



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 09:20 PM UTC

PDB ID : 6XIQ / pdb_00006xiq
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

A user guide is available at

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

The types of validation reports are described at

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

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

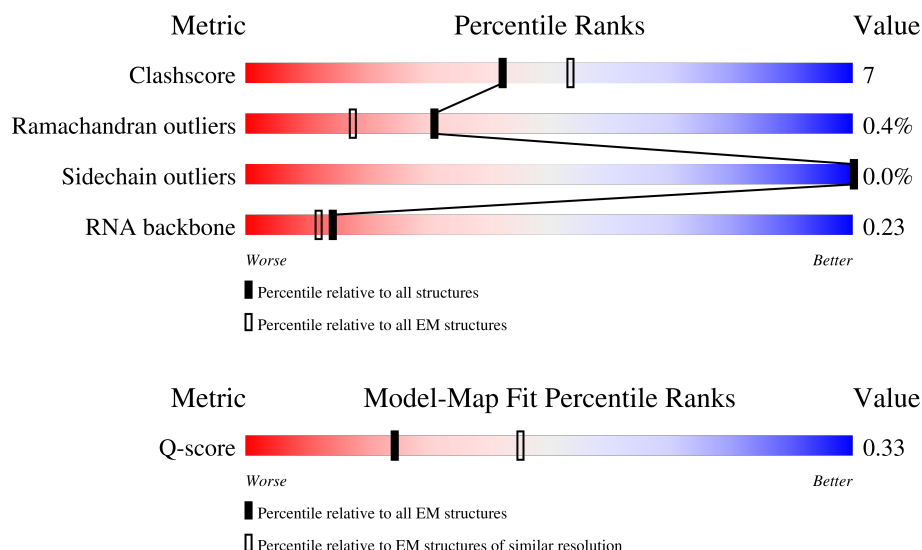
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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.



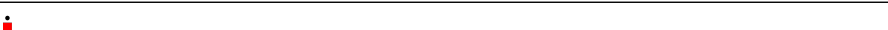
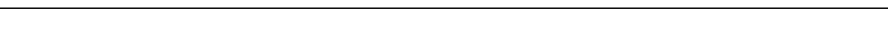
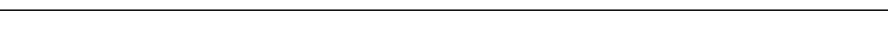
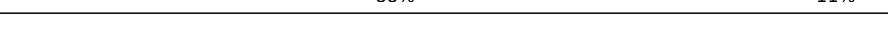
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5410 (3.70 - 4.70)

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

Mol	Chain	Length	Quality of chain
1	A	254	
2	B	387	
3	C	362	

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Mol	Chain	Length	Quality of chain
4	D	297	
5	E	176	
6	F	244	
7	G	256	
8	H	191	
9	I	221	
10	J	174	
11	L	199	
12	M	138	
13	N	204	
14	O	199	
15	P	184	
16	Q	186	
17	R	189	
18	S	172	
19	T	160	
20	U	121	
21	V	137	
22	W	155	
23	X	142	
24	Y	127	
25	Z	136	
26	AA	105	
27	AB	156	
28	1	3395	

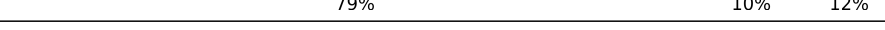
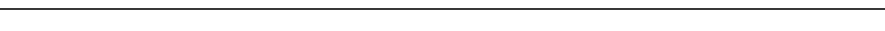
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Mol	Chain	Length	Quality of chain
29	3	121	
30	4	158	
31	P0	312	
32	P2	165	
33	a	149	
34	b	59	
35	c	105	
36	d	113	
37	e	130	
38	f	107	
39	g	121	
40	h	120	
41	i	100	
42	j	88	
43	k	78	
44	l	51	
45	m	128	
46	n	25	
47	o	106	
48	p	92	
49	2	1800	
50	q	252	
51	r	255	
52	s	254	
53	t	240	

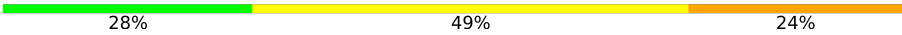
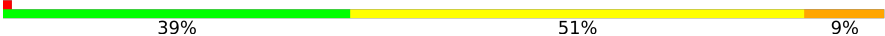
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Mol	Chain	Length	Quality of chain
54	u	261	
55	v	225	
56	w	236	
57	x	190	
58	y	200	
59	z	197	
60	AD	151	
61	AE	138	
62	AF	142	
63	AG	143	
64	AH	136	
65	AI	146	
66	AJ	144	
67	AK	121	
68	AL	87	
69	AM	130	
70	AN	145	
71	AO	135	
72	AP	108	
73	AQ	119	
74	AR	82	
75	AS	67	
76	AT	56	
77	AU	63	
78	AV	319	

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Mol	Chain	Length	Quality of chain
79	AX	76	 28% 49% 24%
79	AZ	76	 39% 51% 9%
80	AY	8	 25% 75%
81	L1	217	 9% 84% 9% 6%

2 Entry composition

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
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
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
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
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
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
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
7	G	233	Total	C	H	N	O	S	0	0
			3681	1151	1877	323	327	3		

- Molecule 8 is a protein called RPL9A isoform 1.

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

- Molecule 9 is a protein called RPL10 isoform 1.

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

- Molecule 10 is a protein called RPL11B isoform 1.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
28	1	3223	Total	C	H	N	O	P	0	0
			103566	30790	34635	12416	22502	3223		

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
29	3	121	Total	C	H	N	O	P	0	0
			3883	1152	1304	461	845	121		

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

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

- Molecule 31 is a protein called RPP0 isoform 1.

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

- Molecule 32 is a protein called RPL12A isoform 1.

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

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

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

- Molecule 34 is a protein called RPL29 isoform 1.

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

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

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

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

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

- Molecule 37 is a protein called RPL32 isoform 1.

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

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

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

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

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

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

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

- 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	S	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
48	p	91	Total	C	H	N	O	S	0	0
			1428	429	734	138	121	6		

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

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

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

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

- Molecule 51 is a protein called RPS1A isoform 1.

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

- Molecule 52 is a protein called RPS2 isoform 1.

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

- Molecule 53 is a protein called RPS3 isoform 1.

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

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

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

- Molecule 55 is a protein called Rps5p.

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

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

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

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

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

- Molecule 58 is a protein called RPS8A isoform 1.

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

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

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

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

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

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

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

- Molecule 62 is a protein called RPS15 isoform 1.

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

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

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

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

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

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

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

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

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

- Molecule 67 is a protein called RPS20 isoform 1.

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

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

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

- Molecule 69 is a protein called RPS22A isoform 1.

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

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

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

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

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

- Molecule 72 is a protein called RPS25A isoform 1.

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

- Molecule 73 is a protein called RPS26B isoform 1.

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

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

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

- Molecule 75 is a protein called RPS28A isoform 1.

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

- 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 (CCD ID: 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	

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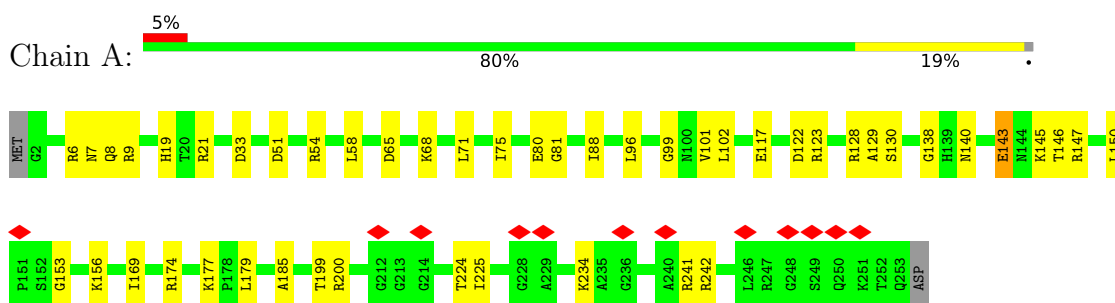
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Mol	Chain	Residues	Atoms		AltConf
82	o	1	Total 1	Zn 1	0
82	p	1	Total 1	Zn 1	0
82	AQ	1	Total 1	Zn 1	0
82	AR	1	Total 1	Zn 1	0
82	AT	1	Total 1	Zn 1	0

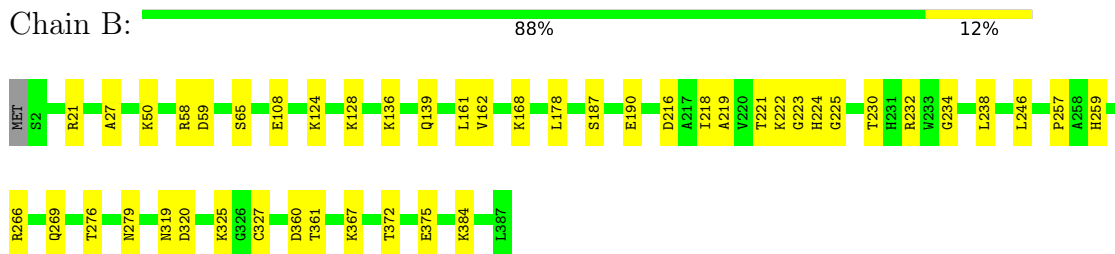
3 Residue-property plots

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.

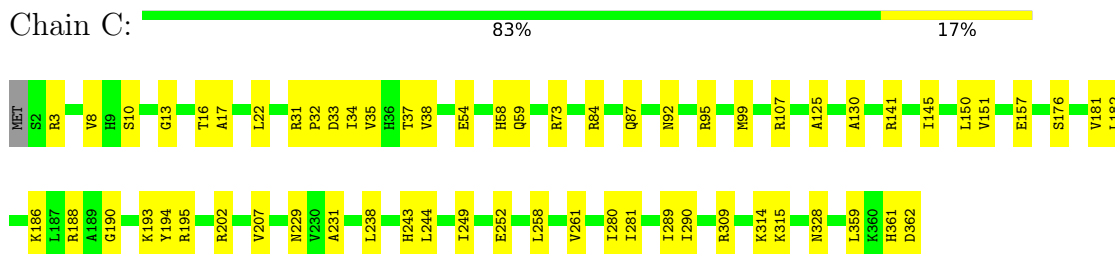
- Molecule 1: 60S ribosomal protein L2-A



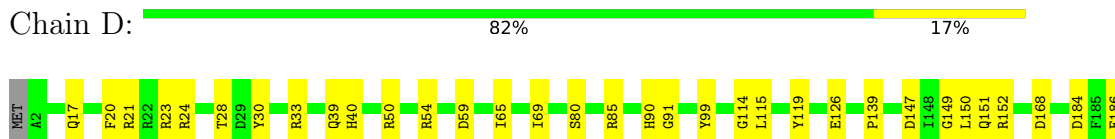
- Molecule 2: RPL3 isoform 1



- Molecule 3: RPL4A isoform 1



- Molecule 4: RPL5 isoform 1





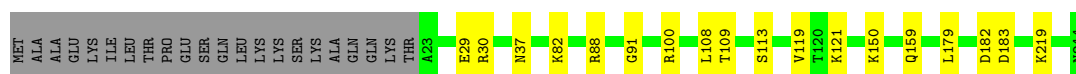
- Molecule 5: 60S ribosomal protein L6-A

Chain E: 80% 9% 11%



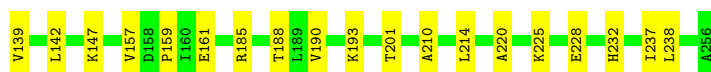
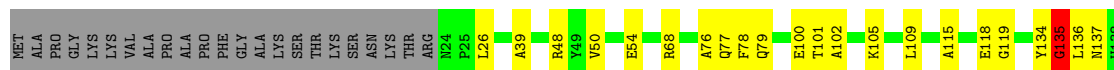
- Molecule 6: 60S ribosomal protein L7-A

Chain F: 84% 7% 9%



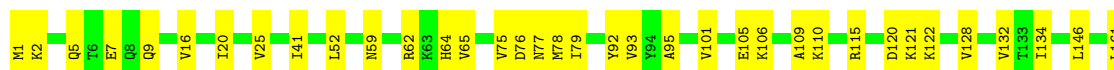
- Molecule 7: RPL8A isoform 1

Chain G: 75% 16% 9%



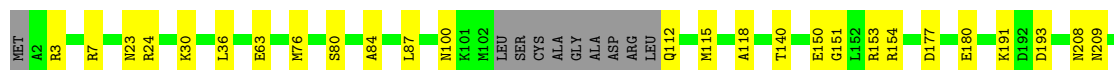
- Molecule 8: RPL9A isoform 1

Chain H: 77% 23%



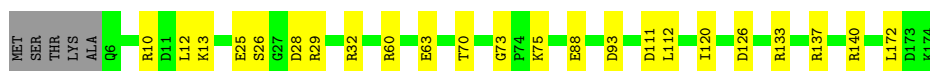
- Molecule 9: RPL10 isoform 1

Chain I: 84% 12% 5%



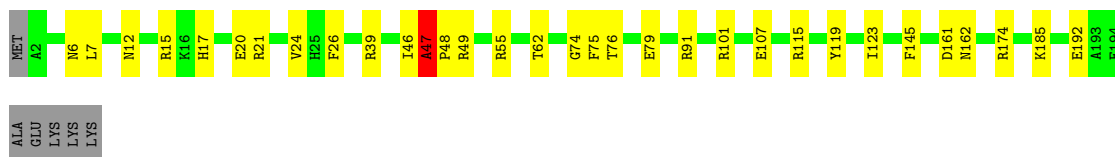
- Molecule 10: RPL11B isoform 1

Chain J: 84% 13%



- Molecule 11: 60S ribosomal protein L13-A

Chain L: 81% 16% ..



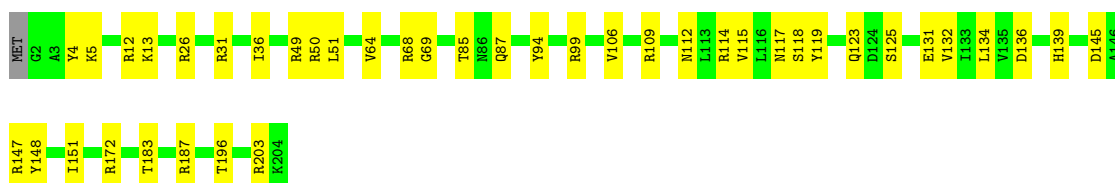
- Molecule 12: 60S ribosomal protein L14-A

Chain M: 83% 15% .



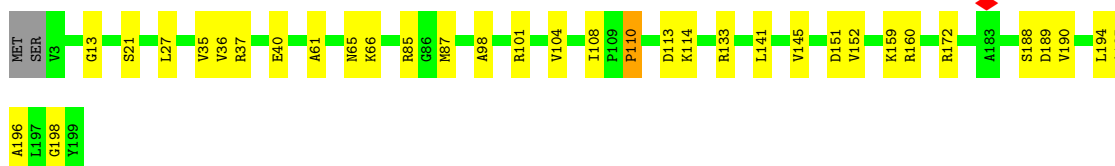
- Molecule 13: 60S ribosomal protein L15-A

Chain N: 79% 20%



- Molecule 14: 60S ribosomal protein L16-A

Chain O: 82% 17% ..



- Molecule 15: 60S ribosomal protein L17-A

Chain P: 86% 13% .



- Molecule 16: 60S ribosomal protein L18-A

Chain Q:  86% 13%



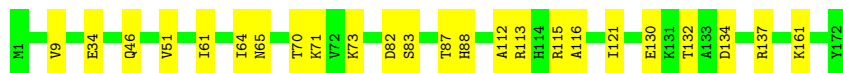
- Molecule 17: 60S ribosomal protein L19-A

Chain R:  88% 11%



- Molecule 18: 60S ribosomal protein L20-A

Chain S:  86% 14%



- Molecule 19: 60S ribosomal protein L21-A

Chain T:  84% 16%



- Molecule 20: 60S ribosomal protein L22-A

Chain U:  77% 6% 17%



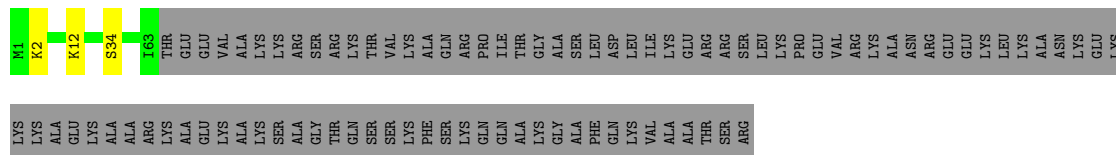
- Molecule 21: 60S ribosomal protein L23-A

Chain V:  84% 15%



- Molecule 22: RPL24A isoform 1

Chain W:  39% 59%



- Molecule 23: 60S ribosomal protein L25

Chain X: 



- Molecule 24: 60S ribosomal protein L26-A

Chain Y: 



- Molecule 25: 60S ribosomal protein L27-A

Chain Z: 



- Molecule 26: 40S ribosomal protein S10-A

Chain AA: 

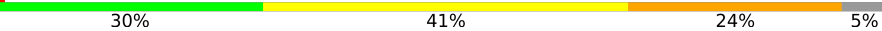


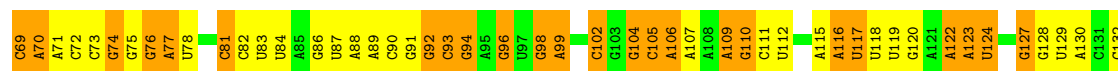
- Molecule 27: 40S ribosomal protein S11-A

Chain AB: 



- Molecule 28: 35S ribosomal RNA

Chain 1: 



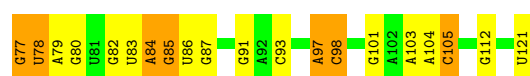
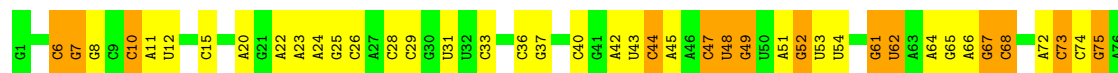


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C2206	C2138	C	A1884	U1818	U1739	C1665	U1595	C1531	G1465	U1331	A1269
A2207	A2139	C	U1885	U1819	U1740	C1666	C1596	U1532	A1467	A1332	U1261
U2208	U2140	G	A1886	U1820	U1741	A1667	C1597	U1533	G1468	C1333	G1262
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U2172	U2172	A	U1855	U1855	U1783	U1704	U1636	A1566	G1433	G1371	U1305
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C2177	C2177	G	U1860	U1860	U1790	G1713	U1641	U1573	U1445	C1376	G1310
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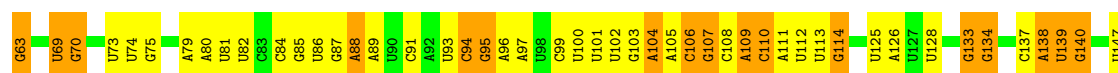
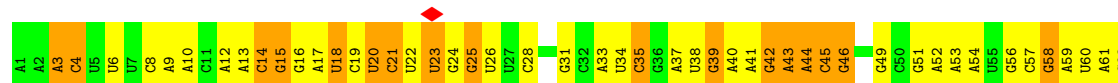
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A3218	C2993	G2993	U2920	A2851	G2784	U2716	A2635	U2565	A2502	U2436	A2296	A2295
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C3235	U3151	A3076	U2932	U2866	A2799	U2730	G2648	C2582	U2514	U2454	A2387	G2311
U3236	U3152	C3077	A2933	U2867	G2800	U2731	A2649	G2583	U2515	U2455	U2388	U2314
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G3240	U3157	U3020	G2937	C2871	A2804	C2737	C2654	U2587	A2519	A2459	C2392	G2324
A3241	C3165	A3087	A2940	G2874	G2805	G2741	A2655	G2588	U2520	A2460	G2393	A2325
G3242	U3169	G3088	A2941	U2875	U2806	G2742	A2656	A2590	A2521	A2461	G2394	G2326
U3251	A3170	C3089	C2942	C2876	U2807	C2743	G2657	A2591	U2522	A2462	G2395	A2327
G3252	U3171	A3090	G2943	C2877	C2808	U2744	G2658	G2592	G2523	G2463	A2396	U2328
U3255	C3172	C3091	U2944	G2878	C2809	G2745	A2667	A2593	G2524	U2464	A2397	C2329
G3256	A3173	G3092	G2945	C2879	A2810	U2746	G2668	C2594	C2526	G2465	A2398	G2330
C3257	U3174	C3093	A2946	U2880	C2811	A2747	U2669	A2595	G2530	G2466	A2399	G2331
U3258	C3175	U3100	U2947	C2881	A2812	U2748	A2674	U2596	U2531	A2467	A2400	A2401
G3259	A3176	G3101	G2950	U2882	G2813	G2749	C2675	U2597	U2532	G2468	A2402	G2335
C3260	C3177	U3102	G2951	U2883	G2814	U2750	A2676	G2598	G2533	G2469	G2403	G2336
G3261	U3179	G3103	G2952	A2887	G2815	G2751	A2677	U2599	A2534	C2470	A2404	C2339
U3262	A3180	C3036	U2954	U2888	A2817	U2752	G2677	C2600	G2535	U2471	G2405	U2340
C3265	C3181	U3037	A2955	G2892	A2819	G2753	A2678	A2601	A2536	U2472	C2406	U2341
G3266	A3182	C3038	C2956	C2893	A2820	G2754	A2679	G2602	U2537	C2473	C2407	U2342
A3267	C3183	U3104	G2957	C2894	C2821	C2755	C2682	G2603	U2538	G2474	U2408	G2409
C3268	A3184	C3039	G2958	G2895	U2822	U2756	C2685	G2604	A2540	C2475	G2409	U2410
U3269	U3185	U3105	G2959	G2896	G2823	G2757	A2686	G2605	U2541	C2476	U2411	G2414
G3270	A3186	U3107	U2960	A2897	G2824	U2760	G2687	G2606	U2542	G2477	C2346	U2347
C3271	C3187	G3108	G2961	U2898	G2825	A2762	U2688	G2607	U2543	C2478	C2347	A2348
U3272	U3190	C3112	G2962	G2899	U2826	U2763	A2689	A2609	U2544	C2479	A2349	U2349
A3273	C3190	A3113	G2963	A2900	U2827	U2764	G2690	U2610	C2545	A2480	U2416	U2349
		A3114	G2964	G2901	G2828	C2765	A2691	U2611	C2546	U2482	G2418	



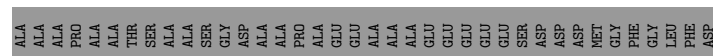
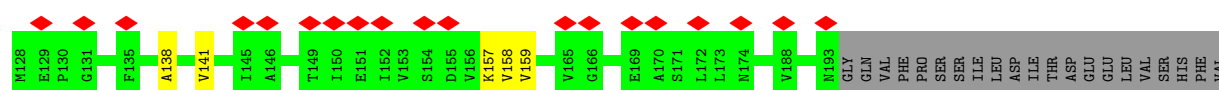
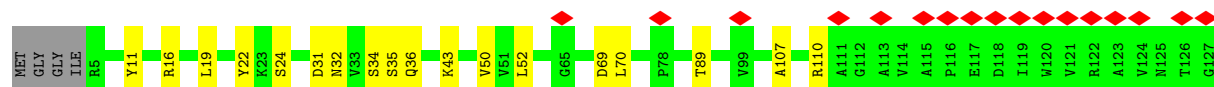
• Molecule 29: 5S ribosomal RNA



• Molecule 30: 5.8S ribosomal RNA

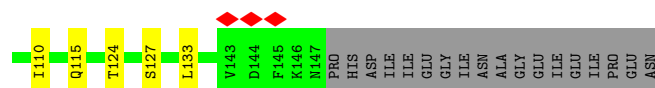
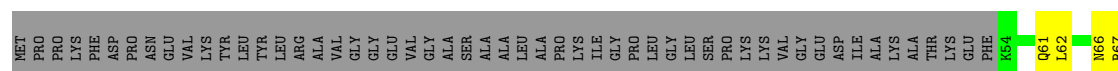


• Molecule 31: RPP0 isoform 1



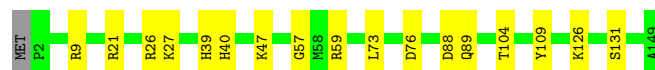
• Molecule 32: RPL12A isoform 1





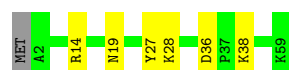
- Molecule 33: 60S ribosomal protein L28

Chain a: 88% 11% .



- Molecule 34: RPL29 isoform 1

Chain b: 88% 10% .



- Molecule 35: 60S ribosomal protein L30

Chain c: 79% 13% 8% .



- Molecule 36: 60S ribosomal protein L31-A

Chain d: 82% 14% .



- Molecule 37: RPL32 isoform 1

Chain e: 92% 6% .



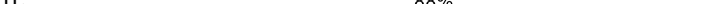
- Molecule 38: 60S ribosomal protein L33-A

Chain f: 85% 14% .

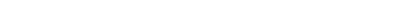


- Molecule 39: 60S ribosomal protein L34-A

Met
A2
Q3
R4
N11
N18
K37
T40
C44
G45
D46
Q52
G53
R80
I89
I90
R91
K102
K113
LYS
SER
GIU
LYS
LYS
ALA
LYS
LYS

- Chain h:  88% 11%

MET
A2
E8
E15
I44
V47
R48
K49
R63
K83
R86
F95
S98
Q113
R114
K115
Y116
A120

- Chain i:  87% 12%

Amino Acid	Relative Abundance (%)
MET	100
T2	10
T5	5
A8	10
I9	5
K13	10
S34	5
T37	10
L57	5
I61	10
K75	5
K84	10
V87	5
M90	10
H100	5

- Chain j: 80% 18% ..

MET	G2	H12	L18 C19	C22 G23	S26	C34	R45	K52	T59	M64	R65 Y66	K75 N76	Q79	T80	G81	S82	A88
-----	----	-----	------------	------------	-----	-----	-----	-----	-----	-----	------------	------------	-----	-----	-----	-----	-----

- Chain k: 76% 23%

MET
A2
D7
Q10
A23
K26
L27
N32
K36
R39
K42
V45
R46
L51
Y52
T53
L65
S68
L73
N76
R77
L78

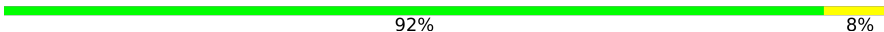
- Chain 1: 80% 18% .

Diagram illustrating the schematic representation of the protein structure of the 12S OMT domain. The structure is shown as a vertical bar with various residues labeled. The residues are grouped into boxes: MET and A2 (grey), R28 (green), L29 (red), R30, T31, and N32 (yellow), R36 and Y37 (green), K40 (yellow), and I51 (red). Arrows indicate the positions of the residues.

- Chain m: 24% 16% 59%

[illegible]

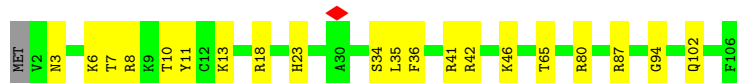
- Molecule 46: RPL41A isoform 1

Chain n:  92% 8%



- Molecule 47: 60S ribosomal protein L42-A

Chain o:  80% 19%



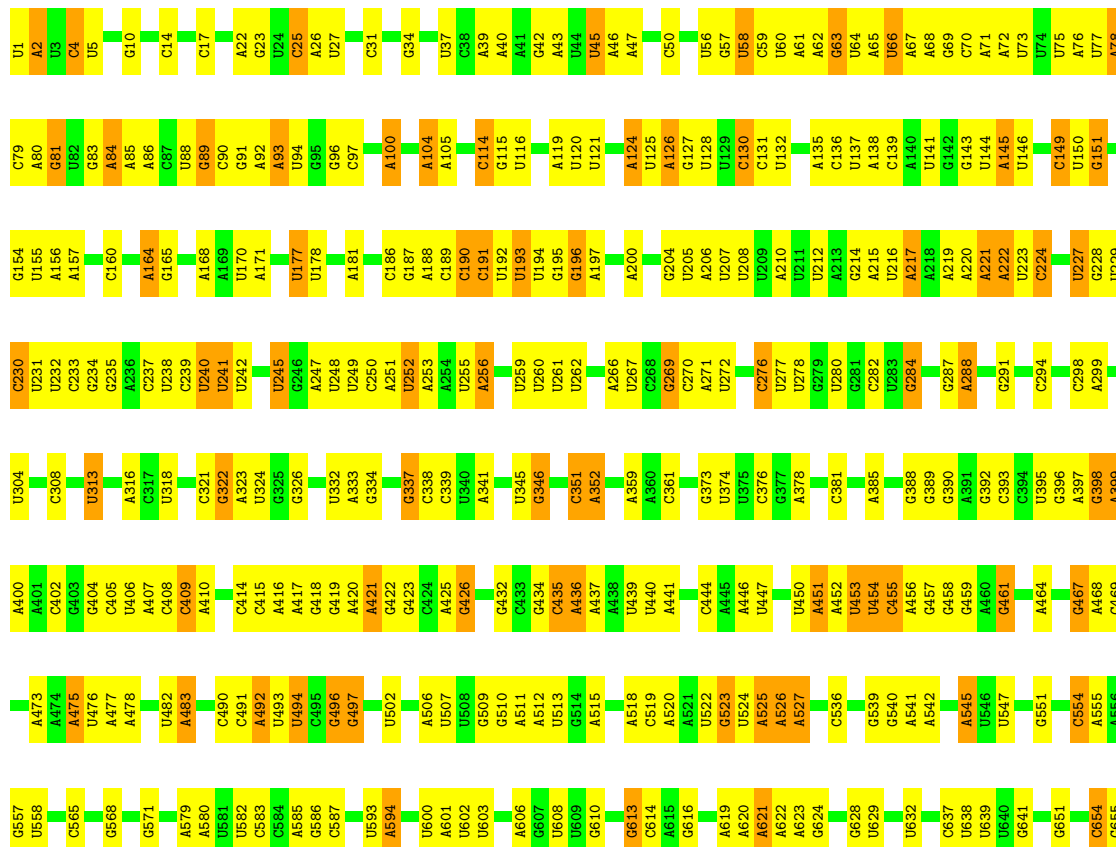
- Molecule 48: 60S ribosomal protein L43-A

Chain p:  89% 10%



- Molecule 49: 18S ribosomal RNA

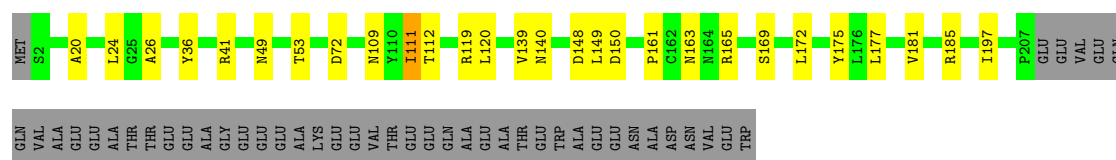
Chain 2:  46% 40% 11%





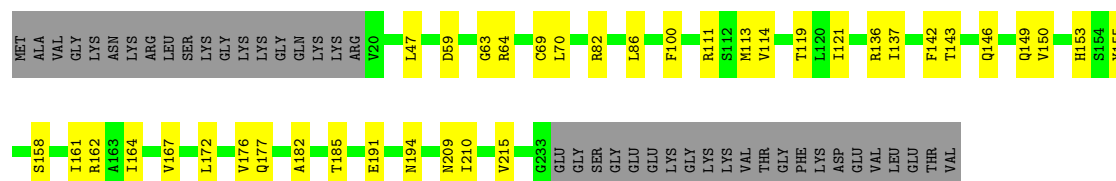
- Molecule 50: 40S ribosomal protein S0-A

Chain q:  71% 11% 18%



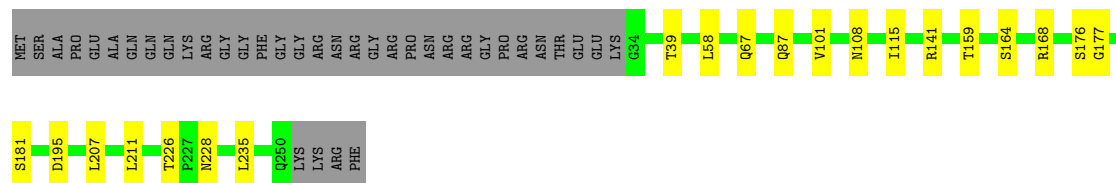
- Molecule 51: RPS1A isoform 1

Chain r:  69% 15% 16%



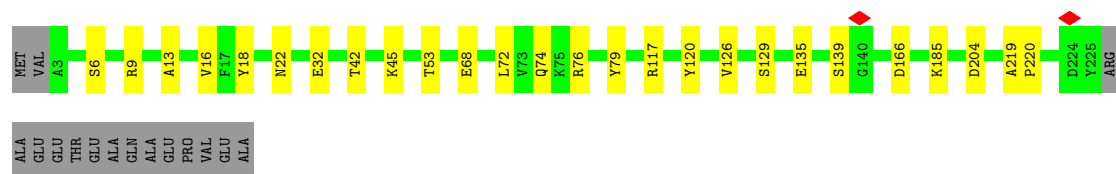
- Molecule 52: RPS2 isoform 1

Chain s:  78% 8% 15%



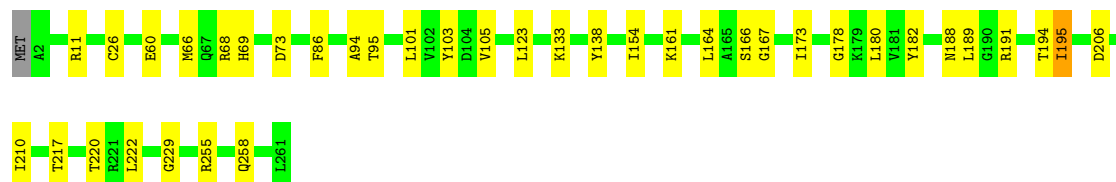
- Molecule 53: RPS3 isoform 1

Chain t:  82% 11% 7%



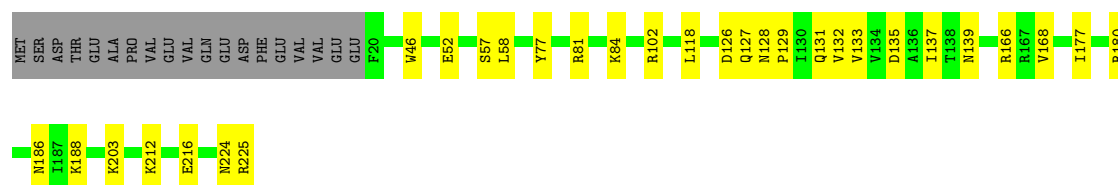
- Molecule 54: 40S ribosomal protein S4-A

Chain u:  85% 14%



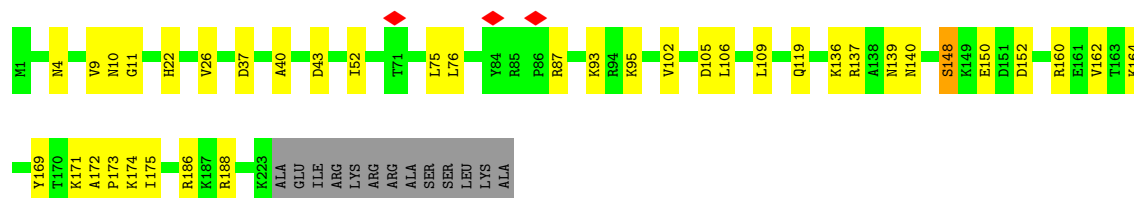
- Molecule 55: Rps5p

Chain v: 



- Molecule 56: 40S ribosomal protein S6-A

Chain w: 



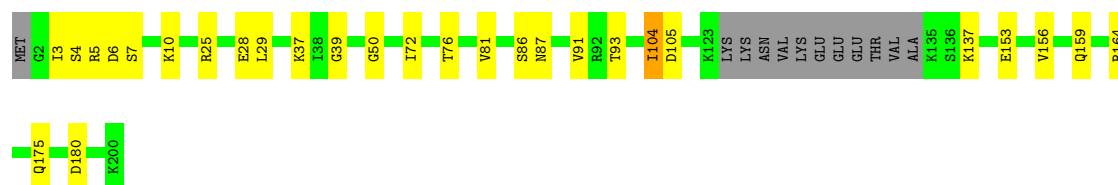
- Molecule 57: 40S ribosomal protein S7-A

Chain x: 



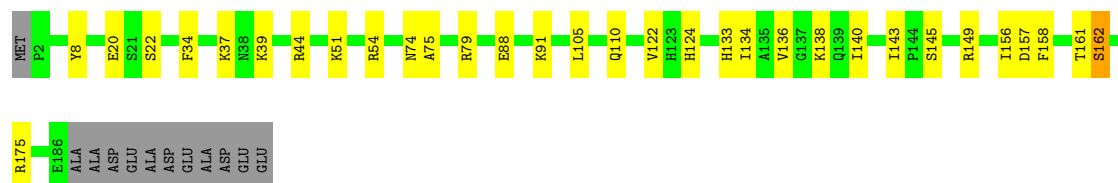
- Molecule 58: RPS8A isoform 1

Chain y: 



- Molecule 59: 40S ribosomal protein S9-A

Chain z: 



- Molecule 60: 40S ribosomal protein S13

Chain AD: 



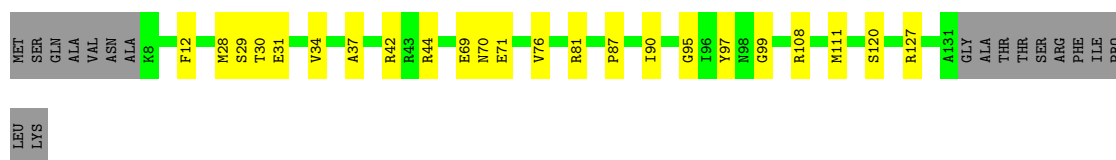
- Molecule 61: 40S ribosomal protein S14-B

Chain AE: 85% 7% 8%



- Molecule 62: RPS15 isoform 1

Chain AF: 71% 16% 13%



- Molecule 63: 40S ribosomal protein S16-A

Chain AG: 87% 12% .



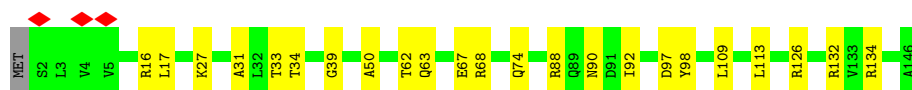
- Molecule 64: 40S ribosomal protein S17-B

Chain AH: 79% 9% 12%



- Molecule 65: 40S ribosomal protein S18-A

Chain AI: 84% 16% .



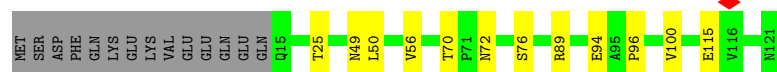
- Molecule 66: 40S ribosomal protein S19-A

Chain AJ: 88% 12% .



- Molecule 67: RPS20 isoform 1

Chain AK:  79% 10% 12%



- Molecule 68: 40S ribosomal protein S21-A

Chain AL:  90% 9%



- Molecule 69: RPS22A isoform 1

Chain AM:  82% 17%



- Molecule 70: 40S ribosomal protein S23-A

Chain AN:  84% 15%



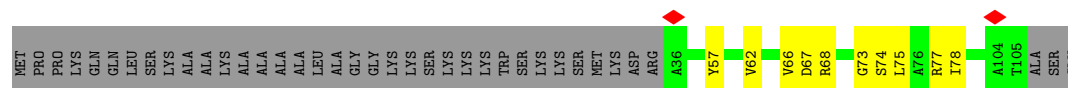
- Molecule 71: 40S ribosomal protein S24-A

Chain AO:  80% 19%



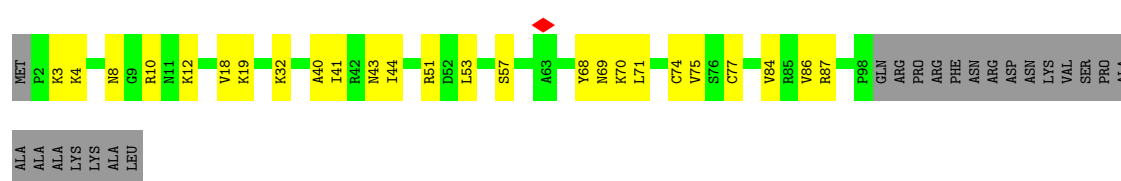
- Molecule 72: RPS25A isoform 1

Chain AP:  56% 9% 35%

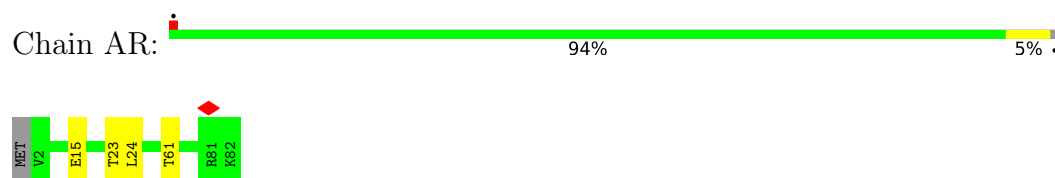


- Molecule 73: RPS26B isoform 1

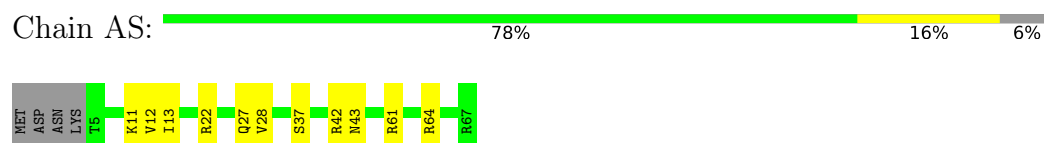
Chain AQ:  61% 21% 18%



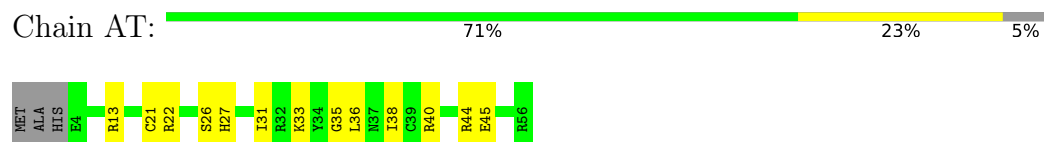
- Molecule 74: 40S ribosomal protein S27-A



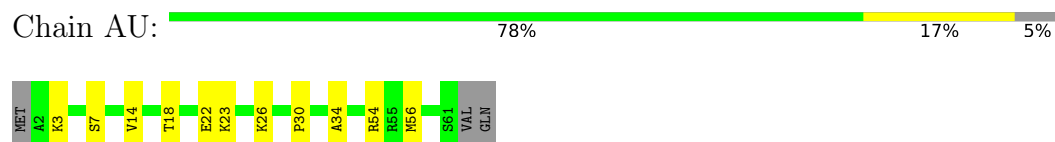
- Molecule 75: RPS28A isoform 1



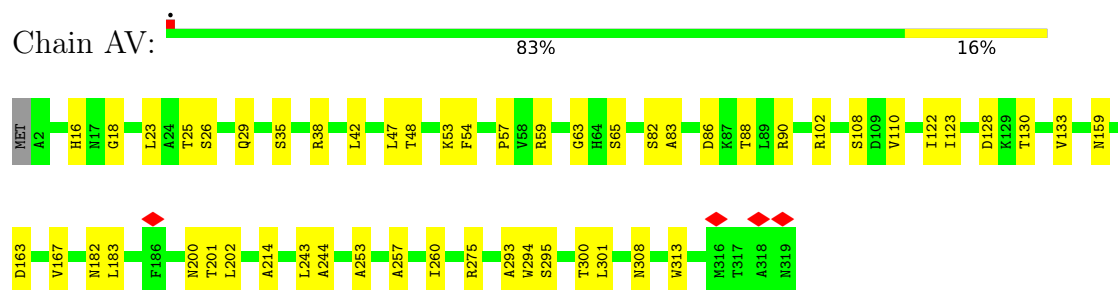
- Molecule 76: RPS29A isoform 1



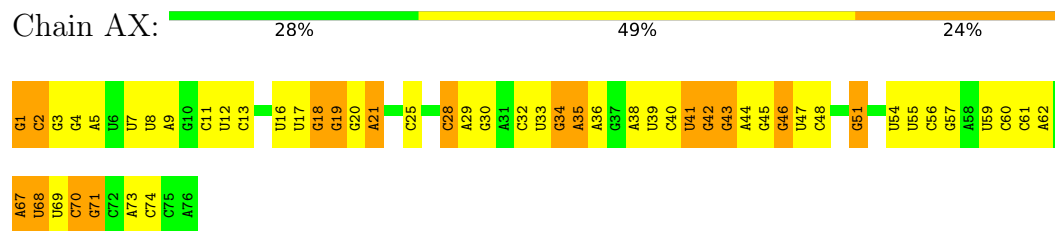
- Molecule 77: 40S ribosomal protein S30-A



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



- Molecule 79: Transfer RNA



- Molecule 79: Transfer RNA

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 ⓘ

5.1 Standard geometry ⓘ

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	0.20	0/1948	0.44	0/2617
2	B	0.19	0/3146	0.41	0/4228
3	C	0.19	0/2800	0.43	0/3790
4	D	0.18	0/2425	0.38	0/3271
5	E	0.18	0/1260	0.36	0/1694
6	F	0.20	0/1821	0.44	0/2451
7	G	0.85	2/1836 (0.1%)	0.49	2/2481 (0.1%)
8	H	0.20	0/1539	0.43	0/2073
9	I	0.18	0/1741	0.40	0/2335
10	J	0.20	0/1374	0.46	0/1842
11	L	0.21	0/1568	0.47	0/2106
12	M	0.19	0/1068	0.36	0/1438
13	N	0.20	0/1757	0.42	0/2354
14	O	0.21	0/1585	0.41	0/2128
15	P	0.18	0/1443	0.40	0/1944
16	Q	0.18	0/1465	0.39	0/1965
17	R	0.19	0/1538	0.40	0/2050
18	S	0.19	0/1481	0.42	0/1990
19	T	0.20	0/1300	0.41	0/1743
20	U	0.19	0/812	0.40	0/1099
21	V	0.19	0/1018	0.41	0/1369
22	W	0.18	0/533	0.33	0/707
23	X	0.16	0/979	0.39	0/1321
24	Y	0.17	0/1004	0.41	0/1341
25	Z	0.18	0/1118	0.40	0/1497
26	AA	0.20	0/789	0.44	0/1067
27	AB	0.18	0/1247	0.41	0/1681
28	1	0.59	12/77157 (0.0%)	0.41	4/120295 (0.0%)
29	3	0.17	0/2883	0.37	0/4491
30	4	1.82	6/3746 (0.2%)	0.44	1/5832 (0.0%)
31	P0	0.23	0/1498	0.47	0/2025
32	P2	0.25	0/728	0.44	0/975

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	a	0.19	0/1204	0.42	0/1612
34	b	0.18	0/473	0.36	0/629
35	c	0.17	0/751	0.37	0/1008
36	d	0.19	0/897	0.39	0/1205
37	e	0.17	0/1041	0.37	0/1394
38	f	0.20	0/868	0.43	0/1168
39	g	0.21	0/890	0.41	0/1189
40	h	0.18	0/978	0.43	0/1301
41	i	0.19	0/778	0.38	0/1034
42	j	2.27	1/696 (0.1%)	0.75	2/923 (0.2%)
43	k	0.17	0/618	0.41	0/826
44	l	0.24	0/443	0.53	0/588
45	m	0.26	0/423	0.49	0/562
46	n	0.19	0/228	0.39	0/293
47	o	0.19	0/860	0.45	0/1136
48	p	0.19	0/701	0.44	0/934
49	2	0.39	4/41539 (0.0%)	0.34	9/64723 (0.0%)
50	q	0.20	0/1617	0.41	0/2215
51	r	0.19	0/1735	0.47	0/2335
52	s	0.18	0/1665	0.42	0/2263
53	t	0.21	0/1759	0.45	0/2368
54	u	0.20	0/2109	0.50	0/2839
55	v	0.21	0/1629	0.47	0/2202
56	w	0.22	0/1814	0.53	0/2425
57	x	0.19	0/1506	0.44	0/2028
58	y	0.22	0/1514	0.52	0/2021
59	z	0.19	0/1519	0.46	0/2035
60	AD	0.19	0/1215	0.48	0/1638
61	AE	0.20	0/901	0.43	0/1217
62	AF	0.22	0/998	0.49	0/1341
63	AG	0.23	0/1125	0.50	0/1510
64	AH	0.19	0/935	0.46	0/1254
65	AI	0.19	0/1211	0.45	0/1628
66	AJ	0.21	0/1130	0.44	0/1517
67	AK	0.21	0/865	0.44	0/1169
68	AL	0.20	0/693	0.49	0/935
69	AM	0.18	0/1038	0.40	0/1395
70	AN	0.20	0/1139	0.47	0/1518
71	AO	0.18	0/1087	0.42	0/1449
72	AP	0.21	0/571	0.44	0/768
73	AQ	0.23	0/782	0.48	0/1047
74	AR	0.17	0/620	0.42	0/838
75	AS	0.21	0/499	0.41	0/670

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	AT	0.20	0/452	0.38	0/600
77	AU	0.20	0/483	0.39	0/643
78	AV	0.18	0/2490	0.39	0/3389
79	AX	0.13	0/1818	0.30	0/2831
79	AZ	0.13	0/1818	0.31	0/2831
80	AY	0.17	0/181	0.40	0/278
81	L1	0.20	0/1634	0.42	0/2195
All	All	0.50	25/220547 (0.0%)	0.41	18/324117 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
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 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	2	1759	C	C1'-N1	69.46	2.52	1.48
42	j	81	GLY	CA-C	59.37	2.35	1.51
28	1	148	G	C6-N1	53.78	2.47	1.39
28	1	148	G	N1-C2	52.97	2.43	1.37
28	1	148	G	C2-N3	52.07	2.36	1.32

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	2	1759	C	C6-N1-C2	-16.88	69.58	120.20
42	j	81	GLY	O-C-N	-15.86	102.09	122.70
49	2	1759	C	N1-C1'-C2'	12.29	130.44	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	2	1759	C	C5-C6-N1	11.53	155.57	121.00
7	G	135	GLY	N-CA-C	9.12	134.81	113.18

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](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1914	1981	1981	40	0
2	B	3075	3142	3142	34	0
3	C	2748	2859	2859	47	0
4	D	2375	2326	2325	36	0
5	E	1239	1326	1326	15	0
6	F	1784	1862	1862	14	0
7	G	1804	1877	1877	48	0
8	H	1518	1587	1587	33	0
9	I	1705	1736	1736	20	0
10	J	1353	1383	1383	16	0
11	L	1543	1608	1608	25	0
12	M	1053	1149	1149	17	0
13	N	1720	1779	1779	34	0
14	O	1555	1659	1659	23	0
15	P	1420	1437	1437	18	0
16	Q	1441	1543	1543	24	0
17	R	1521	1617	1617	20	0
18	S	1445	1487	1487	20	0
19	T	1276	1323	1323	21	0
20	U	796	812	812	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	V	1003	1048	1048	14	0
22	W	521	551	551	2	0
23	X	964	1025	1025	12	0
24	Y	993	1081	1081	14	0
25	Z	1092	1155	1155	20	0
26	AA	772	727	727	4	0
27	AB	1220	1282	1281	11	0
28	1	68931	34635	34637	1006	0
29	3	2579	1304	1304	31	0
30	4	3353	1695	1695	82	0
31	P0	1473	1514	1514	20	0
32	P2	723	774	774	8	0
33	a	1173	1215	1215	13	0
34	b	462	491	491	5	0
35	c	743	797	797	8	0
36	d	883	918	918	12	0
37	e	1020	1090	1090	6	0
38	f	850	880	880	12	0
39	g	880	941	941	10	0
40	h	969	1078	1078	14	0
41	i	771	849	849	7	0
42	j	681	683	683	39	0
43	k	612	682	682	11	0
44	l	436	475	475	7	0
45	m	417	456	456	18	0
46	n	227	273	273	2	0
47	o	847	915	915	15	0
48	p	694	734	734	9	0
49	2	37141	18686	18690	398	0
50	q	1577	1567	1567	19	0
51	r	1709	1784	1784	25	0
52	s	1635	1723	1723	14	0
53	t	1734	1817	1817	16	0
54	u	2068	2154	2154	25	0
55	v	1609	1675	1675	16	0
56	w	1790	1881	1881	27	0
57	x	1481	1572	1572	19	0
58	y	1489	1525	1525	22	0
59	z	1494	1573	1573	22	0
60	AD	1192	1255	1255	18	0
61	AE	891	883	883	8	0
62	AF	977	1002	1002	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	AG	1105	1166	1166	13	0
64	AH	926	930	930	11	0
65	AI	1192	1222	1222	13	0
66	AJ	1112	1124	1124	14	0
67	AK	855	917	917	7	0
68	AL	684	672	672	7	0
69	AM	1021	1060	1060	14	0
70	AN	1121	1196	1196	16	0
71	AO	1073	1132	1132	22	0
72	AP	563	603	603	9	0
73	AQ	769	814	814	20	0
74	AR	610	632	632	2	0
75	AS	497	535	535	7	0
76	AT	442	431	431	9	0
77	AU	475	525	525	8	0
78	AV	2437	2386	2386	37	0
79	AX	1626	820	820	16	0
79	AZ	1626	820	820	10	0
80	AY	164	84	84	0	0
81	L1	1609	1701	1701	14	0
82	AQ	1	0	0	0	0
82	AR	1	0	0	0	0
82	AT	1	0	0	0	0
82	j	1	0	0	0	0
82	m	1	0	0	0	0
82	o	1	0	0	0	0
82	p	1	0	0	0	0
All	All	205275	151628	151632	2244	0

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

The worst 5 of 2244 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2:1759:C:C2	49:2:1759:C:N1	1.71	1.56
30:4:95:G:C4	30:4:95:G:C5	2.13	1.34
28:1:2262:A:C4	28:1:2262:A:C5	2.07	1.33
7:G:135:GLY:CA	7:G:135:GLY:C	2.01	1.33
28:1:148:G:C4	28:1:148:G:C5	2.15	1.32

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	250/254 (98%)	215 (86%)	33 (13%)	2 (1%)	16	52
2	B	384/387 (99%)	339 (88%)	45 (12%)	0	100	100
3	C	359/362 (99%)	314 (88%)	44 (12%)	1 (0%)	36	71
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%)	30	66
8	H	189/191 (99%)	167 (88%)	21 (11%)	1 (0%)	24	62
9	I	207/221 (94%)	185 (89%)	22 (11%)	0	100	100
10	J	167/174 (96%)	139 (83%)	28 (17%)	0	100	100
11	L	191/199 (96%)	154 (81%)	34 (18%)	3 (2%)	7	37
12	M	134/138 (97%)	122 (91%)	11 (8%)	1 (1%)	18	54
13	N	201/204 (98%)	176 (88%)	23 (11%)	2 (1%)	12	47
14	O	195/199 (98%)	177 (91%)	17 (9%)	1 (0%)	24	62
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%)	21	58
20	U	98/121 (81%)	93 (95%)	5 (5%)	0	100	100
21	V	134/137 (98%)	114 (85%)	18 (13%)	2 (2%)	8	38
22	W	61/155 (39%)	57 (93%)	4 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	16	52
26	AA	94/105 (90%)	81 (86%)	12 (13%)	1 (1%)	11	45
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%)	18	54
34	b	56/59 (95%)	46 (82%)	10 (18%)	0	100	100
35	c	95/105 (90%)	87 (92%)	7 (7%)	1 (1%)	11	45
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%)	12	47
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
44	l	48/51 (94%)	41 (85%)	7 (15%)	0	100	100
45	m	50/128 (39%)	37 (74%)	12 (24%)	1 (2%)	6	32
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%)	12	47
51	r	212/255 (83%)	177 (84%)	34 (16%)	1 (0%)	24	62
52	s	215/254 (85%)	195 (91%)	19 (9%)	1 (0%)	24	62
53	t	221/240 (92%)	187 (85%)	34 (15%)	0	100	100
54	u	258/261 (99%)	210 (81%)	47 (18%)	1 (0%)	30	66
55	v	204/225 (91%)	172 (84%)	30 (15%)	2 (1%)	12	47
56	w	221/236 (94%)	171 (77%)	47 (21%)	3 (1%)	9	39
57	x	182/190 (96%)	156 (86%)	26 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
58	y	184/200 (92%)	154 (84%)	28 (15%)	2 (1%)	11	45
59	z	183/197 (93%)	159 (87%)	23 (13%)	1 (0%)	24	62
60	AD	148/151 (98%)	131 (88%)	15 (10%)	2 (1%)	9	39
61	AE	125/138 (91%)	107 (86%)	17 (14%)	1 (1%)	16	52
62	AF	122/142 (86%)	98 (80%)	22 (18%)	2 (2%)	7	37
63	AG	139/143 (97%)	109 (78%)	29 (21%)	1 (1%)	18	54
64	AH	116/136 (85%)	105 (90%)	11 (10%)	0	100	100
65	AI	143/146 (98%)	125 (87%)	17 (12%)	1 (1%)	18	54
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%)	10	42
69	AM	127/130 (98%)	114 (90%)	13 (10%)	0	100	100
70	AN	142/145 (98%)	113 (80%)	28 (20%)	1 (1%)	18	54
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%)	9	41
75	AS	61/67 (91%)	52 (85%)	9 (15%)	0	100	100
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%)	24	62
All	All	11213/12280 (91%)	9675 (86%)	1493 (13%)	45 (0%)	31	66

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 ⓘ

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%)	193 (100%)	0	100	100
2	B	319/323 (99%)	319 (100%)	0	100	100
3	C	288/289 (100%)	288 (100%)	0	100	100
4	D	244/245 (100%)	244 (100%)	0	100	100
5	E	134/153 (88%)	134 (100%)	0	100	100
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%)	171 (100%)	0	100	100
9	I	177/187 (95%)	177 (100%)	0	100	100
10	J	147/151 (97%)	147 (100%)	0	100	100
11	L	154/159 (97%)	154 (100%)	0	100	100
12	M	107/109 (98%)	107 (100%)	0	100	100
13	N	175/176 (99%)	175 (100%)	0	100	100
14	O	160/162 (99%)	160 (100%)	0	100	100
15	P	140/146 (96%)	140 (100%)	0	100	100
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%)	156 (100%)	0	100	100
19	T	136/137 (99%)	136 (100%)	0	100	100
20	U	87/107 (81%)	87 (100%)	0	100	100
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%)	104 (100%)	0	100	100
24	Y	109/110 (99%)	109 (100%)	0	100	100
25	Z	115/116 (99%)	115 (100%)	0	100	100
26	AA	77/98 (79%)	77 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	81 (100%)	0	100	100
33	a	118/119 (99%)	118 (100%)	0	100	100
34	b	46/47 (98%)	46 (100%)	0	100	100
35	c	81/88 (92%)	81 (100%)	0	100	100
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%)	95 (100%)	0	100	100
40	h	104/105 (99%)	104 (100%)	0	100	100
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
47	o	90/91 (99%)	90 (100%)	0	100	100
48	p	71/72 (99%)	71 (100%)	0	100	100
50	q	164/210 (78%)	164 (100%)	0	100	100
51	r	191/224 (85%)	191 (100%)	0	100	100
52	s	176/205 (86%)	176 (100%)	0	100	100
53	t	182/195 (93%)	182 (100%)	0	100	100
54	u	221/222 (100%)	221 (100%)	0	100	100
55	v	173/191 (91%)	173 (100%)	0	100	100
56	w	189/201 (94%)	189 (100%)	0	100	100
57	x	165/170 (97%)	165 (100%)	0	100	100
58	y	150/161 (93%)	150 (100%)	0	100	100
59	z	158/166 (95%)	158 (100%)	0	100	100
60	AD	127/128 (99%)	127 (100%)	0	100	100
61	AE	81/105 (77%)	81 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	AF	101/118 (86%)	101 (100%)	0	100	100
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%)	119 (100%)	0	100	100
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%)	83 (100%)	0	100	100
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%)	47	65
77	AU	51/54 (94%)	51 (100%)	0	100	100
78	AV	259/262 (99%)	259 (100%)	0	100	100
81	L1	185/198 (93%)	185 (100%)	0	100	100
All	All	9492/10318 (92%)	9491 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
76	AT	38	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
50	q	30	GLN
63	AG	100	GLN
51	r	95	ASN
58	y	88	ASN
65	AI	55	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	1	3220/3395 (94%)	1864 (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%)	2771 (51%)	196 (3%)

5 of 2771 RNA backbone outliers are listed below:

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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 [i](#)

There are no chain breaks in this entry.

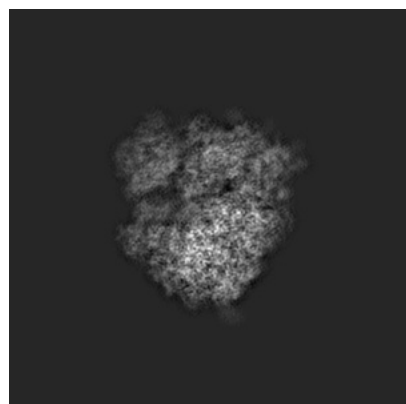
6 Map visualisation [i](#)

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.

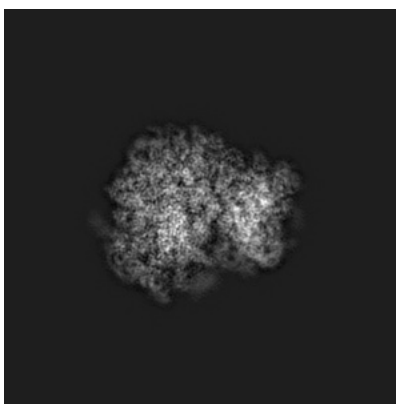
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

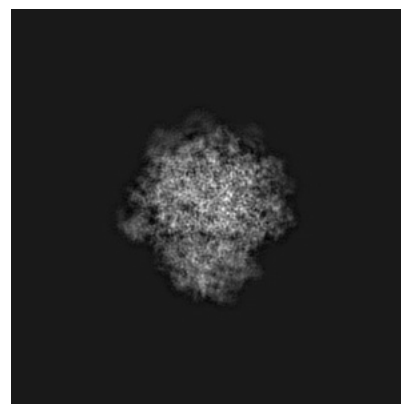
6.1.1 Primary map



X

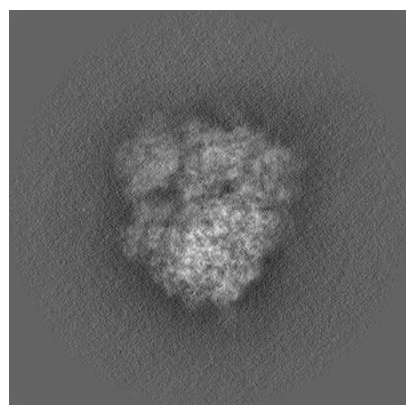


Y

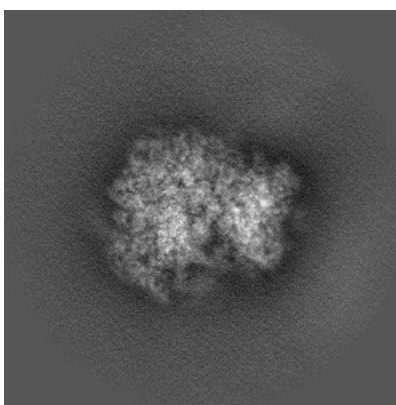


Z

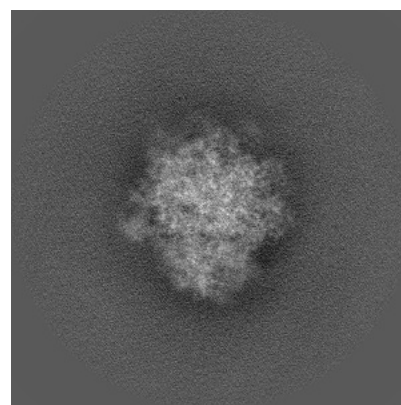
6.1.2 Raw map



X



Y

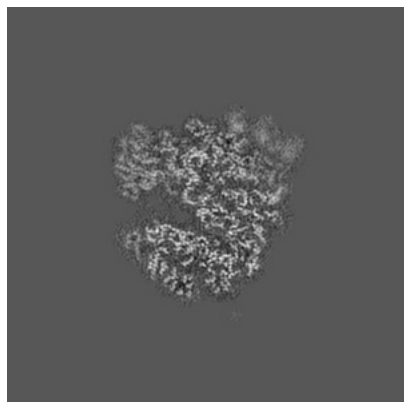


Z

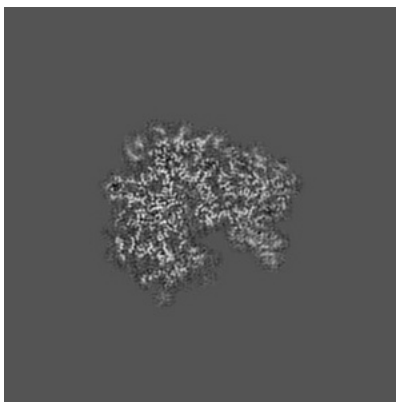
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

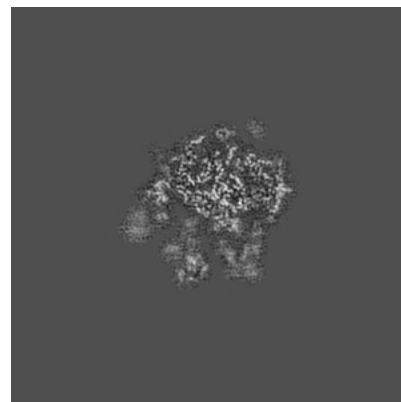
6.2.1 Primary map



X Index: 256

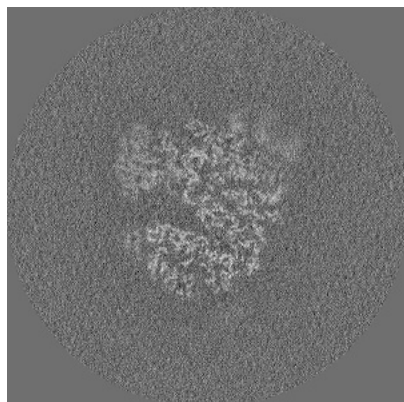


Y Index: 256

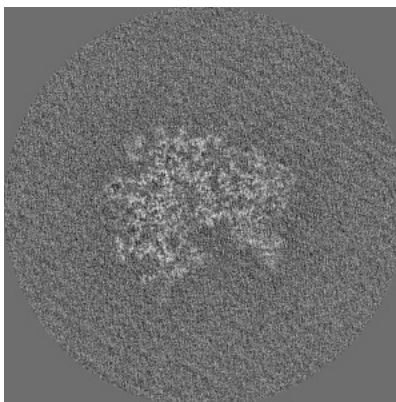


Z Index: 256

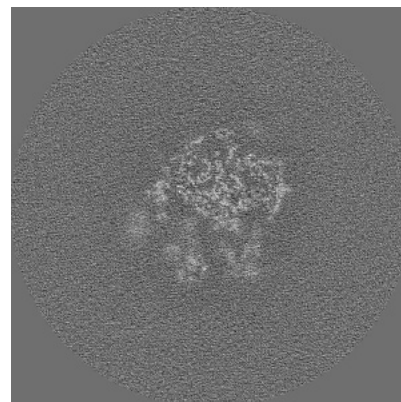
6.2.2 Raw map



X Index: 256



Y Index: 256

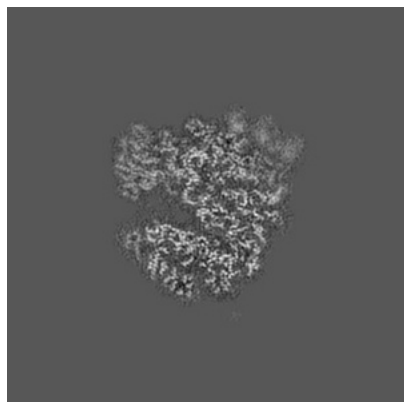


Z Index: 256

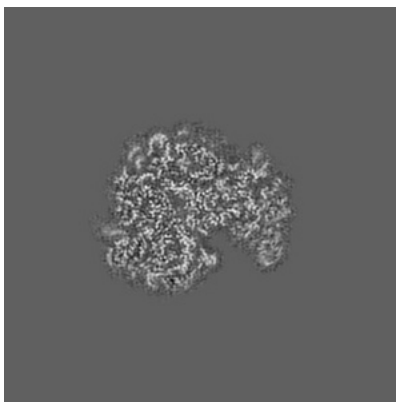
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

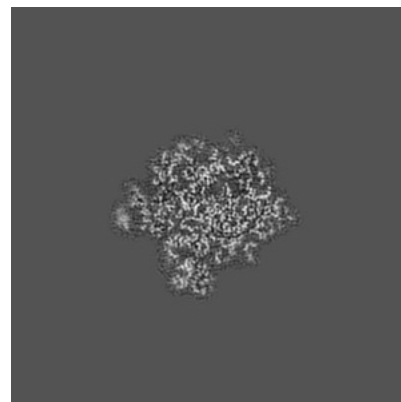
6.3.1 Primary map



X Index: 256

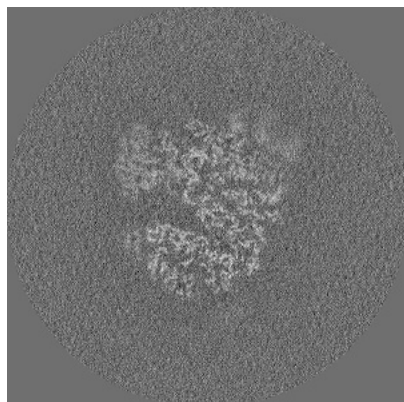


Y Index: 266

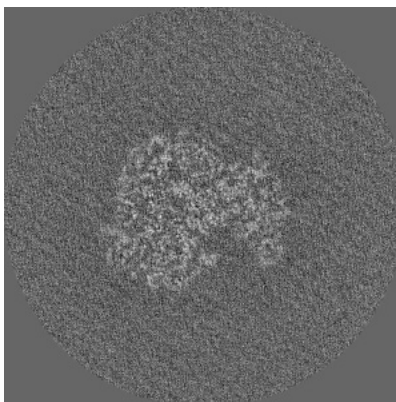


Z Index: 206

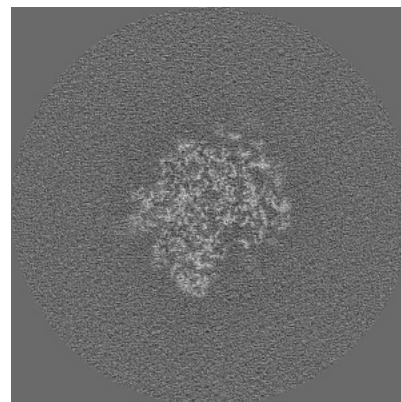
6.3.2 Raw map



X Index: 256



Y Index: 267

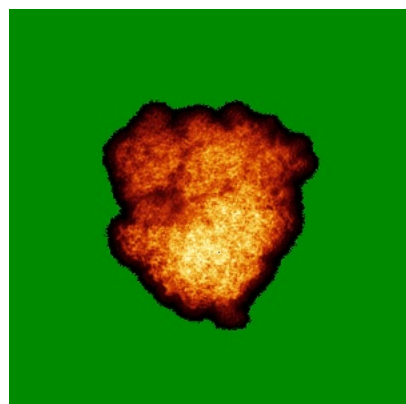


Z Index: 227

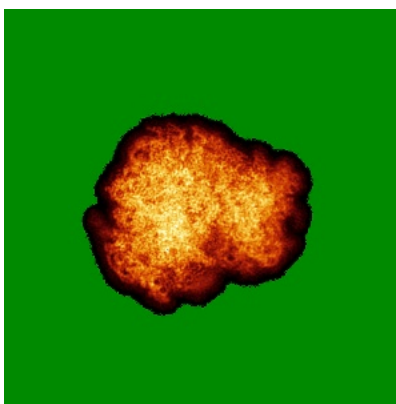
The images above show the largest variance slices of the map in three orthogonal directions.

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

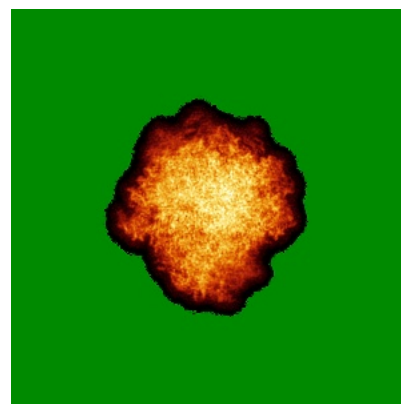
6.4.1 Primary map



X

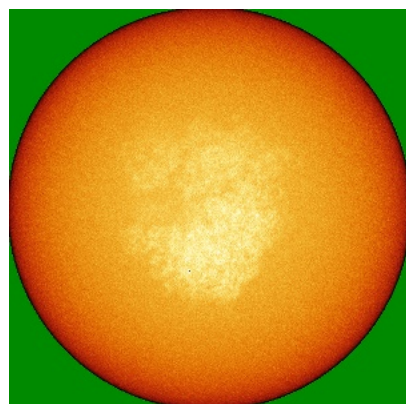


Y

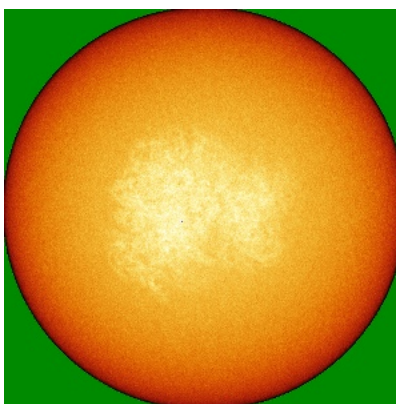


Z

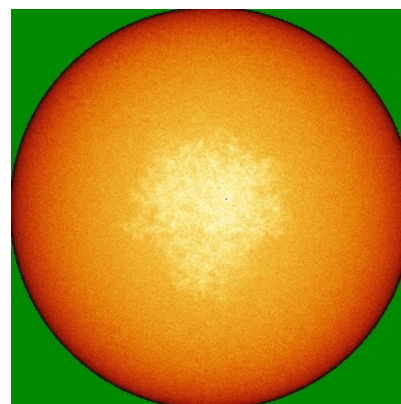
6.4.2 Raw map



X



Y

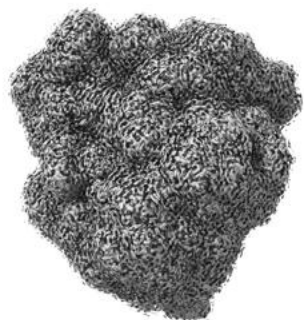


Z

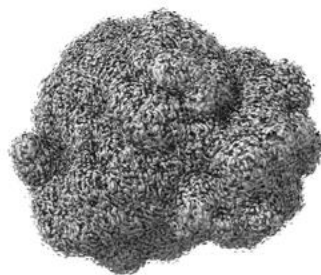
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



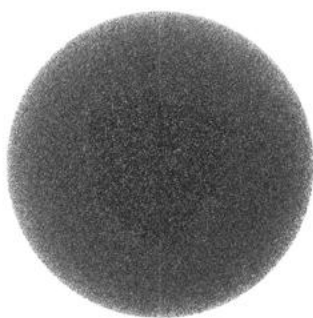
Y



Z

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

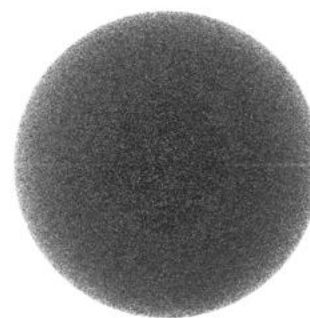
6.5.2 Raw map



X



Y



Z

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

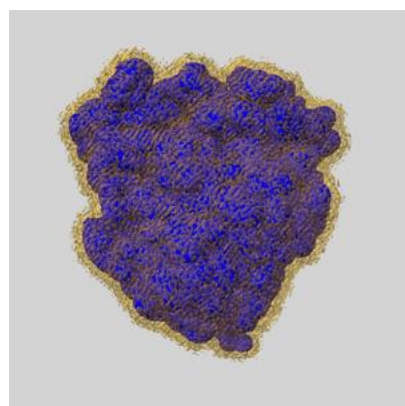
6.6 Mask visualisation [i](#)

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

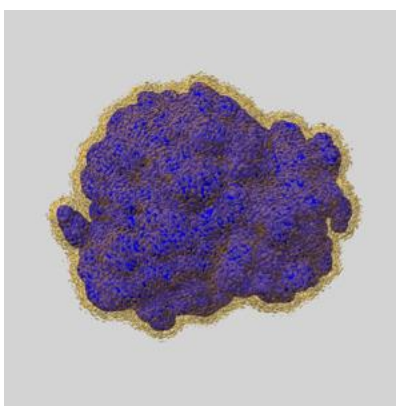
A mask typically either:

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

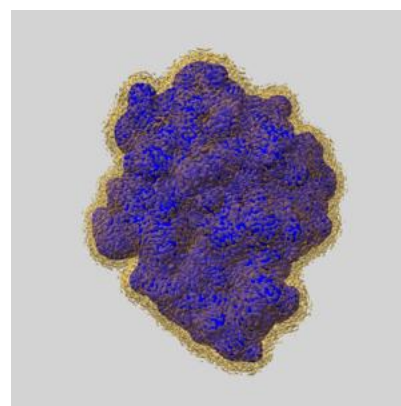
6.6.1 emd_22196_msk_1.map [i](#)



X



Y

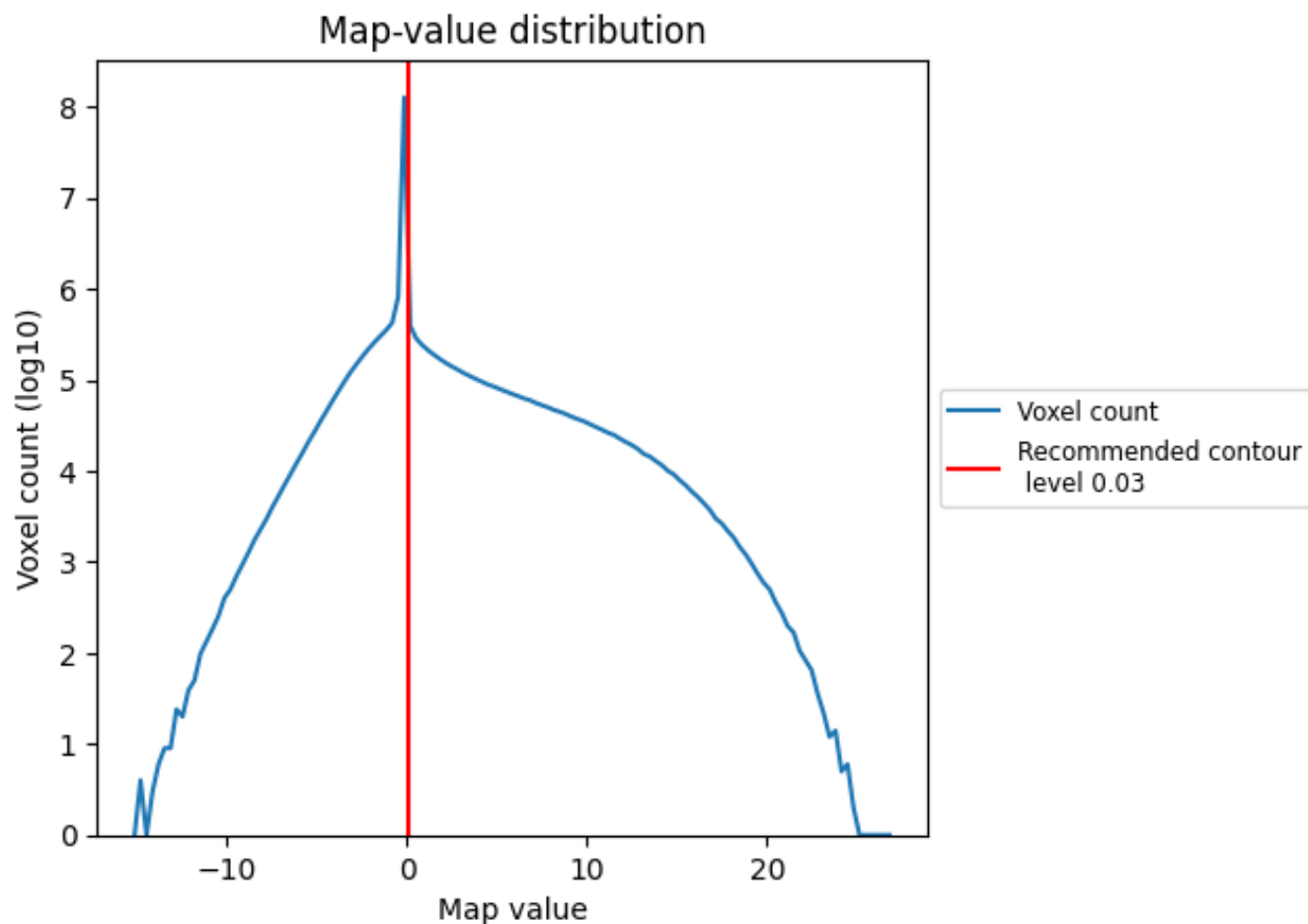


Z

7 Map analysis [i](#)

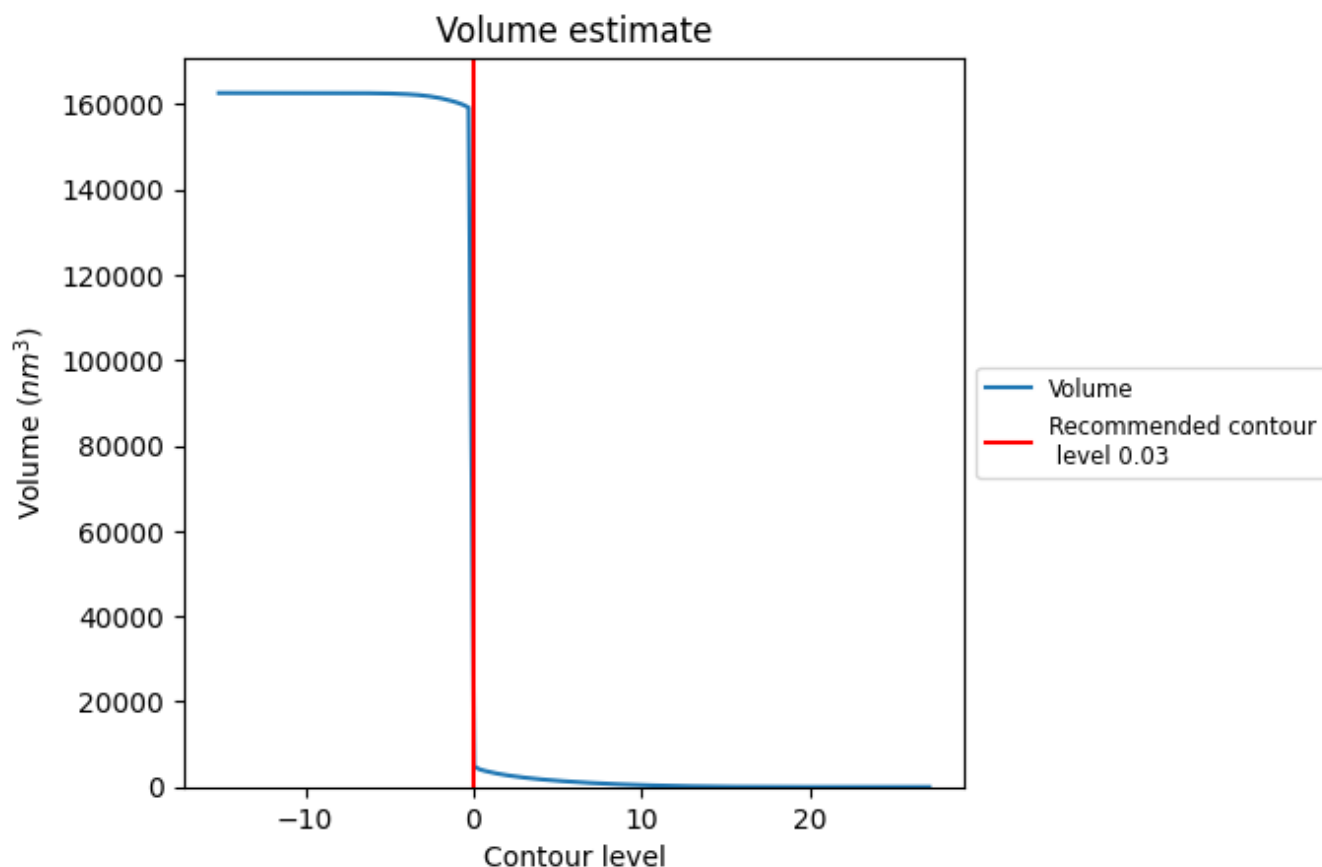
This section contains the results of statistical analysis of the map.

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.

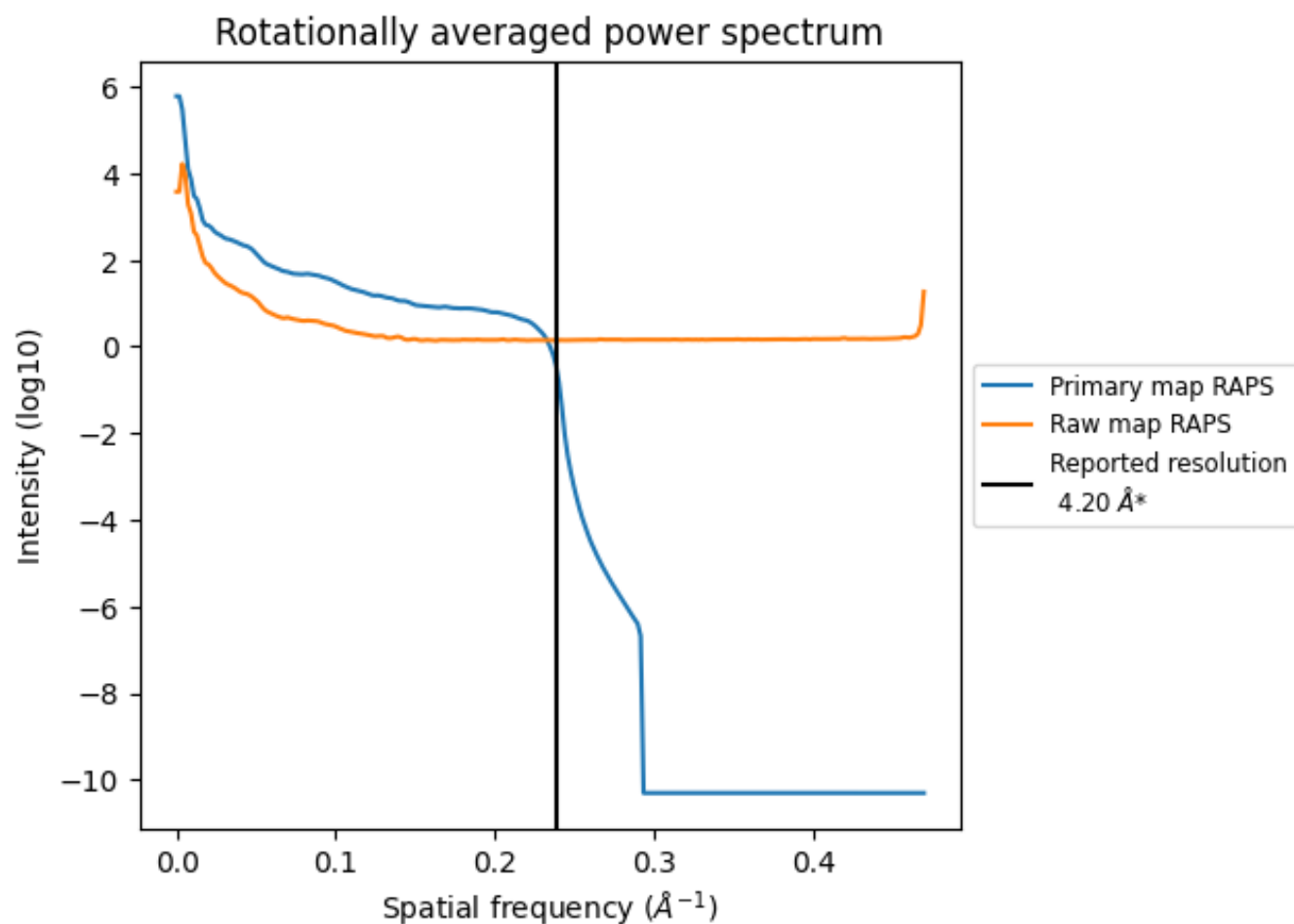
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 11315 nm^3 ; 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 ⓘ

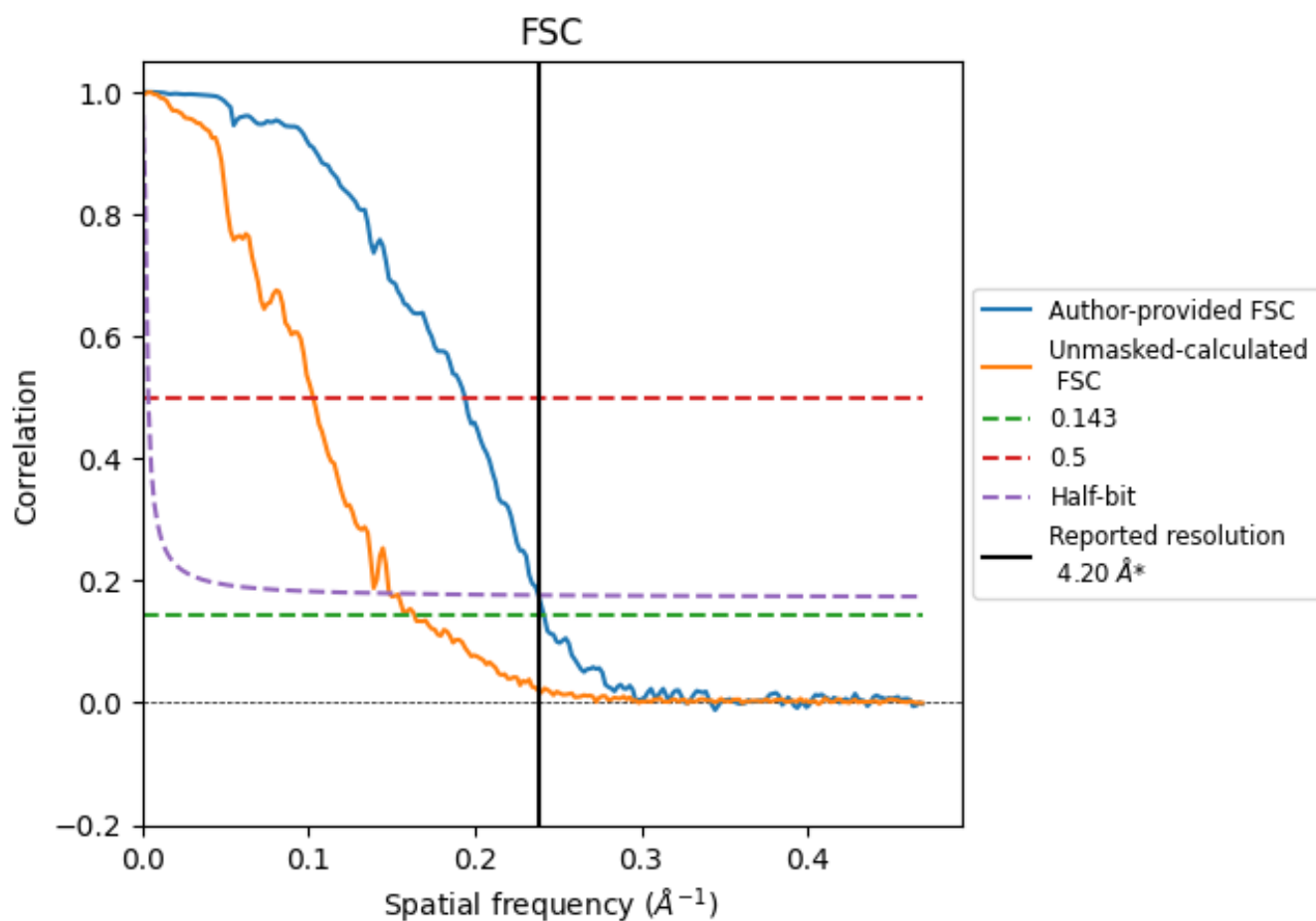


*Reported resolution corresponds to spatial frequency of 0.238 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.238 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

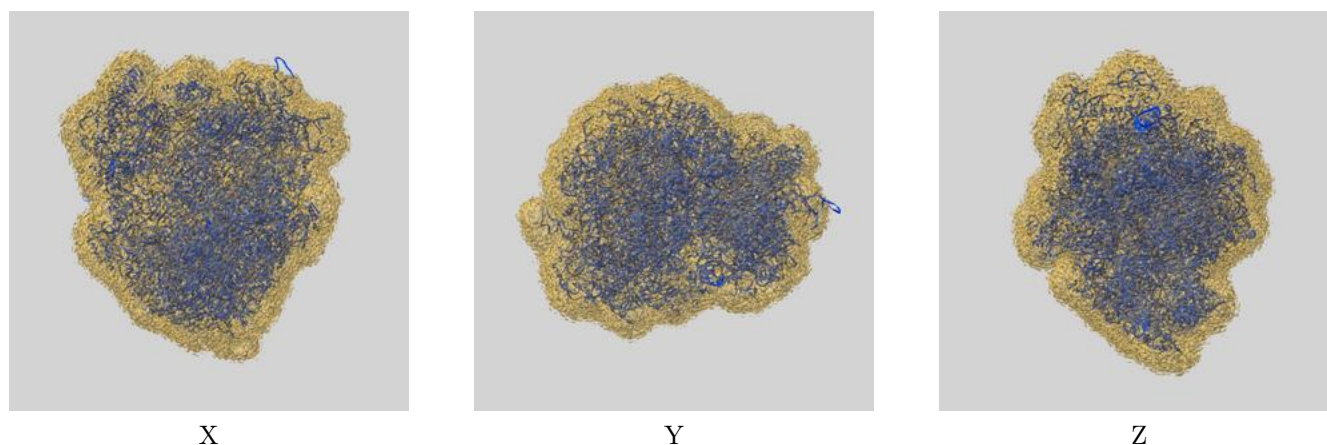
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	4.14	5.15	4.20
Unmasked-calculated*	6.11	9.73	6.72

*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](#)

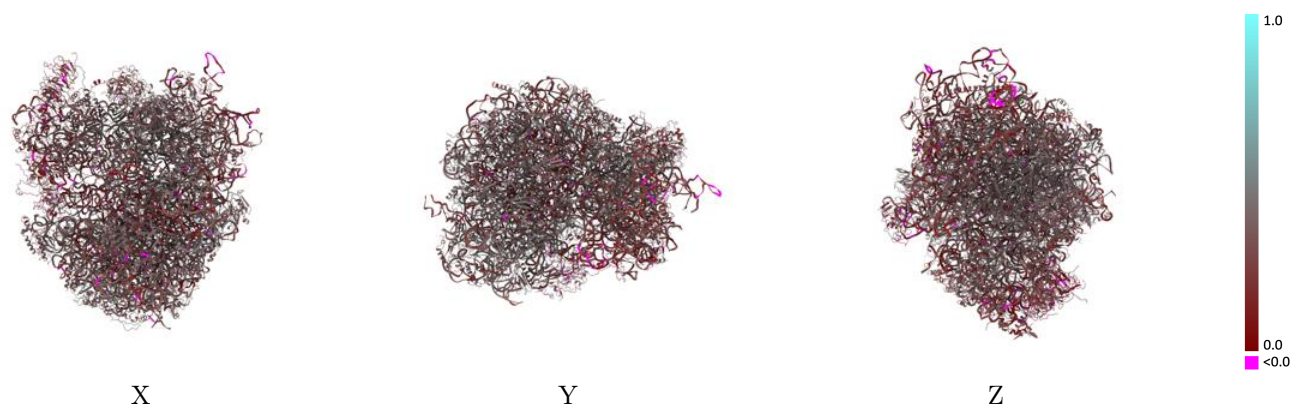
This section contains information regarding the fit between EMDB map EMD-22196 and PDB model 6XIQ. Per-residue inclusion information can be found in section [3](#) on page [20](#).

9.1 Map-model overlay [i](#)



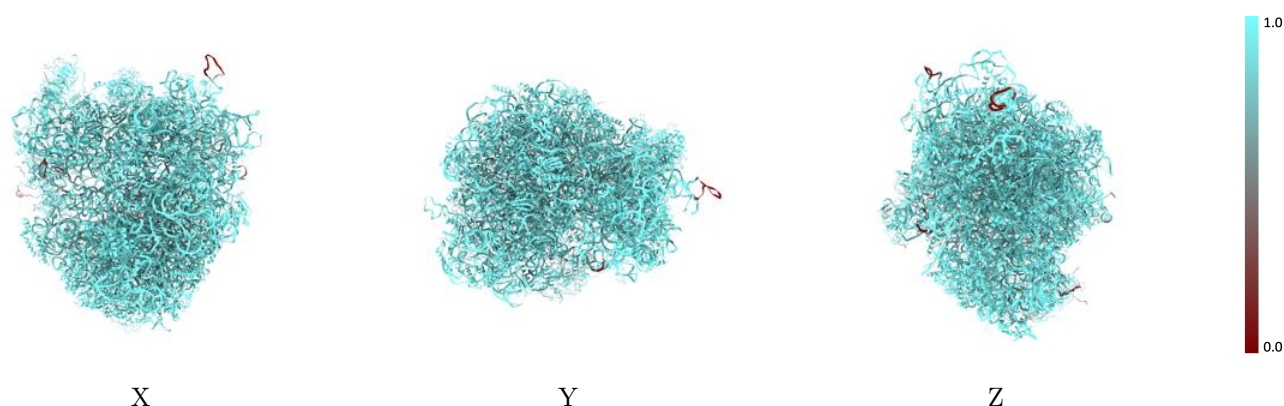
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



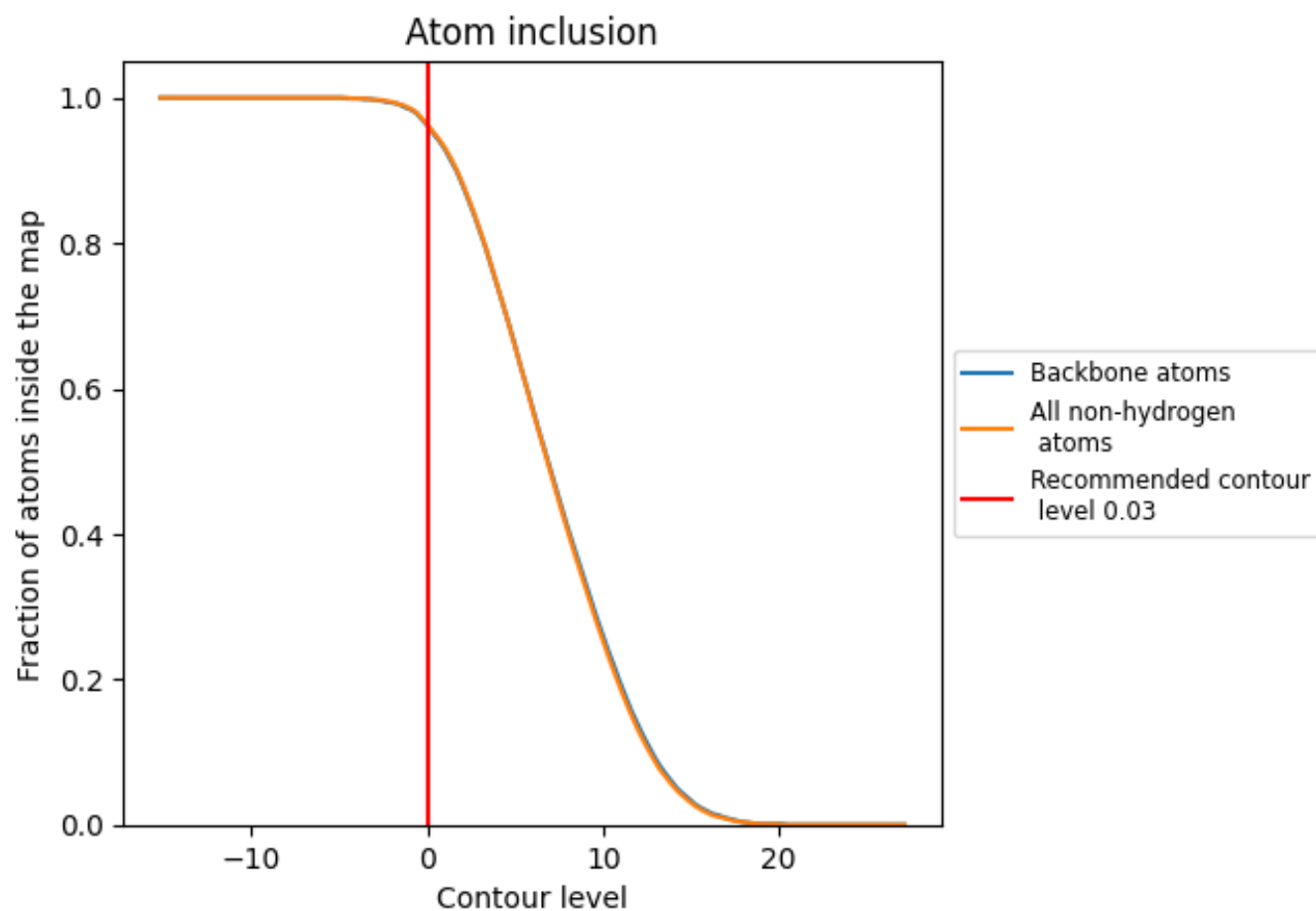
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).

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	Q-score
All	 0.9630	 0.3300
1	 0.9460	 0.3020
2	 0.9800	 0.3130
3	 0.9850	 0.3560
4	 0.9370	 0.3160
A	 0.9130	 0.3910
AA	 0.9880	 0.2740
AB	 0.9730	 0.3670
AD	 0.9730	 0.3810
AE	 0.9760	 0.3990
AF	 0.9810	 0.3200
AG	 0.9620	 0.2480
AH	 0.9760	 0.3200
AI	 0.9730	 0.3100
AJ	 0.9880	 0.2840
AK	 0.9320	 0.2860
AL	 0.9850	 0.3640
AM	 0.9800	 0.4010
AN	 0.9830	 0.3760
AO	 0.9910	 0.2670
AP	 0.9450	 0.2230
AQ	 0.9550	 0.3660
AR	 0.9750	 0.3550
AS	 0.9870	 0.3590
AT	 0.9510	 0.3260
AU	 0.9800	 0.3360
AV	 0.9560	 0.2660
AX	 0.9320	 0.2360
AY	 0.9080	 0.2590
AZ	 0.9100	 0.1690
B	 0.9850	 0.4250
C	 0.9860	 0.4240
D	 0.9860	 0.3640
E	 0.9880	 0.4020
F	 0.9850	 0.4110



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Chain	Atom inclusion	Q-score
G	 0.9780	 0.3790
H	 0.9790	 0.3860
I	 0.9820	 0.4020
J	 0.9850	 0.3620
L	 0.9830	 0.4090
L1	 0.8370	 0.1930
M	 0.9890	 0.3960
N	 0.9790	 0.4210
O	 0.9790	 0.4110
P	 0.9690	 0.4140
P0	 0.7510	 0.2000
P2	 0.8960	 0.2190
Q	 0.9850	 0.4280
R	 0.9820	 0.3940
S	 0.9880	 0.4210
T	 0.9850	 0.4200
U	 0.9940	 0.3910
V	 0.9650	 0.4290
W	 0.9940	 0.4230
X	 0.9930	 0.4360
Y	 0.9930	 0.4230
Z	 0.9850	 0.4050
a	 0.9720	 0.4170
b	 0.9800	 0.3850
c	 0.9810	 0.3940
d	 0.9880	 0.4270
e	 0.9860	 0.4440
f	 0.9830	 0.4430
g	 0.9810	 0.4180
h	 0.9820	 0.3880
i	 0.9790	 0.3870
j	 0.9850	 0.4250
k	 0.9920	 0.3930
l	 0.9610	 0.3970
m	 0.7720	 0.1770
n	 0.9860	 0.4250
o	 0.9720	 0.4050
p	 0.9700	 0.4120
q	 0.9740	 0.3570
r	 0.9760	 0.3740
s	 0.9800	 0.3910
t	 0.9670	 0.3370

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Chain	Atom inclusion	Q-score
u	 0.9800	 0.3090
v	 0.9800	 0.3140
w	 0.9590	 0.2640
x	 0.9810	 0.3390
y	 0.9830	 0.3340
z	 0.9750	 0.2930