



wwPDB EM Validation Summary Report ⓘ

Jun 19, 2026 – 05:01 am BST

PDB ID : 8PJ6 / pdb_00008pj6
EMDB ID : EMD-17701
Title : Structure of human 48S translation initiation complex with initiator tRNA, eIF1A and eIF3 (off-pathway)
Authors : Petrychenko, V.; Yi, S.-H.; Liedtke, D.; Peng, B.Z.; Rodnina, M.V.; Fischer, N.
Deposited on : 2023-06-22
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

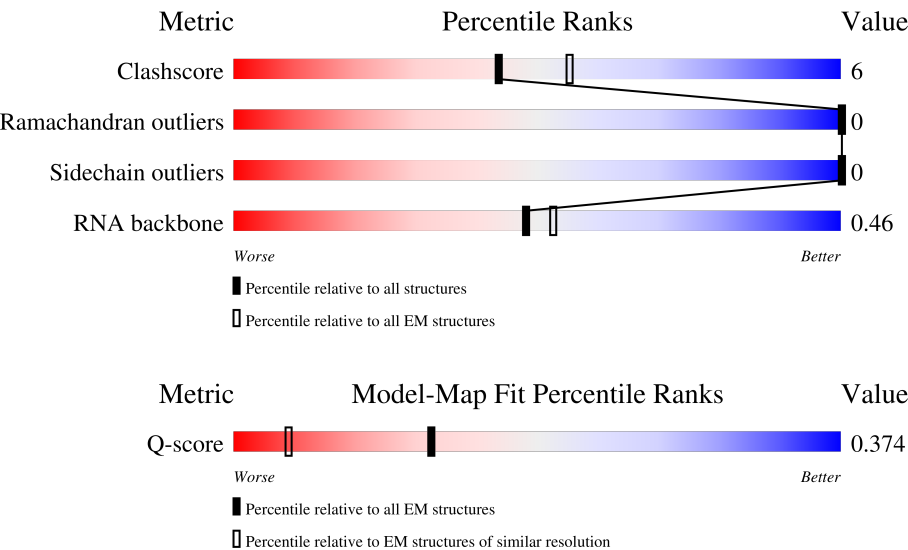
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	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	13054 (2.40 - 3.40)

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	814	70% 67%5%28%
2	2	325	94% 93%6%
3	3	218	79% 98%

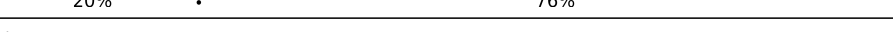
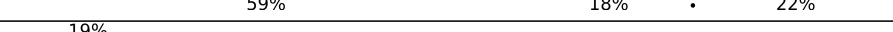
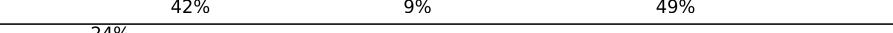
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Mol	Chain	Length	Quality of chain
4	4	357	
5	5	564	
6	6	374	
7	7	255	
8	8	352	
9	9	25	
10	A	1869	
11	B	158	
12	C	263	
13	D	194	
14	E	143	
15	F	59	
16	G	194	
17	H	84	
18	I	151	
19	J	130	
20	K	83	
21	L	293	
22	M	135	
23	N	295	
24	O	264	
25	P	151	
26	Q	115	
27	R	208	
28	S	249	

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Mol	Chain	Length	Quality of chain
29	T	133	
30	V	204	
31	Y	146	
32	Z	243	
33	a	165	
34	b	145	
35	c	317	
36	d	145	
37	e	125	
38	f	152	
39	h	119	
40	i	56	
41	k	156	
42	m	132	
43	n	69	
44	o	320	
45	q	144	
46	u	1382	
47	v	445	
48	w	75	
49	x	548	
50	y	913	

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 106921 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 7 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	56	Total	C	N	O	P	0	0
			1196	537	226	377	56		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	A	1719	Total	C	N	O	P	0	0
			36678	16385	6575	12000	1718		

There is a discrepancy between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	F	59	Total	C	N	O	S	0	0
			468	290	102	75	1		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	131	Total	C	N	O	S	0	0
			1072	682	201	182	7		

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	f	149	Total	C	N	O	S	0	0
			1227	770	249	207	1		

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

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

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

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

- Molecule 41 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	68	Total	C	N	O	S	0	0
			554	349	103	95	7		

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

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

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

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

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

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

- Molecule 45 is a protein called Eukaryotic translation initiation factor 1A, X-chromosomal.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	q	112	Total	C	N	O	S	0	0
			902	560	173	165	4		

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

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

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

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

- Molecule 48 is a RNA chain called Initiator Met-tRNA-i.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	w	73	Total	C	N	O	P	0	0
			1562	698	290	502	72		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
49	x	420	Total	C	N	O	S	0	0
			2826	1743	520	554	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	y	531	Total	C	N	O	S	0	0
			4305	2711	764	797	33		

- Molecule 51 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
51	A	82	Total	Mg	0
			82	82	
51	V	1	Total	Mg	0
			1	1	
51	d	1	Total	Mg	0
			1	1	
51	f	1	Total	Mg	0
			1	1	
51	i	2	Total	Mg	0
			2	2	

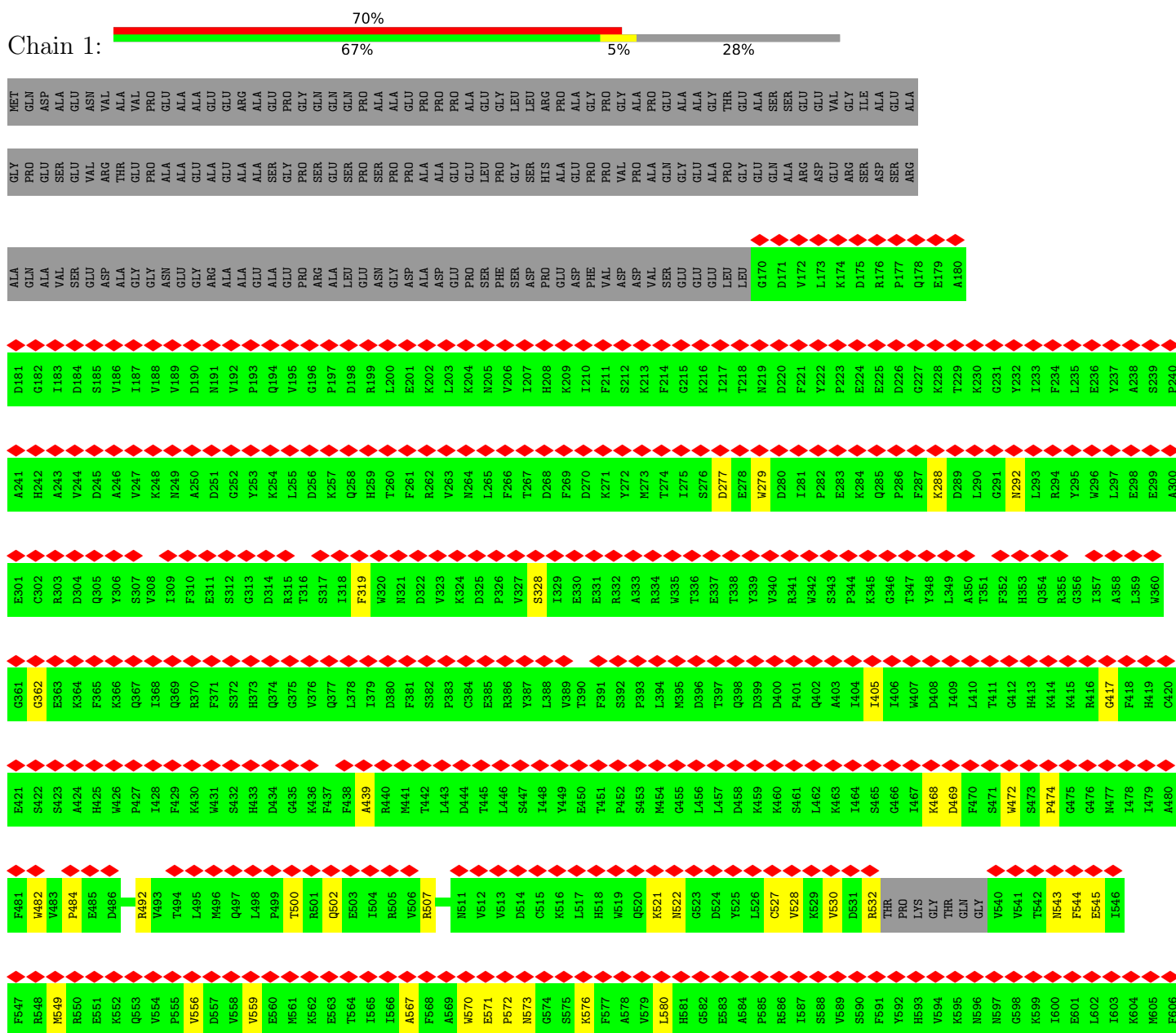
- Molecule 52 is ZINC ION (CCD ID: ZN) (formula: Zn).

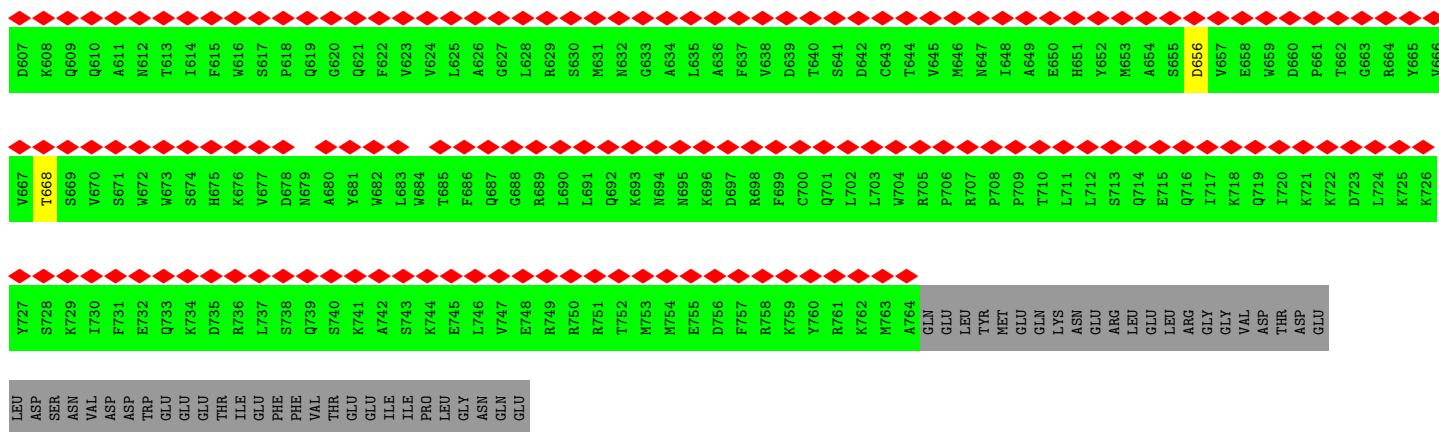
Mol	Chain	Residues	Atoms		AltConf
52	Q	1	Total	Zn	0
			1	1	
52	k	1	Total	Zn	0
			1	1	

3 Residue-property plots

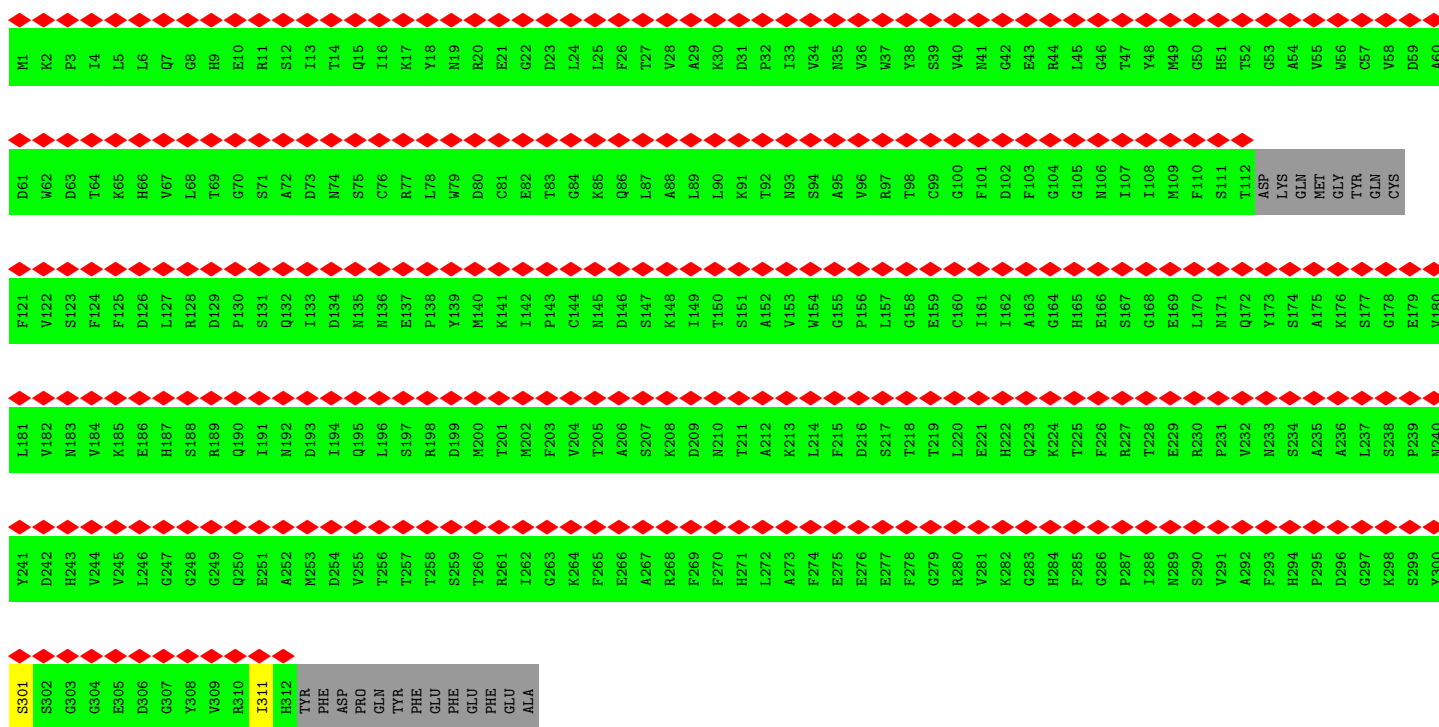
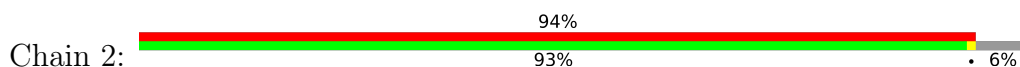
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Eukaryotic translation initiation factor 3 subunit B

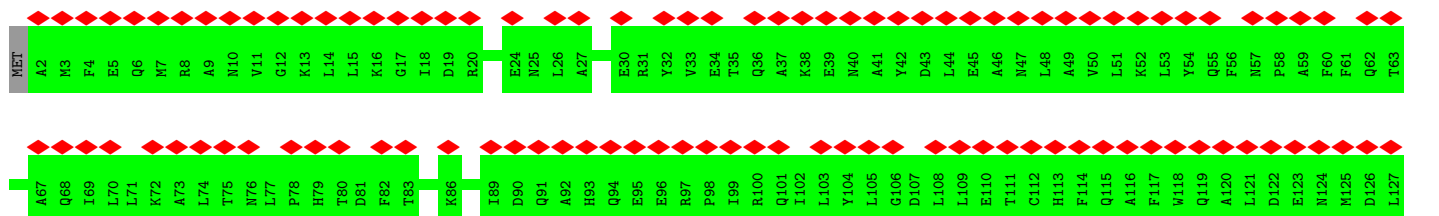
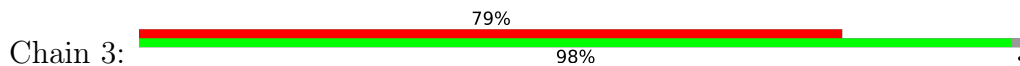


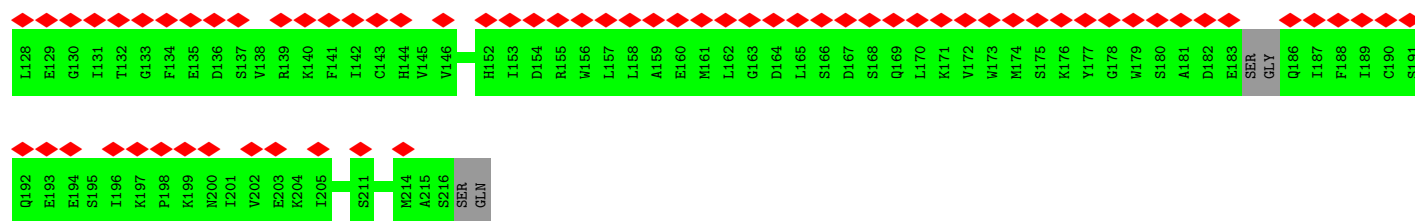


• Molecule 2: Eukaryotic translation initiation factor 3 subunit I

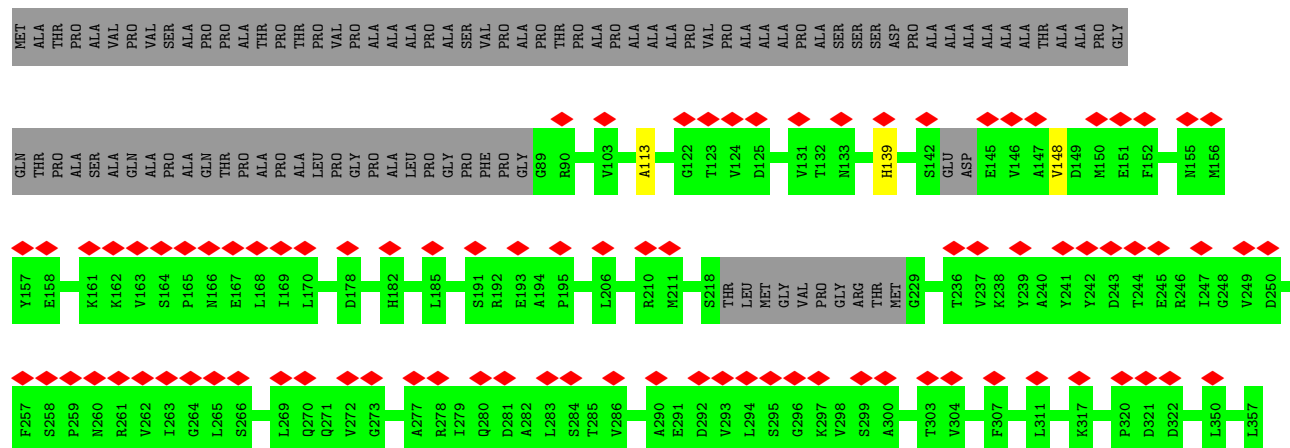


• Molecule 3: Eukaryotic translation initiation factor 3 subunit K

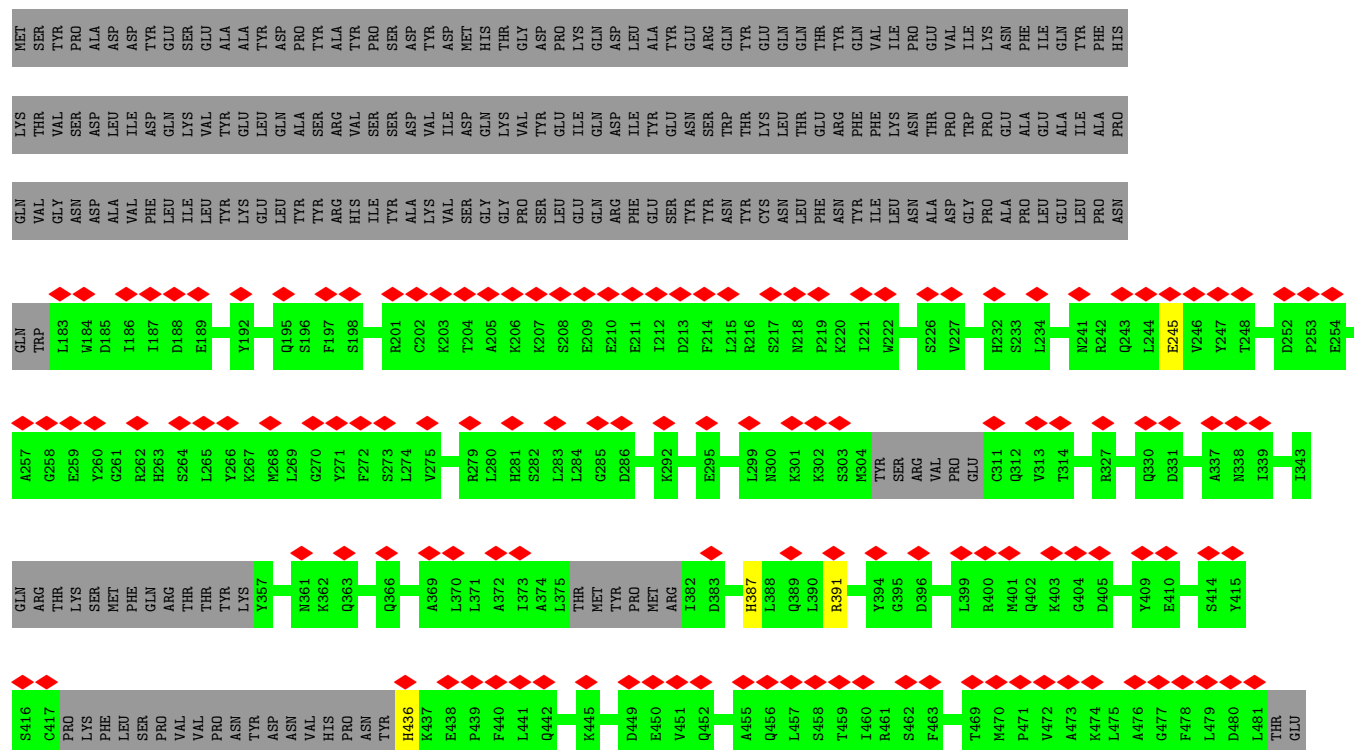


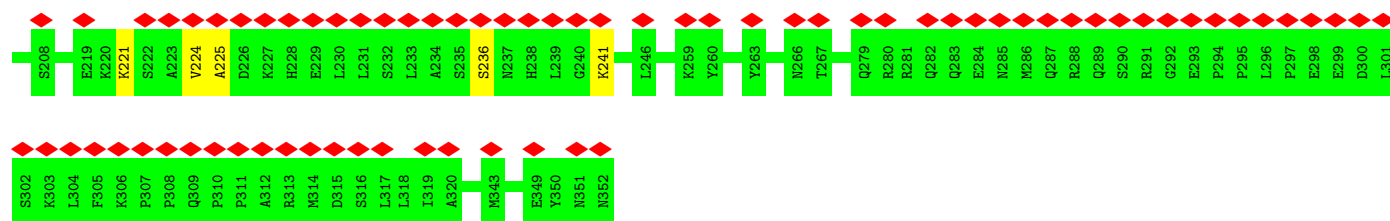


• Molecule 4: Eukaryotic translation initiation factor 3 subunit F



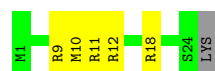
• Molecule 5: Eukaryotic translation initiation factor 3 subunit L





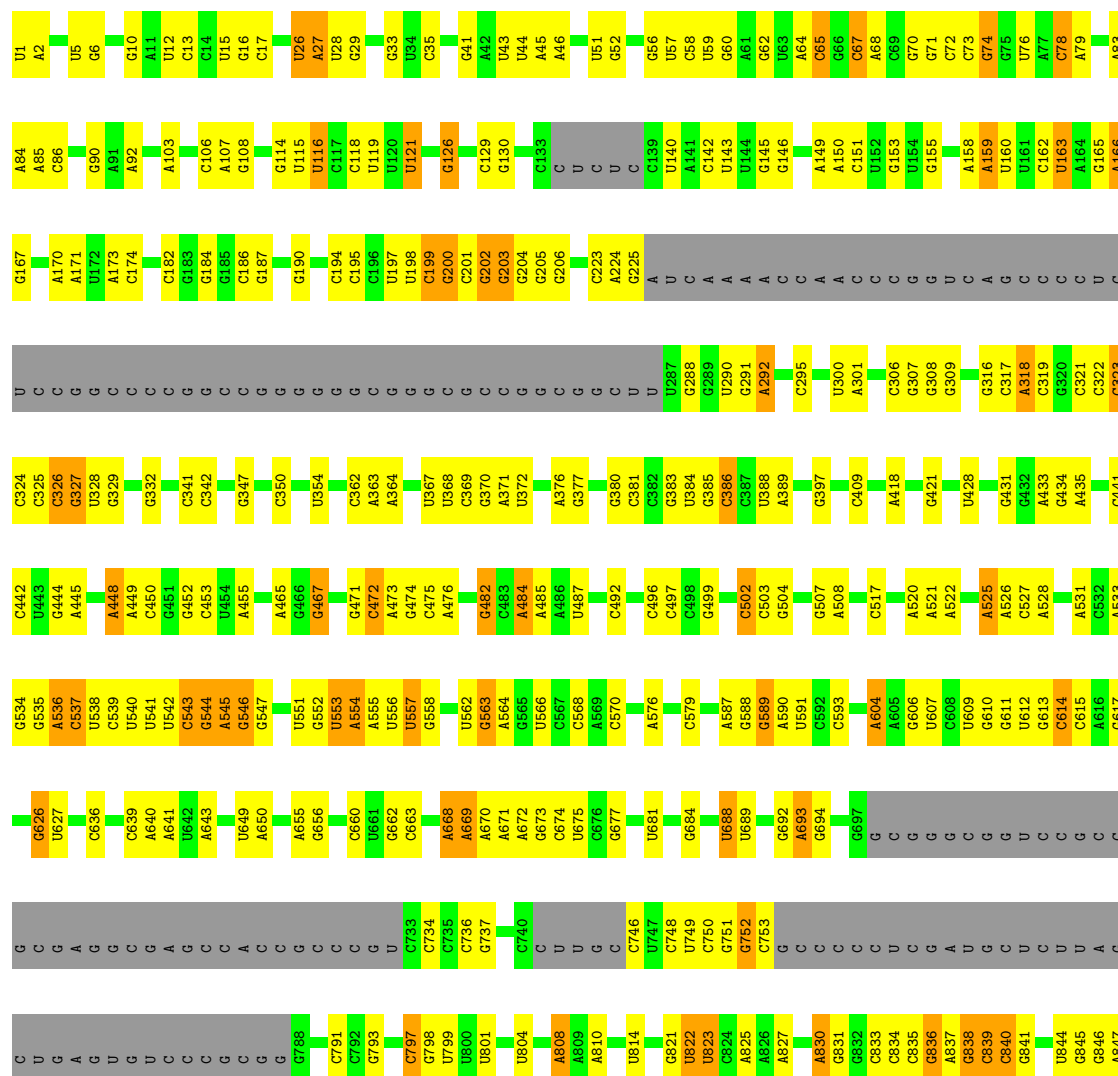
• Molecule 9: 60S ribosomal protein L41

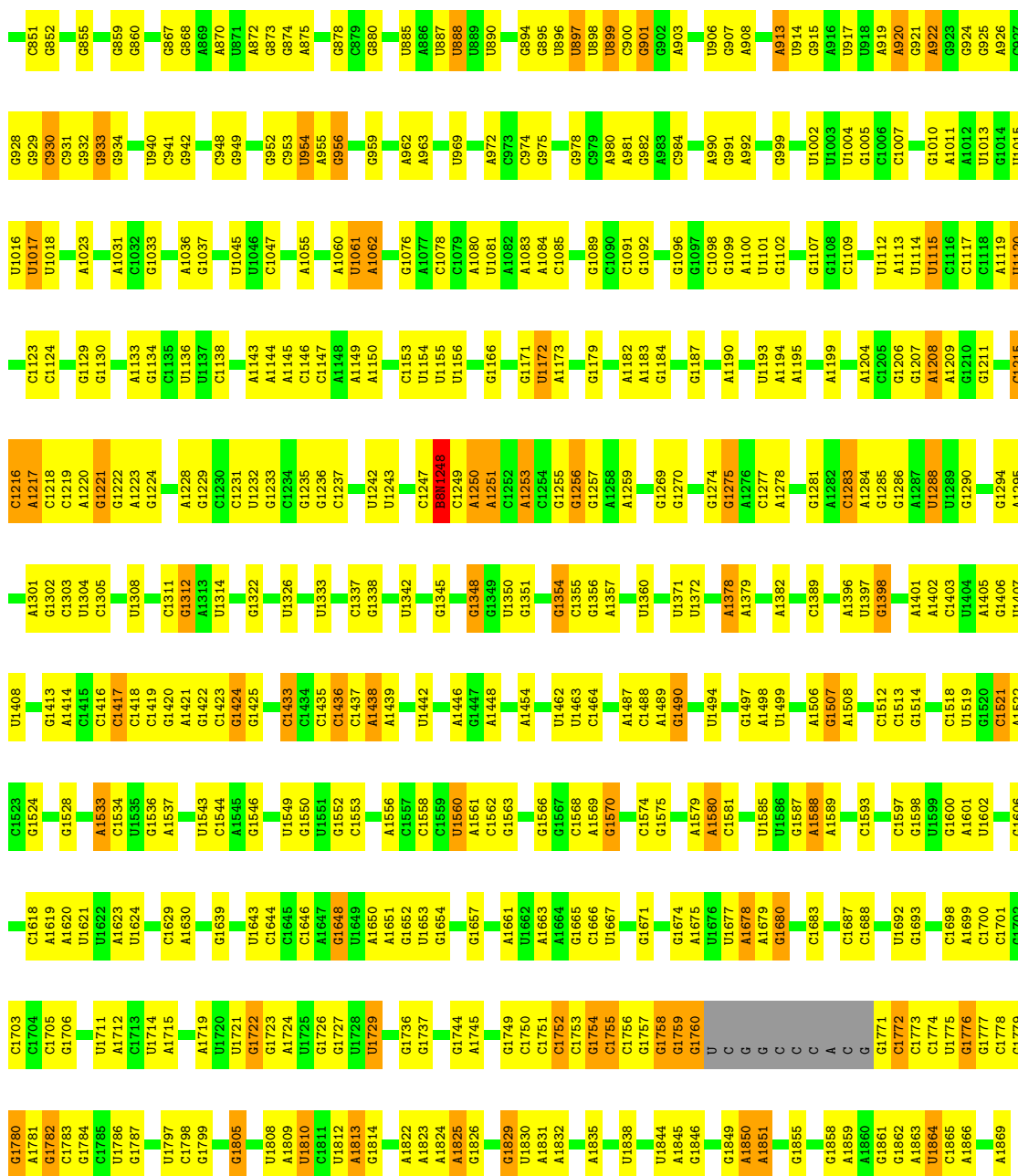
Chain 9: 76% 20% .



• Molecule 10: 18S rRNA

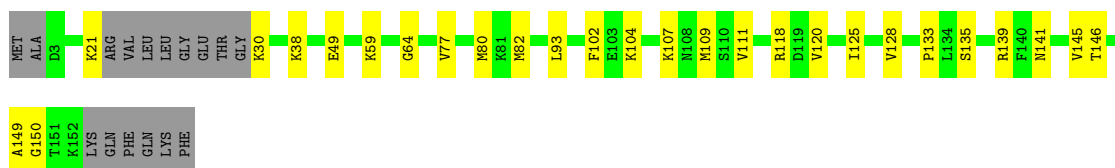
Chain A: 51% 34% 7% 8%





• Molecule 11: 40S ribosomal protein S11

Chain B: 73% 17% 10%

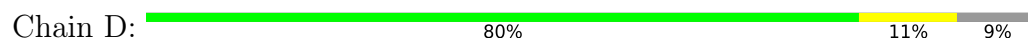


• Molecule 12: 40S ribosomal protein S4, X isoform

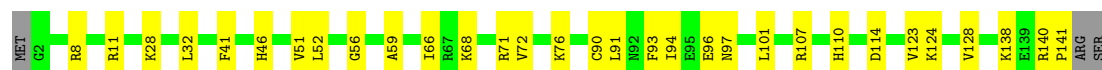
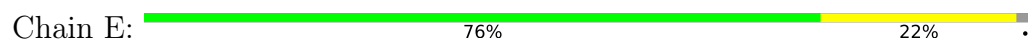
Chain C: 84% 13%



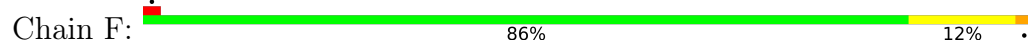
- Molecule 13: 40S ribosomal protein S9



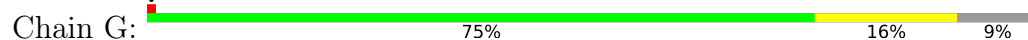
- Molecule 14: 40S ribosomal protein S23



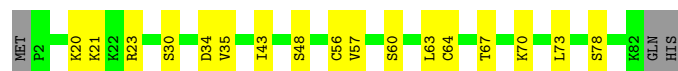
- Molecule 15: 40S ribosomal protein S30



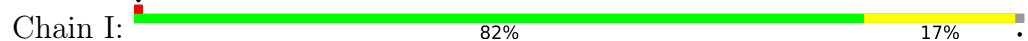
- Molecule 16: 40S ribosomal protein S7



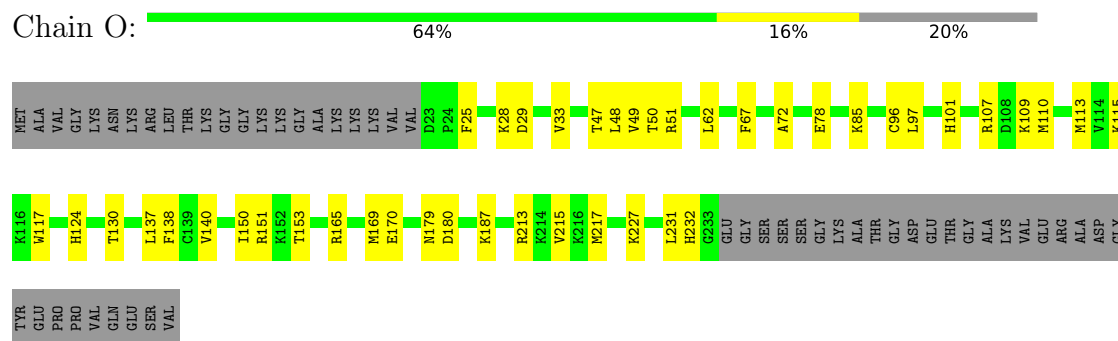
- Molecule 17: 40S ribosomal protein S27



- Molecule 18: 40S ribosomal protein S13



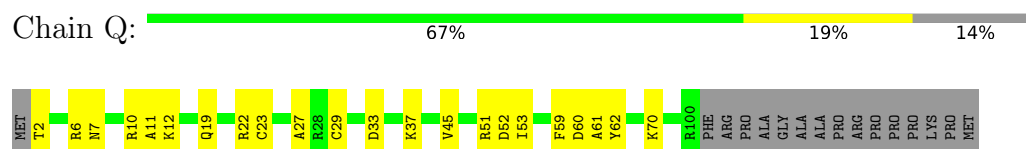
- Molecule 24: 40S ribosomal protein S3a



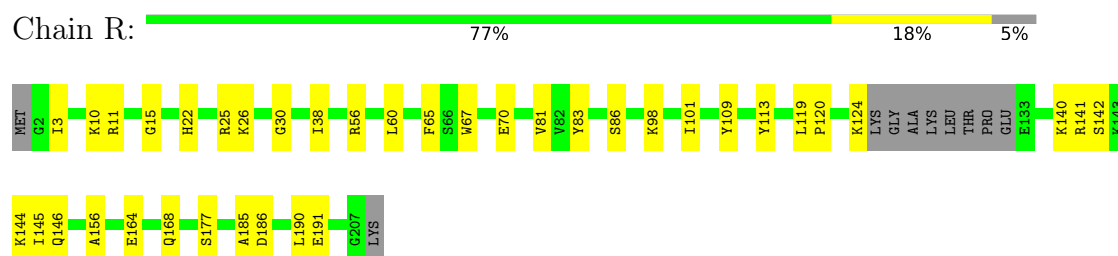
- Molecule 25: 40S ribosomal protein S14



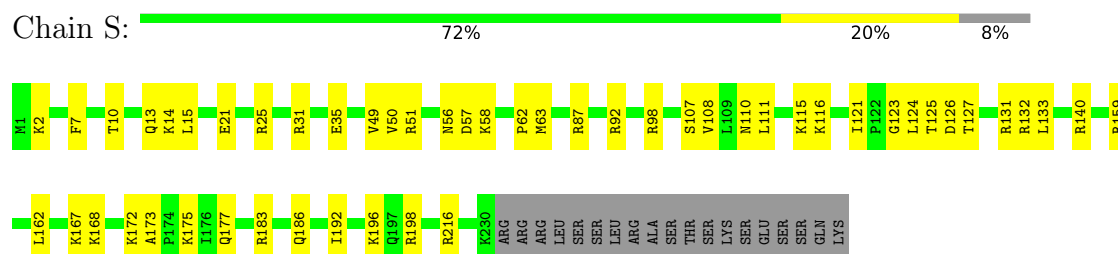
- Molecule 26: 40S ribosomal protein S26



- Molecule 27: 40S ribosomal protein S8



- Molecule 28: 40S ribosomal protein S6



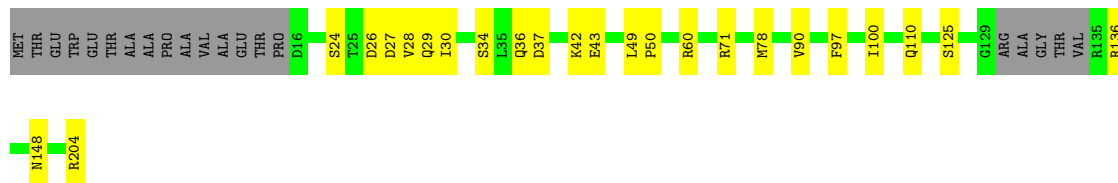
- Molecule 29: 40S ribosomal protein S24

Chain T: 



- Molecule 30: 40S ribosomal protein S5

Chain V: 



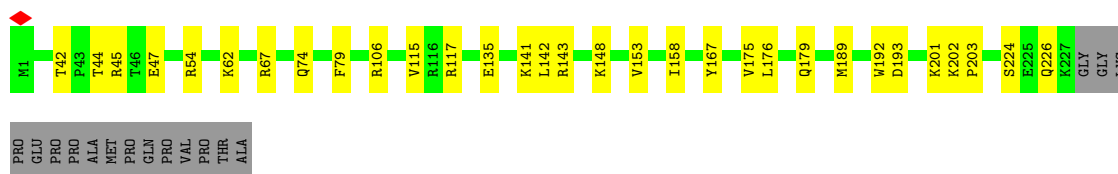
- Molecule 31: 40S ribosomal protein S16

Chain Y: 



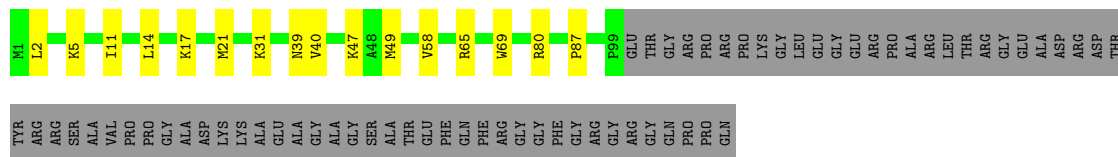
- Molecule 32: 40S ribosomal protein S3

Chain Z: 



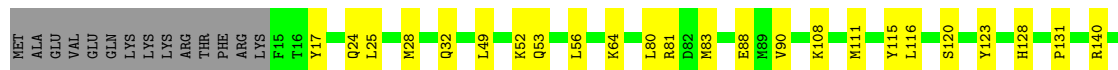
- Molecule 33: 40S ribosomal protein S10

Chain a: 



- Molecule 34: 40S ribosomal protein S15

Chain b: 



P143
L144
K145

- Molecule 35: Receptor of activated protein C kinase 1

Chain c:  78% 21% .

MET T2 M5 L11 L12 G13 H14 L32 S33 S35 R36 M42 W43 K44 L45 T46 R47 Q56 R57 G61 F65 I71 S72 S73 D74 S82 L87 R88 F101 H104 A112 V121 S122 G123 S124 R125 K130 G136 I165 V166 V176

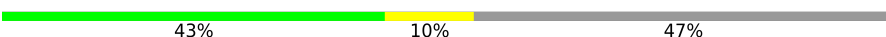
H177 T186 H191 L195 N196 G211 K212 D213 G214 D220 G224 K225 L236 N237 V247 L248 C249 T252 K257 L268 V267 L270 E282 P283 F284 C286 L289 L298 F299 L306 Y307 K308 K309 I314 GLY THR ARG

- Molecule 36: 40S ribosomal protein S19

Chain d:  87% 11% .

MET PRO G3 V4 T5 V6 V9 Q12 D35 G71 K97 L104 L110 K111 M112 R121 K122 R133 V138 A139 A140 K144 HIS

- Molecule 37: 40S ribosomal protein S25

Chain e:  43% 10% 47%

MET PRO PRO G3 V4 T5 V6 V9 Q12 D35 G71 K97 L104 L110 K111 M112 R121 K122 R133 V138 A139 A140 K144 HIS

R76 I79 R80 L83 A84 R85 T110 ARG ASN THR LYS GLY GLY ASP ALA PRO ALA ALA GLY GLU ASP ALA

- Molecule 38: 40S ribosomal protein S18

Chain f:  81% 17% .

MET SER LEU V4 G22 R23 G35 Y40 I50 R55 A56 G57 E58 L59 E63 R66 L84 Y95 S96 Q97 Y98 K106 L114 I117 R121 R124 Q81 V131 T136 R141 R144 T145 K152

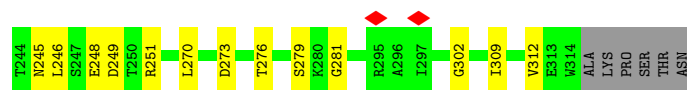
- Molecule 39: 40S ribosomal protein S20

Chain h:  67% 18% 13%

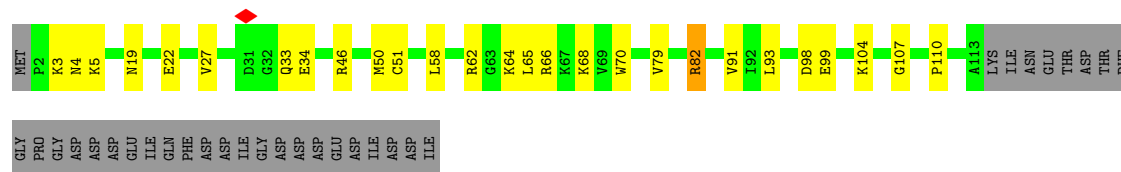
MET ALA PHE LYS THR GLY LYS THR PRO PRO GLU VAL I17 I20 K34 K46 K51 R55 M56 P57 T58 K59 T60 L61 R62 K67 D78 R79 F80 Q81 M82 R83 K86 R87 D90 I97 V98 K99 Q100 I101 A119

- Molecule 40: 40S ribosomal protein S29

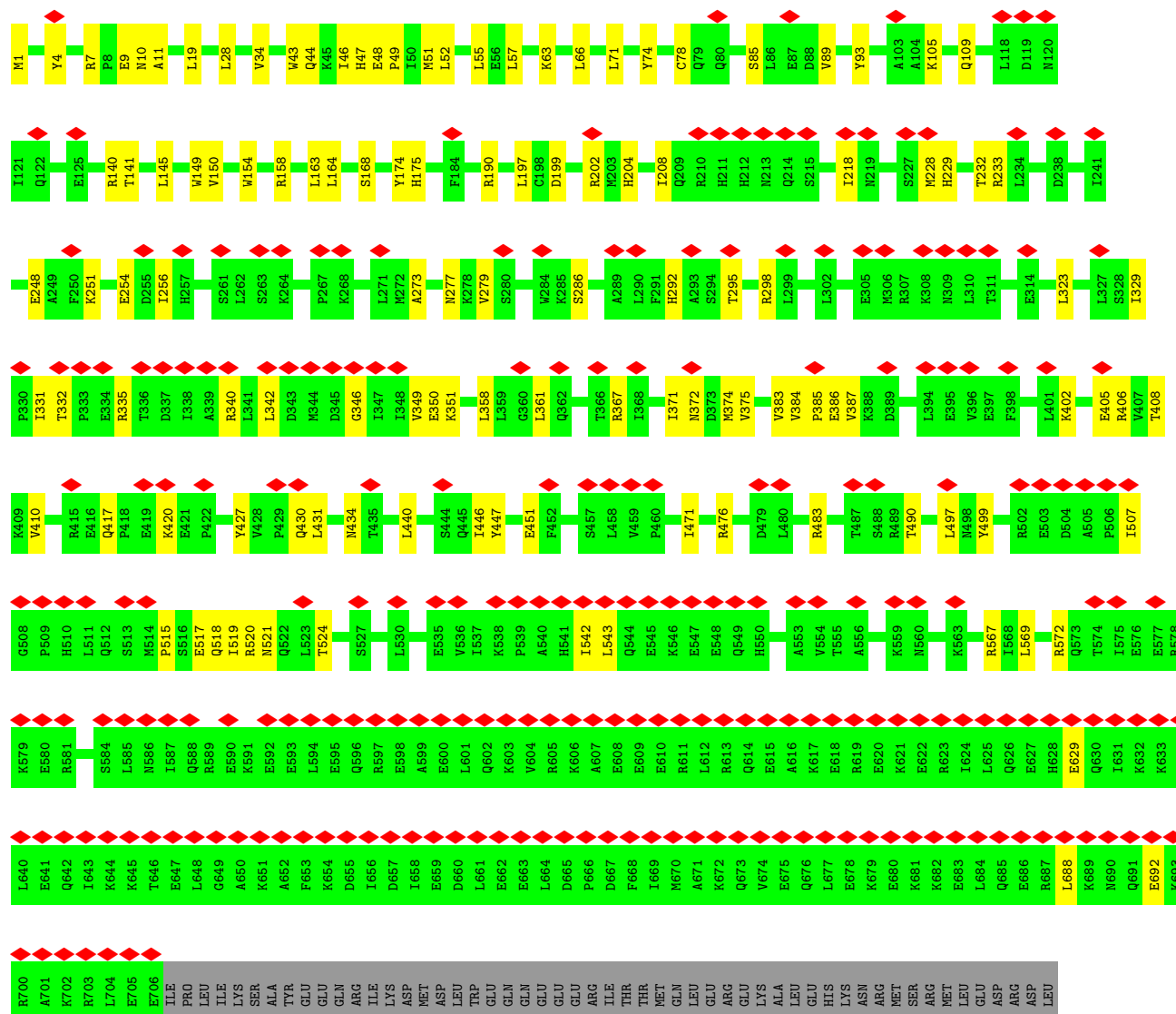
Chain i:  75% 14% 11%



- Molecule 45: Eukaryotic translation initiation factor 1A, X-chromosomal

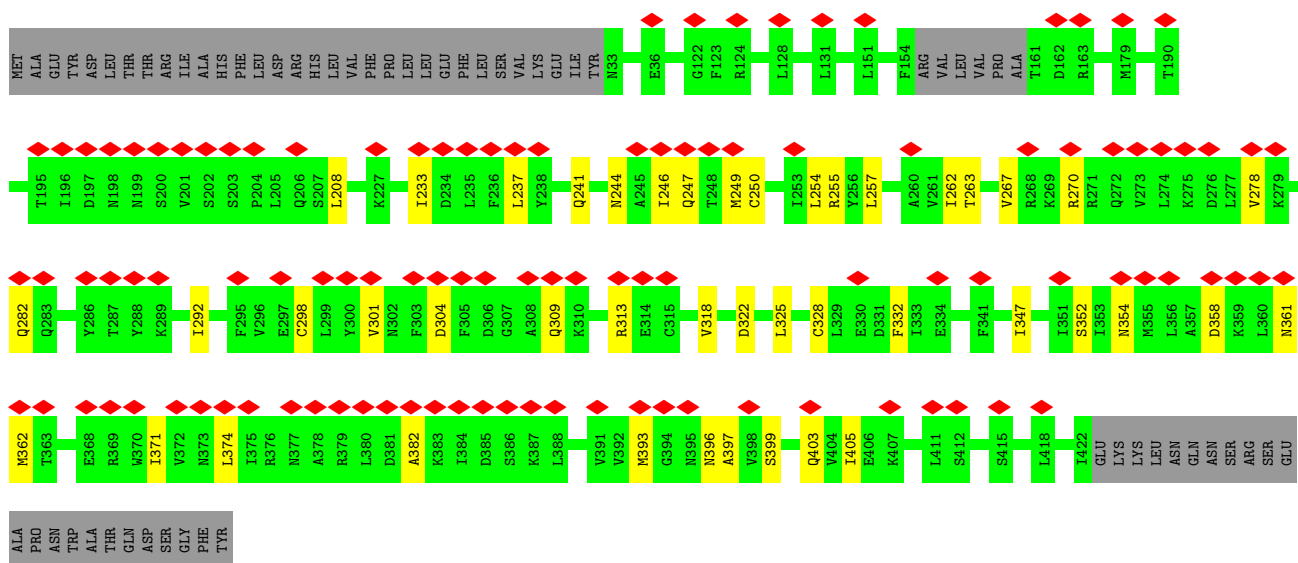
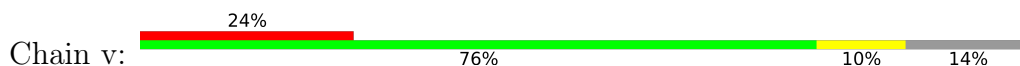


- Molecule 46: Eukaryotic translation initiation factor 3 subunit A



[illegible]

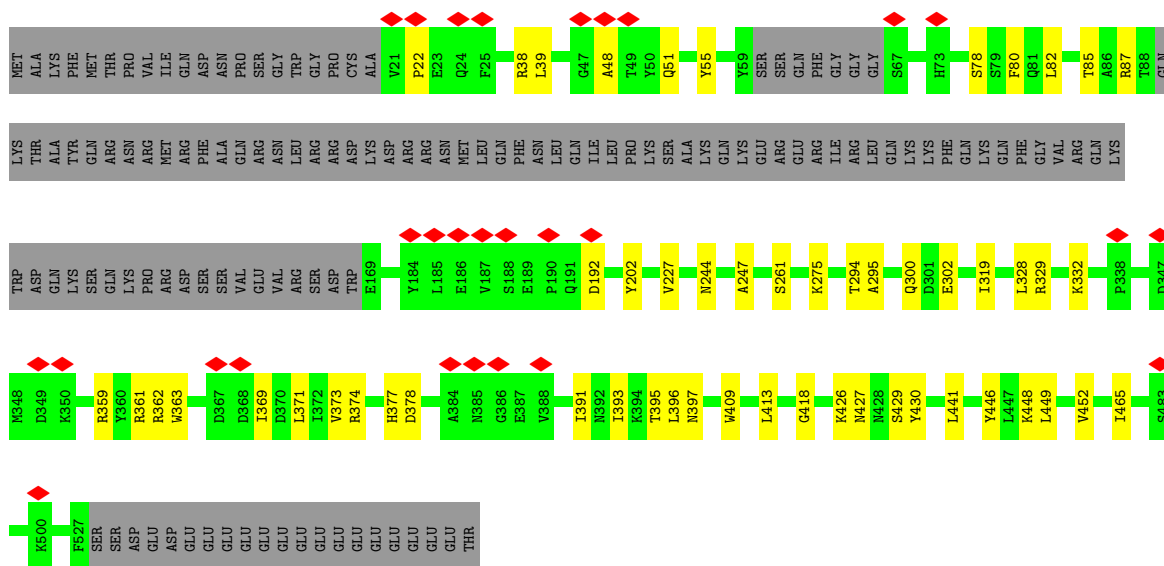
- Molecule 47: Eukaryotic translation initiation factor 3 subunit E



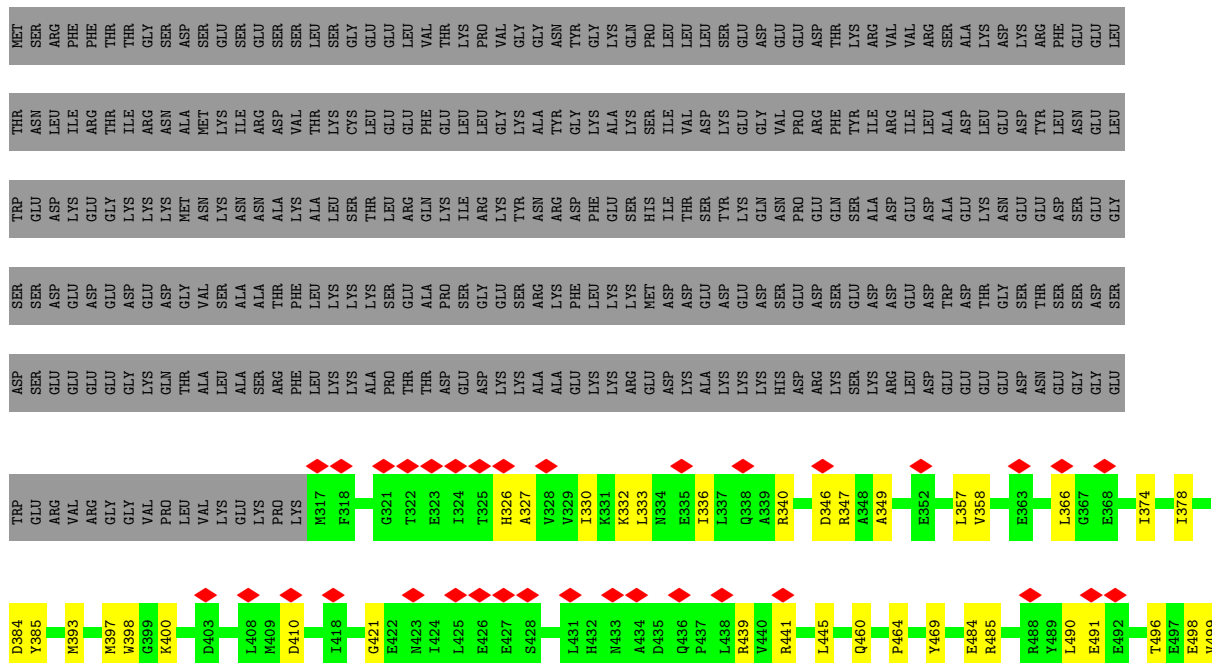
- Molecule 48: Initiator Met-tRNA-i

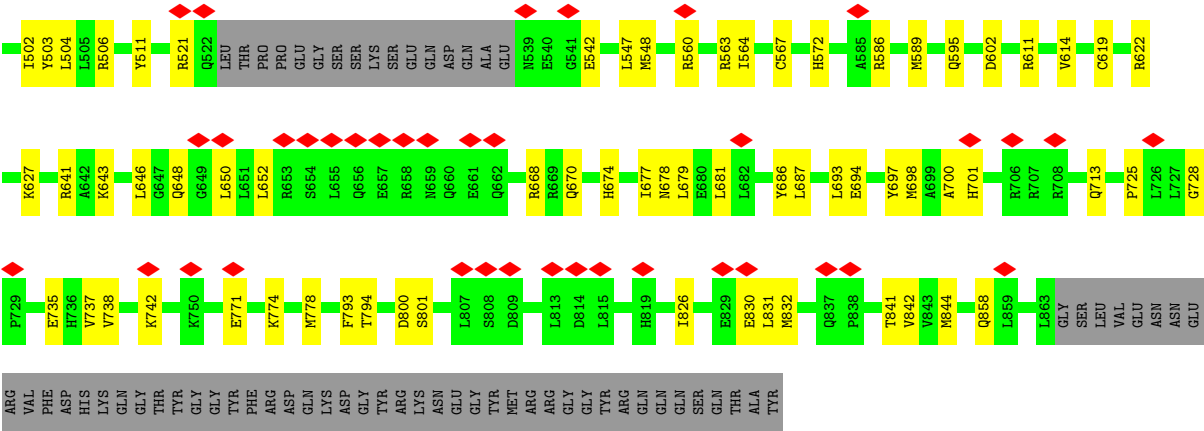
A1	G2	A6	G7	U8	G9	G10	G12	C13	C16	G18	G19	A20	A21	G22	C34	C48	G52	G53	C56	G57	A58	C61	C62	A63	U64	U69	G70	C71	U72	A73	C74	C	A
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Chain x:



Chain y:





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	55368	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.091	Depositor
Minimum map value	-0.016	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0102	Depositor
Map size (Å)	417.59998, 417.59998, 417.59998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMG, PSU, 6MZ, A2M, 5MU, 5MC, JMH, OMC, OMU, ZN, B8N, MG, UR3, 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	0.23	0/3279	0.51	0/4534
2	2	0.14	0/1491	0.34	0/2068
3	3	0.11	0/1055	0.31	0/1469
4	4	0.14	0/1269	0.39	0/1762
5	5	0.13	0/1575	0.35	0/2187
6	6	0.16	0/1926	0.49	1/2669 (0.0%)
7	7	0.16	0/1340	0.40	0/2085
8	8	0.16	0/1569	0.46	0/2183
9	9	0.22	0/231	0.48	0/294
10	A	0.24	0/40290	0.33	0/62786
11	B	0.21	0/1186	0.35	0/1585
12	C	0.23	0/2077	0.44	0/2796
13	D	0.20	0/1502	0.41	0/2008
14	E	0.22	0/1105	0.43	0/1476
15	F	0.25	0/474	0.67	1/623 (0.2%)
16	G	0.21	0/1451	0.52	0/1942
17	H	0.21	0/644	0.41	0/864
18	I	0.20	0/1232	0.41	0/1656
19	J	0.23	0/1051	0.43	0/1406
20	K	0.26	0/623	0.55	0/833
21	L	0.26	0/1743	0.53	0/2354
22	M	0.25	0/1078	0.60	0/1447
23	N	0.24	0/1670	0.50	0/2271
24	O	0.25	0/1742	0.56	1/2330 (0.0%)
25	P	0.24	0/1010	0.54	0/1353
26	Q	0.24	0/805	0.47	0/1079
27	R	0.21	0/1654	0.40	0/2203
28	S	0.18	0/1885	0.41	0/2510
29	T	0.21	0/1032	0.45	0/1371
30	V	0.19	0/1481	0.44	0/1988
31	Y	0.23	0/1142	0.50	1/1528 (0.1%)
32	Z	0.19	0/1793	0.38	0/2414

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	a	0.23	0/859	0.51	0/1159
34	b	0.21	0/1094	0.54	0/1464
35	c	0.22	0/2493	0.51	0/3394
36	d	0.19	0/1123	0.41	0/1504
37	e	0.21	0/529	0.47	0/712
38	f	0.21	0/1245	0.49	0/1665
39	h	0.41	2/827 (0.2%)	0.60	3/1110 (0.3%)
40	i	0.22	0/429	0.36	0/568
41	k	0.63	3/566 (0.5%)	0.78	2/753 (0.3%)
42	m	0.18	0/960	0.50	0/1286
43	n	0.22	0/500	0.50	0/669
44	o	0.20	0/628	0.51	0/846
45	q	0.21	0/913	0.60	2/1213 (0.2%)
46	u	0.20	0/5475	0.53	2/7432 (0.0%)
47	v	0.18	0/2672	0.51	0/3647
48	w	0.20	0/1748	0.36	0/2725
49	x	0.19	0/2869	0.50	2/3918 (0.1%)
50	y	0.19	0/4380	0.51	0/5911
All	All	0.22	5/111715 (0.0%)	0.43	15/160050 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	k	88	PRO	C-N	9.75	1.47	1.33
39	h	99	LYS	C-N	-7.46	1.23	1.33
39	h	100	GLN	C-N	6.48	1.42	1.33
41	k	89	LYS	C-N	-6.04	1.25	1.33
41	k	94	LYS	C-N	5.45	1.41	1.33

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	u	46	ILE	N-CA-C	-7.66	105.84	113.20
46	u	385	PRO	CA-N-CD	-7.52	101.47	112.00
41	k	90	LYS	N-CA-C	-7.10	103.67	112.47
45	q	82	ARG	CA-C-N	6.80	134.54	121.54
45	q	82	ARG	C-N-CA	6.80	134.54	121.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	3258	0	1917	28	0
2	2	1493	0	677	1	0
3	3	1057	0	475	0	0
4	4	1272	0	564	2	0
5	5	1581	0	689	2	0
6	6	1917	0	1096	10	0
7	7	1196	0	609	7	0
8	8	1571	0	683	5	0
9	9	230	0	276	5	0
10	A	36678	0	18526	431	0
11	B	1166	0	1233	19	0
12	C	2035	0	2138	23	0
13	D	1477	0	1589	15	0
14	E	1087	0	1154	17	0
15	F	468	0	516	6	0
16	G	1430	0	1520	25	0
17	H	631	0	657	12	0
18	I	1208	0	1294	23	0
19	J	1034	0	1080	15	0
20	K	617	0	622	10	0
21	L	1707	0	1794	33	0
22	M	1064	0	1118	25	0
23	N	1633	0	1640	24	0
24	O	1715	0	1785	28	0
25	P	997	0	1021	32	0
26	Q	792	0	842	15	0
27	R	1627	0	1706	26	0
28	S	1862	0	2018	41	0
29	T	1015	0	1086	19	0
30	V	1461	0	1511	17	0
31	Y	1124	0	1193	9	0
32	Z	1765	0	1865	23	0
33	a	834	0	861	10	0
34	b	1072	0	1121	21	0
35	c	2436	0	2393	41	0
36	d	1105	0	1138	11	0
37	e	523	0	573	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	f	1227	0	1298	18	0
39	h	817	0	882	16	0
40	i	419	0	415	7	0
41	k	554	0	556	34	0
42	m	950	0	987	22	0
43	n	498	0	525	14	0
44	o	616	0	600	8	0
45	q	902	0	925	23	0
46	u	5383	0	5085	76	0
47	v	2635	0	2207	27	0
48	w	1562	0	794	1	0
49	x	2826	0	2197	35	0
50	y	4305	0	4321	61	0
51	A	82	0	0	0	0
51	V	1	0	0	0	0
51	d	1	0	0	0	0
51	f	1	0	0	0	0
51	i	2	0	0	0	0
52	Q	1	0	0	0	0
52	k	1	0	0	0	0
All	All	106921	0	81772	1164	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 6.

The worst 5 of 1164 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)
10:A:885:U:H3	10:A:901:G:H1	0.98	0.98
1:1:288:LYS:HA	1:1:362:GLY:HA2	1.56	0.88
41:k:87:THR:C	41:k:89:LYS:H	1.81	0.87
10:A:878:G:H1	10:A:908:A:H61	1.26	0.83
10:A:1249:C:H5''	10:A:1250:A:H2'	1.65	0.78

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	584/814 (72%)	535 (92%)	49 (8%)	0	100	100
2	2	300/325 (92%)	297 (99%)	3 (1%)	0	100	100
3	3	209/218 (96%)	204 (98%)	5 (2%)	0	100	100
4	4	251/357 (70%)	232 (92%)	19 (8%)	0	100	100
5	5	307/564 (54%)	293 (95%)	14 (5%)	0	100	100
6	6	348/374 (93%)	308 (88%)	40 (12%)	0	100	100
8	8	313/352 (89%)	282 (90%)	31 (10%)	0	100	100
9	9	22/25 (88%)	22 (100%)	0	0	100	100
11	B	138/158 (87%)	136 (99%)	2 (1%)	0	100	100
12	C	254/263 (97%)	249 (98%)	5 (2%)	0	100	100
13	D	175/194 (90%)	172 (98%)	3 (2%)	0	100	100
14	E	138/143 (96%)	135 (98%)	3 (2%)	0	100	100
15	F	57/59 (97%)	47 (82%)	10 (18%)	0	100	100
16	G	171/194 (88%)	167 (98%)	4 (2%)	0	100	100
17	H	79/84 (94%)	78 (99%)	1 (1%)	0	100	100
18	I	148/151 (98%)	147 (99%)	1 (1%)	0	100	100
19	J	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
20	K	79/83 (95%)	77 (98%)	2 (2%)	0	100	100
21	L	218/293 (74%)	215 (99%)	3 (1%)	0	100	100
22	M	129/135 (96%)	127 (98%)	2 (2%)	0	100	100
23	N	205/295 (70%)	201 (98%)	4 (2%)	0	100	100
24	O	209/264 (79%)	206 (99%)	3 (1%)	0	100	100
25	P	131/151 (87%)	124 (95%)	7 (5%)	0	100	100
26	Q	97/115 (84%)	96 (99%)	1 (1%)	0	100	100
27	R	194/208 (93%)	192 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	S	228/249 (92%)	226 (99%)	2 (1%)	0	100	100
29	T	123/133 (92%)	123 (100%)	0	0	100	100
30	V	180/204 (88%)	179 (99%)	1 (1%)	0	100	100
31	Y	139/146 (95%)	134 (96%)	5 (4%)	0	100	100
32	Z	225/243 (93%)	224 (100%)	1 (0%)	0	100	100
33	a	97/165 (59%)	94 (97%)	3 (3%)	0	100	100
34	b	129/145 (89%)	123 (95%)	6 (5%)	0	100	100
35	c	311/317 (98%)	295 (95%)	16 (5%)	0	100	100
36	d	140/145 (97%)	137 (98%)	3 (2%)	0	100	100
37	e	64/125 (51%)	63 (98%)	1 (2%)	0	100	100
38	f	147/152 (97%)	142 (97%)	5 (3%)	0	100	100
39	h	101/119 (85%)	97 (96%)	4 (4%)	0	100	100
40	i	48/56 (86%)	47 (98%)	1 (2%)	0	100	100
41	k	66/156 (42%)	60 (91%)	6 (9%)	0	100	100
42	m	120/132 (91%)	120 (100%)	0	0	100	100
43	n	61/69 (88%)	58 (95%)	3 (5%)	0	100	100
44	o	75/320 (23%)	73 (97%)	2 (3%)	0	100	100
45	q	110/144 (76%)	100 (91%)	10 (9%)	0	100	100
46	u	705/1382 (51%)	662 (94%)	43 (6%)	0	100	100
47	v	380/445 (85%)	355 (93%)	25 (7%)	0	100	100
49	x	414/548 (76%)	399 (96%)	15 (4%)	0	100	100
50	y	527/913 (58%)	508 (96%)	19 (4%)	0	100	100
All	All	9273/12257 (76%)	8885 (96%)	388 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	
1	1	97/702 (14%)	97 (100%)	0	100	100
6	6	49/335 (15%)	49 (100%)	0	100	100
9	9	23/24 (96%)	23 (100%)	0	100	100
11	B	129/142 (91%)	129 (100%)	0	100	100
12	C	220/225 (98%)	220 (100%)	0	100	100
13	D	158/168 (94%)	158 (100%)	0	100	100
14	E	112/115 (97%)	112 (100%)	0	100	100
15	F	48/48 (100%)	48 (100%)	0	100	100
16	G	159/174 (91%)	159 (100%)	0	100	100
17	H	73/76 (96%)	73 (100%)	0	100	100
18	I	130/131 (99%)	130 (100%)	0	100	100
19	J	112/113 (99%)	112 (100%)	0	100	100
20	K	65/67 (97%)	65 (100%)	0	100	100
21	L	186/225 (83%)	186 (100%)	0	100	100
22	M	119/122 (98%)	119 (100%)	0	100	100
23	N	173/243 (71%)	173 (100%)	0	100	100
24	O	192/231 (83%)	192 (100%)	0	100	100
25	P	104/119 (87%)	104 (100%)	0	100	100
26	Q	86/98 (88%)	86 (100%)	0	100	100
27	R	172/180 (96%)	172 (100%)	0	100	100
28	S	200/218 (92%)	200 (100%)	0	100	100
29	T	107/115 (93%)	107 (100%)	0	100	100
30	V	156/170 (92%)	156 (100%)	0	100	100
31	Y	117/121 (97%)	117 (100%)	0	100	100
32	Z	190/202 (94%)	190 (100%)	0	100	100
33	a	90/136 (66%)	90 (100%)	0	100	100
34	b	117/130 (90%)	117 (100%)	0	100	100
35	c	272/275 (99%)	272 (100%)	0	100	100
36	d	112/115 (97%)	112 (100%)	0	100	100
37	e	58/103 (56%)	58 (100%)	0	100	100
38	f	129/132 (98%)	129 (100%)	0	100	100
39	h	94/107 (88%)	94 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	i	44/49 (90%)	44 (100%)	0	100	100
41	k	61/140 (44%)	61 (100%)	0	100	100
42	m	104/108 (96%)	104 (100%)	0	100	100
43	n	56/62 (90%)	56 (100%)	0	100	100
44	o	64/277 (23%)	64 (100%)	0	100	100
45	q	94/123 (76%)	94 (100%)	0	100	100
46	u	528/1259 (42%)	528 (100%)	0	100	100
47	v	206/406 (51%)	206 (100%)	0	100	100
49	x	206/494 (42%)	206 (100%)	0	100	100
50	y	473/811 (58%)	473 (100%)	0	100	100
All	All	5885/9091 (65%)	5885 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
31	Y	29	ASN
50	y	364	ASN
46	u	79	GLN
50	y	355	GLN
50	y	858	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	1710/1869 (91%)	374 (21%)	6 (0%)
48	w	72/75 (96%)	26 (36%)	0
7	7	55/255 (21%)	34 (61%)	3 (5%)
All	All	1837/2199 (83%)	434 (23%)	9 (0%)

5 of 434 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	7	-30	C
7	7	-29	A
7	7	-28	A

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Mol	Chain	Res	Type
7	7	-27	C
7	7	-26	A

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	A	797	C
10	A	1600	G
10	A	1	U
10	A	291	G
10	A	368	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	OMC	A	1703	10	19,22,23	0.61	0	26,31,34	0.77	1 (3%)
10	UR3	A	1830	10	19,22,23	2.76	7 (36%)	26,32,35	1.51	4 (15%)
10	PSU	A	119	10	18,21,22	0.99	1 (5%)	22,30,33	1.59	4 (18%)
10	PSU	A	1081	10	18,21,22	1.04	1 (5%)	22,30,33	1.83	5 (22%)
10	A2M	A	484	10	22,25,26	3.87	11 (50%)	31,36,39	3.32	13 (41%)
10	MA6	A	1850	10	23,26,27	1.56	2 (8%)	34,38,41	3.07	11 (32%)
10	PSU	A	822	10	18,21,22	1.03	1 (5%)	22,30,33	1.86	6 (27%)
10	A2M	A	166	10	22,25,26	3.96	10 (45%)	31,36,39	3.41	15 (48%)
10	A2M	A	1678	51,10	22,25,26	3.99	11 (50%)	31,36,39	3.47	13 (41%)
10	PSU	A	823	10	18,21,22	1.08	1 (5%)	22,30,33	1.77	4 (18%)
10	OMC	A	174	51,10	19,22,23	0.57	0	26,31,34	0.71	1 (3%)
10	OMC	A	517	10	19,22,23	0.59	0	26,31,34	0.66	0
10	OMU	A	116	10	19,22,23	2.97	5 (26%)	26,31,34	1.58	5 (19%)
10	A2M	A	27	51,10	22,25,26	3.94	11 (50%)	31,36,39	3.32	12 (38%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	OMG	A	683	10	23,26,27	0.56	0	33,38,41	0.54	0
10	OMU	A	121	10	19,22,23	2.95	6 (31%)	26,31,34	1.63	5 (19%)
10	A2M	A	1031	10	22,25,26	3.97	11 (50%)	31,36,39	3.40	14 (45%)
10	PSU	A	612	10	18,21,22	1.00	1 (5%)	22,30,33	1.79	5 (22%)
10	A2M	A	668	51,10	22,25,26	3.90	12 (54%)	31,36,39	3.37	14 (45%)
10	OMG	A	644	10	23,26,27	0.55	0	33,38,41	0.44	0
10	PSU	A	1243	10	18,21,22	1.06	1 (5%)	22,30,33	1.80	4 (18%)
10	OMG	A	509	51,10	23,26,27	0.57	0	33,38,41	0.50	0
10	6MZ	A	1832	51,10	22,25,26	2.39	5 (22%)	30,36,39	2.53	11 (36%)
10	5MU	A	814	10	19,22,23	0.48	0	28,32,35	0.93	2 (7%)
10	B8N	A	1248	10	24,29,30	0.30	0	29,42,45	0.73	1 (3%)
10	MA6	A	1851	10	23,26,27	1.56	2 (8%)	34,38,41	3.13	12 (35%)
10	JMH	A	1219	10	18,22,23	0.25	0	21,32,35	0.25	0
10	A2M	A	159	10	22,25,26	3.91	11 (50%)	31,36,39	3.44	14 (45%)
10	5MC	A	1374	10	18,22,23	0.65	0	26,32,35	0.60	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
10	OMC	A	1703	10	-	2/9/27/28	0/2/2/2
10	UR3	A	1830	10	-	2/7/25/26	0/2/2/2
10	PSU	A	119	10	-	0/7/25/26	0/2/2/2
10	PSU	A	1081	10	-	1/7/25/26	0/2/2/2
10	A2M	A	484	10	-	1/9/27/28	0/3/3/3
10	MA6	A	1850	10	-	0/11/29/30	0/3/3/3
10	PSU	A	822	10	-	2/7/25/26	0/2/2/2
10	A2M	A	166	10	-	0/9/27/28	0/3/3/3
10	A2M	A	1678	51,10	-	0/9/27/28	0/3/3/3
10	PSU	A	823	10	-	0/7/25/26	0/2/2/2
10	OMC	A	174	51,10	-	0/9/27/28	0/2/2/2
10	OMC	A	517	10	-	2/9/27/28	0/2/2/2
10	OMU	A	116	10	-	1/9/27/28	0/2/2/2
10	A2M	A	27	51,10	-	1/9/27/28	0/3/3/3
10	OMG	A	683	10	-	2/9/27/28	0/3/3/3
10	OMU	A	121	10	-	1/9/27/28	0/2/2/2
10	A2M	A	1031	10	-	1/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	PSU	A	612	10	-	0/7/25/26	0/2/2/2
10	A2M	A	668	51,10	-	2/9/27/28	0/3/3/3
10	OMG	A	644	10	-	2/9/27/28	0/3/3/3
10	PSU	A	1243	10	-	2/7/25/26	0/2/2/2
10	OMG	A	509	51,10	-	1/9/27/28	0/3/3/3
10	6MZ	A	1832	51,10	-	0/9/27/28	0/3/3/3
10	5MU	A	814	10	-	0/7/25/26	0/2/2/2
10	B8N	A	1248	10	-	7/16/34/35	0/2/2/2
10	MA6	A	1851	10	-	3/11/29/30	0/3/3/3
10	JMH	A	1219	10	-	0/7/25/26	0/2/2/2
10	A2M	A	159	10	-	2/9/27/28	0/3/3/3
10	5MC	A	1374	10	-	0/7/25/26	0/2/2/2

The worst 5 of 110 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	1031	A2M	C3'-C2'	-12.99	1.24	1.52
10	A	1678	A2M	C3'-C2'	-12.96	1.24	1.52
10	A	166	A2M	C3'-C2'	-12.90	1.24	1.52
10	A	27	A2M	C3'-C2'	-12.85	1.24	1.52
10	A	159	A2M	C3'-C2'	-12.45	1.25	1.52

The worst 5 of 176 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	1851	MA6	N1-C6-N6	-11.94	104.03	117.08
10	A	1850	MA6	N1-C6-N6	-11.75	104.24	117.08
10	A	1678	A2M	C1'-N9-C8	-9.64	105.36	127.14
10	A	159	A2M	C1'-N9-C8	-9.53	105.62	127.14
10	A	1031	A2M	C1'-N9-C8	-9.01	106.79	127.14

There are no chirality outliers.

5 of 35 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	A	27	A2M	C1'-C2'-O2'-CM'
10	A	116	OMU	C1'-C2'-O2'-CM2
10	A	121	OMU	C1'-C2'-O2'-CM2
10	A	159	A2M	C1'-C2'-O2'-CM'
10	A	484	A2M	C1'-C2'-O2'-CM'

There are no ring outliers.

11 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	A	484	A2M	1	0
10	A	1850	MA6	1	0
10	A	166	A2M	1	0
10	A	1678	A2M	1	0
10	A	823	PSU	1	0
10	A	116	OMU	2	0
10	A	27	A2M	1	0
10	A	121	OMU	1	0
10	A	1248	B8N	2	0
10	A	1219	JMH	2	0
10	A	159	A2M	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 89 ligands modelled in this entry, 89 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

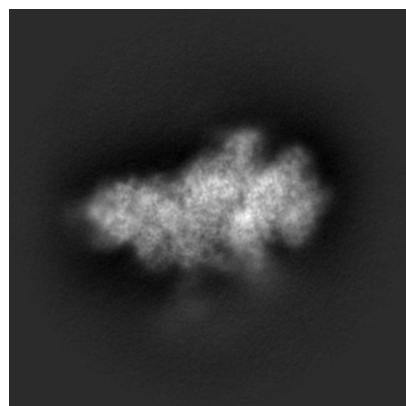
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17701. These allow visual inspection of the internal detail of the map and identification of artifacts.

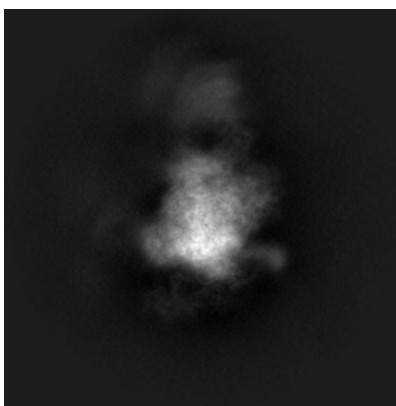
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

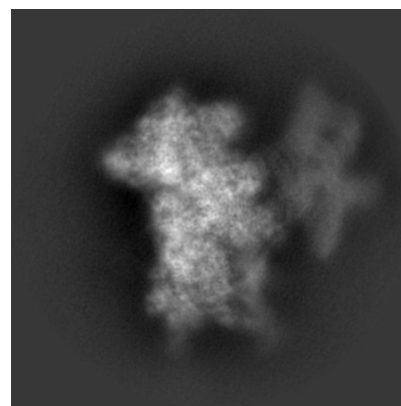
6.1.1 Primary map



X

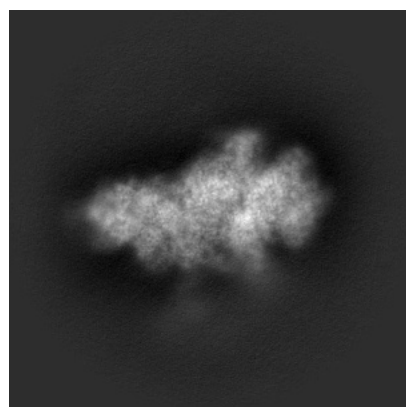


Y

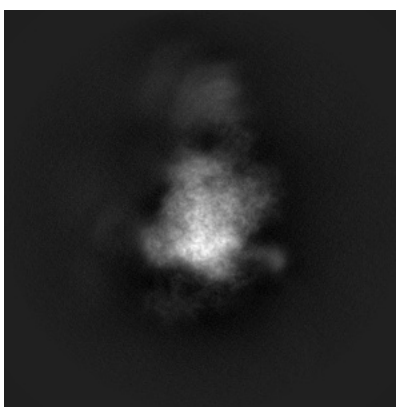


Z

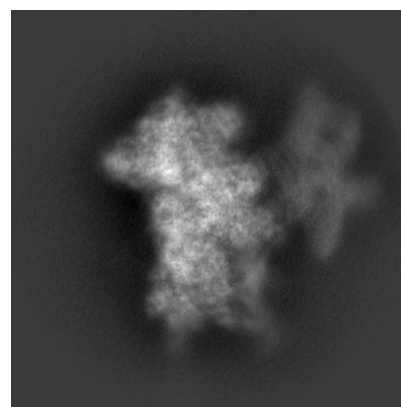
6.1.2 Raw map



X



Y

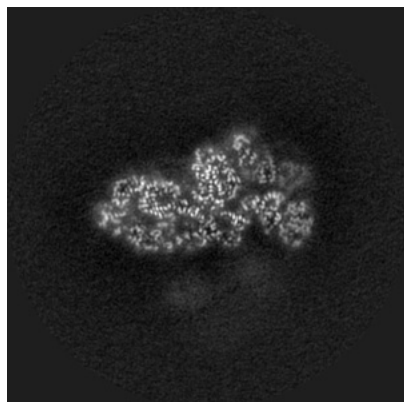


Z

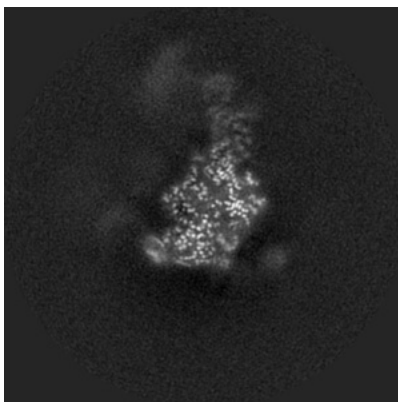
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

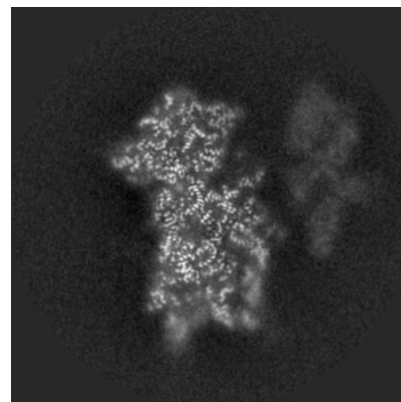
6.2.1 Primary map



X Index: 180

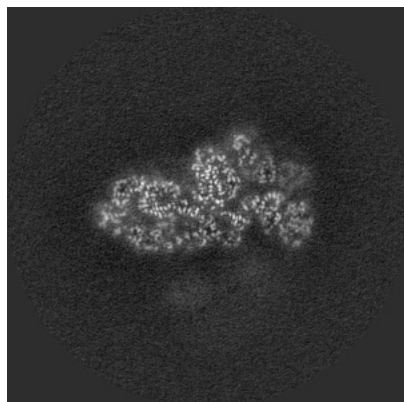


Y Index: 180

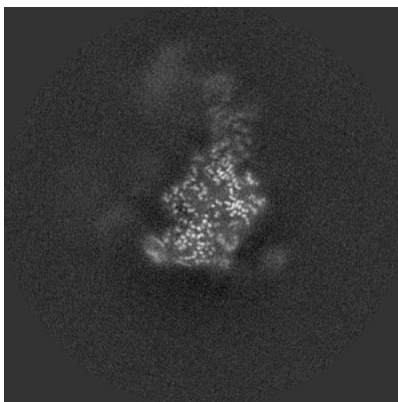


Z Index: 180

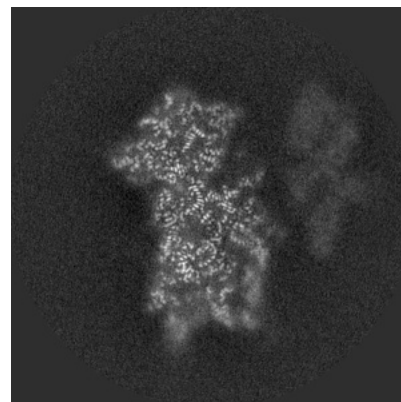
6.2.2 Raw map



X Index: 180



Y Index: 180

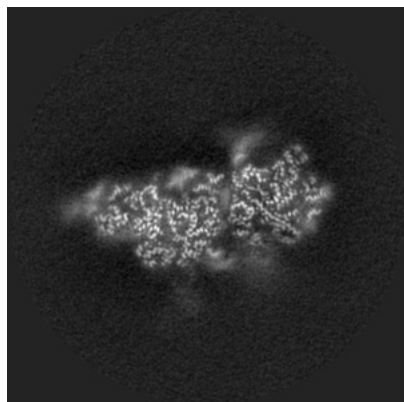


Z Index: 180

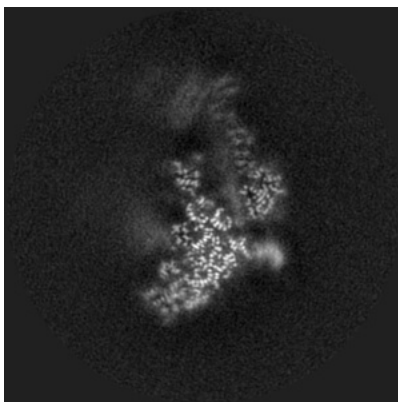
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

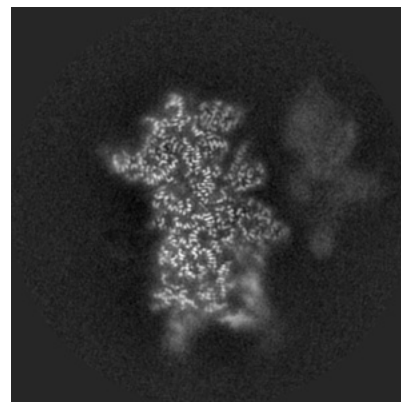
6.3.1 Primary map



X Index: 147

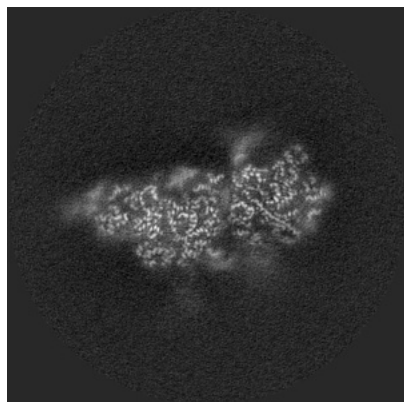


Y Index: 216

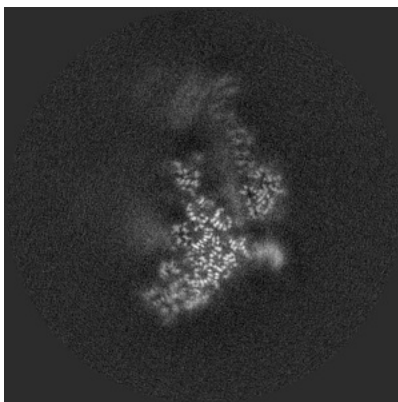


Z Index: 174

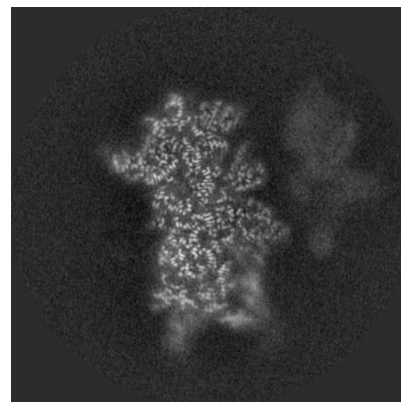
6.3.2 Raw map



X Index: 147



Y Index: 216

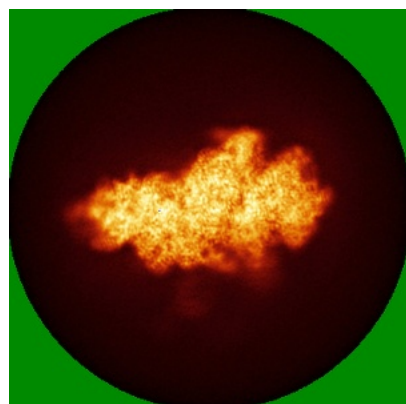


Z Index: 174

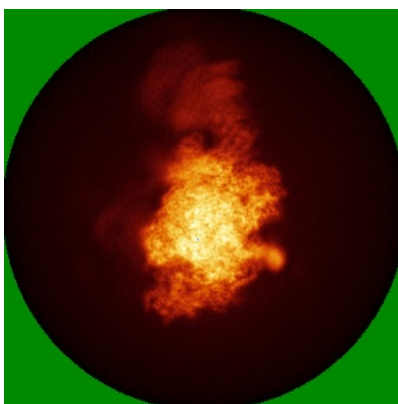
The images above show the largest variance slices of the map in three orthogonal directions.

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

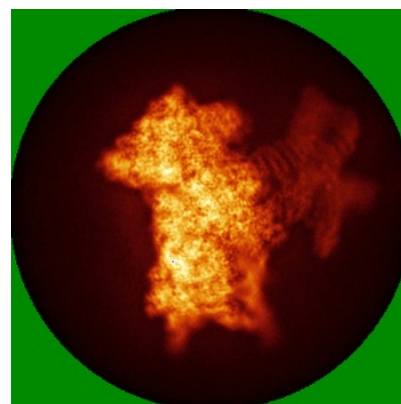
6.4.1 Primary map



X

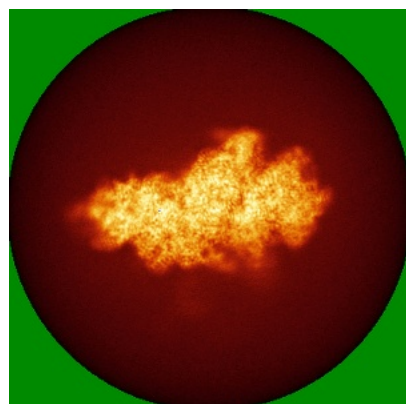


Y

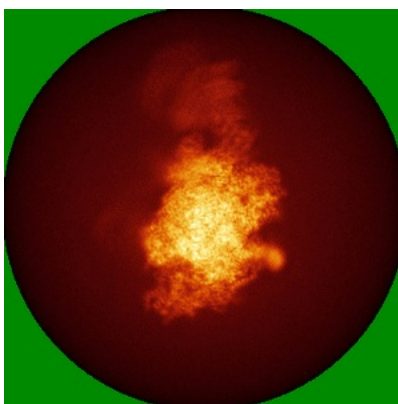


Z

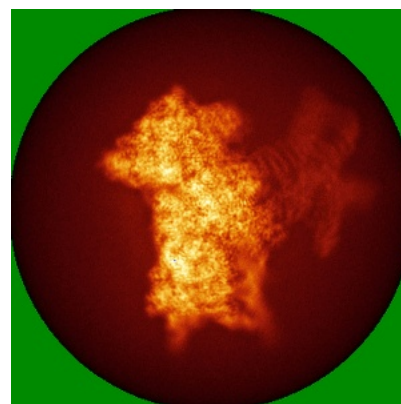
6.4.2 Raw map



X



Y

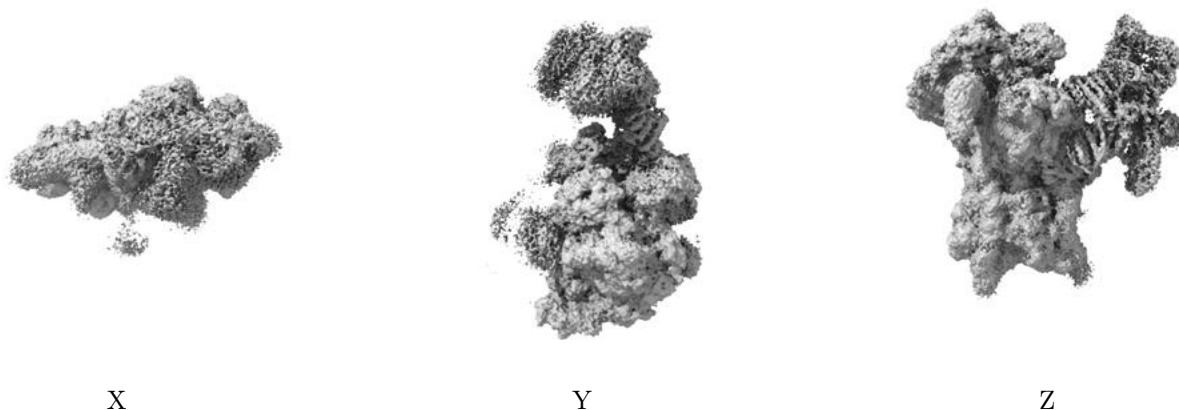


Z

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

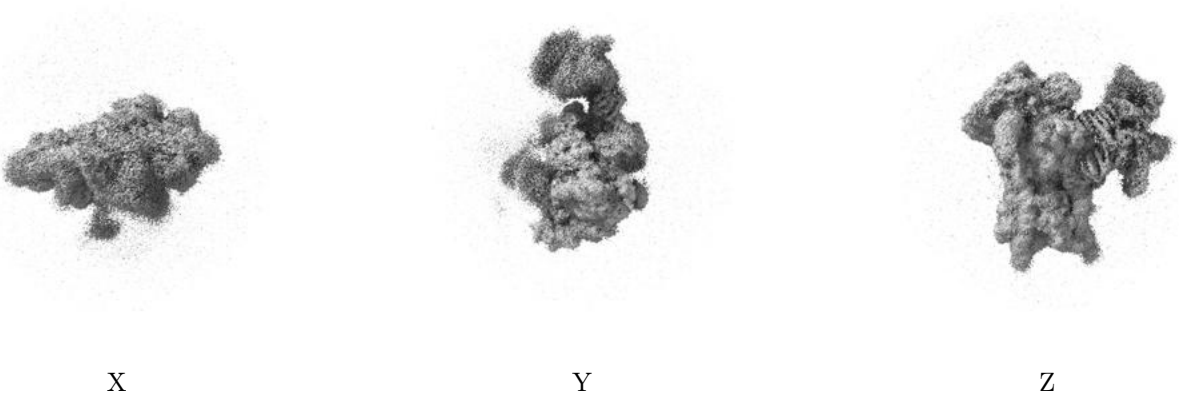
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0102. 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.

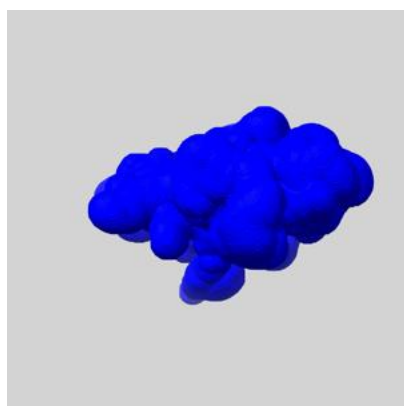
6.6 Mask visualisation [i](#)

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

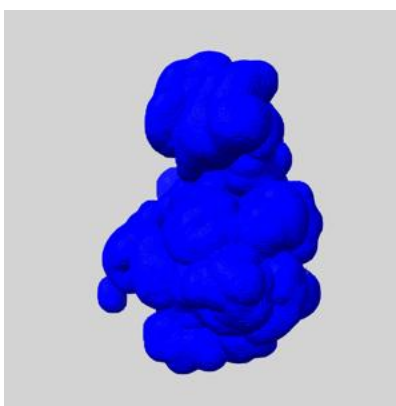
A mask typically either:

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

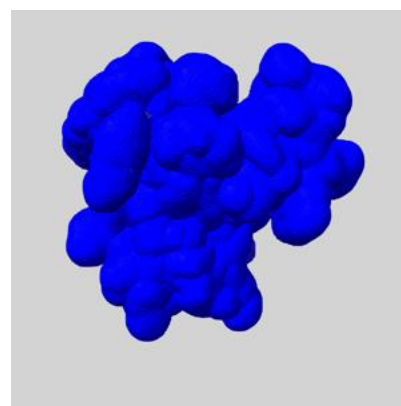
6.6.1 emd_17701_msk_1.map [i](#)



X



Y

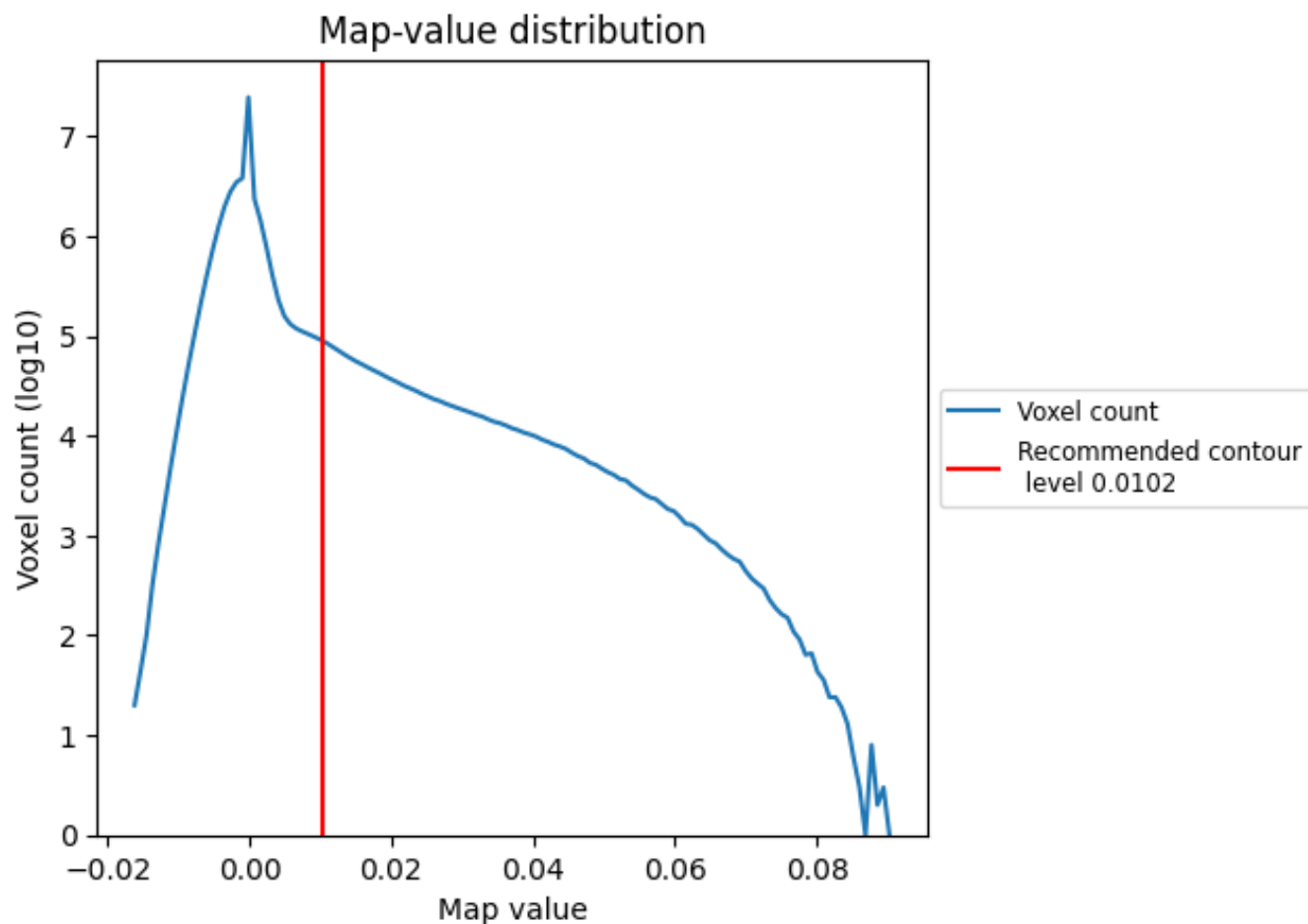


Z

7 Map analysis [i](#)

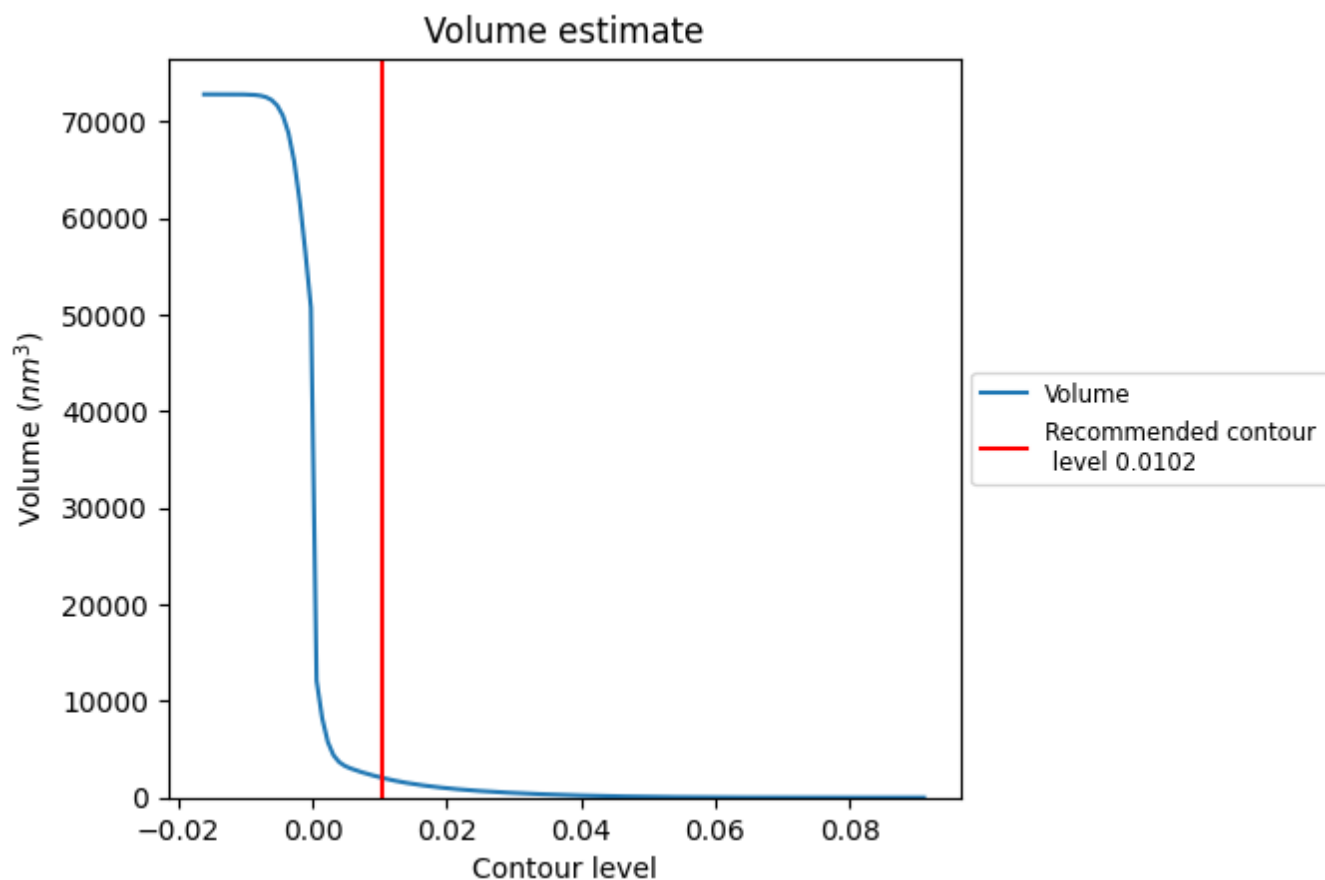
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

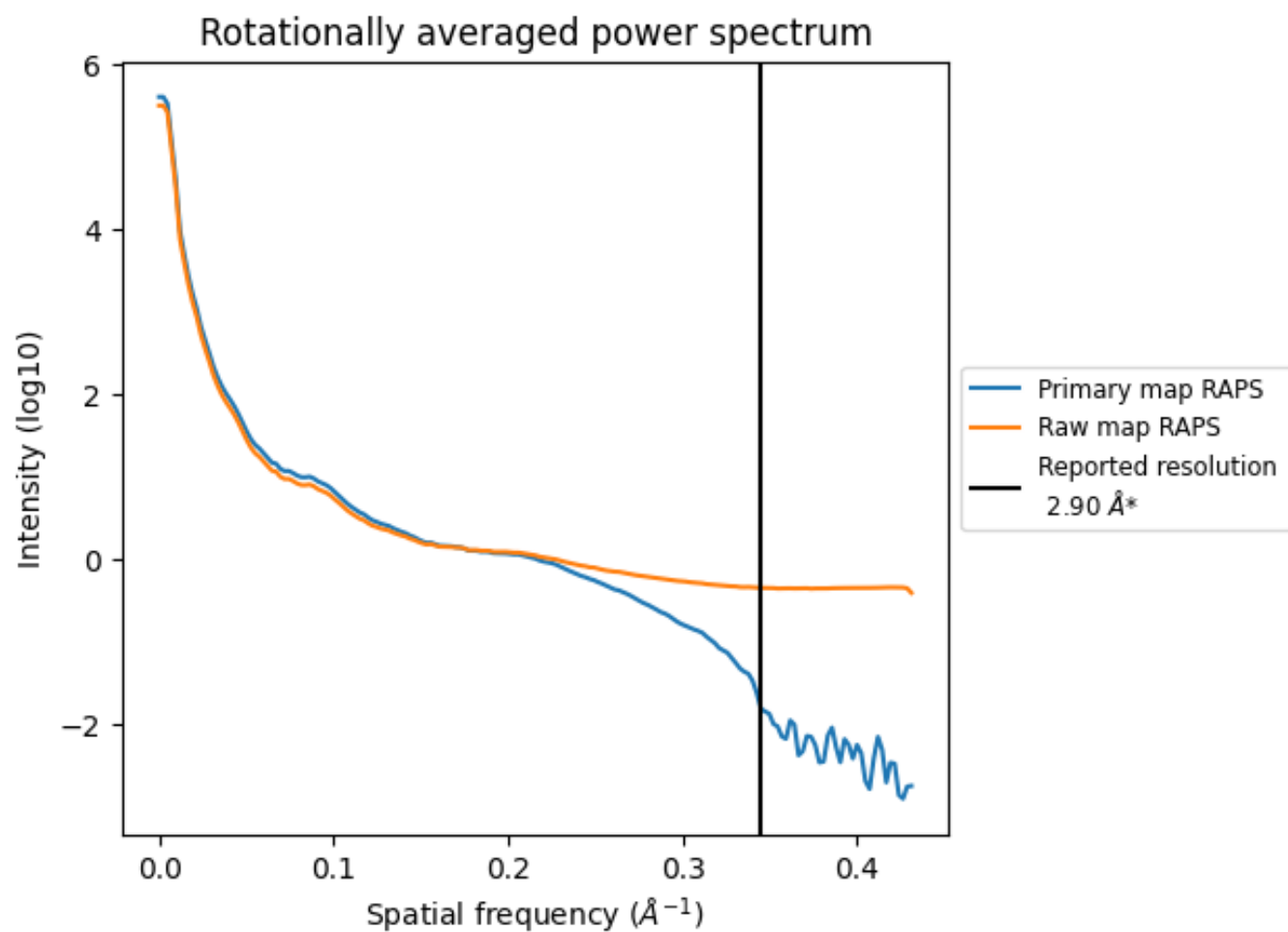
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2072 nm³; this corresponds to an approximate mass of 1872 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 ⓘ

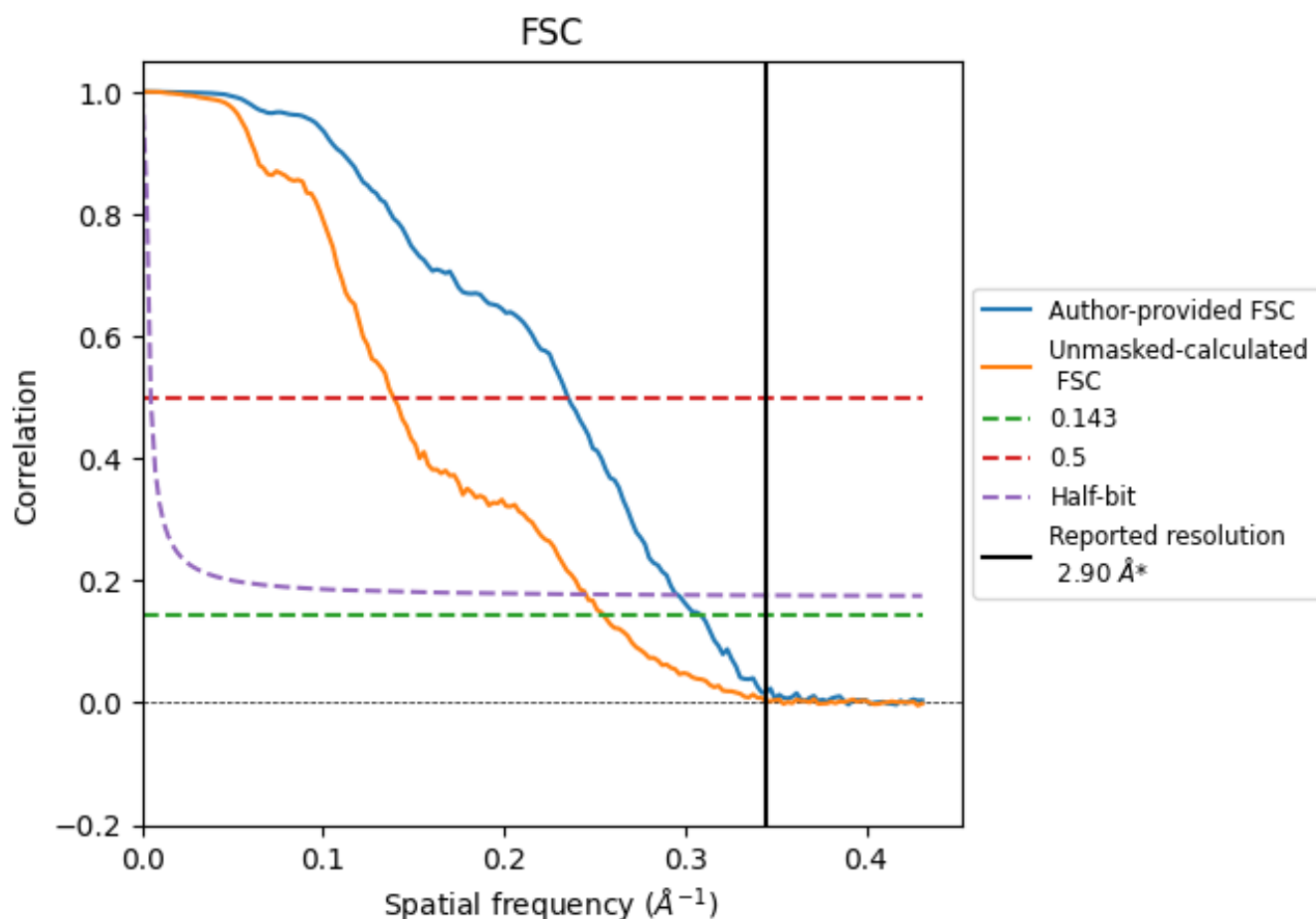


*Reported resolution corresponds to spatial frequency of $0.345 \text{ \AA}^{-1}$

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 0.345 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	3.24	4.25	3.38
Unmasked-calculated*	3.92	7.21	4.08

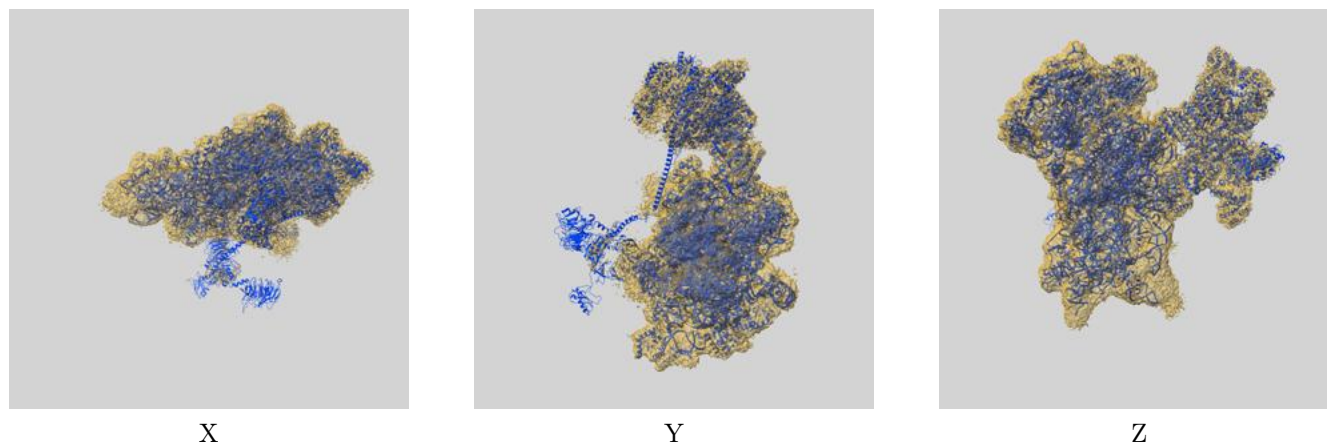
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.24 differs from the reported value 2.9 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.92 differs from the reported value 2.9 by more than 10 %

9 Map-model fit [i](#)

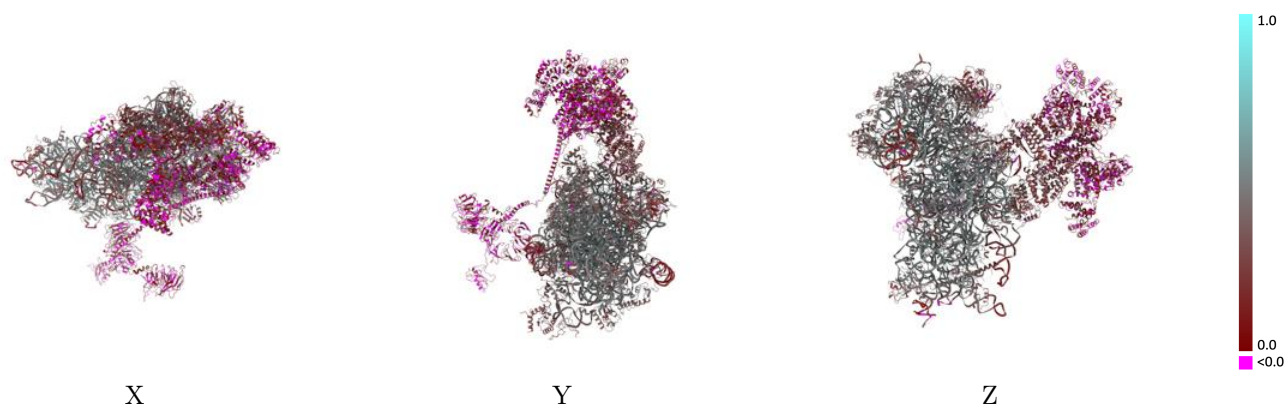
This section contains information regarding the fit between EMDB map EMD-17701 and PDB model 8PJ6. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



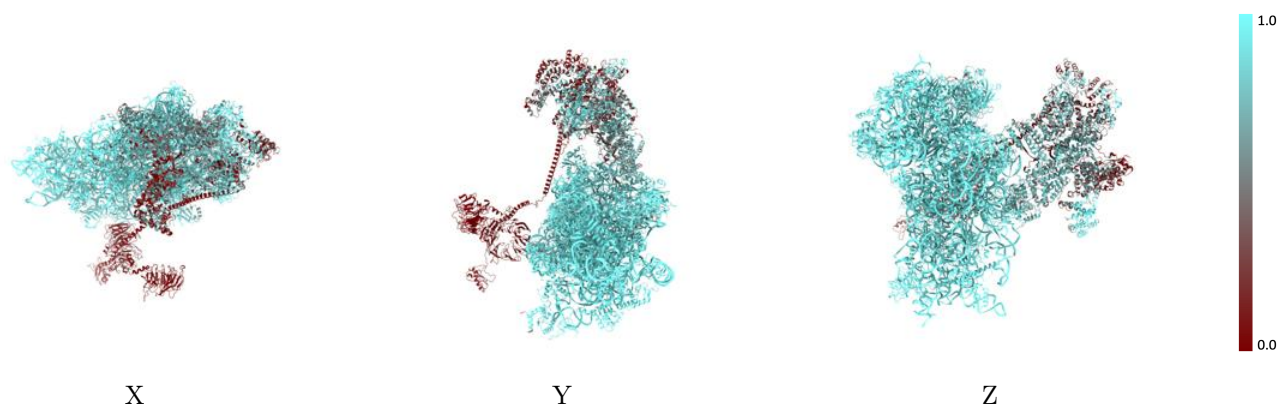
The images above show the 3D surface view of the map at the recommended contour level 0.0102 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



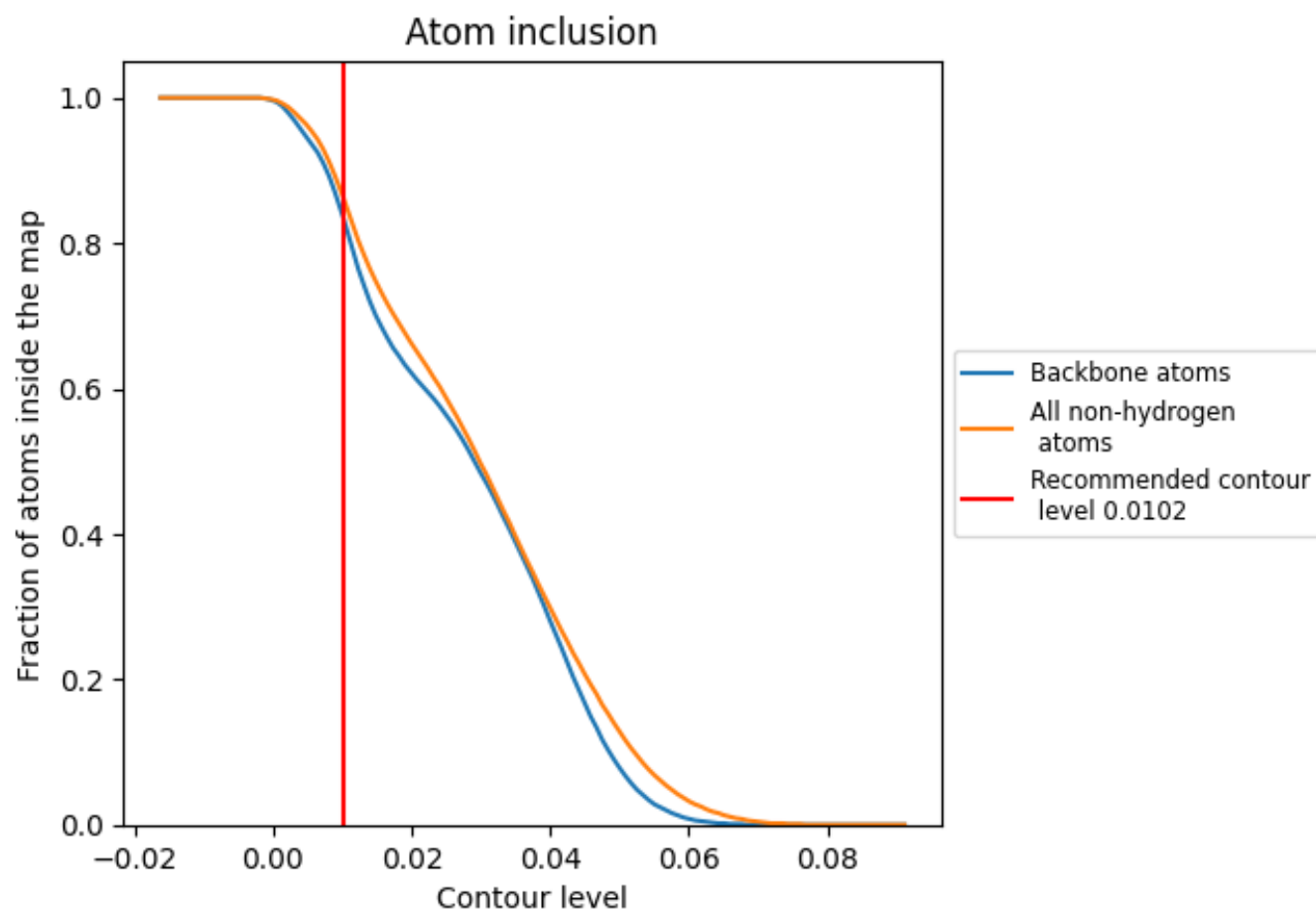
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0102).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 86% 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 (0.0102) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8620	 0.3740
1	 0.0480	 0.1230
2	 0.0000	 0.1160
3	 0.2540	 0.1220
4	 0.6150	 0.1240
5	 0.4660	 0.1170
6	 0.5550	 0.1380
7	 0.7220	 0.2430
8	 0.5440	 0.1010
9	 1.0000	 0.4250
A	 0.9990	 0.4610
B	 0.9950	 0.4940
C	 0.9970	 0.4780
D	 0.9900	 0.4640
E	 0.9990	 0.4890
F	 0.9760	 0.4130
G	 0.9430	 0.3920
H	 0.9760	 0.4540
I	 0.9860	 0.4500
J	 0.9940	 0.4840
K	 0.9780	 0.4460
L	 0.9730	 0.4710
M	 0.9530	 0.4080
N	 0.9800	 0.4530
O	 0.9890	 0.4390
P	 0.9810	 0.4610
Q	 0.9920	 0.4920
R	 0.9990	 0.4510
S	 0.9930	 0.4000
T	 0.9990	 0.4350
V	 0.9880	 0.4590
Y	 0.9970	 0.4770
Z	 0.9650	 0.4390
a	 0.9830	 0.4270
b	 0.9930	 0.4170



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Chain	Atom inclusion	Q-score
c	 0.9910	 0.4260
d	 0.9940	 0.4570
e	 0.9900	 0.4340
f	 0.9920	 0.4300
h	 0.9890	 0.4360
i	 0.9880	 0.5020
k	 0.9960	 0.3130
m	 0.9630	 0.2870
n	 0.9900	 0.4500
o	 0.9110	 0.2080
q	 0.9670	 0.3550
u	 0.5270	 0.2040
v	 0.5880	 0.1420
w	 0.9970	 0.2510
x	 0.8460	 0.2890
y	 0.6840	 0.2590