



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:15 AM UTC

PDB ID : 6SNT / pdb_00006snt
EMDB ID : EMD-10262
Title : Yeast 80S ribosome stalled on SDD1 mRNA.
Authors : Tesina, P.; Buschauer, R.; Cheng, J.; Becker, T.; Beckmann, R.
Deposited on : 2019-08-27
Resolution : 2.80 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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

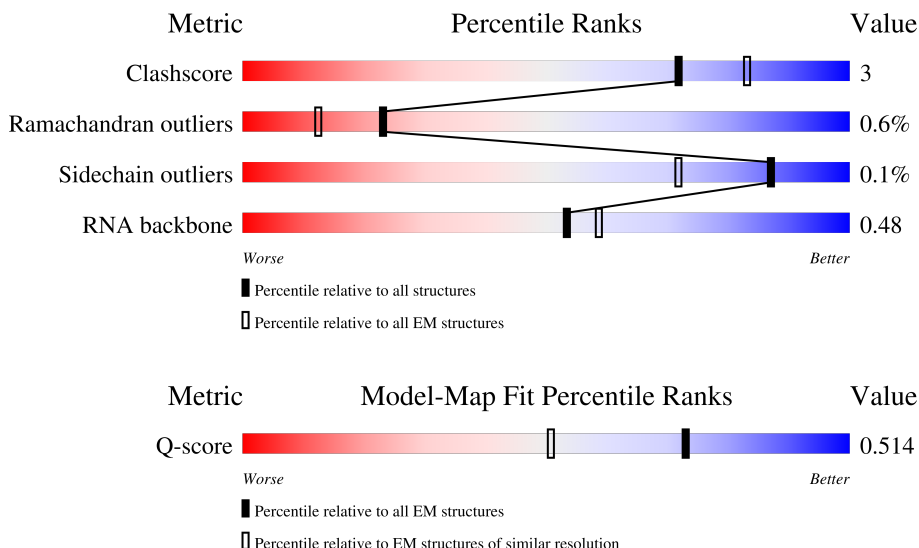
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11806 (2.30 - 3.30)

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

Mol	Chain	Length	Quality of chain
1	2	1800	
2	A	252	
3	B	255	

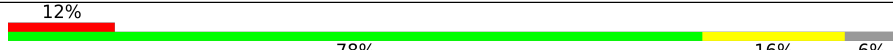
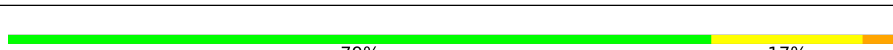
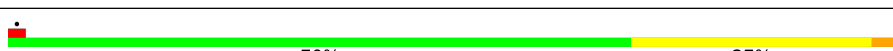
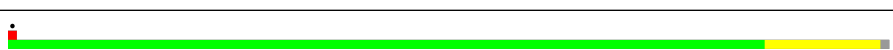
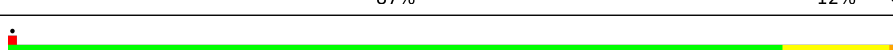
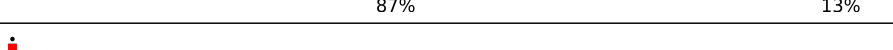
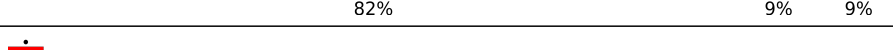
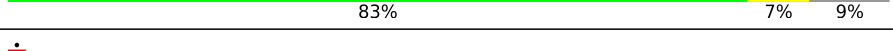
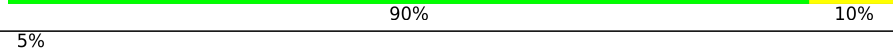
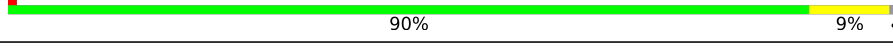
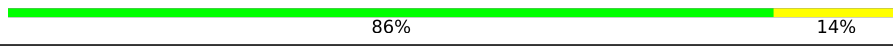
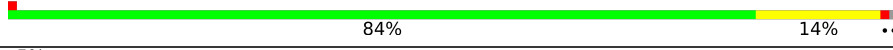
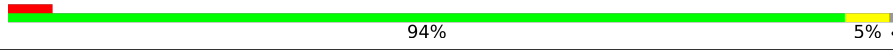
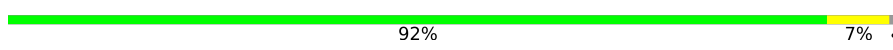
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Mol	Chain	Length	Quality of chain
4	P	142	
5	C	254	
6	D	240	
7	E	261	
8	F	225	
9	G	236	
10	H	190	
11	I	200	
12	J	197	
13	K	105	
14	L	156	
15	M	143	
16	N	151	
17	O	137	
18	Q	143	
19	R	136	
20	S	146	
21	T	144	
22	U	121	
23	V	87	
24	W	130	
25	X	145	
26	Y	135	
27	Z	105	
28	a	119	

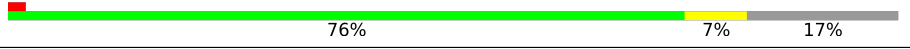
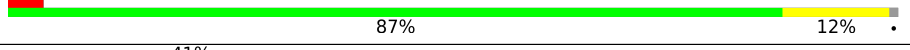
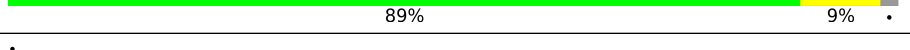
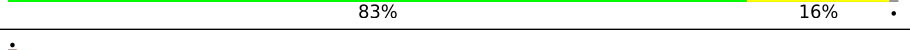
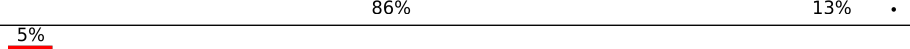
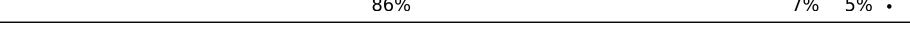
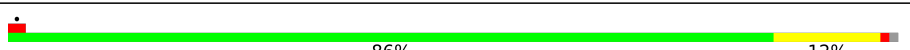
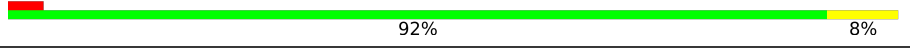
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Mol	Chain	Length	Quality of chain
29	b	82	
30	d	56	
31	e	63	
32	f	152	
33	g	319	
34	c	67	
35	4	121	
36	3	158	
37	h	254	
38	i	387	
39	j	362	
40	k	297	
41	l	167	
42	m	244	
43	n	256	
44	o	191	
45	p	221	
46	q	174	
47	r	199	
48	s	138	
49	t	204	
50	u	199	
51	v	184	
52	w	186	
53	x	189	

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Mol	Chain	Length	Quality of chain
54	y	172	
55	z	160	
56	au	121	
57	AB	137	
58	at	155	
59	as	142	
60	ar	127	
61	aq	136	
62	ap	149	
63	ao	59	
64	an	105	
65	am	113	
66	al	130	
67	ak	107	
68	aj	121	
69	ai	120	
70	ah	100	
71	ag	88	
72	af	78	
73	ae	51	
74	ad	128	
75	ac	25	
76	ab	106	
77	aa	92	
78	1	3396	

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Mol	Chain	Length	Quality of chain
79	5	21	71% 43% 38% 19%
80	NC	233	6% 94%
81	6	76	76% 22%

2 Entry composition [i](#)

There are 83 unique types of molecules in this entry. The entry contains 201787 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 *Saccharomyces cerevisiae* S288C 18S ribosomal RNA (RDN18-1), rRNA.

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

- Molecule 2 is a protein called 40S ribosomal protein S0-A.

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

- Molecule 3 is a protein called 40S ribosomal protein S1-A.

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

- Molecule 4 is a protein called 40S ribosomal protein S15.

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

- Molecule 5 is a protein called 40S ribosomal protein S2.

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

- Molecule 6 is a protein called 40S ribosomal protein S3.

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

- Molecule 7 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 8 is a protein called 40S ribosomal protein S5.

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

- Molecule 9 is a protein called 40S ribosomal protein S6-A.

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

- Molecule 10 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	184	Total	C	N	O	S	0	0
			1473	946	263	264			

- Molecule 11 is a protein called 40S ribosomal protein S8-A.

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

- Molecule 12 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 13 is a protein called 40S ribosomal protein S10-A.

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

- Molecule 14 is a protein called 40S ribosomal protein S11-A.

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

- Molecule 15 is a protein called 40S ribosomal protein S12.

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

- Molecule 16 is a protein called 40S ribosomal protein S13.

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

- Molecule 17 is a protein called 40S ribosomal protein S14-A.

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

- Molecule 18 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 19 is a protein called 40S ribosomal protein S17-B.

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

- Molecule 20 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 21 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 22 is a protein called 40S ribosomal protein S20.

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

- Molecule 23 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 24 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 25 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 26 is a protein called 40S ribosomal protein S24-A.

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

- Molecule 27 is a protein called 40S ribosomal protein S25-A.

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

- Molecule 28 is a protein called 40S ribosomal protein S26-A.

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

- Molecule 29 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 30 is a protein called 40S ribosomal protein S29-A.

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

- Molecule 31 is a protein called 40S ribosomal protein S30-A.

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

- Molecule 32 is a protein called Ubiquitin-40S ribosomal protein S31.

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

- Molecule 33 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

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

- Molecule 34 is a protein called 40S ribosomal protein S28-B.

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

- Molecule 35 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	4	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 36 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	3	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 37 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 38 is a protein called 60S ribosomal protein L3.

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

- Molecule 39 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 40 is a protein called 60S ribosomal protein L5.

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

- Molecule 41 is a protein called 60S ribosomal protein L6-B.

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

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	113	ALA	LYS	conflict	UNP P05739
1	114	ALA	LYS	conflict	UNP P05739
1	115	ALA	GLU	conflict	UNP P05739
1	116	ALA	LYS	conflict	UNP P05739
1	117	ALA	LYS	conflict	UNP P05739
1	118	ALA	GLU	conflict	UNP P05739
1	?	-	ASN	deletion	UNP P05739
1	?	-	LEU	deletion	UNP P05739
1	?	-	PHE	deletion	UNP P05739
1	?	-	PRO	deletion	UNP P05739
1	?	-	GLU	deletion	UNP P05739
1	?	-	GLN	deletion	UNP P05739
1	?	-	GLN	deletion	UNP P05739
1	?	-	THR	deletion	UNP P05739
1	120	ALA	LYS	conflict	UNP P05739
1	132	ALA	THR	conflict	UNP P05739
1	146	ILE	LEU	conflict	UNP P05739
1	173	MET	LEU	conflict	UNP P05739

- Molecule 42 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 43 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 44 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 45 is a protein called 60S ribosomal protein L10.

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

- Molecule 46 is a protein called 60S ribosomal protein L11-A.

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

- Molecule 47 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 48 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 51 is a protein called 60S ribosomal protein L17-A.

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

- Molecule 52 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 53 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 54 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 55 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 56 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 57 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 58 is a protein called 60S ribosomal protein L24-A.

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
at	104	GLN	ASN	conflict	UNP P04449
at	109	GLN	LEU	conflict	UNP P04449
at	112	ASP	ASN	conflict	UNP P04449
at	119	ALA	GLU	conflict	UNP P04449

- Molecule 59 is a protein called 60S ribosomal protein L25.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	ar	125	Total	C	N	O		0	0
			984	620	191	173			

- Molecule 61 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 62 is a protein called 60S ribosomal protein L28.

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

- Molecule 63 is a protein called 60S ribosomal protein L29.

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

- Molecule 64 is a protein called 60S ribosomal protein L30.

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

- Molecule 65 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 66 is a protein called 60S ribosomal protein L32.

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

- Molecule 67 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 68 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 69 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 70 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 71 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 72 is a protein called 60S ribosomal protein L38.

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

- Molecule 73 is a protein called 60S ribosomal protein L39.

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

- Molecule 74 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 75 is a protein called L41-A.

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

- Molecule 76 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 77 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 78 is a RNA chain called *Saccharomyces cerevisiae* S288C 25S ribosomal RNA (RDN25-1), rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	1	3184	Total	C	N	O	P	0	0
			68091	30415	12259	22233	3184		

- Molecule 79 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	5	21	Total	C	N	O	P	0	0
			454	203	88	142	21		

- Molecule 80 is a protein called Uncharacterized protein YEL057C.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	NC	14	Total	C	N	O	S	0	0
			129	85	21	22	1		

- Molecule 81 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	6	76	Total	C	N	O	P	0	0
			1621	723	290	532	76		

- Molecule 82 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
82	2	82	Total	Mg	0
			82	82	
82	E	1	Total	Mg	0
			1	1	
82	F	1	Total	Mg	0
			1	1	
82	T	1	Total	Mg	0
			1	1	
82	1	1	Total	Mg	0
			1	1	
82	6	1	Total	Mg	0
			1	1	

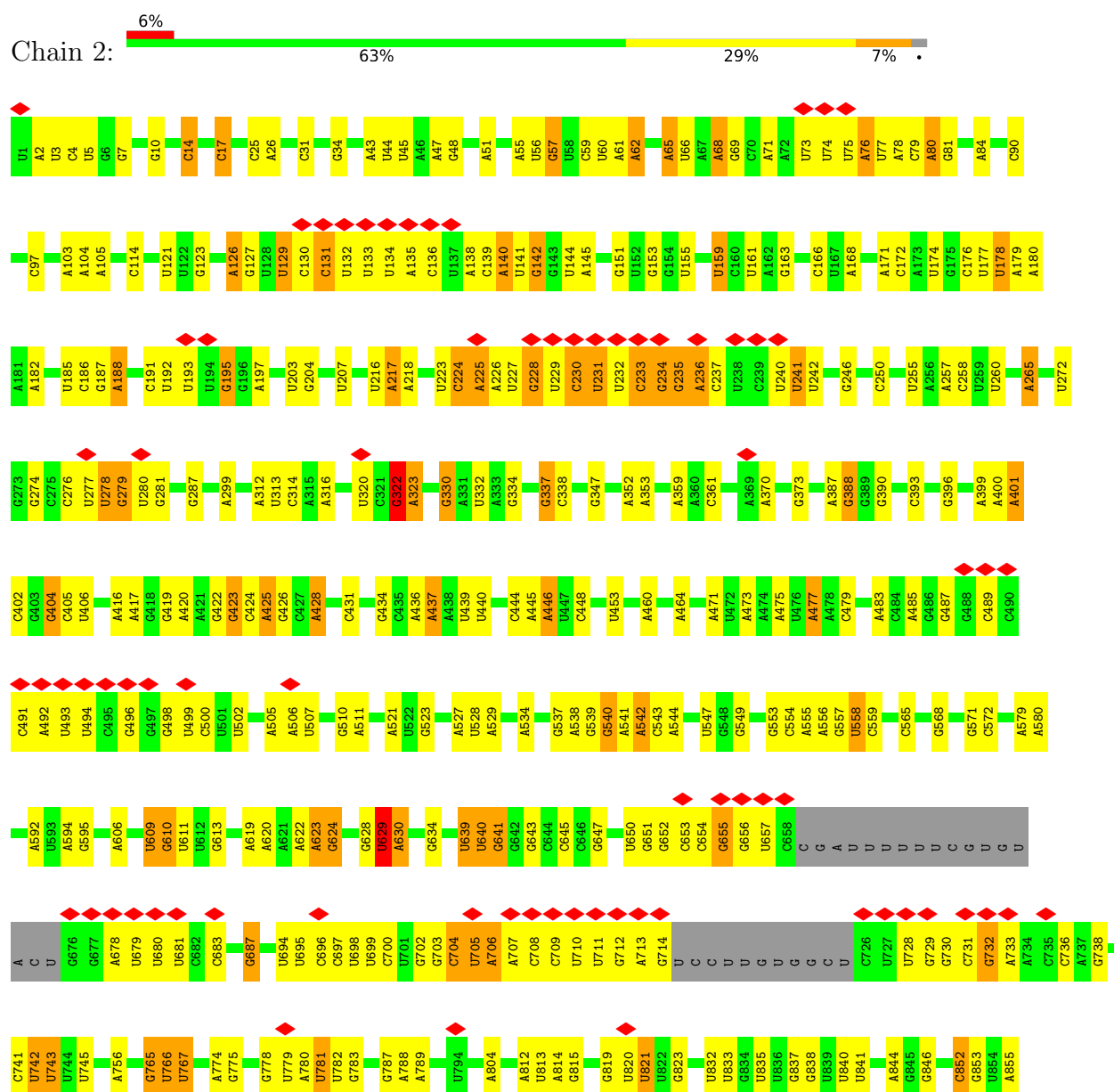
- Molecule 83 is ZINC ION (CCD ID: ZN) (formula: Zn).

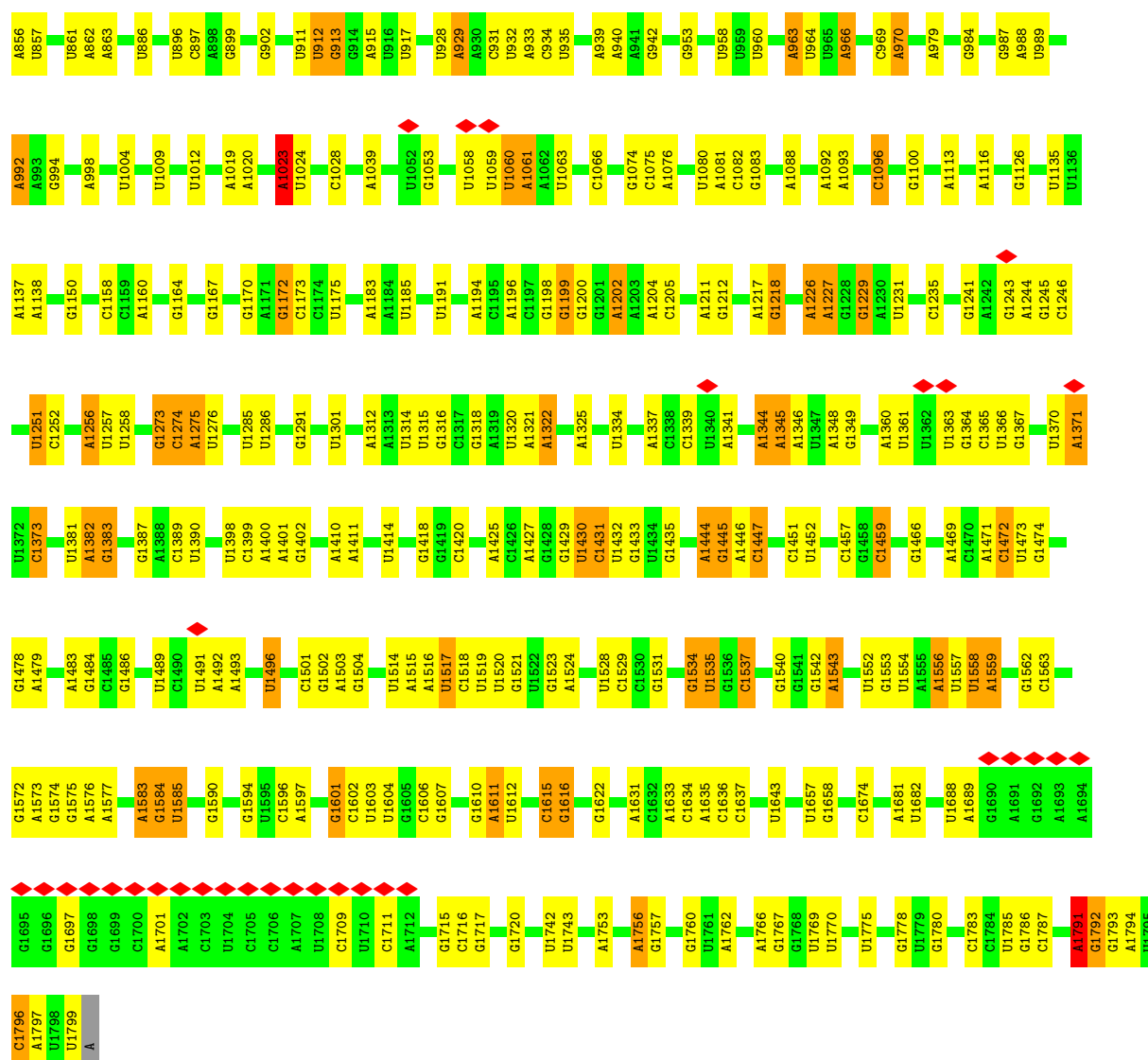
Mol	Chain	Residues	Atoms		AltConf
83	d	1	Total	Zn	0
			1	1	
83	f	1	Total	Zn	0
			1	1	
83	aj	1	Total	Zn	0
			1	1	
83	ag	1	Total	Zn	0
			1	1	
83	ad	1	Total	Zn	0
			1	1	
83	ab	1	Total	Zn	0
			1	1	
83	aa	1	Total	Zn	0
			1	1	

3 Residue-property plots

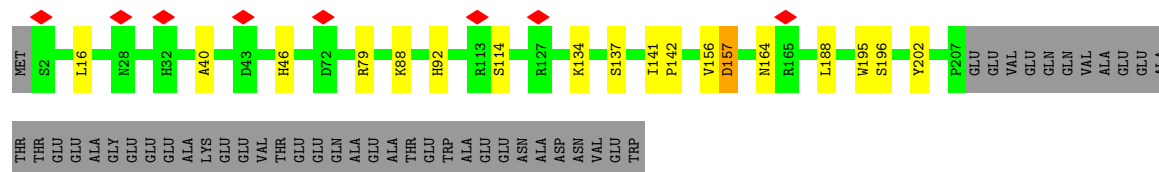
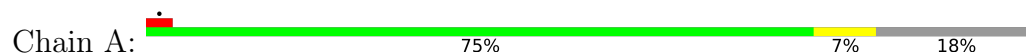
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: *Saccharomyces cerevisiae* S288C 18S ribosomal RNA (RDN18-1), rRNA

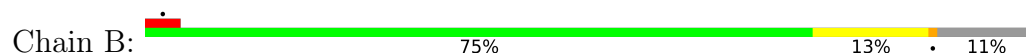


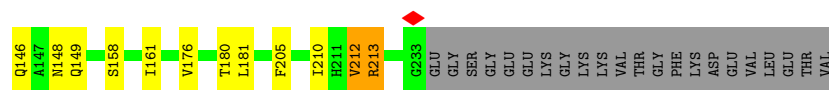


• Molecule 2: 40S ribosomal protein S0-A

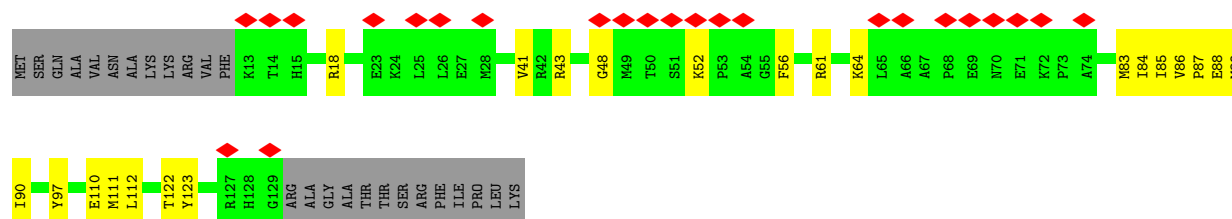


• Molecule 3: 40S ribosomal protein S1-A

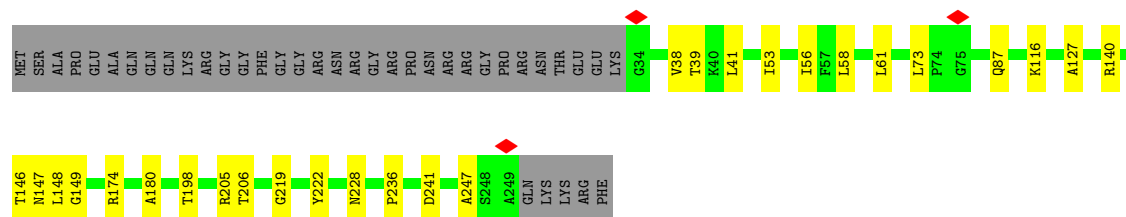
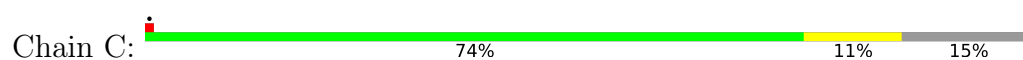




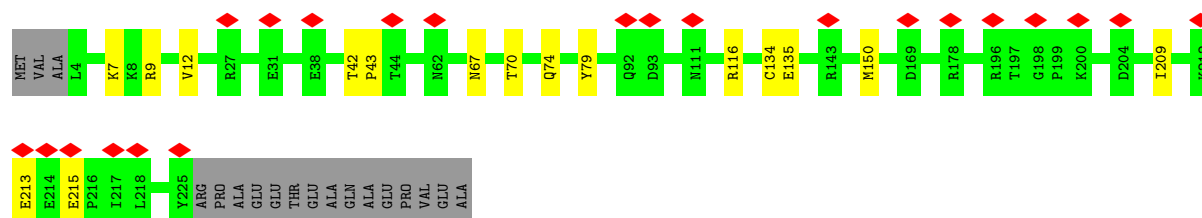
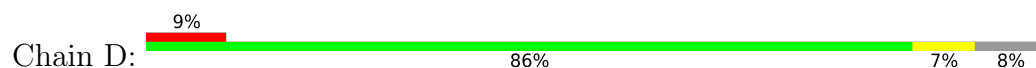
- Molecule 4: 40S ribosomal protein S15



- Molecule 5: 40S ribosomal protein S2



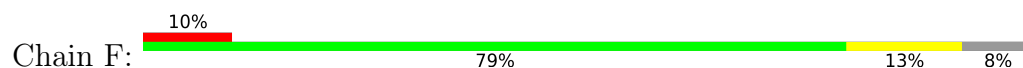
- Molecule 6: 40S ribosomal protein S3

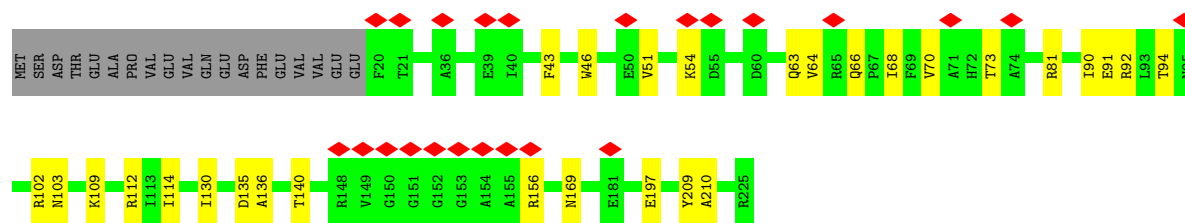


- Molecule 7: 40S ribosomal protein S4-A

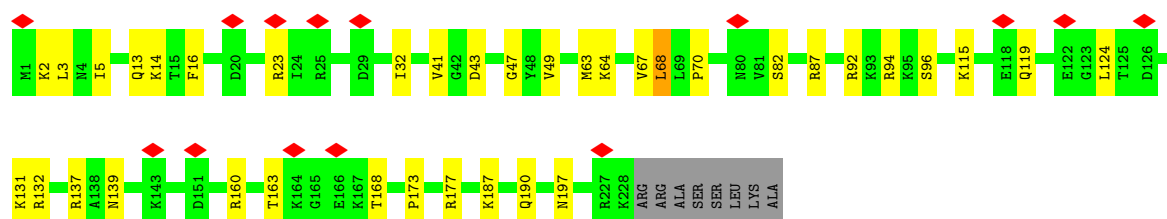
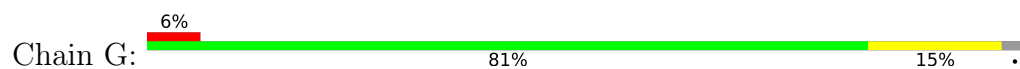


- Molecule 8: 40S ribosomal protein S5

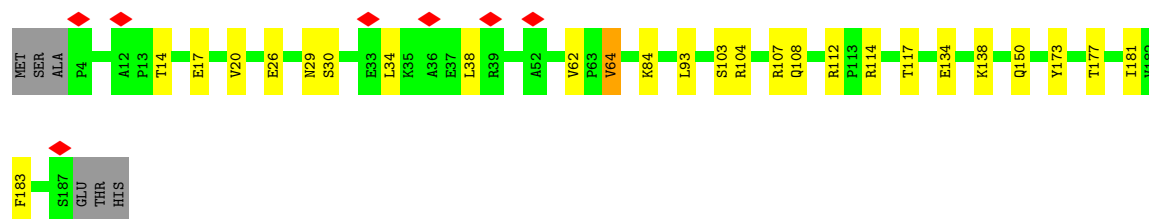
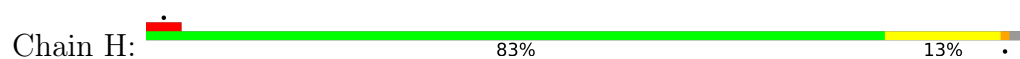




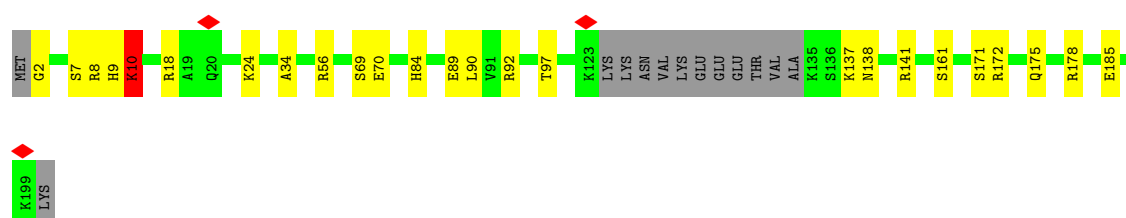
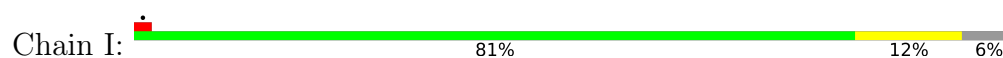
• Molecule 9: 40S ribosomal protein S6-A



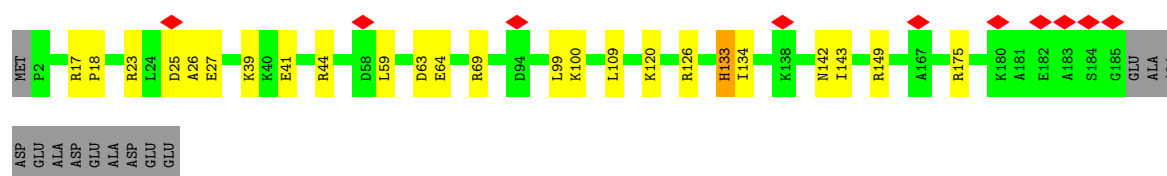
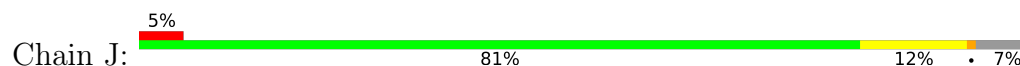
• Molecule 10: 40S ribosomal protein S7-A



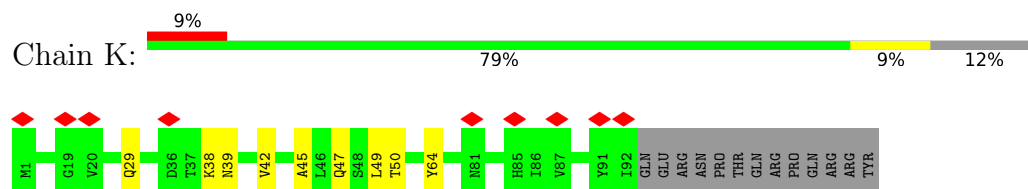
• Molecule 11: 40S ribosomal protein S8-A



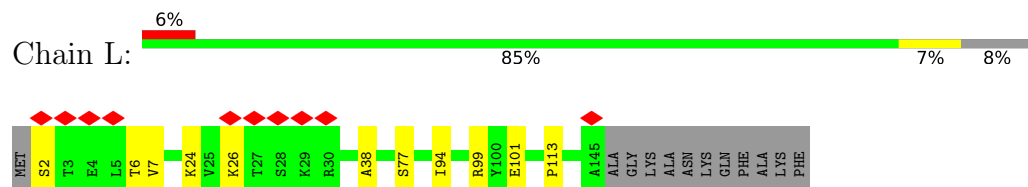
• Molecule 12: 40S ribosomal protein S9-A



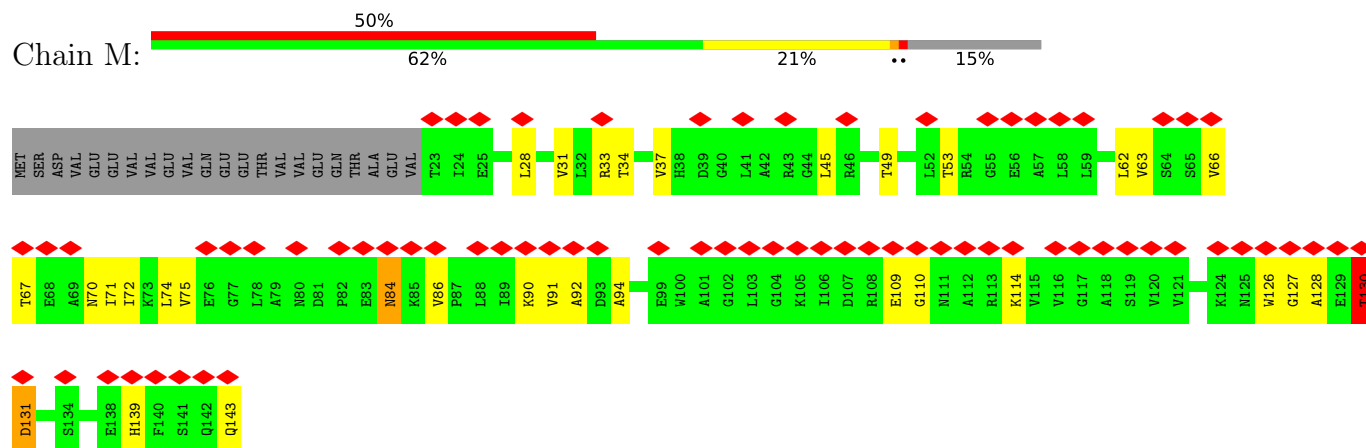
- Molecule 13: 40S ribosomal protein S10-A



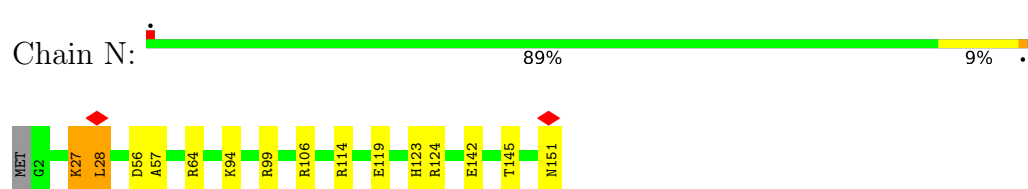
- Molecule 14: 40S ribosomal protein S11-A



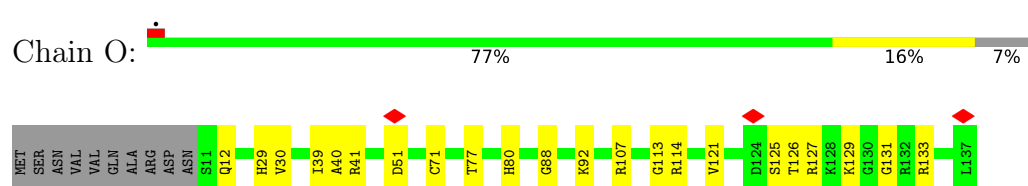
- Molecule 15: 40S ribosomal protein S12



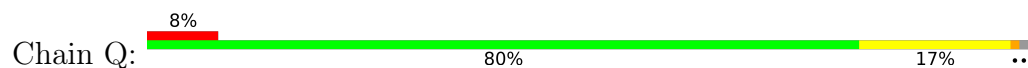
- Molecule 16: 40S ribosomal protein S13

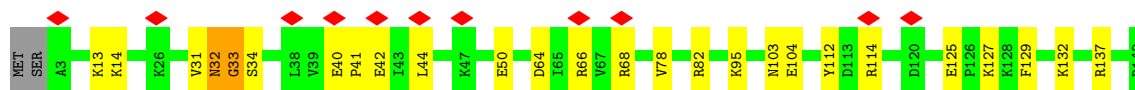


- Molecule 17: 40S ribosomal protein S14-A

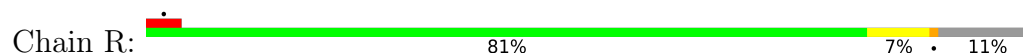


- Molecule 18: 40S ribosomal protein S16-A

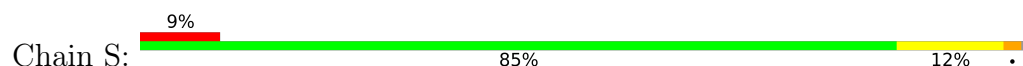




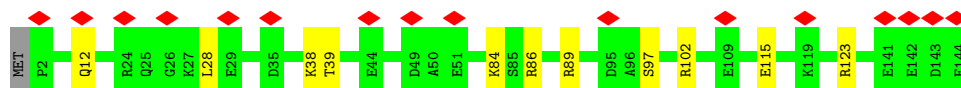
- Molecule 19: 40S ribosomal protein S17-B



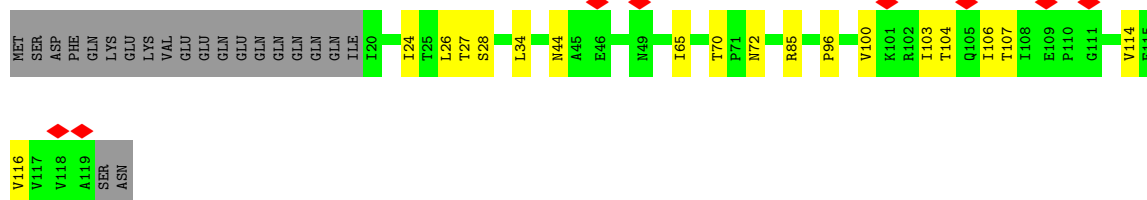
- Molecule 20: 40S ribosomal protein S18-A



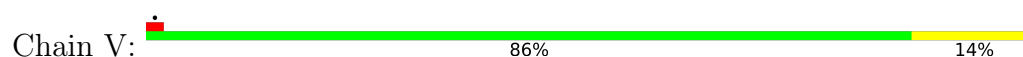
- Molecule 21: 40S ribosomal protein S19-A



- Molecule 22: 40S ribosomal protein S20



- Molecule 23: 40S ribosomal protein S21-A

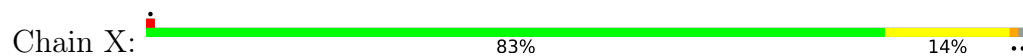


- Molecule 24: 40S ribosomal protein S22-A

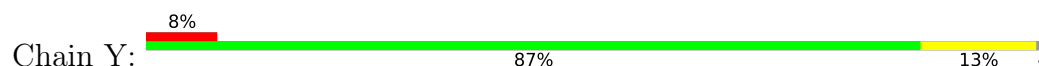




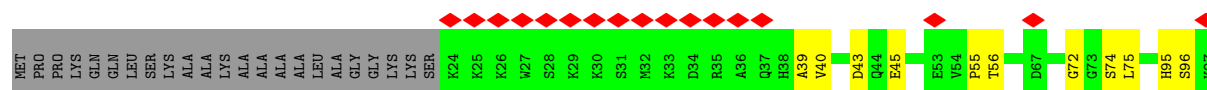
- Molecule 25: 40S ribosomal protein S23-A



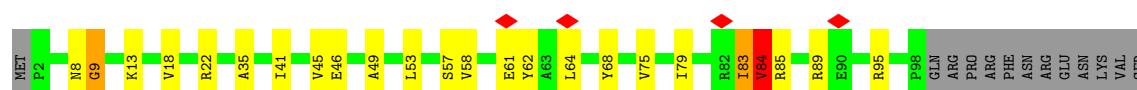
- Molecule 26: 40S ribosomal protein S24-A



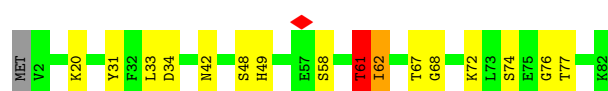
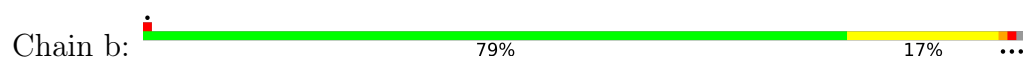
- Molecule 27: 40S ribosomal protein S25-A



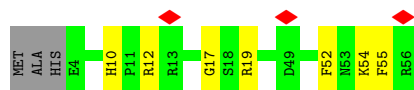
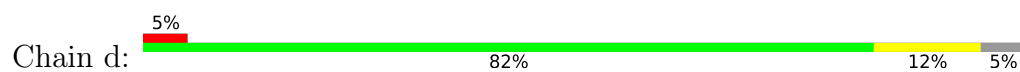
- Molecule 28: 40S ribosomal protein S26-A



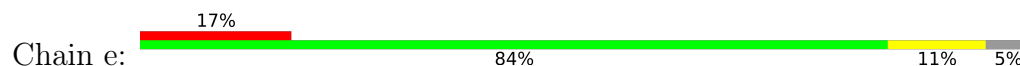
- Molecule 29: 40S ribosomal protein S27-A



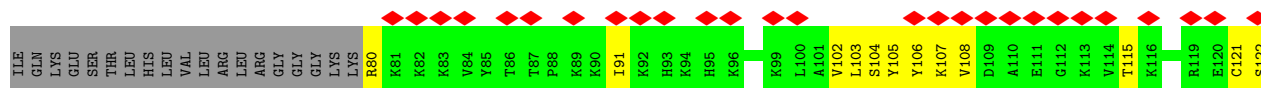
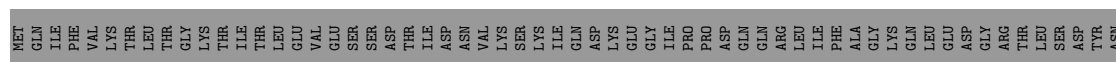
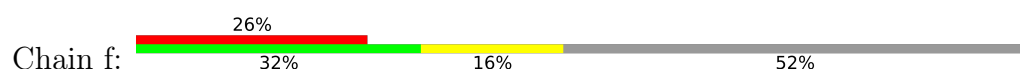
- Molecule 30: 40S ribosomal protein S29-A



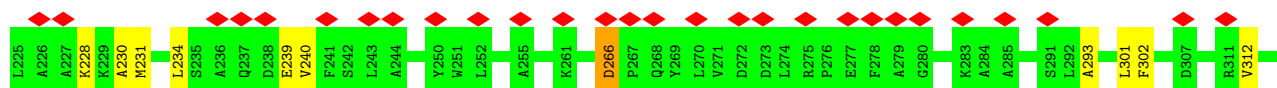
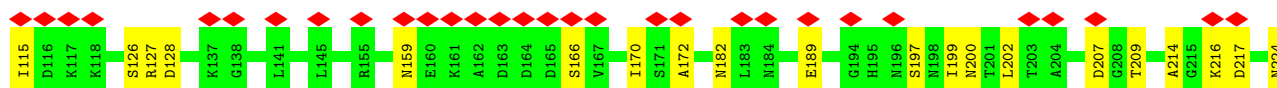
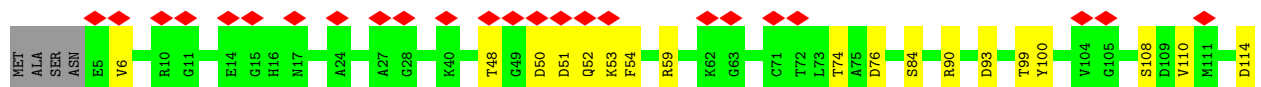
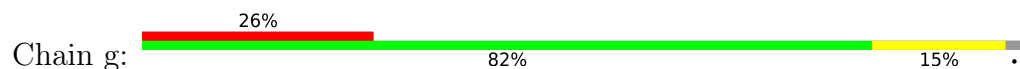
- Molecule 31: 40S ribosomal protein S30-A



- Molecule 32: Ubiquitin-40S ribosomal protein S31

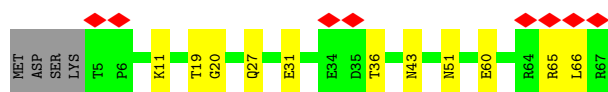


- Molecule 33: Guanine nucleotide-binding protein subunit beta-like protein



- Molecule 34: 40S ribosomal protein S28-B





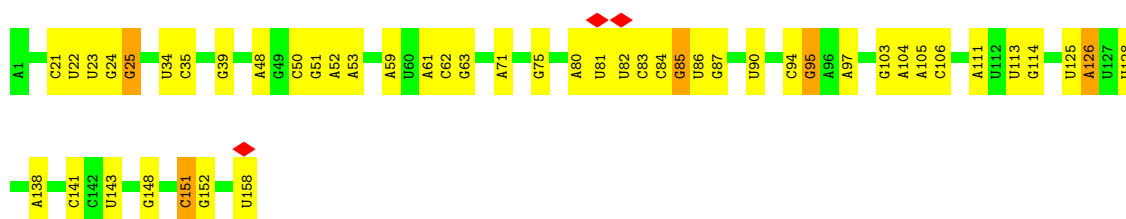
- Molecule 35: 5S rRNA

Chain 4: 79% 17% .



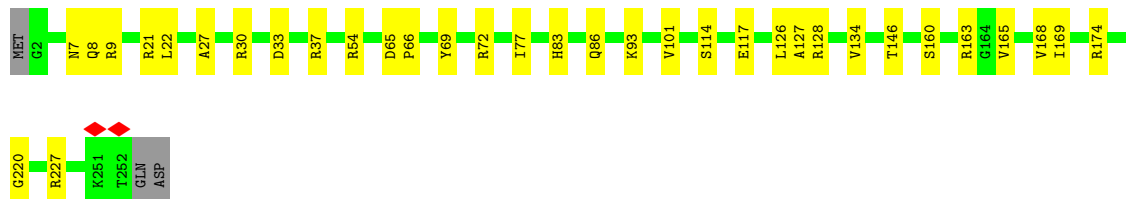
- Molecule 36: 5.8S rRNA

Chain 3: 70% 27% .



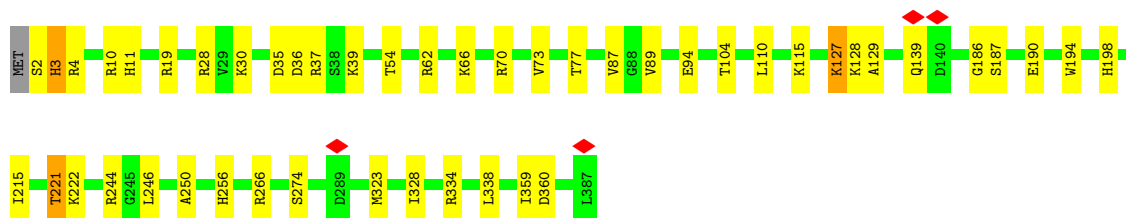
- Molecule 37: 60S ribosomal protein L2-A

Chain h: 85% 13% .



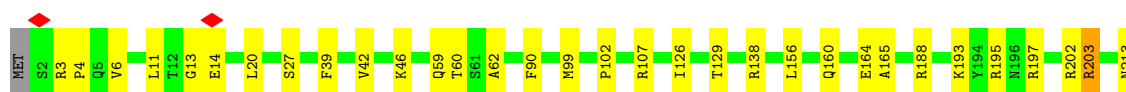
- Molecule 38: 60S ribosomal protein L3

Chain i: 87% 12% .



- Molecule 39: 60S ribosomal protein L4-A

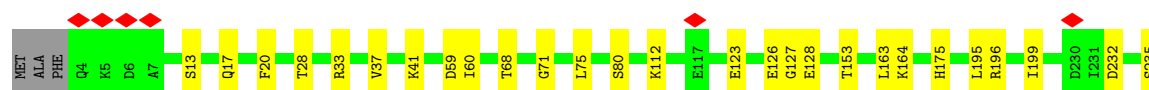
Chain j: 87% 12% .





- Molecule 40: 60S ribosomal protein L5

Chain k: 88% 11%



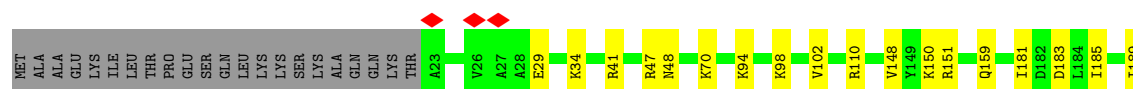
- Molecule 41: 60S ribosomal protein L6-B

Chain l: 87% 13%



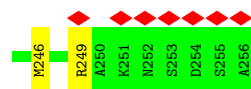
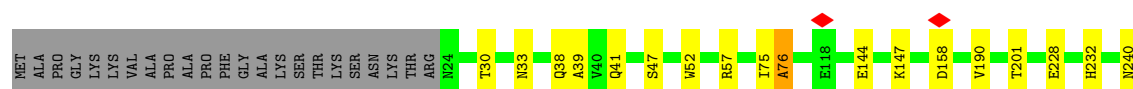
- Molecule 42: 60S ribosomal protein L7-A

Chain m: 82% 9% 9%



- Molecule 43: 60S ribosomal protein L8-A

Chain n: 83% 7% 9%

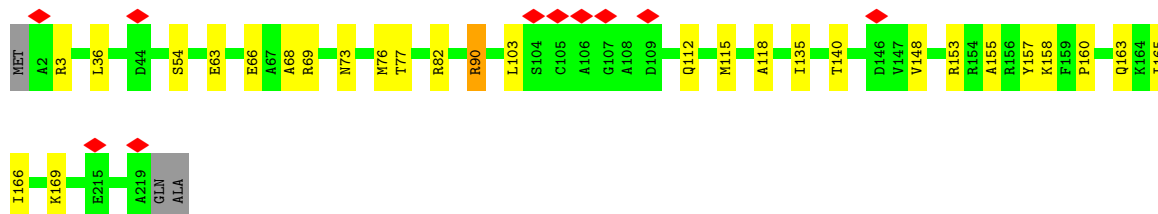
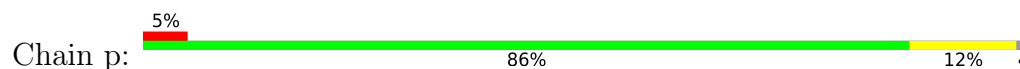


- Molecule 44: 60S ribosomal protein L9-A

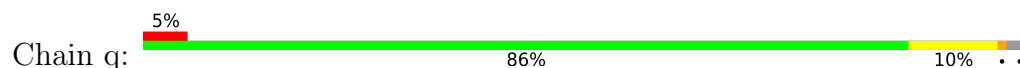
Chain o: 90% 10%



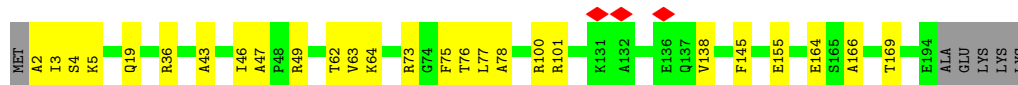
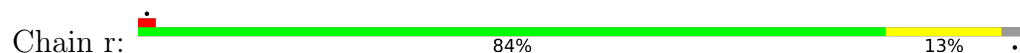
- Molecule 45: 60S ribosomal protein L10



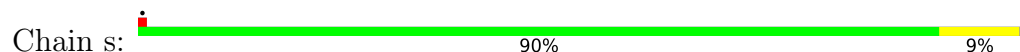
- Molecule 46: 60S ribosomal protein L11-A



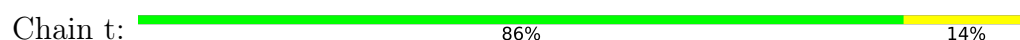
- Molecule 47: 60S ribosomal protein L13-A



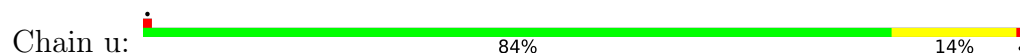
- Molecule 48: 60S ribosomal protein L14-A



- Molecule 49: 60S ribosomal protein L15-A



- Molecule 50: 60S ribosomal protein L16-A

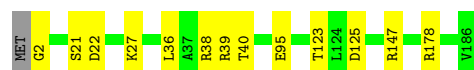




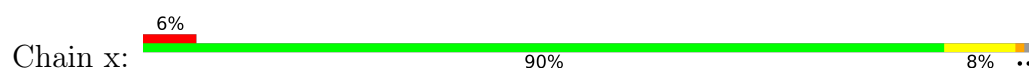
- Molecule 51: 60S ribosomal protein L17-A



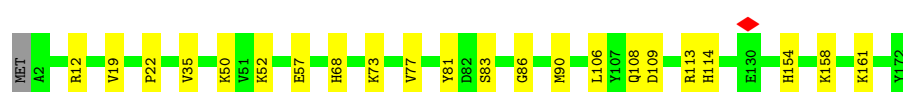
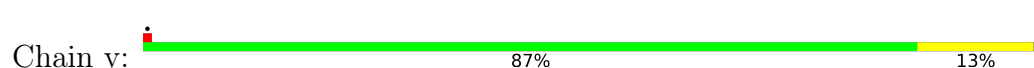
- Molecule 52: 60S ribosomal protein L18-A



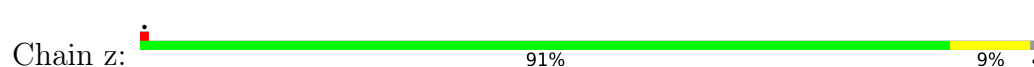
- Molecule 53: 60S ribosomal protein L19-A



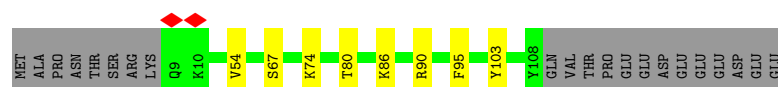
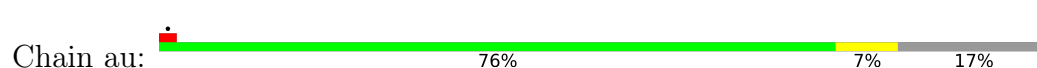
- Molecule 54: 60S ribosomal protein L20-A



- Molecule 55: 60S ribosomal protein L21-A

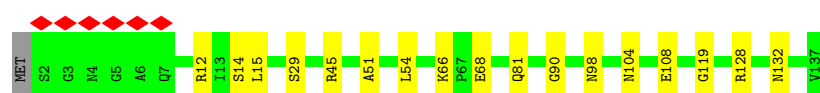


- Molecule 56: 60S ribosomal protein L22-A



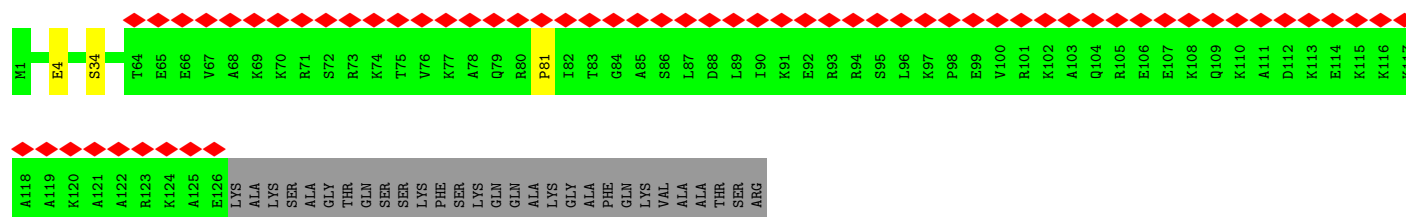
- Molecule 57: 60S ribosomal protein L23-A

Chain AB:  87% 12% .



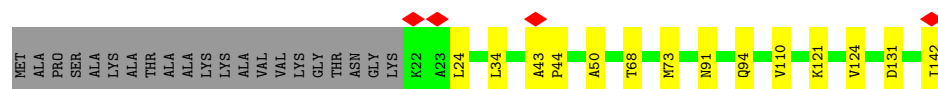
- Molecule 58: 60S ribosomal protein L24-A

Chain at:  41% 79% 19% .



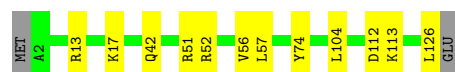
- Molecule 59: 60S ribosomal protein L25

Chain as:  75% 10% 15% .



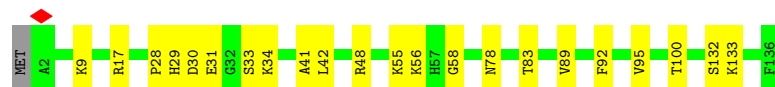
- Molecule 60: 60S ribosomal protein L26-A

Chain ar:  89% 9% .



- Molecule 61: 60S ribosomal protein L27-A

Chain aq:  83% 16% .



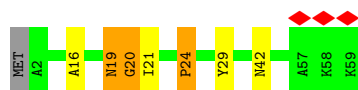
- Molecule 62: 60S ribosomal protein L28

Chain ap:  86% 13% .



- Molecule 63: 60S ribosomal protein L29

Chain ao:  5% 86% 7% 5% .



- Molecule 64: 60S ribosomal protein L30

Chain an: 85% 7% 9%



- Molecule 65: 60S ribosomal protein L31-A

Chain am: 6% 88% 8% .



- Molecule 66: 60S ribosomal protein L32

Chain al: 90% 8% .



- Molecule 67: 60S ribosomal protein L33-A

Chain ak: 91% 8% .



- Molecule 68: 60S ribosomal protein L34-A

Chain aj: 82% 11% 7%



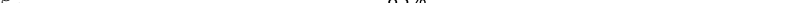
- Molecule 69: 60S ribosomal protein L35-A

Chain ai: 86% 12% ..



- Molecule 70: 60S ribosomal protein L36-A

Diagram illustrating the structure of the T2 domain of the T2 receptor. The structure is shown as a vertical bar with various residues labeled. The residues are: MET (grey), T2 (green), S34 (yellow), N35 (green), R36 (yellow), T37 (yellow), I58 (yellow), R76 (orange), M90 (yellow), R99 (green), and H100 (green). Red diamonds are placed above the MET, R99, and H100 residues.

- Chain ag:  83% 14% 3%

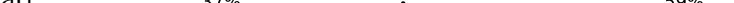


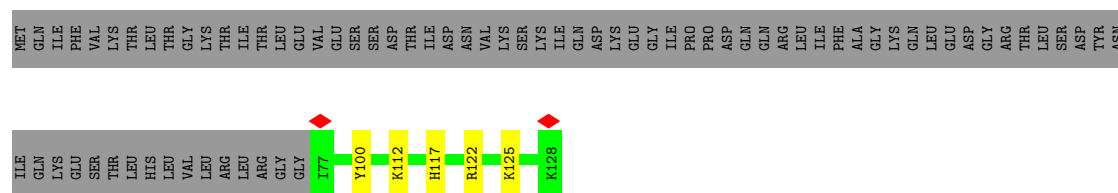
- Chain af:  5% 86% 13%



- Chain ae: 90% 8% .

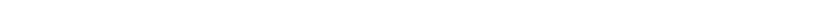


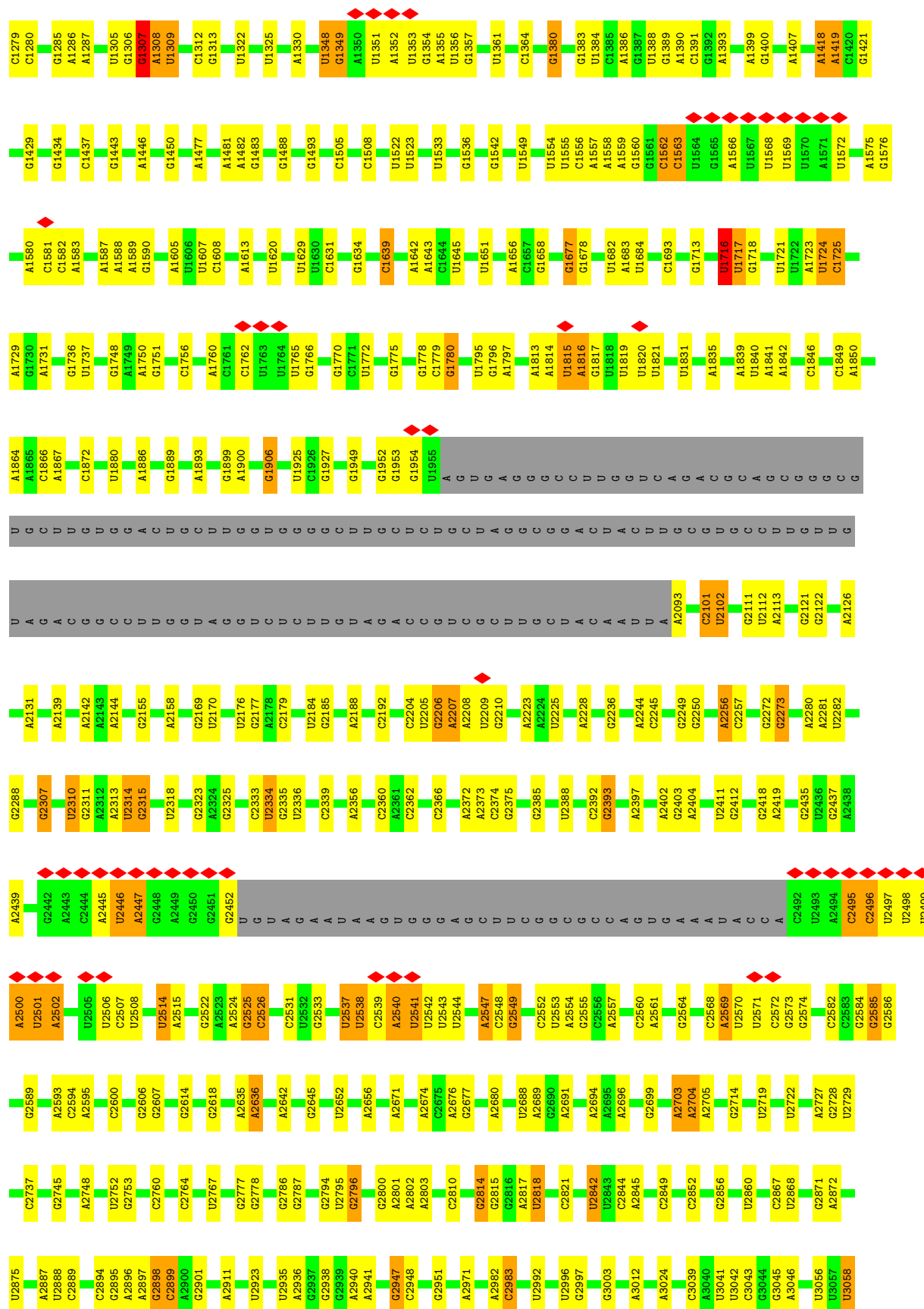
- Chain ad:  37% 5% 58%

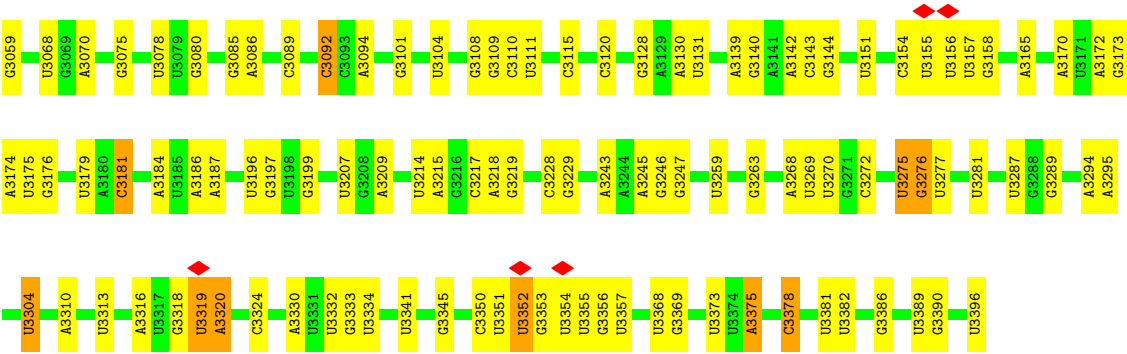


- Chain ac: 92% 8%

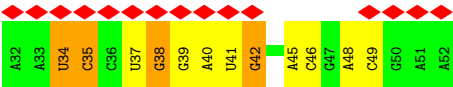


- Chain ab:  90% 7% ...

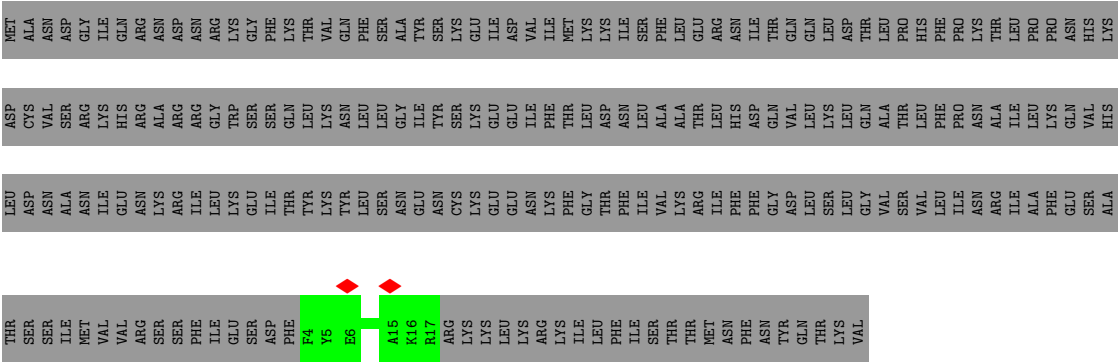




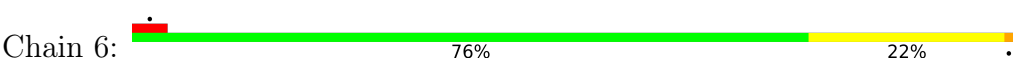
• Molecule 79: mRNA



• Molecule 80: Uncharacterized protein YEL057C



• Molecule 81: tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	214383	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	0.604	Depositor
Minimum map value	-0.255	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.0587	Depositor
Map size (Å)	433.6, 433.6, 433.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 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	0.60	1/42211 (0.0%)	0.45	4/65773 (0.0%)
2	A	0.42	0/1644	0.52	0/2249
3	B	0.46	0/1823	0.62	0/2447
4	P	0.28	0/936	0.53	0/1259
5	C	0.55	0/1656	0.57	0/2251
6	D	0.35	0/1754	0.51	0/2361
7	E	0.52	0/2097	0.59	1/2823 (0.0%)
8	F	0.36	0/1625	0.56	0/2197
9	G	0.37	0/1839	0.60	0/2460
10	H	0.38	0/1498	0.56	0/2019
11	I	0.58	0/1501	0.65	1/2006 (0.0%)
12	J	0.45	0/1504	0.64	0/2016
13	K	0.28	0/769	0.51	0/1039
14	L	0.64	0/1185	0.64	0/1598
15	M	0.29	0/883	0.75	0/1199
16	N	0.56	0/1215	0.65	0/1638
17	O	0.51	0/937	0.64	0/1261
18	Q	0.37	0/1125	0.56	0/1510
19	R	0.34	0/957	0.56	0/1283
20	S	0.31	0/1211	0.55	0/1628
21	T	0.34	0/1130	0.51	0/1517
22	U	0.35	0/807	0.54	0/1091
23	V	0.51	0/682	0.63	0/921
24	W	0.66	0/1038	0.61	1/1395 (0.1%)
25	X	0.57	0/1139	0.63	0/1518
26	Y	0.39	0/1087	0.52	0/1449
27	Z	0.27	0/661	0.58	0/888
28	a	0.60	0/782	0.80	0/1047
29	b	0.49	0/620	0.67	2/838 (0.2%)
30	d	0.40	0/452	0.48	0/600
31	e	0.36	0/480	0.54	0/639
32	f	0.25	0/567	0.67	0/764

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.26	0/2436	0.50	0/3318
34	c	0.38	0/493	0.54	0/663
35	4	0.39	0/2883	0.37	0/4491
36	3	0.61	0/3746	0.45	0/5832
37	h	0.78	0/1933	0.68	0/2598
38	i	0.68	0/3146	0.61	0/4228
39	j	0.67	0/2800	0.61	0/3790
40	k	0.41	0/2400	0.53	0/3239
41	l	0.46	0/1327	0.52	0/1790
42	m	0.63	1/1821 (0.1%)	0.58	0/2451
43	n	0.54	0/1836	0.58	0/2481
44	o	0.46	0/1529	0.50	0/2060
45	p	0.52	0/1801	0.52	0/2416
46	q	0.37	0/1371	0.54	0/1838
47	r	0.64	0/1568	0.71	0/2106
48	s	0.50	0/1068	0.55	0/1438
49	t	0.77	0/1757	0.67	1/2354 (0.0%)
50	u	0.66	0/1585	0.59	0/2128
51	v	0.73	0/1439	0.65	0/1938
52	w	0.64	0/1465	0.58	0/1965
53	x	0.65	0/1532	0.66	0/2043
54	y	0.56	0/1473	0.55	0/1980
55	z	0.54	0/1300	0.53	0/1743
56	au	0.46	0/812	0.54	0/1099
57	AB	0.68	0/1018	0.56	0/1369
58	at	0.53	0/850	0.53	0/1152
59	as	0.63	0/979	0.62	0/1321
60	ar	0.62	0/995	0.55	0/1329
61	aq	0.57	0/1118	0.58	0/1497
62	ap	0.68	0/1204	0.65	0/1612
63	ao	0.50	0/473	0.60	0/629
64	an	0.61	0/745	0.54	0/1001
65	am	0.69	0/890	0.64	0/1196
66	al	0.68	0/1038	0.57	0/1390
67	ak	0.70	0/868	0.59	0/1168
68	aj	0.70	0/890	0.63	0/1189
69	ai	0.57	0/978	0.65	1/1301 (0.1%)
70	ah	0.50	0/772	0.57	0/1026
71	ag	0.77	0/685	0.73	0/908
72	af	0.51	0/618	0.52	0/826
73	ae	0.81	0/443	0.65	0/588
74	ad	0.55	0/423	0.53	0/562
75	ac	0.57	0/230	0.83	0/296

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	ab	0.54	0/836	0.53	0/1104
77	aa	0.70	0/701	0.66	0/934
78	1	0.62	5/76214 (0.0%)	0.47	7/118821 (0.0%)
79	5	0.19	0/509	0.32	0/792
80	NC	0.45	0/132	0.72	0/175
81	6	0.41	2/1810 (0.1%)	0.40	0/2817
All	All	0.58	9/216755 (0.0%)	0.51	18/318676 (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
3	B	0	1
5	C	0	1
7	E	0	1
10	H	0	1
12	J	0	1
14	L	0	2
15	M	0	3
16	N	0	1
17	O	0	1
18	Q	0	3
20	S	0	4
24	W	0	1
25	X	0	2
28	a	0	5
29	b	0	1
32	f	0	2
38	i	0	4
39	j	0	1
43	n	0	2
44	o	0	1
46	q	0	3
47	r	0	1
48	s	0	1
49	t	0	1
50	u	0	1
53	x	0	1
59	as	0	1
60	ar	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
61	aq	0	1
62	ap	0	1
63	ao	0	3
65	am	0	1
69	ai	0	1
76	ab	0	1
All	All	0	56

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	629	U	C5'-C4'	83.80	3.18	1.51
78	1	846	A	C4'-O4'	34.48	2.14	1.45
78	1	846	A	O4'-C1'	33.95	2.09	1.41
78	1	846	A	C3'-C2'	23.21	1.99	1.53
78	1	846	A	C2'-C1'	20.88	1.95	1.53

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	W	28	ARG	C-N-CD	-7.65	103.76	120.60
78	1	846	A	N9-C1'-C2'	6.64	125.67	112.40
78	1	846	A	C5'-C4'-O4'	5.96	121.42	109.50
78	1	846	A	C4'-C3'-C2'	5.54	113.39	102.30
78	1	1307	G	P-O3'-C3'	5.47	128.40	120.20

There are no chirality outliers.

5 of 56 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	B	81	PHE	Peptide
5	C	247	ALA	Peptide
7	E	42	LEU	Peptide
10	H	64	VAL	Peptide
12	J	133	HIS	Peptide

5.2 Too-close contacts [\(i\)](#)

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

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	37739	0	18988	255	0
2	A	1603	0	1610	13	0
3	B	1798	0	1890	23	0
4	P	916	0	941	17	0
5	C	1626	0	1715	18	0
6	D	1729	0	1812	10	0
7	E	2056	0	2140	14	0
8	F	1605	0	1669	20	0
9	G	1815	0	1894	26	0
10	H	1473	0	1555	17	0
11	I	1476	0	1501	19	0
12	J	1479	0	1556	17	0
13	K	752	0	719	5	0
14	L	1159	0	1225	8	0
15	M	875	0	878	19	0
16	N	1192	0	1255	12	0
17	O	926	0	950	18	0
18	Q	1105	0	1166	18	0
19	R	948	0	990	10	0
20	S	1192	0	1222	16	0
21	T	1112	0	1124	10	0
22	U	797	0	863	13	0
23	V	673	0	662	9	0
24	W	1021	0	1060	11	0
25	X	1121	0	1196	16	0
26	Y	1073	0	1132	13	0
27	Z	651	0	682	8	0
28	a	769	0	818	13	0
29	b	610	0	633	11	0
30	d	442	0	428	8	0
31	e	472	0	521	6	0
32	f	556	0	545	15	0
33	g	2383	0	2332	28	0
34	c	491	0	524	7	0
35	4	2579	0	1304	12	0
36	3	3353	0	1695	20	0
37	h	1899	0	1957	25	0
38	i	3075	0	3142	31	0
39	j	2748	0	2859	35	0
40	k	2351	0	2294	24	0
41	l	1305	0	1394	14	0
42	m	1784	0	1862	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	n	1804	0	1877	12	0
44	o	1508	0	1572	12	0
45	p	1764	0	1804	17	0
46	q	1350	0	1381	12	0
47	r	1543	0	1608	19	0
48	s	1053	0	1149	9	0
49	t	1720	0	1779	22	0
50	u	1555	0	1659	17	0
51	v	1416	0	1433	6	0
52	w	1441	0	1543	10	0
53	x	1515	0	1606	15	0
54	y	1437	0	1475	18	0
55	z	1276	0	1323	10	0
56	au	796	0	812	7	0
57	AB	1003	0	1048	12	0
58	at	836	0	709	3	0
59	as	964	0	1025	10	0
60	ar	984	0	1075	9	0
61	aq	1092	0	1155	14	0
62	ap	1173	0	1215	15	0
63	ao	462	0	491	6	0
64	an	737	0	792	6	0
65	am	876	0	912	6	0
66	al	1017	0	1081	9	0
67	ak	850	0	880	7	0
68	aj	880	0	942	10	0
69	ai	969	0	1078	12	0
70	ah	766	0	844	6	0
71	ag	670	0	673	10	0
72	af	612	0	682	6	0
73	ae	436	0	475	5	0
74	ad	417	0	456	4	0
75	ac	229	0	273	2	0
76	ab	824	0	890	6	0
77	aa	694	0	735	10	0
78	1	68091	0	34217	311	0
79	5	454	0	229	4	0
80	NC	129	0	120	0	0
81	6	1621	0	820	2	0
82	1	1	0	0	0	0
82	2	82	0	0	0	0
82	6	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
82	E	1	0	0	0	0
82	F	1	0	0	0	0
82	T	1	0	0	0	0
83	aa	1	0	0	0	0
83	ab	1	0	0	0	0
83	ad	1	0	0	0	0
83	ag	1	0	0	0	0
83	aj	1	0	0	0	0
83	d	1	0	0	0	0
83	f	1	0	0	0	0
All	All	201787	0	148541	1164	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 1164 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:1:846:A:C4'	78:1:846:A:C3'	1.94	1.45
78:1:846:A:C1'	78:1:846:A:C2'	1.95	1.44
78:1:846:A:C3'	78:1:846:A:C2'	1.99	1.39
1:2:629:U:H4'	78:1:846:A:C4'	1.51	1.37
1:2:629:U:C5'	78:1:846:A:O4'	2.00	1.09

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	204/252 (81%)	179 (88%)	23 (11%)	2 (1%)	12	38
3	B	222/255 (87%)	188 (85%)	31 (14%)	3 (1%)	9	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	P	115/142 (81%)	103 (90%)	12 (10%)	0	100	100
5	C	214/254 (84%)	197 (92%)	16 (8%)	1 (0%)	24	55
6	D	220/240 (92%)	210 (96%)	10 (4%)	0	100	100
7	E	256/261 (98%)	229 (90%)	26 (10%)	1 (0%)	30	60
8	F	204/225 (91%)	188 (92%)	16 (8%)	0	100	100
9	G	226/236 (96%)	206 (91%)	16 (7%)	4 (2%)	6	23
10	H	182/190 (96%)	162 (89%)	19 (10%)	1 (0%)	24	55
11	I	183/200 (92%)	165 (90%)	16 (9%)	2 (1%)	11	36
12	J	182/197 (92%)	163 (90%)	17 (9%)	2 (1%)	11	36
13	K	90/105 (86%)	77 (86%)	13 (14%)	0	100	100
14	L	142/156 (91%)	128 (90%)	13 (9%)	1 (1%)	18	47
15	M	119/143 (83%)	79 (66%)	34 (29%)	6 (5%)	1	5
16	N	148/151 (98%)	133 (90%)	13 (9%)	2 (1%)	9	30
17	O	125/137 (91%)	108 (86%)	16 (13%)	1 (1%)	16	44
18	Q	139/143 (97%)	126 (91%)	11 (8%)	2 (1%)	9	30
19	R	117/136 (86%)	107 (92%)	8 (7%)	2 (2%)	7	25
20	S	143/146 (98%)	129 (90%)	10 (7%)	4 (3%)	4	14
21	T	141/144 (98%)	127 (90%)	13 (9%)	1 (1%)	18	47
22	U	98/121 (81%)	89 (91%)	9 (9%)	0	100	100
23	V	85/87 (98%)	73 (86%)	11 (13%)	1 (1%)	10	34
24	W	127/130 (98%)	116 (91%)	11 (9%)	0	100	100
25	X	142/145 (98%)	122 (86%)	19 (13%)	1 (1%)	18	47
26	Y	132/135 (98%)	120 (91%)	11 (8%)	1 (1%)	16	44
27	Z	80/105 (76%)	63 (79%)	17 (21%)	0	100	100
28	a	95/119 (80%)	74 (78%)	17 (18%)	4 (4%)	2	7
29	b	79/82 (96%)	71 (90%)	7 (9%)	1 (1%)	9	31
30	d	51/56 (91%)	49 (96%)	2 (4%)	0	100	100
31	e	58/63 (92%)	50 (86%)	8 (14%)	0	100	100
32	f	71/152 (47%)	43 (61%)	28 (39%)	0	100	100
33	g	310/319 (97%)	282 (91%)	27 (9%)	1 (0%)	36	66
34	c	61/67 (91%)	56 (92%)	5 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	h	249/254 (98%)	232 (93%)	16 (6%)	1 (0%)	30	60
38	i	384/387 (99%)	345 (90%)	37 (10%)	2 (0%)	24	55
39	j	359/362 (99%)	333 (93%)	24 (7%)	2 (1%)	21	51
40	k	292/297 (98%)	275 (94%)	16 (6%)	1 (0%)	36	66
41	l	163/167 (98%)	147 (90%)	16 (10%)	0	100	100
42	m	220/244 (90%)	205 (93%)	15 (7%)	0	100	100
43	n	231/256 (90%)	216 (94%)	15 (6%)	0	100	100
44	o	189/191 (99%)	174 (92%)	15 (8%)	0	100	100
45	p	216/221 (98%)	208 (96%)	8 (4%)	0	100	100
46	q	167/174 (96%)	147 (88%)	20 (12%)	0	100	100
47	r	191/199 (96%)	162 (85%)	26 (14%)	3 (2%)	7	27
48	s	134/138 (97%)	126 (94%)	8 (6%)	0	100	100
49	t	201/204 (98%)	185 (92%)	16 (8%)	0	100	100
50	u	195/199 (98%)	187 (96%)	6 (3%)	2 (1%)	12	38
51	v	181/184 (98%)	167 (92%)	14 (8%)	0	100	100
52	w	183/186 (98%)	174 (95%)	9 (5%)	0	100	100
53	x	186/189 (98%)	178 (96%)	6 (3%)	2 (1%)	11	36
54	y	169/172 (98%)	163 (96%)	6 (4%)	0	100	100
55	z	157/160 (98%)	143 (91%)	14 (9%)	0	100	100
56	au	98/121 (81%)	96 (98%)	2 (2%)	0	100	100
57	AB	134/137 (98%)	132 (98%)	2 (2%)	0	100	100
58	at	124/155 (80%)	113 (91%)	11 (9%)	0	100	100
59	as	119/142 (84%)	110 (92%)	8 (7%)	1 (1%)	16	44
60	ar	123/127 (97%)	115 (94%)	8 (6%)	0	100	100
61	aq	133/136 (98%)	119 (90%)	14 (10%)	0	100	100
62	ap	146/149 (98%)	124 (85%)	20 (14%)	2 (1%)	9	30
63	ao	56/59 (95%)	48 (86%)	6 (11%)	2 (4%)	2	10
64	an	94/105 (90%)	93 (99%)	1 (1%)	0	100	100
65	am	107/113 (95%)	96 (90%)	11 (10%)	0	100	100
66	al	125/130 (96%)	119 (95%)	6 (5%)	0	100	100
67	ak	104/107 (97%)	100 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	aj	110/121 (91%)	106 (96%)	4 (4%)	0	100	100
69	ai	117/120 (98%)	110 (94%)	7 (6%)	0	100	100
70	ah	97/100 (97%)	90 (93%)	7 (7%)	0	100	100
71	ag	83/88 (94%)	76 (92%)	7 (8%)	0	100	100
72	af	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
73	ae	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
74	ad	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
75	ac	23/25 (92%)	23 (100%)	0	0	100	100
76	ab	101/106 (95%)	95 (94%)	6 (6%)	0	100	100
77	aa	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
80	NC	12/233 (5%)	9 (75%)	3 (25%)	0	100	100
All	All	10996/12101 (91%)	10006 (91%)	928 (8%)	62 (1%)	23	51

5 of 62 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	E	43	PRO
9	G	68	LEU
11	I	10	LYS
28	a	84	VAL
37	h	126	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	170/210 (81%)	170 (100%)	0	100	100
3	B	200/224 (89%)	200 (100%)	0	100	100
4	P	95/118 (80%)	95 (100%)	0	100	100
5	C	175/205 (85%)	175 (100%)	0	100	100
6	D	182/195 (93%)	182 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	E	220/222 (99%)	220 (100%)	0	100	100
8	F	172/191 (90%)	171 (99%)	1 (1%)	78	92
9	G	189/201 (94%)	189 (100%)	0	100	100
10	H	163/170 (96%)	163 (100%)	0	100	100
11	I	148/161 (92%)	148 (100%)	0	100	100
12	J	156/166 (94%)	156 (100%)	0	100	100
13	K	77/98 (79%)	77 (100%)	0	100	100
14	L	129/137 (94%)	129 (100%)	0	100	100
15	M	88/119 (74%)	88 (100%)	0	100	100
16	N	127/128 (99%)	127 (100%)	0	100	100
17	O	91/105 (87%)	91 (100%)	0	100	100
18	Q	117/119 (98%)	117 (100%)	0	100	100
19	R	101/124 (82%)	101 (100%)	0	100	100
20	S	128/129 (99%)	128 (100%)	0	100	100
21	T	115/116 (99%)	115 (100%)	0	100	100
22	U	93/114 (82%)	93 (100%)	0	100	100
23	V	71/74 (96%)	71 (100%)	0	100	100
24	W	110/111 (99%)	110 (100%)	0	100	100
25	X	119/120 (99%)	119 (100%)	0	100	100
26	Y	112/113 (99%)	112 (100%)	0	100	100
27	Z	67/87 (77%)	67 (100%)	0	100	100
28	a	83/101 (82%)	83 (100%)	0	100	100
29	b	70/71 (99%)	70 (100%)	0	100	100
30	d	47/49 (96%)	47 (100%)	0	100	100
31	e	50/54 (93%)	50 (100%)	0	100	100
32	f	56/135 (42%)	56 (100%)	0	100	100
33	g	250/262 (95%)	249 (100%)	1 (0%)	84	94
34	c	55/60 (92%)	55 (100%)	0	100	100
37	h	190/196 (97%)	190 (100%)	0	100	100
38	i	321/323 (99%)	318 (99%)	3 (1%)	70	89
39	j	288/289 (100%)	287 (100%)	1 (0%)	86	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	k	241/245 (98%)	241 (100%)	0	100	100
41	l	138/138 (100%)	138 (100%)	0	100	100
42	m	186/205 (91%)	186 (100%)	0	100	100
43	n	187/208 (90%)	186 (100%)	1 (0%)	81	93
44	o	168/171 (98%)	168 (100%)	0	100	100
45	p	185/187 (99%)	184 (100%)	1 (0%)	81	93
46	q	146/150 (97%)	146 (100%)	0	100	100
47	r	154/159 (97%)	154 (100%)	0	100	100
48	s	107/109 (98%)	107 (100%)	0	100	100
49	t	175/176 (99%)	175 (100%)	0	100	100
50	u	160/162 (99%)	160 (100%)	0	100	100
51	v	138/146 (94%)	136 (99%)	2 (1%)	59	85
52	w	150/151 (99%)	150 (100%)	0	100	100
53	x	152/154 (99%)	152 (100%)	0	100	100
54	y	155/156 (99%)	155 (100%)	0	100	100
55	z	136/137 (99%)	136 (100%)	0	100	100
56	au	87/107 (81%)	87 (100%)	0	100	100
57	AB	104/105 (99%)	104 (100%)	0	100	100
58	at	56/128 (44%)	56 (100%)	0	100	100
59	as	104/118 (88%)	104 (100%)	0	100	100
60	ar	108/110 (98%)	108 (100%)	0	100	100
61	aq	115/116 (99%)	115 (100%)	0	100	100
62	ap	118/119 (99%)	118 (100%)	0	100	100
63	ao	46/47 (98%)	46 (100%)	0	100	100
64	an	81/88 (92%)	81 (100%)	0	100	100
65	am	92/97 (95%)	92 (100%)	0	100	100
66	al	108/111 (97%)	108 (100%)	0	100	100
67	ak	90/91 (99%)	90 (100%)	0	100	100
68	aj	95/103 (92%)	95 (100%)	0	100	100
69	ai	104/105 (99%)	102 (98%)	2 (2%)	50	81
70	ah	80/82 (98%)	79 (99%)	1 (1%)	61	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
71	ag	69/71 (97%)	69 (100%)	0	100	100
72	af	68/69 (99%)	68 (100%)	0	100	100
73	ae	45/46 (98%)	45 (100%)	0	100	100
74	ad	47/116 (40%)	47 (100%)	0	100	100
75	ac	22/23 (96%)	22 (100%)	0	100	100
76	ab	87/91 (96%)	87 (100%)	0	100	100
77	aa	71/72 (99%)	71 (100%)	0	100	100
80	NC	13/215 (6%)	13 (100%)	0	100	100
All	All	9213/10181 (90%)	9200 (100%)	13 (0%)	87	97

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	p	90	ARG
51	v	29	THR
70	ah	76	ARG
69	ai	81	ARG
69	ai	94	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 80 such sidechains are listed below:

Mol	Chain	Res	Type
57	AB	98	ASN
65	am	56	ASN
60	ar	26	GLN
63	ao	12	GLN
67	ak	75	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1768/1800 (98%)	486 (27%)	47 (2%)
35	4	120/121 (99%)	16 (13%)	1 (0%)
36	3	157/158 (99%)	31 (19%)	1 (0%)
78	1	3180/3396 (93%)	629 (19%)	45 (1%)
79	5	20/21 (95%)	8 (40%)	1 (5%)
81	6	73/76 (96%)	14 (19%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	5318/5572 (95%)	1184 (22%)	95 (1%)

5 of 1184 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	14	C
1	2	17	C
1	2	25	C

5 of 95 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
78	1	846	A
78	1	1607	U
78	1	916	G
78	1	1307	G
78	1	2101	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 94 ligands modelled in this entry, 94 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
41	1	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	120:ALA	C	129:GLU	N	12.16

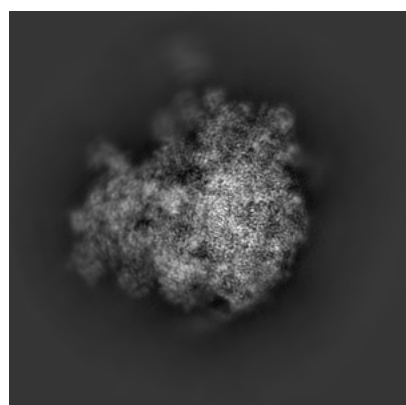
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10262. These allow visual inspection of the internal detail of the map and identification of artifacts.

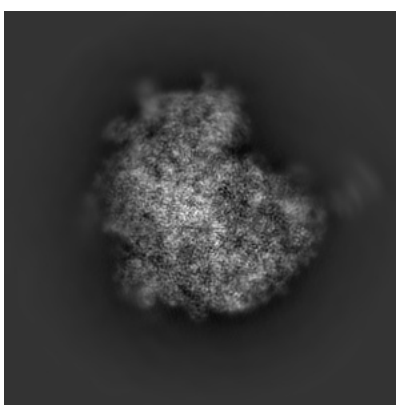
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

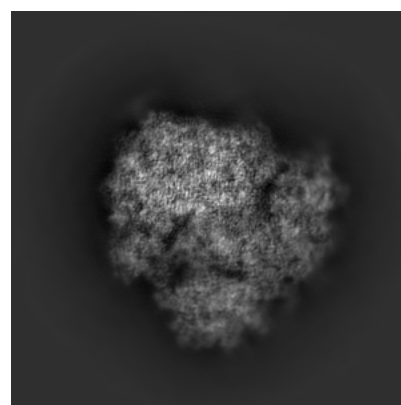
6.1.1 Primary map



X



Y

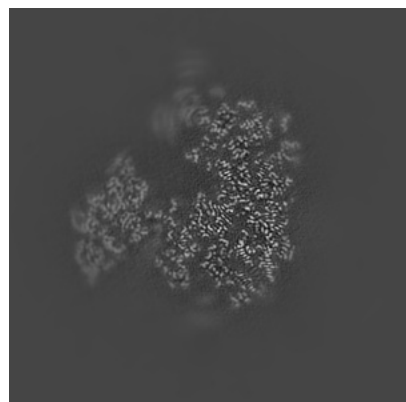


Z

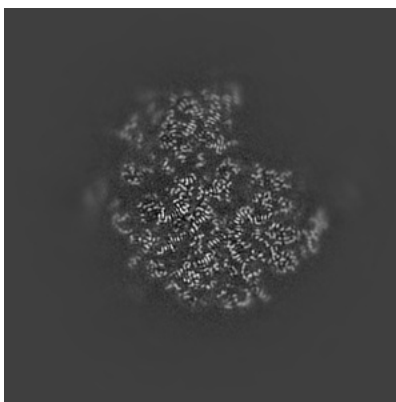
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

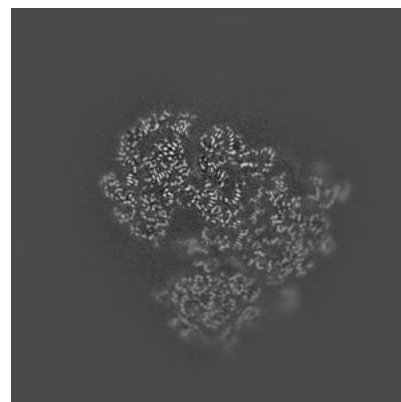
6.2.1 Primary map



X Index: 200



Y Index: 200

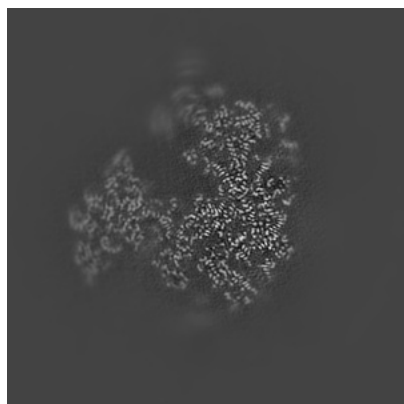


Z Index: 200

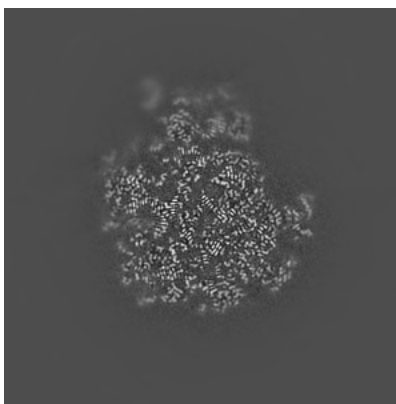
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

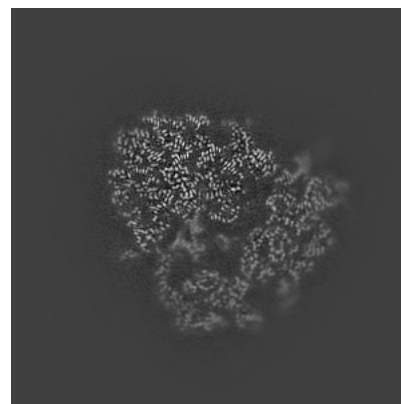
6.3.1 Primary map



X Index: 198



Y Index: 233

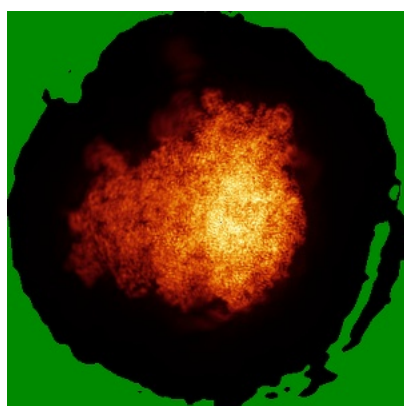


Z Index: 211

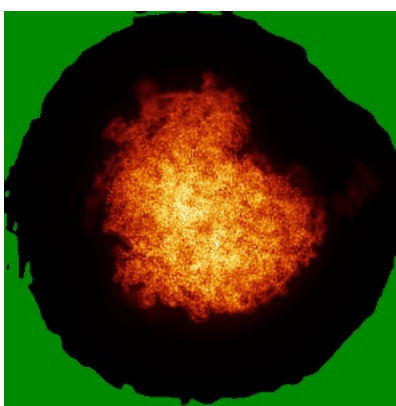
The images above show the largest variance slices of the map in three orthogonal directions.

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

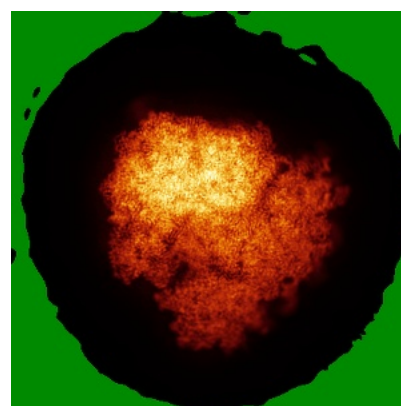
6.4.1 Primary map



X



Y

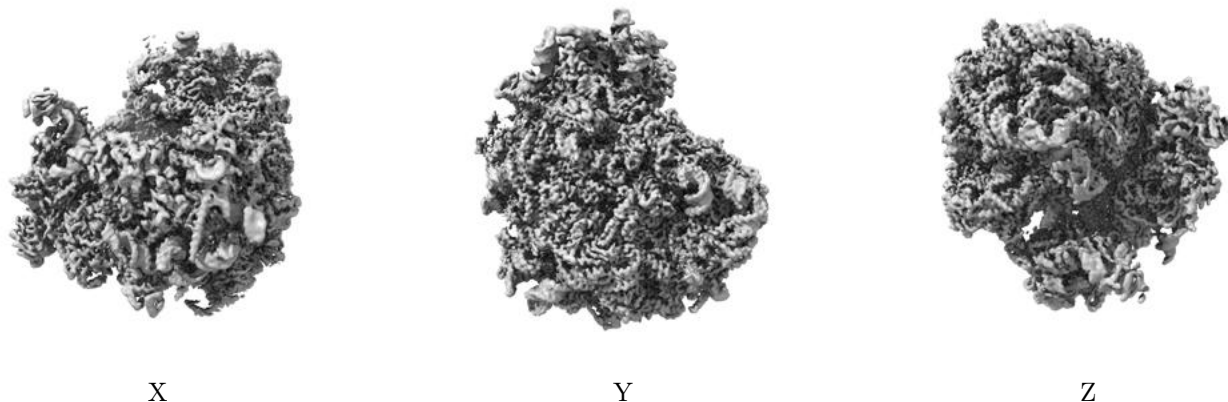


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0587. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

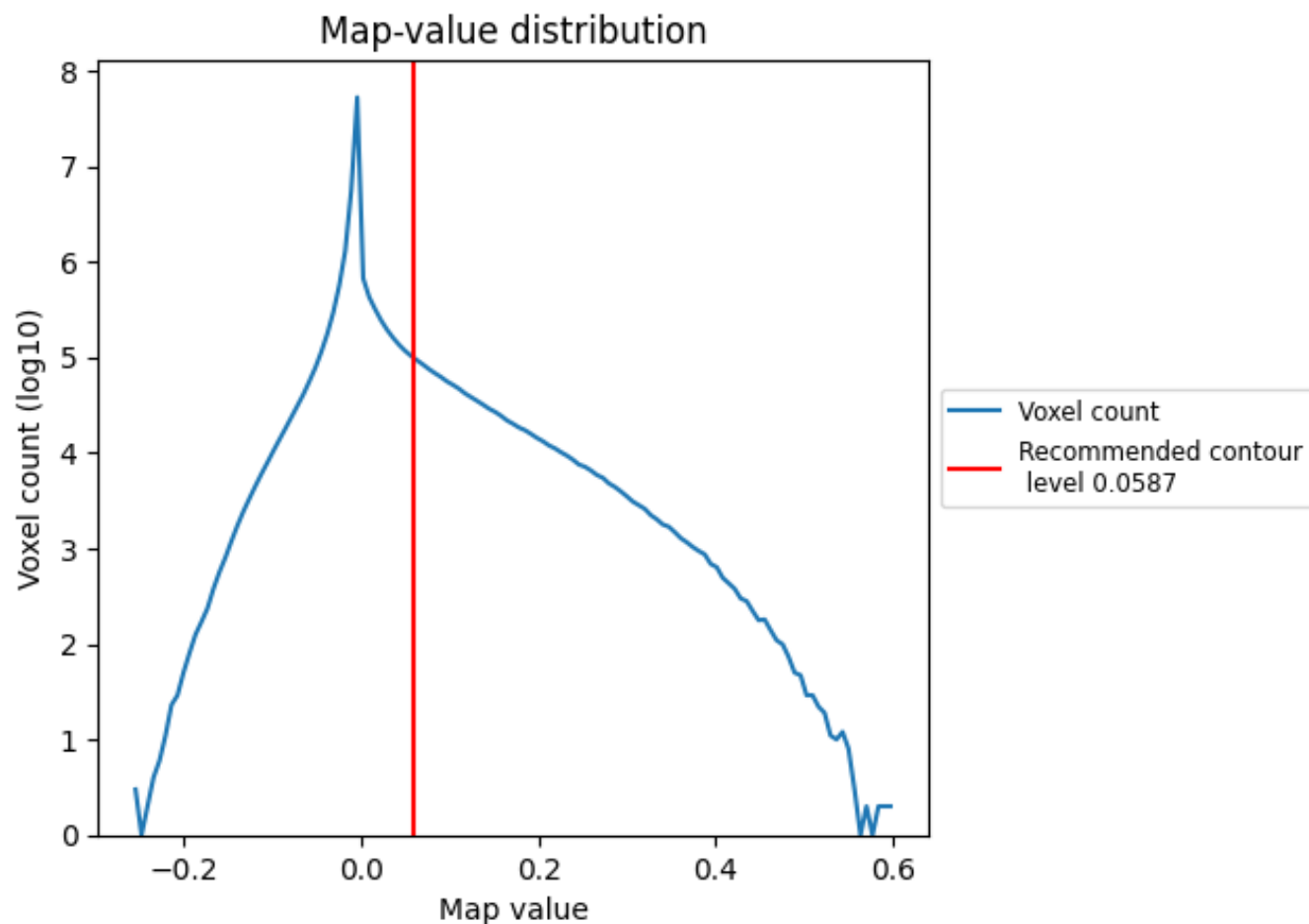
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

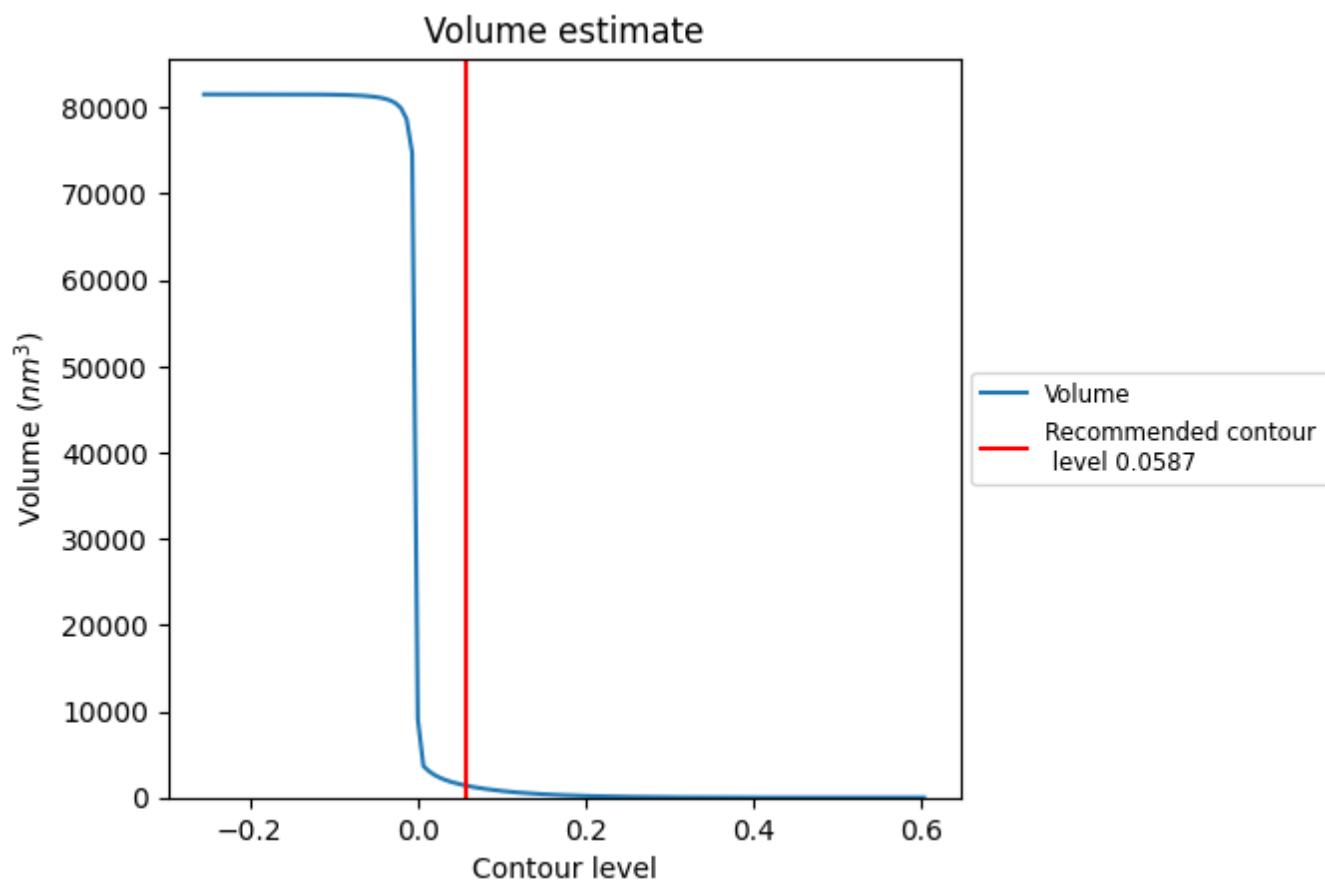
This section contains the results of statistical analysis of the map.

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.

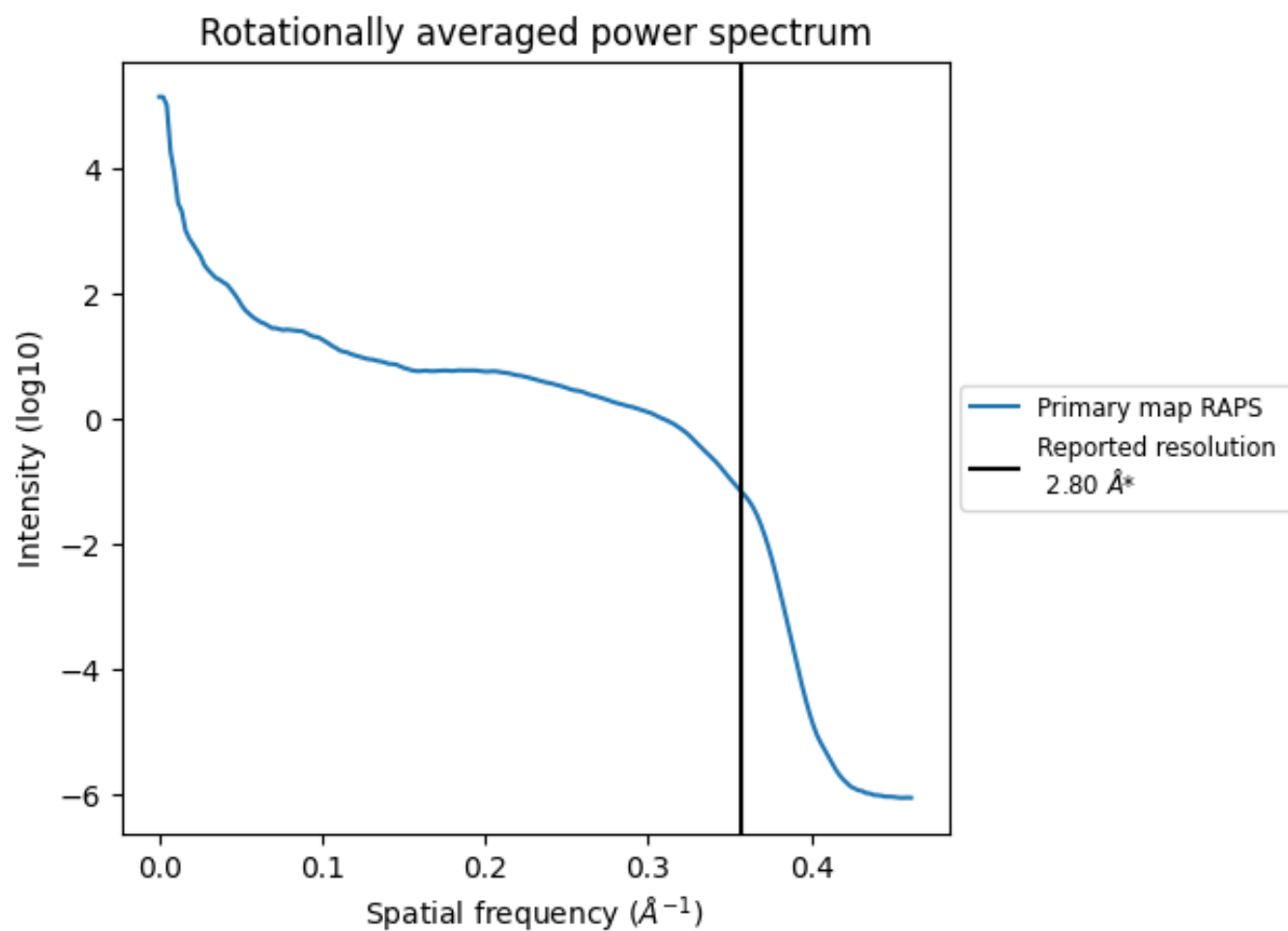
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1374 nm³; this corresponds to an approximate mass of 1241 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

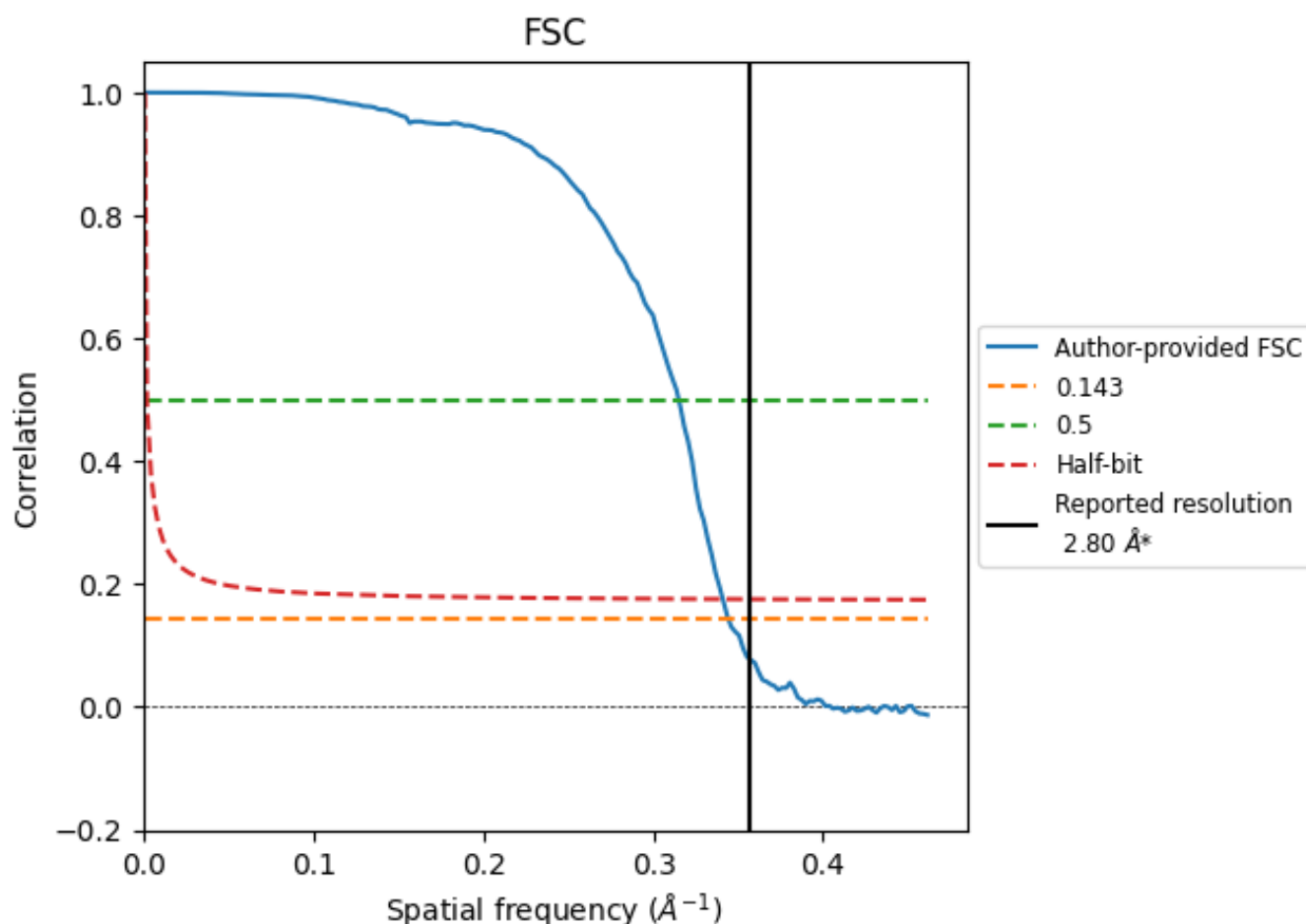


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

8.2 Resolution estimates [i](#)

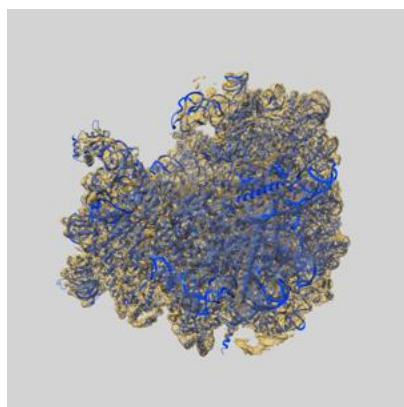
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.90	3.17	2.93
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

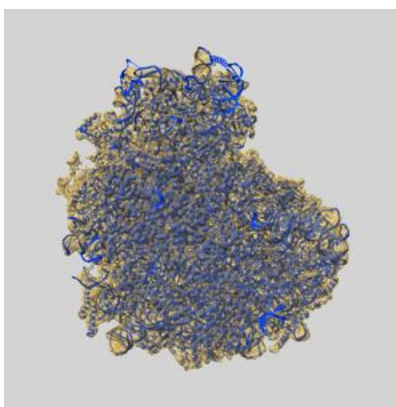
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10262 and PDB model 6SNT. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

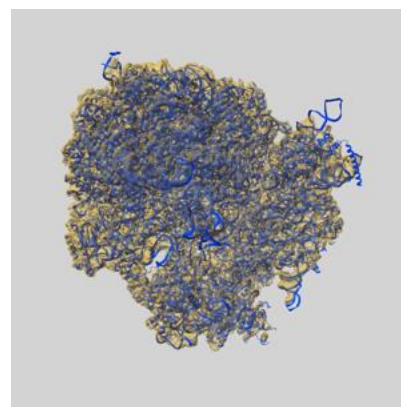
9.1 Map-model overlay [i](#)



X



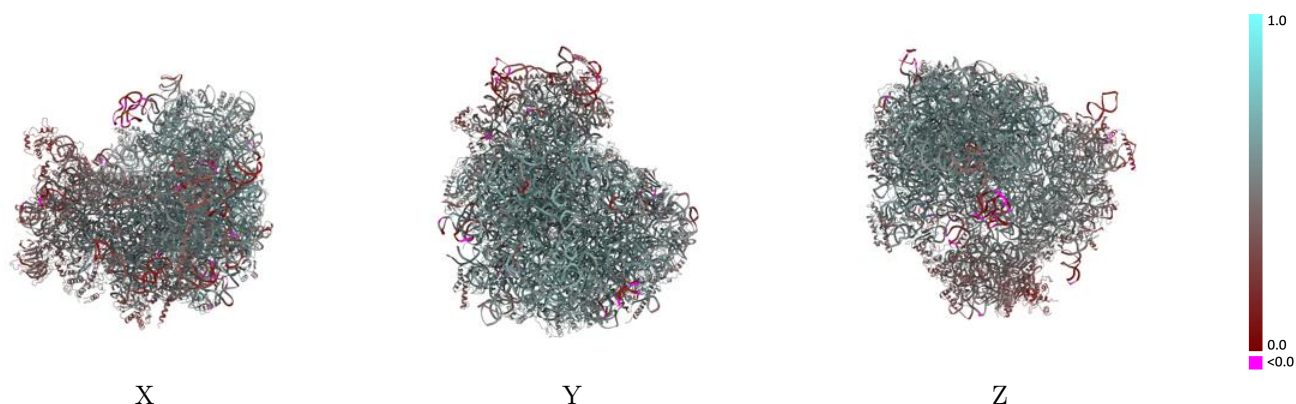
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0587 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

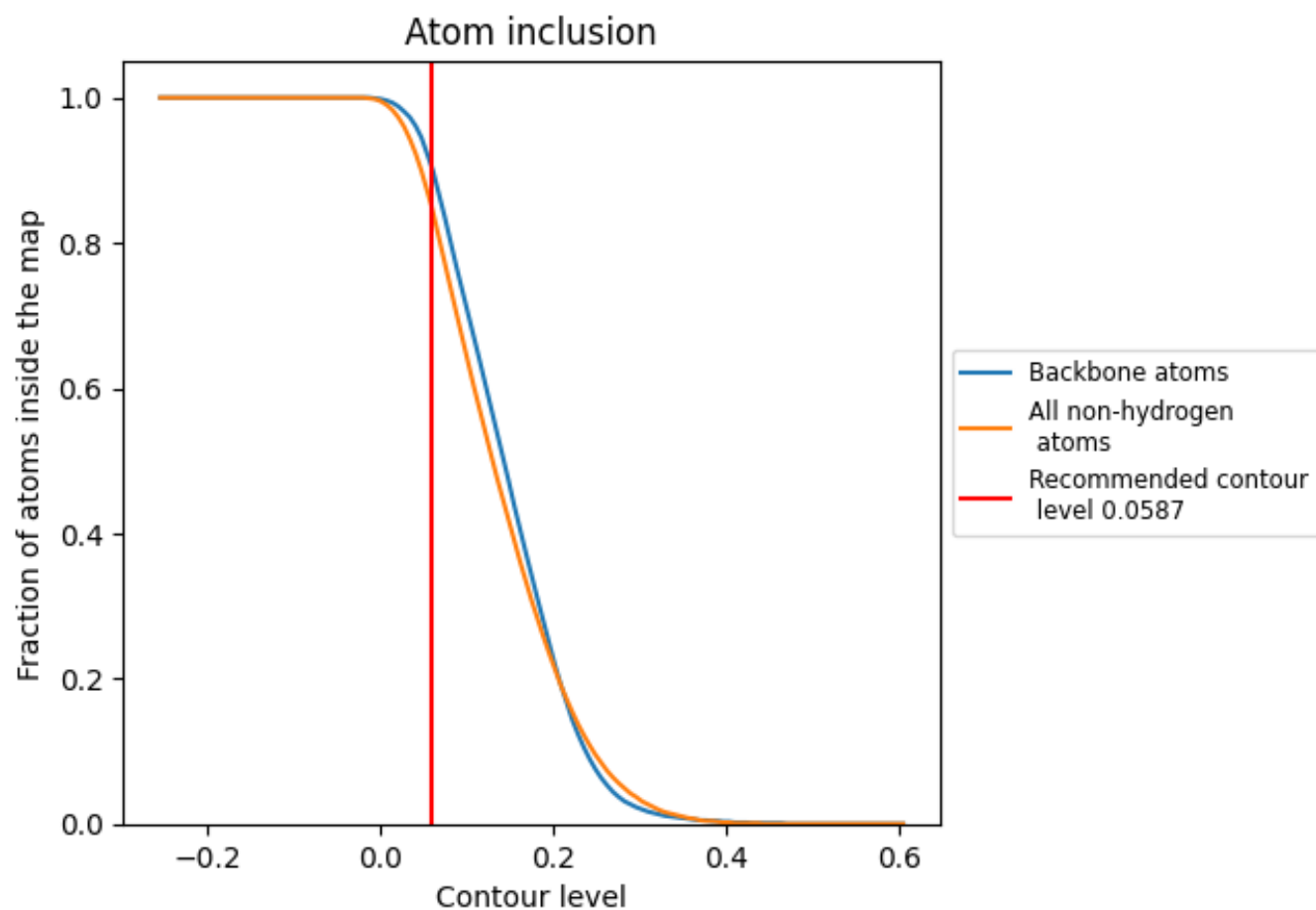


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 85% 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 (0.0587) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8520	 0.5140
1	 0.9380	 0.5620
2	 0.8770	 0.4690
3	 0.9610	 0.5880
4	 0.9760	 0.5400
5	 0.2420	 0.2200
6	 0.8850	 0.4480
A	 0.7190	 0.4390
AB	 0.8530	 0.5790
B	 0.7410	 0.4840
C	 0.7410	 0.4840
D	 0.6030	 0.3990
E	 0.7350	 0.4780
F	 0.6210	 0.4040
G	 0.7190	 0.4160
H	 0.6820	 0.4130
I	 0.8000	 0.5230
J	 0.7040	 0.4360
K	 0.6020	 0.3420
L	 0.7860	 0.5390
M	 0.3310	 0.2330
N	 0.7830	 0.5040
NC	 0.6670	 0.5250
O	 0.7810	 0.5030
P	 0.5890	 0.3720
Q	 0.6360	 0.4150
R	 0.6730	 0.4010
S	 0.6470	 0.3850
T	 0.6380	 0.3820
U	 0.6270	 0.3900
V	 0.7350	 0.4680
W	 0.7640	 0.5170
X	 0.7470	 0.5190
Y	 0.7030	 0.4180
Z	 0.5270	 0.3520



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Chain	Atom inclusion	Q-score
a	 0.7790	 0.5070
aa	 0.8190	 0.5770
ab	 0.8150	 0.5490
ac	 0.6970	 0.5440
ad	 0.8140	 0.5480
ae	 0.8940	 0.6030
af	 0.7530	 0.4860
ag	 0.9130	 0.6110
ah	 0.8000	 0.5100
ai	 0.8090	 0.5260
aj	 0.8350	 0.5600
ak	 0.8920	 0.5880
al	 0.8720	 0.5860
am	 0.8400	 0.5570
an	 0.8280	 0.5350
ao	 0.7880	 0.5260
ap	 0.8870	 0.5780
aq	 0.8340	 0.5240
ar	 0.8750	 0.5630
as	 0.8430	 0.5590
at	 0.5330	 0.4270
au	 0.8080	 0.4910
b	 0.7540	 0.4860
c	 0.6200	 0.4420
d	 0.7410	 0.4520
e	 0.6140	 0.4390
f	 0.3810	 0.2200
g	 0.5330	 0.3460
h	 0.8860	 0.6020
i	 0.8850	 0.5680
j	 0.8700	 0.5600
k	 0.7880	 0.4740
l	 0.8210	 0.5110
m	 0.8560	 0.5450
n	 0.8050	 0.5010
o	 0.8270	 0.5270
p	 0.7950	 0.5290
q	 0.7450	 0.4630
r	 0.8510	 0.5380
s	 0.8610	 0.5250
t	 0.9040	 0.5970
u	 0.8630	 0.5610

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Chain	Atom inclusion	Q-score
v	 0.8530	 0.5720
w	 0.8630	 0.5610
x	 0.7900	 0.5230
y	 0.8440	 0.5500
z	 0.8480	 0.5540