



## wwPDB EM Validation Summary Report ⓘ

Dec 19, 2022 – 03:42 pm GMT

PDB ID : 7NRD  
EMDB ID : EMD-12535  
Title : Structure of the yeast Gen1 bound to a colliding stalled 80S ribosome with MBF1, A/P-tRNA and P/E-tRNA  
Authors : Pochopien, A.A.; Beckert, B.; Wilson, D.N.  
Deposited on : 2021-03-03  
Resolution : 4.36 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:

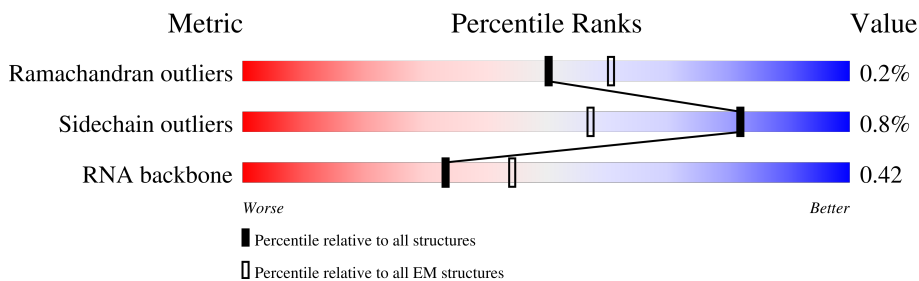
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

# 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 4.36 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	S2	1800	
2	SA	223	
3	SB	206	
4	SC	92	
5	SD	124	
6	SE	119	
7	SF	141	
8	SG	125	

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Mol	Chain	Length	Quality of chain
9	SH	145	10% 99%
10	SI	143	6% 100%
11	SJ	101	5% 94% 6%
12	SK	69	12% 100%
13	SL	63	10% 100%
14	SM	53	• 100%
15	SN	73	23% 96%
16	SO	313	23% 99%
17	SP	206	• 95% 5%
18	SQ	216	15% 98%
19	SR	217	• 99%
20	SS	260	• 98%
21	ST	218	8% 100%
22	SU	185	14% 97%
23	SV	188	• 98%
24	SW	185	9% 100%
25	SX	146	5% 96%
26	SY	150	• 99%
27	SZ	128	11% 99%
28	Sa	87	8% 100%
29	Sb	129	• 98%
30	Sc	144	• 97%
31	Sd	134	5% 97%
32	Se	97	7% 96%
33	Sf	81	11% 98%

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Mol	Chain	Length	Quality of chain
34	Sg	44	7% 98%
35	Sh	120	6% 98%
36	S3	32	28% 28% 41% 31%
37	Sn	75	47% 55% 33% 12%
38	Sm	77	5% 71% 25%
39	LA	3394	53% 34% 7% 6%
40	LB	121	75% 23%
41	LC	158	65% 33%
42	LD	251	96%
43	LE	386	8% 99%
44	LF	361	5% 99%
45	LG	294	19% 99%
46	LH	167	9% 100%
47	LI	222	9% 100%
48	LJ	233	23% 98%
49	LK	191	21% 99%
50	LL	218	37% 99%
51	LM	169	38% 99%
52	LN	193	11% 98%
53	LO	136	12% 99%
54	LP	203	98%
55	LQ	197	6% 98%
56	LR	183	6% 100%
57	LS	185	99%
58	LT	188	17% 97%

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Mol	Chain	Length	Quality of chain
59	LU	171	19% 100%
60	LV	159	16% 99%
61	LW	100	35% 99%
62	LX	136	7% 100%
63	LY	61	10% 100%
64	LZ	121	• 100%
65	La	125	7% 99%
66	Lb	135	19% 99%
67	Lc	148	6% 97%
68	Ld	58	7% 93% 7%
69	Le	96	8% 96%
70	Lf	109	23% 98%
71	Lg	127	• 99%
72	Lh	106	5% 99%
73	Li	112	12% 100%
74	Lj	119	6% 97%
75	Lk	99	19% 100%
76	Ll	81	• 98%
77	Lm	77	18% 100%
78	Ln	50	• 98%
79	Lo	52	21% 100%
80	Lp	25	8% 88% 12%
81	Lq	103	15% 100%
82	Lr	91	• 97% ••

## 2 Entry composition [i](#)

There are 82 unique types of molecules in this entry. The entry contains 204032 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 TPA\_inf: Saccharomyces cerevisiae S288C chromosome XII, complete sequence.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	S2	1783	37990	16984	6722	12501	1783	0	0

- Molecule 2 is a protein called 40S ribosomal protein S3.

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

- Molecule 3 is a protein called 40S ribosomal protein S5.

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

- Molecule 4 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	SC	92	741	478	121	140	2	0	0

- Molecule 5 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	SD	124	890	560	156	172	2	0	0

- Molecule 6 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	SE	119	939	595	176	161	7	0	0

- Molecule 7 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 8 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	SG	125	1001	625	188	186	2	0	0

- Molecule 9 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 10 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 11 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	SJ	101	805	512	145	147	1	0	0

- Molecule 12 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	SK	69	558	357	103	98	0	0

- Molecule 13 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 14 is a protein called 40S ribosomal protein S29-A.

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

- Molecule 15 is a protein called Ubiquitin-40S ribosomal protein S31.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SN	97	ALA	LYS	conflict	UNP P05759

- Molecule 16 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SO	313	Total	C	N	O	S	0	0
			2403	1521	411	463	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SO	161	ALA	LYS	conflict	UNP P38011

- Molecule 17 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SP	206	Total	C	N	O	S	0	0
			1583	1017	281	283	2		

- Molecule 18 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SQ	216	Total	C	N	O	S	0	0
			1722	1091	312	315	4		

- Molecule 19 is a protein called 40S ribosomal protein S2.

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



- Molecule 20 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 21 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	ST	218	1755	1102	337	313	3	0	0

- Molecule 22 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
22	SU	185	1486	954	266	266	0	0

- Molecule 23 is a protein called 40S ribosomal protein S8-A.

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

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SV	?	-	LYS	deletion	UNP P0CX39
SV	?	-	LYS	deletion	UNP P0CX39
SV	?	-	ASN	deletion	UNP P0CX39
SV	?	-	VAL	deletion	UNP P0CX39
SV	?	-	LYS	deletion	UNP P0CX39
SV	?	-	GLU	deletion	UNP P0CX39
SV	?	-	GLU	deletion	UNP P0CX39
SV	?	-	GLU	deletion	UNP P0CX39
SV	?	-	THR	deletion	UNP P0CX39
SV	?	-	VAL	deletion	UNP P0CX39
SV	?	-	ALA	deletion	UNP P0CX39

- Molecule 24 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 25 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	SX	146	1168	747	221	197	3	0	0

- Molecule 26 is a protein called 40S ribosomal protein S13.

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

- Molecule 27 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	SZ	128	949	582	188	176	3	0	0

- Molecule 28 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 29 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 30 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 31 is a protein called 40S ribosomal protein S24-A.

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

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

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

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

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

- Molecule 34 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
34	Sg	44	355	227	72	56	0	0

- Molecule 35 is a protein called Multiprotein-bridging factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	Sh	120	928	563	185	179	1	0	0

- Molecule 36 is a RNA chain called mRNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
36	S3	32	652	294	87	239	32	0	0

- Molecule 37 is a RNA chain called tRNA (75-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
37	Sn	75	1606	716	297	518	75	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Sn	10	A	G	conflict	GB 176433

- Molecule 38 is a RNA chain called tRNA (77-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
38	Sm	77	1625	722	292	534	77	0	0

- Molecule 39 is a RNA chain called 25S rRNA (3184-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
39	LA	3184	68091	30415	12259	22233	3184	0	0

- Molecule 40 is a RNA chain called 5S rRNA (121-MER).

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

- Molecule 41 is a RNA chain called 5.8S rRNA (158-MER).

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

- Molecule 42 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 43 is a protein called 60S ribosomal protein L3.

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

- Molecule 44 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 45 is a protein called 60S ribosomal protein L5.

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

- Molecule 46 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	LH	167	1307	843	234	230		0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LH	?	-	ASN	deletion	UNP P05739
LH	?	-	LEU	deletion	UNP P05739
LH	?	-	PHE	deletion	UNP P05739
LH	?	-	PRO	deletion	UNP P05739
LH	?	-	GLU	deletion	UNP P05739
LH	?	-	GLN	deletion	UNP P05739
LH	?	-	GLN	deletion	UNP P05739
LH	?	-	THR	deletion	UNP P05739

- Molecule 47 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 48 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L10.

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

- Molecule 51 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	LM	169	1346	843	252	247	4	0	0

- Molecule 52 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 53 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 54 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 55 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 56 is a protein called 60S ribosomal protein L17-A.

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

- Molecule 57 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 58 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	LT	188	1515	932	323	260		0	0

- Molecule 59 is a protein called 60S ribosomal protein L20-A.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	LV	159	1272	802	245	221	4	0	0

- Molecule 61 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 62 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 63 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	LY	61	509	328	100	80	1	0	0

- Molecule 64 is a protein called 60S ribosomal protein L25.

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

- Molecule 65 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 66 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	Lb	135	1080	701	199	180		0	0

- Molecule 67 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	Lc	148	1169	747	231	188	3	0	0

- Molecule 68 is a protein called 60S ribosomal protein L29.

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

- Molecule 69 is a protein called 60S ribosomal protein L30.

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

- Molecule 70 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 71 is a protein called 60S ribosomal protein L32.



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

- Molecule 72 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 73 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 74 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 75 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 76 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	Ll	81	645	393	141	106	5	0	0

- Molecule 77 is a protein called 60S ribosomal protein L38.

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

- Molecule 78 is a protein called 60S ribosomal protein L39.

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

- Molecule 79 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Lo	52	Total	C	N	O	S	0	0
			410	254	86	65	5		

- Molecule 80 is a protein called 60S ribosomal protein L41-B.

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

- Molecule 81 is a protein called 60S ribosomal protein L42-A.

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

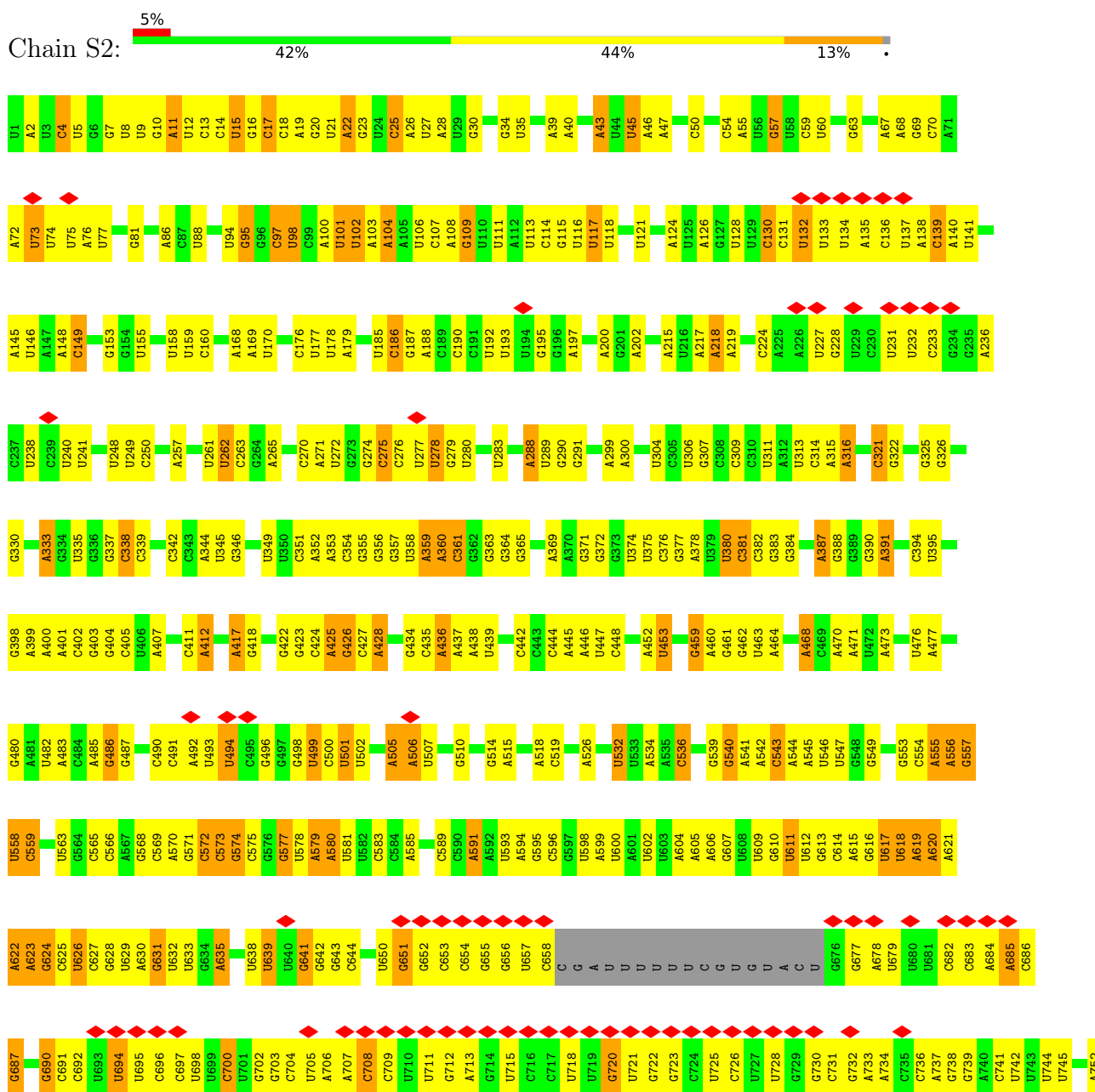
- Molecule 82 is a protein called 60S ribosomal protein L43-A.

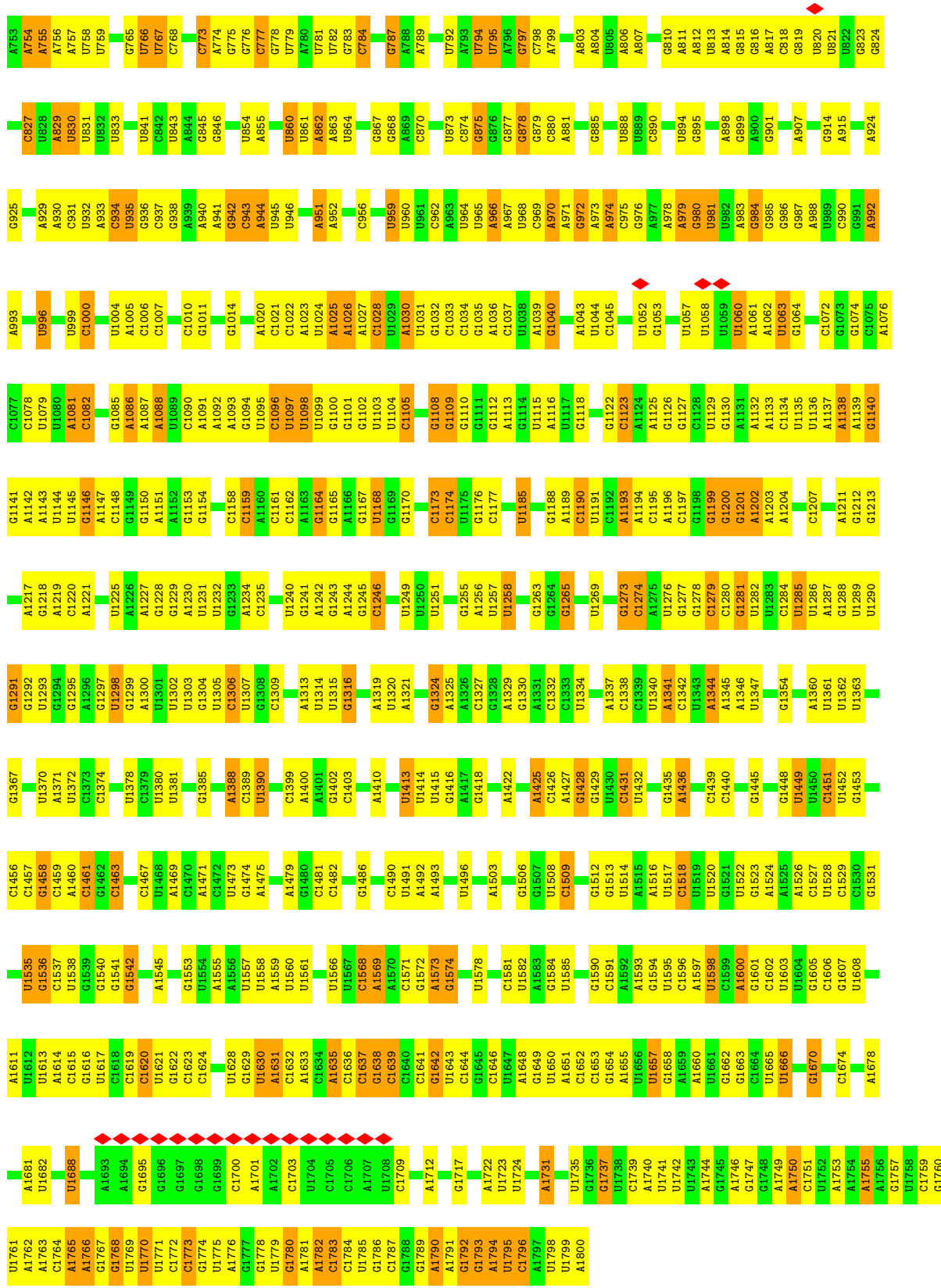
Mol	Chain	Residues	Atoms					AltConf	Trace
82	Lr	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

### 3 Residue-property plots

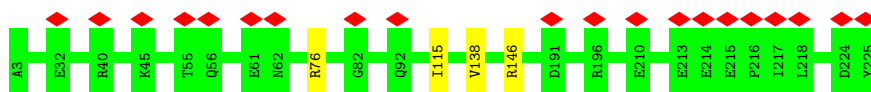
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: TPA\_inf: *Saccharomyces cerevisiae* S288C chromosome XII, complete sequence

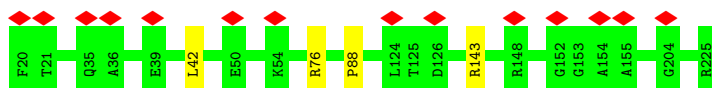




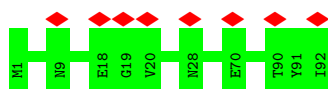
• Molecule 2: 40S ribosomal protein S3



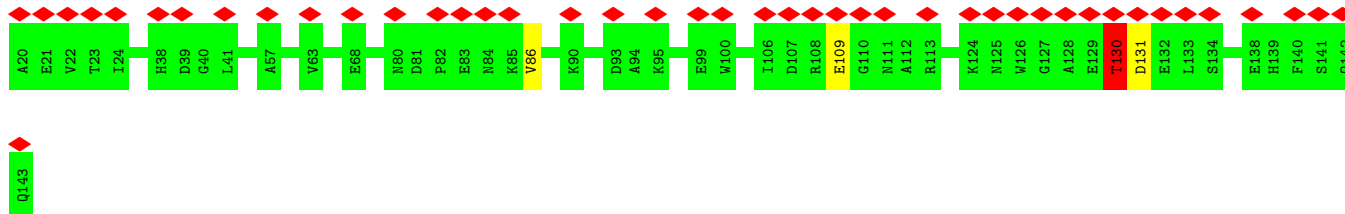
- Molecule 3: 40S ribosomal protein S5



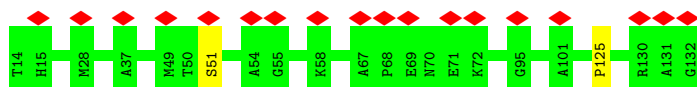
- Molecule 4: 40S ribosomal protein S10-A



- Molecule 5: 40S ribosomal protein S12



- Molecule 6: 40S ribosomal protein S15

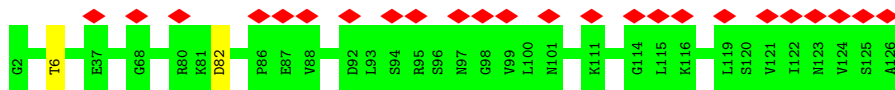


- Molecule 7: 40S ribosomal protein S16-A

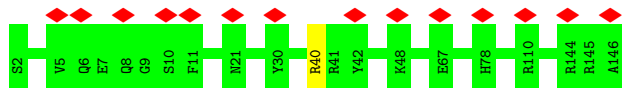


- Molecule 8: 40S ribosomal protein S17-B

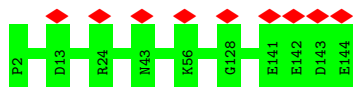




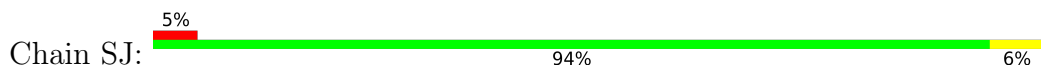
- Molecule 9: 40S ribosomal protein S18-A



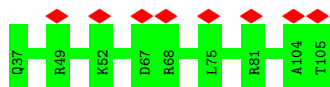
- Molecule 10: 40S ribosomal protein S19-A



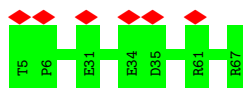
- Molecule 11: 40S ribosomal protein S20



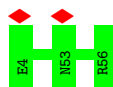
- Molecule 12: 40S ribosomal protein S25-A



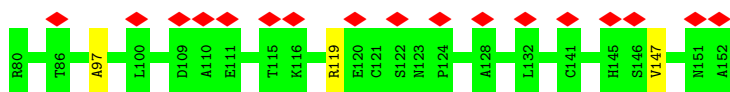
- Molecule 13: 40S ribosomal protein S28-A



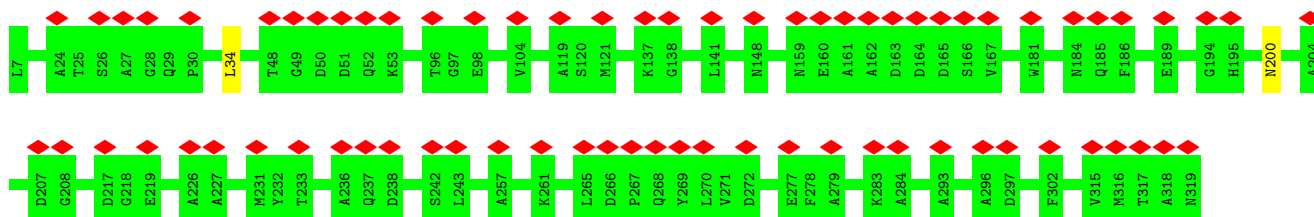
- Molecule 14: 40S ribosomal protein S29-A



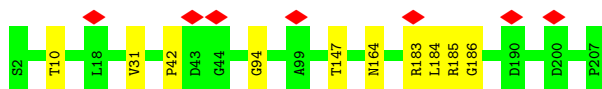
- Molecule 15: Ubiquitin-40S ribosomal protein S31



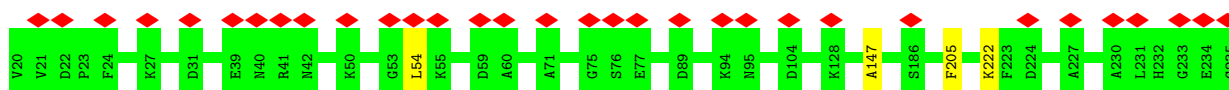
- Molecule 16: Guanine nucleotide-binding protein subunit beta-like protein



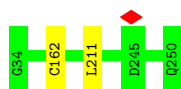
- Molecule 17: 40S ribosomal protein S0-A



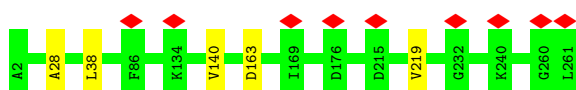
- Molecule 18: 40S ribosomal protein S1-A



- Molecule 19: 40S ribosomal protein S2

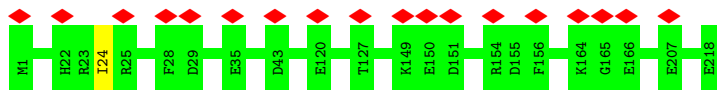


- Molecule 20: 40S ribosomal protein S4-A

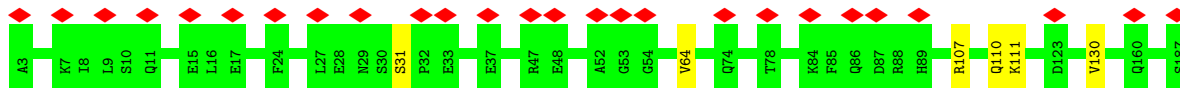


- Molecule 21: 40S ribosomal protein S6-A

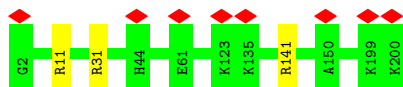




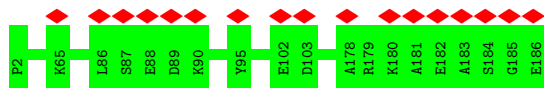
- Molecule 22: 40S ribosomal protein S7-A



- Molecule 23: 40S ribosomal protein S8-A



- Molecule 24: 40S ribosomal protein S9-A



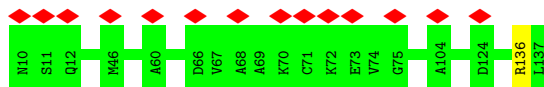
- Molecule 25: 40S ribosomal protein S11-A



- Molecule 26: 40S ribosomal protein S13

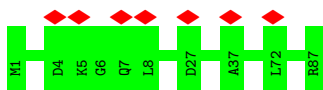


- Molecule 27: 40S ribosomal protein S14-B



- Molecule 28: 40S ribosomal protein S21-A

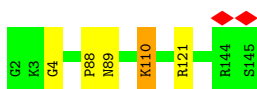




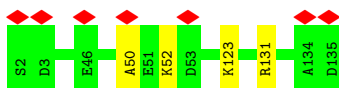
- Molecule 29: 40S ribosomal protein S22-A



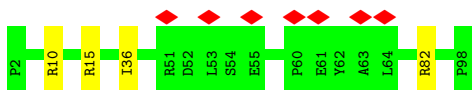
- Molecule 30: 40S ribosomal protein S23-A



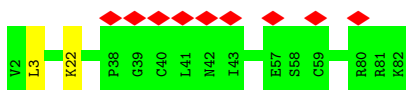
- Molecule 31: 40S ribosomal protein S24-A



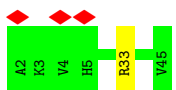
- Molecule 32: 40S ribosomal protein S26-B



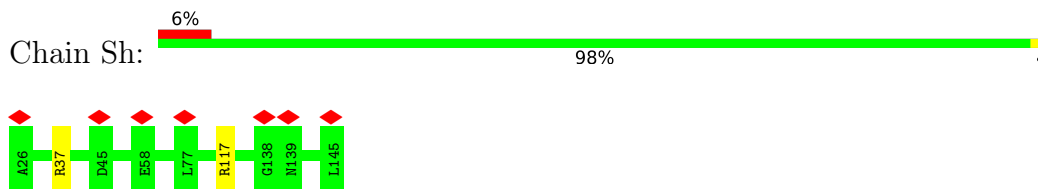
- Molecule 33: 40S ribosomal protein S27-A



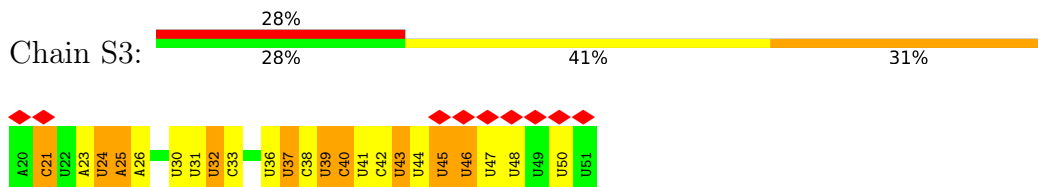
- Molecule 34: 40S ribosomal protein S30-A



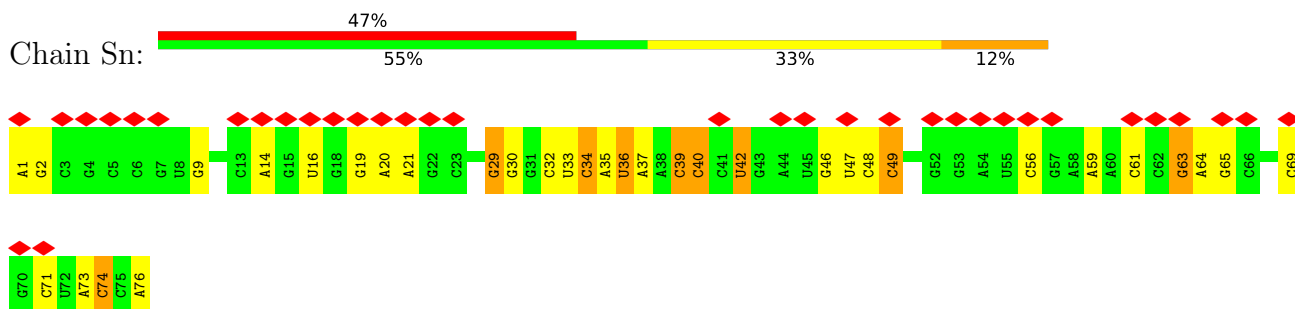
• Molecule 35: Multiprotein-bridging factor 1



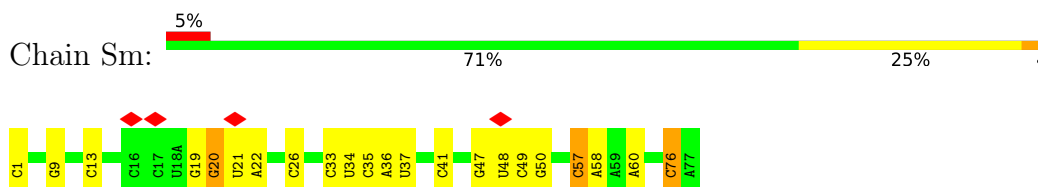
• Molecule 36: mRNA (32-MER)



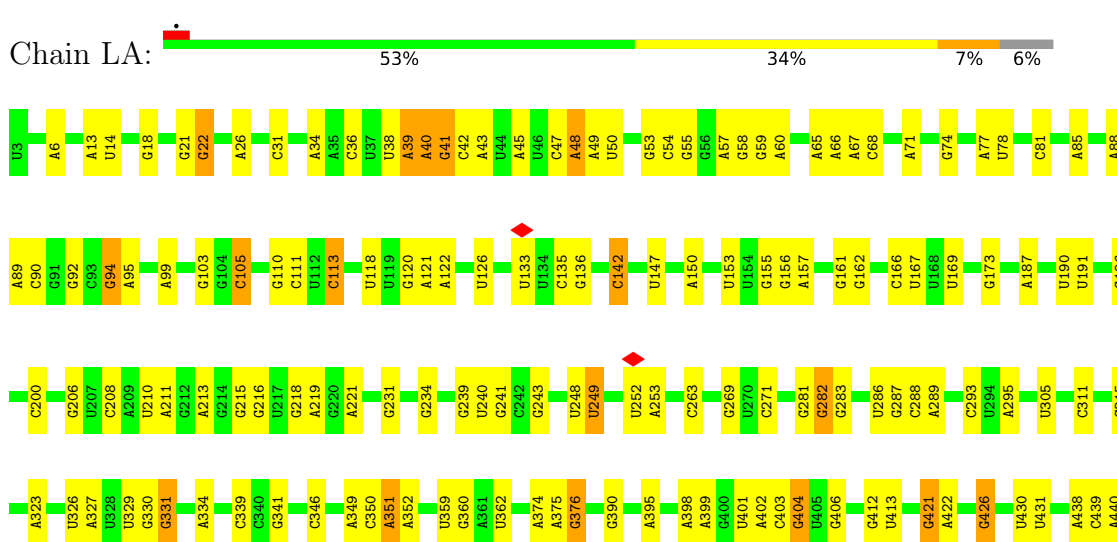
• Molecule 37: tRNA (75-MER)

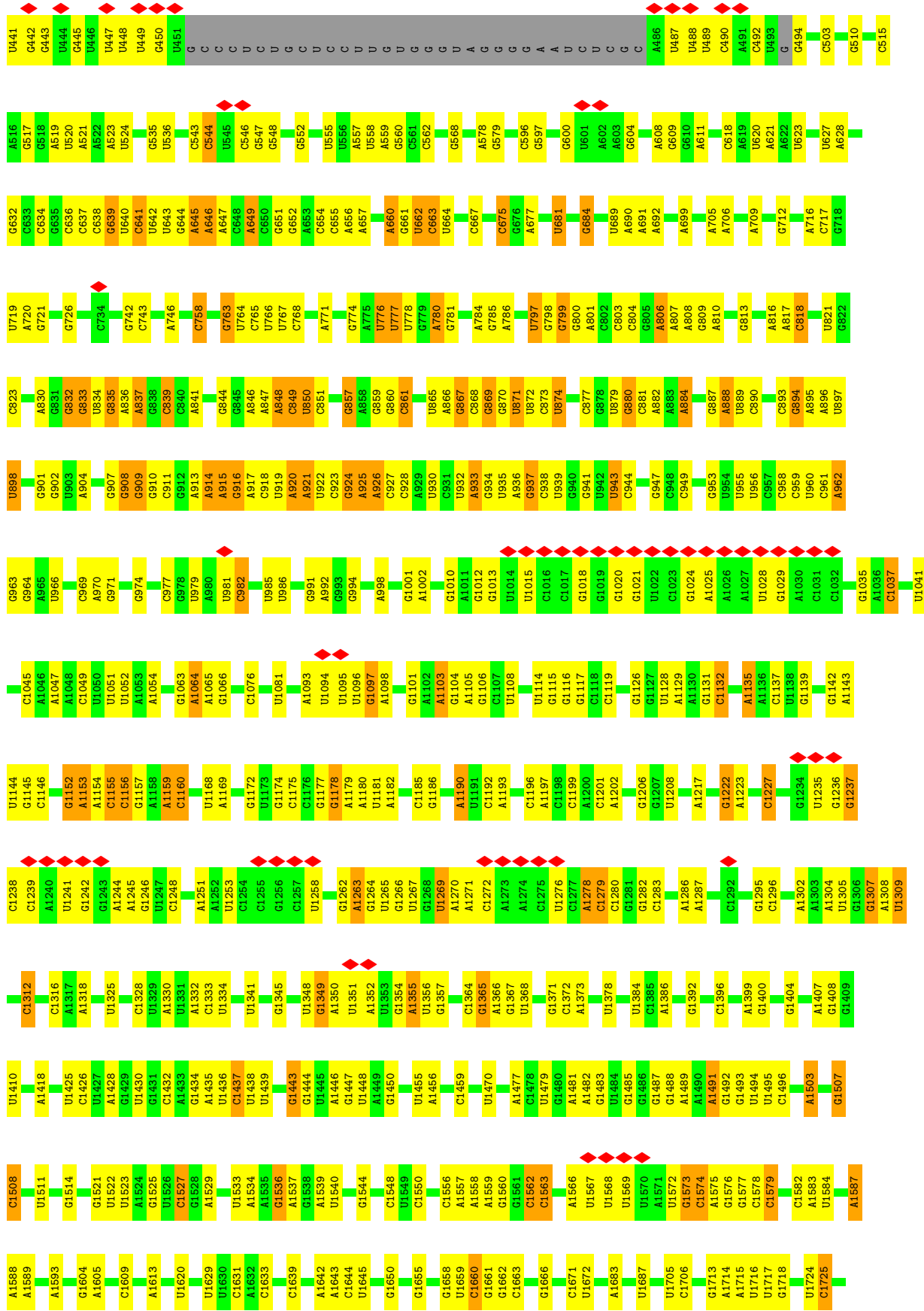


• Molecule 38: tRNA (77-MER)

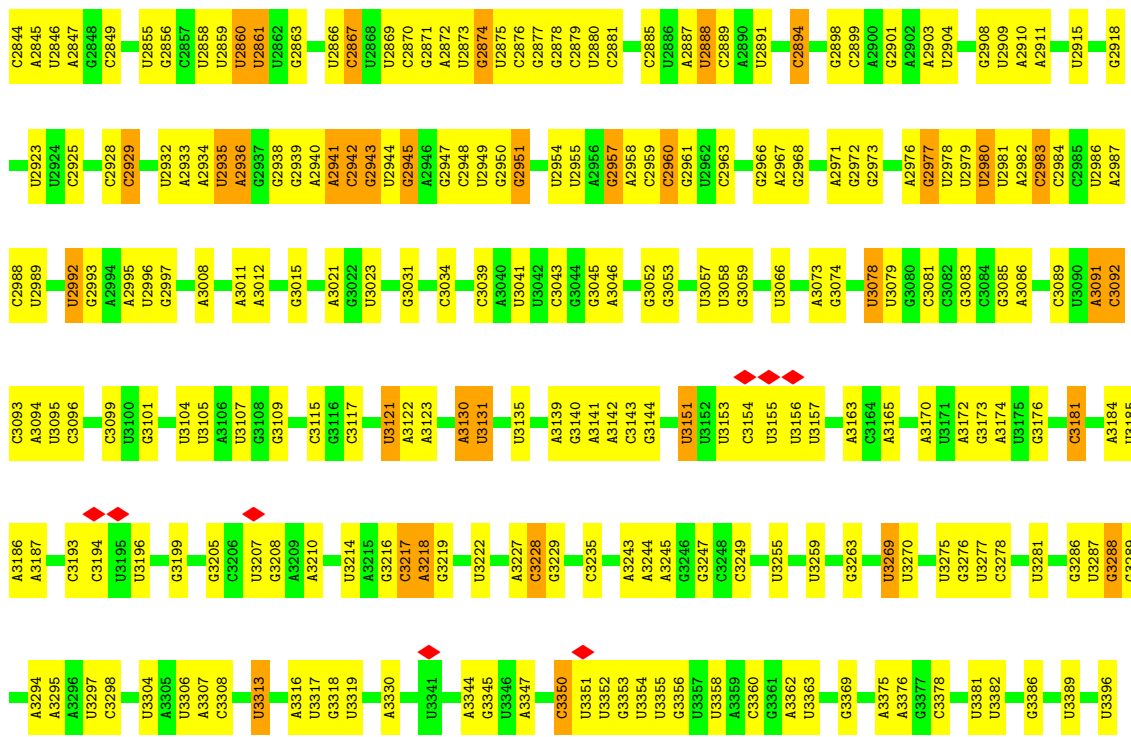


• Molecule 39: 25S rRNA (3184-MER)

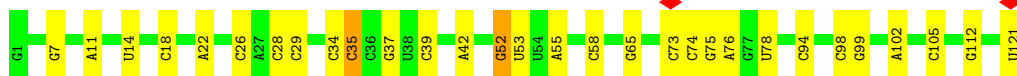
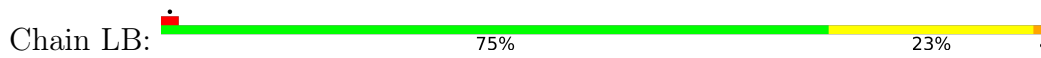




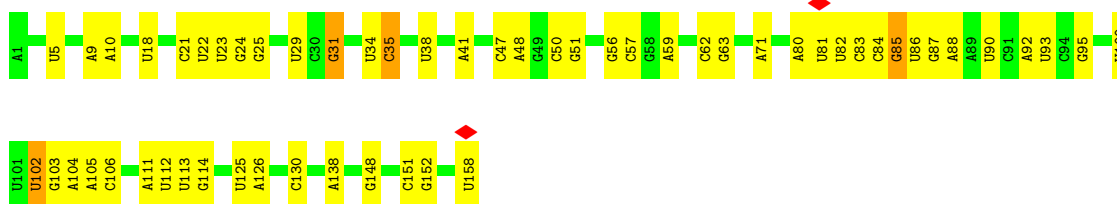
A visualization of EM validation metrics for EMD-12535, 7NRD. The data is organized into 12 columns, each representing a different validation metric (e.g., C1730, U1837, U1912, C2116, A2183, U2268, G2335, A2404, C2546, U2652, G2753, G2754, C2755, U2759, C2760, A2761, U2762, G2763, C2764, U2765, C2772, G2777, C2778, A2779, U2780, U2783, C2787, U2795, G2796, C2797, U2798, A2799, G2800, U2801, A2802, C2803, U2805, C2810, A2811, C2812, U2813, G2814, C2815, A2816, U2818, A2819, C2820, U2821, C2822, U2827, C2832, U2836, C2837, A2840, U2841, C2836, A2837, U2844, C2843, U2844). Each cell contains a numerical value and a color-coded box indicating its quality level. Red diamonds above certain cells indicate specific validation warnings. A large grey block is present in the lower-middle section of the table.



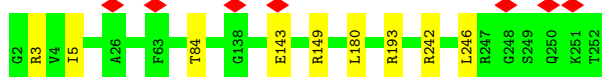
• Molecule 40: 5S rRNA (121-MER)



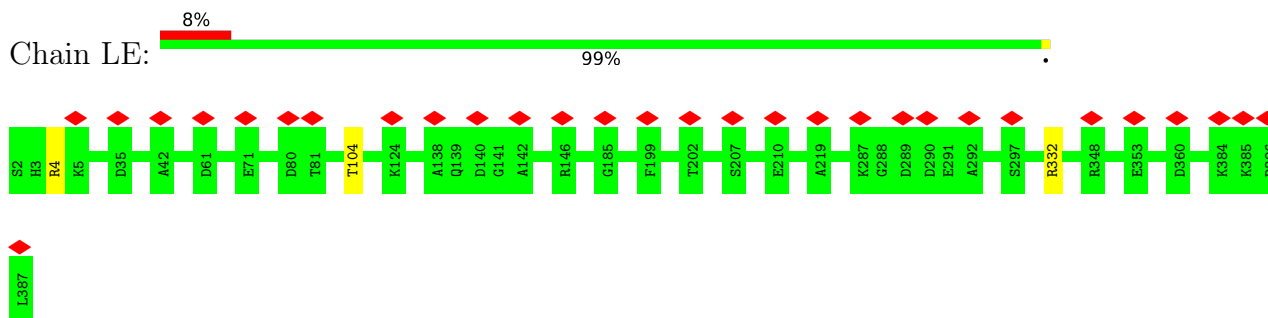
• Molecule 41: 5.8S rRNA (158-MER)



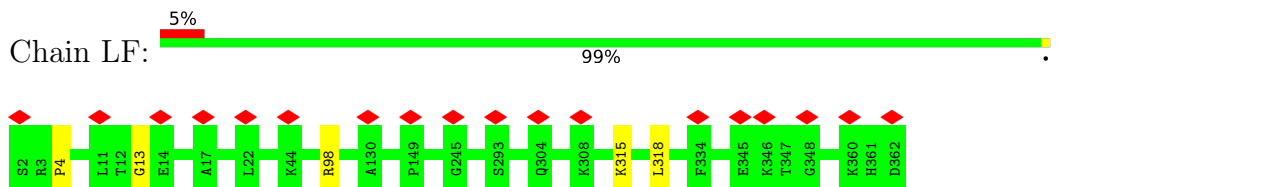
• Molecule 42: 60S ribosomal protein L2-A



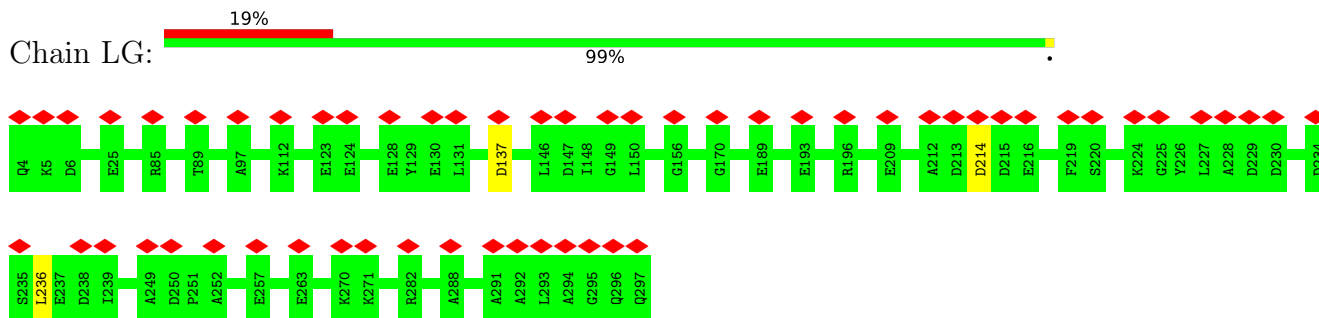
• Molecule 43: 60S ribosomal protein L3



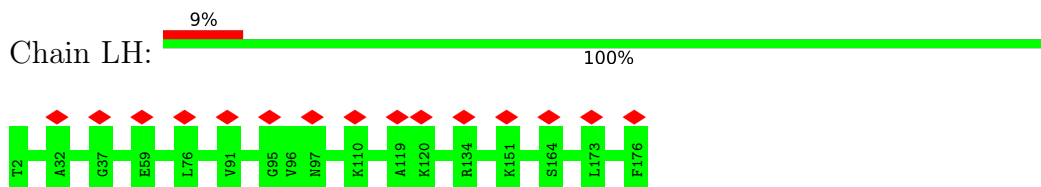
- Molecule 44: 60S ribosomal protein L4-A



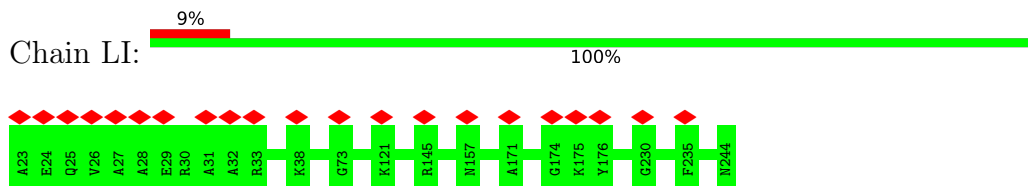
- Molecule 45: 60S ribosomal protein L5



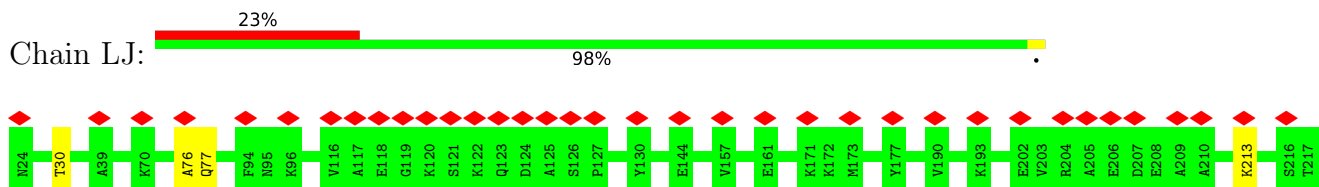
- Molecule 46: 60S ribosomal protein L6-B

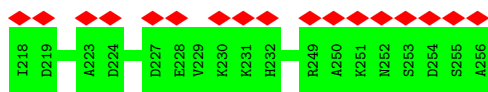


- Molecule 47: 60S ribosomal protein L7-A

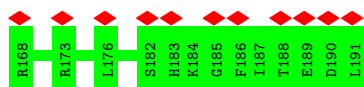
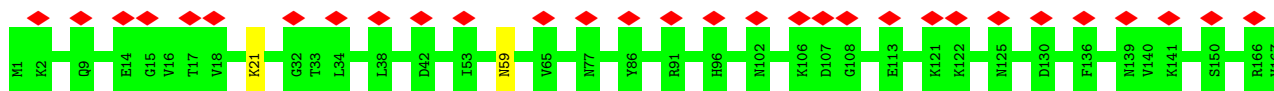


- Molecule 48: 60S ribosomal protein L8-A

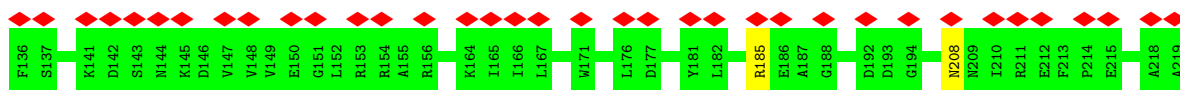
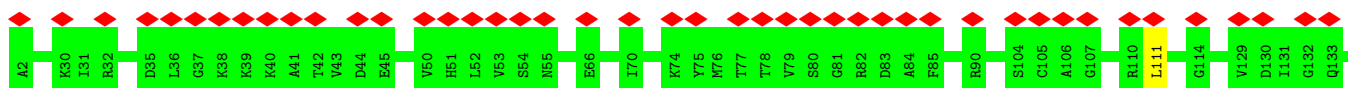




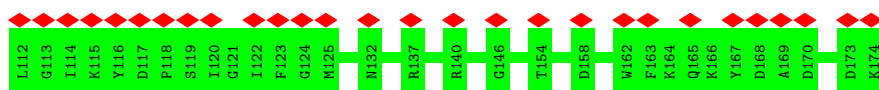
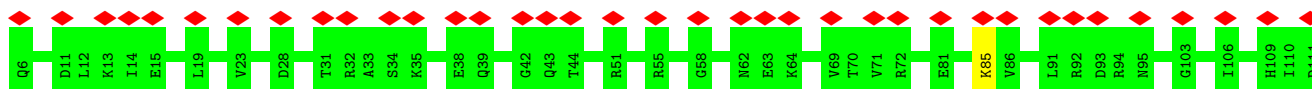
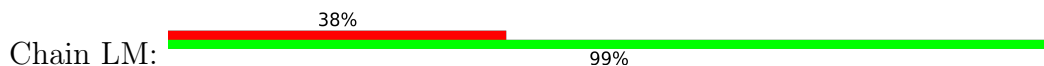
- Molecule 49: 60S ribosomal protein L9-A



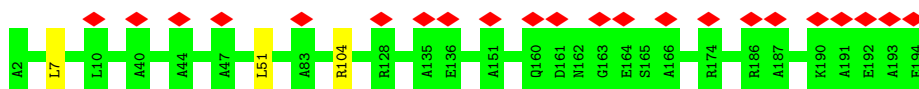
- Molecule 50: 60S ribosomal protein L10



- Molecule 51: 60S ribosomal protein L11-B

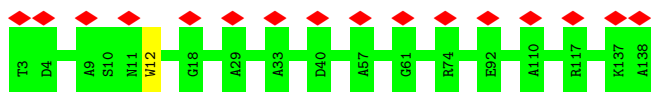


- Molecule 52: 60S ribosomal protein L13-A

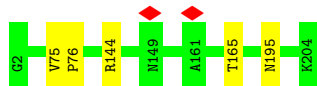


- Molecule 53: 60S ribosomal protein L14-A

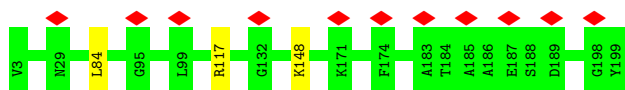




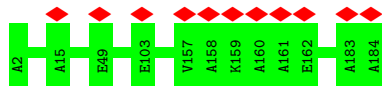
- Molecule 54: 60S ribosomal protein L15-A



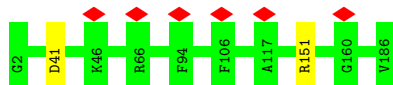
- Molecule 55: 60S ribosomal protein L16-A



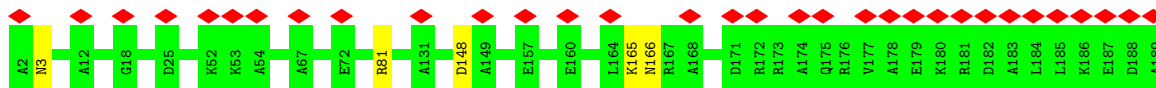
- Molecule 56: 60S ribosomal protein L17-A



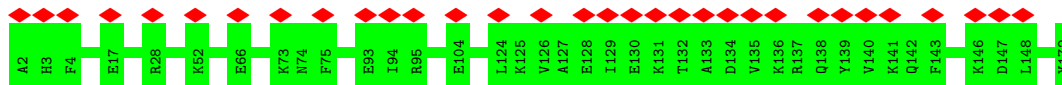
- Molecule 57: 60S ribosomal protein L18-A



- Molecule 58: 60S ribosomal protein L19-A

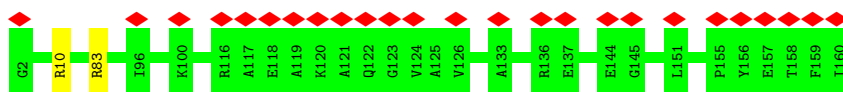


- Molecule 59: 60S ribosomal protein L20-A

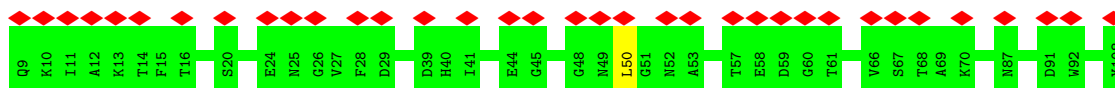


- Molecule 60: 60S ribosomal protein L21-A

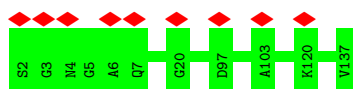




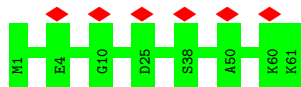
- Molecule 61: 60S ribosomal protein L22-A



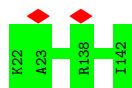
- Molecule 62: 60S ribosomal protein L23-A



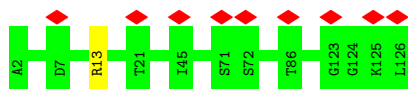
- Molecule 63: 60S ribosomal protein L24-A



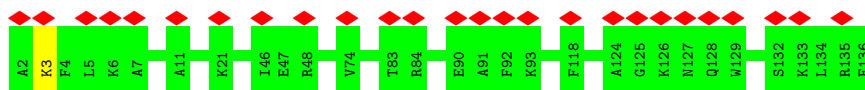
- Molecule 64: 60S ribosomal protein L25



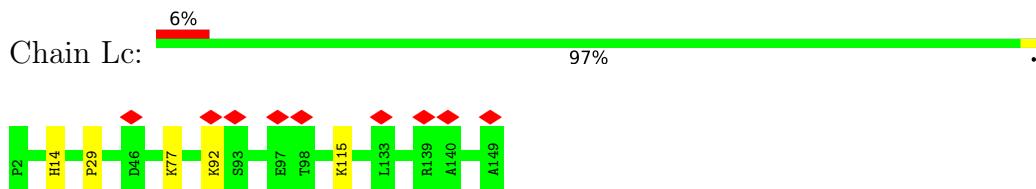
- Molecule 65: 60S ribosomal protein L26-A



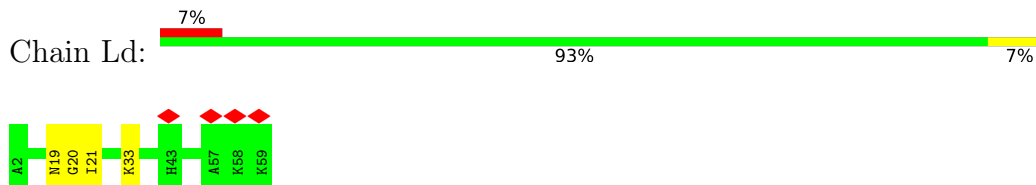
- Molecule 66: 60S ribosomal protein L27-A



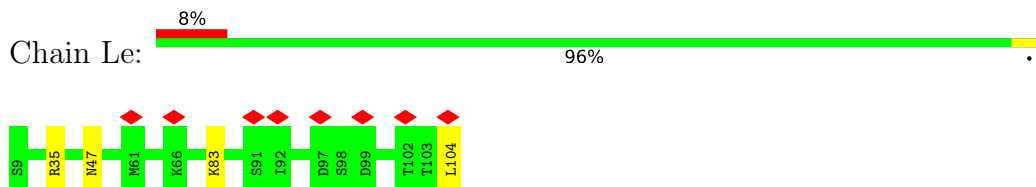
- Molecule 67: 60S ribosomal protein L28



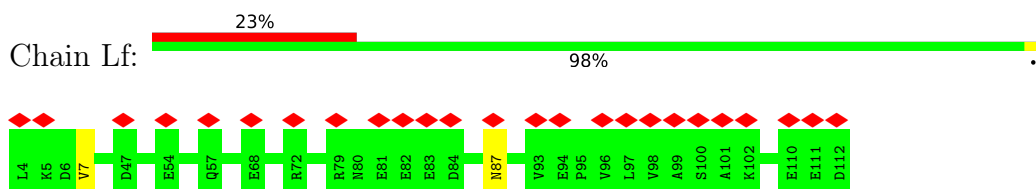
- Molecule 68: 60S ribosomal protein L29



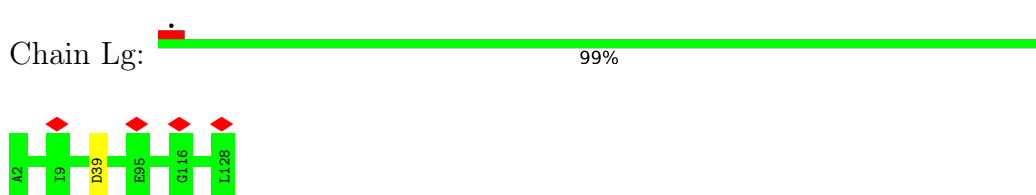
- Molecule 69: 60S ribosomal protein L30



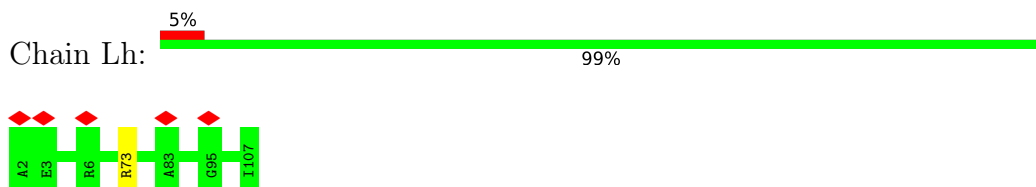
- Molecule 70: 60S ribosomal protein L31-A



- Molecule 71: 60S ribosomal protein L32

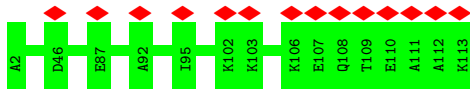


- Molecule 72: 60S ribosomal protein L33-A

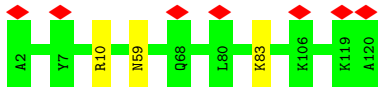


- Molecule 73: 60S ribosomal protein L34-A

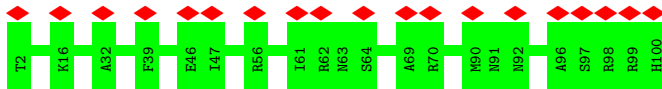




- Molecule 74: 60S ribosomal protein L35-A



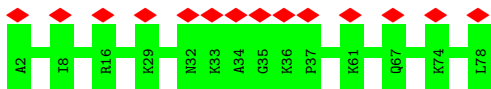
- Molecule 75: 60S ribosomal protein L36-A



- Molecule 76: 60S ribosomal protein L37-A



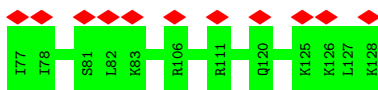
- Molecule 77: 60S ribosomal protein L38



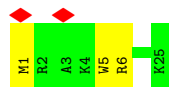
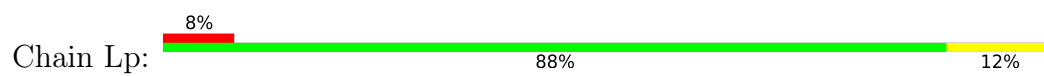
- Molecule 78: 60S ribosomal protein L39



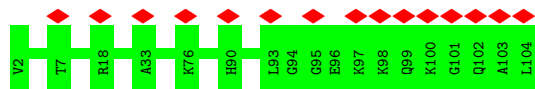
- Molecule 79: Ubiquitin-60S ribosomal protein L40



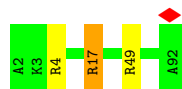
- Molecule 80: 60S ribosomal protein L41-B



- Molecule 81: 60S ribosomal protein L42-A



- Molecule 82: 60S ribosomal protein L43-A



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	30016	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 ( $e^-/\text{\AA}^2$ )	2.5	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	0.508	Depositor
Minimum map value	-0.313	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	758.8, 758.8, 758.8	wwPDB
Map dimensions	700, 700, 700	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

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	S2	1.49	417/42491 (1.0%)	1.63	1117/66211 (1.7%)
2	SA	0.51	0/1759	0.72	0/2368
3	SB	0.44	0/1629	0.68	1/2202 (0.0%)
4	SC	0.52	0/757	0.65	0/1022
5	SD	0.30	0/898	0.61	0/1220
6	SE	0.49	0/959	0.65	0/1288
7	SF	0.63	0/1125	0.82	0/1510
8	SG	0.49	0/1011	0.70	0/1355
9	SH	0.38	0/1211	0.66	0/1628
10	SI	0.48	0/1130	0.65	0/1517
11	SJ	0.56	0/815	0.73	0/1102
12	SK	0.39	0/566	0.62	0/761
13	SL	0.39	0/499	0.72	0/670
14	SM	0.61	0/452	0.85	0/600
15	SN	0.38	0/567	0.69	0/764
16	SO	0.42	0/2456	0.68	1/3343 (0.0%)
17	SP	0.58	0/1623	0.77	0/2222
18	SQ	0.56	0/1748	0.75	1/2352 (0.0%)
19	SR	0.72	1/1665 (0.1%)	0.82	1/2263 (0.0%)
20	SS	0.58	0/2109	0.75	1/2839 (0.0%)
21	ST	0.37	0/1779	0.60	0/2379
22	SU	0.42	0/1511	0.67	0/2036
23	SV	0.54	0/1514	0.69	0/2021
24	SW	0.53	0/1519	0.66	0/2035
25	SX	0.79	2/1194 (0.2%)	0.79	1/1610 (0.1%)
26	SY	0.55	0/1215	0.70	0/1638
27	SZ	0.54	0/960	0.72	0/1290
28	Sa	0.65	0/693	0.75	0/935
29	Sb	0.87	0/1038	0.86	1/1395 (0.1%)
30	Sc	0.81	1/1139 (0.1%)	0.91	1/1518 (0.1%)
31	Sd	0.50	0/1087	0.70	0/1449
32	Se	0.73	0/782	0.93	0/1047
33	Sf	0.44	0/620	0.74	1/838 (0.1%)
34	Sg	0.53	0/361	0.71	0/478

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	Sh	0.41	0/934	0.66	0/1251
36	S3	0.98	1/721 (0.1%)	1.69	26/1114 (2.3%)
37	Sn	0.66	1/1796 (0.1%)	1.52	44/2799 (1.6%)
38	Sm	0.73	1/1814 (0.1%)	1.19	15/2824 (0.5%)
39	LA	1.15	201/76214 (0.3%)	1.45	1276/118821 (1.1%)
40	LB	0.67	0/2883	1.19	24/4491 (0.5%)
41	LC	0.91	1/3746 (0.0%)	1.28	28/5832 (0.5%)
42	LD	0.74	0/1933	0.85	4/2598 (0.2%)
43	LE	0.50	0/3146	0.67	0/4228
44	LF	0.48	0/2800	0.67	1/3790 (0.0%)
45	LG	0.36	0/2400	0.63	3/3239 (0.1%)
46	LH	0.34	0/1329	0.57	0/1794
47	LI	0.45	0/1821	0.60	0/2451
48	LJ	0.37	0/1836	0.62	0/2481
49	LK	0.37	0/1529	0.62	0/2060
50	LL	0.38	0/1801	0.61	0/2416
51	LM	0.35	0/1367	0.62	0/1834
52	LN	0.42	0/1568	0.62	2/2106 (0.1%)
53	LO	0.34	0/1068	0.57	0/1438
54	LP	0.64	0/1757	0.76	0/2354
55	LQ	0.53	0/1585	0.71	1/2128 (0.0%)
56	LR	0.48	0/1439	0.63	0/1938
57	LS	0.41	0/1465	0.65	1/1965 (0.1%)
58	LT	0.45	0/1532	0.62	1/2043 (0.0%)
59	LU	0.42	0/1473	0.60	0/1980
60	LV	0.44	0/1296	0.63	0/1739
61	LW	0.33	0/812	0.64	1/1099 (0.1%)
62	LX	0.57	0/1018	0.77	0/1369
63	LY	0.43	0/521	0.64	0/691
64	LZ	0.43	0/979	0.59	0/1321
65	La	0.34	0/995	0.57	0/1329
66	Lb	0.37	0/1106	0.55	0/1485
67	Lc	0.52	0/1200	0.69	0/1607
68	Ld	0.42	0/473	0.65	0/629
69	Le	0.51	1/745 (0.1%)	0.64	1/1001 (0.1%)
70	Lf	0.39	0/890	0.61	0/1196
71	Lg	0.50	0/1038	0.67	0/1390
72	Lh	0.51	0/868	0.70	0/1168
73	Li	0.55	0/890	0.71	0/1189
74	Lj	0.31	0/978	0.59	0/1301
75	Lk	0.33	0/772	0.57	0/1026
76	Ll	0.73	1/660 (0.2%)	0.78	0/875
77	Lm	0.35	0/618	0.64	0/826

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
78	Ln	0.51	0/443	0.70	1/588 (0.2%)
79	Lo	0.38	0/416	0.55	0/553
80	Lp	0.78	0/230	1.19	1/296 (0.3%)
81	Lq	0.45	0/836	0.61	0/1104
82	Lr	0.73	0/701	0.77	0/934
All	All	1.01	628/219324 (0.3%)	1.26	2556/322597 (0.8%)

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
3	SB	0	2
5	SD	0	2
6	SE	0	2
7	SF	0	2
11	SJ	0	4
15	SN	0	2
17	SP	0	5
18	SQ	0	1
20	SS	0	1
22	SU	0	4
29	Sb	0	2
30	Sc	0	2
31	Sd	0	1
32	Se	0	1
35	Sh	0	1
42	LD	0	2
43	LE	0	1
44	LF	0	2
48	LJ	0	3
49	LK	0	1
53	LO	0	1
54	LP	0	2
55	LQ	0	1
67	Lc	0	2
68	Ld	0	1
70	Lf	0	1
71	Lg	0	1
74	Lj	0	1
80	Lp	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
82	Lr	0	1
All	All	0	54

The worst 5 of 628 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	Sm	1	C	OP3-P	-10.95	1.48	1.61
1	S2	382	C	N1-C6	-9.77	1.31	1.37
39	LA	2957	G	C5-C4	-9.75	1.31	1.38
1	S2	622	A	N9-C4	-9.53	1.32	1.37
1	S2	619	A	N9-C4	-9.47	1.32	1.37

The worst 5 of 2556 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S2	1159	C	N1-C2-O2	15.23	128.04	118.90
39	LA	823	C	C6-N1-C2	-14.08	114.67	120.30
1	S2	1159	C	C2-N1-C1'	13.77	133.94	118.80
1	S2	13	C	C6-N1-C2	-13.61	114.86	120.30
1	S2	13	C	C5-C6-N1	12.72	127.36	121.00

There are no chirality outliers.

5 of 54 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	SB	76	ARG	Peptide
3	SB	88	PRO	Peptide
5	SD	130	THR	Peptide
5	SD	86	VAL	Peptide
6	SE	51	SER	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

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	SA	221/223 (99%)	199 (90%)	22 (10%)	0	100	100
3	SB	204/206 (99%)	184 (90%)	20 (10%)	0	100	100
4	SC	90/92 (98%)	83 (92%)	7 (8%)	0	100	100
5	SD	122/124 (98%)	105 (86%)	14 (12%)	3 (2%)	5	35
6	SE	117/119 (98%)	100 (86%)	17 (14%)	0	100	100
7	SF	139/141 (99%)	122 (88%)	17 (12%)	0	100	100
8	SG	123/125 (98%)	108 (88%)	14 (11%)	1 (1%)	19	60
9	SH	143/145 (99%)	126 (88%)	17 (12%)	0	100	100
10	SI	141/143 (99%)	126 (89%)	15 (11%)	0	100	100
11	SJ	99/101 (98%)	86 (87%)	13 (13%)	0	100	100
12	SK	67/69 (97%)	59 (88%)	8 (12%)	0	100	100
13	SL	61/63 (97%)	51 (84%)	10 (16%)	0	100	100
14	SM	51/53 (96%)	43 (84%)	8 (16%)	0	100	100
15	SN	71/73 (97%)	51 (72%)	20 (28%)	0	100	100
16	SO	311/313 (99%)	278 (89%)	33 (11%)	0	100	100
17	SP	204/206 (99%)	171 (84%)	30 (15%)	3 (2%)	10	46
18	SQ	214/216 (99%)	185 (86%)	28 (13%)	1 (0%)	29	68
19	SR	215/217 (99%)	193 (90%)	22 (10%)	0	100	100
20	SS	258/260 (99%)	214 (83%)	43 (17%)	1 (0%)	34	72
21	ST	216/218 (99%)	196 (91%)	20 (9%)	0	100	100
22	SU	183/185 (99%)	159 (87%)	23 (13%)	1 (0%)	29	68
23	SV	184/188 (98%)	167 (91%)	17 (9%)	0	100	100
24	SW	183/185 (99%)	161 (88%)	22 (12%)	0	100	100
25	SX	144/146 (99%)	118 (82%)	24 (17%)	2 (1%)	11	47
26	SY	148/150 (99%)	132 (89%)	16 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	SZ	126/128 (98%)	105 (83%)	21 (17%)	0	100	100
28	Sa	85/87 (98%)	76 (89%)	9 (11%)	0	100	100
29	Sb	127/129 (98%)	112 (88%)	15 (12%)	0	100	100
30	Sc	142/144 (99%)	114 (80%)	28 (20%)	0	100	100
31	Sd	132/134 (98%)	114 (86%)	17 (13%)	1 (1%)	19	60
32	Se	95/97 (98%)	80 (84%)	14 (15%)	1 (1%)	14	52
33	Sf	79/81 (98%)	68 (86%)	11 (14%)	0	100	100
34	Sg	42/44 (96%)	35 (83%)	7 (17%)	0	100	100
35	Sh	118/120 (98%)	106 (90%)	12 (10%)	0	100	100
42	LD	249/251 (99%)	213 (86%)	36 (14%)	0	100	100
43	LE	384/386 (100%)	344 (90%)	40 (10%)	0	100	100
44	LF	359/361 (99%)	325 (90%)	33 (9%)	1 (0%)	41	76
45	LG	292/294 (99%)	261 (89%)	31 (11%)	0	100	100
46	LH	163/167 (98%)	147 (90%)	16 (10%)	0	100	100
47	LI	220/222 (99%)	206 (94%)	14 (6%)	0	100	100
48	LJ	231/233 (99%)	211 (91%)	20 (9%)	0	100	100
49	LK	189/191 (99%)	173 (92%)	16 (8%)	0	100	100
50	LL	216/218 (99%)	197 (91%)	19 (9%)	0	100	100
51	LM	167/169 (99%)	147 (88%)	20 (12%)	0	100	100
52	LN	191/193 (99%)	170 (89%)	21 (11%)	0	100	100
53	LO	134/136 (98%)	125 (93%)	9 (7%)	0	100	100
54	LP	201/203 (99%)	178 (89%)	22 (11%)	1 (0%)	29	68
55	LQ	195/197 (99%)	182 (93%)	13 (7%)	0	100	100
56	LR	181/183 (99%)	164 (91%)	17 (9%)	0	100	100
57	LS	183/185 (99%)	167 (91%)	16 (9%)	0	100	100
58	LT	186/188 (99%)	179 (96%)	7 (4%)	0	100	100
59	LU	169/171 (99%)	160 (95%)	9 (5%)	0	100	100
60	LV	157/159 (99%)	140 (89%)	17 (11%)	0	100	100
61	LW	98/100 (98%)	91 (93%)	7 (7%)	0	100	100
62	LX	134/136 (98%)	120 (90%)	14 (10%)	0	100	100
63	LY	59/61 (97%)	54 (92%)	5 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
64	LZ	119/121 (98%)	111 (93%)	8 (7%)	0	100	100
65	La	123/125 (98%)	114 (93%)	9 (7%)	0	100	100
66	Lb	133/135 (98%)	118 (89%)	15 (11%)	0	100	100
67	Lc	146/148 (99%)	126 (86%)	19 (13%)	1 (1%)	22	62
68	Ld	56/58 (97%)	46 (82%)	9 (16%)	1 (2%)	8	42
69	Le	94/96 (98%)	92 (98%)	2 (2%)	0	100	100
70	Lf	107/109 (98%)	96 (90%)	11 (10%)	0	100	100
71	Lg	125/127 (98%)	113 (90%)	12 (10%)	0	100	100
72	Lh	104/106 (98%)	98 (94%)	6 (6%)	0	100	100
73	Li	110/112 (98%)	100 (91%)	10 (9%)	0	100	100
74	Lj	117/119 (98%)	113 (97%)	4 (3%)	0	100	100
75	Lk	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
76	Ll	79/81 (98%)	71 (90%)	8 (10%)	0	100	100
77	Lm	75/77 (97%)	73 (97%)	2 (3%)	0	100	100
78	Ln	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
79	Lo	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
80	Lp	23/25 (92%)	23 (100%)	0	0	100	100
81	Lq	101/103 (98%)	91 (90%)	10 (10%)	0	100	100
82	Lr	89/91 (98%)	81 (91%)	8 (9%)	0	100	100
All	All	11009/11163 (99%)	9830 (89%)	1161 (10%)	18 (0%)	50	81

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	SQ	147	ALA
20	SS	163	ASP
31	Sd	52	LYS
5	SD	131	ASP
8	SG	82	ASP

### 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	
2	SA	182/182 (100%)	178 (98%)	4 (2%)	52	71
3	SB	173/173 (100%)	172 (99%)	1 (1%)	86	92
4	SC	73/85 (86%)	73 (100%)	0	100	100
5	SD	88/100 (88%)	87 (99%)	1 (1%)	73	85
6	SE	98/98 (100%)	98 (100%)	0	100	100
7	SF	117/117 (100%)	115 (98%)	2 (2%)	60	78
8	SG	113/113 (100%)	112 (99%)	1 (1%)	78	88
9	SH	128/128 (100%)	127 (99%)	1 (1%)	81	89
10	SI	115/115 (100%)	115 (100%)	0	100	100
11	SJ	94/94 (100%)	92 (98%)	2 (2%)	53	72
12	SK	61/61 (100%)	61 (100%)	0	100	100
13	SL	56/56 (100%)	56 (100%)	0	100	100
14	SM	47/47 (100%)	47 (100%)	0	100	100
15	SN	56/63 (89%)	55 (98%)	1 (2%)	59	77
16	SO	255/256 (100%)	254 (100%)	1 (0%)	91	94
17	SP	165/173 (95%)	163 (99%)	2 (1%)	71	84
18	SQ	192/192 (100%)	191 (100%)	1 (0%)	88	93
19	SR	176/176 (100%)	176 (100%)	0	100	100
20	SS	221/221 (100%)	219 (99%)	2 (1%)	78	88
21	ST	187/187 (100%)	186 (100%)	1 (0%)	88	93
22	SU	165/165 (100%)	164 (99%)	1 (1%)	86	92
23	SV	150/150 (100%)	147 (98%)	3 (2%)	55	74
24	SW	158/158 (100%)	158 (100%)	0	100	100
25	SX	129/129 (100%)	127 (98%)	2 (2%)	62	79
26	SY	127/127 (100%)	126 (99%)	1 (1%)	81	89
27	SZ	97/97 (100%)	96 (99%)	1 (1%)	76	86
28	Sa	74/74 (100%)	74 (100%)	0	100	100
29	Sb	110/110 (100%)	110 (100%)	0	100	100
30	Sc	119/119 (100%)	117 (98%)	2 (2%)	60	78
31	Sd	112/112 (100%)	110 (98%)	2 (2%)	59	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	Se	83/83 (100%)	81 (98%)	2 (2%)	49	69
33	Sf	70/70 (100%)	69 (99%)	1 (1%)	67	81
34	Sg	37/37 (100%)	36 (97%)	1 (3%)	44	66
35	Sh	101/101 (100%)	100 (99%)	1 (1%)	76	86
42	LD	190/193 (98%)	187 (98%)	3 (2%)	62	79
43	LE	318/322 (99%)	316 (99%)	2 (1%)	86	92
44	LF	288/288 (100%)	287 (100%)	1 (0%)	92	95
45	LG	241/243 (99%)	241 (100%)	0	100	100
46	LH	139/146 (95%)	139 (100%)	0	100	100
47	LI	186/186 (100%)	186 (100%)	0	100	100
48	LJ	187/191 (98%)	186 (100%)	1 (0%)	88	93
49	LK	168/171 (98%)	167 (99%)	1 (1%)	86	92
50	LL	185/185 (100%)	182 (98%)	3 (2%)	62	79
51	LM	145/147 (99%)	144 (99%)	1 (1%)	84	90
52	LN	154/154 (100%)	153 (99%)	1 (1%)	86	92
53	LO	107/107 (100%)	107 (100%)	0	100	100
54	LP	175/175 (100%)	173 (99%)	2 (1%)	73	85
55	LQ	160/160 (100%)	159 (99%)	1 (1%)	86	92
56	LR	138/145 (95%)	138 (100%)	0	100	100
57	LS	150/150 (100%)	149 (99%)	1 (1%)	84	90
58	LT	152/153 (99%)	148 (97%)	4 (3%)	46	67
59	LU	155/155 (100%)	155 (100%)	0	100	100
60	LV	135/136 (99%)	133 (98%)	2 (2%)	65	80
61	LW	87/87 (100%)	87 (100%)	0	100	100
62	LX	104/104 (100%)	104 (100%)	0	100	100
63	LY	54/54 (100%)	54 (100%)	0	100	100
64	LZ	104/105 (99%)	104 (100%)	0	100	100
65	La	108/108 (100%)	107 (99%)	1 (1%)	78	88
66	Lb	112/115 (97%)	111 (99%)	1 (1%)	78	88
67	Lc	117/118 (99%)	115 (98%)	2 (2%)	60	78
68	Ld	46/46 (100%)	44 (96%)	2 (4%)	29	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	Le	81/81 (100%)	79 (98%)	2 (2%)	47	68
70	Lf	92/96 (96%)	91 (99%)	1 (1%)	73	85
71	Lg	108/109 (99%)	108 (100%)	0	100	100
72	Lh	90/90 (100%)	89 (99%)	1 (1%)	73	85
73	Li	95/95 (100%)	95 (100%)	0	100	100
74	Lj	104/104 (100%)	102 (98%)	2 (2%)	57	75
75	Lk	80/81 (99%)	80 (100%)	0	100	100
76	Ll	67/67 (100%)	66 (98%)	1 (2%)	65	80
77	Lm	68/68 (100%)	68 (100%)	0	100	100
78	Ln	45/45 (100%)	45 (100%)	0	100	100
79	Lo	45/47 (96%)	45 (100%)	0	100	100
80	Lp	22/23 (96%)	22 (100%)	0	100	100
81	Lq	87/88 (99%)	87 (100%)	0	100	100
82	Lr	71/71 (100%)	68 (96%)	3 (4%)	30	55
All	All	9289/9378 (99%)	9213 (99%)	76 (1%)	82	89

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
58	LT	166	ASN
74	Lj	59	ASN
60	LV	83	ARG
68	Ld	33	LYS
82	Lr	49	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 101 such sidechains are listed below:

Mol	Chain	Res	Type
44	LF	45	ASN
50	LL	209	ASN
81	Lq	3	ASN
44	LF	221	ASN
48	LJ	137	ASN

### 5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	S2	1781/1800 (98%)	648 (36%)	40 (2%)
36	S3	31/32 (96%)	21 (67%)	2 (6%)
37	Sn	74/75 (98%)	27 (36%)	0
38	Sm	75/77 (97%)	15 (20%)	0
39	LA	3180/3394 (93%)	918 (28%)	33 (1%)
40	LB	120/121 (99%)	20 (16%)	1 (0%)
41	LC	157/158 (99%)	41 (26%)	2 (1%)
All	All	5418/5657 (95%)	1690 (31%)	78 (1%)

5 of 1690 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	S2	2	A
1	S2	4	C
1	S2	5	U
1	S2	11	A
1	S2	15	U

5 of 78 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
39	LA	2138	A
39	LA	3228	C
39	LA	2445	A
39	LA	2801	A
40	LB	52	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
23	SV	1
46	LH	1
30	Sc	1
69	Le	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	SV	123:LYS	C	135:LYS	N	22.74
1	LH	120:LYS	C	129:GLU	N	12.42
1	Sc	4:GLY	C	5:LYS	N	1.20
1	Le	47:ASN	C	48:THR	N	1.19

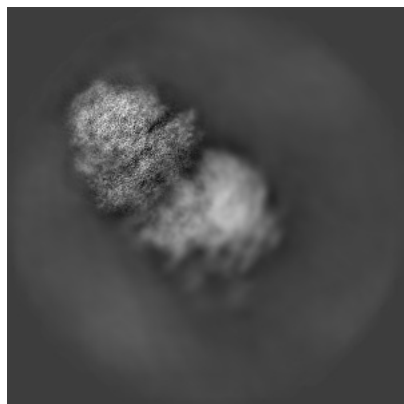
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12535. These allow visual inspection of the internal detail of the map and identification of artifacts.

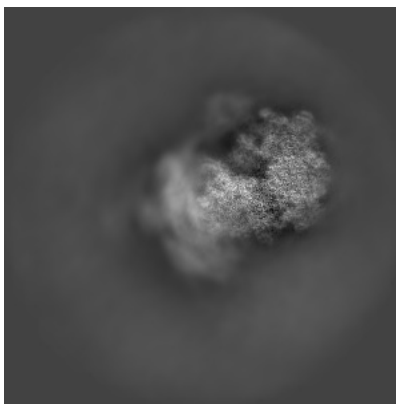
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

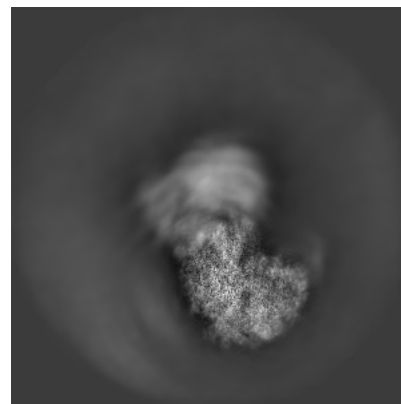
#### 6.1.1 Primary map



X

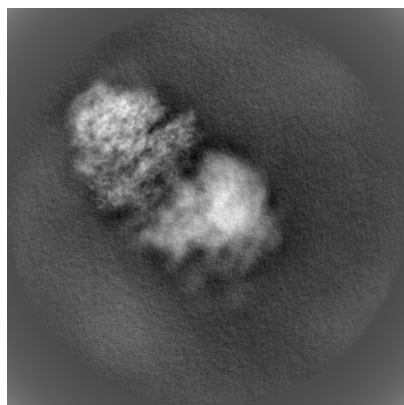


Y

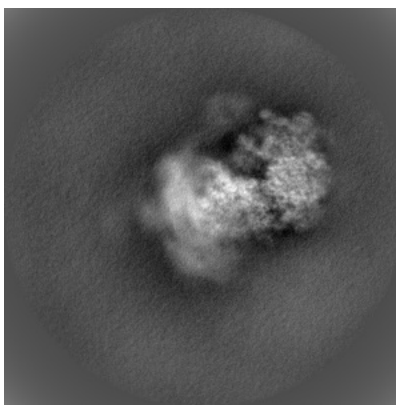


Z

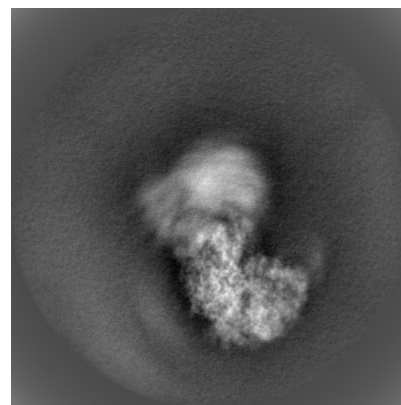
#### 6.1.2 Raw map



X



Y

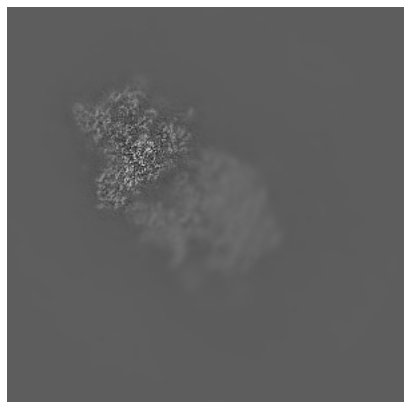


Z

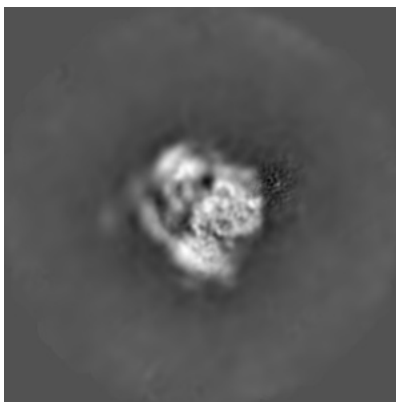
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

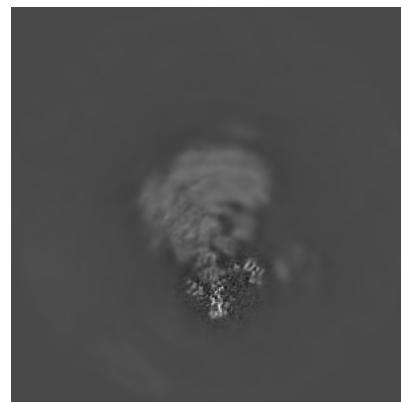
### 6.2.1 Primary map



X Index: 350

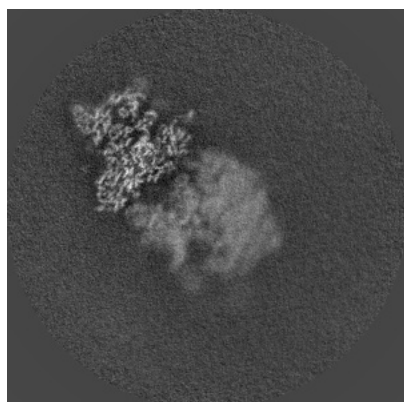


Y Index: 350

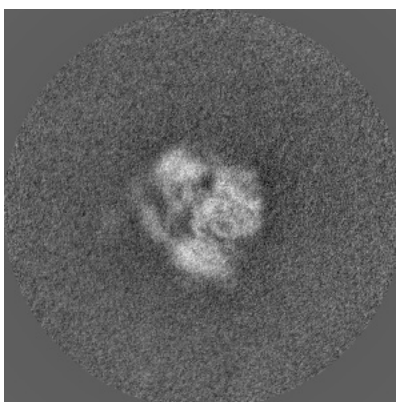


Z Index: 350

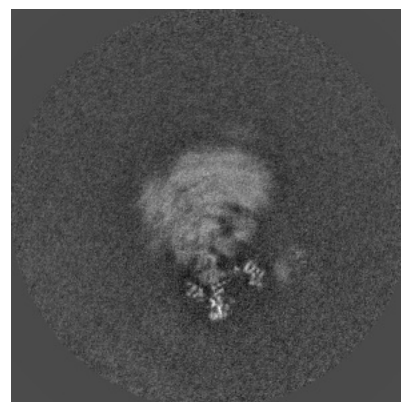
### 6.2.2 Raw map



X Index: 350



Y Index: 350

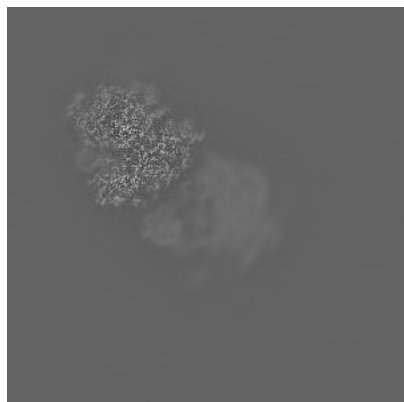


Z Index: 350

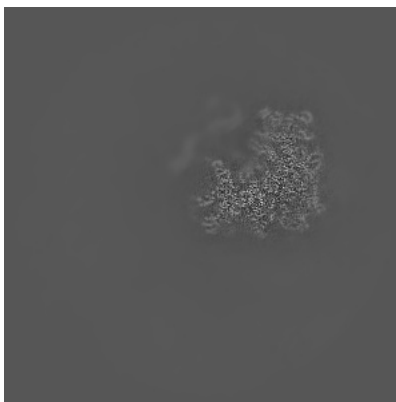
The images above show central slices of the map in three orthogonal directions.

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

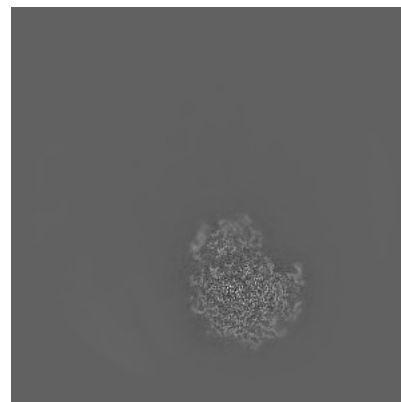
### 6.3.1 Primary map



X Index: 383

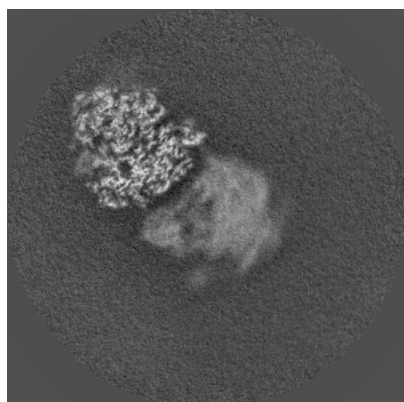


Y Index: 212

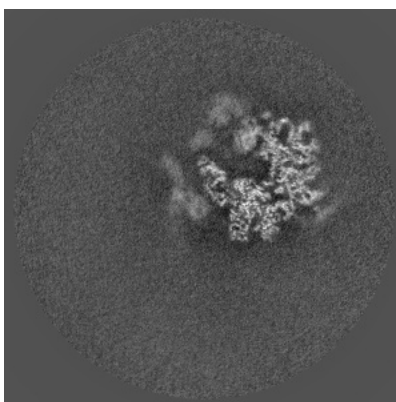


Z Index: 489

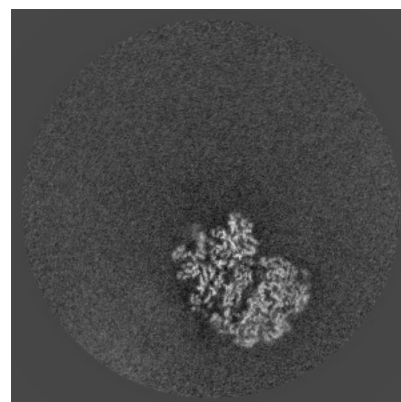
### 6.3.2 Raw map



X Index: 388



Y Index: 239



Z Index: 466

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

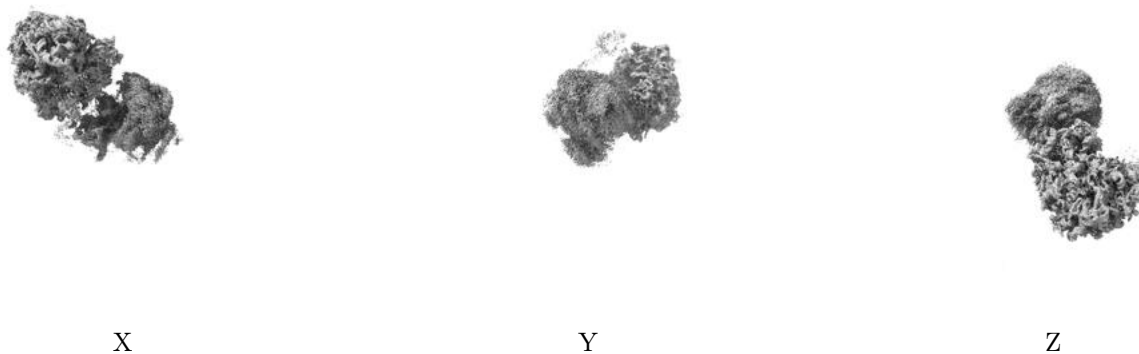
## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



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

### 6.4.2 Raw map



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

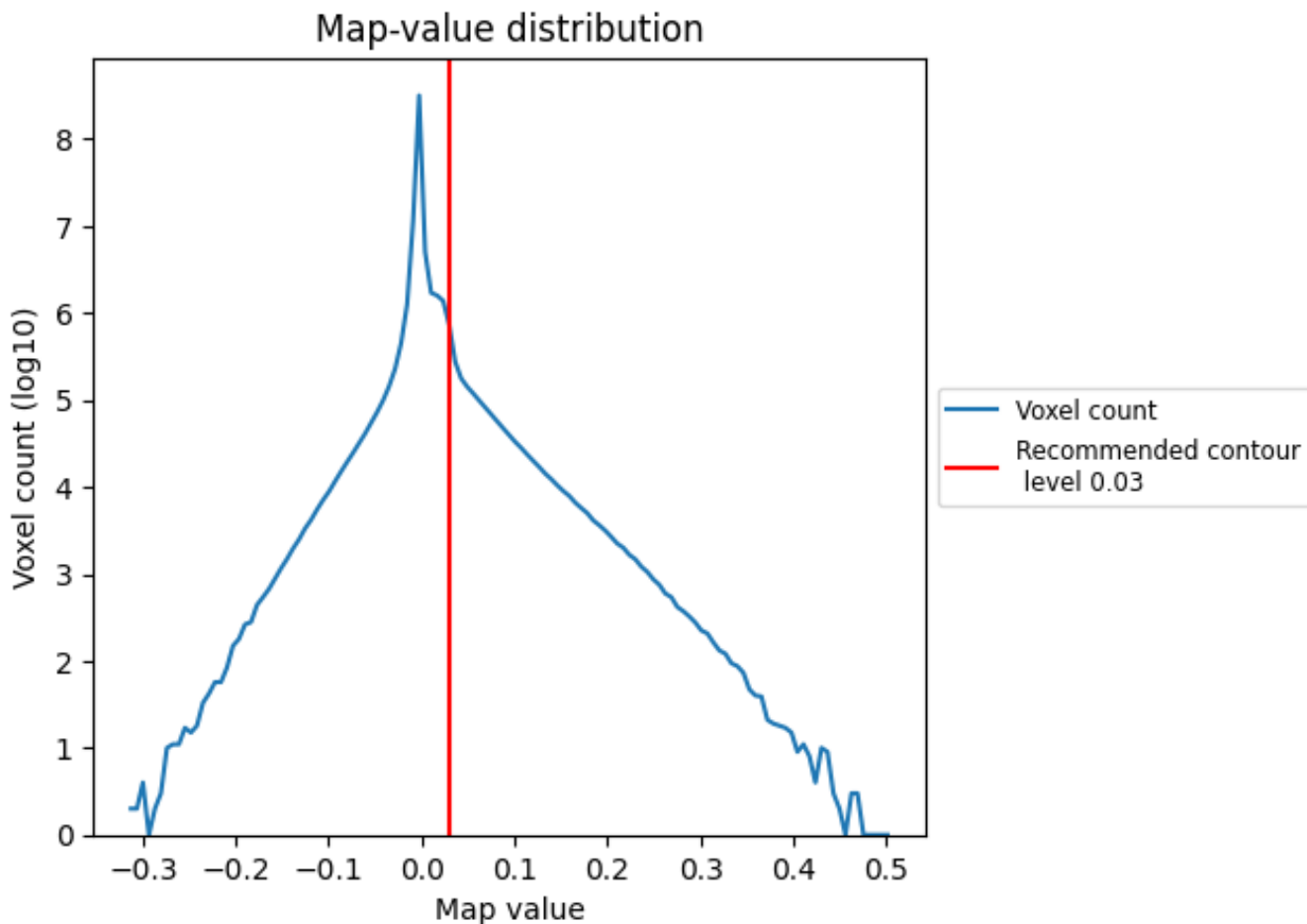
## 6.5 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

## 7 Map analysis [i](#)

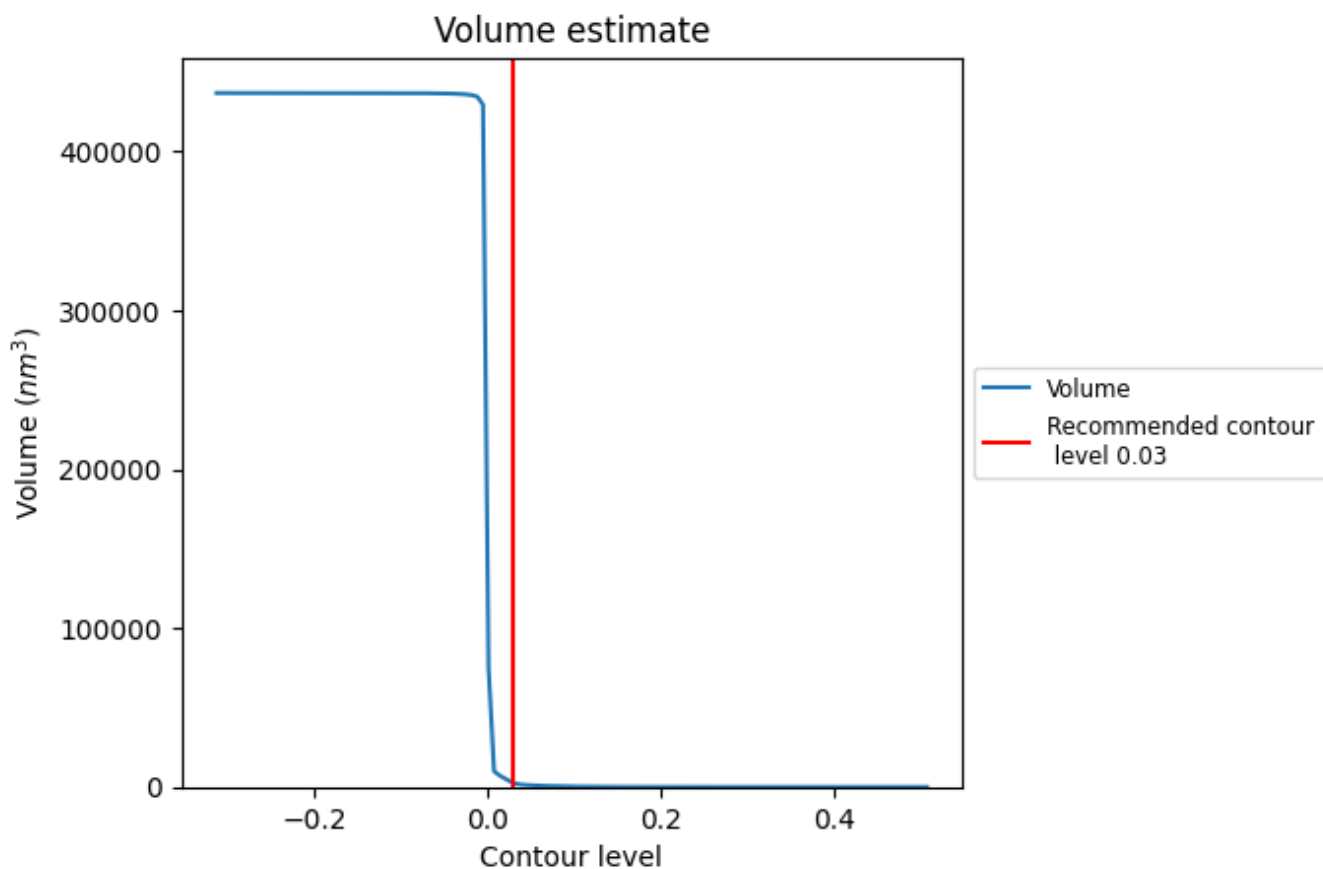
This section contains the results of statistical analysis of the map.

### 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.

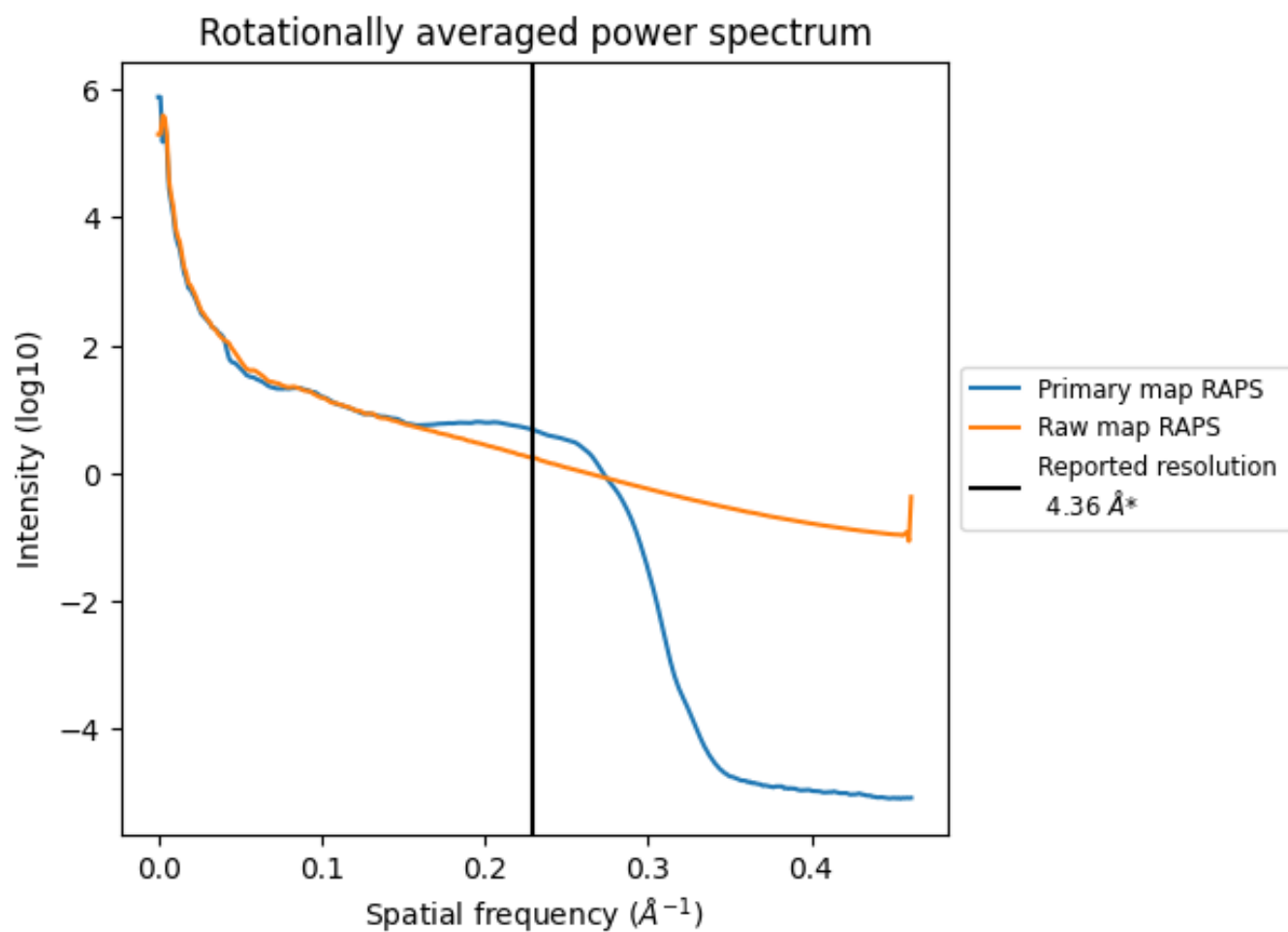
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2684 nm<sup>3</sup>; this corresponds to an approximate mass of 2425 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



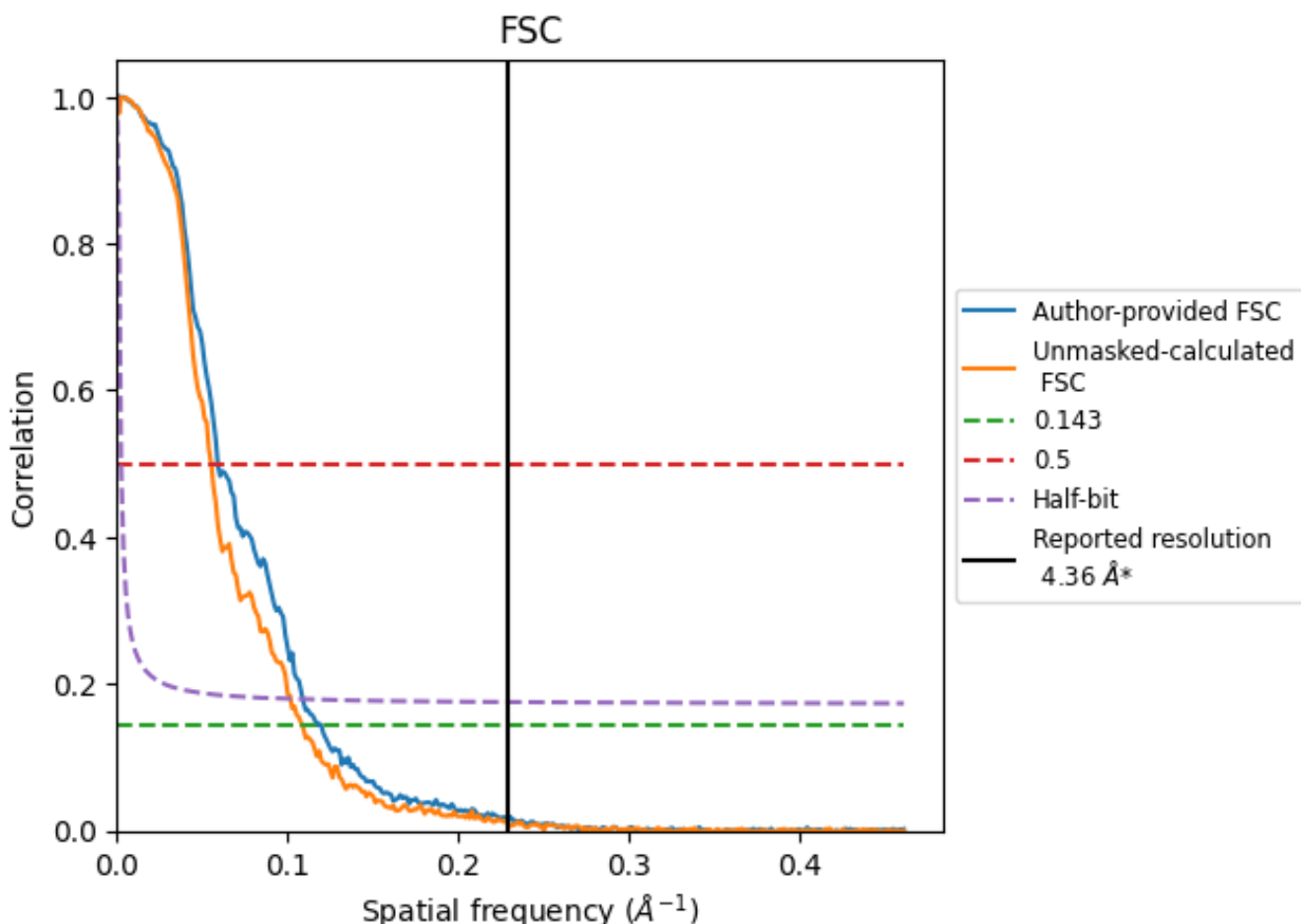
\*Reported resolution corresponds to spatial frequency of  $0.229 \text{ \AA}^{-1}$



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

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.229 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	4.36	-	-
Author-provided FSC curve	8.35	16.89	9.17
Unmasked-calculated*	9.21	18.08	9.82

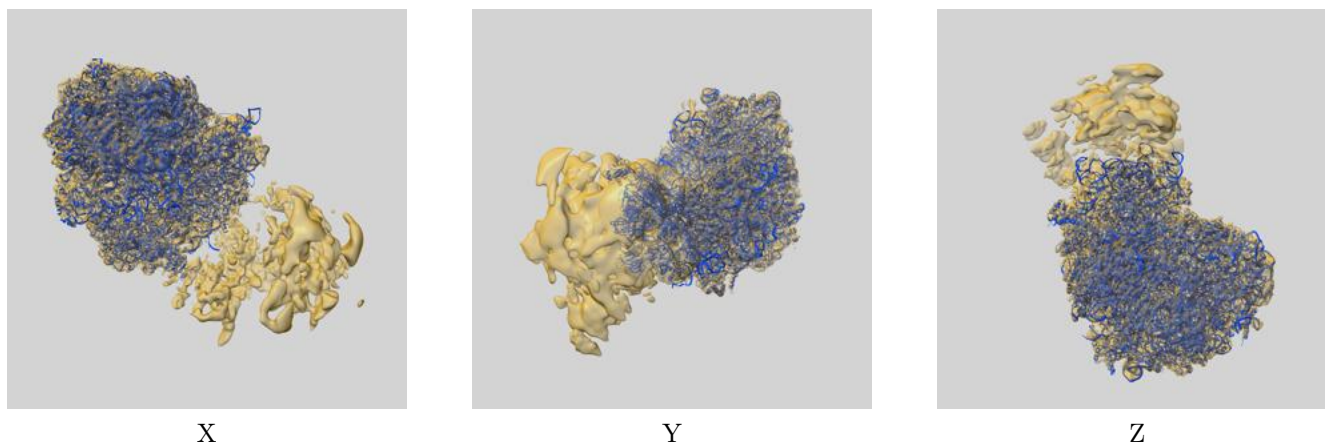
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 8.35 differs from the reported value 4.36 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 9.21 differs from the reported value 4.36 by more than 10 %

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

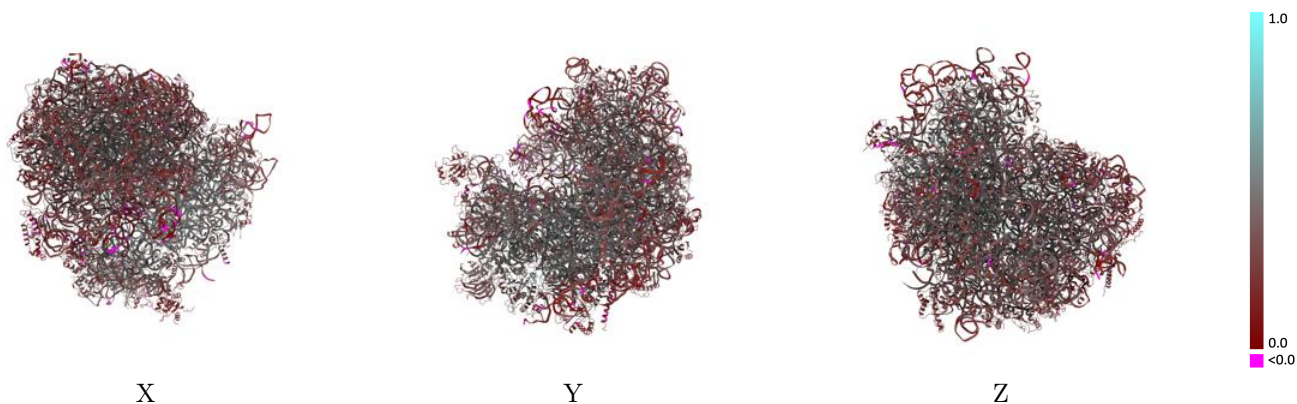
This section contains information regarding the fit between EMDB map EMD-12535 and PDB model 7NRD. Per-residue inclusion information can be found in section [3](#) on page [19](#).

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



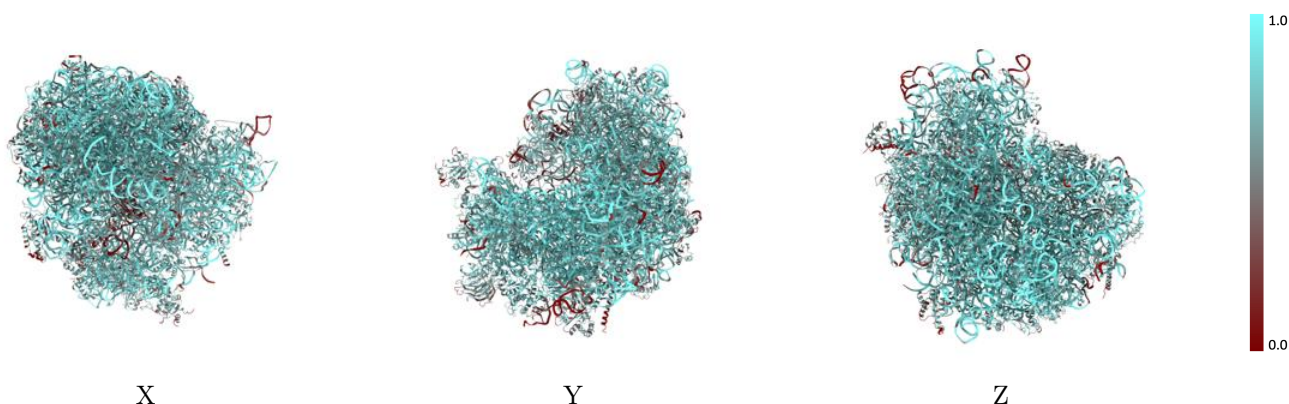
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



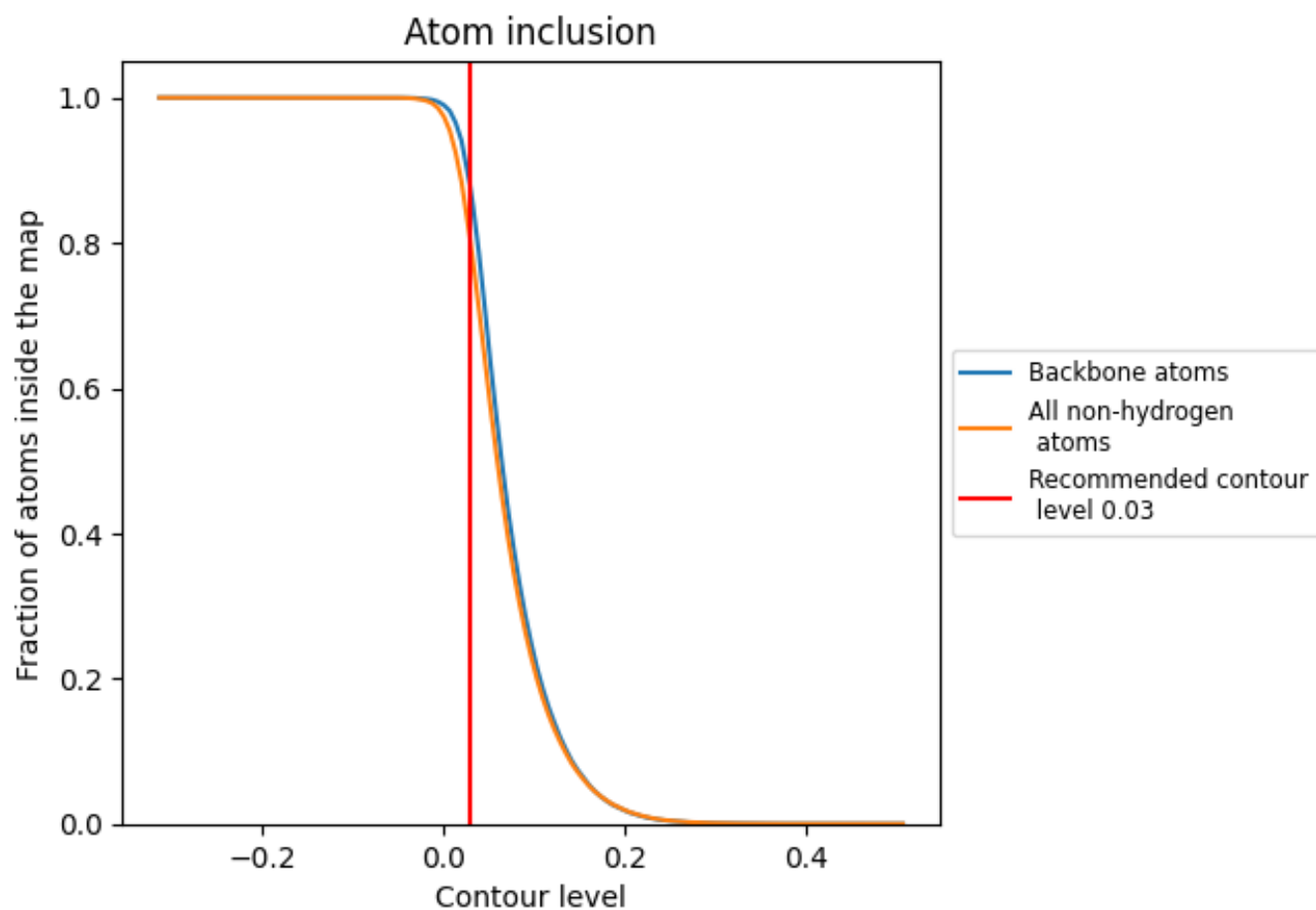
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 81% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary





















































































The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8066	 0.3630
LA	 0.8840	 0.3670
LB	 0.9124	 0.3100
LC	 0.9120	 0.3670
LD	 0.8293	 0.4600
LE	 0.7144	 0.3550
LF	 0.7748	 0.3420
LG	 0.6329	 0.2290
LH	 0.7002	 0.2580
LI	 0.6860	 0.3250
LJ	 0.5576	 0.2920
LK	 0.5777	 0.2820
LL	 0.5102	 0.2650
LM	 0.4878	 0.1750
LN	 0.7115	 0.3320
LO	 0.6998	 0.2610
LP	 0.8021	 0.4030
LQ	 0.7338	 0.3460
LR	 0.7533	 0.3640
LS	 0.7728	 0.3450
LT	 0.6832	 0.3360
LU	 0.6291	 0.3130
LV	 0.6926	 0.3350
LW	 0.5102	 0.2420
LX	 0.7538	 0.4220
LY	 0.7120	 0.3670
LZ	 0.7675	 0.3670
La	 0.7618	 0.3100
Lb	 0.5807	 0.2800
Lc	 0.7909	 0.3760
Ld	 0.7677	 0.3590
Le	 0.6648	 0.3510
Lf	 0.5788	 0.3070
Lg	 0.7851	 0.3760
Lh	 0.7674	 0.3600















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Chain	Atom inclusion	Q-score
Li	 0.7156	 0.3860
Lj	 0.7094	 0.3040
Lk	 0.6311	 0.2990
Ll	 0.8918	 0.4450
Lm	 0.6294	 0.2560
Ln	 0.8120	 0.4160
Lo	 0.5707	 0.3260
Lp	 0.7067	 0.3810
Lq	 0.6596	 0.3450
Lr	 0.8191	 0.4470
S2	 0.8899	 0.4030
S3	 0.5844	 0.3100
SA	 0.7052	 0.3950
SB	 0.7097	 0.3340
SC	 0.6919	 0.3470
SD	 0.4761	 0.2010
SE	 0.6861	 0.3390
SF	 0.7627	 0.3710
SG	 0.6434	 0.3380
SH	 0.7019	 0.3370
SI	 0.7613	 0.3450
SJ	 0.7456	 0.3730
SK	 0.6476	 0.2720
SL	 0.6751	 0.3650
SM	 0.8203	 0.4310
SN	 0.6077	 0.2430
SO	 0.5924	 0.3060
SP	 0.7692	 0.3990
SQ	 0.6773	 0.3940
SR	 0.8340	 0.4640
SS	 0.7835	 0.4150
ST	 0.6945	 0.3130
SU	 0.6417	 0.3160
SV	 0.7925	 0.3750
SW	 0.7198	 0.3970
SX	 0.8100	 0.4430
SY	 0.8234	 0.4240
SZ	 0.7225	 0.4050
Sa	 0.7590	 0.4110
Sb	 0.8968	 0.4820
Sc	 0.8812	 0.4840
Sd	 0.7272	 0.3560

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Chain	Atom inclusion	Q-score
Se	 0.8227	 0.4590
Sf	 0.7338	 0.3990
Sg	 0.8047	 0.4270
Sh	 0.7118	 0.3420
Sm	 0.8062	 0.3000
Sn	 0.4826	 0.1880