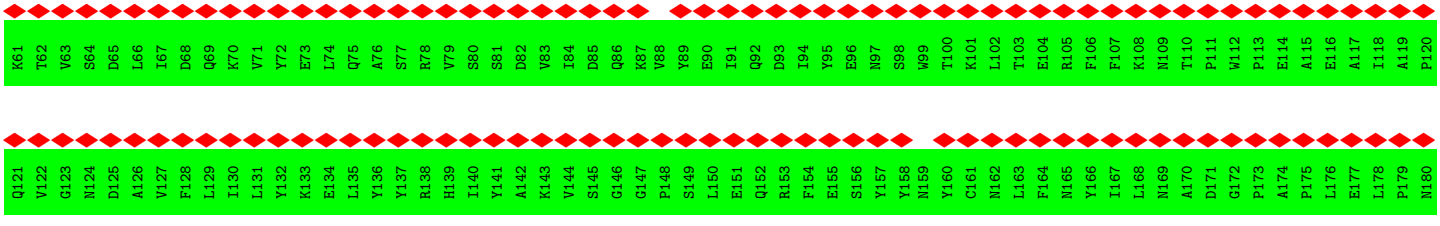


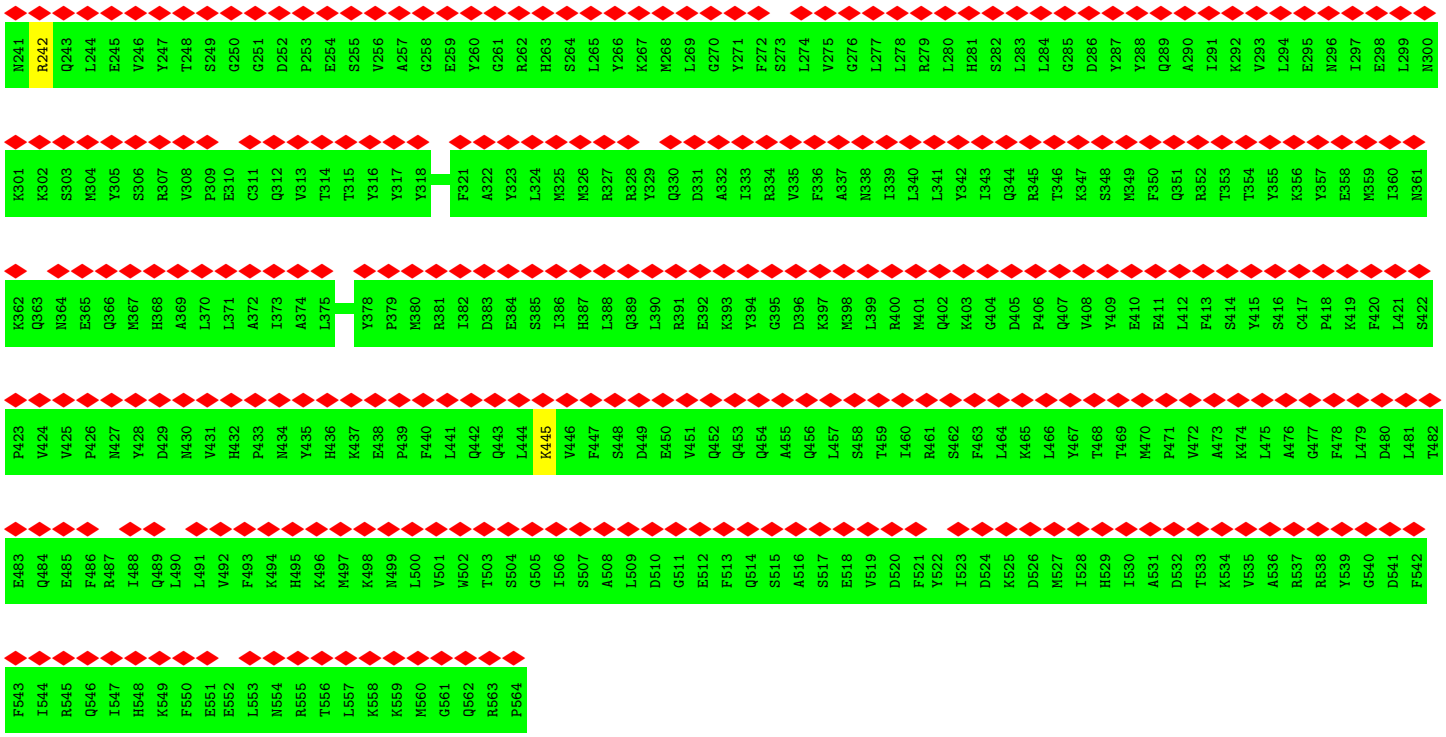
• Molecule 5: Eukaryotic translation initiation factor 3 subunit L

Chain 5:



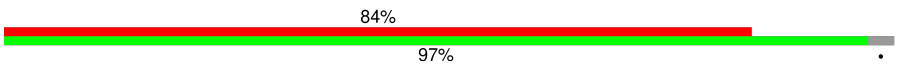


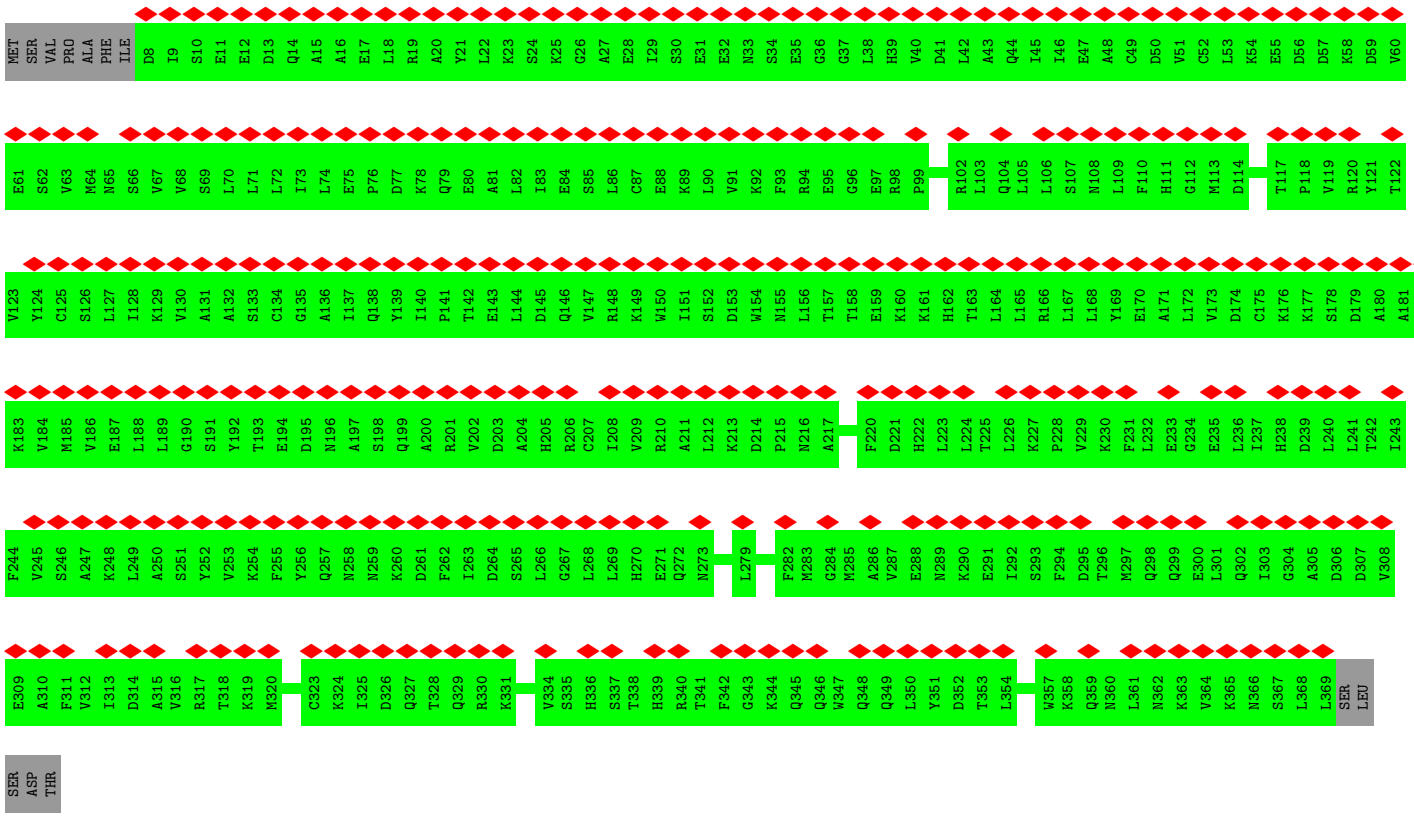




• Molecule 6: Eukaryotic translation initiation factor 3 subunit M

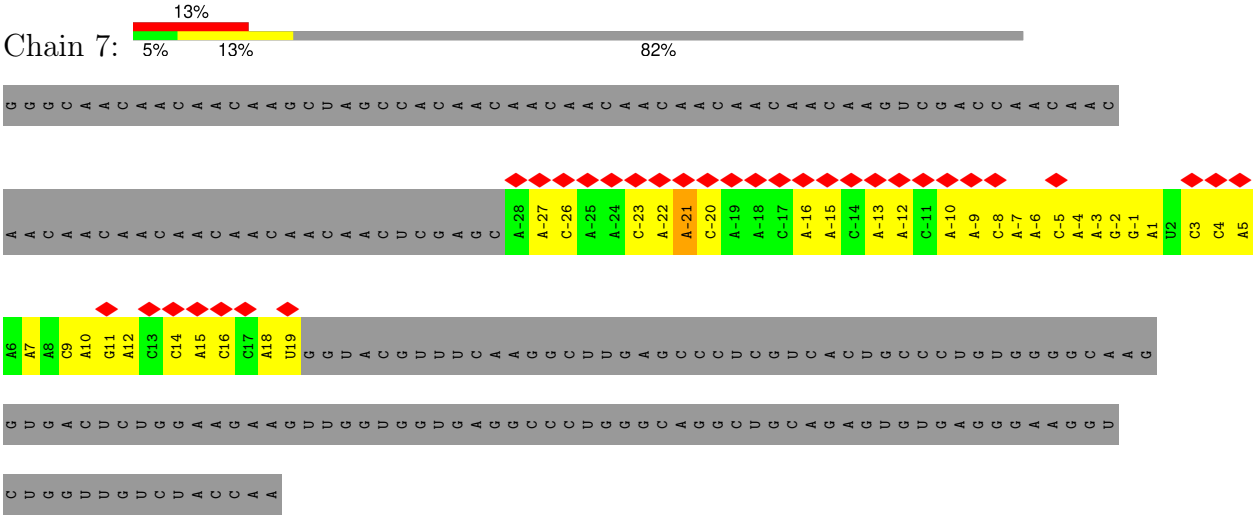
Chain 6:





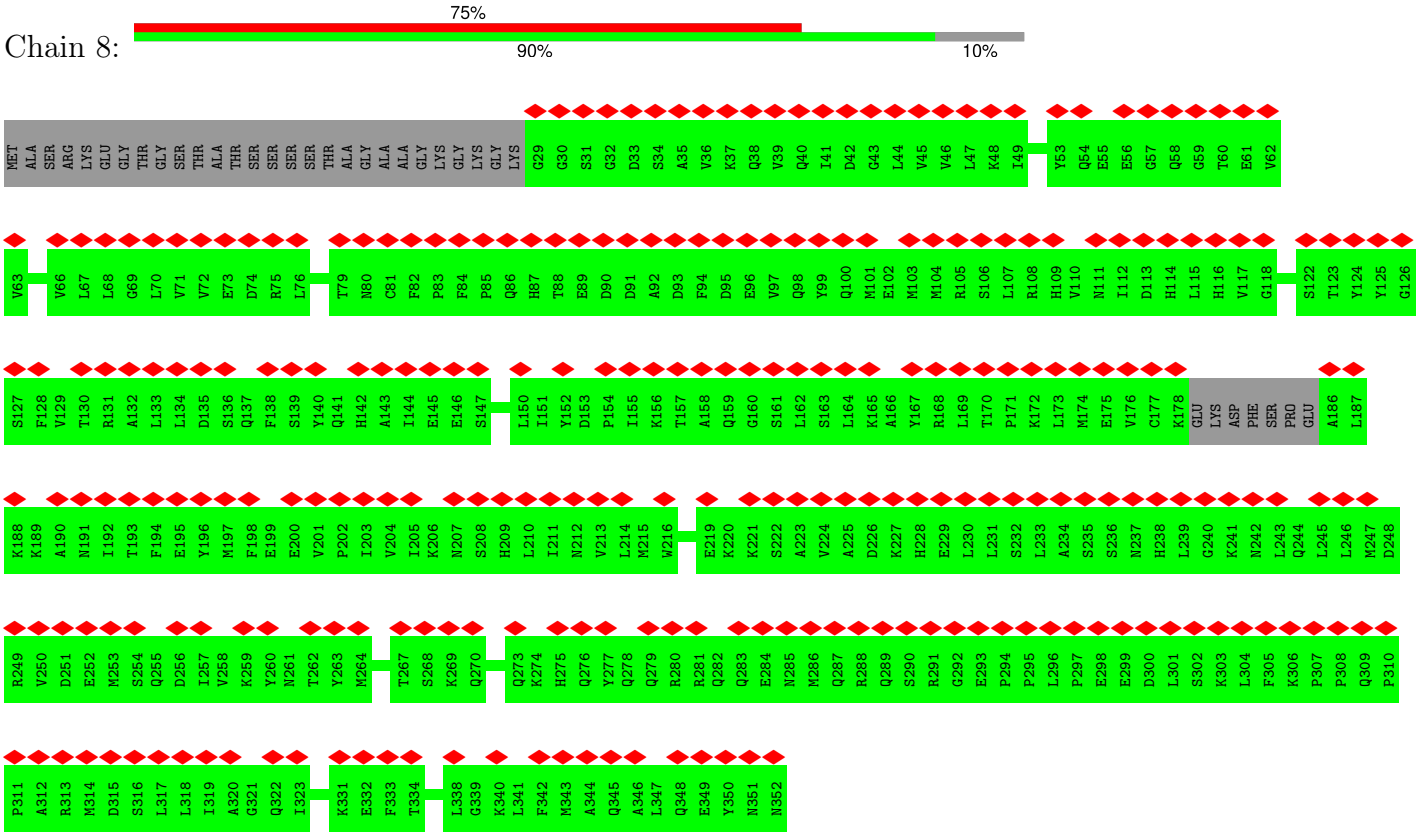
• Molecule 7: mRNA

Chain 7:



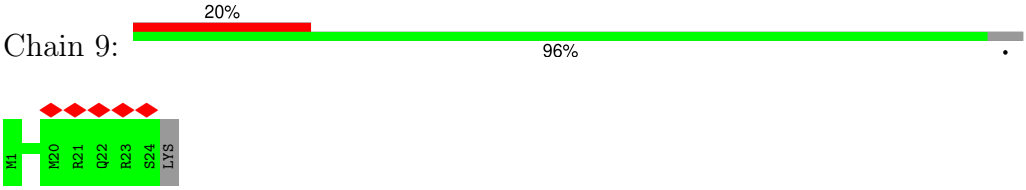
• Molecule 8: Eukaryotic translation initiation factor 3 subunit H

Chain 8:



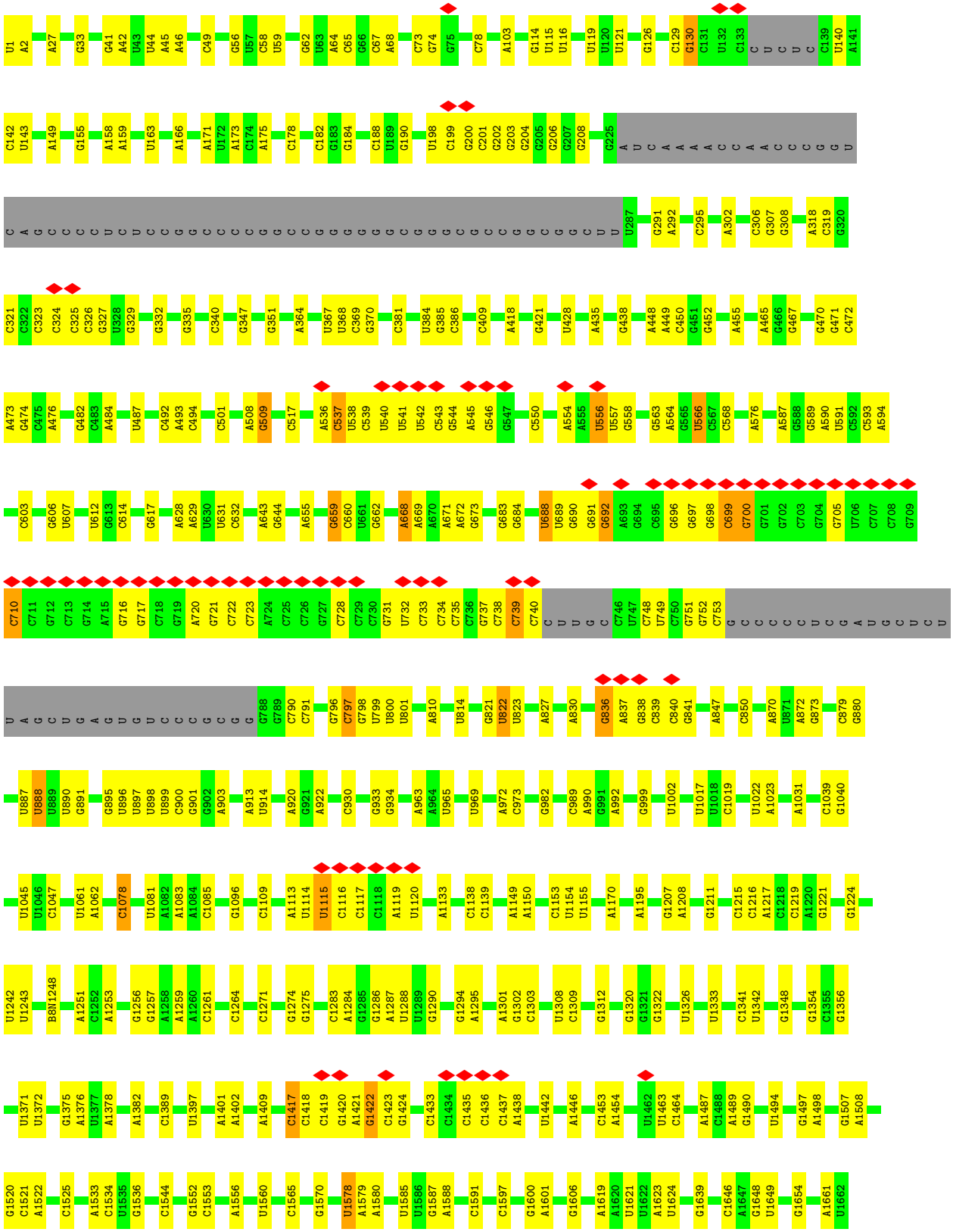
• Molecule 9: 60S ribosomal protein L41

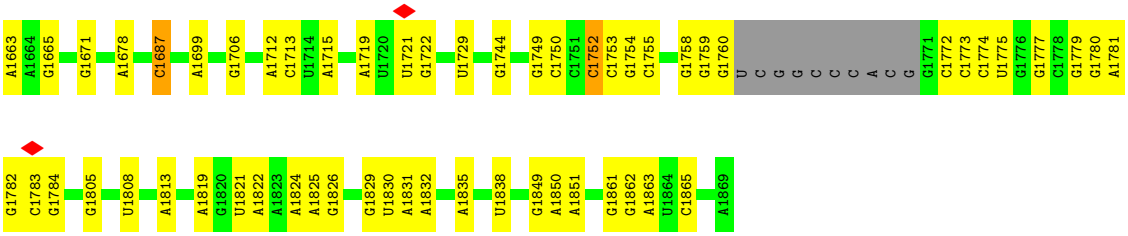
Chain 9:



• Molecule 10: 18S rRNA

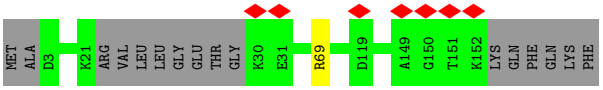
Chain A:





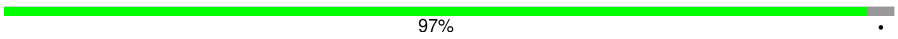
• Molecule 11: 40S ribosomal protein S11

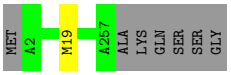
Chain B:



• Molecule 12: 40S ribosomal protein S4, X isoform

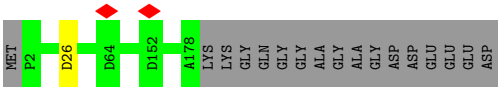
Chain C:





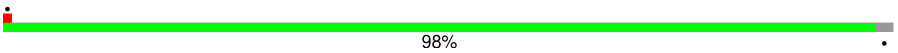
• Molecule 13: 40S ribosomal protein S9

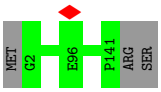
Chain D:



• Molecule 14: 40S ribosomal protein S23

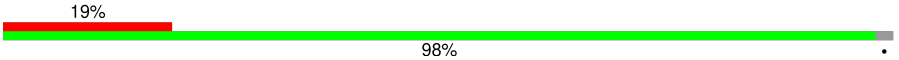
Chain E:

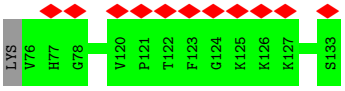




• Molecule 15: 40S ribosomal protein S30

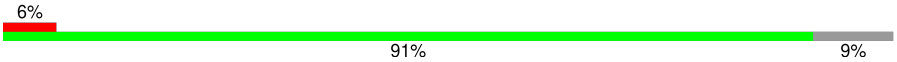
Chain F:

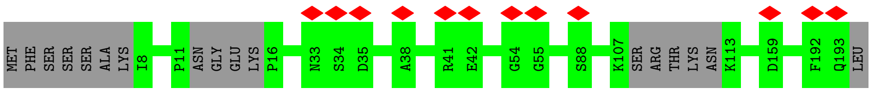




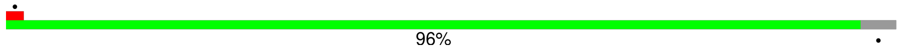
• Molecule 16: 40S ribosomal protein S7

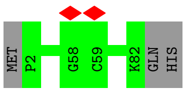
Chain G:



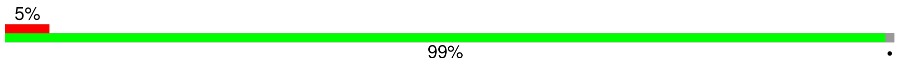


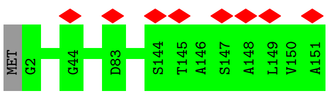
• Molecule 17: 40S ribosomal protein S27

Chain H: 

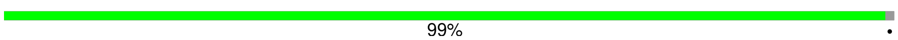


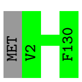
• Molecule 18: 40S ribosomal protein S13

Chain I: 

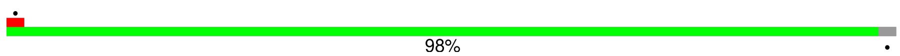


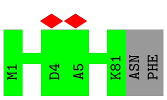
• Molecule 19: 40S ribosomal protein S15a

Chain J: 



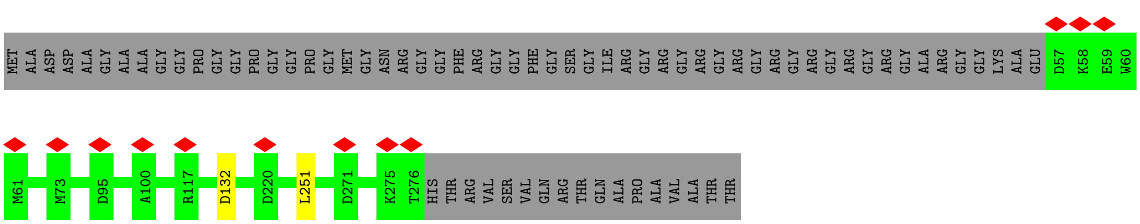
• Molecule 20: 40S ribosomal protein S21

Chain K: 



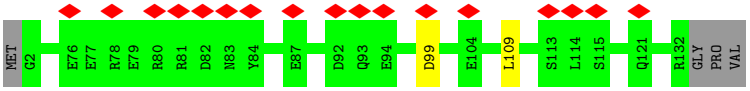
• Molecule 21: 40S ribosomal protein S2

Chain L: 



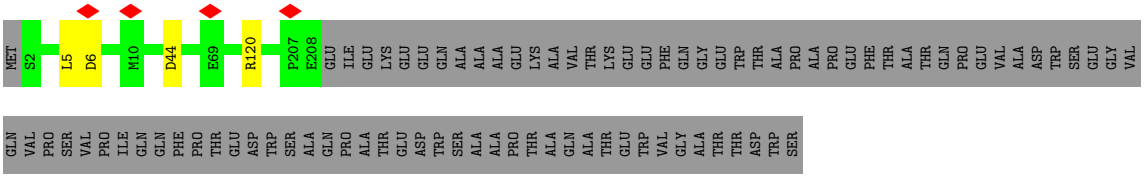
• Molecule 22: 40S ribosomal protein S17

Chain M: 



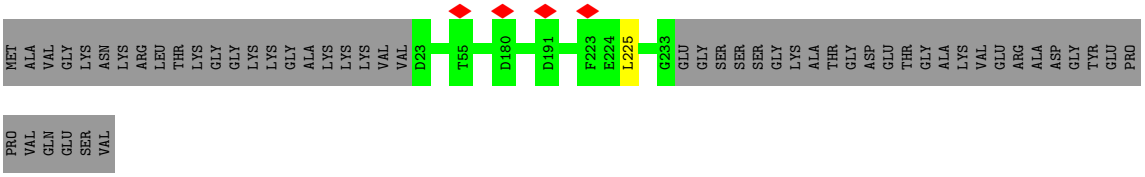
• Molecule 23: 40S ribosomal protein SA

Chain N:



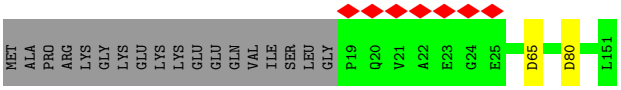
• Molecule 24: 40S ribosomal protein S3a

Chain O:



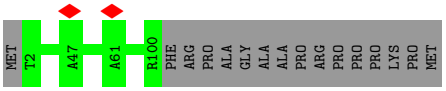
• Molecule 25: 40S ribosomal protein S14

Chain P:



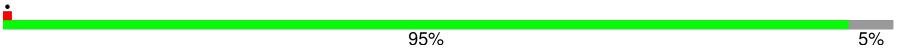
• Molecule 26: 40S ribosomal protein S26

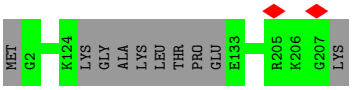
Chain Q:



• Molecule 27: 40S ribosomal protein S8

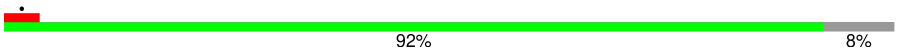
Chain R:

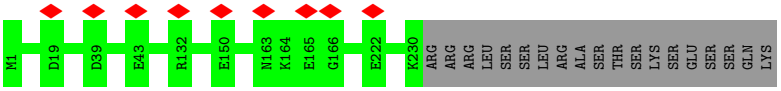




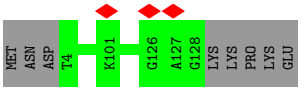
• Molecule 28: 40S ribosomal protein S6

Chain S:

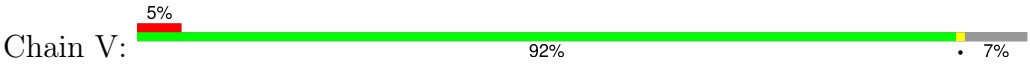


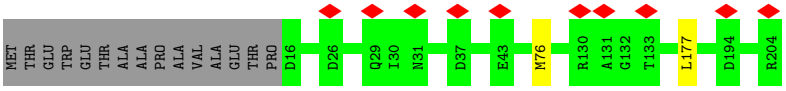


• Molecule 29: 40S ribosomal protein S24

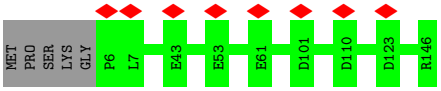


• Molecule 30: 40S ribosomal protein S5

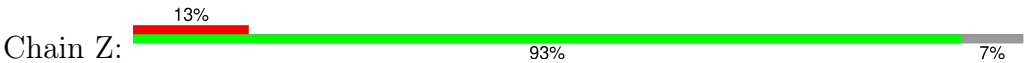


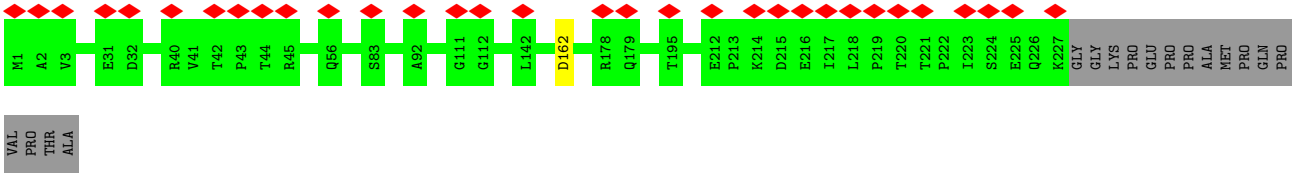


• Molecule 31: 40S ribosomal protein S16

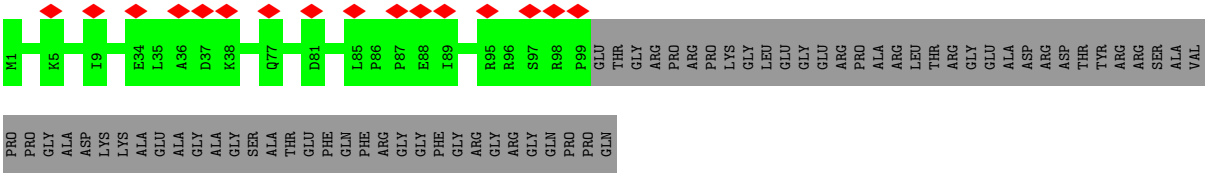


• Molecule 32: 40S ribosomal protein S3

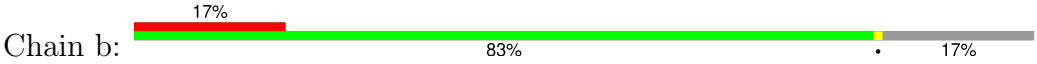


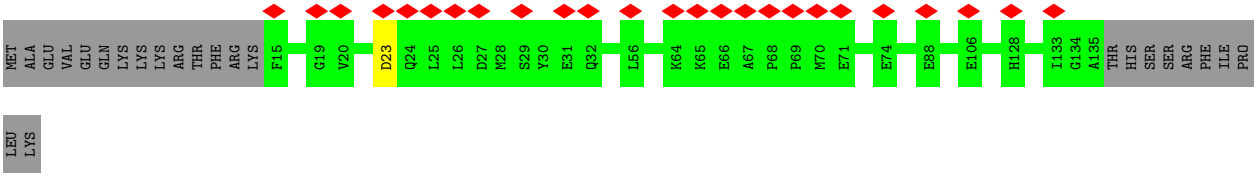


• Molecule 33: 40S ribosomal protein S10

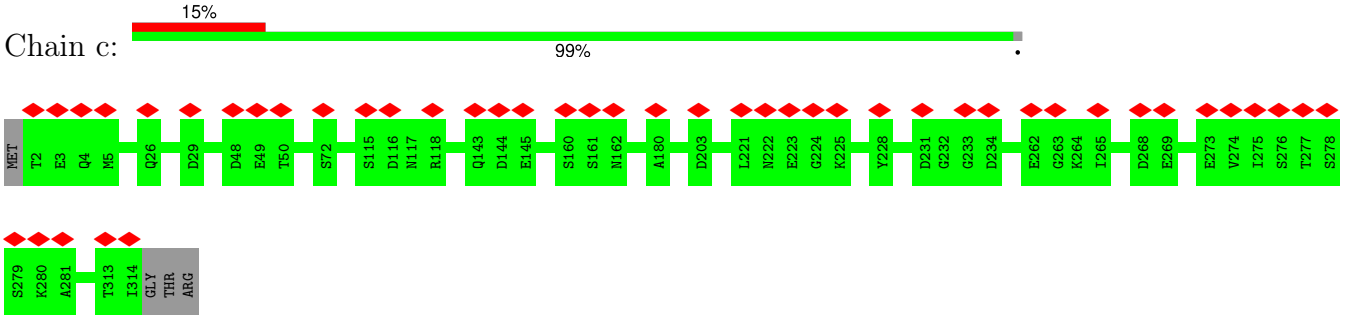


• Molecule 34: 40S ribosomal protein S15

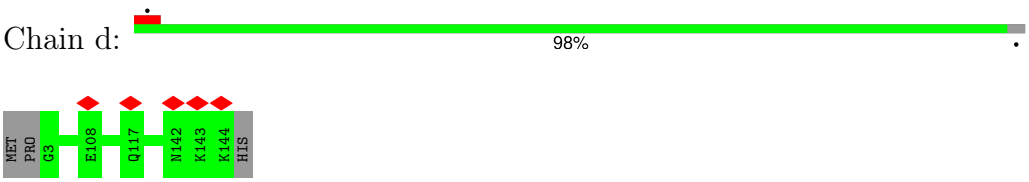




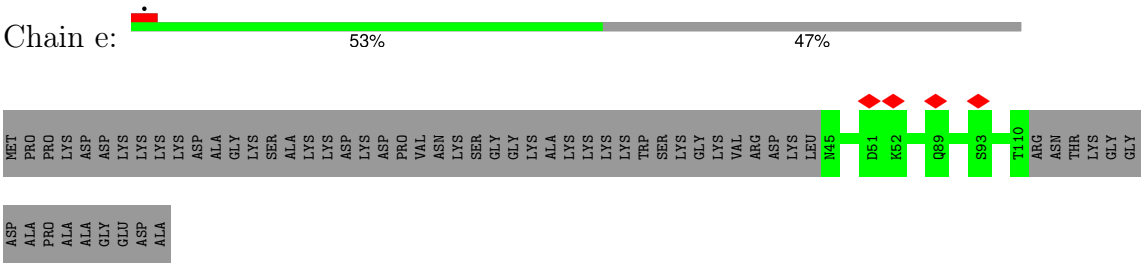
• Molecule 35: Receptor of activated protein C kinase 1



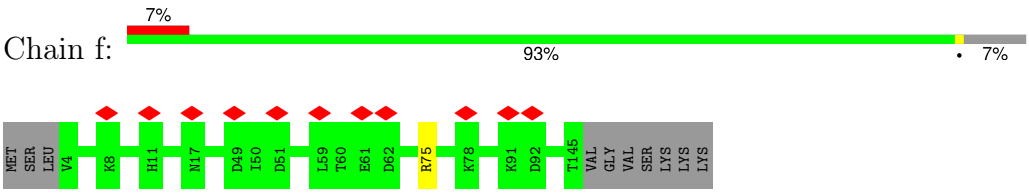
• Molecule 36: 40S ribosomal protein S19



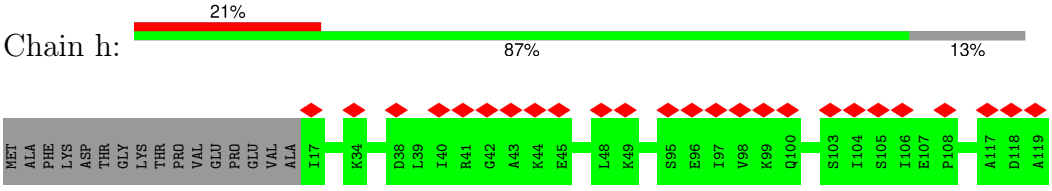
• Molecule 37: 40S ribosomal protein S25



• Molecule 38: 40S ribosomal protein S18

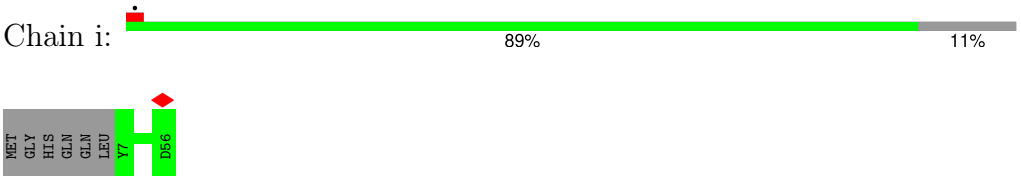


• Molecule 39: 40S ribosomal protein S20



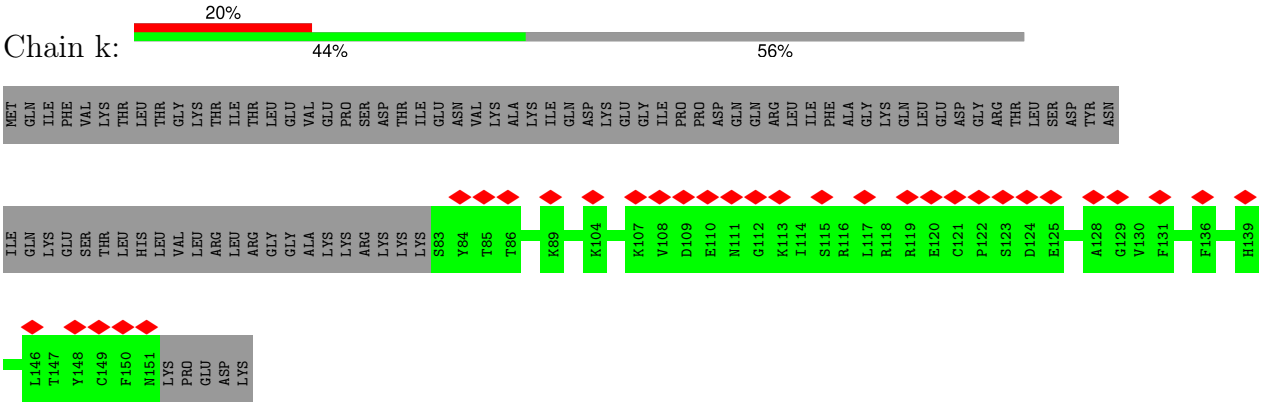
• Molecule 40: 40S ribosomal protein S29

Chain i:



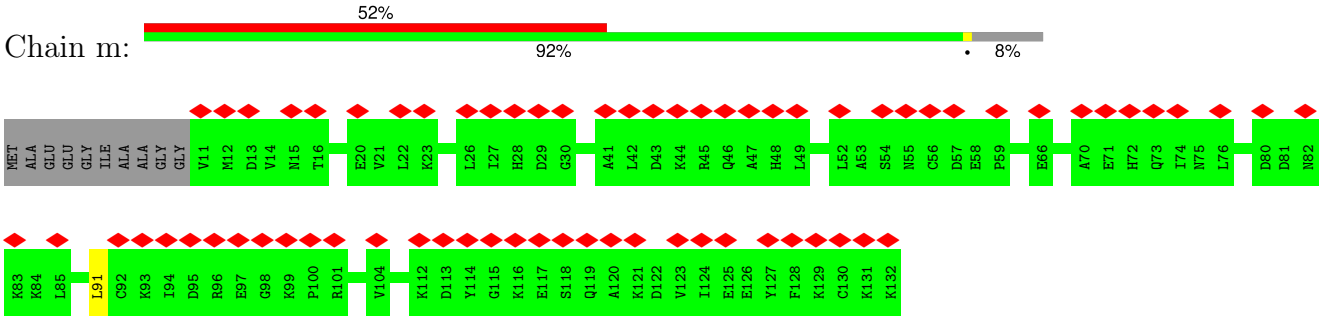
• Molecule 41: Ubiquitin

Chain k:



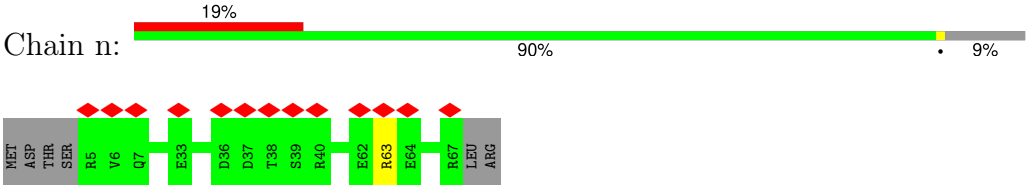
• Molecule 42: 40S ribosomal protein S12

Chain m:



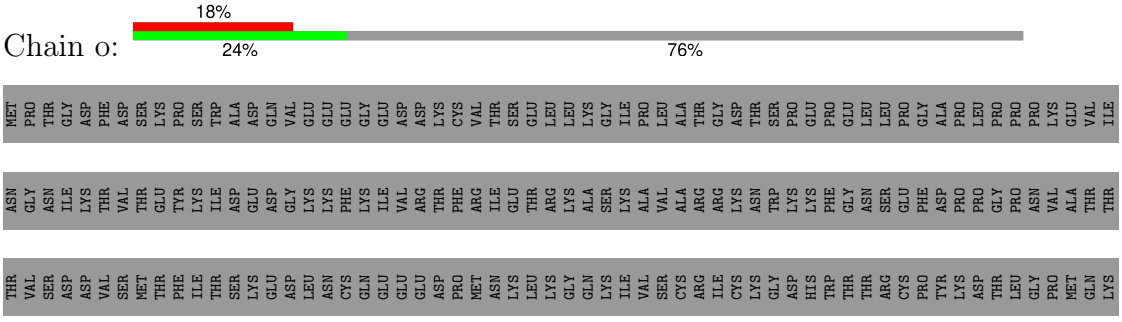
• Molecule 43: 40S ribosomal protein S28

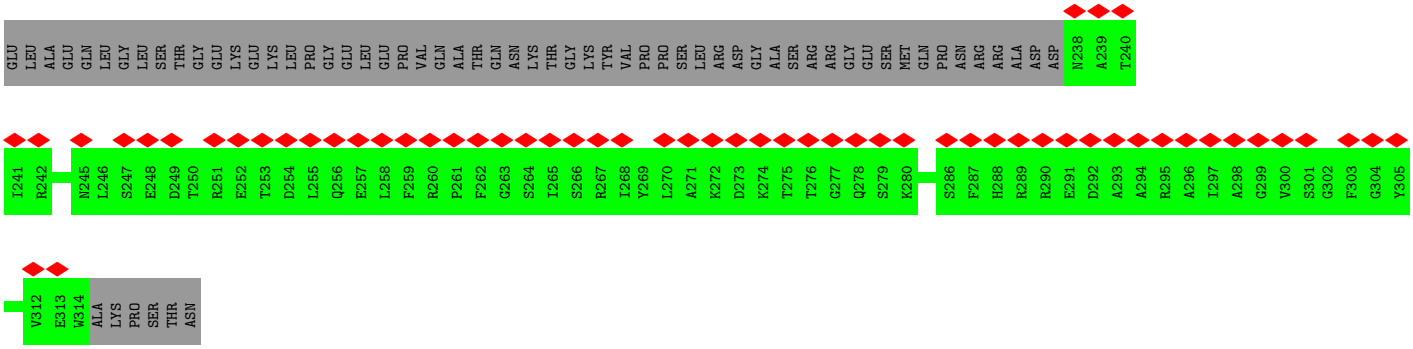
Chain n:



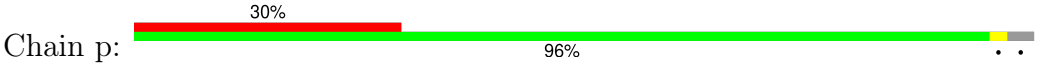
• Molecule 44: Eukaryotic translation initiation factor 3 subunit G

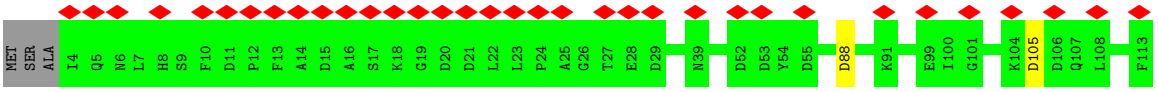
Chain o:



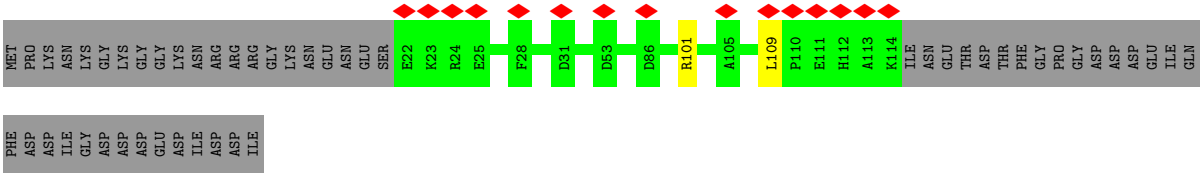


• Molecule 45: Eukaryotic translation initiation factor 1

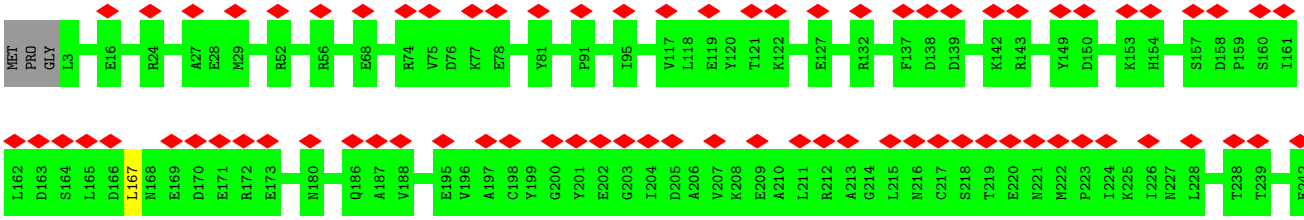




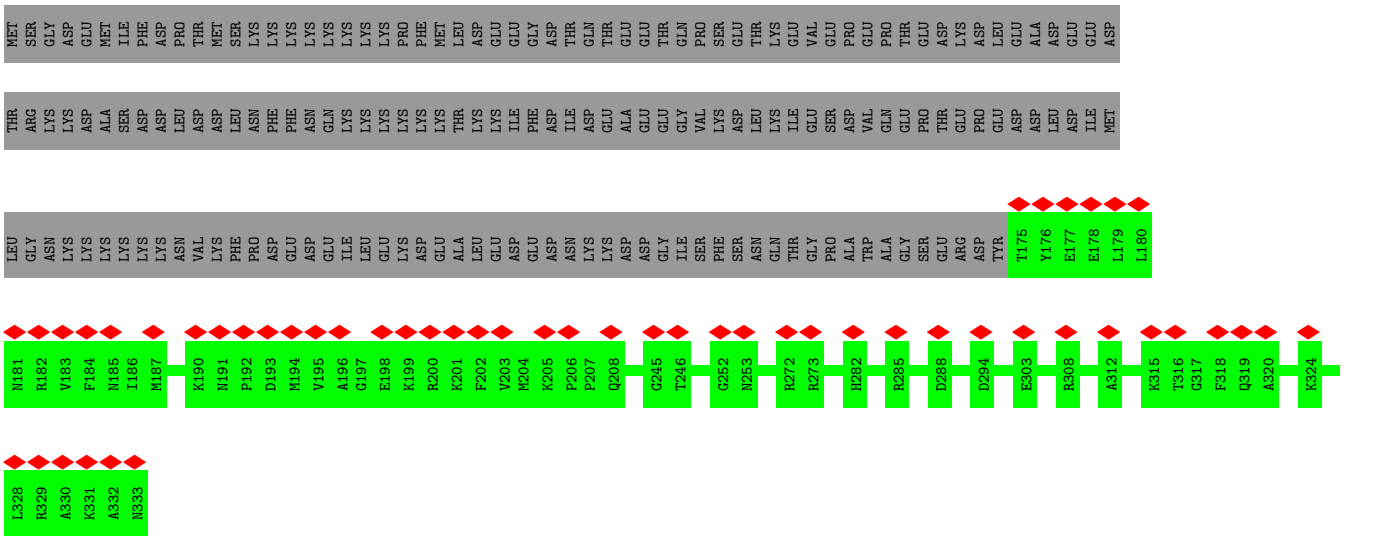
• Molecule 46: Eukaryotic translation initiation factor 1A, X-chromosomal



• Molecule 47: Eukaryotic translation initiation factor 2 subunit 1

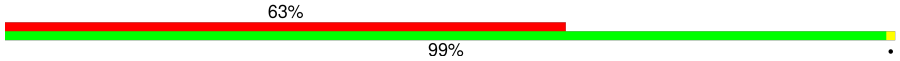


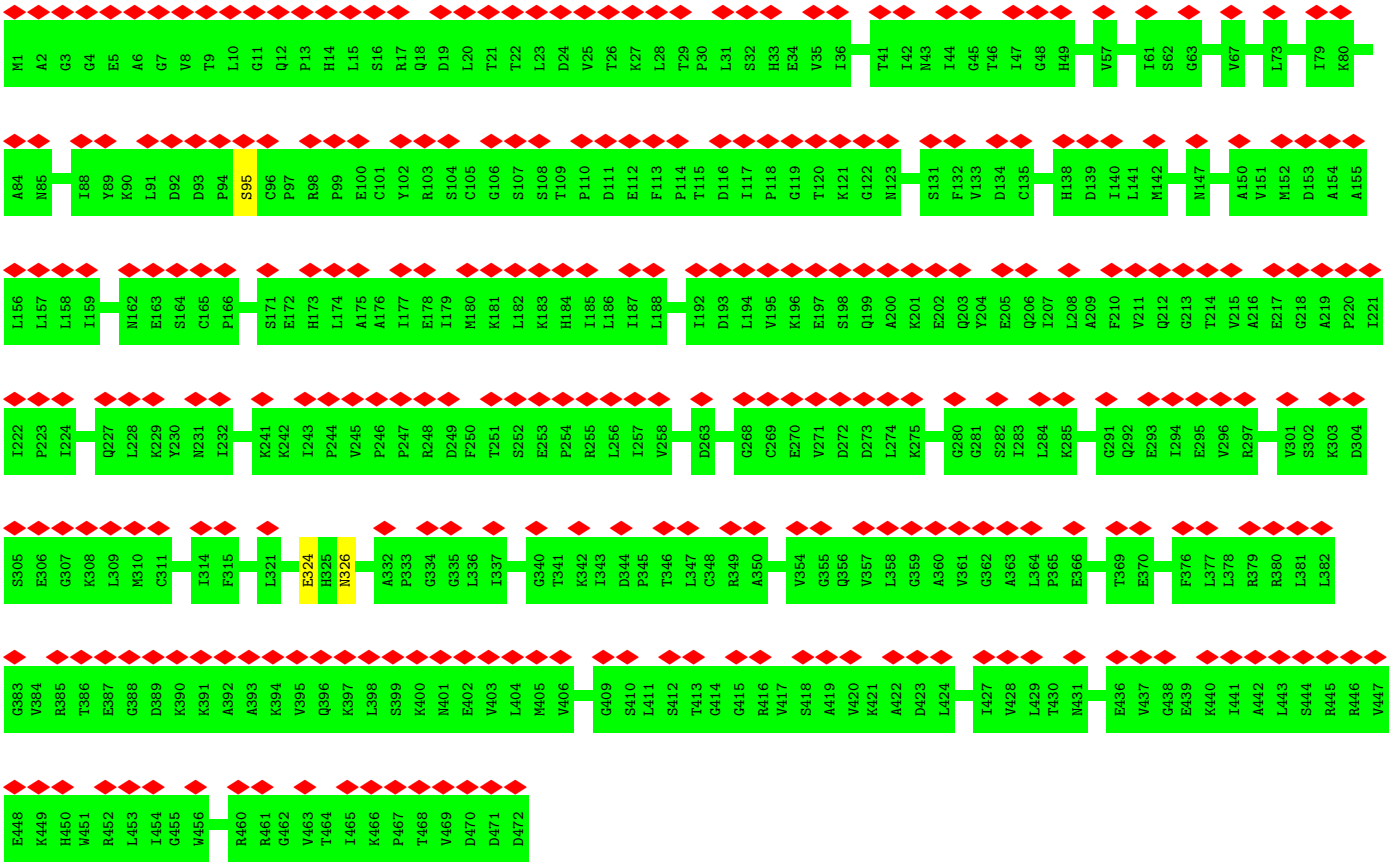
• Molecule 48: Eukaryotic translation initiation factor 2 subunit 2



• Molecule 49: Eukaryotic translation initiation factor 2 subunit 3

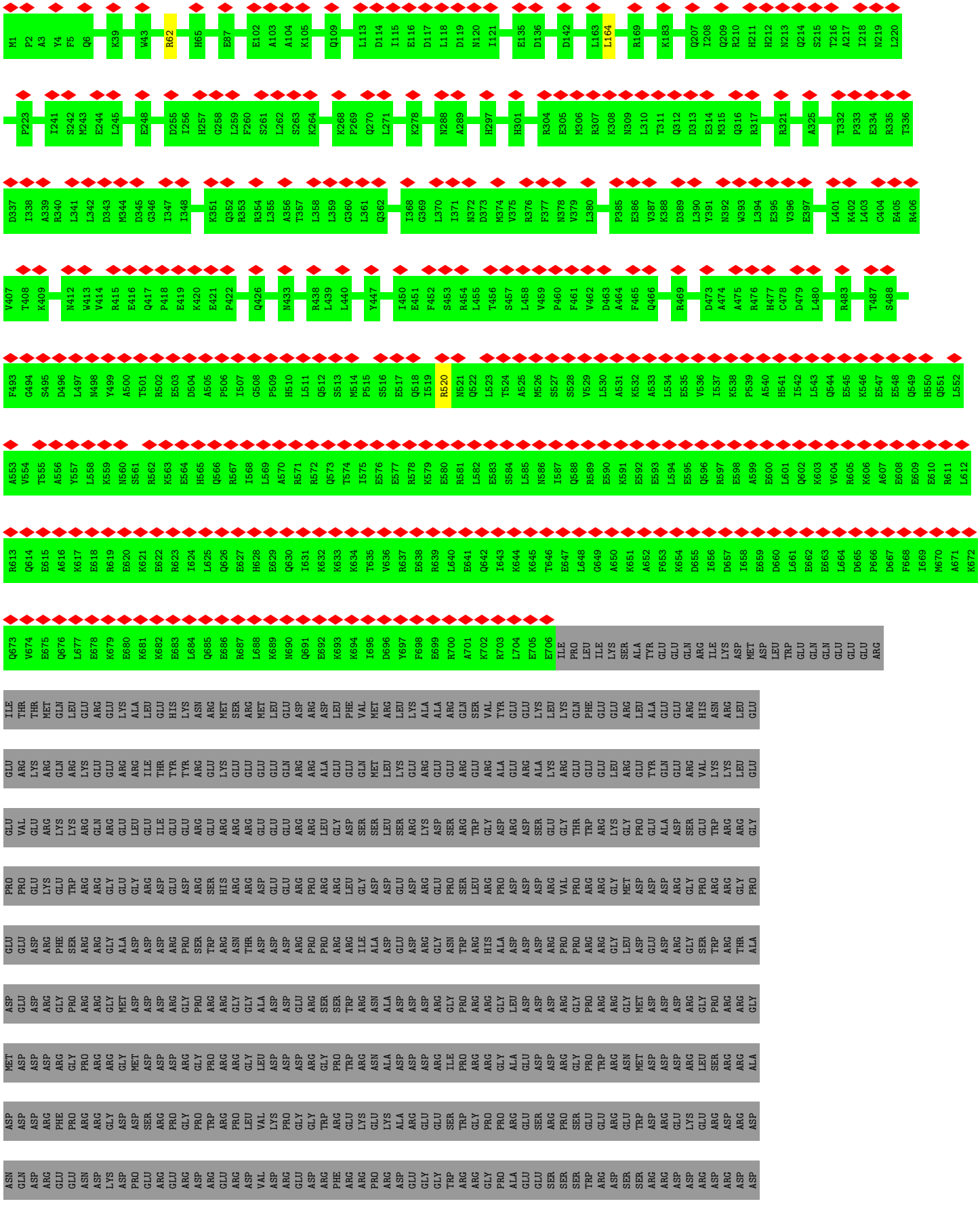
Chain t:

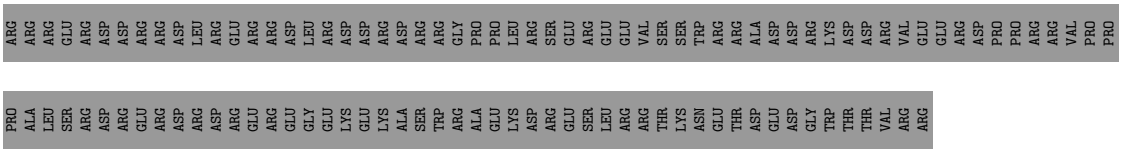




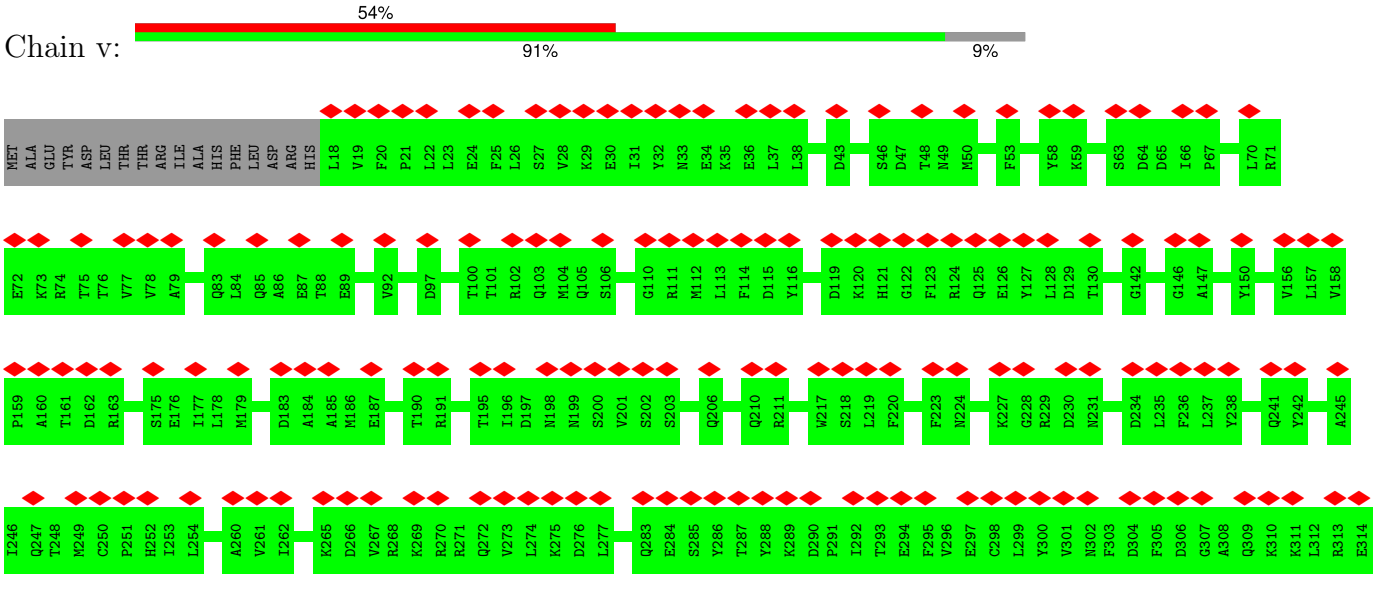
• Molecule 50: Eukaryotic translation initiation factor 3 subunit A

Chain u:

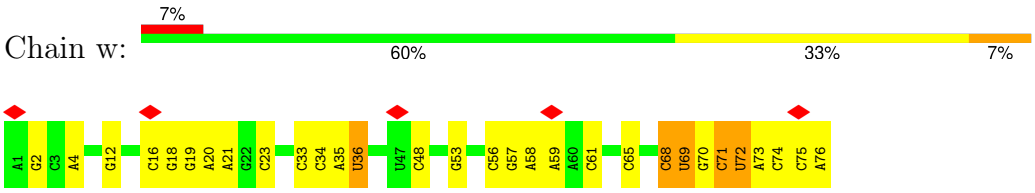

M1 P2 A3 Y4 F5 Q6 K39 W43 R62 H65 E87 E102 A103 A104 K105 Q109 L113 D114 I115 E116 D117 L118 D119 N120 I121 E135 D136 D142 L163 L164 R169 K183 Q207 I208 Q209 R210 H211 H212 N213 Q214 S215 T216 A217 I218 N219 L220
P223 T241 S242 M243 E244 L245 E248 D255 I256 H257 G258 L259 F260 S261 L262 S263 K264 K268 P269 Q270 L271 K278 N288 A289 H297 H301 R304 E305 M306 R307 K308 N309 L310 T311 Q312 D313 E314 M315 Q316 R317 R321 A325 T332 P333 E334 R335 T336
D337 I338 A339 R340 L341 L342 D343 M344 D345 G346 I347 I348 K351 Q352 R353 R354 L355 A356 T357 L358 L359 G360 L361 Q362 I368 G369 L370 I371 N372 D373 M374 V375 R376 F377 N378 V379 L380 P385 E386 V387 K388 D389 L390 Y391 N392 W393 L394 E395 V396 E397 L401 K402 L403 C404 E405 R406
V407 T408 K409 N412 W413 V414 R415 E416 Q417 P418 E419 K420 E421 P422 Q426 N433 R438 L439 L440 Y447 I450 E451 F452 S453 R454 L455 T456 S457 L458 V459 P460 F461 V462 D463 A464 F465 Q466 R469 D473 A474 A475 R476 H477 C478 D479 L480 R483 T487 S488
F493 G494 S495 D496 L497 N498 Y499 A500 T501 R502 E503 D504 A505 P506 I507 G508 P509 H510 L511 Q512 S513 M514 P515 S516 E517 Q518 I519 R520 N521 Q522 L523 T524 A525 M526 S527 S528 V529 L530 A531 K532 A533 L534 E535 V536 I537 K538 P539 A540 H541 I542 L543 Q544 E545 K546 E547 E548 Q549 H550 Q551 L552
A553 V554 T555 A556 Y557 L558 K559 N560 S561 R562 K563 E564 H565 Q566 R567 I568 L569 A570 R571 R572 Q573 T574 I575 E576 E577 R578 K579 E580 R581 L582 E583 S584 L585 N586 I587 Q588 R589 E590 K591 E592 E593 L594 E595 Q596 R597 E598 A599 E600 L601 Q602 K603 V604 R605 K606 A607 E608 E609 E610 R611 L612
R613 Q614 E615 A616 K617 E618 R619 E620 K621 E622 R623 I624 L625 Q626 E627 H628 E629 Q630 I631 K632 K633 K634 T635 V636 R637 E638 R639 L640 E641 Q642 I643 K644 K645 T646 E647 L648 G649 A650 K651 A652 F653 K654 D655 I656 D657 I658 E659 D660 L661 E662 E663 L664 D665 P666 D667 F668 I669 M670 A671 K672
Q673 V674 E675 Q676 L677 E678 K679 E680 K681 K682 E683 L684 Q685 E686 R687 L688 K689 N690 Q691 E692 K693 K694 I695 D696 Y697 F698 E699 R700 A701 K702 R703 L704 E705 E706 ILE PRO LEU ILE LYS SER ALA TYR GLU GLU GLN ARG ILE LYS ASP MET ASP LEU TRP GLU GLN GLN GLU GLU GLU ARG
ILE THR THR MET GLN LEU GLU ARG GLU LYS ALA LEU GLU HIS LYS ASN ARG MET SER ARG MET LEU GLU ASP ARG ASP LEU PHE VAL MET ARG LEU LYS ALA ALA ARG GLN SER VAL TYR GLU GLU LYS LEU LYS GLN PHE GLU GLU ARG LEU ALA GLU GLU ARG HIS ASN ARG LEU GLU
GLU ARG LYS ARG GLN ARG LYS GLU GLU ARG ARG ILE THR TYR TYR ARG GLU LYS GLU GLU GLU GLN ARG ARG ALA GLU GLU GLN MET LEU LYS GLU ARG GLU GLU ARG GLU ALA LYS ARG GLU GLU GLU LEU ARG GLU TYR GLN GLU ARG VAL LYS LYS LEU GLU
GLU VAL GLU ARG LYS LYS ARG GLN ARG GLU LEU GLU ILE GLU GLU ARG GLU ARG ARG GLU GLU ARG ARG LEU GLY ASP SER SER LEU SER ARG LYS ASP SER ARG TRP GLY ASP ARG ASP SER GLU GLY THR TRP ARG LYS GLY PRO GLU ALA ASP SER GLU TRP ARG ARG GLY
PRO PRO GLU LYS GLU TRP ARG ARG GLY GLU GLY ARG ASP GLU ASP ARG HIS ARG ARG ASP GLU GLU ARG PRO ARG ARG LEU GLY ASP ASP GLU ASP ARG PRO SER LEU ARG PRO ASP ASP ASP ARG VAL PRO ARG ARG GLY ASP ASP ARG GLY PRO ARG ARG GLY PRO
GLU GLU ASP ARG PHE SER ARG ARG GLY ALA ASP ASP ASP ARG PRO PRO ARG ARG ILE ALA ASP GLU ASP ARG GLY ASN TRP ASP HIS ALA ASP ASP ASP ARG PRO ARG ARG LEU GLY SER TRP ARG THR ALA
ASP GLU ASP ARG GLY PRO ARG ARG GLY PRO ARG ARG GLY MET ASP ASP ARG GLY PRO ARG ARG GLY ASN ALA ASP ASP ASP ARG GLY PRO ARG ARG GLY LEU ASP ASP ASP ARG GLY PRO ARG ARG GLY
MET ASP ASP ARG GLY PRO ARG GLY LEU ASP ASP ASP ARG GLY PRO ARG ARG GLY ALA GLU ASP ASP ARG GLY PRO TRP ARG ASN MET ASP ASP ASP ARG LEU SER ARG ARG ALA
ASP ASP ASP ARG PHE PRO ARG GLY ASP SER ARG PRO ARG GLU LYS GLU ALA ARG GLU GLU SER TRP ASP ARG ARG ASP ARG ASP
ASN GLN ASP ARG GLU GLU ASN ASP LYS ASP PRO GLU ARG GLU ARG ASP VAL ASP ARG GLU ASP ARG PHE ARG ARG PRO ARG ASP GLU GLY GLY TRP ARG ARG GLY PRO ALA GLU GLU SER SER SER TRP ARG ASP SER SER ARG ARG ASP ARG ASP ASP ASP ARG ASP



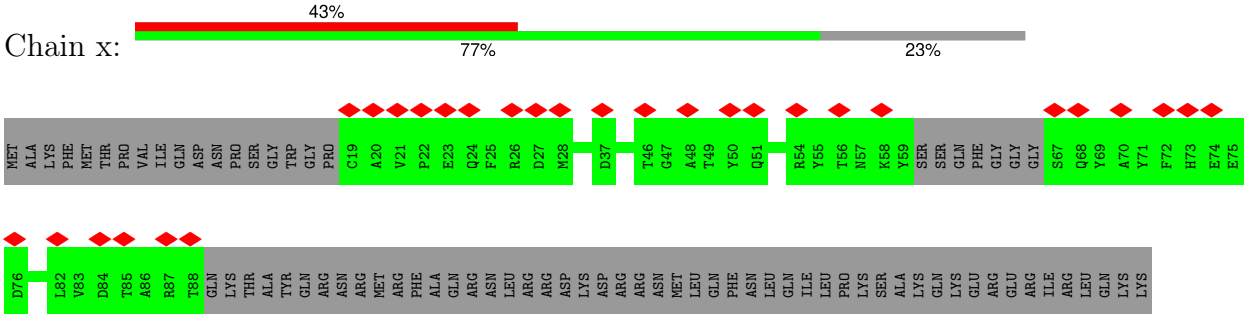
• Molecule 51: Eukaryotic translation initiation factor 3 subunit E

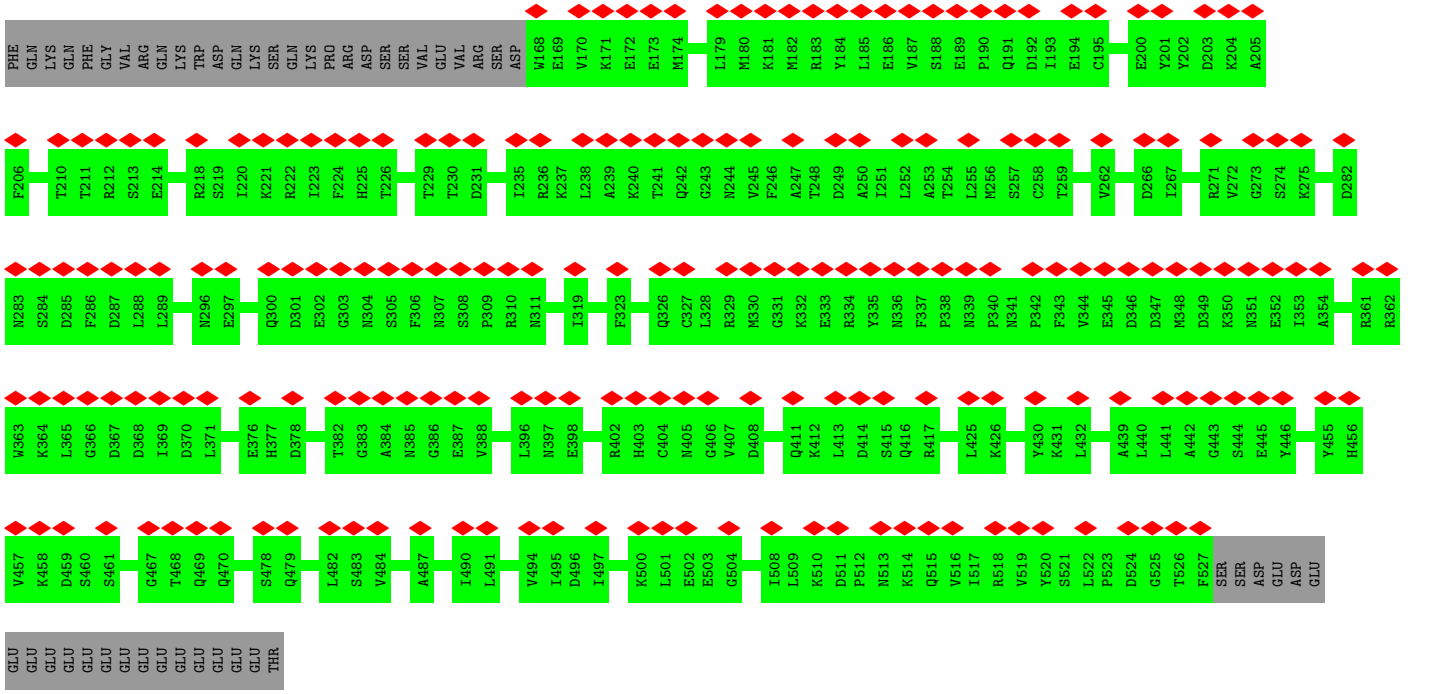


• Molecule 52: Initiator Met-tRNA-i



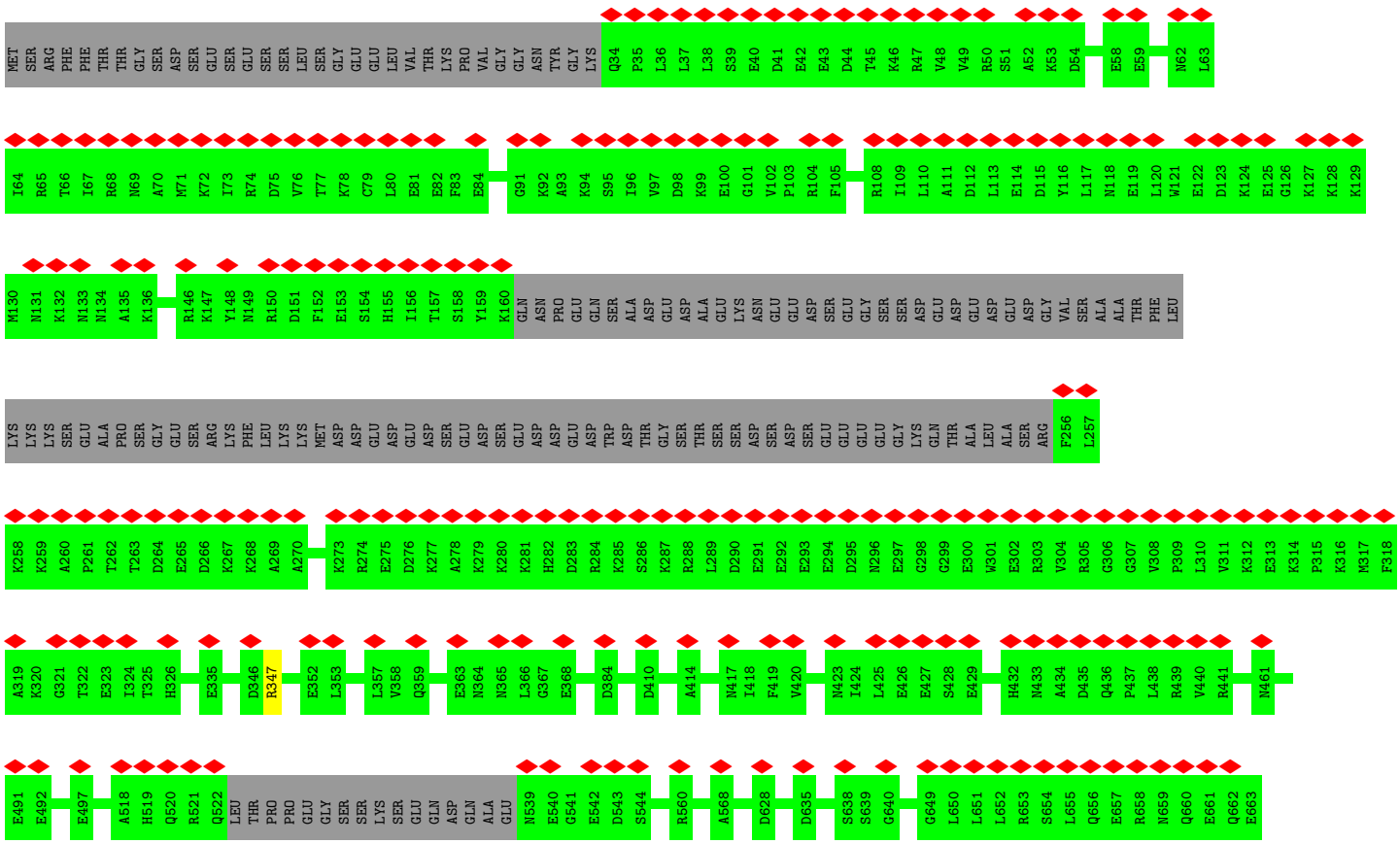
• Molecule 53: Eukaryotic translation initiation factor 3 subunit D

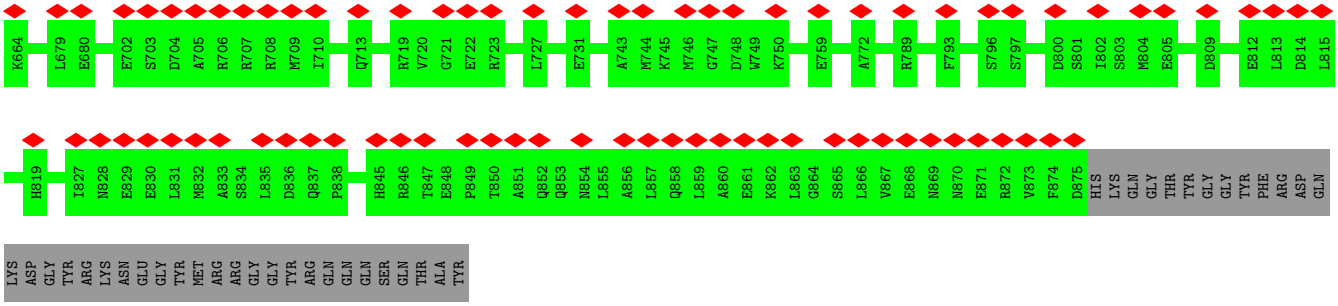




• Molecule 54: Eukaryotic translation initiation factor 3 subunit C

Chain y:




K664 L679 E680 E702 S703 D704 A705 R706 R707 R708 M709 I710 Q713 R719 V720 G721 E722 R723 L727 E731 A743 M744 K745 M746 G747 D748 W749 K750 E759 A772 R789 F793 S796 S797 D800 S801 I802 S803 M804 E805 D809 E812 L813 D814 L815
H819 T827 N828 E829 E830 L831 M832 A833 S834 L835 D836 Q837 P838 H845 R846 T847 E848 P849 T850 A851 Q852 Q853 N854 L855 A856 L857 Q858 L859 A860 E861 K862 L863 G864 S865 L866 V867 E868 N869 N870 E871 R872 V873 F874 D875 HIS LYS GLN GLY THR TYR GLY GLY TYR PHE ARG ASP GLN
LYS ASP GLY TYR ARG LYS ASN GLU GLY TYR MET ARG ARG GLY GLY TYR ARG GLN GLN GLN SER GLN THR ALA TYR

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	92749	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 ($e^-/Å^2$)	45	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	24.146	Depositor
Minimum map value	-8.937	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	4	Depositor
Map size (Å)	417.74402, 417.74402, 417.74402	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.96700007, 0.96700007, 0.96700007	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: OMG, PSU, OMU, 6MZ, GTP, UR3, A2M, ZN, MA6, 5MC, 5MU, JMH, MG, B8N, OMC

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	1	0.26	0/3279	0.52	0/4534
2	2	0.24	0/1491	0.47	0/2068
3	3	0.23	0/1055	0.37	0/1469
4	4	0.24	0/1269	0.40	0/1762
5	5	0.25	0/4458	0.50	0/6027
6	6	0.25	0/2212	0.48	0/3034
7	7	0.21	0/1126	0.78	1/1750 (0.1%)
8	8	0.24	0/1572	0.42	0/2187
9	9	0.28	0/231	0.74	0/294
10	A	0.37	0/41130	0.96	118/64100 (0.2%)
11	B	0.32	0/1186	0.59	0/1585
12	C	0.30	0/2077	0.62	2/2796 (0.1%)
13	D	0.30	0/1502	0.61	1/2008 (0.0%)
14	E	0.29	0/1105	0.54	0/1476
15	F	0.25	0/465	0.58	0/612
16	G	0.28	0/1451	0.56	0/1942
17	H	0.30	0/644	0.57	0/864
18	I	0.29	0/1232	0.54	0/1656
19	J	0.30	0/1051	0.59	0/1406
20	K	0.29	0/623	0.57	0/833
21	L	0.32	0/1743	0.62	2/2354 (0.1%)
22	M	0.34	0/1078	0.70	2/1447 (0.1%)
23	N	0.30	0/1670	0.63	3/2271 (0.1%)
24	O	0.30	0/1742	0.61	1/2330 (0.0%)
25	P	0.32	0/1010	0.72	2/1353 (0.1%)
26	Q	0.32	0/805	0.62	0/1079
27	R	0.29	0/1654	0.57	0/2203
28	S	0.29	0/1885	0.59	0/2510
29	T	0.29	0/1032	0.57	0/1371
30	V	0.28	0/1516	0.61	2/2037 (0.1%)
31	Y	0.30	0/1142	0.62	0/1528
32	Z	0.29	0/1793	0.59	1/2414 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	a	0.29	0/859	0.53	0/1159
34	b	0.29	0/1008	0.62	1/1348 (0.1%)
35	c	0.26	0/2493	0.57	0/3394
36	d	0.27	0/1123	0.56	0/1504
37	e	0.26	0/529	0.58	0/712
38	f	0.27	0/1194	0.61	0/1599
39	h	0.30	0/827	0.66	0/1110
40	i	0.28	0/429	0.62	0/568
41	k	0.31	0/571	0.64	0/760
42	m	0.26	0/960	0.57	1/1286 (0.1%)
43	n	0.31	0/500	0.74	0/669
44	o	0.26	0/628	0.59	0/846
45	p	0.30	0/843	0.70	2/1134 (0.2%)
46	q	0.30	0/764	0.70	1/1020 (0.1%)
47	r	0.27	0/2167	0.55	1/2943 (0.0%)
48	s	0.31	0/1295	0.65	0/1739
49	t	0.28	0/3644	0.60	1/4929 (0.0%)
50	u	0.26	0/5475	0.55	1/7432 (0.0%)
51	v	0.26	0/2778	0.54	0/3797
52	w	0.37	0/1795	1.13	15/2798 (0.5%)
53	x	0.26	0/2885	0.55	0/3940
54	y	0.27	0/5744	0.56	0/7761
All	All	0.31	0/124740	0.75	158/177748 (0.1%)

There are no bond length outliers.

The worst 5 of 158 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
10	A	1453	C	C2-N1-C1'	10.83	130.71	118.80
10	A	1453	C	N1-C2-O2	10.79	125.37	118.90
10	A	1115	U	C2-N1-C1'	8.89	128.37	117.70
10	A	888	U	C2-N1-C1'	8.70	128.14	117.70
10	A	501	C	C2-N1-C1'	8.63	128.29	118.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	1	584/814 (72%)	541 (93%)	43 (7%)	0	100	100
2	2	300/325 (92%)	296 (99%)	4 (1%)	0	100	100
3	3	209/218 (96%)	197 (94%)	12 (6%)	0	100	100
4	4	251/357 (70%)	240 (96%)	11 (4%)	0	100	100
5	5	518/564 (92%)	508 (98%)	10 (2%)	0	100	100
6	6	360/374 (96%)	347 (96%)	13 (4%)	0	100	100
8	8	313/352 (89%)	293 (94%)	20 (6%)	0	100	100
9	9	22/25 (88%)	22 (100%)	0	0	100	100
11	B	138/158 (87%)	135 (98%)	3 (2%)	0	100	100
12	C	254/263 (97%)	248 (98%)	6 (2%)	0	100	100
13	D	175/194 (90%)	172 (98%)	3 (2%)	0	100	100
14	E	138/143 (96%)	133 (96%)	5 (4%)	0	100	100
15	F	56/59 (95%)	48 (86%)	8 (14%)	0	100	100
16	G	171/194 (88%)	164 (96%)	7 (4%)	0	100	100
17	H	79/84 (94%)	75 (95%)	4 (5%)	0	100	100
18	I	148/151 (98%)	148 (100%)	0	0	100	100
19	J	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
20	K	79/83 (95%)	73 (92%)	6 (8%)	0	100	100
21	L	218/293 (74%)	212 (97%)	6 (3%)	0	100	100
22	M	129/135 (96%)	125 (97%)	4 (3%)	0	100	100
23	N	205/295 (70%)	196 (96%)	9 (4%)	0	100	100
24	O	209/264 (79%)	202 (97%)	7 (3%)	0	100	100
25	P	131/151 (87%)	121 (92%)	10 (8%)	0	100	100
26	Q	97/115 (84%)	95 (98%)	2 (2%)	0	100	100
27	R	194/208 (93%)	189 (97%)	5 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	S	228/249 (92%)	223 (98%)	5 (2%)	0	100	100
29	T	123/133 (92%)	123 (100%)	0	0	100	100
30	V	187/204 (92%)	174 (93%)	13 (7%)	0	100	100
31	Y	139/146 (95%)	134 (96%)	5 (4%)	0	100	100
32	Z	225/243 (93%)	219 (97%)	6 (3%)	0	100	100
33	a	97/165 (59%)	90 (93%)	7 (7%)	0	100	100
34	b	119/145 (82%)	117 (98%)	2 (2%)	0	100	100
35	c	311/317 (98%)	292 (94%)	19 (6%)	0	100	100
36	d	140/145 (97%)	138 (99%)	2 (1%)	0	100	100
37	e	64/125 (51%)	63 (98%)	1 (2%)	0	100	100
38	f	140/152 (92%)	134 (96%)	6 (4%)	0	100	100
39	h	101/119 (85%)	97 (96%)	4 (4%)	0	100	100
40	i	48/56 (86%)	46 (96%)	2 (4%)	0	100	100
41	k	67/157 (43%)	55 (82%)	12 (18%)	0	100	100
42	m	120/132 (91%)	116 (97%)	4 (3%)	0	100	100
43	n	61/69 (88%)	55 (90%)	6 (10%)	0	100	100
44	o	75/320 (23%)	70 (93%)	5 (7%)	0	100	100
45	p	108/113 (96%)	96 (89%)	12 (11%)	0	100	100
46	q	91/144 (63%)	87 (96%)	4 (4%)	0	100	100
47	r	294/315 (93%)	276 (94%)	18 (6%)	0	100	100
48	s	157/333 (47%)	138 (88%)	19 (12%)	0	100	100
49	t	470/472 (100%)	431 (92%)	39 (8%)	0	100	100
50	u	705/1382 (51%)	672 (95%)	33 (5%)	0	100	100
51	v	403/445 (91%)	377 (94%)	26 (6%)	0	100	100
53	x	417/548 (76%)	396 (95%)	21 (5%)	0	100	100
54	y	725/913 (79%)	697 (96%)	28 (4%)	0	100	100
All	All	10720/13491 (80%)	10218 (95%)	502 (5%)	0	100	100

There are no Ramachandran outliers to report.

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
1	1	97/702 (14%)	96 (99%)	1 (1%)	73 83
5	5	477/515 (93%)	475 (100%)	2 (0%)	89 93
6	6	112/335 (33%)	112 (100%)	0	100 100
8	8	1/310 (0%)	1 (100%)	0	100 100
9	9	23/24 (96%)	23 (100%)	0	100 100
11	B	129/142 (91%)	128 (99%)	1 (1%)	79 87
12	C	220/225 (98%)	220 (100%)	0	100 100
13	D	158/168 (94%)	158 (100%)	0	100 100
14	E	112/115 (97%)	112 (100%)	0	100 100
15	F	47/48 (98%)	47 (100%)	0	100 100
16	G	159/174 (91%)	159 (100%)	0	100 100
17	H	73/76 (96%)	73 (100%)	0	100 100
18	I	130/131 (99%)	130 (100%)	0	100 100
19	J	112/113 (99%)	112 (100%)	0	100 100
20	K	65/67 (97%)	65 (100%)	0	100 100
21	L	186/225 (83%)	186 (100%)	0	100 100
22	M	119/122 (98%)	119 (100%)	0	100 100
23	N	173/243 (71%)	172 (99%)	1 (1%)	84 90
24	O	192/231 (83%)	192 (100%)	0	100 100
25	P	104/119 (87%)	104 (100%)	0	100 100
26	Q	86/98 (88%)	86 (100%)	0	100 100
27	R	172/180 (96%)	172 (100%)	0	100 100
28	S	200/218 (92%)	200 (100%)	0	100 100
29	T	107/115 (93%)	107 (100%)	0	100 100
30	V	159/170 (94%)	159 (100%)	0	100 100
31	Y	117/121 (97%)	117 (100%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
32	Z	190/202 (94%)	190 (100%)	0	100 100
33	a	90/136 (66%)	90 (100%)	0	100 100
34	b	107/130 (82%)	107 (100%)	0	100 100
35	c	272/275 (99%)	272 (100%)	0	100 100
36	d	112/115 (97%)	112 (100%)	0	100 100
37	e	58/103 (56%)	58 (100%)	0	100 100
38	f	123/132 (93%)	122 (99%)	1 (1%)	79 87
39	h	94/107 (88%)	94 (100%)	0	100 100
40	i	44/49 (90%)	44 (100%)	0	100 100
41	k	61/140 (44%)	61 (100%)	0	100 100
42	m	104/108 (96%)	104 (100%)	0	100 100
43	n	56/62 (90%)	55 (98%)	1 (2%)	54 73
44	o	64/277 (23%)	64 (100%)	0	100 100
45	p	79/96 (82%)	79 (100%)	0	100 100
46	q	79/123 (64%)	78 (99%)	1 (1%)	65 78
47	r	190/280 (68%)	190 (100%)	0	100 100
48	s	142/304 (47%)	142 (100%)	0	100 100
49	t	397/397 (100%)	395 (100%)	2 (0%)	86 91
50	u	528/1259 (42%)	526 (100%)	2 (0%)	89 93
51	v	206/406 (51%)	205 (100%)	1 (0%)	86 91
53	x	207/494 (42%)	207 (100%)	0	100 100
54	y	569/811 (70%)	568 (100%)	1 (0%)	92 96
All	All	7302/10993 (66%)	7288 (100%)	14 (0%)	91 96

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	q	101	ARG
49	t	324	GLU
54	y	347	ARG
50	u	520	ARG
51	v	414	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
53	x	322	ASN
54	y	819	HIS
45	p	111	HIS
49	t	169	GLN
50	u	110	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	1741/1869 (93%)	410 (23%)	8 (0%)
52	w	74/75 (98%)	28 (37%)	0
7	7	46/255 (18%)	34 (73%)	4 (8%)
All	All	1861/2199 (84%)	472 (25%)	12 (0%)

5 of 472 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	7	-27	A
7	7	-26	C
7	7	-23	C
7	7	-22	A
7	7	-21	A

5 of 12 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	A	606	G
10	A	688	U
10	A	1600	G
10	A	731	G
7	7	-4	A

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

29 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	$\#\|Z\|>2$
10	OMG	A	683	10	19,26,27	1.18	2 (10%)	21,38,41	0.88	1 (4%)
10	A2M	A	668	55,10	18,25,26	4.55	9 (50%)	20,36,39	4.28	7 (35%)
10	OMU	A	116	10	19,22,23	3.03	6 (31%)	25,31,34	1.75	5 (20%)
10	MA6	A	1850	10	19,26,27	1.91	3 (15%)	18,38,41	3.23	3 (16%)
10	OMC	A	517	10	19,22,23	0.53	0	25,31,34	0.65	0
10	JMH	A	1219	55,10	18,22,23	2.91	5 (27%)	23,32,35	1.50	3 (13%)
10	5MU	A	814	10	19,22,23	0.46	0	27,32,35	1.37	4 (14%)
10	A2M	A	1031	10	18,25,26	4.67	8 (44%)	20,36,39	4.12	6 (30%)
10	PSU	A	823	10	18,21,22	1.14	1 (5%)	21,30,33	1.85	4 (19%)
10	A2M	A	27	55,10	18,25,26	4.64	8 (44%)	20,36,39	4.02	6 (30%)
10	OMC	A	174	55,10	19,22,23	0.54	0	25,31,34	0.70	0
10	OMG	A	509	55,10	19,26,27	1.18	2 (10%)	21,38,41	0.85	1 (4%)
10	5MC	A	1374	10	19,22,23	0.57	0	26,32,35	0.72	0
10	PSU	A	1243	10	18,21,22	1.14	1 (5%)	21,30,33	1.91	4 (19%)
10	PSU	A	119	10	18,21,22	1.00	1 (5%)	21,30,33	1.73	4 (19%)
10	A2M	A	159	10	18,25,26	4.65	8 (44%)	20,36,39	4.09	6 (30%)
10	OMG	A	644	10	19,26,27	1.19	2 (10%)	21,38,41	0.79	1 (4%)
10	6MZ	A	1832	55,10	17,25,26	1.44	1 (5%)	15,36,39	2.96	5 (33%)
10	UR3	A	1830	10	19,22,23	2.84	8 (42%)	26,32,35	1.76	4 (15%)
10	PSU	A	1081	10	18,21,22	1.05	1 (5%)	21,30,33	1.84	5 (23%)
10	OMU	A	121	10	19,22,23	3.01	6 (31%)	25,31,34	1.78	5 (20%)
10	A2M	A	1678	10	18,25,26	4.70	9 (50%)	20,36,39	4.31	6 (30%)
10	OMC	A	1703	10	19,22,23	0.53	0	25,31,34	0.69	0
10	PSU	A	822	10	18,21,22	1.09	1 (5%)	21,30,33	1.85	5 (23%)
10	PSU	A	612	10	18,21,22	1.03	1 (5%)	21,30,33	1.87	5 (23%)
10	A2M	A	484	10	18,25,26	4.53	9 (50%)	20,36,39	3.95	6 (30%)
10	B8N	A	1248	10	25,29,30	3.40	9 (36%)	28,42,45	1.98	7 (25%)
10	MA6	A	1851	10	19,26,27	1.89	2 (10%)	18,38,41	3.22	3 (16%)
10	A2M	A	166	10	18,25,26	4.70	8 (44%)	20,36,39	4.19	8 (40%)

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
10	OMG	A	683	10	-	2/5/27/28	0/3/3/3
10	A2M	A	668	55,10	-	2/5/27/28	0/3/3/3
10	OMU	A	116	10	-	1/9/27/28	0/2/2/2
10	MA6	A	1850	10	-	1/7/29/30	0/3/3/3
10	OMC	A	517	10	-	2/9/27/28	0/2/2/2
10	JMH	A	1219	55,10	-	1/7/25/26	0/2/2/2
10	5MU	A	814	10	-	1/7/25/26	0/2/2/2
10	A2M	A	1031	10	-	1/5/27/28	0/3/3/3
10	PSU	A	823	10	-	0/7/25/26	0/2/2/2
10	A2M	A	27	55,10	-	2/5/27/28	0/3/3/3
10	OMC	A	174	55,10	-	0/9/27/28	0/2/2/2
10	OMG	A	509	55,10	-	1/5/27/28	0/3/3/3
10	5MC	A	1374	10	-	0/7/25/26	0/2/2/2
10	PSU	A	1243	10	-	2/7/25/26	0/2/2/2
10	PSU	A	119	10	-	1/7/25/26	0/2/2/2
10	A2M	A	159	10	-	2/5/27/28	0/3/3/3
10	OMG	A	644	10	-	3/5/27/28	0/3/3/3
10	6MZ	A	1832	55,10	-	0/5/27/28	0/3/3/3
10	UR3	A	1830	10	-	2/7/25/26	0/2/2/2
10	PSU	A	1081	10	-	1/7/25/26	0/2/2/2
10	OMU	A	121	10	-	0/9/27/28	0/2/2/2
10	A2M	A	1678	10	-	1/5/27/28	0/3/3/3
10	OMC	A	1703	10	-	0/9/27/28	0/2/2/2
10	PSU	A	822	10	-	2/7/25/26	0/2/2/2
10	PSU	A	612	10	-	0/7/25/26	0/2/2/2
10	A2M	A	484	10	-	0/5/27/28	0/3/3/3
10	B8N	A	1248	10	-	9/16/34/35	0/2/2/2
10	MA6	A	1851	10	-	3/7/29/30	0/3/3/3
10	A2M	A	166	10	-	1/5/27/28	0/3/3/3

The worst 5 of 111 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	166	A2M	C3'-C2'	-13.15	1.24	1.53
10	A	1678	A2M	C3'-C2'	-13.09	1.24	1.53
10	A	1031	A2M	C3'-C2'	-13.07	1.24	1.53
10	A	27	A2M	C3'-C2'	-12.97	1.24	1.53
10	A	159	A2M	C3'-C2'	-12.89	1.24	1.53

The worst 5 of 114 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
10	A	1851	MA6	N1-C6-N6	-11.28	103.80	116.83
10	A	1850	MA6	N1-C6-N6	-11.20	103.89	116.83
10	A	1678	A2M	C1'-N9-C4	10.87	145.74	126.64
10	A	159	A2M	C1'-N9-C4	10.65	145.35	126.64
10	A	484	A2M	C1'-N9-C4	10.59	145.24	126.64

There are no chirality outliers.

5 of 41 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	A	27	A2M	C1'-C2'-O2'-CM'
10	A	116	OMU	C1'-C2'-O2'-CM2
10	A	159	A2M	C1'-C2'-O2'-CM'
10	A	668	A2M	O4'-C4'-C5'-O5'
10	A	668	A2M	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 95 ligands modelled in this entry, 93 are monoatomic - leaving 2 for Mogul analysis.

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	$\#\|Z\| > 2$
58	MET	w	101	-	6,7,8	0.66	0	2,7,9	0.53	0
57	GTP	t	501	55	29,34,34	1.25	2 (6%)	35,54,54	1.25	4 (11%)

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
58	MET	w	101	-	-	1/5/6/8	-
57	GTP	t	501	55	-	7/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	t	501	GTP	C5-C6	-4.08	1.39	1.47
57	t	501	GTP	C2-N3	2.19	1.38	1.33

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
57	t	501	GTP	C8-N7-C5	3.70	108.84	102.55
57	t	501	GTP	C2-N1-C6	-2.97	119.67	125.11
57	t	501	GTP	C5-C6-N1	2.88	119.57	114.07
57	t	501	GTP	O6-C6-C5	-2.06	120.24	124.32

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	t	501	GTP	C5'-O5'-PA-O3A
57	t	501	GTP	C5'-O5'-PA-O1A
57	t	501	GTP	C5'-O5'-PA-O2A
58	w	101	MET	O-C-CA-CB
57	t	501	GTP	C3'-C4'-C5'-O5'

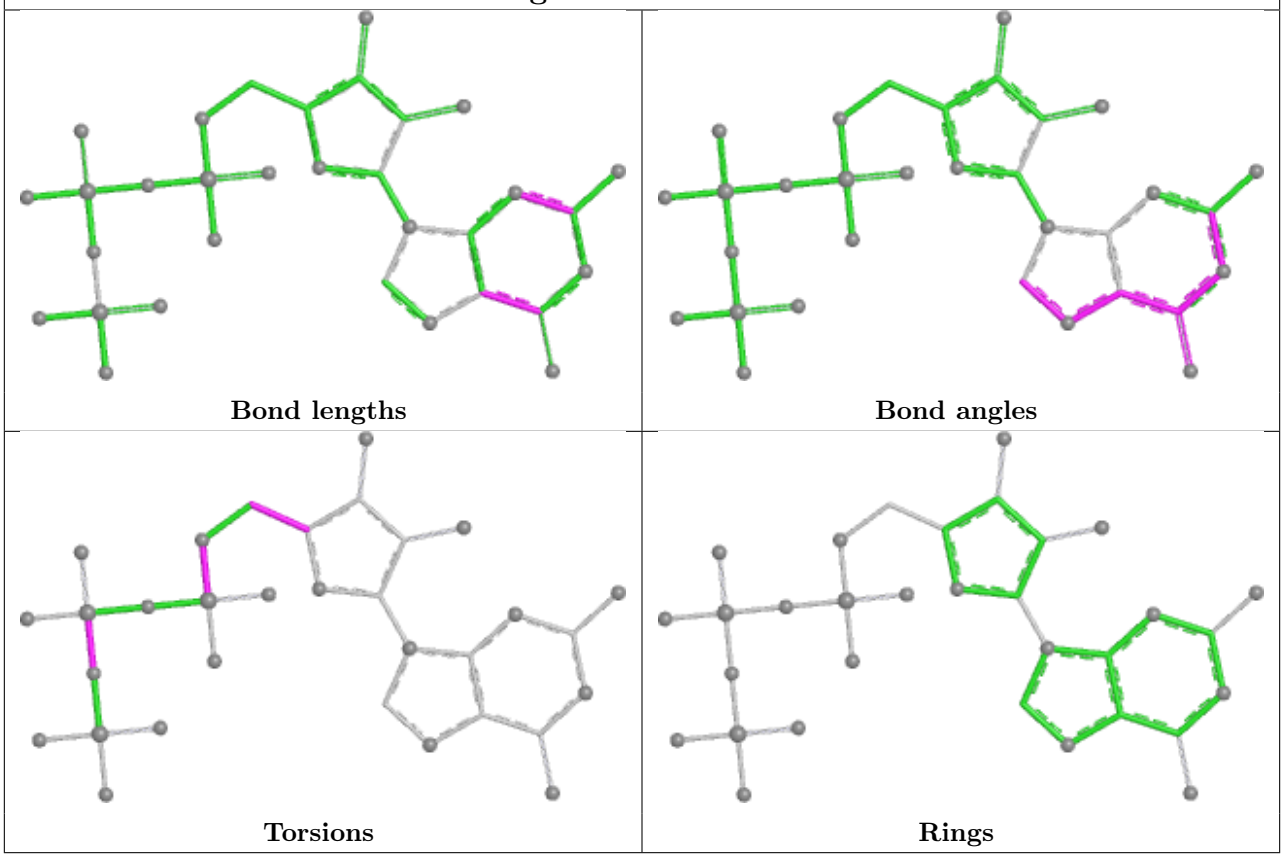
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand GTP t 501



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.

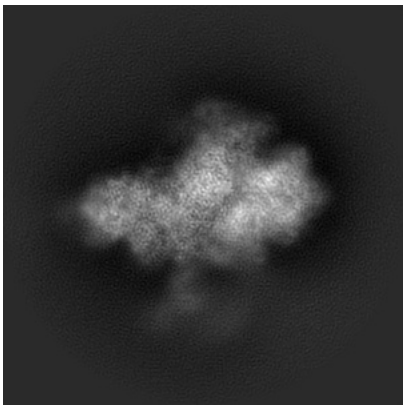
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-17696. These allow visual inspection of the internal detail of the map and identification of artifacts.

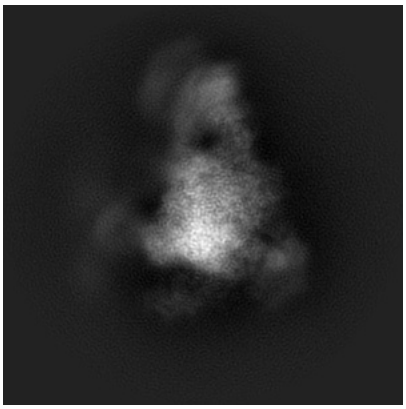
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

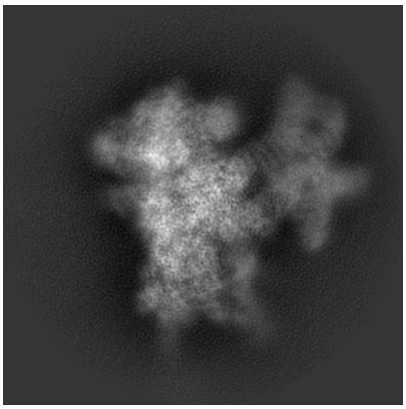
6.1.1 Primary map



X

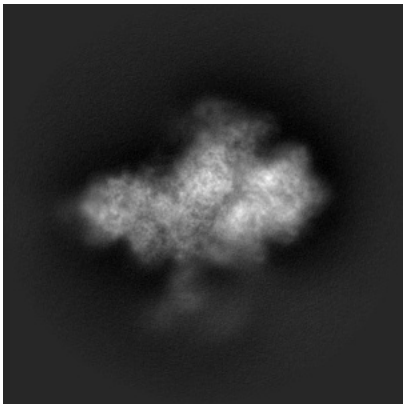


Y

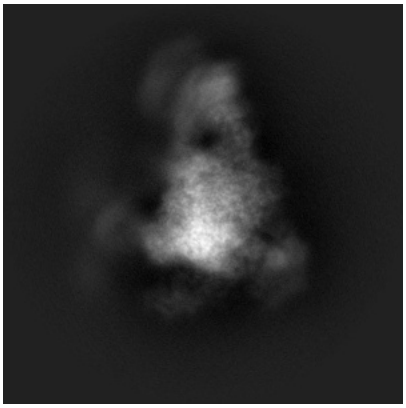


Z

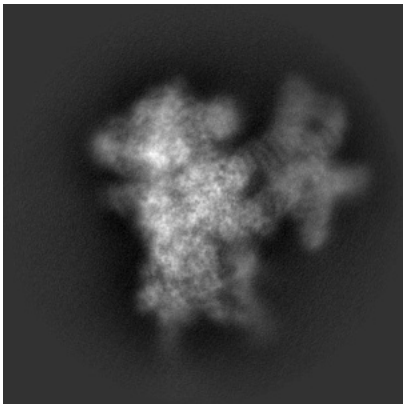
6.1.2 Raw map



X



Y

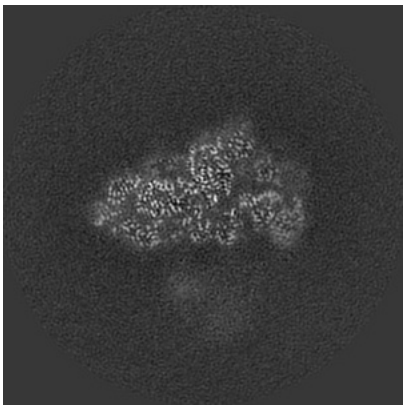


Z

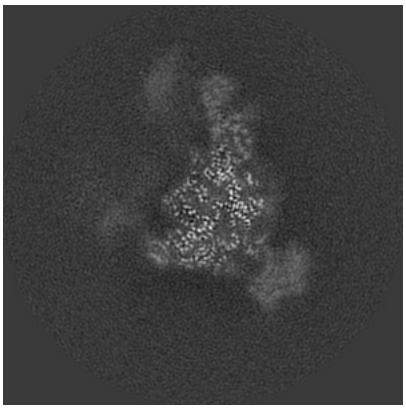
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

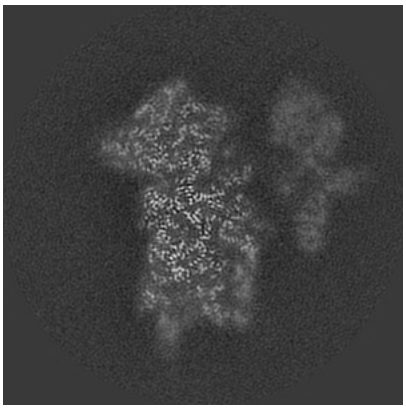
6.2.1 Primary map



X Index: 216

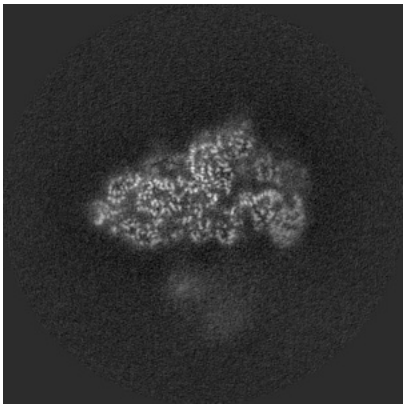


Y Index: 216

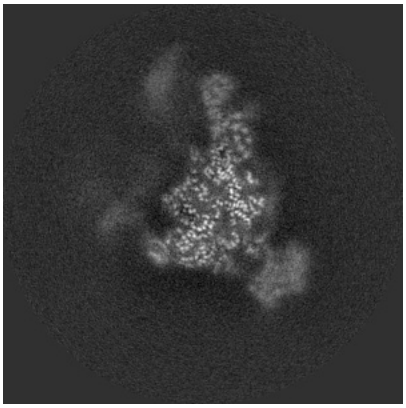


Z Index: 216

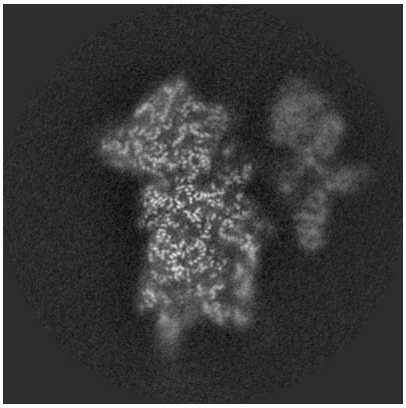
6.2.2 Raw map



X Index: 180



Y Index: 180

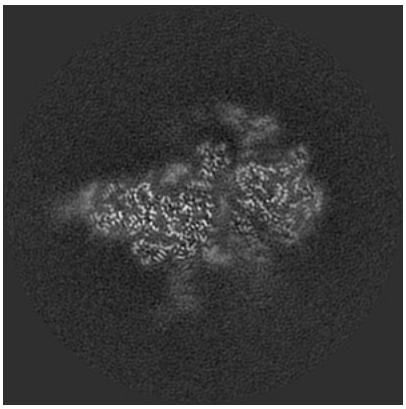


Z Index: 180

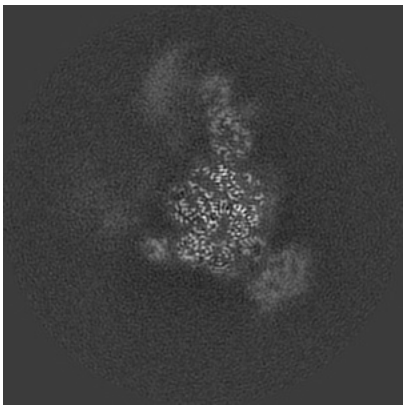
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

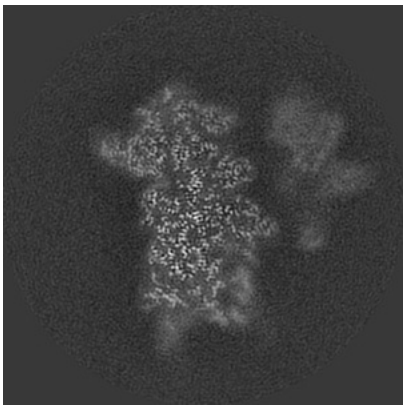
6.3.1 Primary map



X Index: 175

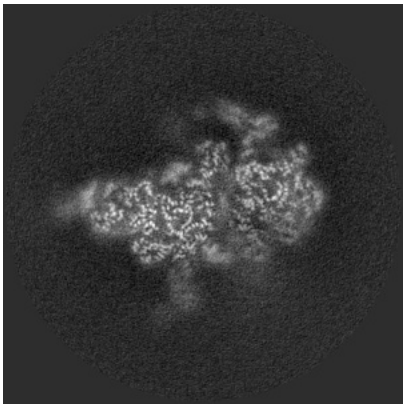


Y Index: 221

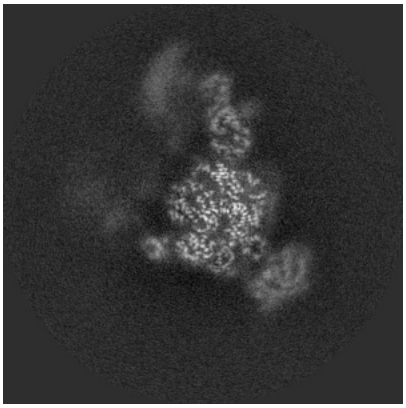


Z Index: 210

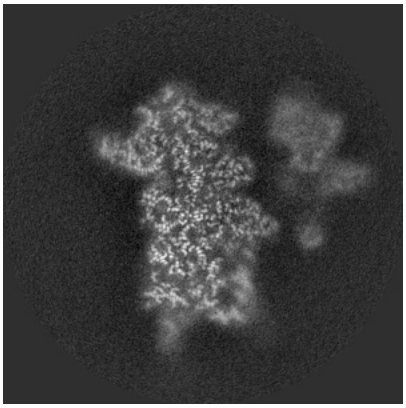
6.3.2 Raw map



X Index: 145



Y Index: 185

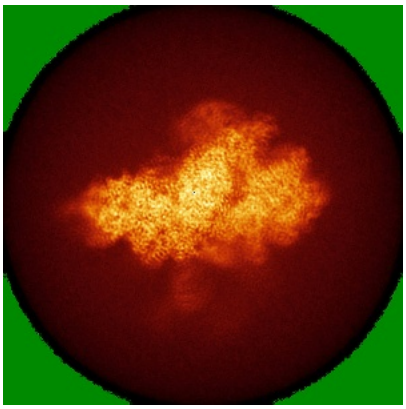


Z Index: 174

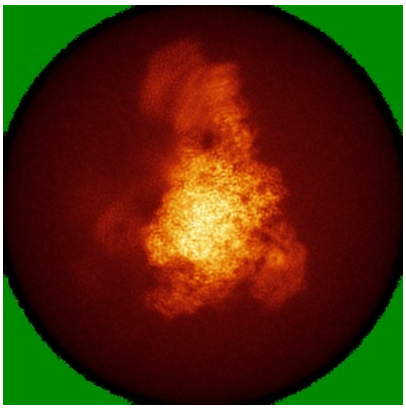
The images above show the largest variance slices of the map in three orthogonal directions.

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

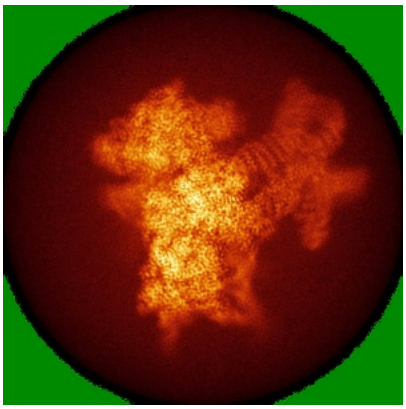
6.4.1 Primary map



X

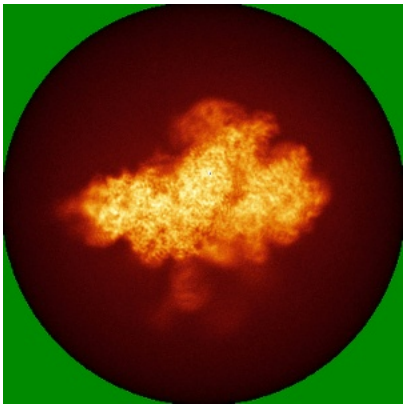


Y

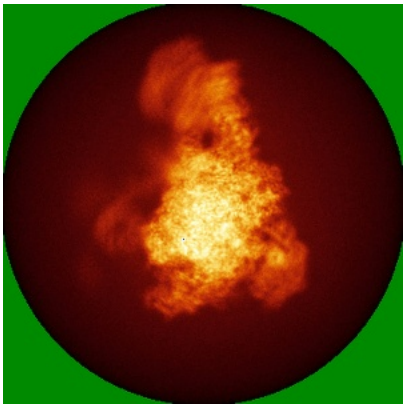


Z

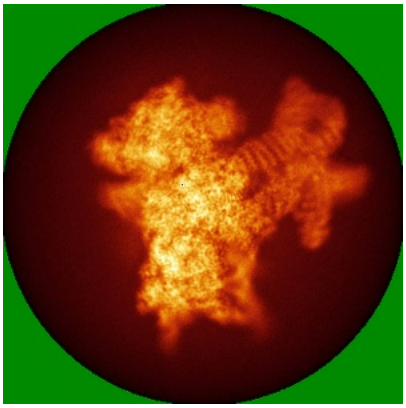
6.4.2 Raw map



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 4.0. 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.

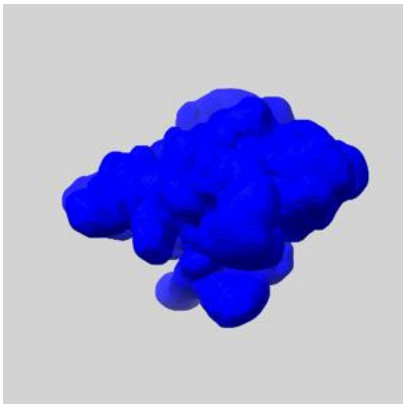
6.6 Mask visualisation

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

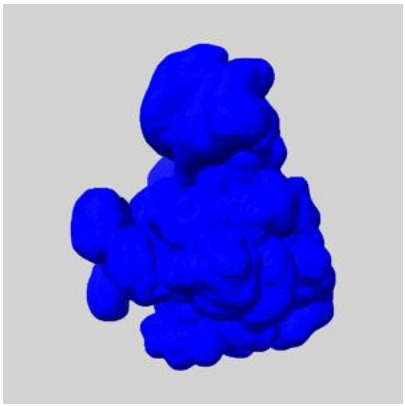
A mask typically either:

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

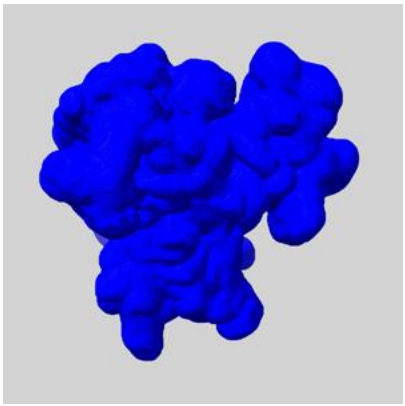
6.6.1 emd_17696_msk_1.map



X



Y

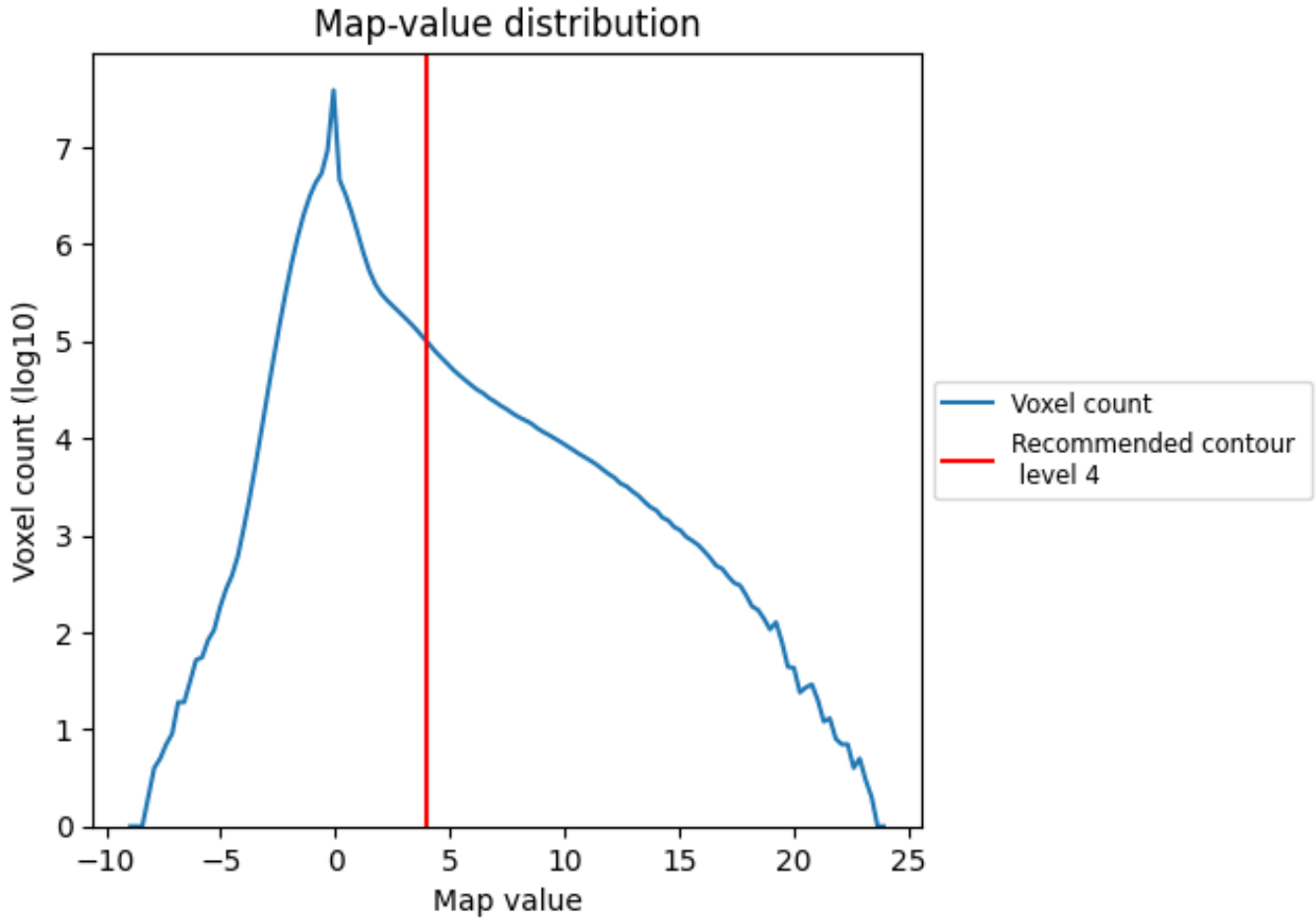


Z

7 Map analysis

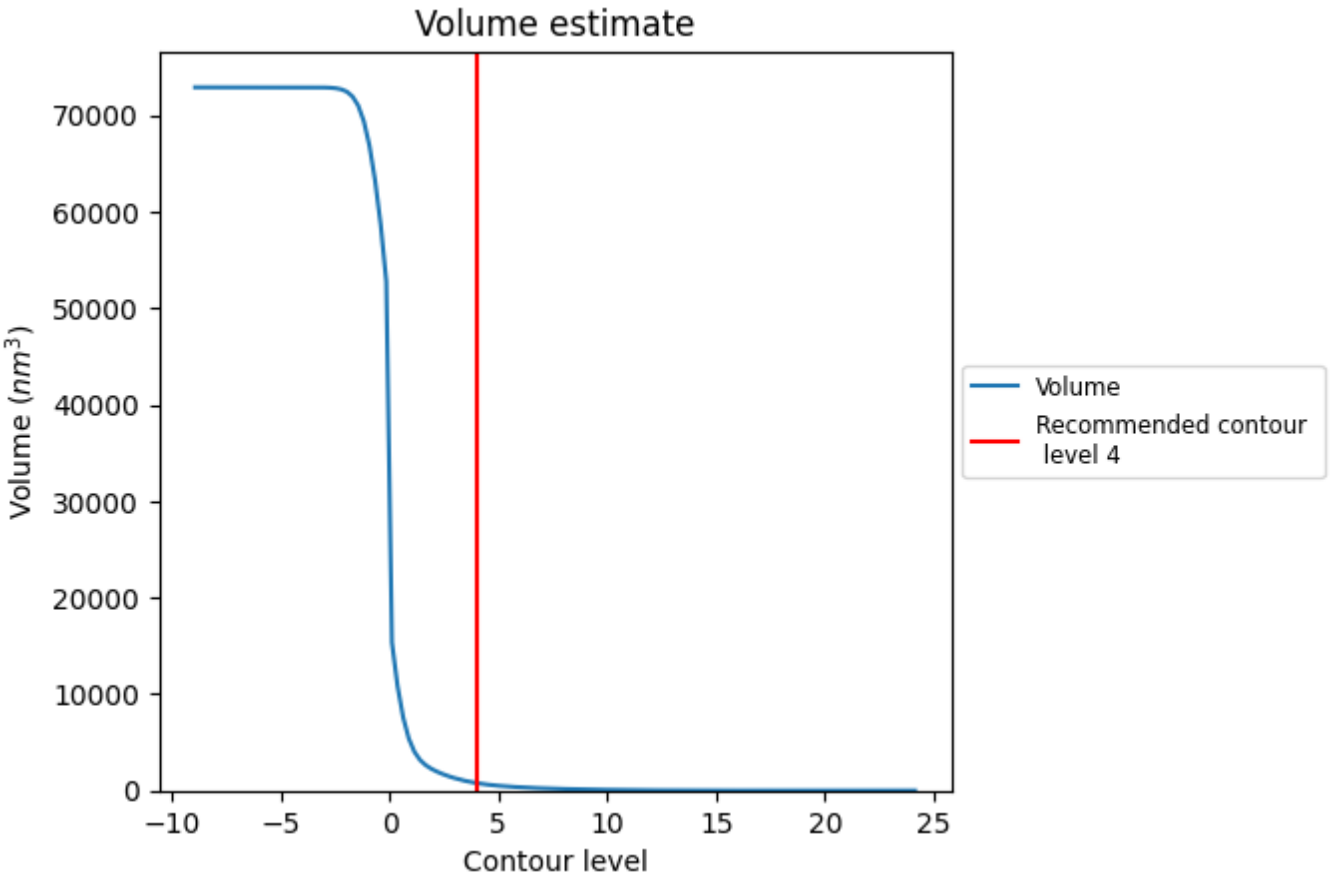
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

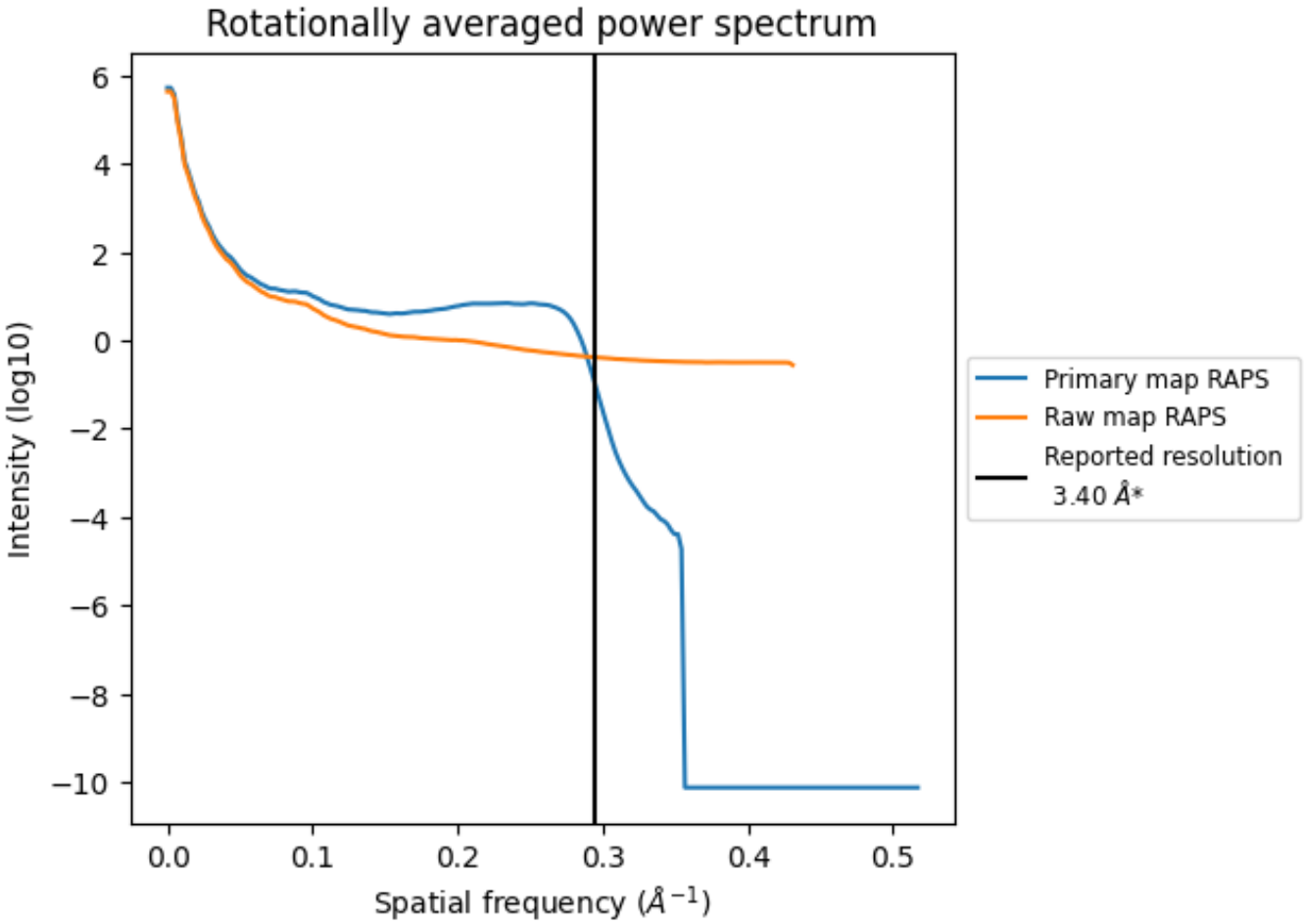
7.2 Volume estimate (i)



The volume at the recommended contour level is 777 nm^3; this corresponds to an approximate mass of 702 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)

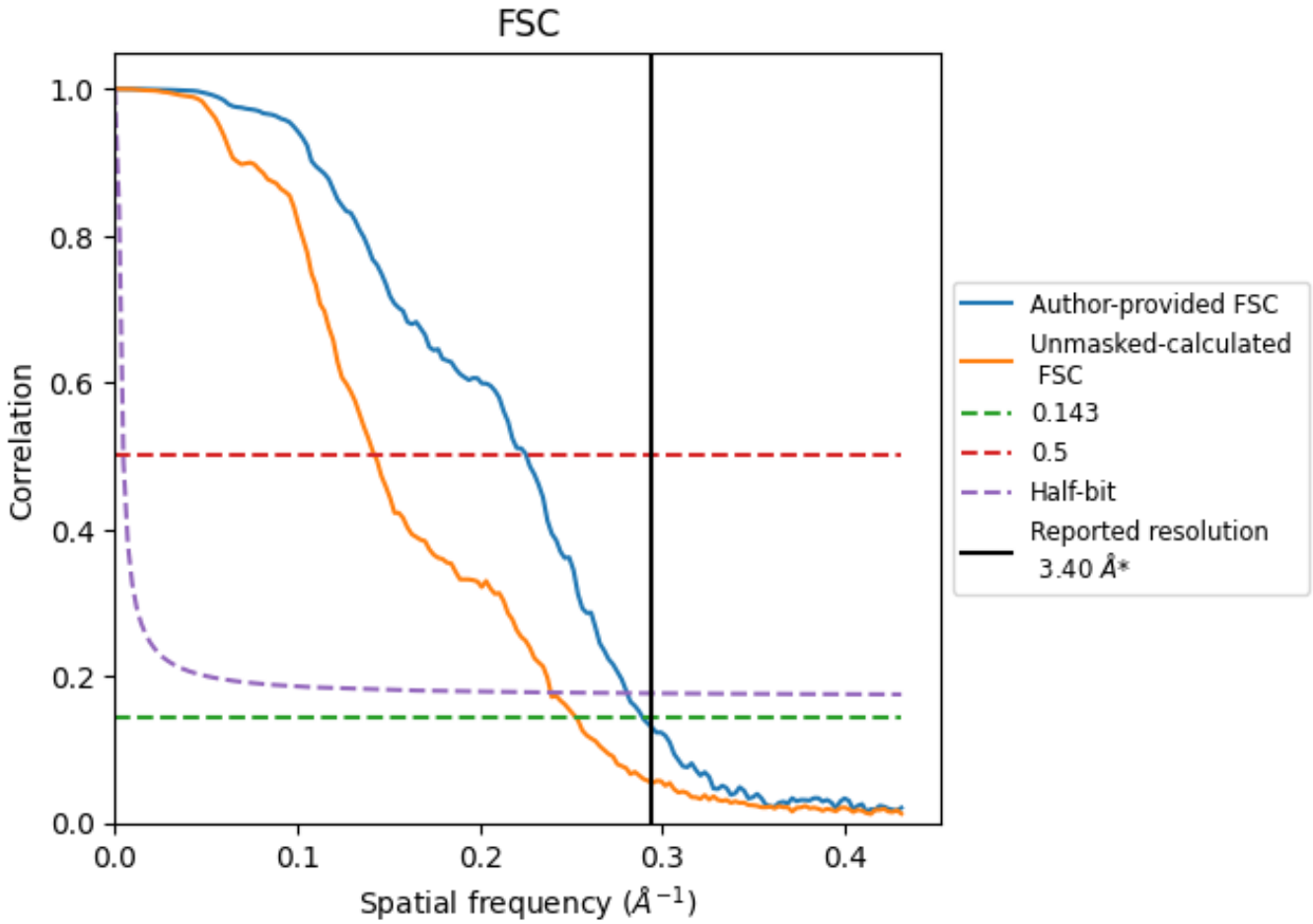


*Reported resolution corresponds to spatial frequency of 0.294 $Å^{-1}$

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.294 Å^{-1}

8.2 Resolution estimates (i)

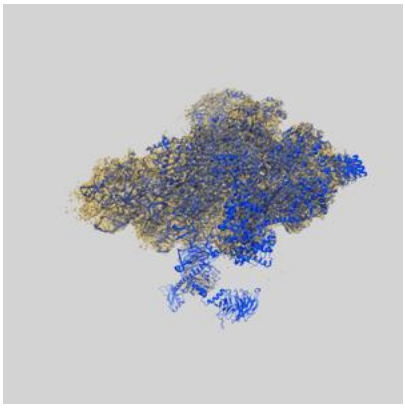
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.46	4.43	3.56
Unmasked-calculated*	3.96	7.02	4.19

*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 3.96 differs from the reported value 3.4 by more than 10 %

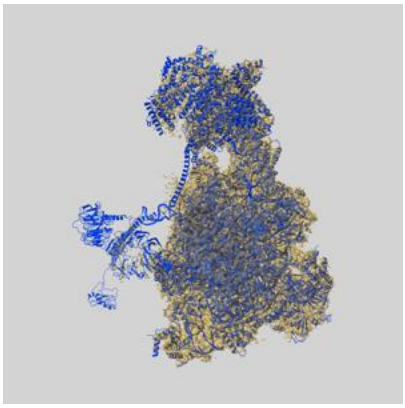
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-17696 and PDB model 8PJ1. Per-residue inclusion information can be found in section 3 on page 15.

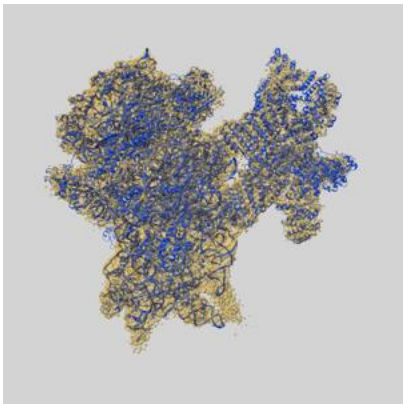
9.1 Map-model overlay



X



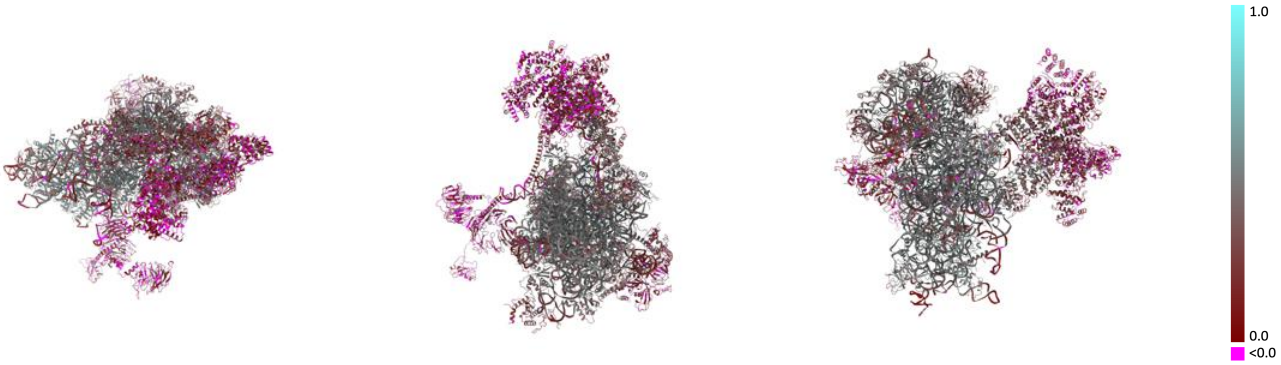
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 4.0 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.

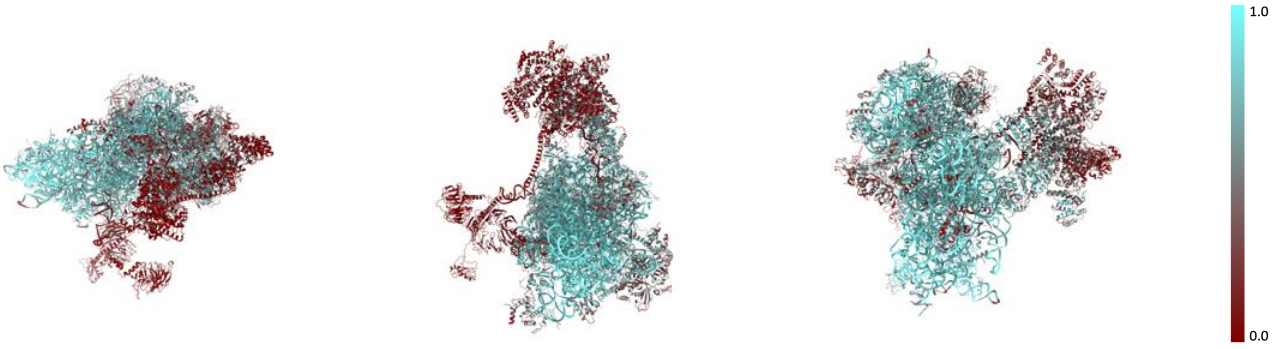
9.2 Q-score mapped to coordinate model



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.

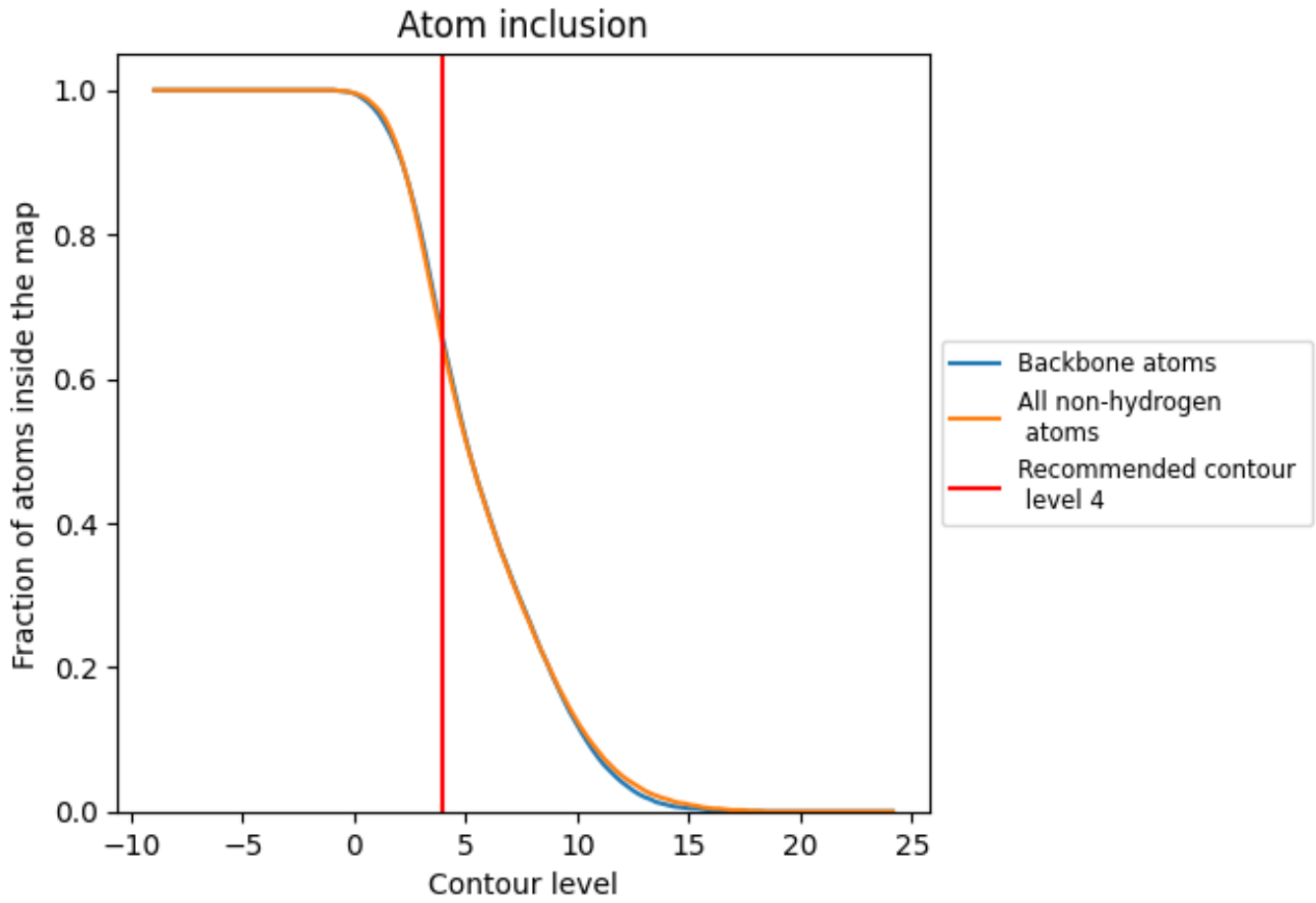
9.3 Atom inclusion mapped to coordinate model



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 (4).

9.4 Atom inclusion (i)



At the recommended contour level, 65% of all backbone atoms, 64% 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 (4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6440	0.3680
1	0.0360	0.1280
2	0.0010	0.1030
3	0.0860	0.0960
4	0.1970	0.1250
5	0.0910	0.0960
6	0.2010	0.1480
7	0.2940	0.2100
8	0.2170	0.1350
9	0.6790	0.4710
A	0.9040	0.4360
B	0.8380	0.5120
C	0.8510	0.5170
D	0.8220	0.5000
E	0.8480	0.5240
F	0.7070	0.4540
G	0.7250	0.4520
H	0.7820	0.4910
I	0.8020	0.4990
J	0.8410	0.5180
K	0.7740	0.4930
L	0.7640	0.4920
M	0.6780	0.4520
N	0.7880	0.4960
O	0.7900	0.4840
P	0.7840	0.4810
Q	0.8440	0.5230
R	0.8540	0.4880
S	0.8060	0.4460
T	0.8690	0.5030
V	0.7300	0.4670
Y	0.7770	0.4750
Z	0.6300	0.4460
a	0.6600	0.4140
b	0.6490	0.4180

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
c	0.6500	0.4070
d	0.7950	0.4590
e	0.6990	0.4350
f	0.7070	0.4220
h	0.6220	0.4380
i	0.8530	0.4940
k	0.4480	0.2430
m	0.3430	0.2390
n	0.5900	0.4560
o	0.2420	0.2490
p	0.5620	0.4100
q	0.6710	0.4500
r	0.5010	0.3140
s	0.4910	0.3350
t	0.3330	0.1900
u	0.4040	0.2780
v	0.3690	0.1990
w	0.8210	0.2820
x	0.4000	0.3140
y	0.4760	0.3240