



wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 06:42 PM UTC

PDB ID : 6FYY / pdb_00006fyy
EMDB ID : EMD-4328
Title : Structure of a partial yeast 48S preinitiation complex with eIF5 N-terminal domain (model C2)
Authors : Llacer, J.L.; Hussain, T.; Gordiyenko, Y.; Ramakrishnan, V.
Deposited on : 2018-03-12
Resolution : 3.02 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

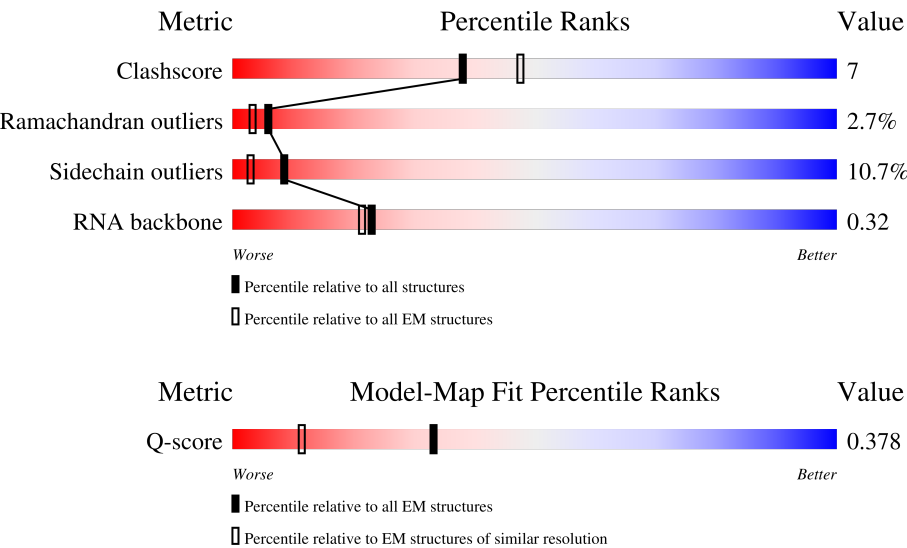
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.02 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	13913 (2.52 - 3.52)

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

Mol	Chain	Length	Quality of chain
1	1	76	67% 49% 24% 20% 7%
2	2	1798	12% 40% 44% 13%
3	3	49	49% 14% 37% 12% 37%

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Mol	Chain	Length	Quality of chain
4	A	254	
5	B	255	
6	C	259	
7	D	237	
8	E	261	
9	F	227	
10	G	236	
11	H	190	
12	I	201	
13	J	188	
14	K	106	
15	L	156	
16	M	134	
17	N	151	
18	O	137	
19	P	142	
20	Q	143	
21	R	136	
22	S	146	
23	T	144	
24	U	117	
25	V	87	
26	W	130	
27	X	145	
28	Y	135	

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Mol	Chain	Length	Quality of chain
29	Z	108	
30	a	119	
31	b	82	
32	c	67	
33	d	56	
34	e	63	
35	f	150	
36	g	326	
37	h	25	
38	i	153	
39	j	304	
40	k	527	
41	l	285	
42	m	405	
43	o	964	
44	p	763	
45	q	812	
46	r	274	
47	s	347	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	C4J	2	1190	X	-	-	-

2 Entry composition

There are 51 unique types of molecules in this entry. The entry contains 104316 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 RNA chain called tRNAi.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	75	Total	C	N	O	P	0	0
			1639	734	298	531	76		

- Molecule 2 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1780	Total	C	N	O	P	0	0
			37812	16904	6659	12469	1780		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	676	G	U	conflict	GB 49642208
2	678	U	G	conflict	GB 49642208
2	1190	C4J	U	conflict	GB 49642208

- Molecule 3 is a RNA chain called mRNA (31-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	31	Total	C	N	O	P	4	0
			719	324	108	252	35		

- Molecule 4 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	219	Total	C	N	O	S	0	0
			1702	1085	299	316	2		

- Molecule 5 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	225	Total	C	N	O	S	0	0
			1797	1135	330	329	3		

- Molecule 6 is a protein called KLLA0F09812p.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	220	Total	C	N	O	S	0	0
			1648	1053	291	300	4		

- Molecule 7 is a protein called KLLA0D08305p.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	227	Total	C	N	O	S	0	0
			1774	1126	320	323	5		

- Molecule 8 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	260	Total	C	N	O	S	0	0
			2078	1322	393	359	4		

- Molecule 9 is a protein called KLLA0D10659p.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	206	Total	C	N	O	S	0	0
			1609	1008	298	300	3		

- Molecule 10 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	230	Total	C	N	O	S	0	0
			1832	1146	352	330	4		

- Molecule 11 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	H	184	Total	C	N	O	0	0
			1483	950	270	263		

- Molecule 12 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	188	Total	C	N	O	S	0	0
			1489	923	300	265	1		

- Molecule 13 is a protein called KLLA0E23673p.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	182	Total	C	N	O	S	0	0
			1471	929	287	254	1		

- Molecule 14 is a protein called KLLA0B08173p.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	96	Total	C	N	O	S	0	0
			809	533	129	146	1		

- Molecule 15 is a protein called KLLA0A10483p.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	155	Total	C	N	O	S	0	0
			1248	798	237	210	3		

- Molecule 16 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	117	Total	C	N	O		0	0
			885	553	161	171			

- Molecule 17 is a protein called KLLA0F18040p.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	151	Total	C	N	O	S	0	0
			1195	761	224	207	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	129	Total	C	N	O	S	0	0
			955	585	191	176	3		

- Molecule 19 is a protein called KLLA0F07843p.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	P	117	Total	C	N	O	S	0	0
			923	592	165	161	5		

- Molecule 20 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	Q	141	Total	C	N	O	0	0
			1105	709	204	192		

- Molecule 21 is a protein called KLLA0B01474p.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	R	130	Total	C	N	O	S	0	0
			1033	643	194	193	3		

- Molecule 22 is a protein called KLLA0B01562p.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	S	145	Total	C	N	O	S	0	0
			1189	739	239	209	2		

- Molecule 23 is a protein called KLLA0A07194p.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	T	143	Total	C	N	O	0	0
			1110	693	210	207		

- Molecule 24 is a protein called KLLA0F25542p.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	U	106	Total	C	N	O	S	0	0
			845	540	152	152	1		

- Molecule 25 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	V	87	Total	C	N	O	S	0	0
			687	424	126	135	2		

- Molecule 26 is a protein called 40S ribosomal protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	W	129	Total	C	N	O	S	0	0
			1021	651	187	180	3		

- Molecule 27 is a protein called KLLA0B11231p.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	X	144	Total	C	N	O	S	0	0
			1119	708	218	191	2		

- Molecule 28 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Y	134	Total	C	N	O	S	0	0
			1061	665	207	189			

- Molecule 29 is a protein called KLLA0B06182p.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	78	Total	C	N	O	S	0	0
			594	376	111	106	1		

- Molecule 30 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	103	Total	C	N	O	S	0	0
			812	500	173	134	5		

- Molecule 31 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	81	Total	C	N	O	S	0	0
			609	379	112	113	5		

- Molecule 32 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	c	64	Total	C	N	O	S	0	0
			499	308	99	91	1		

- Molecule 33 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	55	Total	C	N	O	S	0	0
			461	289	93	78	1		

- Molecule 34 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	e	60	Total	C	N	O	S	0	0
			472	295	96	80	1		

- Molecule 35 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	f	74	Total	C	N	O	S	0	0
			584	374	111	95	4		

- Molecule 36 is a protein called KLLA0E12277p.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	320	Total	C	N	O	S	0	0
			2469	1561	432	471	5		

- Molecule 37 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	h	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 38 is a protein called Eukaryotic translation initiation factor 1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	i	121	Total	C	N	O	S	0	0
			958	587	183	183	5		

- Molecule 39 is a protein called Eukaryotic translation initiation factor 2 subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	j	249	Total	C	N	O	S	0	0
			2006	1283	333	382	8		

- Molecule 40 is a protein called Eukaryotic translation initiation factor 2 subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	396	Total	C	N	O	S	0	0
			3034	1932	542	544	16		

- Molecule 41 is a protein called Eukaryotic translation initiation factor 2 subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	128	Total	C	N	O	S	0	0
			1036	661	186	182	7		

- Molecule 42 is a protein called Eukaryotic translation initiation factor 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	m	147	Total	C	N	O	S	0	0
			1140	724	201	208	7		

- Molecule 43 is a protein called Eukaryotic translation initiation factor 3 subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	529	Total	C	N	O	S	0	0
			4070	2597	697	769	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	647	Total	C	N	O	S	0	0
			5114	3274	880	942	18		

- Molecule 45 is a protein called eIF3c, Eukaryotic translation initiation factor 3 subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	q	621	Total	C	N	O	S	0	0
			4827	3076	813	926	12		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
46	r	49	Total	C	N	O	0	0
			392	240	76	76		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
47	s	330	Total	C	N	O	S	0	0
			2606	1661	429	507	9		

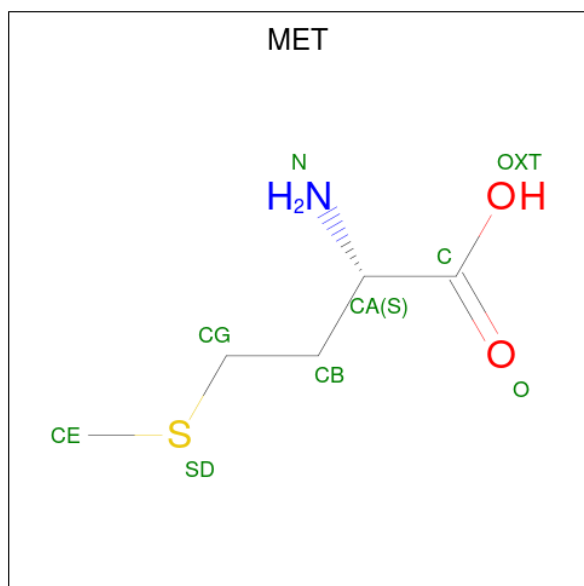
- Molecule 48 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
48	2	116	Total	Mg	0
			116	116	
48	k	1	Total	Mg	0
			1	1	

- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn).

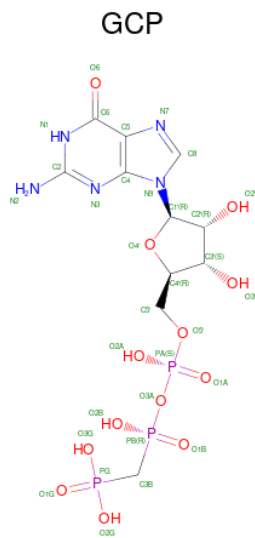
Mol	Chain	Residues	Atoms		AltConf
49	a	1	Total	Zn	0
			1	1	
49	b	1	Total	Zn	0
			1	1	
49	f	1	Total	Zn	0
			1	1	
49	l	1	Total	Zn	0
			1	1	
49	m	1	Total	Zn	0
			1	1	

- Molecule 50 is METHIONINE (CCD ID: MET) (formula: C₅H₁₁NO₂S).



Mol	Chain	Residues	Atoms					AltConf
50	k	1	Total	C	N	O	S	0
			8	5	1	1	1	

- Molecule 51 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).

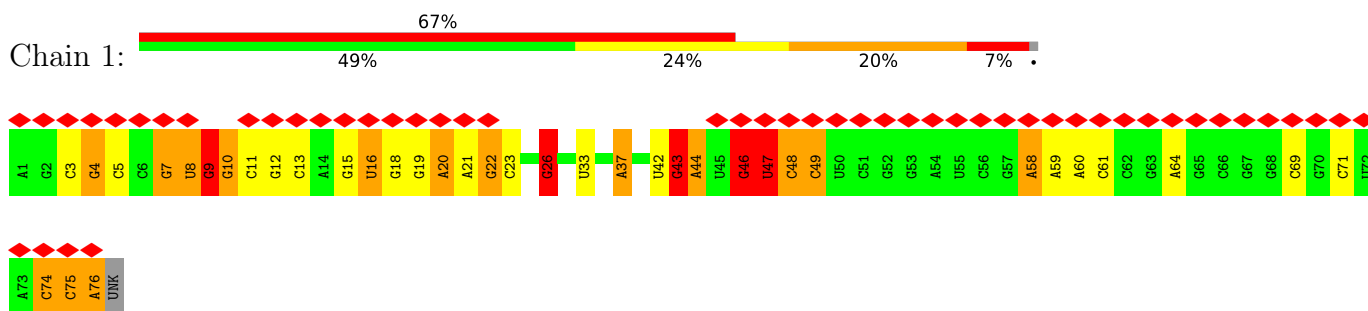


Mol	Chain	Residues	Atoms					AltConf
51	k	1	Total	C	N	O	P	0
			32	11	5	13	3	

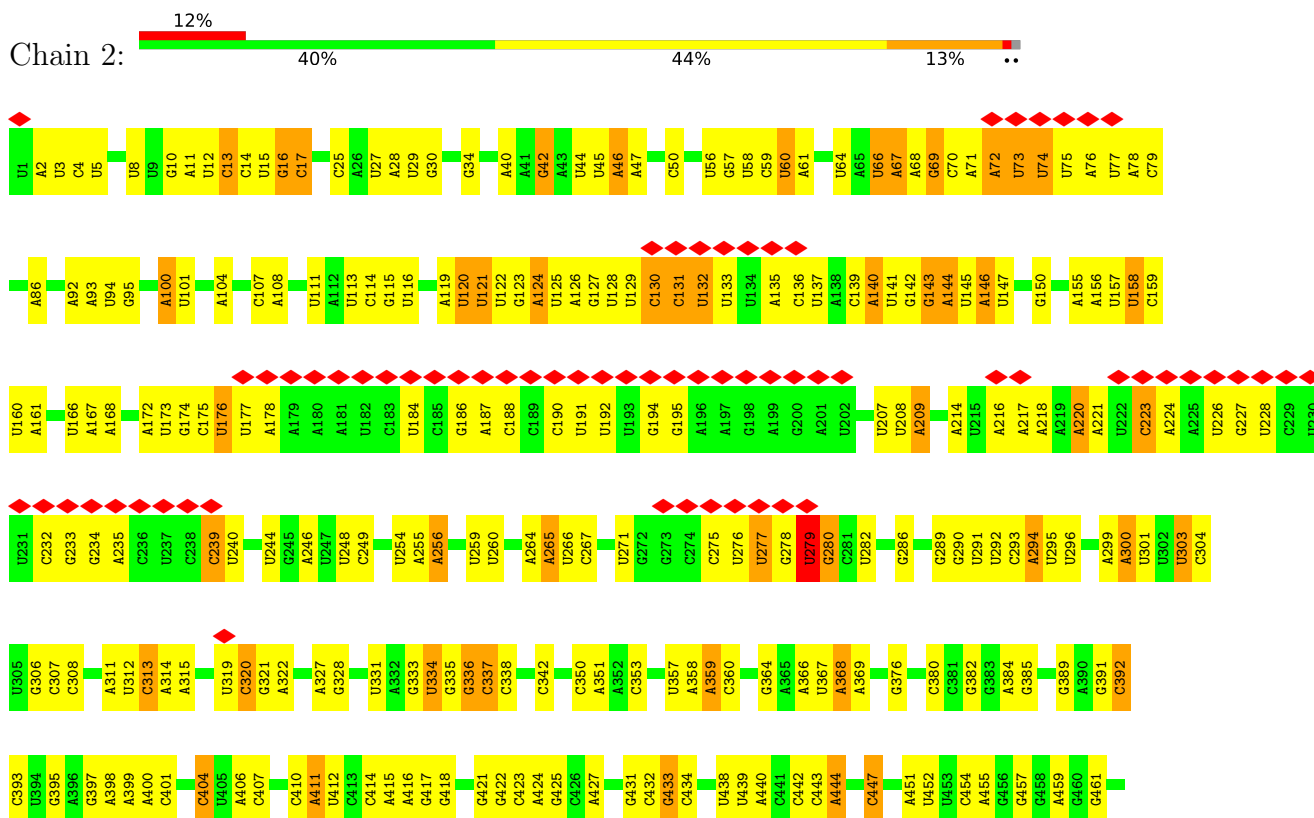
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

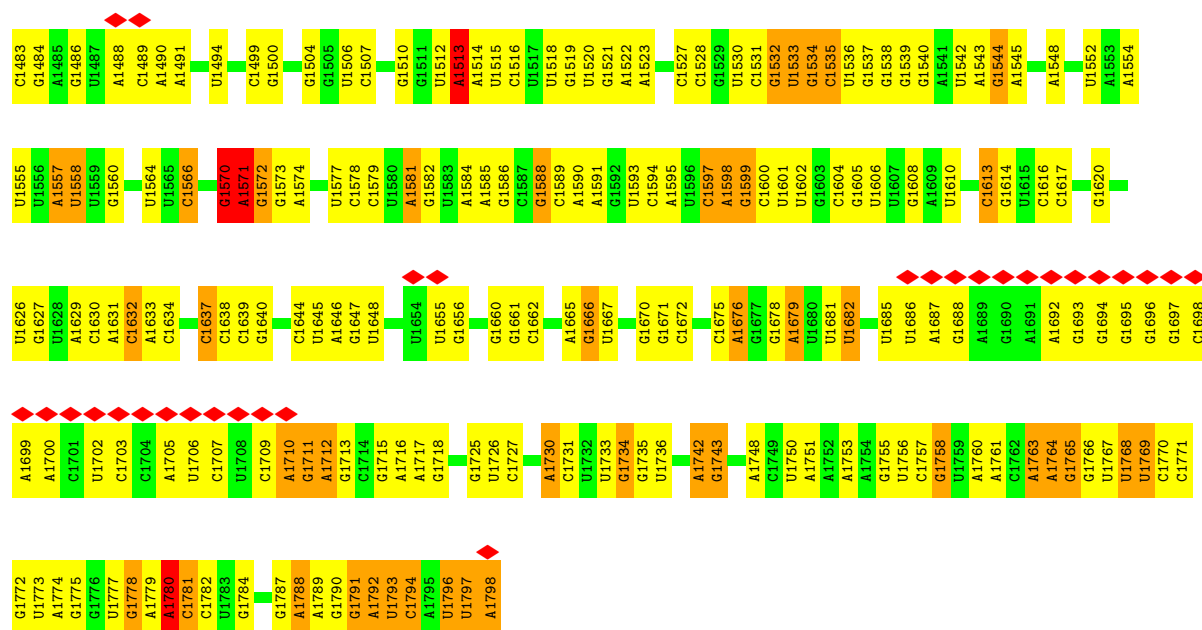
• Molecule 1: tRNAi



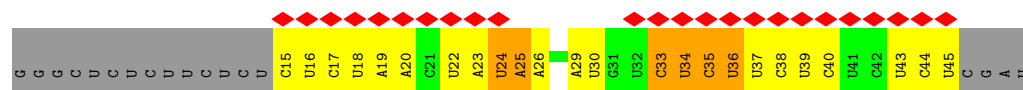
• Molecule 2: 18S ribosomal RNA



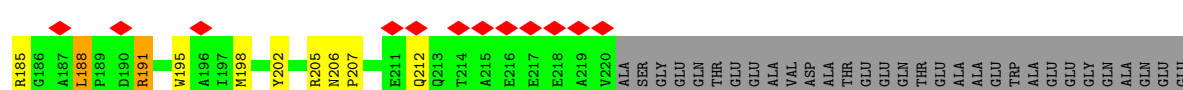
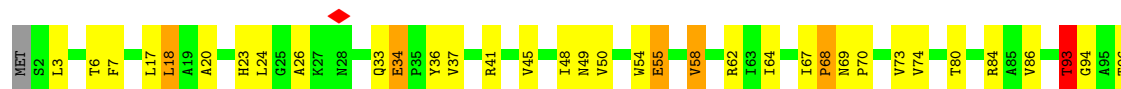




• Molecule 3: mRNA (31-MER)

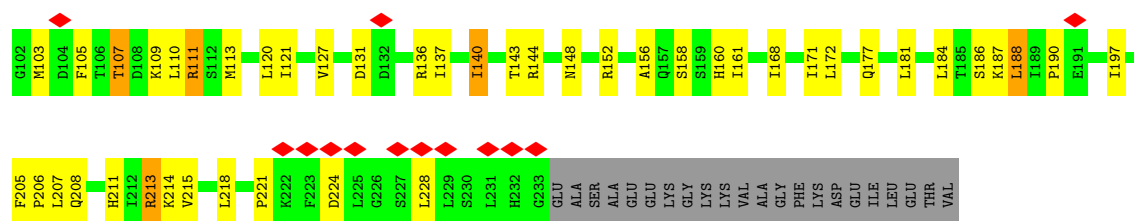


• Molecule 4: 40S ribosomal protein S0

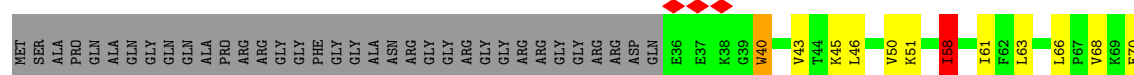


• Molecule 5: 40S ribosomal protein S1

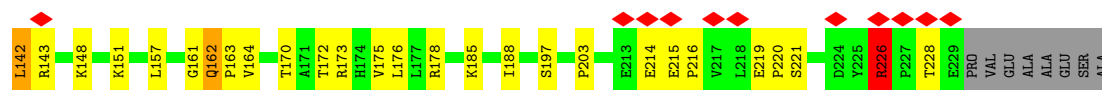
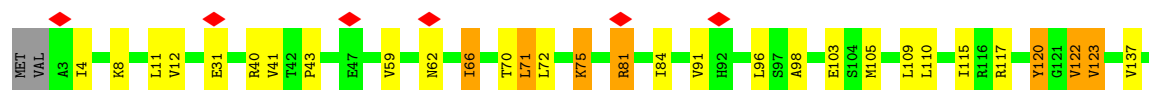




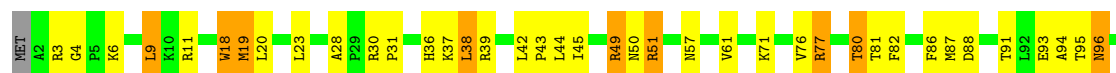
• Molecule 6: KLLA0F09812p



• Molecule 7: KLLA0D08305p

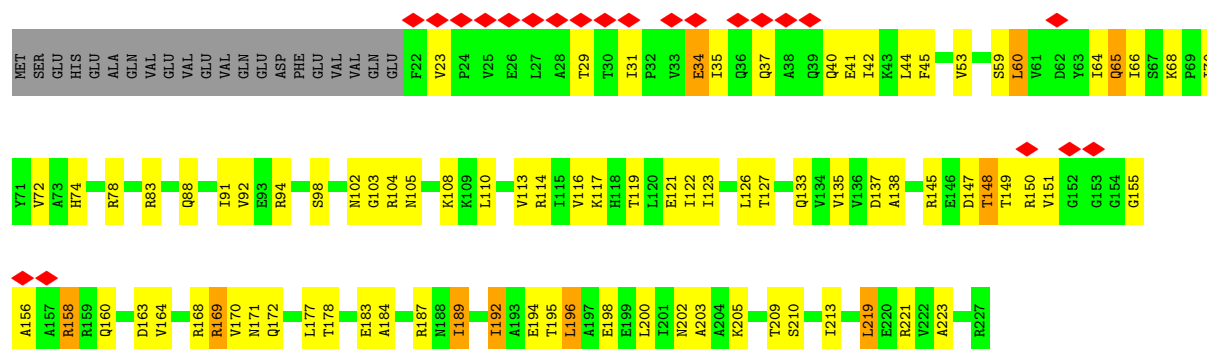


• Molecule 8: 40S ribosomal protein S4

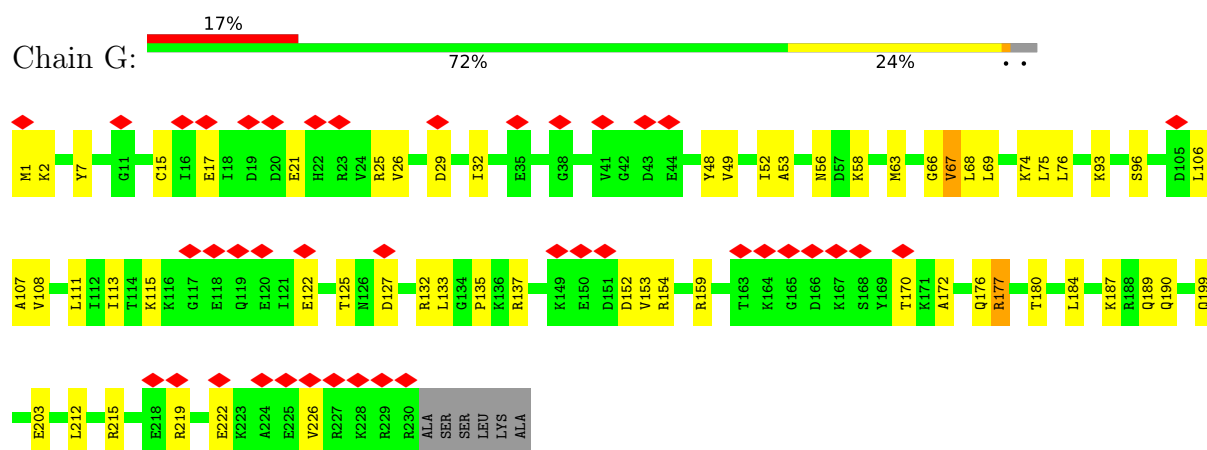


• Molecule 9: KLLA0D10659p

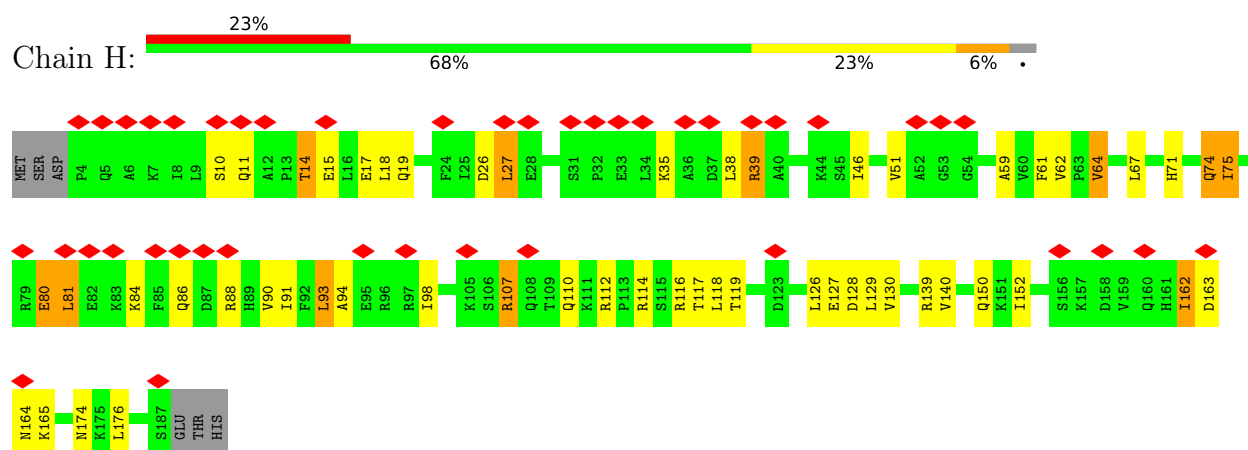




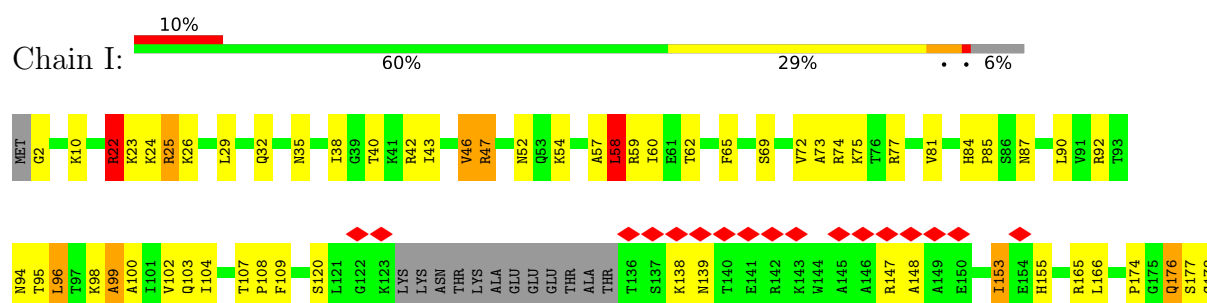
• Molecule 10: 40S ribosomal protein S6



• Molecule 11: 40S ribosomal protein S7



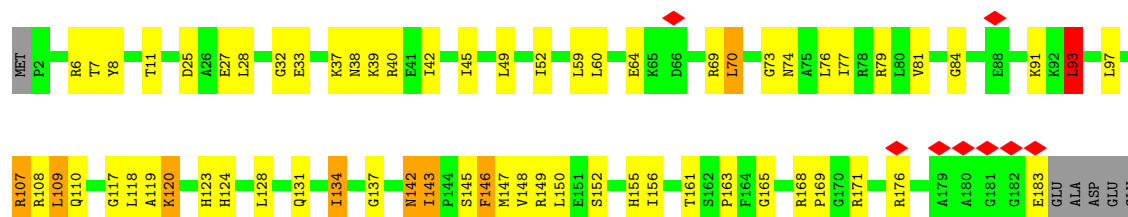
• Molecule 12: 40S ribosomal protein S8





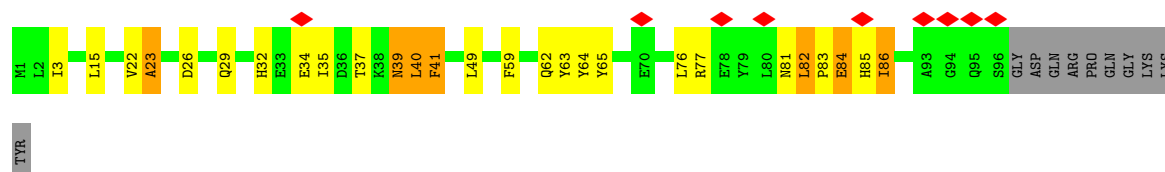
• Molecule 13: KLLA0E23673p

Chain J: 62% 30%



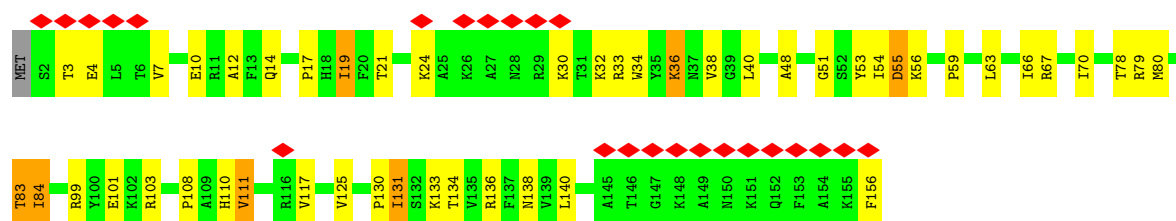
• Molecule 14: KLLA0B08173p

Chain K: 8% 65% 19% 7% 9%



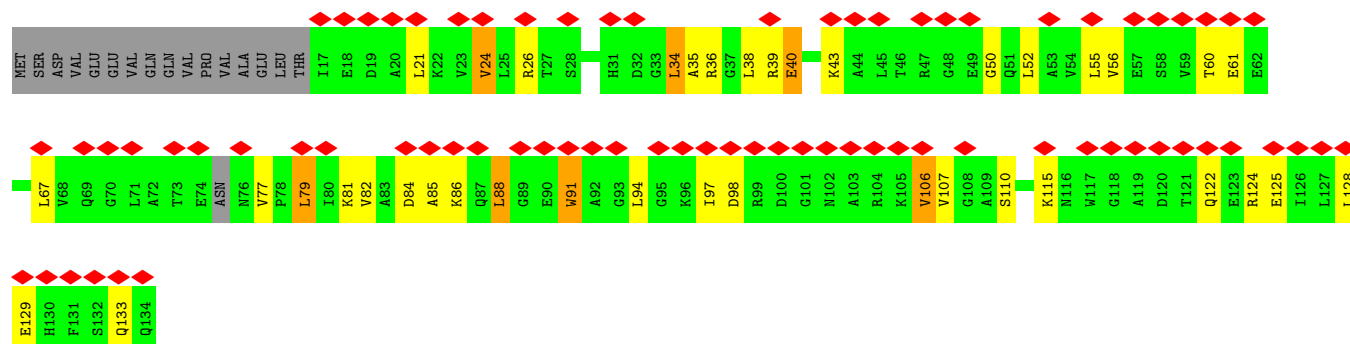
• Molecule 15: KLLA0A10483p

Chain L: 15% 68% 27%

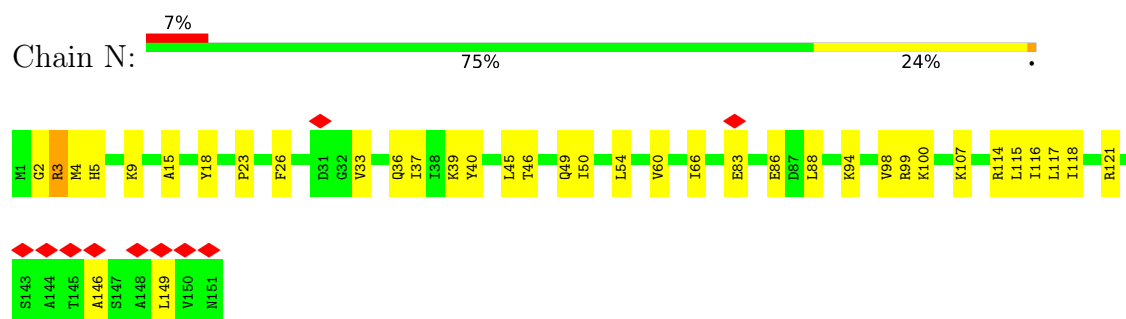


• Molecule 16: 40S ribosomal protein S12

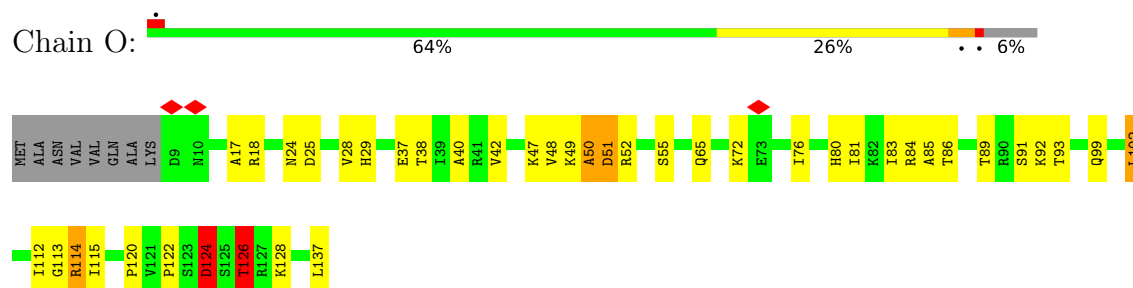
Chain M: 56% 58% 24% 5% 13%



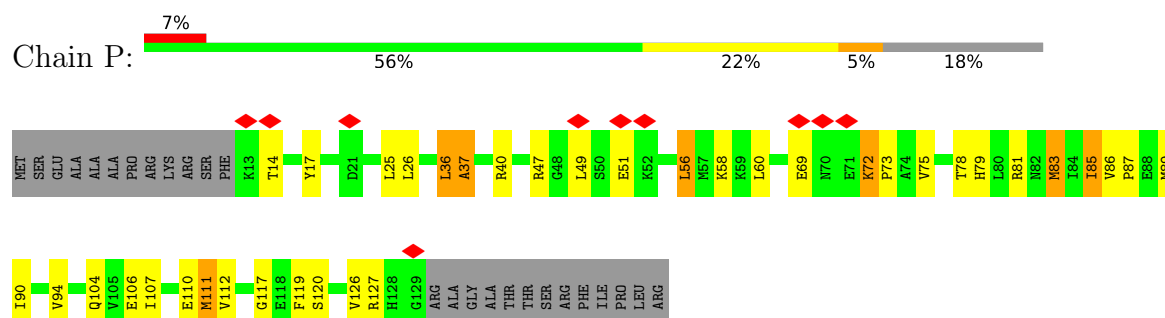
- Molecule 17: KLLA0F18040p



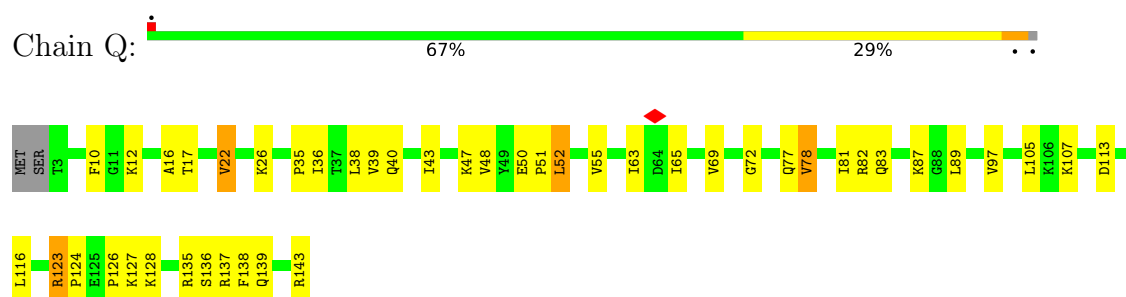
- Molecule 18: 40S ribosomal protein S14



- Molecule 19: KLLA0F07843p

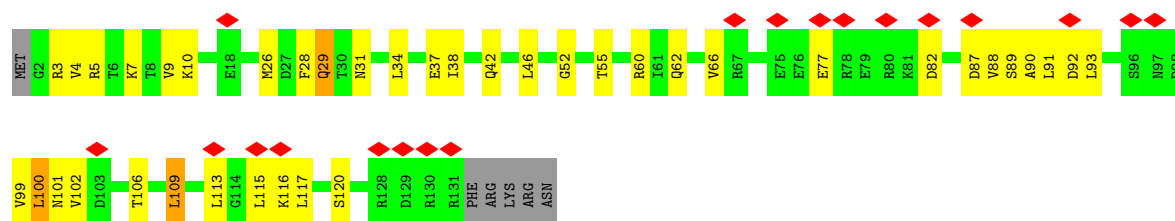


- Molecule 20: 40S ribosomal protein S16

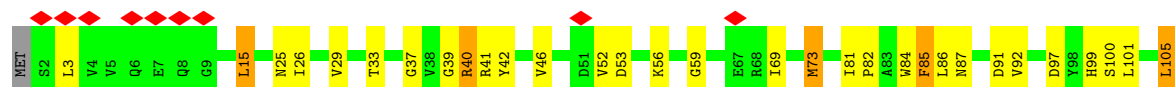


- Molecule 21: KLLA0B01474p

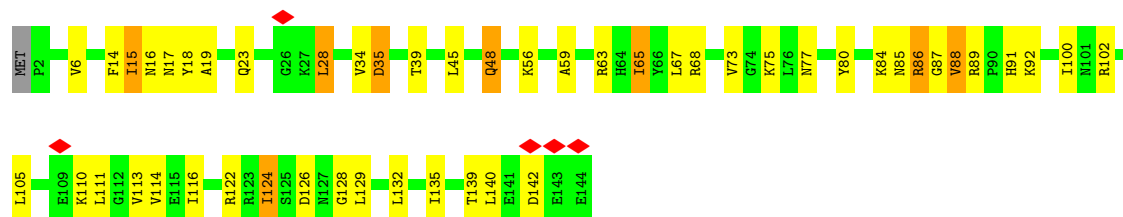




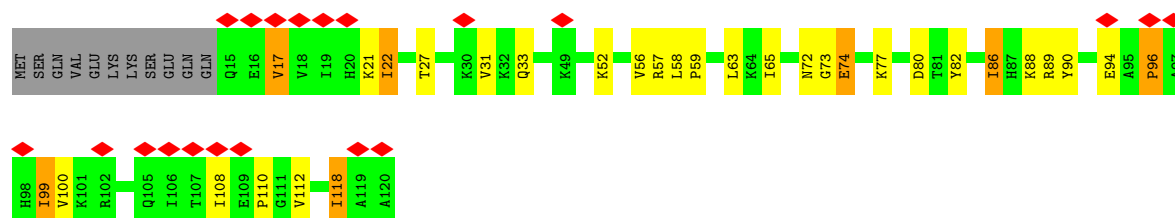
• Molecule 22: KLLA0B01562p



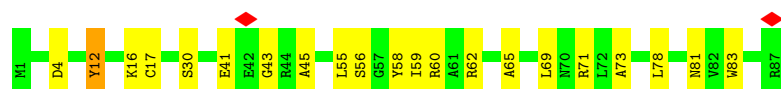
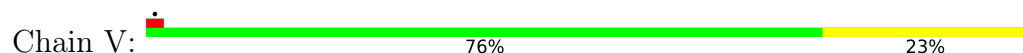
• Molecule 23: KLLA0A07194p



• Molecule 24: KLLA0F25542p

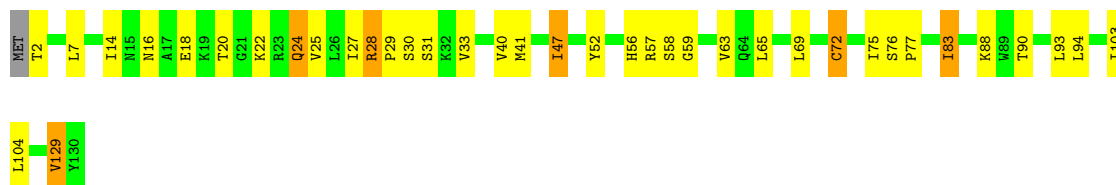


• Molecule 25: 40S ribosomal protein S21



• Molecule 26: 40S ribosomal protein S22

Chain W: 



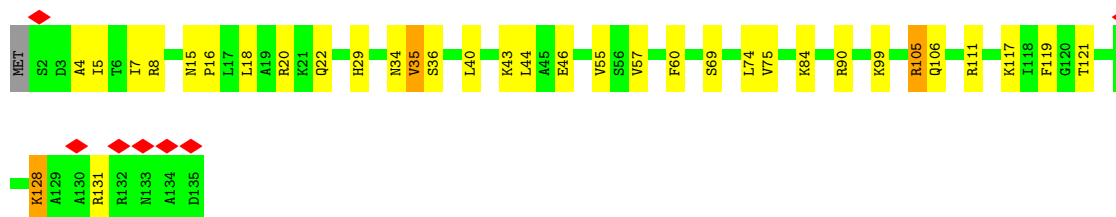
- Molecule 27: KLLA0B11231p

Chain X: 



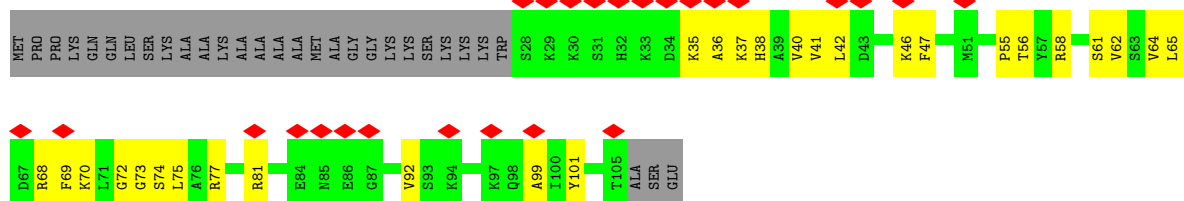
- Molecule 28: 40S ribosomal protein S24

Chain Y: 



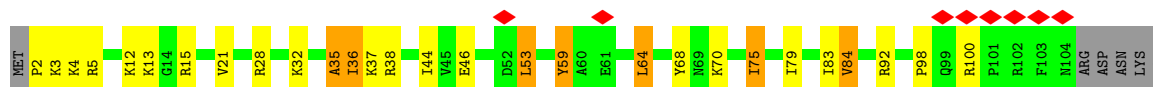
- Molecule 29: KLLA0B06182p

Chain Z: 



- Molecule 30: 40S ribosomal protein S26

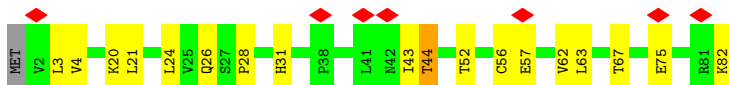
Chain a: 



SER
PRO
ALA
ASP
ALA
ALA
LYS
LYS
ALA
LEU

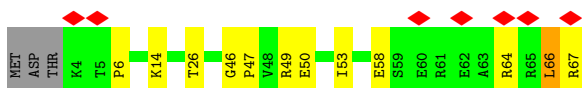
- Molecule 31: 40S ribosomal protein S27

Chain b: 



- Molecule 32: 40S ribosomal protein S28

Chain c: 



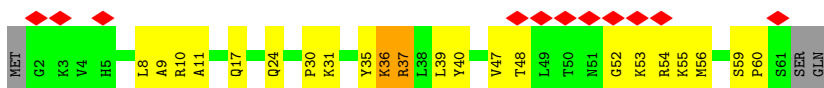
- Molecule 33: 40S ribosomal protein S29

Chain d: 



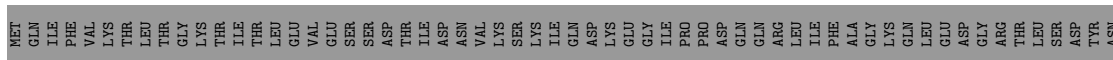
- Molecule 34: 40S ribosomal protein S30

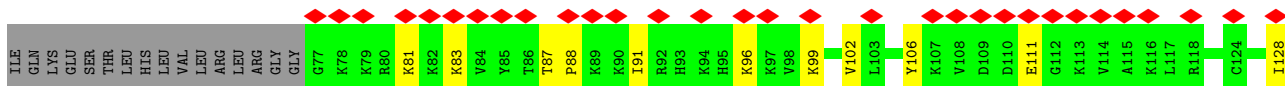
Chain e: 

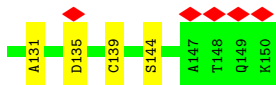


- Molecule 35: Ubiquitin-40S ribosomal protein S27a

Chain f: 

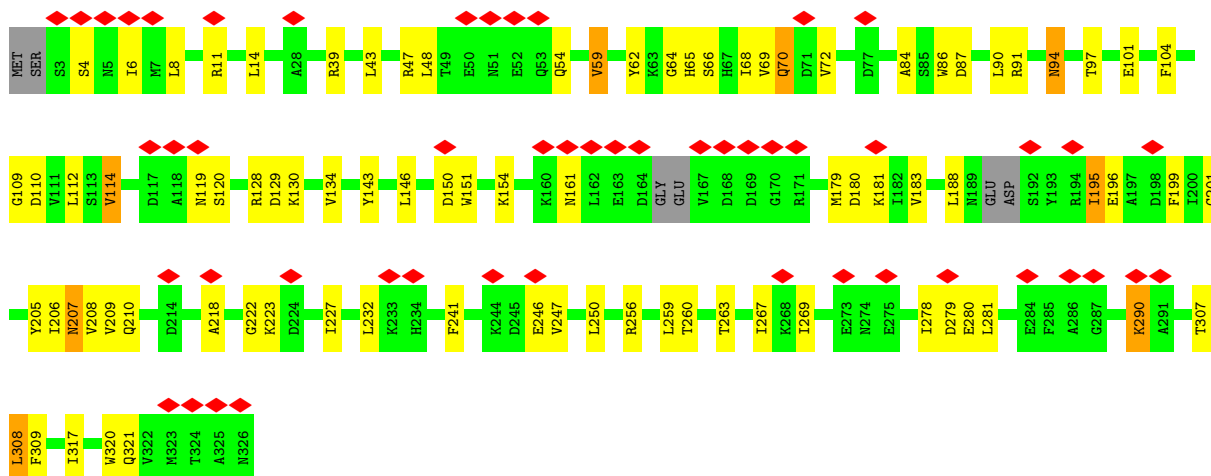




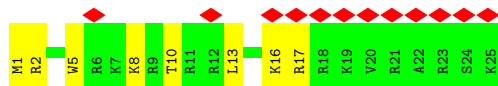


- Molecule 36: KLLA0E12277p

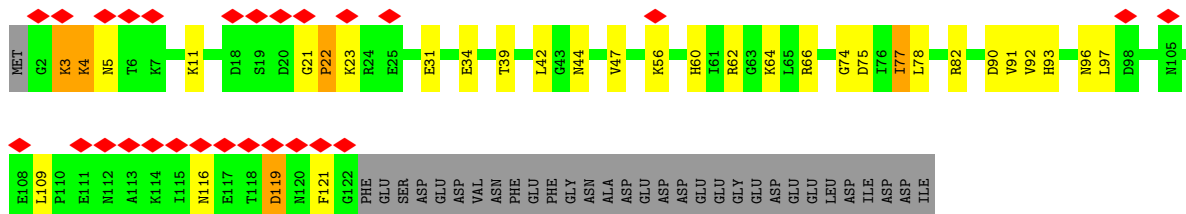
Chain g: 



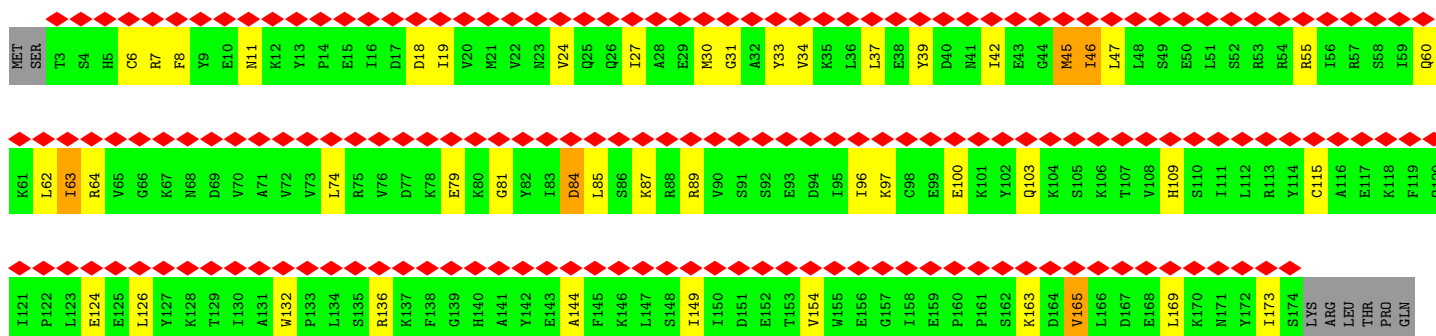
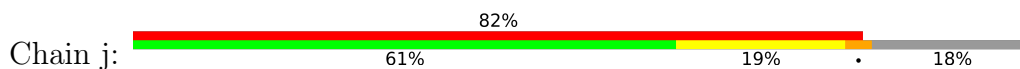
- Molecule 37: 60S ribosomal protein L41-A



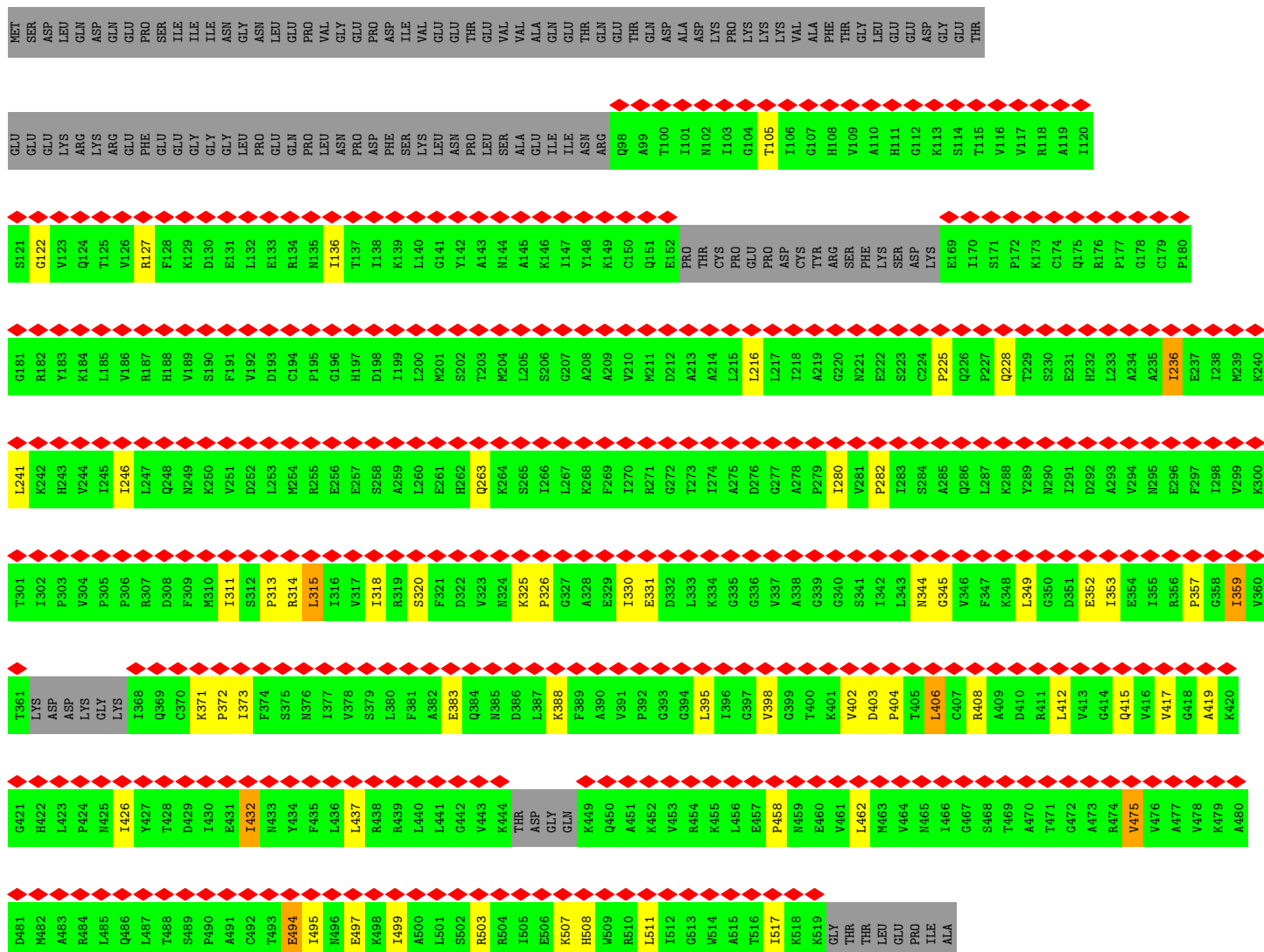
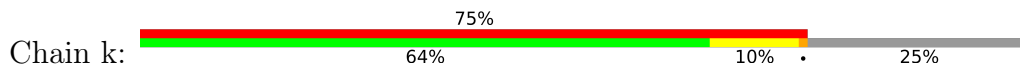
- Molecule 38: Eukaryotic translation initiation factor 1A



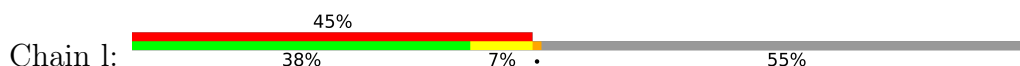
- Molecule 39: Eukaryotic translation initiation factor 2 subunit alpha

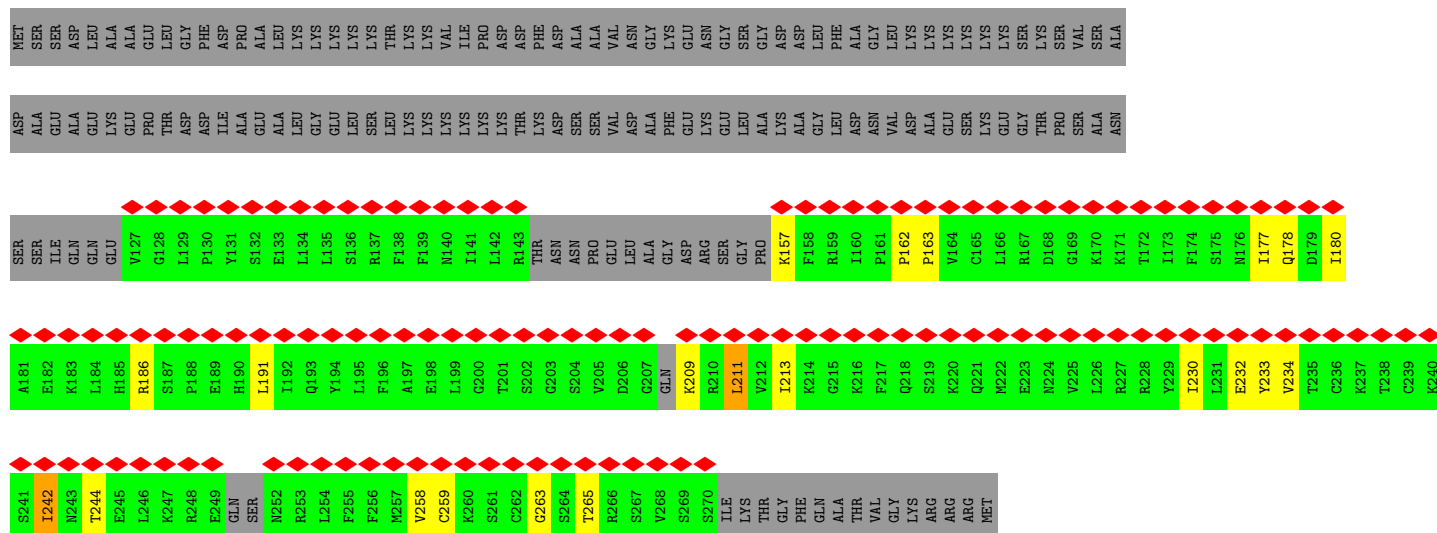


- Molecule 40: Eukaryotic translation initiation factor 2 subunit gamma

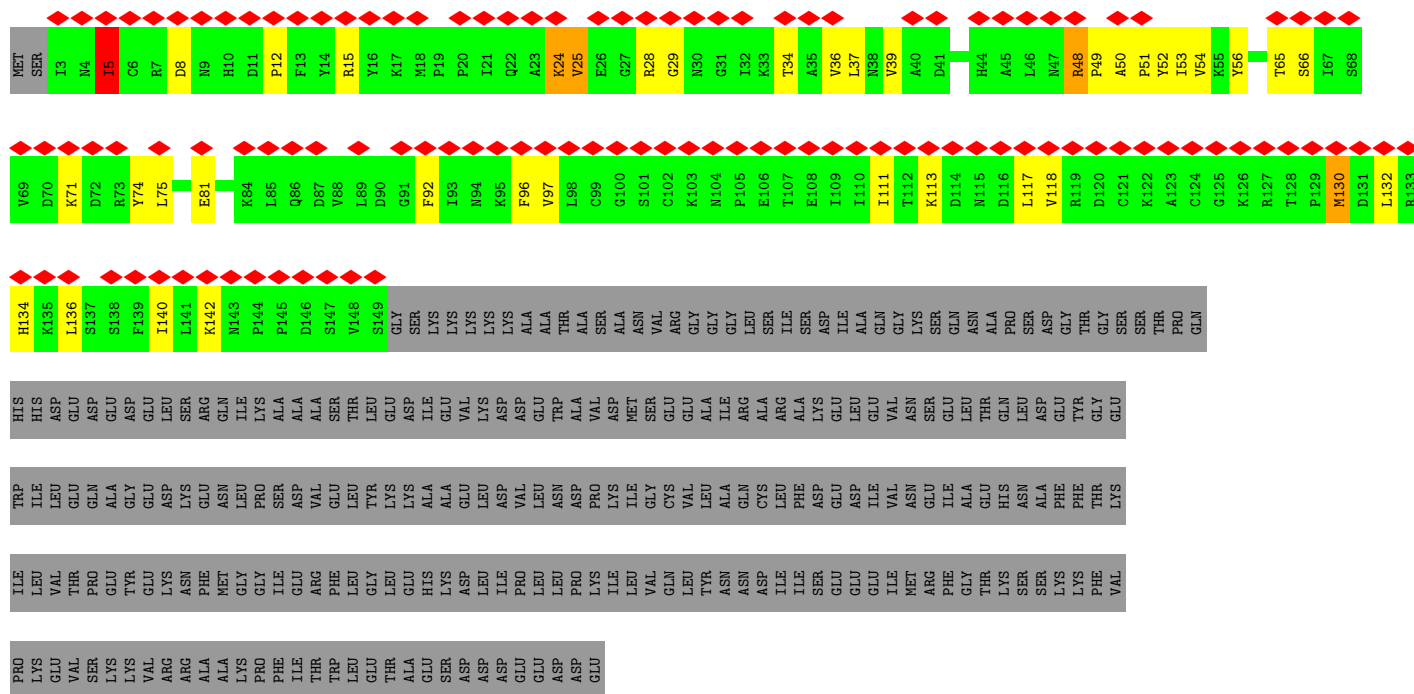


- Molecule 41: Eukaryotic translation initiation factor 2 subunit beta

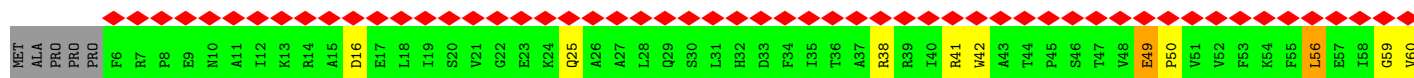




• Molecule 42: Eukaryotic translation initiation factor 5



• Molecule 43: Eukaryotic translation initiation factor 3 subunit A

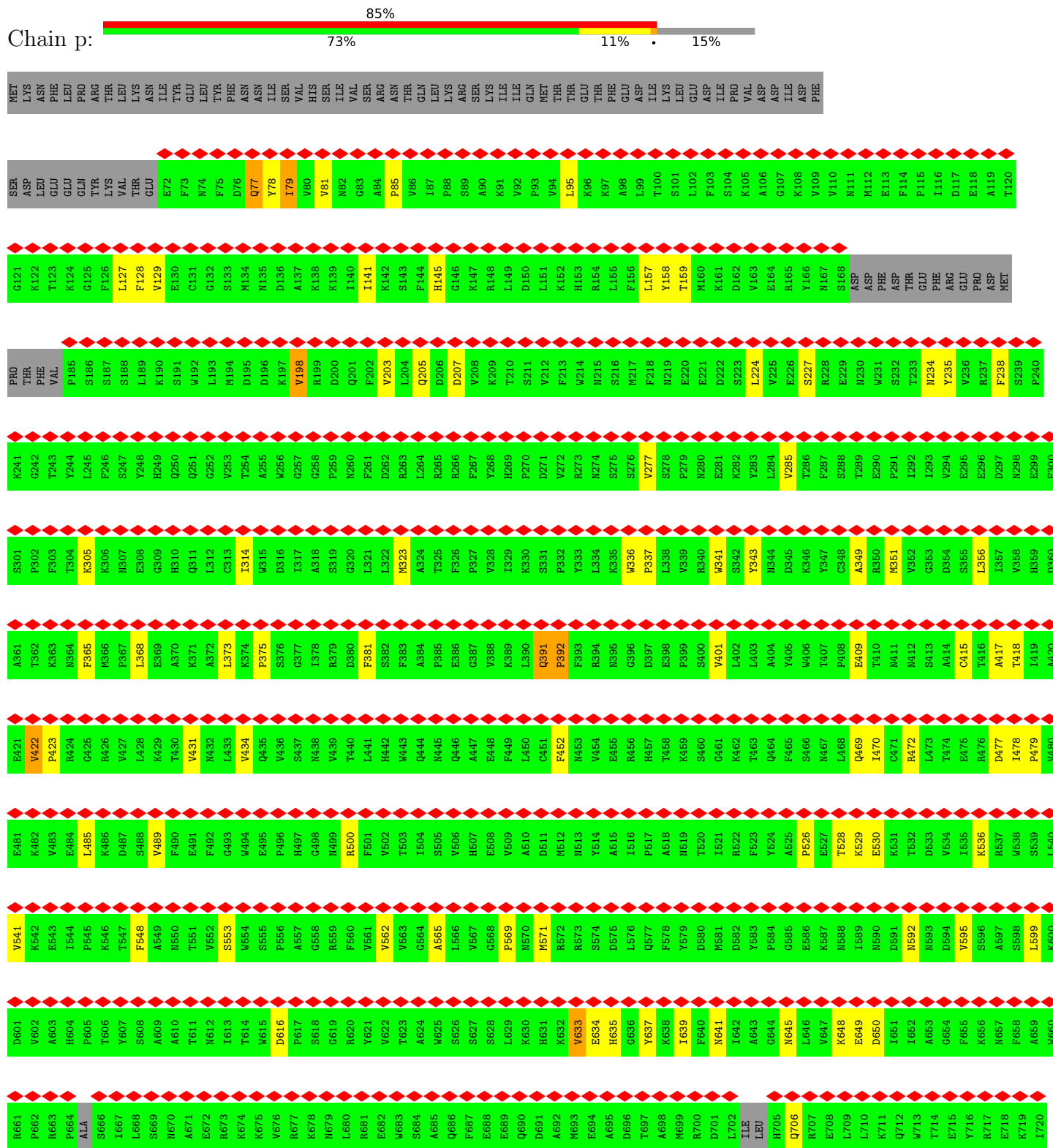




LYS
GLY
GLY
ARG

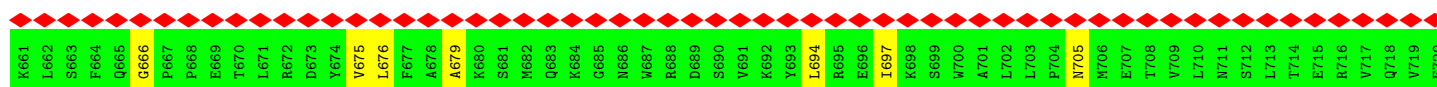
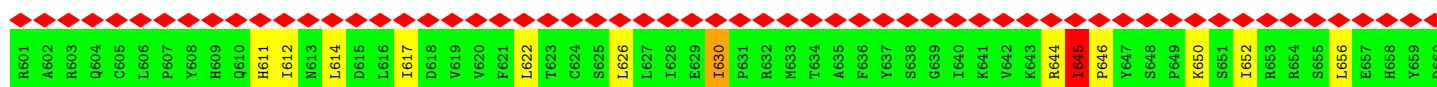
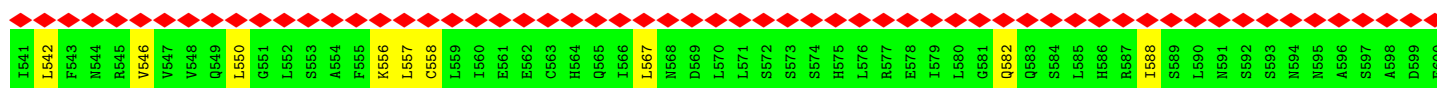
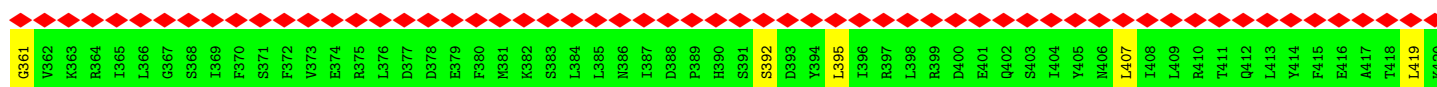
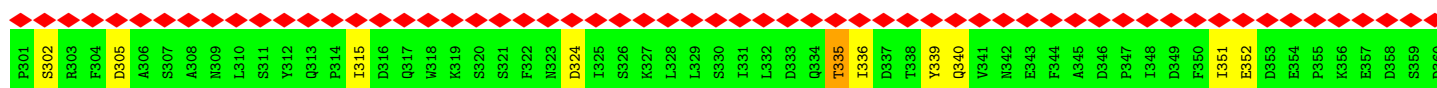
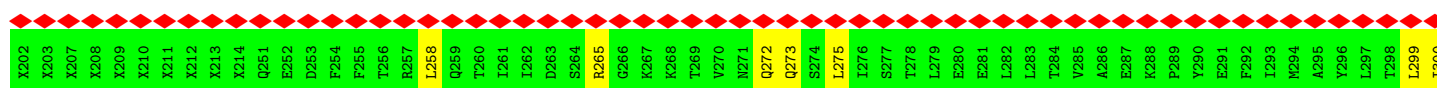
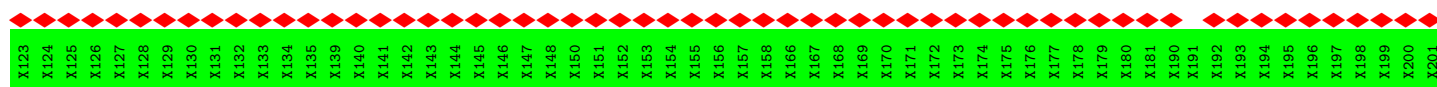
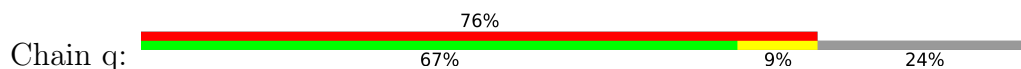
● Molecule 44: Eukaryotic translation initiation factor 3 subunit B

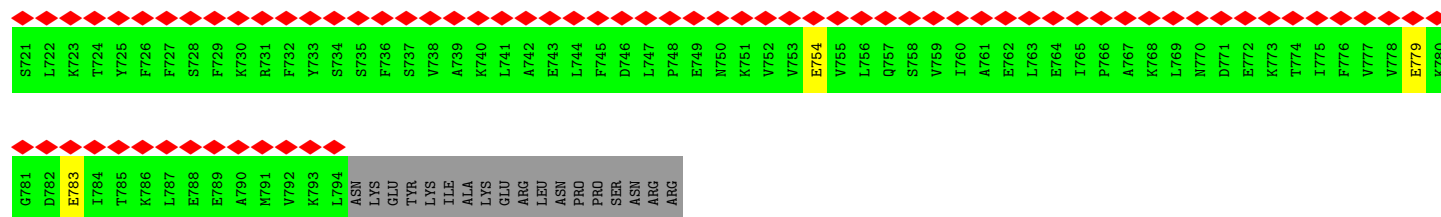
Chain p:



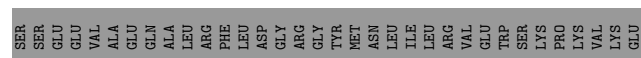
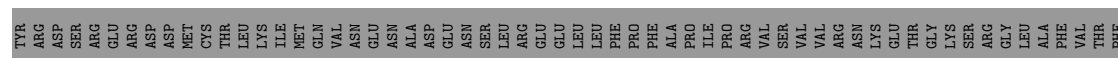
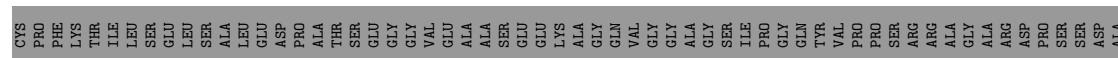
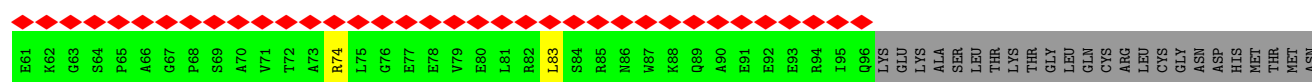
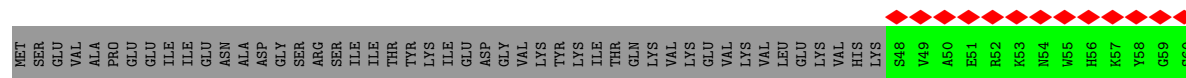


• Molecule 45: eIF3c, Eukaryotic translation initiation factor 3 subunit C

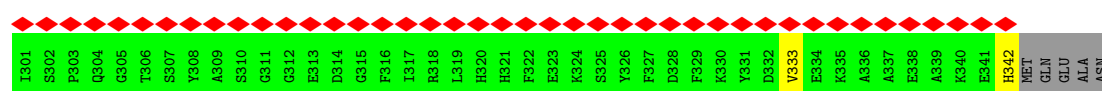
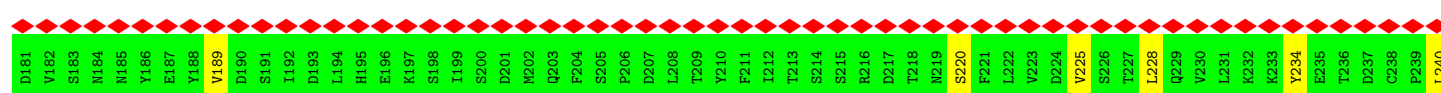
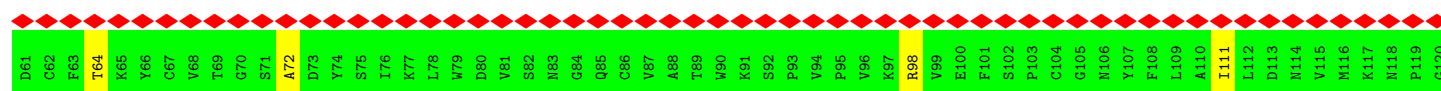
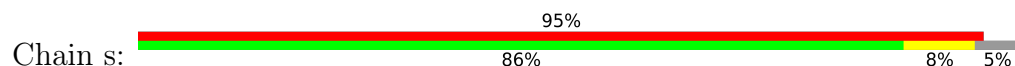




• Molecule 46: Eukaryotic translation initiation factor 3 subunit G



• Molecule 47: Eukaryotic translation initiation factor 3 subunit I



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	157868	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	104478	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	1.157	Depositor
Minimum map value	-0.645	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.037	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	402.0, 402.0, 402.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.34, 1.34, 1.34	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 7MG, AYA, 2MG, 1MG, GCP, MG, M2G, 5MC, PSU, 1MA, H2U, C4J, ZN, T6A, RIA, MA6

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	0.40	1/1529 (0.1%)	0.79	4/2376 (0.2%)
2	2	0.37	0/41987	0.76	42/65416 (0.1%)
3	3	0.39	0/797	0.77	0/1233
4	A	0.54	0/1742	1.05	0/2383
5	B	0.48	0/1813	0.98	2/2438 (0.1%)
6	C	0.51	0/1678	1.01	2/2277 (0.1%)
7	D	0.52	0/1800	1.01	2/2421 (0.1%)
8	E	0.48	0/2122	0.92	1/2861 (0.0%)
9	F	0.53	0/1628	1.08	0/2198
10	G	0.54	0/1855	0.98	2/2479 (0.1%)
11	H	0.56	0/1507	1.04	0/2028
12	I	0.47	0/1515	0.95	0/2029
13	J	0.51	0/1495	1.10	4/2001 (0.2%)
14	K	0.55	0/831	1.09	4/1123 (0.4%)
15	L	0.50	0/1276	0.85	1/1718 (0.1%)
16	M	0.63	0/891	1.04	1/1201 (0.1%)
17	N	0.51	0/1218	1.06	0/1638
18	O	0.53	0/966	1.02	2/1297 (0.2%)
19	P	0.52	0/942	1.05	2/1269 (0.2%)
20	Q	0.50	0/1125	0.99	0/1510
21	R	0.61	0/1044	1.08	0/1402
22	S	0.53	0/1208	1.03	0/1624
23	T	0.50	0/1129	1.08	0/1520
24	U	0.55	0/857	0.99	0/1158
25	V	0.48	0/696	0.92	1/938 (0.1%)
26	W	0.48	0/1039	1.03	0/1399
27	X	0.52	0/1137	0.92	1/1516 (0.1%)
28	Y	0.47	0/1075	0.93	0/1433
29	Z	0.51	0/603	0.98	0/814
30	a	0.53	0/825	0.98	1/1106 (0.1%)
31	b	0.48	0/619	0.84	0/837
32	c	0.52	0/501	0.91	2/673 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	d	0.43	0/473	0.90	0/629
34	e	0.53	0/480	0.98	0/640
35	f	0.53	0/597	0.88	0/795
36	g	0.49	0/2523	0.83	0/3434
37	h	0.42	0/234	1.10	0/300
38	i	0.50	0/969	0.96	0/1287
39	j	0.60	0/2034	1.01	0/2737
40	k	0.61	0/3079	0.94	0/4157
41	l	0.60	0/1051	0.92	0/1402
42	m	0.57	0/1164	0.99	0/1575
43	o	0.59	0/4140	1.13	6/5608 (0.1%)
44	p	0.61	0/5245	0.89	2/7115 (0.0%)
45	q	0.62	2/4523 (0.0%)	1.11	6/6114 (0.1%)
46	r	0.54	0/399	0.89	0/535
47	s	0.59	0/2669	0.85	0/3611
All	All	0.49	3/109030 (0.0%)	0.90	88/156255 (0.1%)

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
2	2	1	0
20	Q	0	1
44	p	0	2
All	All	1	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
45	q	630	ILE	CA-CB	5.35	1.57	1.54
45	q	300	ILE	CA-CB	5.07	1.57	1.53
1	1	37	T6A	O3'-P	5.04	1.61	1.56

The worst 5 of 88 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1470	C	C2'-C3'-O3'	9.22	123.33	109.50
2	2	1206	C	C2'-C3'-O3'	8.99	122.98	109.50
2	2	1080	A	C4'-C3'-O3'	8.78	122.57	109.40
2	2	277	U	C2'-C3'-O3'	8.34	122.01	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	p	528	THR	N-CA-C	8.31	119.96	111.07

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	2	1190	C4J	C4'

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
20	Q	40	GLN	Peptide
44	p	336	TRP	Peptide
44	p	391	GLN	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	1639	0	852	16	0
2	2	37812	0	19023	599	0
3	3	719	0	371	55	0
4	A	1702	0	1695	38	0
5	B	1797	0	1870	26	0
6	C	1648	0	1727	34	0
7	D	1774	0	1855	21	0
8	E	2078	0	2157	52	0
9	F	1609	0	1679	38	0
10	G	1832	0	1919	20	0
11	H	1483	0	1579	24	0
12	I	1489	0	1504	34	0
13	J	1471	0	1554	36	0
14	K	809	0	810	10	0
15	L	1248	0	1311	31	0
16	M	885	0	917	16	0
17	N	1195	0	1263	17	0
18	O	955	0	987	22	0
19	P	923	0	960	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	Q	1105	0	1170	18	0
21	R	1033	0	1082	19	0
22	S	1189	0	1211	27	0
23	T	1110	0	1124	31	0
24	U	845	0	913	16	0
25	V	687	0	682	12	0
26	W	1021	0	1056	25	0
27	X	1119	0	1198	20	0
28	Y	1061	0	1111	14	0
29	Z	594	0	590	12	0
30	a	812	0	855	22	0
31	b	609	0	630	6	0
32	c	499	0	536	4	0
33	d	461	0	448	13	0
34	e	472	0	508	8	0
35	f	584	0	601	4	0
36	g	2469	0	2403	34	0
37	h	233	0	284	8	0
38	i	958	0	957	10	0
39	j	2006	0	2066	27	0
40	k	3034	0	3195	25	0
41	l	1036	0	1079	9	0
42	m	1140	0	1141	15	0
43	o	4070	0	3936	75	0
44	p	5114	0	4934	47	0
45	q	4827	0	4561	26	0
46	r	392	0	382	1	0
47	s	2606	0	2528	16	0
48	2	116	0	0	0	0
48	k	1	0	0	0	0
49	a	1	0	0	0	0
49	b	1	0	0	0	0
49	f	1	0	0	0	0
49	l	1	0	0	0	0
49	m	1	0	0	0	0
50	k	8	0	8	0	0
51	k	32	0	14	0	0
All	All	104316	0	85236	1386	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 1386 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)
3:3:16[A]:U:O2	43:o:38:ARG:HA	1.17	1.28
2:2:28:A:N1	2:2:597:U:C4	2.08	1.21
2:2:760:A:N1	2:2:789:U:C4	2.13	1.16
2:2:28:A:N1	2:2:597:U:O4	1.82	1.13
2:2:760:A:N1	2:2:789:U:O4	1.82	1.11

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	
4	A	217/254 (85%)	192 (88%)	16 (7%)	9 (4%)	2	12
5	B	220/255 (86%)	191 (87%)	19 (9%)	10 (4%)	2	11
6	C	218/259 (84%)	197 (90%)	16 (7%)	5 (2%)	5	23
7	D	225/237 (95%)	211 (94%)	8 (4%)	6 (3%)	4	20
8	E	258/261 (99%)	233 (90%)	21 (8%)	4 (2%)	7	32
9	F	204/227 (90%)	173 (85%)	21 (10%)	10 (5%)	1	10
10	G	228/236 (97%)	211 (92%)	15 (7%)	2 (1%)	14	46
11	H	182/190 (96%)	161 (88%)	14 (8%)	7 (4%)	2	13
12	I	184/201 (92%)	162 (88%)	12 (6%)	10 (5%)	1	8
13	J	180/188 (96%)	152 (84%)	20 (11%)	8 (4%)	2	11
14	K	94/106 (89%)	83 (88%)	8 (8%)	3 (3%)	3	17
15	L	153/156 (98%)	132 (86%)	17 (11%)	4 (3%)	4	21
16	M	113/134 (84%)	85 (75%)	20 (18%)	8 (7%)	1	4
17	N	149/151 (99%)	139 (93%)	9 (6%)	1 (1%)	18	51
18	O	127/137 (93%)	107 (84%)	13 (10%)	7 (6%)	1	8
19	P	115/142 (81%)	98 (85%)	11 (10%)	6 (5%)	1	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	Q	139/143 (97%)	125 (90%)	11 (8%)	3 (2%)	5	24
21	R	128/136 (94%)	110 (86%)	11 (9%)	7 (6%)	1	8
22	S	143/146 (98%)	127 (89%)	13 (9%)	3 (2%)	5	25
23	T	141/144 (98%)	132 (94%)	7 (5%)	2 (1%)	9	34
24	U	104/117 (89%)	90 (86%)	9 (9%)	5 (5%)	2	10
25	V	85/87 (98%)	80 (94%)	2 (2%)	3 (4%)	3	15
26	W	127/130 (98%)	115 (91%)	7 (6%)	5 (4%)	2	13
27	X	142/145 (98%)	126 (89%)	12 (8%)	4 (3%)	4	19
28	Y	132/135 (98%)	123 (93%)	5 (4%)	4 (3%)	3	18
29	Z	76/108 (70%)	62 (82%)	10 (13%)	4 (5%)	1	8
30	a	101/119 (85%)	84 (83%)	11 (11%)	6 (6%)	1	7
31	b	79/82 (96%)	68 (86%)	9 (11%)	2 (2%)	4	21
32	c	62/67 (92%)	55 (89%)	5 (8%)	2 (3%)	3	17
33	d	53/56 (95%)	48 (91%)	5 (9%)	0	100	100
34	e	58/63 (92%)	44 (76%)	9 (16%)	5 (9%)	0	2
35	f	72/150 (48%)	57 (79%)	13 (18%)	2 (3%)	4	19
36	g	314/326 (96%)	276 (88%)	29 (9%)	9 (3%)	3	18
37	h	23/25 (92%)	23 (100%)	0	0	100	100
38	i	119/153 (78%)	102 (86%)	11 (9%)	6 (5%)	1	9
39	j	243/304 (80%)	213 (88%)	25 (10%)	5 (2%)	5	25
40	k	388/527 (74%)	333 (86%)	47 (12%)	8 (2%)	5	25
41	l	120/285 (42%)	109 (91%)	11 (9%)	0	100	100
42	m	145/405 (36%)	126 (87%)	17 (12%)	2 (1%)	9	34
43	o	519/964 (54%)	483 (93%)	30 (6%)	6 (1%)	10	38
44	p	637/763 (84%)	583 (92%)	43 (7%)	11 (2%)	7	30
45	q	538/812 (66%)	490 (91%)	39 (7%)	9 (2%)	7	30
46	r	47/274 (17%)	43 (92%)	4 (8%)	0	100	100
47	s	326/347 (94%)	311 (95%)	15 (5%)	0	100	100
All	All	7928/10147 (78%)	7065 (89%)	650 (8%)	213 (3%)	6	20

5 of 213 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	C	141	VAL
7	D	220	PRO
9	F	104	ARG
11	H	64	VAL
11	H	74	GLN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	A	180/211 (85%)	149 (83%)	31 (17%)	2	10
5	B	201/228 (88%)	178 (89%)	23 (11%)	5	22
6	C	177/203 (87%)	152 (86%)	25 (14%)	3	15
7	D	188/196 (96%)	157 (84%)	31 (16%)	2	11
8	E	223/224 (100%)	182 (82%)	41 (18%)	1	8
9	F	174/194 (90%)	141 (81%)	33 (19%)	1	8
10	G	192/200 (96%)	162 (84%)	30 (16%)	2	12
11	H	164/170 (96%)	135 (82%)	29 (18%)	2	9
12	I	147/159 (92%)	123 (84%)	24 (16%)	2	11
13	J	153/158 (97%)	132 (86%)	21 (14%)	3	16
14	K	88/96 (92%)	77 (88%)	11 (12%)	4	19
15	L	136/137 (99%)	122 (90%)	14 (10%)	7	27
16	M	93/109 (85%)	82 (88%)	11 (12%)	5	21
17	N	128/128 (100%)	118 (92%)	10 (8%)	11	38
18	O	97/104 (93%)	80 (82%)	17 (18%)	2	9
19	P	99/119 (83%)	84 (85%)	15 (15%)	3	13
20	Q	117/119 (98%)	101 (86%)	16 (14%)	3	16
21	R	116/124 (94%)	105 (90%)	11 (10%)	8	30
22	S	127/129 (98%)	110 (87%)	17 (13%)	4	17
23	T	117/118 (99%)	99 (85%)	18 (15%)	2	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	U	96/107 (90%)	80 (83%)	16 (17%)	2	11
25	V	73/73 (100%)	71 (97%)	2 (3%)	39	70
26	W	110/111 (99%)	101 (92%)	9 (8%)	10	36
27	X	119/120 (99%)	104 (87%)	15 (13%)	4	19
28	Y	108/109 (99%)	95 (88%)	13 (12%)	5	20
29	Z	59/88 (67%)	52 (88%)	7 (12%)	5	21
30	a	85/100 (85%)	77 (91%)	8 (9%)	8	30
31	b	71/72 (99%)	61 (86%)	10 (14%)	3	15
32	c	55/59 (93%)	48 (87%)	7 (13%)	4	18
33	d	47/48 (98%)	40 (85%)	7 (15%)	3	14
34	e	51/55 (93%)	43 (84%)	8 (16%)	2	12
35	f	60/133 (45%)	52 (87%)	8 (13%)	4	17
36	g	264/272 (97%)	234 (89%)	30 (11%)	5	22
37	h	23/23 (100%)	20 (87%)	3 (13%)	4	18
38	i	100/130 (77%)	83 (83%)	17 (17%)	2	10
39	j	224/274 (82%)	194 (87%)	30 (13%)	4	17
40	k	332/449 (74%)	311 (94%)	21 (6%)	16	46
41	l	119/246 (48%)	114 (96%)	5 (4%)	26	59
42	m	125/352 (36%)	105 (84%)	20 (16%)	2	12
43	o	406/846 (48%)	378 (93%)	28 (7%)	14	43
44	p	544/693 (78%)	533 (98%)	11 (2%)	48	75
45	q	506/523 (97%)	482 (95%)	24 (5%)	23	56
46	r	40/232 (17%)	39 (98%)	1 (2%)	42	71
47	s	287/301 (95%)	282 (98%)	5 (2%)	53	77
All	All	6821/8542 (80%)	6088 (89%)	733 (11%)	8	25

5 of 733 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
27	X	100	ASP
38	i	23	LYS
28	Y	99	LYS
27	X	94	ASN
33	d	39	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 167 such sidechains are listed below:

Mol	Chain	Res	Type
40	k	286	GLN
44	p	215	ASN
40	k	384	GLN
42	m	134	HIS
44	p	712	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	72/76 (94%)	29 (40%)	8 (11%)
2	2	1777/1798 (98%)	659 (37%)	72 (4%)
3	3	27/49 (55%)	16 (59%)	4 (14%)
All	All	1876/1923 (97%)	704 (37%)	84 (4%)

5 of 704 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	4	G
1	1	5	C
1	1	8	U
1	1	9	1MG
1	1	10	2MG

5 of 84 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	1320	A
2	2	1599	G
2	2	1343	A
2	2	1513	A
2	2	1678	G

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

24 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
1	T6A	1	37	1	31,34,35	1.41	4 (12%)	43,49,52	2.53	17 (39%)
2	7MG	2	1573	2,1	23,26,27	1.52	7 (30%)	27,39,42	2.75	6 (22%)
1	M2G	1	26	1	24,27,28	1.43	4 (16%)	33,40,43	2.06	7 (21%)
1	5MC	1	49	1	19,22,23	2.02	2 (10%)	26,32,35	1.37	4 (15%)
1	RIA	1	64	1	35,38,39	0.33	0	50,57,60	0.69	0
1	H2U	1	47	1	18,21,22	0.85	0	19,30,33	1.37	3 (15%)
2	2MG	2	1570	2	23,26,27	1.27	3 (13%)	33,38,41	2.28	7 (21%)
2	PSU	2	465	2	18,21,22	1.55	3 (16%)	21,30,33	2.04	5 (23%)
1	7MG	1	46	1	23,26,27	1.43	4 (17%)	27,39,42	2.73	9 (33%)
1	H2U	1	16	1	18,21,22	0.84	1 (5%)	19,30,33	1.68	3 (15%)
1	5MC	1	48	1	19,22,23	1.70	2 (10%)	26,32,35	1.27	3 (11%)
1	1MG	1	9	1	23,26,27	1.41	3 (13%)	33,39,42	2.09	8 (24%)
1	1MA	1	58	1	21,25,26	1.55	5 (23%)	30,37,40	1.96	5 (16%)
2	PSU	2	120	2	18,21,22	1.42	2 (11%)	21,30,33	2.08	4 (19%)
2	C4J	2	1190	2	25,29,30	0.88	1 (4%)	28,42,45	1.04	1 (3%)
1	2MG	1	10	1	23,26,27	1.29	3 (13%)	33,38,41	2.25	7 (21%)
2	2MG	2	1426	2,48	23,26,27	1.19	3 (13%)	33,38,41	3.38	12 (36%)
5	AYA	B	2	-	6,7,8	0.67	0	6,8,10	0.96	0
2	PSU	2	998	2	18,21,22	1.45	3 (16%)	21,30,33	2.08	4 (19%)
2	5MC	2	1637	2	19,22,23	1.85	2 (10%)	26,32,35	1.39	6 (23%)
2	MA6	2	1780	2	23,26,27	1.68	6 (26%)	33,38,41	2.36	10 (30%)
2	PSU	2	1289	2	18,21,22	1.51	3 (16%)	21,30,33	2.05	4 (19%)
2	5MC	2	1006	2	19,22,23	1.38	2 (10%)	26,32,35	1.70	6 (23%)
2	PSU	2	766	2	18,21,22	1.40	2 (11%)	21,30,33	2.27	5 (23%)

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
1	T6A	1	37	1	-	5/23/41/42	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	7MG	2	1573	2,1	-	2/7/37/38	0/3/3/3
1	M2G	1	26	1	-	2/11/29/30	0/3/3/3
1	5MC	1	49	1	-	2/7/25/26	0/2/2/2
1	RIA	1	64	1	-	3/17/51/52	0/4/4/4
1	H2U	1	47	1	-	4/7/38/39	0/2/2/2
2	2MG	2	1570	2	-	0/9/27/28	0/3/3/3
2	PSU	2	465	2	-	0/7/25/26	0/2/2/2
1	7MG	1	46	1	-	1/7/37/38	0/3/3/3
1	H2U	1	16	1	-	2/7/38/39	0/2/2/2
1	5MC	1	48	1	-	3/7/25/26	0/2/2/2
1	1MG	1	9	1	-	3/7/25/26	0/3/3/3
1	1MA	1	58	1	-	0/7/25/26	0/3/3/3
2	PSU	2	120	2	-	0/7/25/26	0/2/2/2
2	C4J	2	1190	2	1/1/7/7	0/16/34/35	0/2/2/2
1	2MG	1	10	1	-	2/9/27/28	0/3/3/3
2	2MG	2	1426	2,48	-	3/9/27/28	0/3/3/3
5	AYA	B	2	-	-	0/5/6/8	-
2	PSU	2	998	2	-	0/7/25/26	0/2/2/2
2	5MC	2	1637	2	-	1/7/25/26	0/2/2/2
2	MA6	2	1780	2	-	5/11/29/30	0/3/3/3
2	PSU	2	1289	2	-	0/7/25/26	0/2/2/2
2	5MC	2	1006	2	-	0/7/25/26	0/2/2/2
2	PSU	2	766	2	-	1/7/25/26	0/2/2/2

The worst 5 of 65 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	49	5MC	C5-C4	7.46	1.49	1.44
2	2	1637	5MC	C5-C4	6.77	1.49	1.44
1	1	48	5MC	C5-C4	5.95	1.48	1.44
2	2	1780	MA6	C5-C4	4.82	1.47	1.39
1	1	37	T6A	C5-C4	4.73	1.47	1.39

The worst 5 of 136 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1426	2MG	N1-C2-N2	10.66	127.44	116.56
2	2	1573	7MG	N9-C4-N3	9.04	138.71	125.46
2	2	1426	2MG	C2-N3-C4	8.92	123.16	112.00
1	1	46	7MG	N9-C4-N3	8.92	138.53	125.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	37	T6A	C12-N11-C10	8.57	136.24	121.99

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	2	1190	C4J	C4'

5 of 39 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	2	1780	MA6	O4'-C4'-C5'-O5'
2	2	1780	MA6	C5-C6-N6-C10
2	2	1780	MA6	N1-C6-N6-C10
1	1	9	1MG	O4'-C4'-C5'-O5'
1	1	10	2MG	O4'-C4'-C5'-O5'

There are no ring outliers.

12 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	37	T6A	2	0
1	1	26	M2G	1	0
1	1	47	H2U	1	0
2	2	1570	2MG	1	0
1	1	46	7MG	1	0
1	1	9	1MG	1	0
2	2	120	PSU	1	0
2	2	1426	2MG	3	0
5	B	2	AYA	1	0
2	2	1637	5MC	2	0
2	2	1780	MA6	1	0
2	2	1289	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 124 ligands modelled in this entry, 122 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	$\# Z > 2$
51	GCP	k	603	-	32,34,34	1.79	9 (28%)	49,54,54	1.78	8 (16%)
50	MET	k	601	-	6,7,8	0.48	0	2,7,9	0.06	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
51	GCP	k	603	-	-	1/19/38/38	0/3/3/3
50	MET	k	601	-	-	1/5/6/8	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	k	603	GCP	PG-O1G	5.54	1.61	1.50
51	k	603	GCP	C5-C4	3.46	1.48	1.38
51	k	603	GCP	PB-O3A	2.95	1.61	1.58
51	k	603	GCP	PG-O3G	-2.93	1.48	1.55
51	k	603	GCP	PG-O2G	2.88	1.61	1.55

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	k	603	GCP	C5-C4-N3	-6.33	118.31	128.39
51	k	603	GCP	C2-N3-C4	5.27	121.38	112.30
51	k	603	GCP	N9-C4-N3	4.68	135.31	125.95
51	k	603	GCP	C6-C5-N7	3.25	136.20	130.29
51	k	603	GCP	PB-O3A-PA	-2.89	122.93	132.37

There are no chirality outliers.

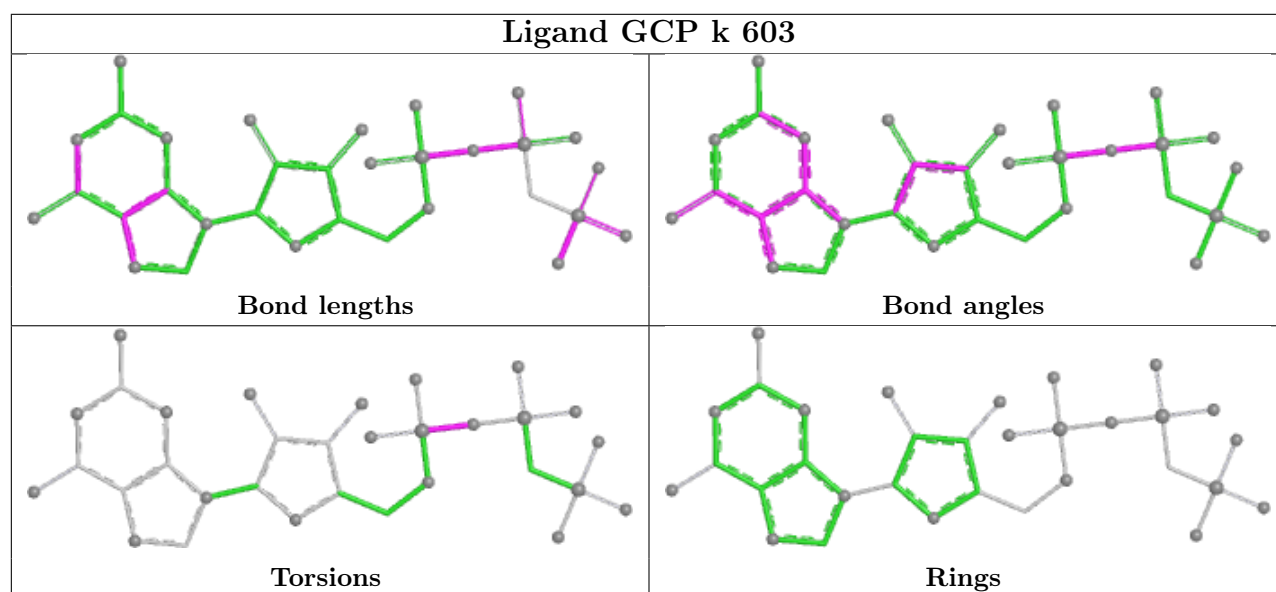
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
50	k	601	MET	CA-CB-CG-SD
51	k	603	GCP	PB-O3A-PA-O1A

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 than 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.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
45	q	8
2	2	1
1	1	1
44	p	1
5	B	1

The worst 5 of 12 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	q	214:UNK	C	251:GLN	N	50.55
1	q	158:UNK	C	166:UNK	N	17.71
1	q	181:UNK	C	190:UNK	N	14.31
1	q	135:UNK	C	139:UNK	N	7.79
1	q	203:UNK	C	207:UNK	N	6.84

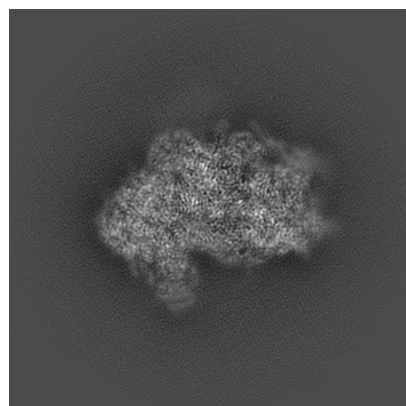
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4328. These allow visual inspection of the internal detail of the map and identification of artifacts.

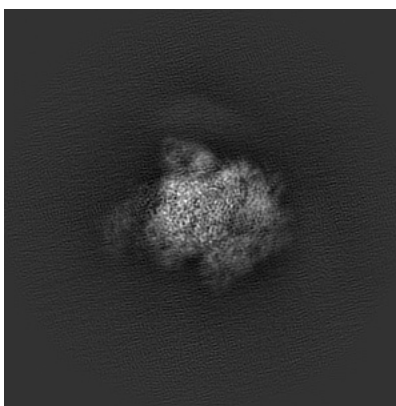
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

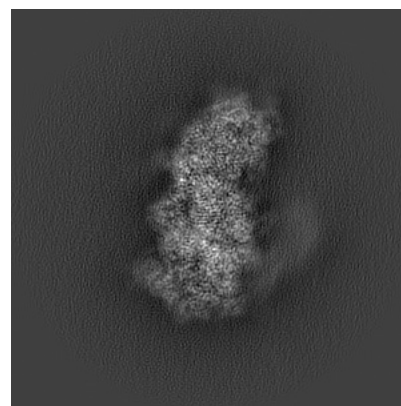
6.1.1 Primary map



X

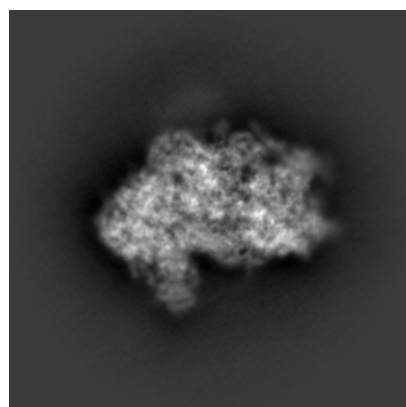


Y

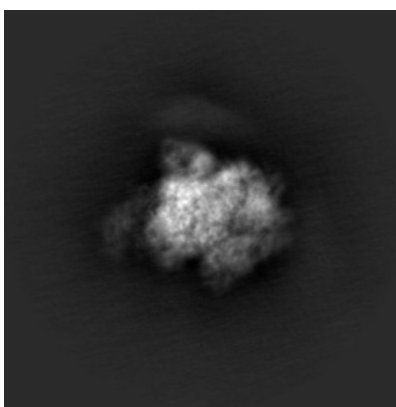


Z

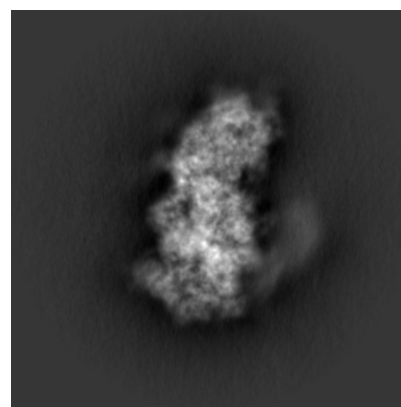
6.1.2 Raw map



X



Y

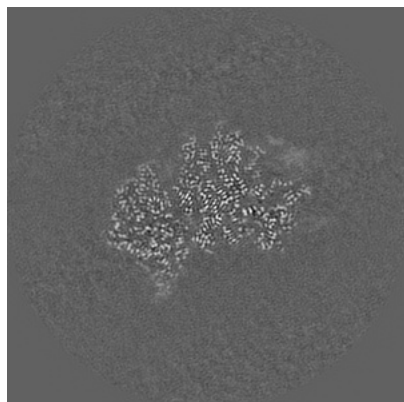


Z

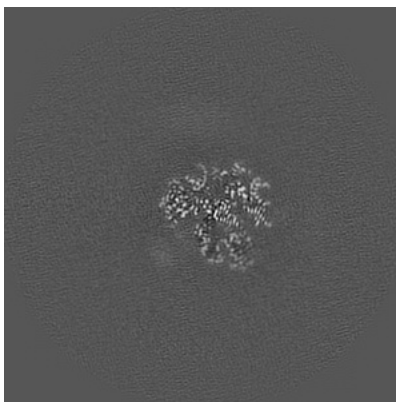
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

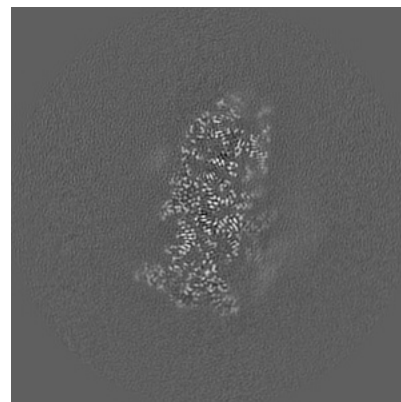
6.2.1 Primary map



X Index: 150

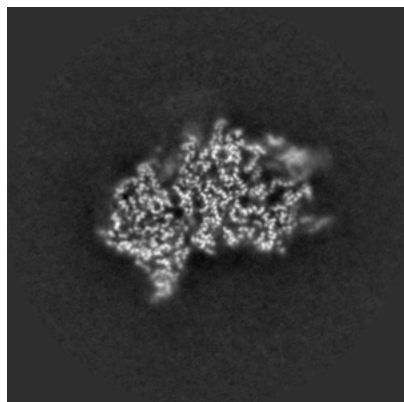


Y Index: 150

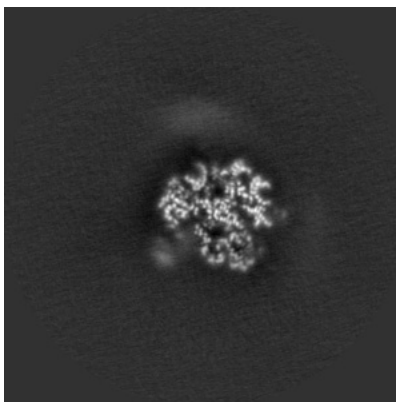


Z Index: 150

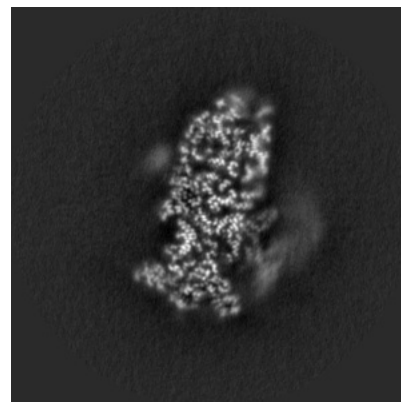
6.2.2 Raw map



X Index: 150



Y Index: 150

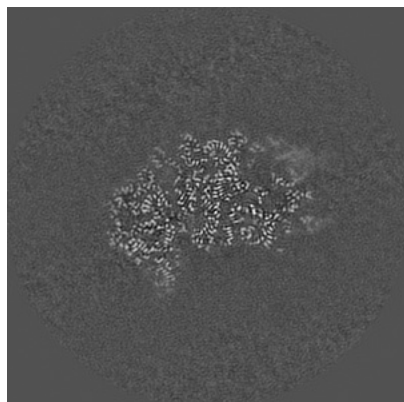


Z Index: 150

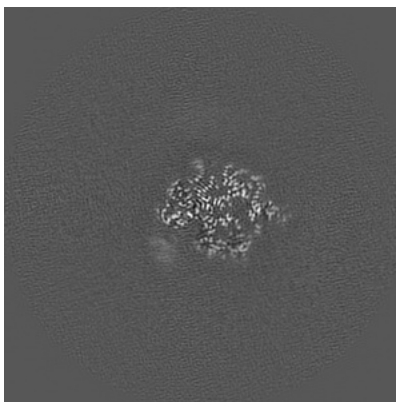
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

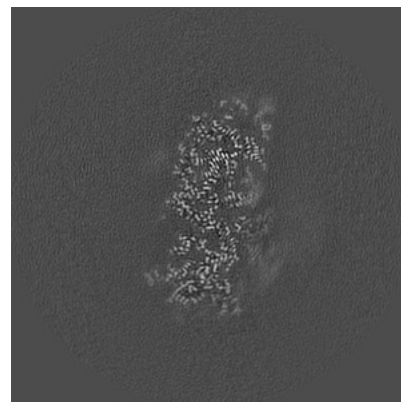
6.3.1 Primary map



X Index: 152

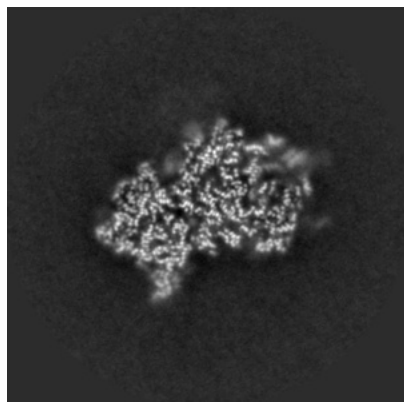


Y Index: 155

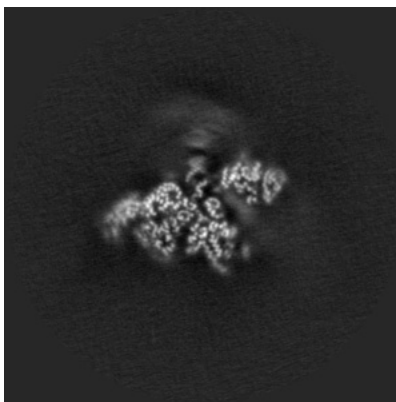


Z Index: 147

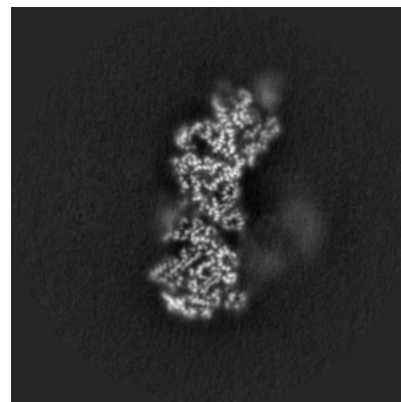
6.3.2 Raw map



X Index: 148



Y Index: 119

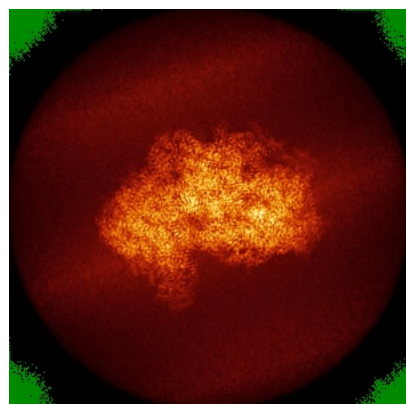


Z Index: 132

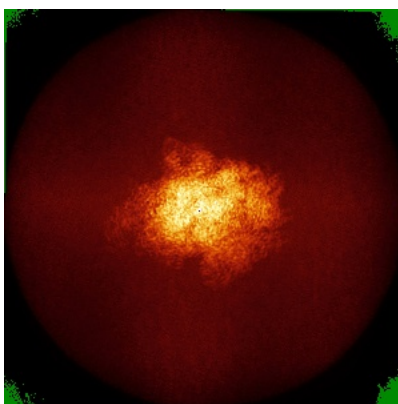
The images above show the largest variance slices of the map in three orthogonal directions.

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

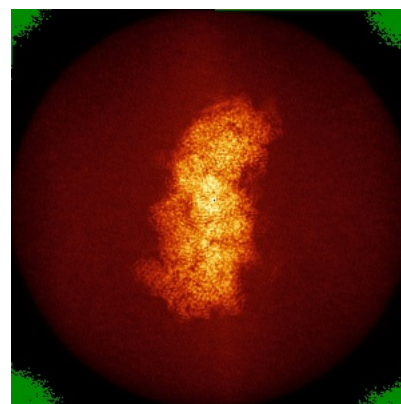
6.4.1 Primary map



X



Y

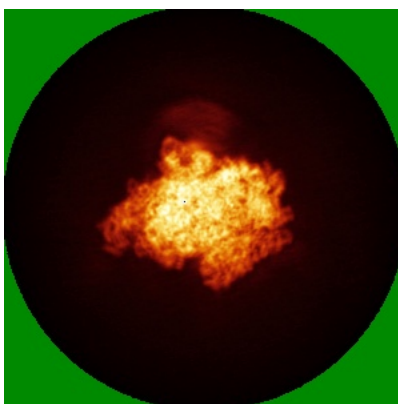


Z

6.4.2 Raw map



X



Y

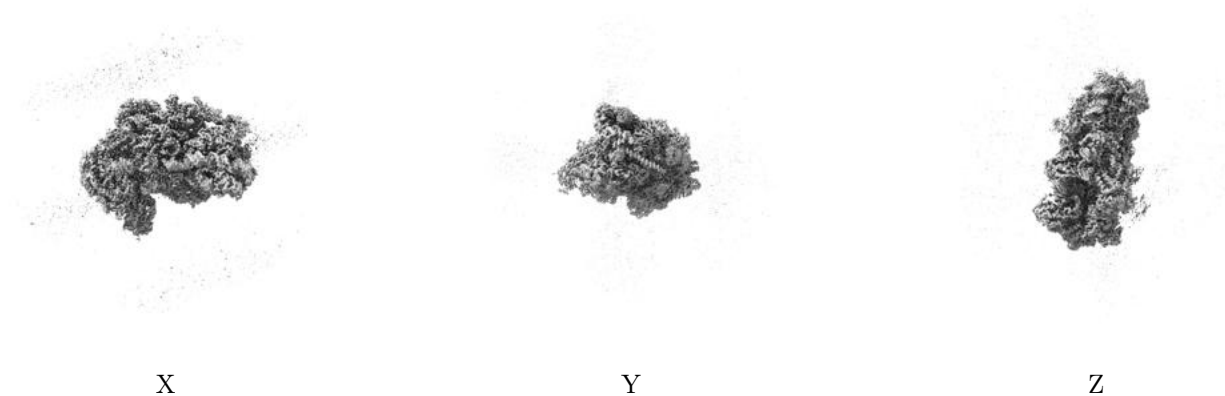


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.12. 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



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

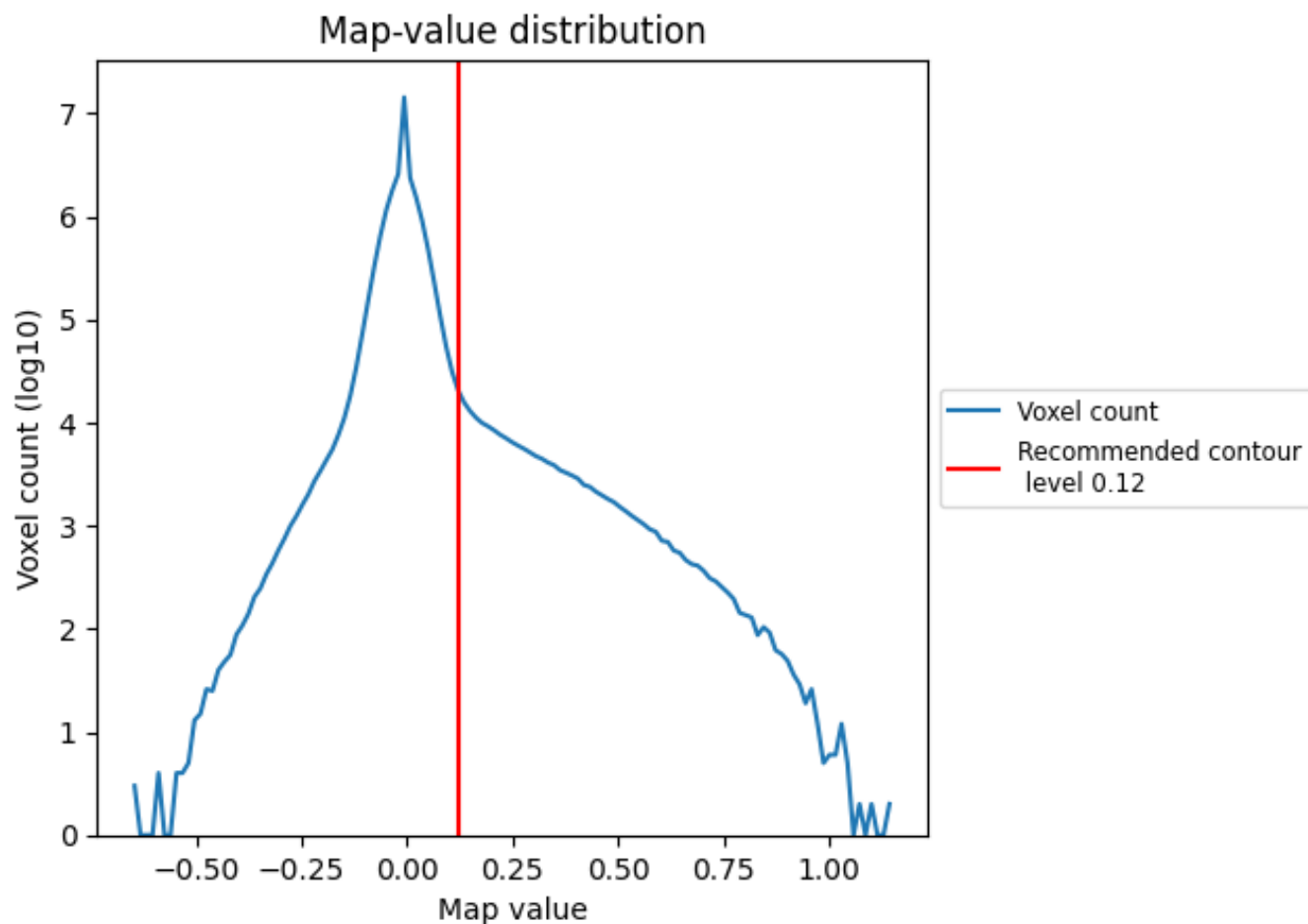
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

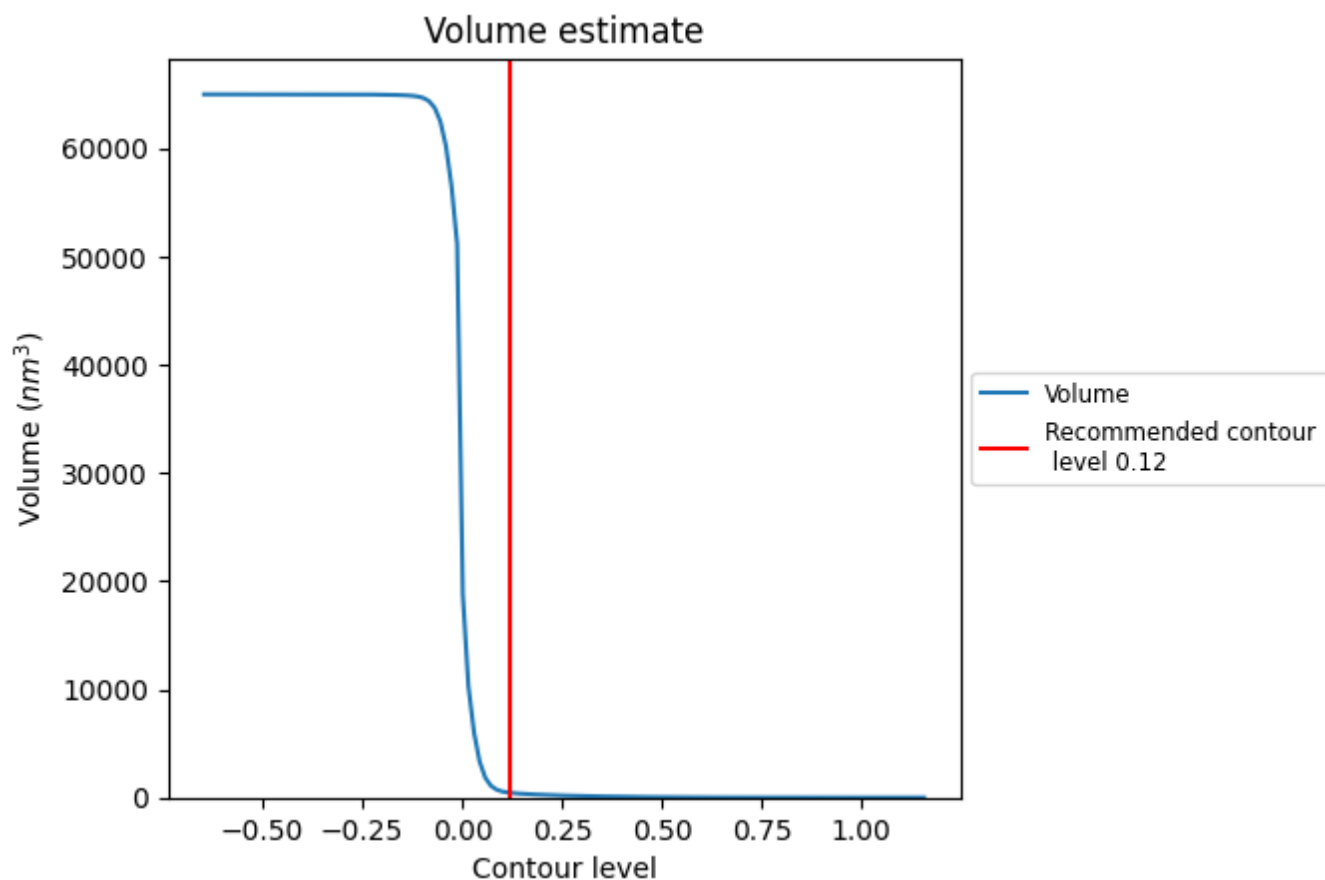
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

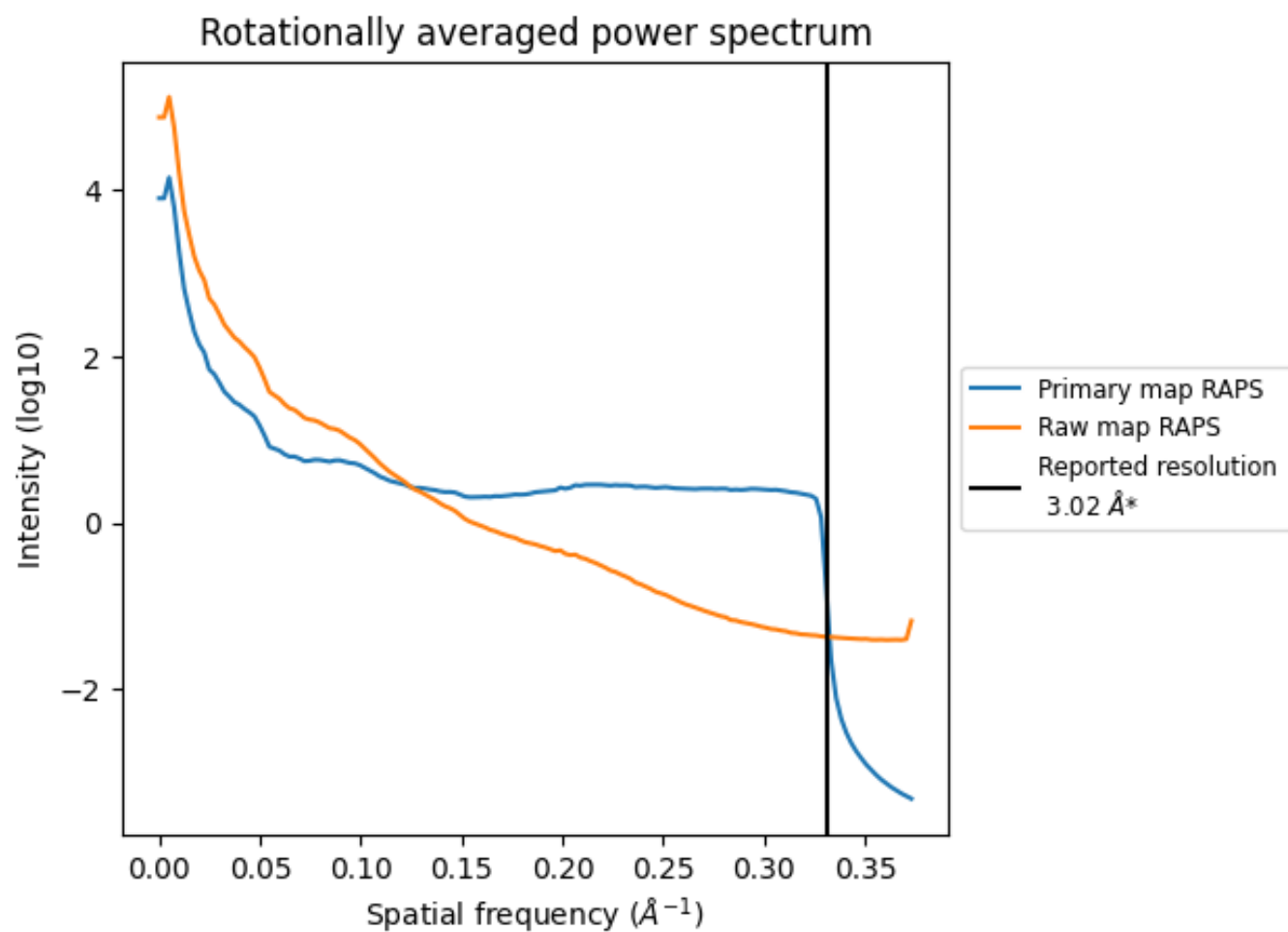
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 447 nm³; this corresponds to an approximate mass of 404 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

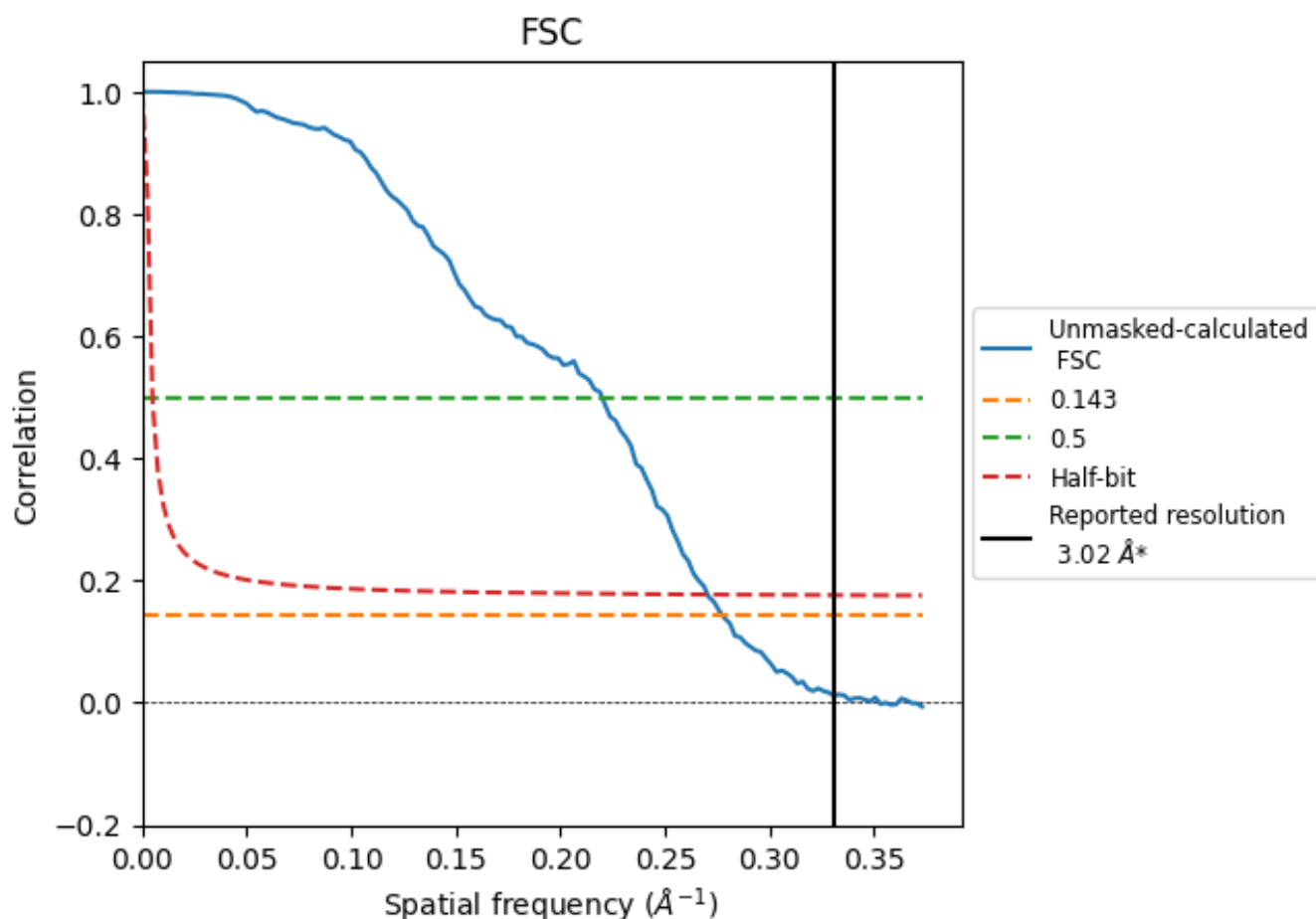


*Reported resolution corresponds to spatial frequency of 0.331 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.331 Å⁻¹

8.2 Resolution estimates [i](#)

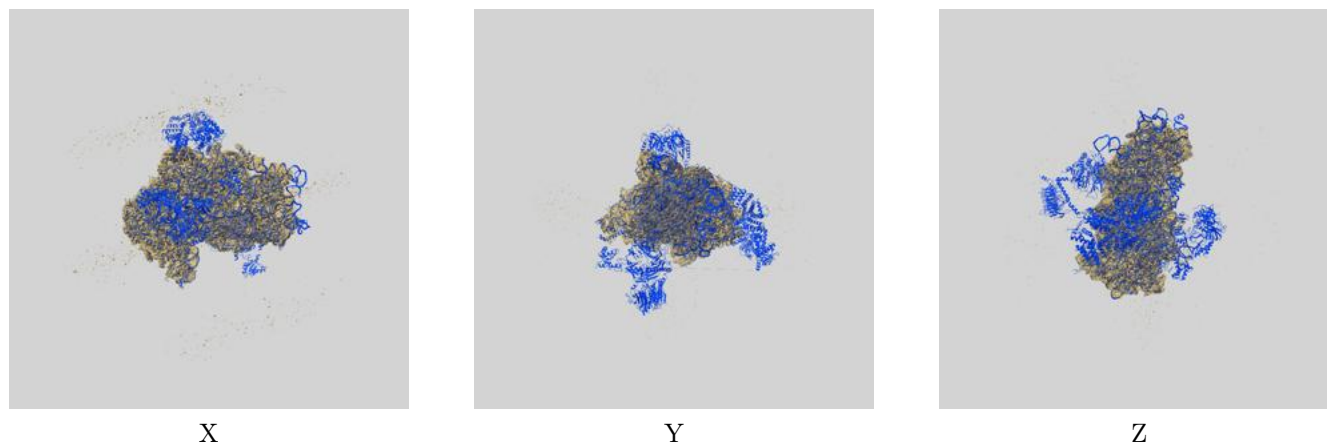
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.02	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.60	4.55	3.70

*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 3.60 differs from the reported value 3.02 by more than 10 %

9 Map-model fit [i](#)

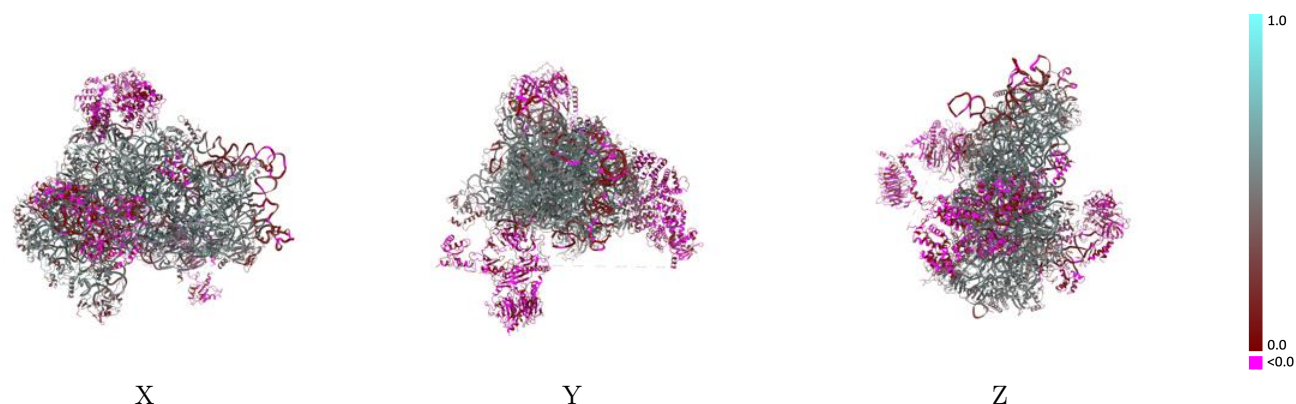
This section contains information regarding the fit between EMDB map EMD-4328 and PDB model 6FYY. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



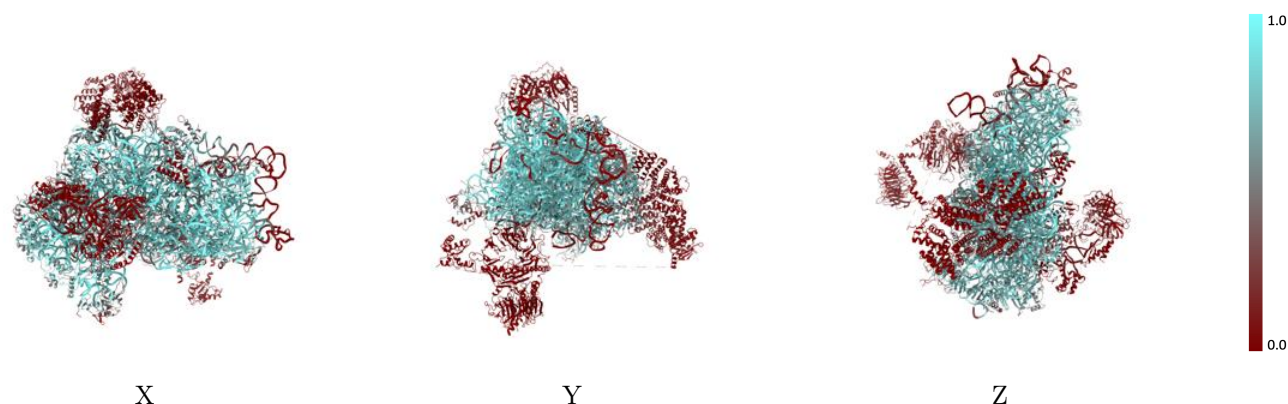
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



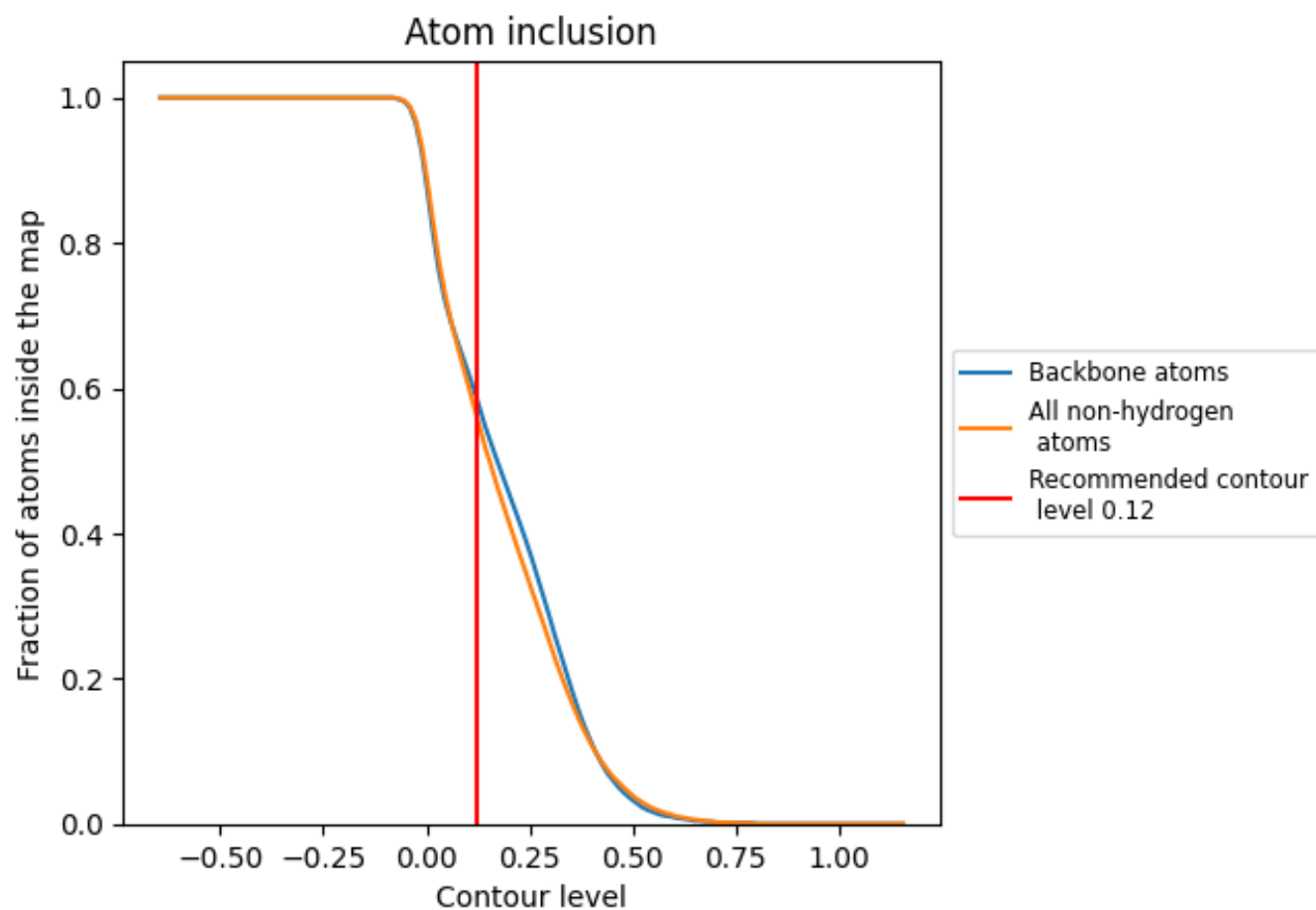
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.12).

9.4 Atom inclusion [i](#)



At the recommended contour level, 59% of all backbone atoms, 57% 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 (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5660	 0.3780
1	 0.3120	 0.2600
2	 0.8100	 0.4820
3	 0.2570	 0.2510
A	 0.7070	 0.4840
B	 0.6630	 0.4590
C	 0.7640	 0.5220
D	 0.6750	 0.4700
E	 0.7960	 0.5310
F	 0.6620	 0.4770
G	 0.6330	 0.4360
H	 0.5630	 0.4250
I	 0.7200	 0.4870
J	 0.7650	 0.5110
K	 0.6910	 0.4620
L	 0.6960	 0.4930
M	 0.2850	 0.2570
N	 0.7520	 0.5110
O	 0.7400	 0.5100
P	 0.7040	 0.4800
Q	 0.7480	 0.5120
R	 0.6330	 0.4600
S	 0.7000	 0.4680
T	 0.7690	 0.5010
U	 0.5920	 0.4170
V	 0.7360	 0.5000
W	 0.8000	 0.5420
X	 0.8050	 0.5470
Y	 0.7550	 0.5010
Z	 0.4990	 0.3820
a	 0.7570	 0.5150
b	 0.6890	 0.4940
c	 0.6620	 0.4980
d	 0.8580	 0.5620
e	 0.6790	 0.4730



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Chain	Atom inclusion	Q-score
f	 0.4190	 0.3750
g	 0.6160	 0.4590
h	 0.4720	 0.4180
i	 0.6140	 0.4750
j	 0.0030	 0.1410
k	 0.0010	 0.0430
l	 0.0010	 0.0530
m	 0.2220	 0.3860
o	 0.0000	 0.0240
p	 0.0000	 0.0450
q	 0.0010	 0.0430
r	 0.0000	 0.0090
s	 0.0000	 0.0250