



## wwPDB EM Validation Summary Report ⓘ

Feb 22, 2023 – 09:18 am GMT

PDB ID : 7ZUW  
EMDB ID : EMD-14978  
Title : Structure of RQT (C1) bound to the stalled ribosome in a disome unit from *S. cerevisiae*  
Authors : Best, K.M.; Ikeuchi, K.; Kater, L.; Best, D.M.; Musial, J.; Matsuo, Y.; Berninghausen, O.; Becker, T.; Inada, T.; Beckmann, R.  
Deposited on : 2022-05-13  
Resolution : 4.30 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.32.1

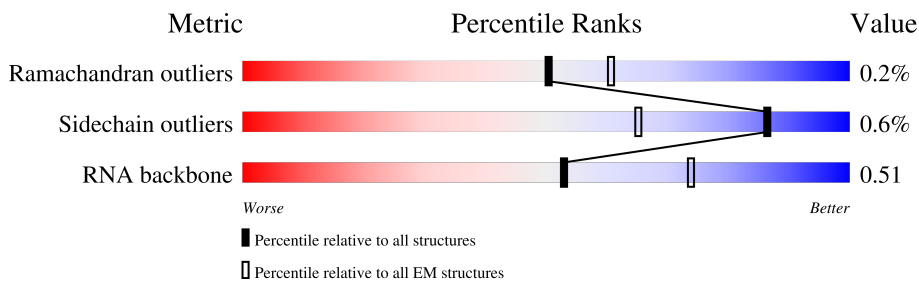
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.30 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	2	1800	
2	3	158	
3	4	121	
4	5	3396	
5	6	76	
6	AA	206	
7	AB	255	
8	AC	216	

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Mol	Chain	Length	Quality of chain
9	AD	222	5% 100%
10	AE	258	98%
11	AF	206	100%
12	AG	228	98%
13	AH	184	99%
14	AI	200	92% 6%
15	AJ	184	99%
16	AK	92	100%
17	AL	144	99%
18	AM	121	10% 97%
19	AN	150	100%
20	AO	127	100%
21	AP	117	99%
22	AQ	141	99%
23	AR	136	89% 11%
24	AS	145	99%
25	AT	143	99%
26	AU	100	98%
27	AV	87	97%
28	AW	129	100%
29	AX	144	99%
30	AY	134	99%
31	AZ	82	16% 100%
32	Aa	97	98%
33	Ab	81	100%

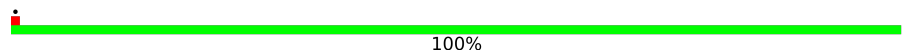
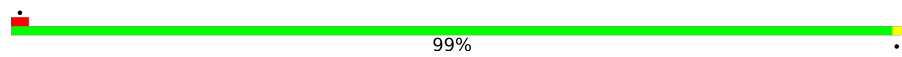
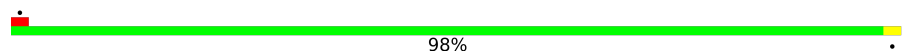
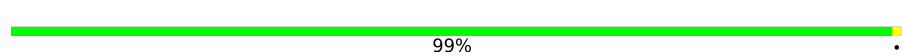
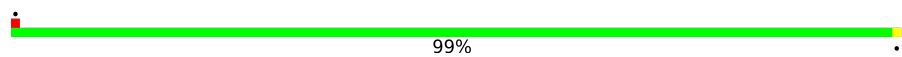
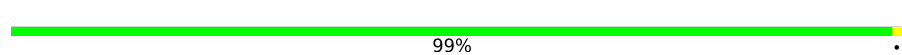
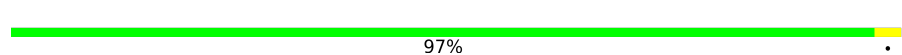



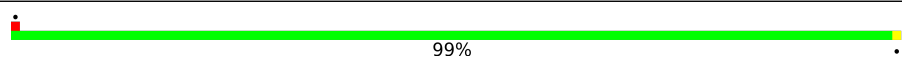
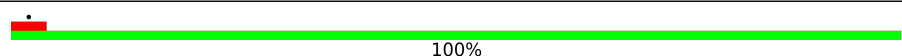



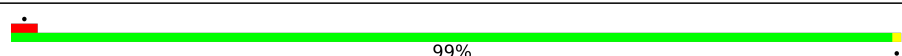
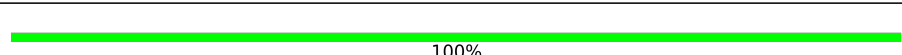
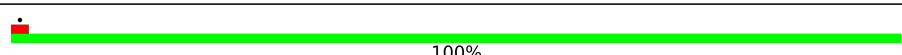
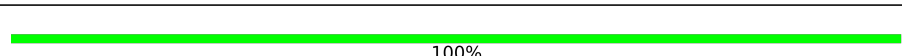
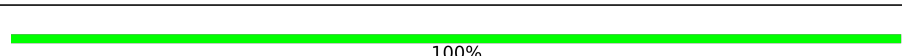
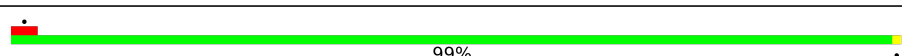

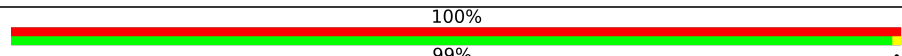
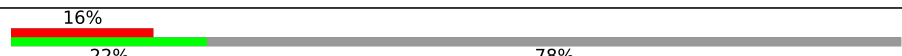
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Mol	Chain	Length	Quality of chain
34	Ac	63	5% 98%
35	Ad	53	98%
36	Ae	60	5% 98%
37	Af	73	11% 99%
38	Ag	312	96% 99%
39	BA	251	100%
40	BB	386	99%
41	BC	361	99%
42	BD	294	100%
43	BE	176	94% 5%
44	BF	222	100%
45	BG	233	99%
46	BH	191	100%
47	BI	218	100%
48	BJ	169	100%
49	BK	193	97%
50	BL	136	100%
51	BM	203	100%
52	BN	197	98%
53	BO	183	100%
54	BP	185	99%
55	BQ	188	99%
56	BR	171	100%
57	BS	159	100%
58	BT	100	99%

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Mol	Chain	Length	Quality of chain
59	BU	136	 100%
60	BV	126	 99%
61	BW	121	 98%
62	BX	125	 99%
63	BY	135	 99%
64	BZ	148	 99%
65	Ba	58	 97%
66	Bb	96	 100%
67	Bc	109	 100%
68	Bd	127	 100%
69	Be	106	 99%
70	Bf	112	 100%
71	Bg	119	 100%
72	Bh	99	 100%
73	Bi	85	 100%
74	Bj	77	 99%
75	Bk	50	 100%
76	Bl	52	 100%
77	Bm	25	 100%
78	Bn	103	 100%
79	Bo	91	 99%
80	CA	1967	 50% 88% 11%
81	CB	297	 100% 99%
82	CC	530	 16% 22% 78%

## 2 Entry composition [i](#)

There are 84 unique types of molecules in this entry. The entry contains 218071 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	2	1771	37739	16872	6683	12413	1771	0	0

- Molecule 2 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	3	158	3353	1500	586	1109	158	0	0

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	4	121	2579	1152	461	845	121	0	0

- Molecule 4 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	5	3163	67650	30218	12191	22078	3163	0	0

- Molecule 5 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	6	76	1619	722	288	533	76	0	0

- Molecule 6 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	AA	206	1603	1030	284	287	2	0	0

- Molecule 7 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	AB	226	1798	1139	330	325	4	0	0

- Molecule 8 is a protein called RPS2 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	AC	216	1626	1042	287	295	2	0	0

- Molecule 9 is a protein called RPS3 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	AD	222	1729	1098	312	313	6	0	0

- Molecule 10 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	AE	258	2056	1308	387	358	3	0	0

- Molecule 11 is a protein called Rps5p.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	AF	206	1605	1005	299	298	3	0	0

- Molecule 12 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	AG	228	1815	1138	351	323	3	0	0

- Molecule 13 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	AH	184	1473	946	263	264	0	0

- Molecule 14 is a protein called 40S ribosomal protein S8-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	AI	187	1476	916	295	263	2	0	0

- Molecule 15 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	AJ	184	1479	935	285	258	1	0	0

- Molecule 16 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	AK	92	752	487	122	141	2	0	0

- Molecule 17 is a protein called 40S ribosomal protein S11-A.

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

- Molecule 18 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	AM	121	875	551	153	169	2	0	0

- Molecule 19 is a protein called 40S ribosomal protein S13.

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

- Molecule 20 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	AO	127	926	569	185	169	3	0	0

- Molecule 21 is a protein called RPS15 isoform 1.



Mol	Chain	Residues	Atoms					AltConf	Trace
21	AP	117	Total	C	N	O	S	0	0
			916	583	171	155	7		

- Molecule 22 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AQ	141	Total	C	N	O	S	0	0
			1105	708	203	194			

- Molecule 23 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AR	121	Total	C	N	O	S	0	0
			948	596	179	171	2		

- Molecule 24 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 25 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 26 is a protein called RPS20 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AU	100	Total	C	N	O	S	0	0
			797	506	144	146	1		

- Molecule 27 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AV	87	Total	C	N	O	S	0	0
			673	415	125	131	2		

- Molecule 28 is a protein called RPS22A isoform 1.

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

- Molecule 29 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 30 is a protein called 40S ribosomal protein S24-A.

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

- Molecule 31 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	AZ	82	Total	C	N	O	0	0
			651	416	123	112		

- Molecule 32 is a protein called 40S ribosomal protein S26.

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

- Molecule 33 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 34 is a protein called RPS28A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ac	63	Total	C	N	O	S	0	0
			491	303	96	91	1		

- Molecule 35 is a protein called RPS29A isoform 1.

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

- Molecule 36 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Ae	60	Total	C	N	O	S	0	0
			472	298	97	76	1		

- Molecule 37 is a protein called RPS31 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Af	73	Total	C	N	O	S	0	0
			556	352	105	95	4		

- Molecule 38 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ag	312	Total	C	N	O	S	0	0
			2383	1514	409	452	8		

- Molecule 39 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BA	251	Total	C	N	O	S	0	0
			1899	1182	385	331	1		

- Molecule 40 is a protein called 60S ribosomal protein L3.

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

- Molecule 41 is a protein called RPL4A isoform 1.

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

- Molecule 42 is a protein called RPL5 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BD	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 43 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BE	167	Total	C	N	O	S	0	0
			1305	841	234	229	1		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BE	146	ILE	LEU	conflict	UNP P05739
BE	173	MET	LEU	conflict	UNP P05739

- Molecule 44 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 45 is a protein called 60S ribosomal protein L8.

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

- Molecule 46 is a protein called RPL9A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BH	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 47 is a protein called RPL10 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BI	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 48 is a protein called RPL11B isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	BJ	169	1350	846	253	247	4	0	0

- Molecule 49 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	BK	193	1543	962	315	266		0	0

- Molecule 50 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 51 is a protein called Ribosomal protein L15.

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

- Molecule 52 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 53 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	BO	183	1416	879	284	253		0	0

- Molecule 54 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 55 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
55	BQ	188	1515	932	323	260	0	0

- Molecule 56 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	BR	171	1437	925	266	243	3	0	0

- Molecule 57 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 58 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
58	BT	100	796	516	131	149	0	0

- Molecule 59 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 60 is a protein called RPL24A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	BV	126	836	525	165	145	1	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BV	104	GLN	ASN	conflict	UNP A0A6A5PY83
BV	109	GLN	LEU	conflict	UNP A0A6A5PY83
BV	112	ASP	ASN	conflict	UNP A0A6A5PY83
BV	119	ALA	GLU	conflict	UNP A0A6A5PY83

- Molecule 61 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	BW	121	964	620	169	173	2	0	0

- Molecule 62 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	BX	125	984	620	191	173		0	0

- Molecule 63 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	BY	135	1092	710	202	180		0	0

- Molecule 64 is a protein called 60S ribosomal protein L28.

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

- Molecule 65 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	Ba	58	462	289	100	73		0	0

- Molecule 66 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	Bb	96	737	476	123	137	1	0	0

- Molecule 67 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	Bc	109	876	556	167	152	1	0	0

- Molecule 68 is a protein called RPL32 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	Bd	127	1017	644	205	167	1	0	0

- Molecule 69 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 70 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 71 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 72 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	Bh	99	766	478	154	132	2	0	0

- Molecule 73 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	Bi	85	670	408	146	111	5	0	0

- Molecule 74 is a protein called RPL38 isoform 1.

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

- Molecule 75 is a protein called 60S ribosomal protein L39.



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

- Molecule 76 is a protein called 60S ribosomal protein L40-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Bl	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 77 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Bm	25	Total	C	N	O	S	0	0
			229	139	62	27	1		

- Molecule 78 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Bn	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 79 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 80 is a protein called RQC trigger complex helicase SLH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	CA	1742	Total	C	N	O	S	0	0
			14008	8959	2378	2596	75		

- Molecule 81 is a protein called CUE3 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	CB	297	Total	C	N	O	S	0	0
			2415	1568	414	427	6		

- Molecule 82 is a protein called RQC trigger complex subunit RQT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
82	CC	114	886	539	167	172	8	0	0

- Molecule 83 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
83	2	84	Total 84	Mg 84	0
83	AC	1	Total 1	Mg 1	0
83	AQ	1	Total 1	Mg 1	0

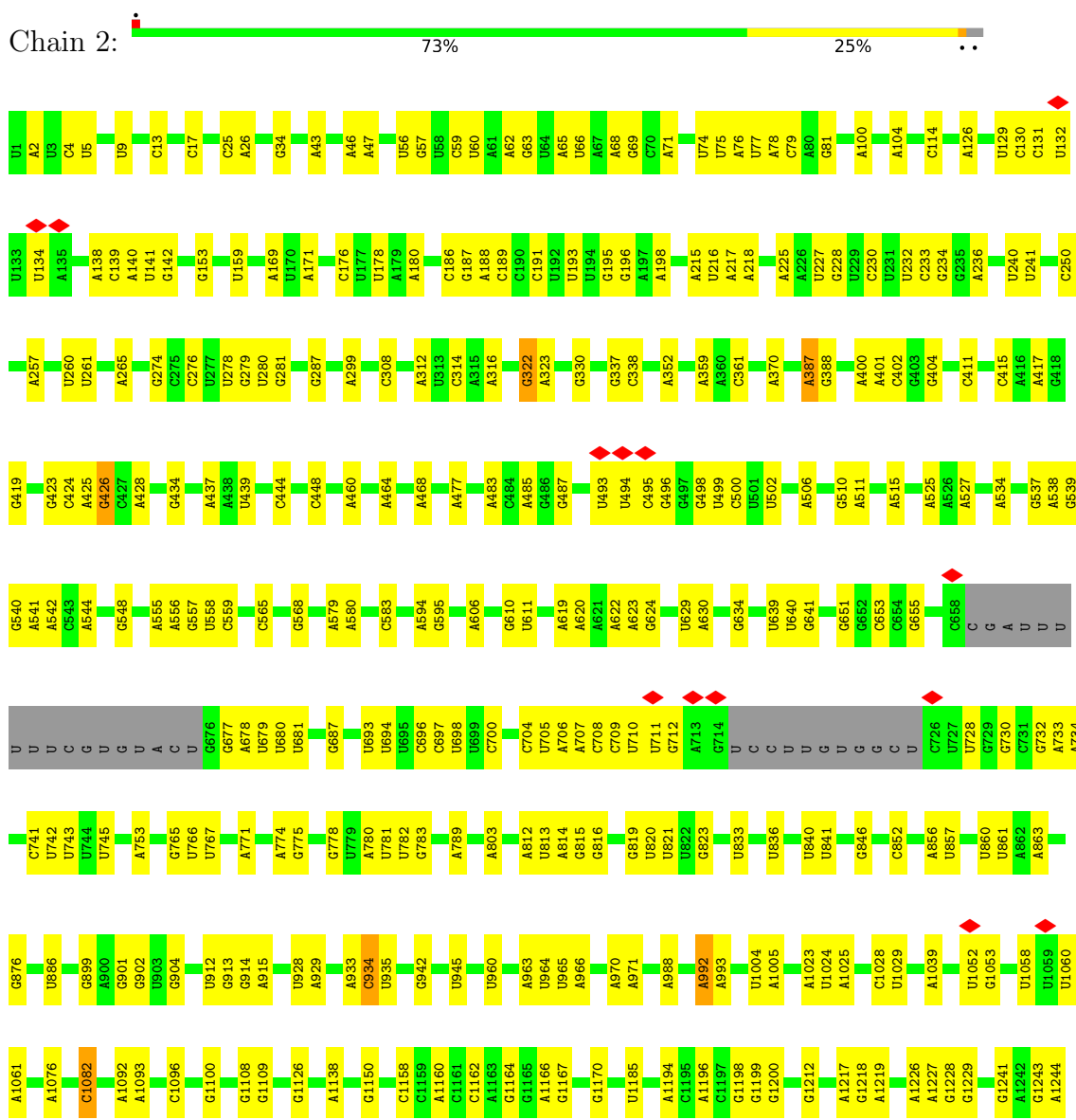
- Molecule 84 is ZINC ION (three-letter code: ZN) (formula: Zn).

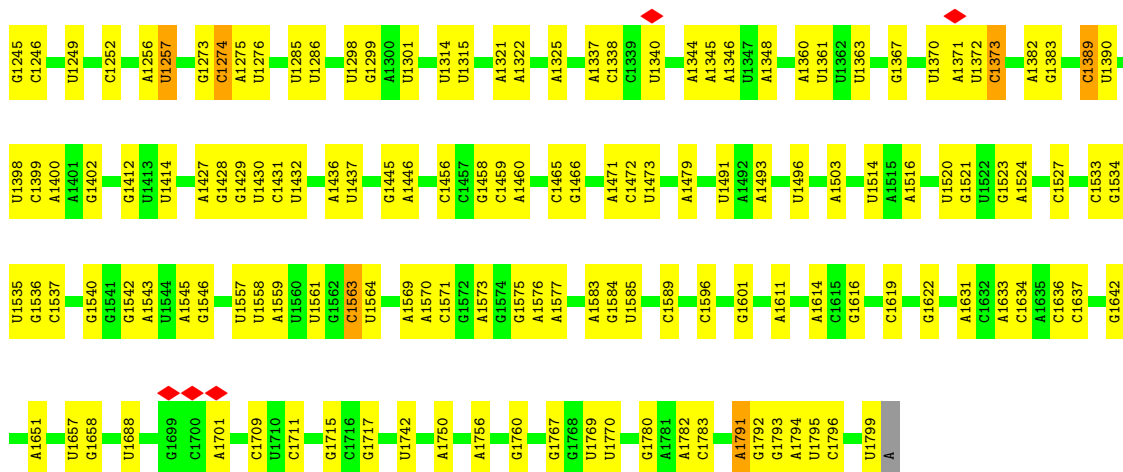
Mol	Chain	Residues	Atoms		AltConf
84	Ad	1	Total 1	Zn 1	0
84	Af	1	Total 1	Zn 1	0
84	Bf	1	Total 1	Zn 1	0
84	Bi	1	Total 1	Zn 1	0
84	Bl	1	Total 1	Zn 1	0
84	Bn	1	Total 1	Zn 1	0
84	Bo	1	Total 1	Zn 1	0
84	CC	2	Total 2	Zn 2	0

### 3 Residue-property plots [i](#)

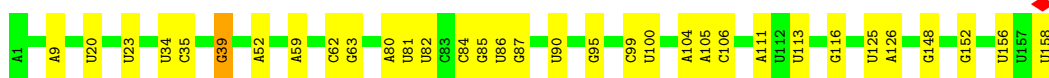
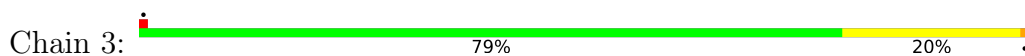
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 18S ribosomal RNA

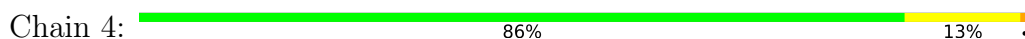




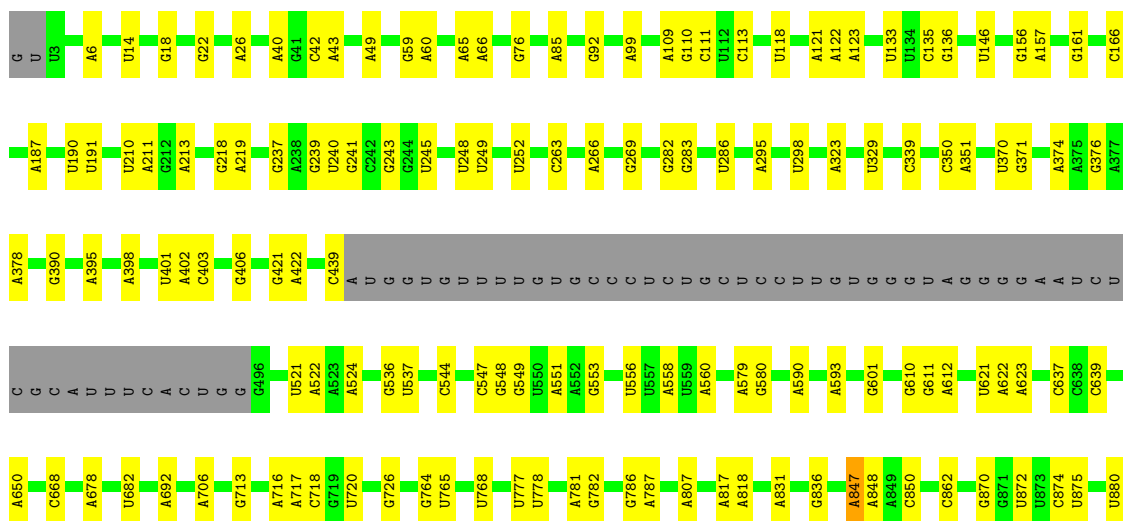
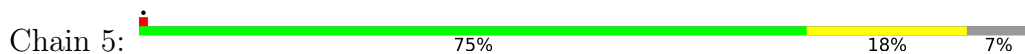
• Molecule 2: 5.8S ribosomal RNA



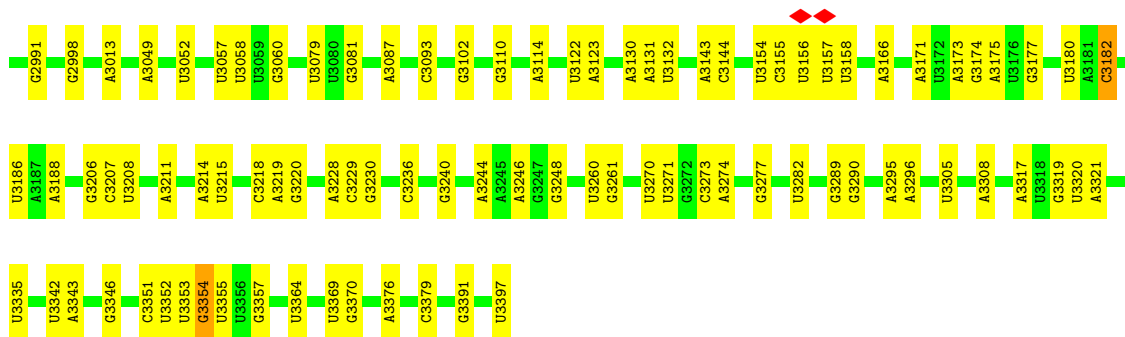
• Molecule 3: 5S ribosomal RNA



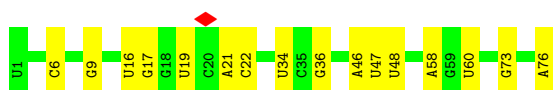
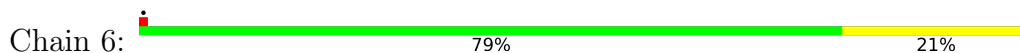
• Molecule 4: 25S ribosomal RNA



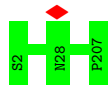
A2804	U2618	C2408	U2226	C	A1798	C1664	G1346	A1065	A1066	A889
C2811	A2627	U2412	C2238	U	A1815	U1568	U1349	A1066	A1066	A896
G2815	U2630	G2419	A2245	C	U1816	U1569	G1350	G1073	A896	A897
G2816	A2495	A2420	C2246	A	A1817	U1570	A1351	U1082	A897	G908
G2817	A2637	A	G2247	U	G1818	U1573	U1352	A1094	G908	G909
A2818	G2436	U	G2247	U	U1819	G1574	U1353	U1095	A915	A915
C2822	A2440	A2094	G2250	G	U1820	C1575	U1354	U1096	A916	A916
C2837	U2499	A2101	A2253	G	U1821	G1576	G1355	U1097	A917	A917
U2843	U2500	C2102	A2257	G	U1822	G1577	U1356	U1098	A918	A918
U2844	A2501	U2103	A2258	G	A1840	A1581	U1357	U1099	A919	A919
C2845	U2657	U2113	G2273	C	A1843	A1584	G1358	A1104	A922	A922
U2846	A2658	A2114	G2274	C	C1847	A1588	U1228	A1105	U923	U923
U2847	A2678	C2115	U2282	U	A1865	A1589	G1227	G1116	C924	C924
G2848	U2682	G2122	U2283	G	A1866	A1590	G1227	G1117	G995	G995
G2849	A2690	G2123	U2284	U	C1867	A1594	G1227	G1118	A926	A926
C2850	A2691	G2127	G2288	G	A1868	A1595	U1254	G1127	G938	G938
G2857	A2692	A2127	G2289	G	U1872	U1596	C1255	A1130	U940	U940
U2861	A2697	A2132	G2308	A	U1879	C1597	C1256	A1131	C945	C945
G2872	G2700	U2141	U2311	U	G1879	G1605	U0259	G1132	C960	C960
U2873	U2507	U2142	G2314	C	A1880	A1606	G1263	C1133	U961	U961
G2874	C3508	A2143	U2315	G	U1881	U1621	A1264	A1134	G975	G975
G2875	U2509	A2144	G2316	C	A1884	U1630	U1266	A1144	U980	U980
U2876	U2515	A2145	U2336	U	U1895	U1646	G1267	U1145	G995	G995
G2887	A2516	A2146	U2337	G	A1896	U1718	A1275	A1154	U996	U996
U2888	G2523	A2159	G2338	G	G1907	A1643	U1279	A1155	A1003	A1003
G2889	C2523	U2147	G2339	U	G1908	A1644	C1280	C1156	G1011	G1011
C2890	U2542	A2171	U2337	U	A1909	A1645	C1281	A1180	U1016	U1016
G2899	U2543	G2172	C2351	G	U1926	G1646	G1286	A1181	C1017	C1017
A2912	C3547	A2183	A2357	G	C1927	U1718	A1287	U1182	G1025	G1025
U2924	G2550	G2186	A2374	C	A1931	U1725	G1288	A1191	A1026	A1026
C2929	U2551	U2187	C2375	U	U1932	C1726	C1281	U1192	U1029	U1029
U2936	C2552	G2188	G2376	G	A1933	U1765	A1288	C1193	G1030	G1030
A2937	U2552	A2189	A2377	U	G1936	U1766	G1296	A1194	C1033	C1033
G2938	C2553	G2193	C2377	U	C1952	G1752	U1306	C1197	A1037	A1037
G2939	A2562	U2194	G2378	G	G1953	G1752	U1310	A1200	U1042	U1042
U2951	U2570	C2205	A2379	C	G1954	U1765	G1314	C1202	A1048	A1048
A2952	U2571	U2206	C2379	A	U1955	U1766	A1331	A1201	A1049	A1049
G2953	U2572	G2207	G2376	C	A	G1767	U1332	A1206	C1050	C1050
C2954	C2573	A2208	A2389	C	U	G1771	A1331	A1207	G1208	G1208
U2955	G2574	U2211	C2394	C	G	G1771	A1331	A1208	U1209	U1209
G2956	U2575	G2211	A2398	G	A	G1771	A1331	A1209		
A2957	U2576	A2223	G2399	C	U	G1771	A1331	A1209		
C2958	C2577	A2224	C2399	C	U	G1771	A1331	A1209		
U2959	G2578	A2225	G2399	C	G	G1771	A1331	A1209		
G2961	U2579	A2225	A2403	C	A	G1771	A1331	A1209		
C2962	U2580	A2225	A2404	C	U	G1771	A1331	A1209		
U2963	G2581	A2225	G2405	C	G	G1771	A1331	A1209		
A2964	U2582	A2225	A2405	C	G	G1771	A1331	A1209		
C2965	G2583	A2225	G2405	C	G	G1771	A1331	A1209		



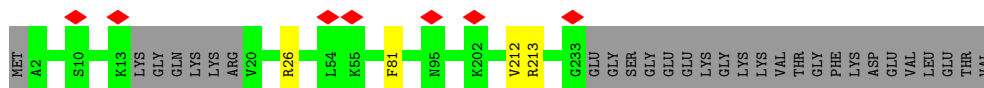
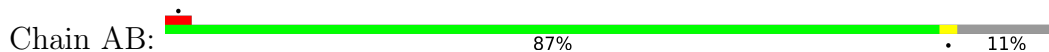
• Molecule 5: tRNA



• Molecule 6: 40S ribosomal protein S0-A



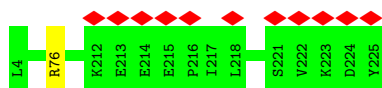
• Molecule 7: 40S ribosomal protein S1-A



• Molecule 8: RPS2 isoform 1



• Molecule 9: RPS3 isoform 1



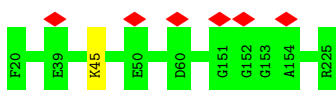
• Molecule 10: 40S ribosomal protein S4-A

Chain AE:  98%



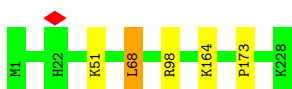
- Molecule 11: Rps5p

Chain AF:  100%



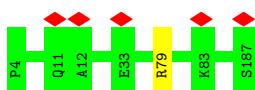
- Molecule 12: 40S ribosomal protein S6-A

Chain AG:  98%



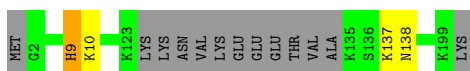
- Molecule 13: 40S ribosomal protein S7-A

Chain AH:  99%



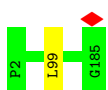
- Molecule 14: 40S ribosomal protein S8-B

Chain AI:  92% 6%



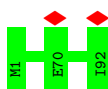
- Molecule 15: 40S ribosomal protein S9-A

Chain AJ:  99%

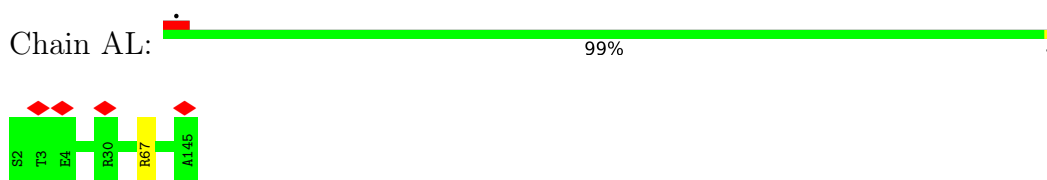


- Molecule 16: 40S ribosomal protein S10-A

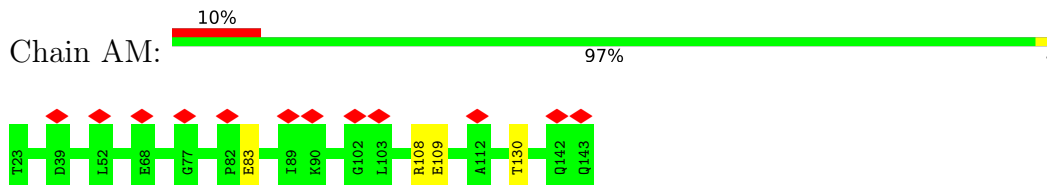
Chain AK:  100%



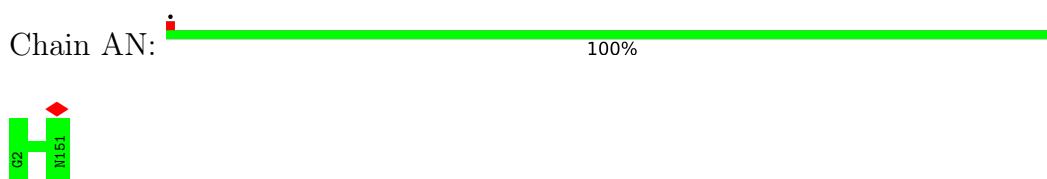
- Molecule 17: 40S ribosomal protein S11-A



- Molecule 18: 40S ribosomal protein S12



- Molecule 19: 40S ribosomal protein S13

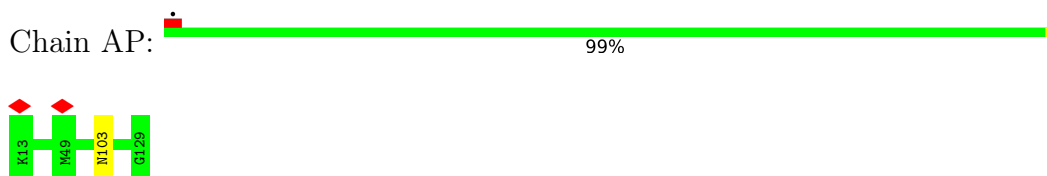


- Molecule 20: 40S ribosomal protein S14-B

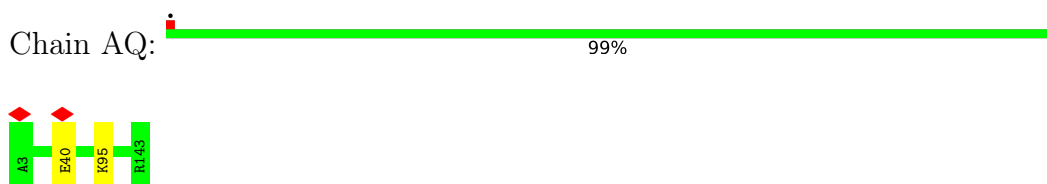


There are no outlier residues recorded for this chain.

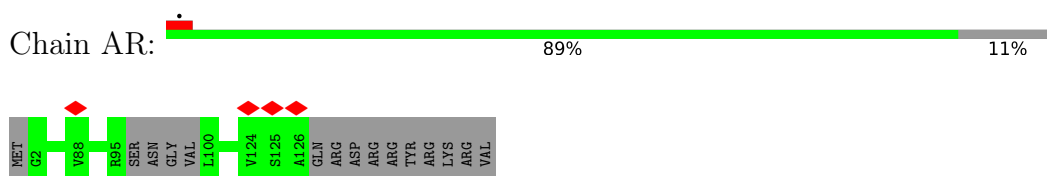
- Molecule 21: RPS15 isoform 1



- Molecule 22: 40S ribosomal protein S16-A



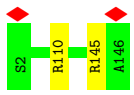
- Molecule 23: 40S ribosomal protein S17-A





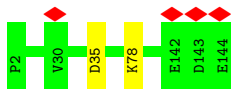
- Molecule 24: 40S ribosomal protein S18-A

Chain AS:  99%



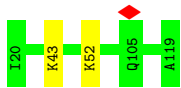
- Molecule 25: 40S ribosomal protein S19-A

Chain AT:  99%



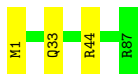
- Molecule 26: RPS20 isoform 1

Chain AU:  98%



- Molecule 27: 40S ribosomal protein S21-A

Chain AV:  97%



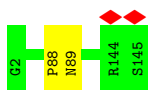
- Molecule 28: RPS22A isoform 1

Chain AW:  100%

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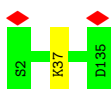
- Molecule 29: 40S ribosomal protein S23-A

Chain AX:  99%

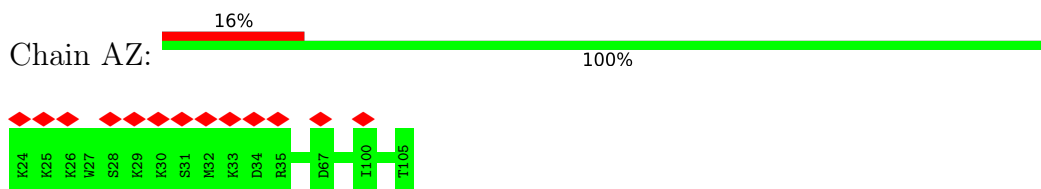


- Molecule 30: 40S ribosomal protein S24-A

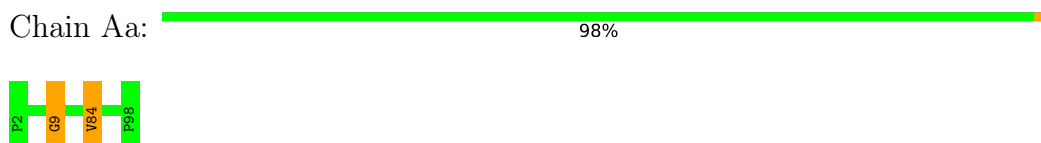
Chain AY:  99%



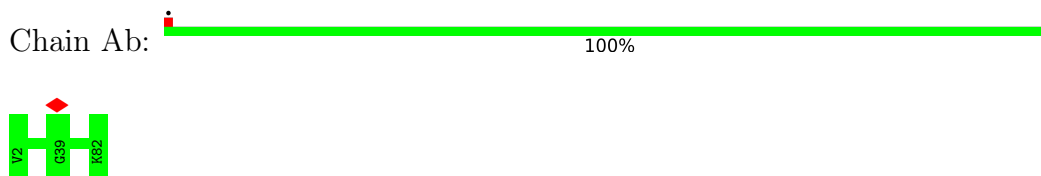
- Molecule 31: 40S ribosomal protein S25



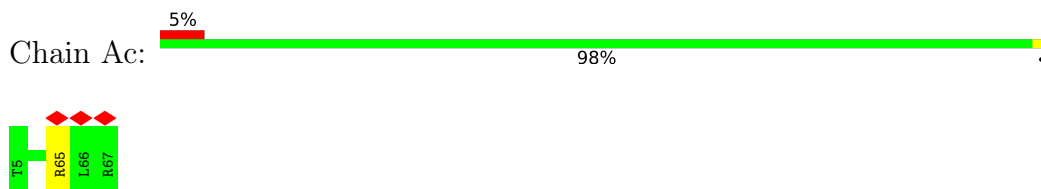
- Molecule 32: 40S ribosomal protein S26



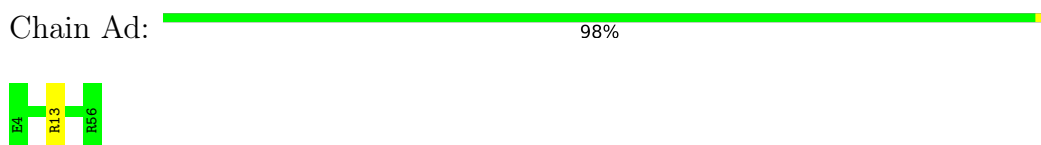
- Molecule 33: 40S ribosomal protein S27-A



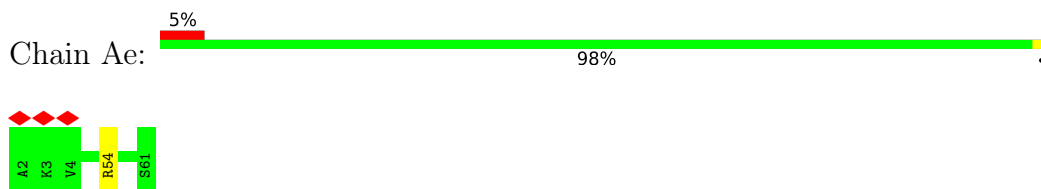
- Molecule 34: RPS28A isoform 1



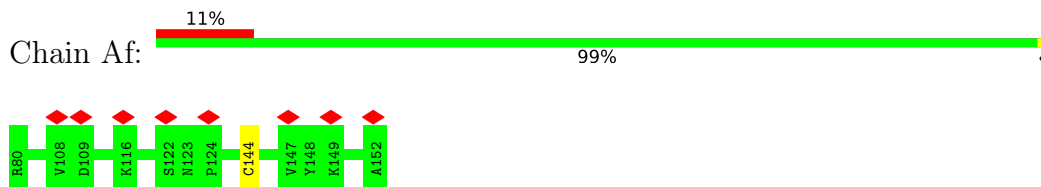
- Molecule 35: RPS29A isoform 1



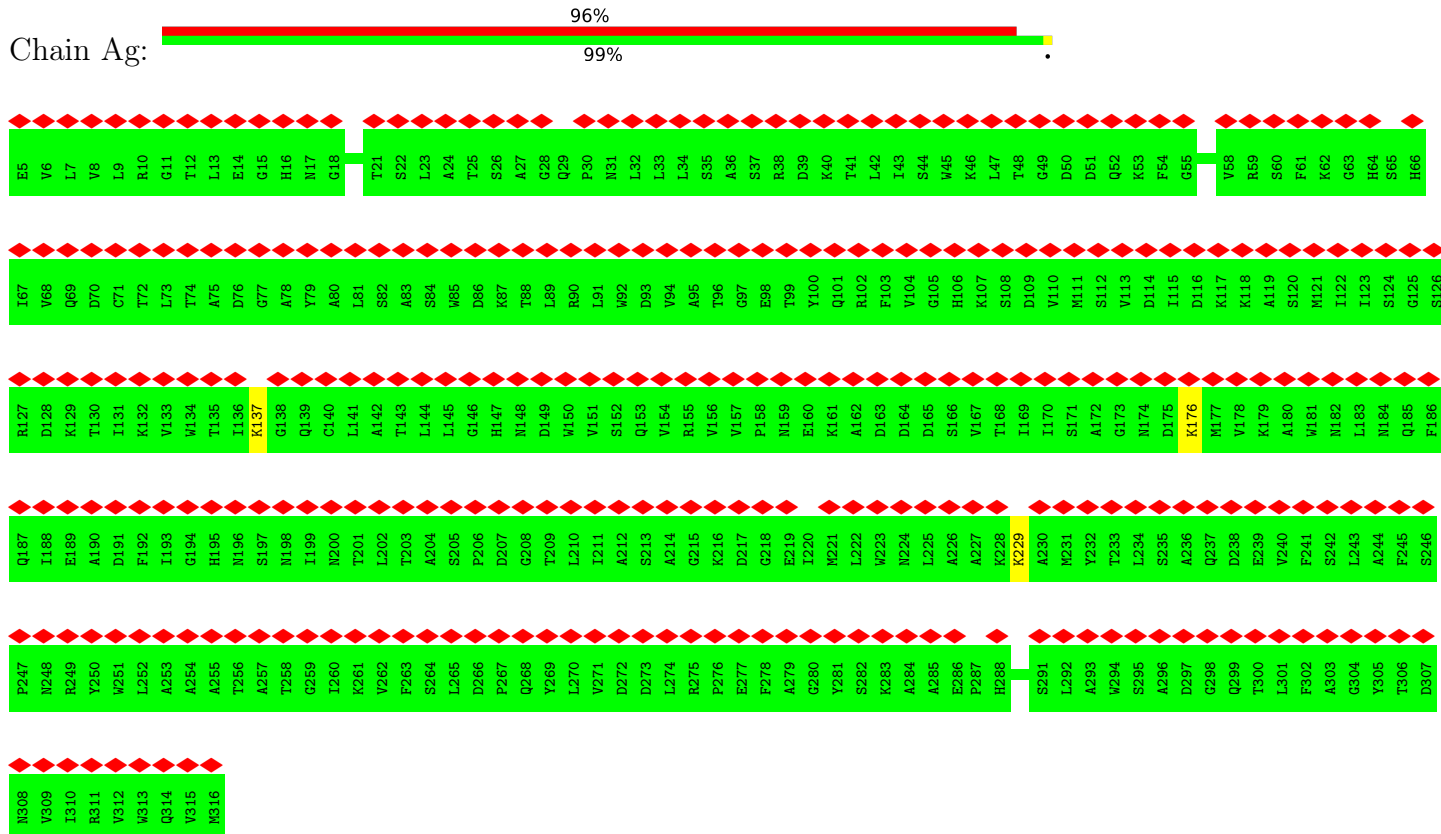
- Molecule 36: 40S ribosomal protein S30-A



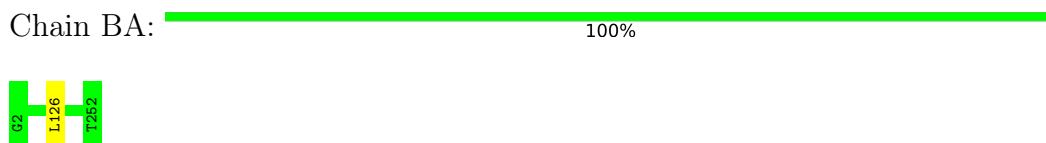
- Molecule 37: RPS31 isoform 1



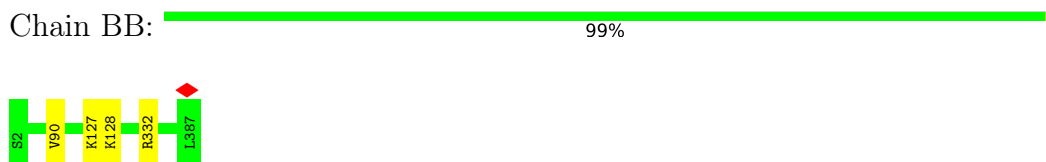
- Molecule 38: Guanine nucleotide-binding protein subunit beta-like protein



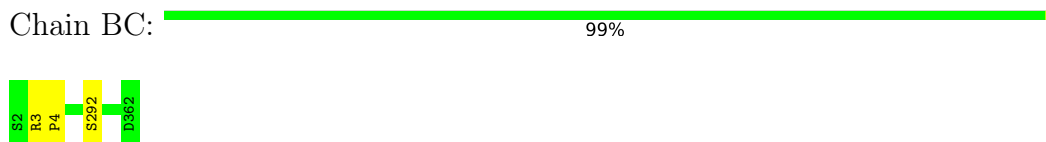
- Molecule 39: 60S ribosomal protein L2-A



- Molecule 40: 60S ribosomal protein L3

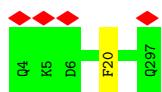


- Molecule 41: RPL4A isoform 1



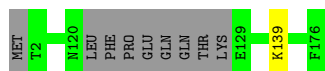
- Molecule 42: RPL5 isoform 1





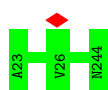
- Molecule 43: 60S ribosomal protein L6-B

Chain BE: 94% 5%



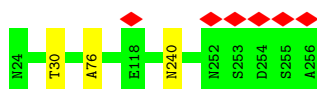
- Molecule 44: 60S ribosomal protein L7-A

Chain BF: 100%



- Molecule 45: 60S ribosomal protein L8

Chain BG: 99%



- Molecule 46: RPL9A isoform 1

Chain BH: 100%



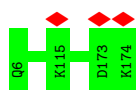
- Molecule 47: RPL10 isoform 1

Chain BI: 100%



- Molecule 48: RPL11B isoform 1

Chain BJ: 100%



- Molecule 49: 60S ribosomal protein L13-A

Chain BK:  97%



- Molecule 50: 60S ribosomal protein L14-A

Chain BL:  100%



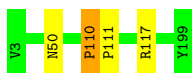
- Molecule 51: Ribosomal protein L15

Chain BM:  100%



- Molecule 52: 60S ribosomal protein L16-A

Chain BN:  98%



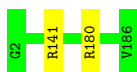
- Molecule 53: 60S ribosomal protein L17-A

Chain BO:  100%



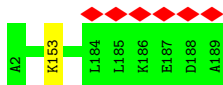
- Molecule 54: 60S ribosomal protein L18-A

Chain BP:  99%



- Molecule 55: 60S ribosomal protein L19-A

Chain BQ:  99%



- Molecule 56: 60S ribosomal protein L20-A

Chain BR:  100%

There are no outlier residues recorded for this chain.

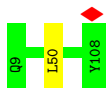
- Molecule 57: 60S ribosomal protein L21-A

Chain BS:  100%

There are no outlier residues recorded for this chain.

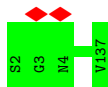
- Molecule 58: 60S ribosomal protein L22-A

Chain BT:  99%



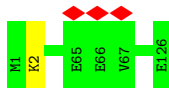
- Molecule 59: 60S ribosomal protein L23-A

Chain BU:  100%



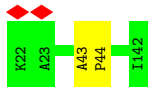
- Molecule 60: RPL24A isoform 1

Chain BV:  99%



- Molecule 61: 60S ribosomal protein L25

Chain BW:  98%



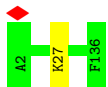
- Molecule 62: 60S ribosomal protein L26-A

Chain BX:  99%



- Molecule 63: 60S ribosomal protein L27-A

Chain BY:  99%



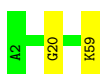
- Molecule 64: 60S ribosomal protein L28

Chain BZ: 99%



- Molecule 65: 60S ribosomal protein L29

Chain Ba: 97%



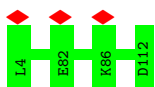
- Molecule 66: 60S ribosomal protein L30

Chain Bb: 100%

There are no outlier residues recorded for this chain.

- Molecule 67: 60S ribosomal protein L31-A

Chain Bc: 100%



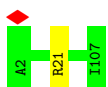
- Molecule 68: RPL32 isoform 1

Chain Bd: 100%



- Molecule 69: 60S ribosomal protein L33-A

Chain Be: 99%



- Molecule 70: 60S ribosomal protein L34-A

Chain Bf: 100%



- Molecule 71: 60S ribosomal protein L35-A



- Molecule 72: 60S ribosomal protein L36-A

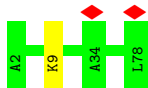


- Molecule 73: 60S ribosomal protein L37-A



There are no outlier residues recorded for this chain.

- Molecule 74: RPL38 isoform 1



- Molecule 75: 60S ribosomal protein L39



There are no outlier residues recorded for this chain.

- Molecule 76: 60S ribosomal protein L40-A



- Molecule 77: 60S ribosomal protein L41

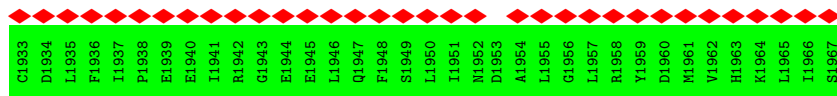


There are no outlier residues recorded for this chain.

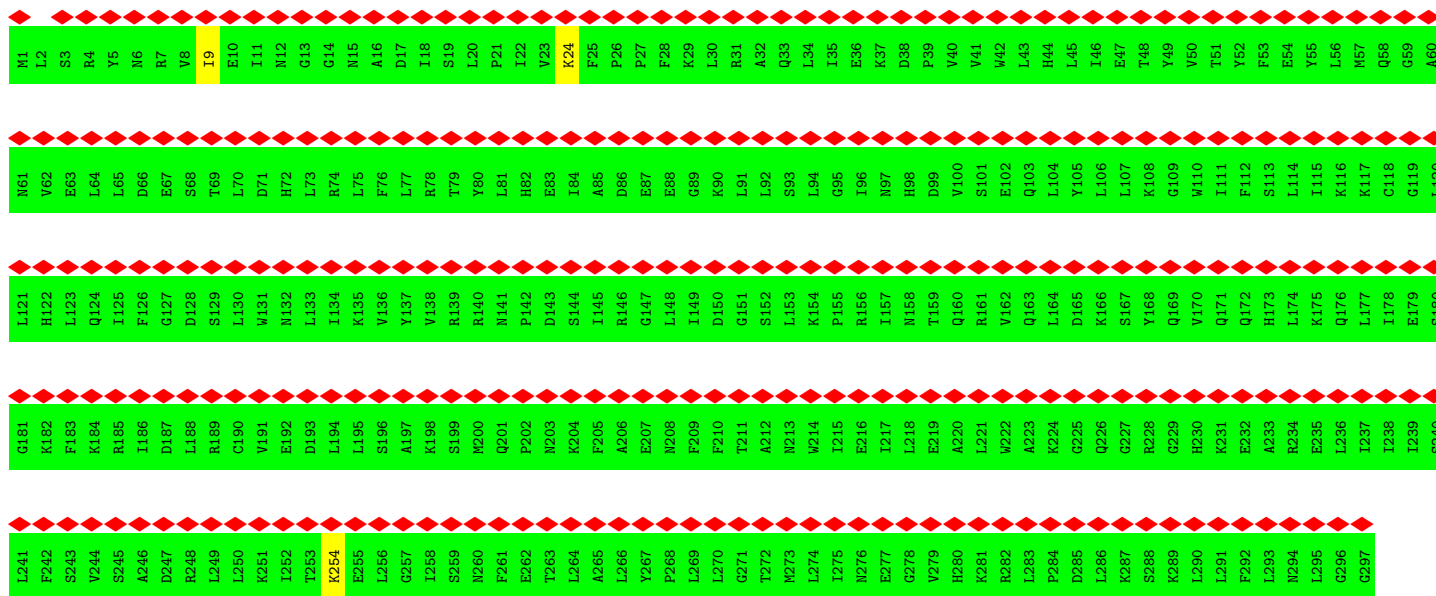




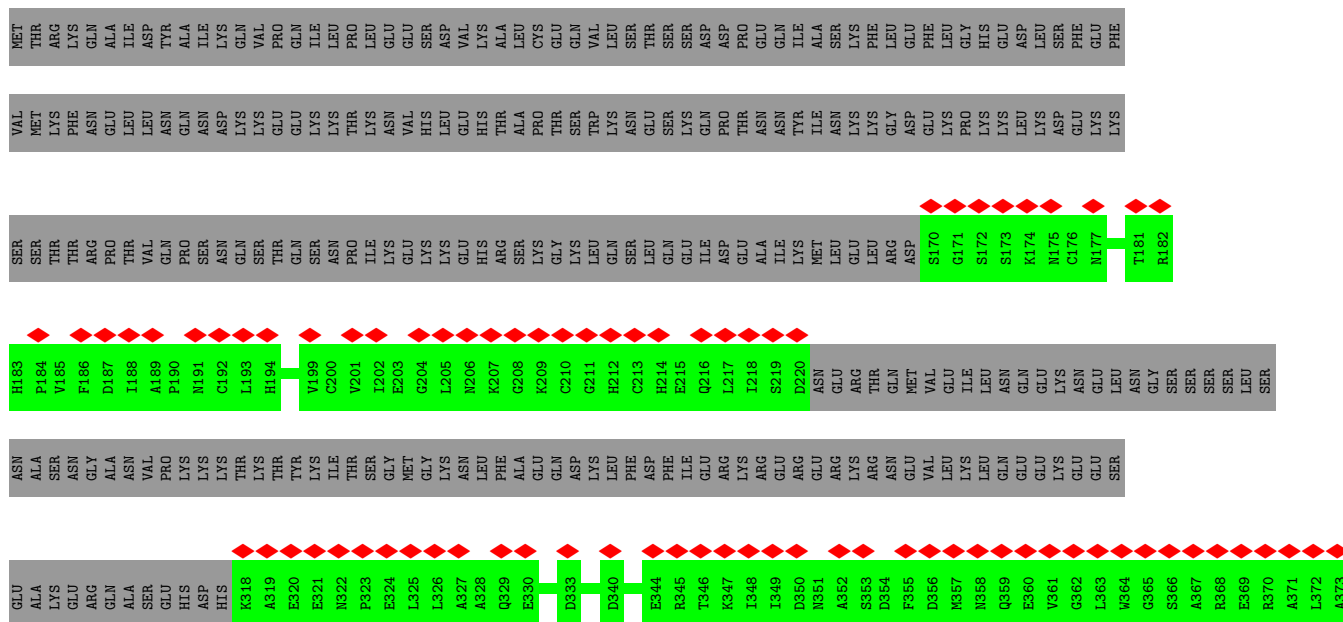
G708	G709	K710	D713	S720	L721	D728	E729	A730	E731	L734	M739	F740	R744	K745	T749	Y750	G751	W754	W759	Q762	L763	Y764	E765	R766	R767	R768	K769	M770	R777	L778	H779	A780	L781	F786	D787	E788	F793	F805	Y806	L807	L808	E813	C819																																																		
R822	A823	A826	L829	M834	F838	D839	G840	I841	K842	R843	E845	E846	R849	K852	S855	D856	I863	C864	S865	D866	F888	D889	S890	R968	D959	T960	K961	E977	L1048	L1060	S1073	D1074	T1113	K1114	L1115	L1116	K1117	L1118	R1119	P1120	L1121	P1122																																																			
T1123	S1124	A1125	L1126	Q1127	N1128	P1129	L1130	I1131	E1132	S1133	I1134	Y1135	P1136	F1137	K1138	M1146	T1147	F1148	N1155	F1159	T1164	G1165	S1166	G1167	K1168	A1172	E1173	H1178	A1179	F1180	K1181	T1182	F1183	P1184	K1185	G1186	K1187	I1188	Y1189	V1190	I1191	A1192	P1193	L1197	D1203	D1204	W1205	R1206	K1207	I1209																																											
T1210	P1211	V1212	T1213	K1214	D1215	K1216	V1217	V1218	E1219	L1220	T1221	G1222	S1224	L1225	P1226	D1227	P1228	K1229	D1230	V1231	H1232	D1233	A1234	L1235	I1236	V1237	I1238	P1241	F1244	I1247	W1251	Q1252	T1253	R1254	K1255	F1256	V1257	Q1258	D1259	V1260	S1261	L1262	I1263	M1265	E1267	I1268	A1272	S1273	D1274	R1275	G1276																																										
M1281	R1285	T1283	K1284	Q1285	P1286	V1287	R1288	L1289	L1300	V1306	K1319	D1320	L1323	P1327	S1328	S1329	V1330	R1331	P1332	V1333	P1334	I1339	D1340	G1341	F1342	P1343	D1344	A1347	F1348	K1353	T1354	M1355	F1360	M1361	Q1365	H1366	D1369	K1370	P1371	L1373	I1374	F1375	V1376	A1377	S1378	Q1381	R1382	T1385	L1392	M1395	E1396	D1397	N1398	P1399	R1400	F1402	L1403	N1404	I1405	D1406	D1407	E1408	E1409	E1410	L1411	Y1413	Y1414	L1415	S1416	Q1417	V1418	F1419	T1419	D1420	L1427	I1431	L1432	H1434	H1435	A1436	L1438	V1439	Q1440	K1441	D1442	R1443	I1444	F1450	Q1451	K1452	N1453	K1454	I1457
L1458	I1459	A1460	T1461	S1462	T1463	L1464	A1465	M1466	G1467	V1468	N1469	L1470	P1471	A1472	H1473	K1478	G1479	T1480	K1481	F1482	F1483	D1484	A1485	K1486	I1487	E1488	D1489	Y1490	R1491	D1492	M1493	D1494	L1495	T1496	L1499	Q1500	M1501	M1502	G1503	R1504	A1505	A1509	T1512	T1513	G1514	L1515	A1516	S1523	K1524	K1525	Y1526	V1534																																									
S1540	H1543	K1544	V1545	L1546	D1547	D1548	H1549	L1550	G1551	A1552	E1553	S1556	G1557	S1558	I1559	T1560	M1561	K1562	Q1563	W1571	Y1585	D1589	D1590	T1591	S1592	T1593	A1594	E1598	H1599	D1605	L1608	E1609	M1610	L1611	R1612	E1613	S1614	G1616	L1617	L1618	L1619	H1620	G1621	D1622	D1623	A1626	T1627	P1628																																													
F1629	L1630	S1631	I1632	S1633	Y1636	I1637	I1638	S1639	H1640	L1641	T1642	I1643	R1644	Q1645	L1646	L1647	K1648	Q1649	I1650	H1651	D1652	H1653	F1656	Q1657	E1658	V1659	L1660	R1661	W1662	L1663	S1664	L1665	A1666	V1667	E1668	M1670	E1671	L1672	P1673	V1674	R1675	G1676	G1677	E1678	I1679	I1680	M1681	M1682	E1683	E1684	M1685	S1686	Q1687	Q1688	Y1691																																						
S1692	V1693	E1694	S1695	T1696	F1697	T1698	D1699	E1700	F1701	E1702	L1703	P1704	M1705	W1706	D1707	P1708	H1709	V1710	K1711	T1712	F1713	L1714	L1715	L1716	Q1717	A1718	H1719	L1720	S1721	R1722	V1723	D1724	L1725	P1726	I1727	A1728	D1729	Y1730	I1731	Q1732	D1733	T1734	V1735	S1736	L1737	L1738	D1739	L1742	R1743	I1744	L1745	Q1746	A1747	I1748	I1749	D1750	V1751	A1752																																			
S1753	E1754	L1755	G1756	Y1757	F1758	H1759	T1760	V1761	L1762	T1763	M1764	I1765	K1766	M1767	M1768	Q1769	C1770	I1771	K1772	Q1773	G1774	Y1775	W1776	Y1777	E1778	D1779	L1780	P1781	V1782	S1783	Y1784	L1785	P1786	G1787	L1788	Q1789	L1790	R1791	R1792	I1793	K1794	L1795	Y1796	T1797	F1798	S1799	E1800	Q1801	G1802	I1804	E1805	M1806	T1807	P1808	Q1809	Q1810	K1811	K1812																																			
K1813	K1814	L1815	L1816	L1817	L1818	E1819	E1820	I1821	L1822	R1823	F1824	G1825	Y1826	K1827	K1828	C1829	I1830	M1831	V1832	F1833	G1834	Y1835	L1836	L1837	F1838	G1839	M1840	T1841	E1842	S1843	E1844	D1845	L1846	K1847	K1848	R1849	F1850	V1851	S1852	V1853	C1854	Q1855	R1856	L1857	P1858	V1859	L1860	E1861	F1862	M1863	K1864	F1865	M1866	I1867	P1868	E1869	N1870	N1871	E1872																																		
L1873	L1874	T1875	F1876	S1877	L1878	K1879	H1880	L1881	S1882	S1883	K1884	H1885	N1886	N1887	K1888	F1889	E1890	V1891	Y1892	C1893	D1894	K1895	F1896	R1897	K1898	I1899	Q1900	E1901	L1902	L1903	W1904	F1905	L1906	I1907	G1908	H1909	G1910	V1911	D1912	E1913	L1914	L1915	M1916	I1917	K1918	R1919	Q1920	Q1921	P1922	K1923	Q1924	M1925	N1926	K1927	E1928	V1929	I1930	I1931	E1932																																		



● Molecule 81: CUE3 isoform 1



● Molecule 82: RQC trigger complex subunit RQT4





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	17885	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 ( $e^-/\text{\AA}^2$ )	44	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	4.383	Depositor
Minimum map value	-1.015	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.109	Depositor
Recommended contour level	0.3	Depositor
Map size ( $\text{\AA}$ )	585.19995, 585.19995, 585.19995	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.045, 1.045, 1.045	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, MG

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	2	0.93	1/42211 (0.0%)	0.94	40/65773 (0.1%)
2	3	1.07	0/3746	0.93	2/5832 (0.0%)
3	4	0.92	0/2883	0.95	5/4491 (0.1%)
4	5	1.16	6/75723 (0.0%)	0.97	50/118057 (0.0%)
5	6	0.66	0/1808	0.86	2/2816 (0.1%)
6	AA	0.39	0/1644	0.56	0/2249
7	AB	0.39	0/1823	0.60	0/2447
8	AC	0.47	0/1656	0.58	0/2251
9	AD	0.40	0/1754	0.58	0/2361
10	AE	0.45	0/2097	0.60	1/2823 (0.0%)
11	AF	0.37	0/1625	0.59	0/2197
12	AG	0.37	0/1839	0.60	1/2460 (0.0%)
13	AH	0.34	0/1498	0.56	0/2019
14	AI	0.49	0/1501	0.66	0/2006
15	AJ	0.44	0/1504	0.61	0/2016
16	AK	0.40	0/769	0.62	0/1039
17	AL	0.52	0/1185	0.57	0/1598
18	AM	0.28	0/883	0.59	0/1199
19	AN	0.46	0/1215	0.60	0/1638
20	AO	0.42	0/937	0.68	0/1261
21	AP	0.33	0/936	0.59	0/1259
22	AQ	0.40	0/1125	0.61	0/1510
23	AR	0.34	0/957	0.61	0/1283
24	AS	0.36	0/1211	0.61	0/1628
25	AT	0.35	0/1130	0.62	1/1517 (0.1%)
26	AU	0.39	0/807	0.56	0/1091
27	AV	0.45	0/682	0.62	0/921
28	AW	0.47	0/1038	0.63	0/1395
29	AX	0.52	0/1139	0.63	0/1518
30	AY	0.42	0/1087	0.59	0/1449
31	AZ	0.31	0/661	0.64	0/888
32	Aa	0.45	0/782	0.68	0/1047

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Ab	0.40	0/620	0.62	0/838
34	Ac	0.39	0/493	0.73	0/663
35	Ad	0.46	0/452	0.64	0/600
36	Ae	0.37	0/480	0.62	0/639
37	Af	0.31	0/567	0.59	0/764
38	Ag	0.27	0/2436	0.55	0/3318
39	BA	0.56	0/1933	0.64	0/2598
40	BB	0.52	0/3146	0.60	0/4228
41	BC	0.52	0/2800	0.61	0/3790
42	BD	0.43	0/2400	0.55	0/3239
43	BE	0.40	0/1327	0.53	0/1790
44	BF	0.53	0/1821	0.55	0/2451
45	BG	0.39	0/1836	0.54	0/2481
46	BH	0.45	0/1529	0.58	0/2060
47	BI	0.52	0/1801	0.60	0/2416
48	BJ	0.39	0/1371	0.60	0/1838
49	BK	0.45	0/1568	0.63	0/2106
50	BL	0.39	0/1068	0.57	0/1438
51	BM	0.57	0/1757	0.63	0/2354
52	BN	0.54	0/1585	0.58	0/2128
53	BO	0.57	0/1439	0.62	0/1938
54	BP	0.52	0/1465	0.64	0/1965
55	BQ	0.47	0/1532	0.60	0/2043
56	BR	0.53	0/1473	0.61	0/1980
57	BS	0.52	0/1300	0.59	0/1743
58	BT	0.45	0/812	0.62	1/1099 (0.1%)
59	BU	0.57	0/1018	0.61	0/1369
60	BV	0.45	0/850	0.55	0/1152
61	BW	0.48	0/979	0.60	0/1321
62	BX	0.47	0/995	0.61	0/1329
63	BY	0.41	0/1118	0.55	0/1497
64	BZ	0.57	0/1204	0.62	0/1612
65	Ba	0.41	0/473	0.55	0/629
66	Bb	0.46	0/745	0.50	0/1001
67	Bc	0.52	0/890	0.63	0/1196
68	Bd	0.54	0/1038	0.61	0/1390
69	Be	0.58	0/868	0.61	0/1168
70	Bf	0.50	0/890	0.61	0/1189
71	Bg	0.42	0/978	0.57	0/1301
72	Bh	0.37	0/772	0.60	0/1026
73	Bi	0.59	0/685	0.65	0/908
74	Bj	0.37	0/618	0.58	0/826
75	Bk	0.51	0/443	0.64	0/588

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	B1	0.48	0/423	0.64	0/562
77	Bm	0.51	0/230	0.77	0/296
78	Bn	0.49	0/836	0.60	0/1104
79	Bo	0.58	0/701	0.62	0/934
80	CA	0.27	0/14309	0.49	0/19348
81	CB	0.23	0/2463	0.46	0/3324
82	CC	0.24	0/897	0.53	0/1203
All	All	0.84	7/233290 (0.0%)	0.82	103/340819 (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
7	AB	0	1
10	AE	0	1
12	AG	0	1
14	AI	0	1
18	AM	0	3
22	AQ	0	1
29	AX	0	1
32	Aa	0	2
37	Af	0	1
38	Ag	0	1
40	BB	0	1
41	BC	0	1
45	BG	0	2
49	BK	0	1
52	BN	0	1
61	BW	0	1
64	BZ	0	1
65	Ba	0	1
All	All	0	22

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	5	2408	C	N1-C6	-6.41	1.33	1.37
4	5	1134	A	N9-C4	-6.33	1.34	1.37
4	5	2183	A	N9-C4	-6.12	1.34	1.37
4	5	889	A	N9-C4	-6.04	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	5	2186	G	C5-C4	-5.39	1.34	1.38

The worst 5 of 103 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	934	C	C2-N1-C1'	8.82	128.50	118.80
1	2	1533	C	N3-C2-O2	-7.92	116.35	121.90
4	5	3058	U	N3-C2-O2	-7.83	116.72	122.20
1	2	1527	C	C2-N1-C1'	7.82	127.40	118.80
1	2	934	C	N1-C2-O2	7.45	123.37	118.90

There are no chirality outliers.

5 of 22 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	AB	81	PHE	Peptide
10	AE	42	LEU	Peptide
12	AG	68	LEU	Peptide
14	AI	9	HIS	Peptide
18	AM	83	GLU	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
6	AA	204/206 (99%)	186 (91%)	18 (9%)	0	100 100
7	AB	222/255 (87%)	207 (93%)	13 (6%)	2 (1%)	17 56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	AC	214/216 (99%)	204 (95%)	10 (5%)	0	100	100
9	AD	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
10	AE	256/258 (99%)	237 (93%)	18 (7%)	1 (0%)	34	72
11	AF	204/206 (99%)	197 (97%)	7 (3%)	0	100	100
12	AG	226/228 (99%)	212 (94%)	13 (6%)	1 (0%)	34	72
13	AH	182/184 (99%)	171 (94%)	11 (6%)	0	100	100
14	AI	183/200 (92%)	167 (91%)	14 (8%)	2 (1%)	14	52
15	AJ	182/184 (99%)	171 (94%)	10 (6%)	1 (0%)	29	68
16	AK	90/92 (98%)	86 (96%)	4 (4%)	0	100	100
17	AL	142/144 (99%)	134 (94%)	8 (6%)	0	100	100
18	AM	119/121 (98%)	95 (80%)	23 (19%)	1 (1%)	19	60
19	AN	148/150 (99%)	141 (95%)	7 (5%)	0	100	100
20	AO	125/127 (98%)	114 (91%)	11 (9%)	0	100	100
21	AP	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
22	AQ	139/141 (99%)	127 (91%)	12 (9%)	0	100	100
23	AR	117/136 (86%)	113 (97%)	4 (3%)	0	100	100
24	AS	143/145 (99%)	130 (91%)	13 (9%)	0	100	100
25	AT	141/143 (99%)	130 (92%)	11 (8%)	0	100	100
26	AU	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
27	AV	85/87 (98%)	72 (85%)	13 (15%)	0	100	100
28	AW	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
29	AX	142/144 (99%)	129 (91%)	12 (8%)	1 (1%)	22	62
30	AY	132/134 (98%)	124 (94%)	7 (5%)	1 (1%)	19	60
31	AZ	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
32	Aa	95/97 (98%)	77 (81%)	16 (17%)	2 (2%)	7	39
33	Ab	79/81 (98%)	72 (91%)	7 (9%)	0	100	100
34	Ac	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
35	Ad	51/53 (96%)	49 (96%)	2 (4%)	0	100	100
36	Ae	58/60 (97%)	54 (93%)	4 (7%)	0	100	100
37	Af	71/73 (97%)	62 (87%)	9 (13%)	0	100	100
38	Ag	310/312 (99%)	300 (97%)	10 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	BA	249/251 (99%)	236 (95%)	12 (5%)	1 (0%)	34	72
40	BB	384/386 (100%)	361 (94%)	22 (6%)	1 (0%)	41	76
41	BC	359/361 (99%)	338 (94%)	19 (5%)	2 (1%)	25	65
42	BD	292/294 (99%)	280 (96%)	11 (4%)	1 (0%)	41	76
43	BE	163/176 (93%)	158 (97%)	5 (3%)	0	100	100
44	BF	220/222 (99%)	209 (95%)	11 (5%)	0	100	100
45	BG	231/233 (99%)	217 (94%)	14 (6%)	0	100	100
46	BH	189/191 (99%)	183 (97%)	6 (3%)	0	100	100
47	BI	216/218 (99%)	210 (97%)	6 (3%)	0	100	100
48	BJ	167/169 (99%)	154 (92%)	13 (8%)	0	100	100
49	BK	191/193 (99%)	176 (92%)	13 (7%)	2 (1%)	15	54
50	BL	134/136 (98%)	126 (94%)	8 (6%)	0	100	100
51	BM	201/203 (99%)	189 (94%)	12 (6%)	0	100	100
52	BN	195/197 (99%)	189 (97%)	4 (2%)	2 (1%)	15	54
53	BO	181/183 (99%)	172 (95%)	9 (5%)	0	100	100
54	BP	183/185 (99%)	174 (95%)	9 (5%)	0	100	100
55	BQ	186/188 (99%)	177 (95%)	9 (5%)	0	100	100
56	BR	169/171 (99%)	165 (98%)	4 (2%)	0	100	100
57	BS	157/159 (99%)	147 (94%)	10 (6%)	0	100	100
58	BT	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
59	BU	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
60	BV	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
61	BW	119/121 (98%)	114 (96%)	4 (3%)	1 (1%)	19	60
62	BX	123/125 (98%)	121 (98%)	2 (2%)	0	100	100
63	BY	133/135 (98%)	129 (97%)	4 (3%)	0	100	100
64	BZ	146/148 (99%)	135 (92%)	10 (7%)	1 (1%)	22	62
65	Ba	56/58 (97%)	49 (88%)	7 (12%)	0	100	100
66	Bb	94/96 (98%)	93 (99%)	1 (1%)	0	100	100
67	Bc	107/109 (98%)	99 (92%)	8 (8%)	0	100	100
68	Bd	125/127 (98%)	120 (96%)	5 (4%)	0	100	100
69	Be	104/106 (98%)	102 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
70	Bf	110/112 (98%)	107 (97%)	3 (3%)	0	100	100
71	Bg	117/119 (98%)	113 (97%)	4 (3%)	0	100	100
72	Bh	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
73	Bi	83/85 (98%)	80 (96%)	3 (4%)	0	100	100
74	Bj	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
75	Bk	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
76	Bl	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
77	Bm	23/25 (92%)	23 (100%)	0	0	100	100
78	Bn	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
79	Bo	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
80	CA	1738/1967 (88%)	1664 (96%)	70 (4%)	4 (0%)	47	81
81	CB	295/297 (99%)	291 (99%)	3 (1%)	1 (0%)	41	76
82	CC	110/530 (21%)	107 (97%)	3 (3%)	0	100	100
All	All	13127/14000 (94%)	12439 (95%)	660 (5%)	28 (0%)	50	81

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	AI	10	LYS
32	Aa	84	VAL
52	BN	111[A]	PRO
80	CA	224	THR
80	CA	621	VAL

### 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	
6	AA	170/173 (98%)	170 (100%)	0	100	100
7	AB	200/224 (89%)	199 (100%)	1 (0%)	88	93
8	AC	175/175 (100%)	175 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	AD	182/182 (100%)	181 (100%)	1 (0%)	88	93
10	AE	220/220 (100%)	218 (99%)	2 (1%)	78	88
11	AF	172/173 (99%)	171 (99%)	1 (1%)	86	92
12	AG	189/195 (97%)	186 (98%)	3 (2%)	62	79
13	AH	163/165 (99%)	162 (99%)	1 (1%)	86	92
14	AI	148/161 (92%)	146 (99%)	2 (1%)	67	81
15	AJ	156/157 (99%)	156 (100%)	0	100	100
16	AK	77/85 (91%)	77 (100%)	0	100	100
17	AL	129/129 (100%)	128 (99%)	1 (1%)	81	89
18	AM	88/98 (90%)	88 (100%)	0	100	100
19	AN	127/127 (100%)	127 (100%)	0	100	100
20	AO	91/96 (95%)	91 (100%)	0	100	100
21	AP	95/98 (97%)	94 (99%)	1 (1%)	73	85
22	AQ	117/117 (100%)	116 (99%)	1 (1%)	78	88
23	AR	101/124 (82%)	101 (100%)	0	100	100
24	AS	128/128 (100%)	126 (98%)	2 (2%)	62	79
25	AT	115/115 (100%)	114 (99%)	1 (1%)	78	88
26	AU	93/93 (100%)	91 (98%)	2 (2%)	52	71
27	AV	71/74 (96%)	68 (96%)	3 (4%)	30	55
28	AW	110/110 (100%)	110 (100%)	0	100	100
29	AX	119/119 (100%)	119 (100%)	0	100	100
30	AY	112/112 (100%)	112 (100%)	0	100	100
31	AZ	67/73 (92%)	67 (100%)	0	100	100
32	Aa	83/83 (100%)	83 (100%)	0	100	100
33	Ab	70/70 (100%)	70 (100%)	0	100	100
34	Ac	55/56 (98%)	54 (98%)	1 (2%)	59	77
35	Ad	47/47 (100%)	46 (98%)	1 (2%)	53	72
36	Ae	50/51 (98%)	49 (98%)	1 (2%)	55	73
37	Af	56/64 (88%)	56 (100%)	0	100	100
38	Ag	250/257 (97%)	248 (99%)	2 (1%)	81	89
39	BA	190/193 (98%)	190 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	BB	321/322 (100%)	319 (99%)	2 (1%)	86	92
41	BC	288/288 (100%)	288 (100%)	0	100	100
42	BD	241/243 (99%)	241 (100%)	0	100	100
43	BE	138/155 (89%)	137 (99%)	1 (1%)	84	90
44	BF	186/186 (100%)	186 (100%)	0	100	100
45	BG	187/191 (98%)	186 (100%)	1 (0%)	88	93
46	BH	168/171 (98%)	168 (100%)	0	100	100
47	BI	185/185 (100%)	185 (100%)	0	100	100
48	BJ	146/147 (99%)	146 (100%)	0	100	100
49	BK	154/154 (100%)	152 (99%)	2 (1%)	69	82
50	BL	107/107 (100%)	107 (100%)	0	100	100
51	BM	175/175 (100%)	174 (99%)	1 (1%)	86	92
52	BN	160/160 (100%)	158 (99%)	2 (1%)	69	82
53	BO	138/145 (95%)	138 (100%)	0	100	100
54	BP	150/150 (100%)	148 (99%)	2 (1%)	69	82
55	BQ	152/153 (99%)	151 (99%)	1 (1%)	84	90
56	BR	155/155 (100%)	155 (100%)	0	100	100
57	BS	136/136 (100%)	136 (100%)	0	100	100
58	BT	87/87 (100%)	87 (100%)	0	100	100
59	BU	104/104 (100%)	104 (100%)	0	100	100
60	BV	56/107 (52%)	55 (98%)	1 (2%)	59	77
61	BW	104/105 (99%)	104 (100%)	0	100	100
62	BX	108/108 (100%)	107 (99%)	1 (1%)	78	88
63	BY	115/115 (100%)	114 (99%)	1 (1%)	78	88
64	BZ	118/118 (100%)	118 (100%)	0	100	100
65	Ba	46/46 (100%)	45 (98%)	1 (2%)	52	71
66	Bb	81/81 (100%)	81 (100%)	0	100	100
67	Bc	92/96 (96%)	92 (100%)	0	100	100
68	Bd	108/109 (99%)	108 (100%)	0	100	100
69	Be	90/90 (100%)	89 (99%)	1 (1%)	73	85
70	Bf	95/95 (100%)	95 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
71	Bg	104/104 (100%)	104 (100%)	0	100	100
72	Bh	80/81 (99%)	80 (100%)	0	100	100
73	Bi	69/69 (100%)	69 (100%)	0	100	100
74	Bj	68/68 (100%)	67 (98%)	1 (2%)	65	80
75	Bk	45/45 (100%)	45 (100%)	0	100	100
76	Bl	47/47 (100%)	47 (100%)	0	100	100
77	Bm	22/23 (96%)	22 (100%)	0	100	100
78	Bn	87/88 (99%)	87 (100%)	0	100	100
79	Bo	71/71 (100%)	70 (99%)	1 (1%)	67	81
80	CA	1560/1770 (88%)	1545 (99%)	15 (1%)	76	86
81	CB	266/266 (100%)	264 (99%)	2 (1%)	81	89
82	CC	97/482 (20%)	97 (100%)	0	100	100
All	All	11123/11942 (93%)	11060 (99%)	63 (1%)	86	92

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
40	BB	332	ARG
80	CA	1146	MET
52	BN	117[A]	ARG
80	CA	849	LYS
80	CA	1441	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
80	CA	261	ASN
80	CA	1096	HIS
80	CA	1773	GLN
41	BC	221	ASN
33	Ab	19	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1768/1800 (98%)	433 (24%)	36 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	3	157/158 (99%)	31 (19%)	1 (0%)
3	4	120/121 (99%)	14 (11%)	1 (0%)
4	5	3159/3396 (93%)	584 (18%)	32 (1%)
5	6	75/76 (98%)	14 (18%)	0
All	All	5279/5551 (95%)	1076 (20%)	70 (1%)

5 of 1076 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	5	U
1	2	9	U
1	2	17	C

5 of 70 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	5	2496	C
4	5	2538	U
4	5	3229	C
1	2	1256	A
1	2	1226	A

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 95 ligands modelled in this entry, 95 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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

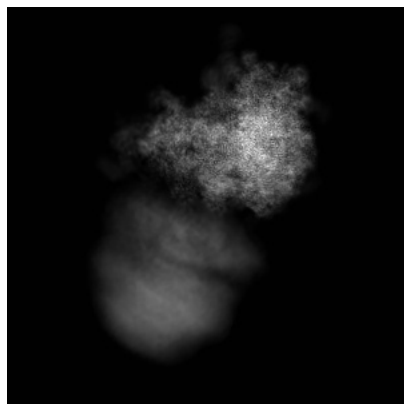
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14978. These allow visual inspection of the internal detail of the map and identification of artifacts.

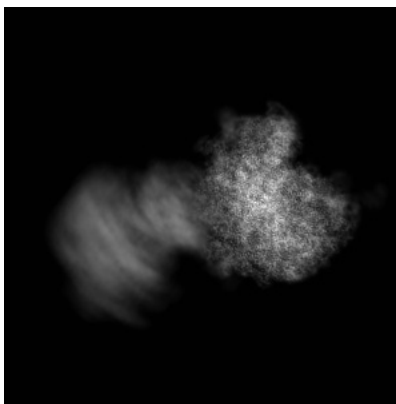
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

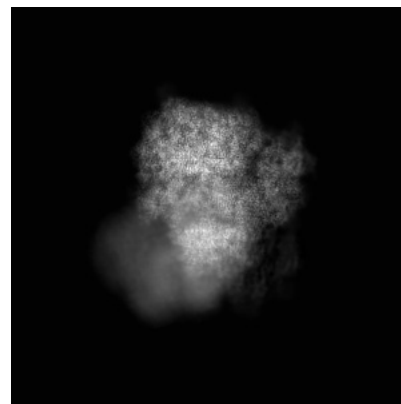
#### 6.1.1 Primary map



X

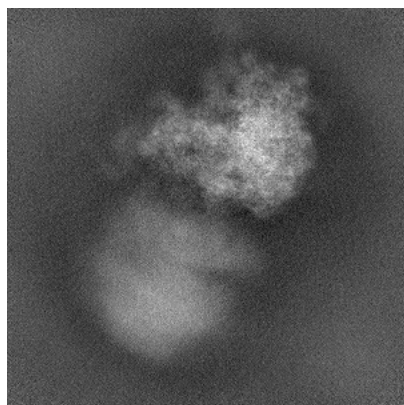


Y

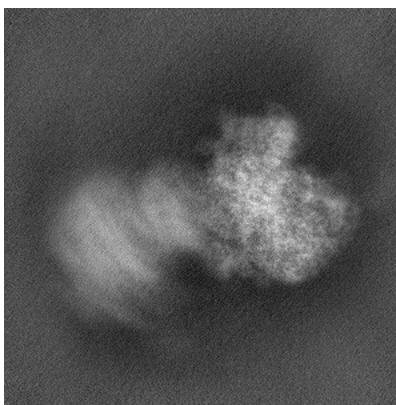


Z

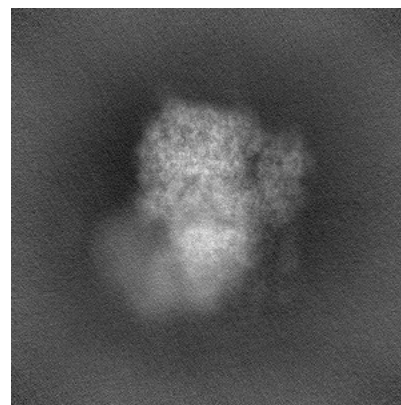
#### 6.1.2 Raw map



X



Y

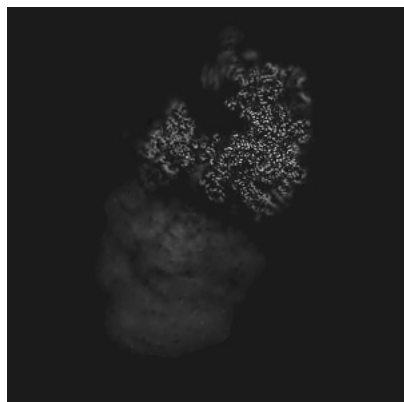


Z

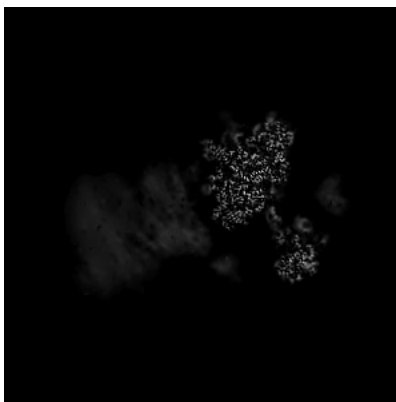
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

### 6.2.1 Primary map



X Index: 280

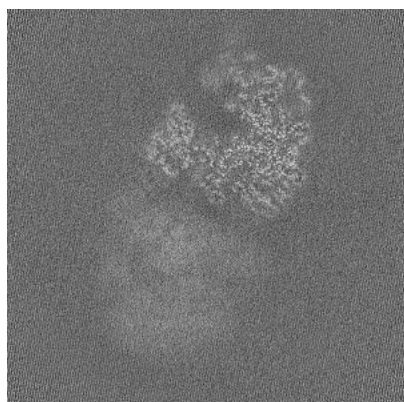


Y Index: 280

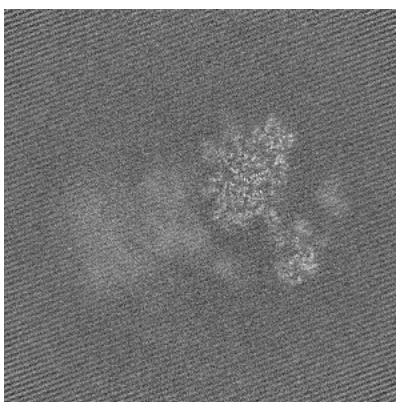


Z Index: 280

### 6.2.2 Raw map



X Index: 280



Y Index: 280

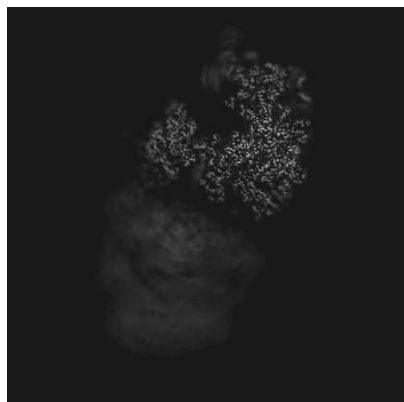


Z Index: 280

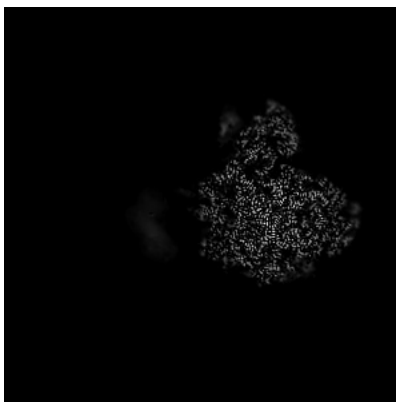
The images above show central slices of the map in three orthogonal directions.

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

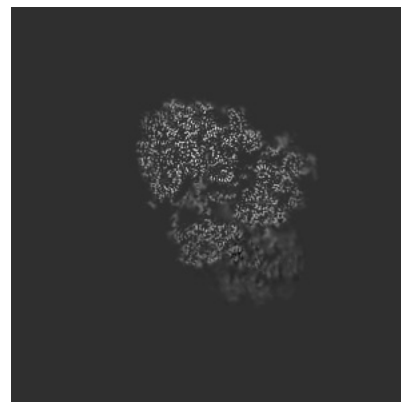
### 6.3.1 Primary map



X Index: 281

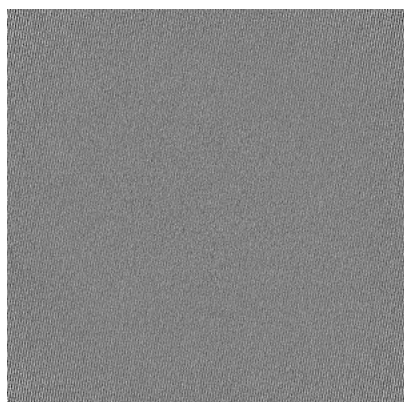


Y Index: 345

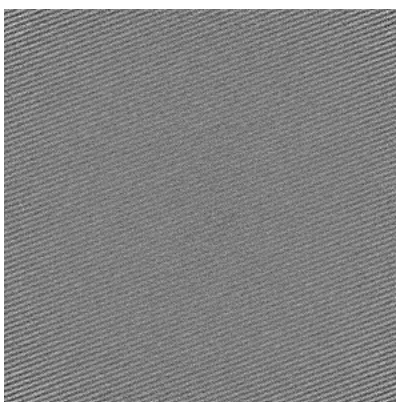


Z Index: 380

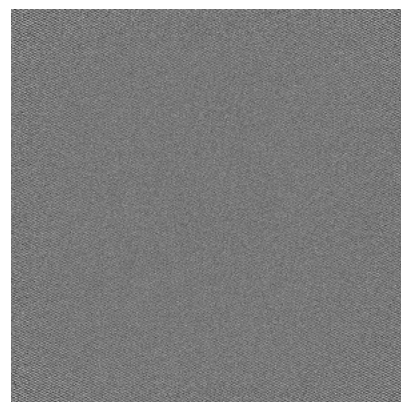
### 6.3.2 Raw map



X Index: 0



Y Index: 0

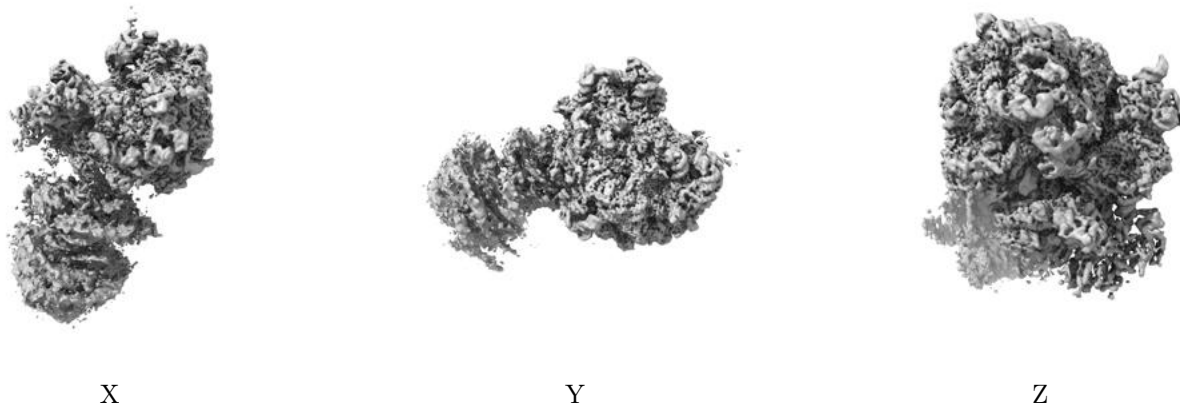


Z Index: 0

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

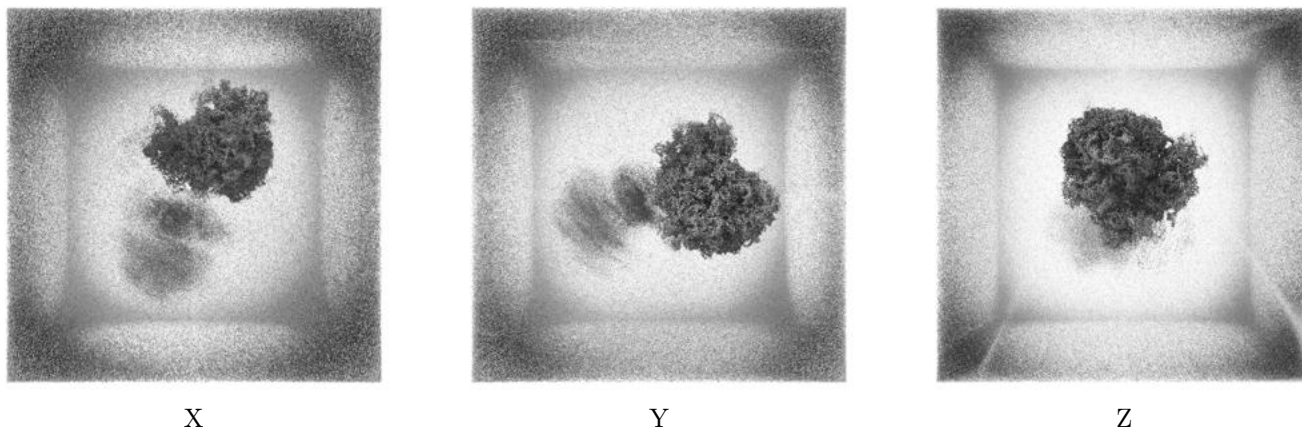
## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 Raw map



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

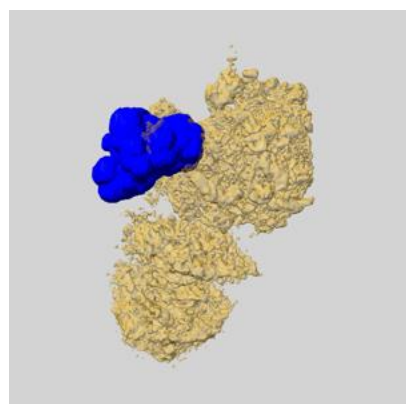
## 6.5 Mask visualisation [i](#)

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

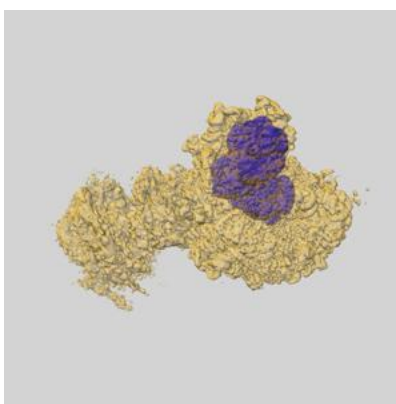
A mask typically either:

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

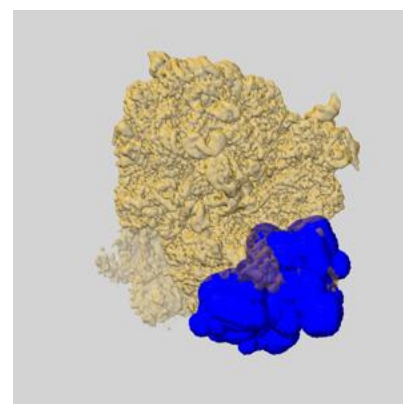
### 6.5.1 emd\_14978\_msk\_1.map [i](#)



X

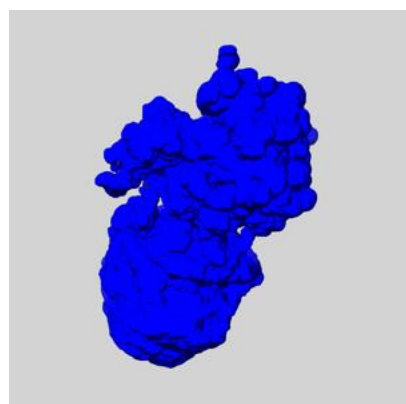


Y

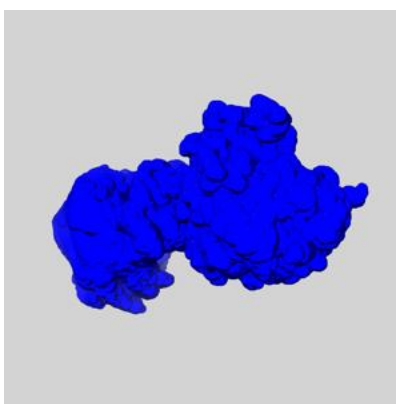


Z

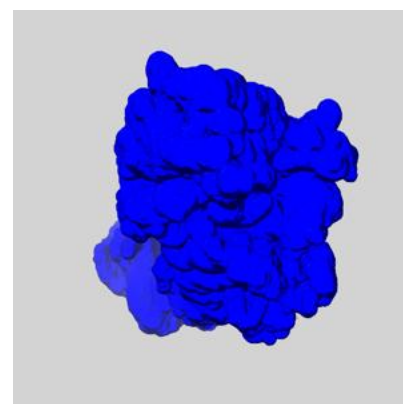
### 6.5.2 emd\_14978\_msk\_2.map [i](#)



X



Y

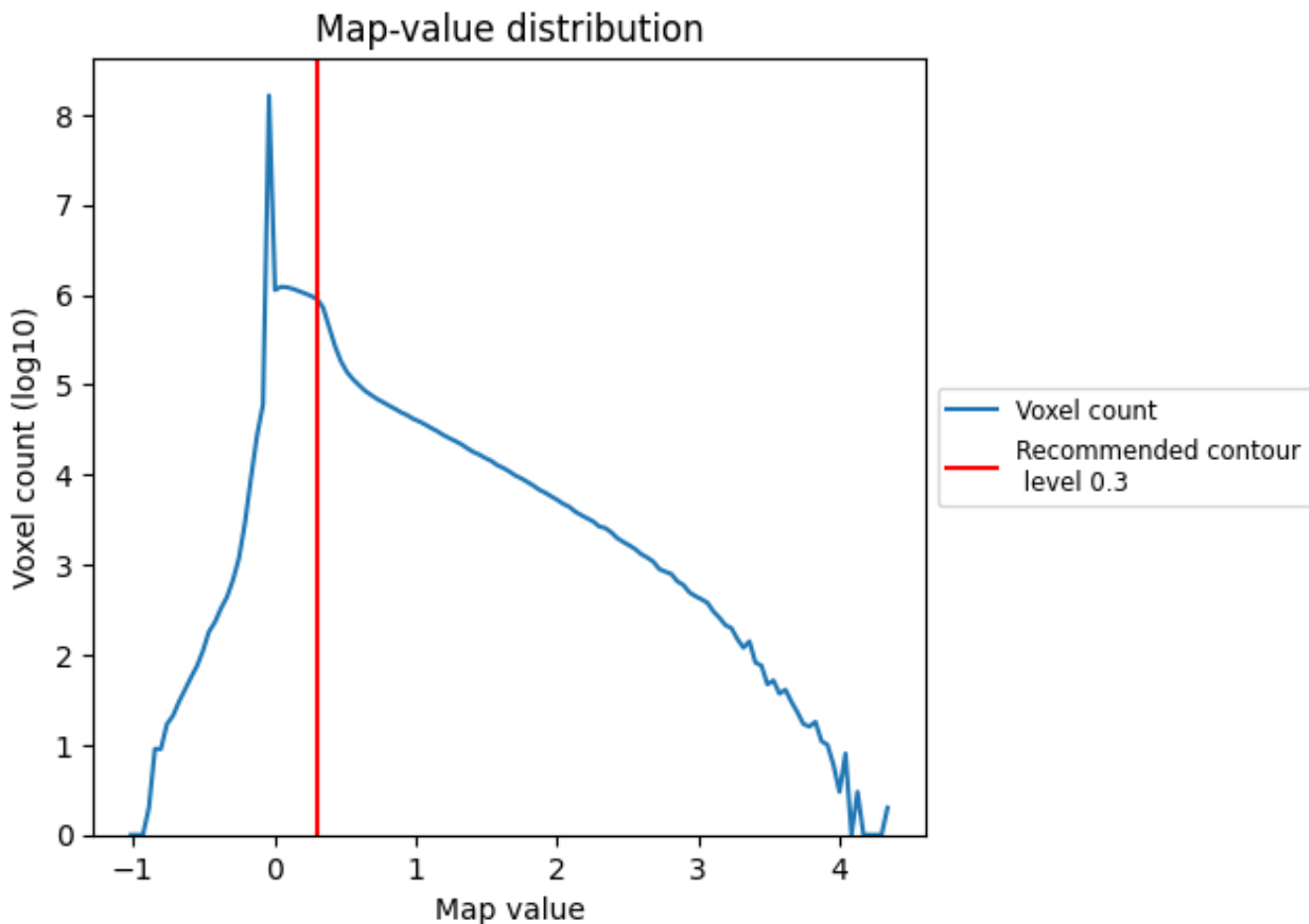


Z

## 7 Map analysis [i](#)

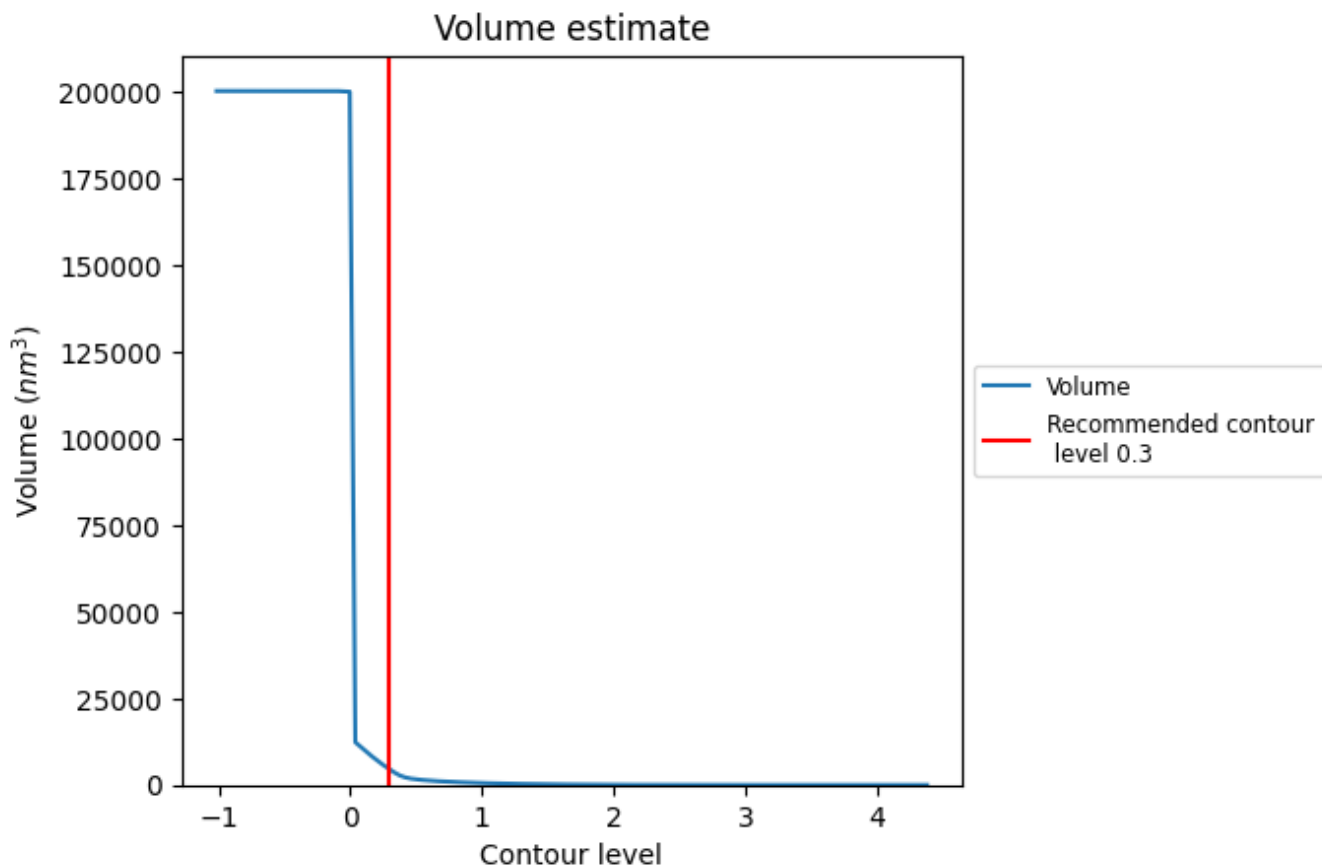
This section contains the results of statistical analysis of the map.

### 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 [\(i\)](#)

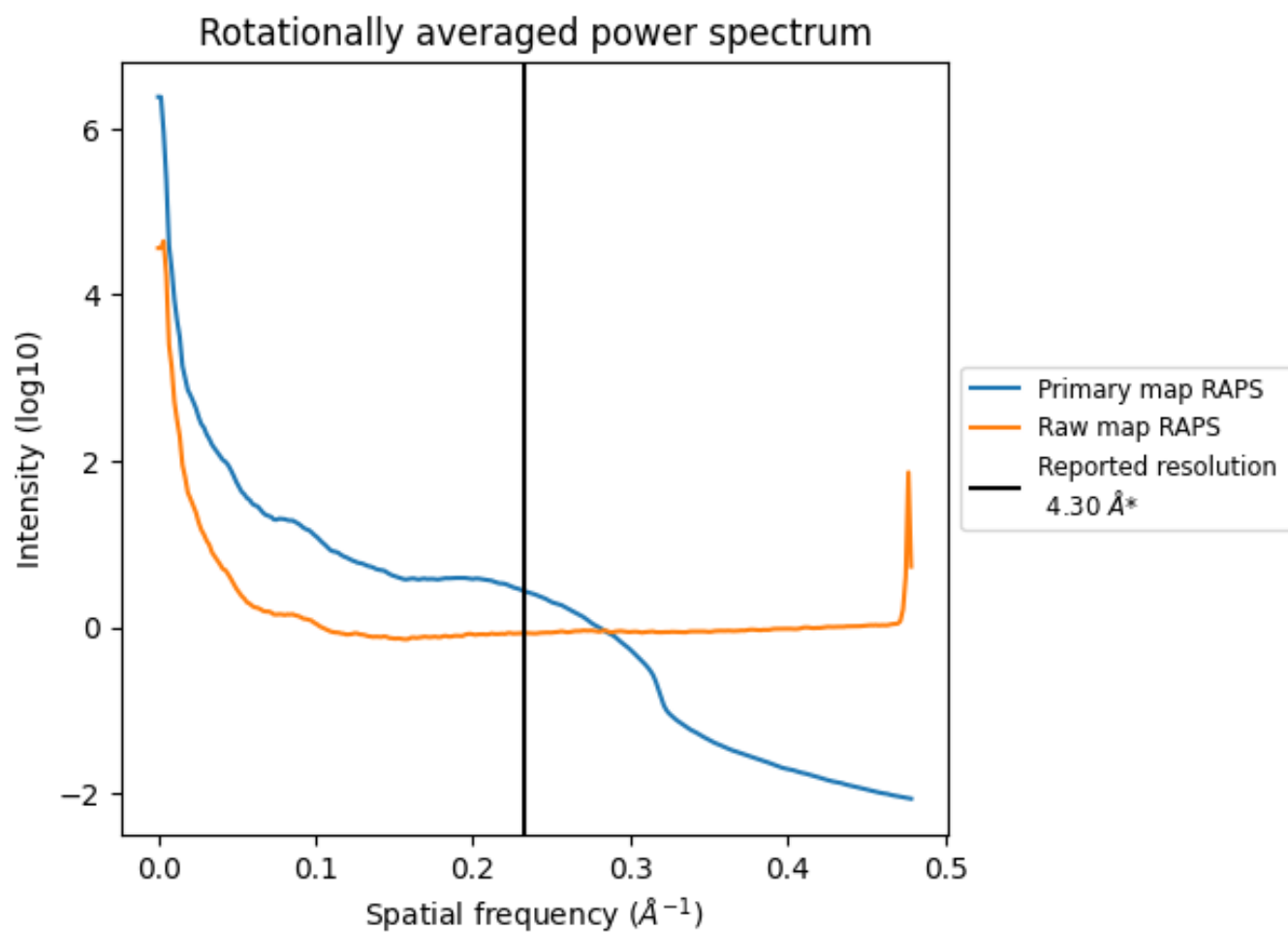


The volume at the recommended contour level is 4493  $\text{nm}^3$ ; this corresponds to an approximate mass of 4059 kDa.

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

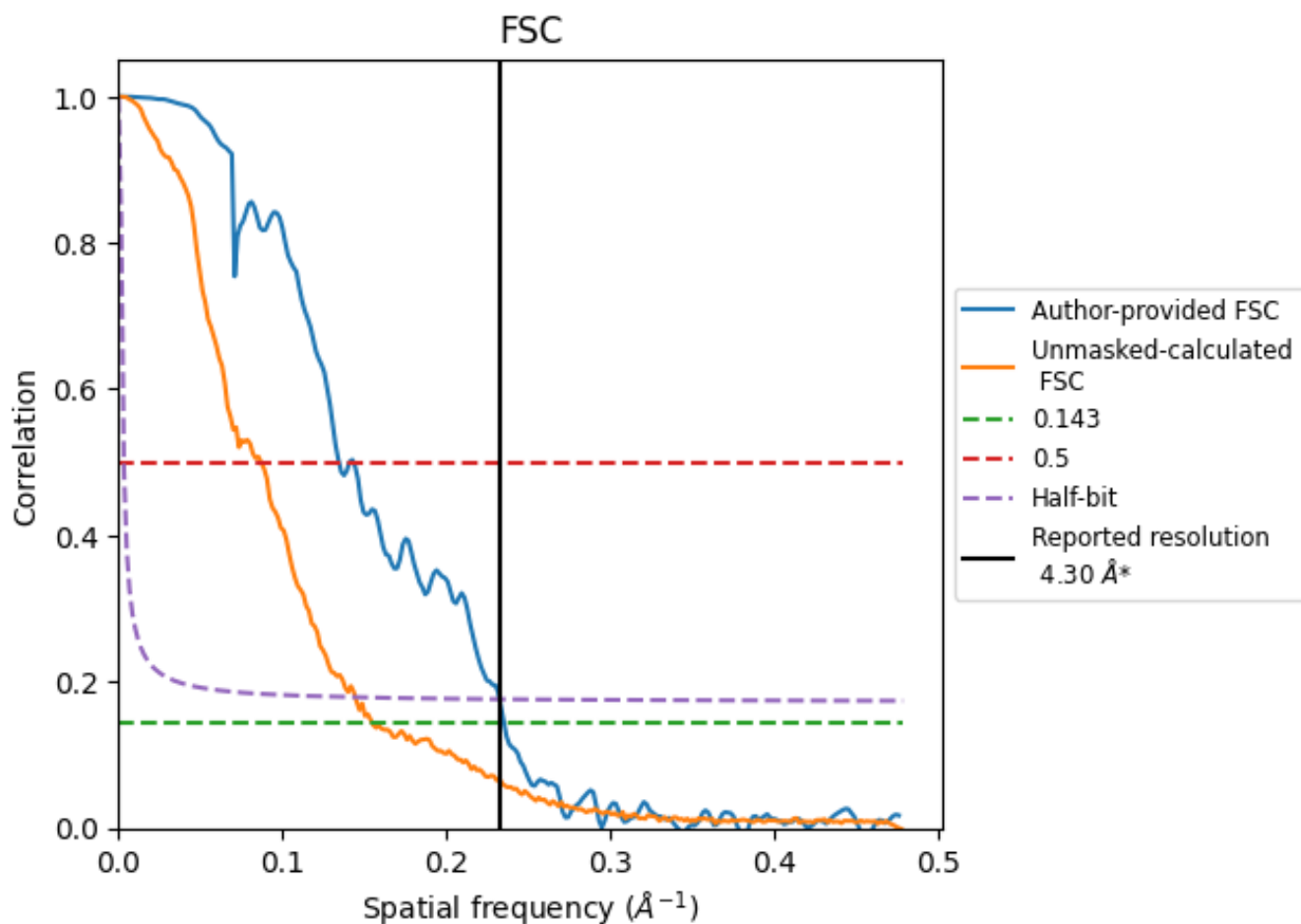


\*Reported resolution corresponds to spatial frequency of 0.233 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.233 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

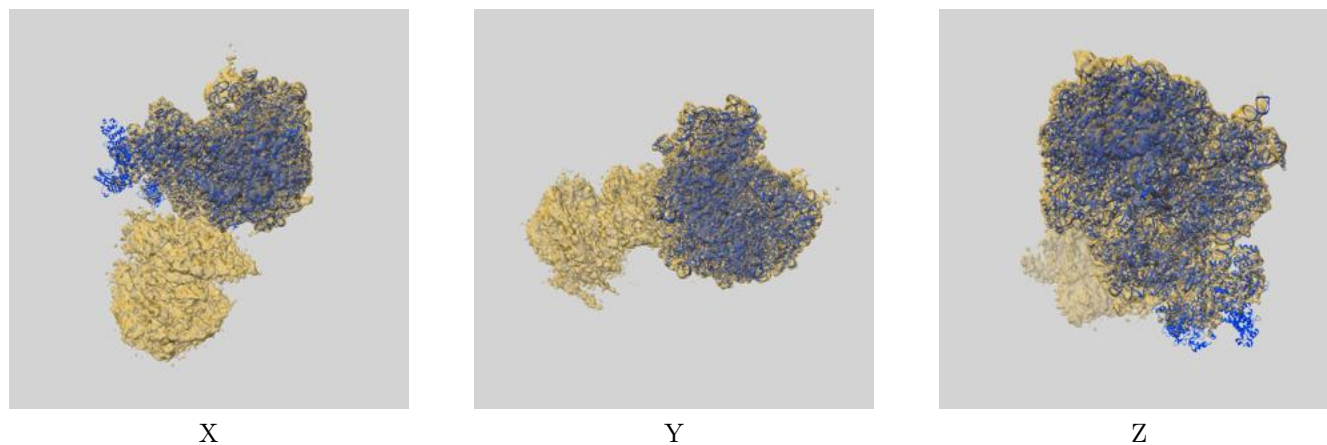
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	4.25	7.43	4.30
Unmasked-calculated*	6.46	11.49	6.92

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.46 differs from the reported value 4.3 by more than 10 %

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

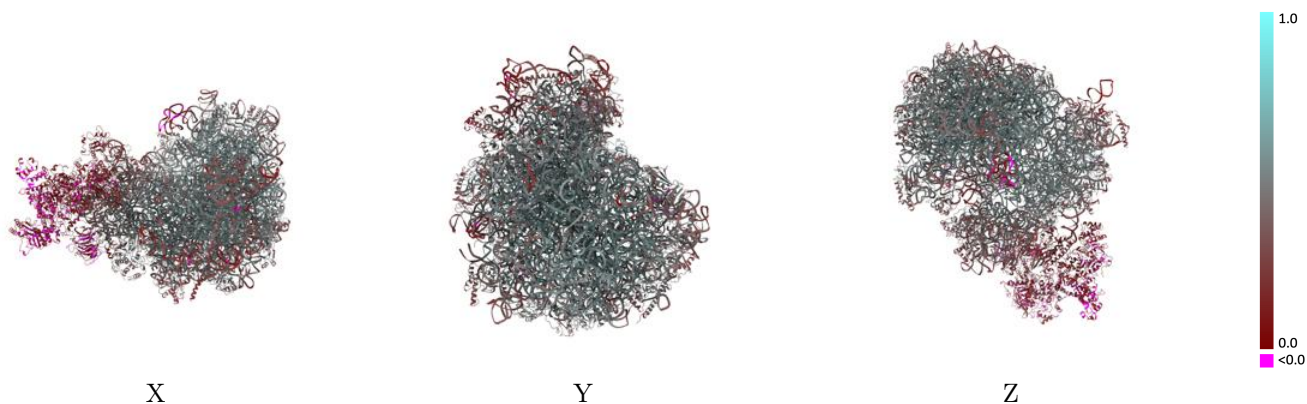
This section contains information regarding the fit between EMDB map EMD-14978 and PDB model 7ZUW. Per-residue inclusion information can be found in section [3](#) on page [19](#).

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



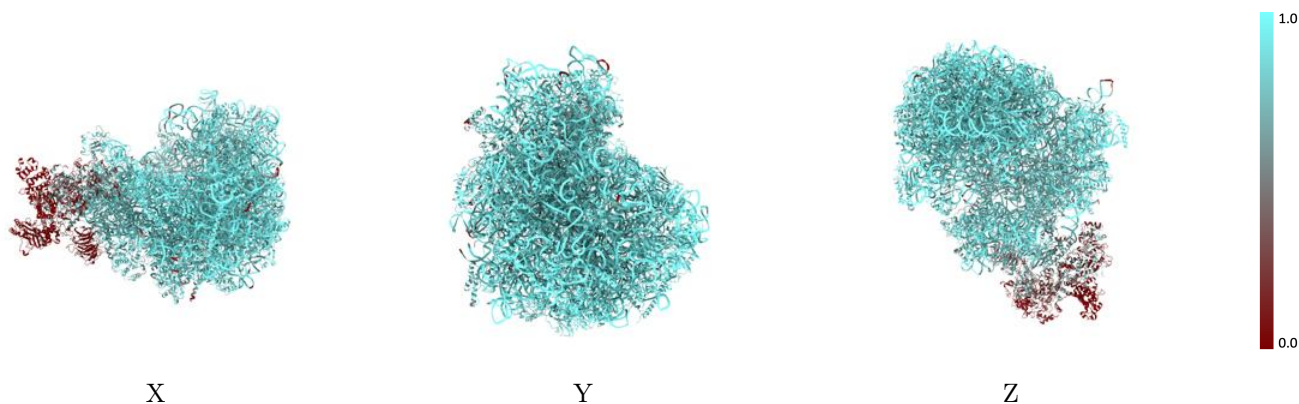
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



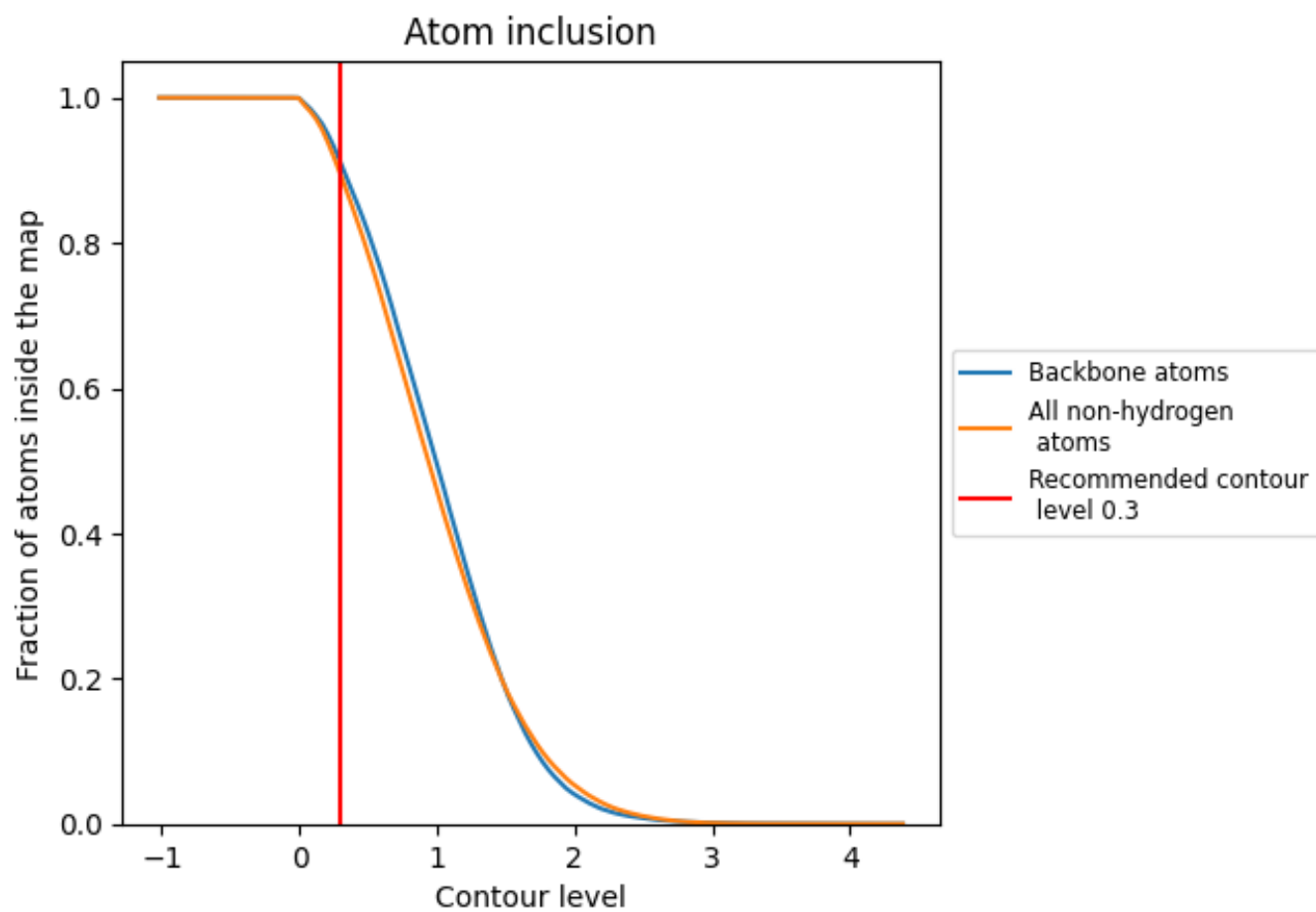
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.3).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 89% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary





















































































The table lists the average atom inclusion at the recommended contour level (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8942	 0.4470
2	 0.9704	 0.4490
3	 0.9875	 0.5060
4	 0.9934	 0.4820
5	 0.9794	 0.5100
6	 0.9660	 0.3900
AA	 0.8951	 0.4260
AB	 0.8511	 0.4360
AC	 0.9319	 0.4800
AD	 0.8652	 0.3930
AE	 0.9535	 0.4910
AF	 0.8551	 0.3850
AG	 0.9108	 0.3870
AH	 0.8331	 0.3740
AI	 0.9592	 0.4980
AJ	 0.9496	 0.4460
AK	 0.8970	 0.3180
AL	 0.9220	 0.5140
AM	 0.7538	 0.2070
AN	 0.9143	 0.4800
AO	 0.9185	 0.4910
AP	 0.9101	 0.3570
AQ	 0.8833	 0.3830
AR	 0.8232	 0.3630
AS	 0.9047	 0.3610
AT	 0.8807	 0.3400
AU	 0.8862	 0.3600
AV	 0.9081	 0.4500
AW	 0.9559	 0.5190
AX	 0.9698	 0.5350
AY	 0.9443	 0.4420
AZ	 0.7326	 0.3040
Aa	 0.9202	 0.4790
Ab	 0.8602	 0.4290
Ac	 0.8013	 0.4040



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Chain	Atom inclusion	Q-score
Ad	 0.9693	 0.4690
Ae	 0.8838	 0.4330
Af	 0.8217	 0.2180
Ag	 0.0695	 0.1180
BA	 0.9592	 0.5570
BB	 0.9756	 0.5300
BC	 0.9672	 0.5180
BD	 0.9156	 0.4200
BE	 0.9281	 0.4320
BF	 0.9673	 0.5180
BG	 0.8674	 0.4130
BH	 0.9419	 0.4780
BI	 0.9415	 0.4950
BJ	 0.9017	 0.4000
BK	 0.9449	 0.4840
BL	 0.9513	 0.4520
BM	 0.9731	 0.5520
BN	 0.9696	 0.5230
BO	 0.9672	 0.5300
BP	 0.9771	 0.5400
BQ	 0.9196	 0.4810
BR	 0.9527	 0.5150
BS	 0.9653	 0.5140
BT	 0.9361	 0.4360
BU	 0.9561	 0.5600
BV	 0.9415	 0.4570
BW	 0.9501	 0.4830
BX	 0.9718	 0.4800
BY	 0.9169	 0.4450
BZ	 0.9527	 0.5280
Ba	 0.9491	 0.5030
Bb	 0.9352	 0.4890
Bc	 0.9541	 0.5040
Bd	 0.9738	 0.5520
Be	 0.9610	 0.5490
Bf	 0.9167	 0.5050
Bg	 0.9512	 0.4680
Bh	 0.9014	 0.4400
Bi	 0.9953	 0.5690
Bj	 0.9165	 0.4040
Bk	 0.9831	 0.5650
Bl	 0.9505	 0.5160

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Chain	Atom inclusion	Q-score
Bm	 0.9856	 0.5870
Bn	 0.9429	 0.5110
Bo	 0.9388	 0.5410
CA	 0.3623	 0.1550
CB	 0.0059	 0.0480
CC	 0.2122	 0.1450