



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 11:00 AM UTC

PDB ID : 6XIR / pdb_00006xir
EMDB ID : EMD-22198
Title : Cryo-EM Structure of K63 Ubiquitinated Yeast Translocating Ribosome under Oxidative Stress
Authors : Zhou, Y.; Bartesaghi, A.; Silva, G.M.
Deposited on : 2020-06-21
Resolution : 3.20 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:

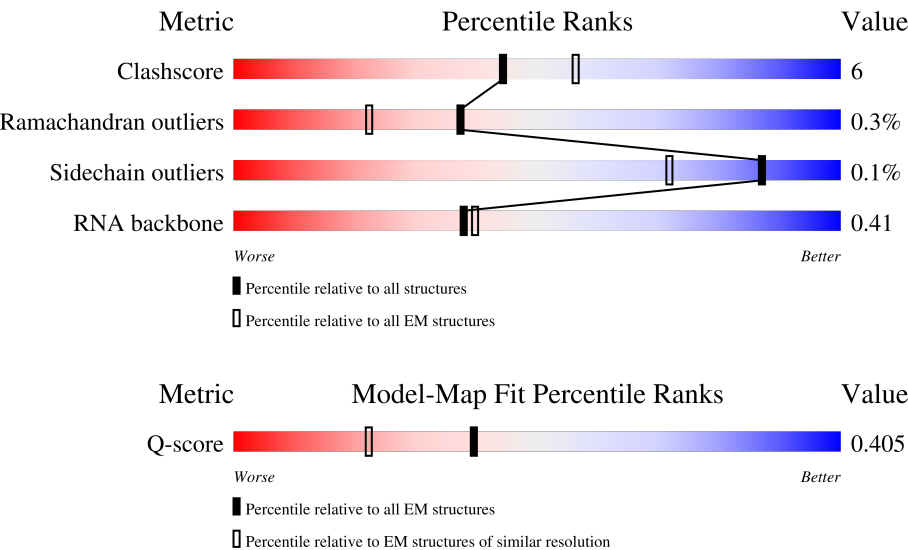
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.20 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.



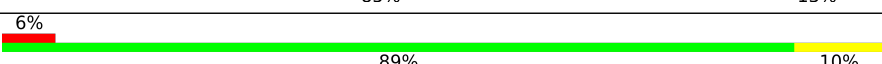
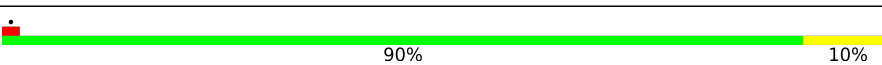
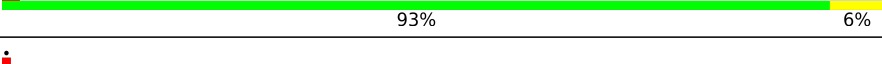
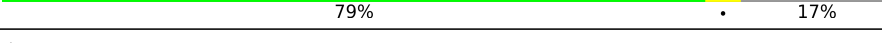
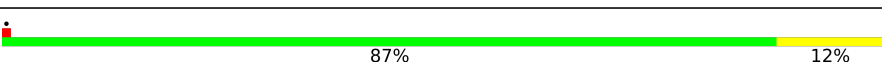
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	

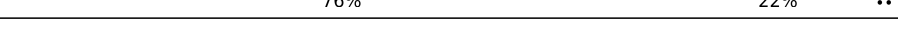
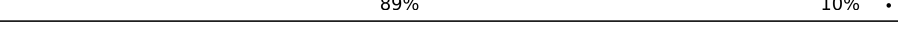
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Mol	Chain	Length	Quality of chain
4	D	297	
5	E	176	
6	F	244	
7	G	256	
8	H	191	
9	I	221	
10	J	174	
11	L	199	
12	M	138	
13	N	204	
14	O	199	
15	P	184	
16	Q	186	
17	R	189	
18	S	172	
19	T	160	
20	U	121	
21	V	137	
22	W	155	
23	X	142	
24	Y	127	
25	Z	136	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

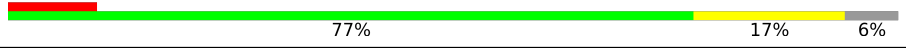
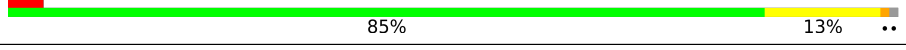
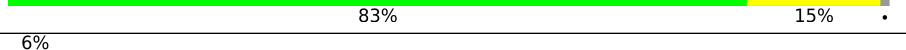
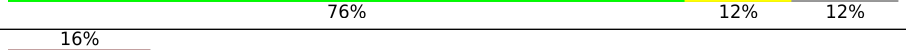
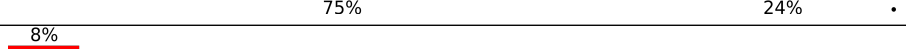
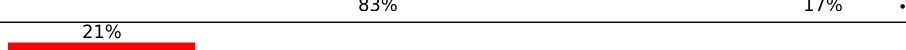
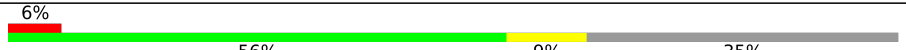
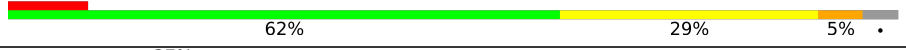
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Mol	Chain	Length	Quality of chain
29	3	121	
30	4	158	
31	a	149	
32	b	59	
33	c	105	
34	d	113	
35	e	130	
36	f	107	
37	g	121	
38	h	120	
39	i	100	
40	j	88	
41	k	78	
42	l	51	
43	n	25	
44	o	106	
45	p	92	
46	2	1800	
47	q	252	
48	r	255	
49	s	254	
50	t	240	
51	u	261	
52	v	225	
53	w	236	

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

2 Entry composition

There are 76 unique types of molecules in this entry. The entry contains 197132 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	252	Total	C	N	O	S	0	0
			1914	1191	388	334	1		

- Molecule 2 is a protein called RPL3 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 3 is a protein called RPL4A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 4 is a protein called RPL5 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	296	Total	C	N	O	S	0	0
			2375	1501	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	N	O	S	0	0
			1239	800	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	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 7 is a protein called RPL8A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 8 is a protein called RPL9A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 9 is a protein called RPL10 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	211	Total	C	N	O	S	0	0
			1705	1083	322	294	6		

- Molecule 10 is a protein called RPL11B isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	169	Total	C	N	O	S	0	0
			1353	847	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	N	O		0	0
			1543	962	315	266			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	136	Total	C	N	O	S	0	0
			1053	675	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	N	O	S	0	0
			1720	1077	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	N	O	S	0	0
			1555	1003	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	N	O		0	0
			1420	882	281	257			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	185	Total	C	N	O	S	0	0
			1441	908	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	N	O		0	0
			1521	935	326	260			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	172	Total	C	N	O	S	0	0
			1445	930	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	N	O	S	0	0
			1276	805	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	N	O		0	0
			796	516	131	149			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 22 is a protein called RPL24A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	63	Total	C	N	O	S	0	0
			521	336	102	82	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	121	Total	C	N	O	S	0	0
			964	620	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	N	O		0	0
			993	625	192	176			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	135	Total	C	N	O		0	0
			1092	710	202	180			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AA	96	Total	C	N	O	S	0	0
			772	499	126	145	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AB	144	Total	C	N	O	S	0	0
			1159	742	219	195	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	1	3113	Total	C	N	O	P	0	0
			66567	29735	11981	21738	3113		

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	N	O	P	0	0
			2579	1152	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	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 31 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 32 is a protein called RPL29 isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	b	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 33 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 34 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	109	Total	C	N	O	S	0	0
			883	559	167	156	1		

- Molecule 35 is a protein called RPL32 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 36 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 37 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 38 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 39 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 40 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 41 is a protein called RPL38 isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	k	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 42 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 43 is a protein called RPL41A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	25	Total	C	N	O	S	0	0
			227	139	60	27	1		

- Molecule 44 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 45 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	p	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 46 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	2	1708	Total	C	N	O	P	0	0
			36409	16277	6464	11960	1708		

- Molecule 47 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	206	Total	C	N	O	S	0	0
			1577	1014	278	283	2		

- Molecule 48 is a protein called RPS1A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	r	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 49 is a protein called RPS2 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 50 is a protein called RPS3 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 51 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	u	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 52 is a protein called Rps5p.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	v	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 53 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	w	223	Total	C	N	O	S	0	0
			1790	1123	346	318	3		

- Molecule 54 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	x	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 55 is a protein called RPS8A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	y	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 56 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	z	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 57 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AD	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 58 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AE	127	Total	C	N	O	S	0	0
			891	545	182	163	1		

- Molecule 59 is a protein called RPS15 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AF	124	Total	C	N	O	S	0	0
			977	622	182	166	7		

- Molecule 60 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
60	AG	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 61 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AH	120	Total	C	N	O	S	0	0
			926	577	177	170	2		

- Molecule 62 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AI	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 63 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AJ	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 64 is a protein called RPS20 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AK	107	Total	C	N	O	S	0	0
			855	539	156	159	1		

- Molecule 65 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AL	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 66 is a protein called RPS22A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AM	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 67 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	AN	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 68 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
68	AO	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 69 is a protein called RPS25A isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
69	AP	70	Total	C	N	O	0	0
			563	360	104	99		

- Molecule 70 is a protein called RPS26B isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
70	AQ	97	Total	C	N	O	S	0
			769	475	160	129	5	0

- Molecule 71 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
71	AR	81	Total	C	N	O	S	0
			610	382	110	113	5	0

- Molecule 72 is a protein called RPS28A isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
72	AS	63	Total	C	N	O	S	0
			497	306	99	91	1	0

- Molecule 73 is a protein called RPS29A isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
73	AT	53	Total	C	N	O	S	0
			442	274	92	72	4	0

- Molecule 74 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
74	AV	318	Total	C	N	O	S	0
			2437	1541	418	470	8	0

- Molecule 75 is a RNA chain called Transfer RNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
75	AX	73	Total	C	N	O	P	0
			1564	697	282	512	73	0
75	AZ	73	Total	C	N	O	P	0
			1564	697	282	512	73	0

- Molecule 76 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by

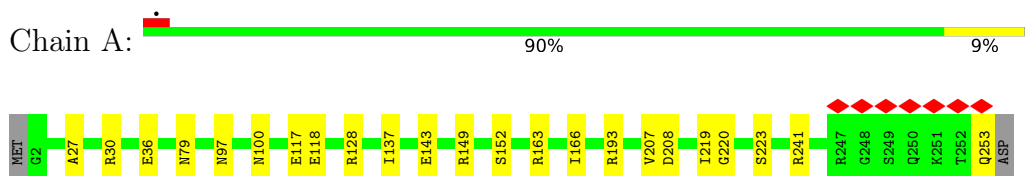
depositor).

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

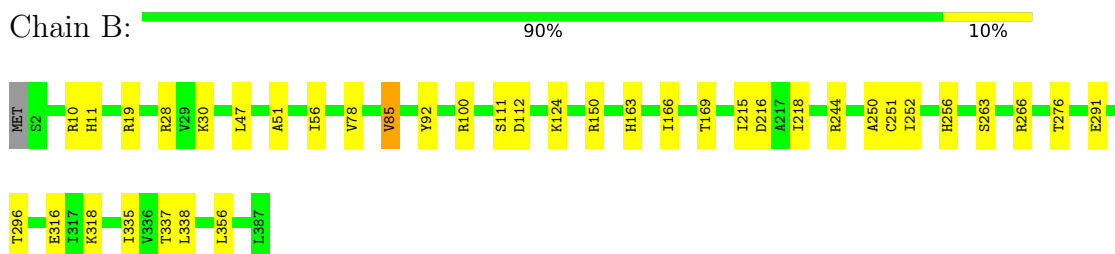
3 Residue-property plots [i](#)

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.

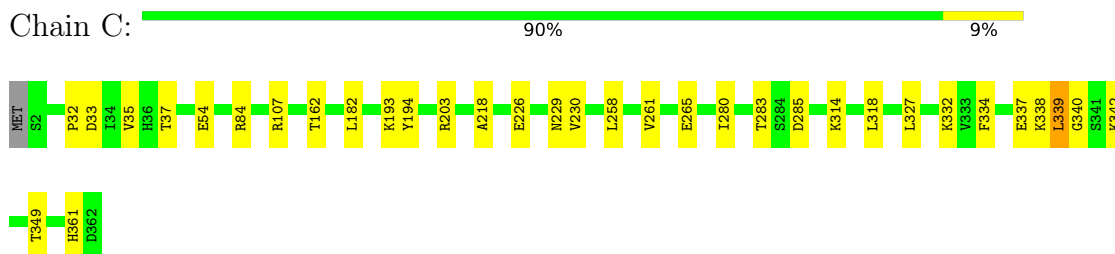
- Molecule 1: 60S ribosomal protein L2-A



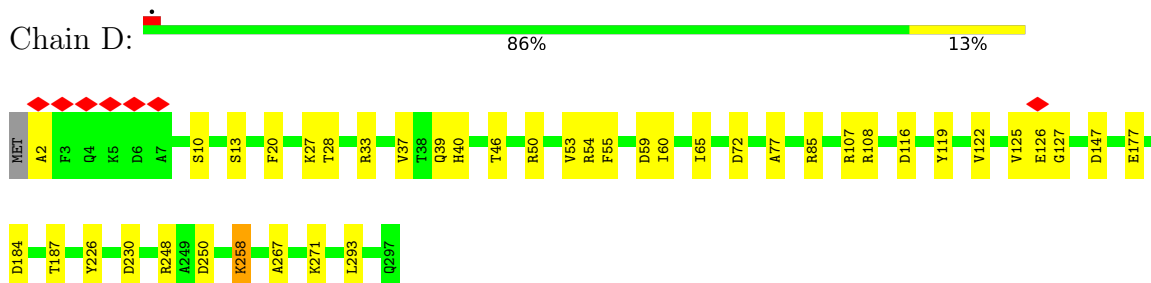
- Molecule 2: RPL3 isoform 1



- Molecule 3: RPL4A isoform 1

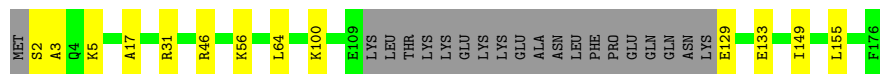


- Molecule 4: RPL5 isoform 1



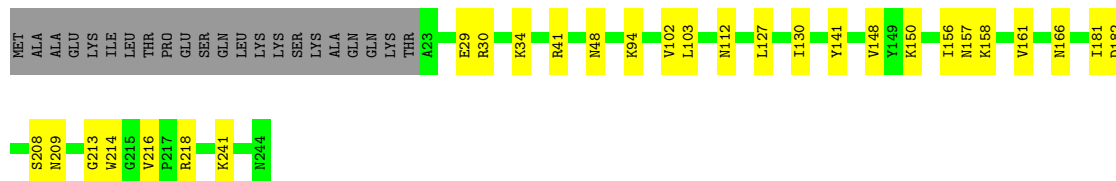
- Molecule 5: 60S ribosomal protein L6-A

Chain E:  81% 7% 11%



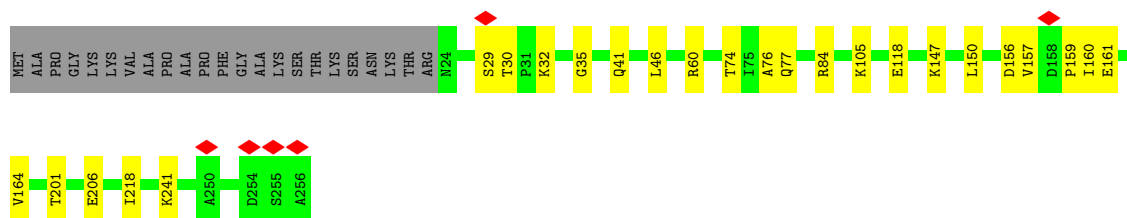
- Molecule 6: 60S ribosomal protein L7-A

Chain F:  80% 11% 9%



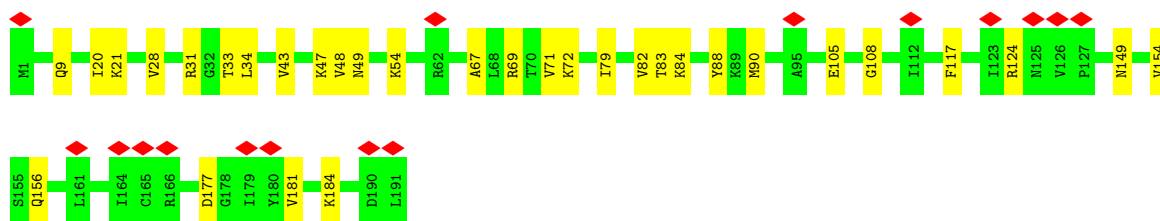
- Molecule 7: RPL8A isoform 1

Chain G:  81% 10% 9%



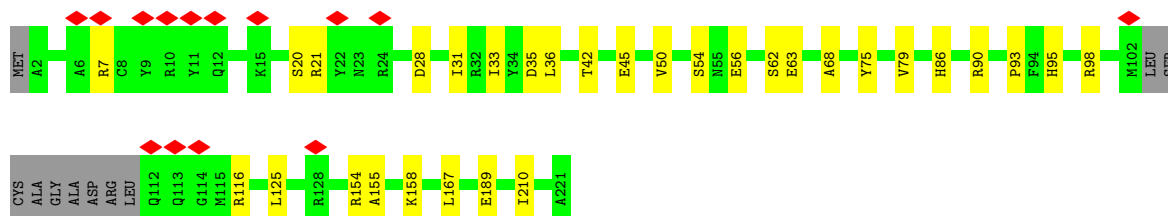
- Molecule 8: RPL9A isoform 1

Chain H:  8% 83% 17%

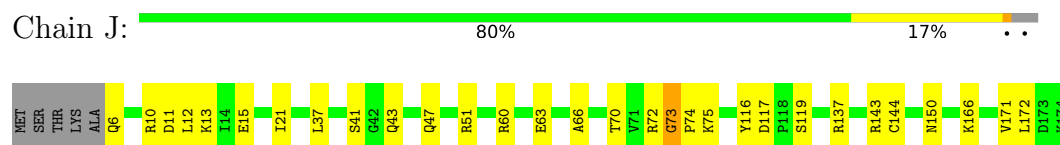


- Molecule 9: RPL10 isoform 1

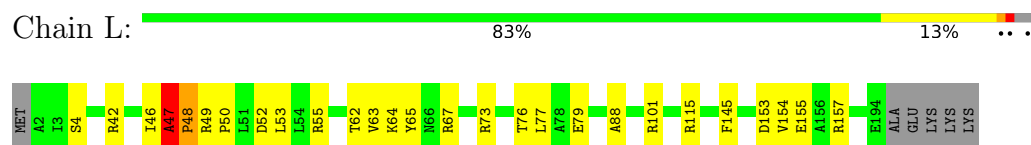
Chain I:  6% 81% 14% 5%



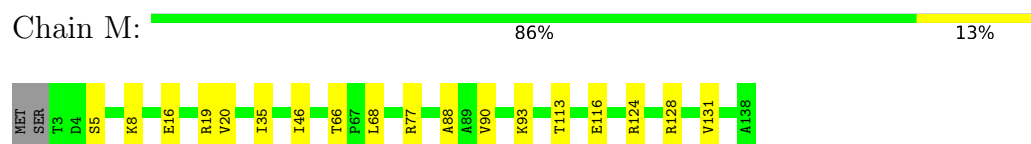
- Molecule 10: RPL11B isoform 1



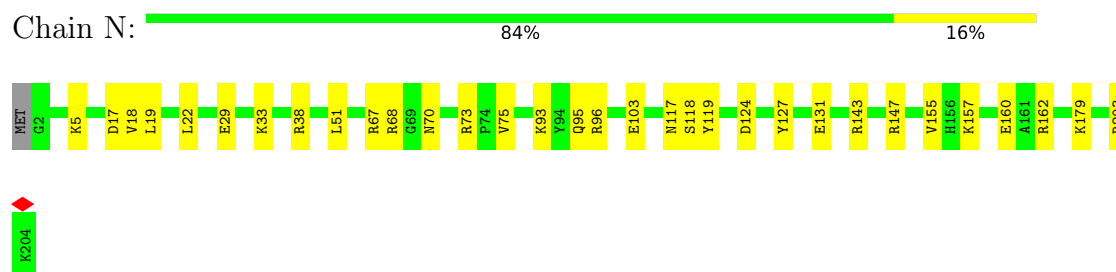
- Molecule 11: 60S ribosomal protein L13-A



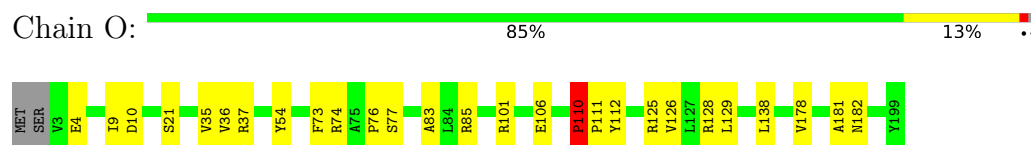
- Molecule 12: 60S ribosomal protein L14-A



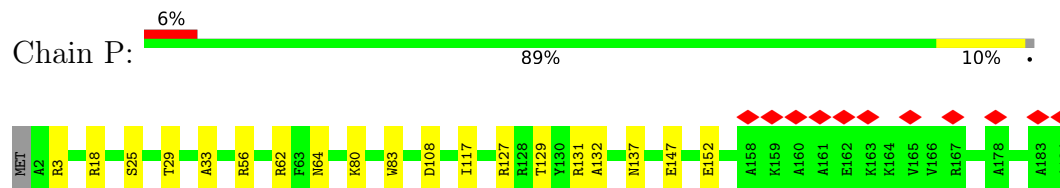
- Molecule 13: 60S ribosomal protein L15-A



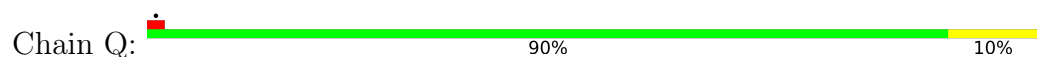
- Molecule 14: 60S ribosomal protein L16-A



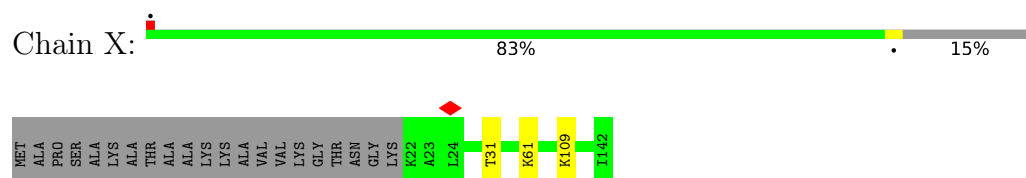
- Molecule 15: 60S ribosomal protein L17-A



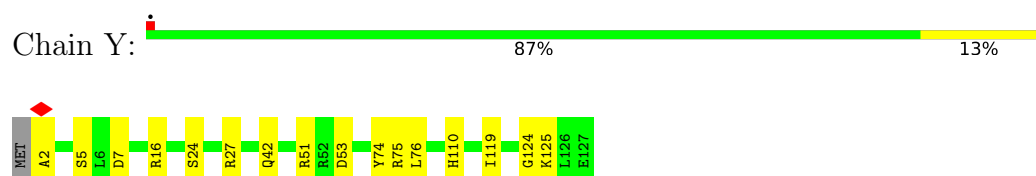
- Molecule 16: 60S ribosomal protein L18-A



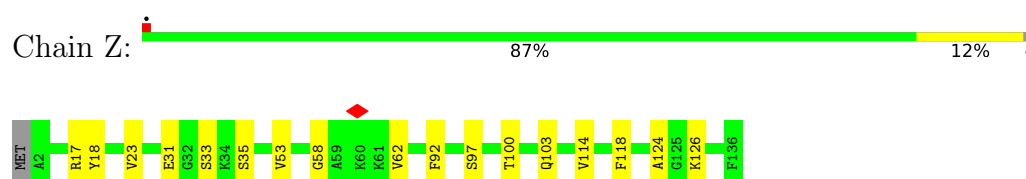
- Molecule 23: 60S ribosomal protein L25



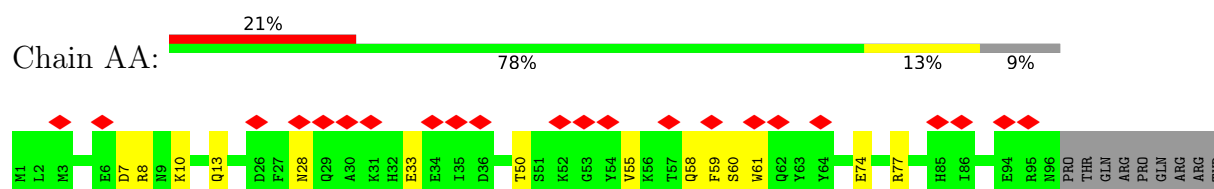
- Molecule 24: 60S ribosomal protein L26-A



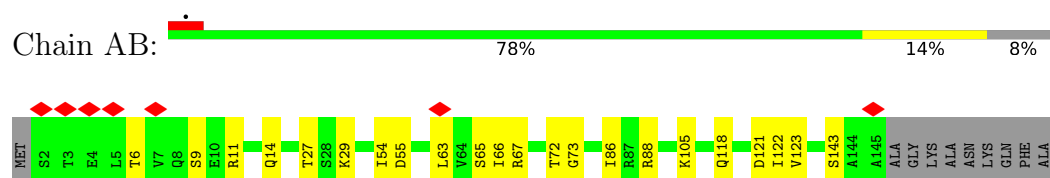
- Molecule 25: 60S ribosomal protein L27-A



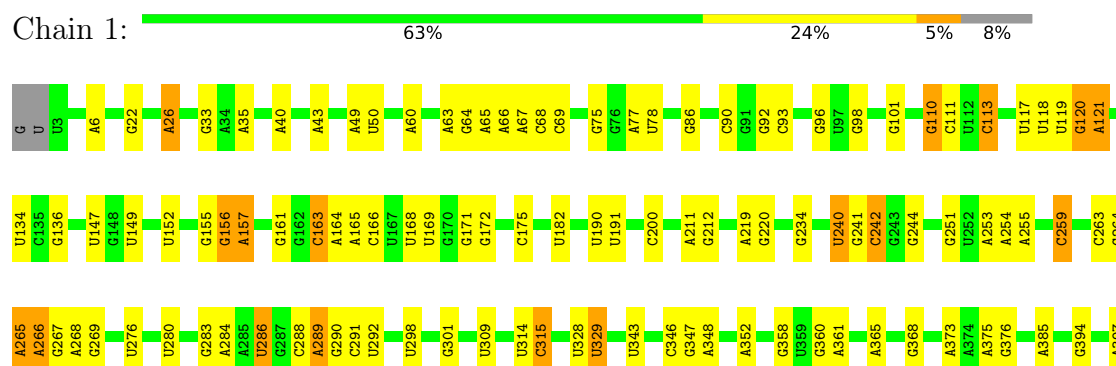
- Molecule 26: 40S ribosomal protein S10-A



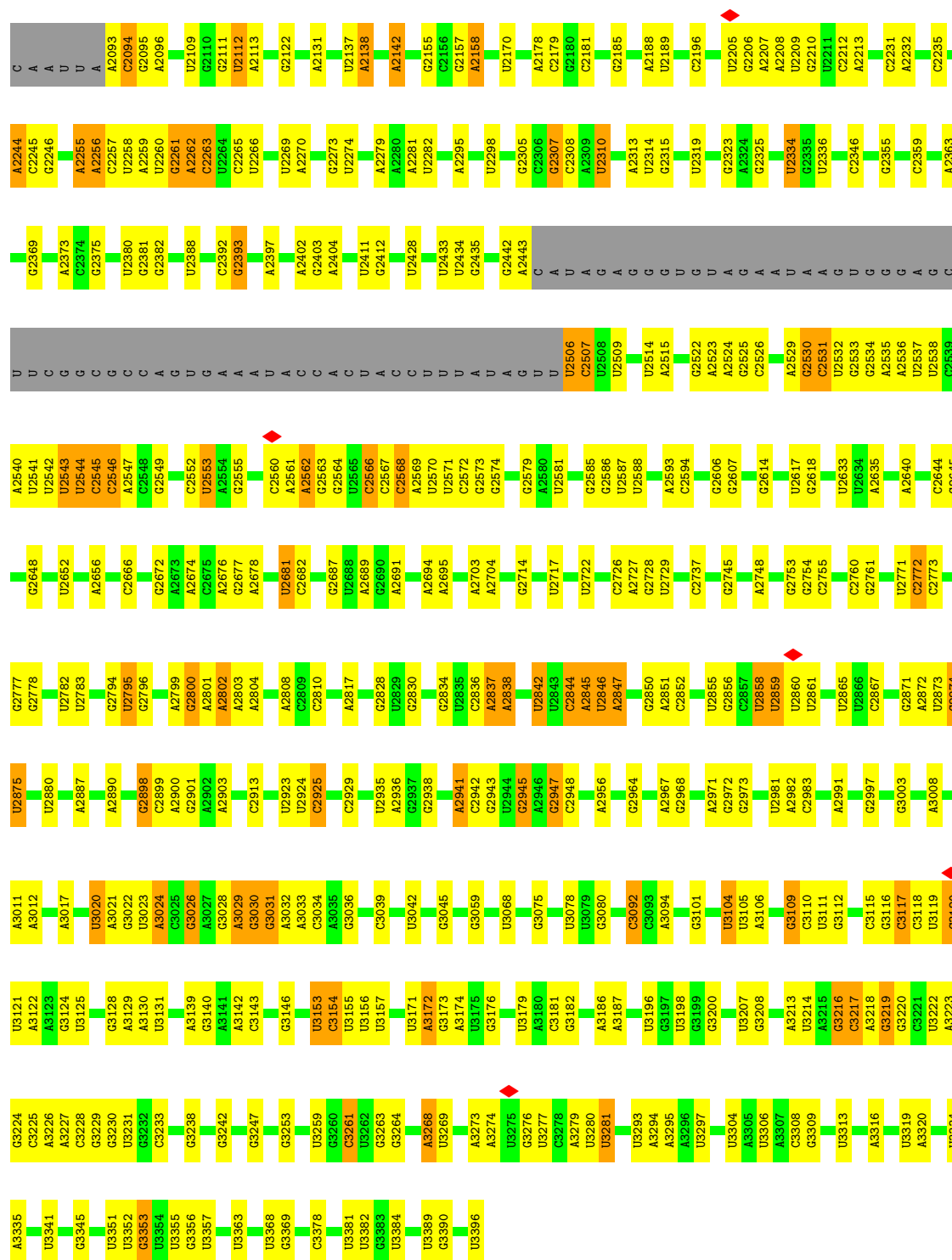
- Molecule 27: 40S ribosomal protein S11-A



- Molecule 28: 35S ribosomal RNA





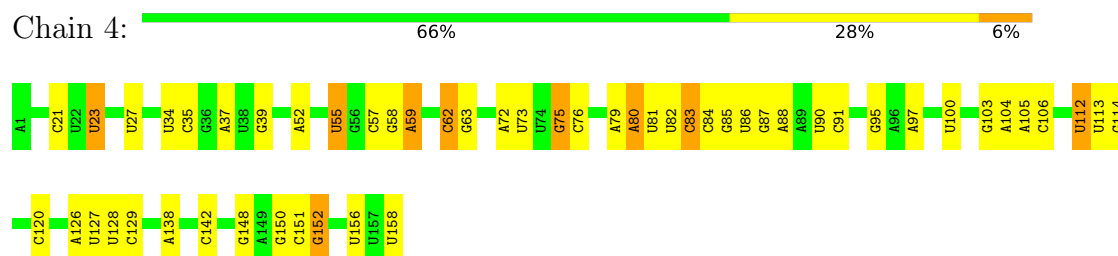


• Molecule 29: 5S ribosomal RNA

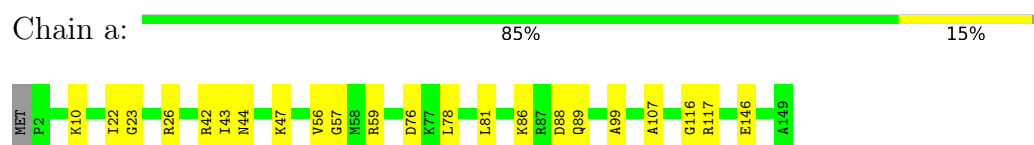
Chain 3: 73% 25%



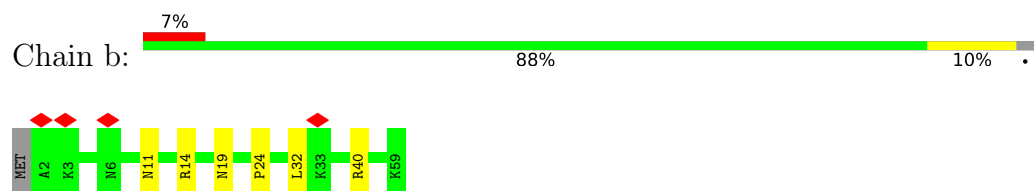
- Molecule 30: 5.8S ribosomal RNA



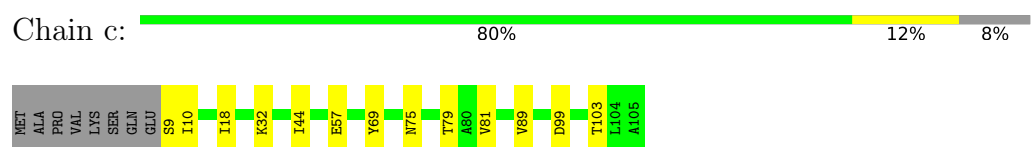
- Molecule 31: 60S ribosomal protein L28



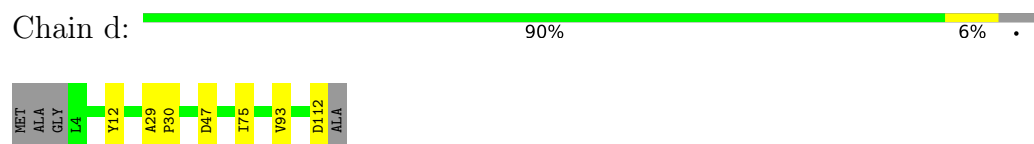
- Molecule 32: RPL29 isoform 1



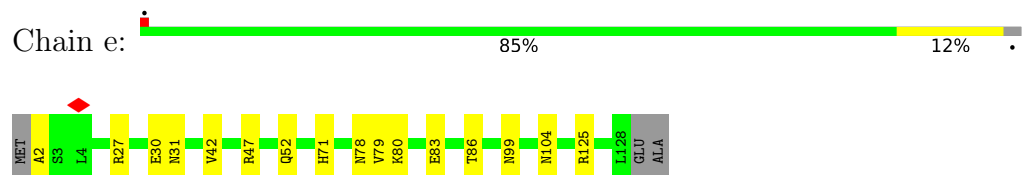
- Molecule 33: 60S ribosomal protein L30



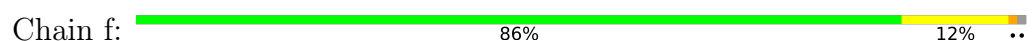
- Molecule 34: 60S ribosomal protein L31-A

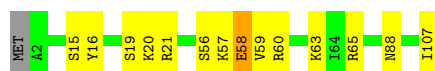


- Molecule 35: RPL32 isoform 1

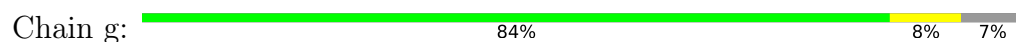


- Molecule 36: 60S ribosomal protein L33-A





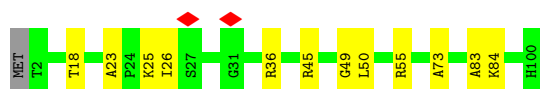
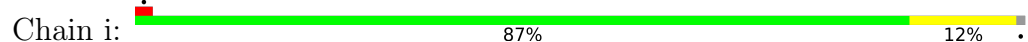
- Molecule 37: 60S ribosomal protein L34-A



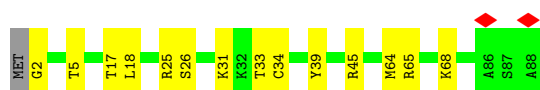
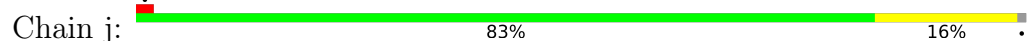
- Molecule 38: 60S ribosomal protein L35-A



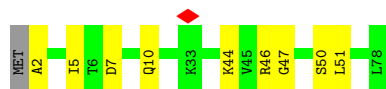
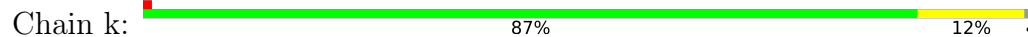
- Molecule 39: 60S ribosomal protein L36-A



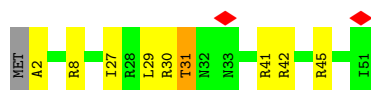
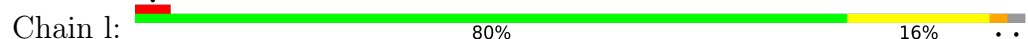
- Molecule 40: 60S ribosomal protein L37-A



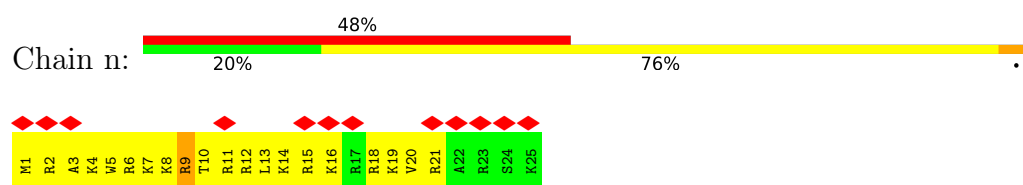
- Molecule 41: RPL38 isoform 1



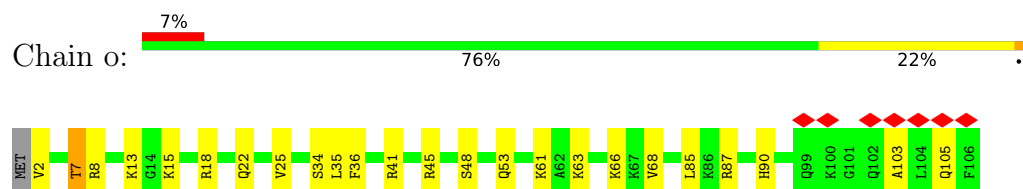
- Molecule 42: 60S ribosomal protein L39



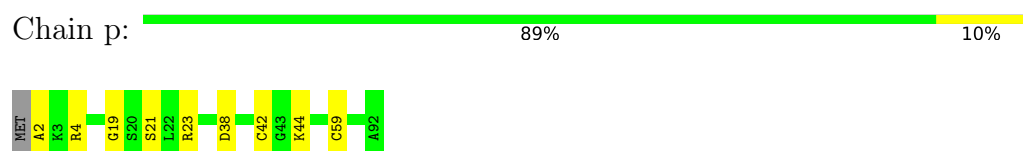
- Molecule 43: RPL41A isoform 1



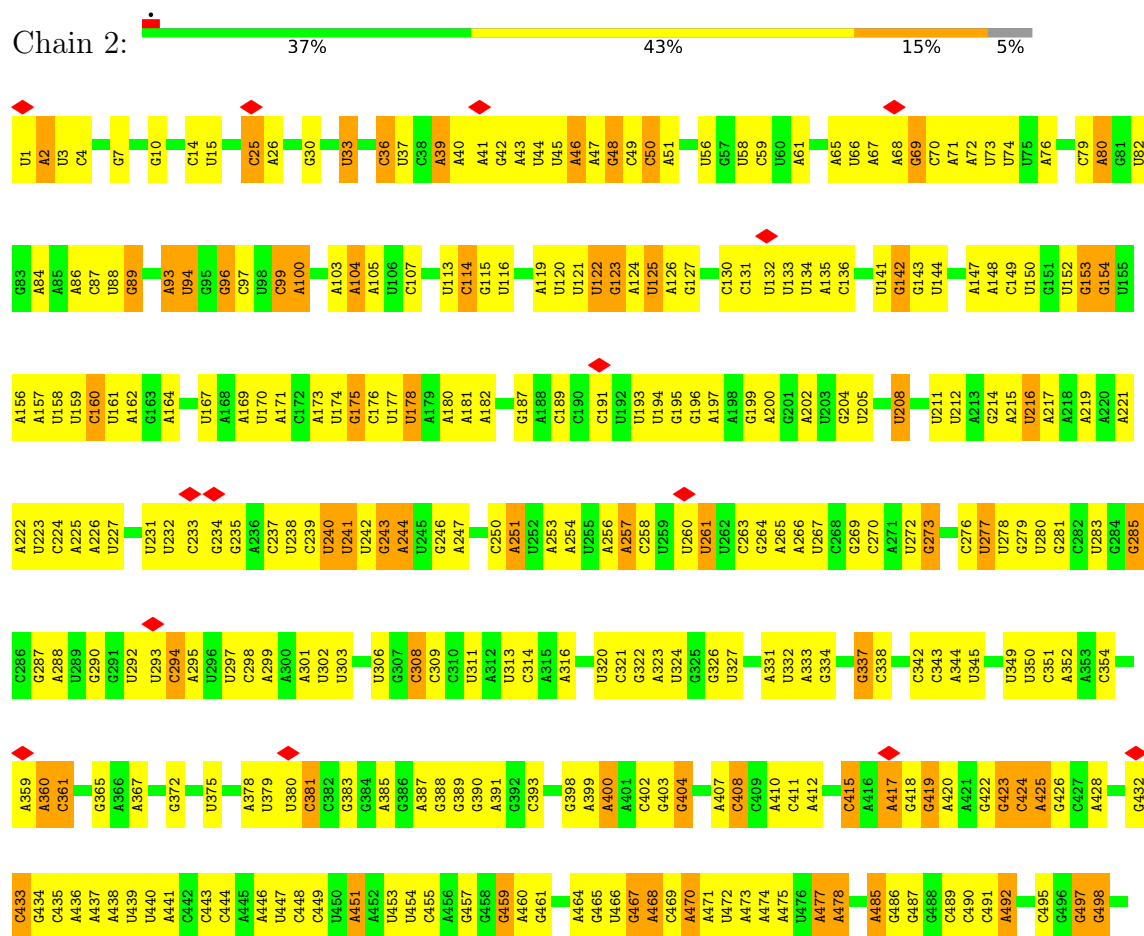
• Molecule 44: 60S ribosomal protein L42-A



• Molecule 45: 60S ribosomal protein L43-A

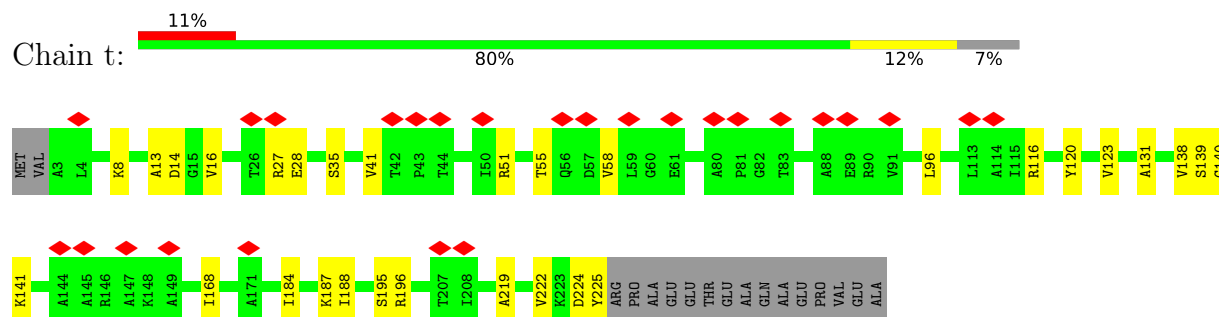


• Molecule 46: 18S ribosomal RNA

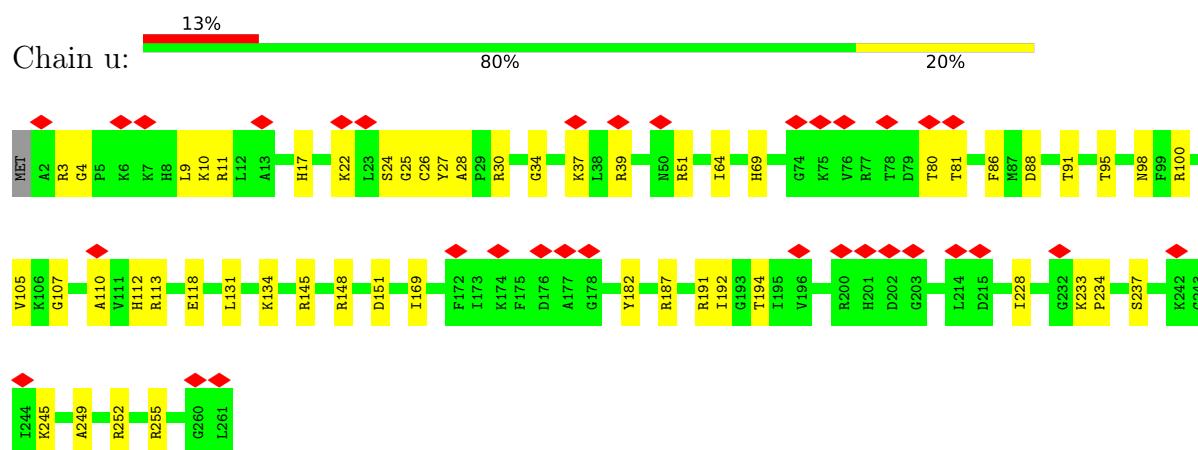


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U1496	U1497	A1425	C1359	U1286	A1223	A1151	U1052	U932	G834	A769	A707	G647	U502
U1498	U1499	G1426	A1360	A1287	U1224	C1156	U1053	A933	U835	A770	C	G648	U503
G1501	G1502	G1427	U1361	G1288	A	A1157	G1053	A934	U836	A771	U	U649	U504
U1503	U1504	U1428	U1362	G1289	G	C1158	U1054	C934	G837	G772	U	G650	A505
G1505	G1506	G1429	U1363	G1295	A	C1159	U1055	U935	G838	A773	G	G651	A506
U1507	U1508	U1430	U1366	U1298	G	A1160	U1056	A940	U841	A774	A	G652	U507
C1509	U1510	U1431	G1367	U1299	A	C1161	U	A941	C842	C777	G	C	U508
U1511	U1512	U1432	U1368	A1300	U	A1162	U	G942	A943	A778	G	C	G509
G1513	U1514	G1433	U1369	U1301	G	A1163	U	A951	U844	G779	C	G	G510
U1517	U1518	U1434	U1370	U1302	A	G1164	U	A952	C848	A780	C	U	A511
C1519	U1520	U1435	A1371	U1303	C	G1165	A	A956	C849	U781	U	C	A512
U1521	U1522	U1436	U1372	U1307	A	A1166	U1057	U960	U850	U782	U	C	U513
G1523	U1524	U1437	C1373	G1306	G	U1167	A1052	U961	A851	A783	G	G	G514
A1525	A1526	G1438	A1374	C1309	A	U1168	G1053	A963	U852	C784	U	A	A515
G1527	U1528	U1439	A1375	U1310	U	G1169	G1054	A964	C852	U785	G	U	C519
U1529	U1530	C1440	C1376	U1311	G	A1170	A1055	U965	G853	C786	G	U	C518
G1533	G1534	C1441	U1377	U1312	U	A1171	C1056	A966	U854	A787	U	U	G523
U1535	U1536	U1442	C1378	A1312	G	C1172	C1070	A967	U855	A788	C	U	U524
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U1545	U1546	U1447	U1383	U1319	C	U1181	U1106	A989	U861	U794	G	U	A534
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A1559	U1560	U1451	U1389	G1327	C	C1190	U1097	A993	A865	A799	G	U	G540
U1561	U1562	U1452	U1390	U1328	U	U1191	U1098	A994	U869	U800	A	U	A541
G1563	G1564	U1453	U1391	A1329	U	C1192	U1099	C1000	U872	G802	U	U	A542
U1565	U1566	U1454	U1392	U1330	G	U1193	G1100	U1004	U873	A803	U	U	A544
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U1591	U1592	U1467	U1412	A1344	U	C1208	G1130	U1031	G913	U821	C896	U696	C565
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U1597	U1598	U1470	U1415	U1347	U	C1211	A1138	C1034	U920	U826	U699	U700	U640
U1599	U1600	U1471	U1416	G1348	U	C1212	A1142	G1035	U921	A829	U701	G702	G642
U1601	U1602	U1472	U1417	U1349	U	C1213	A1147	U1038	U922	U831	U756	G703	G643
U1603	U1604	U1473	U1418	U1350	U	C1214	U1147	U1039	U923	U832	U767	C704	G571
U1605	U1606	U1474	U1419	U1351	U	C1215	U1148	G1042	U924	U833	U768	U705	C572
U1607	U1608	U1475	U1420	U1352	U	C1216	U1149	U1043	U925	U834	U769	U706	
U1609	U1610	U1476	U1421	U1353	U	C1217	U1150	U1044	U926	U835	U770	U707	
U1611	U1612	U1477	U1422	U1354	U	C1218	U1151	U1045	U927	U836	U771	U708	
U1613	U1614	U1478	U1423	U1355	U	C1219	U1152	U1046	U928	U837	U772	U709	
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U1617	U1618	U1480	U1425	U1357	U	C1221	U1154	U1048	U930	U839	U774	U711	
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U1631	U1632	U1487	U1432	U1364	U	C1228	U1161	U1055	U937	U846	U781	U718	
U1633	U1634	U1488	U1433	U1365	U	C1229	U1162	U1056	U938	U847	U782	U719	
U1635	U1636	U1489	U1434	U1366	U	C1230	U1163	U1057	U939	U848	U783	U720	
U1637	U1638	U1490	U1435	U1367	U	C1231	U1164	U1058	U940	U849	U784	U721	
U1639	U1640	U1491	U1436	U1368	U	C1232	U1165	U1059	U941	U850	U785	U722	
U1641	U1642	U1492	U1437	U1369	U	C1233	U1166	U1060	U942	U851	U786	U723	
U1643	U1644	U1493	U1438	U1370	U	C1234	U1167	U1061	U943	U852	U787	U724	
U1645	U1646	U1494	U1439	U1371	U	C1235	U1168	U1062	U944	U853	U788	U725	
U1647	U1648	U1495	U1440	U1372	U	C1236	U1169	U1063	U945	U854	U789	U726	
U1649	U1650	U1496	U1441	U1373	U	C1237	U1170	U1064	U946	U855	U790	U727	
U1651	U1652	U1497	U1442	U1374	U	C1238	U1171	U1065	U947	U856	U791	U728	
U1653	U1654	U1498	U1443	U1375	U	C1239	U1172	U1066	U948	U857	U792	U729	
U1655	U1656	U1499	U1444	U1376	U	C1240	U1173	U1067	U949	U858	U793	U730	
U1657	U1658	U1500	U1445	U1377	U	C1241	U1174	U1068	U950	U859	U794	U731	
U1659	U1660	U1501	U1446	U1378	U	C1242	U1175	U1069	U951	U860	U795	U732	
U1661	U1662	U1502	U1447	U1379	U	C1243	U1176	U1070	U952	U861	U796	U733	
U1663	U1664	U1503	U1448	U1380	U	C1244	U1177	U1071	U953	U862	U797	U734	
U1665	U1666	U1504	U1449	U1381	U	C1245	U1178	U1072	U954	U863	U798	U735	
U1667	U1668	U1505	U1450	U1382	U	C1246	U1179	U1073	U955	U864	U799	U736	
U1669	U1670	U1506	U1451	U1383	U	C1247	U1180	U1074	U956	U865	U800	U737	
U1671	U1672	U1507	U1452	U1384	U	C1248	U1181	U1075	U957	U866	U801	U738	
U1673	U1674	U1508	U1453	U1385	U	C1249	U1182	U1076	U958	U867	U802	U739	
U1675	U1676	U1509	U1454	U1386	U	C1250	U1183	U1077	U959	U868	U803	U740	
U1677	U1678	U1510	U1455	U1387	U	C1251	U1184	U1078	U960	U869	U804	U741	
U1679	U1680	U1511	U1456	U1388	U	C1252	U1185	U1079	U961	U870	U805	U742	
U1681	U1682	U1512	U1457	U1389	U	C1253	U1186	U1080	U962	U871	U806	U743	
U1683	U1684	U1513	U1458	U1390	U	C1254	U1187	U1081	U963	U872	U807	U744	
U1685	U1686	U1514	U1459	U1391	U	C1255	U1188	U1082	U964	U873	U808	U745	
U1687	U1688	U1515	U1460	U1392	U	C1256	U1189	U1083	U965	U874	U809	U746	
U1689	U1690	U1516	U1461	U1393	U	C1257	U1190	U1084	U966	U875	U810	U747	
U1691	U1692	U1517	U1462	U1394	U	C1258	U1191	U1085	U967	U876	U811	U748	
U1693	U1694	U1518	U1463	U1395	U	C1259	U1192	U1086	U968	U877	U812	U749	
U1695	U1696	U1519	U1464	U1396	U	C1260	U1193	U1087	U969	U878	U813	U750	
U1697	U1698	U1520	U1465	U1397	U	C1261	U1194	U1088	U970	U879			

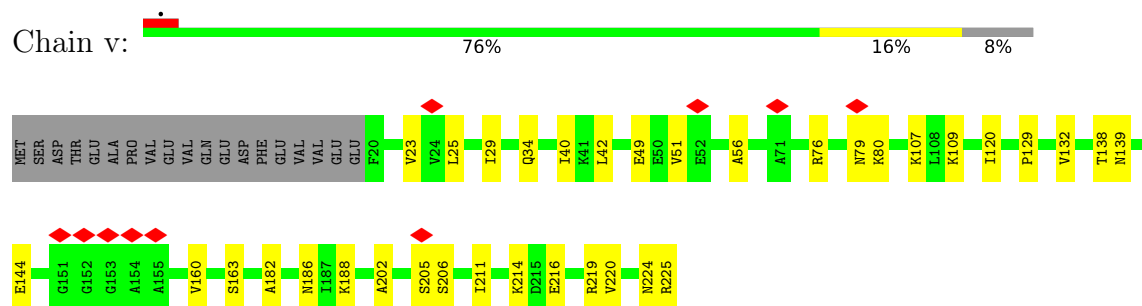
- Molecule 50: RPS3 isoform 1



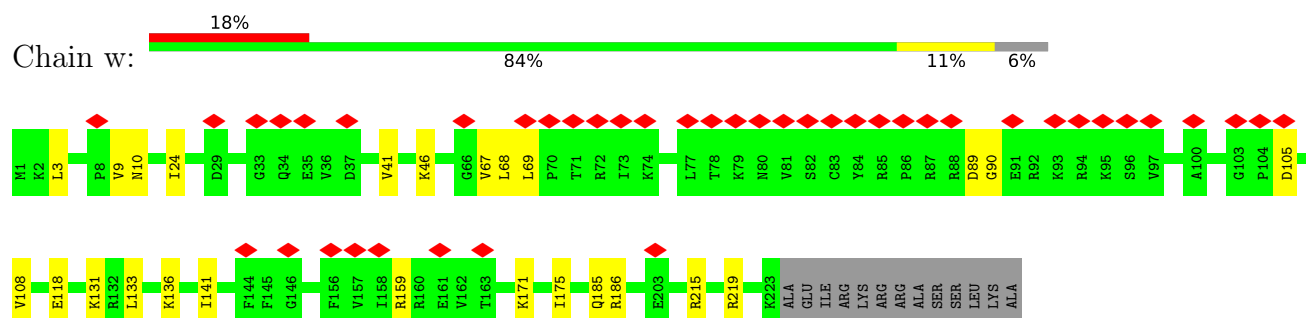
- Molecule 51: 40S ribosomal protein S4-A



- Molecule 52: Rps5p

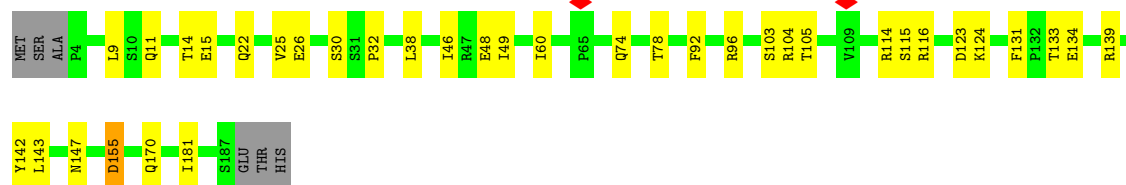


- Molecule 53: 40S ribosomal protein S6-A



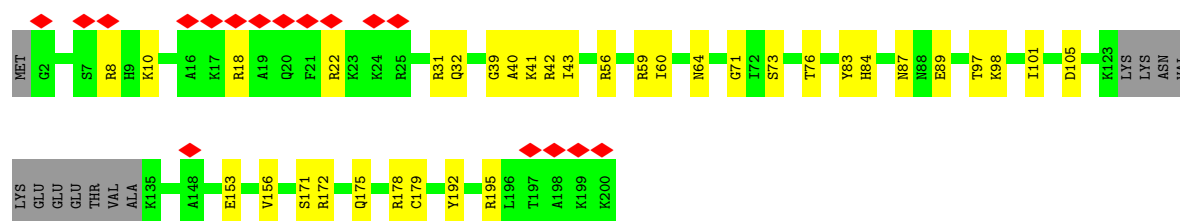
- Molecule 54: 40S ribosomal protein S7-A

Chain x:  78% 18% ..



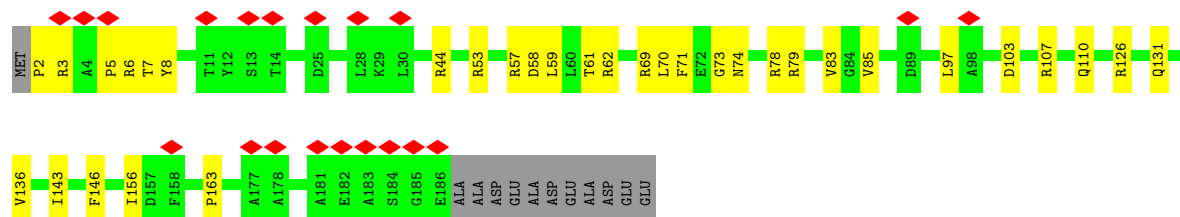
- Molecule 55: RPS8A isoform 1

Chain y:  8% 76% 18% 6%



- Molecule 56: 40S ribosomal protein S9-A

Chain z:  10% 77% 17% 6%



- Molecule 57: 40S ribosomal protein S13

Chain AD:  85% 13% ..



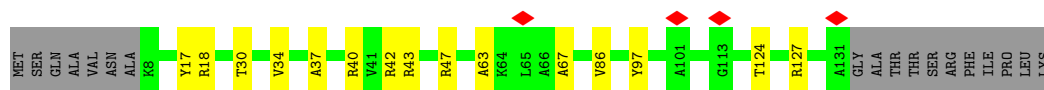
- Molecule 58: 40S ribosomal protein S14-B

Chain AE:  83% 9% 8%

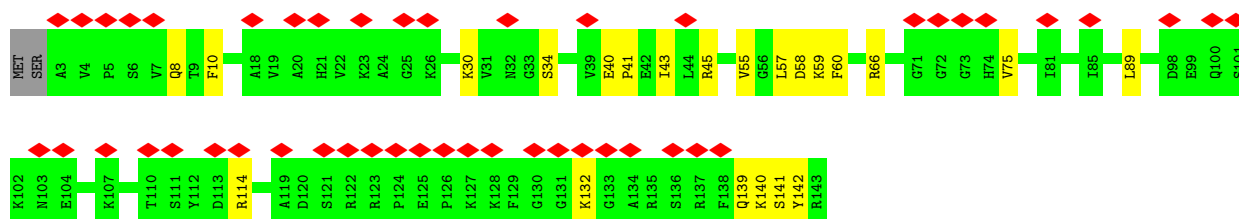
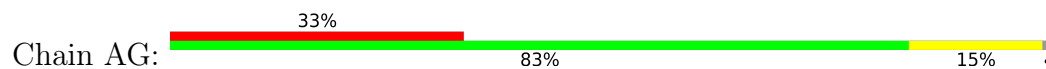


- Molecule 59: RPS15 isoform 1

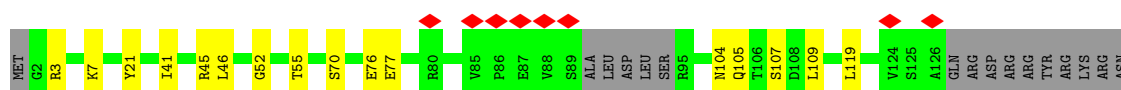
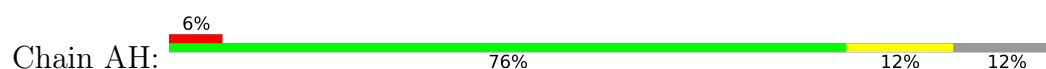
Chain AF:  77% 11% 13%



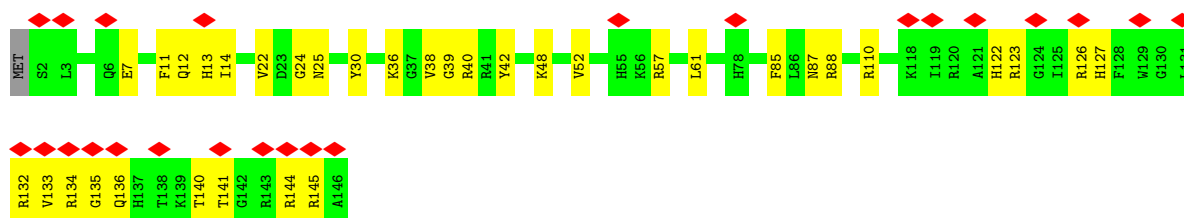
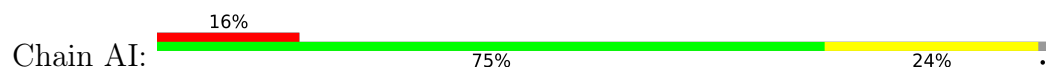
- Molecule 60: 40S ribosomal protein S16-A



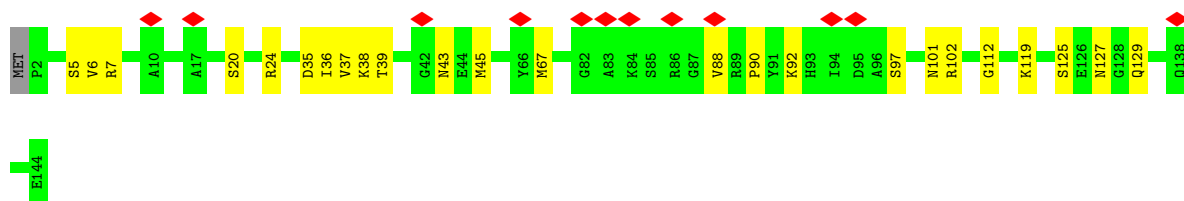
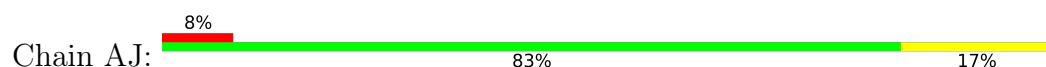
- Molecule 61: 40S ribosomal protein S17-B



- Molecule 62: 40S ribosomal protein S18-A

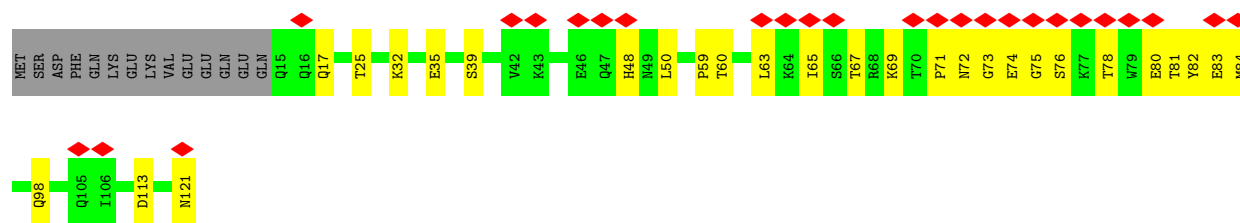


- Molecule 63: 40S ribosomal protein S19-A

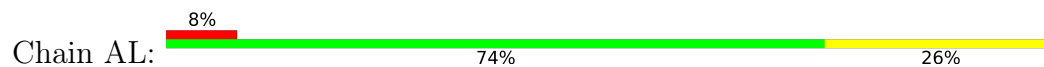


- Molecule 64: RPS20 isoform 1

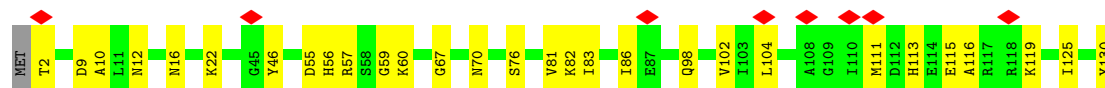
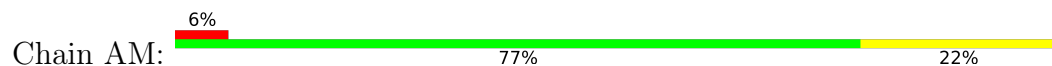




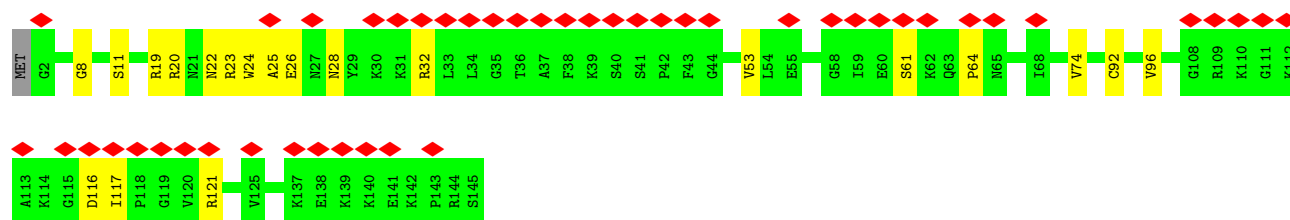
- Molecule 65: 40S ribosomal protein S21-A



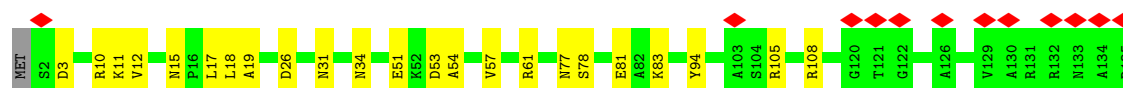
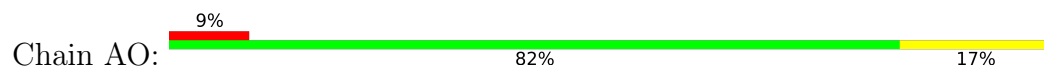
- Molecule 66: RPS22A isoform 1



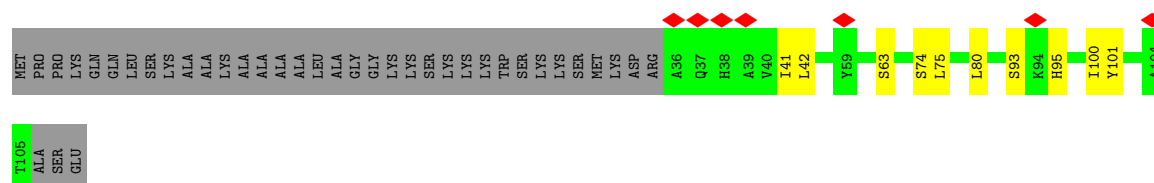
- Molecule 67: 40S ribosomal protein S23-A



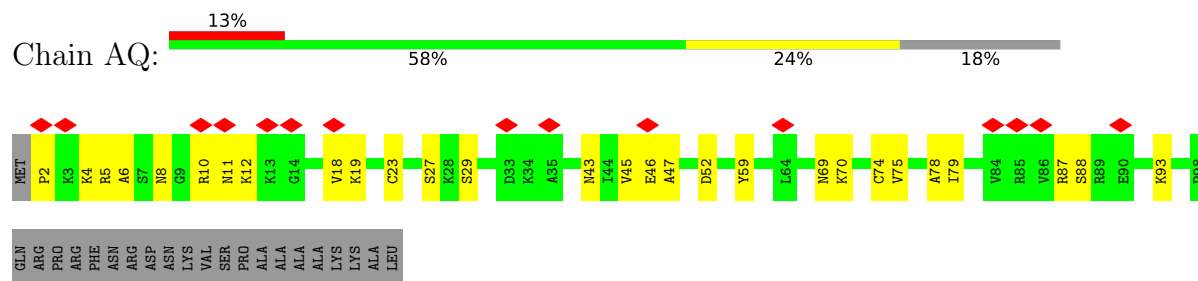
- Molecule 68: 40S ribosomal protein S24-A



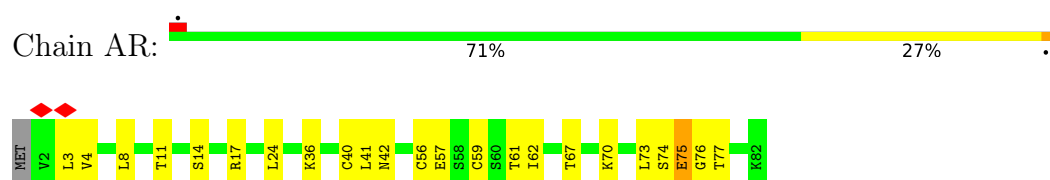
- Molecule 69: RPS25A isoform 1



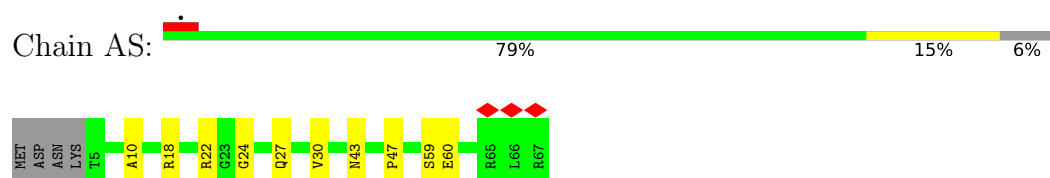
- Molecule 70: RPS26B isoform 1



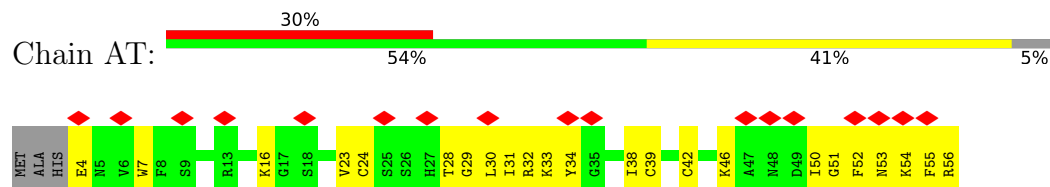
- Molecule 71: 40S ribosomal protein S27-A



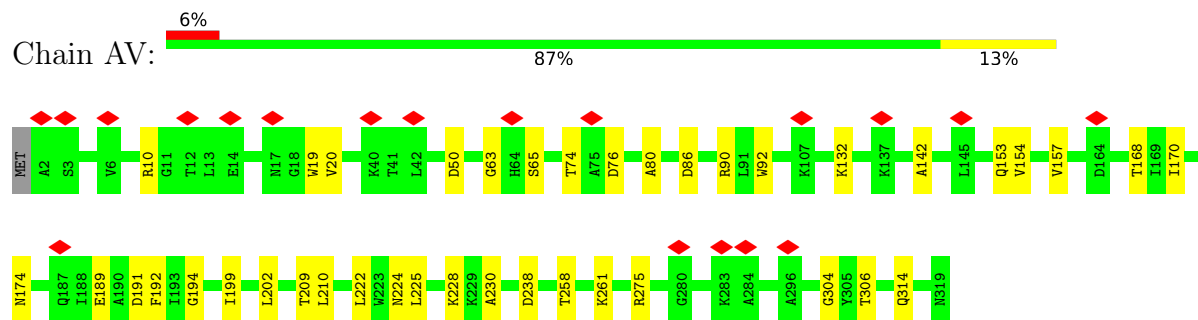
- Molecule 72: RPS28A isoform 1



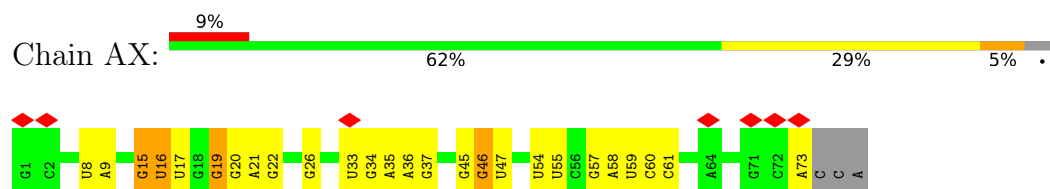
- Molecule 73: RPS29A isoform 1



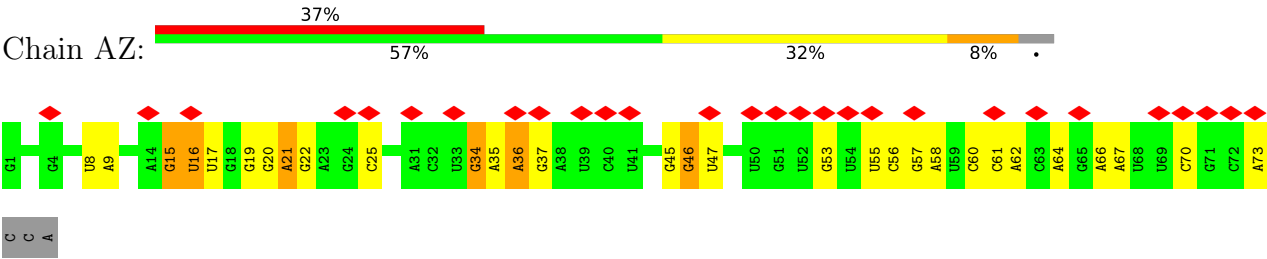
- Molecule 74: Guanine nucleotide-binding protein subunit beta-like protein



- Molecule 75: Transfer RNA



● Molecule 75: Transfer RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	87939	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 ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	44.862	Depositor
Minimum map value	-22.382	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.6	Depositor
Map size (Å)	652.8, 652.8, 652.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.36, 1.36, 1.36	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	0.49	0/1948	0.59	0/2617
2	B	0.48	0/3146	0.55	0/4228
3	C	0.46	0/2800	0.59	0/3790
4	D	0.33	0/2425	0.55	0/3271
5	E	0.36	0/1260	0.49	0/1694
6	F	0.49	0/1821	0.60	0/2451
7	G	0.36	0/1836	0.53	0/2481
8	H	0.27	0/1539	0.54	0/2073
9	I	0.26	0/1741	0.51	0/2335
10	J	0.27	0/1374	0.55	0/1842
11	L	0.43	0/1568	0.63	0/2106
12	M	0.37	0/1068	0.52	0/1438
13	N	0.48	0/1757	0.58	0/2354
14	O	0.50	0/1585	0.54	0/2128
15	P	0.45	0/1443	0.53	0/1944
16	Q	0.47	0/1465	0.55	0/1965
17	R	0.41	0/1538	0.53	0/2050
18	S	0.38	0/1481	0.53	0/1990
19	T	0.40	0/1300	0.52	0/1743
20	U	0.31	0/812	0.54	0/1099
21	V	0.44	0/1018	0.54	0/1369
22	W	0.43	0/533	0.50	0/707
23	X	0.41	0/979	0.48	0/1321
24	Y	0.41	0/1004	0.53	0/1341
25	Z	0.34	0/1118	0.52	0/1497
26	AA	0.27	0/789	0.53	0/1067
27	AB	0.25	0/1185	0.54	0/1598
28	1	0.35	0/74506	0.39	0/116154
29	3	0.30	0/2883	0.34	0/4491
30	4	0.35	0/3746	0.37	0/5832
31	a	0.47	0/1204	0.61	2/1612 (0.1%)
32	b	0.34	0/473	0.54	0/629

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.37	0/751	0.51	0/1008
34	d	0.44	0/897	0.50	0/1205
35	e	0.45	0/1041	0.53	0/1394
36	f	0.50	0/868	0.58	0/1168
37	g	0.42	0/890	0.58	1/1189 (0.1%)
38	h	0.38	0/978	0.54	0/1301
39	i	0.38	0/778	0.54	0/1034
40	j	0.46	0/696	0.61	0/923
41	k	0.33	0/618	0.48	0/826
42	l	0.42	0/443	0.62	0/588
43	n	0.41	0/228	0.83	0/293
44	o	0.34	0/860	0.59	0/1136
45	p	0.42	0/701	0.58	0/934
46	2	0.18	0/40725	0.36	0/63454
47	q	0.28	0/1617	0.58	0/2215
48	r	0.27	0/1735	0.59	0/2335
49	s	0.29	0/1665	0.57	0/2263
50	t	0.25	0/1759	0.60	0/2368
51	u	0.27	0/2109	0.56	0/2839
52	v	0.26	0/1629	0.61	0/2202
53	w	0.29	0/1814	0.61	0/2425
54	x	0.29	0/1506	0.60	0/2028
55	y	0.26	0/1514	0.63	0/2021
56	z	0.26	0/1519	0.58	0/2035
57	AD	0.29	0/1215	0.67	0/1638
58	AE	0.26	0/901	0.56	0/1217
59	AF	0.27	0/998	0.55	0/1341
60	AG	0.28	0/1125	0.55	0/1510
61	AH	0.27	0/935	0.61	0/1254
62	AI	0.26	0/1211	0.54	0/1628
63	AJ	0.26	0/1130	0.53	0/1517
64	AK	0.26	0/865	0.54	0/1169
65	AL	0.28	0/693	0.56	0/935
66	AM	0.26	0/1038	0.54	0/1395
67	AN	0.27	0/1139	0.61	0/1518
68	AO	0.26	0/1087	0.56	0/1449
69	AP	0.26	0/571	0.56	0/768
70	AQ	0.30	0/782	0.63	0/1047
71	AR	0.24	0/620	0.58	0/838
72	AS	0.26	0/499	0.50	0/670
73	AT	0.31	0/452	0.52	0/600
74	AV	0.22	0/2490	0.48	0/3389
75	AX	0.14	0/1749	0.31	0/2724

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	AZ	0.13	0/1749	0.31	0/2724
All	All	0.33	0/211935	0.45	3/311732 (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	2
4	D	0	1
6	F	0	1
7	G	0	2
10	J	0	3
11	L	0	1
14	O	0	2
16	Q	0	1
19	T	0	1
21	V	0	2
36	f	0	2
38	h	0	1
40	j	0	2
43	n	0	1
44	o	0	2
47	q	0	1
48	r	0	1
51	u	0	3
53	w	0	1
54	x	0	1
55	y	0	1
56	z	0	1
57	AD	0	2
58	AE	0	2
70	AQ	0	4
71	AR	0	1
All	All	0	43

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	g	81	CYS	CA-CB-SG	5.84	127.84	114.40
31	a	47	LYS	CA-C-N	5.20	131.47	121.54
31	a	47	LYS	C-N-CA	5.20	131.47	121.54

There are no chirality outliers.

5 of 43 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	143	GLU	Peptide
3	C	182	LEU	Peptide
3	C	318	LEU	Peptide
4	D	258	LYS	Peptide
6	F	157	ASN	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	0	1981	17	0
2	B	3075	0	3142	32	0
3	C	2748	0	2859	25	0
4	D	2375	0	2325	30	0
5	E	1239	0	1326	9	0
6	F	1784	0	1862	23	0
7	G	1804	0	1877	17	0
8	H	1518	0	1587	19	0
9	I	1705	0	1736	27	0
10	J	1353	0	1383	23	0
11	L	1543	0	1608	21	0
12	M	1053	0	1149	15	0
13	N	1720	0	1779	26	0
14	O	1555	0	1659	17	0
15	P	1420	0	1437	14	0
16	Q	1441	0	1543	14	0
17	R	1521	0	1617	16	0
18	S	1445	0	1487	14	0
19	T	1276	0	1323	8	0
20	U	796	0	812	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	V	1003	0	1048	10	0
22	W	521	0	551	4	0
23	X	964	0	1025	3	0
24	Y	993	0	1081	10	0
25	Z	1092	0	1155	10	0
26	AA	772	0	727	10	0
27	AB	1159	0	1225	20	0
28	1	66567	0	33454	383	0
29	3	2579	0	1304	15	0
30	4	3353	0	1695	21	0
31	a	1173	0	1215	17	0
32	b	462	0	491	6	0
33	c	743	0	797	8	0
34	d	883	0	918	5	0
35	e	1020	0	1090	11	0
36	f	850	0	880	9	0
37	g	880	0	941	7	0
38	h	969	0	1078	6	0
39	i	771	0	849	9	0
40	j	681	0	683	8	0
41	k	612	0	682	7	0
42	l	436	0	475	7	0
43	n	227	0	268	239	0
44	o	847	0	914	14	0
45	p	694	0	734	8	0
46	2	36409	0	18314	746	0
47	q	1577	0	1567	23	0
48	r	1709	0	1784	28	0
49	s	1635	0	1723	42	0
50	t	1734	0	1817	40	0
51	u	2068	0	2154	69	0
52	v	1609	0	1675	28	0
53	w	1790	0	1881	17	0
54	x	1481	0	1572	30	0
55	y	1489	0	1525	28	0
56	z	1494	0	1573	83	0
57	AD	1192	0	1255	12	0
58	AE	891	0	883	15	0
59	AF	977	0	1002	11	0
60	AG	1105	0	1166	42	0
61	AH	926	0	930	15	0
62	AI	1192	0	1221	98	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	AJ	1112	0	1124	49	0
64	AK	855	0	917	117	0
65	AL	684	0	672	22	0
66	AM	1021	0	1060	31	0
67	AN	1121	0	1196	14	0
68	AO	1073	0	1132	18	0
69	AP	563	0	603	26	0
70	AQ	769	0	817	39	0
71	AR	610	0	633	23	0
72	AS	497	0	535	23	0
73	AT	442	0	430	108	0
74	AV	2437	0	2386	31	0
75	AX	1564	0	787	5	0
75	AZ	1564	0	787	19	0
76	AQ	1	0	0	0	0
76	AR	1	0	0	0	0
76	AT	1	0	0	0	0
76	j	1	0	0	0	0
76	o	1	0	0	0	0
76	p	1	0	0	0	0
All	All	197132	0	144893	2043	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 2043 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)
43:n:9:ARG:HG3	46:2:1789:G:C6	1.13	1.64
43:n:10:THR:CB	46:2:1026:A:H2'	1.24	1.62
64:AK:80:GLU:HG3	73:AT:52:PHE:CE2	1.19	1.60
46:2:1543:A:C3'	62:AI:132:ARG:HH12	1.22	1.49
43:n:7:LYS:N	46:2:1027:A:C5'	1.70	1.48

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	250/254 (98%)	238 (95%)	12 (5%)	0	100	100
2	B	384/387 (99%)	357 (93%)	27 (7%)	0	100	100
3	C	359/362 (99%)	320 (89%)	38 (11%)	1 (0%)	36	68
4	D	294/297 (99%)	267 (91%)	26 (9%)	1 (0%)	36	68
5	E	152/176 (86%)	142 (93%)	10 (7%)	0	100	100
6	F	220/244 (90%)	201 (91%)	18 (8%)	1 (0%)	24	59
7	G	231/256 (90%)	211 (91%)	20 (9%)	0	100	100
8	H	189/191 (99%)	164 (87%)	25 (13%)	0	100	100
9	I	207/221 (94%)	192 (93%)	15 (7%)	0	100	100
10	J	167/174 (96%)	144 (86%)	23 (14%)	0	100	100
11	L	191/199 (96%)	162 (85%)	25 (13%)	4 (2%)	5	31
12	M	134/138 (97%)	122 (91%)	12 (9%)	0	100	100
13	N	201/204 (98%)	183 (91%)	18 (9%)	0	100	100
14	O	195/199 (98%)	177 (91%)	16 (8%)	2 (1%)	12	45
15	P	181/184 (98%)	169 (93%)	12 (7%)	0	100	100
16	Q	183/186 (98%)	173 (94%)	10 (6%)	0	100	100
17	R	186/189 (98%)	174 (94%)	12 (6%)	0	100	100
18	S	170/172 (99%)	158 (93%)	12 (7%)	0	100	100
19	T	157/160 (98%)	142 (90%)	15 (10%)	0	100	100
20	U	98/121 (81%)	91 (93%)	7 (7%)	0	100	100
21	V	134/137 (98%)	122 (91%)	11 (8%)	1 (1%)	18	52
22	W	61/155 (39%)	58 (95%)	3 (5%)	0	100	100
23	X	119/142 (84%)	115 (97%)	4 (3%)	0	100	100
24	Y	124/127 (98%)	115 (93%)	9 (7%)	0	100	100
25	Z	133/136 (98%)	118 (89%)	15 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	AA	94/105 (90%)	79 (84%)	15 (16%)	0	100	100
27	AB	142/156 (91%)	123 (87%)	19 (13%)	0	100	100
31	a	146/149 (98%)	125 (86%)	20 (14%)	1 (1%)	18	52
32	b	56/59 (95%)	47 (84%)	9 (16%)	0	100	100
33	c	95/105 (90%)	86 (90%)	9 (10%)	0	100	100
34	d	107/113 (95%)	101 (94%)	6 (6%)	0	100	100
35	e	125/130 (96%)	116 (93%)	8 (6%)	1 (1%)	16	50
36	f	104/107 (97%)	97 (93%)	5 (5%)	2 (2%)	6	33
37	g	110/121 (91%)	101 (92%)	9 (8%)	0	100	100
38	h	117/120 (98%)	105 (90%)	12 (10%)	0	100	100
39	i	97/100 (97%)	81 (84%)	16 (16%)	0	100	100
40	j	85/88 (97%)	73 (86%)	11 (13%)	1 (1%)	10	42
41	k	75/78 (96%)	69 (92%)	6 (8%)	0	100	100
42	l	48/51 (94%)	40 (83%)	6 (12%)	2 (4%)	2	16
43	n	23/25 (92%)	16 (70%)	7 (30%)	0	100	100
44	o	103/106 (97%)	83 (81%)	20 (19%)	0	100	100
45	p	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
47	q	204/252 (81%)	166 (81%)	36 (18%)	2 (1%)	12	45
48	r	212/255 (83%)	184 (87%)	28 (13%)	0	100	100
49	s	215/254 (85%)	195 (91%)	20 (9%)	0	100	100
50	t	221/240 (92%)	198 (90%)	23 (10%)	0	100	100
51	u	258/261 (99%)	204 (79%)	53 (20%)	1 (0%)	30	62
52	v	204/225 (91%)	178 (87%)	26 (13%)	0	100	100
53	w	221/236 (94%)	173 (78%)	47 (21%)	1 (0%)	24	59
54	x	182/190 (96%)	160 (88%)	22 (12%)	0	100	100
55	y	184/200 (92%)	159 (86%)	25 (14%)	0	100	100
56	z	183/197 (93%)	166 (91%)	17 (9%)	0	100	100
57	AD	148/151 (98%)	130 (88%)	14 (10%)	4 (3%)	4	25
58	AE	125/138 (91%)	114 (91%)	11 (9%)	0	100	100
59	AF	122/142 (86%)	107 (88%)	15 (12%)	0	100	100
60	AG	139/143 (97%)	122 (88%)	17 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	AH	116/136 (85%)	102 (88%)	14 (12%)	0	100	100
62	AI	143/146 (98%)	125 (87%)	18 (13%)	0	100	100
63	AJ	141/144 (98%)	131 (93%)	10 (7%)	0	100	100
64	AK	105/121 (87%)	95 (90%)	10 (10%)	0	100	100
65	AL	85/87 (98%)	71 (84%)	14 (16%)	0	100	100
66	AM	127/130 (98%)	115 (91%)	11 (9%)	1 (1%)	16	50
67	AN	142/145 (98%)	119 (84%)	23 (16%)	0	100	100
68	AO	132/135 (98%)	109 (83%)	23 (17%)	0	100	100
69	AP	68/108 (63%)	60 (88%)	8 (12%)	0	100	100
70	AQ	95/119 (80%)	62 (65%)	32 (34%)	1 (1%)	11	43
71	AR	79/82 (96%)	64 (81%)	14 (18%)	1 (1%)	9	40
72	AS	61/67 (91%)	55 (90%)	6 (10%)	0	100	100
73	AT	51/56 (91%)	43 (84%)	8 (16%)	0	100	100
74	AV	316/319 (99%)	287 (91%)	29 (9%)	0	100	100
All	All	10615/11395 (93%)	9433 (89%)	1154 (11%)	28 (0%)	37	68

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	339	LEU
14	O	111	PRO
36	f	58	GLU
47	q	113	ARG
11	L	48	PRO

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	321/323 (99%)	320 (100%)	1 (0%)	86	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	170 (99%)	1 (1%)	78	84
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%)	113 (98%)	2 (2%)	53	75
26	AA	77/98 (79%)	76 (99%)	1 (1%)	61	78
27	AB	129/137 (94%)	129 (100%)	0	100	100
31	a	118/119 (99%)	118 (100%)	0	100	100
32	b	46/47 (98%)	46 (100%)	0	100	100
33	c	81/88 (92%)	81 (100%)	0	100	100
34	d	94/97 (97%)	94 (100%)	0	100	100
35	e	109/111 (98%)	109 (100%)	0	100	100
36	f	90/91 (99%)	90 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	g	95/103 (92%)	95 (100%)	0	100	100
38	h	104/105 (99%)	104 (100%)	0	100	100
39	i	81/82 (99%)	81 (100%)	0	100	100
40	j	70/71 (99%)	70 (100%)	0	100	100
41	k	68/69 (99%)	68 (100%)	0	100	100
42	l	45/46 (98%)	45 (100%)	0	100	100
43	n	22/23 (96%)	22 (100%)	0	100	100
44	o	90/91 (99%)	90 (100%)	0	100	100
45	p	71/72 (99%)	70 (99%)	1 (1%)	59	77
47	q	164/210 (78%)	164 (100%)	0	100	100
48	r	191/224 (85%)	191 (100%)	0	100	100
49	s	176/205 (86%)	175 (99%)	1 (1%)	78	84
50	t	182/195 (93%)	182 (100%)	0	100	100
51	u	221/222 (100%)	221 (100%)	0	100	100
52	v	173/191 (91%)	173 (100%)	0	100	100
53	w	189/201 (94%)	189 (100%)	0	100	100
54	x	165/170 (97%)	165 (100%)	0	100	100
55	y	150/161 (93%)	150 (100%)	0	100	100
56	z	158/166 (95%)	158 (100%)	0	100	100
57	AD	127/128 (99%)	127 (100%)	0	100	100
58	AE	81/105 (77%)	81 (100%)	0	100	100
59	AF	101/118 (86%)	101 (100%)	0	100	100
60	AG	117/119 (98%)	117 (100%)	0	100	100
61	AH	94/124 (76%)	94 (100%)	0	100	100
62	AI	128/129 (99%)	128 (100%)	0	100	100
63	AJ	115/116 (99%)	115 (100%)	0	100	100
64	AK	100/114 (88%)	100 (100%)	0	100	100
65	AL	74/74 (100%)	74 (100%)	0	100	100
66	AM	110/111 (99%)	110 (100%)	0	100	100
67	AN	119/120 (99%)	119 (100%)	0	100	100
68	AO	112/113 (99%)	111 (99%)	1 (1%)	70	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	AP	61/89 (68%)	61 (100%)	0	100	100
70	AQ	83/100 (83%)	83 (100%)	0	100	100
71	AR	70/71 (99%)	70 (100%)	0	100	100
72	AS	56/60 (93%)	56 (100%)	0	100	100
73	AT	47/49 (96%)	47 (100%)	0	100	100
74	AV	259/262 (99%)	259 (100%)	0	100	100
All	All	8966/9560 (94%)	8958 (100%)	8 (0%)	87	91

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
68	AO	34	ASN
49	s	201	ASN
26	AA	28	ASN
25	Z	103	GLN
45	p	42	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
62	AI	12	GLN
74	AV	52	GLN
63	AJ	48	GLN
67	AN	27	ASN
40	j	69	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	1	3109/3395 (91%)	680 (21%)	7 (0%)
29	3	120/121 (99%)	20 (16%)	0
30	4	157/158 (99%)	37 (23%)	0
46	2	1703/1800 (94%)	807 (47%)	13 (0%)
75	AX	72/76 (94%)	22 (30%)	0
75	AZ	72/76 (94%)	23 (31%)	0
All	All	5233/5626 (93%)	1589 (30%)	20 (0%)

5 of 1589 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
28	1	6	A
28	1	22	G
28	1	26	A
28	1	35	A
28	1	40	A

5 of 20 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
46	2	1366	U
46	2	1665	U
46	2	1755	A
46	2	1748	G
28	1	2874	G

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 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.

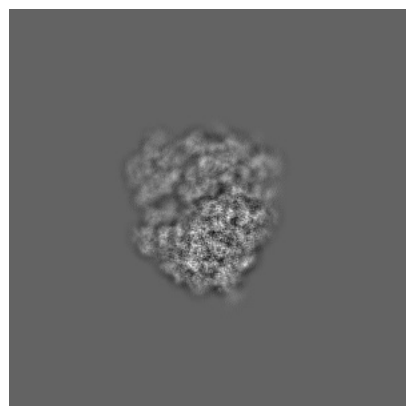
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22198. These allow visual inspection of the internal detail of the map and identification of artifacts.

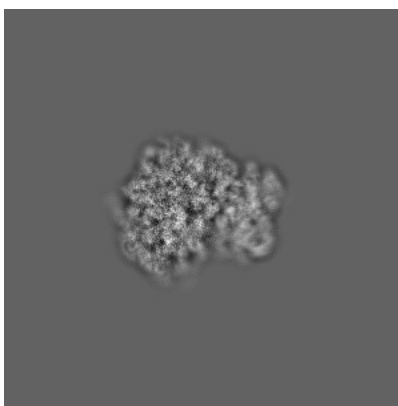
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

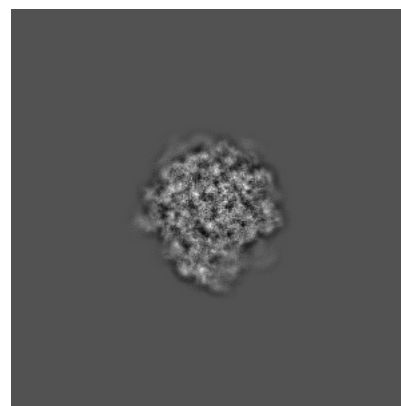
6.1.1 Primary map



X

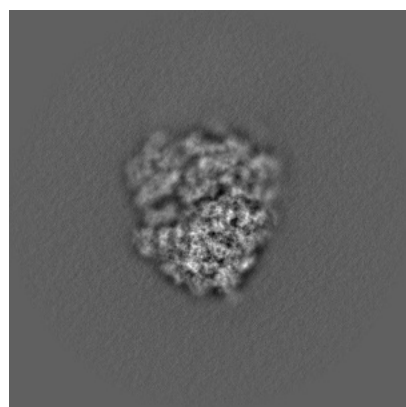


Y

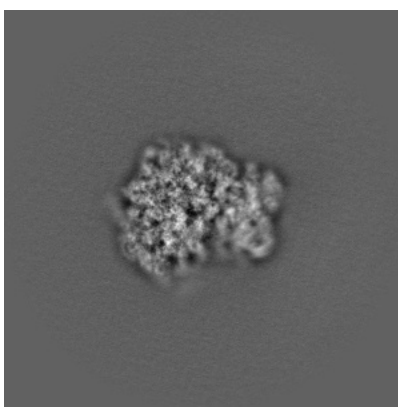


Z

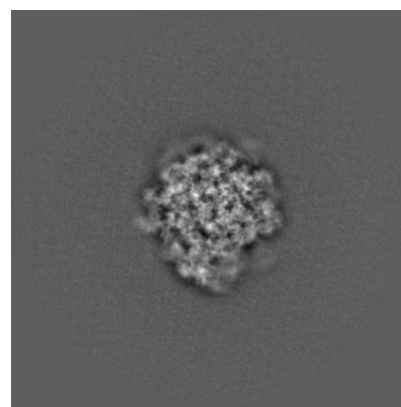
6.1.2 Raw map



X



Y

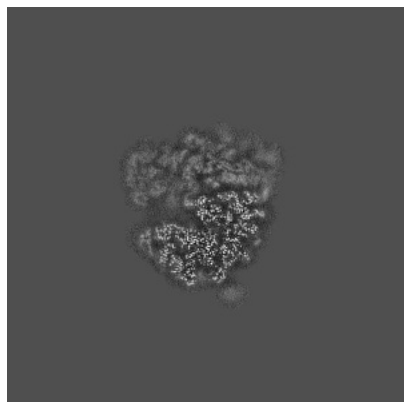


Z

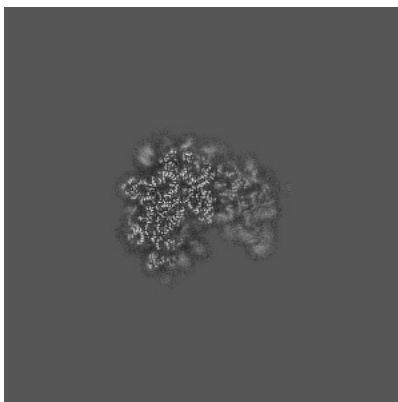
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

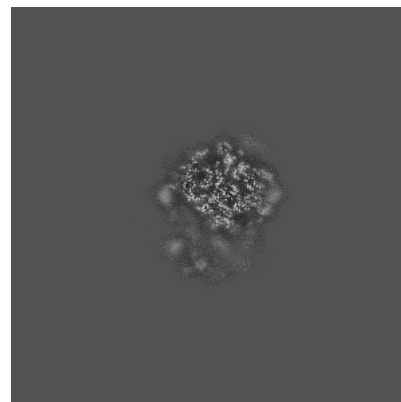
6.2.1 Primary map



X Index: 240

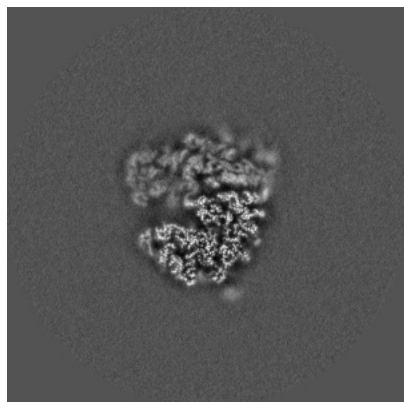


Y Index: 240

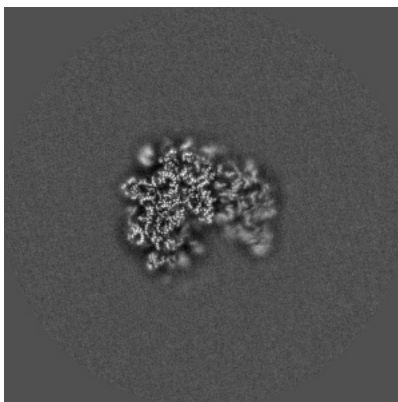


Z Index: 240

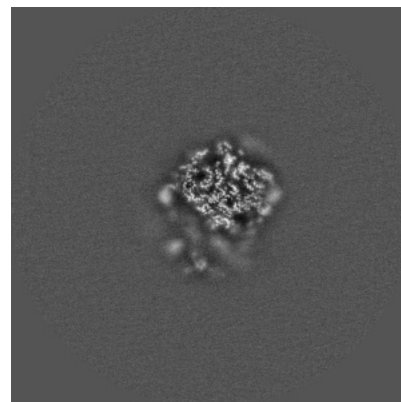
6.2.2 Raw map



X Index: 240



Y Index: 240

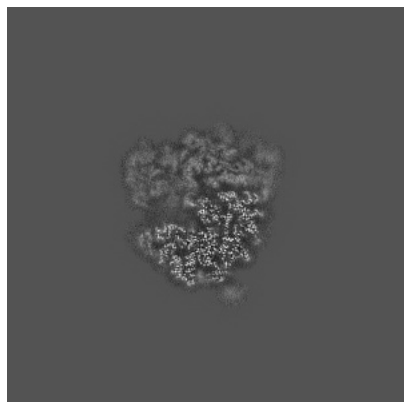


Z Index: 240

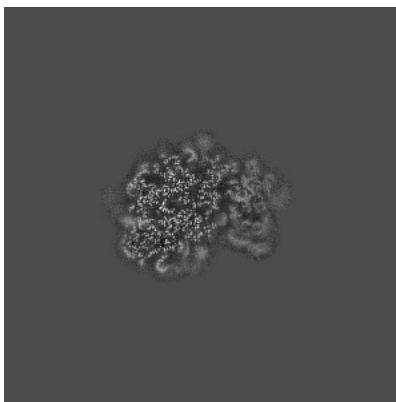
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

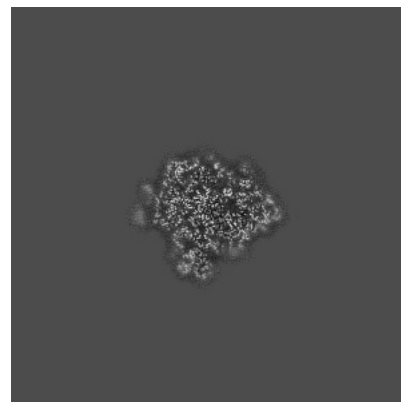
6.3.1 Primary map



X Index: 239

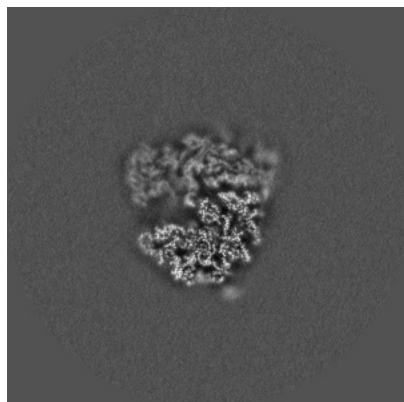


Y Index: 257

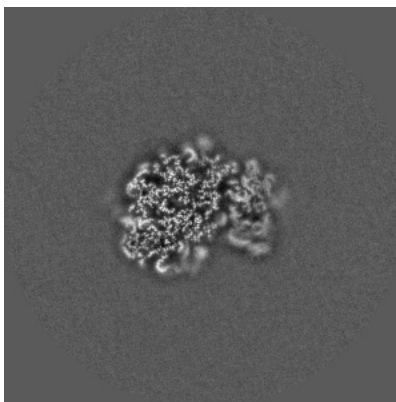


Z Index: 195

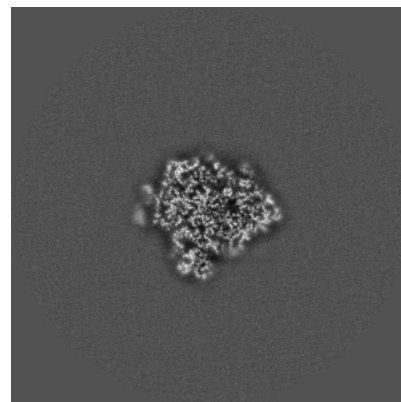
6.3.2 Raw map



X Index: 238



Y Index: 257

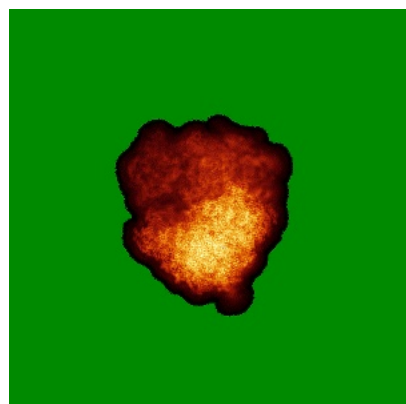


Z Index: 195

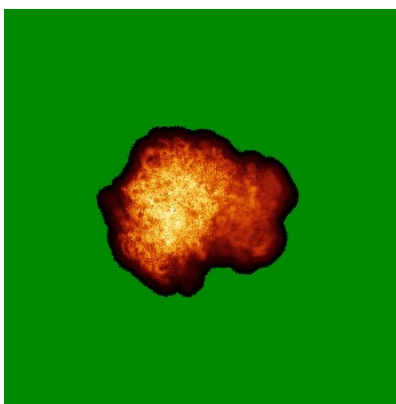
The images above show the largest variance slices of the map in three orthogonal directions.

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

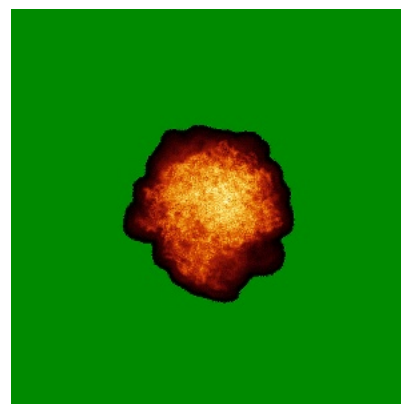
6.4.1 Primary map



X

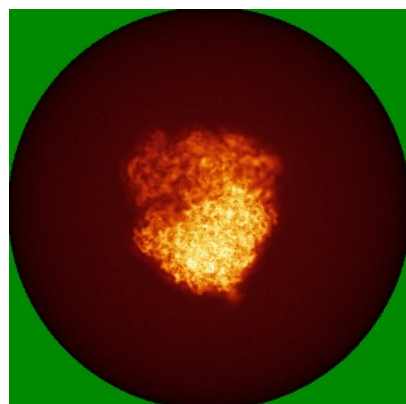


Y

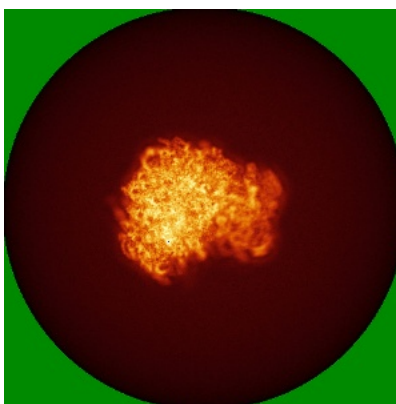


Z

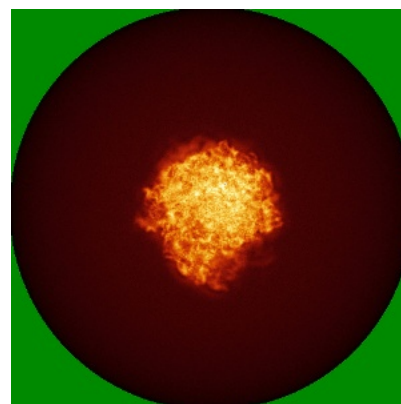
6.4.2 Raw map



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](#)

This section was not generated.

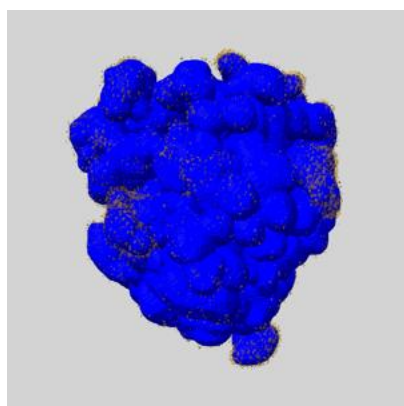
6.6 Mask visualisation [i](#)

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

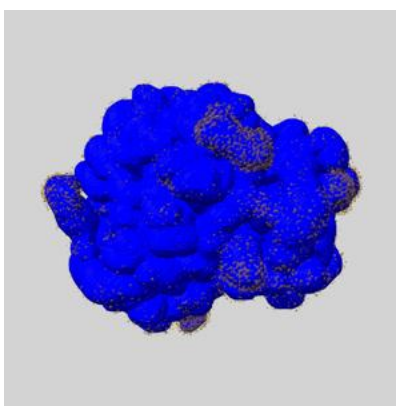
A mask typically either:

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

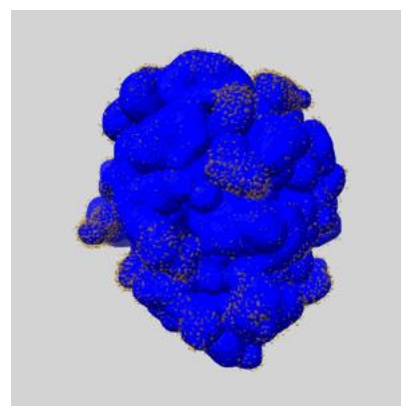
6.6.1 emd_22198_msk_1.map [i](#)



X



Y

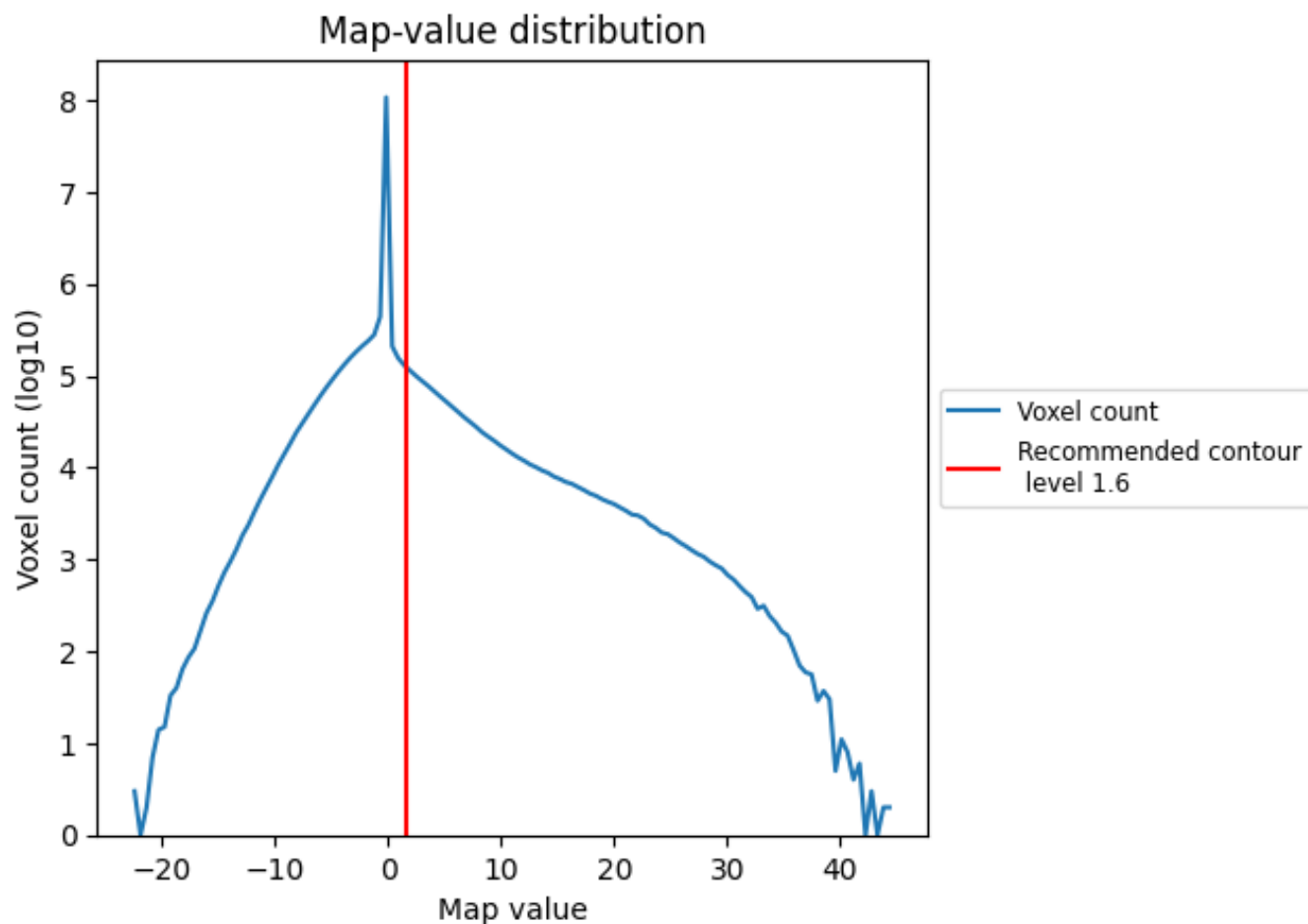


Z

7 Map analysis [i](#)

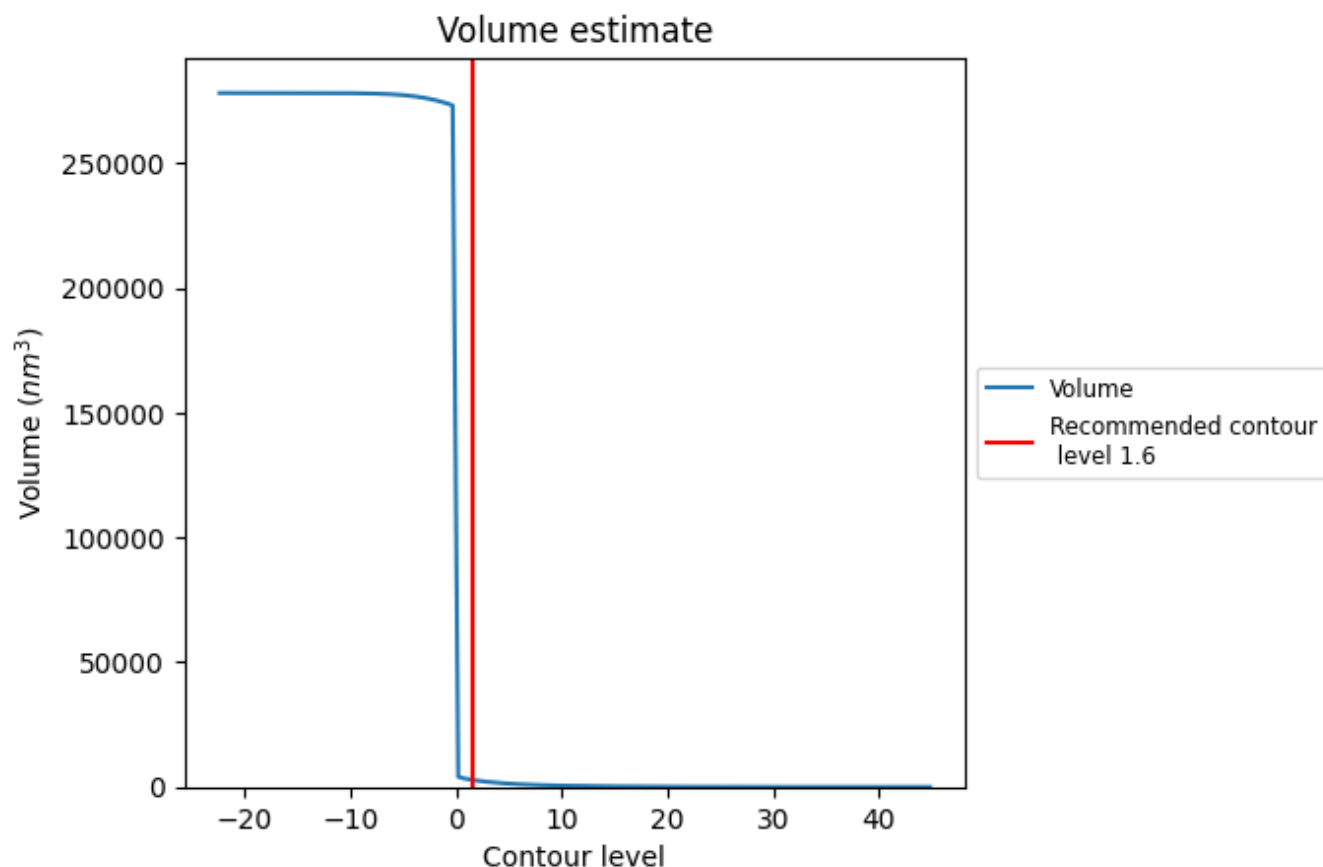
This section contains the results of statistical analysis of the map.

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.

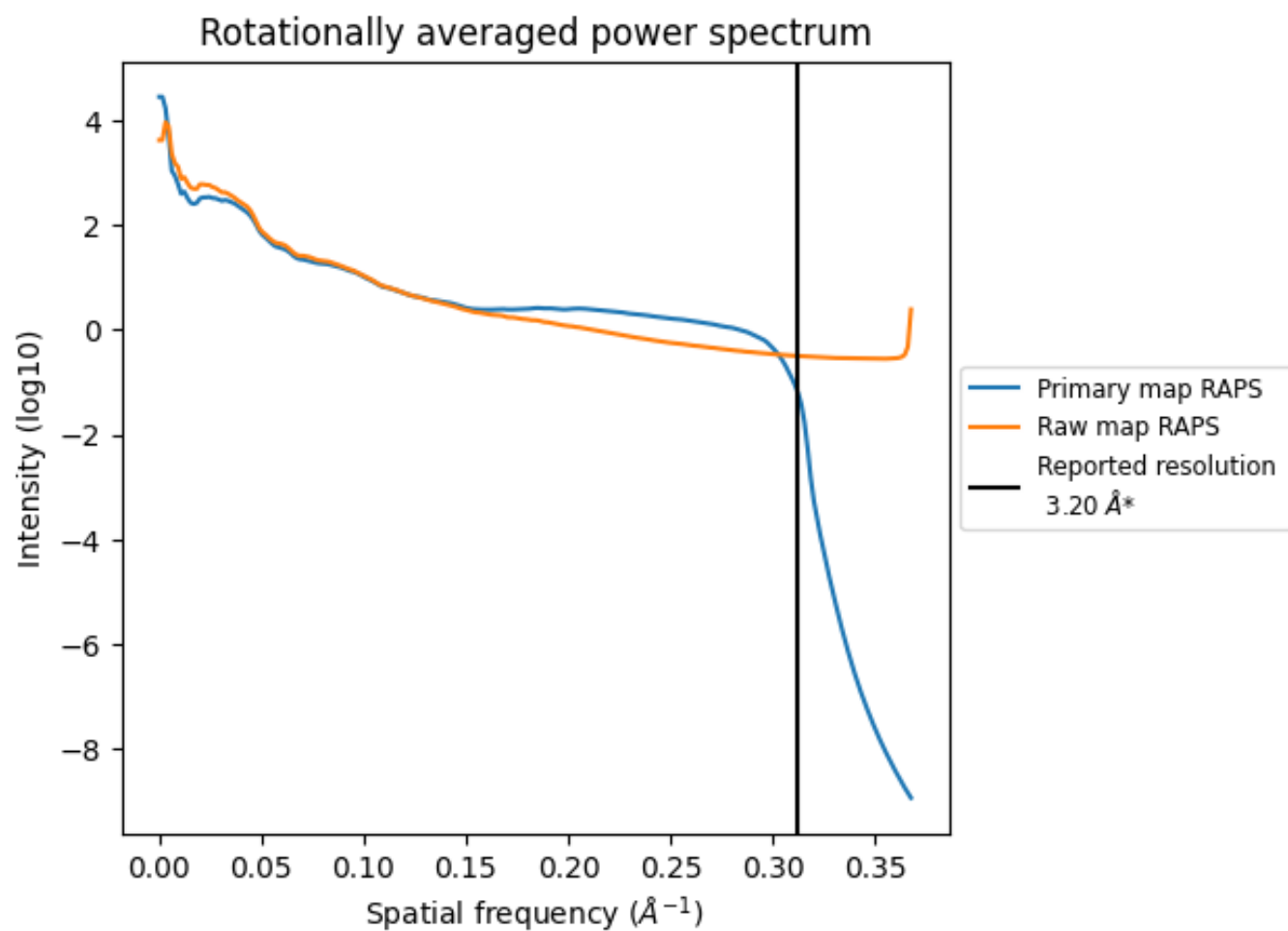
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2788 nm^3 ; this corresponds to an approximate mass of 2518 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 ⓘ

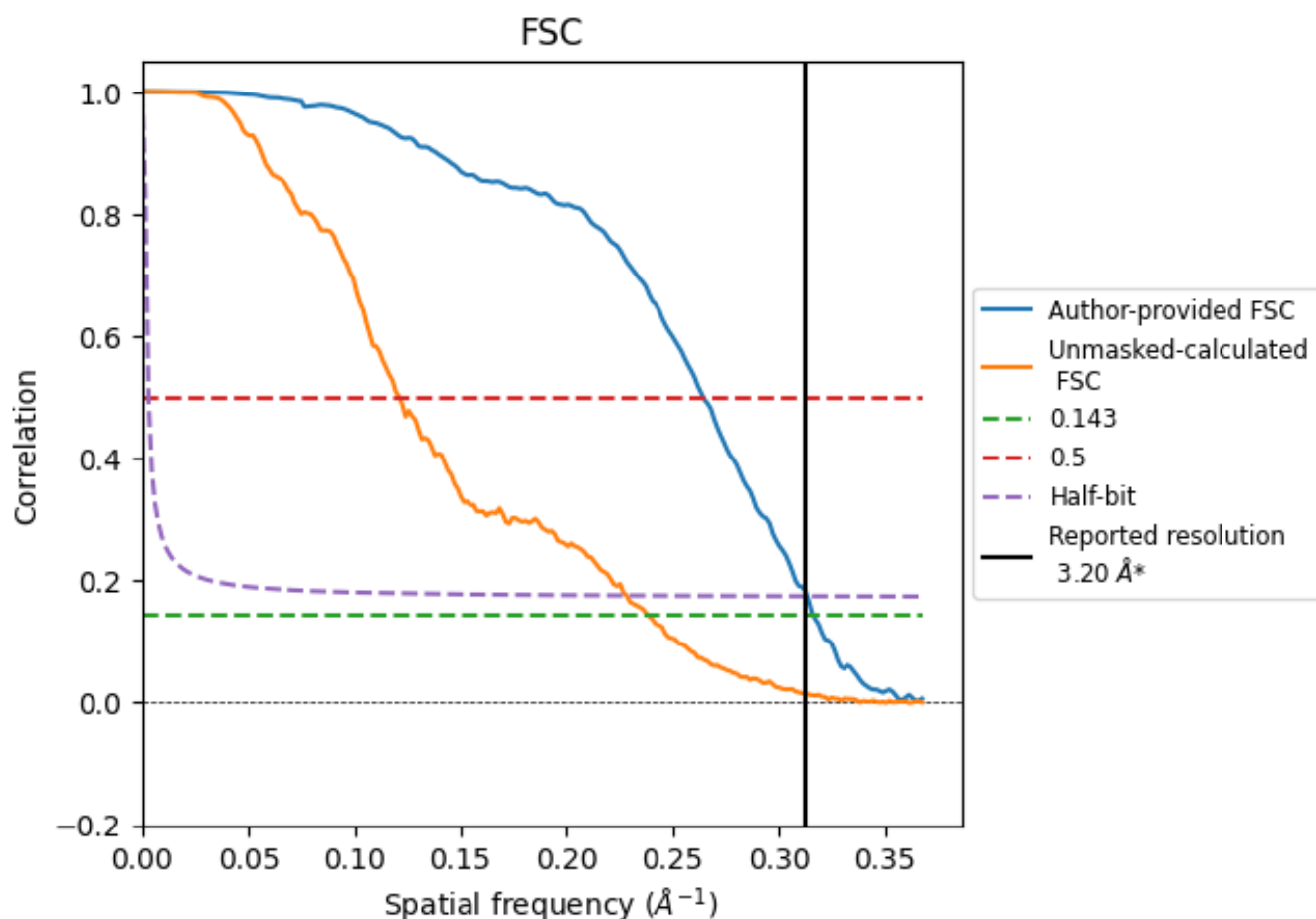


*Reported resolution corresponds to spatial frequency of 0.312 $\text{\AA}^{-1}$

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 0.312 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

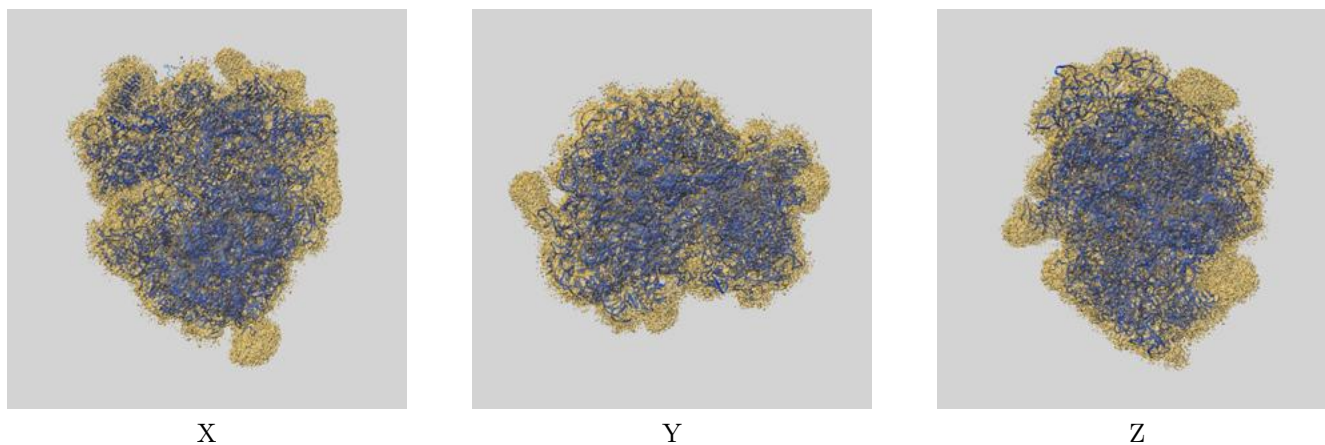
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.16	3.78	3.19
Unmasked-calculated*	4.19	8.25	4.38

*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 4.19 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

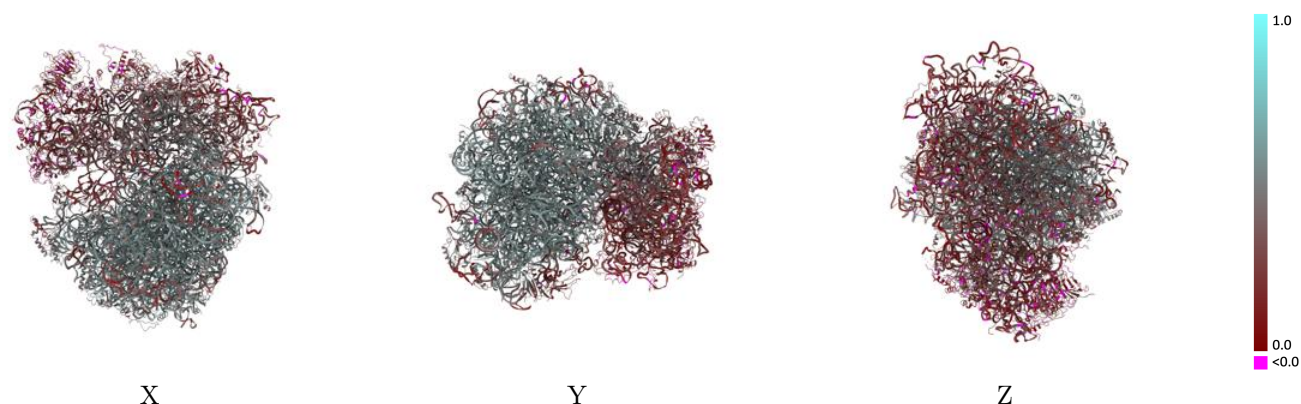
This section contains information regarding the fit between EMDB map EMD-22198 and PDB model 6XIR. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 1.6 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](#)

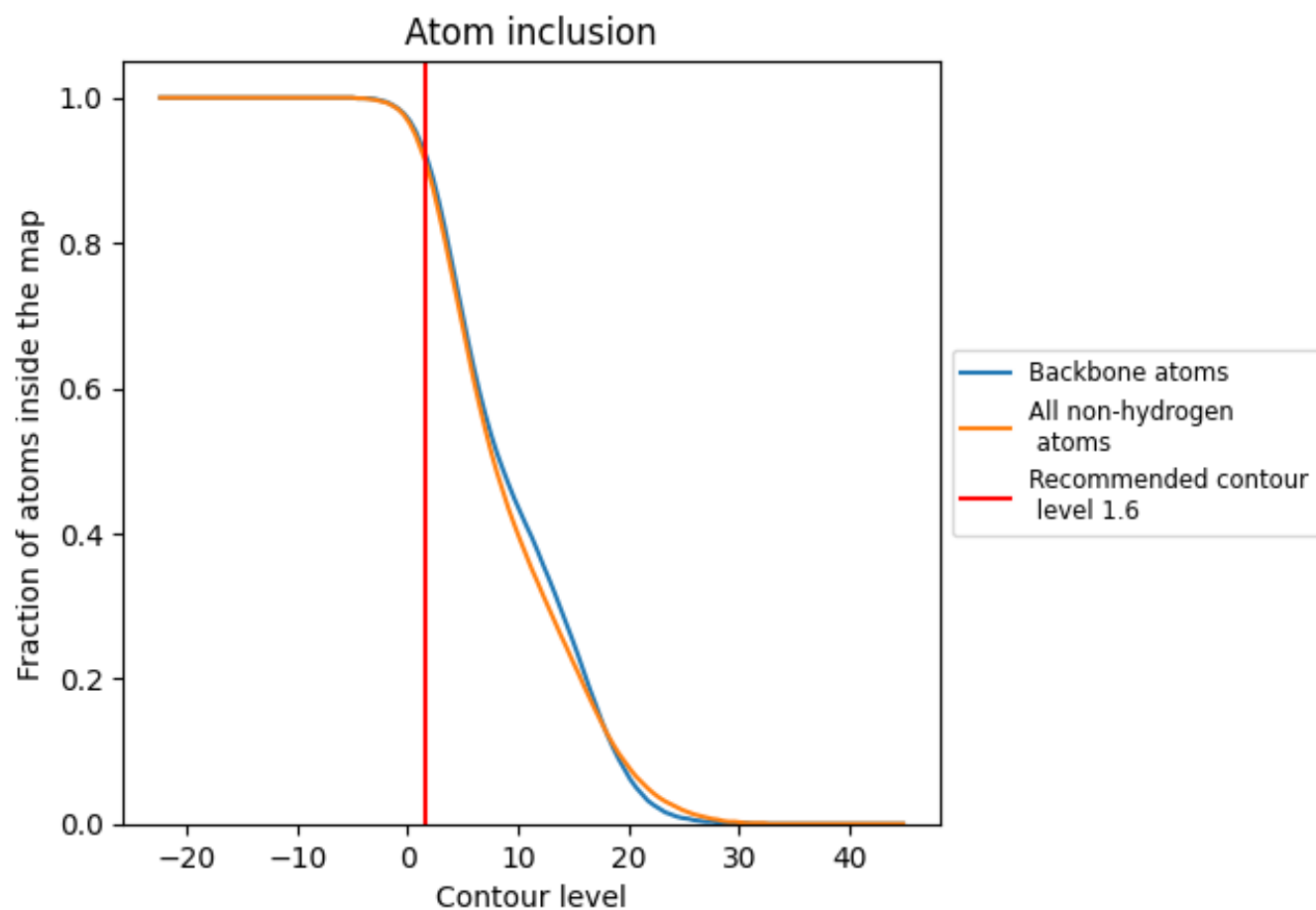


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 91% 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 (1.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9130	 0.4050
1	 0.9840	 0.4910
2	 0.8980	 0.2740
3	 0.9990	 0.5000
4	 0.9860	 0.5060
A	 0.9030	 0.5470
AA	 0.6560	 0.1760
AB	 0.8470	 0.3740
AD	 0.8620	 0.3890
AE	 0.9050	 0.4360
AF	 0.8630	 0.2210
AG	 0.5970	 0.1940
AH	 0.8430	 0.2600
AI	 0.7090	 0.1080
AJ	 0.8060	 0.2200
AK	 0.6540	 0.1760
AL	 0.8390	 0.3140
AM	 0.7980	 0.3400
AN	 0.5990	 0.2360
AO	 0.8530	 0.2020
AP	 0.8260	 0.2530
AQ	 0.6920	 0.3610
AR	 0.9190	 0.3470
AS	 0.8830	 0.3040
AT	 0.5380	 0.1300
AV	 0.8500	 0.2030
AX	 0.7230	 0.2110
AZ	 0.4880	 0.0760
B	 0.9580	 0.5460
C	 0.9580	 0.5360
D	 0.9340	 0.4330
E	 0.9600	 0.4980
F	 0.9500	 0.5220
G	 0.9290	 0.4670
H	 0.8330	 0.3160



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Chain	Atom inclusion	Q-score
I	 0.8260	 0.4120
J	 0.9490	 0.3660
L	 0.9590	 0.5110
M	 0.9510	 0.4900
N	 0.8970	 0.5520
O	 0.9480	 0.5300
P	 0.8950	 0.5140
Q	 0.9350	 0.5400
R	 0.9490	 0.4830
S	 0.9240	 0.5190
T	 0.9170	 0.5200
U	 0.9800	 0.4540
V	 0.9220	 0.5210
W	 0.9430	 0.5250
X	 0.9400	 0.5310
Y	 0.9660	 0.5190
Z	 0.9530	 0.4440
a	 0.9450	 0.5470
b	 0.8430	 0.4850
c	 0.9630	 0.4700
d	 0.9510	 0.5220
e	 0.9080	 0.5410
f	 0.9510	 0.5560
g	 0.9120	 0.5240
h	 0.9400	 0.4850
i	 0.9210	 0.4660
j	 0.9050	 0.5460
k	 0.9500	 0.4810
l	 0.8460	 0.5280
n	 0.4470	 0.0030
o	 0.8430	 0.5010
p	 0.9420	 0.5170
q	 0.8170	 0.2390
r	 0.9050	 0.3870
s	 0.7770	 0.2580
t	 0.7410	 0.2330
u	 0.7800	 0.2230
v	 0.8290	 0.3060
w	 0.6810	 0.2230
x	 0.9070	 0.2580
y	 0.8230	 0.2900
z	 0.7790	 0.2110