wwPDB EM Validation Summary Report

Oct 28, 2026 – 05:31 pm GMT

PDB ID	:	9SJ4 / pdb_00009sj4
EMDB ID	:	EMD-54937
Title	:	Structure of a circMbl 48S translation initiation complex in the scanning state
Authors	:	Zuber, P.K.; Li, X.; Du, Y.; Gordiyenko, Y.; Haddad, T.F.M.; Ramakrishnan, V.
Deposited on	:	2025-08-29
Resolution	:	3.10 Å(reported)
Based on initial models	:	6ZMW, 1YFG

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:

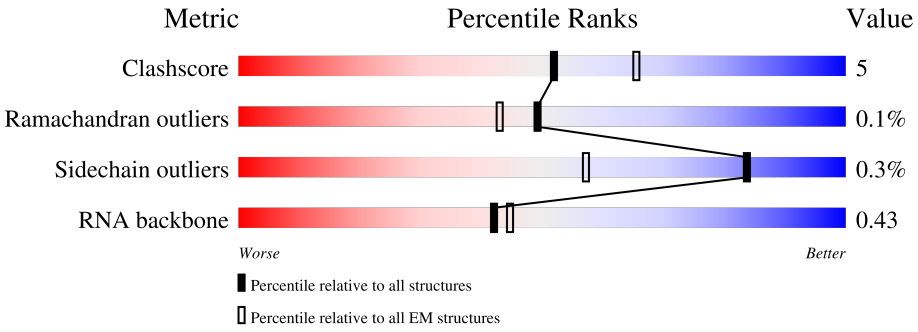
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

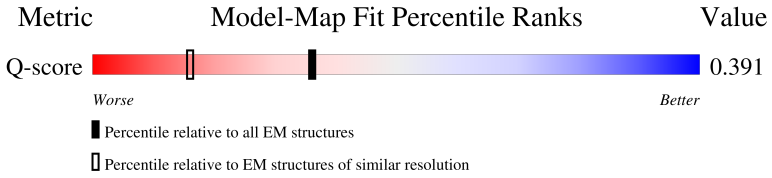
1 Overall quality at a glance

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

The reported resolution of this entry is 3.10 Å.

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





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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

Mol	Chain	Length	Quality of chain
1	A	1382	36% 47% 6% 47%
2	B	445	76% 82% 9% 9%
3	D	315	42% 71% 16% 13%

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Mol	Chain	Length	Quality of chain
4	E	472	66% 72% 25%
5	F	325	100% 97%
6	G	147	34% 46% 14% 41%
7	H	116	9% 56% 17% 27%
8	I	814	70% 61% 9% 29%
9	J	913	36% 59% 11% 29%
10	L	194	79% 12% 8%
11	M	84	75% 19%
12	N	83	94% 6%
13	O	293	67% 8% 25%
14	P	264	66% 14% 20%
15	Q	295	63% 9% 27%
16	R	115	79% 7% 14%
17	S	249	76% 16% 8%
18	T	151	74% 13% 12%
19	U	333	34% 35% 6% 59%
20	V	151	89% 10%
21	W	1869	57% 28% 7% 8%
22	X	158	84% 6% 10%
23	Y	263	90% 7%
24	Z	194	72% 19% 9%
25	7	320	24% 22% 76%
26	9	25	12% 72% 24%
27	a	143	91% 7%
28	b	59	15% 85% 12%

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Mol	Chain	Length	Quality of chain
29	c	130	92% 8%
30	d	208	75% 19% 5%
31	e	133	80% 14% 6%
32	f	204	68% 22% 10%
33	g	146	76% 20%
34	h	243	10% 73% 20% 7%
35	i	165	10% 47% 13% 40%
36	j	145	12% 60% 17% 22%
37	k	317	23% 69% 29%
38	m	125	10% 50% 6% 44%
39	o	56	77% 21%
40	p	80	28% 55% 11% 34%
41	q	132	56% 79% 14% 8%
42	s	69	13% 86% 6% 9%
43	v	135	5% 82% 15%
44	w	119	9% 76% 10% 13%
45	x	548	72% 66% 12% 23%
46	6	374	88% 80% 12% 6%
47	4	357	68% 69% 28%
48	8	352	88% 86% 5% 10%
49	3	218	97% 98%
50	l	145	83% 14%
51	y	75	5% 55% 29% 12%
52	n	152	11% 74% 20% 7%
53	z	774	100%

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Mol	Chain	Length	Quality of chain
54	5	564	

2 Entry composition (i)

There are 57 unique types of molecules in this entry. The entry contains 113724 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 A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	733	Total	C	N	O	S	1	0
			5518	3460	1009	1026	23		

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

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

- Molecule 3 is a protein called Eukaryotic translation initiation factor 2 subunit 1.

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

- Molecule 4 is a protein called Eukaryotic translation initiation factor 2 subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	E	356	Total	C	N	O	0	0
			1750	1038	356	356		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
5	F	325	Total	C	N	O	0	0
			1598	947	325	326		

- Molecule 6 is a protein called Eukaryotic translation initiation factor 1A, X-chromosomal.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	87	Total	C	N	O	S	0	0
			705	446	128	127	4		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-2	GLY	-	expression tag	UNP P47813
G	-1	ALA	-	expression tag	UNP P47813
G	0	HIS	-	expression tag	UNP P47813

- Molecule 7 is a protein called Eukaryotic translation initiation factor 1.

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

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	-2	GLY	-	expression tag	UNP P41567
H	-1	ALA	-	expression tag	UNP P41567
H	0	HIS	-	expression tag	UNP P41567

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	575	Total	C	N	O	S	0	0
			4569	2935	788	828	18		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	645	Total	C	N	O	S	0	0
			4940	3096	888	923	33		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	178	Total	C	N	O	S	0	0
			1439	923	262	253	1		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q	214	Total	C	N	O	S	0	0
			1695	1077	297	313	8		

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

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

- Molecule 17 is a protein called 40S ribosomal protein S6.

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

- Molecule 18 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	133	Total	C	N	O	S	0	0
			998	610	196	186	6		

- Molecule 19 is a protein called Eukaryotic translation initiation factor 2 subunit 2.

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

- Molecule 20 is a protein called 40S ribosomal protein S13.

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

- Molecule 21 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	1716	Total	C	N	O	P	0	0
			36675	16396	6572	11991	1716		

- Molecule 22 is a protein called 40S ribosomal protein S11.

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

- Molecule 23 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	257	Total	C	N	O	S	0	0
			2041	1305	379	349	8		

- Molecule 24 is a protein called 40S ribosomal protein S9.

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

- Molecule 25 is a protein called Eukaryotic translation initiation factor 3 subunit G.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	7	77	Total	C	N	O	0	0
			616	389	111	116		

- Molecule 26 is a protein called 60S ribosomal protein L41.

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

- Molecule 27 is a protein called 40S ribosomal protein S23.

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

- Molecule 28 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	57	Total	C	N	O	S	0	0
			452	279	99	73	1		

- Molecule 29 is a protein called 40S ribosomal protein S15a.

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

- Molecule 30 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	198	Total	C	N	O	S	0	0
			1628	1021	322	280	5		

- Molecule 31 is a protein called 40S ribosomal protein S24.

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

- Molecule 32 is a protein called 40S ribosomal protein S5.

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

- Molecule 33 is a protein called 40S ribosomal protein S16.

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

- Molecule 34 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	225	Total	C	N	O	S	0	0
			1752	1117	315	313	7		

- Molecule 35 is a protein called 40S ribosomal protein S10.

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

- Molecule 36 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	j	113	Total	C	N	O	S	0	0
			936	596	172	161	7		

- Molecule 37 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 38 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	70	Total	C	N	O	S	0	0
			559	360	102	96	1		

- Molecule 39 is a protein called 40S ribosomal protein S29.

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

- Molecule 40 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

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

- Molecule 41 is a protein called 40S ribosomal protein S12.

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

- Molecule 42 is a protein called 40S ribosomal protein S28.

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

- Molecule 43 is a protein called 40S ribosomal protein S17.

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

- Molecule 44 is a protein called 40S ribosomal protein S20.

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

- Molecule 45 is a protein called Eukaryotic translation initiation factor 3 subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	x	423	Total	C	N	O	S	0	0
			2838	1749	522	557	10		

- Molecule 46 is a protein called Eukaryotic translation initiation factor 3 subunit M.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	6	350	Total	C	N	O	S	0	0
			2099	1287	395	410	7		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
47	4	257	Total	C	N	O	0	0
			1272	757	257	258		

- Molecule 48 is a protein called Eukaryotic translation initiation factor 3 subunit H.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	8	317	Total	C	N	O	0	0
			1574	937	318	319		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
49	3	213	Total	C	N	O	0	0
			1057	631	213	213		

- Molecule 50 is a protein called 40S ribosomal protein S19.

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

- Molecule 51 is a RNA chain called tRNAi-Met.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	y	73	Total	C	N	O	P	0	0
			1597	715	290	518	74		

- Molecule 52 is a protein called 40S ribosomal protein S18.

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

- Molecule 53 is a RNA chain called circMbl-FLAG.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	z	3	Total	C	N	O	P	0	0
			67	30	15	19	3		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
54	5	319	Total	C	N	O	0	0
			1581	943	319	319		

- Molecule 55 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
55	R	1	Total	Zn	0
			1	1	
55	o	1	Total	Zn	0
			1	1	
55	p	1	Total	Zn	0
			1	1	

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	S	1	Total	Mg	0
			1	1	
56	W	75	Total	Mg	0
			75	75	

- Molecule 57 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
57	W	1	Total	K	0
			1	1	

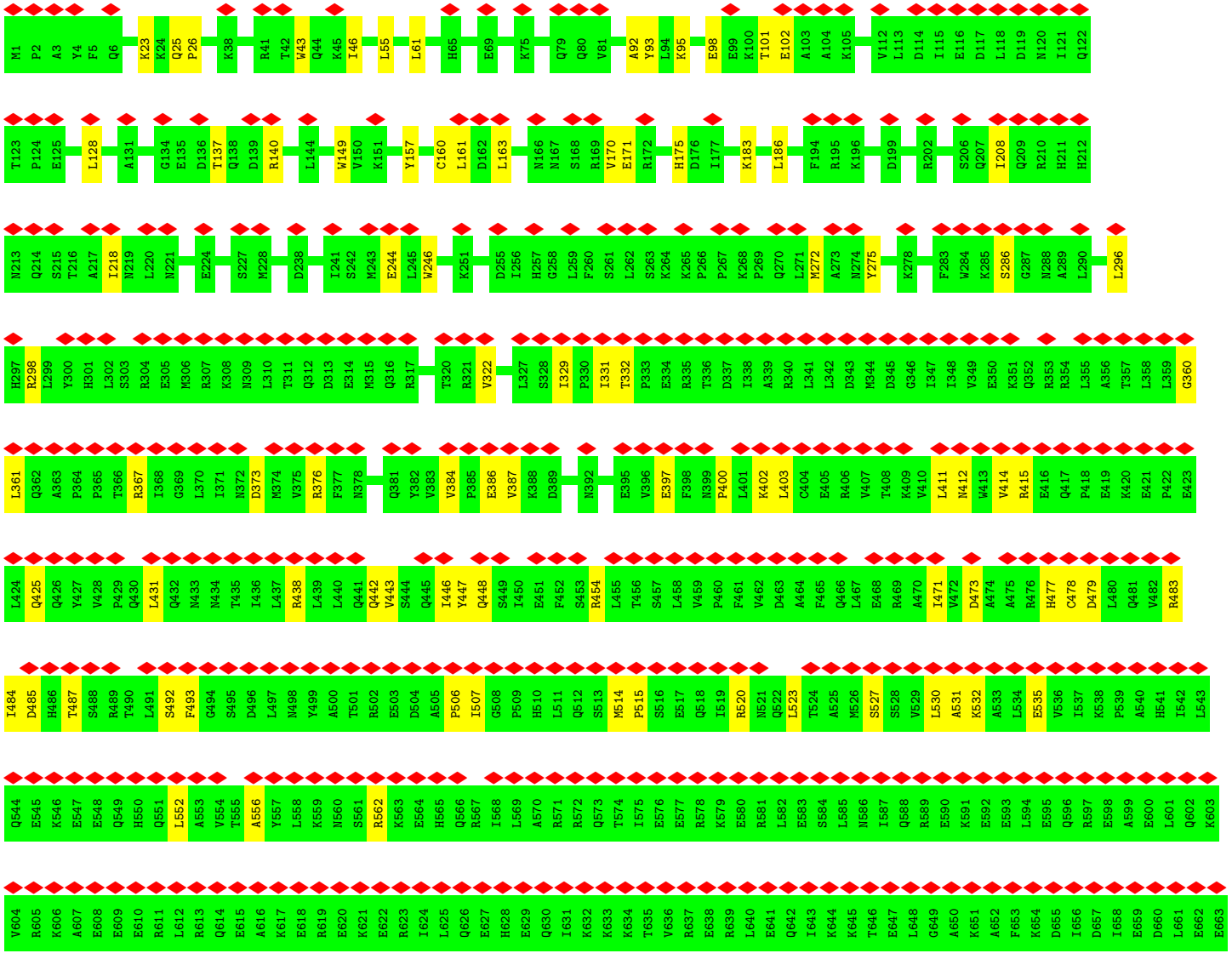
3 Residue-property plots (i)

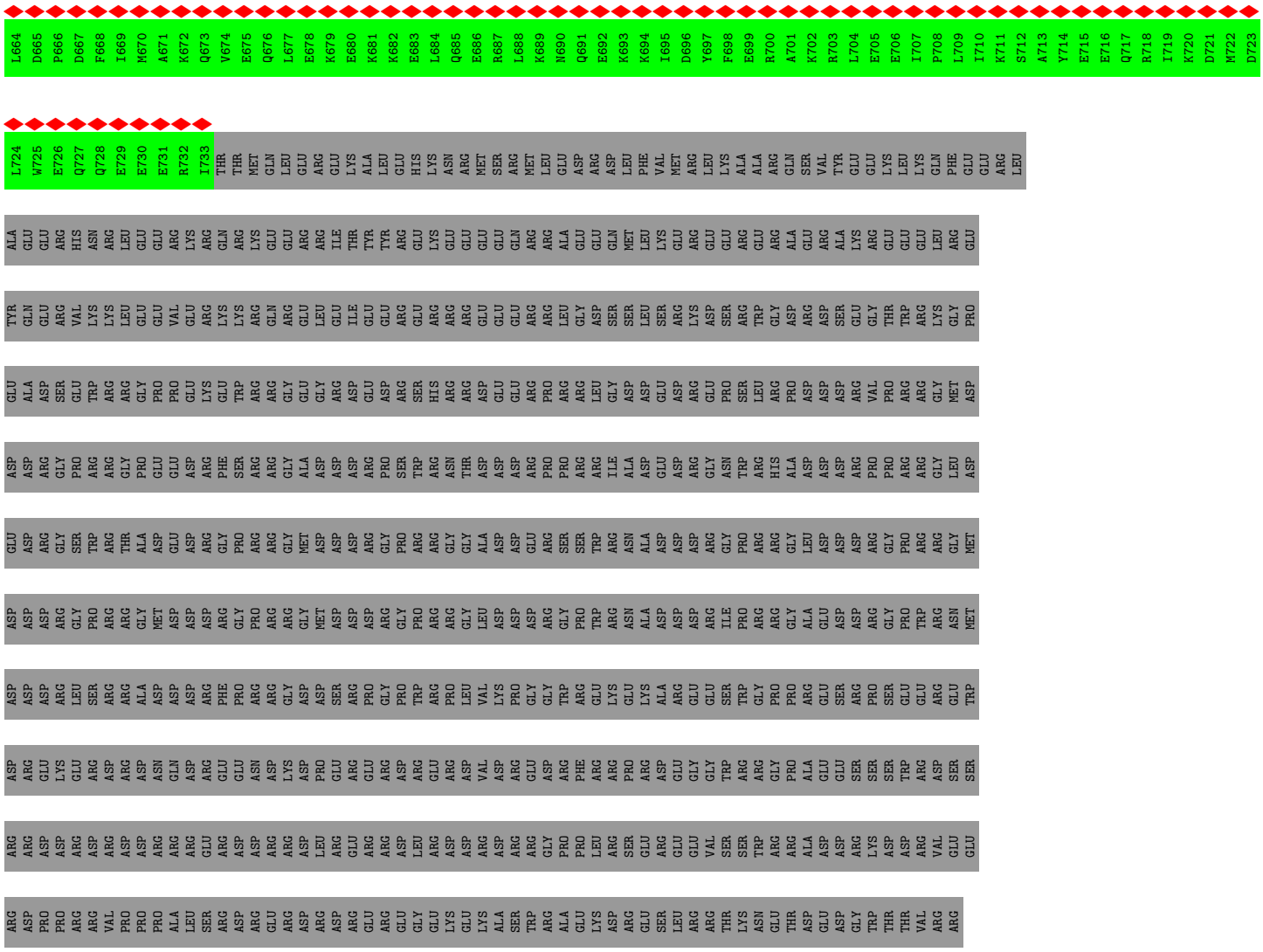
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 A

Chain A:



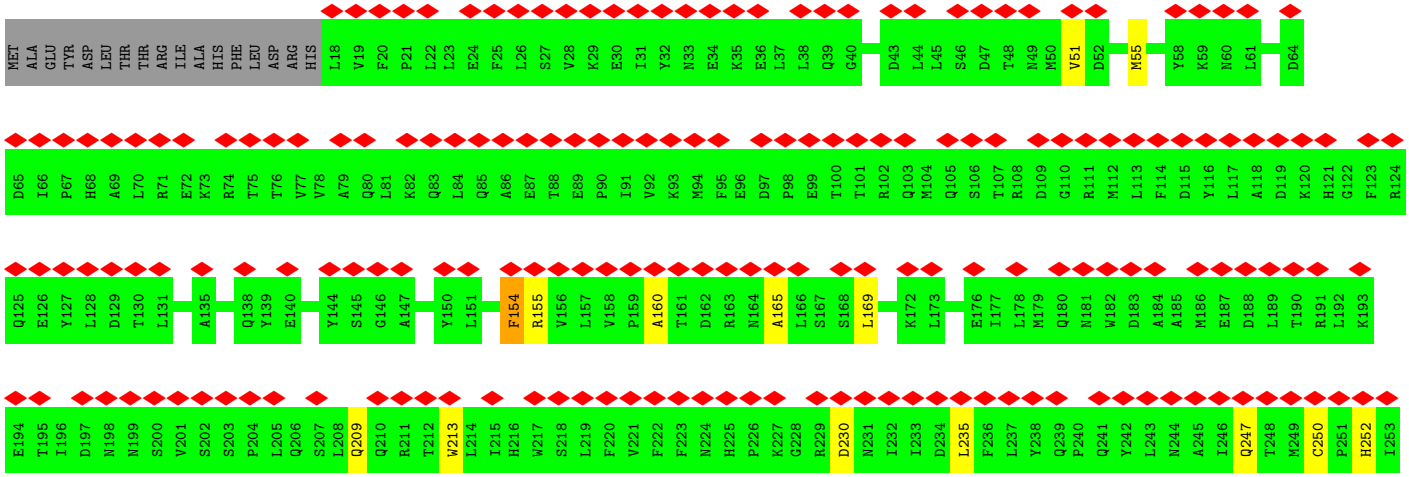




• Molecule 2: Eukaryotic translation initiation factor 3 subunit E

Chain B:



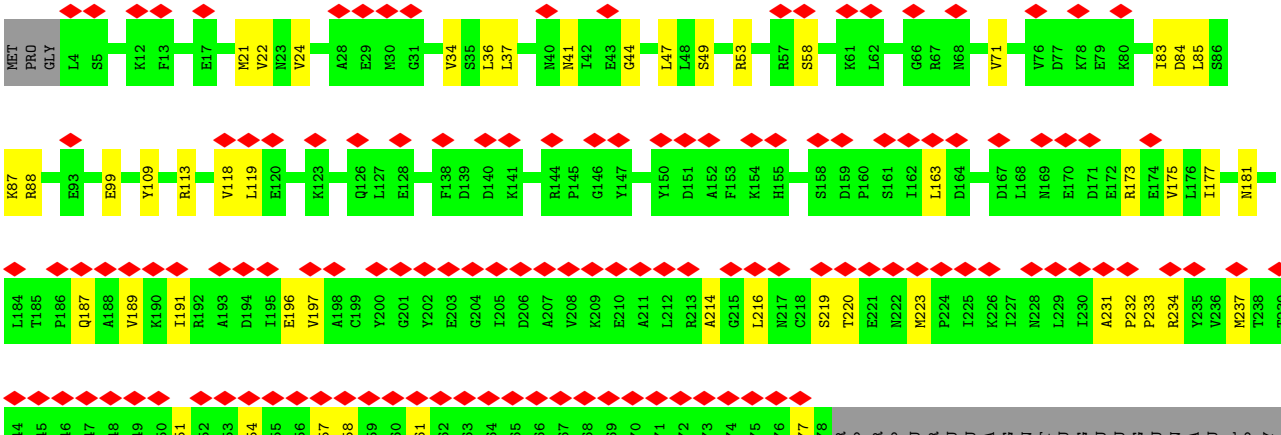




• Molecule 3: Eukaryotic translation initiation factor 2 subunit 1

Chain D:

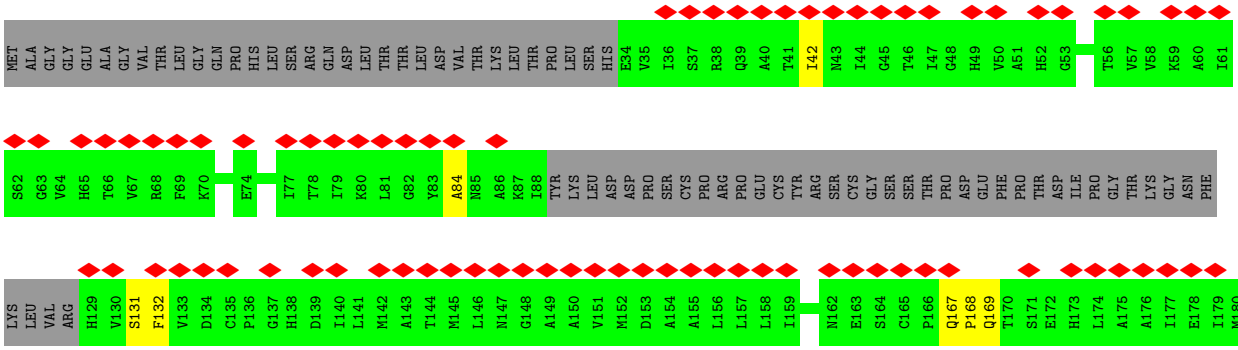


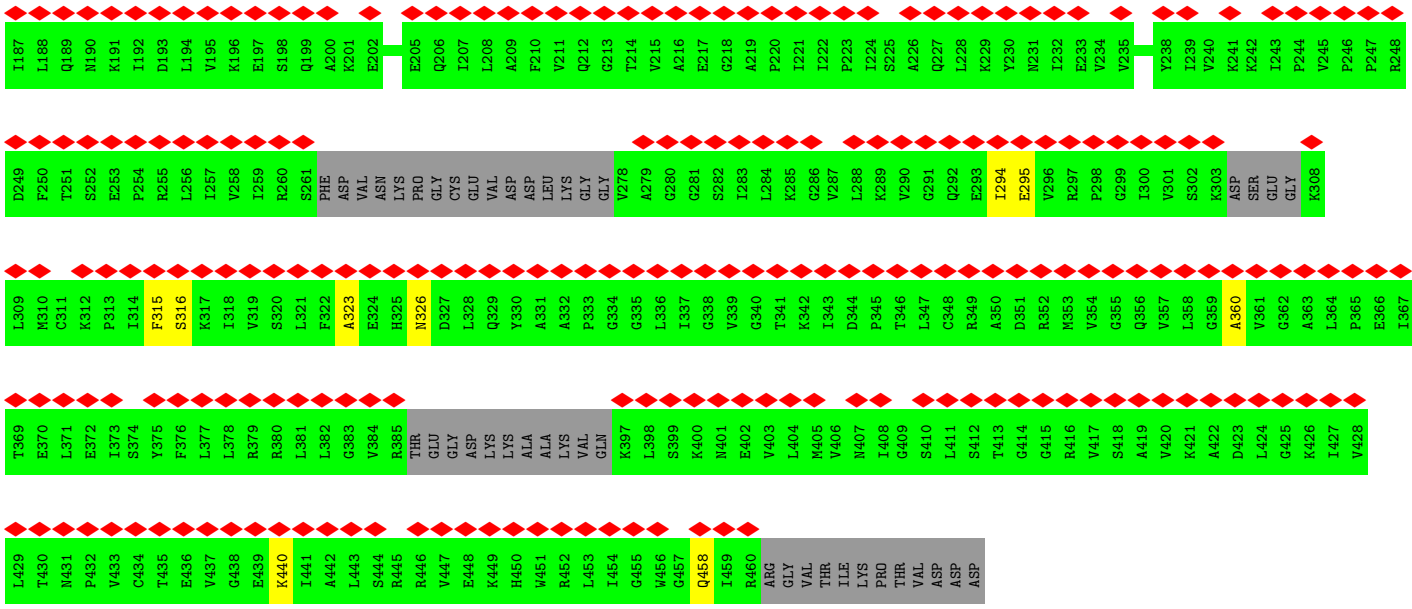


• Molecule 4: Eukaryotic translation initiation factor 2 subunit 3

Chain E:



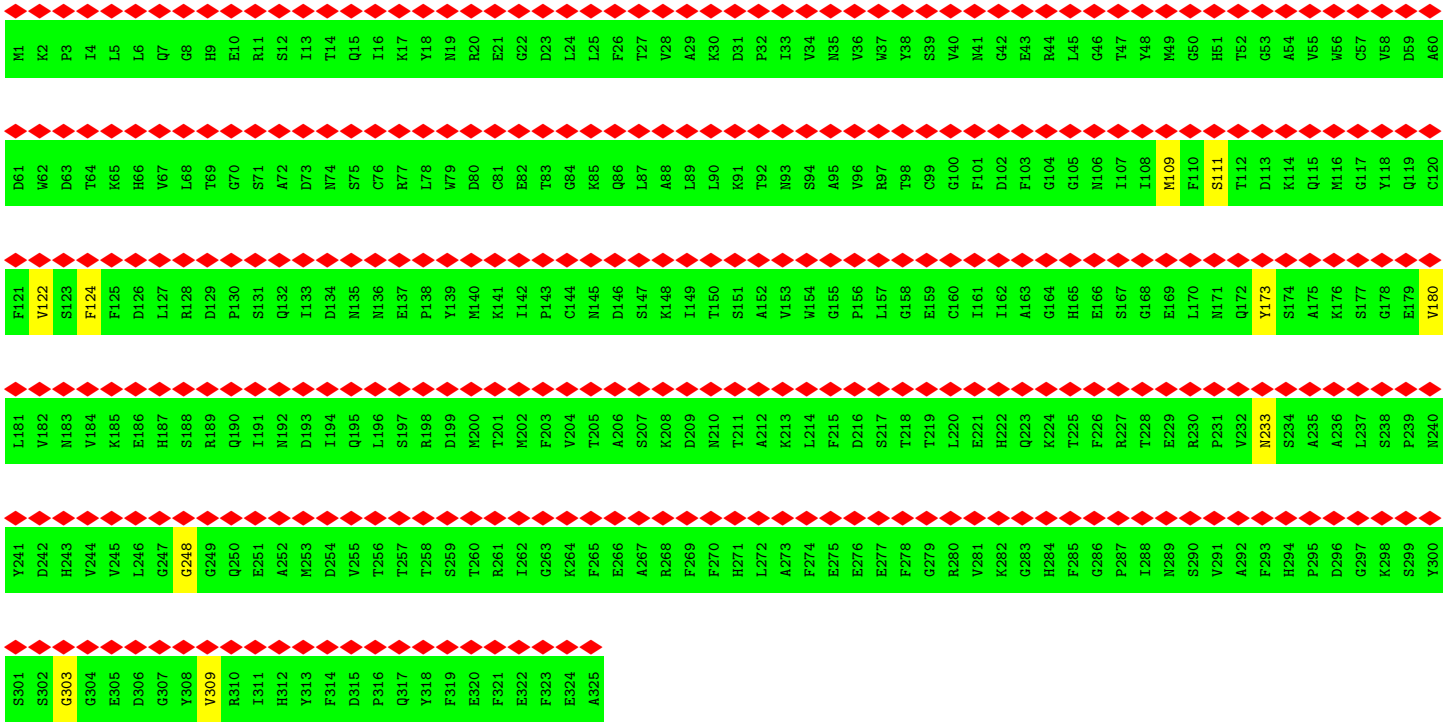




• Molecule 5: Eukaryotic translation initiation factor 3 subunit I

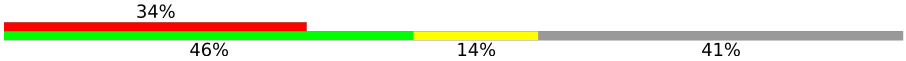
Chain F:

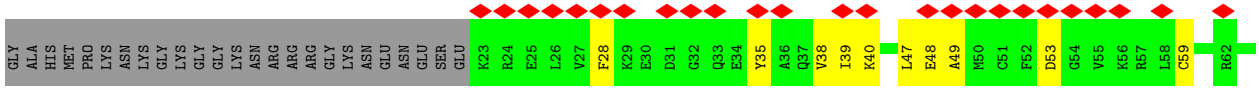


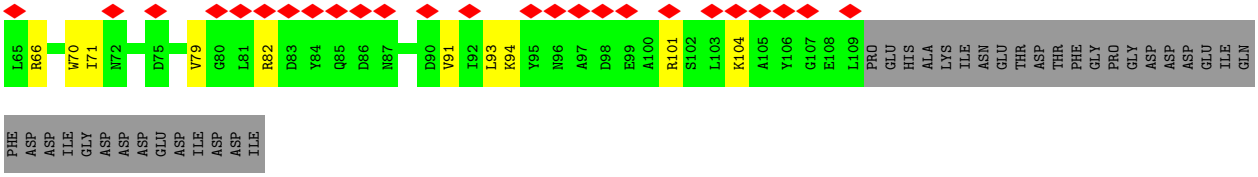


• Molecule 6: Eukaryotic translation initiation factor 1A, X-chromosomal

Chain G:



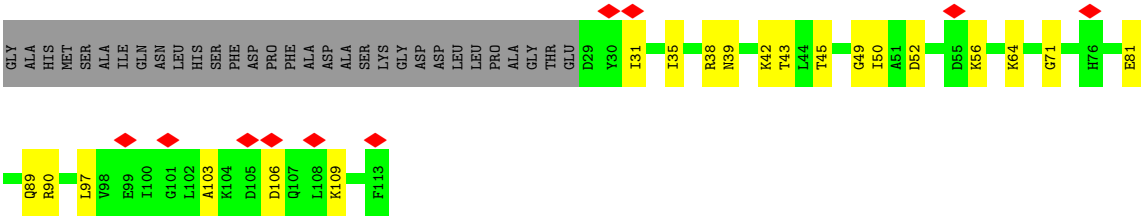




• Molecule 7: Eukaryotic translation initiation factor 1

Chain H:

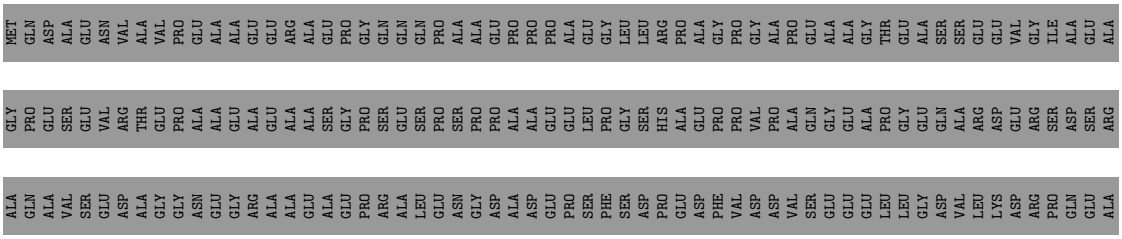


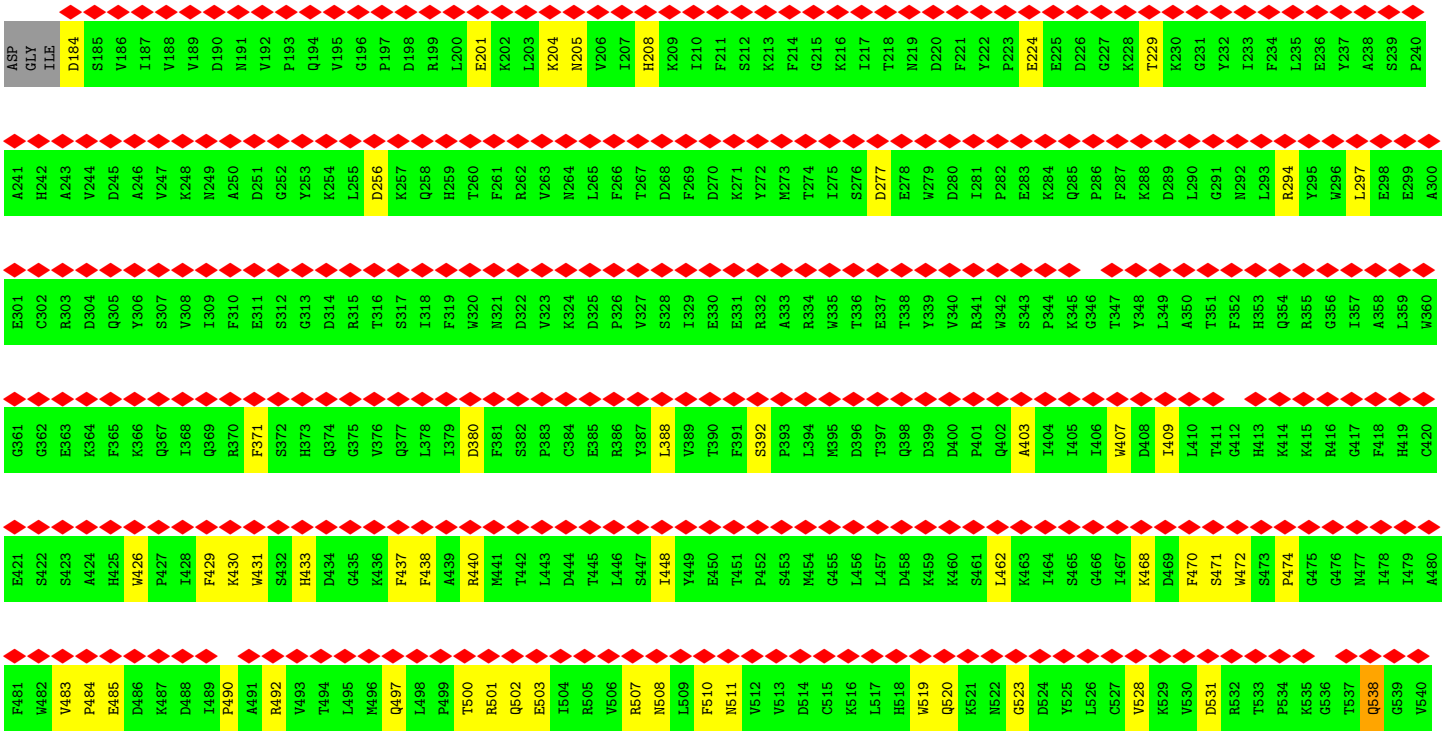


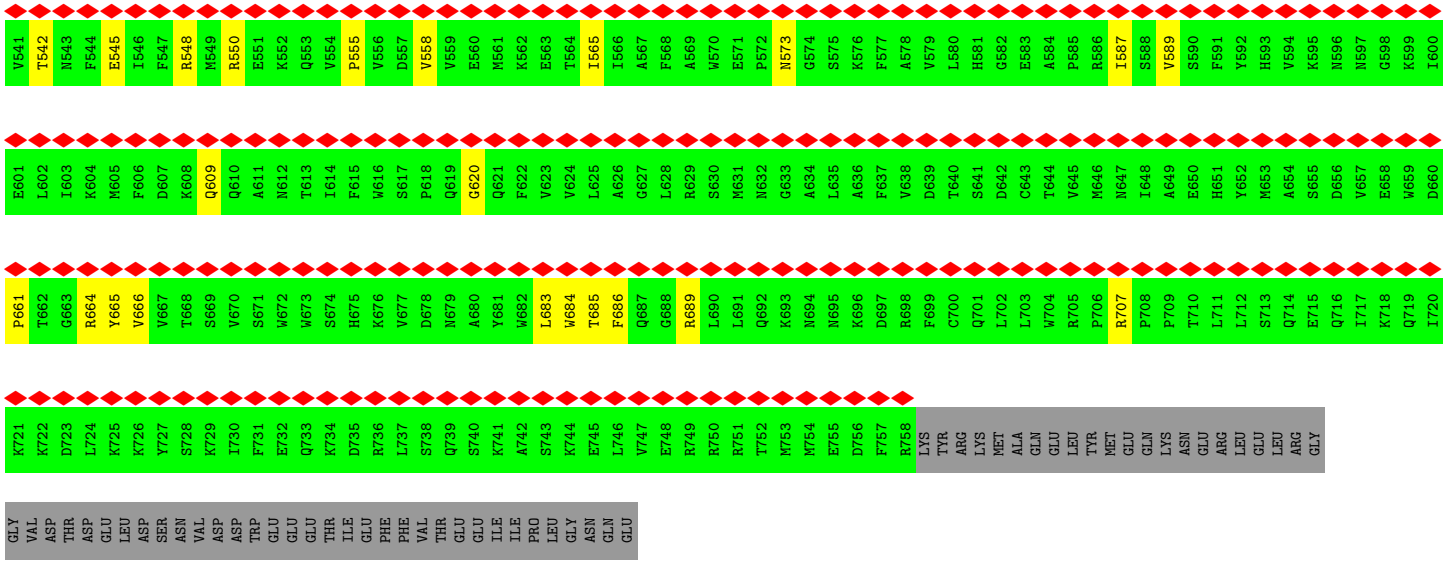
• Molecule 8: Eukaryotic translation initiation factor 3 subunit B

Chain I:





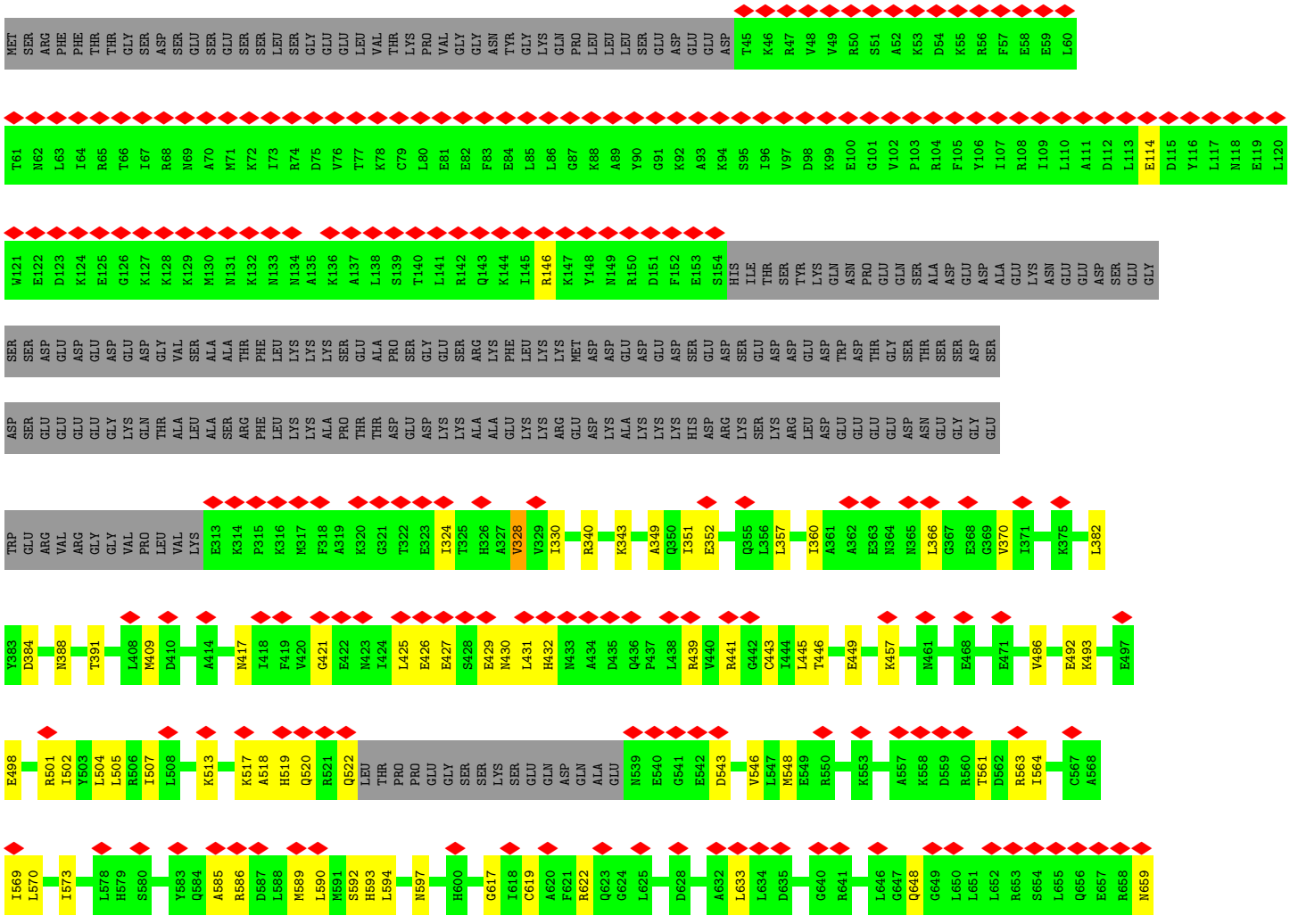


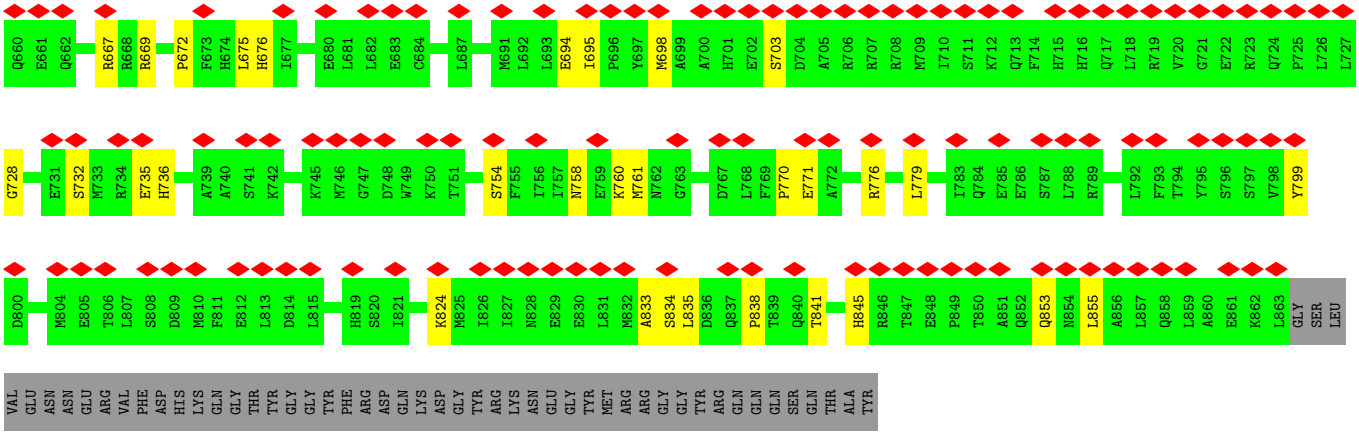


• Molecule 9: Eukaryotic translation initiation factor 3 subunit C

Chain J:



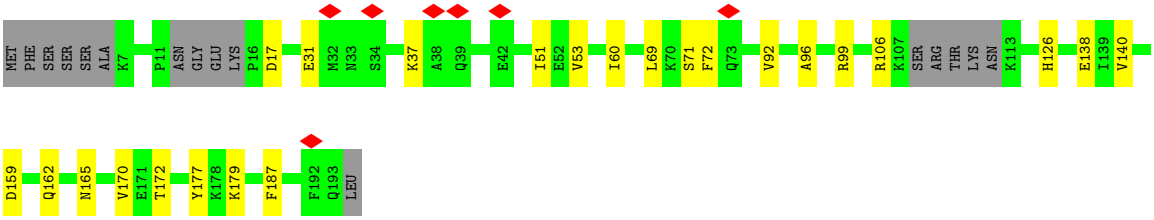




• Molecule 10: 40S ribosomal protein S7

Chain L:

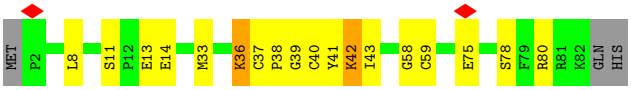




• Molecule 11: 40S ribosomal protein S27

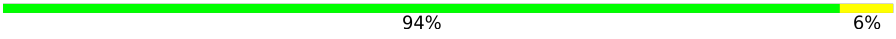
Chain M:

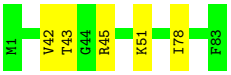




• Molecule 12: 40S ribosomal protein S21

Chain N:

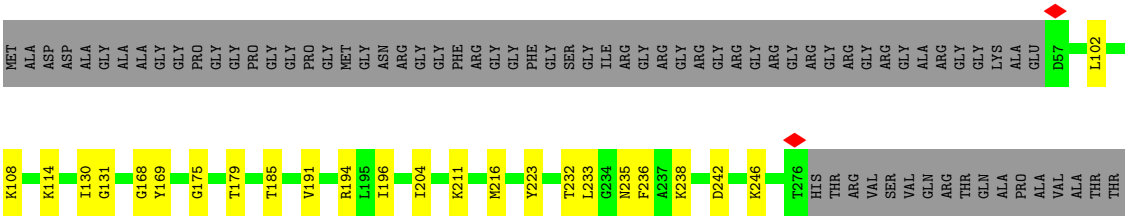




• Molecule 13: 40S ribosomal protein S2

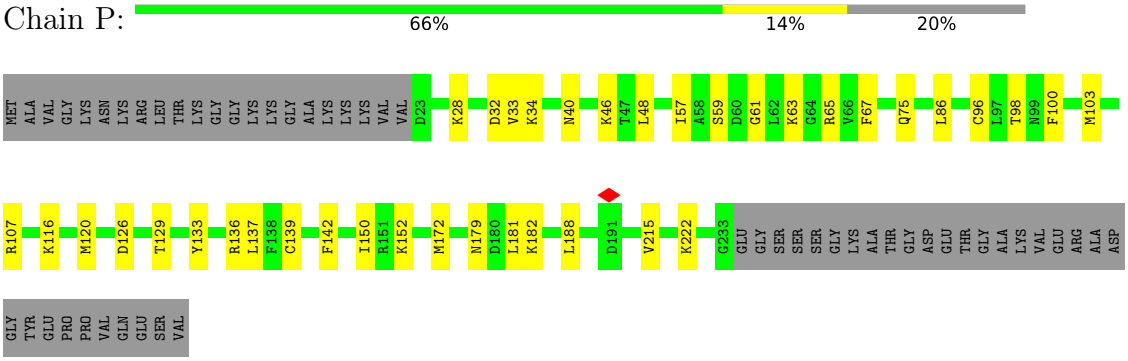
Chain O:





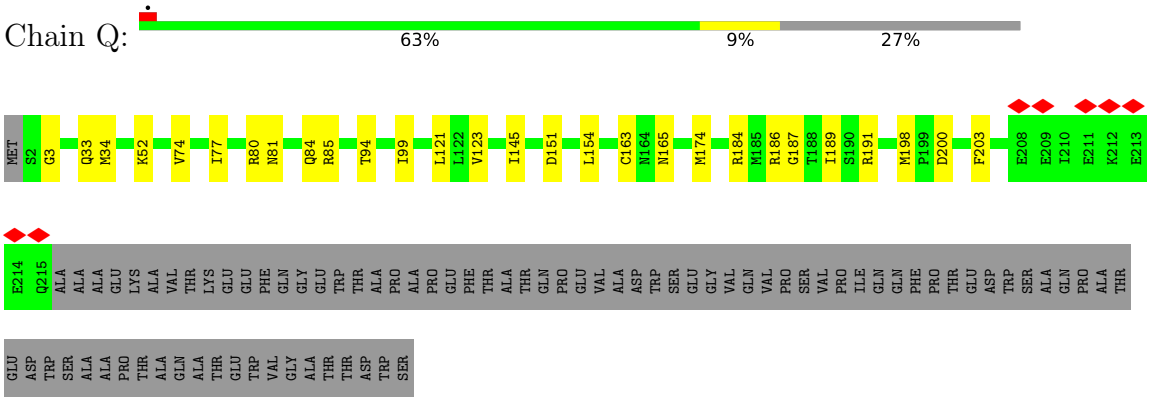
• Molecule 14: 40S ribosomal protein S3a

Chain P:



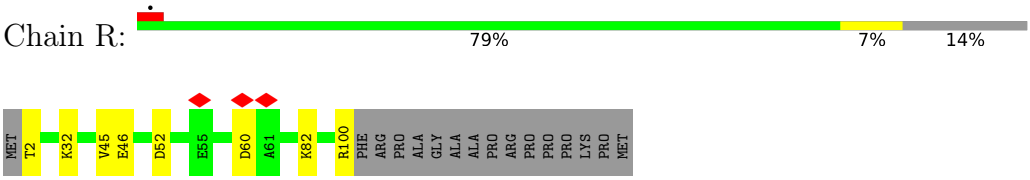
• Molecule 15: 40S ribosomal protein SA

Chain Q:



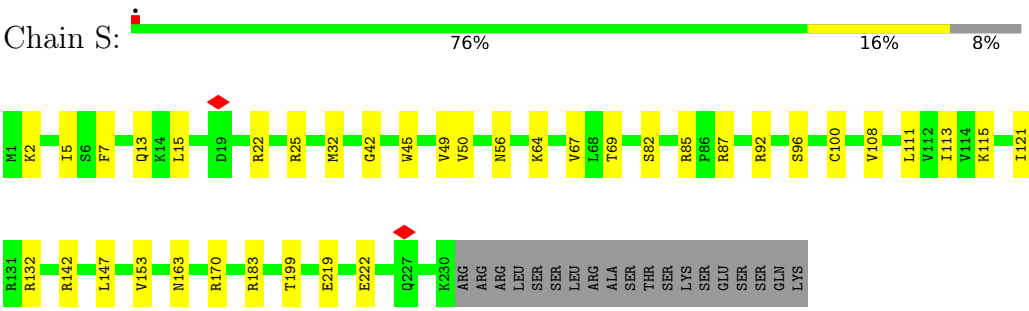
• Molecule 16: 40S ribosomal protein S26

Chain R:



• Molecule 17: 40S ribosomal protein S6

Chain S:



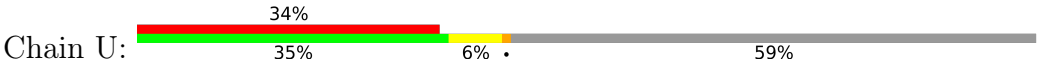
• Molecule 18: 40S ribosomal protein S14

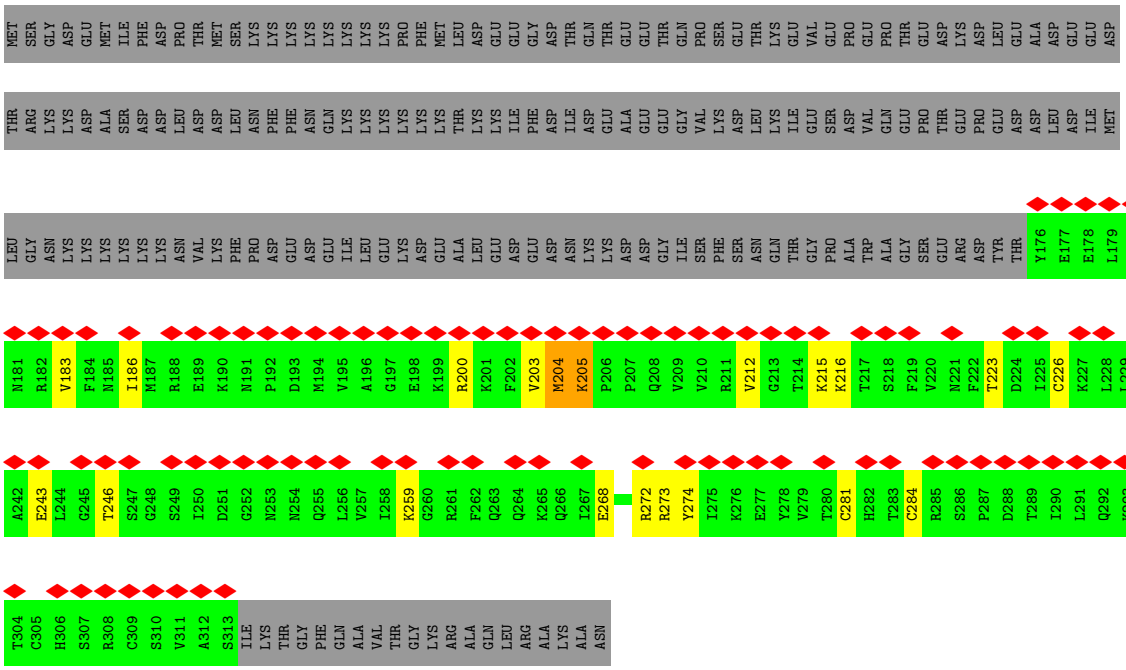
Chain T:



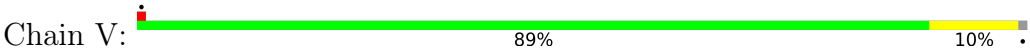


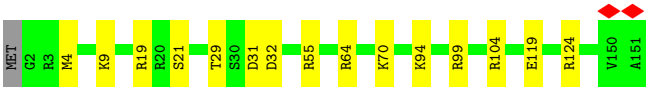
• Molecule 19: Eukaryotic translation initiation factor 2 subunit 2





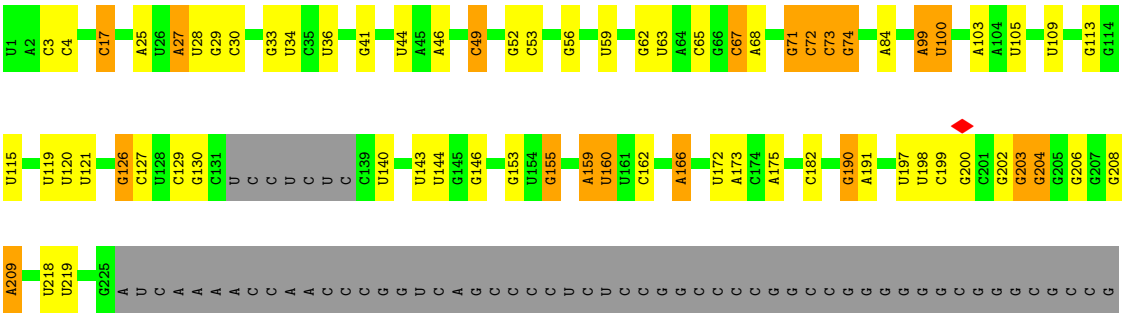
• Molecule 20: 40S ribosomal protein S13

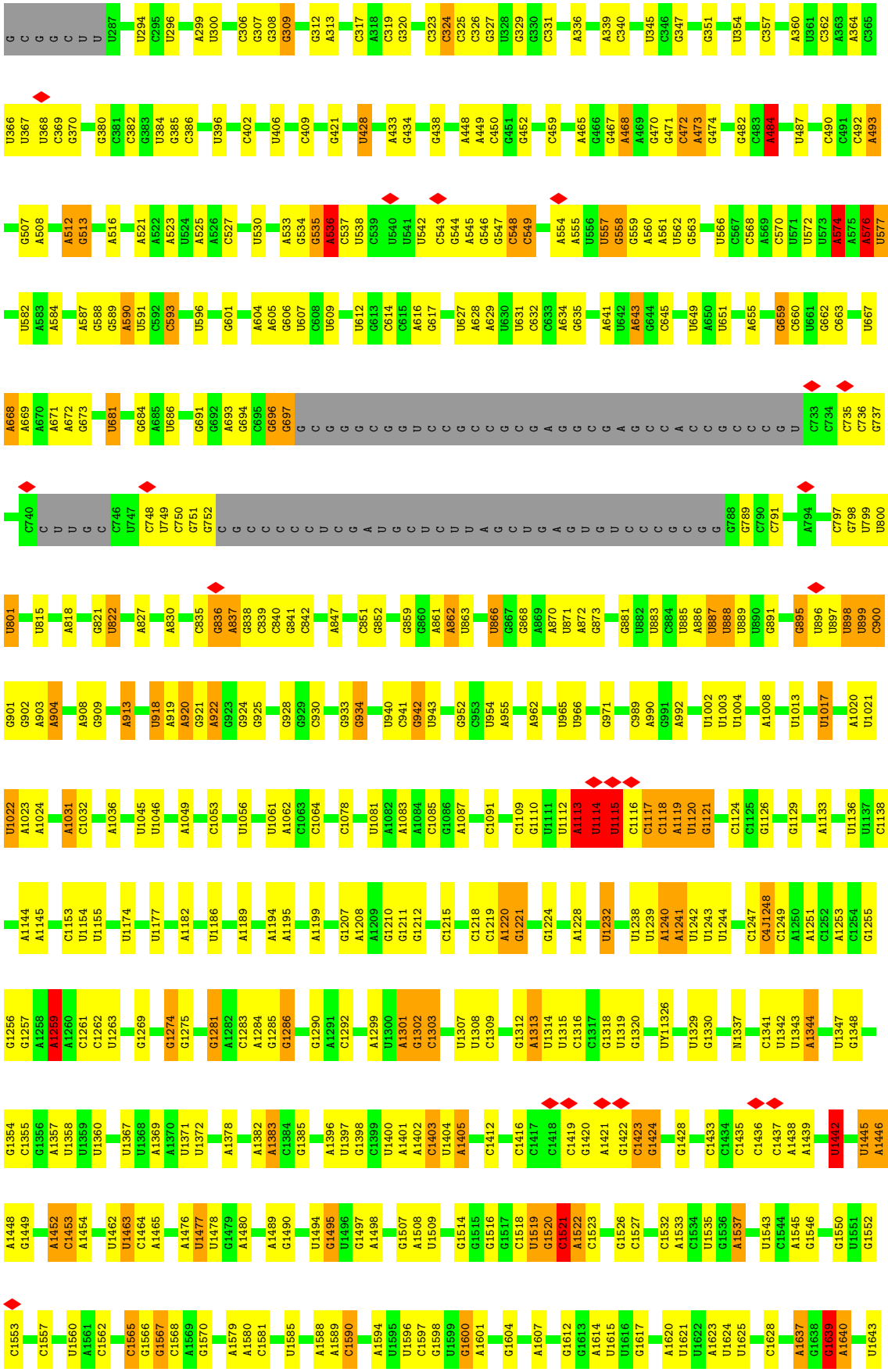


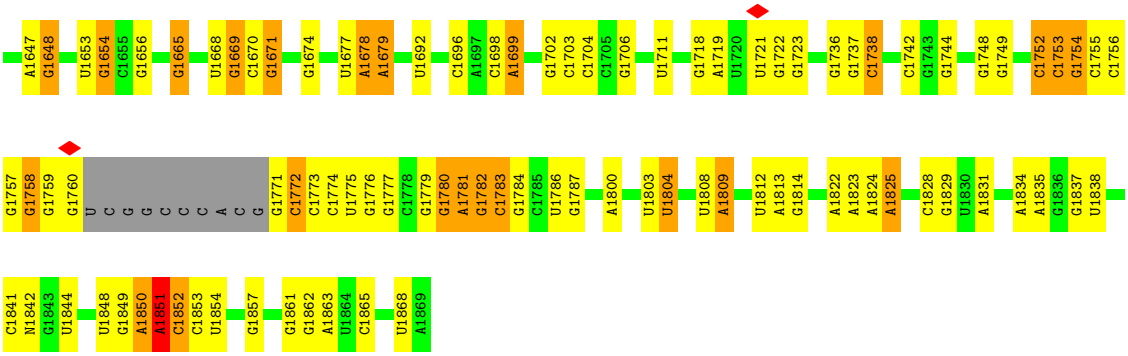


• Molecule 21: 18S rRNA

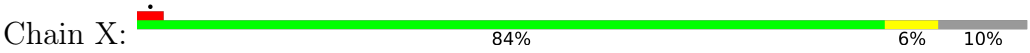


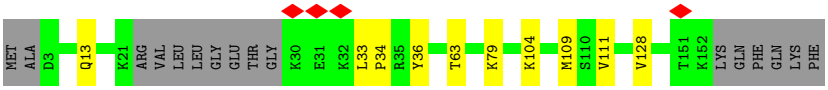




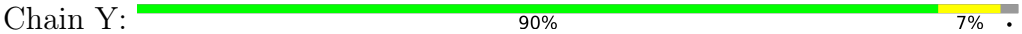


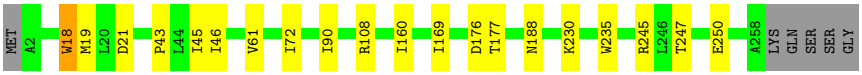
• Molecule 22: 40S ribosomal protein S11





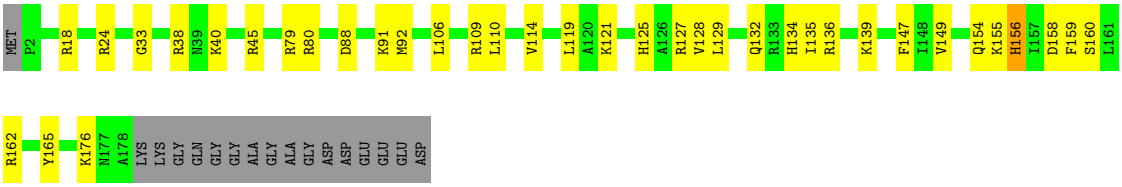
• Molecule 23: Small ribosomal subunit protein eS4, X isoform





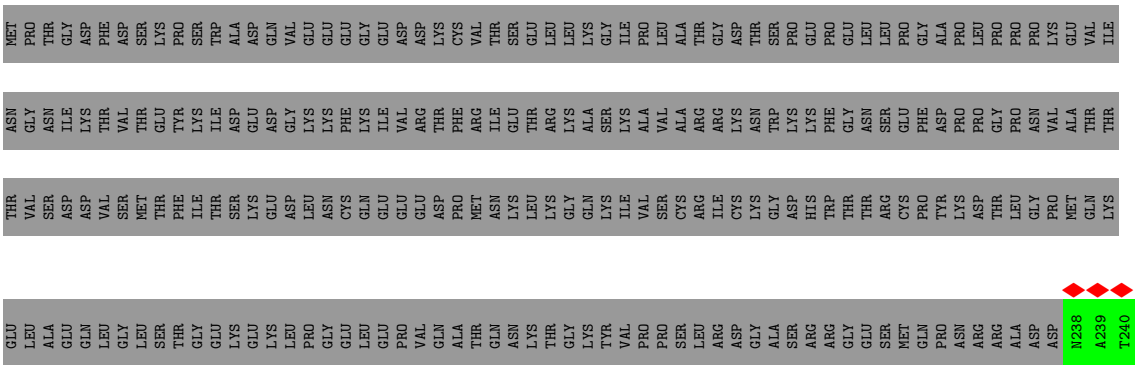
• Molecule 24: 40S ribosomal protein S9





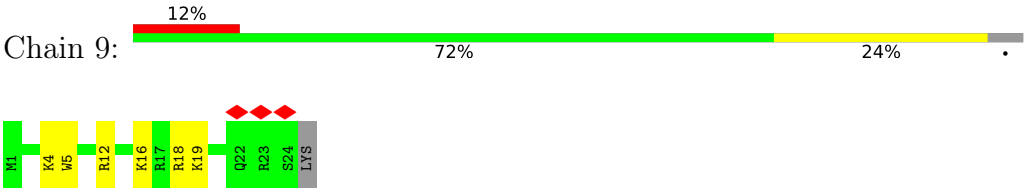
• Molecule 25: Eukaryotic translation initiation factor 3 subunit G



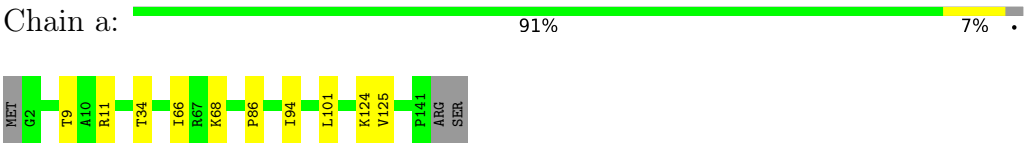




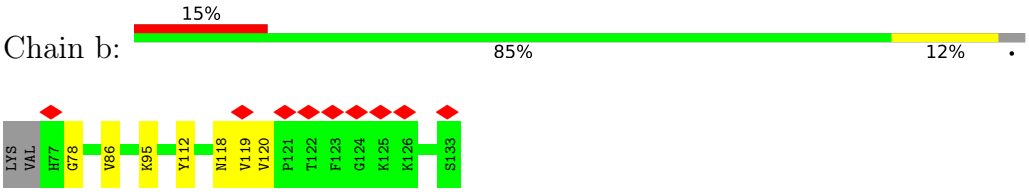
• Molecule 26: 60S ribosomal protein L41



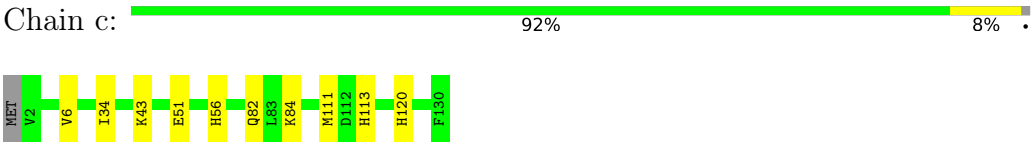
• Molecule 27: 40S ribosomal protein S23



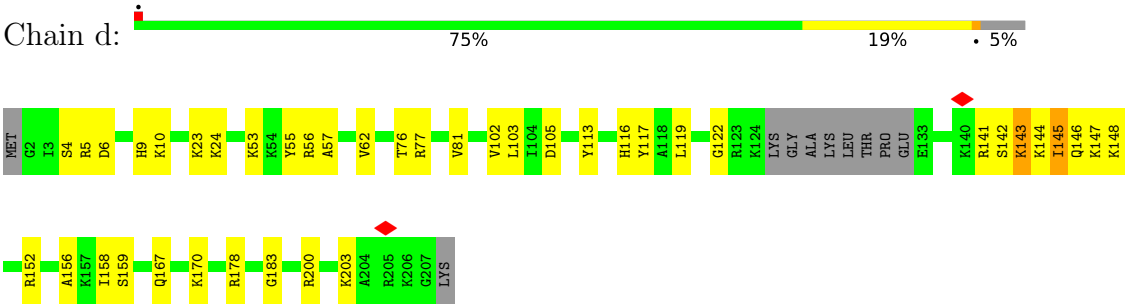
• Molecule 28: 40S ribosomal protein S30



• Molecule 29: 40S ribosomal protein S15a

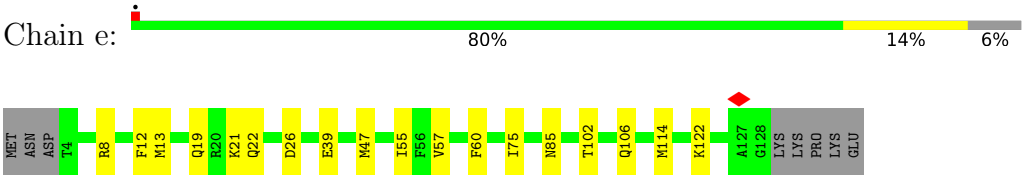


• Molecule 30: 40S ribosomal protein S8



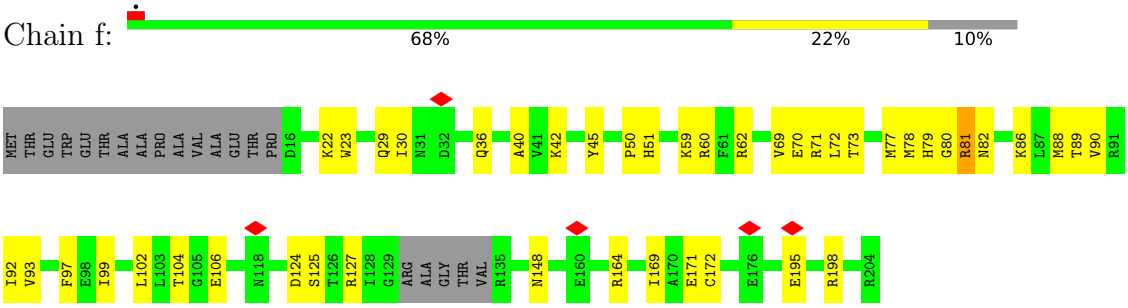
• Molecule 31: 40S ribosomal protein S24

Chain e:



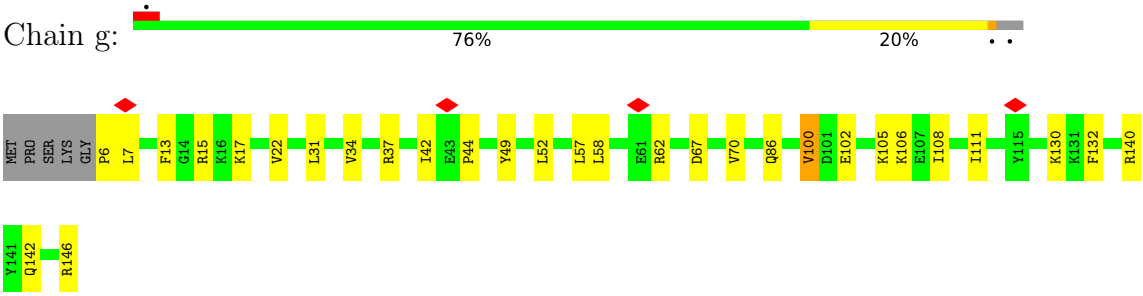
• Molecule 32: 40S ribosomal protein S5

Chain f:



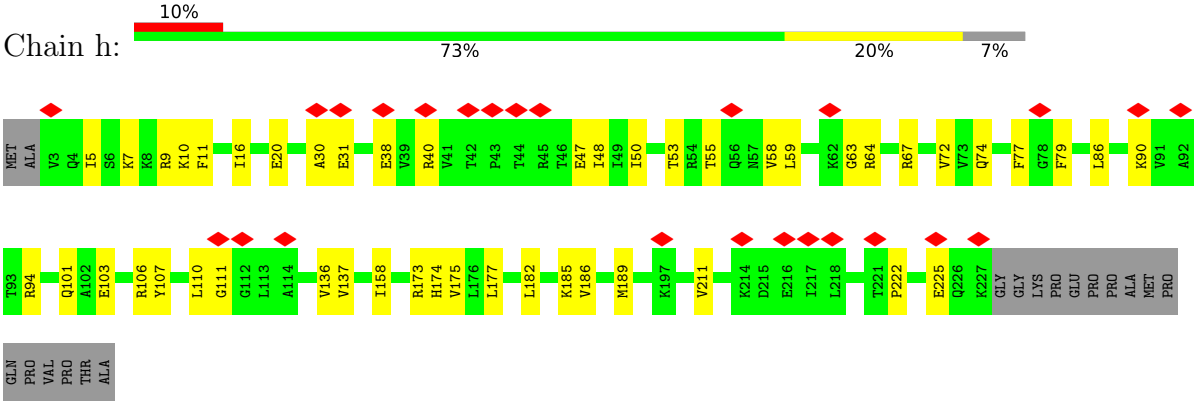
• Molecule 33: 40S ribosomal protein S16

Chain g:



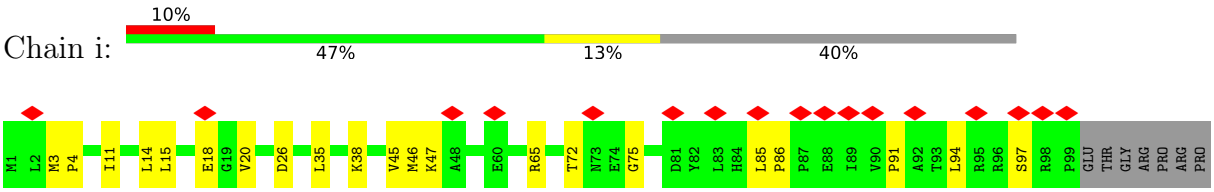
• Molecule 34: 40S ribosomal protein S3

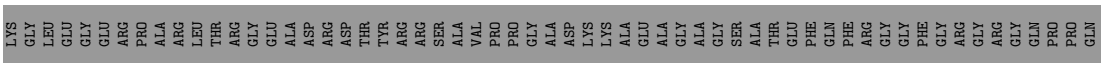
Chain h:



• Molecule 35: 40S ribosomal protein S10

Chain i:

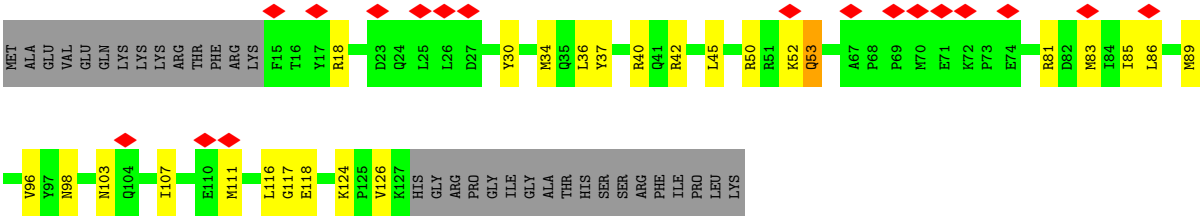




• Molecule 36: 40S ribosomal protein S15

Chain j:

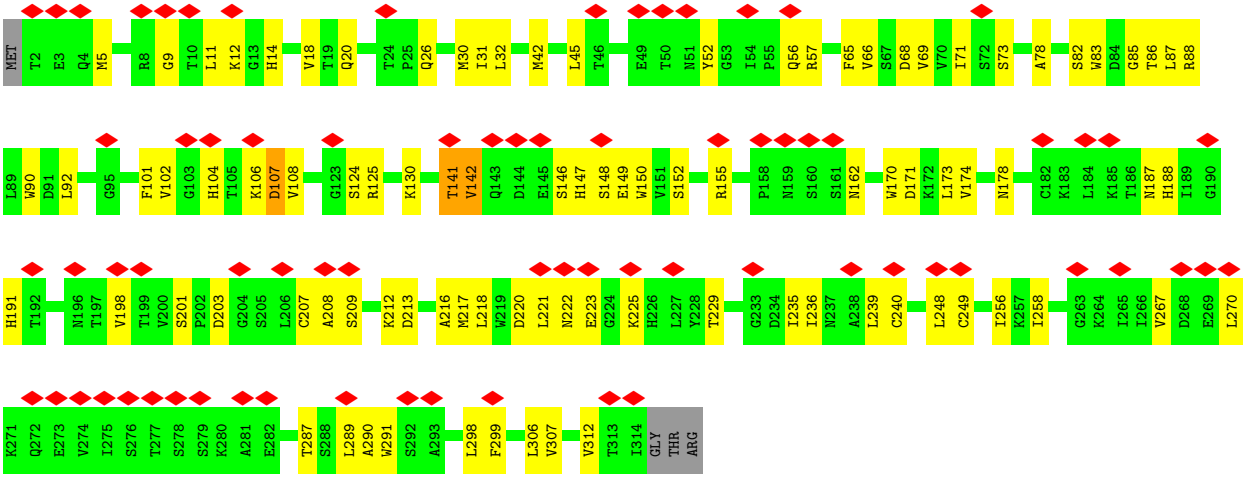




• Molecule 37: Receptor of activated protein C kinase 1

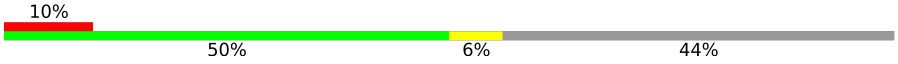
Chain k:

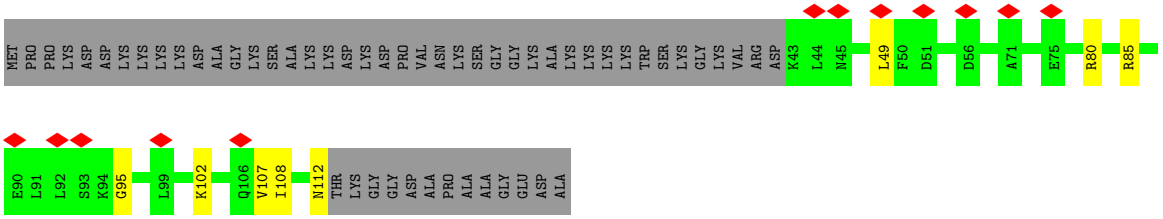




• Molecule 38: 40S ribosomal protein S25

Chain m:

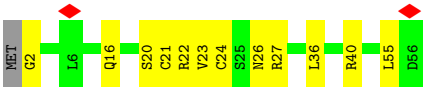




• Molecule 39: 40S ribosomal protein S29

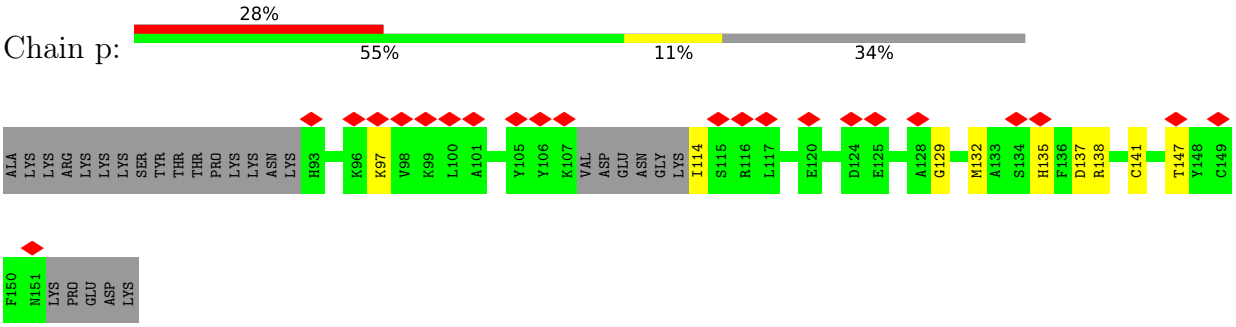
Chain o:





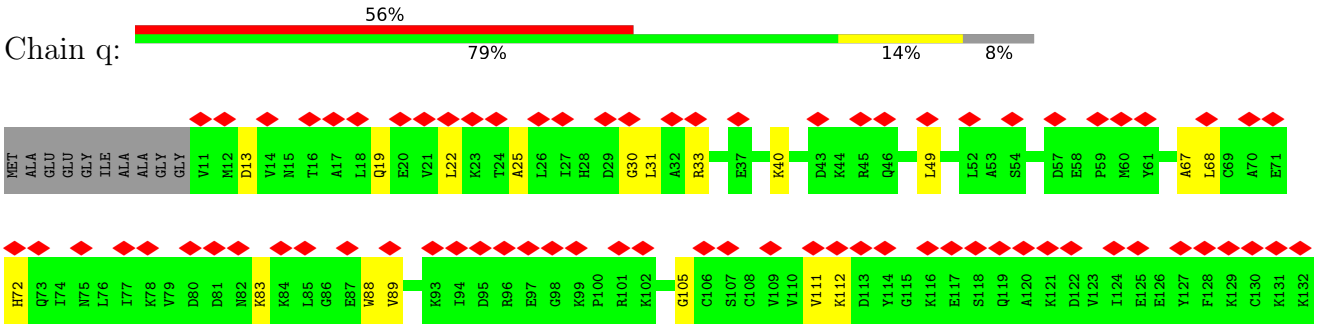
• Molecule 40: Ubiquitin-ribosomal protein eS31 fusion protein

Chain p:



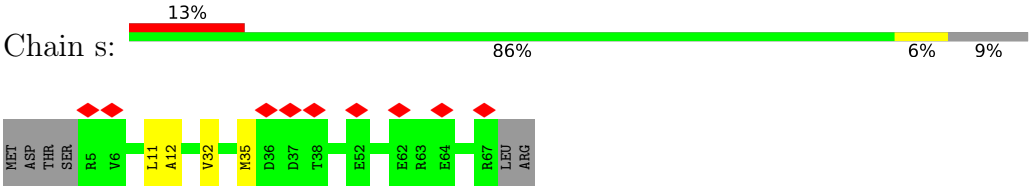
• Molecule 41: 40S ribosomal protein S12

Chain q:



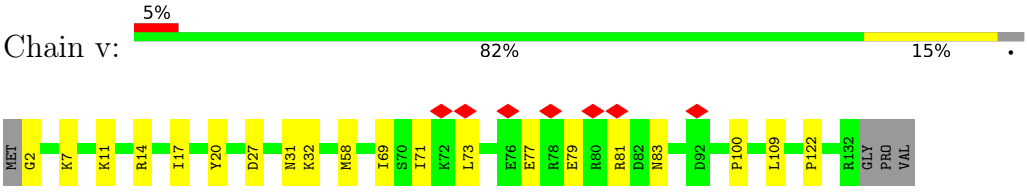
• Molecule 42: 40S ribosomal protein S28

Chain s:



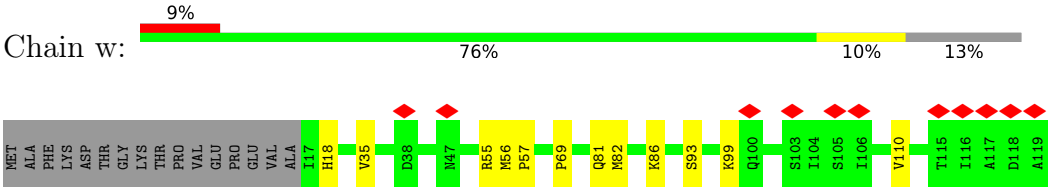
• Molecule 43: 40S ribosomal protein S17

Chain v:



• Molecule 44: 40S ribosomal protein S20

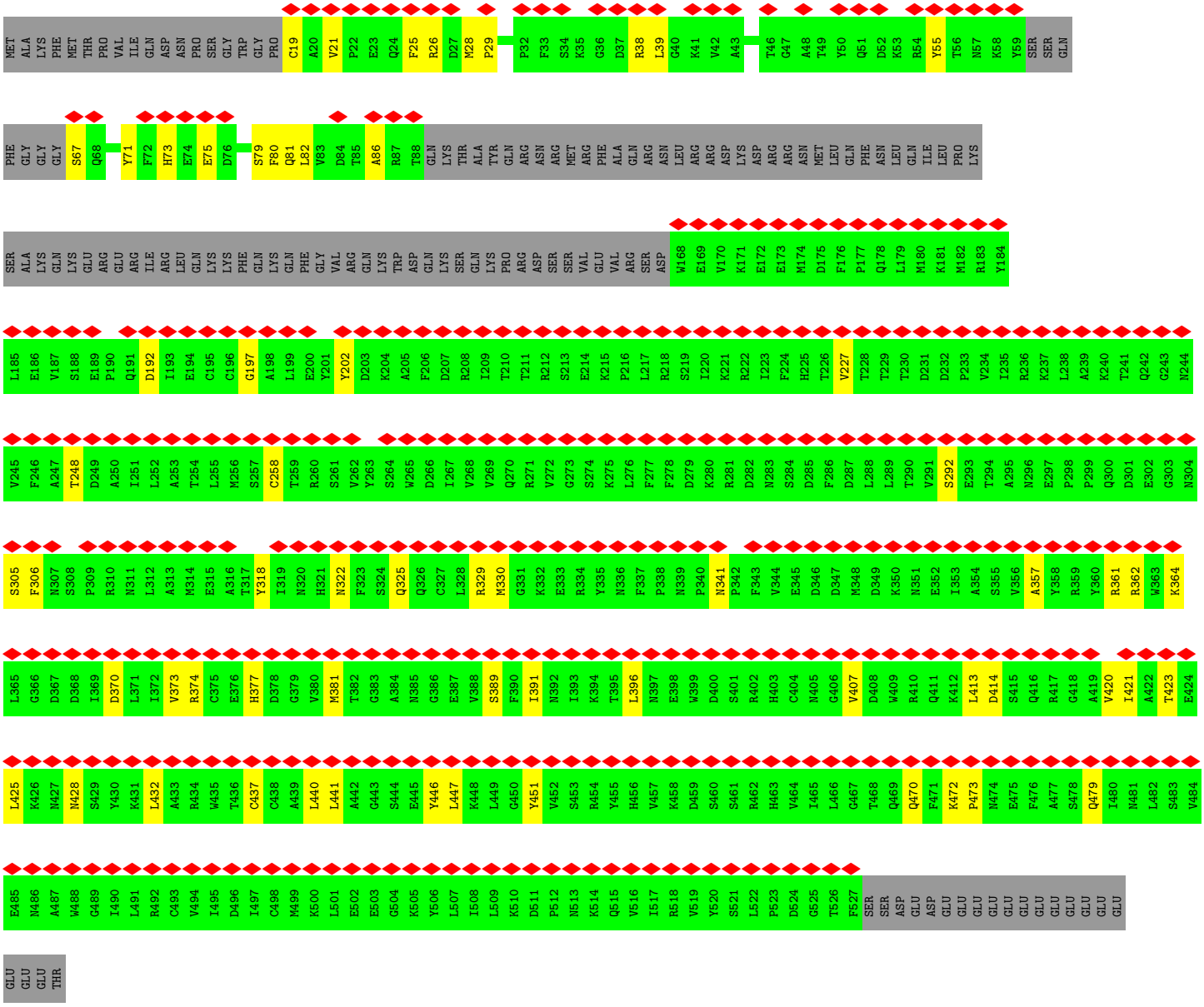
Chain w:



• Molecule 45: Eukaryotic translation initiation factor 3 subunit D

Chain x:

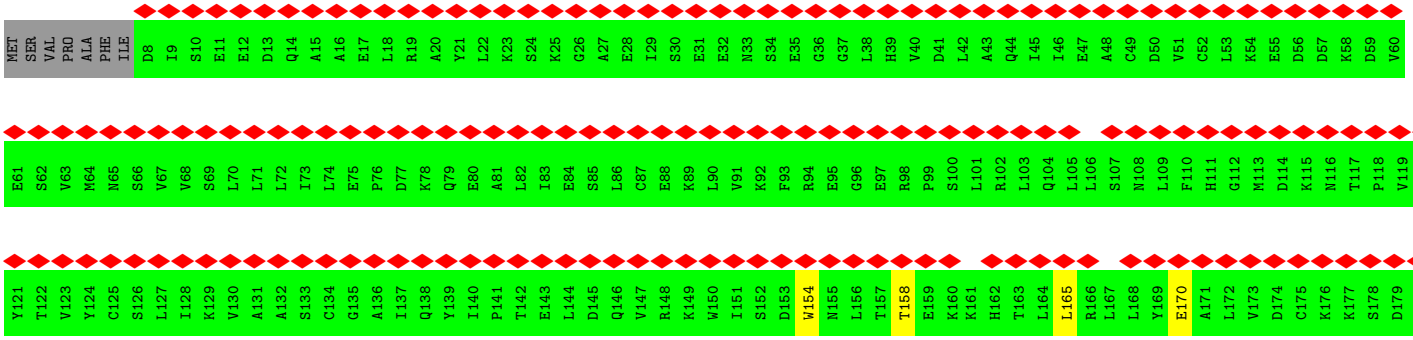




• Molecule 46: Eukaryotic translation initiation factor 3 subunit M

Chain 6:



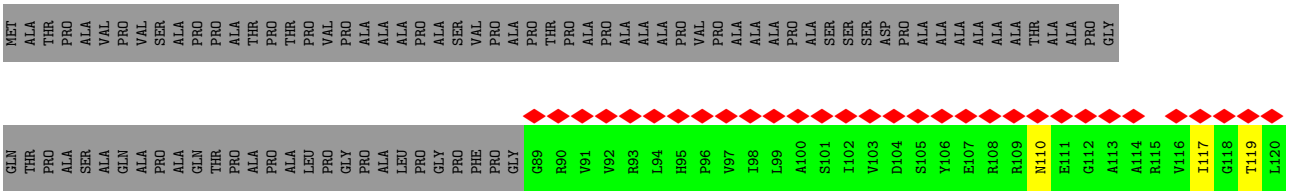




• Molecule 47: Eukaryotic translation initiation factor 3 subunit F

Chain 4:

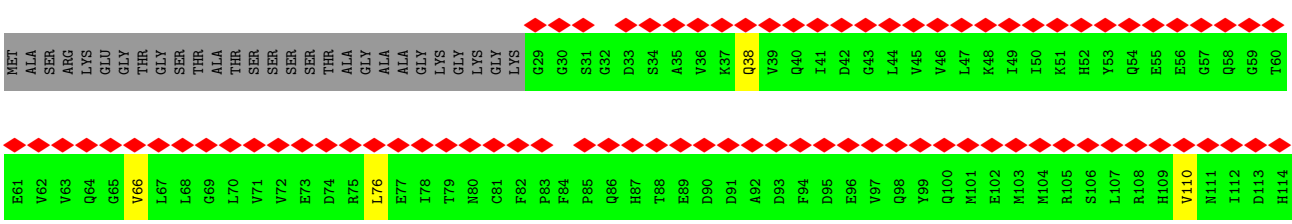


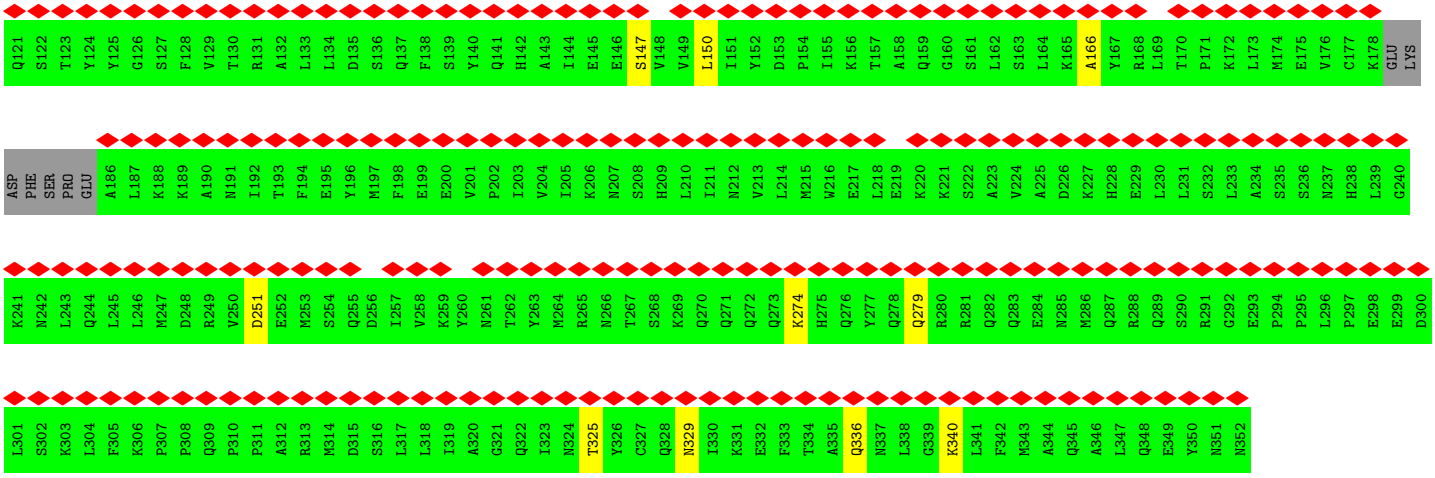


• Molecule 48: Eukaryotic translation initiation factor 3 subunit H

Chain 8:

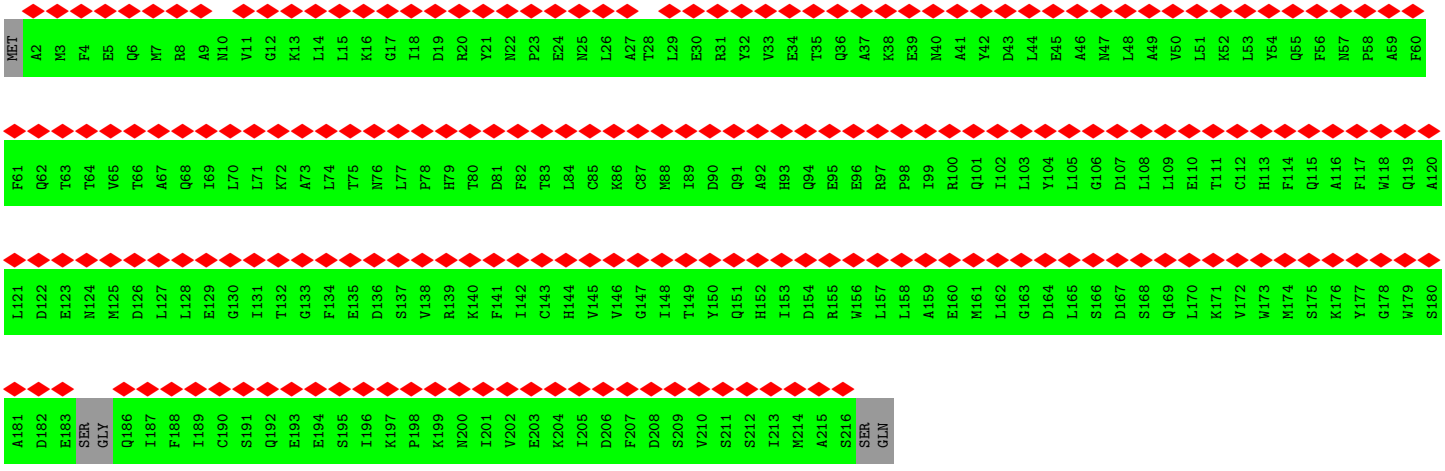




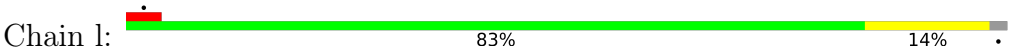


• Molecule 49: Eukaryotic translation initiation factor 3 subunit K





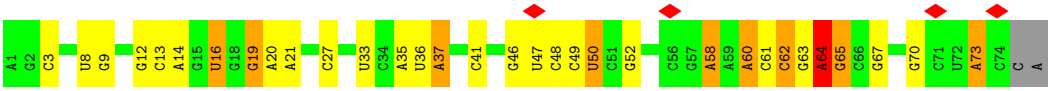
• Molecule 50: 40S ribosomal protein S19





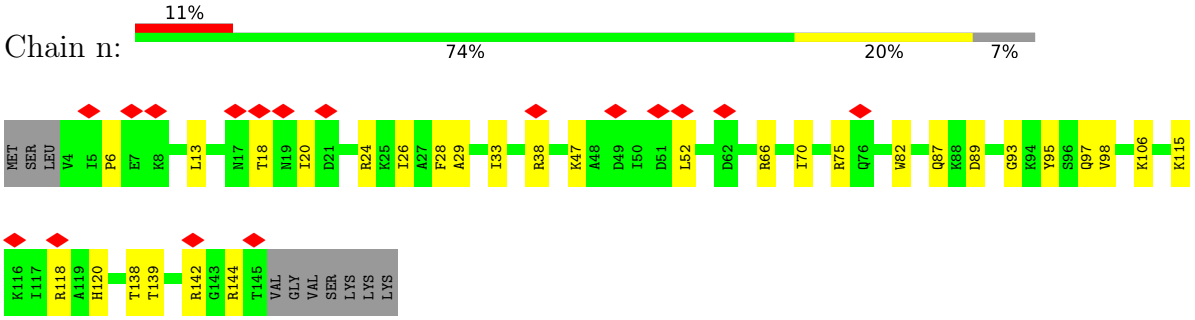
• Molecule 51: tRNAi-Met





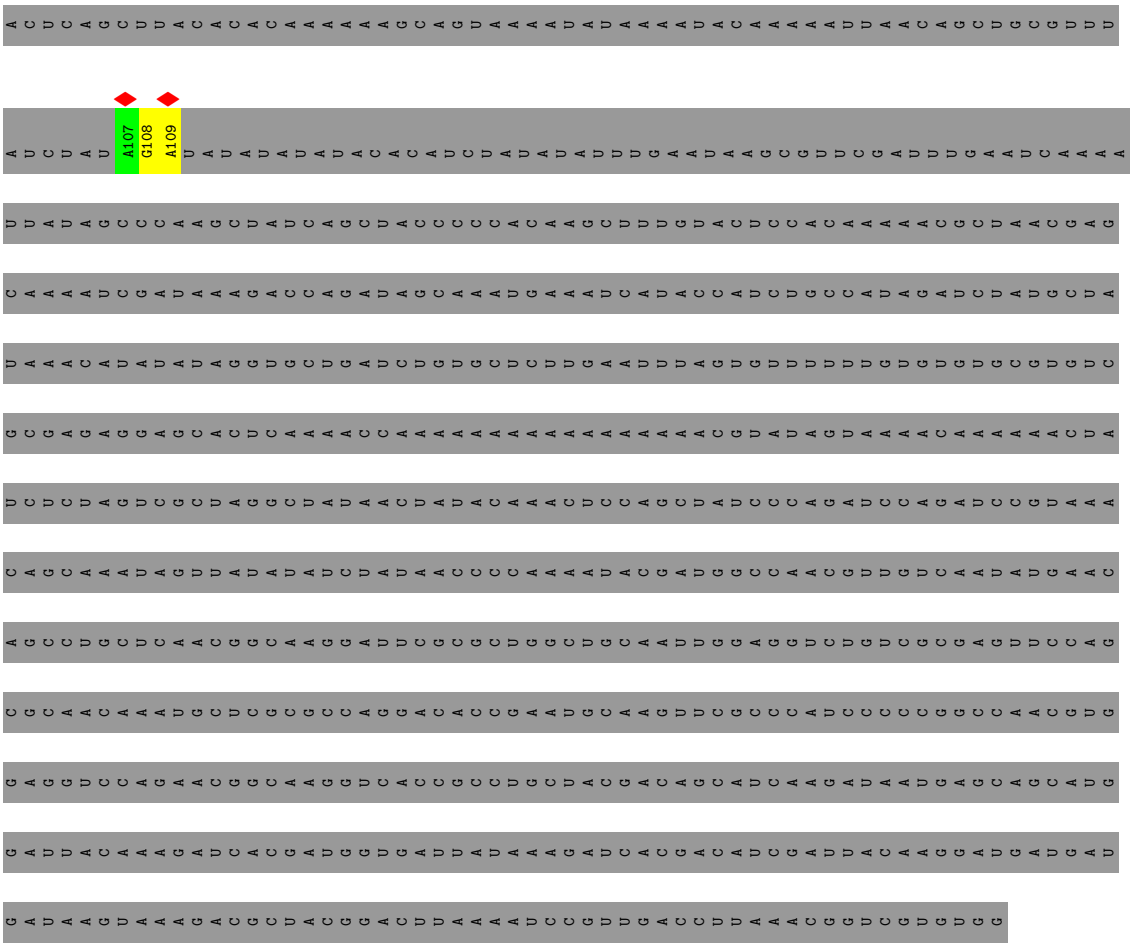
• Molecule 52: 40S ribosomal protein S18

Chain n:



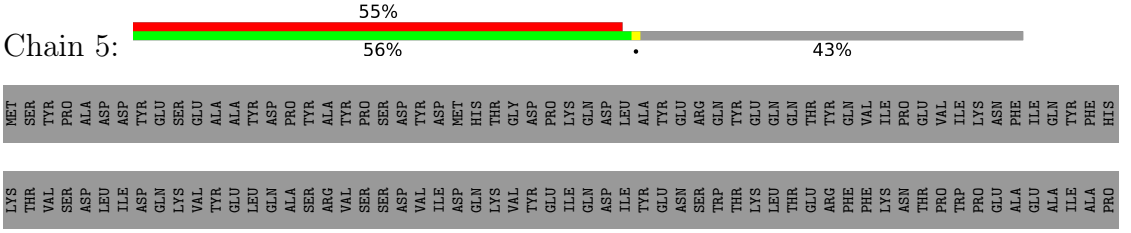
• Molecule 53: circMbl-FLAG

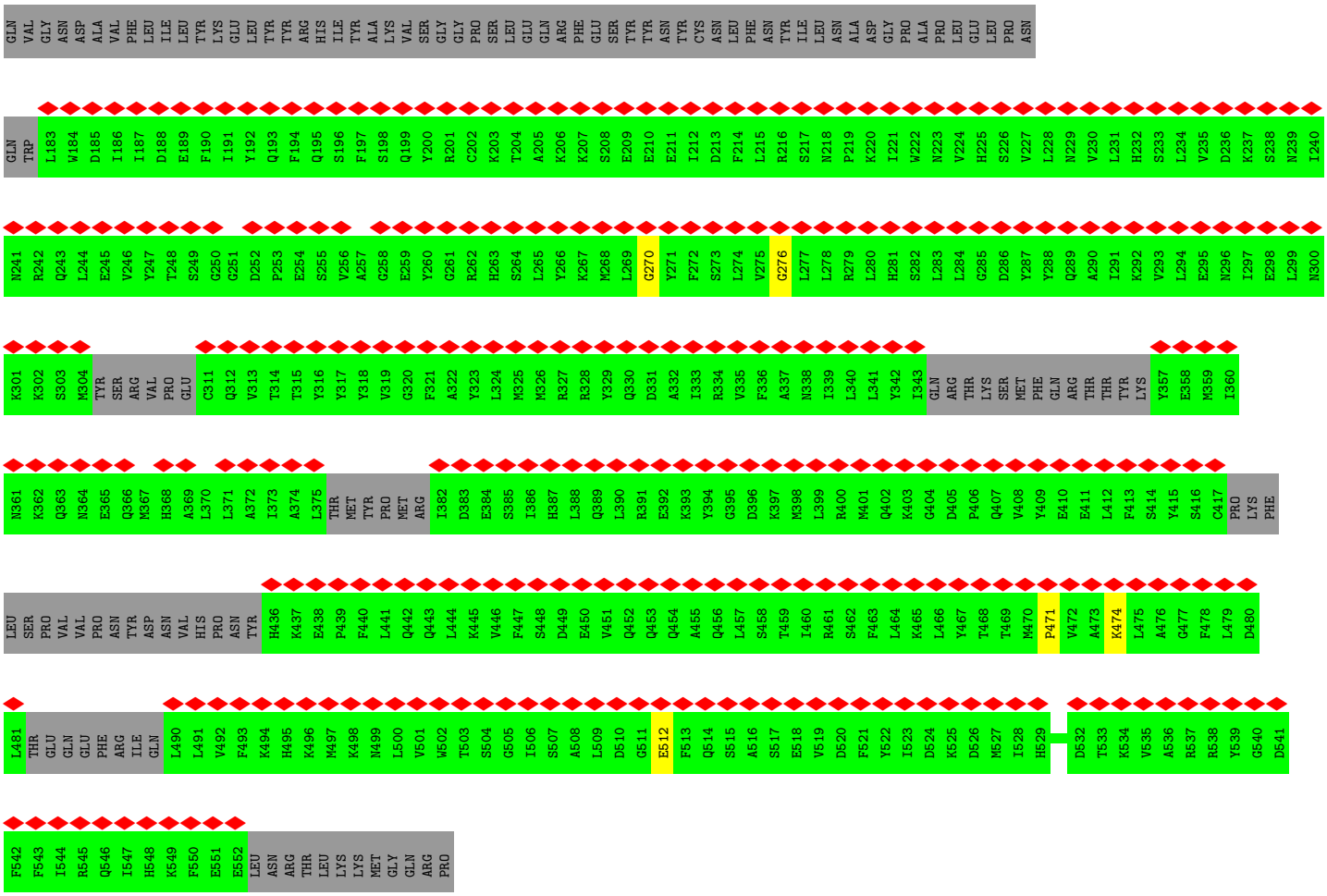
Chain z:



• Molecule 54: Eukaryotic translation initiation factor 3 subunit L

Chain 5:




GLN VAL GLY ASN ASP ALA VAL PHE LEU ILE LEU TYR LYS GLU LEU TYR TYR ARG HIS ILE TYR ALA LYS VAL SER GLY GLY PRO SER LEU GLU GLN ARG PHE GLU SER TYR TYR ASN TYR CYS ASN LEU PHE ASN TYR ILE LEU ASN ALA ASP GLY PRO ALA PRO LEU GLU LEU PRO ASN
GLN TRP L183 W184 D185 I186 I187 D188 E189 F190 I191 Y192 Q193 F194 Q195 S196 F197 S198 Q199 Y200 R201 C202 K203 T204 A205 K206 K207 S208 E209 E210 E211 I212 D213 F214 L215 R216 S217 N218 P219 K220 I221 W222 N223 V224 H225 S226 V227 L228 N229 V230 L231 H232 S233 L234 V235 D236 K237 S238 N239 I240
N241 R242 Q243 L244 E245 V246 Y247 T248 S249 G250 G251 D252 P253 E254 S255 V256 A257 G258 E259 Y260 G261 R262 H263 S264 L265 Y266 K267 M268 L269 G270 Y271 F272 S273 L274 V275 G276 L277 L278 R279 L280 H281 S282 L283 L284 G285 D286 Y287 Y288 Q289 A290 I291 K292 V293 L294 E295 N296 I297 E298 L299 N300
K301 K302 S303 M304 TYR SER ARG VAL PRO GLU C311 Q312 V313 T314 T315 Y316 Y317 Y318 V319 G320 F321 A322 Y323 L324 M325 M326 R327 R328 Y329 Q330 D331 A332 I333 R334 V335 F336 A337 N338 I339 L340 L341 Y342 I343 GLN ARG THR LYS SER MET PHE GLN ARG THR THR TYR LYS Y357 E358 M359 I360
N361 K362 Q363 N364 E365 Q366 M367 H368 A369 L370 L371 A372 I373 A374 L375 THR MET TYR PRO MET ARG I382 D383 E384 S385 I386 H387 L388 Q389 L390 R391 E392 K393 Y394 G395 D396 K397 M398 L399 R400 M401 Q402 K403 G404 D405 P406 Q407 V408 Y409 E410 E411 L412 F413 S414 Y415 S416 C417 PRO LYS PHE
LEU SER PRO VAL VAL PRO ASN TYR ASP ASN VAL HIS PRO ASN TYR H436 K437 E438 P439 F440 L441 Q442 Q443 L444 K445 V446 F447 S448 D449 E450 V451 Q452 Q453 Q454 A455 Q456 L457 S458 T459 I460 R461 S462 F463 L464 K465 L466 Y467 T468 T469 M470 P471 V472 A473 K474 L475 A476 G477 F478 L479 D480
L481 THR GLU GLN GLU PHE ARG ILE GLN L490 L491 V492 F493 K494 H495 K496 M497 K498 N499 L500 V501 W502 T503 S504 G505 I506 S507 A508 L509 D510 G511 E512 F513 Q514 S515 A516 S517 E518 V519 D520 F521 Y522 I523 D524 K525 D526 M527 I528 H529 D532 T533 K534 V535 A536 R537 R538 Y539 G540 D541
F542 P543 I544 R545 Q546 I547 H548 K549 P550 E551 E552 LEU ASN ARG THR LEU LYS LYS MET GLY GLN ARG PRO

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21721	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	40.0	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.034	Depositor
Minimum map value	-0.012	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0045	Depositor
Map size (Å)	494.4, 494.4, 494.4	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.824, 0.824, 0.824	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 4AC, 7MG, M2G, K, RIA, MG, MA6, JMH, OMG, 2MG, 1MA, ZN, G7M, C4J, H2U, OMC, OMU, UY1, T6A, 5MC, PSU, 1MG, 5MU, A2M, 6MZ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.26	0/5610	0.66	1/7621 (0.0%)
2	B	0.30	0/2778	0.66	0/3797
3	D	0.24	0/2247	0.53	0/3029
4	E	0.13	0/1745	0.36	0/2417
5	F	0.13	0/1597	0.34	0/2216
6	G	0.25	0/713	0.62	0/951
7	H	0.42	0/701	0.82	0/936
8	I	0.23	0/4696	0.54	0/6379
9	J	0.22	0/5018	0.61	5/6791 (0.1%)
10	L	0.28	0/1460	0.57	0/1953
11	M	0.37	0/644	0.66	0/864
12	N	0.28	0/643	0.53	0/860
13	O	0.27	0/1743	0.48	0/2354
14	P	0.28	0/1742	0.57	0/2330
15	Q	0.26	0/1732	0.48	0/2353
16	R	0.28	0/805	0.50	0/1079
17	S	0.22	0/1885	0.51	0/2510
18	T	0.31	0/1011	0.62	0/1355
19	U	0.29	0/1142	0.65	0/1534
20	V	0.24	0/1232	0.40	0/1656
21	W	0.56	6/38756 (0.0%)	0.89	33/60400 (0.1%)
22	X	0.26	0/1186	0.39	0/1585
23	Y	0.36	0/2083	0.58	1/2805 (0.0%)
24	Z	0.31	0/1502	0.56	4/2008 (0.2%)
25	7	0.26	0/628	0.66	0/846
26	9	0.30	0/231	0.57	0/294
27	a	0.36	0/1105	0.53	0/1476
28	b	0.27	0/458	0.64	0/602
29	c	0.38	0/1051	0.66	2/1406 (0.1%)
30	d	0.27	0/1655	0.52	1/2205 (0.0%)
31	e	0.22	0/1032	0.45	0/1371

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	f	0.36	0/1481	0.71	1/1988 (0.1%)
33	g	0.30	0/1142	0.65	0/1528
34	h	0.23	0/1780	0.52	0/2397
35	i	0.26	0/859	0.64	0/1159
36	j	0.22	0/953	0.58	0/1274
37	k	0.31	0/2493	0.62	2/3394 (0.1%)
38	m	0.18	0/565	0.47	0/759
39	o	0.39	0/470	0.60	0/623
40	p	0.17	0/444	0.47	0/588
41	q	0.22	0/960	0.57	0/1286
42	s	0.27	0/500	0.60	0/669
43	v	0.22	0/1078	0.51	0/1447
44	w	0.21	0/827	0.48	0/1110
45	x	0.24	0/2881	0.61	0/3936
46	6	0.36	0/2115	0.71	4/2905 (0.1%)
47	4	0.13	0/1269	0.36	0/1762
48	8	0.14	0/1572	0.44	0/2187
49	3	0.11	0/1055	0.34	0/1469
50	l	0.19	0/1123	0.49	0/1504
51	y	0.43	1/1484 (0.1%)	0.84	1/2311 (0.0%)
52	n	0.20	0/1194	0.47	0/1599
53	z	0.26	0/75	0.68	0/115
54	5	0.12	0/1575	0.38	0/2187
All	All	0.39	7/116726 (0.0%)	0.70	55/166180 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	D	0	1
18	T	0	1
All	All	0	2

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	y	64	RIA	O3'-P	5.70	1.61	1.56
21	W	468	A2M	O3'-P	5.57	1.61	1.56
21	W	1031	A2M	O3'-P	5.44	1.61	1.56
21	W	1383	A2M	O3'-P	5.43	1.61	1.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	W	576	A2M	O3'-P	5.41	1.61	1.56

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	170	VAL	N-CA-C	-7.20	104.25	111.88
9	J	694	GLU	CA-C-N	7.19	124.77	120.24
9	J	694	GLU	C-N-CA	7.19	124.77	120.24
37	k	141	THR	CA-C-N	6.56	133.77	121.97
37	k	141	THR	C-N-CA	6.56	133.77	121.97

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	D	232	PRO	Peptide
18	T	147	ARG	Sidechain

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	A	5518	0	5141	63	0
2	B	2740	0	2251	27	0
3	D	2215	0	2266	36	0
4	E	1750	0	806	8	0
5	F	1598	0	723	5	0
6	G	705	0	729	13	0
7	H	691	0	706	13	0
8	I	4569	0	4317	50	0
9	J	4940	0	4682	68	0
10	L	1439	0	1533	15	0
11	M	631	0	657	16	0
12	N	636	0	637	4	0
13	O	1707	0	1794	14	0
14	P	1715	0	1785	26	0
15	Q	1695	0	1696	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	R	792	0	841	8	0
17	S	1862	0	2018	29	0
18	T	998	0	1021	21	0
19	U	1123	0	1153	12	0
20	V	1208	0	1294	13	0
21	W	36675	0	18554	240	0
22	X	1166	0	1233	8	0
23	Y	2041	0	2143	11	0
24	Z	1477	0	1589	28	0
25	7	616	0	600	5	0
26	9	230	0	276	5	0
27	a	1087	0	1154	6	0
28	b	452	0	494	5	0
29	c	1034	0	1080	6	0
30	d	1628	0	1706	27	0
31	e	1015	0	1086	11	0
32	f	1461	0	1511	31	0
33	g	1124	0	1193	24	0
34	h	1752	0	1848	33	0
35	i	834	0	861	15	0
36	j	936	0	981	17	0
37	k	2436	0	2389	62	0
38	m	559	0	616	6	0
39	o	459	0	448	12	0
40	p	435	0	434	8	0
41	q	950	0	985	12	0
42	s	498	0	525	4	0
43	v	1064	0	1118	12	0
44	w	817	0	882	10	0
45	x	2838	0	2198	47	0
46	6	2099	0	1435	33	0
47	4	1272	0	564	7	0
48	8	1574	0	687	9	0
49	3	1057	0	475	0	0
50	l	1105	0	1138	13	0
51	y	1597	0	828	20	0
52	n	1176	0	1233	21	0
53	z	67	0	34	0	0
54	5	1581	0	689	3	0
55	R	1	0	0	0	0
55	o	1	0	0	0	0
55	p	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	S	1	0	0	0	0
56	W	75	0	0	0	0
57	W	1	0	0	0	0
All	All	113724	0	89037	1024	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 5.

The worst 5 of 1024 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)
21:W:1113:A:H62	21:W:1118:C:H2'	1.35	0.92
21:W:1301:A:HO2'	39:o:2:GLY:N	1.71	0.88
32:f:92:ILE:HD13	32:f:169:ILE:HD13	1.64	0.80
21:W:1532:C:H3'	21:W:1637:A:H62	1.49	0.78
8:I:538:GLN:HA	8:I:538:GLN:HE21	1.47	0.77

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	732/1382 (53%)	685 (94%)	47 (6%)	0	100 100
2	B	403/445 (91%)	365 (91%)	37 (9%)	1 (0%)	43 73
3	D	273/315 (87%)	259 (95%)	14 (5%)	0	100 100
4	E	346/472 (73%)	318 (92%)	27 (8%)	1 (0%)	36 67
5	F	323/325 (99%)	310 (96%)	13 (4%)	0	100 100
6	G	85/147 (58%)	74 (87%)	11 (13%)	0	100 100
7	H	83/116 (72%)	76 (92%)	7 (8%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	I	573/814 (70%)	536 (94%)	37 (6%)	0	100	100
9	J	639/913 (70%)	606 (95%)	33 (5%)	0	100	100
10	L	172/194 (89%)	161 (94%)	11 (6%)	0	100	100
11	M	79/84 (94%)	74 (94%)	5 (6%)	0	100	100
12	N	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
13	O	218/293 (74%)	215 (99%)	3 (1%)	0	100	100
14	P	209/264 (79%)	196 (94%)	13 (6%)	0	100	100
15	Q	212/295 (72%)	204 (96%)	8 (4%)	0	100	100
16	R	97/115 (84%)	96 (99%)	1 (1%)	0	100	100
17	S	228/249 (92%)	218 (96%)	10 (4%)	0	100	100
18	T	131/151 (87%)	123 (94%)	8 (6%)	0	100	100
19	U	136/333 (41%)	117 (86%)	19 (14%)	0	100	100
20	V	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
22	X	138/158 (87%)	133 (96%)	5 (4%)	0	100	100
23	Y	255/263 (97%)	249 (98%)	5 (2%)	1 (0%)	30	61
24	Z	175/194 (90%)	171 (98%)	4 (2%)	0	100	100
25	7	75/320 (23%)	66 (88%)	9 (12%)	0	100	100
26	9	22/25 (88%)	22 (100%)	0	0	100	100
27	a	138/143 (96%)	133 (96%)	4 (3%)	1 (1%)	18	49
28	b	55/59 (93%)	50 (91%)	4 (7%)	1 (2%)	6	28
29	c	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
30	d	194/208 (93%)	183 (94%)	9 (5%)	2 (1%)	12	41
31	e	123/133 (92%)	122 (99%)	1 (1%)	0	100	100
32	f	180/204 (88%)	171 (95%)	8 (4%)	1 (1%)	21	52
33	g	139/146 (95%)	132 (95%)	6 (4%)	1 (1%)	18	49
34	h	223/243 (92%)	216 (97%)	7 (3%)	0	100	100
35	i	97/165 (59%)	90 (93%)	7 (7%)	0	100	100
36	j	111/145 (77%)	109 (98%)	2 (2%)	0	100	100
37	k	311/317 (98%)	277 (89%)	32 (10%)	2 (1%)	21	52
38	m	68/125 (54%)	64 (94%)	4 (6%)	0	100	100
39	o	53/56 (95%)	50 (94%)	3 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	p	49/80 (61%)	43 (88%)	6 (12%)	0	100	100
41	q	120/132 (91%)	107 (89%)	13 (11%)	0	100	100
42	s	61/69 (88%)	57 (93%)	4 (7%)	0	100	100
43	v	129/135 (96%)	121 (94%)	8 (6%)	0	100	100
44	w	101/119 (85%)	93 (92%)	8 (8%)	0	100	100
45	x	417/548 (76%)	372 (89%)	44 (11%)	1 (0%)	43	73
46	6	348/374 (93%)	308 (88%)	39 (11%)	1 (0%)	36	67
47	4	251/357 (70%)	238 (95%)	13 (5%)	0	100	100
48	8	313/352 (89%)	291 (93%)	22 (7%)	0	100	100
49	3	209/218 (96%)	199 (95%)	10 (5%)	0	100	100
50	l	140/145 (97%)	134 (96%)	6 (4%)	0	100	100
52	n	140/152 (92%)	136 (97%)	4 (3%)	0	100	100
54	5	307/564 (54%)	298 (97%)	9 (3%)	0	100	100
All	All	10237/13420 (76%)	9611 (94%)	613 (6%)	13 (0%)	49	78

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	E	168	PRO
30	d	143	LYS
32	f	81	ARG
37	k	142	VAL
46	6	290	LYS

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	A	528/1259 (42%)	528 (100%)	0	100	100
2	B	206/406 (51%)	206 (100%)	0	100	100
3	D	247/280 (88%)	247 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	G	74/124 (60%)	74 (100%)	0	100	100
7	H	74/97 (76%)	74 (100%)	0	100	100
8	I	470/702 (67%)	469 (100%)	1 (0%)	87	89
9	J	489/811 (60%)	489 (100%)	0	100	100
10	L	160/174 (92%)	159 (99%)	1 (1%)	78	83
11	M	73/76 (96%)	70 (96%)	3 (4%)	27	59
12	N	67/67 (100%)	67 (100%)	0	100	100
13	O	186/225 (83%)	186 (100%)	0	100	100
14	P	192/231 (83%)	192 (100%)	0	100	100
15	Q	180/243 (74%)	180 (100%)	0	100	100
16	R	86/98 (88%)	86 (100%)	0	100	100
17	S	200/218 (92%)	200 (100%)	0	100	100
18	T	104/119 (87%)	104 (100%)	0	100	100
19	U	128/304 (42%)	125 (98%)	3 (2%)	44	70
20	V	130/131 (99%)	130 (100%)	0	100	100
22	X	129/142 (91%)	129 (100%)	0	100	100
23	Y	220/225 (98%)	220 (100%)	0	100	100
24	Z	158/168 (94%)	157 (99%)	1 (1%)	78	83
25	7	64/277 (23%)	64 (100%)	0	100	100
26	9	23/24 (96%)	23 (100%)	0	100	100
27	a	112/115 (97%)	112 (100%)	0	100	100
28	b	46/48 (96%)	46 (100%)	0	100	100
29	c	112/113 (99%)	112 (100%)	0	100	100
30	d	172/180 (96%)	172 (100%)	0	100	100
31	e	107/115 (93%)	107 (100%)	0	100	100
32	f	156/170 (92%)	154 (99%)	2 (1%)	61	77
33	g	117/121 (97%)	116 (99%)	1 (1%)	70	80
34	h	189/202 (94%)	189 (100%)	0	100	100
35	i	90/136 (66%)	90 (100%)	0	100	100
36	j	103/130 (79%)	102 (99%)	1 (1%)	68	79
37	k	272/275 (99%)	271 (100%)	1 (0%)	84	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
38	m	62/103 (60%)	62 (100%)	0	100 100
39	o	48/49 (98%)	47 (98%)	1 (2%)	47 71
40	p	47/72 (65%)	47 (100%)	0	100 100
41	q	104/108 (96%)	104 (100%)	0	100 100
42	s	56/62 (90%)	56 (100%)	0	100 100
43	v	119/122 (98%)	119 (100%)	0	100 100
44	w	94/107 (88%)	94 (100%)	0	100 100
45	x	206/494 (42%)	206 (100%)	0	100 100
46	6	100/335 (30%)	96 (96%)	4 (4%)	28 60
48	8	1/310 (0%)	1 (100%)	0	100 100
50	l	112/115 (97%)	112 (100%)	0	100 100
52	n	123/132 (93%)	123 (100%)	0	100 100
All	All	6736/10015 (67%)	6717 (100%)	19 (0%)	84 87

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	o	16	GLN
46	6	261	ASP
46	6	280	LEU
46	6	260	LYS
24	Z	154	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
9	J	713	GLN
41	q	82	ASN
20	V	58	HIS
37	k	285	GLN
45	x	307	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
21	W	1708/1869 (91%)	434 (25%)	23 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	y	72/75 (96%)	19 (26%)	0
53	z	2/774 (0%)	2 (100%)	0
All	All	1782/2718 (65%)	455 (25%)	23 (1%)

5 of 455 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
21	W	17	C
21	W	25	A
21	W	33	G
21	W	41	G
21	W	44	U

5 of 23 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
21	W	1423	C
21	W	1463	U
21	W	1452	A
21	W	1519	U
21	W	1113	A

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

106 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	$\#\|Z\| > 2$
21	4AC	W	1842	21	21,24,25	0.50	0	29,34,37	0.47	0
21	PSU	W	119	21	18,21,22	1.00	1 (5%)	22,30,33	0.68	0
21	PSU	W	100	21	18,21,22	1.01	1 (5%)	22,30,33	0.77	0
51	H2U	y	16	51	18,21,22	0.51	0	21,30,33	0.75	1 (4%)
21	PSU	W	1081	21	18,21,22	1.07	2 (11%)	22,30,33	0.76	0
21	PSU	W	296	21	18,21,22	1.01	1 (5%)	22,30,33	0.74	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
21	PSU	W	918	21	18,21,22	1.05	2 (11%)	22,30,33	0.84	1 (4%)
21	A2M	W	1678	21	22,25,26	0.27	0	31,36,39	1.50	3 (9%)
51	7MG	y	46	51	22,26,27	1.12	1 (4%)	29,39,42	0.73	1 (3%)
21	UY1	W	1326	21,56	19,22,23	0.96	1 (5%)	22,31,34	0.62	0
21	PSU	W	1232	21	18,21,22	1.01	1 (5%)	22,30,33	0.77	0
51	1MA	y	58	51	21,25,26	0.40	0	31,37,40	0.66	0
21	PSU	W	1360	21	18,21,22	1.01	1 (5%)	22,30,33	0.76	0
51	RIA	y	64	51	35,38,39	0.38	0	53,57,60	0.62	0
21	PSU	W	1056	21	18,21,22	1.01	1 (5%)	22,30,33	0.68	0
51	5MC	y	49	51	18,22,23	0.40	0	26,32,35	0.53	0
21	A2M	W	99	21,56	22,25,26	0.22	0	31,36,39	1.45	3 (9%)
21	OMG	W	644	21	23,26,27	0.39	0	33,38,41	0.43	0
21	PSU	W	1045	21	18,21,22	0.99	1 (5%)	22,30,33	0.72	0
21	OMC	W	1703	21	19,22,23	0.33	0	26,31,34	0.36	0
21	OMU	W	116	21	19,22,23	0.43	0	26,31,34	0.67	0
21	PSU	W	815	21	18,21,22	1.01	1 (5%)	22,30,33	0.73	0
21	PSU	W	651	21	18,21,22	1.01	1 (5%)	22,30,33	0.73	0
21	PSU	W	1186	21	18,21,22	1.01	1 (5%)	22,30,33	0.78	0
21	PSU	W	612	21	18,21,22	1.01	1 (5%)	22,30,33	0.70	0
21	OMG	W	436	21	23,26,27	0.41	0	33,38,41	0.49	0
21	5MU	W	814	21	19,22,23	0.49	0	28,32,35	0.69	0
21	PSU	W	863	21	18,21,22	1.02	1 (5%)	22,30,33	0.67	0
21	A2M	W	576	21	22,25,26	0.22	0	31,36,39	1.41	2 (6%)
51	1MG	y	9	51	22,26,27	0.52	0	33,39,42	0.67	0
21	MA6	W	1851	21	23,26,27	0.31	0	34,38,41	0.76	1 (2%)
51	2MG	y	10	51	23,26,27	0.40	0	32,38,41	0.41	0
21	4AC	W	1337	21	21,24,25	0.47	0	29,34,37	0.81	1 (3%)
21	OMU	W	1442	21	19,22,23	0.54	0	26,31,34	0.82	1 (3%)
51	M2G	y	26	51	24,27,28	0.46	0	35,40,43	0.39	0
21	MA6	W	1850	21	23,26,27	0.33	0	34,38,41	0.65	1 (2%)
21	PSU	W	218	21	18,21,22	0.97	1 (5%)	22,30,33	0.72	0
21	PSU	W	63	21	18,21,22	1.01	1 (5%)	22,30,33	0.82	0
21	PSU	W	34	21	18,21,22	0.99	1 (5%)	22,30,33	0.72	0
21	5MC	W	1374	21	18,22,23	0.41	0	26,32,35	0.54	0
21	PSU	W	1238	21	18,21,22	0.99	1 (5%)	22,30,33	0.75	0
21	A2M	W	1031	21	22,25,26	0.23	0	31,36,39	1.50	3 (9%)
21	PSU	W	1367	21	18,21,22	1.00	1 (5%)	22,30,33	0.71	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
21	OMC	W	517	21	19,22,23	0.50	0	26,31,34	0.65	0
21	OMG	W	867	21	23,26,27	0.39	0	33,38,41	0.42	0
21	OMG	W	1328	21	23,26,27	0.35	0	33,38,41	0.38	0
21	PSU	W	1136	21	18,21,22	0.99	1 (5%)	22,30,33	0.73	0
21	OMC	W	1272	21	19,22,23	0.48	0	26,31,34	0.68	0
21	PSU	W	1177	21	18,21,22	1.00	1 (5%)	22,30,33	0.74	0
21	OMU	W	172	21	19,22,23	0.33	0	26,31,34	1.00	1 (3%)
21	PSU	W	1596	21	18,21,22	0.98	1 (5%)	22,30,33	0.75	0
21	OMC	W	462	21	19,22,23	0.47	0	26,31,34	0.66	0
21	PSU	W	109	21	18,21,22	0.99	1 (5%)	22,30,33	0.71	0
21	PSU	W	966	21	18,21,22	1.00	1 (5%)	22,30,33	0.73	0
21	PSU	W	667	21	18,21,22	1.06	1 (5%)	22,30,33	0.71	0
21	OMU	W	1288	21	19,22,23	0.51	0	26,31,34	0.80	0
21	PSU	W	822	21	18,21,22	1.00	2 (11%)	22,30,33	0.76	1 (4%)
21	PSU	W	609	21	18,21,22	0.97	1 (5%)	22,30,33	0.71	0
21	PSU	W	1003	21	18,21,22	1.01	1 (5%)	22,30,33	0.70	0
21	A2M	W	159	21	22,25,26	0.24	0	31,36,39	0.92	3 (9%)
21	OMG	W	601	21	23,26,27	0.39	0	33,38,41	0.38	0
21	PSU	W	1004	21	18,21,22	1.03	1 (5%)	22,30,33	0.73	0
21	OMG	W	1490	21,56	23,26,27	0.34	0	33,38,41	0.43	0
21	PSU	W	1046	21	18,21,22	1.01	1 (5%)	22,30,33	0.66	0
21	A2M	W	484	21	22,25,26	0.18	0	31,36,39	1.15	3 (9%)
21	6MZ	W	1832	21,56	22,25,26	0.49	0	30,36,39	0.61	0
21	G7M	W	1639	21,51	23,26,27	0.69	1 (4%)	35,39,42	0.80	1 (2%)
21	OMU	W	1804	21	19,22,23	0.46	0	26,31,34	0.75	1 (3%)
21	A2M	W	166	21	22,25,26	0.23	0	31,36,39	1.43	3 (9%)
21	JMH	W	1219	21,56	18,22,23	0.60	1 (5%)	21,32,35	0.70	0
21	PSU	W	406	21	18,21,22	1.00	1 (5%)	22,30,33	0.77	0
21	OMG	W	509	21,56	23,26,27	0.39	0	33,38,41	0.43	0
21	PSU	W	1625	21	18,21,22	1.01	1 (5%)	22,30,33	0.67	0
21	PSU	W	1174	21	18,21,22	1.01	1 (5%)	22,30,33	0.72	0
21	PSU	W	1347	21	18,21,22	0.99	1 (5%)	22,30,33	0.75	0
21	C4J	W	1248	21	24,29,30	0.80	1 (4%)	29,42,45	0.73	0
21	OMU	W	121	21	19,22,23	0.45	0	26,31,34	0.61	0
21	PSU	W	801	21	18,21,22	0.99	1 (5%)	22,30,33	0.65	0
21	A2M	W	590	21	22,25,26	0.28	0	31,36,39	1.05	4 (12%)
21	A2M	W	468	21	22,25,26	0.23	0	31,36,39	1.44	3 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
21	PSU	W	681	21	18,21,22	1.03	1 (5%)	22,30,33	0.74	0
51	5MC	y	48	51	18,22,23	0.33	0	26,32,35	0.54	0
21	PSU	W	1445	21	18,21,22	0.87	1 (5%)	22,30,33	0.65	0
21	A2M	W	512	21	22,25,26	0.23	0	31,36,39	1.42	4 (12%)
21	PSU	W	866	21	18,21,22	1.04	1 (5%)	22,30,33	0.63	0
21	OMC	W	1391	21	19,22,23	0.49	0	26,31,34	0.68	0
51	T6A	y	37	51	31,34,35	0.52	0	44,49,52	0.92	2 (4%)
21	PSU	W	366	21	18,21,22	0.99	1 (5%)	22,30,33	0.74	0
21	PSU	W	36	21	18,21,22	1.02	1 (5%)	22,30,33	0.71	0
21	PSU	W	572	21	18,21,22	0.99	1 (5%)	22,30,33	0.73	0
21	OMG	W	1447	21	23,26,27	0.29	0	33,38,41	0.37	0
21	PSU	W	300	21	18,21,22	0.99	1 (5%)	22,30,33	0.78	0
21	PSU	W	1643	21	18,21,22	0.99	1 (5%)	22,30,33	0.69	0
51	H2U	y	47	51	18,21,22	0.55	0	21,30,33	0.52	0
21	PSU	W	649	21	18,21,22	1.02	1 (5%)	22,30,33	0.76	0
21	A2M	W	668	21,56	22,25,26	0.19	0	31,36,39	1.02	2 (6%)
21	A2M	W	27	21,56	22,25,26	0.21	0	31,36,39	1.44	3 (9%)
21	PSU	W	1692	21	18,21,22	0.87	1 (5%)	22,30,33	0.70	0
21	OMC	W	174	21,56	19,22,23	0.48	0	26,31,34	0.64	0
21	OMG	W	683	21	23,26,27	0.42	0	33,38,41	0.46	0
21	PSU	W	105	21	18,21,22	1.03	1 (5%)	22,30,33	0.72	0
21	OMU	W	354	21	19,22,23	0.48	0	26,31,34	0.82	1 (3%)
21	PSU	W	1244	21	18,21,22	0.87	1 (5%)	22,30,33	0.57	0
21	PSU	W	686	21	18,21,22	1.00	1 (5%)	22,30,33	0.73	0
21	OMU	W	428	21	19,22,23	0.35	0	26,31,34	0.51	0
21	A2M	W	1383	21	22,25,26	0.22	0	31,36,39	1.57	3 (9%)

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
21	4AC	W	1842	21	-	4/11/29/30	0/2/2/2
21	PSU	W	119	21	-	0/7/25/26	0/2/2/2
21	PSU	W	100	21	-	2/7/25/26	0/2/2/2
51	H2U	y	16	51	-	3/7/38/39	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
21	PSU	W	1081	21	-	1/7/25/26	0/2/2/2
21	PSU	W	296	21	-	2/7/25/26	0/2/2/2
21	PSU	W	918	21	-	0/7/25/26	0/2/2/2
21	A2M	W	1678	21	-	1/9/27/28	0/3/3/3
51	7MG	y	46	51	-	3/7/37/38	0/3/3/3
21	UY1	W	1326	21,56	-	1/9/27/28	0/2/2/2
21	PSU	W	1232	21	-	0/7/25/26	0/2/2/2
51	1MA	y	58	51	-	0/7/25/26	0/3/3/3
21	PSU	W	1360	21	-	0/7/25/26	0/2/2/2
51	RIA	y	64	51	-	8/17/51/52	0/4/4/4
21	PSU	W	1056	21	-	0/7/25/26	0/2/2/2
51	5MC	y	49	51	-	0/7/25/26	0/2/2/2
21	A2M	W	99	21,56	-	1/9/27/28	0/3/3/3
21	OMG	W	644	21	-	2/9/27/28	0/3/3/3
21	PSU	W	1045	21	-	0/7/25/26	0/2/2/2
21	OMC	W	1703	21	-	1/9/27/28	0/2/2/2
21	OMU	W	116	21	-	0/9/27/28	0/2/2/2
21	PSU	W	815	21	-	0/7/25/26	0/2/2/2
21	PSU	W	651	21	-	0/7/25/26	0/2/2/2
21	PSU	W	1186	21	-	0/7/25/26	0/2/2/2
21	PSU	W	612	21	-	0/7/25/26	0/2/2/2
21	OMG	W	436	21	-	0/9/27/28	0/3/3/3
21	5MU	W	814	21	-	0/7/25/26	0/2/2/2
21	PSU	W	863	21	-	0/7/25/26	0/2/2/2
21	A2M	W	576	21	-	2/9/27/28	0/3/3/3
51	1MG	y	9	51	-	0/7/25/26	0/3/3/3
21	MA6	W	1851	21	-	2/11/29/30	0/3/3/3
51	2MG	y	10	51	-	0/9/27/28	0/3/3/3
21	4AC	W	1337	21	-	0/11/29/30	0/2/2/2
21	OMU	W	1442	21	-	3/9/27/28	0/2/2/2
51	M2G	y	26	51	-	2/11/29/30	0/3/3/3
21	MA6	W	1850	21	-	0/11/29/30	0/3/3/3
21	PSU	W	218	21	-	0/7/25/26	0/2/2/2
21	PSU	W	63	21	-	0/7/25/26	0/2/2/2
21	PSU	W	34	21	-	0/7/25/26	0/2/2/2
21	5MC	W	1374	21	-	0/7/25/26	0/2/2/2
21	PSU	W	1238	21	-	0/7/25/26	0/2/2/2
21	A2M	W	1031	21	-	1/9/27/28	0/3/3/3
21	PSU	W	1367	21	-	0/7/25/26	0/2/2/2
21	OMC	W	517	21	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
21	OMG	W	867	21	-	0/9/27/28	0/3/3/3
21	OMG	W	1328	21	-	0/9/27/28	0/3/3/3
21	PSU	W	1136	21	-	0/7/25/26	0/2/2/2
21	OMC	W	1272	21	-	0/9/27/28	0/2/2/2
21	PSU	W	1177	21	-	0/7/25/26	0/2/2/2
21	OMU	W	172	21	-	1/9/27/28	0/2/2/2
21	PSU	W	1596	21	-	0/7/25/26	0/2/2/2
21	OMC	W	462	21	-	0/9/27/28	0/2/2/2
21	PSU	W	109	21	-	0/7/25/26	0/2/2/2
21	PSU	W	966	21	-	0/7/25/26	0/2/2/2
21	PSU	W	667	21	-	0/7/25/26	0/2/2/2
21	OMU	W	1288	21	-	1/9/27/28	0/2/2/2
21	PSU	W	822	21	-	2/7/25/26	0/2/2/2
21	PSU	W	609	21	-	0/7/25/26	0/2/2/2
21	PSU	W	1003	21	-	0/7/25/26	0/2/2/2
21	A2M	W	159	21	-	1/9/27/28	0/3/3/3
21	OMG	W	601	21	-	0/9/27/28	0/3/3/3
21	PSU	W	1004	21	-	0/7/25/26	0/2/2/2
21	OMG	W	1490	21,56	-	3/9/27/28	0/3/3/3
21	PSU	W	1046	21	-	0/7/25/26	0/2/2/2
21	A2M	W	484	21	-	3/9/27/28	0/3/3/3
21	6MZ	W	1832	21,56	-	0/9/27/28	0/3/3/3
21	G7M	W	1639	21,51	-	2/7/25/26	0/3/3/3
21	OMU	W	1804	21	-	0/9/27/28	0/2/2/2
21	A2M	W	166	21	-	1/9/27/28	0/3/3/3
21	JMH	W	1219	21,56	-	0/7/25/26	0/2/2/2
21	PSU	W	406	21	-	0/7/25/26	0/2/2/2
21	OMG	W	509	21,56	-	1/9/27/28	0/3/3/3
21	PSU	W	1625	21	-	0/7/25/26	0/2/2/2
21	PSU	W	1174	21	-	0/7/25/26	0/2/2/2
21	PSU	W	1347	21	-	0/7/25/26	0/2/2/2
21	C4J	W	1248	21	-	3/16/34/35	0/2/2/2
21	OMU	W	121	21	-	0/9/27/28	0/2/2/2
21	PSU	W	801	21	-	2/7/25/26	0/2/2/2
21	A2M	W	590	21	-	4/9/27/28	0/3/3/3
21	A2M	W	468	21	-	3/9/27/28	0/3/3/3
21	PSU	W	681	21	-	0/7/25/26	0/2/2/2
51	5MC	y	48	51	-	0/7/25/26	0/2/2/2
21	PSU	W	1445	21	-	0/7/25/26	0/2/2/2
21	A2M	W	512	21	-	4/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
21	PSU	W	866	21	-	2/7/25/26	0/2/2/2
21	OMC	W	1391	21	-	0/9/27/28	0/2/2/2
51	T6A	y	37	51	-	5/23/41/42	0/3/3/3
21	PSU	W	366	21	-	0/7/25/26	0/2/2/2
21	PSU	W	36	21	-	0/7/25/26	0/2/2/2
21	PSU	W	572	21	-	0/7/25/26	0/2/2/2
21	OMG	W	1447	21	-	1/9/27/28	0/3/3/3
21	PSU	W	300	21	-	0/7/25/26	0/2/2/2
21	PSU	W	1643	21	-	0/7/25/26	0/2/2/2
51	H2U	y	47	51	-	5/7/38/39	0/2/2/2
21	PSU	W	649	21	-	0/7/25/26	0/2/2/2
21	A2M	W	668	21,56	-	4/9/27/28	0/3/3/3
21	A2M	W	27	21,56	-	3/9/27/28	0/3/3/3
21	PSU	W	1692	21	-	0/7/25/26	0/2/2/2
21	OMC	W	174	21,56	-	0/9/27/28	0/2/2/2
21	OMG	W	683	21	-	0/9/27/28	0/3/3/3
21	PSU	W	105	21	-	0/7/25/26	0/2/2/2
21	OMU	W	354	21	-	0/9/27/28	0/2/2/2
21	PSU	W	1244	21	-	0/7/25/26	0/2/2/2
21	PSU	W	686	21	-	0/7/25/26	0/2/2/2
21	OMU	W	428	21	-	5/9/27/28	0/2/2/2
21	A2M	W	1383	21	-	1/9/27/28	0/3/3/3

The worst 5 of 56 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	y	46	7MG	C5-N7	4.70	1.41	1.35
21	W	1232	PSU	C6-C5	3.45	1.39	1.35
21	W	105	PSU	C6-C5	3.43	1.39	1.35
21	W	866	PSU	C6-C5	3.42	1.39	1.35
21	W	1625	PSU	C6-C5	3.42	1.39	1.35

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
21	W	1678	A2M	O3'-C3'-C2'	5.75	127.50	111.17
21	W	1383	A2M	O3'-C3'-C4'	5.46	126.85	111.05
21	W	1383	A2M	C2'-C1'-N9	-5.13	104.90	113.53
21	W	468	A2M	O3'-C3'-C4'	5.03	125.59	111.05
21	W	166	A2M	O3'-C3'-C4'	4.99	125.49	111.05

There are no chirality outliers.

5 of 96 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
21	W	27	A2M	C1'-C2'-O2'-CM'
21	W	99	A2M	C1'-C2'-O2'-CM'
21	W	100	PSU	C3'-C4'-C5'-O5'
21	W	159	A2M	C1'-C2'-O2'-CM'
21	W	166	A2M	C1'-C2'-O2'-CM'

There are no ring outliers.

26 monomers are involved in 38 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
21	W	1842	4AC	2	0
21	W	918	PSU	1	0
21	W	1678	A2M	1	0
21	W	1232	PSU	1	0
51	y	58	1MA	1	0
51	y	64	RIA	3	0
21	W	99	A2M	1	0
21	W	1703	OMC	2	0
21	W	576	A2M	1	0
21	W	1851	MA6	1	0
21	W	1442	OMU	1	0
21	W	1850	MA6	2	0
21	W	1031	A2M	1	0
21	W	601	OMG	1	0
21	W	484	A2M	1	0
21	W	1639	G7M	2	0
21	W	1804	OMU	1	0
21	W	166	A2M	1	0
21	W	121	OMU	1	0
21	W	468	A2M	2	0
21	W	681	PSU	1	0
21	W	1445	PSU	1	0
21	W	1447	OMG	7	0
21	W	27	A2M	1	0
21	W	428	OMU	1	0
21	W	1383	A2M	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 80 ligands modelled in this entry, 80 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.

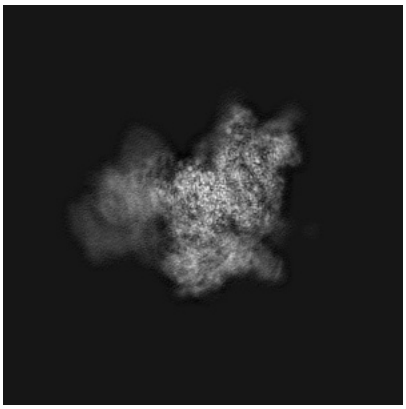
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-54937. These allow visual inspection of the internal detail of the map and identification of artifacts.

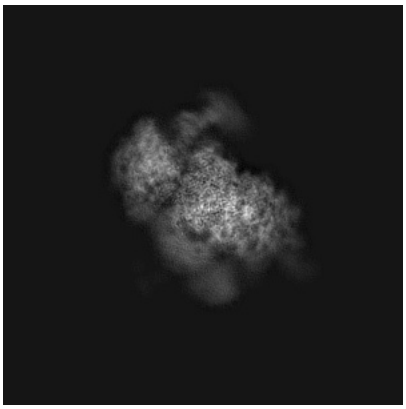
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

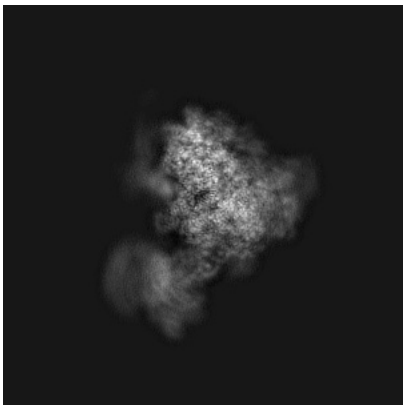
6.1.1 Primary map



X

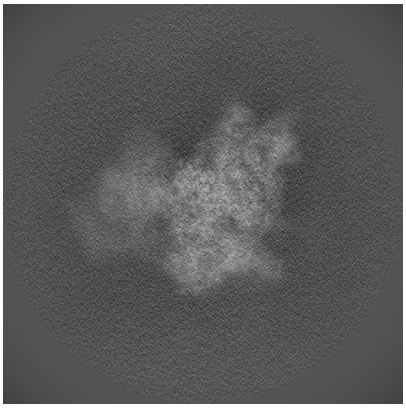


Y

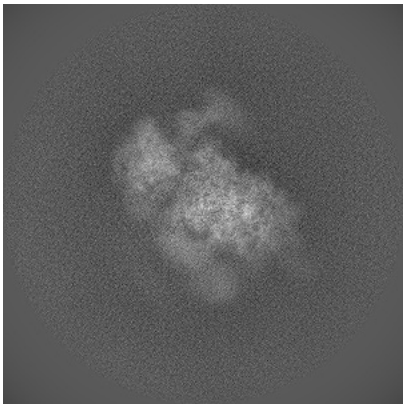


Z

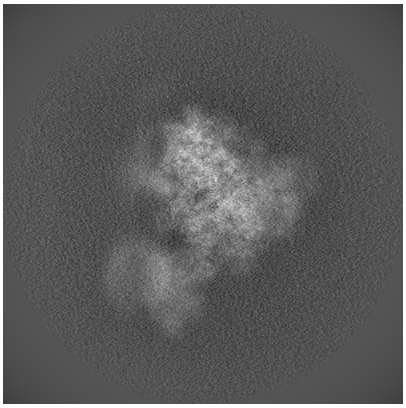
6.1.2 Raw map



X



Y

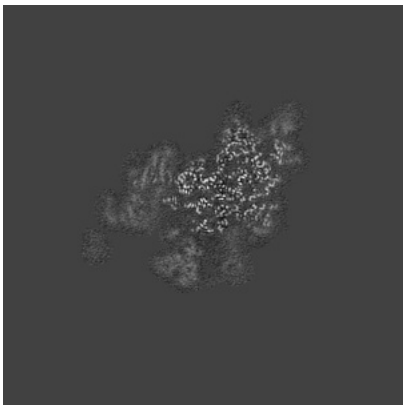


Z

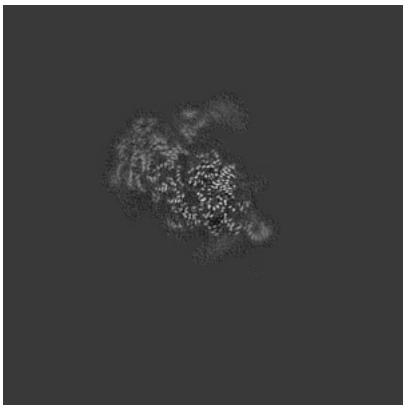
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

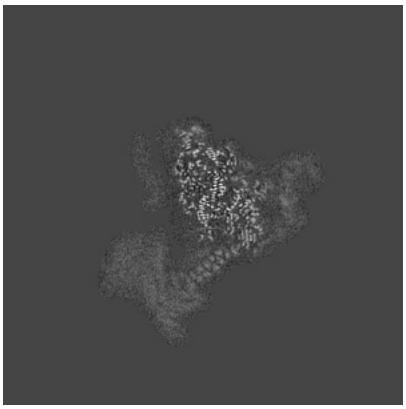
6.2.1 Primary map



X Index: 300

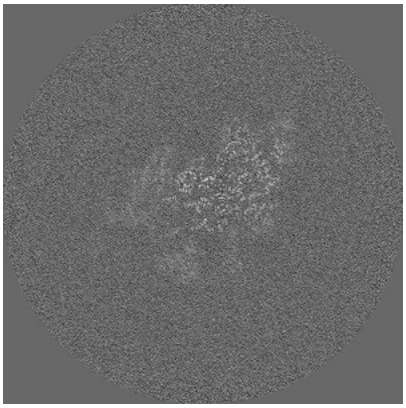


Y Index: 300

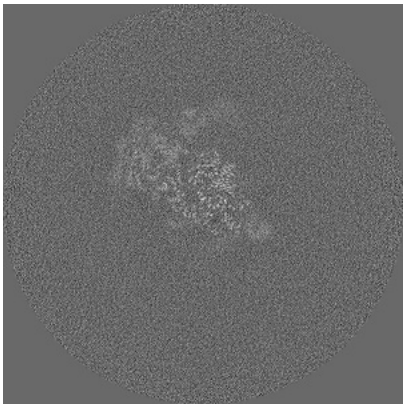


Z Index: 300

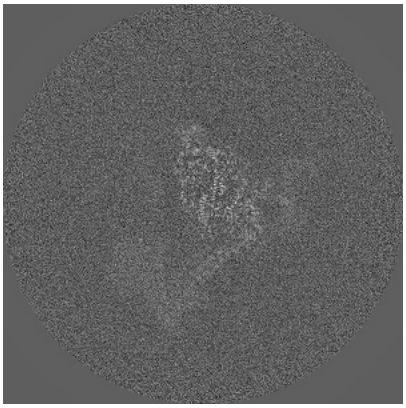
6.2.2 Raw map



X Index: 300



Y Index: 300

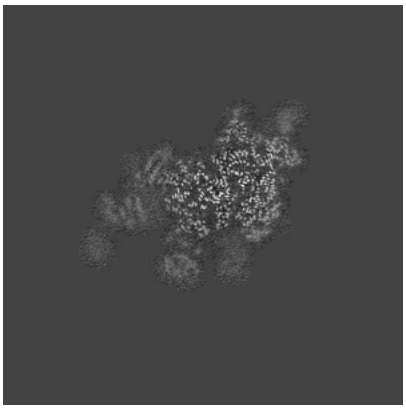


Z Index: 300

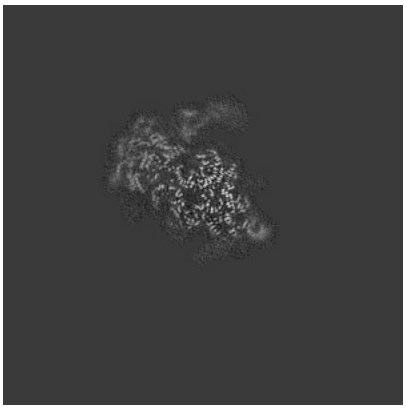
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

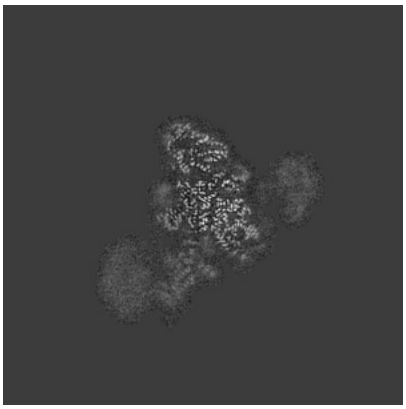
6.3.1 Primary map



X Index: 293

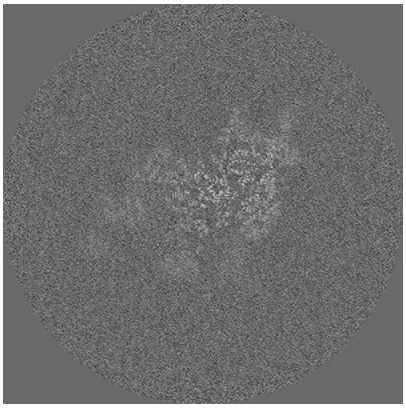


Y Index: 297

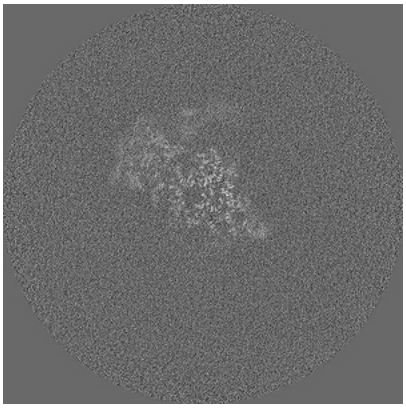


Z Index: 327

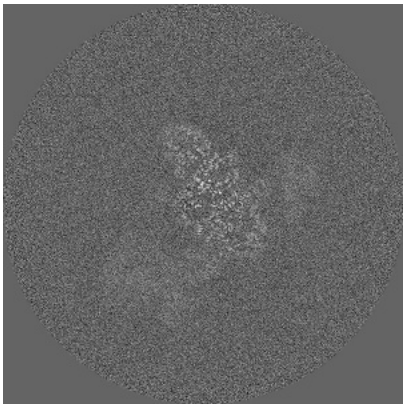
6.3.2 Raw map



X Index: 293



Y Index: 297

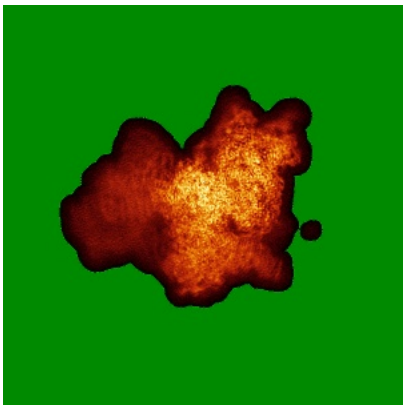


Z Index: 313

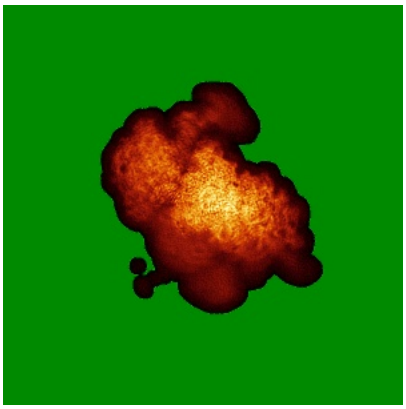
The images above show the largest variance slices of the map in three orthogonal directions.

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

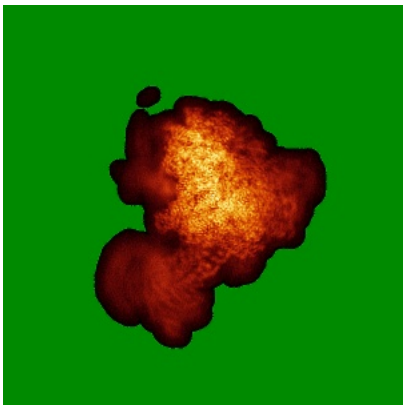
6.4.1 Primary map



X

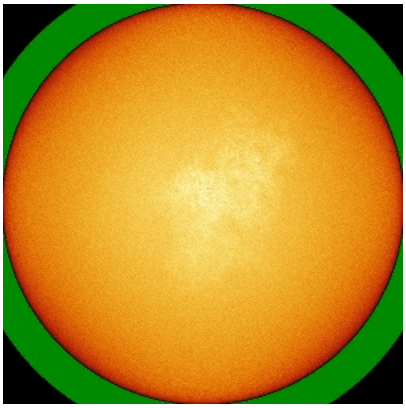


Y

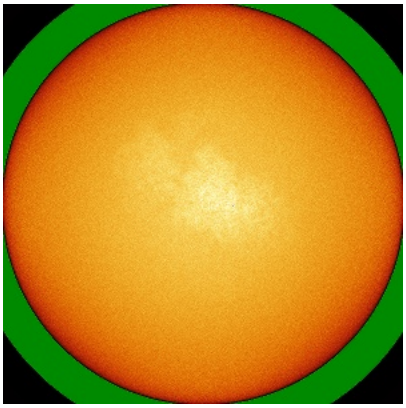


Z

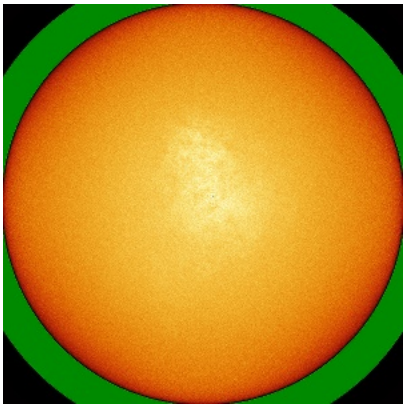
6.4.2 Raw map



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)

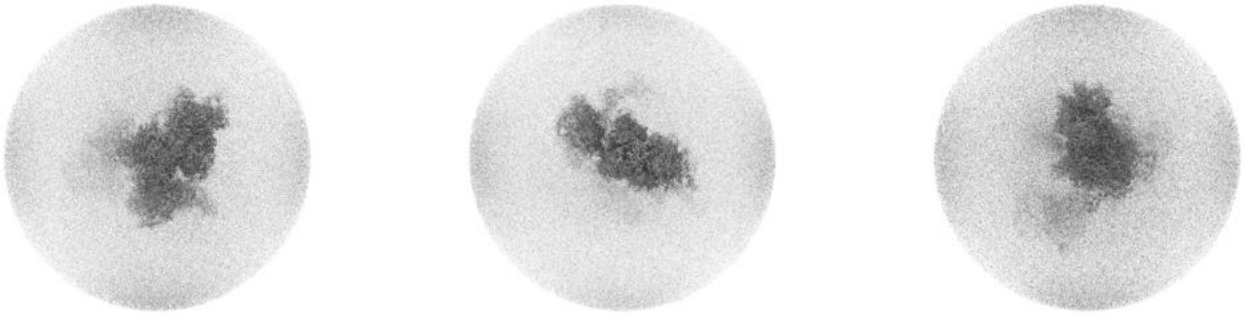
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0045. 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.

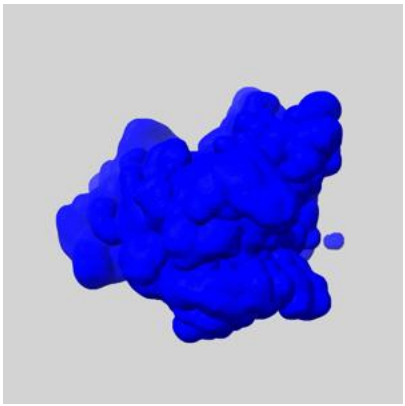
6.6 Mask visualisation

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

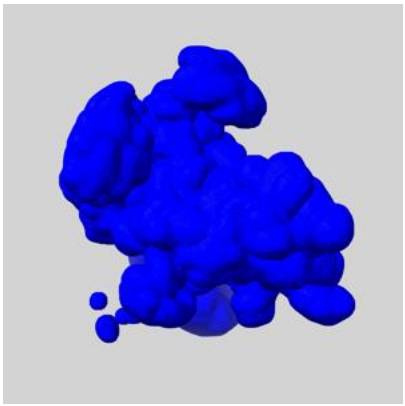
A mask typically either:

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

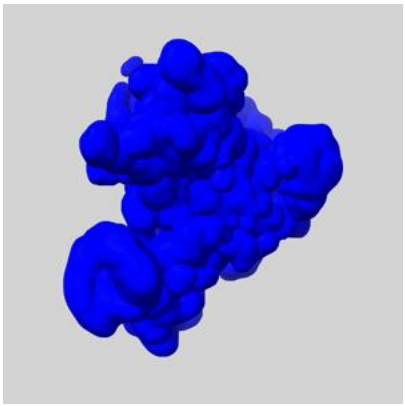
6.6.1 emd_54937_msk_1.map



X



Y

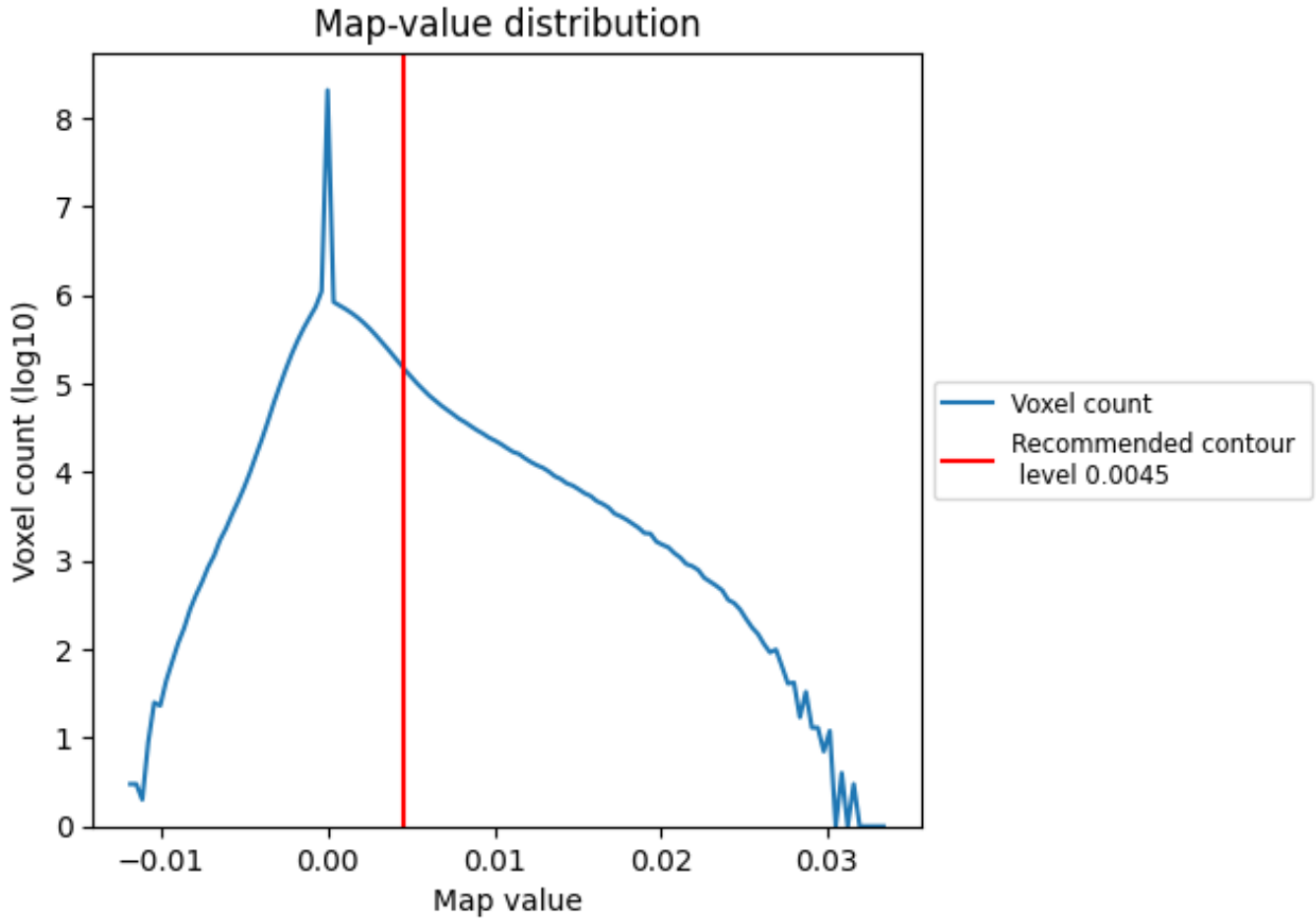


Z

7 Map analysis

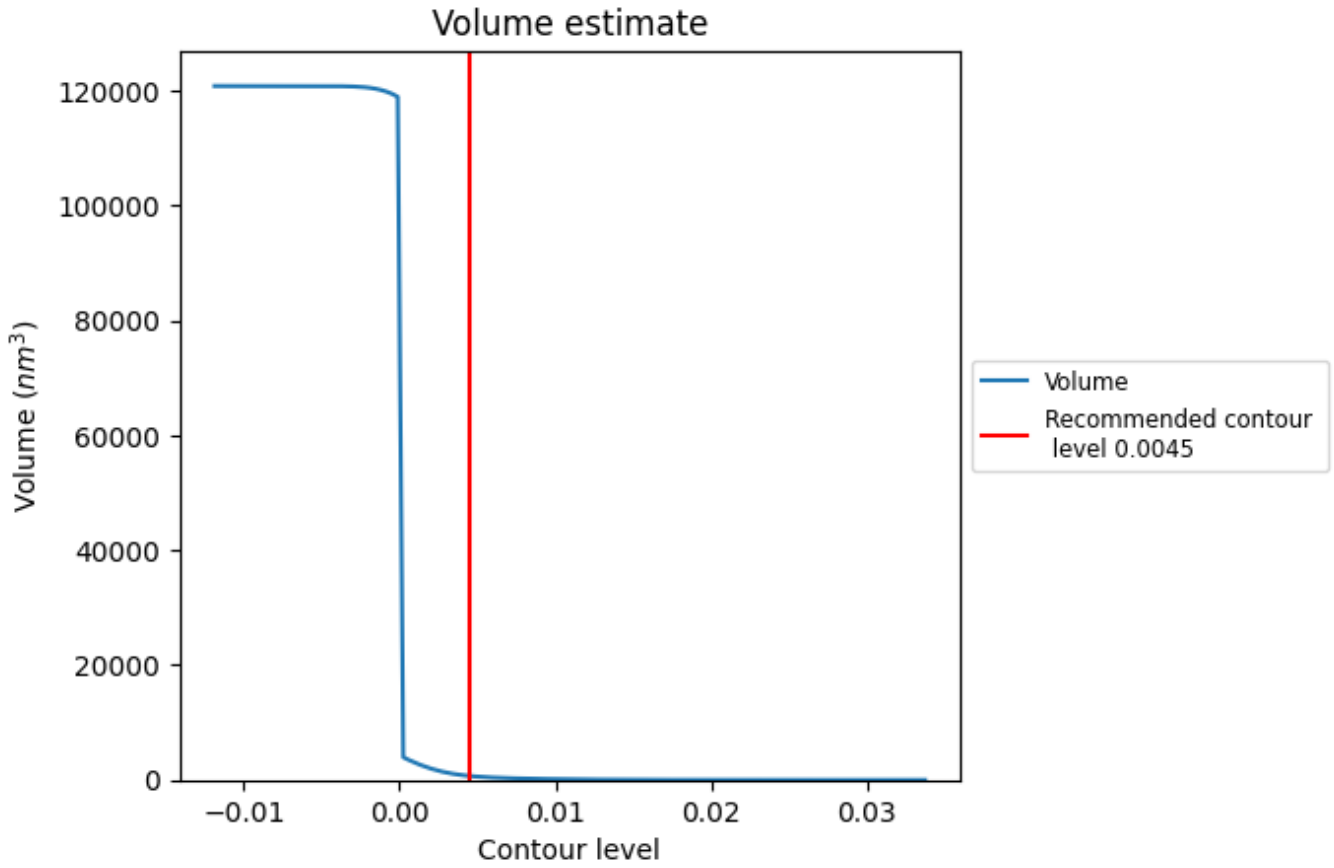
This section contains the results of statistical analysis of the map.

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.

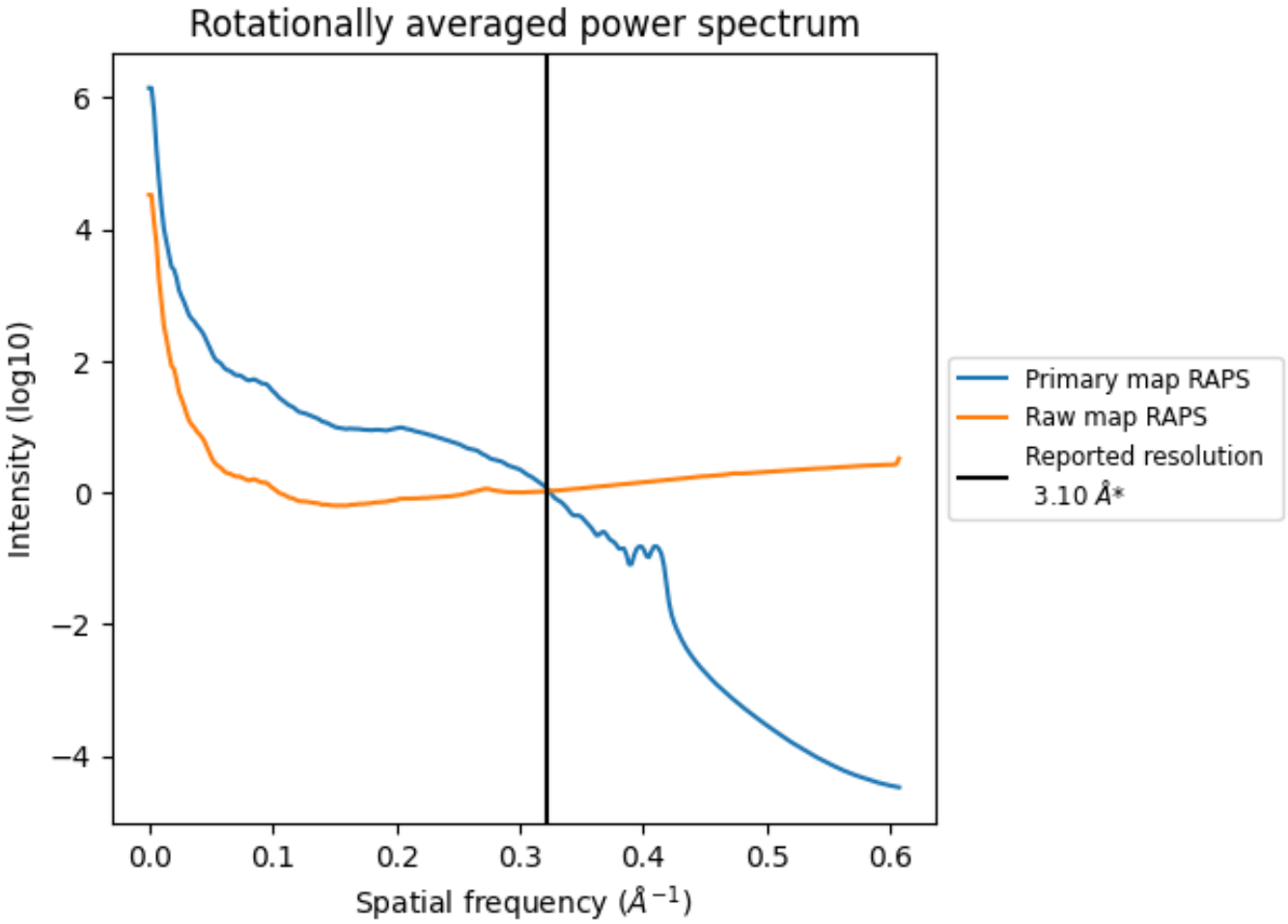
7.2 Volume estimate (i)



The volume at the recommended contour level is 695 nm^3; this corresponds to an approximate mass of 628 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)

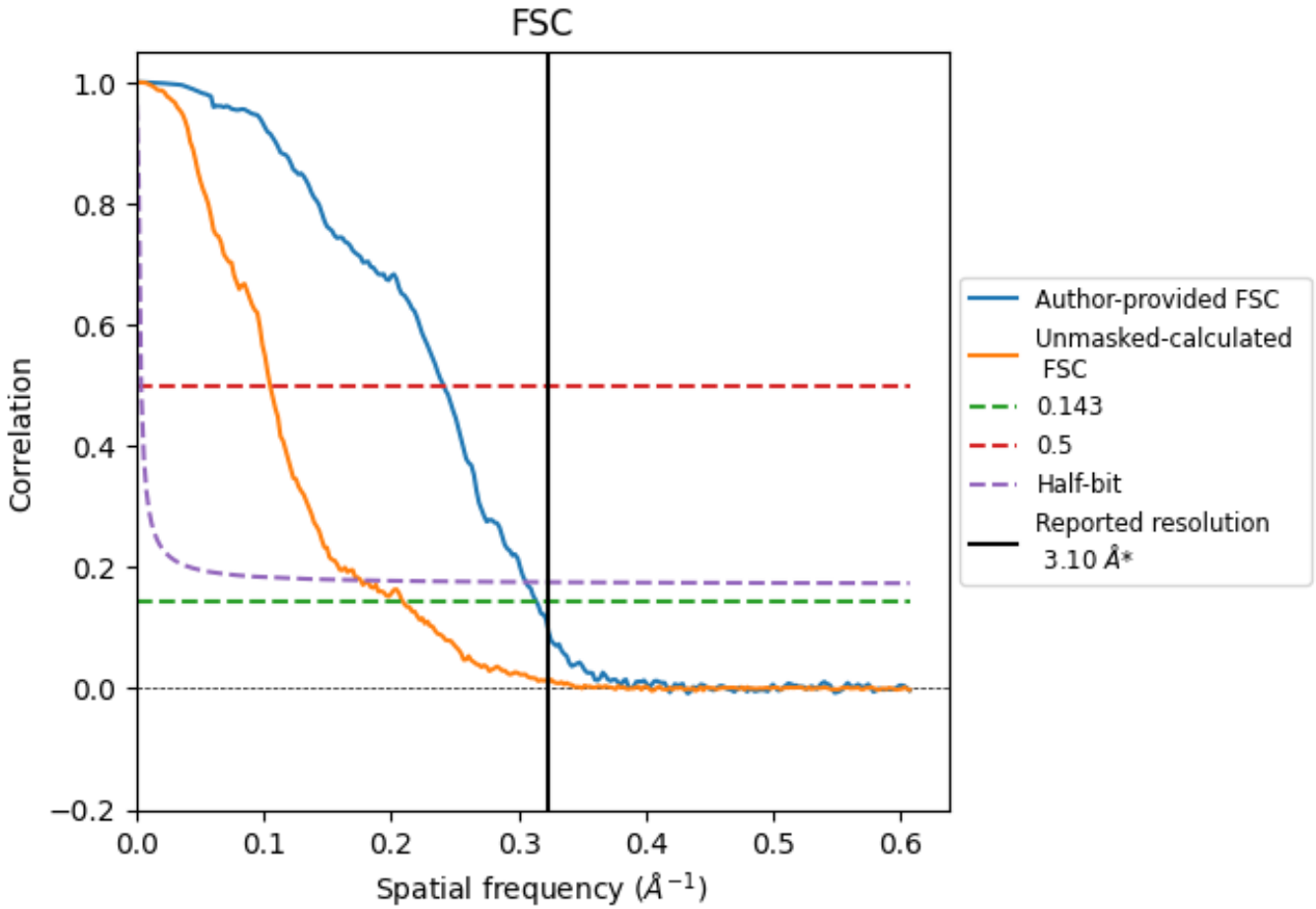


*Reported resolution corresponds to spatial frequency of 0.323 Å^{-1}

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 0.323 Å^{-1}

8.2 Resolution estimates (i)

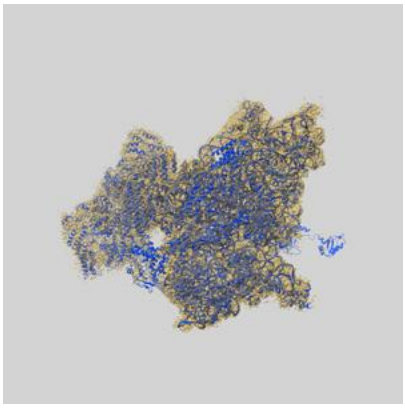
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.18	4.15	3.27
Unmasked-calculated*	4.78	9.51	5.68

*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 4.78 differs from the reported value 3.1 by more than 10 %

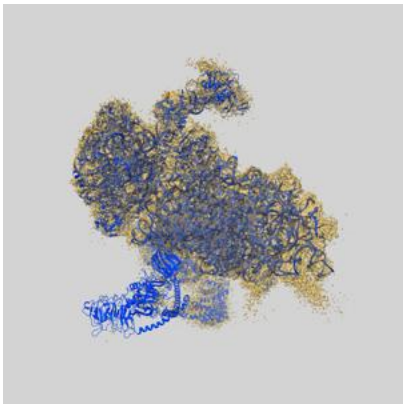
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-54937 and PDB model 9SJ4. Per-residue inclusion information can be found in section 3 on page 15.

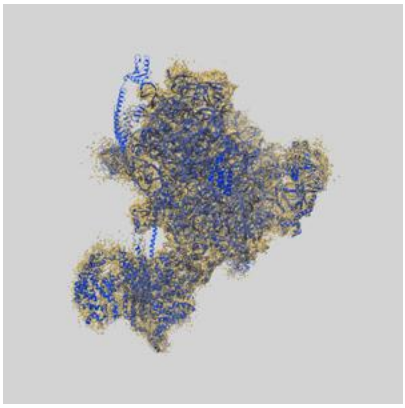
9.1 Map-model overlay



X



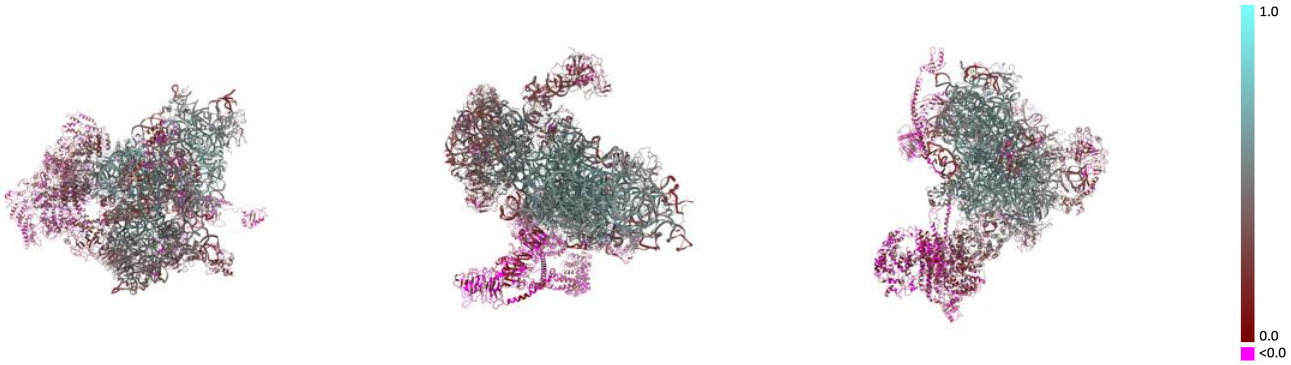
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0045 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.

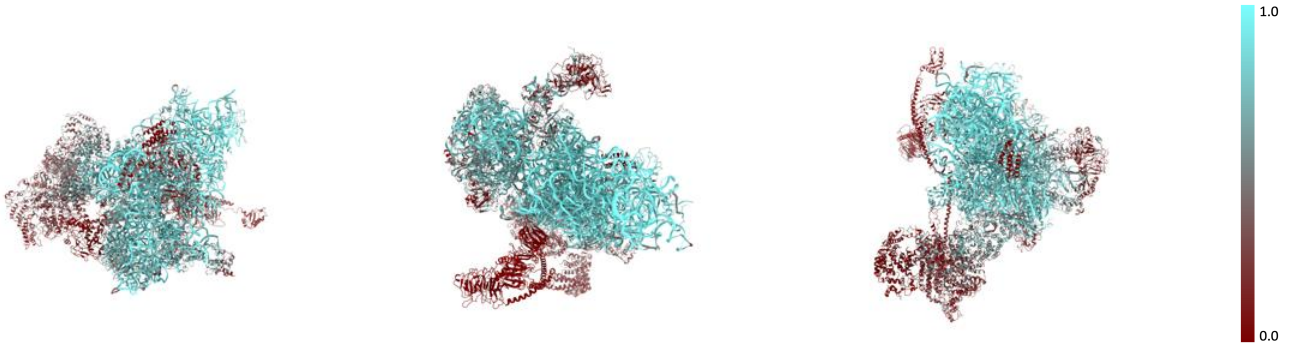
9.2 Q-score mapped to coordinate model



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.

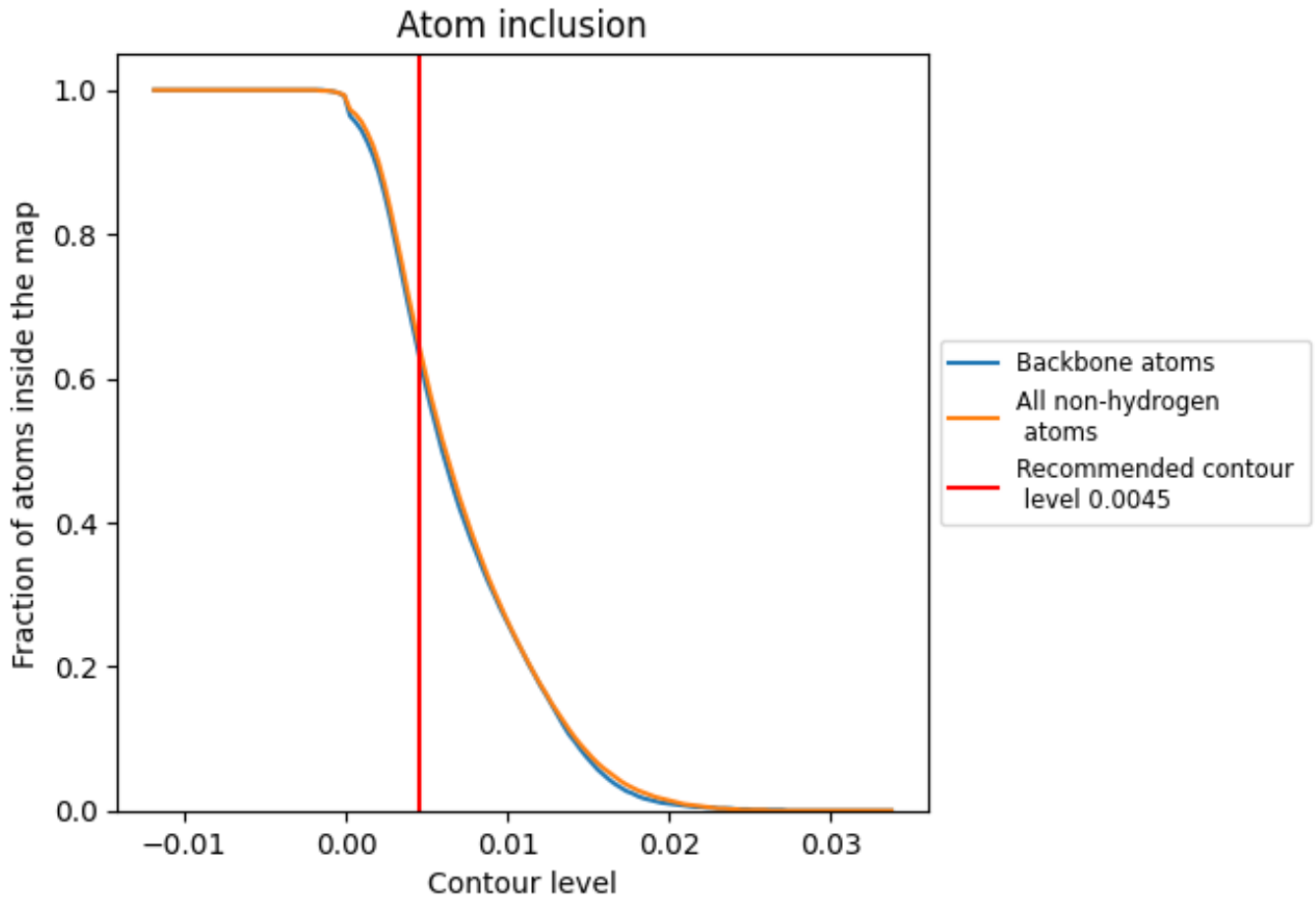
9.3 Atom inclusion mapped to coordinate model



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 (0.0045).

9.4 Atom inclusion (i)



At the recommended contour level, 63% of all backbone atoms, 65% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6470	0.3910
3	0.0800	0.0770
4	0.1460	0.1090
5	0.0960	0.0750
6	0.1410	0.0880
7	0.0800	0.2090
8	0.1110	0.0660
9	0.8130	0.5370
A	0.3100	0.2050
B	0.2270	0.1210
D	0.4170	0.3210
E	0.2150	0.2400
F	0.0000	0.0080
G	0.3450	0.2880
H	0.6720	0.4430
I	0.0140	0.0860
J	0.4050	0.2530
L	0.7580	0.4680
M	0.8470	0.5350
N	0.8710	0.5510
O	0.8720	0.5760
P	0.8500	0.5170
Q	0.8390	0.5420
R	0.8790	0.5620
S	0.8470	0.4660
T	0.8610	0.5260
U	0.2230	0.2820
V	0.8770	0.5550
W	0.9360	0.5110
X	0.8870	0.5700
Y	0.9020	0.5690
Z	0.8700	0.5560
a	0.9100	0.5820
b	0.7390	0.5020
c	0.9160	0.5960



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Chain	Atom inclusion	Q-score
d	0.8740	0.5180
e	0.8860	0.5310
f	0.7470	0.4690
g	0.7810	0.4700
h	0.6660	0.4460
i	0.6400	0.3820
j	0.6640	0.3780
k	0.5750	0.3380
l	0.7530	0.4200
m	0.6350	0.3690
n	0.6470	0.3750
o	0.8050	0.4960
p	0.4790	0.2710
q	0.3320	0.2730
s	0.6630	0.4740
v	0.7420	0.4900
w	0.6880	0.4550
x	0.1250	0.2400
y	0.7590	0.3540
z	0.2540	0.3800