



wwPDB EM Validation Summary Report ⓘ

Oct 13, 2024 – 08:42 AM EDT

PDB ID : 6XIR
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:

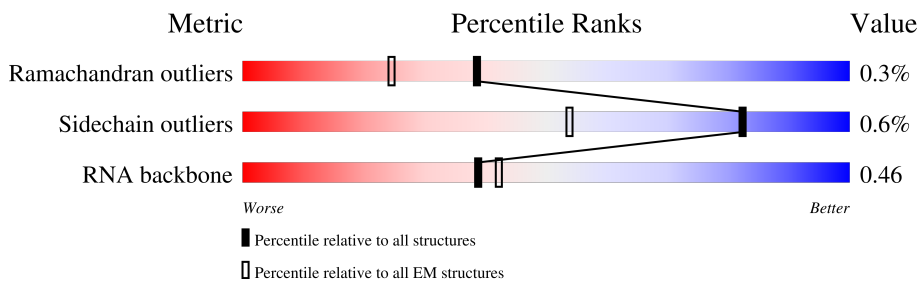
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	98%
2	B	387	98%
3	C	362	98%
4	D	297	99%
5	E	176	88% 11%
6	F	244	90% 9%
7	G	256	90% 9%
8	H	191	8% 98%

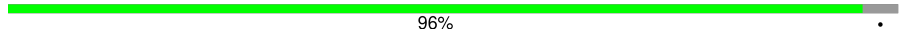
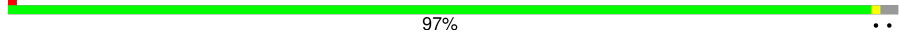
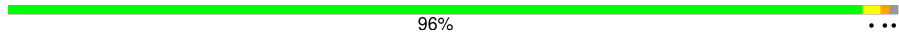

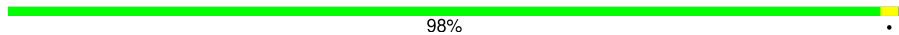
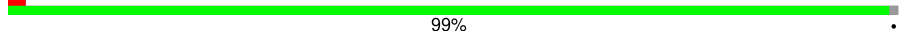
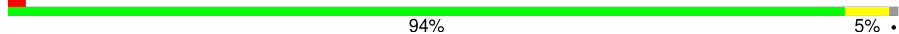
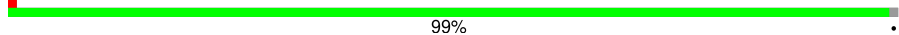


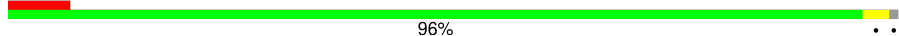






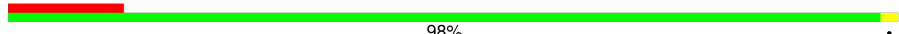

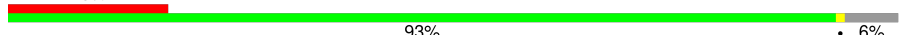
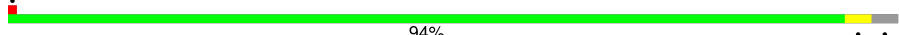




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Mol	Chain	Length	Quality of chain
9	I	221	6% 94% 5%
10	J	174	95%
11	L	199	94%
12	M	138	98%
13	N	204	100%
14	O	199	97%
15	P	184	6% 98%
16	Q	186	98%
17	R	189	98%
18	S	172	100%
19	T	160	99%
20	U	121	83% 17%
21	V	137	97%
22	W	155	40% 59%
23	X	142	85% 15%
24	Y	127	98%
25	Z	136	96%
26	AA	105	21% 90% 9%
27	AB	156	92% 8%
28	1	3395	71% 20% 8%
29	3	121	83% 16%
30	4	158	76% 24%
31	a	149	97%
32	b	59	7% 95%
33	c	105	90% 8%


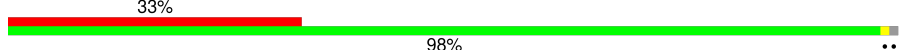
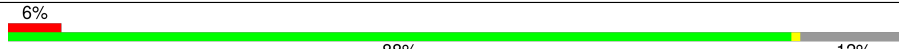
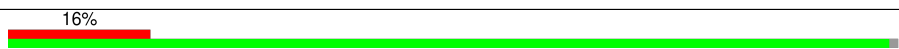
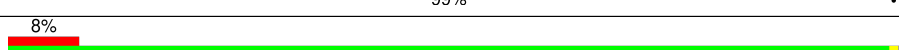
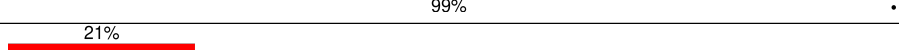
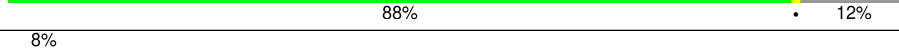
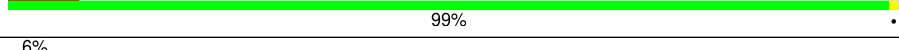
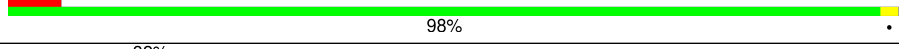
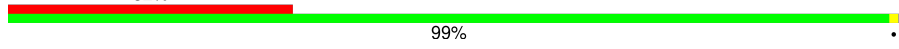
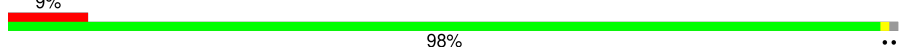



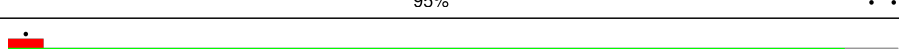
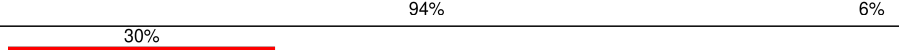
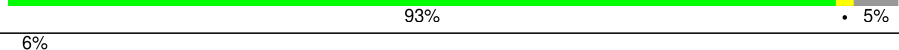
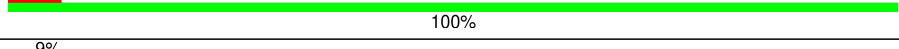
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Mol	Chain	Length	Quality of chain
34	d	113	 96%
35	e	130	 97%
36	f	107	 96%
37	g	121	 91% 7%
38	h	120	 98%
39	i	100	 99%
40	j	88	 94% 5%
41	k	78	 99%
42	l	51	 94%
43	n	25	 48% 84% 16%
44	o	106	 7% 96%
45	p	92	 99%
46	2	1800	 49% 44% 5%
47	q	252	 10% 81% 18%
48	r	255	 83% 16%
49	s	254	 8% 85% 15%
50	t	240	 11% 92% 7%
51	u	261	 13% 98%
52	v	225	 18% 91% 8%
53	w	236	 18% 93% 6%
54	x	190	 94%
55	y	200	 8% 92% 6%
56	z	197	 10% 93% 6%
57	AD	151	 95%
58	AE	138	 91% 8%

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Mol	Chain	Length	Quality of chain
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 [i](#)

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
			Total	C	N	O	S		
1	A	252	1914	1191	388	334	1	0	0

- Molecule 2 is a protein called RPL3 isoform 1.

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

- Molecule 3 is a protein called RPL4A isoform 1.

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

- Molecule 4 is a protein called RPL5 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	296	2375	1501	414	458	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	156	1239	800	222	216	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	222	1784	1151	324	308	1	0	0

- Molecule 7 is a protein called RPL8A isoform 1.

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

- Molecule 8 is a protein called RPL9A isoform 1.

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

- Molecule 9 is a protein called RPL10 isoform 1.

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

- Molecule 10 is a protein called RPL11B isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	169	1353	847	253	249	4	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	L	193	1543	962	315	266	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	M	136	1053	675	199	177	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	N	203	1720	1077	361	281	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	O	197	1555	1003	289	262	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	P	183	1420	882	281	257		0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	Q	185	1441	908	290	241	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	R	188	1521	935	326	260		0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	S	172	1445	930	267	244	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	T	159	1276	805	246	221	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	U	100	796	516	131	149		0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	136	Total	C	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
			Total	C	N	O	P		
28	1	3113	66567	29735	11981	21738	3113	0	0

There is a discrepancy between the modelled and reference sequences:

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
29	3	121	2579	1152	461	845	121	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
30	4	158	3353	1500	586	1109	158	0	0

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

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

- Molecule 32 is a protein called RPL29 isoform 1.

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

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

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

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

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

- Molecule 35 is a protein called RPL32 isoform 1.

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
55	y	188	1489	925	298	264	2	0	0

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

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

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

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

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

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

- Molecule 59 is a protein called RPS15 isoform 1.

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

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

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

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

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

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

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

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

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

- Molecule 64 is a protein called RPS20 isoform 1.

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

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

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

- Molecule 66 is a protein called RPS22A isoform 1.

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

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

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

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

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

- 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	0
			769	475	160	129	5		

- 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	0
			610	382	110	113	5		

- Molecule 72 is a protein called RPS28A isoform 1.

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

- Molecule 73 is a protein called RPS29A isoform 1.

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

- 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	0
			2437	1541	418	470	8		

- Molecule 75 is a RNA chain called Transfer RNA.

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

- Molecule 76 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of

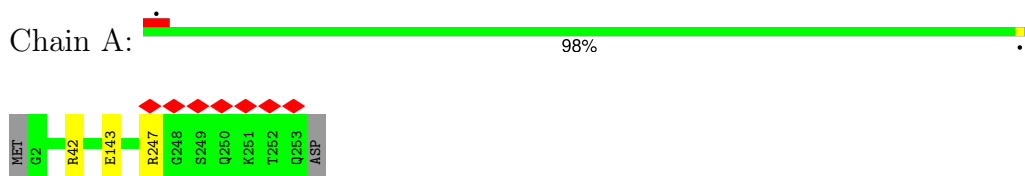
Interest" by depositor).

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

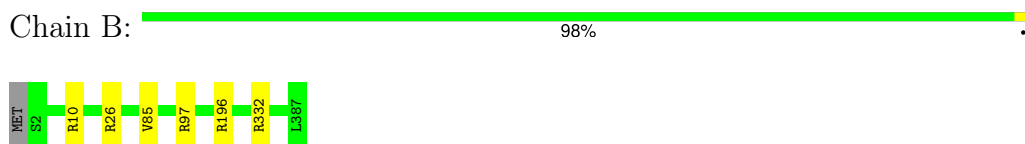
3 Residue-property plots [i](#)

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.

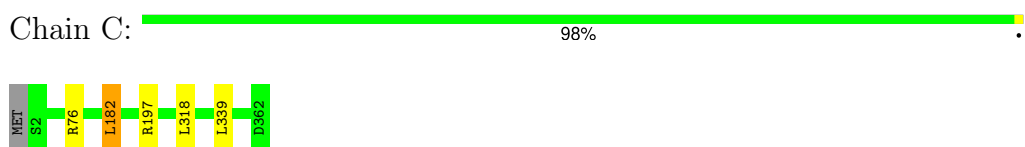
- Molecule 1: 60S ribosomal protein L2-A



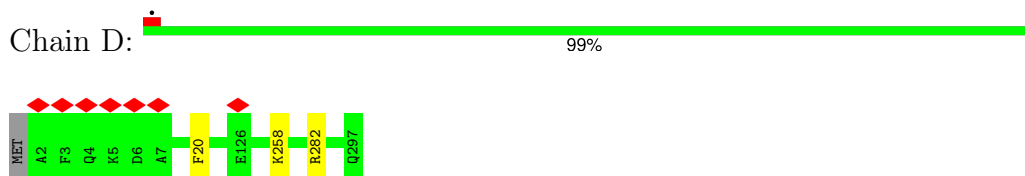
- Molecule 2: RPL3 isoform 1



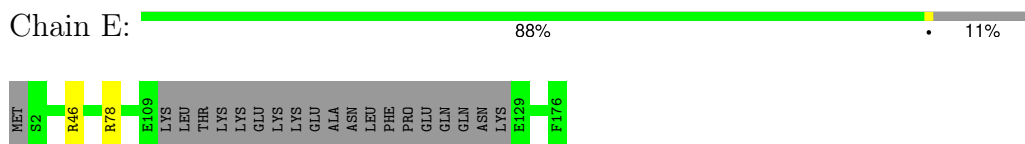
- Molecule 3: RPL4A isoform 1




- Molecule 4: RPL5 isoform 1

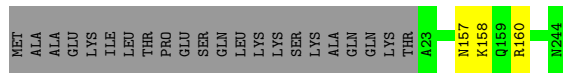


- Molecule 5: 60S ribosomal protein L6-A



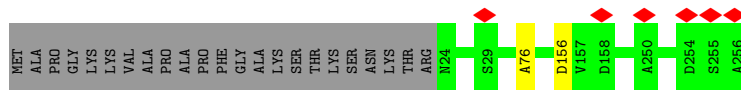
- Molecule 6: 60S ribosomal protein L7-A

Chain F:  90% 9%



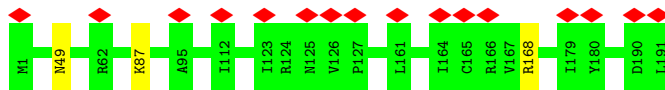
• Molecule 7: RPL8A isoform 1

Chain G:  90% 9%

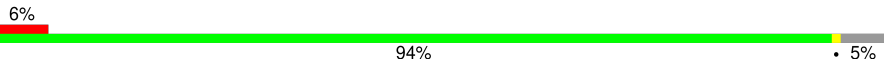


• Molecule 8: RPL9A isoform 1

Chain H:  8% 98% 5%



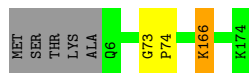
• Molecule 9: RPL10 isoform 1

Chain I:  6% 94% 5%



• Molecule 10: RPL11B isoform 1

Chain J:  95%



• Molecule 11: 60S ribosomal protein L13-A

Chain L:  94%



• Molecule 12: 60S ribosomal protein L14-A

Chain M:  98%



• Molecule 13: 60S ribosomal protein L15-A

Chain N:  100%



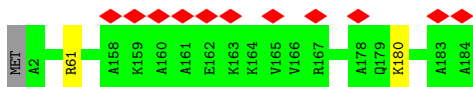
- Molecule 14: 60S ribosomal protein L16-A

Chain O:  97%



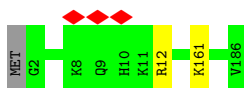
- Molecule 15: 60S ribosomal protein L17-A

Chain P:  98%



- Molecule 16: 60S ribosomal protein L18-A

Chain Q:  98%



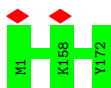
- Molecule 17: 60S ribosomal protein L19-A

Chain R:  98%



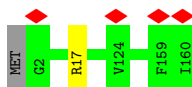
- Molecule 18: 60S ribosomal protein L20-A

Chain S:  100%

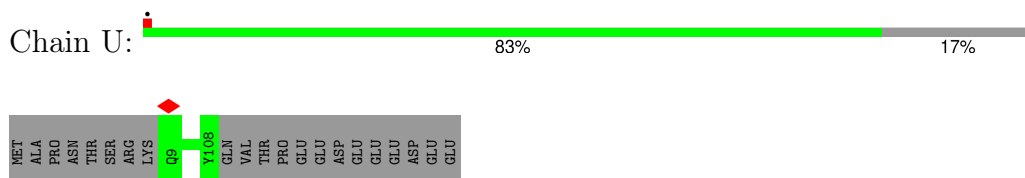


- Molecule 19: 60S ribosomal protein L21-A

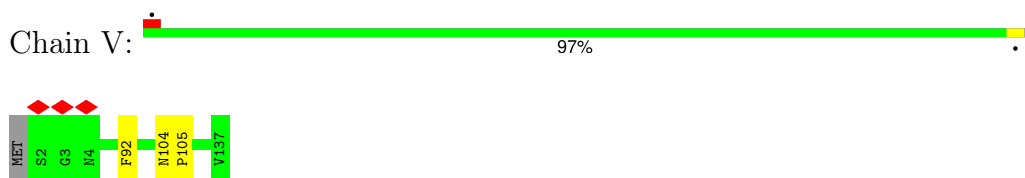
Chain T:  99%



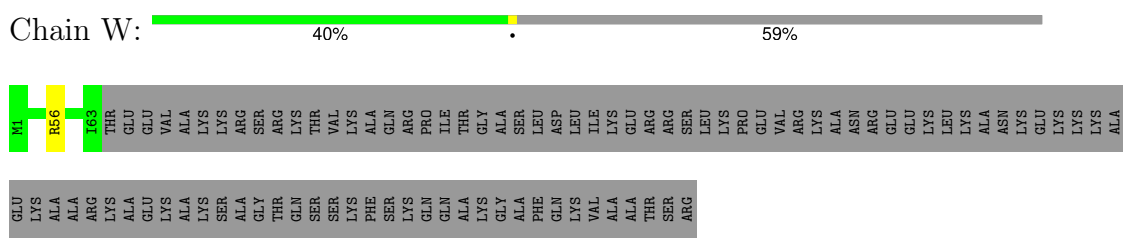
• Molecule 20: 60S ribosomal protein L22-A



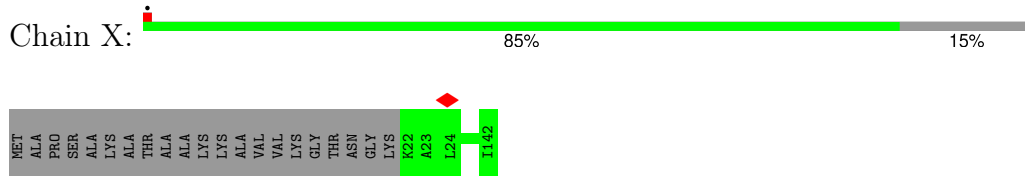
• Molecule 21: 60S ribosomal protein L23-A



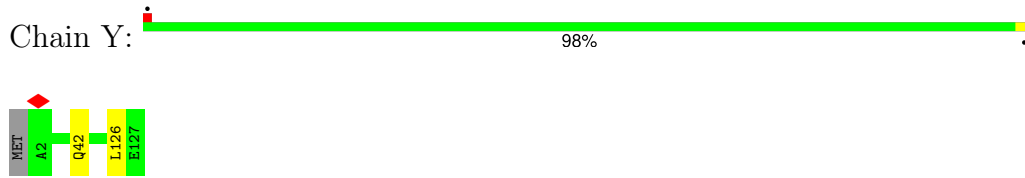
• Molecule 22: RPL24A isoform 1



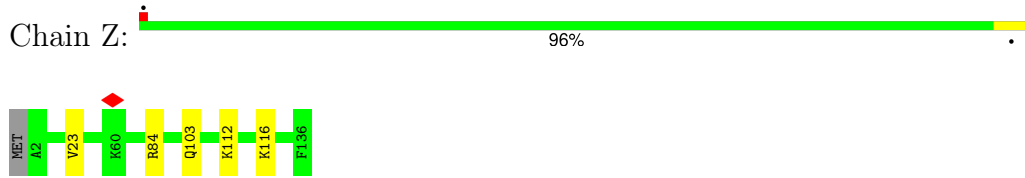
• Molecule 23: 60S ribosomal protein L25



• Molecule 24: 60S ribosomal protein L26-A

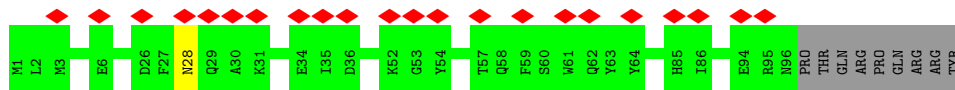


• Molecule 25: 60S ribosomal protein L27-A

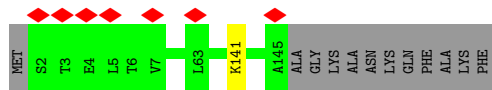


• Molecule 26: 40S ribosomal protein S10-A

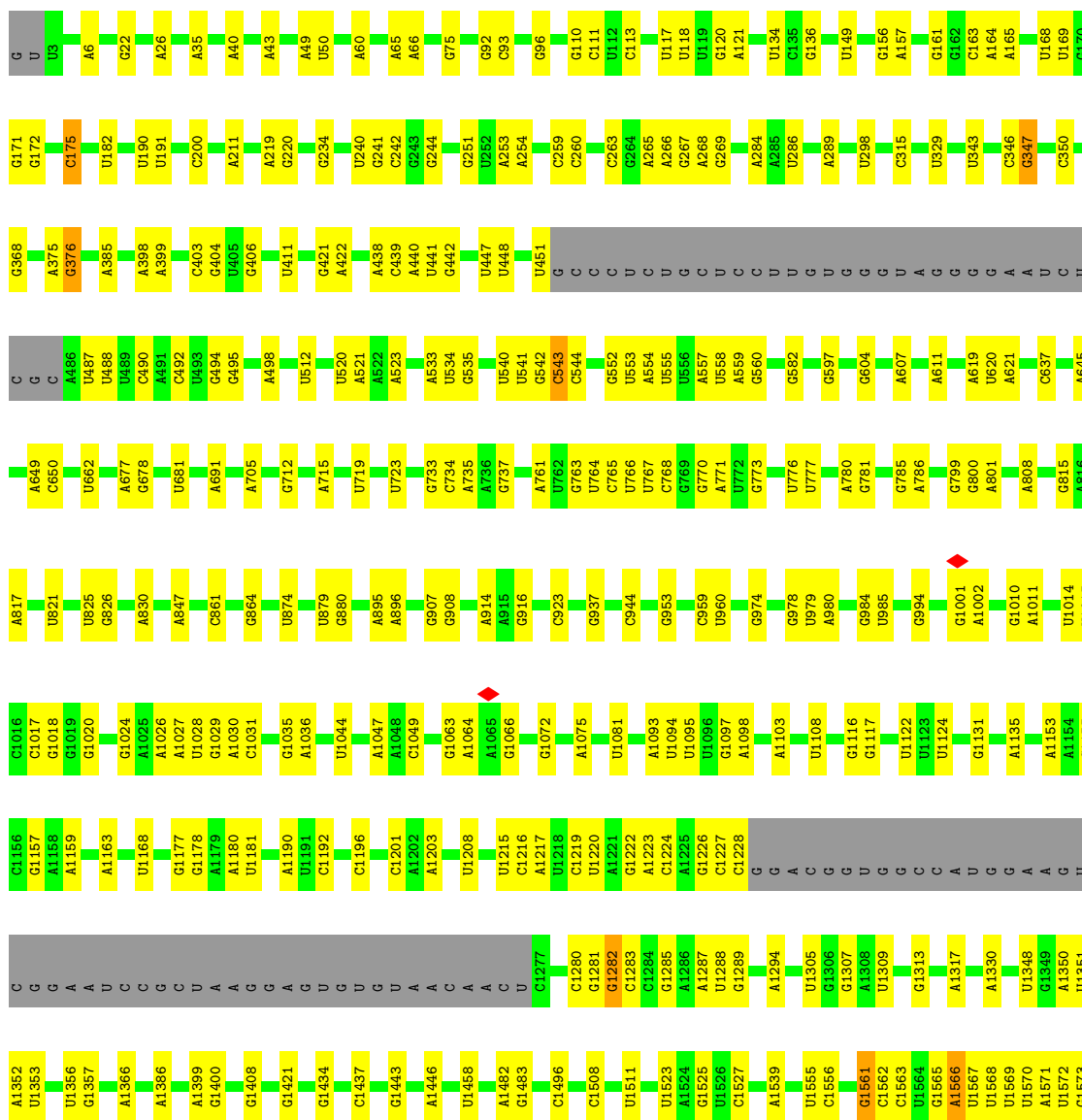


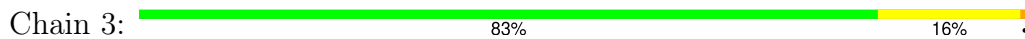


• Molecule 27: 40S ribosomal protein S11-A

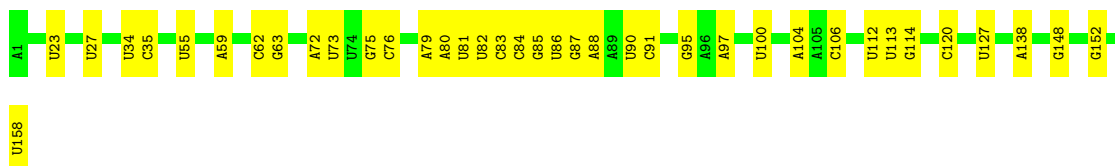


• Molecule 28: 35S ribosomal RNA





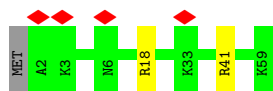
• Molecule 30: 5.8S ribosomal RNA



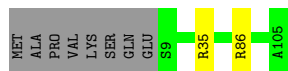
• Molecule 31: 60S ribosomal protein L28



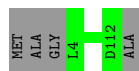
• Molecule 32: RPL29 isoform 1



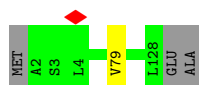
• Molecule 33: 60S ribosomal protein L30



• Molecule 34: 60S ribosomal protein L31-A



• Molecule 35: RPL32 isoform 1



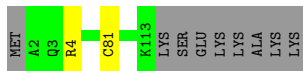
- Molecule 36: 60S ribosomal protein L33-A

Chain f:  96%



- Molecule 37: 60S ribosomal protein L34-A

Chain g:  91%



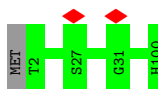
- Molecule 38: 60S ribosomal protein L35-A

Chain h:  98%



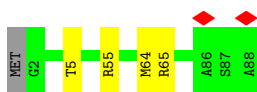
- Molecule 39: 60S ribosomal protein L36-A

Chain i:  99%



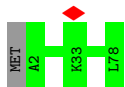
- Molecule 40: 60S ribosomal protein L37-A

Chain j:  94%



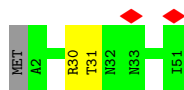
- Molecule 41: RPL38 isoform 1

Chain k:  99%

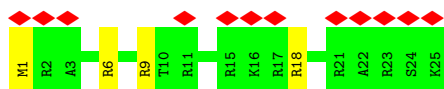
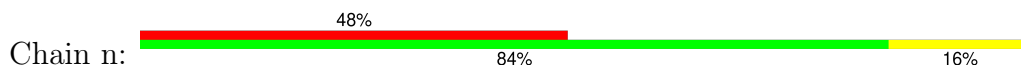


- Molecule 42: 60S ribosomal protein L39

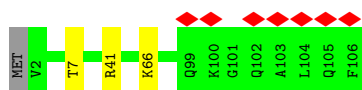
Chain l:  94%



• Molecule 43: RPL41A isoform 1



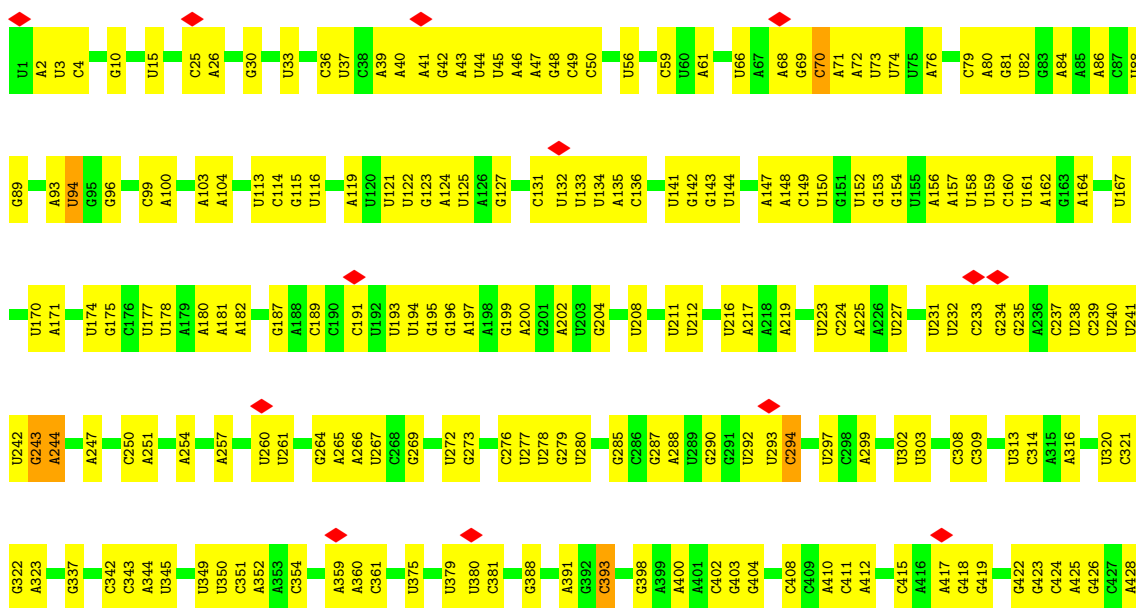
• Molecule 44: 60S ribosomal protein L42-A

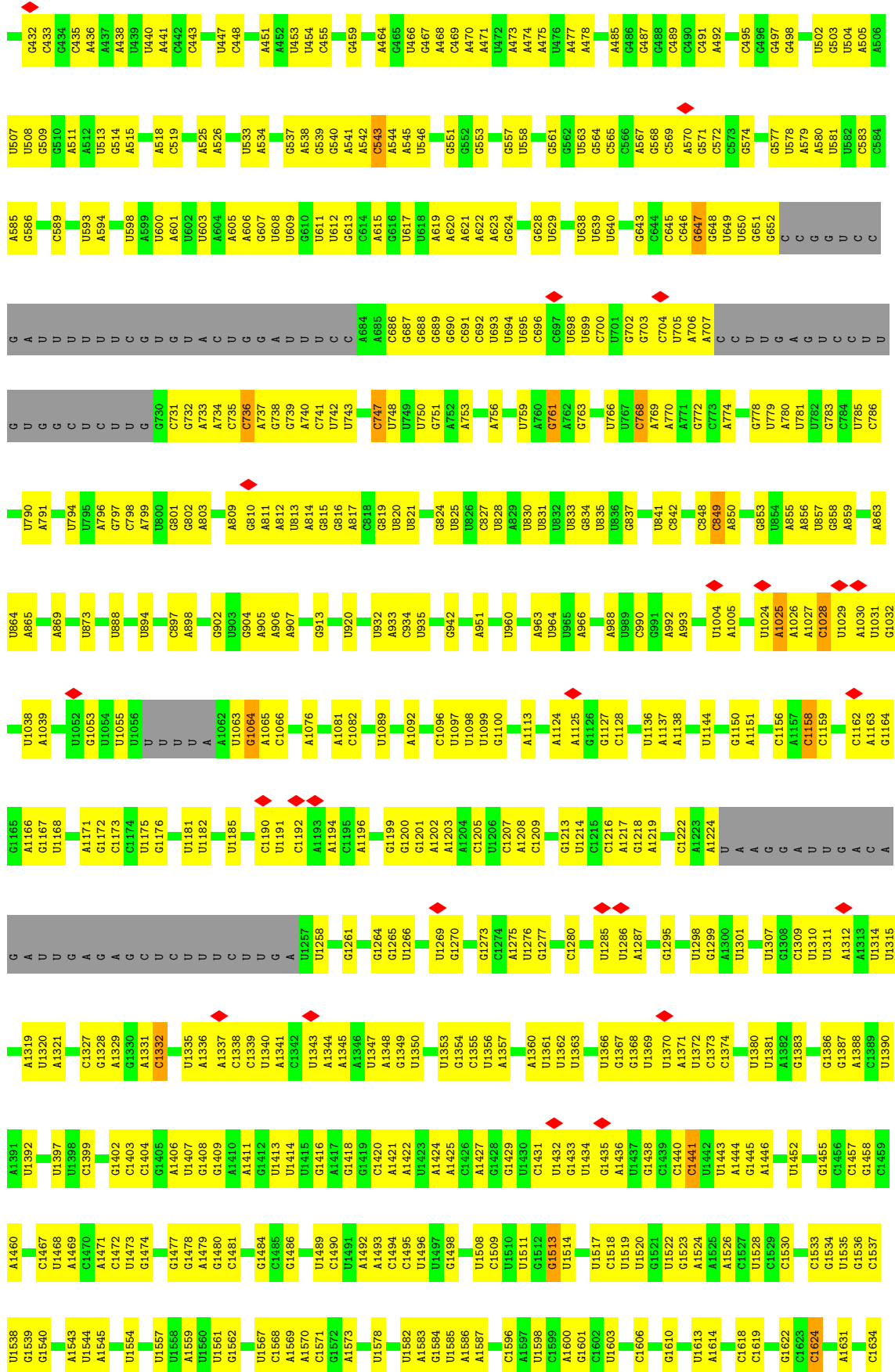


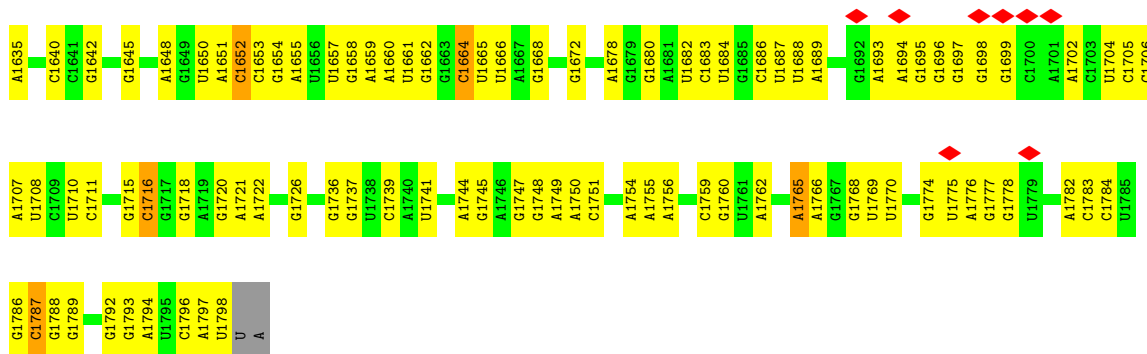
• Molecule 45: 60S ribosomal protein L43-A



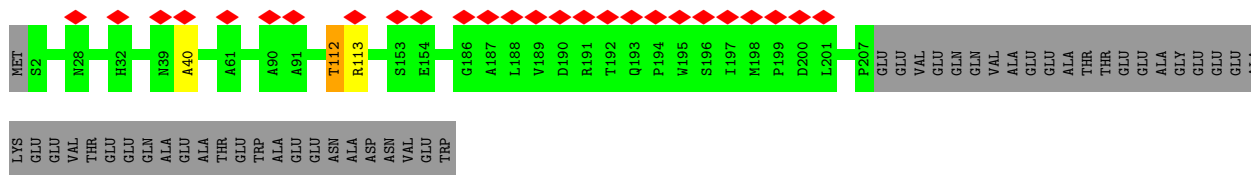
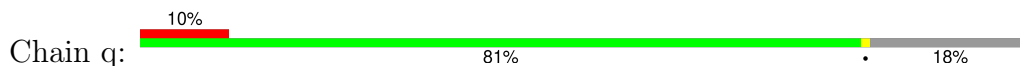
• Molecule 46: 18S ribosomal RNA



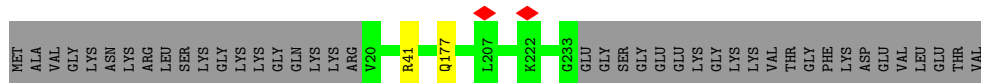
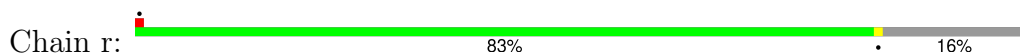




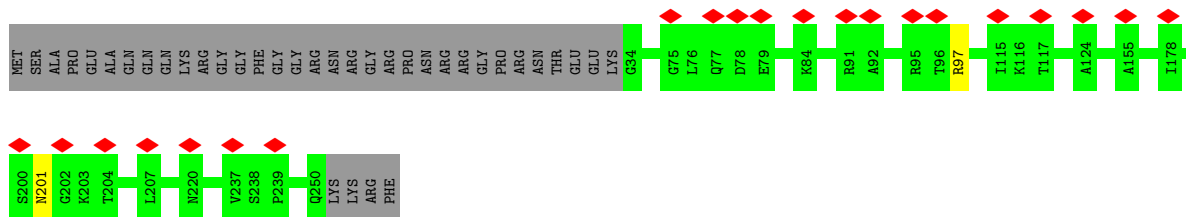
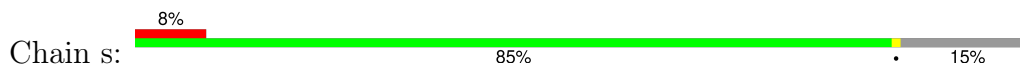
● Molecule 47: 40S ribosomal protein S0-A



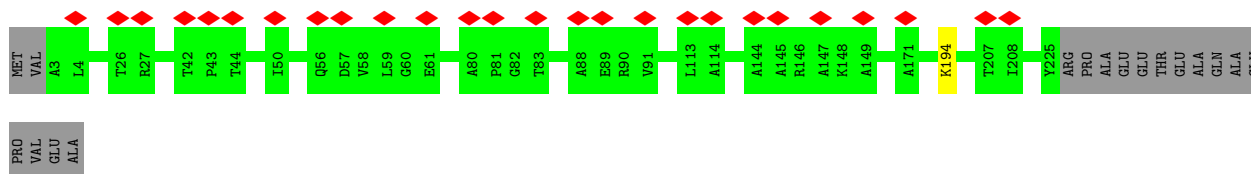
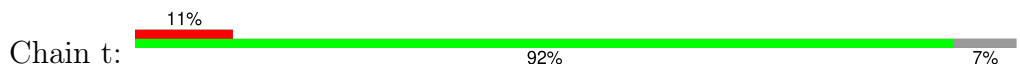
● Molecule 48: RPS1A isoform 1



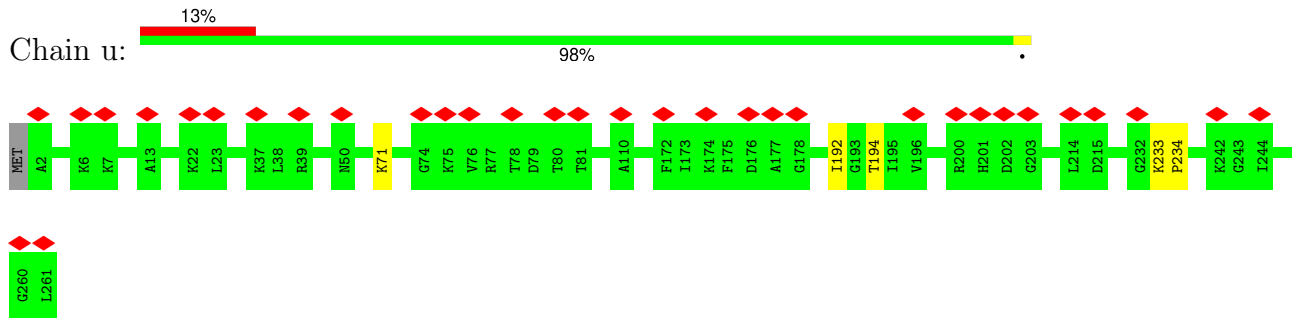
● Molecule 49: RPS2 isoform 1



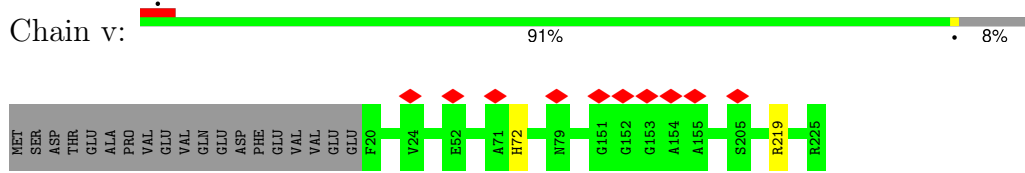
● Molecule 50: RPS3 isoform 1



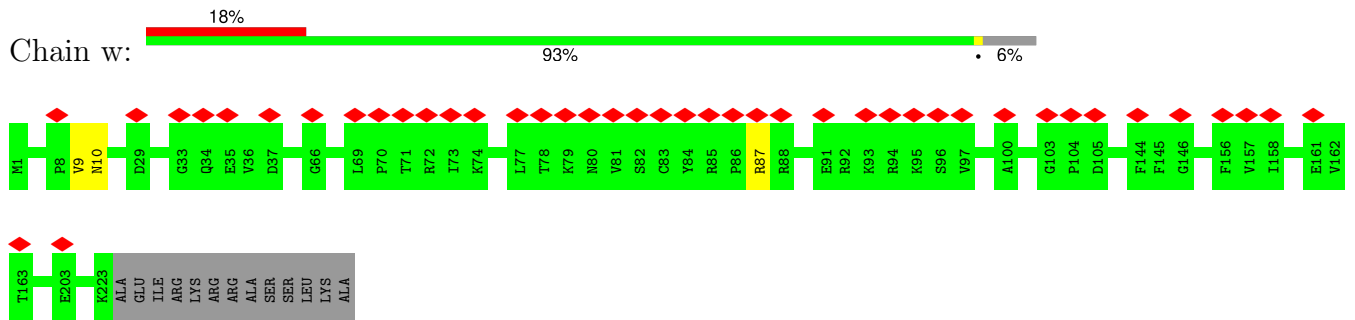
● Molecule 51: 40S ribosomal protein S4-A



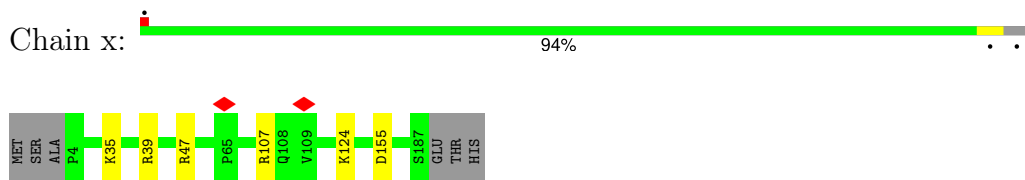
• Molecule 52: Rps5p



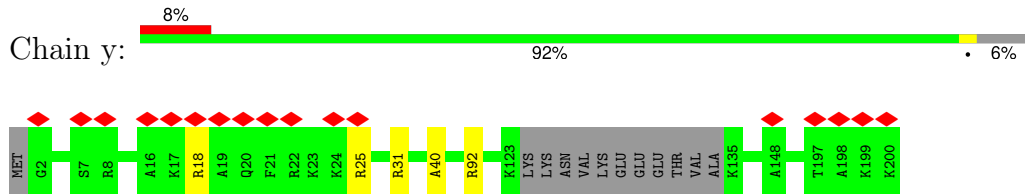
• Molecule 53: 40S ribosomal protein S6-A



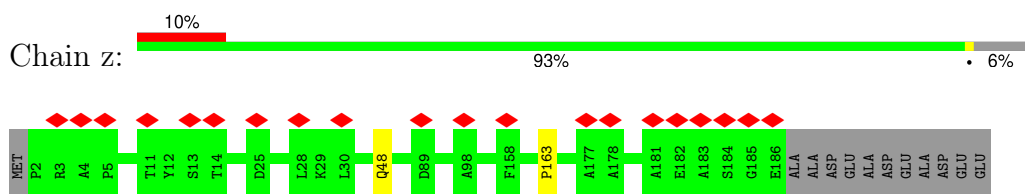
• Molecule 54: 40S ribosomal protein S7-A



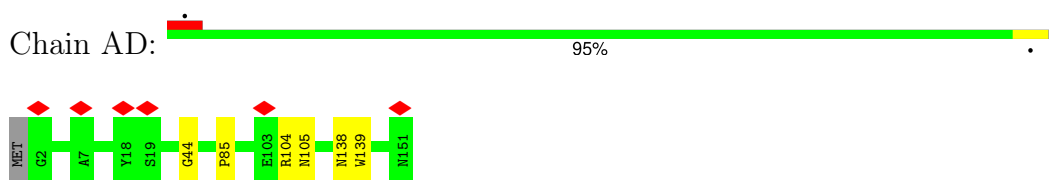
• Molecule 55: RPS8A isoform 1



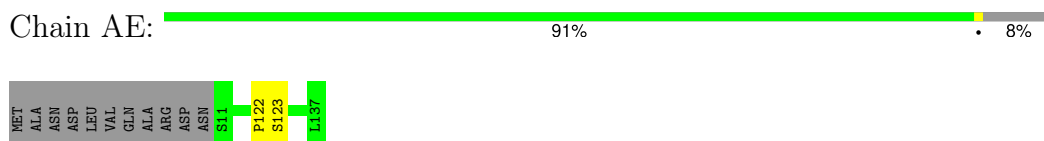
• Molecule 56: 40S ribosomal protein S9-A



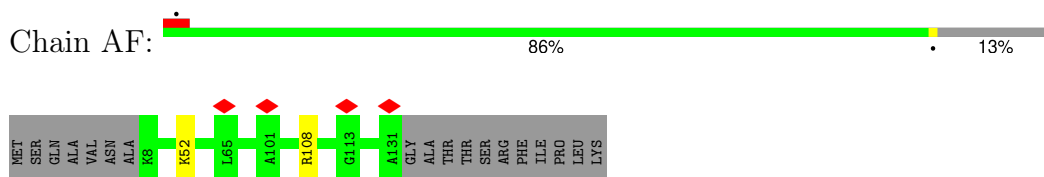
- Molecule 57: 40S ribosomal protein S13



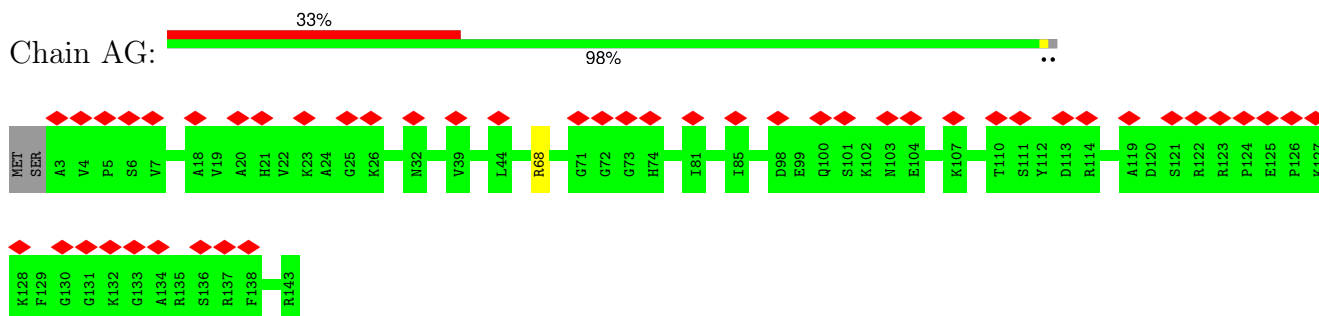
- Molecule 58: 40S ribosomal protein S14-B



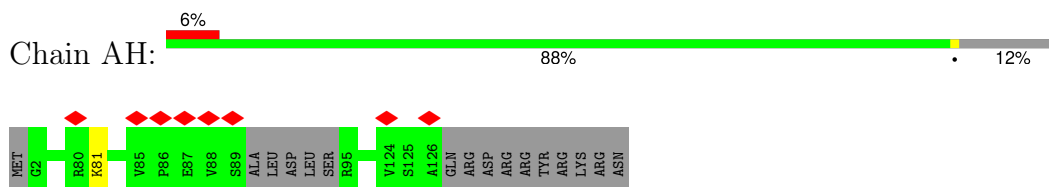
- Molecule 59: RPS15 isoform 1



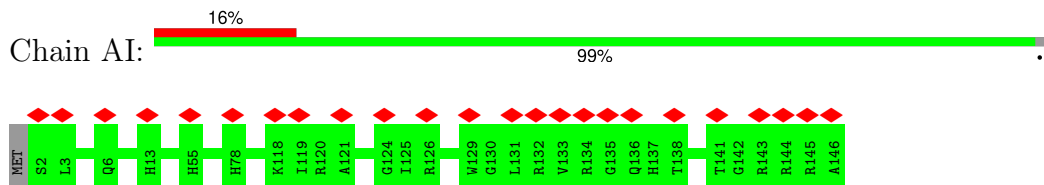
- Molecule 60: 40S ribosomal protein S16-A



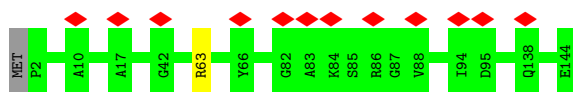
- Molecule 61: 40S ribosomal protein S17-B



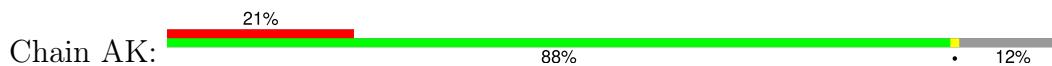
- Molecule 62: 40S ribosomal protein S18-A



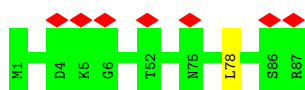
- Molecule 63: 40S ribosomal protein S19-A



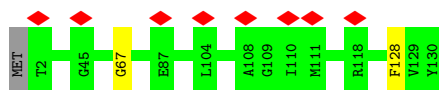
- Molecule 64: RPS20 isoform 1



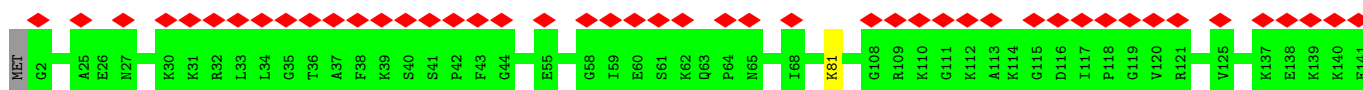
- Molecule 65: 40S ribosomal protein S21-A



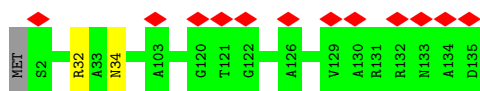
- Molecule 66: RPS22A isoform 1



- Molecule 67: 40S ribosomal protein S23-A

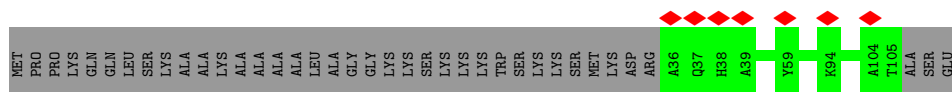


- Molecule 68: 40S ribosomal protein S24-A

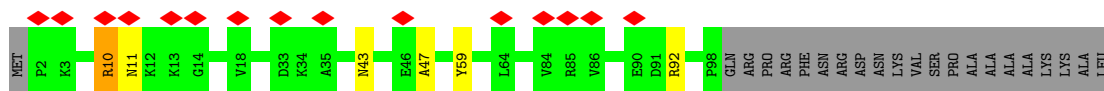
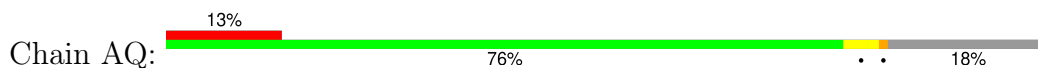


- Molecule 69: RPS25A isoform 1

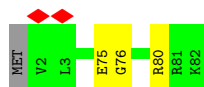




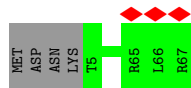
• Molecule 70: RPS26B isoform 1



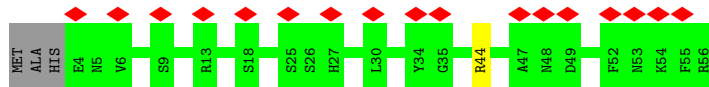
• Molecule 71: 40S ribosomal protein S27-A



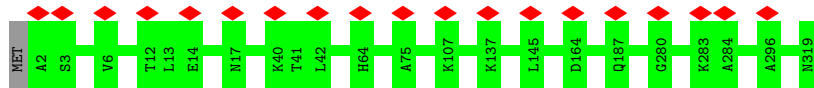
• Molecule 72: RPS28A isoform 1



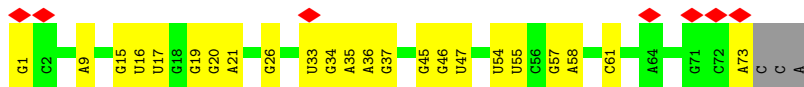
• Molecule 73: RPS29A isoform 1



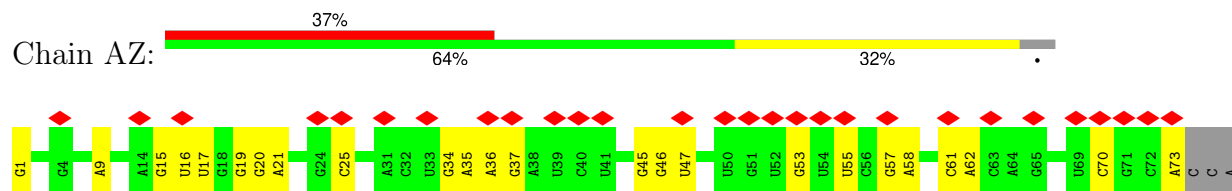
• Molecule 74: Guanine nucleotide-binding protein subunit beta-like protein



• 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 i

5.1 Standard geometry i

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.53	0/1948	0.72	1/2617 (0.0%)
2	B	0.53	0/3146	0.70	2/4228 (0.0%)
3	C	0.50	0/2800	0.71	3/3790 (0.1%)
4	D	0.40	0/2425	0.66	1/3271 (0.0%)
5	E	0.42	0/1260	0.63	1/1694 (0.1%)
6	F	0.53	0/1821	0.66	1/2451 (0.0%)
7	G	0.41	0/1836	0.60	0/2481
8	H	0.32	0/1539	0.64	0/2073
9	I	0.32	0/1741	0.66	1/2335 (0.0%)
10	J	0.33	0/1374	0.68	0/1842
11	L	0.46	0/1568	0.76	1/2106 (0.0%)
12	M	0.41	0/1068	0.65	0/1438
13	N	0.54	0/1757	0.76	0/2354
14	O	0.55	0/1585	0.67	1/2128 (0.0%)
15	P	0.50	0/1443	0.67	1/1944 (0.1%)
16	Q	0.49	0/1465	0.73	0/1965
17	R	0.44	0/1538	0.73	2/2050 (0.1%)
18	S	0.45	0/1481	0.64	0/1990
19	T	0.46	0/1300	0.66	0/1743
20	U	0.38	0/812	0.61	0/1099
21	V	0.49	0/1018	0.68	0/1369
22	W	0.49	0/533	0.68	1/707 (0.1%)
23	X	0.48	0/979	0.63	0/1321
24	Y	0.43	0/1004	0.69	1/1341 (0.1%)
25	Z	0.43	0/1118	0.61	1/1497 (0.1%)
26	AA	0.32	0/789	0.57	0/1067
27	AB	0.31	0/1185	0.67	0/1598
28	1	0.75	1/74506 (0.0%)	1.00	90/116154 (0.1%)
29	3	0.65	0/2883	0.94	1/4491 (0.0%)
30	4	0.73	0/3746	0.98	4/5832 (0.1%)
31	a	0.50	0/1204	0.69	1/1612 (0.1%)
32	b	0.37	0/473	0.66	2/629 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.44	0/751	0.64	1/1008 (0.1%)
34	d	0.49	0/897	0.68	0/1205
35	e	0.49	0/1041	0.67	0/1394
36	f	0.57	0/868	0.72	0/1168
37	g	0.47	0/890	0.75	1/1189 (0.1%)
38	h	0.41	0/978	0.71	1/1301 (0.1%)
39	i	0.40	0/778	0.70	0/1034
40	j	0.50	0/696	0.78	1/923 (0.1%)
41	k	0.38	0/618	0.63	0/826
42	l	0.44	0/443	0.79	0/588
43	n	0.40	0/228	1.10	1/293 (0.3%)
44	o	0.40	0/860	0.69	1/1136 (0.1%)
45	p	0.49	0/701	0.73	0/934
46	2	0.36	0/40725	0.94	58/63454 (0.1%)
47	q	0.31	0/1617	0.65	1/2215 (0.0%)
48	r	0.32	0/1735	0.68	0/2335
49	s	0.32	0/1665	0.62	0/2263
50	t	0.31	0/1759	0.69	0/2368
51	u	0.31	0/2109	0.66	0/2839
52	v	0.30	0/1629	0.66	1/2202 (0.0%)
53	w	0.32	0/1814	0.72	1/2425 (0.0%)
54	x	0.33	0/1506	0.69	1/2028 (0.0%)
55	y	0.31	0/1514	0.73	2/2021 (0.1%)
56	z	0.32	0/1519	0.69	0/2035
57	AD	0.34	0/1215	0.73	0/1638
58	AE	0.31	0/901	0.70	0/1217
59	AF	0.32	0/998	0.66	0/1341
60	AG	0.33	0/1125	0.64	0/1510
61	AH	0.31	0/935	0.67	0/1254
62	AI	0.31	0/1211	0.66	0/1628
63	AJ	0.33	0/1130	0.66	0/1517
64	AK	0.30	0/865	0.64	0/1169
65	AL	0.33	0/693	0.68	0/935
66	AM	0.32	0/1038	0.68	1/1395 (0.1%)
67	AN	0.31	0/1139	0.68	0/1518
68	AO	0.32	0/1087	0.69	1/1449 (0.1%)
69	AP	0.30	0/571	0.62	0/768
70	AQ	0.33	0/782	0.78	1/1047 (0.1%)
71	AR	0.30	0/620	0.67	0/838
72	AS	0.31	0/499	0.73	0/670
73	AT	0.33	0/452	0.73	1/600 (0.2%)
74	AV	0.29	0/2490	0.60	0/3389
75	AX	0.39	1/1749 (0.1%)	0.87	0/2724

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	AZ	0.36	1/1749 (0.1%)	0.86	0/2724
All	All	0.55	3/211935 (0.0%)	0.88	190/311732 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
3	C	0	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

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
75	AX	1	G	OP3-P	-10.70	1.48	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
75	AZ	1	G	OP3-P	-10.61	1.48	1.61
28	1	1561	G	O3'-P	5.90	1.68	1.61

The worst 5 of 190 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	2	94	U	C2-N3-C4	19.84	138.90	127.00
28	1	2545	C	C6-N1-C2	-11.16	115.84	120.30
28	1	1872	C	C6-N1-C2	-10.62	116.05	120.30
46	2	94	U	N1-C2-N3	9.80	120.78	114.90
46	2	94	U	N3-C4-C5	9.37	120.22	114.60

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](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	250/254 (98%)	238 (95%)	12 (5%)	0	100	100
2	B	384/387 (99%)	357 (93%)	27 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	359/362 (99%)	320 (89%)	38 (11%)	1 (0%)	37	69
4	D	294/297 (99%)	267 (91%)	26 (9%)	1 (0%)	37	69
5	E	152/176 (86%)	142 (93%)	10 (7%)	0	100	100
6	F	220/244 (90%)	201 (91%)	18 (8%)	1 (0%)	25	60
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%)	13	47
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%)	19	54
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
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%)	19	54
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	51
36	f	104/107 (97%)	97 (93%)	5 (5%)	2 (2%)	6	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	11	43
41	k	75/78 (96%)	69 (92%)	6 (8%)	0	100	100
42	l	48/51 (94%)	40 (83%)	6 (12%)	2 (4%)	2	17
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%)	13	47
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	64
52	v	204/225 (91%)	178 (87%)	26 (13%)	0	100	100
53	w	221/236 (94%)	173 (78%)	47 (21%)	1 (0%)	25	60
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	26
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
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	51
67	AN	142/145 (98%)	119 (84%)	23 (16%)	0	100	100
68	AO	132/135 (98%)	109 (83%)	23 (17%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	AP	68/108 (63%)	60 (88%)	8 (12%)	0	100	100
70	AQ	95/119 (80%)	62 (65%)	32 (34%)	1 (1%)	12	44
71	AR	79/82 (96%)	64 (81%)	14 (18%)	1 (1%)	10	41
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%)	38	69

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 [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	193/196 (98%)	192 (100%)	1 (0%)	86	93
2	B	321/323 (99%)	317 (99%)	4 (1%)	67	85
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%)	133 (99%)	1 (1%)	81	92
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%)	168 (98%)	3 (2%)	54	77
9	I	177/187 (95%)	175 (99%)	2 (1%)	70	86
10	J	147/151 (97%)	146 (99%)	1 (1%)	81	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	L	154/159 (97%)	153 (99%)	1 (1%)	84	92
12	M	107/109 (98%)	106 (99%)	1 (1%)	75	89
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%)	139 (99%)	1 (1%)	81	92
16	Q	150/151 (99%)	149 (99%)	1 (1%)	81	92
17	R	153/154 (99%)	152 (99%)	1 (1%)	81	92
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%)	108 (99%)	1 (1%)	75	89
25	Z	115/116 (99%)	111 (96%)	4 (4%)	31	63
26	AA	77/98 (79%)	76 (99%)	1 (1%)	65	83
27	AB	129/137 (94%)	128 (99%)	1 (1%)	79	90
31	a	118/119 (99%)	117 (99%)	1 (1%)	79	90
32	b	46/47 (98%)	46 (100%)	0	100	100
33	c	81/88 (92%)	80 (99%)	1 (1%)	67	85
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
37	g	95/103 (92%)	94 (99%)	1 (1%)	70	86
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%)	20 (91%)	2 (9%)	7	29
44	o	90/91 (99%)	90 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	p	71/72 (99%)	71 (100%)	0	100	100
47	q	164/210 (78%)	164 (100%)	0	100	100
48	r	191/224 (85%)	190 (100%)	1 (0%)	86	93
49	s	176/205 (86%)	174 (99%)	2 (1%)	70	86
50	t	182/195 (93%)	181 (100%)	1 (0%)	86	93
51	u	221/222 (100%)	220 (100%)	1 (0%)	86	93
52	v	173/191 (91%)	172 (99%)	1 (1%)	84	92
53	w	189/201 (94%)	189 (100%)	0	100	100
54	x	165/170 (97%)	161 (98%)	4 (2%)	44	71
55	y	150/161 (93%)	148 (99%)	2 (1%)	65	83
56	z	158/166 (95%)	157 (99%)	1 (1%)	84	92
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%)	99 (98%)	2 (2%)	50	75
60	AG	117/119 (98%)	116 (99%)	1 (1%)	75	89
61	AH	94/124 (76%)	93 (99%)	1 (1%)	70	86
62	AI	128/129 (99%)	128 (100%)	0	100	100
63	AJ	115/116 (99%)	114 (99%)	1 (1%)	75	89
64	AK	100/114 (88%)	99 (99%)	1 (1%)	73	87
65	AL	74/74 (100%)	73 (99%)	1 (1%)	62	82
66	AM	110/111 (99%)	110 (100%)	0	100	100
67	AN	119/120 (99%)	118 (99%)	1 (1%)	79	90
68	AO	112/113 (99%)	111 (99%)	1 (1%)	75	89
69	AP	61/89 (68%)	61 (100%)	0	100	100
70	AQ	83/100 (83%)	82 (99%)	1 (1%)	67	85
71	AR	70/71 (99%)	69 (99%)	1 (1%)	62	82
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%)	8913 (99%)	53 (1%)	82	92

5 of 53 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
43	n	18	ARG
54	x	35	LYS
67	AN	81	LYS
48	r	41	ARG
50	t	194	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
63	AJ	101	ASN
63	AJ	129	GLN
68	AO	77	ASN
65	AL	70	ASN
51	u	98	ASN

5.3.3 RNA [i](#)

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

Continued on next page...

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Mol	Chain	Res	Type
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 [i](#)

There are no chain breaks in this entry.

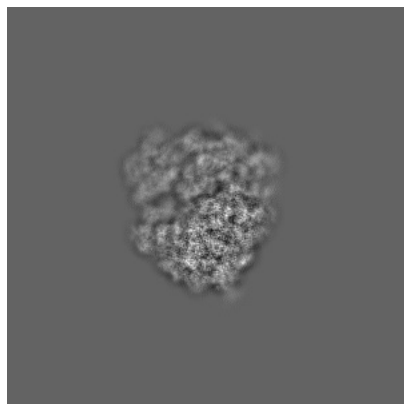
6 Map visualisation [i](#)

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.

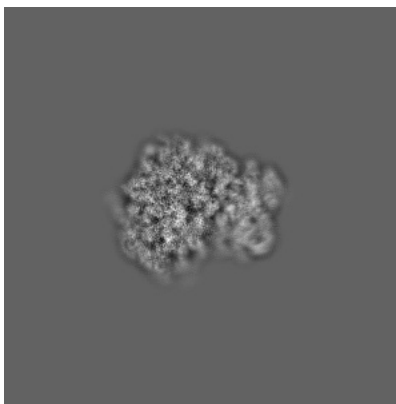
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

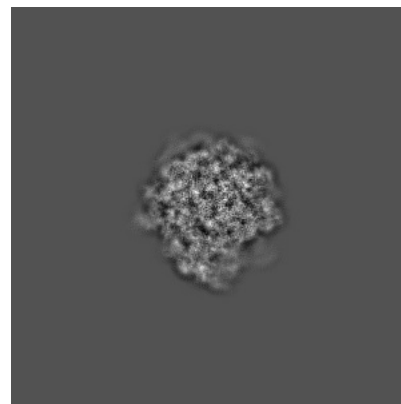
6.1.1 Primary map



X

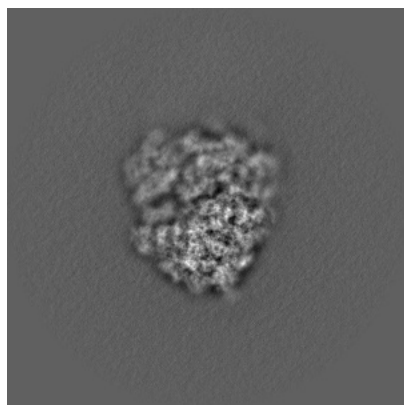


Y

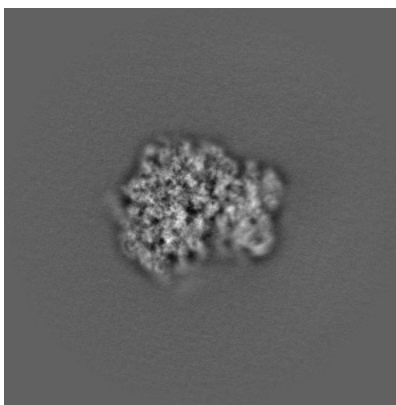


Z

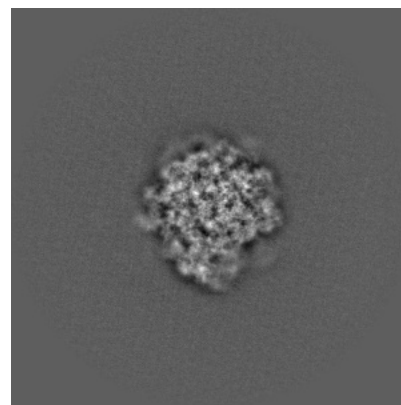
6.1.2 Raw map



X



Y

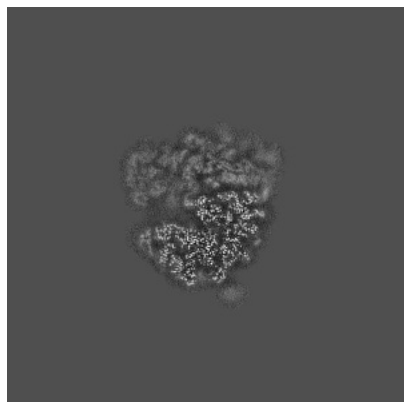


Z

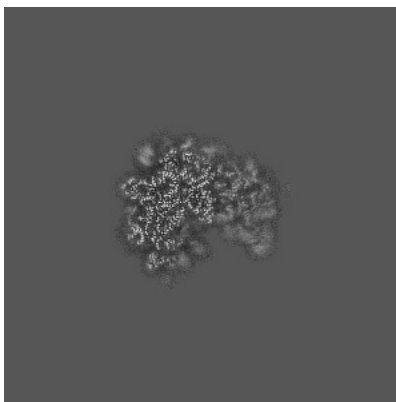
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

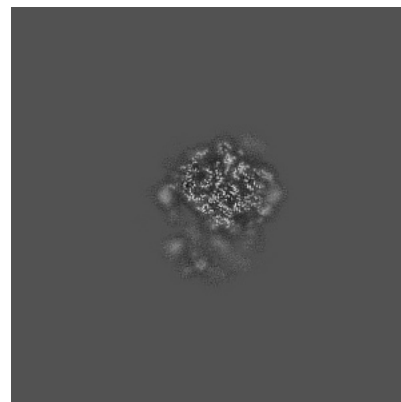
6.2.1 Primary map



X Index: 240

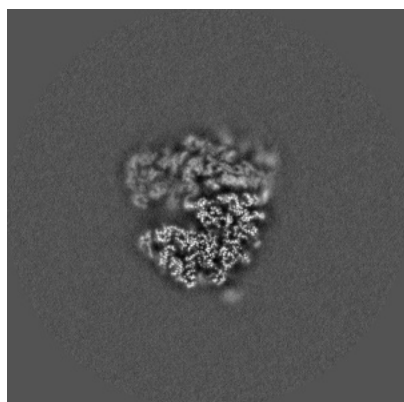


Y Index: 240

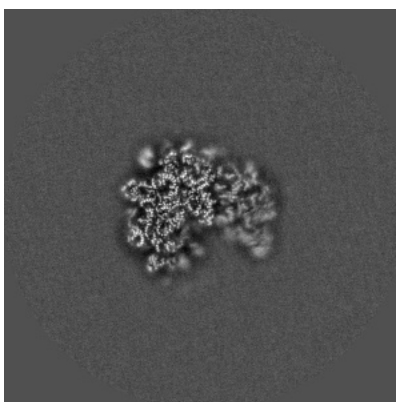


Z Index: 240

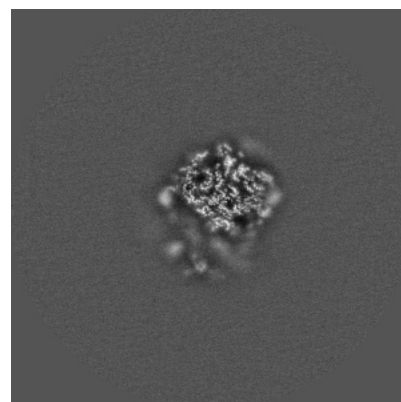
6.2.2 Raw map



X Index: 240



Y Index: 240

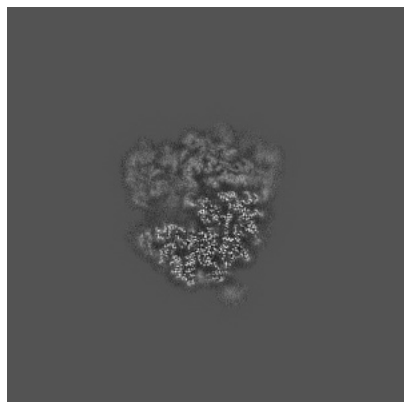


Z Index: 240

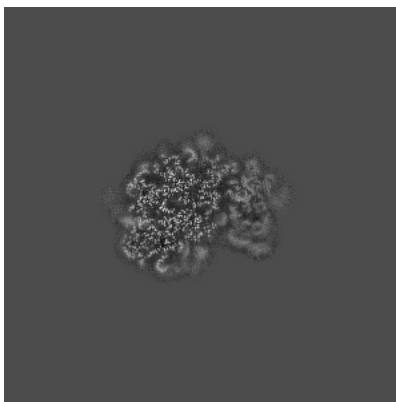
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

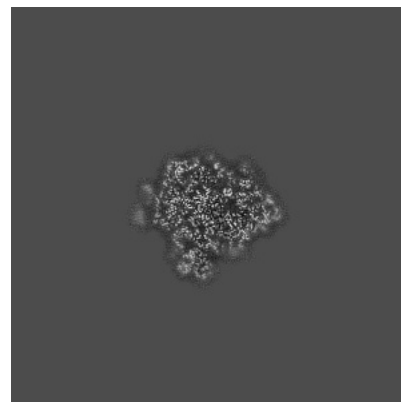
6.3.1 Primary map



X Index: 239

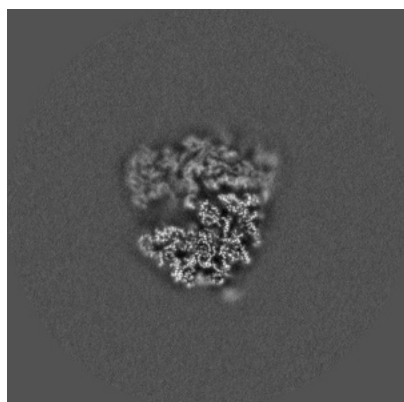


Y Index: 257

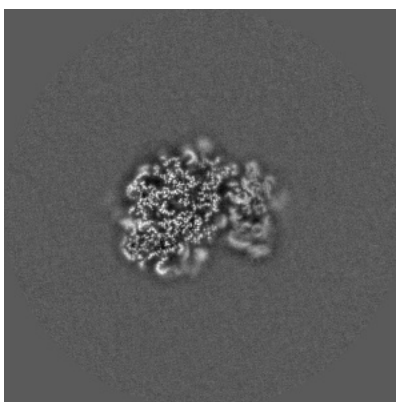


Z Index: 195

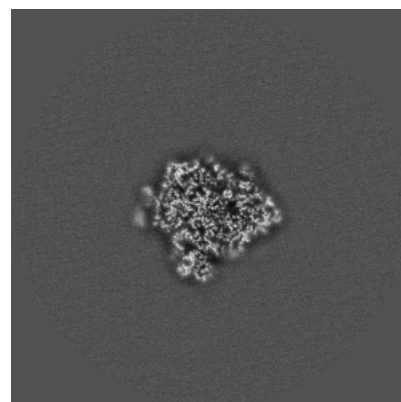
6.3.2 Raw map



X Index: 238



Y Index: 257

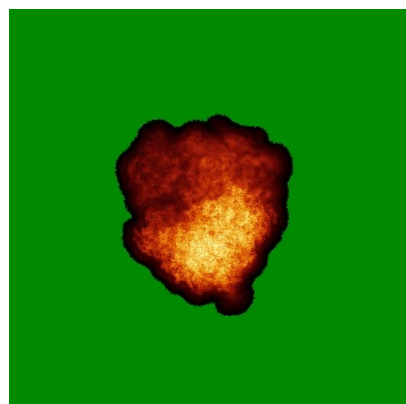


Z Index: 195

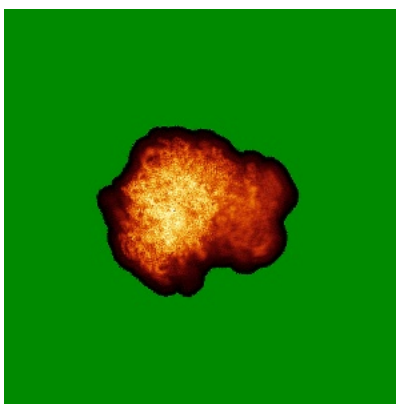
The images above show the largest variance slices of the map in three orthogonal directions.

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

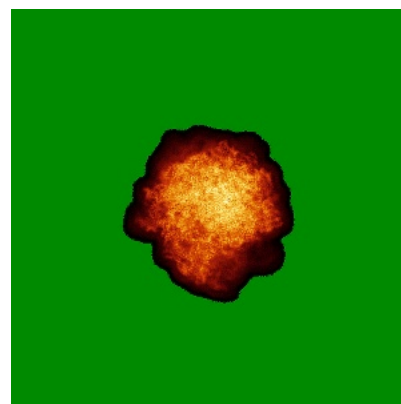
6.4.1 Primary map



X

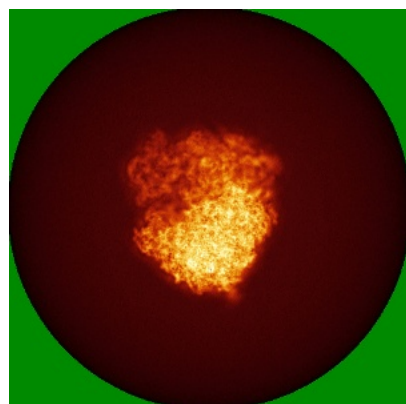


Y

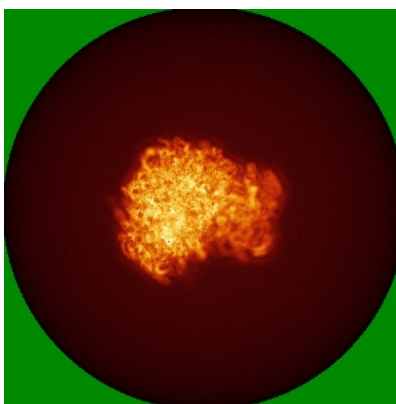


Z

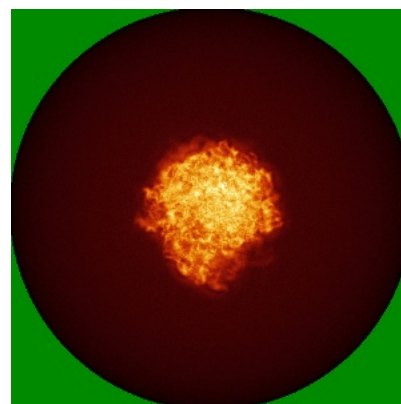
6.4.2 Raw map



X



Y

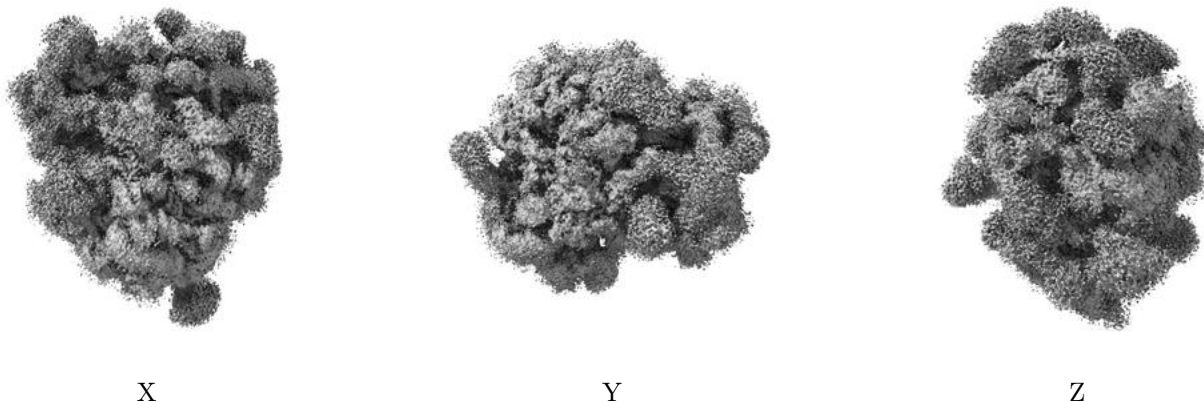


Z

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.

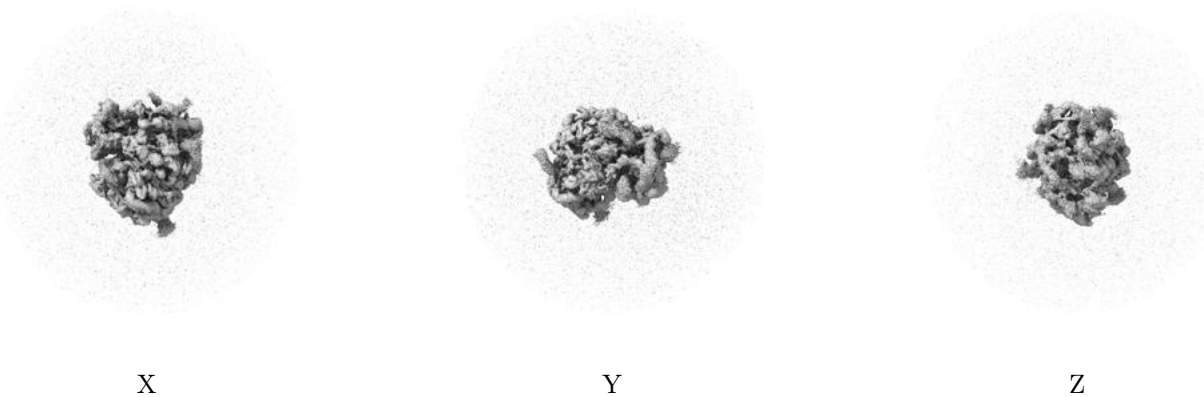
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.6. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

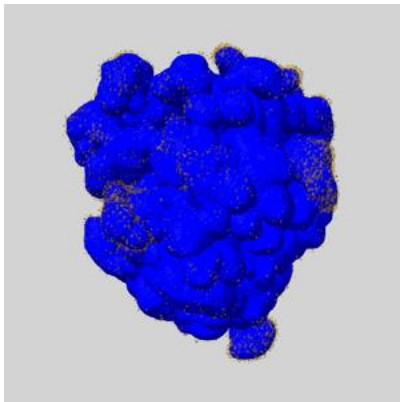
6.6 Mask visualisation [i](#)

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

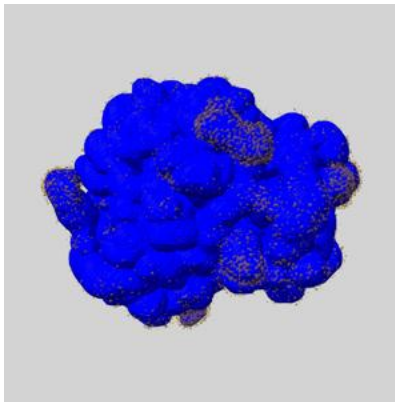
A mask typically either:

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

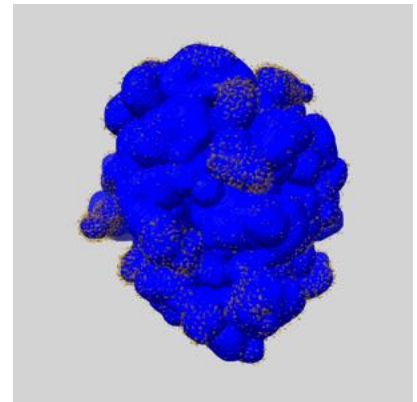
6.6.1 emd_22198_msk_1.map [i](#)



X



Y

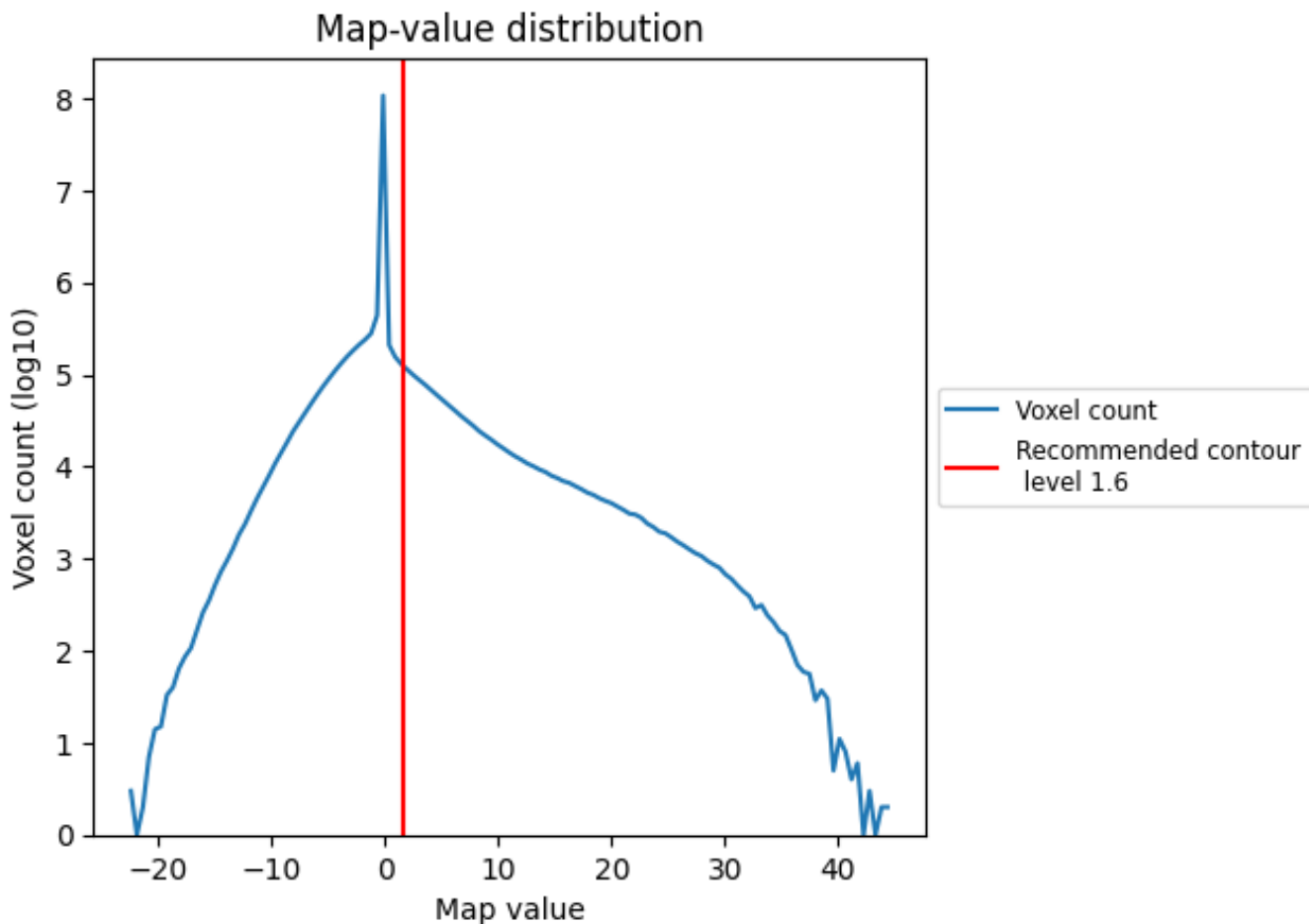


Z

7 Map analysis [i](#)

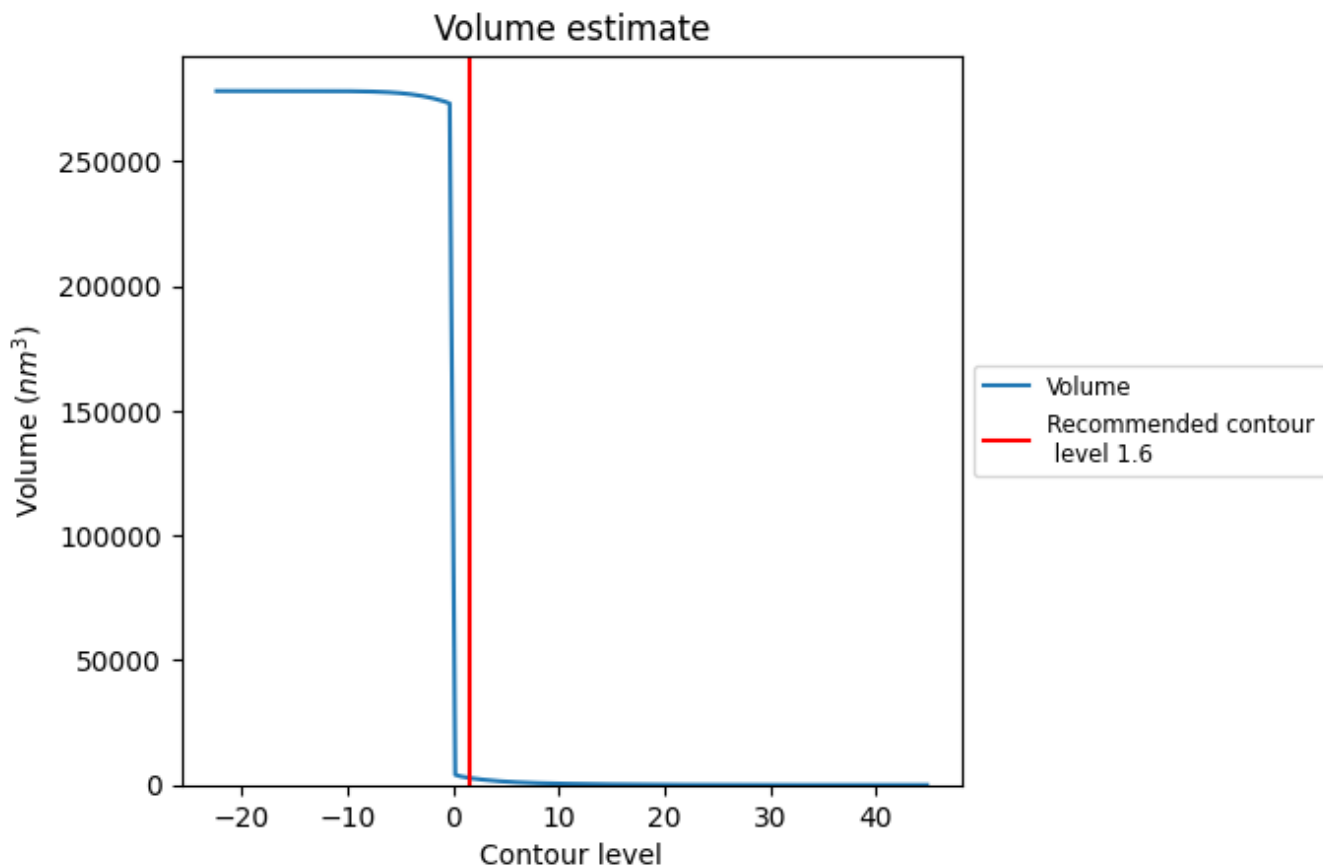
This section contains the results of statistical analysis of the map.

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.

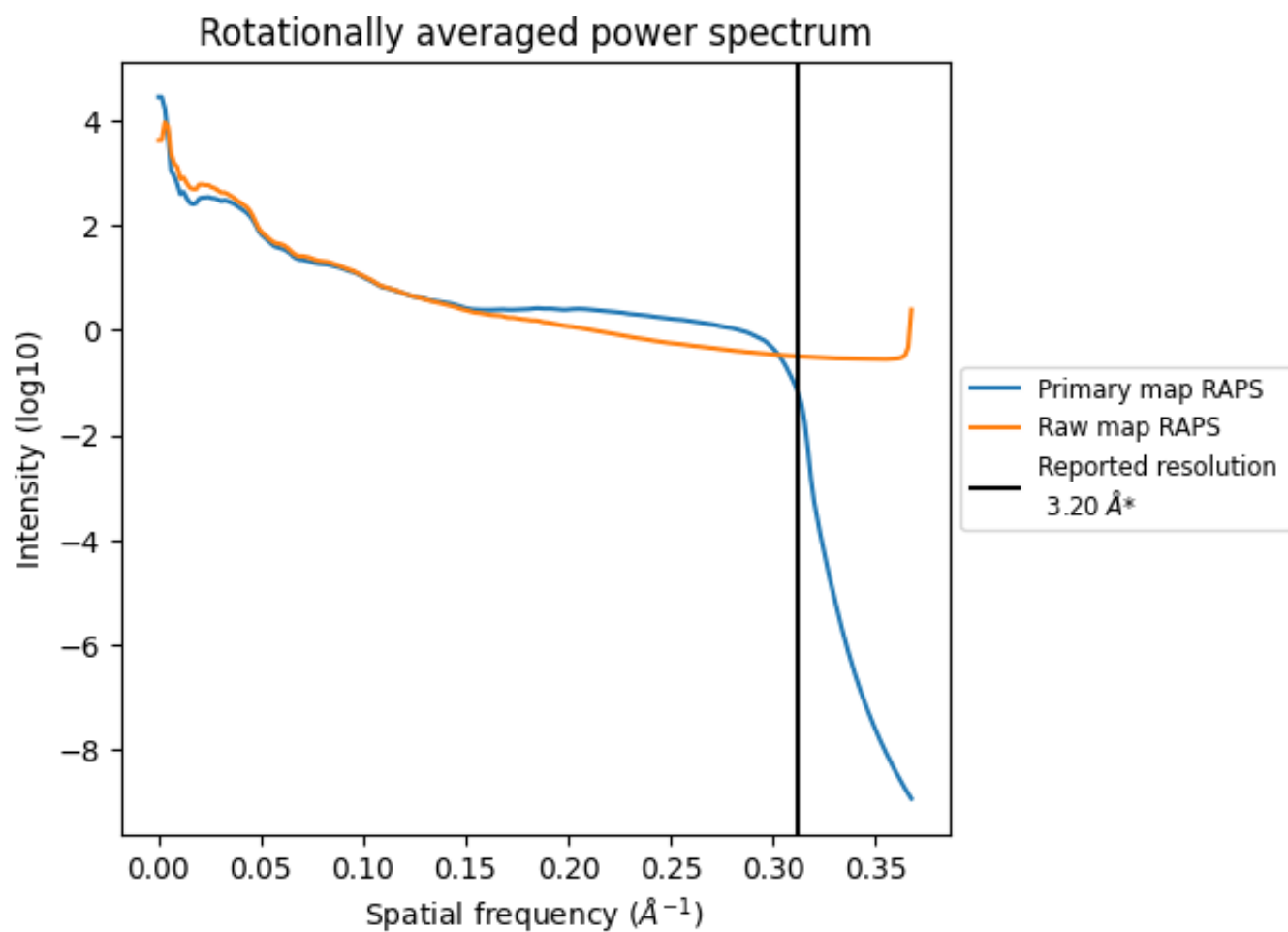
7.2 Volume estimate [\(i\)](#)



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 i

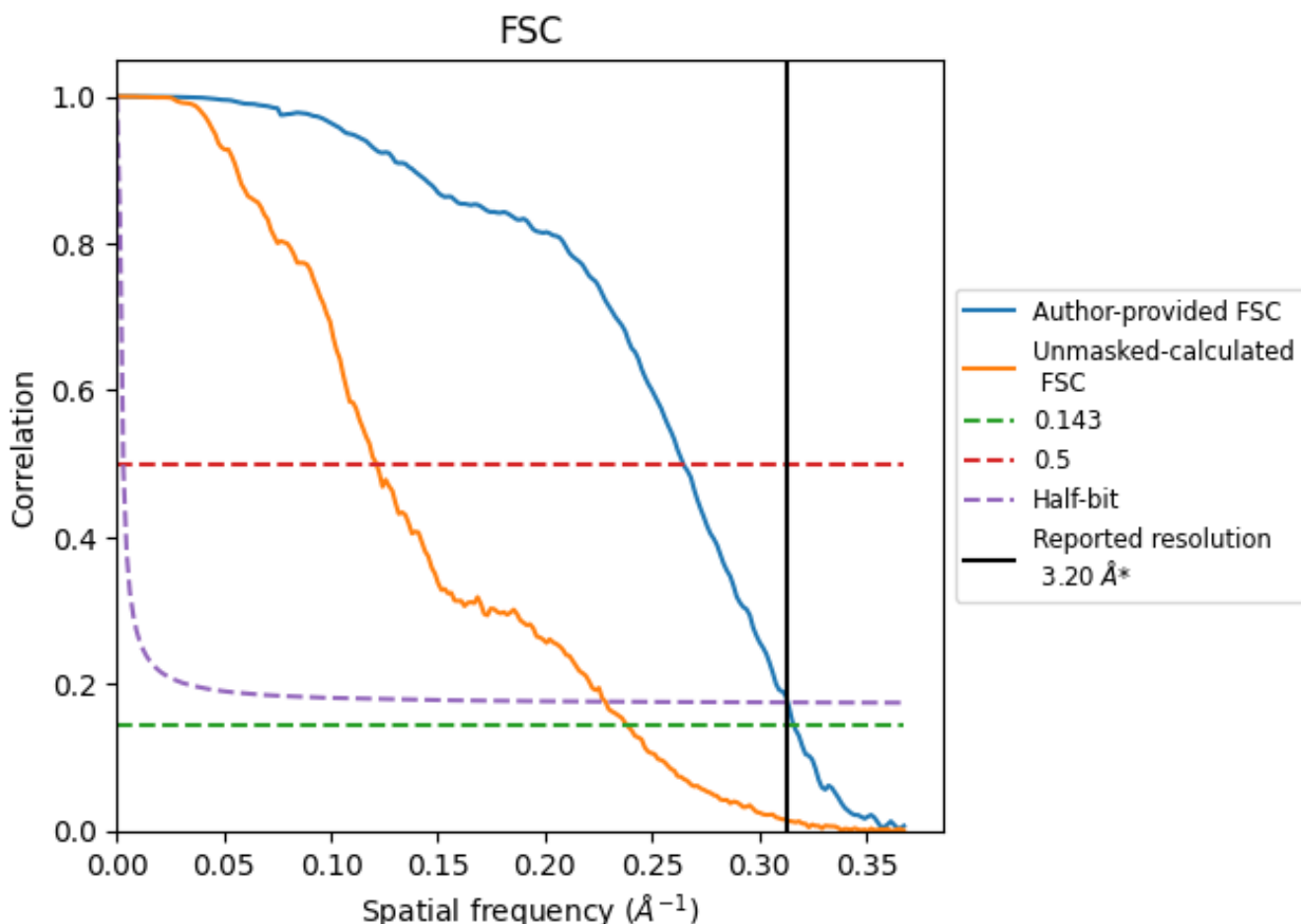


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 Å⁻¹

8.2 Resolution estimates

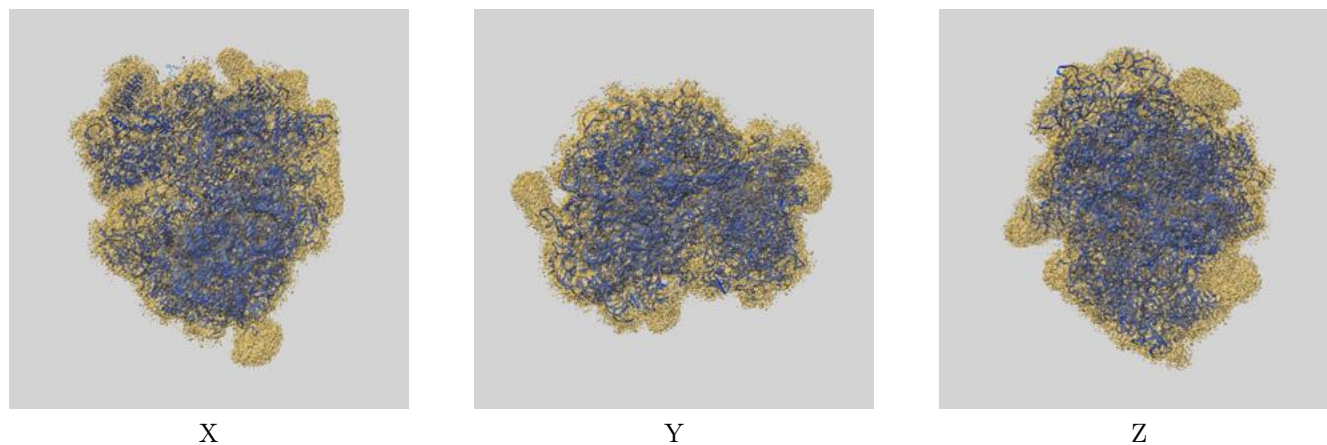
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.16	3.78	3.19
Unmasked-calculated*	4.19	8.25	4.38

*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](#)

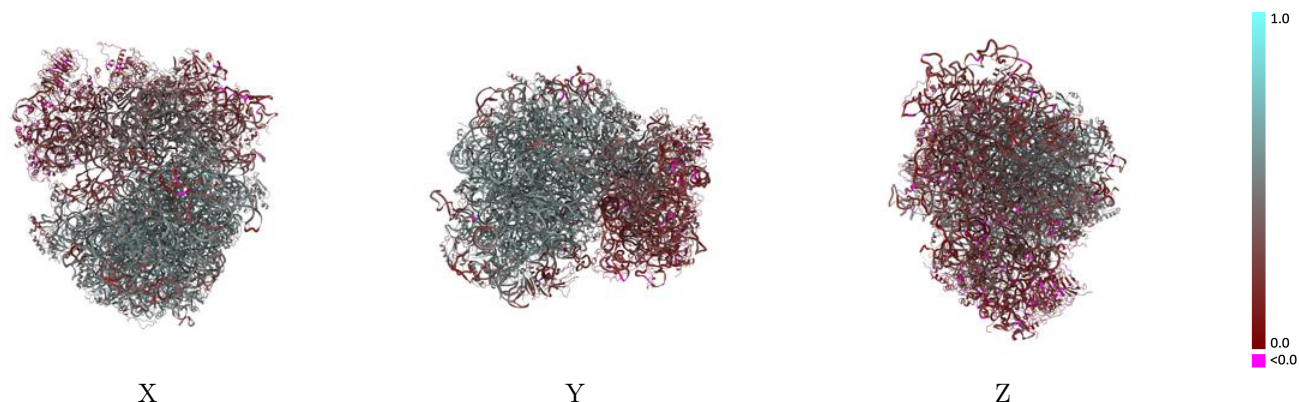
This section contains information regarding the fit between EMDB map EMD-22198 and PDB model 6XIR. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)



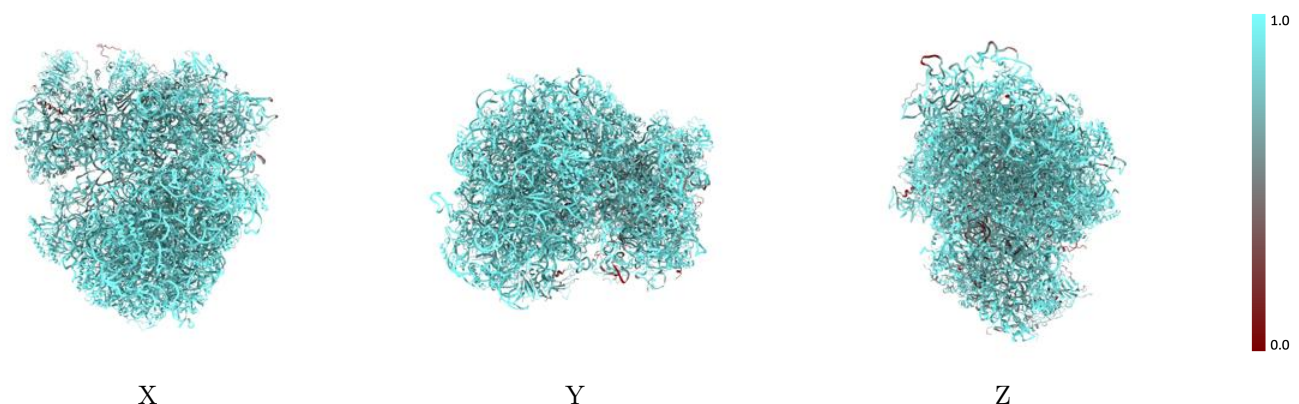
The images above show the 3D surface view of the map at the recommended contour level 1.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



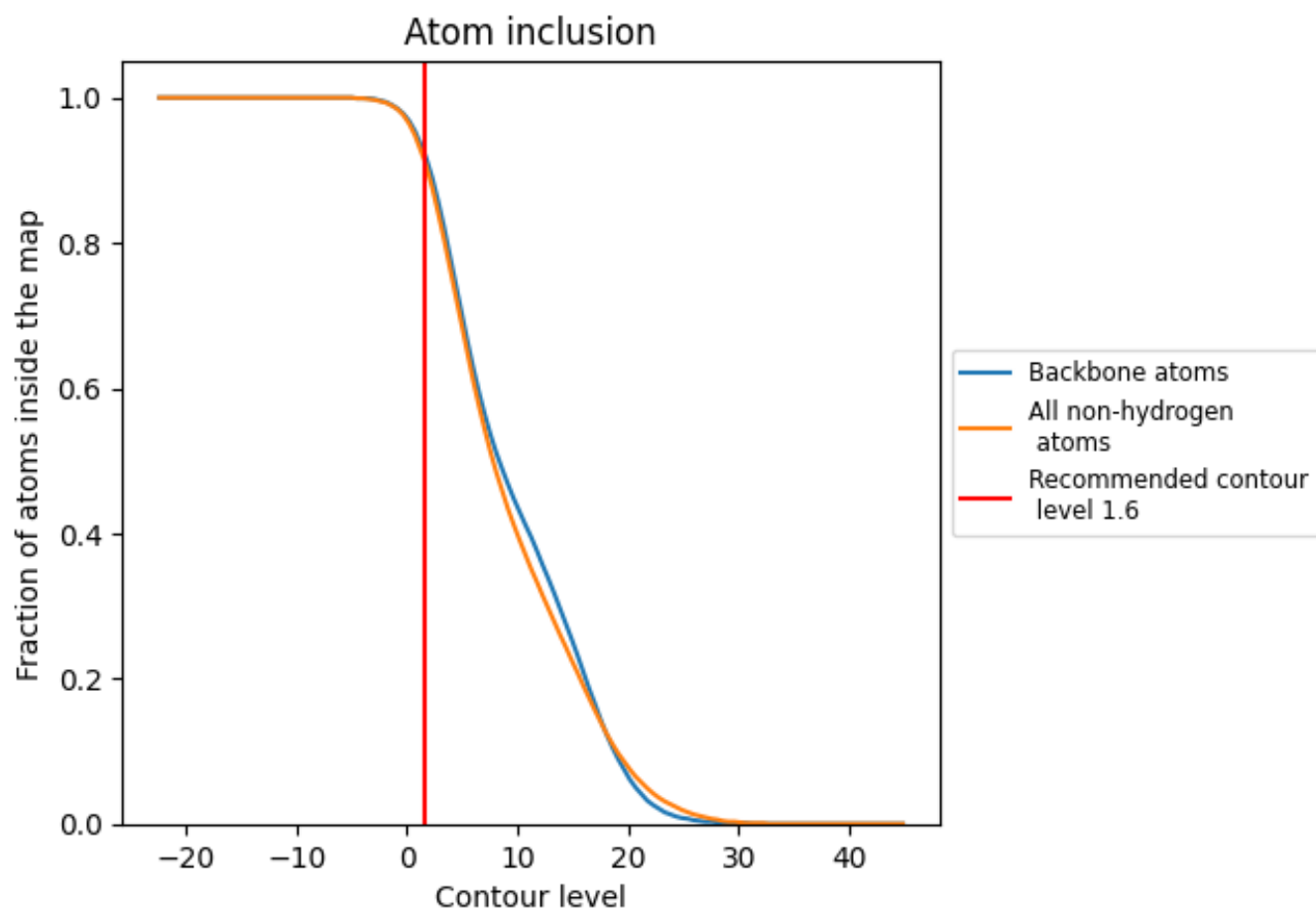
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (1.6).







































































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



Continued on next page...

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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