



## wwPDB EM Validation Summary Report ⓘ

Nov 27, 2022 – 04:54 PM EST

PDB ID : 6XIQ  
EMDB ID : EMD-22196  
Title : Cryo-EM Structure of K63R Ubiquitin Mutant Ribosome under Oxidative Stress  
Authors : Zhou, Y.; Bartesaghi, A.; Silva, G.M.  
Deposited on : 2020-06-21  
Resolution : 4.20 Å (reported)  
Based on initial model : 6GQ1

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 ⓘ 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 ⓘ](#)) were used in the production of this report:

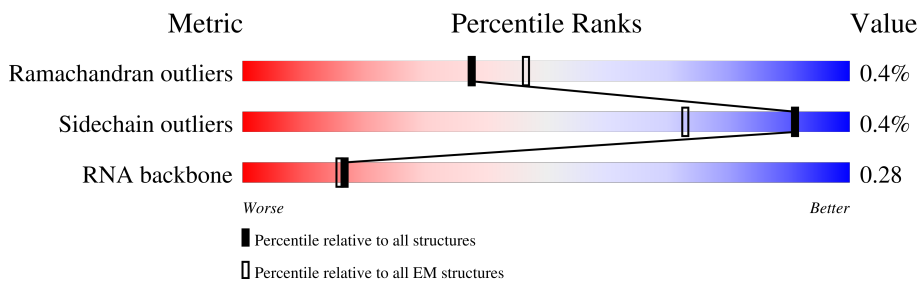
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 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 4.20 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  $\geq 3$ , 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	A	254	
2	B	387	
3	C	362	
4	D	297	
5	E	176	
6	F	244	
7	G	256	
8	H	191	

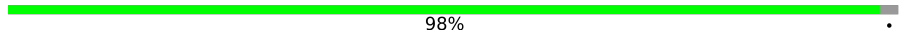

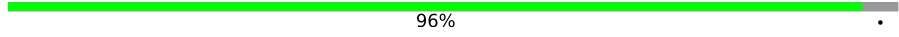
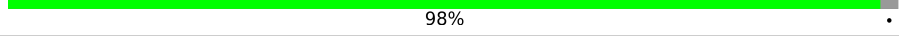
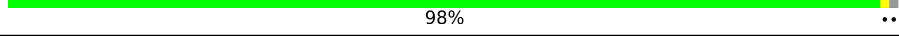

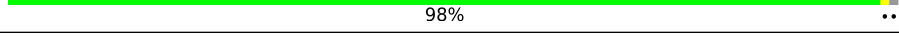
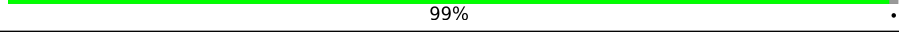
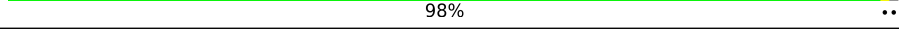
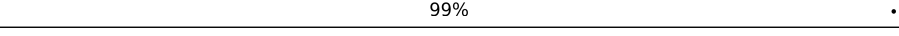
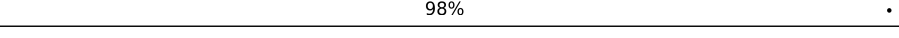
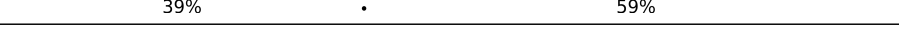
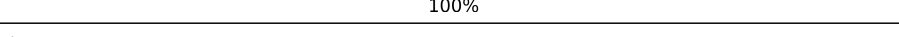
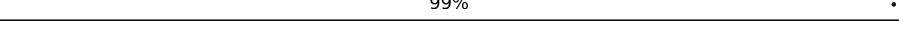
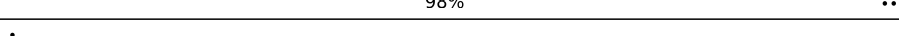

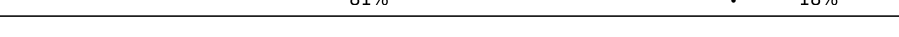

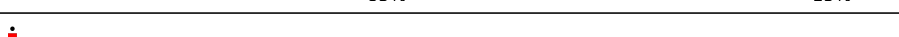






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Mol	Chain	Length	Quality of chain
9	I	221	95% 5%
10	J	174	97% ..
11	L	199	95% ..
12	M	138	98% ..
13	N	204	98% .
14	O	199	98% ...
15	P	184	99% ..
16	Q	186	99% .
17	R	189	99% .
18	S	172	99% .
19	T	160	99% ..
20	U	121	81% . 17%
21	V	137	98% ..
22	W	155	41% 59%
23	X	142	85% . 15%
24	Y	127	98% ..
25	Z	136	99% ..
26	AA	105	90% . 9%
27	AB	156	98% .
28	1	3395	38% 55% . 5%
29	3	121	57% 41% .
30	4	158	43% 54% .
31	P0	312	12% 61% 39%
32	P2	165	56% . 43%
33	a	149	98% ..

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Mol	Chain	Length	Quality of chain
34	b	59	 98%
35	c	105	 90% 8%
36	d	113	 96%
37	e	130	 98%
38	f	107	 98%
39	g	121	 91% 7%
40	h	120	 98%
41	i	100	 99%
42	j	88	 98%
43	k	78	 99%
44	l	51	 98%
45	m	128	 39% 59%
46	n	25	 100%
47	o	106	 99%
48	p	92	 98%
49	2	1800	 58% 38%
50	q	252	 81% 18%
51	r	255	 83% 16%
52	s	254	 85% 15%
53	t	240	 92% 7%
54	u	261	 99%
55	v	225	 90% 8%
56	w	236	 93% 6%
57	x	190	 96%
58	y	200	 92% 6%

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Mol	Chain	Length	Quality of chain
59	z	197	92% 6%
60	AD	151	98%
61	AE	138	91% 8%
62	AF	142	86% 13%
63	AG	143	98%
64	AH	136	88% 12%
65	AI	146	99%
66	AJ	144	99%
67	AK	121	88% 12%
68	AL	87	99%
69	AM	130	99%
70	AN	145	98%
71	AO	135	99%
72	AP	108	65% 35%
73	AQ	119	81% 18%
74	AR	82	98%
75	AS	67	94% 6%
76	AT	56	93% 5%
77	AU	63	94% 5%
78	AV	319	100%
79	AX	76	30% 67%
79	AZ	76	45% 55%
80	AY	8	25% 75%
81	L1	217	94% 6%

## 2 Entry composition [i](#)

There are 82 unique types of molecules in this entry. The entry contains 356903 atoms, of which 151628 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 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	A	252	Total	C	H	N	O	S	0	0
			3895	1191	1981	388	334	1		

- Molecule 2 is a protein called RPL3 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
2	B	386	Total	C	H	N	O	S	0	0
			6217	1950	3142	584	533	8		

- Molecule 3 is a protein called RPL4A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
3	C	361	Total	C	H	N	O	S	0	0
			5607	1729	2859	522	494	3		

- Molecule 4 is a protein called RPL5 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
4	D	296	Total	C	H	N	O	S	0	0
			4701	1501	2326	414	458	2		

- Molecule 5 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
5	E	156	Total	C	H	N	O	S	0	0
			2565	800	1326	222	216	1		

- Molecule 6 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
6	F	222	Total	C	H	N	O	S	0	0
			3646	1151	1862	324	308	1		

- Molecule 7 is a protein called RPL8A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
7	G	233	3681	1151	1877	323	327	3	0	0

- Molecule 8 is a protein called RPL9A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
8	H	191	3105	963	1587	274	277	4	0	0

- Molecule 9 is a protein called RPL10 isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
9	I	211	3441	1083	1736	322	294	6	0	0

- Molecule 10 is a protein called RPL11B isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
10	J	169	2736	847	1383	253	249	4	0	0

- Molecule 11 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
11	L	193	3151	962	1608	315	266	0	0

- Molecule 12 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
12	M	136	2202	675	1149	199	177	2	0	0

- Molecule 13 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
13	N	203	3499	1077	1779	361	281	1	0	0

- Molecule 14 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
14	O	197	3214	1003	1659	289	262	1	0	0

- Molecule 15 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
15	P	183	2857	882	1437	281	257		0	0

- Molecule 16 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
16	Q	185	2984	908	1543	290	241	2	0	0

- Molecule 17 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
17	R	188	3138	935	1617	326	260		0	0

- Molecule 18 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
18	S	172	2932	930	1487	267	244	4	0	0

- Molecule 19 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
19	T	159	2599	805	1323	246	221	4	0	0

- Molecule 20 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
20	U	100	1608	516	812	131	149		0	0

- Molecule 21 is a protein called 60S ribosomal protein L23-A.



Mol	Chain	Residues	Atoms					AltConf	Trace	
21	V	136	Total	C	H	N	O	S	0	0
			2051	628	1048	189	179	7		

- Molecule 22 is a protein called RPL24A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
22	W	63	Total	C	H	N	O	S	0	0
			1072	336	551	102	82	1		

- Molecule 23 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace	
23	X	121	Total	C	H	N	O	S	0	0
			1989	620	1025	169	173	2		

- Molecule 24 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
24	Y	126	Total	C	H	N	O		0	0
			2074	625	1081	192	176			

- Molecule 25 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
25	Z	135	Total	C	H	N	O		0	0
			2247	710	1155	202	180			

- Molecule 26 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
26	AA	96	Total	C	H	N	O	S	0	0
			1499	499	727	126	145	2		

- Molecule 27 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
27	AB	153	Total	C	H	N	O	S	0	0
			2502	780	1282	231	206	3		

- Molecule 28 is a RNA chain called 35S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
28	1	3223	103566	30790	34635	12416	22502	3223	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	?	-	G	deletion	GB 380294104

- Molecule 29 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
29	3	121	3883	1152	1304	461	845	121	0	0

- Molecule 30 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
30	4	158	5048	1500	1695	586	1109	158	0	0

- Molecule 31 is a protein called RPP0 isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
31	P0	189	2987	942	1514	257	270	4	0	0

- Molecule 32 is a protein called RPL12A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
32	P2	94	1497	448	774	138	135	2	0	0

- Molecule 33 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
33	a	148	2388	749	1215	231	190	3	0	0

- Molecule 34 is a protein called RPL29 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
34	b	58	953	289	491	100	73	0	0

- Molecule 35 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
35	c	97	1540	479	797	124	139	1	0	0

- Molecule 36 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
36	d	109	1801	559	918	167	156	1	0	0

- Molecule 37 is a protein called RPL32 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
37	e	127	2110	647	1090	205	167	1	0	0

- Molecule 38 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
38	f	106	1730	540	880	165	144	1	0	0

- Molecule 39 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
39	g	112	1821	545	941	179	152	4	0	0

- Molecule 40 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
40	h	119	2047	615	1078	186	167	1	0	0

- Molecule 41 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
41	i	99	Total	C	H	N	O	S	0	0
			1620	481	849	156	132	2		

- Molecule 42 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
42	j	87	Total	C	H	N	O	S	0	0
			1364	414	683	148	114	5		

- Molecule 43 is a protein called RPL38 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	k	77	Total	C	H	N	O	0	0
			1294	391	682	115	106		

- Molecule 44 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace	
44	l	50	Total	C	H	N	O	S	0	0
			911	272	475	97	65	2		

- Molecule 45 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace	
45	m	52	Total	C	H	N	O	S	0	0
			873	259	456	86	67	5		

- Molecule 46 is a protein called RPL41A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
46	n	25	Total	C	H	N	O	S	0	0
			500	139	273	60	27	1		

- Molecule 47 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
47	o	105	Total	C	H	N	O	S	0	0
			1762	534	915	170	138	5		

- Molecule 48 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
48	p	91	1428	429	734	138	121	6	0	0

- Molecule 49 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
49	2	1743	55827	16603	18686	6578	12217	1743	0	0

- Molecule 50 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
50	q	206	3144	1014	1567	278	283	2	0	0

- Molecule 51 is a protein called RPS1A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
51	r	214	3493	1084	1784	310	311	4	0	0

- Molecule 52 is a protein called RPS2 isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
52	s	217	3358	1047	1723	289	297	2	0	0

- Molecule 53 is a protein called RPS3 isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
53	t	223	3551	1101	1817	313	314	6	0	0

- Molecule 54 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
54	u	260	4222	1316	2154	389	360	3	0	0

- Molecule 55 is a protein called Rps5p.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
55	v	206	3284	1007	1675	300	299	3	0	0

- Molecule 56 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
56	w	223	3671	1123	1881	346	318	3	0	0

- Molecule 57 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
57	x	184	3053	951	1572	265	265	0	0

- Molecule 58 is a protein called RPS8A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
58	y	188	3014	925	1525	298	264	2	0	0

- Molecule 59 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
59	z	185	3067	943	1573	289	261	1	0	0

- Molecule 60 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
60	AD	150	2447	759	1255	224	207	2	0	0

- Molecule 61 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
61	AE	127	1774	545	883	182	163	1	0	0

- Molecule 62 is a protein called RPS15 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
62	AF	124	1979	622	1002	182	166	7	0	0

- Molecule 63 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
63	AG	141	2271	708	1166	203	194		0	0

- Molecule 64 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
64	AH	120	1856	577	930	177	170	2	0	0

- Molecule 65 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
65	AI	145	2414	743	1222	237	210	2	0	0

- Molecule 66 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
66	AJ	143	2236	694	1124	208	208	2	0	0

- Molecule 67 is a protein called RPS20 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
67	AK	107	1772	539	917	156	159	1	0	0

- Molecule 68 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
68	AL	87	1356	420	672	125	137	2	0	0

- Molecule 69 is a protein called RPS22A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
69	AM	129	2081	650	1060	188	180	3	0	0

- Molecule 70 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
70	AN	144	2317	708	1196	220	191	2	0	0

- Molecule 71 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
71	AO	134	2205	676	1132	208	189		0	0

- Molecule 72 is a protein called RPS25A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
72	AP	70	1166	360	603	104	99		0	0

- Molecule 73 is a protein called RPS26B isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
73	AQ	97	1583	475	814	160	129	5	0	0

- Molecule 74 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
74	AR	81	1242	382	632	110	113	5	0	0

- Molecule 75 is a protein called RPS28A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
75	AS	63	1032	306	535	99	91	1	0	0

- Molecule 76 is a protein called RPS29A isoform 1.



Mol	Chain	Residues	Atoms						AltConf	Trace
76	AT	53	Total	C	H	N	O	S	0	0
			873	274	431	92	72	4		

- Molecule 77 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
77	AU	60	Total	C	H	N	O	S	0	0
			1000	299	525	98	77	1		

- Molecule 78 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
78	AV	318	Total	C	H	N	O	S	0	0
			4823	1541	2386	418	470	8		

- Molecule 79 is a RNA chain called Transfer RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
79	AX	76	Total	C	H	N	O	P	0	0
			2446	725	820	293	532	76		
79	AZ	76	Total	C	H	N	O	P	0	0
			2446	725	820	293	532	76		

- Molecule 80 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
80	AY	8	Total	C	H	N	O	P	0	0
			248	74	84	23	59	8		

- Molecule 81 is a protein called RPL1A isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
81	L1	204	Total	C	H	N	O	S	0	0
			3310	1031	1701	279	290	9		

- Molecule 82 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
82	j	1	Total	Zn	0
			1	1	
82	m	1	Total	Zn	0
			1	1	

*Continued on next page...*

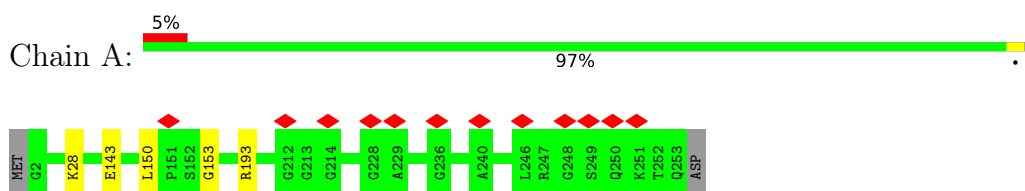
*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>AltConf</b>
82	o	1	Total 1	Zn 1	0
82	p	1	Total 1	Zn 1	0
82	AQ	1	Total 1	Zn 1	0
82	AR	1	Total 1	Zn 1	0
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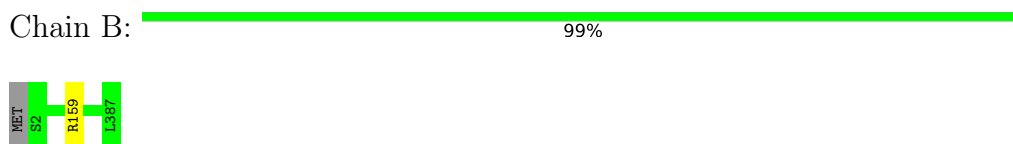
### 3 Residue-property plots [i](#)

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

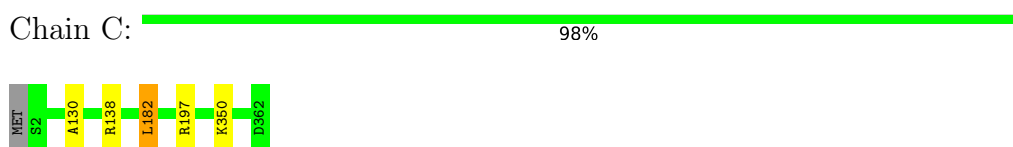
- Molecule 1: 60S ribosomal protein L2-A



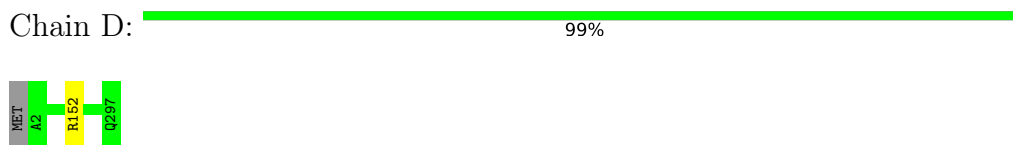
- Molecule 2: RPL3 isoform 1



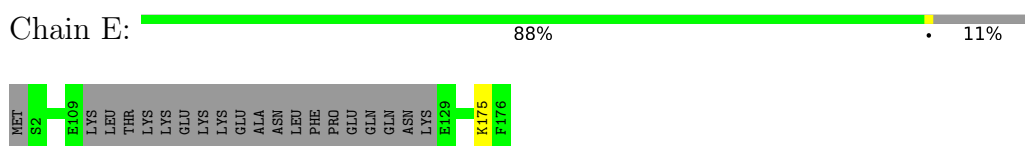
- Molecule 3: RPL4A isoform 1



- Molecule 4: RPL5 isoform 1

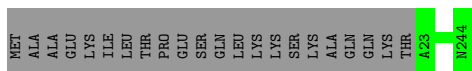


- Molecule 5: 60S ribosomal protein L6-A



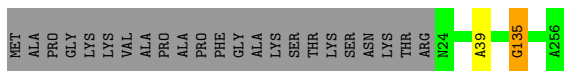
- Molecule 6: 60S ribosomal protein L7-A

Chain F:  91% 9%



- Molecule 7: RPL8A isoform 1

Chain G:  90% 9%



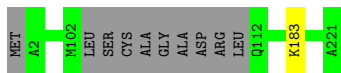
- Molecule 8: RPL9A isoform 1

Chain H:  99%



- Molecule 9: RPL10 isoform 1

Chain I:  95% 5%



- Molecule 10: RPL11B isoform 1

Chain J:  97%



- Molecule 11: 60S ribosomal protein L13-A

Chain L:  95%



- Molecule 12: 60S ribosomal protein L14-A

Chain M:  98%

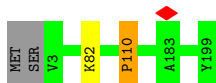


- Molecule 13: 60S ribosomal protein L15-A

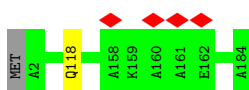
Chain N:  98%



- Molecule 14: 60S ribosomal protein L16-A



- Molecule 15: 60S ribosomal protein L17-A



- Molecule 16: 60S ribosomal protein L18-A



- Molecule 17: 60S ribosomal protein L19-A



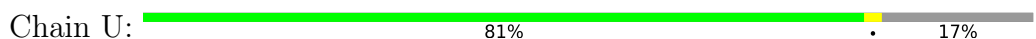
- Molecule 18: 60S ribosomal protein L20-A

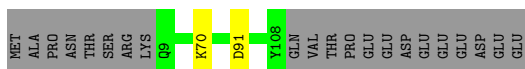


- Molecule 19: 60S ribosomal protein L21-A



- Molecule 20: 60S ribosomal protein L22-A





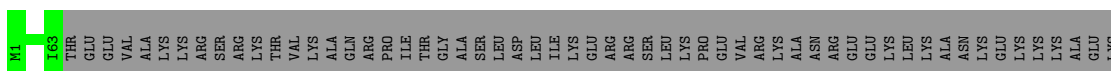
- Molecule 21: 60S ribosomal protein L23-A

Chain V: 98%



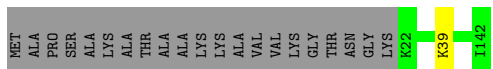
- Molecule 22: RPL24A isoform 1

Chain W: 41% 59%



- Molecule 23: 60S ribosomal protein L25

Chain X: 85% 15%



- Molecule 24: 60S ribosomal protein L26-A

Chain Y: 98%



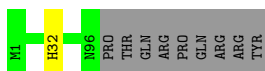
- Molecule 25: 60S ribosomal protein L27-A

Chain Z: 99%



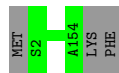
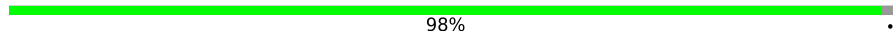
- Molecule 26: 40S ribosomal protein S10-A

Chain AA: 90% 9%



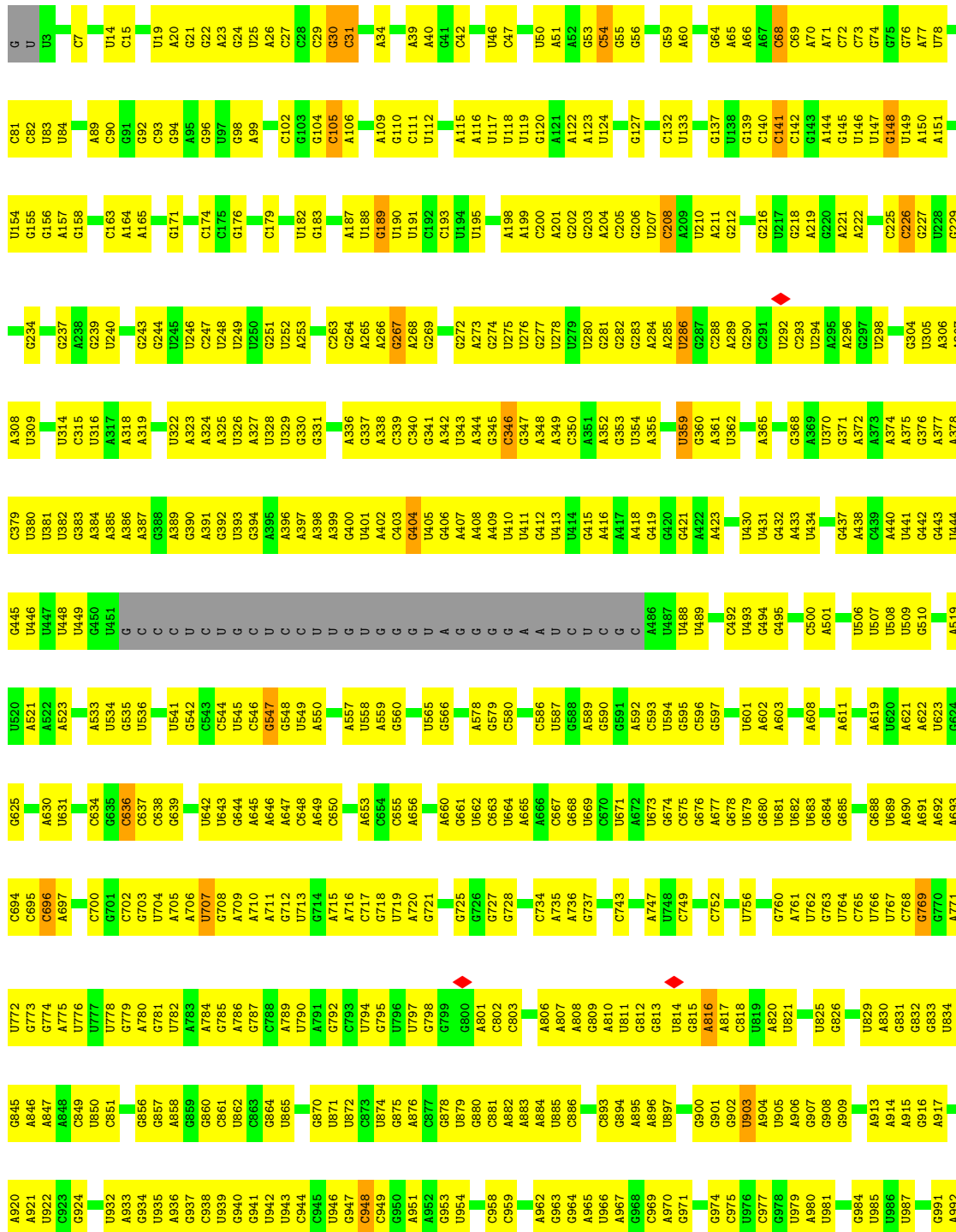
- Molecule 27: 40S ribosomal protein S11-A

Chain AB:



● Molecule 28: 35S ribosomal RNA

Chain 1:







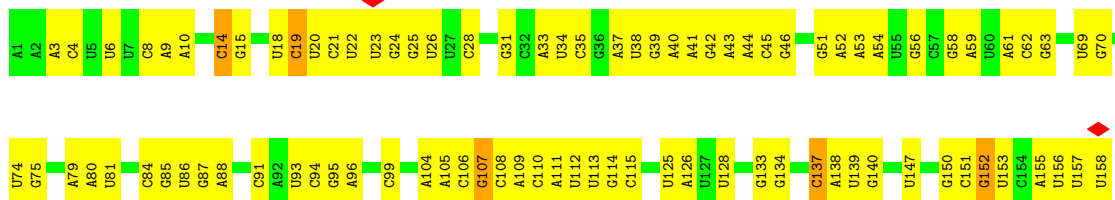
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G2756	U2757	C2760	G2761	U2762	U2763	C2764	G2765	U2766	U2767	U2768	C2772	C2773	C2774	U2775	U2776	U2777	C2778	A2779	U2780	U2781	U2782	U2783	C2784	A2785	C2786	U2787	C2788	G2794	U2795	U2796	C2797	U2798	U2799	G2800	A2801	A2802	A2803	A2804	G2805	U2806	U2807	A2808	C2809	C2810	A2811	C2812	A2813	G2814	G2815	G2816	U2817	U2818	A2819	A2820	U2821	U2822
G2823	G2824	C2825	U2826	U2827	C2832	A2833	U2834	U2835	A2836	A2837	A2838	C2844	A2845	U2846	A2847	G2850	U2854	U2855	U2856	C2863	A2864	U2865	U2866	C2867	U2868	C2876	U2877	G2878	U2879	U2880	U2881	U2882	U2883	A2887	U2891	U2892	C2893	U2894	U2895	U2896	U2897	U2898	U2899	A2900												
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C2756	U2757	C2760	G2761	U2762	U2763	C2764	G2765	U2766	U2767	U2768	C2772	C2773	C2774	U2775	U2776	U2777	C2778	A2779	U2780	U2781	U2782	U2783	C2784	A2785	C2786	U2787	C2788	G2794	U2795	U2796	C2797	U2798	U2799	G2800	A2801	A2802	A2803	A2804	G2805	U2806	U2807	A2808	C2809	C2810	A2811	C2812	A2813	G2814	G2815	G2816	U2817	U2818	A2819	A2820	U2821	U2822
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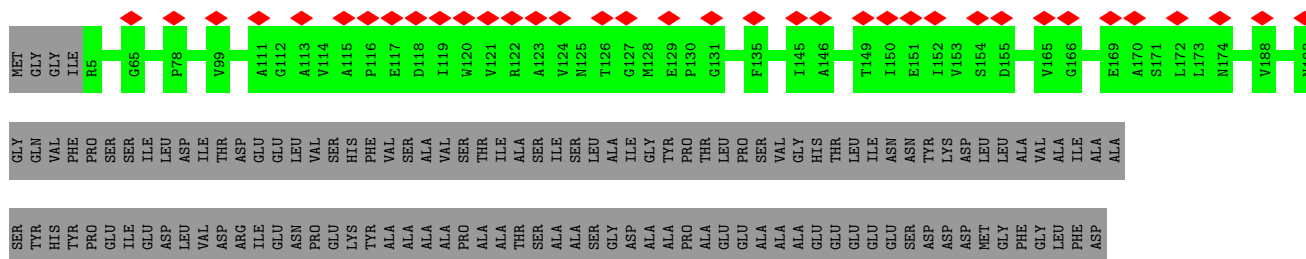
• Molecule 29: 5S ribosomal RNA



• Molecule 30: 5.8S ribosomal RNA

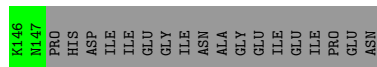
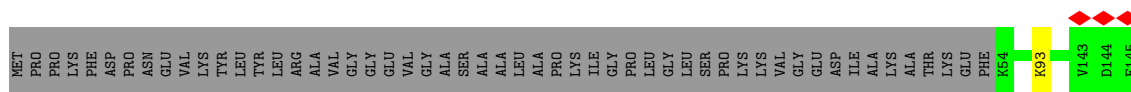


• Molecule 31: RPP0 isoform 1



• Molecule 32: RPL12A isoform 1





- Molecule 33: 60S ribosomal protein L28

Chain a: 98% ..



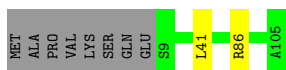
- Molecule 34: RPL29 isoform 1

Chain b: 98% .



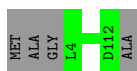
- Molecule 35: 60S ribosomal protein L30

Chain c: 90% . 8%



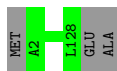
- Molecule 36: 60S ribosomal protein L31-A

Chain d: 96% .



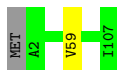
- Molecule 37: RPL32 isoform 1

Chain e: 98% .

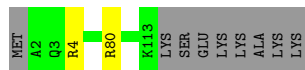
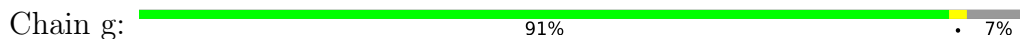


- Molecule 38: 60S ribosomal protein L33-A

Chain f: 98% ..



- Molecule 39: 60S ribosomal protein L34-A



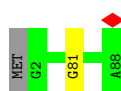
- Molecule 40: 60S ribosomal protein L35-A



- Molecule 41: 60S ribosomal protein L36-A



- Molecule 42: 60S ribosomal protein L37-A



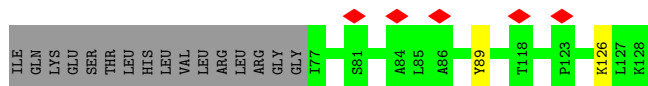
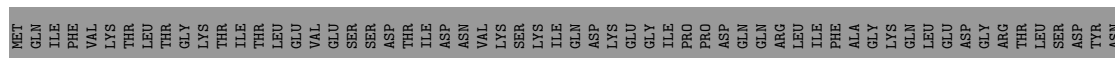
- Molecule 43: RPL38 isoform 1



- Molecule 44: 60S ribosomal protein L39



- Molecule 45: 60S ribosomal protein L40

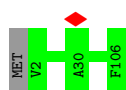


• Molecule 46: RPL41A isoform 1

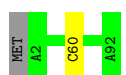


There are no outlier residues recorded for this chain.

• Molecule 47: 60S ribosomal protein L42-A



• Molecule 48: 60S ribosomal protein L43-A



• Molecule 49: 18S ribosomal RNA

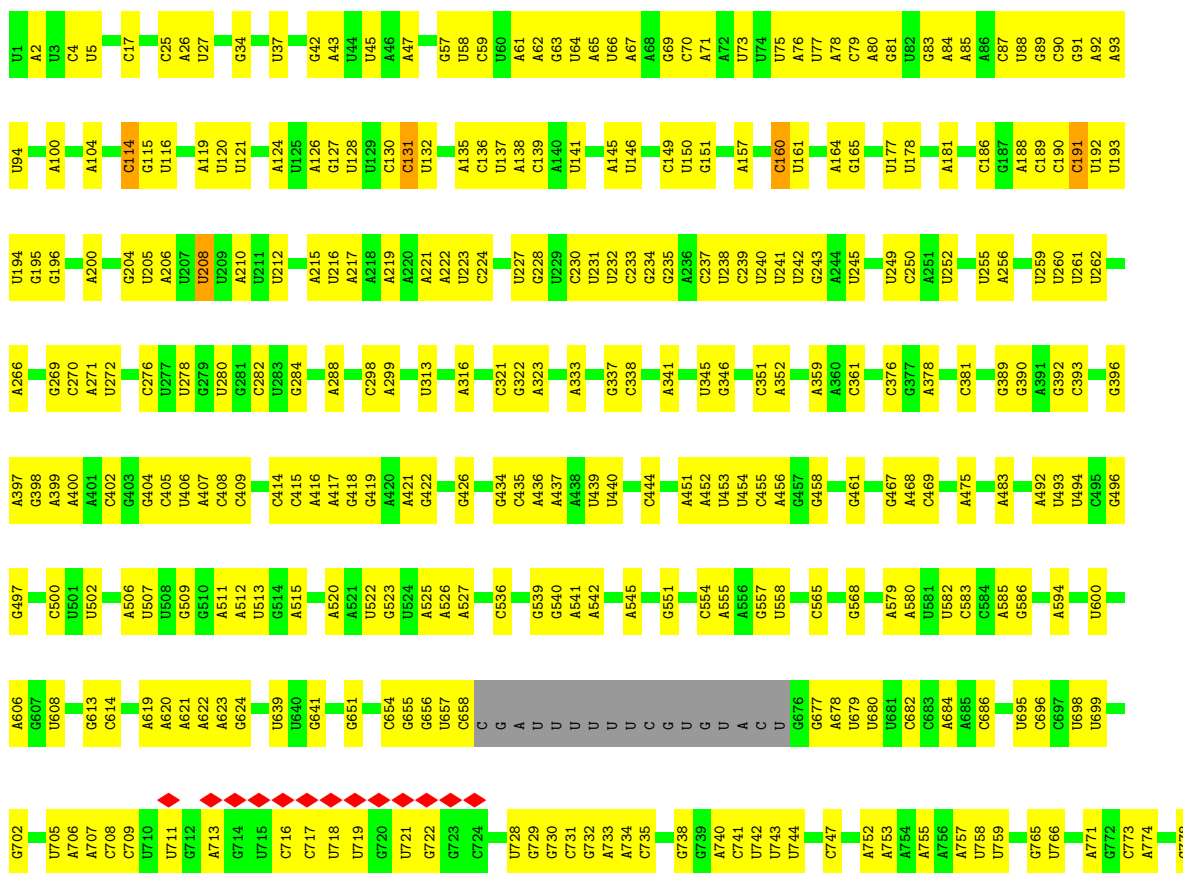
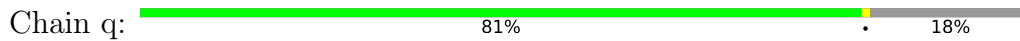


Table showing residue IDs and their corresponding quality metrics (A, B, C, G) for various chains.

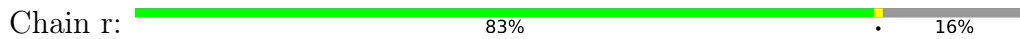
U779 A760	A865	C1016	A1138 A1139	G	A1386	C1404	G1507	U1612	C1706 A1707 U1708
A783	A884	C1021	G1150	C	A1337	U1407	U1508	U1613	A1709
C784	A884	C1021	C1150	A	A1338	A1410	C1509	A1614	C1708
U789	A894	A1025	C1158	C	C1339	A1411	U1510	C1615	U1710
A799	C895	A1026	C1159	A	U1340	A1412	G1512	U1616	C1711
U794	G896	A1027	C1162	U	A1341	C1412	G1513	C1618	A1712
A799	C897	A1028	C1163	U	C1342	U1413	U1514	C1619	G1713
G802	A898	A1029	C1164	G	U1343	U1414	A1515	C1620	U1714
A803	U903	A1030	C1165	A	A1344	U1415	U1516	G1622	G1715
A804	U912	A1031	C1166	C	A1345	A1427	U1517	G1622	C1716
U805	G913	G1032	G1167	C	A1346	G1428	U1518	A1631	G1717
A806	C914	A1039	C1174	U	A1347	U1432	U1519	A1631	G1718
A807	U917	U1052	U1181	C	U1348	U1433	A1520	C1634	A1719
G810	U918	G1053	U1182	U	U1349	U1434	A1521	A1635	G1720
A811	A919	U1054	U1183	U	G1351	U1434	U1522	A1635	A1721
A812	U920	U1055	U1184	U	U1352	C1440	G1523	U1636	A1722
U813	U921	U1056	U1185	U	U1353	C1441	A1524	C1637	U1723
U814	G925	U	C1190	A	U1356	G1445	C1527	G1638	U1724
U815	A926	U	C1191	A	A1357	A1446	C1530	A1651	U1725
G815	C927	U	C1192	C	G1358	C1447	U1531	U1656	C1729
U820	U928	A1062	C1193	A	A1359	C1457	U1532	U1657	A1730
U821	A929	U1063	C1194	C	U1361	G1458	G1533	G1658	A1731
U829	U931	A930	C1199	U	U1362	G1459	U1534	C1664	G1745
U830	A933	G1064	G1200	C	U1363	A1460	G1535	G1670	G1746
U831	C934	A1076	G1201	C	U1366	G1467	A1537	G1671	G1747
U832	U935	A1081	G1202	U	G1367	A1471	U1538	G1672	A1755
U833	A944	A1091	A1203	U	A1371	C1472	U1539	G1673	A1756
G834	U951	A1092	C1204	C	C1372	U1473	G1540	C1677	G1757
U835	U960	A1097	C1205	U	C1373	G1474	G1542	C1678	U1788
U841	U961	U1098	C1206	A	C1375	A1479	A1550	A1680	C1759
C842	C962	U1099	C1207	C	C1376	G1480	U1557	A1681	A1763
U843	G962	G1100	C1212	C	U1377	C1481	U1558	U1682	A1766
U844	U965	G1101	C1213	U	C1378	A1482	U1559	U1683	G1767
G845	A966	U1113	U1214	C	C1379	C1485	U1560	U1684	G1768
G846	A970	A1118	C1215	C	U1381	C1485	U1561	G1685	U1769
C848	A973	C1123	A1217	C	A1382	U1489	A1569	C1686	U1770
A850	U973	A1124	G1218	U	G1383	U1490	G1575	U1687	U1779
U851	A988	C1128	U1219	U	A1384	U1491	A1582	U1688	G1780
C852	A992	G1126	C1220	A	G1387	A1492	U1583	A1689	A1781
G853	A993	U1131	A1221	C	A1388	A1493	G1584	A1694	C1783
U854	U1001	A1132	C1222	C	C1389	C1494	A1594	G1695	C1784
U857	U1004	U1135	A1223	C	U1390	G1495	A1596	G1696	G1782
A862	U1005	U1136	A	U	A1391	U1496	U1597	G1697	G1783
U864	A1137	U1136	U	C	U1392	U1497	G1590	C1698	A1784
		A1137	A	U	U1393	G1498	U1596	C1699	C1784
		U1137	A	U	U1398	C1501	C1596	C1700	G1792
		A1137	U	U	C1399	G1502	A1600	A1701	G1793
		A1137	U	U	A1400	G1504	A1611	A1702	A1794
		A1137	U	U	A1401	G1504	A1611	C1703	U1795
		A1137	U	U	A1401	G1504	A1611	U1704	C1796
		A1137	U	U	A1401	G1504	A1611	U1705	A1797
		A1137	U	U	A1401	G1504	A1611	U1705	U1798
		A1137	U	U	A1401	G1504	A1611	U1705	U
		A1137	U	U	A1401	G1504	A1611	U1705	A

Molecule 50: 40S ribosomal protein S0-A



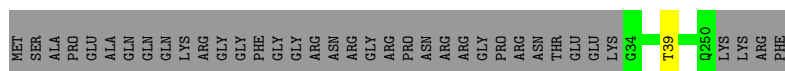
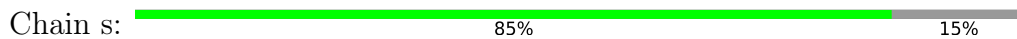
MET	S2	M109	Y110	I111	P207	GLU	VAL	GLY	GLN	VAL	GLY	GLY	GLY	VAL	THR	THR	GLY	GLY	GLY	GLU	GLY	GLY	GLY	ALA	LYS	GLY	GLY	VAL	THR	GLY	GLY	GLN	ALA	GLY	GLY	ALA	ALA	THR	GLY	GLY	LEU	THR	ASP	ASP	ASN	ASN	VAL	TRP
-----	----	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Molecule 51: RPS1A isoform 1

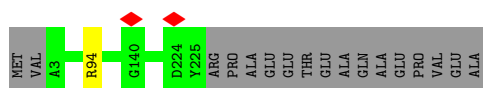


MET	ALA	VAL	GLY	LYS	ASN	LYS	ARG	LEU	SER	LYS	GLY	LYS	LYS	GLY	GLN	VAL	VAL	GLN	ALA	LYS	LYS	LYS	ARG	ARG	Y29	L61	F62	G63	K166	G233	GLU	GLY	SER	GLY	GLY	GLY	LYS	LYS	LYS	LYS	VAL	THR	GLY	PHE	LYS	ASP	VAL	VAL	LEU	GLU	THR	THR	VAL
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

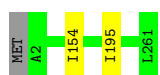
Molecule 52: RPS2 isoform 1



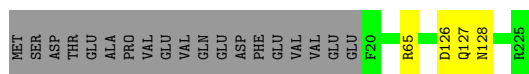
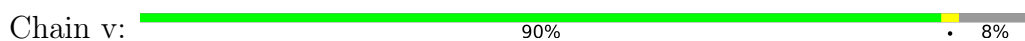
• Molecule 53: RPS3 isoform 1



• Molecule 54: 40S ribosomal protein S4-A



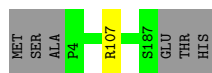
• Molecule 55: Rps5p



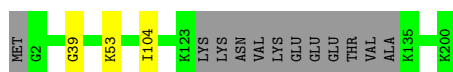
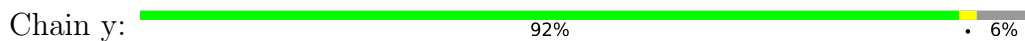
• Molecule 56: 40S ribosomal protein S6-A




• Molecule 57: 40S ribosomal protein S7-A

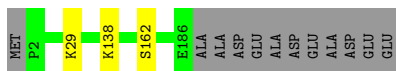


• Molecule 58: RPS8A isoform 1



• Molecule 59: 40S ribosomal protein S9-A

Chain z:  92% • 6%



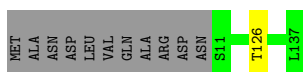
- Molecule 60: 40S ribosomal protein S13

Chain AD:  98% ..




- Molecule 61: 40S ribosomal protein S14-B

Chain AE:  91% • 8%



- Molecule 62: RPS15 isoform 1

Chain AF:  86% .. 13%




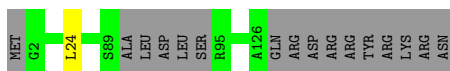
- Molecule 63: 40S ribosomal protein S16-A

Chain AG:  98% ..



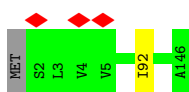
- Molecule 64: 40S ribosomal protein S17-B

Chain AH:  88% • 12%



- Molecule 65: 40S ribosomal protein S18-A

Chain AI:  99% ..




- Molecule 66: 40S ribosomal protein S19-A

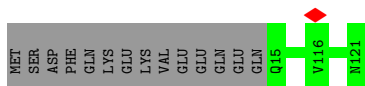


Chain AJ:  99%



- Molecule 67: RPS20 isoform 1

Chain AK:  88% 12%



- Molecule 68: 40S ribosomal protein S21-A

Chain AL:  99%



- Molecule 69: RPS22A isoform 1

Chain AM:  99%



- Molecule 70: 40S ribosomal protein S23-A

Chain AN:  98%



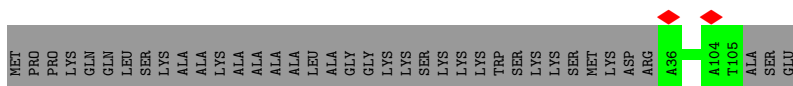
- Molecule 71: 40S ribosomal protein S24-A

Chain AO:  99%

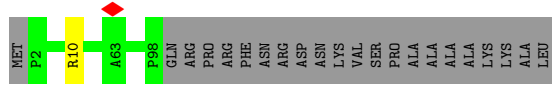
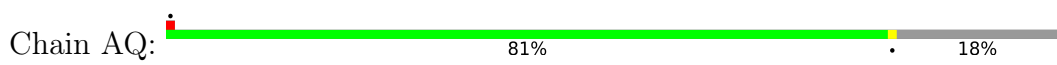


- Molecule 72: RPS25A isoform 1

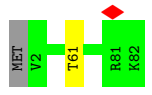
Chain AP:  65% 35%



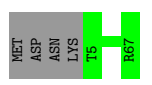
- Molecule 73: RPS26B isoform 1



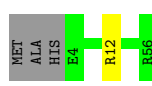
• Molecule 74: 40S ribosomal protein S27-A



• Molecule 75: RPS28A isoform 1



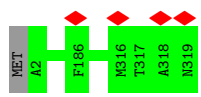
• Molecule 76: RPS29A isoform 1



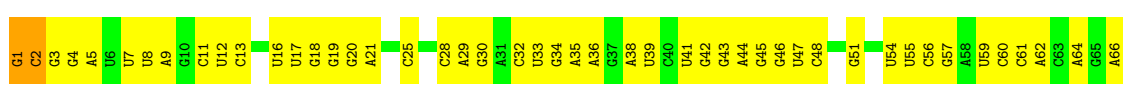
• Molecule 77: 40S ribosomal protein S30-A

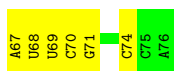


• Molecule 78: Guanine nucleotide-binding protein subunit beta-like protein



• Molecule 79: Transfer RNA





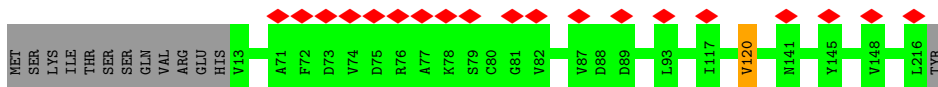
• Molecule 79: Transfer RNA



• Molecule 80: mRNA



• Molecule 81: RPL1A isoform 1



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	9629	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 ( $e^-/\text{\AA}^2$ )	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	27.135	Depositor
Minimum map value	-15.154	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	545.792, 545.792, 545.792	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.066, 1.066, 1.066	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section:  
ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.27	0/1948	0.60	0/2617
2	B	0.27	0/3146	0.55	0/4228
3	C	0.27	0/2800	0.54	1/3790 (0.0%)
4	D	0.28	0/2425	0.53	0/3271
5	E	0.27	0/1260	0.53	0/1694
6	F	0.29	0/1821	0.52	0/2451
7	G	0.78	2/1836 (0.1%)	0.57	2/2481 (0.1%)
8	H	0.27	0/1539	0.56	0/2073
9	I	0.27	0/1741	0.55	0/2335
10	J	0.27	0/1374	0.59	0/1842
11	L	0.27	0/1568	0.57	0/2106
12	M	0.26	0/1068	0.52	0/1438
13	N	0.27	0/1757	0.58	0/2354
14	O	0.29	0/1585	0.54	0/2128
15	P	0.27	0/1443	0.53	0/1944
16	Q	0.26	0/1465	0.54	0/1965
17	R	0.27	0/1538	0.57	0/2050
18	S	0.28	0/1481	0.56	0/1990
19	T	0.28	0/1300	0.53	0/1743
20	U	0.29	0/812	0.53	1/1099 (0.1%)
21	V	0.27	0/1018	0.55	0/1369
22	W	0.28	0/533	0.56	0/707
23	X	0.27	0/979	0.50	0/1321
24	Y	0.25	0/1004	0.56	0/1341
25	Z	0.28	0/1118	0.50	0/1497
26	AA	0.31	0/789	0.53	0/1067
27	AB	0.27	0/1247	0.55	0/1681
28	1	1.52	15/77157 (0.0%)	1.05	259/120295 (0.2%)
29	3	0.36	0/2883	0.91	2/4491 (0.0%)
30	4	4.75	8/3746 (0.2%)	1.40	28/5832 (0.5%)
31	P0	0.29	0/1498	0.55	0/2025
32	P2	0.26	0/728	0.54	0/975

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	a	0.26	0/1204	0.56	0/1612
34	b	0.27	0/473	0.50	0/629
35	c	0.27	0/751	0.53	0/1008
36	d	0.26	0/897	0.55	0/1205
37	e	0.26	0/1041	0.52	0/1394
38	f	0.28	0/868	0.58	0/1168
39	g	0.29	0/890	0.61	0/1189
40	h	0.28	0/978	0.53	0/1301
41	i	0.27	0/778	0.53	0/1034
42	j	2.01	1/696 (0.1%)	0.80	3/923 (0.3%)
43	k	0.27	0/618	0.56	0/826
44	l	0.29	0/443	0.65	0/588
45	m	0.27	0/423	0.55	0/562
46	n	0.26	0/228	0.64	0/293
47	o	0.28	0/860	0.57	0/1136
48	p	0.27	0/701	0.62	0/934
49	2	0.53	6/41539 (0.0%)	1.08	65/64723 (0.1%)
50	q	0.27	0/1617	0.52	0/2215
51	r	0.26	0/1735	0.58	1/2335 (0.0%)
52	s	0.27	0/1665	0.54	0/2263
53	t	0.28	0/1759	0.55	0/2368
54	u	0.26	0/2109	0.57	0/2839
55	v	0.27	0/1629	0.56	0/2202
56	w	0.28	0/1814	0.60	0/2425
57	x	0.28	0/1506	0.54	0/2028
58	y	0.27	0/1514	0.59	0/2021
59	z	0.26	0/1519	0.55	0/2035
60	AD	0.27	0/1215	0.57	0/1638
61	AE	0.26	0/901	0.57	0/1217
62	AF	0.28	0/998	0.55	0/1341
63	AG	0.28	0/1125	0.54	0/1510
64	AH	0.27	0/935	0.58	1/1254 (0.1%)
65	AI	0.25	0/1211	0.56	0/1628
66	AJ	0.28	0/1130	0.58	0/1517
67	AK	0.26	0/865	0.53	0/1169
68	AL	0.28	0/693	0.56	0/935
69	AM	0.26	0/1038	0.55	0/1395
70	AN	0.27	0/1139	0.58	0/1518
71	AO	0.27	0/1087	0.55	0/1449
72	AP	0.27	0/571	0.53	0/768
73	AQ	0.27	0/782	0.59	0/1047
74	AR	0.25	0/620	0.50	0/838
75	AS	0.28	0/499	0.58	0/670

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	AT	0.27	0/452	0.59	0/600
77	AU	0.27	0/483	0.53	0/643
78	AV	0.25	0/2490	0.52	0/3389
79	AX	0.36	1/1818 (0.1%)	0.85	1/2831 (0.0%)
79	AZ	0.35	1/1818 (0.1%)	0.86	0/2831
80	AY	0.24	0/181	0.98	0/278
81	L1	0.27	0/1634	0.53	0/2195
All	All	1.14	34/220547 (0.0%)	0.90	364/324117 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
3	C	0	1
7	G	0	1
11	L	0	1
14	O	0	1
39	g	0	1
45	m	0	1
54	u	0	1
55	v	0	1
81	L1	0	1
All	All	0	10

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	1	148	G	C6-N1	153.66	2.47	1.39
28	1	148	G	N3-C4	144.30	2.36	1.35
30	4	95	G	N3-C4	138.97	2.32	1.35
30	4	95	G	C6-N1	136.18	2.34	1.39
28	1	2262	A	N3-C4	134.62	2.15	1.34

The worst 5 of 364 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	2	1759	C	C6-N1-C2	-126.81	69.58	120.30
49	2	1759	C	C5-C6-N1	69.15	155.57	121.00
49	2	1759	C	N3-C2-O2	-38.63	94.86	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	1	148	G	C4-C5-N7	-38.09	95.56	110.80
28	1	2262	A	N1-C2-N3	-35.62	111.49	129.30

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	150	LEU	Peptide
3	C	182	LEU	Peptide
7	G	135	GLY	Mainchain
11	L	47	ALA	Peptide
14	O	110	PRO	Peptide

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

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

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	250/254 (98%)	215 (86%)	33 (13%)	2 (1%)	19	60
2	B	384/387 (99%)	339 (88%)	45 (12%)	0	100	100
3	C	359/362 (99%)	314 (88%)	44 (12%)	1 (0%)	41	76
4	D	294/297 (99%)	263 (90%)	31 (10%)	0	100	100
5	E	152/176 (86%)	134 (88%)	18 (12%)	0	100	100
6	F	220/244 (90%)	198 (90%)	22 (10%)	0	100	100
7	G	231/256 (90%)	208 (90%)	22 (10%)	1 (0%)	34	72
8	H	189/191 (99%)	167 (88%)	21 (11%)	1 (0%)	29	68
9	I	207/221 (94%)	185 (89%)	22 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	J	167/174 (96%)	139 (83%)	28 (17%)	0	100	100
11	L	191/199 (96%)	154 (81%)	34 (18%)	3 (2%)	9	45
12	M	134/138 (97%)	122 (91%)	11 (8%)	1 (1%)	22	62
13	N	201/204 (98%)	176 (88%)	23 (11%)	2 (1%)	15	54
14	O	195/199 (98%)	177 (91%)	17 (9%)	1 (0%)	29	68
15	P	181/184 (98%)	169 (93%)	12 (7%)	0	100	100
16	Q	183/186 (98%)	168 (92%)	15 (8%)	0	100	100
17	R	186/189 (98%)	175 (94%)	11 (6%)	0	100	100
18	S	170/172 (99%)	148 (87%)	22 (13%)	0	100	100
19	T	157/160 (98%)	139 (88%)	17 (11%)	1 (1%)	25	64
20	U	98/121 (81%)	93 (95%)	5 (5%)	0	100	100
21	V	134/137 (98%)	114 (85%)	18 (13%)	2 (2%)	10	46
22	W	61/155 (39%)	57 (93%)	4 (7%)	0	100	100
23	X	119/142 (84%)	107 (90%)	12 (10%)	0	100	100
24	Y	124/127 (98%)	117 (94%)	7 (6%)	0	100	100
25	Z	133/136 (98%)	117 (88%)	15 (11%)	1 (1%)	19	60
26	AA	94/105 (90%)	81 (86%)	12 (13%)	1 (1%)	14	52
27	AB	151/156 (97%)	129 (85%)	22 (15%)	0	100	100
31	P0	187/312 (60%)	143 (76%)	44 (24%)	0	100	100
32	P2	92/165 (56%)	70 (76%)	22 (24%)	0	100	100
33	a	146/149 (98%)	122 (84%)	23 (16%)	1 (1%)	22	62
34	b	56/59 (95%)	46 (82%)	10 (18%)	0	100	100
35	c	95/105 (90%)	87 (92%)	7 (7%)	1 (1%)	14	52
36	d	107/113 (95%)	96 (90%)	11 (10%)	0	100	100
37	e	125/130 (96%)	111 (89%)	14 (11%)	0	100	100
38	f	104/107 (97%)	89 (86%)	14 (14%)	1 (1%)	15	54
39	g	110/121 (91%)	98 (89%)	12 (11%)	0	100	100
40	h	117/120 (98%)	105 (90%)	12 (10%)	0	100	100
41	i	97/100 (97%)	82 (84%)	15 (16%)	0	100	100
42	j	85/88 (97%)	74 (87%)	11 (13%)	0	100	100
43	k	75/78 (96%)	69 (92%)	6 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	l	48/51 (94%)	41 (85%)	7 (15%)	0	100	100
45	m	50/128 (39%)	37 (74%)	12 (24%)	1 (2%)	7	40
46	n	23/25 (92%)	21 (91%)	2 (9%)	0	100	100
47	o	103/106 (97%)	84 (82%)	19 (18%)	0	100	100
48	p	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
50	q	204/252 (81%)	173 (85%)	29 (14%)	2 (1%)	15	54
51	r	212/255 (83%)	177 (84%)	34 (16%)	1 (0%)	29	68
52	s	215/254 (85%)	195 (91%)	19 (9%)	1 (0%)	29	68
53	t	221/240 (92%)	187 (85%)	34 (15%)	0	100	100
54	u	258/261 (99%)	210 (81%)	47 (18%)	1 (0%)	34	72
55	v	204/225 (91%)	172 (84%)	30 (15%)	2 (1%)	15	54
56	w	221/236 (94%)	171 (77%)	47 (21%)	3 (1%)	11	47
57	x	182/190 (96%)	156 (86%)	26 (14%)	0	100	100
58	y	184/200 (92%)	154 (84%)	28 (15%)	2 (1%)	14	52
59	z	183/197 (93%)	159 (87%)	23 (13%)	1 (0%)	29	68
60	AD	148/151 (98%)	131 (88%)	15 (10%)	2 (1%)	11	47
61	AE	125/138 (91%)	107 (86%)	17 (14%)	1 (1%)	19	60
62	AF	122/142 (86%)	98 (80%)	22 (18%)	2 (2%)	9	45
63	AG	139/143 (97%)	109 (78%)	29 (21%)	1 (1%)	22	62
64	AH	116/136 (85%)	105 (90%)	11 (10%)	0	100	100
65	AI	143/146 (98%)	125 (87%)	17 (12%)	1 (1%)	22	62
66	AJ	141/144 (98%)	123 (87%)	18 (13%)	0	100	100
67	AK	105/121 (87%)	84 (80%)	21 (20%)	0	100	100
68	AL	85/87 (98%)	68 (80%)	16 (19%)	1 (1%)	13	50
69	AM	127/130 (98%)	114 (90%)	13 (10%)	0	100	100
70	AN	142/145 (98%)	113 (80%)	28 (20%)	1 (1%)	22	62
71	AO	132/135 (98%)	119 (90%)	13 (10%)	0	100	100
72	AP	68/108 (63%)	53 (78%)	15 (22%)	0	100	100
73	AQ	95/119 (80%)	69 (73%)	26 (27%)	0	100	100
74	AR	79/82 (96%)	65 (82%)	13 (16%)	1 (1%)	12	48
75	AS	61/67 (91%)	52 (85%)	9 (15%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
76	AT	51/56 (91%)	46 (90%)	5 (10%)	0	100	100
77	AU	58/63 (92%)	51 (88%)	7 (12%)	0	100	100
78	AV	316/319 (99%)	269 (85%)	47 (15%)	0	100	100
81	L1	202/217 (93%)	155 (77%)	46 (23%)	1 (0%)	29	68
All	All	11213/12280 (91%)	9675 (86%)	1493 (13%)	45 (0%)	38	72

5 of 45 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	L	47	ALA
11	L	48	PRO
11	L	62	THR
14	O	110	PRO
50	q	111	ILE

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

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	193/196 (98%)	191 (99%)	2 (1%)	76	86
2	B	319/323 (99%)	318 (100%)	1 (0%)	92	95
3	C	288/289 (100%)	285 (99%)	3 (1%)	76	86
4	D	244/245 (100%)	243 (100%)	1 (0%)	91	94
5	E	134/153 (88%)	133 (99%)	1 (1%)	84	90
6	F	186/205 (91%)	186 (100%)	0	100	100
7	G	187/208 (90%)	187 (100%)	0	100	100
8	H	171/171 (100%)	170 (99%)	1 (1%)	86	92
9	I	177/187 (95%)	176 (99%)	1 (1%)	86	92
10	J	147/151 (97%)	146 (99%)	1 (1%)	84	90
11	L	154/159 (97%)	154 (100%)	0	100	100
12	M	107/109 (98%)	107 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	N	175/176 (99%)	174 (99%)	1 (1%)	86	92
14	O	160/162 (99%)	159 (99%)	1 (1%)	86	92
15	P	140/146 (96%)	139 (99%)	1 (1%)	84	90
16	Q	150/151 (99%)	150 (100%)	0	100	100
17	R	153/154 (99%)	153 (100%)	0	100	100
18	S	156/156 (100%)	154 (99%)	2 (1%)	69	82
19	T	136/137 (99%)	136 (100%)	0	100	100
20	U	87/107 (81%)	86 (99%)	1 (1%)	73	84
21	V	104/105 (99%)	104 (100%)	0	100	100
22	W	55/129 (43%)	55 (100%)	0	100	100
23	X	104/118 (88%)	103 (99%)	1 (1%)	76	86
24	Y	109/110 (99%)	108 (99%)	1 (1%)	78	87
25	Z	115/116 (99%)	115 (100%)	0	100	100
26	AA	77/98 (79%)	77 (100%)	0	100	100
27	AB	133/137 (97%)	133 (100%)	0	100	100
31	P0	160/254 (63%)	160 (100%)	0	100	100
32	P2	81/136 (60%)	80 (99%)	1 (1%)	71	83
33	a	118/119 (99%)	117 (99%)	1 (1%)	81	89
34	b	46/47 (98%)	46 (100%)	0	100	100
35	c	81/88 (92%)	80 (99%)	1 (1%)	71	83
36	d	94/97 (97%)	94 (100%)	0	100	100
37	e	109/111 (98%)	109 (100%)	0	100	100
38	f	90/91 (99%)	90 (100%)	0	100	100
39	g	95/103 (92%)	94 (99%)	1 (1%)	73	84
40	h	104/105 (99%)	103 (99%)	1 (1%)	76	86
41	i	81/82 (99%)	81 (100%)	0	100	100
42	j	70/71 (99%)	70 (100%)	0	100	100
43	k	68/69 (99%)	68 (100%)	0	100	100
44	l	45/46 (98%)	45 (100%)	0	100	100
45	m	47/116 (40%)	47 (100%)	0	100	100
46	n	22/23 (96%)	22 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	o	90/91 (99%)	90 (100%)	0	100	100
48	p	71/72 (99%)	70 (99%)	1 (1%)	67	80
50	q	164/210 (78%)	164 (100%)	0	100	100
51	r	191/224 (85%)	190 (100%)	1 (0%)	88	93
52	s	176/205 (86%)	176 (100%)	0	100	100
53	t	182/195 (93%)	181 (100%)	1 (0%)	88	93
54	u	221/222 (100%)	221 (100%)	0	100	100
55	v	173/191 (91%)	172 (99%)	1 (1%)	86	92
56	w	189/201 (94%)	188 (100%)	1 (0%)	88	93
57	x	165/170 (97%)	164 (99%)	1 (1%)	86	92
58	y	150/161 (93%)	149 (99%)	1 (1%)	84	90
59	z	158/166 (95%)	156 (99%)	2 (1%)	69	82
60	AD	127/128 (99%)	127 (100%)	0	100	100
61	AE	81/105 (77%)	81 (100%)	0	100	100
62	AF	101/118 (86%)	100 (99%)	1 (1%)	76	86
63	AG	117/119 (98%)	117 (100%)	0	100	100
64	AH	94/124 (76%)	94 (100%)	0	100	100
65	AI	128/129 (99%)	128 (100%)	0	100	100
66	AJ	115/116 (99%)	115 (100%)	0	100	100
67	AK	100/114 (88%)	100 (100%)	0	100	100
68	AL	74/74 (100%)	74 (100%)	0	100	100
69	AM	110/111 (99%)	110 (100%)	0	100	100
70	AN	119/120 (99%)	118 (99%)	1 (1%)	81	89
71	AO	112/113 (99%)	112 (100%)	0	100	100
72	AP	61/89 (68%)	61 (100%)	0	100	100
73	AQ	83/100 (83%)	82 (99%)	1 (1%)	71	83
74	AR	70/71 (99%)	70 (100%)	0	100	100
75	AS	56/60 (93%)	56 (100%)	0	100	100
76	AT	47/49 (96%)	46 (98%)	1 (2%)	53	71
77	AU	51/54 (94%)	50 (98%)	1 (2%)	55	73
78	AV	259/262 (99%)	259 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
81	L1	185/198 (93%)	185 (100%)	0	100	100
All	All	9492/10318 (92%)	9454 (100%)	38 (0%)	91	94

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
56	w	94	ARG
73	AQ	10	ARG
57	x	107	ARG
59	z	138	LYS
77	AU	10	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
24	Y	81	GLN
34	b	19	ASN
45	m	120	GLN
12	M	126	GLN
8	H	9	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	1	3220/3395 (94%)	1863 (57%)	158 (4%)
29	3	120/121 (99%)	49 (40%)	5 (4%)
30	4	157/158 (99%)	86 (54%)	9 (5%)
49	2	1739/1800 (96%)	675 (38%)	20 (1%)
79	AX	76/76 (100%)	51 (67%)	3 (3%)
79	AZ	75/76 (98%)	40 (53%)	1 (1%)
80	AY	7/8 (87%)	6 (85%)	0
All	All	5394/5634 (95%)	2770 (51%)	196 (3%)

5 of 2770 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
28	1	7	C
28	1	14	U
28	1	15	C

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Mol	Chain	Res	Type
28	1	19	U
28	1	20	A

5 of 196 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
28	1	2520	A
28	1	2981	U
28	1	2633	U
28	1	2816	G
28	1	3113	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](#)

Of 7 ligands modelled in this entry, 7 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

There are no chain breaks in this entry.



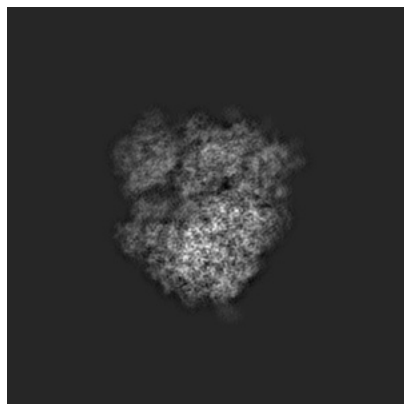
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22196. These allow visual inspection of the internal detail of the map and identification of artifacts.

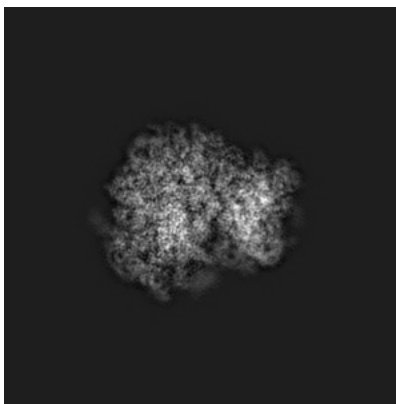
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

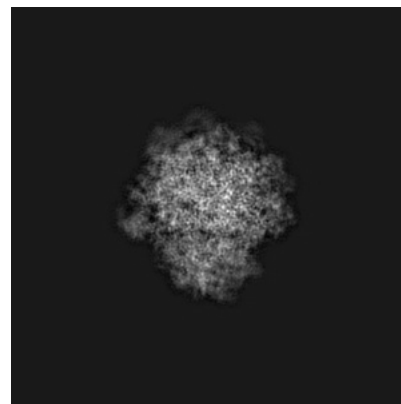
#### 6.1.1 Primary map



X

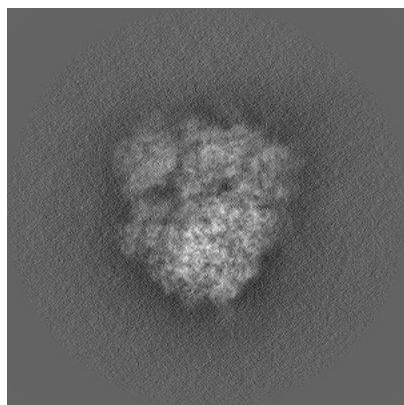


Y

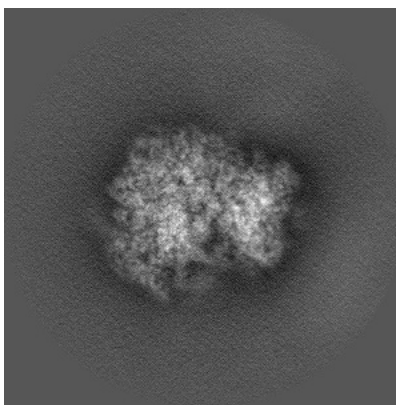


Z

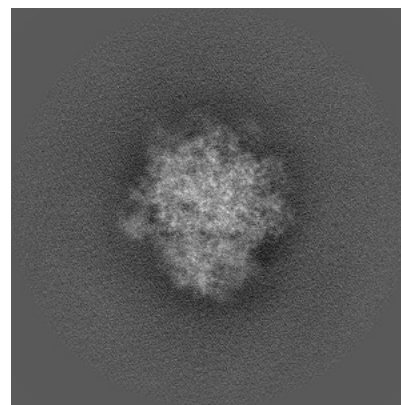
#### 6.1.2 Raw map



X



Y

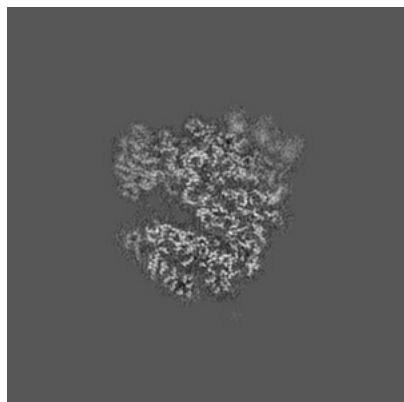


Z

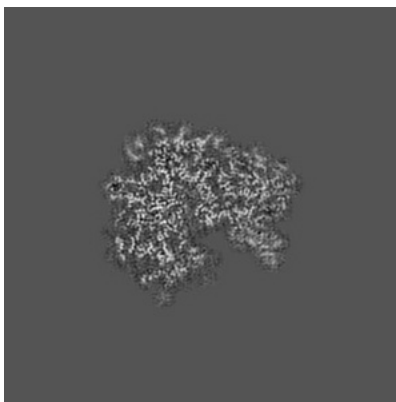
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

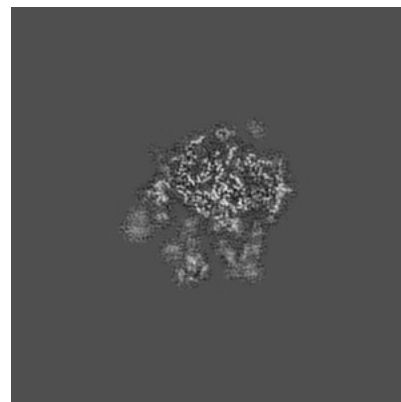
### 6.2.1 Primary map



X Index: 256

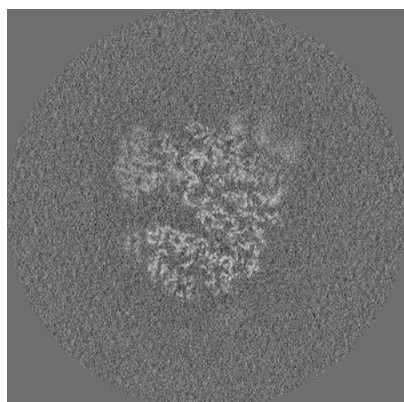


Y Index: 256

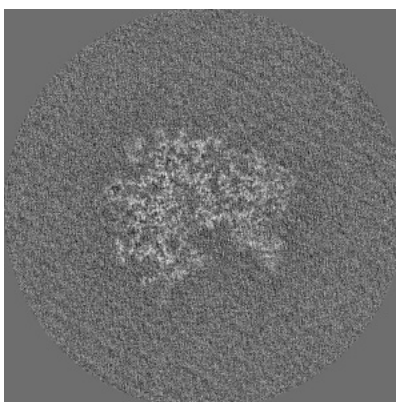


Z Index: 256

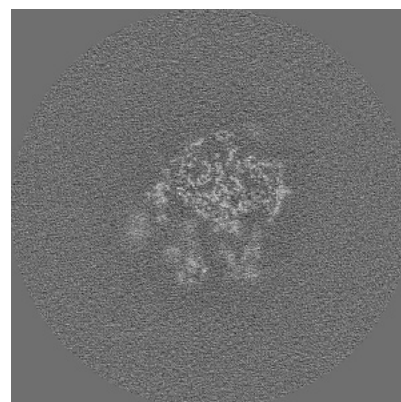
### 6.2.2 Raw map



X Index: 256



Y Index: 256

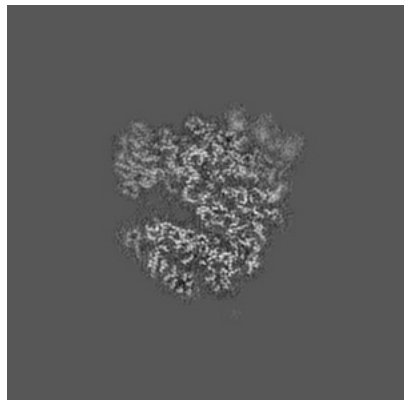


Z Index: 256

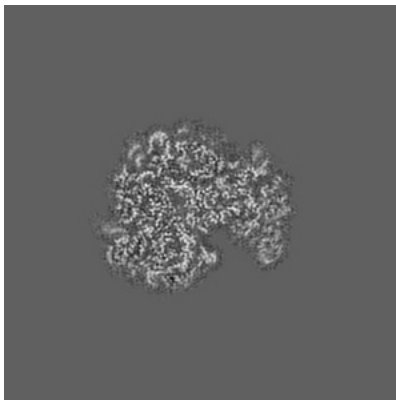
The images above show central slices of the map in three orthogonal directions.

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

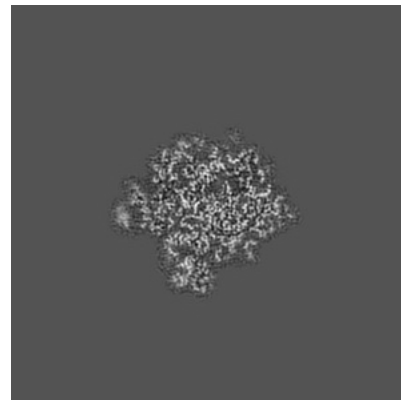
### 6.3.1 Primary map



X Index: 256

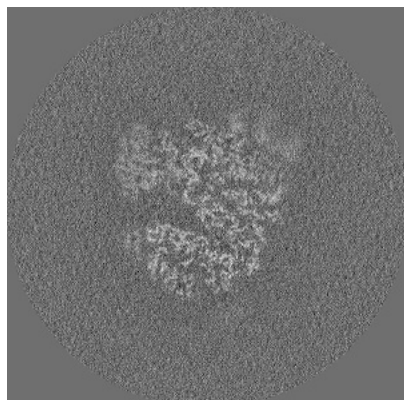


Y Index: 266

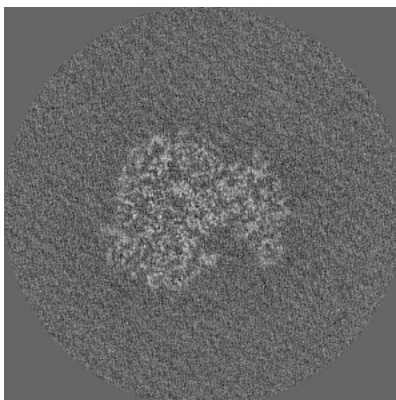


Z Index: 206

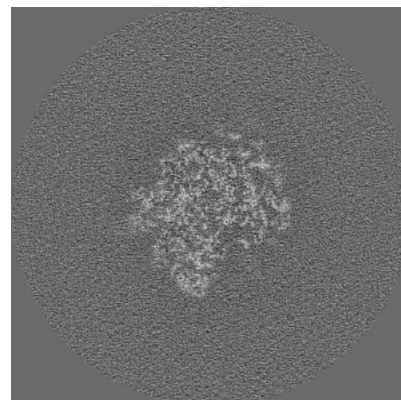
### 6.3.2 Raw map



X Index: 256



Y Index: 267

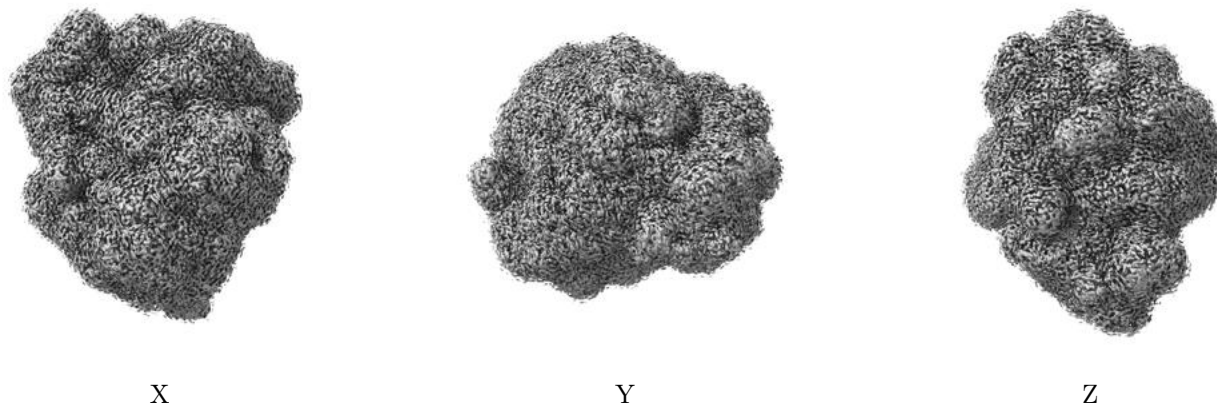


Z Index: 227

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

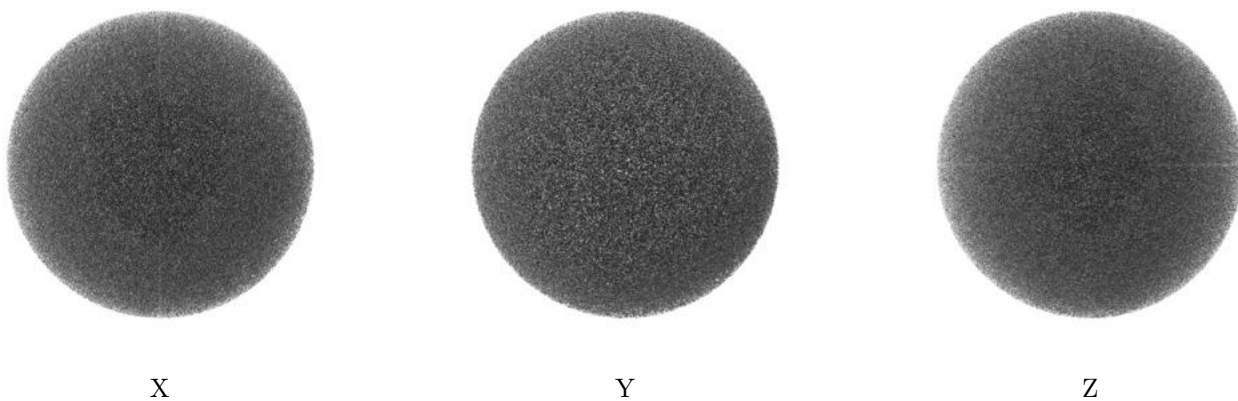
## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 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.

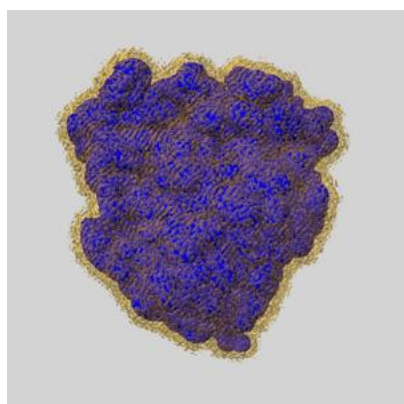
## 6.5 Mask visualisation [i](#)

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

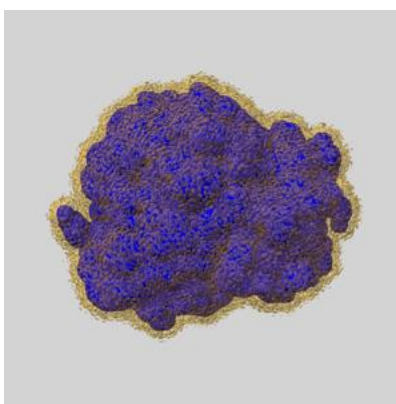
A mask typically either:

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

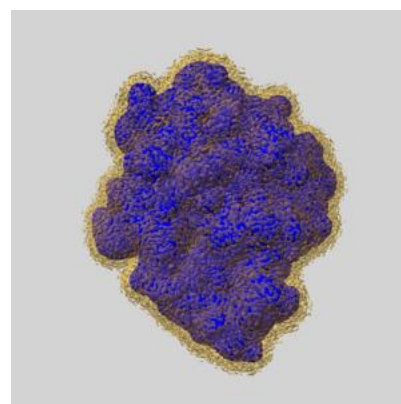
### 6.5.1 emd\_22196\_msk\_1.map [i](#)



X



Y



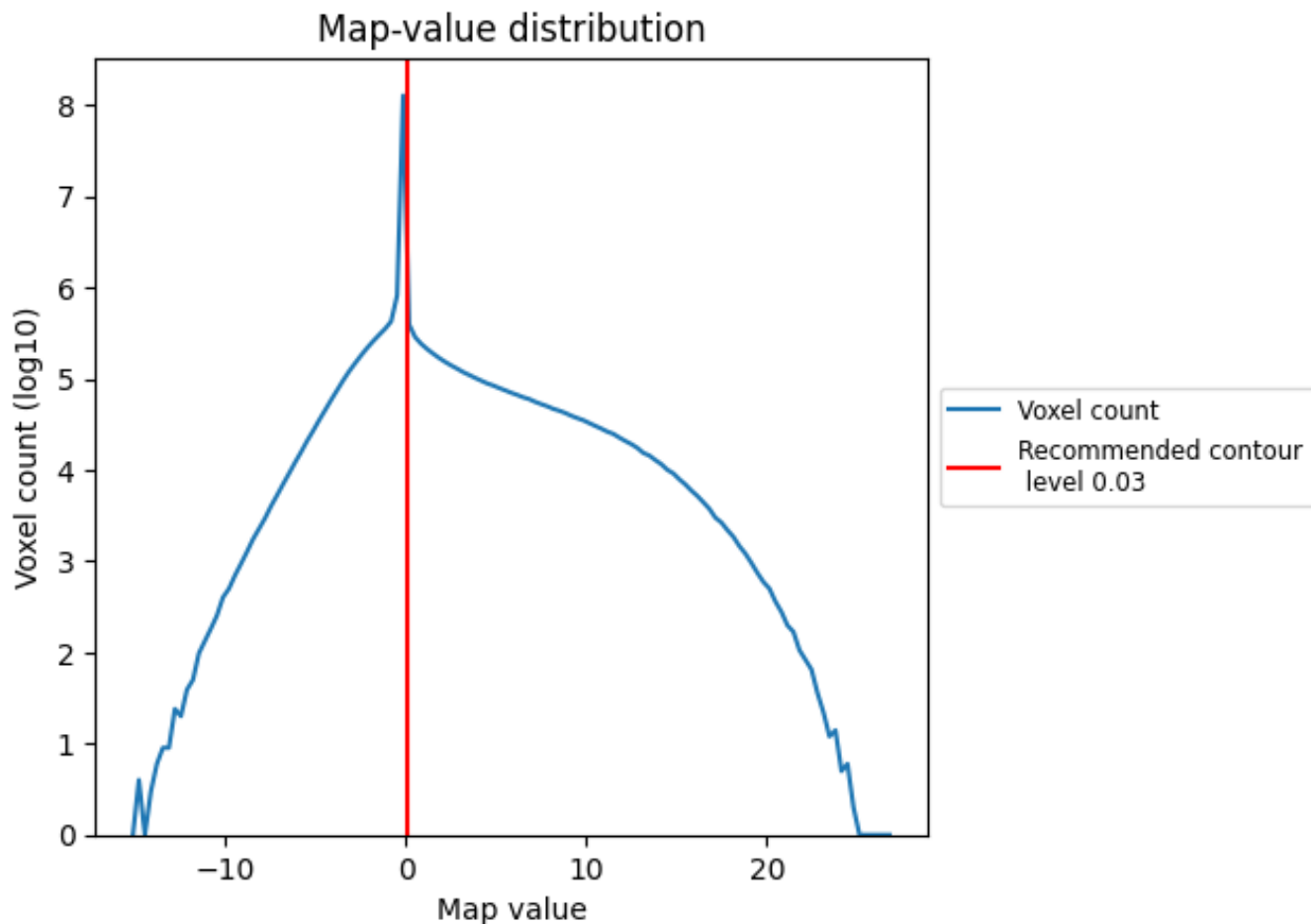
Z



## 7 Map analysis [i](#)

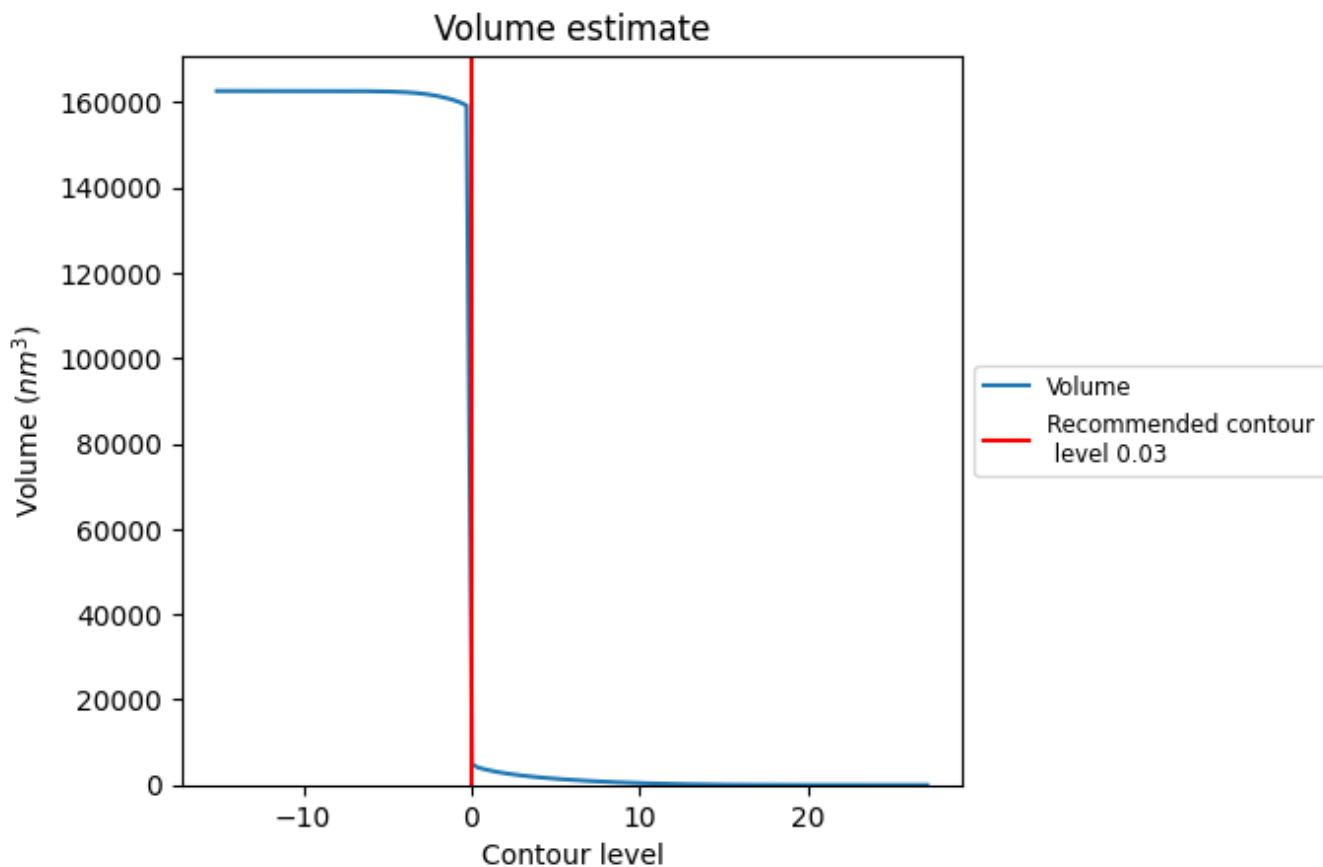
This section contains the results of statistical analysis of the map.

### 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.

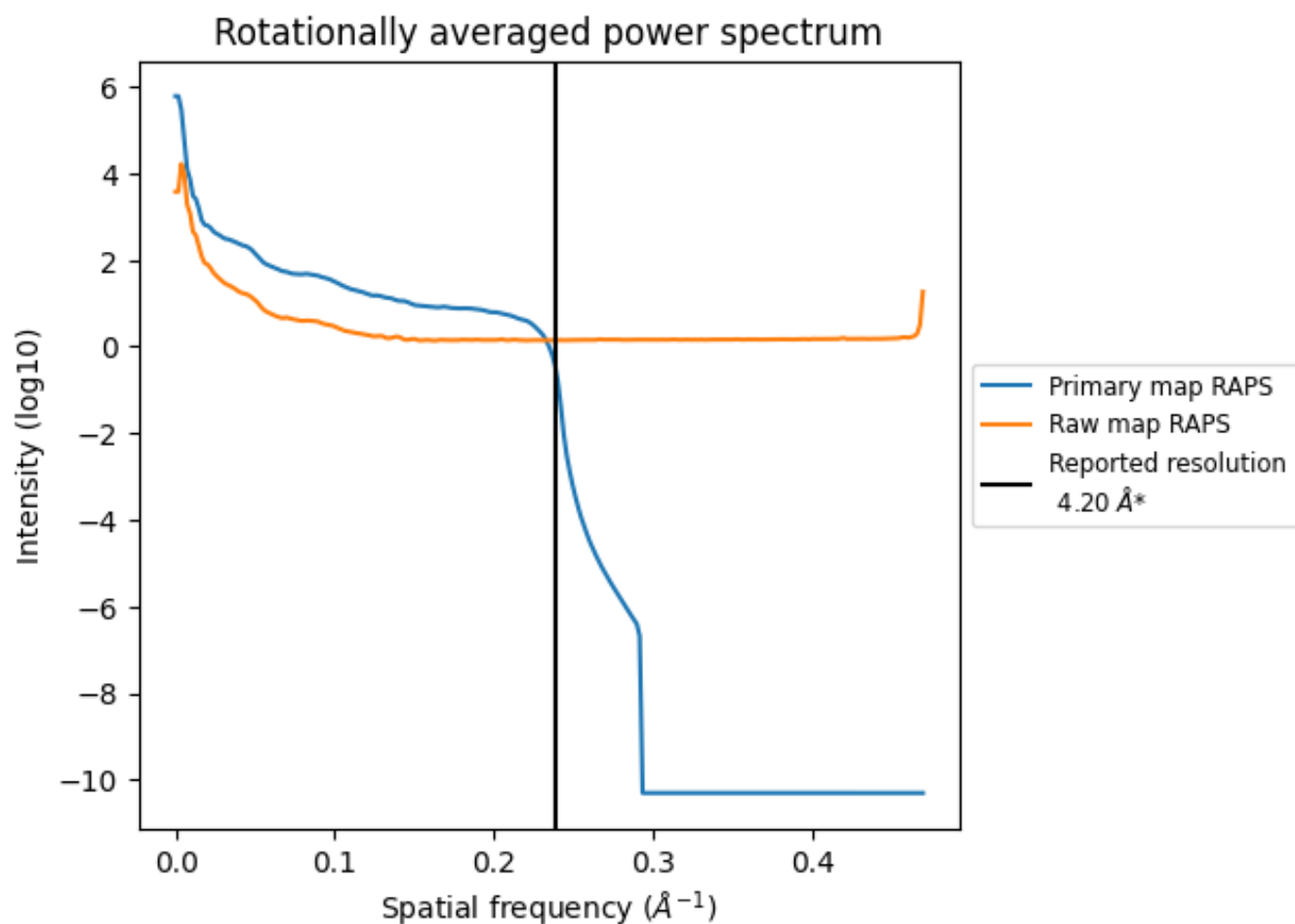
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 11315 nm<sup>3</sup>; this corresponds to an approximate mass of 10221 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](#)



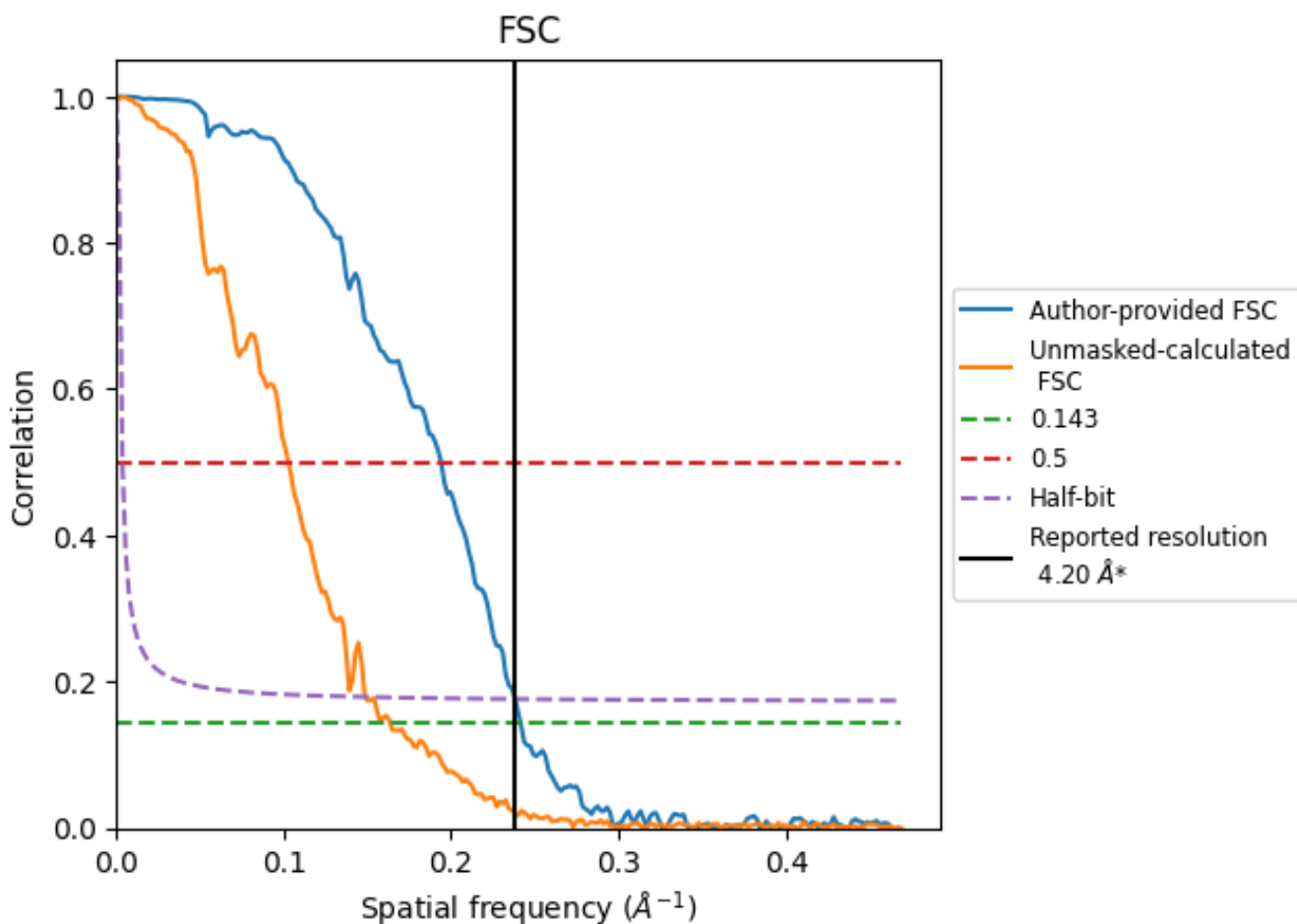
\*Reported resolution corresponds to spatial frequency of 0.238 Å<sup>-1</sup>



## 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 0.238 Å<sup>-1</sup>

## 8.2 Resolution estimates

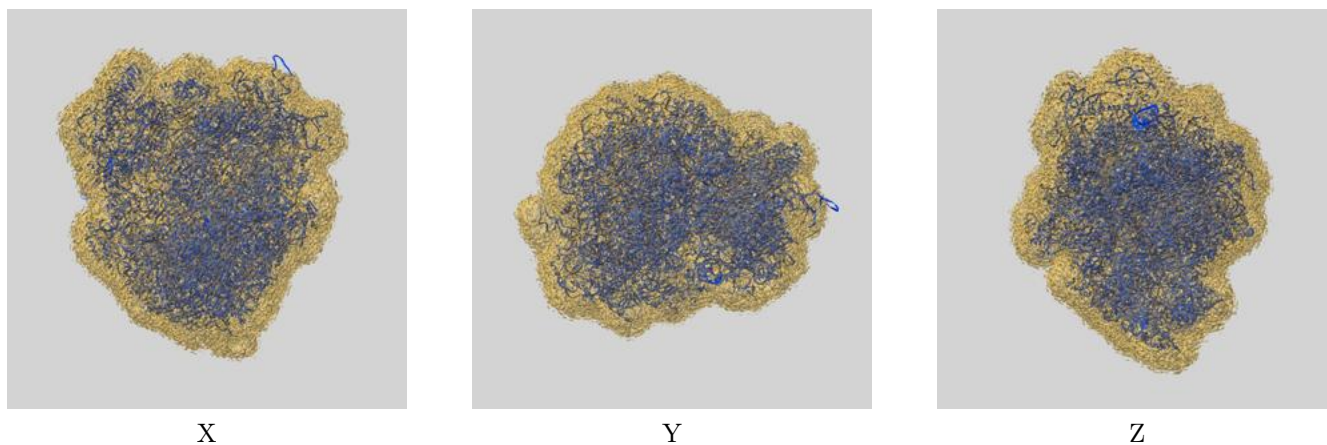
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	4.14	5.15	4.20
Unmasked-calculated*	6.11	9.73	6.72

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.11 differs from the reported value 4.2 by more than 10 %

## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-22196 and PDB model 6XIQ. Per-residue inclusion information can be found in section 3 on page 19.

### 9.1 Map-model overlay [i](#)

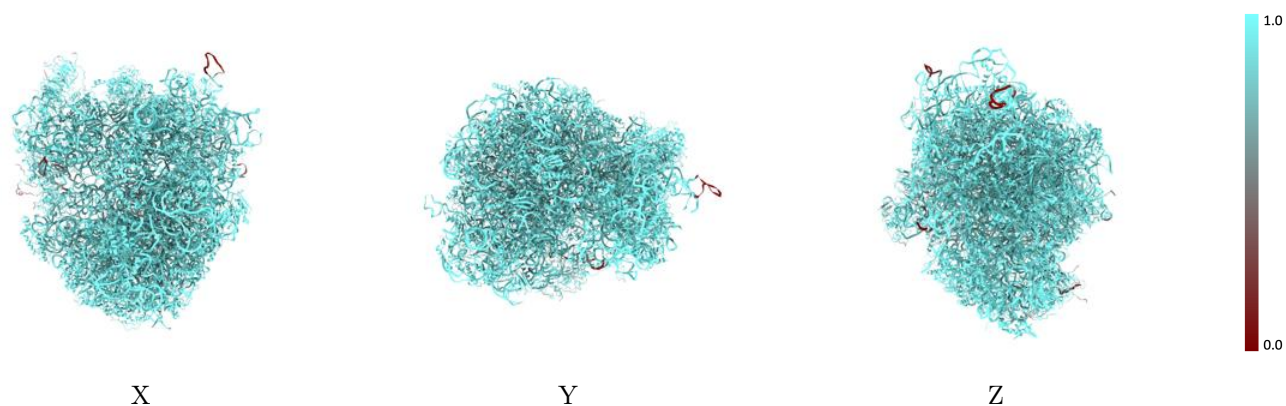


The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

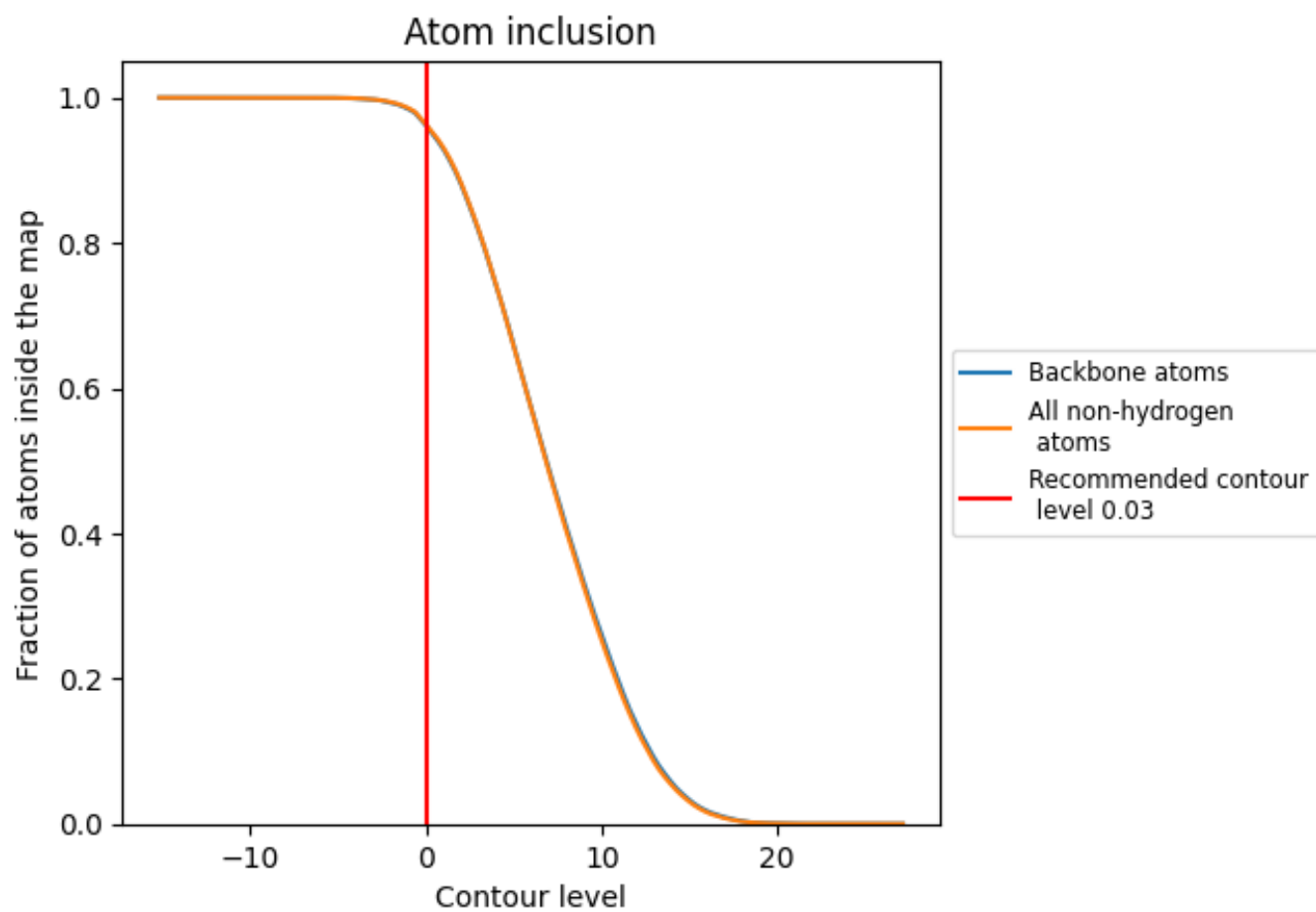
This section was not generated.

## 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 (0.03).




































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion
All	 0.9625
1	 0.9455
2	 0.9797
3	 0.9849
4	 0.9374
A	 0.9126
AA	 0.9881
AB	 0.9731
AD	 0.9732
AE	 0.9756
AF	 0.9810
AG	 0.9620
AH	 0.9756
AI	 0.9731
AJ	 0.9880
AK	 0.9321
AL	 0.9849
AM	 0.9800
AN	 0.9826
AO	 0.9914
AP	 0.9452
AQ	 0.9554
AR	 0.9751
AS	 0.9874
AT	 0.9505
AU	 0.9804
AV	 0.9558
AX	 0.9317
AY	 0.9085
AZ	 0.9102
B	 0.9853
C	 0.9859
D	 0.9862
E	 0.9876
F	 0.9851









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Chain	Atom inclusion
G	 0.9780
H	 0.9792
I	 0.9824
J	 0.9848
L	 0.9825
L1	 0.8369
M	 0.9893
N	 0.9786
O	 0.9789
P	 0.9688
P0	 0.7514
P2	 0.8956
Q	 0.9849
R	 0.9822
S	 0.9879
T	 0.9847
U	 0.9936
V	 0.9653
W	 0.9941
X	 0.9926
Y	 0.9928
Z	 0.9851
a	 0.9720
b	 0.9801
c	 0.9808
d	 0.9883
e	 0.9859
f	 0.9829
g	 0.9812
h	 0.9820
i	 0.9785
j	 0.9848
k	 0.9917
l	 0.9614
m	 0.7723
n	 0.9856
o	 0.9723
p	 0.9701
q	 0.9741
r	 0.9762
s	 0.9795
t	 0.9668

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<b>Chain</b>	<b>Atom inclusion</b>
u	 0.9801
v	 0.9803
w	 0.9585
x	 0.9807
y	 0.9833
z	 0.9750