



## wwPDB EM Validation Summary Report i

Nov 19, 2022 – 10:20 pm GMT

PDB ID : 5K0Y  
EMDB ID : EMD-8190  
Title : m48S late-stage initiation complex, purified from rabbit reticulocytes lysates, displaying eIF2 ternary complex and eIF3 i and g subunits relocated to the intersubunit face  
Authors : Simonetti, A.; Brito Querido, J.; Myasnikov, A.G.; Mancera-Martinez, E.; Renaud, A.; Kuhn, L.; Hashem, Y.  
Deposited on : 2016-05-17  
Resolution : 5.80 Å(reported)  
Based on initial model : 4KZY

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the i symbol.

The types of validation reports are described at  
<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

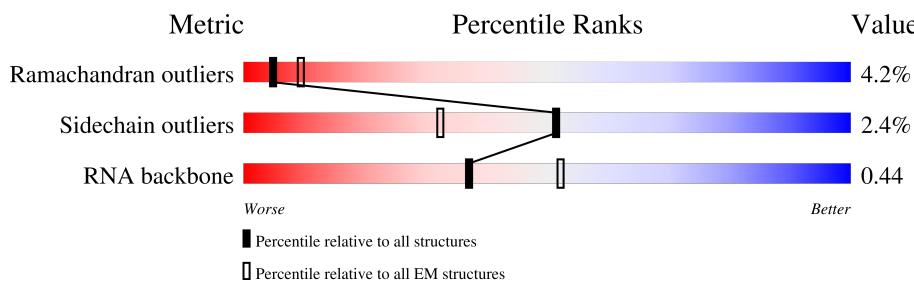
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

# 1 Overall quality at a glance

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

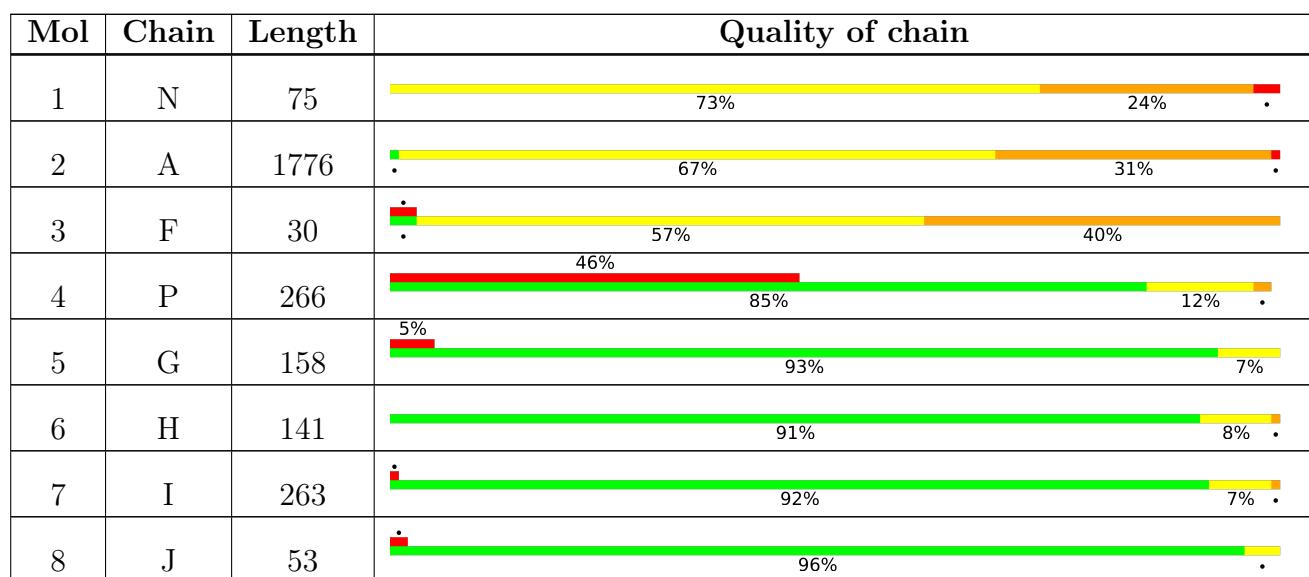
The reported resolution of this entry is 5.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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



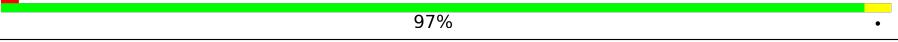
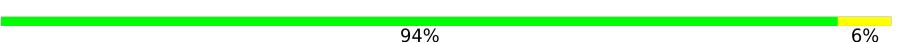
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Mol	Chain	Length	Quality of chain
9	K	182	94% 5% •
10	L	137	91% 8% •
11	M	38	89% 97% •
12	O	77	78% 99% •
13	Q	142	94% 6% •
14	R	141	92% 7% •
15	S	422	75% 92% 7% •
16	T	329	89% 94% 5% •
17	U	191	93% 6% •
18	V	59	7% 92% 8% •
19	W	75	93% 7% •
20	X	190	7% 89% 9% ..
21	Y	84	88% 11% •
22	Z	150	97% •
23	a	129	95% 5% •
24	b	82	82% 17% •
25	c	226	95% •
26	d	17	88% 100% •
27	e	126	6% 96% ..
28	f	208	93% 7% •
29	g	227	94% 6% •
30	h	104	88% 12% •
31	i	215	94% 6% •
32	j	136	93% 5% •
33	k	99	92% 8% •

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Mol	Chain	Length	Quality of chain		
34	l	64		97%	.
35	m	313		92%	7% .
36	n	127		84%	13% .
37	o	206		94%	6%
38	p	71		80%	17% .
39	q	237		94%	6%
40	r	124		90%	10% .
41	s	131		89%	10% .
42	t	98		81%	17% .

## 2 Entry composition i

There are 42 unique types of molecules in this entry. The entry contains 88157 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 tRNA.

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

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	73	C	-	expression tag	REF 655840029
N	74	C	-	expression tag	REF 655840029
N	75	A	-	expression tag	REF 655840029

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	A	1776	37881	16910	6782	12414	1775	0	0

There are 685 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	U	-	expression tag	REF 283837872
A	2	A	-	expression tag	REF 283837872
A	3	C	-	expression tag	REF 283837872
A	4	C	-	expression tag	REF 283837872
A	5	U	-	expression tag	REF 283837872
A	6	G	-	expression tag	REF 283837872
A	7	G	-	expression tag	REF 283837872
A	8	U	-	expression tag	REF 283837872
A	9	U	-	expression tag	REF 283837872
A	10	G	-	expression tag	REF 283837872
A	11	A	-	expression tag	REF 283837872
A	12	U	-	expression tag	REF 283837872
A	13	C	-	expression tag	REF 283837872
A	14	C	-	expression tag	REF 283837872

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Chain	Residue	Modelled	Actual	Comment	Reference
A	15	U	-	expression tag	REF 283837872
A	16	G	-	expression tag	REF 283837872
A	17	C	-	expression tag	REF 283837872
A	18	C	-	expression tag	REF 283837872
A	19	A	-	expression tag	REF 283837872
A	20	G	-	expression tag	REF 283837872
A	21	U	-	expression tag	REF 283837872
A	22	A	-	expression tag	REF 283837872
A	23	G	-	expression tag	REF 283837872
A	24	C	-	expression tag	REF 283837872
A	25	A	-	expression tag	REF 283837872
A	26	U	-	expression tag	REF 283837872
A	27	A	-	expression tag	REF 283837872
A	28	U	-	expression tag	REF 283837872
A	29	G	-	expression tag	REF 283837872
A	30	C	-	expression tag	REF 283837872
A	31	U	-	expression tag	REF 283837872
A	32	U	-	expression tag	REF 283837872
A	33	G	-	expression tag	REF 283837872
A	34	U	-	expression tag	REF 283837872
A	35	C	-	expression tag	REF 283837872
A	36	U	-	expression tag	REF 283837872
A	37	C	-	expression tag	REF 283837872
A	38	A	-	expression tag	REF 283837872
A	39	A	-	expression tag	REF 283837872
A	40	A	-	expression tag	REF 283837872
A	41	G	-	expression tag	REF 283837872
A	42	A	-	expression tag	REF 283837872
A	43	U	-	expression tag	REF 283837872
A	44	U	-	expression tag	REF 283837872
A	45	A	-	expression tag	REF 283837872
A	46	A	-	expression tag	REF 283837872
A	47	G	-	expression tag	REF 283837872
A	48	C	-	expression tag	REF 283837872
A	49	C	-	expression tag	REF 283837872
A	50	A	-	expression tag	REF 283837872
A	51	U	-	expression tag	REF 283837872
A	52	G	-	expression tag	REF 283837872
A	53	C	-	expression tag	REF 283837872
A	54	A	-	expression tag	REF 283837872
A	55	U	-	expression tag	REF 283837872
A	56	G	-	expression tag	REF 283837872

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Chain	Residue	Modelled	Actual	Comment	Reference
A	57	U	-	expression tag	REF 283837872
A	58	C	-	expression tag	REF 283837872
A	59	U	-	expression tag	REF 283837872
A	60	A	-	expression tag	REF 283837872
A	61	A	-	expression tag	REF 283837872
A	62	G	-	expression tag	REF 283837872
A	63	U	-	expression tag	REF 283837872
A	64	A	-	expression tag	REF 283837872
A	65	C	-	expression tag	REF 283837872
A	66	G	-	expression tag	REF 283837872
A	67	C	-	expression tag	REF 283837872
A	68	A	-	expression tag	REF 283837872
A	69	C	-	expression tag	REF 283837872
A	70	G	-	expression tag	REF 283837872
A	71	G	-	expression tag	REF 283837872
A	72	C	-	expression tag	REF 283837872
A	73	C	-	expression tag	REF 283837872
A	74	G	-	expression tag	REF 283837872
A	75	G	-	expression tag	REF 283837872
A	76	U	-	expression tag	REF 283837872
A	77	A	-	expression tag	REF 283837872
A	78	C	-	expression tag	REF 283837872
A	79	A	-	expression tag	REF 283837872
A	80	G	-	expression tag	REF 283837872
A	81	U	-	expression tag	REF 283837872
A	82	G	-	expression tag	REF 283837872
A	83	A	-	expression tag	REF 283837872
A	84	A	-	expression tag	REF 283837872
A	85	A	-	expression tag	REF 283837872
A	86	C	-	expression tag	REF 283837872
A	87	U	-	expression tag	REF 283837872
A	88	G	-	expression tag	REF 283837872
A	89	C	-	expression tag	REF 283837872
A	90	G	-	expression tag	REF 283837872
A	91	A	-	expression tag	REF 283837872
A	92	A	-	expression tag	REF 283837872
A	93	U	-	expression tag	REF 283837872
A	94	G	-	expression tag	REF 283837872
A	95	G	-	expression tag	REF 283837872
A	96	C	-	expression tag	REF 283837872
A	97	U	-	expression tag	REF 283837872
A	98	C	-	expression tag	REF 283837872

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Chain	Residue	Modelled	Actual	Comment	Reference
A	99	A	-	expression tag	REF 283837872
A	100	U	-	expression tag	REF 283837872
A	101	U	-	expression tag	REF 283837872
A	102	A	-	expression tag	REF 283837872
A	103	A	-	expression tag	REF 283837872
A	104	A	-	expression tag	REF 283837872
A	105	U	-	expression tag	REF 283837872
A	106	C	-	expression tag	REF 283837872
A	107	A	-	expression tag	REF 283837872
A	108	G	-	expression tag	REF 283837872
A	109	U	-	expression tag	REF 283837872
A	110	U	-	expression tag	REF 283837872
A	111	A	-	expression tag	REF 283837872
A	112	U	-	expression tag	REF 283837872
A	113	G	-	expression tag	REF 283837872
A	114	G	-	expression tag	REF 283837872
A	115	U	-	expression tag	REF 283837872
A	116	U	-	expression tag	REF 283837872
A	117	C	-	expression tag	REF 283837872
A	118	C	-	expression tag	REF 283837872
A	119	U	-	expression tag	REF 283837872
A	120	U	-	expression tag	REF 283837872
A	121	U	-	expression tag	REF 283837872
A	122	G	-	expression tag	REF 283837872
A	123	G	-	expression tag	REF 283837872
A	124	U	-	expression tag	REF 283837872
A	125	C	-	expression tag	REF 283837872
A	126	G	-	expression tag	REF 283837872
A	127	C	-	expression tag	REF 283837872
A	128	U	-	expression tag	REF 283837872
A	129	C	-	expression tag	REF 283837872
A	130	G	-	expression tag	REF 283837872
A	131	C	-	expression tag	REF 283837872
A	132	U	-	expression tag	REF 283837872
A	133	C	-	expression tag	REF 283837872
A	134	C	-	expression tag	REF 283837872
A	135	U	-	expression tag	REF 283837872
A	136	C	-	expression tag	REF 283837872
A	137	U	-	expression tag	REF 283837872
A	138	C	-	expression tag	REF 283837872
A	139	C	-	expression tag	REF 283837872
A	140	U	-	expression tag	REF 283837872

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Chain	Residue	Modelled	Actual	Comment	Reference
A	141	A	-	expression tag	REF 283837872
A	142	C	-	expression tag	REF 283837872
A	143	U	-	expression tag	REF 283837872
A	144	U	-	expression tag	REF 283837872
A	145	G	-	expression tag	REF 283837872
A	146	G	-	expression tag	REF 283837872
A	147	A	-	expression tag	REF 283837872
A	148	U	-	expression tag	REF 283837872
A	149	A	-	expression tag	REF 283837872
A	150	A	-	expression tag	REF 283837872
A	151	C	-	expression tag	REF 283837872
A	152	U	-	expression tag	REF 283837872
A	153	G	-	expression tag	REF 283837872
A	154	U	-	expression tag	REF 283837872
A	155	G	-	expression tag	REF 283837872
A	156	G	-	expression tag	REF 283837872
A	157	U	-	expression tag	REF 283837872
A	158	A	-	expression tag	REF 283837872
A	159	A	-	expression tag	REF 283837872
A	160	U	-	expression tag	REF 283837872
A	161	U	-	expression tag	REF 283837872
A	162	C	-	expression tag	REF 283837872
A	163	U	-	expression tag	REF 283837872
A	164	A	-	expression tag	REF 283837872
A	165	G	-	expression tag	REF 283837872
A	166	A	-	expression tag	REF 283837872
A	167	G	-	expression tag	REF 283837872
A	168	C	-	expression tag	REF 283837872
A	169	U	-	expression tag	REF 283837872
A	170	A	-	expression tag	REF 283837872
A	171	A	-	expression tag	REF 283837872
A	172	U	-	expression tag	REF 283837872
A	173	A	-	expression tag	REF 283837872
A	174	C	-	expression tag	REF 283837872
A	175	A	-	expression tag	REF 283837872
A	176	U	-	expression tag	REF 283837872
A	177	G	-	expression tag	REF 283837872
A	178	C	-	expression tag	REF 283837872
A	179	C	-	expression tag	REF 283837872
A	180	G	-	expression tag	REF 283837872
A	181	A	-	expression tag	REF 283837872
A	182	C	-	expression tag	REF 283837872

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Chain	Residue	Modelled	Actual	Comment	Reference
A	183	G	-	expression tag	REF 283837872
A	184	G	-	expression tag	REF 283837872
A	185	C	-	expression tag	REF 283837872
A	186	G	-	expression tag	REF 283837872
A	187	C	-	expression tag	REF 283837872
A	188	U	-	expression tag	REF 283837872
A	189	G	-	expression tag	REF 283837872
A	190	A	-	expression tag	REF 283837872
A	191	C	-	expression tag	REF 283837872
A	192	U	-	expression tag	REF 283837872
A	193	C	-	expression tag	REF 283837872
A	194	C	-	expression tag	REF 283837872
A	195	C	-	expression tag	REF 283837872
A	196	U	-	expression tag	REF 283837872
A	197	U	-	expression tag	REF 283837872
A	198	U	-	expression tag	REF 283837872
A	199	G	-	expression tag	REF 283837872
A	200	U	-	expression tag	REF 283837872
A	201	G	-	expression tag	REF 283837872
A	202	U	-	expression tag	REF 283837872
A	203	G	-	expression tag	REF 283837872
A	204	G	-	expression tag	REF 283837872
A	205	G	-	expression tag	REF 283837872
A	206	A	-	expression tag	REF 283837872
A	207	U	-	expression tag	REF 283837872
A	208	G	-	expression tag	REF 283837872
A	209	C	-	expression tag	REF 283837872
A	210	G	-	expression tag	REF 283837872
A	211	U	-	expression tag	REF 283837872
A	212	G	-	expression tag	REF 283837872
A	213	C	-	expression tag	REF 283837872
A	214	A	-	expression tag	REF 283837872
A	215	U	-	expression tag	REF 283837872
A	216	U	-	expression tag	REF 283837872
A	217	U	-	expression tag	REF 283837872
A	218	A	-	expression tag	REF 283837872
A	219	U	-	expression tag	REF 283837872
A	220	C	-	expression tag	REF 283837872
A	221	A	-	expression tag	REF 283837872
A	222	G	-	expression tag	REF 283837872
A	223	A	-	expression tag	REF 283837872
A	224	U	-	expression tag	REF 283837872

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Chain	Residue	Modelled	Actual	Comment	Reference
A	225	C	-	expression tag	REF 283837872
A	226	A	-	expression tag	REF 283837872
A	227	A	-	expression tag	REF 283837872
A	228	A	-	expression tag	REF 283837872
A	229	A	-	expression tag	REF 283837872
A	230	C	-	expression tag	REF 283837872
A	231	C	-	expression tag	REF 283837872
A	232	A	-	expression tag	REF 283837872
A	233	A	-	expression tag	REF 283837872
A	234	C	-	expression tag	REF 283837872
A	235	C	-	expression tag	REF 283837872
A	236	C	-	expression tag	REF 283837872
A	237	G	-	expression tag	REF 283837872
A	238	G	-	expression tag	REF 283837872
A	239	U	-	expression tag	REF 283837872
A	240	C	-	expression tag	REF 283837872
A	241	A	-	expression tag	REF 283837872
A	242	G	-	expression tag	REF 283837872
A	243	C	-	expression tag	REF 283837872
A	267	G	-	expression tag	REF 283837872
A	268	G	-	expression tag	REF 283837872
A	269	C	-	expression tag	REF 283837872
A	270	G	-	expression tag	REF 283837872
A	271	G	-	expression tag	REF 283837872
A	272	C	-	expression tag	REF 283837872
A	273	G	-	expression tag	REF 283837872
A	274	G	-	expression tag	REF 283837872
A	275	C	-	expression tag	REF 283837872
A	276	U	-	expression tag	REF 283837872
A	277	U	-	expression tag	REF 283837872
A	278	U	-	expression tag	REF 283837872
A	279	G	-	expression tag	REF 283837872
A	280	G	-	expression tag	REF 283837872
A	281	U	-	expression tag	REF 283837872
A	282	G	-	expression tag	REF 283837872
A	283	A	-	expression tag	REF 283837872
A	284	C	-	expression tag	REF 283837872
A	285	U	-	expression tag	REF 283837872
A	286	C	-	expression tag	REF 283837872
A	287	U	-	expression tag	REF 283837872
A	288	A	-	expression tag	REF 283837872
A	289	G	-	expression tag	REF 283837872

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Chain	Residue	Modelled	Actual	Comment	Reference
A	290	A	-	expression tag	REF 283837872
A	291	U	-	expression tag	REF 283837872
A	292	A	-	expression tag	REF 283837872
A	293	A	-	expression tag	REF 283837872
A	294	C	-	expression tag	REF 283837872
A	295	C	-	expression tag	REF 283837872
A	296	U	-	expression tag	REF 283837872
A	297	C	-	expression tag	REF 283837872
A	298	G	-	expression tag	REF 283837872
A	299	G	-	expression tag	REF 283837872
A	300	G	-	expression tag	REF 283837872
A	301	C	-	expression tag	REF 283837872
A	302	C	-	expression tag	REF 283837872
A	303	G	-	expression tag	REF 283837872
A	304	A	-	expression tag	REF 283837872
A	305	U	-	expression tag	REF 283837872
A	306	C	-	expression tag	REF 283837872
A	307	G	-	expression tag	REF 283837872
A	308	C	-	expression tag	REF 283837872
A	309	A	-	expression tag	REF 283837872
A	310	G	-	expression tag	REF 283837872
A	311	C	-	expression tag	REF 283837872
A	312	C	-	expression tag	REF 283837872
A	313	C	-	expression tag	REF 283837872
A	314	U	-	expression tag	REF 283837872
A	315	C	-	expression tag	REF 283837872
A	316	C	-	expression tag	REF 283837872
A	317	G	-	expression tag	REF 283837872
A	318	U	-	expression tag	REF 283837872
A	319	G	-	expression tag	REF 283837872
A	320	G	-	expression tag	REF 283837872
A	321	C	-	expression tag	REF 283837872
A	322	G	-	expression tag	REF 283837872
A	323	G	-	expression tag	REF 283837872
A	324	C	-	expression tag	REF 283837872
A	325	G	-	expression tag	REF 283837872
A	326	A	-	expression tag	REF 283837872
A	327	C	-	expression tag	REF 283837872
A	328	G	-	expression tag	REF 283837872
A	329	A	-	expression tag	REF 283837872
A	330	C	-	expression tag	REF 283837872
A	331	C	-	expression tag	REF 283837872

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Chain	Residue	Modelled	Actual	Comment	Reference
A	332	C	-	expression tag	REF 283837872
A	333	A	-	expression tag	REF 283837872
A	334	U	-	expression tag	REF 283837872
A	335	U	-	expression tag	REF 283837872
A	336	C	-	expression tag	REF 283837872
A	337	G	-	expression tag	REF 283837872
A	338	A	-	expression tag	REF 283837872
A	339	A	-	expression tag	REF 283837872
A	340	C	-	expression tag	REF 283837872
A	341	G	-	expression tag	REF 283837872
A	342	U	-	expression tag	REF 283837872
A	343	C	-	expression tag	REF 283837872
A	344	U	-	expression tag	REF 283837872
A	345	G	-	expression tag	REF 283837872
A	346	C	-	expression tag	REF 283837872
A	347	C	-	expression tag	REF 283837872
A	348	C	-	expression tag	REF 283837872
A	349	U	-	expression tag	REF 283837872
A	350	A	-	expression tag	REF 283837872
A	351	U	-	expression tag	REF 283837872
A	352	C	-	expression tag	REF 283837872
A	353	A	-	expression tag	REF 283837872
A	354	A	-	expression tag	REF 283837872
A	355	C	-	expression tag	REF 283837872
A	356	U	-	expression tag	REF 283837872
A	357	U	-	expression tag	REF 283837872
A	358	U	-	expression tag	REF 283837872
A	359	C	-	expression tag	REF 283837872
A	360	G	-	expression tag	REF 283837872
A	361	A	-	expression tag	REF 283837872
A	362	U	-	expression tag	REF 283837872
A	363	G	-	expression tag	REF 283837872
A	364	G	-	expression tag	REF 283837872
A	365	U	-	expression tag	REF 283837872
A	366	A	-	expression tag	REF 283837872
A	367	G	-	expression tag	REF 283837872
A	368	U	-	expression tag	REF 283837872
A	369	C	-	expression tag	REF 283837872
A	370	G	-	expression tag	REF 283837872
A	371	C	-	expression tag	REF 283837872
A	372	C	-	expression tag	REF 283837872
A	373	G	-	expression tag	REF 283837872

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Chain	Residue	Modelled	Actual	Comment	Reference
A	374	U	-	expression tag	REF 283837872
A	375	G	-	expression tag	REF 283837872
A	376	C	-	expression tag	REF 283837872
A	377	C	-	expression tag	REF 283837872
A	378	U	-	expression tag	REF 283837872
A	379	A	-	expression tag	REF 283837872
A	380	C	-	expression tag	REF 283837872
A	381	C	-	expression tag	REF 283837872
A	382	A	-	expression tag	REF 283837872
A	383	U	-	expression tag	REF 283837872
A	384	G	-	expression tag	REF 283837872
A	385	G	-	expression tag	REF 283837872
A	386	U	-	expression tag	REF 283837872
A	387	G	-	expression tag	REF 283837872
A	388	A	-	expression tag	REF 283837872
A	389	C	-	expression tag	REF 283837872
A	390	C	-	expression tag	REF 283837872
A	391	A	-	expression tag	REF 283837872
A	392	C	-	expression tag	REF 283837872
A	393	G	-	expression tag	REF 283837872
A	394	G	-	expression tag	REF 283837872
A	395	G	-	expression tag	REF 283837872
A	396	U	-	expression tag	REF 283837872
A	397	G	-	expression tag	REF 283837872
A	398	A	-	expression tag	REF 283837872
A	399	C	-	expression tag	REF 283837872
A	400	G	-	expression tag	REF 283837872
A	401	G	-	expression tag	REF 283837872
A	402	G	-	expression tag	REF 283837872
A	403	G	-	expression tag	REF 283837872
A	404	A	-	expression tag	REF 283837872
A	405	A	-	expression tag	REF 283837872
A	406	U	-	expression tag	REF 283837872
A	407	C	-	expression tag	REF 283837872
A	408	A	-	expression tag	REF 283837872
A	409	G	-	expression tag	REF 283837872
A	410	G	-	expression tag	REF 283837872
A	411	G	-	expression tag	REF 283837872
A	412	U	-	expression tag	REF 283837872
A	413	U	-	expression tag	REF 283837872
A	414	C	-	expression tag	REF 283837872
A	415	G	-	expression tag	REF 283837872

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Chain	Residue	Modelled	Actual	Comment	Reference
A	416	A	-	expression tag	REF 283837872
A	417	U	-	expression tag	REF 283837872
A	418	U	-	expression tag	REF 283837872
A	419	C	-	expression tag	REF 283837872
A	420	C	-	expression tag	REF 283837872
A	421	G	-	expression tag	REF 283837872
A	422	G	-	expression tag	REF 283837872
A	423	A	-	expression tag	REF 283837872
A	424	G	-	expression tag	REF 283837872
A	425	A	-	expression tag	REF 283837872
A	426	G	-	expression tag	REF 283837872
A	427	G	-	expression tag	REF 283837872
A	428	G	-	expression tag	REF 283837872
A	429	A	-	expression tag	REF 283837872
A	430	G	-	expression tag	REF 283837872
A	431	C	-	expression tag	REF 283837872
A	432	C	-	expression tag	REF 283837872
A	433	U	-	expression tag	REF 283837872
A	434	G	-	expression tag	REF 283837872
A	435	A	-	expression tag	REF 283837872
A	436	G	-	expression tag	REF 283837872
A	437	A	-	expression tag	REF 283837872
A	438	A	-	expression tag	REF 283837872
A	439	A	-	expression tag	REF 283837872
A	440	C	-	expression tag	REF 283837872
A	441	G	-	expression tag	REF 283837872
A	442	G	-	expression tag	REF 283837872
A	443	C	-	expression tag	REF 283837872
A	444	U	-	expression tag	REF 283837872
A	445	A	-	expression tag	REF 283837872
A	446	C	-	expression tag	REF 283837872
A	447	C	-	expression tag	REF 283837872
A	448	A	-	expression tag	REF 283837872
A	449	C	-	expression tag	REF 283837872
A	450	A	-	expression tag	REF 283837872
A	451	U	-	expression tag	REF 283837872
A	452	C	-	expression tag	REF 283837872
A	453	C	-	expression tag	REF 283837872
A	454	A	-	expression tag	REF 283837872
A	455	A	-	expression tag	REF 283837872
A	456	G	-	expression tag	REF 283837872
A	457	G	-	expression tag	REF 283837872

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Chain	Residue	Modelled	Actual	Comment	Reference
A	458	A	-	expression tag	REF 283837872
A	459	A	-	expression tag	REF 283837872
A	460	G	-	expression tag	REF 283837872
A	461	G	-	expression tag	REF 283837872
A	462	C	-	expression tag	REF 283837872
A	463	A	-	expression tag	REF 283837872
A	464	G	-	expression tag	REF 283837872
A	465	C	-	expression tag	REF 283837872
A	466	A	-	expression tag	REF 283837872
A	467	G	-	expression tag	REF 283837872
A	468	G	-	expression tag	REF 283837872
A	469	C	-	expression tag	REF 283837872
A	470	G	-	expression tag	REF 283837872
A	471	C	-	expression tag	REF 283837872
A	472	G	-	expression tag	REF 283837872
A	473	C	-	expression tag	REF 283837872
A	474	A	-	expression tag	REF 283837872
A	475	A	-	expression tag	REF 283837872
A	476	A	-	expression tag	REF 283837872
A	477	U	-	expression tag	REF 283837872
A	478	U	-	expression tag	REF 283837872
A	479	A	-	expression tag	REF 283837872
A	480	C	-	expression tag	REF 283837872
A	481	C	-	expression tag	REF 283837872
A	482	C	-	expression tag	REF 283837872
A	483	A	-	expression tag	REF 283837872
A	484	C	-	expression tag	REF 283837872
A	485	U	-	expression tag	REF 283837872
A	486	C	-	expression tag	REF 283837872
A	487	C	-	expression tag	REF 283837872
A	488	C	-	expression tag	REF 283837872
A	489	G	-	expression tag	REF 283837872
A	490	A	-	expression tag	REF 283837872
A	491	C	-	expression tag	REF 283837872
A	492	C	-	expression tag	REF 283837872
A	493	C	-	expression tag	REF 283837872
A	494	G	-	expression tag	REF 283837872
A	495	G	-	expression tag	REF 283837872
A	496	G	-	expression tag	REF 283837872
A	497	G	-	expression tag	REF 283837872
A	498	A	-	expression tag	REF 283837872
A	499	G	-	expression tag	REF 283837872

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Chain	Residue	Modelled	Actual	Comment	Reference
A	500	G	-	expression tag	REF 283837872
A	501	U	-	expression tag	REF 283837872
A	502	A	-	expression tag	REF 283837872
A	503	G	-	expression tag	REF 283837872
A	504	U	-	expression tag	REF 283837872
A	505	G	-	expression tag	REF 283837872
A	506	A	-	expression tag	REF 283837872
A	507	C	-	expression tag	REF 283837872
A	508	G	-	expression tag	REF 283837872
A	509	A	-	expression tag	REF 283837872
A	510	A	-	expression tag	REF 283837872
A	511	A	-	expression tag	REF 283837872
A	512	A	-	expression tag	REF 283837872
A	513	A	-	expression tag	REF 283837872
A	514	U	-	expression tag	REF 283837872
A	515	A	-	expression tag	REF 283837872
A	516	A	-	expression tag	REF 283837872
A	517	C	-	expression tag	REF 283837872
A	518	A	-	expression tag	REF 283837872
A	519	A	-	expression tag	REF 283837872
A	520	U	-	expression tag	REF 283837872
A	521	A	-	expression tag	REF 283837872
A	522	C	-	expression tag	REF 283837872
A	523	A	-	expression tag	REF 283837872
A	524	G	-	expression tag	REF 283837872
A	525	G	-	expression tag	REF 283837872
A	526	A	-	expression tag	REF 283837872
A	527	C	-	expression tag	REF 283837872
A	528	U	-	expression tag	REF 283837872
A	529	C	-	expression tag	REF 283837872
A	530	U	-	expression tag	REF 283837872
A	531	U	-	expression tag	REF 283837872
A	532	U	-	expression tag	REF 283837872
A	533	C	-	expression tag	REF 283837872
A	534	G	-	expression tag	REF 283837872
A	535	A	-	expression tag	REF 283837872
A	536	G	-	expression tag	REF 283837872
A	537	G	-	expression tag	REF 283837872
A	538	C	-	expression tag	REF 283837872
A	539	C	-	expression tag	REF 283837872
A	540	C	-	expression tag	REF 283837872
A	541	U	-	expression tag	REF 283837872

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Chain	Residue	Modelled	Actual	Comment	Reference
A	542	G	-	expression tag	REF 283837872
A	543	U	-	expression tag	REF 283837872
A	544	A	-	expression tag	REF 283837872
A	545	A	-	expression tag	REF 283837872
A	546	U	-	expression tag	REF 283837872
A	547	U	-	expression tag	REF 283837872
A	548	G	-	expression tag	REF 283837872
A	549	G	-	expression tag	REF 283837872
A	550	A	-	expression tag	REF 283837872
A	551	A	-	expression tag	REF 283837872
A	552	U	-	expression tag	REF 283837872
A	553	G	-	expression tag	REF 283837872
A	554	A	-	expression tag	REF 283837872
A	555	G	-	expression tag	REF 283837872
A	556	U	-	expression tag	REF 283837872
A	557	C	-	expression tag	REF 283837872
A	558	C	-	expression tag	REF 283837872
A	559	A	-	expression tag	REF 283837872
A	560	C	-	expression tag	REF 283837872
A	561	U	-	expression tag	REF 283837872
A	562	U	-	expression tag	REF 283837872
A	563	U	-	expression tag	REF 283837872
A	564	A	-	expression tag	REF 283837872
A	565	A	-	expression tag	REF 283837872
A	566	A	-	expression tag	REF 283837872
A	567	U	-	expression tag	REF 283837872
A	568	C	-	expression tag	REF 283837872
A	569	C	-	expression tag	REF 283837872
A	570	U	-	expression tag	REF 283837872
A	571	U	-	expression tag	REF 283837872
A	572	U	-	expression tag	REF 283837872
A	573	A	-	expression tag	REF 283837872
A	574	A	-	expression tag	REF 283837872
A	575	C	-	expression tag	REF 283837872
A	576	G	-	expression tag	REF 283837872
A	577	A	-	expression tag	REF 283837872
A	578	G	-	expression tag	REF 283837872
A	579	G	-	expression tag	REF 283837872
A	580	A	-	expression tag	REF 283837872
A	581	U	-	expression tag	REF 283837872
A	582	C	-	expression tag	REF 283837872
A	583	C	-	expression tag	REF 283837872

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Chain	Residue	Modelled	Actual	Comment	Reference
A	584	A	-	expression tag	REF 283837872
A	585	U	-	expression tag	REF 283837872
A	586	U	-	expression tag	REF 283837872
A	587	G	-	expression tag	REF 283837872
A	588	G	-	expression tag	REF 283837872
A	589	A	-	expression tag	REF 283837872
A	590	G	-	expression tag	REF 283837872
A	591	G	-	expression tag	REF 283837872
A	592	G	-	expression tag	REF 283837872
A	593	C	-	expression tag	REF 283837872
A	594	A	-	expression tag	REF 283837872
A	595	A	-	expression tag	REF 283837872
A	596	G	-	expression tag	REF 283837872
A	597	U	-	expression tag	REF 283837872
A	598	C	-	expression tag	REF 283837872
A	599	U	-	expression tag	REF 283837872
A	600	G	-	expression tag	REF 283837872
A	601	G	-	expression tag	REF 283837872
A	602	U	-	expression tag	REF 283837872
A	603	C	-	expression tag	REF 283837872
A	604	G	-	expression tag	REF 283837872
A	605	C	-	expression tag	REF 283837872
A	606	A	-	expression tag	REF 283837872
A	607	G	-	expression tag	REF 283837872
A	608	C	-	expression tag	REF 283837872
A	609	A	-	expression tag	REF 283837872
A	610	G	-	expression tag	REF 283837872
A	611	C	-	expression tag	REF 283837872
A	612	C	-	expression tag	REF 283837872
A	613	G	-	expression tag	REF 283837872
A	614	C	-	expression tag	REF 283837872
A	615	G	-	expression tag	REF 283837872
A	616	G	-	expression tag	REF 283837872
A	617	U	-	expression tag	REF 283837872
A	618	A	-	expression tag	REF 283837872
A	619	A	-	expression tag	REF 283837872
A	620	U	-	expression tag	REF 283837872
A	621	U	-	expression tag	REF 283837872
A	622	C	-	expression tag	REF 283837872
A	623	C	-	expression tag	REF 283837872
A	624	A	-	expression tag	REF 283837872
A	625	G	-	expression tag	REF 283837872

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Chain	Residue	Modelled	Actual	Comment	Reference
A	626	C	-	expression tag	REF 283837872
A	627	U	-	expression tag	REF 283837872
A	628	C	-	expression tag	REF 283837872
A	629	C	-	expression tag	REF 283837872
A	630	A	-	expression tag	REF 283837872
A	631	A	-	expression tag	REF 283837872
A	632	U	-	expression tag	REF 283837872
A	633	A	-	expression tag	REF 283837872
A	634	G	-	expression tag	REF 283837872
A	635	C	-	expression tag	REF 283837872
A	636	G	-	expression tag	REF 283837872
A	637	U	-	expression tag	REF 283837872
A	638	A	-	expression tag	REF 283837872
A	639	U	-	expression tag	REF 283837872
A	640	A	-	expression tag	REF 283837872
A	641	U	-	expression tag	REF 283837872
A	642	U	-	expression tag	REF 283837872
A	643	A	-	expression tag	REF 283837872
A	644	A	-	expression tag	REF 283837872
A	645	A	-	expression tag	REF 283837872
A	646	G	-	expression tag	REF 283837872
A	647	U	-	expression tag	REF 283837872
A	648	U	-	expression tag	REF 283837872
A	649	G	-	expression tag	REF 283837872
A	650	C	-	expression tag	REF 283837872
A	651	U	-	expression tag	REF 283837872
A	652	G	-	expression tag	REF 283837872
A	653	C	-	expression tag	REF 283837872
A	654	A	-	expression tag	REF 283837872
A	655	G	-	expression tag	REF 283837872
A	656	U	-	expression tag	REF 283837872
A	657	U	-	expression tag	REF 283837872
A	658	A	-	expression tag	REF 283837872
A	659	A	-	expression tag	REF 283837872
A	660	A	-	expression tag	REF 283837872
A	661	A	-	expression tag	REF 283837872
A	662	A	-	expression tag	REF 283837872
A	663	G	-	expression tag	REF 283837872
A	664	C	-	expression tag	REF 283837872
A	665	U	-	expression tag	REF 283837872
A	666	C	-	expression tag	REF 283837872
A	667	G	-	expression tag	REF 283837872

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Chain	Residue	Modelled	Actual	Comment	Reference
A	668	U	-	expression tag	REF 283837872
A	669	A	-	expression tag	REF 283837872
A	670	G	-	expression tag	REF 283837872
A	671	U	-	expression tag	REF 283837872
A	672	U	-	expression tag	REF 283837872
A	673	G	-	expression tag	REF 283837872
A	674	G	-	expression tag	REF 283837872
A	675	A	-	expression tag	REF 283837872
A	676	U	-	expression tag	REF 283837872
A	677	C	-	expression tag	REF 283837872
A	678	U	-	expression tag	REF 283837872
A	679	U	-	expression tag	REF 283837872
A	683	G	-	expression tag	REF 283837872
A	684	A	-	expression tag	REF 283837872
A	685	G	-	expression tag	REF 283837872
A	686	G	-	expression tag	REF 283837872
A	687	G	-	expression tag	REF 283837872
A	730	C	-	expression tag	REF 283837872
A	731	C	-	expression tag	REF 283837872
A	732	C	-	expression tag	REF 283837872
A	733	G	-	expression tag	REF 283837872
A	734	C	-	expression tag	REF 283837872
A	735	C	-	expression tag	REF 283837872
A	736	C	-	expression tag	REF 283837872
A	744	C	-	expression tag	REF 283837872
A	745	U	-	expression tag	REF 283837872
A	746	C	-	expression tag	REF 283837872
A	747	G	-	expression tag	REF 283837872
A	748	G	-	expression tag	REF 283837872
A	749	C	-	expression tag	REF 283837872
A	750	G	-	expression tag	REF 283837872
A	751	C	-	expression tag	REF 283837872
A	752	C	-	expression tag	REF 283837872
A	753	C	-	expression tag	REF 283837872
A	754	C	-	expression tag	REF 283837872
A	755	C	-	expression tag	REF 283837872
A	756	U	-	expression tag	REF 283837872
A	757	C	-	expression tag	REF 283837872
A	758	G	-	expression tag	REF 283837872
A	759	A	-	expression tag	REF 283837872
A	760	U	-	expression tag	REF 283837872

- Molecule 3 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	30	Total	C	N	O	P	0	0

- Molecule 4 is a protein called Eukaryotic translation initiation factor 2 subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	P	266	Total	C	N	O	S	0	0

- Molecule 5 is a protein called ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	158	Total	C	N	O	S	0	0

- Molecule 6 is a protein called ribosomal protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	H	141	Total	C	N	O	S	0	0

- Molecule 7 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	263	Total	C	N	O	S	0	0

- Molecule 8 is a protein called ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	53	Total	C	N	O	S	0	0

- Molecule 9 is a protein called Ribosomal protein S9 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	182	Total	C	N	O	S	0	0

- Molecule 10 is a protein called ribosomal protein uS13.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	L	137	Total C	N	O	S	0	0
			1140	714	231	194	1	

- Molecule 11 is a protein called Eukaryotic translation initiation factor 3 subunit G.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	M	38	Total C	N	O	S	0	0
			288	177	45	64	2	

- Molecule 12 is a protein called Eukaryotic translation initiation factor 3 subunit G.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	O	77	Total C	N	O		0	0
			614	388	110	116		

- Molecule 13 is a protein called ribosomal protein uS12.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	Q	142	Total C	N	O	S	0	0
			1107	698	220	185	4	

- Molecule 14 is a protein called ribosomal protein eS19.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	R	141	Total C	N	O	S	0	0
			1113	701	213	196	3	

- Molecule 15 is a protein called eukaryotic initiation factor 2 Gamma subunit (eIF2-Gamma).

Mol	Chain	Residues	Atoms				AltConf	Trace
15	S	422	Total C	N	O	S	0	0
			3214	2044	561	592	17	

- Molecule 16 is a protein called Eukaryotic translation initiation factor 3 subunit I.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	T	329	Total C	N	O	S	0	0
			2605	1640	447	503	15	

- Molecule 17 is a protein called ribosomal protein uS7.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	U	191	Total	C 1509	N 943	O 286	S 273	0 7

- Molecule 18 is a protein called ribosomal protein eS30.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	V	59	Total	C 473	N 293	O 104	S 75	0 1

- Molecule 19 is a protein called ribosomal protein eS25.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	W	75	Total	C 599	N 382	O 111	S 105	0 1

- Molecule 20 is a protein called ribosomal protein eS7.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	X	190	Total	C 1530	N 975	O 281	S 273	0 1

- Molecule 21 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	Y	84	Total	C 659	N 413	O 122	S 116	0 8

- Molecule 22 is a protein called ribosomal protein uS15.

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

- Molecule 23 is a protein called ribosomal protein uS8.

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

- Molecule 24 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	b	82	Total	C	N	O	S	0	0

- Molecule 25 is a protein called ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	c	226	Total	C	N	O	S	0	0

- Molecule 26 is a protein called eukaryotic initiation factor 2 subunit Beta (eIF2-Beta).

Mol	Chain	Residues	Atoms					AltConf	Trace
26	d	17	Total	C	N	O	S	0	0

- Molecule 27 is a protein called ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	e	126	Total	C	N	O	S	0	0

- Molecule 28 is a protein called ribosomal protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	f	208	Total	C	N	O	S	0	0

- Molecule 29 is a protein called ribosomal protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	g	227	Total	C	N	O	S	0	0

- Molecule 30 is a protein called ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	h	104	Total	C	N	O	S	0	0

- Molecule 31 is a protein called ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	i	215	1742	1107	309	311	15	0	0

- Molecule 32 is a protein called ribosomal protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	j	136	1016	621	199	190	6	0	0

- Molecule 33 is a protein called ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	k	99	790	491	162	131	6	0	0

- Molecule 34 is a protein called ribosomal protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	l	64	507	308	102	95	2	0	0

- Molecule 35 is a protein called ribosomal protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	m	313	2437	1535	424	466	12	0	0

- Molecule 36 is a protein called ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	n	127	1061	673	201	180	7	0	0

- Molecule 37 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	o	206	1680	1054	329	292	5	0	0

- Molecule 38 is a protein called ribosomal protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	p	71	Total	C	N	O	S	0	0

- Molecule 39 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	q	237	Total	C	N	O	S	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	r	124	Total	C	N	O	S	0	0

- Molecule 41 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	s	131	Total	C	N	O	S	0	0

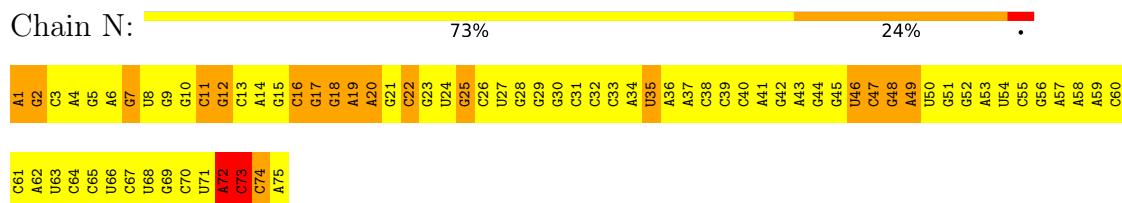
- Molecule 42 is a protein called ribosomal protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	t	98	Total	C	N	O	S	0	0

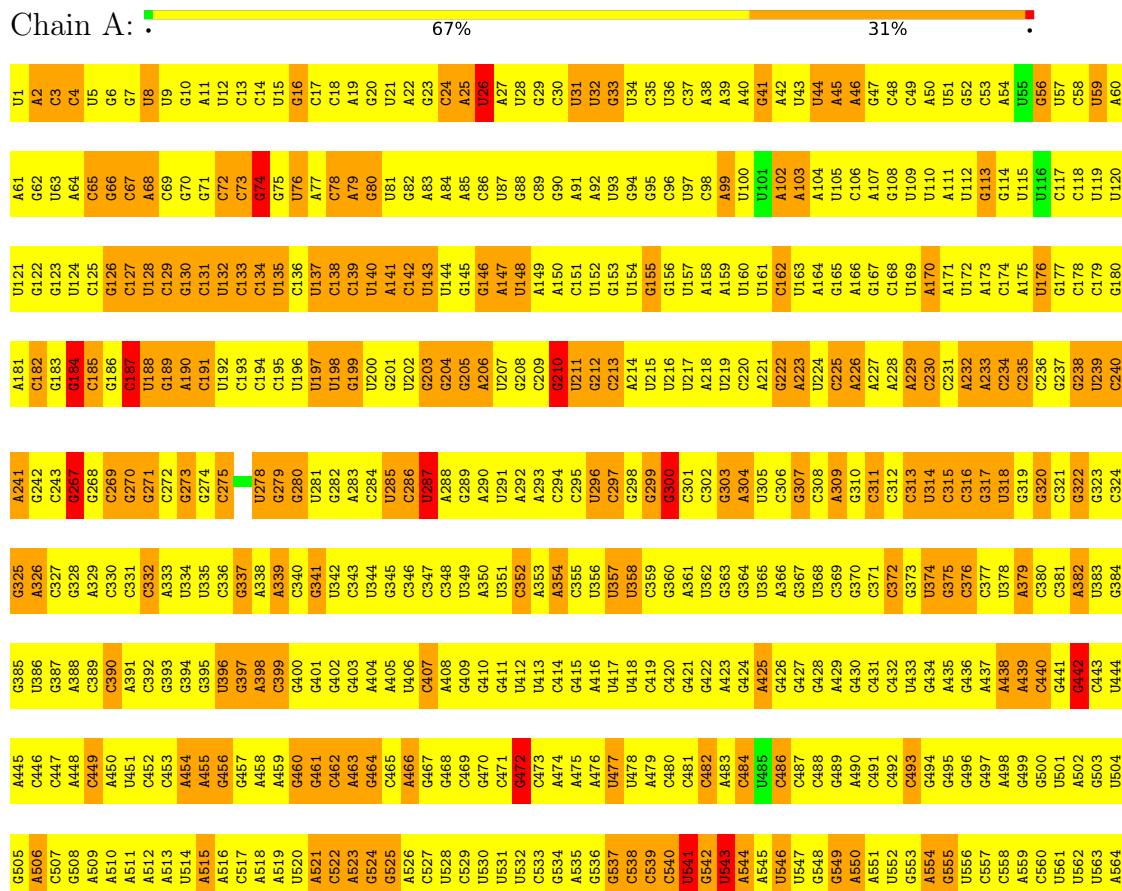
### 3 Residue-property plots

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: tRNA



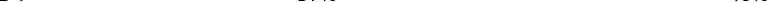
- Molecule 2: 18S ribosomal RNA



G1649	G1469	A1529	A1289	C1049	A1169	A1109	A809	C889	G889
C1650	C1530	U1530	C1410	C1350	A1470	A1170	U1110	C930	G930
G1651	C1531	U1531	C1411	C1351	A1471	C1171	C1231	A1050	C990
C1652	A1532	U1532	A1472	C1352	A1473	C1172	C1232	C1233	A1051
G1653	C1533	U1533	C1413	A1353	C1234	C1173	C1113	C1053	A991
U1554	C1534	U1534	C1414	A1354	C1235	C1174	C1114	A1054	A994
C1655	G1535	G1535	C1415	A1355	C1236	C1175	C1115	C1055	G995
A1556	C1536	U1536	A1475	C1416	A1482	C1176	C1116	A1056	C996
C1657	A1537	U1537	A1477	A1417	C1237	A1177	C1117	A1057	A997
A1558	C1538	U1538	C1418	A1358	C1238	A1178	A1118	A1058	A998
A1659	C1539	A1479	C1419	A1359	C1239	A1179	C1119	C1059	U999
G1660	A1540	U1540	C1420	C1360	C1240	C1180	C1120	A1060	A940
C1661	G1541	G1601	A1481	C1421	C1361	C1181	C1121	A1061	G1001
C1662	A1542	C1542	A1482	A1422	C1362	C1182	C1122	C1062	A942
C1663	A1543	U1603	C1483	C1423	C1363	C1183	C1123	C1063	A943
G1664	A1544	C1604	A1484	A1424	C1364	C1184	C1124	A1064	C944
C1665	A1545	C1605	A1485	C1425	C1365	C1185	C1125	A1065	G945
G1666	A1546	C1606	A1486	C1426	C1366	C1186	C1126	A1066	A946
C1667	A1547	C1607	A1487	A1427	C1367	C1187	C1127	A1067	C947
C1668	A1548	C1608	A1488	C1428	C1368	C1188	C1128	A1068	A948
C1669	A1549	C1609	A1489	C1429	C1369	C1189	C1129	A1069	C949
C1670	A1550	C1610	A1490	C1430	C1370	C1190	C1130	C1070	A1010
A1671	C1551	A1491	C1431	C1371	C1366	C1191	C1131	A951	A951
C1672	A1552	C1612	A1492	C1432	C1372	C1192	C1132	C1072	A1012
A1673	C1553	C1613	C1493	C1433	C1373	C1193	C1133	A1073	A1013
A1674	A1614	A1674	A1494	A1434	C1374	C1194	C1134	C1074	A1014
G1675	A1675	A1675	C1495	A1435	C1375	C1195	C1135	C1075	C1015
C1676	A1556	C1556	A1556	A1436	C1376	C1196	C1136	A1076	A1016
C1677	C1677	C1677	A1497	A1437	C1377	C1197	C1137	C1077	C1017
C1678	A1618	C1558	C1498	C1438	C1378	C1198	C1138	C1078	A1018
C1679	A1619	C1559	C1499	C1439	C1379	C1199	C1139	A1079	A1019
C1680	A1620	C1620	C1490	C1440	C1380	C1260	C1200	A1080	A900
C1681	C1621	C1621	A1561	A1441	C1381	C1261	C1201	C1081	C1021
C1682	C1622	C1622	A1562	A1442	A1382	C1262	C1202	C1082	C1022
C1683	C1623	C1623	A1563	A1443	C1383	C1263	C1203	C1083	C1023
C1684	C1624	C1624	A1564	A1444	C1384	C1264	C1204	A1084	A1024
C1685	C1625	C1625	A1565	C1445	C1385	C1265	C1205	A1085	C1025
C1686	A1626	C1626	A1566	C1446	C1386	C1266	C1206	A1086	A1046
C1687	C1627	C1627	A1567	A1447	C1387	C1267	C1207	C1087	A1027
C1688	A1628	C1628	A1568	A1448	C1388	C1268	C1208	C1088	C1028
C1689	C1629	C1629	A1569	C1449	C1389	C1269	C1209	C1089	C1029
C1690	C1630	C1630	A1570	A1450	C1390	C1270	C1210	A1090	A1030
C1691	C1631	C1631	A1571	A1451	C1391	C1331	C1271	C1091	A1031
C1692	C1632	C1632	A1572	A1452	C1392	C1332	C1272	C1092	C1032
C1693	C1633	C1633	A1573	A1453	C1393	C1333	C1273	C1093	C1033
C1694	C1634	C1634	A1574	A1454	C1394	C1334	C1274	C1094	C1034
C1695	C1635	C1635	A1575	C1455	C1395	C1335	C1275	C1095	C1035
C1696	C1636	C1636	A1576	C1456	C1396	C1336	C1276	C1096	C1036
C1697	C1637	C1637	A1577	A1457	C1397	C1337	C1277	C1097	C1037
C1698	C1638	C1638	A1578	A1458	C1398	C1338	C1278	C1098	C1038
C1699	C1639	C1639	A1579	A1459	C1399	C1339	C1279	C1099	C1039
C1700	C1640	C1640	A1580	C1450	C1390	C1340	C1280	C1090	C1040
C1691	C1641	C1641	A1581	A1461	C1391	C1341	C1281	C1091	C1041
C1692	C1642	C1642	A1582	C1462	C1392	C1342	C1282	C1092	C1042
C1693	C1643	C1643	A1583	C1463	C1393	C1343	C1283	C1093	C1043
C1694	C1644	C1644	A1584	C1464	C1394	C1344	C1284	C1094	C1044
C1695	C1645	C1645	A1585	A1465	C1395	C1345	C1285	C1095	C1045
C1696	C1646	C1646	A1586	C1466	C1396	C1346	C1286	C1096	C1046
C1697	C1647	C1647	A1587	C1467	C1397	C1347	C1287	C1097	C1047
C1698	C1648	C1648	A1588	C1468	C1398	C1348	C1288	C1098	C1048



- Molecule 3: mRNA

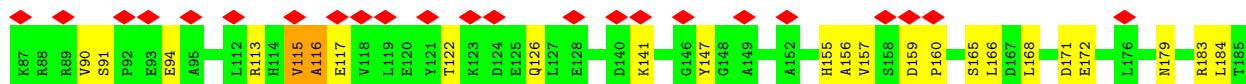
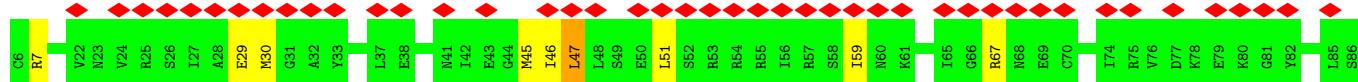
Chain F:  57% 40%



- Molecule 4: Eukaryotic translation initiation factor 2 subunit 1

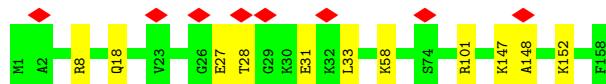
A horizontal bar chart titled "Chain P" showing the percentage distribution across three categories. The bars are colored red, green, and orange. The values are labeled above each bar: 46% (red), 85% (green), and 12% (orange). The total length of the bars is 100%.

Category	Percentage
Red	46%
Green	85%
Orange	12%

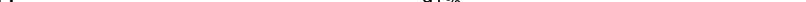


- Molecule 5: ribosomal protein uS17

Chain G: 5% 93% 7%

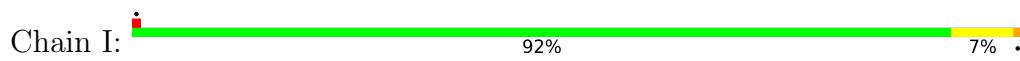


- Molecule 6: ribosomal protein uS9

Chain H:  91% 8%



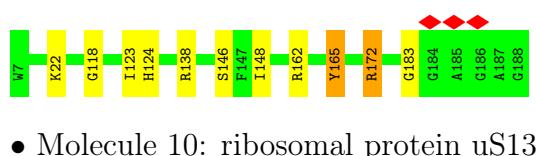
- Molecule 7: 40S ribosomal protein S4



- Molecule 8: ribosomal protein uS14



- Molecule 9: Ribosomal protein S9 (Predicted)



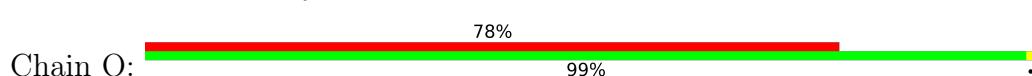
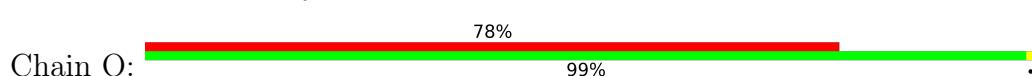
- Molecule 10: ribosomal protein uS13



- Molecule 11: Eukaryotic translation initiation factor 3 subunit G



- Molecule 12: Eukaryotic translation initiation factor 3 subunit G



- Molecule 13: ribosomal protein uS12

Chain Q:  94% 6%



- Molecule 14: ribosomal protein eS19

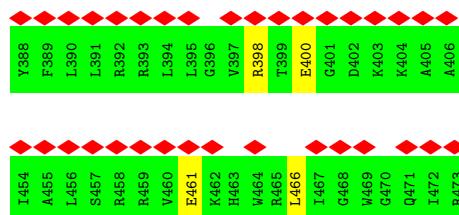
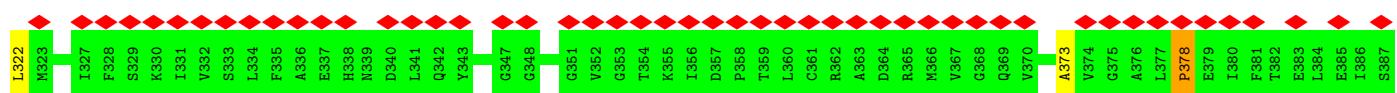
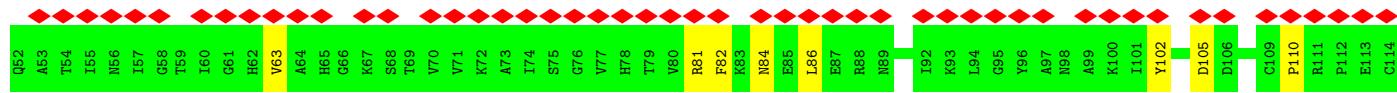
Chain R: 92% 7% •

A horizontal progress bar consisting of a green segment followed by a yellow segment. The green segment is labeled '92%' in white text. To its right is a yellow segment labeled '7%' in black text, followed by a small black dot.



- Molecule 15: eukaryotic initiation factor 2 Gamma subunit (eIF2-Gamma)

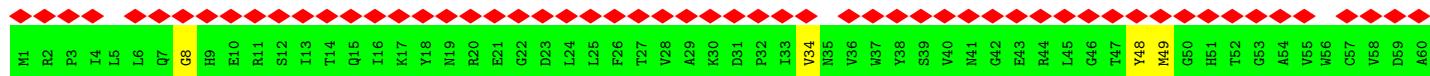
Chain S: 92% 75% 7% •

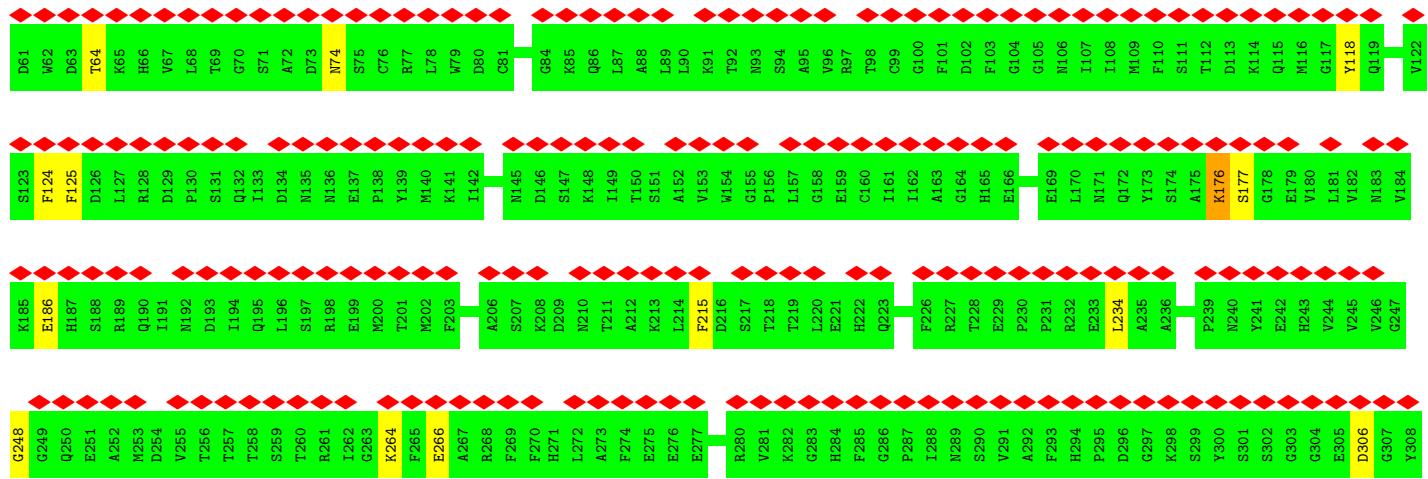


- Molecule 16: Eukaryotic translation initiation factor 3 subunit I

Chain T: 89%

The figure shows a horizontal progress bar for 'Chain T'. The bar is mostly red, with a green segment on the right side. The total length of the bar is indicated by a yellow tick mark at the far right. The red segment ends at the 89% mark, while the green segment begins at the 94% mark. The text 'Chain T:' is positioned to the left of the bar.





- Molecule 17: ribosomal protein uS7

Chain U:  93% 6%

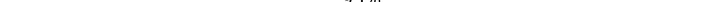


- Molecule 18: ribosomal protein eS30

Chain V: 7% 92% 8%



- Molecule 19: ribosomal protein eS25

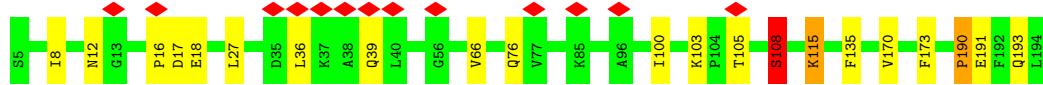
Chain W:  93% 7%



- Molecule 20: ribosomal protein eS7

Chain X: 99%

A horizontal progress bar for 'Chain X' is shown at the bottom of the screen. The bar is mostly green, with a small yellow segment at the far right. The text 'Chain X:' is to the left of the bar. Above the bar, the value '99%' is displayed in black text. To the right of the bar, there is some very small, illegible text.

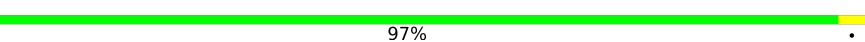


- Molecule 21: 40S ribosomal protein S27

Chain Y:  11% •



- Molecule 22: ribosomal protein uS15

Chain Z:  •



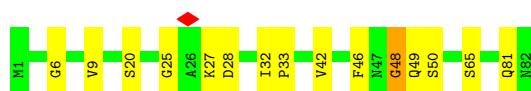
- Molecule 23: ribosomal protein uS8

Chain a:  5% •



- Molecule 24: 40S ribosomal protein S21

Chain b:  17% •



- Molecule 25: ribosomal protein uS5

Chain c:  •

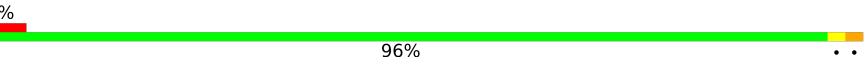


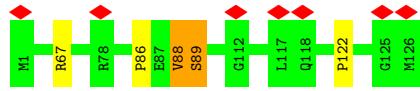
- Molecule 26: eukaryotic initiation factor 2 subunit Beta (eIF2-Beta)

Chain d:  100%

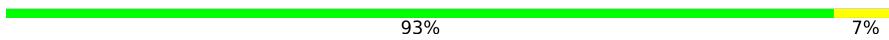


- Molecule 27: ribosomal protein eS17

Chain e:  96% •

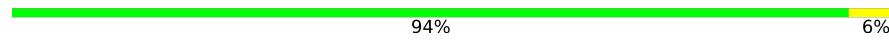


- Molecule 28: ribosomal protein uS2

Chain f:  93% 7%



- Molecule 29: ribosomal protein uS3

Chain g:  94% 6%

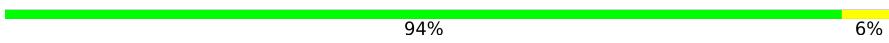


- Molecule 30: ribosomal protein uS10

Chain h:  88% 12%

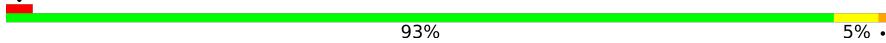


- Molecule 31: ribosomal protein eS1

Chain i:  94% 6%

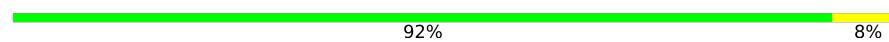


- Molecule 32: ribosomal protein uS11

Chain j:  93% 5%

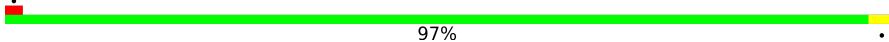


- Molecule 33: ribosomal protein eS26

Chain k:  92% 8%



- Molecule 34: ribosomal protein eS28

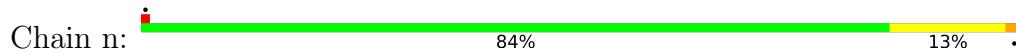
Chain l:  97% 3%



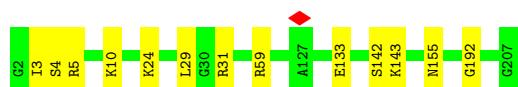
- Molecule 35: ribosomal protein RACK1



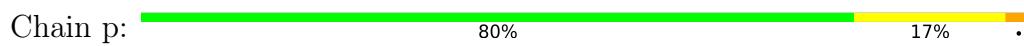
- Molecule 36: ribosomal protein uS19



- Molecule 37: 40S ribosomal protein S8



- Molecule 38: ribosomal protein eS31



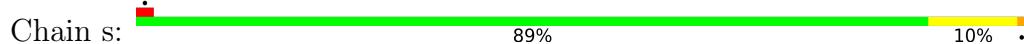
- Molecule 39: 40S ribosomal protein S6



- Molecule 40: 40S ribosomal protein S12



- Molecule 41: 40S ribosomal protein S24





- Molecule 42: ribosomal protein eS10

Chain t: 81% 17%



## 4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	475000	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 ( $e^-/\text{\AA}^2$ )	24	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.400	Depositor
Minimum map value	-0.107	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	440.0, 440.0, 440.0	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.2, 2.2, 2.2	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

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	N	1.68	9/1795 (0.5%)	2.61	215/2798 (7.7%)
2	A	1.62	35/42353 (0.1%)	2.56	5098/66010 (7.7%)
3	F	1.59	0/709	2.51	91/1103 (8.3%)
4	P	1.00	0/2178	1.08	3/2935 (0.1%)
5	G	1.02	0/1319	1.01	0/1761
6	H	1.04	0/1142	1.07	3/1528 (0.2%)
7	I	0.98	0/2125	1.06	5/2856 (0.2%)
8	J	1.12	0/455	0.98	0/603
9	K	1.08	0/1523	1.00	2/2031 (0.1%)
10	L	1.06	0/1158	1.04	1/1548 (0.1%)
11	M	0.81	0/293	0.94	0/396
12	O	1.03	0/626	1.01	0/842
13	Q	0.99	0/1125	0.98	0/1500
14	R	0.99	0/1133	1.05	5/1517 (0.3%)
15	S	0.91	0/3267	1.01	2/4415 (0.0%)
16	T	0.96	0/2669	1.07	8/3608 (0.2%)
17	U	0.99	0/1531	0.98	0/2059
18	V	1.10	0/478	1.04	1/628 (0.2%)
19	W	0.97	0/605	1.04	0/810
20	X	0.96	0/1553	1.04	4/2079 (0.2%)
21	Y	0.94	0/673	1.01	0/902
22	Z	0.98	0/1232	0.94	0/1656
23	a	1.01	0/1051	0.98	0/1406
24	b	0.98	0/627	1.08	0/839
25	c	0.91	0/1779	1.02	3/2399 (0.1%)
26	d	0.98	0/149	0.79	0/197
27	e	0.99	0/1032	1.03	0/1383
28	f	0.96	0/1680	1.05	2/2283 (0.1%)
29	g	0.99	0/1793	1.04	2/2412 (0.1%)
30	h	0.99	0/832	1.08	0/1117
31	i	0.91	0/1770	1.02	0/2367
32	j	1.04	0/1029	1.08	0/1380
33	k	1.07	0/803	1.06	1/1076 (0.1%)
34	l	1.13	0/509	1.05	0/680

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	m	0.92	0/2494	1.13	3/3394 (0.1%)
36	n	1.03	0/1080	1.04	0/1437
37	o	1.04	0/1709	1.05	1/2278 (0.0%)
38	p	0.99	0/594	1.09	1/786 (0.1%)
39	q	1.07	0/1947	1.08	4/2590 (0.2%)
40	r	0.89	0/968	1.04	2/1296 (0.2%)
41	s	0.99	0/1083	1.10	0/1437
42	t	0.96	0/852	1.13	4/1147 (0.3%)
All	All	1.33	44/93723 (0.0%)	1.98	5461/135489 (4.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	N	0	6
2	A	1	68
4	P	0	17
5	G	0	4
6	H	0	2
7	I	1	2
9	K	0	3
10	L	0	6
14	R	0	1
15	S	0	5
16	T	0	1
17	U	0	3
18	V	0	1
19	W	0	2
20	X	0	6
21	Y	0	3
23	a	0	1
24	b	0	5
25	c	0	1
27	e	0	3
28	f	0	2
29	g	0	1
30	h	0	5
31	i	0	3
32	j	0	1
35	m	0	7

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Mol	Chain	#Chirality outliers	#Planarity outliers
36	n	0	3
37	o	0	4
38	p	0	7
40	r	0	1
41	s	1	4
42	t	0	7
All	All	3	185

The worst 5 of 44 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	211	U	C2-N3	6.75	1.42	1.37
2	A	524	G	O3'-P	-6.71	1.53	1.61
2	A	1186	A	N7-C5	-6.68	1.35	1.39
2	A	749	C	O3'-P	-6.62	1.53	1.61
1	N	14	A	N7-C5	-6.52	1.35	1.39

The worst 5 of 5461 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	730	C	P-O3'-C3'	22.13	146.25	119.70
2	A	883	U	P-O3'-C3'	21.96	146.05	119.70
2	A	748	G	P-O3'-C3'	21.66	145.69	119.70
2	A	524	G	P-O3'-C3'	21.53	145.53	119.70
2	A	1627	G	P-O3'-C3'	21.22	145.16	119.70

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	794	G	C4'
7	I	171	ASP	CA
41	s	86	GLU	CA

5 of 185 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	N	1	A	Sidechain
1	N	12	G	Sidechain
1	N	2	G	Sidechain
1	N	22	C	Sidechain
1	N	72	A	Sidechain

## 5.2 Too-close contacts [\(i\)](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	N	1604	0	816	0	0
2	A	37881	0	19145	0	0
3	F	635	0	327	0	0
4	P	2147	0	2191	0	0
5	G	1296	0	1374	0	0
6	H	1124	0	1193	0	0
7	I	2083	0	2189	0	0
8	J	445	0	442	0	0
9	K	1499	0	1608	0	0
10	L	1140	0	1191	0	0
11	M	288	0	269	0	0
12	O	614	0	599	0	0
13	Q	1107	0	1179	0	0
14	R	1113	0	1149	0	0
15	S	3214	0	3354	0	0
16	T	2605	0	2474	0	0
17	U	1509	0	1563	0	0
18	V	473	0	524	0	0
19	W	599	0	656	0	0
20	X	1530	0	1627	0	0
21	Y	659	0	683	0	0
22	Z	1208	0	1294	0	0
23	a	1034	0	1080	0	0
24	b	620	0	622	0	0
25	c	1743	0	1836	0	0
26	d	147	0	146	0	0
27	e	1020	0	1075	0	0
28	f	1643	0	1646	0	0
29	g	1765	0	1863	0	0
30	h	822	0	887	0	0
31	i	1742	0	1815	0	0
32	j	1016	0	1039	0	0
33	k	790	0	839	0	0
34	l	507	0	536	0	0
35	m	2437	0	2393	0	0
36	n	1061	0	1120	0	0
37	o	1680	0	1762	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	p	582	0	599	0	0
39	q	1924	0	2089	0	0
40	r	958	0	993	0	0
41	s	1065	0	1137	0	0
42	t	828	0	854	0	0
All	All	88157	0	70178	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

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	P	264/266 (99%)	220 (83%)	26 (10%)	18 (7%)	1 14
5	G	156/158 (99%)	135 (86%)	17 (11%)	4 (3%)	5 31
6	H	139/141 (99%)	125 (90%)	7 (5%)	7 (5%)	2 20
7	I	261/263 (99%)	235 (90%)	14 (5%)	12 (5%)	2 21
8	J	51/53 (96%)	45 (88%)	4 (8%)	2 (4%)	3 23
9	K	180/182 (99%)	156 (87%)	18 (10%)	6 (3%)	4 26
10	L	135/137 (98%)	118 (87%)	11 (8%)	6 (4%)	2 22
11	M	36/38 (95%)	31 (86%)	5 (14%)	0	100 100
12	O	75/77 (97%)	70 (93%)	5 (7%)	0	100 100
13	Q	140/142 (99%)	119 (85%)	15 (11%)	6 (4%)	2 22
14	R	139/141 (99%)	130 (94%)	7 (5%)	2 (1%)	11 46
15	S	420/422 (100%)	364 (87%)	41 (10%)	15 (4%)	3 25
16	T	327/329 (99%)	292 (89%)	29 (9%)	6 (2%)	8 40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
17	U	189/191 (99%)	169 (89%)	13 (7%)	7 (4%)	3 24
18	V	57/59 (97%)	46 (81%)	8 (14%)	3 (5%)	2 19
19	W	73/75 (97%)	61 (84%)	11 (15%)	1 (1%)	11 46
20	X	188/190 (99%)	163 (87%)	11 (6%)	14 (7%)	1 13
21	Y	82/84 (98%)	71 (87%)	5 (6%)	6 (7%)	1 13
22	Z	148/150 (99%)	137 (93%)	9 (6%)	2 (1%)	11 46
23	a	127/129 (98%)	118 (93%)	6 (5%)	3 (2%)	6 33
24	b	80/82 (98%)	65 (81%)	6 (8%)	9 (11%)	0 7
25	c	224/226 (99%)	209 (93%)	9 (4%)	6 (3%)	5 31
26	d	15/17 (88%)	15 (100%)	0	0	100 100
27	e	124/126 (98%)	110 (89%)	11 (9%)	3 (2%)	6 33
28	f	206/208 (99%)	174 (84%)	24 (12%)	8 (4%)	3 23
29	g	225/227 (99%)	203 (90%)	14 (6%)	8 (4%)	3 25
30	h	102/104 (98%)	86 (84%)	12 (12%)	4 (4%)	3 23
31	i	213/215 (99%)	188 (88%)	17 (8%)	8 (4%)	3 24
32	j	134/136 (98%)	107 (80%)	19 (14%)	8 (6%)	1 16
33	k	97/99 (98%)	87 (90%)	7 (7%)	3 (3%)	4 27
34	l	62/64 (97%)	57 (92%)	5 (8%)	0	100 100
35	m	311/313 (99%)	278 (89%)	23 (7%)	10 (3%)	4 26
36	n	125/127 (98%)	103 (82%)	10 (8%)	12 (10%)	0 9
37	o	204/206 (99%)	182 (89%)	14 (7%)	8 (4%)	3 23
38	p	69/71 (97%)	47 (68%)	14 (20%)	8 (12%)	0 6
39	q	235/237 (99%)	211 (90%)	16 (7%)	8 (3%)	3 26
40	r	122/124 (98%)	103 (84%)	12 (10%)	7 (6%)	1 17
41	s	129/131 (98%)	113 (88%)	7 (5%)	9 (7%)	1 14
42	t	96/98 (98%)	76 (79%)	10 (10%)	10 (10%)	0 8
All	All	5960/6038 (99%)	5219 (88%)	492 (8%)	249 (4%)	5 22

5 of 249 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	P	115	VAL
4	P	166	LEU

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Mol	Chain	Res	Type
4	P	172	GLU
4	P	223	MET
6	H	19	ALA

### 5.3.2 Protein sidechains [\(i\)](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
4	P	238/238 (100%)	231 (97%)	7 (3%)	42 64
5	G	142/142 (100%)	139 (98%)	3 (2%)	53 72
6	H	117/117 (100%)	113 (97%)	4 (3%)	37 60
7	I	225/225 (100%)	219 (97%)	6 (3%)	44 65
8	J	47/47 (100%)	47 (100%)	0	100 100
9	K	157/157 (100%)	154 (98%)	3 (2%)	57 75
10	L	119/119 (100%)	119 (100%)	0	100 100
11	M	35/35 (100%)	34 (97%)	1 (3%)	42 64
12	O	63/63 (100%)	62 (98%)	1 (2%)	62 79
13	Q	114/114 (100%)	111 (97%)	3 (3%)	46 66
14	R	113/113 (100%)	107 (95%)	6 (5%)	22 47
15	S	354/354 (100%)	340 (96%)	14 (4%)	31 55
16	T	281/281 (100%)	273 (97%)	8 (3%)	43 64
17	U	161/161 (100%)	156 (97%)	5 (3%)	40 62
18	V	49/49 (100%)	49 (100%)	0	100 100
19	W	66/66 (100%)	64 (97%)	2 (3%)	41 63
20	X	170/170 (100%)	168 (99%)	2 (1%)	71 83
21	Y	76/76 (100%)	74 (97%)	2 (3%)	46 66
22	Z	130/130 (100%)	128 (98%)	2 (2%)	65 80
23	a	112/112 (100%)	110 (98%)	2 (2%)	59 77
24	b	67/67 (100%)	65 (97%)	2 (3%)	41 63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	c	187/187 (100%)	184 (98%)	3 (2%)	62	79
26	d	17/17 (100%)	17 (100%)	0	100	100
27	e	114/114 (100%)	113 (99%)	1 (1%)	78	87
28	f	174/174 (100%)	171 (98%)	3 (2%)	60	78
29	g	190/190 (100%)	187 (98%)	3 (2%)	62	79
30	h	94/94 (100%)	91 (97%)	3 (3%)	39	62
31	i	196/196 (100%)	195 (100%)	1 (0%)	88	93
32	j	106/106 (100%)	104 (98%)	2 (2%)	57	75
33	k	87/87 (100%)	83 (95%)	4 (5%)	27	52
34	l	57/57 (100%)	55 (96%)	2 (4%)	36	59
35	m	272/272 (100%)	265 (97%)	7 (3%)	46	66
36	n	116/116 (100%)	108 (93%)	8 (7%)	15	40
37	o	177/177 (100%)	177 (100%)	0	100	100
38	p	64/64 (100%)	64 (100%)	0	100	100
39	q	207/207 (100%)	203 (98%)	4 (2%)	57	75
40	r	104/104 (100%)	100 (96%)	4 (4%)	33	57
41	s	113/113 (100%)	111 (98%)	2 (2%)	59	77
42	t	89/89 (100%)	85 (96%)	4 (4%)	27	52
All	All	5200/5200 (100%)	5076 (98%)	124 (2%)	51	69

5 of 124 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	U	130	ARG
39	q	13	GLN
24	b	32	ILE
36	n	100	LYS
41	s	17	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [\(i\)](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	N	74/75 (98%)	16 (21%)	3 (4%)
2	A	1772/1776 (99%)	499 (28%)	113 (6%)
3	F	29/30 (96%)	11 (37%)	2 (6%)
All	All	1875/1881 (99%)	526 (28%)	118 (6%)

5 of 526 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	N	7	G
1	N	11	C
1	N	16	C
1	N	17	G
1	N	18	G

5 of 118 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A	807	A
2	A	1774	G
2	A	1249	A
2	A	1763	C
2	A	1615	A

## 5.4 Non-standard residues in protein, DNA, RNA chains [\(i\)](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [\(i\)](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [\(i\)](#)

There are no ligands in this entry.

## 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
2	A	5

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	736:C	O3'	744:C	P	29.45
1	A	679:U	O3'	683:G	P	18.26
1	A	761:G	O3'	774:U	P	17.60
1	A	687:G	O3'	730:C	P	14.44
1	A	243:C	O3'	267:G	P	13.79

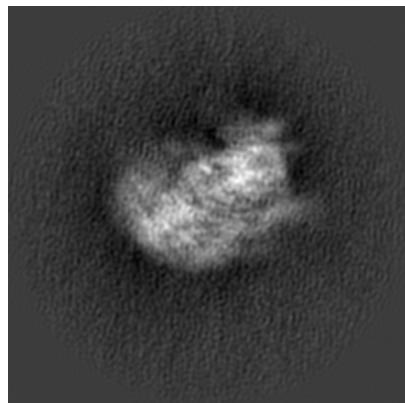
## 6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-8190. These allow visual inspection of the internal detail of the map and identification of artifacts.

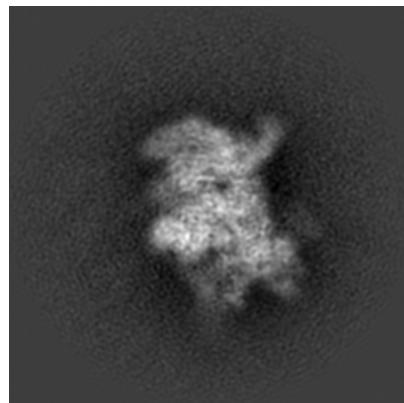
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections (i)

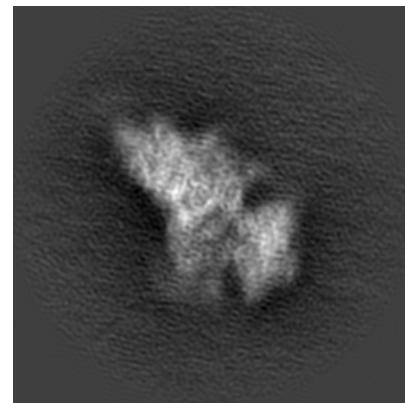
#### 6.1.1 Primary map



X



Y

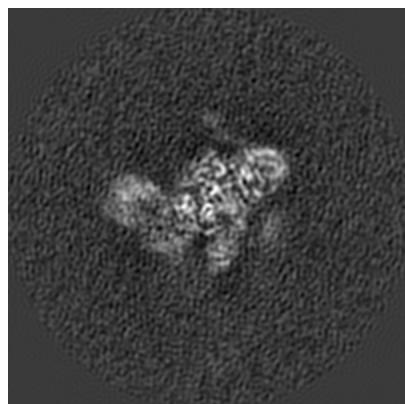


Z

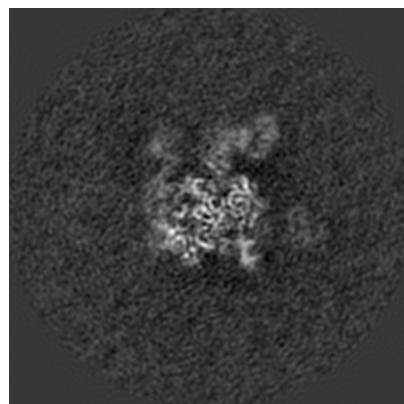
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices (i)

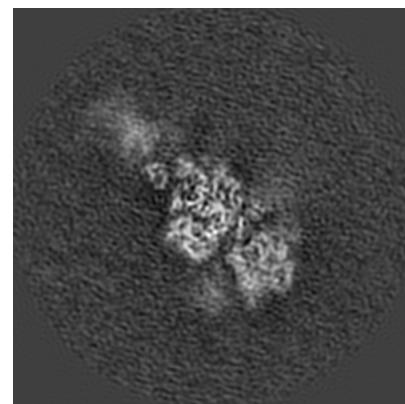
#### 6.2.1 Primary map



X Index: 100



Y Index: 100

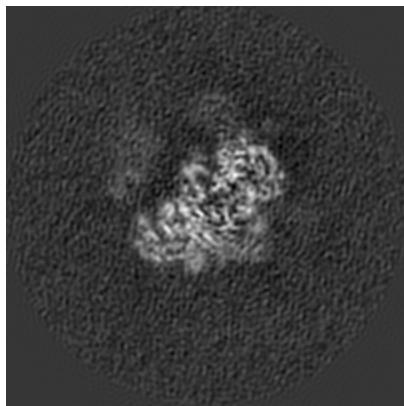


Z Index: 100

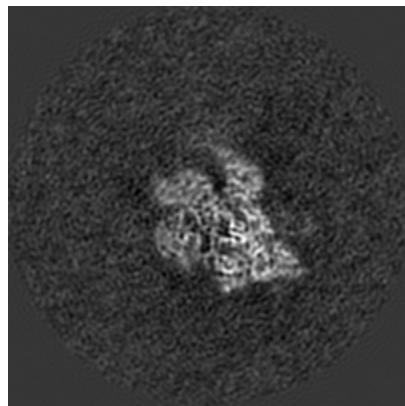
The images above show central slices of the map in three orthogonal directions.

### 6.3 Largest variance slices [\(i\)](#)

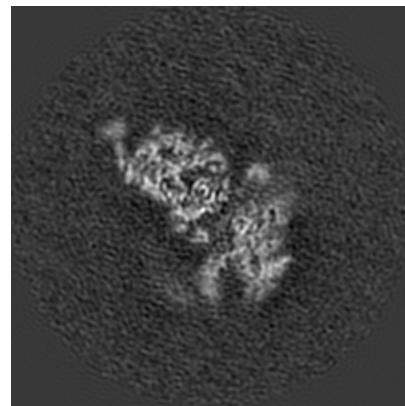
#### 6.3.1 Primary map



X Index: 85



Y Index: 113



Z Index: 108

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

### 6.4 Orthogonal surface views [\(i\)](#)

#### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

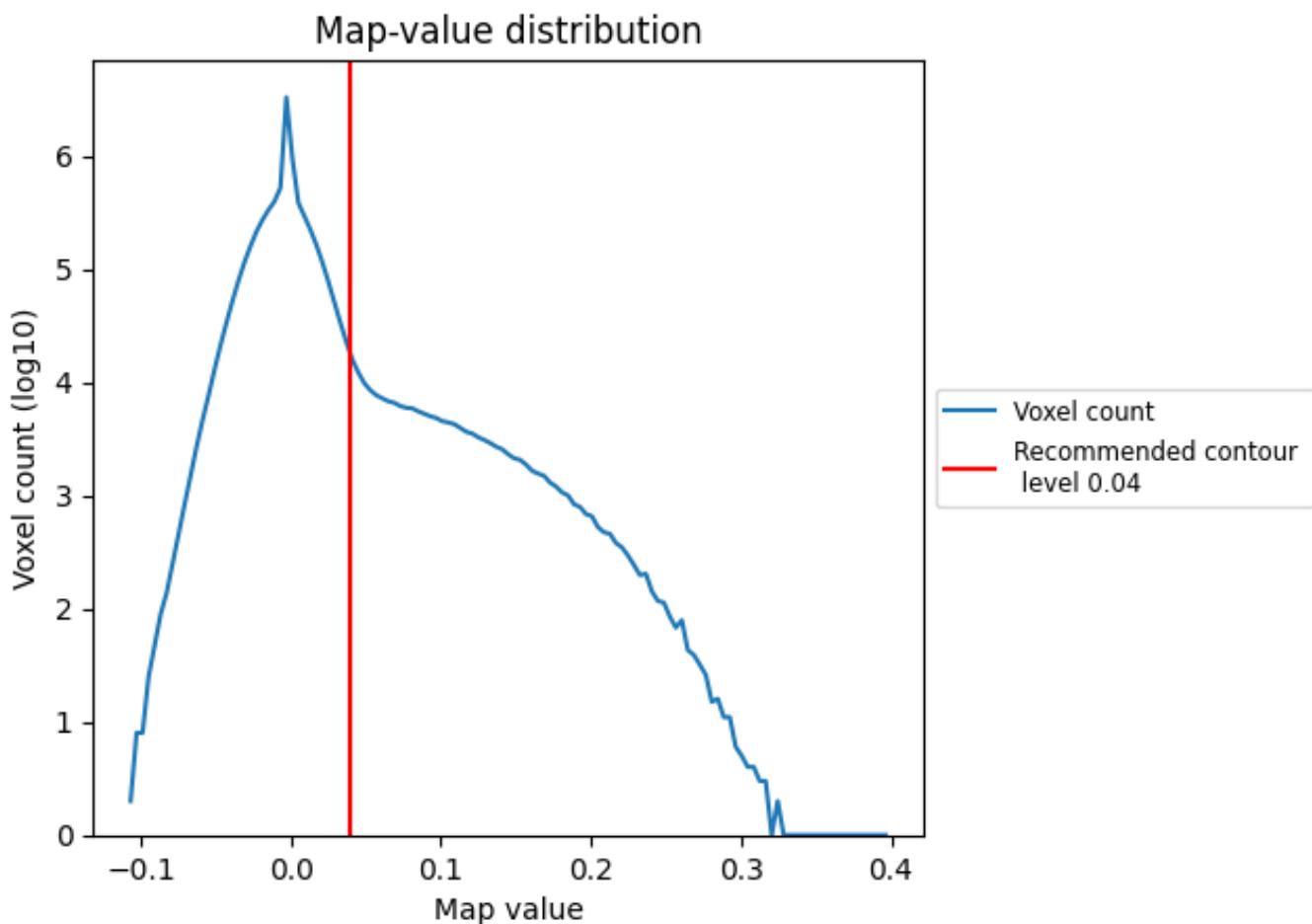
## 6.5 Mask visualisation

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

## 7 Map analysis (i)

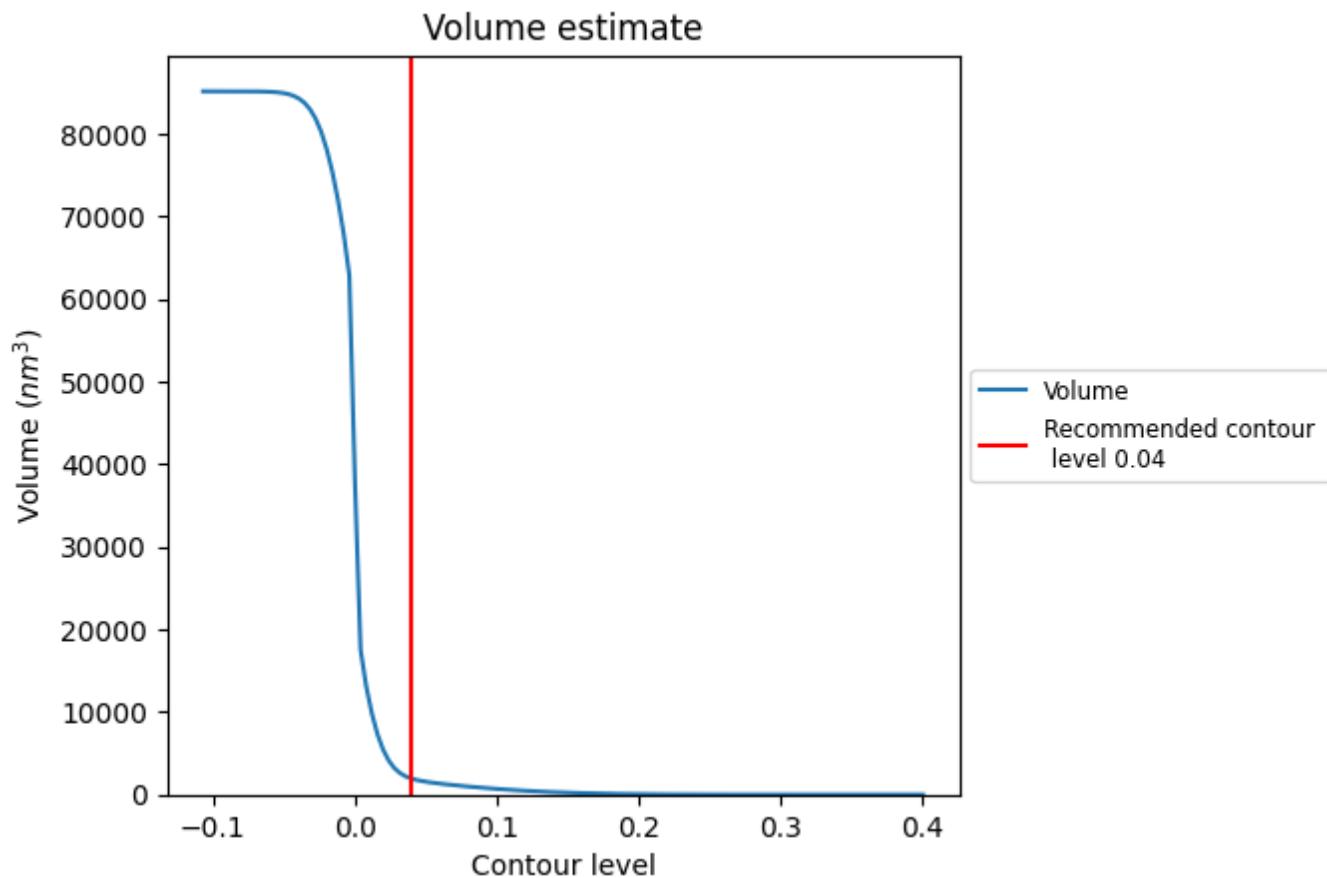
This section contains the results of statistical analysis of the map.

### 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.

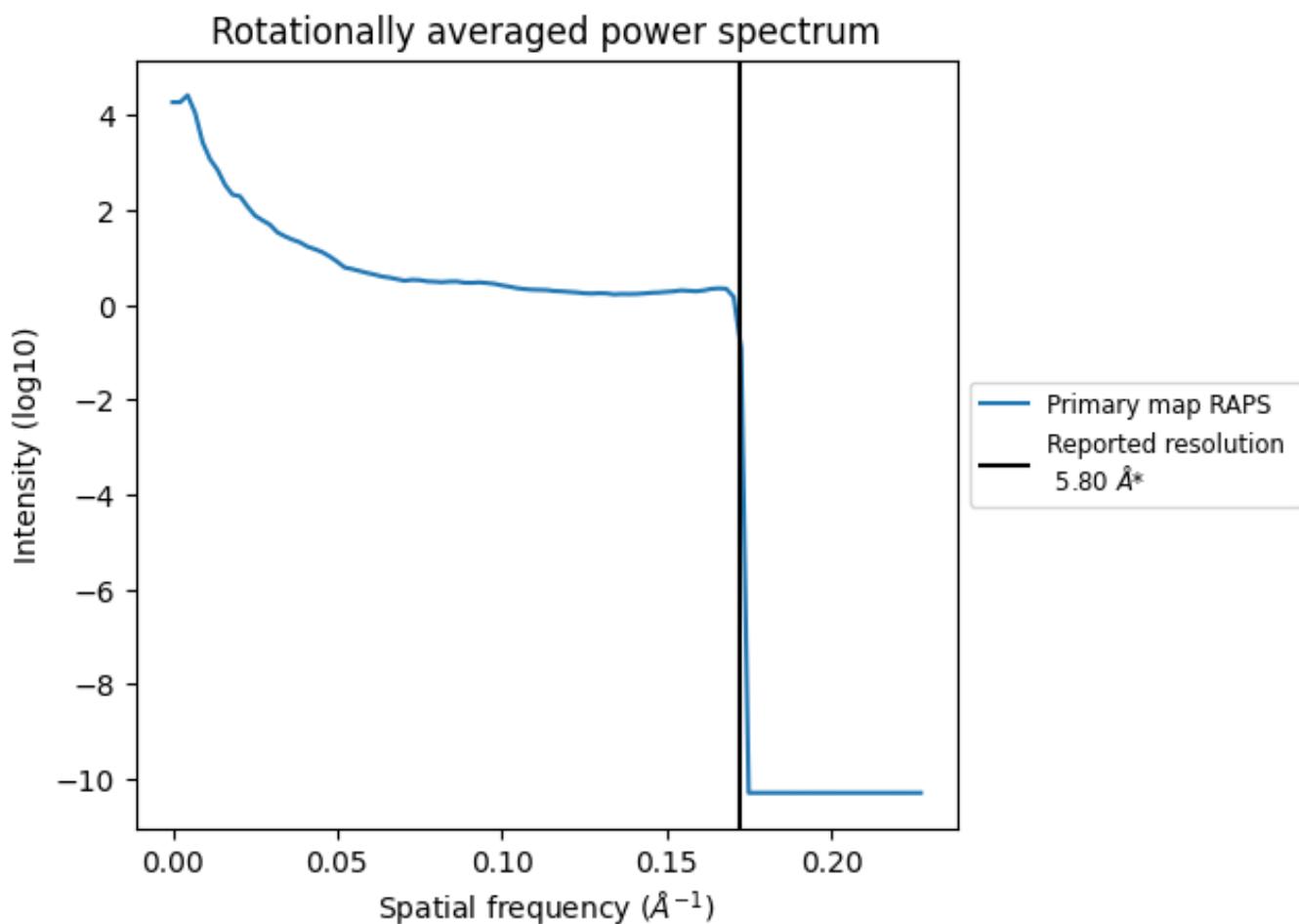
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is  $1932 \text{ nm}^3$ ; this corresponds to an approximate mass of  $1746 \text{ kDa}$ .

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

### 7.3 Rotationally averaged power spectrum [\(i\)](#)



\*Reported resolution corresponds to spatial frequency of  $0.172 \text{ \AA}^{-1}$

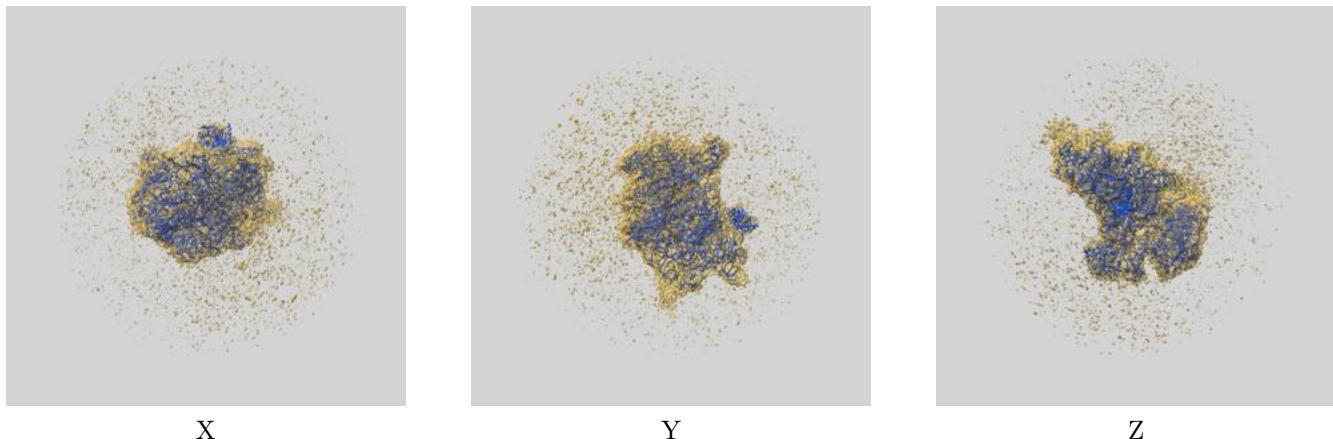
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

## 9 Map-model fit (i)

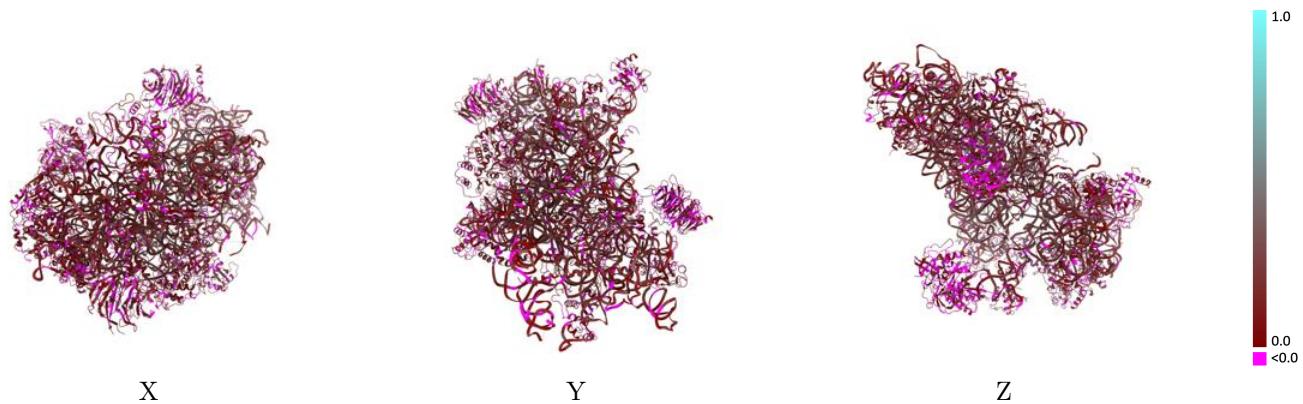
This section contains information regarding the fit between EMDB map EMD-8190 and PDB model 5K0Y. Per-residue inclusion information can be found in section 3 on page 28.

### 9.1 Map-model overlay (i)



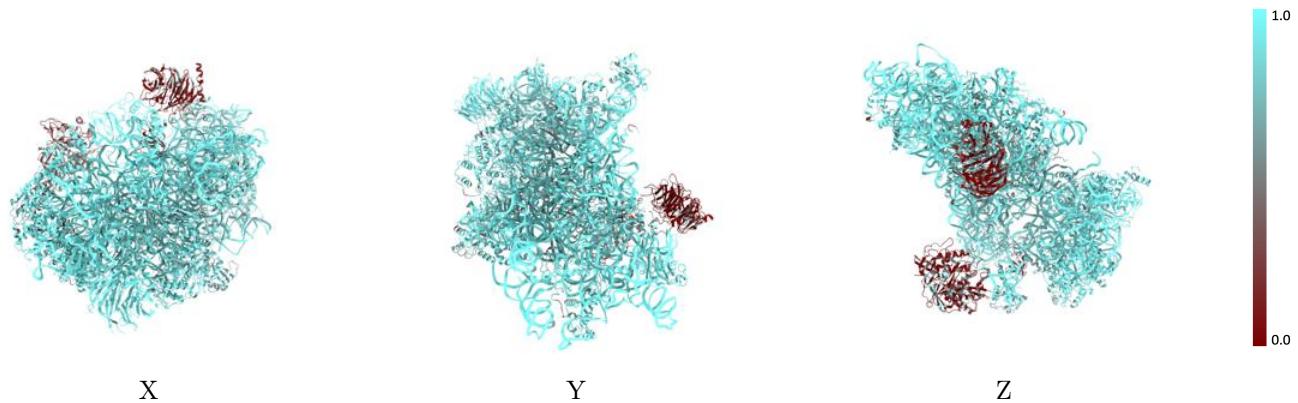
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



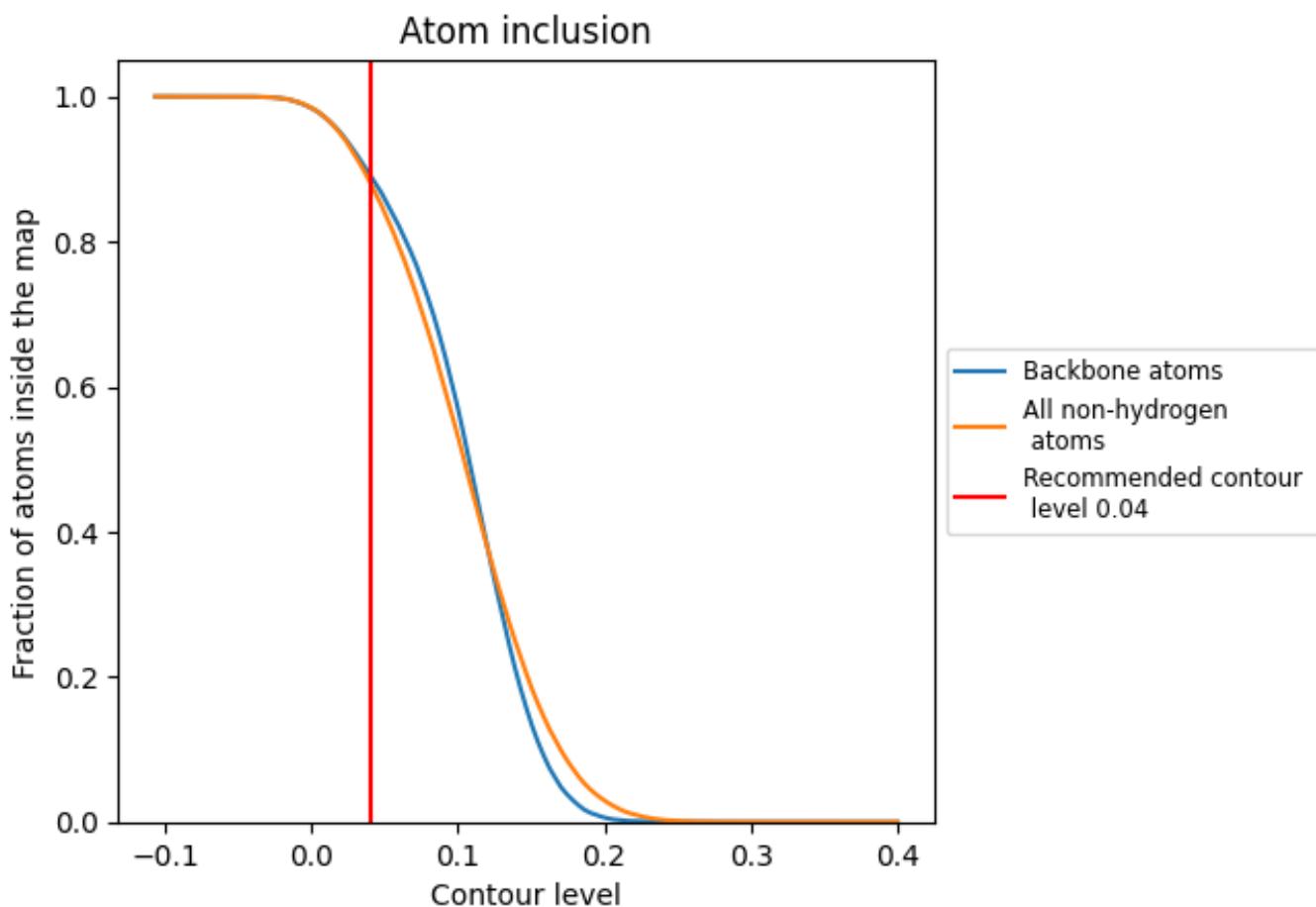
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

## 9.4 Atom inclusion [\(i\)](#)



At the recommended contour level, 89% of all backbone atoms, 88% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8817	0.1410
A	0.9915	0.1880
F	0.7890	0.0970
G	0.8469	0.1270
H	0.9540	0.1200
I	0.9199	0.1450
J	0.9063	0.0990
K	0.9133	0.1380
L	0.9508	0.1050
M	0.1632	0.1060
N	0.9133	0.1420
O	0.2044	0.0100
P	0.4785	0.0450
Q	0.9093	0.1400
R	0.9603	0.1210
S	0.2385	0.0250
T	0.1134	0.0300
U	0.9285	0.1280
V	0.8706	0.1170
W	0.9469	0.1020
X	0.8021	0.1010
Y	0.9459	0.1200
Z	0.9266	0.1270
a	0.8158	0.1300
b	0.9290	0.1300
c	0.8698	0.1380
d	0.1329	0.0070
e	0.8679	0.1070
f	0.9326	0.1350
g	0.8891	0.1340
h	0.9014	0.1180
i	0.9650	0.1250
j	0.9331	0.1060
k	0.9106	0.1170
l	0.9363	0.1310



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Chain	Atom inclusion	Q-score
m	0.9645	0.1020
n	0.9474	0.0890
o	0.9372	0.1160
p	0.9718	0.0690
q	0.9628	0.1210
r	0.9025	0.0880
s	0.9364	0.1350
t	0.9566	0.1240