



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 05:21 AM UTC

PDB ID : 8CMJ / pdb_00008cmj
EMDB ID : EMD-16729
Title : Translocation intermediate 4 (TI-4*) of 80S *S. cerevisiae* ribosome with eEF2
in the absence of sordarin
Authors : Milicevic, N.; Jenner, L.; Myasnikov, A.; Yusupov, M.; Yusupova, G.
Deposited on : 2023-02-20
Resolution : 3.79 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:

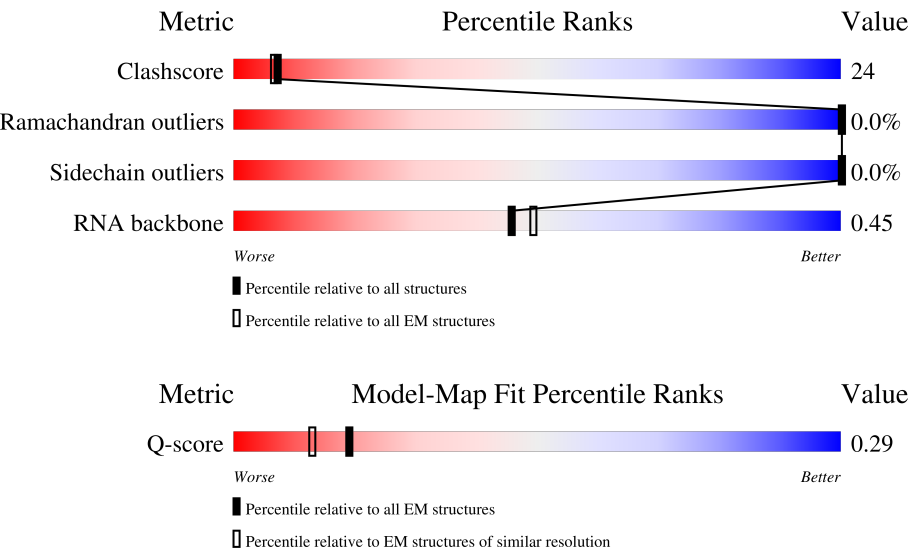
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.79 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.



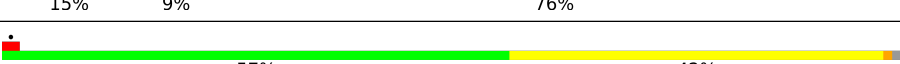
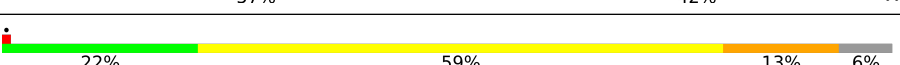
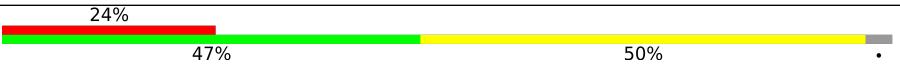
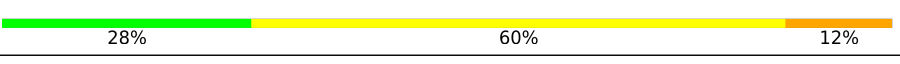
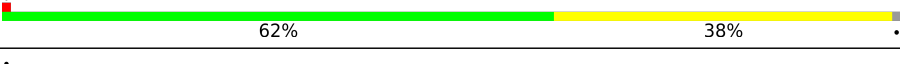
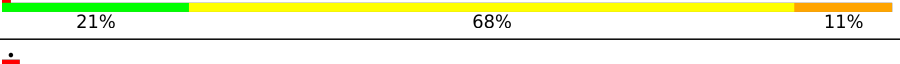
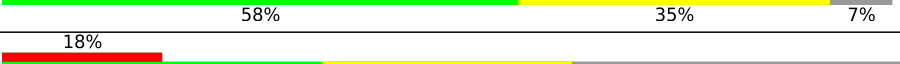
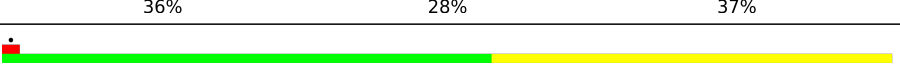
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10018 (3.29 - 4.29)

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	0	135	13% 51% 48% .
2	1	108	60% 32% 32% 35%
3	2	119	42% 39% 18%

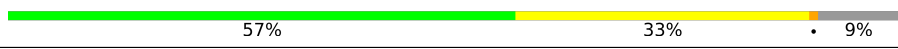
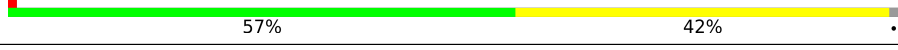
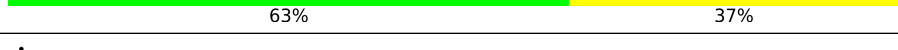
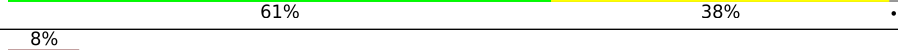
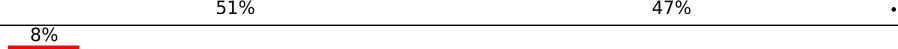
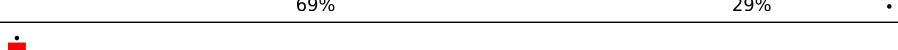
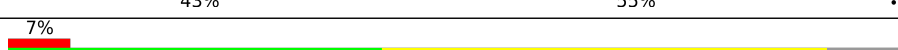
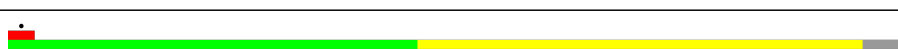
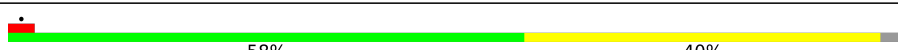
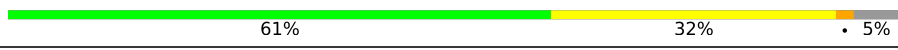
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Mol	Chain	Length	Quality of chain
4	3	82	
5	4	67	
6	5	56	
7	6	63	
8	7	319	
9	8	152	
10	A	199	
11	AA	3396	
12	Aa	842	
13	B	184	
14	BB	121	
15	C	186	
16	CC	158	
17	D	189	
18	DD	312	
19	E	172	
20	EE	254	
21	Ee	165	
22	F	160	
23	FF	387	
24	G	121	
25	GG	362	
26	H	137	
27	HH	297	
28	I	155	

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Mol	Chain	Length	Quality of chain
29	II	176	
30	J	142	
31	JJ	244	
32	K	127	
33	KK	256	
34	L	136	
35	LL	191	
36	M	149	
37	MM	221	
38	N	59	
39	NN	174	
40	O	105	
41	OO	199	
42	P	113	
43	PP	138	
44	Q	130	
45	QQ	204	
46	R	107	
47	S	121	
48	T	120	
49	U	100	
50	V	88	
51	W	78	
52	X	51	
53	Y	128	

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Mol	Chain	Length	Quality of chain
54	Z	25	
55	a	106	
56	b	92	
57	c	1800	
58	d	252	
59	e	255	
60	f	254	
61	g	240	
62	h	261	
63	i	225	
64	j	236	
65	k	190	
66	l	200	
67	m	197	
68	n	105	
69	o	156	
70	p	151	
71	q	137	
72	r	142	
73	s	143	
74	t	136	
75	u	146	
76	v	144	
77	w	121	
78	x	87	

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Mol	Chain	Length	Quality of chain
79	y	130	
80	z	145	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
11	OMU	AA	2724	-	-	X	-
57	OMG	c	562	-	-	X	-

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 202630 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	0	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 2 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	70	Total	C	N	O	0	0
			563	360	104	99		

- Molecule 3 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 4 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 5 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 6 is a protein called HLJ1_G0030400.mRNA.1.CDS.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	49	Total	C	N	O	S	0	0
			404	249	86	65	4		

- Molecule 7 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	53	Total	C	N	O	S	0	0
			427	269	88	69	1		

- Molecule 8 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	318	Total	C	N	O	S	0	0
			2436	1541	418	469	8		

- Molecule 9 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	8	36	Total	C	N	O	S	0	0
			276	173	54	45	4		

- Molecule 10 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 11 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AA	3197	Total	C	N	O	P	0	0
			68429	30589	12334	22309	3197		

- Molecule 12 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Aa	816	Total	C	N	O	S	0	0
			6368	4051	1088	1198	31		

- Molecule 13 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	B	154	Total	C	N	O	0	0
			1222	761	237	224		

- Molecule 14 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 15 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 16 is a RNA chain called 5.8S ribosomal RNA.

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
17	D	176	Total	C	N	O	0	0
			1423	875	308	240		

- Molecule 18 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	DD	197	Total	C	N	O	S	0	0
			1531	980	266	281	4		

- Molecule 19 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 20 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 21 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Ee	158	Total	C	N	O	S	0	0
			1196	750	216	228	2		

- Molecule 22 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 23 is a protein called 60S ribosomal protein L3.

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

- Molecule 24 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	G	97	Total	C	N	O		0	0
			770	499	126	145			

- Molecule 25 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 26 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	H	129	Total	C	N	O	S	0	0
			963	607	180	169	7		

- Molecule 27 is a protein called 60S ribosomal protein L5.

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

- Molecule 28 is a protein called 60S ribosomal protein L24-A.

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

- Molecule 29 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	II	155	Total	C	N	O	S	0	0
			1230	795	221	213	1		

- Molecule 30 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	J	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

- Molecule 31 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 32 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	K	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 33 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 34 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 35 is a protein called RPL9A isoform 1.

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

- Molecule 36 is a protein called 60S ribosomal protein L28.

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

- Molecule 37 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	MM	215	Total	C	N	O	S	0	0
			1743	1102	331	303	7		

- Molecule 38 is a protein called 60S ribosomal protein L29.

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

- Molecule 39 is a protein called 60S ribosomal protein L11-A.

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

- Molecule 40 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	O	97	Total	C	N	O	S	0	0
			742	479	124	138	1		

- Molecule 41 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 42 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 43 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 44 is a protein called 60S ribosomal protein L32.

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

- Molecule 45 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 46 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 47 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S	109	Total	C	N	O	S	0	0
			861	533	175	149	4		

- Molecule 48 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	V	84	Total	C	N	O	S	0	0
			665	405	145	110	5		

- Molecule 51 is a protein called 60S ribosomal protein L38.

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

- Molecule 52 is a protein called 60S ribosomal protein L39.

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

- Molecule 53 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 54 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Z	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 55 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	a	102	Total	C	N	O	S	0	0
			819	514	166	134	5		

- Molecule 56 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 57 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	c	1608	Total	C	N	O	P	0	0
			34321	15360	6093	11260	1608		

- Molecule 58 is a protein called 40S ribosomal protein S0-A.

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

- Molecule 59 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	e	212	Total	C	N	O	S	0	0
			1689	1073	303	309	4		

- Molecule 60 is a protein called 40S ribosomal protein S2.

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

- Molecule 61 is a protein called RPS3 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	g	183	Total	C	N	O	S	0	0
			1412	893	260	253	6		

- Molecule 62 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 63 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	i	199	Total	C	N	O	S	0	0
			1572	987	290	292	3		

- Molecule 64 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	j	219	Total	C	N	O	S	0	0
			1766	1108	341	314	3		

- Molecule 65 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	k	184	Total	C	N	O	S	0	0
			1481	951	265	265			

- Molecule 66 is a protein called 40S ribosomal protein S8-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	l	184	Total	C	N	O	S	0	0
			1457	906	291	258	2		

- Molecule 67 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 68 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	n	33	Total	C	N	O	S	0	0
			300	199	46	55			

- Molecule 69 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	o	142	Total	C	N	O	S	0	0
			1146	735	217	191	3		

- Molecule 70 is a protein called 40S ribosomal protein S13.

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

- Molecule 71 is a protein called 40S ribosomal protein S14-A.

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

- Molecule 72 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	r	91	Total	C	N	O	S	0	0
			732	469	138	120	5		

- Molecule 73 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	s	136	Total	C	N	O		0	0
			1069	686	195	188			

- Molecule 74 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	t	121	Total	C	N	O	S	0	0
			961	599	182	178	2		

- Molecule 75 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 76 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 77 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	w	100	Total	C	N	O	S	0	0
			800	509	144	146	1		

- Molecule 78 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 79 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 80 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 81 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
81	2	1	Total	Zn	0
			1	1	
81	5	1	Total	Zn	0
			1	1	
81	8	1	Total	Zn	0
			1	1	
81	S	1	Total	Zn	0
			1	1	
81	V	1	Total	Zn	0
			1	1	
81	Y	1	Total	Zn	0
			1	1	
81	a	1	Total	Zn	0
			1	1	
81	b	1	Total	Zn	0
			1	1	

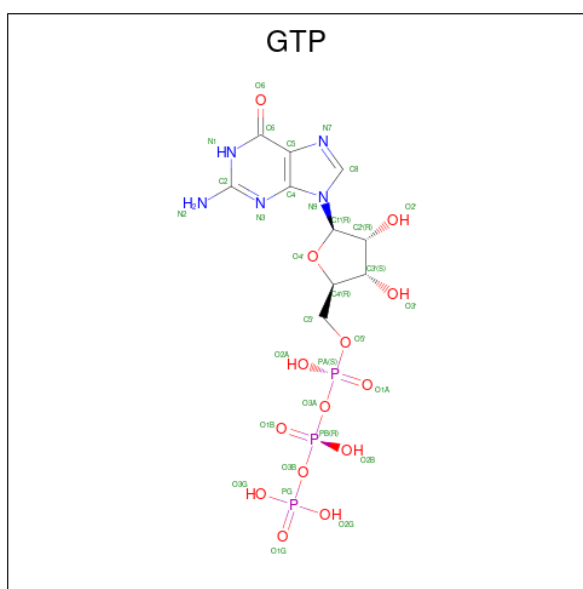
- Molecule 82 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
82	AA	119	Total	Mg	0
			119	119	
82	Aa	1	Total	Mg	0
			1	1	
82	BB	3	Total	Mg	0
			3	3	
82	CC	3	Total	Mg	0
			3	3	
82	H	1	Total	Mg	0
			1	1	
82	JJ	1	Total	Mg	0
			1	1	
82	c	25	Total	Mg	0
			25	25	

- Molecule 83 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
83	AA	9	Total	K	0
			9	9	
83	EE	1	Total	K	0
			1	1	

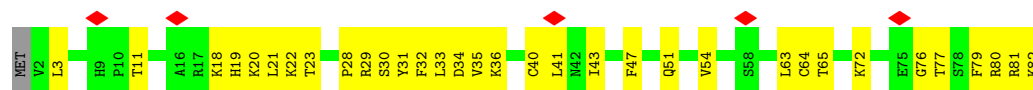
- Molecule 84 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



Mol	Chain	Residues	Atoms					AltConf
84	Aa	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 85 is water.

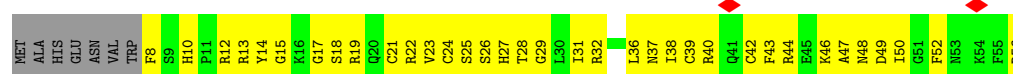
Mol	Chain	Residues	Atoms		AltConf
85	AA	71	Total 71	O 71	0
85	B	1	Total 1	O 1	0
85	CC	8	Total 8	O 8	0
85	F	1	Total 1	O 1	0
85	JJ	1	Total 1	O 1	0
85	R	1	Total 1	O 1	0
85	V	1	Total 1	O 1	0
85	c	18	Total 18	O 18	0



- Molecule 5: 40S ribosomal protein S28-A



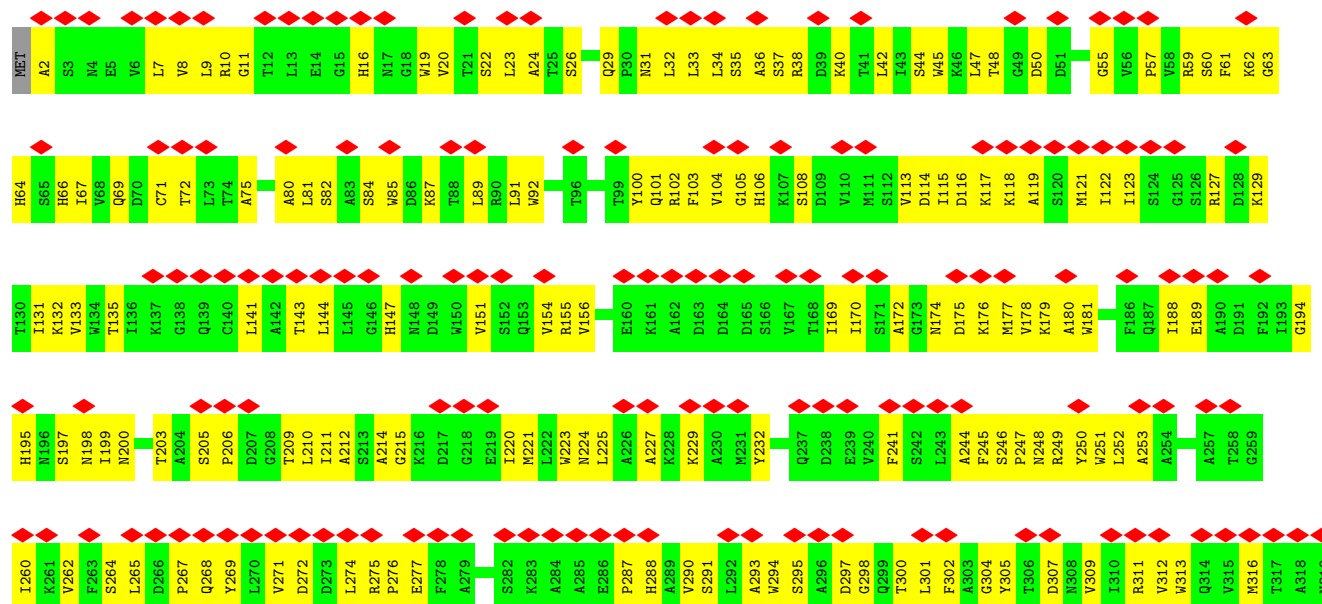
- Molecule 6: HLJ1_G0030400.mRNA.1.CDS.1



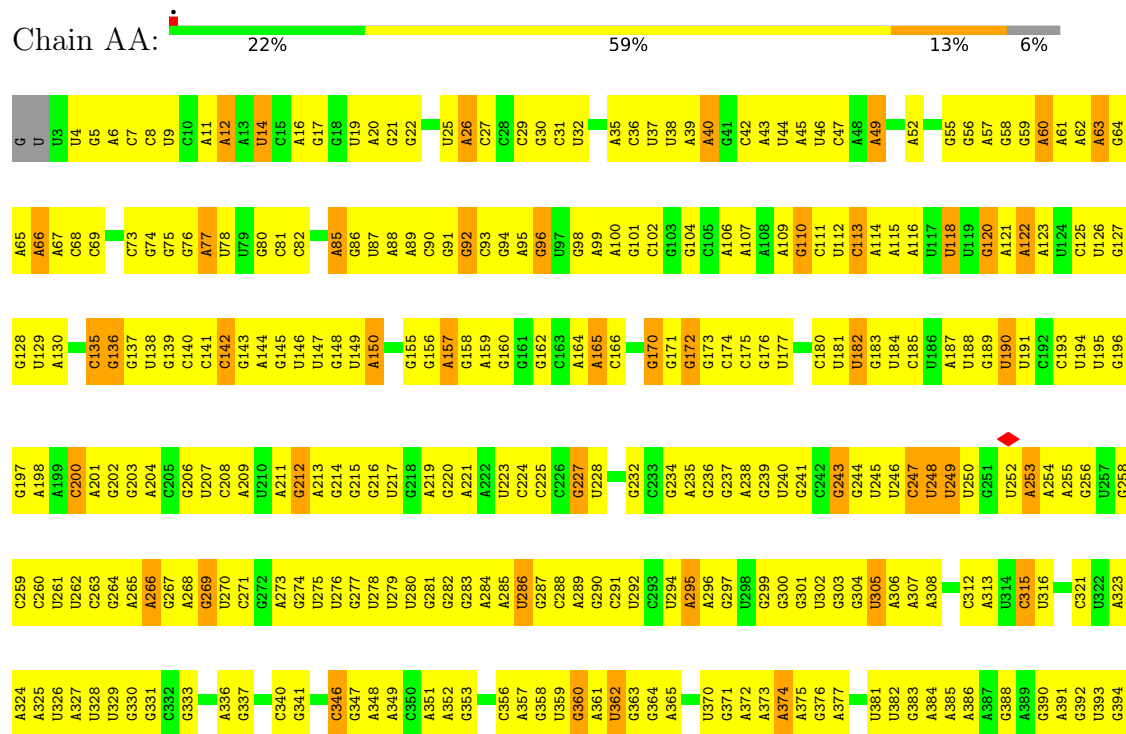
- Molecule 7: 40S ribosomal protein S30-A



- Molecule 8: Guanine nucleotide-binding protein subunit beta-like protein



- Molecule 9: Ubiquitin-40S ribosomal protein S31

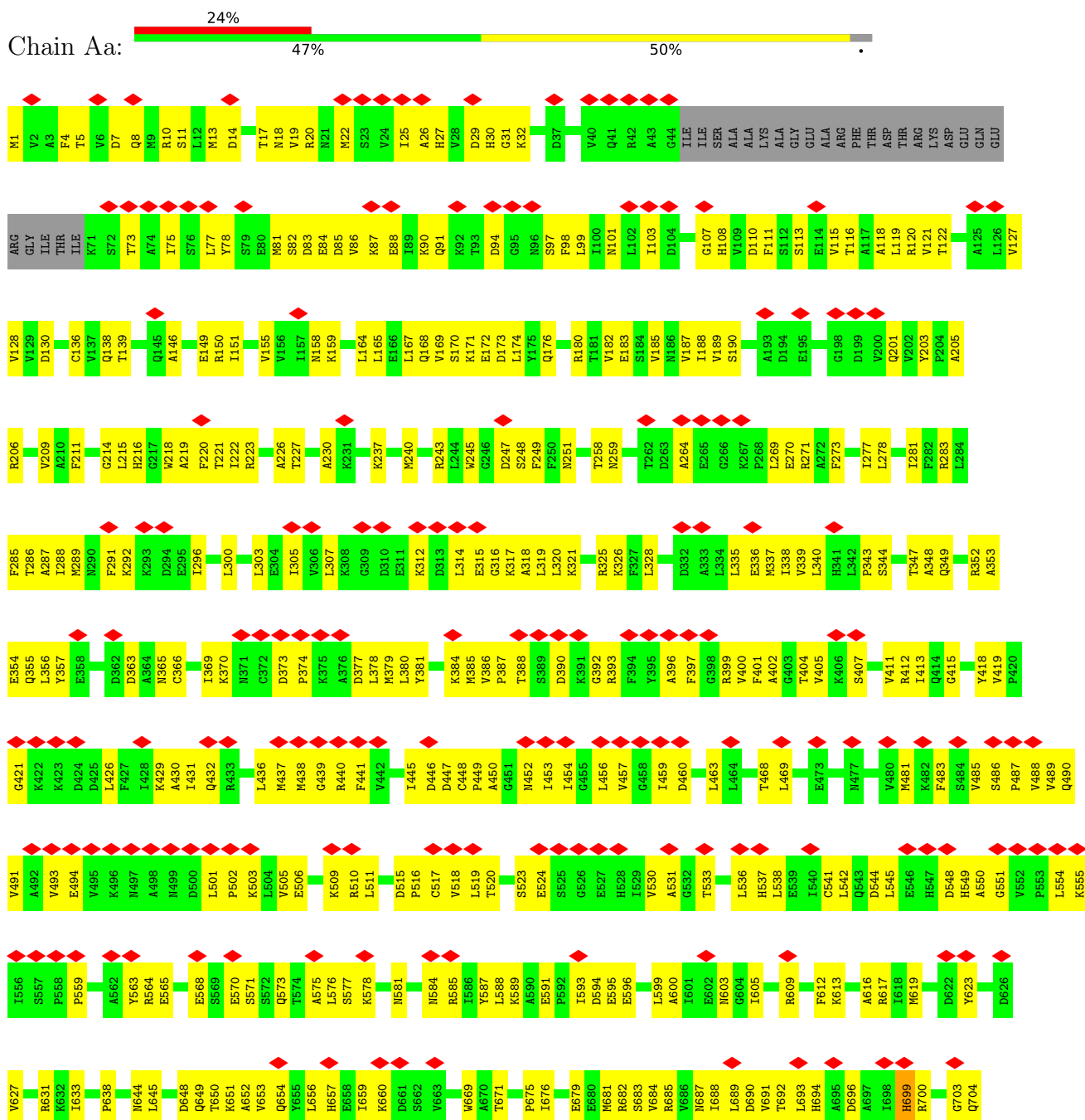


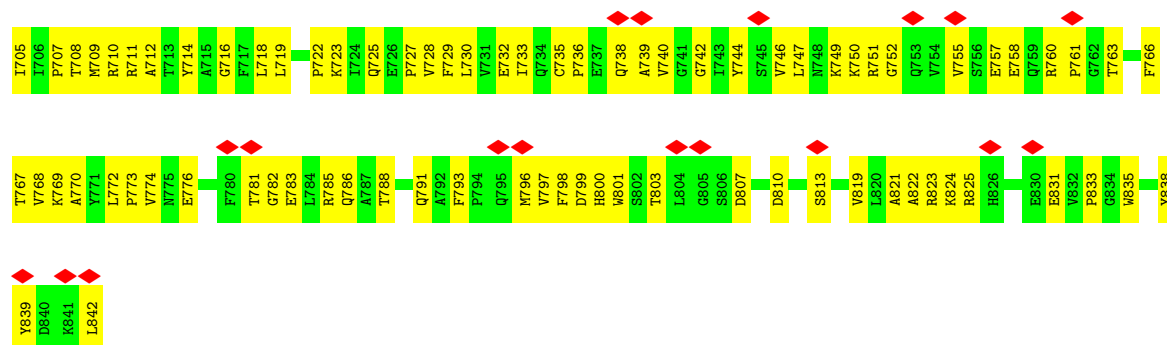
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G1289	A1102	G1228	G1166	A971	G908	G838	A709	A646	A585	U524	U525	A397
A1290	A1103	G1229	U1167	A972	G909	C839	U777	A647	C586	C526	C527	A398
A1291	G1104	A1230	U1168	A973	G910	C840	G778	A648	U587	C526	C527	A399
	A1105	G1231	U1169	A974	C911		G779	A649	G588	A527	A528	C400
A1294	G1106	C1232	A1170		G912	G845	A780	A650	A589	U528	U529	U401
G1295	C1107	G1233	G1171	G978	A913	A846	G781	G651	G590	A529	A530	A402
C1296	U1108	G1234	U1172	U979	A914	A847	A782	G652	G591	G530	G531	C403
	U1109	U1235	A1173	A980	A915	A848	A783		A592	U531	U532	G406
U1299	U1110	U1236	G1174	U981	G916	C849	A784	A655	C593	A532	A533	A407
G1300	U1111	U1237	A1047	C982	A917	U850	G785	A656	U594	A534	A535	A408
A1301	A1112	C1238	A1048	A983	C918	C851	A786	A657	U595	U536	U537	A409
A1302	G1113	C1239	C1049	U919	U919	U852	G787	G658	C596	G535	G536	U410
A1303	U1050	U1240	U1050	A920	G853	G854		A660	G597	A537	A538	U411
A1304	U1051	U1241	U1051	A921	G854	G855	A789	A661	C599	G538	G539	G412
U1305	U1052	G1242	A1052	U922	U855	U856	A790	U662	G600	A540	A541	U413
G1306	A1053	G1243	G1117	C923	G856	G857	G791	G663	U601	U540	U541	U414
G1307	U1054	A1244	G1118	G924	G857	G858	G792	U664	A602	G542	G543	G415
A1308	A1055	A1245	C1119	A925	A858	U859	C793	U665	A603	G544	G545	A416
	U1056	A1246	A1120	A926	U859	G859	U794	A666	G604	C544	C545	A417
U1309	U1057	U1247		A927	G860	C861	U795	C667	U605	U546	U547	A418
G1310	A1058	U1248	U1125	G993	C927	U862	G796	G668	C606	U548	U549	G419
G1311	G1058	G1249	G1126	G994	C928	C862	U797		A607	C546	C547	G420
G1312	U1059	G1250	U1127	U995	U929	U863	U797		A608	G547	G548	G421
	A1061	A1251	U1128	A996	U930	C863	G798		A609	U549	U550	A422
U1315	A1062	C1252	U1129	A997	U931		G799	U671	G609	G549	G550	A423
G1316	U1063	U1253	A1130	U998	U932	U870	A800	A672	G610	U551	U552	A424
A1317	G1063	C1254	G1131	C1000	G934	U871	G801	A673	G611	U553	U554	U429
	A1064	A1255	C1132		U935		C802	G674	A612	U555	U556	U430
U1322	A1065	G1256	U1133		A936	U874	C803	G675	G613	U557	U558	U431
G1323	U1066	G1257	G1134	U1004	G937	C875	C804	G676	G614	A559	A560	A433
U1324	A1067	C1258	A1135	G1005	U938	C876	C805	G677	U615	G560	G561	U434
U1325	A1068	U1259	U1136	A1006	C938	A876	A806	G678	G616	C562	C563	C435
C1326	U1071	A1260	G1137	U1007	U939	C877	A807	U679	U617	U564	U565	A436
C1328	U1072	G1261	U1138	U1008	G940	G878	A808	G680	C618	A498	A499	G437
U1329	U1073	G1262	U1139	A1009	U943	U879	A810	U682	G619	C500	C501	A438
A1330	U1074	A1263	G1140	G1010	C944	C880	U811	U683	U620	U502	U503	A439
U1331	A1075	A1264	G1141	A1011	C945	C881	G812	U684	A621	A504	A505	A440
A1332	C1076	U1265	C1142	G1012	U946	A882	U813	G685	G622	G506	G507	A441
C1333	U1077	G1266	A1143	G1013	U947	A883	U814	G686	U623	U508	U509	A442
U1334	U1078	U1267	A1144	U1014	G948	A884	G815	U687	G624	U510	U511	A443
C1335	A1079	G1268	G1145	U1015	C949	A885	A816	G688	G625	U512	U513	A444
U1336	A1080	U1269	U1081	C1016	G950	C889	A817	U689	U626	U514	U515	A445
A1337	U1081	A1270	U1146	C1017	A951	C890	C818	A690	U627	U516	U517	A446
C1338	G1147	C1271	G1148	G1018	A952	C891	U819	A691	U628	U518	U519	A447
C1339	G1149	A1272	G1150	G1019	G953	U892	C820	A692	A629	U520	U521	A448
G1340	C1086	U1273	A1151	G1020	U954	C893	U821	C700	G630	U522	U523	A449
U1341	G1087		U1152	U1021		C894	G822	G701	C631	U524	U525	A450
C1342	U1088		G1153	U1022	C958	A895	C823	G702	C632	U526	U527	A451
A1343	G1089		A1154	G1023	C959	A896	U824	G703	G633	U528	U529	A452
G1344	C1277		C1155	G1024	U960	U897	U825	U704	C634	U530	U531	A453
G1345	A1278		U1156	A1025	C961	U898	G826	U705	G635	U532	U533	A454
G1346	C1280		G1157	A1026	A962	U899	C765	U706	C636	U534	U535	A455
U1347	U1281		G1158	A1027	G963	G900	U766	G707	C637	U536	U537	A456
U1348	A1282		A1159	U1028	A965	G901	U767	G708	C638	U538	U539	A457
G1349	G1222		C1160	G1029	U966	G902	U768	U709	C639	U540	U541	A458
A1350	A1223		G1161	A1030	U967	U903	C769	U710	C640	U542	U543	A459
U1351	C1284			A1031	U968	U904	G770	U711	C641	U544	U545	A460
A1352	A1285			U1033	G968	U905	G835			U546	U547	A461
	A1286			U1034						U548	U549	A462





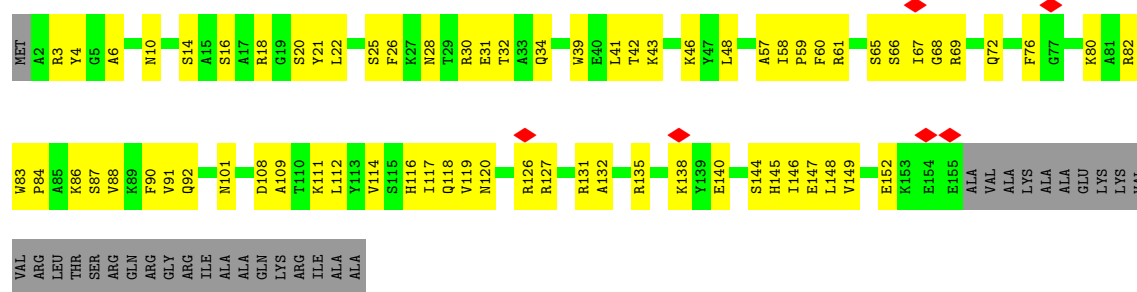
- Molecule 12: Elongation factor 2





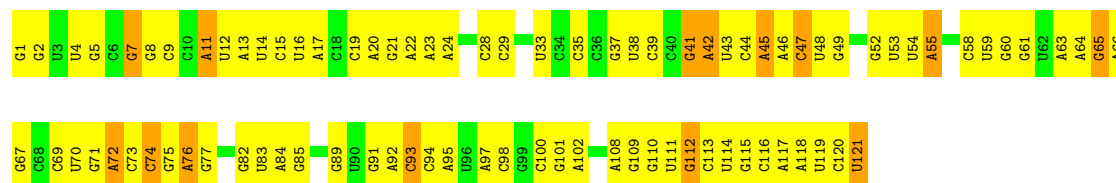
- Molecule 13: 60S ribosomal protein L17-A

Chain B: 46% 38% 16%



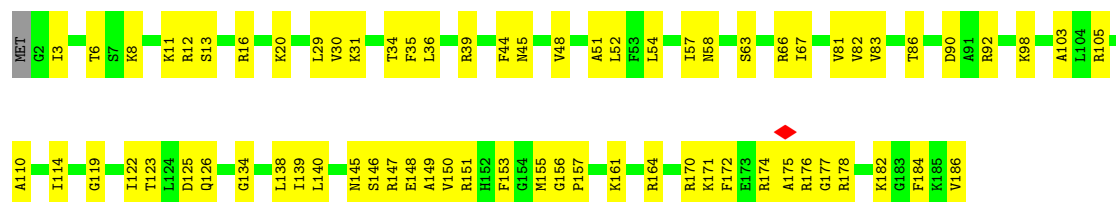
- Molecule 14: 5S ribosomal RNA

Chain BB: 28% 60% 12%



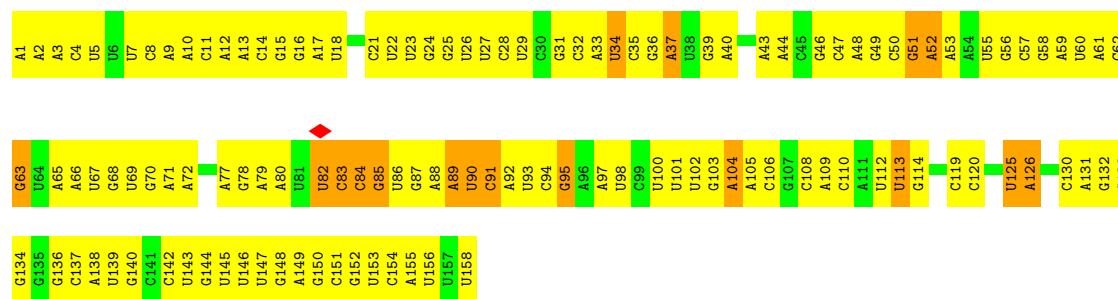
- Molecule 15: 60S ribosomal protein L18-A

Chain C: 62% 38% 0%

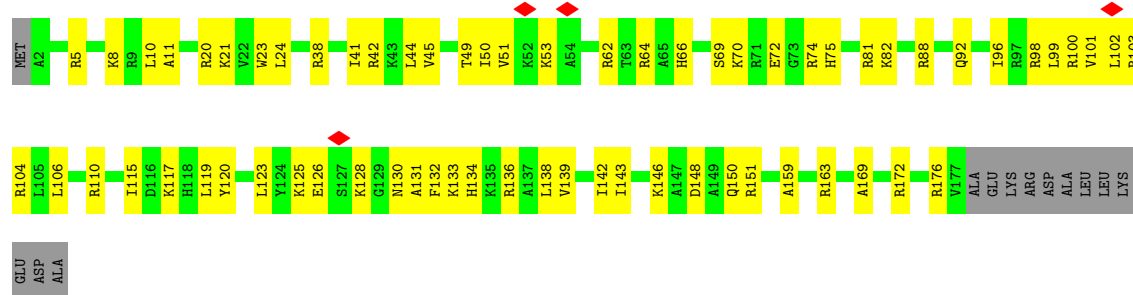


- Molecule 16: 5.8S ribosomal RNA

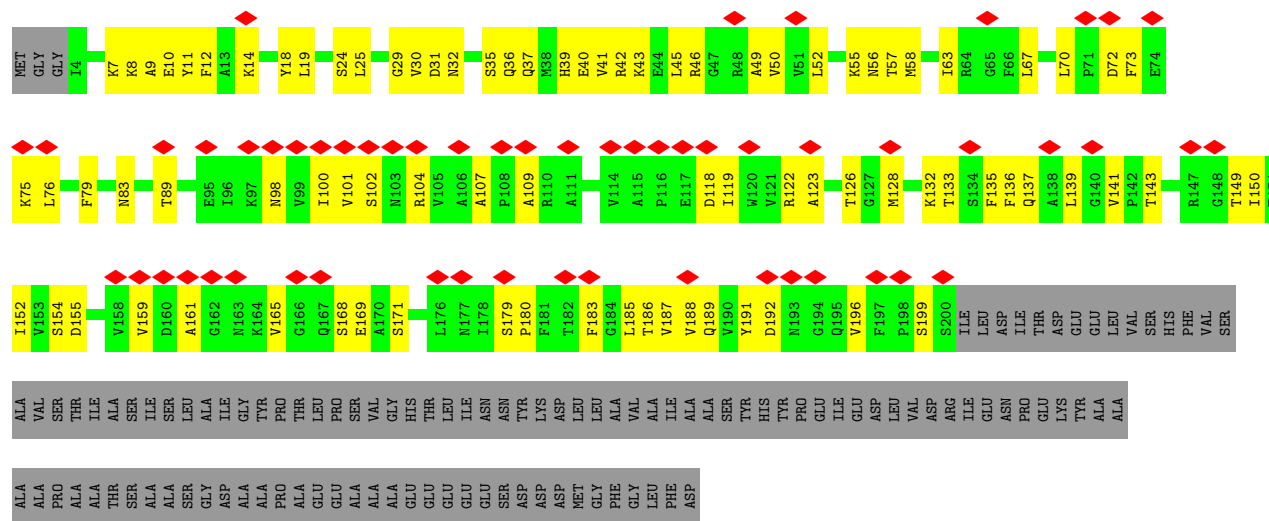
Chain CC: 21% 68% 11%



• Molecule 17: 60S ribosomal protein L19-A

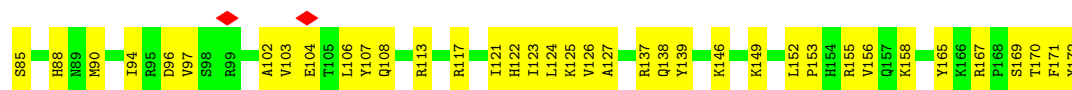


• Molecule 18: 60S acidic ribosomal protein P0

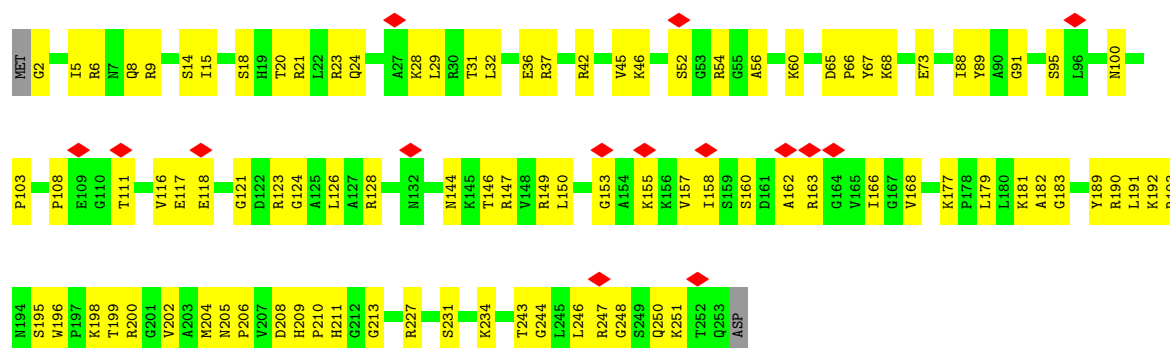


• Molecule 19: 60S ribosomal protein L20-A

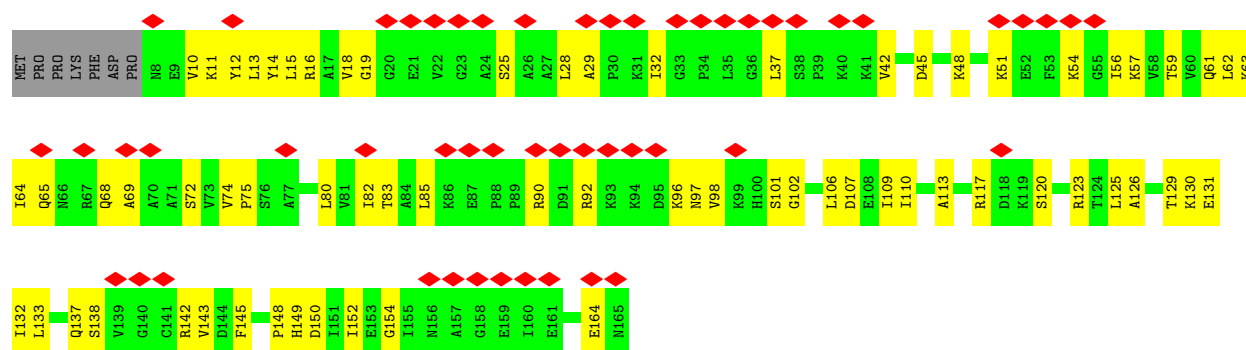




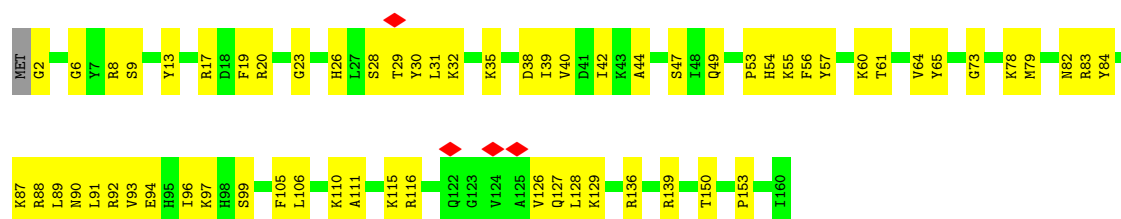
• Molecule 20: 60S ribosomal protein L2-A



• Molecule 21: 60S ribosomal protein L12-A

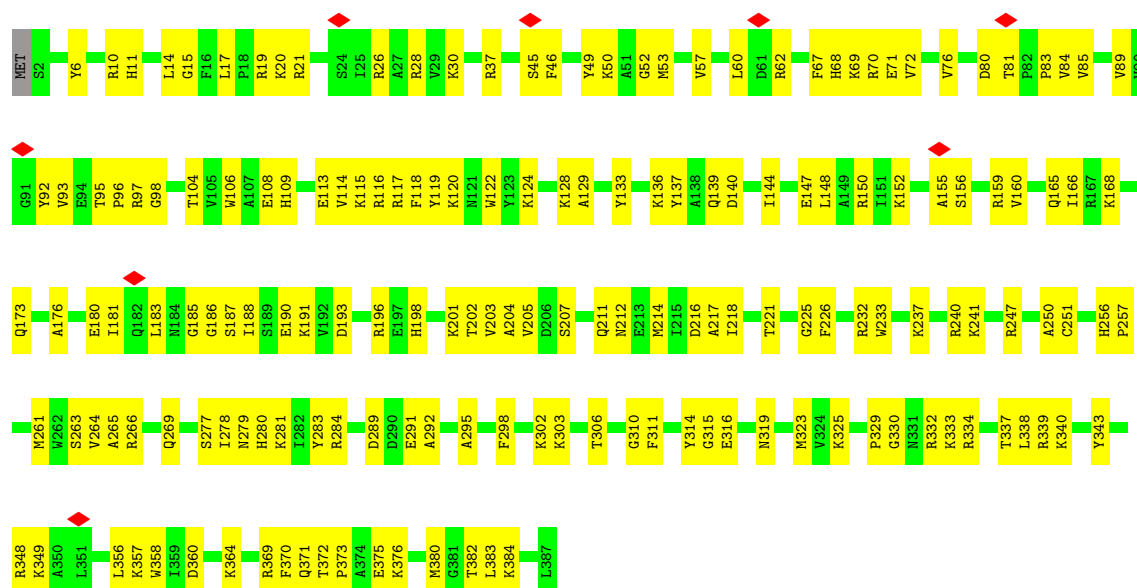


• Molecule 22: 60S ribosomal protein L21-A

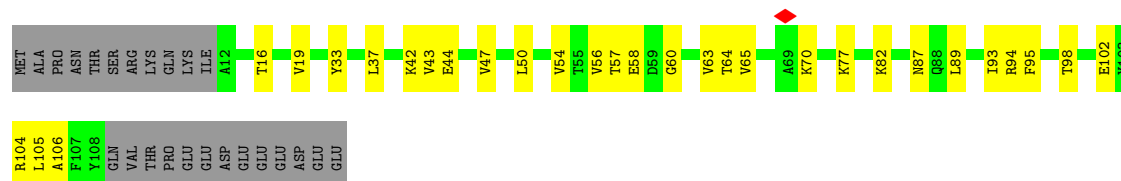


• Molecule 23: 60S ribosomal protein L3

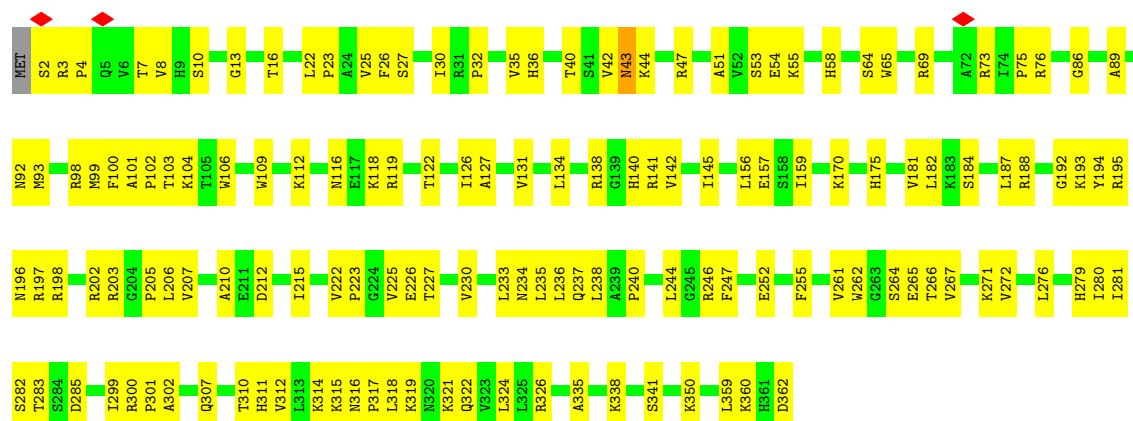




• Molecule 24: 60S ribosomal protein L22-A

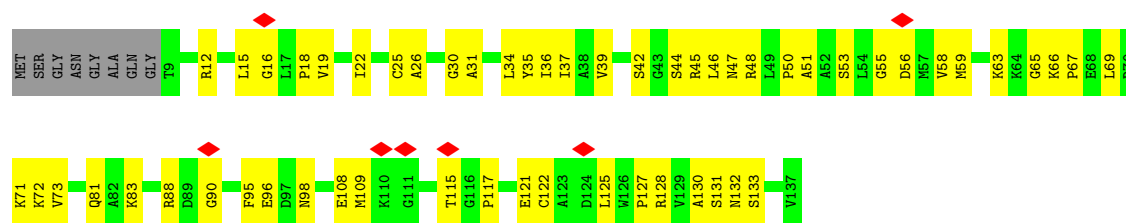


• Molecule 25: 60S ribosomal protein L4-A

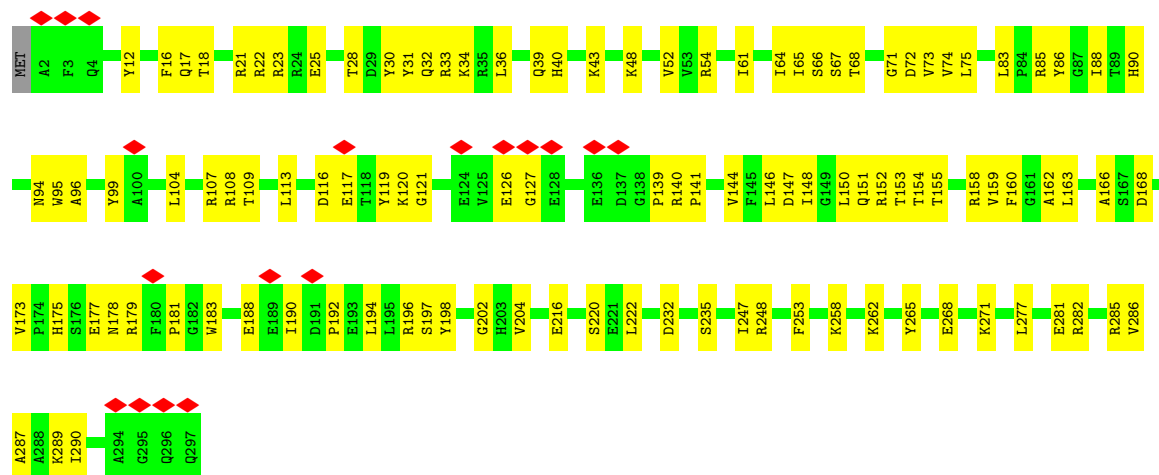


• Molecule 26: 60S ribosomal protein L23-A

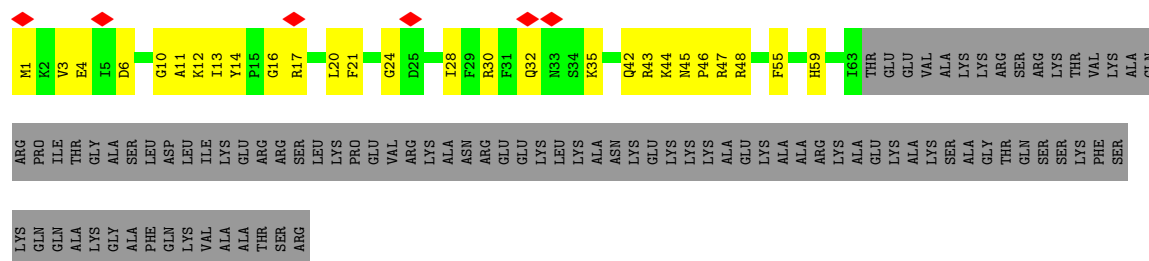




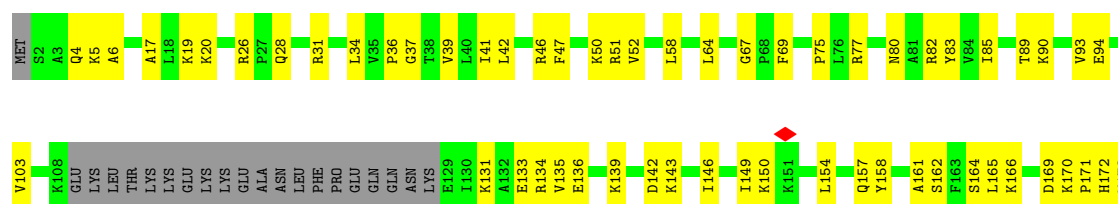
• Molecule 27: 60S ribosomal protein L5



• Molecule 28: 60S ribosomal protein L24-A

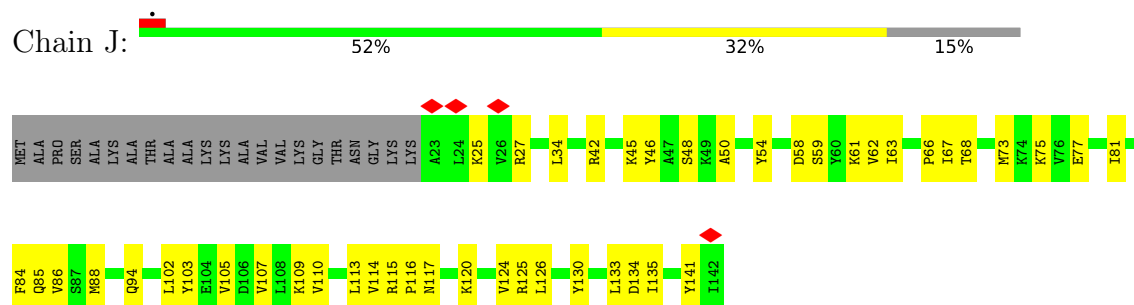


• Molecule 29: 60S ribosomal protein L6-A

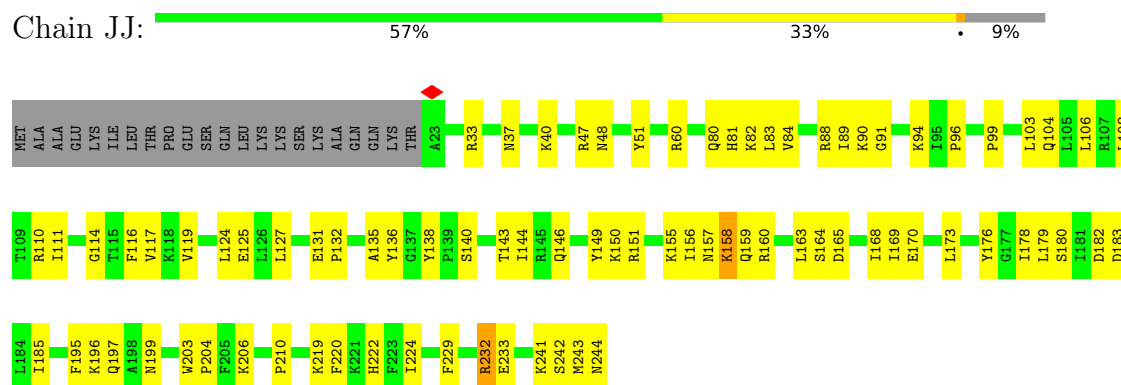




- Molecule 30: 60S ribosomal protein L25



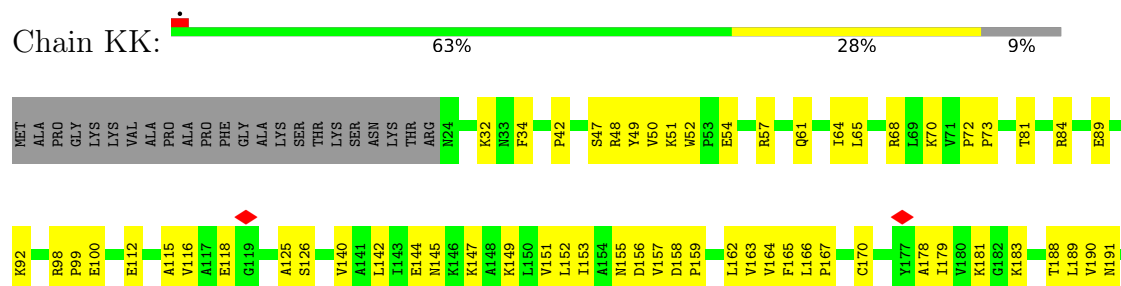
- Molecule 31: 60S ribosomal protein L7-A

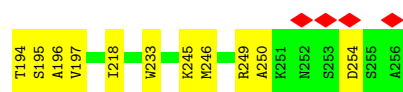


- Molecule 32: 60S ribosomal protein L26-A



- Molecule 33: 60S ribosomal protein L8-A

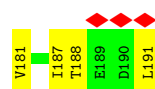
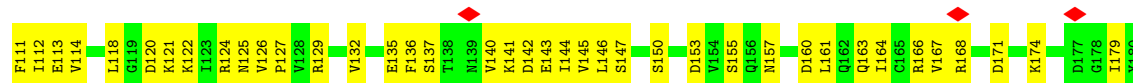




- Molecule 34: 60S ribosomal protein L27-A



- Molecule 35: RPL9A isoform 1

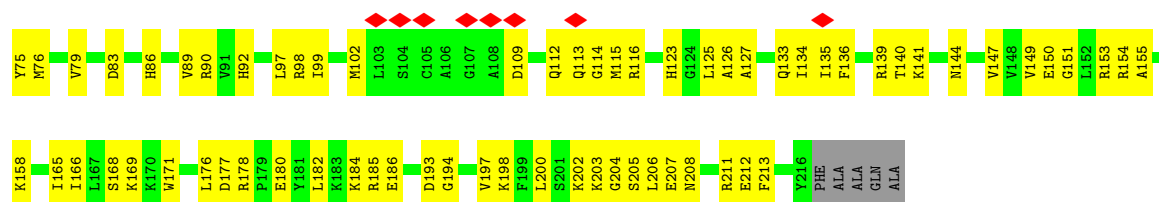


- Molecule 36: 60S ribosomal protein L28



- Molecule 37: 60S ribosomal protein L10

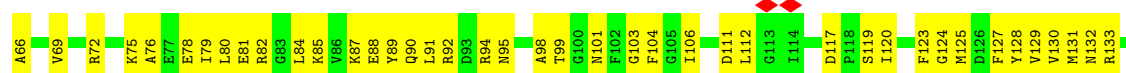




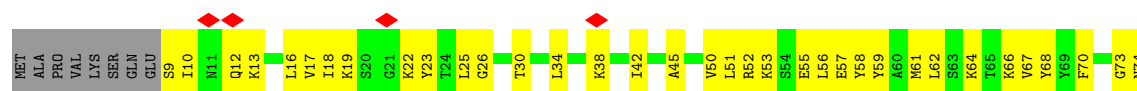
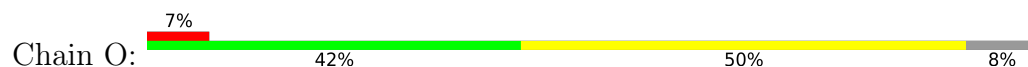
• Molecule 38: 60S ribosomal protein L29



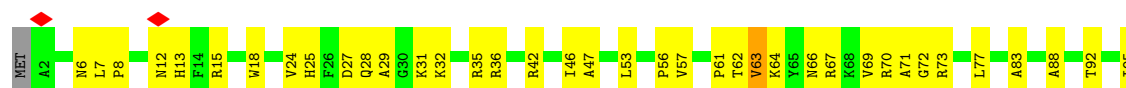
• Molecule 39: 60S ribosomal protein L11-A



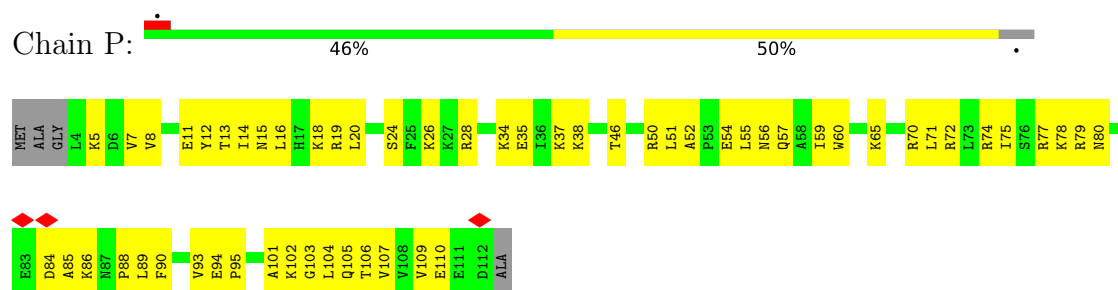
• Molecule 40: 60S ribosomal protein L30



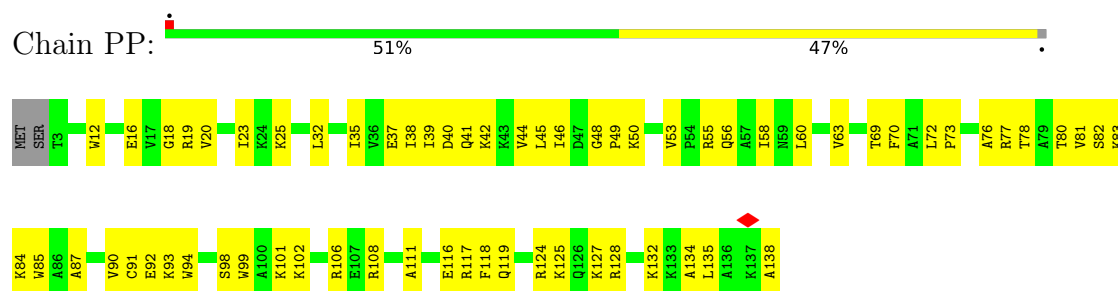
• Molecule 41: 60S ribosomal protein L13-A



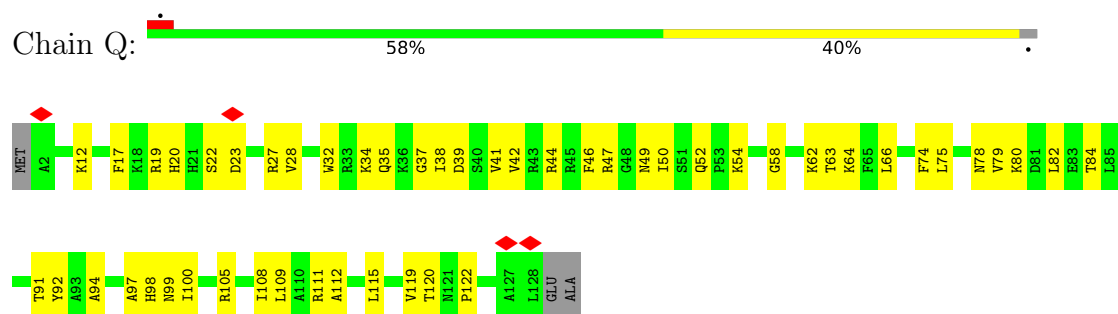
- Molecule 42: 60S ribosomal protein L31-A



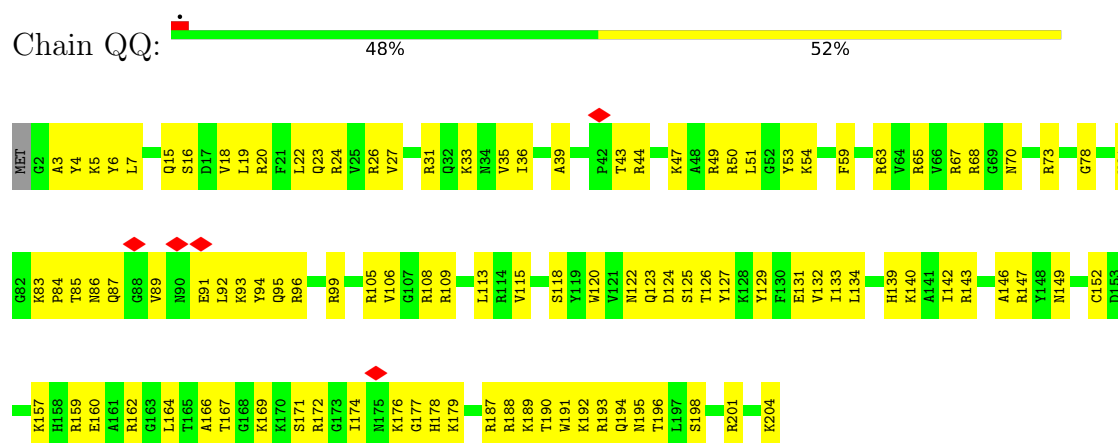
- Molecule 43: 60S ribosomal protein L14-A



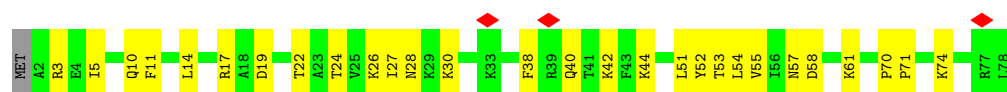
- Molecule 44: 60S ribosomal protein L32



- Molecule 45: 60S ribosomal protein L15-A



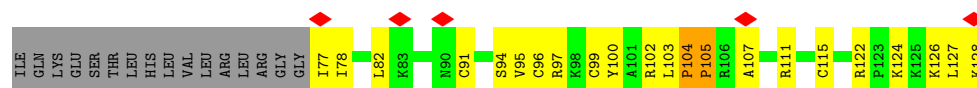
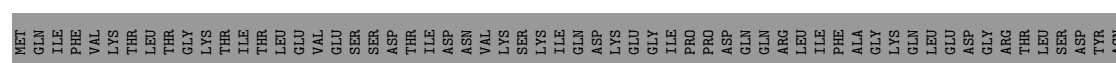
- Molecule 46: 60S ribosomal protein L33-A



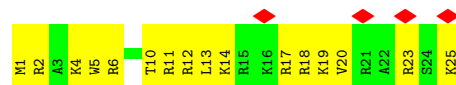
- Molecule 52: 60S ribosomal protein L39



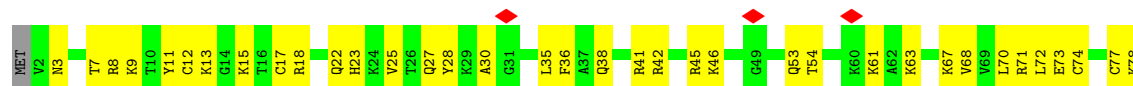
- Molecule 53: Ubiquitin-60S ribosomal protein L40



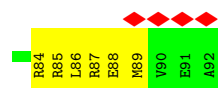
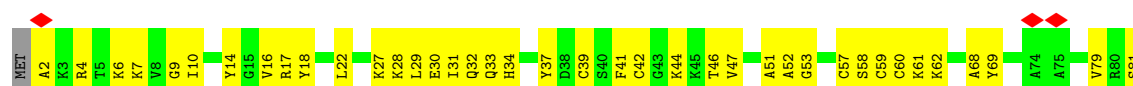
- Molecule 54: 60S ribosomal protein L41



- Molecule 55: 60S ribosomal protein L42-A



- Molecule 56: 60S ribosomal protein L43-A



Chain c:

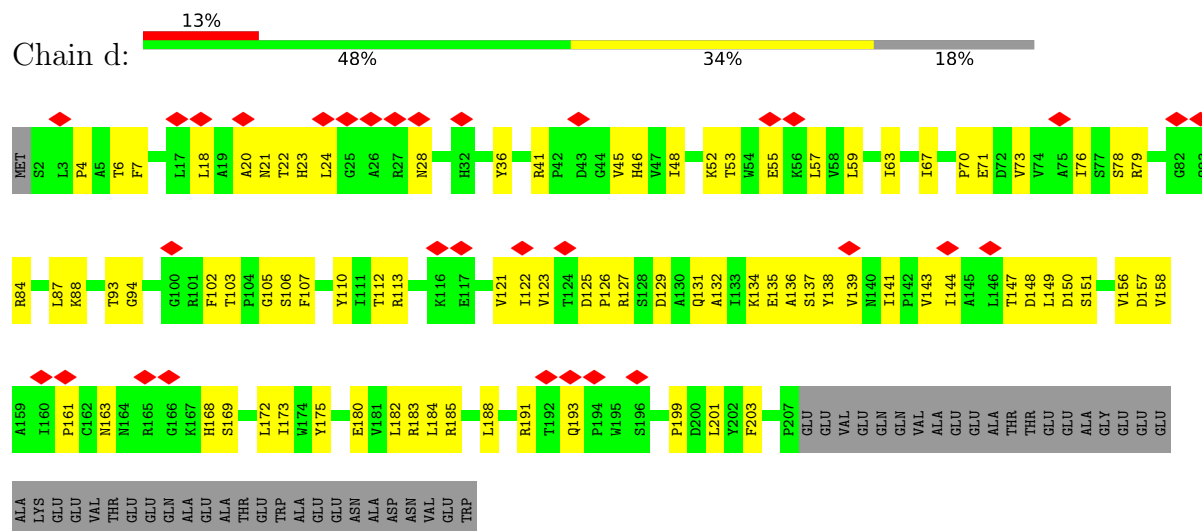
16% 53% 19% 11%

The diagram illustrates a network structure with nodes and connections. The nodes are organized into columns labeled A through U and rows labeled 1 through 990. The nodes are color-coded based on their category: green (16%), yellow (53%), orange (19%), and red (11%). The connections are represented by lines between nodes, showing a complex web of relationships. The diagram is a visual representation of a complex network structure.

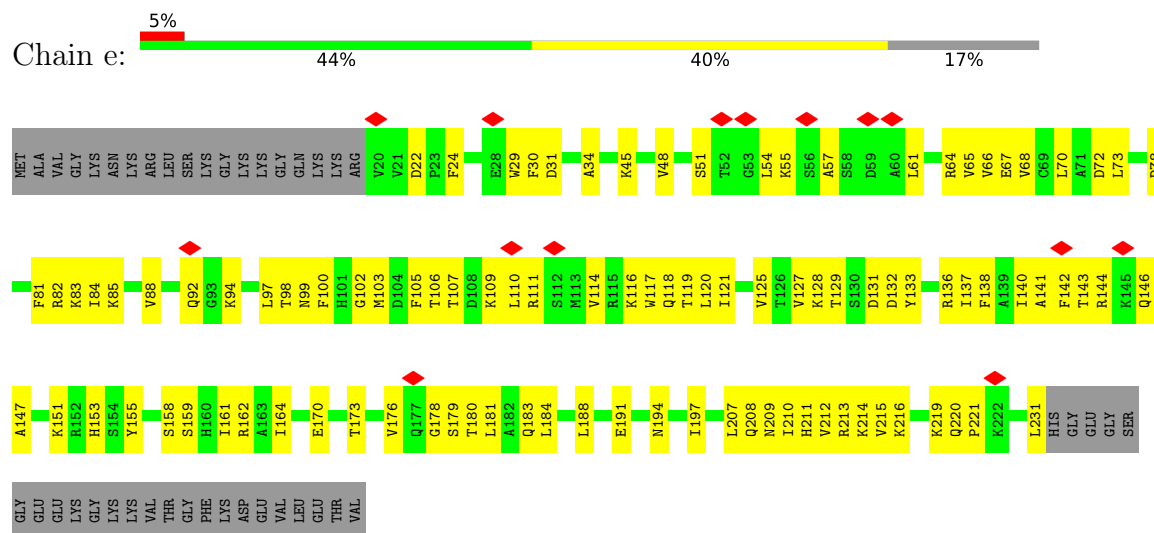
C	G1641	U1579	G1453	U1390	G1330	G1267	G1207	A1147	U1080	C1016	G954	A892
U	G1642	U1580	G1454	A1391	A1331	G1268	A1208	C1146	A1081	U1017	A955	U893
C	G1643	U1581	G1455	U1392	C1332	U1269	C1209	G1150	G1083	U1018	C956	U894
C	G1644	U1582	G1456	C1393	C1333	G1270	C1210	G1151	G1084	A1019	G957	G895
A	G1645	A1583	C1457	G1394	U1334	G1271	A1211	A1152	A1085	C1022	U958	U896
U	G1646	U1584	C1458	U1335	U1335	G1272	G1212	G1153	G1086	C1023	U959	C937
C	G1647	G1521	C1459	A1336	A1336	G1273	G1213	G1154	A1087	A1026	U960	A898
U	A1648	A1522	A1460	A1337	A1337	C1274	U1214	G1155	A1088	U1027	U961	G899
C	A1649	A1523	G1461	U1338	C1338	A1275	C1215	A1156	A1089	C1028	C962	A900
A	A1650	A1524	G1462	C1339	C1339	U1276	C1216	C1157	G1090	U1029	U963	G901
G	A1651	A1525	G1463	U1340	U1340	G1277	A1217	C1158	A1091	C1030	U964	G902
G	A1652	A1526	A1401	A1341	A1341	G1278	G1218	C1159	A1092	U1031	U965	U903
G1715	A1653	A1527	G1464	A1400	U1342	C1279	A1219	A1160	A1093	A1032	A966	G904
C1716	A1654	A1528	G1465	C1403	U1343	G1280	C1220	A1161	A1094	G1033	A967	A905
G1717	A1655	C1530	G1466	C1404	A1344	C1281	A1221	C1162	U1095	C1034	U968	A906
G1718	A1656	G1531	G1467	A1405	A1345	C1282	C1222	G1163	G1096	G1035	C969	A907
G1719	A1657	U1532	U1468	G1406	A1346	U1283	A1223	G1164	U1097	A1036	U970	U908
A1720	A1658	C1533	A1469	A1407	U1347	U1286	A1224	G1165	G1098	A1037	A971	U909
A1721	A1659	G1534	C1470	U1408	A1348	A1287	U1225	A1166	U1099	U1038	G972	C910
A1722	A1660	U1535	A1471	G1409	U1349	G1288	A1226	G1167	U1099	A1039	A973	U911
U1723	A1661	G1536	C1472	A1410	U1350	U1289	A1227	U1168	G1100	G1040	A974	U912
U1724	A1662	U1537	U1473	G1411	G1351	U1290	G1228	G1169	C1041	G1042	C975	G913
U1725	A1663	U1538	G1474	A1412	G1352	G1291	G1229	G1170	U104	A1043	G976	G914
G1726	A1664	G1539	A1475	G1413	U1353	G1292	A1230	A1171	G105	U1044	A977	A915
G1727	A1665	G1540	C1476	U1414	G1354	G1294	U1231	G1172	U106	C1045	A978	U916
A1728	A1666	U1541	G1477	U1415	C1355	G1295	U1232	C1173	G107	U1046	A979	U917
G1729	A1667	G1542	A1478	A1416	U1356	U1296	G1233	C1174	G108	G1047	G980	U918
A1730	A1668	A1543	A1479	G1417	A1357	A1296	A1234	U1175	U109	U1048	U981	A919
A1731	A1669	U1544	C1480	A1418	G1358	G1297	C1235	G1176	G110	G1049	U982	U920
A1732	A1670	U1545	C1481	G1419	C1359	U1298	A1236	C1177	G111	U1049	A983	U921
C1733	A1671	G1546	C1482	C1420	U1360	G1299	G1237	G1178	G1112	G1050	G987	G922
U1734	A1672	A1547	A1483	A1421	U1361	A1300	U1238	C1179	A1113	G1051	A988	A923
U1735	A1673	G1548	G1484	A1422	U1362	U1301	U1239	C1180	G1114	U1052	U989	A924
U1736	A1674	C1549	G1485	A1423	U1363	U1302	U1240	U1182	U1115	G1053	G990	G925
G1737	A1675	U1550	U1486	A1424	G1364	G1303	G1241	A1183	A1116	U1054	C991	U926
U1738	A1676	U1551	A1487	A1425	C1365	G1304	A1242	A1184	G1123	U1055	A992	U928
A1739	A1677	U1552	C1488	A1426	U1366	C1305	G1243	A1185	U1066	U1056	A993	A929
C1739	A1678	G1553	U1489	C1427	G1367	C1306	A1244	U1186	U1067	U1057	G994	A930
A1740	A1679	U1554	U1490	G1428	U1367	U1307	G1245	U1187	U1068	U1058	A995	C931
U1741	A1680	U1555	A1491	U1430	C1368	G1308	C1246	G1188	G1127	U1069	U996	U932
U1742	A1681	A1556	U1492	U1431	U1369	U1310	G1247	A1189	C1128	A1061	A998	A933
U1743	A1682	U1557	U1493	G1432	A1371	A1312	U1248	C1190	U1129	A1062	U999	U935
A1744	A1683	U1558	U1494	U1433	U1372	G1313	U1249	B8N1191	G1130	U1063	C1000	G936
G1745	A1684	A1559	A1495	G1434	U1373	U1314	U1250	C1192	A1131	G1064	A1001	C937
U1746	A1685	U1560	U1496	A1435	C1374	G1315	U1251	A1193	A1132	A1065	G1002	G938
U1747	A1686	U1561	U1497	U1436	A1375	G1316	C1252	C1194	A1133	C1066	A1003	A939
U1748	A1687	G1562	U1498	U1437	C1376	G1317	U1253	C1195	A1134	C1067	U1004	A940
A	U	G1563	C1500	U1438	U1377	G1318	U1254	A1196	U1135	C1068	A1005	A944
U1752	A	U1564	C1501	G1439	U1378	G1319	A1256	C1197	U1136	C1069	C1006	U945
A1753	A	C1565	C1502	U1440	U1379	A1321	U1257	G1198	A1137	C1070	C1007	U946
A1754	A	U1566	G1503	C1441	C1379	A1322	U1258	G1199	A1138	U1071	G1008	U947
A1755	A	U1567	U1504	U1442	U1380	A1323	U1259	G1200	G1141	C1072	C1010	G948
G1756	A	U1568	G1505	U1443	U1381	G1324	G1260	A1201	A1142	G1073	G1011	G949
U1757	A	C1569	U1506	A1444	U1382	A1325	G1261	A1202	A1143	G1074	U1012	C950
C1759	A	U1570	U1507	G1445	A1383	A1326	U1262	A1203	A1144	C1075	U1013	A951
A1760	A	C1571	U1508	A1446	U1384	A1327	G1263	A1204	U1145	A1076	G1014	A952
U1761	A	U1572	U1509	C1447	A1385	G1328	U1264	A1205	G1146	U1079	U1015	G953
A1762	A	A1573	G1510	U1448	G1386	A1329	U1265	U1206				
A1763	A	G1512	U1511	U1450	G1387							
C1764	A	U1514	U1515	U1451	A1388							
		A1576		U1452	C1389							



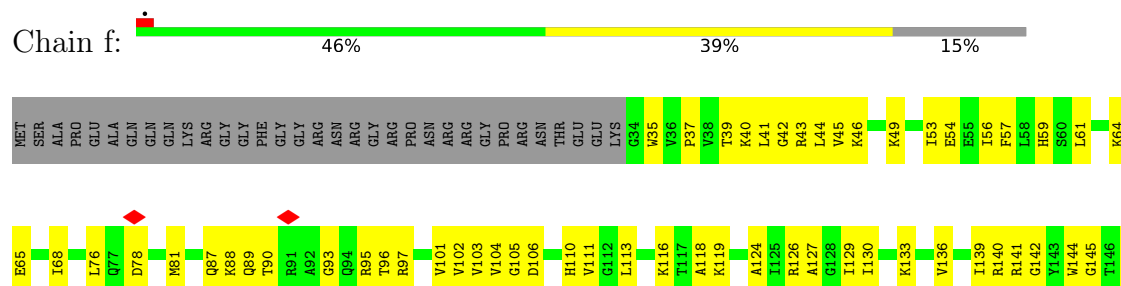
• Molecule 58: 40S ribosomal protein S0-A

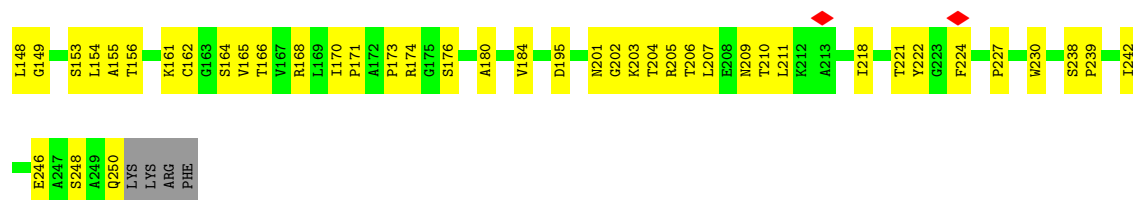


• Molecule 59: 40S ribosomal protein S1-A

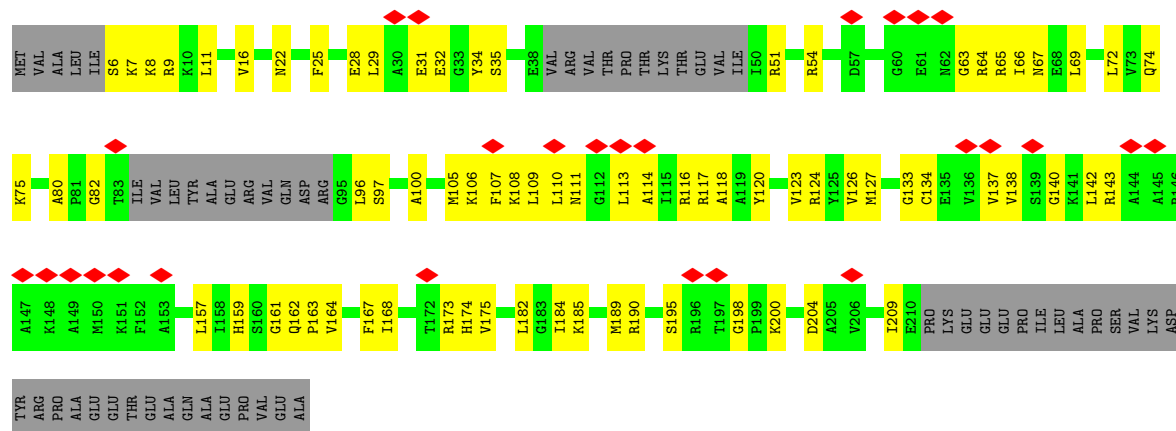
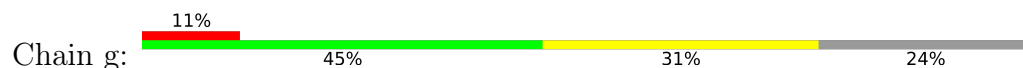


• Molecule 60: 40S ribosomal protein S2

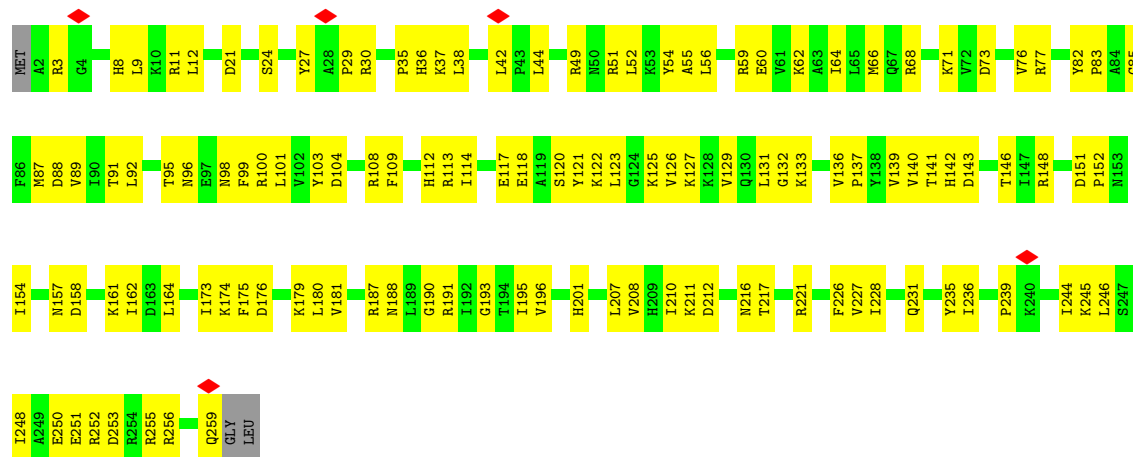




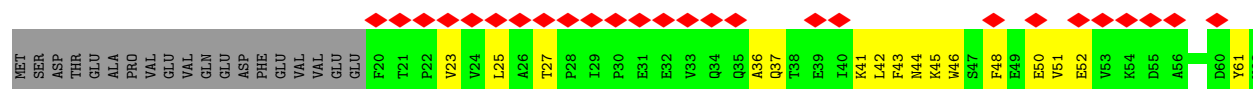
• Molecule 61: RPS3 isoform 1

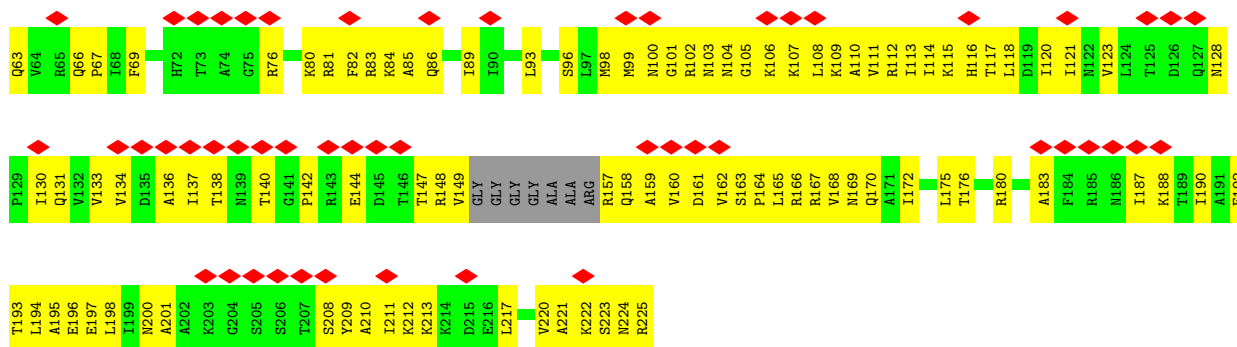


• Molecule 62: 40S ribosomal protein S4-A

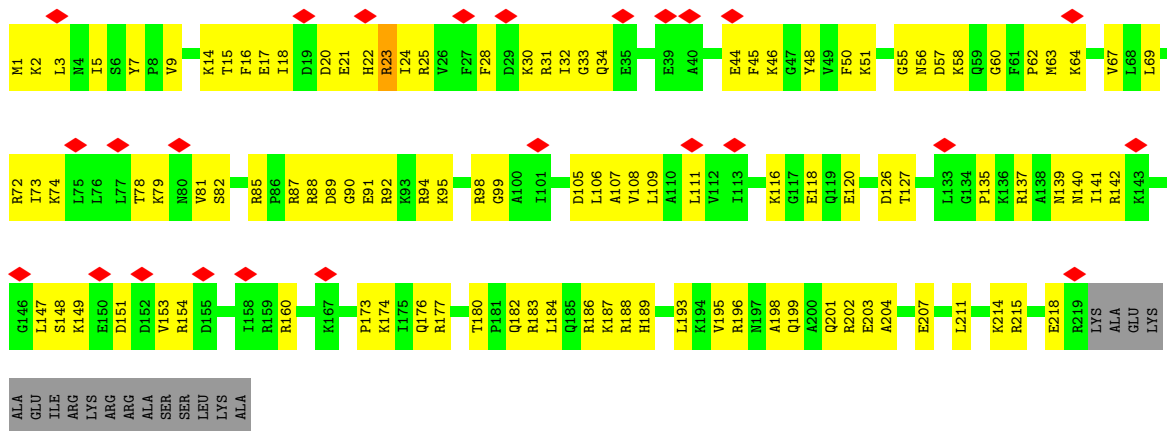


• Molecule 63: 40S ribosomal protein S5

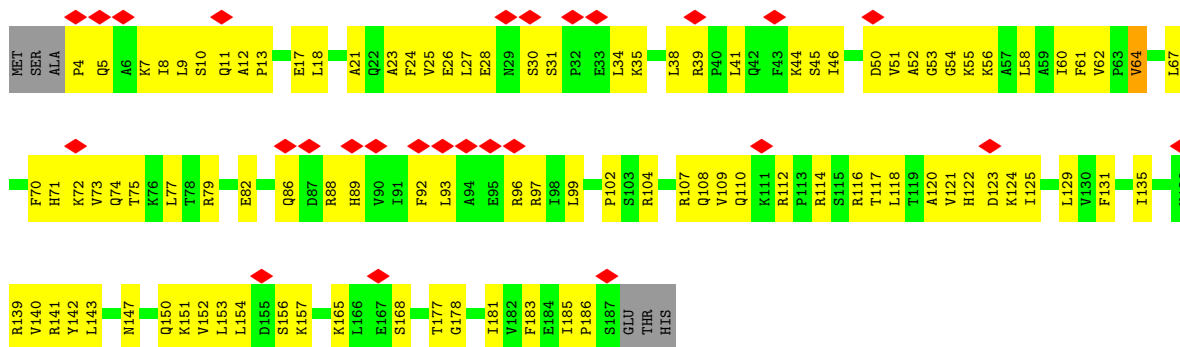
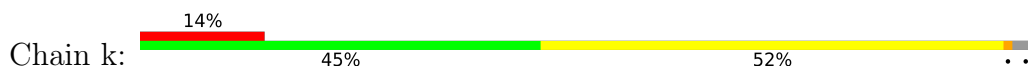




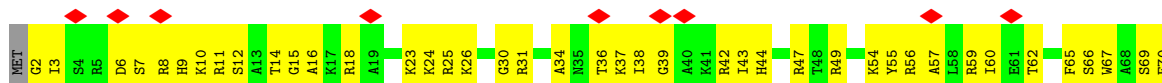
• Molecule 64: 40S ribosomal protein S6-A

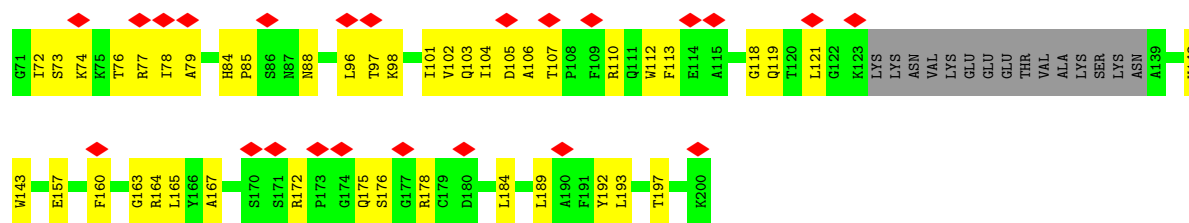


• Molecule 65: 40S ribosomal protein S7-A



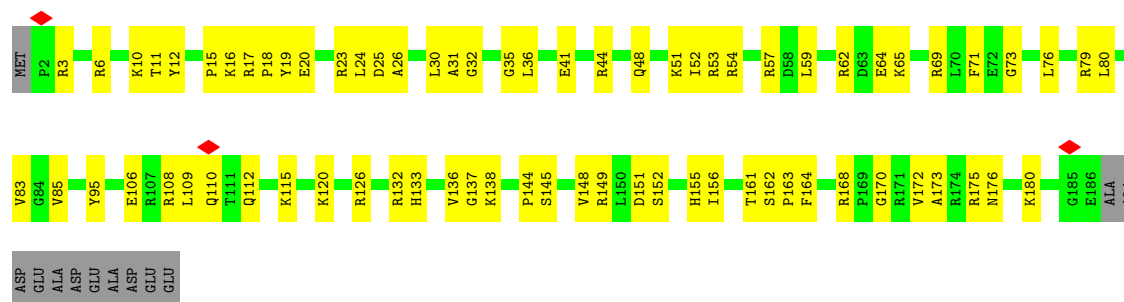
• Molecule 66: 40S ribosomal protein S8-B





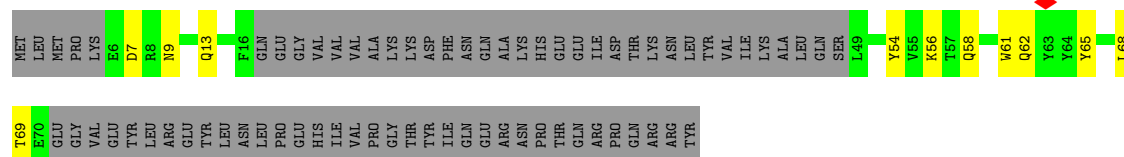
- Molecule 67: 40S ribosomal protein S9-A

Chain m: 57% 37% 6%



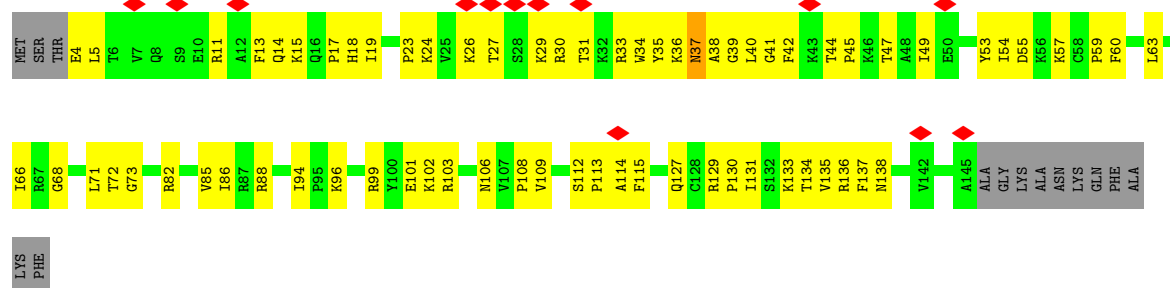
- Molecule 68: 40S ribosomal protein S10-A

Chain n: 21% 10% 69%



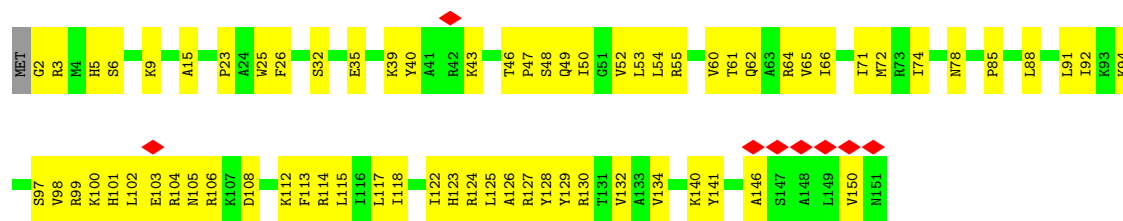
- Molecule 69: 40S ribosomal protein S11-A

Chain o: 8% 47% 44% 9%

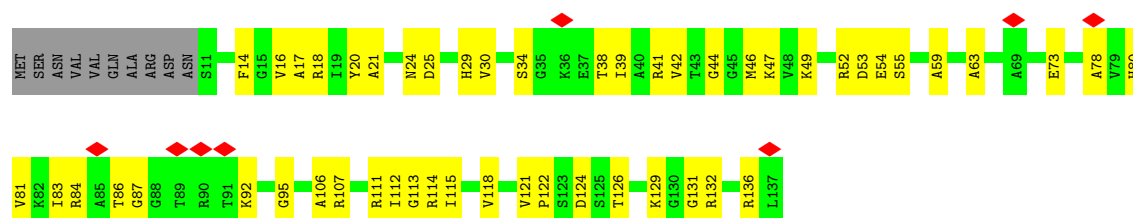


- Molecule 70: 40S ribosomal protein S13

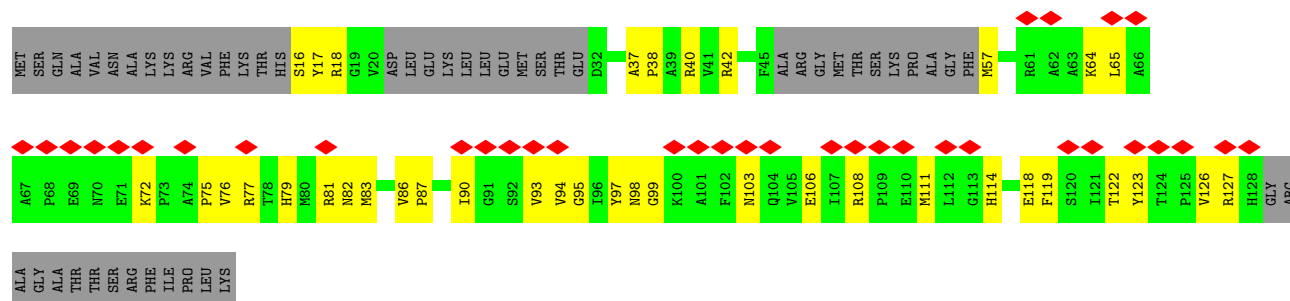
Chain p: 5% 53% 46%



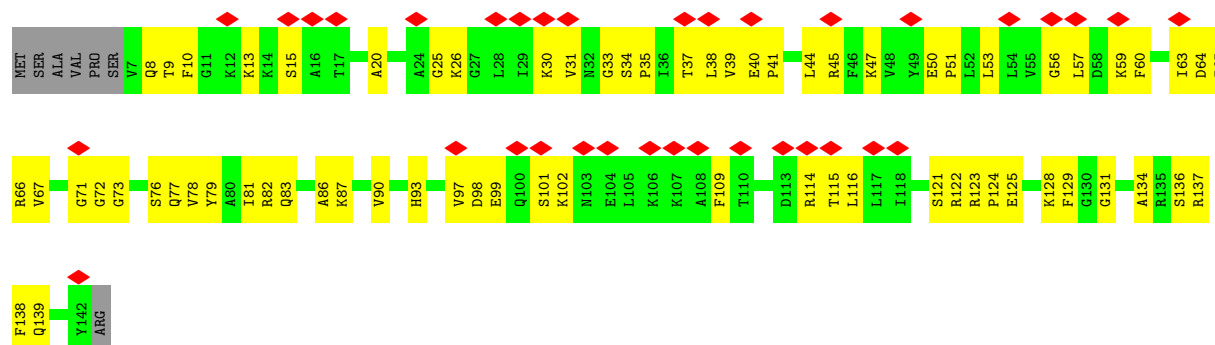
• Molecule 71: 40S ribosomal protein S14-A



• Molecule 72: 40S ribosomal protein S15

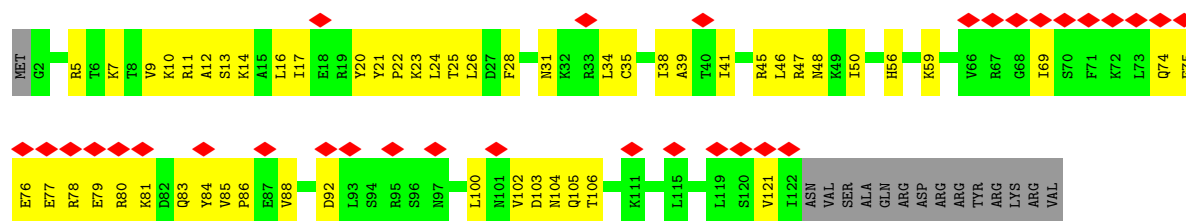


• Molecule 73: 40S ribosomal protein S16-A

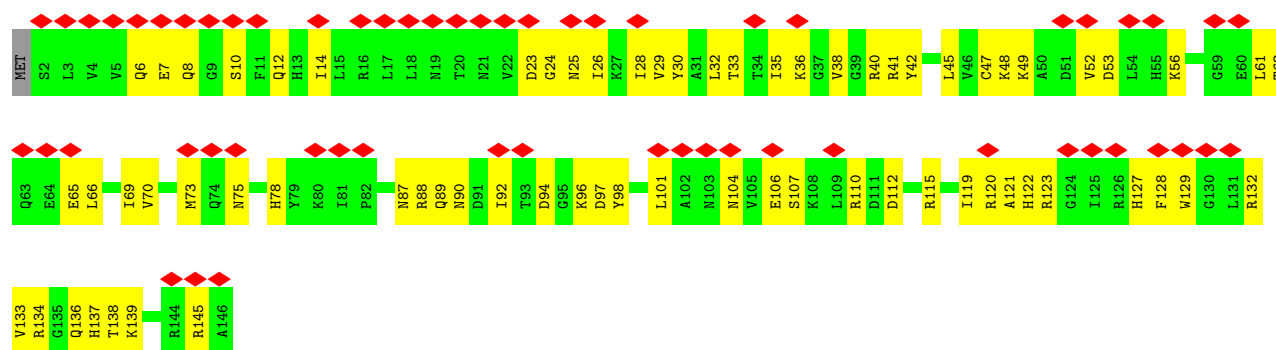
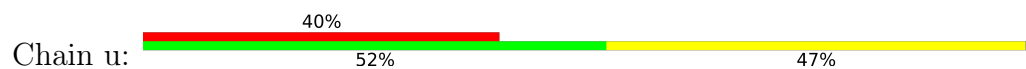


• Molecule 74: 40S ribosomal protein S17-A

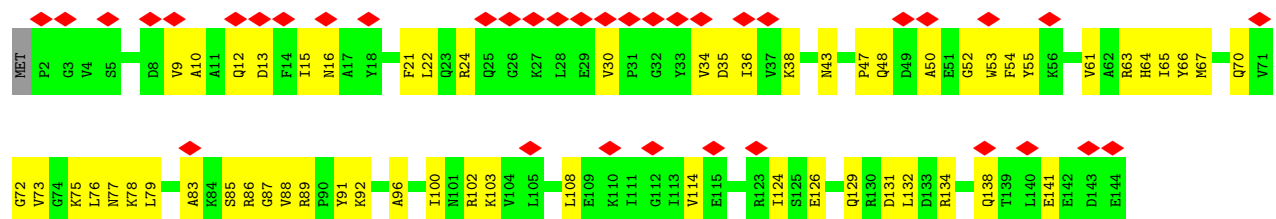




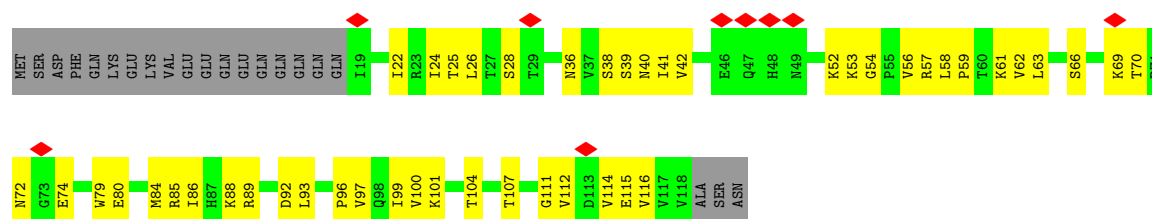
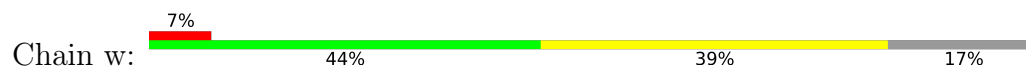
• Molecule 75: 40S ribosomal protein S18-A



• Molecule 76: 40S ribosomal protein S19-A



• Molecule 77: 40S ribosomal protein S20

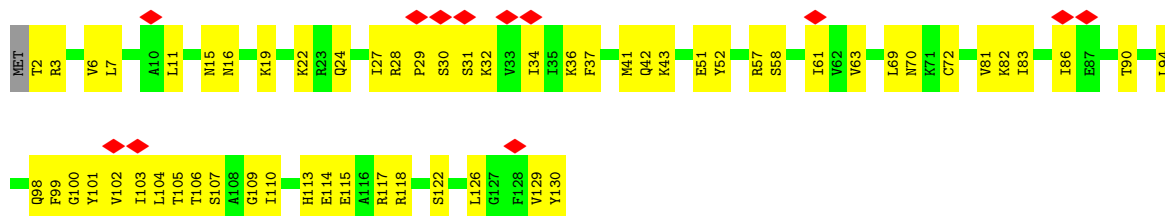


• Molecule 78: 40S ribosomal protein S21-A

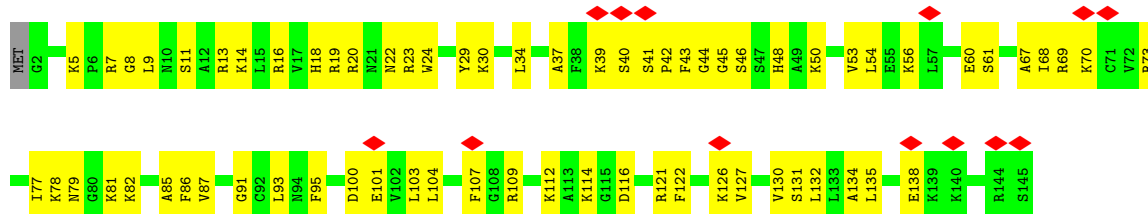




- Molecule 79: 40S ribosomal protein S22-A



- Molecule 80: 40S ribosomal protein S23-A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	38558	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	1000	Depositor
Magnification	165000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.659	Depositor
Minimum map value	-0.906	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.044	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	638.88, 638.88, 638.88	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.452, 1.452, 1.452	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, B8N, GTP, UR3, 1MA, K, A2M, OMG, MG, DDE, OMU, 5MC, G7M, 4AC, OMC, MA6

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	0	0.18	0/1087	0.44	0/1449
2	1	0.19	0/571	0.57	0/768
3	2	0.20	0/782	0.44	0/1047
4	3	0.19	0/620	0.46	0/838
5	4	0.16	0/499	0.37	0/670
6	5	0.16	0/412	0.37	0/544
7	6	0.60	2/433 (0.5%)	1.14	6/575 (1.0%)
8	7	0.33	1/2489 (0.0%)	0.65	4/3389 (0.1%)
9	8	0.18	0/279	0.54	0/369
10	A	0.22	0/1585	0.39	0/2128
11	AA	0.21	2/75545 (0.0%)	0.30	0/117782
12	Aa	0.17	0/6470	0.41	0/8759
13	B	0.24	0/1245	0.42	0/1676
14	BB	0.19	0/2883	0.29	0/4491
15	C	0.18	0/1465	0.38	0/1965
16	CC	0.20	0/3746	0.29	0/5832
17	D	0.20	0/1440	0.40	0/1921
18	DD	0.15	0/1558	0.37	0/2107
19	E	0.23	0/1481	0.44	0/1990
20	EE	0.21	0/1948	0.41	0/2617
21	Ee	0.17	0/1210	0.47	0/1627
22	F	0.19	0/1300	0.38	0/1743
23	FF	0.20	0/3146	0.37	0/4228
24	G	0.17	0/786	0.40	0/1065
25	GG	0.20	0/2800	0.36	0/3790
26	H	0.21	0/978	0.41	0/1316
27	HH	0.18	0/2425	0.36	0/3271
28	I	0.22	0/533	0.43	0/707
29	II	0.20	0/1251	0.39	0/1682
30	J	0.19	0/974	0.39	0/1314
31	JJ	0.24	0/1821	0.44	2/2451 (0.1%)
32	K	0.19	0/1004	0.36	0/1341

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	KK	0.16	0/1836	0.33	0/2481
34	L	0.19	0/1118	0.40	0/1497
35	LL	0.22	0/1539	0.40	0/2073
36	M	0.18	0/1204	0.38	0/1612
37	MM	0.19	0/1779	0.36	0/2386
38	N	0.17	0/473	0.39	0/629
39	NN	0.18	0/1374	0.44	0/1842
40	O	0.22	0/750	0.46	0/1008
41	OO	0.18	0/1568	0.39	0/2106
42	P	0.21	0/897	0.44	0/1205
43	PP	0.19	0/1068	0.35	0/1438
44	Q	0.19	0/1041	0.34	0/1394
45	QQ	0.18	0/1757	0.35	0/2354
46	R	0.24	0/868	0.43	0/1168
47	S	0.20	0/871	0.39	0/1164
48	T	0.18	0/978	0.35	0/1301
49	U	0.18	0/778	0.40	0/1034
50	V	0.21	0/680	0.51	0/901
51	W	0.18	0/618	0.39	0/826
52	X	0.23	0/443	0.50	0/588
53	Y	0.21	0/423	0.55	0/562
54	Z	0.24	0/234	0.62	0/300
55	a	0.18	0/831	0.48	0/1097
56	b	0.21	0/701	0.44	0/934
57	c	0.20	2/37760 (0.0%)	0.38	23/58811 (0.0%)
58	d	0.18	0/1623	0.43	0/2222
59	e	0.21	0/1714	0.48	0/2308
60	f	0.20	0/1665	0.45	0/2263
61	g	0.18	0/1429	0.44	0/1913
62	h	0.20	0/2097	0.44	0/2823
63	i	0.19	0/1591	0.47	0/2151
64	j	0.18	0/1790	0.45	0/2393
65	k	0.19	0/1506	0.51	0/2028
66	l	0.22	0/1482	0.49	0/1980
67	m	0.18	0/1519	0.38	0/2035
68	n	0.20	0/309	0.38	0/416
69	o	0.20	0/1172	0.43	0/1580
70	p	0.21	0/1215	0.44	0/1638
71	q	0.18	0/901	0.47	1/1217 (0.1%)
72	r	0.19	0/747	0.51	0/1002
73	s	0.21	0/1088	0.54	0/1459
74	t	0.18	0/971	0.47	0/1303
75	u	0.17	0/1211	0.45	0/1628

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	v	0.15	0/1130	0.41	0/1517
77	w	0.16	0/810	0.47	0/1095
78	x	0.20	0/693	0.46	0/935
79	y	0.21	0/1038	0.44	0/1395
80	z	0.20	0/1139	0.45	0/1518
All	All	0.20	7/215195 (0.0%)	0.38	36/314982 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
7	6	0	1
31	JJ	0	2
34	L	0	1
50	V	0	1
53	Y	0	1
64	j	0	1
65	k	0	1
69	o	0	1
73	s	0	1
All	All	0	10

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	7	287	PRO	CG-CD	-13.15	1.06	1.50
7	6	19	PRO	CG-CD	-8.02	1.23	1.50
57	c	619	A2M	O3'-P	5.23	1.61	1.56
57	c	541	A2M	O3'-P	5.21	1.61	1.56
7	6	18	THR	N-CA	-5.07	1.40	1.46

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	7	287	PRO	N-CD-CG	-18.44	75.55	103.20
7	6	18	THR	N-CA-CB	-13.11	92.55	110.77
8	7	287	PRO	CA-CB-CG	-12.41	80.92	104.50
7	6	19	PRO	N-CD-CG	-10.68	87.18	103.20
57	c	1591	C	C4'-C3'-O3'	-9.81	94.68	109.40

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	6	17	GLN	Mainchain
31	JJ	158	LYS	Peptide
31	JJ	232	ARG	Peptide
34	L	102	GLU	Peptide
50	V	64	MET	Peptide

5.2 Too-close contacts

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	0	1073	0	1132	68	0
2	1	563	0	603	29	0
3	2	769	0	815	47	0
4	3	610	0	633	38	0
5	4	497	0	535	28	0
6	5	404	0	398	33	0
7	6	427	0	476	39	0
8	7	2436	0	2386	146	0
9	8	276	0	289	11	0
10	A	1555	0	1659	79	0
11	AA	68429	0	34442	2642	0
12	Aa	6368	0	6435	358	0
13	B	1222	0	1231	71	0
14	BB	2579	0	1304	107	0
15	C	1441	0	1543	70	0
16	CC	3353	0	1695	137	0
17	D	1423	0	1510	66	0
18	DD	1531	0	1571	72	0
19	E	1445	0	1487	73	0
20	EE	1914	0	1981	88	0
21	Ee	1196	0	1257	69	0
22	F	1276	0	1323	70	0
23	FF	3075	0	3142	169	0
24	G	770	0	780	23	0
25	GG	2748	0	2859	142	0
26	H	963	0	1015	54	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	HH	2375	0	2325	95	0
28	I	521	0	551	28	0
29	II	1230	0	1320	61	0
30	J	959	0	1023	46	0
31	JJ	1784	0	1862	85	0
32	K	993	0	1081	53	0
33	KK	1804	0	1877	62	0
34	L	1092	0	1155	43	0
35	LL	1518	0	1587	66	0
36	M	1173	0	1215	60	0
37	MM	1743	0	1785	95	0
38	N	462	0	491	20	0
39	NN	1353	0	1383	98	0
40	O	742	0	797	53	0
41	OO	1543	0	1608	65	0
42	P	883	0	918	49	0
43	PP	1053	0	1149	54	0
44	Q	1020	0	1090	37	0
45	QQ	1720	0	1779	107	0
46	R	850	0	880	38	0
47	S	861	0	918	53	0
48	T	969	0	1078	39	0
49	U	771	0	849	40	0
50	V	665	0	668	35	0
51	W	612	0	682	26	0
52	X	436	0	475	28	0
53	Y	417	0	455	27	0
54	Z	233	0	284	28	0
55	a	819	0	886	63	0
56	b	694	0	734	40	0
57	c	34321	0	17287	1679	0
58	d	1583	0	1578	77	0
59	e	1689	0	1763	105	0
60	f	1635	0	1723	90	0
61	g	1412	0	1473	63	0
62	h	2056	0	2140	134	0
63	i	1572	0	1639	119	0
64	j	1766	0	1859	103	0
65	k	1481	0	1572	89	0
66	l	1457	0	1488	102	0
67	m	1494	0	1573	66	0
68	n	300	0	279	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
69	o	1146	0	1213	71	0
70	p	1192	0	1255	69	0
71	q	891	0	883	53	0
72	r	732	0	760	53	0
73	s	1069	0	1127	72	0
74	t	961	0	999	55	0
75	u	1192	0	1222	67	0
76	v	1112	0	1124	58	0
77	w	800	0	869	40	0
78	x	684	0	672	32	0
79	y	1021	0	1060	56	0
80	z	1121	0	1196	73	0
81	2	1	0	0	0	0
81	5	1	0	0	0	0
81	8	1	0	0	0	0
81	S	1	0	0	0	0
81	V	1	0	0	0	0
81	Y	1	0	0	0	0
81	a	1	0	0	0	0
81	b	1	0	0	0	0
82	AA	119	0	0	0	0
82	Aa	1	0	0	0	0
82	BB	3	0	0	0	0
82	CC	3	0	0	0	0
82	H	1	0	0	0	0
82	JJ	1	0	0	0	0
82	c	25	0	0	0	0
83	AA	9	0	0	0	0
83	EE	1	0	0	0	0
84	Aa	32	0	12	7	0
85	AA	71	0	0	1	0
85	B	1	0	0	0	0
85	CC	8	0	0	0	0
85	F	1	0	0	0	0
85	JJ	1	0	0	0	0
85	R	1	0	0	0	0
85	V	1	0	0	0	0
85	c	18	0	0	0	0
All	All	202630	0	152172	8200	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 24.

The worst 5 of 8200 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)
11:AA:1237:G:N1	11:AA:1251:A:C2	2.01	1.28
57:c:1550:A:N6	57:c:1562:G:H21	1.32	1.28
57:c:1550:A:H62	57:c:1562:G:N2	1.31	1.28
6:5:21:CYS:SG	6:5:39:CYS:N	2.12	1.21
57:c:1541:G:N2	57:c:1570:A:H62	1.36	1.20

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	
1	0	132/135 (98%)	126 (96%)	6 (4%)	0	100	100
2	1	68/108 (63%)	61 (90%)	7 (10%)	0	100	100
3	2	95/119 (80%)	90 (95%)	5 (5%)	0	100	100
4	3	79/82 (96%)	73 (92%)	6 (8%)	0	100	100
5	4	61/67 (91%)	59 (97%)	2 (3%)	0	100	100
6	5	47/56 (84%)	45 (96%)	2 (4%)	0	100	100
7	6	51/63 (81%)	48 (94%)	3 (6%)	0	100	100
8	7	316/319 (99%)	298 (94%)	18 (6%)	0	100	100
9	8	32/152 (21%)	19 (59%)	13 (41%)	0	100	100
10	A	195/199 (98%)	193 (99%)	2 (1%)	0	100	100
12	Aa	811/842 (96%)	794 (98%)	17 (2%)	0	100	100
13	B	152/184 (83%)	152 (100%)	0	0	100	100
15	C	183/186 (98%)	182 (100%)	1 (0%)	0	100	100
17	D	174/189 (92%)	170 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	DD	195/312 (62%)	192 (98%)	3 (2%)	0	100	100
19	E	170/172 (99%)	166 (98%)	4 (2%)	0	100	100
20	EE	250/254 (98%)	248 (99%)	2 (1%)	0	100	100
21	Ee	156/165 (94%)	148 (95%)	8 (5%)	0	100	100
22	F	157/160 (98%)	155 (99%)	2 (1%)	0	100	100
23	FF	384/387 (99%)	373 (97%)	11 (3%)	0	100	100
24	G	95/121 (78%)	95 (100%)	0	0	100	100
25	GG	359/362 (99%)	350 (98%)	9 (2%)	0	100	100
26	H	127/137 (93%)	127 (100%)	0	0	100	100
27	HH	294/297 (99%)	285 (97%)	9 (3%)	0	100	100
28	I	61/155 (39%)	61 (100%)	0	0	100	100
29	II	151/176 (86%)	150 (99%)	1 (1%)	0	100	100
30	J	118/142 (83%)	114 (97%)	4 (3%)	0	100	100
31	JJ	220/244 (90%)	212 (96%)	7 (3%)	1 (0%)	24	57
32	K	124/127 (98%)	123 (99%)	1 (1%)	0	100	100
33	KK	231/256 (90%)	226 (98%)	5 (2%)	0	100	100
34	L	133/136 (98%)	129 (97%)	3 (2%)	1 (1%)	16	48
35	LL	189/191 (99%)	184 (97%)	5 (3%)	0	100	100
36	M	146/149 (98%)	141 (97%)	5 (3%)	0	100	100
37	MM	213/221 (96%)	207 (97%)	6 (3%)	0	100	100
38	N	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
39	NN	167/174 (96%)	159 (95%)	8 (5%)	0	100	100
40	O	95/105 (90%)	95 (100%)	0	0	100	100
41	OO	191/199 (96%)	180 (94%)	10 (5%)	1 (0%)	24	57
42	P	107/113 (95%)	105 (98%)	2 (2%)	0	100	100
43	PP	134/138 (97%)	131 (98%)	3 (2%)	0	100	100
44	Q	125/130 (96%)	123 (98%)	2 (2%)	0	100	100
45	QQ	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
46	R	104/107 (97%)	103 (99%)	1 (1%)	0	100	100
47	S	107/121 (88%)	107 (100%)	0	0	100	100
48	T	117/120 (98%)	115 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	U	97/100 (97%)	91 (94%)	6 (6%)	0	100	100
50	V	82/88 (93%)	79 (96%)	2 (2%)	1 (1%)	10	40
51	W	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
52	X	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
53	Y	50/128 (39%)	47 (94%)	2 (4%)	1 (2%)	6	32
54	Z	23/25 (92%)	23 (100%)	0	0	100	100
55	a	100/106 (94%)	97 (97%)	3 (3%)	0	100	100
56	b	89/92 (97%)	88 (99%)	1 (1%)	0	100	100
58	d	204/252 (81%)	193 (95%)	11 (5%)	0	100	100
59	e	210/255 (82%)	196 (93%)	14 (7%)	0	100	100
60	f	215/254 (85%)	201 (94%)	14 (6%)	0	100	100
61	g	177/240 (74%)	170 (96%)	7 (4%)	0	100	100
62	h	256/261 (98%)	244 (95%)	12 (5%)	0	100	100
63	i	195/225 (87%)	186 (95%)	9 (5%)	0	100	100
64	j	217/236 (92%)	217 (100%)	0	0	100	100
65	k	182/190 (96%)	172 (94%)	10 (6%)	0	100	100
66	l	180/200 (90%)	169 (94%)	11 (6%)	0	100	100
67	m	183/197 (93%)	175 (96%)	8 (4%)	0	100	100
68	n	29/105 (28%)	29 (100%)	0	0	100	100
69	o	140/156 (90%)	133 (95%)	7 (5%)	0	100	100
70	p	148/151 (98%)	145 (98%)	3 (2%)	0	100	100
71	q	125/137 (91%)	119 (95%)	6 (5%)	0	100	100
72	r	85/142 (60%)	80 (94%)	5 (6%)	0	100	100
73	s	134/143 (94%)	126 (94%)	8 (6%)	0	100	100
74	t	119/136 (88%)	114 (96%)	5 (4%)	0	100	100
75	u	143/146 (98%)	134 (94%)	9 (6%)	0	100	100
76	v	141/144 (98%)	137 (97%)	4 (3%)	0	100	100
77	w	98/121 (81%)	98 (100%)	0	0	100	100
78	x	85/87 (98%)	81 (95%)	4 (5%)	0	100	100
79	y	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
80	z	142/145 (98%)	132 (93%)	10 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	11672/13056 (89%)	11284 (97%)	383 (3%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
31	JJ	159	GLN
50	V	65	ARG
34	L	102	GLU
53	Y	105	PRO
41	OO	63	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	112/113 (99%)	112 (100%)	0	100	100
2	1	61/89 (68%)	61 (100%)	0	100	100
3	2	83/101 (82%)	83 (100%)	0	100	100
4	3	70/71 (99%)	70 (100%)	0	100	100
5	4	56/60 (93%)	56 (100%)	0	100	100
6	5	43/49 (88%)	43 (100%)	0	100	100
7	6	46/54 (85%)	46 (100%)	0	100	100
8	7	259/262 (99%)	259 (100%)	0	100	100
9	8	30/135 (22%)	30 (100%)	0	100	100
10	A	160/162 (99%)	159 (99%)	1 (1%)	78	79
12	Aa	694/714 (97%)	694 (100%)	0	100	100
13	B	125/146 (86%)	125 (100%)	0	100	100
15	C	150/151 (99%)	150 (100%)	0	100	100
17	D	143/154 (93%)	143 (100%)	0	100	100
18	DD	167/254 (66%)	167 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	E	156/156 (100%)	156 (100%)	0	100	100
20	EE	193/196 (98%)	193 (100%)	0	100	100
21	Ee	129/136 (95%)	129 (100%)	0	100	100
22	F	136/137 (99%)	136 (100%)	0	100	100
23	FF	320/323 (99%)	319 (100%)	1 (0%)	86	84
24	G	84/107 (78%)	84 (100%)	0	100	100
25	GG	288/289 (100%)	287 (100%)	1 (0%)	86	84
26	H	101/105 (96%)	101 (100%)	0	100	100
27	HH	244/245 (100%)	244 (100%)	0	100	100
28	I	55/129 (43%)	55 (100%)	0	100	100
29	II	133/153 (87%)	133 (100%)	0	100	100
30	J	104/118 (88%)	104 (100%)	0	100	100
31	JJ	186/205 (91%)	186 (100%)	0	100	100
32	K	109/110 (99%)	109 (100%)	0	100	100
33	KK	187/208 (90%)	187 (100%)	0	100	100
34	L	115/116 (99%)	115 (100%)	0	100	100
35	LL	171/171 (100%)	171 (100%)	0	100	100
36	M	118/119 (99%)	118 (100%)	0	100	100
37	MM	184/187 (98%)	184 (100%)	0	100	100
38	N	46/47 (98%)	46 (100%)	0	100	100
39	NN	147/150 (98%)	147 (100%)	0	100	100
40	O	81/88 (92%)	81 (100%)	0	100	100
41	OO	154/159 (97%)	154 (100%)	0	100	100
42	P	94/97 (97%)	94 (100%)	0	100	100
43	PP	107/109 (98%)	107 (100%)	0	100	100
44	Q	109/111 (98%)	109 (100%)	0	100	100
45	QQ	175/176 (99%)	175 (100%)	0	100	100
46	R	90/91 (99%)	90 (100%)	0	100	100
47	S	94/103 (91%)	94 (100%)	0	100	100
48	T	104/105 (99%)	103 (99%)	1 (1%)	68	74
49	U	81/82 (99%)	81 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	V	69/71 (97%)	69 (100%)	0	100	100
51	W	68/69 (99%)	68 (100%)	0	100	100
52	X	45/46 (98%)	45 (100%)	0	100	100
53	Y	47/116 (40%)	47 (100%)	0	100	100
54	Z	23/23 (100%)	23 (100%)	0	100	100
55	a	87/91 (96%)	87 (100%)	0	100	100
56	b	71/72 (99%)	71 (100%)	0	100	100
58	d	165/210 (79%)	165 (100%)	0	100	100
59	e	189/224 (84%)	189 (100%)	0	100	100
60	f	176/205 (86%)	176 (100%)	0	100	100
61	g	145/195 (74%)	145 (100%)	0	100	100
62	h	220/222 (99%)	220 (100%)	0	100	100
63	i	172/191 (90%)	172 (100%)	0	100	100
64	j	188/201 (94%)	188 (100%)	0	100	100
65	k	165/170 (97%)	165 (100%)	0	100	100
66	l	146/161 (91%)	146 (100%)	0	100	100
67	m	158/166 (95%)	158 (100%)	0	100	100
68	n	32/98 (33%)	32 (100%)	0	100	100
69	o	127/137 (93%)	127 (100%)	0	100	100
70	p	127/128 (99%)	127 (100%)	0	100	100
71	q	81/105 (77%)	81 (100%)	0	100	100
72	r	77/118 (65%)	77 (100%)	0	100	100
73	s	113/119 (95%)	113 (100%)	0	100	100
74	t	105/124 (85%)	105 (100%)	0	100	100
75	u	128/129 (99%)	128 (100%)	0	100	100
76	v	115/116 (99%)	115 (100%)	0	100	100
77	w	94/114 (82%)	94 (100%)	0	100	100
78	x	74/74 (100%)	74 (100%)	0	100	100
79	y	110/111 (99%)	110 (100%)	0	100	100
80	z	119/120 (99%)	119 (100%)	0	100	100
All	All	9930/10969 (90%)	9926 (100%)	4 (0%)	100	100

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	A	14	HIS
23	FF	104	THR
25	GG	43	ASN
48	T	108	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 106 such sidechains are listed below:

Mol	Chain	Res	Type
41	OO	28	GLN
49	U	12	ASN
76	v	16	ASN
42	P	17	HIS
46	R	26	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	AA	3193/3396 (94%)	636 (19%)	21 (0%)
14	BB	120/121 (99%)	18 (15%)	1 (0%)
16	CC	157/158 (99%)	28 (17%)	1 (0%)
57	c	1598/1800 (88%)	472 (29%)	0
All	All	5068/5475 (92%)	1154 (22%)	23 (0%)

5 of 1154 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	AA	4	U
11	AA	6	A
11	AA	12	A
11	AA	14	U
11	AA	26	A

5 of 23 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	AA	2490	C
11	AA	2570	U
11	AA	2501	U
11	AA	2971	A

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Mol	Chain	Res	Type
11	AA	1348	U

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

67 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
11	OMC	AA	2337	11	19,22,23	0.59	0	25,31,34	0.81	1 (4%)
11	A2M	AA	649	11	22,25,26	3.22	10 (45%)	30,36,39	2.95	11 (36%)
11	OMG	AA	2791	11	23,26,27	0.51	0	32,38,41	0.54	0
11	A2M	AA	1449	82,11	22,25,26	3.24	10 (45%)	30,36,39	2.98	12 (40%)
11	OMU	AA	2729	11	19,22,23	3.06	8 (42%)	25,31,34	1.85	4 (16%)
57	4AC	c	1773	57	21,24,25	3.45	10 (47%)	28,34,37	1.71	6 (21%)
11	OMG	AA	2922	11	23,26,27	0.50	0	32,38,41	0.47	0
11	A2M	AA	1133	82,11	22,25,26	3.26	10 (45%)	30,36,39	3.04	11 (36%)
11	A2M	AA	2946	82,11	22,25,26	3.24	9 (40%)	30,36,39	3.00	11 (36%)
57	OMG	c	1572	57	23,26,27	0.49	0	32,38,41	0.52	0
11	A2M	AA	807	11	22,25,26	3.22	10 (45%)	30,36,39	2.96	13 (43%)
11	1MA	AA	2142	82,11	21,25,26	0.51	0	30,37,40	0.83	1 (3%)
57	G7M	c	1575	57	23,26,27	2.69	8 (34%)	34,39,42	2.34	11 (32%)
11	OMG	AA	2815	11	23,26,27	0.48	0	32,38,41	0.59	0
11	A2M	AA	2281	11	22,25,26	3.25	10 (45%)	30,36,39	3.17	14 (46%)
11	5MC	AA	2870	83,11	19,22,23	0.67	0	26,32,35	0.57	0
11	A2M	AA	2220	11	22,25,26	3.20	10 (45%)	30,36,39	2.97	10 (33%)
11	OMG	AA	867	83,11	23,26,27	0.50	0	32,38,41	0.48	0
12	DDE	Aa	699	12	18,20,21	1.04	1 (5%)	17,28,30	0.84	1 (5%)
57	A2M	c	100	82,57	22,25,26	3.24	10 (45%)	30,36,39	3.03	11 (36%)
57	OMC	c	414	57	19,22,23	0.61	0	25,31,34	1.10	2 (8%)
57	OMG	c	562	57	23,26,27	0.52	0	32,38,41	0.71	0
11	OMC	AA	1437	82,11	19,22,23	0.60	0	25,31,34	1.37	3 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
11	OMG	AA	1450	11	23,26,27	0.48	0	32,38,41	0.47	0
11	5MC	AA	2278	82,11	19,22,23	0.56	0	26,32,35	0.68	0
11	OMC	AA	650	11	19,22,23	0.53	0	25,31,34	0.81	1 (4%)
11	OMU	AA	2921	11	19,22,23	3.05	8 (42%)	25,31,34	1.82	5 (20%)
57	OMU	c	578	57	19,22,23	3.11	8 (42%)	25,31,34	1.80	5 (20%)
57	OMG	c	1271	57	23,26,27	0.47	0	32,38,41	0.47	0
11	A2M	AA	2280	11	22,25,26	3.23	9 (40%)	30,36,39	2.94	10 (33%)
11	OMG	AA	908	11	23,26,27	0.53	0	32,38,41	0.51	0
11	UR3	AA	2634	11	19,22,23	2.79	7 (36%)	26,32,35	1.60	2 (7%)
11	OMG	AA	2288	11	23,26,27	0.51	0	32,38,41	0.47	0
57	OMG	c	1126	57	23,26,27	0.52	0	32,38,41	0.49	0
57	A2M	c	28	57	22,25,26	3.24	9 (40%)	30,36,39	3.01	11 (36%)
11	OMG	AA	805	11	23,26,27	0.48	0	32,38,41	0.48	0
11	A2M	AA	2256	11	22,25,26	3.16	9 (40%)	30,36,39	3.18	15 (50%)
57	A2M	c	619	82,57	22,25,26	3.27	10 (45%)	30,36,39	2.97	11 (36%)
57	MA6	c	1782	57	23,26,27	1.41	4 (17%)	33,38,41	3.27	12 (36%)
11	OMC	AA	2197	83,11	19,22,23	0.53	0	25,31,34	0.67	0
11	OMG	AA	2793	11	23,26,27	0.52	0	32,38,41	0.45	0
11	OMU	AA	2724	11	19,22,23	3.07	8 (42%)	25,31,34	1.86	6 (24%)
57	OMC	c	1007	57	19,22,23	0.53	0	25,31,34	0.70	0
11	OMU	AA	1888	11	19,22,23	3.08	8 (42%)	25,31,34	1.82	5 (20%)
57	A2M	c	420	57	22,25,26	3.23	10 (45%)	30,36,39	3.04	12 (40%)
57	MA6	c	1781	57	23,26,27	1.42	4 (17%)	33,38,41	3.21	10 (30%)
57	A2M	c	796	57	22,25,26	3.25	10 (45%)	30,36,39	3.08	11 (36%)
57	A2M	c	436	57	22,25,26	3.22	9 (40%)	30,36,39	2.89	10 (33%)
11	OMC	AA	663	11	19,22,23	0.56	0	25,31,34	0.70	0
57	B8N	c	1191	57	25,29,30	3.40	7 (28%)	28,42,45	1.92	7 (25%)
57	A2M	c	974	57	22,25,26	3.24	10 (45%)	30,36,39	3.01	12 (40%)
11	A2M	AA	876	11	22,25,26	3.25	10 (45%)	30,36,39	3.03	10 (33%)
11	OMG	AA	2619	11	23,26,27	0.49	0	32,38,41	0.46	0
57	OMG	c	1428	57	23,26,27	0.47	0	32,38,41	0.56	0
11	A2M	AA	2640	11	22,25,26	3.21	10 (45%)	30,36,39	2.94	10 (33%)
57	4AC	c	1280	57	21,24,25	3.51	10 (47%)	28,34,37	1.87	7 (25%)
57	OMU	c	1269	57	19,22,23	3.17	8 (42%)	25,31,34	1.76	5 (20%)
11	OMU	AA	2421	11	19,22,23	3.07	8 (42%)	25,31,34	1.80	5 (20%)
11	A2M	AA	817	82,11	22,25,26	3.24	10 (45%)	30,36,39	3.00	12 (40%)
11	OMC	AA	2959	11	19,22,23	0.53	0	25,31,34	0.68	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
11	OMU	AA	898	11	19,22,23	3.09	8 (42%)	25,31,34	1.83	5 (20%)
57	OMC	c	1639	82,57	19,22,23	0.54	0	25,31,34	0.68	0
11	OMU	AA	2347	11	19,22,23	3.05	8 (42%)	25,31,34	1.86	4 (16%)
11	OMC	AA	2948	11	19,22,23	0.59	0	25,31,34	1.06	2 (8%)
11	OMU	AA	2417	11	19,22,23	3.04	8 (42%)	25,31,34	1.83	5 (20%)
57	A2M	c	541	57	22,25,26	3.23	10 (45%)	30,36,39	2.84	11 (36%)
11	1MA	AA	645	82,11	21,25,26	0.50	0	30,37,40	0.75	1 (3%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	OMC	AA	2337	11	-	3/9/27/28	0/2/2/2
11	A2M	AA	649	11	-	1/9/27/28	0/3/3/3
11	OMG	AA	2791	11	-	0/9/27/28	0/3/3/3
11	A2M	AA	1449	82,11	-	0/9/27/28	0/3/3/3
11	OMU	AA	2729	11	-	1/9/27/28	0/2/2/2
57	4AC	c	1773	57	-	2/11/29/30	0/2/2/2
11	OMG	AA	2922	11	-	2/9/27/28	0/3/3/3
11	A2M	AA	1133	82,11	-	0/9/27/28	0/3/3/3
11	A2M	AA	2946	82,11	-	3/9/27/28	0/3/3/3
57	OMG	c	1572	57	-	3/9/27/28	0/3/3/3
11	A2M	AA	807	11	-	6/9/27/28	0/3/3/3
11	1MA	AA	2142	82,11	-	0/7/25/26	0/3/3/3
57	G7M	c	1575	57	-	1/7/25/26	0/3/3/3
11	OMG	AA	2815	11	-	1/9/27/28	0/3/3/3
11	A2M	AA	2281	11	-	3/9/27/28	0/3/3/3
11	5MC	AA	2870	83,11	-	5/7/25/26	0/2/2/2
11	A2M	AA	2220	11	-	1/9/27/28	0/3/3/3
11	OMG	AA	867	83,11	-	0/9/27/28	0/3/3/3
12	DDE	Aa	699	12	-	11/20/21/23	0/1/1/1
57	A2M	c	100	82,57	-	0/9/27/28	0/3/3/3
57	OMC	c	414	57	-	3/9/27/28	0/2/2/2
57	OMG	c	562	57	-	3/9/27/28	0/3/3/3
11	OMC	AA	1437	82,11	-	5/9/27/28	0/2/2/2
11	OMG	AA	1450	11	-	3/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	5MC	AA	2278	82,11	-	2/7/25/26	0/2/2/2
11	OMC	AA	650	11	-	1/9/27/28	0/2/2/2
11	OMU	AA	2921	11	-	1/9/27/28	0/2/2/2
57	OMU	c	578	57	-	0/9/27/28	0/2/2/2
57	OMG	c	1271	57	-	2/9/27/28	0/3/3/3
11	A2M	AA	2280	11	-	2/9/27/28	0/3/3/3
11	OMG	AA	908	11	-	3/9/27/28	0/3/3/3
11	UR3	AA	2634	11	-	0/7/25/26	0/2/2/2
11	OMG	AA	2288	11	-	0/9/27/28	0/3/3/3
57	OMG	c	1126	57	-	1/9/27/28	0/3/3/3
57	A2M	c	28	57	-	3/9/27/28	0/3/3/3
11	OMG	AA	805	11	-	1/9/27/28	0/3/3/3
11	A2M	AA	2256	11	-	2/9/27/28	0/3/3/3
57	A2M	c	619	82,57	-	2/9/27/28	0/3/3/3
57	MA6	c	1782	57	-	1/11/29/30	0/3/3/3
11	OMC	AA	2197	83,11	-	2/9/27/28	0/2/2/2
11	OMG	AA	2793	11	-	1/9/27/28	0/3/3/3
11	OMU	AA	2724	11	-	1/9/27/28	0/2/2/2
57	OMC	c	1007	57	-	0/9/27/28	0/2/2/2
11	OMU	AA	1888	11	-	0/9/27/28	0/2/2/2
57	A2M	c	420	57	-	3/9/27/28	0/3/3/3
57	MA6	c	1781	57	-	0/11/29/30	0/3/3/3
57	A2M	c	796	57	-	1/9/27/28	0/3/3/3
57	A2M	c	436	57	-	0/9/27/28	0/3/3/3
11	OMC	AA	663	11	-	1/9/27/28	0/2/2/2
57	B8N	c	1191	57	-	5/16/34/35	0/2/2/2
57	A2M	c	974	57	-	0/9/27/28	0/3/3/3
11	A2M	AA	876	11	-	0/9/27/28	0/3/3/3
11	OMG	AA	2619	11	-	0/9/27/28	0/3/3/3
57	OMG	c	1428	57	-	3/9/27/28	0/3/3/3
11	A2M	AA	2640	11	-	1/9/27/28	0/3/3/3
57	4AC	c	1280	57	-	6/11/29/30	0/2/2/2
57	OMU	c	1269	57	-	5/9/27/28	0/2/2/2
11	OMU	AA	2421	11	-	1/9/27/28	0/2/2/2
11	A2M	AA	817	82,11	-	1/9/27/28	0/3/3/3
11	OMC	AA	2959	11	-	1/9/27/28	0/2/2/2
11	OMU	AA	898	11	-	2/9/27/28	0/2/2/2
57	OMC	c	1639	82,57	-	0/9/27/28	0/2/2/2
11	OMU	AA	2347	11	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	OMC	AA	2948	11	-	3/9/27/28	0/2/2/2
11	OMU	AA	2417	11	-	0/9/27/28	0/2/2/2
57	A2M	c	541	57	-	3/9/27/28	0/3/3/3
11	1MA	AA	645	82,11	-	2/7/25/26	0/3/3/3

The worst 5 of 326 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	c	28	A2M	C3'-C4'	-9.23	1.29	1.53
11	AA	1133	A2M	C3'-C4'	-9.06	1.30	1.53
11	AA	1449	A2M	C3'-C4'	-9.06	1.30	1.53
57	c	619	A2M	C3'-C4'	-9.02	1.30	1.53
57	c	974	A2M	C3'-C4'	-9.00	1.30	1.53

The worst 5 of 344 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	c	1782	MA6	N1-C6-N6	-12.00	102.23	116.86
57	c	1781	MA6	N1-C6-N6	-11.82	102.45	116.86
57	c	1782	MA6	C5-C6-N6	8.07	138.11	125.33
57	c	1781	MA6	C5-C6-N6	7.93	137.88	125.33
11	AA	817	A2M	N6-C6-N1	-6.98	102.83	118.38

There are no chirality outliers.

5 of 120 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	AA	649	A2M	C1'-C2'-O2'-CM'
11	AA	663	OMC	C1'-C2'-O2'-CM2
11	AA	805	OMG	C1'-C2'-O2'-CM2
11	AA	807	A2M	C1'-C2'-O2'-CM'
11	AA	898	OMU	C1'-C2'-O2'-CM2

There are no ring outliers.

58 monomers are involved in 129 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	AA	2337	OMC	1	0
11	AA	649	A2M	2	0
11	AA	2791	OMG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	AA	1449	A2M	1	0
11	AA	2729	OMU	3	0
57	c	1773	4AC	4	0
11	AA	2922	OMG	1	0
11	AA	1133	A2M	1	0
11	AA	2946	A2M	1	0
57	c	1572	OMG	1	0
11	AA	807	A2M	1	0
57	c	1575	G7M	2	0
11	AA	2815	OMG	3	0
11	AA	2281	A2M	1	0
11	AA	2870	5MC	1	0
11	AA	2220	A2M	4	0
12	Aa	699	DDE	3	0
57	c	100	A2M	1	0
57	c	414	OMC	2	0
57	c	562	OMG	11	0
11	AA	650	OMC	2	0
11	AA	2921	OMU	2	0
57	c	578	OMU	2	0
57	c	1271	OMG	3	0
11	AA	2280	A2M	1	0
11	AA	908	OMG	3	0
11	AA	2634	UR3	3	0
11	AA	2288	OMG	2	0
57	c	1126	OMG	1	0
57	c	28	A2M	1	0
11	AA	805	OMG	2	0
11	AA	2256	A2M	3	0
57	c	1782	MA6	1	0
11	AA	2197	OMC	1	0
11	AA	2793	OMG	1	0
11	AA	2724	OMU	8	0
11	AA	1888	OMU	1	0
57	c	420	A2M	2	0
57	c	1781	MA6	3	0
57	c	796	A2M	2	0
57	c	436	A2M	1	0
11	AA	663	OMC	3	0
57	c	974	A2M	2	0
11	AA	876	A2M	3	0
57	c	1428	OMG	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	AA	2640	A2M	4	0
57	c	1280	4AC	1	0
57	c	1269	OMU	2	0
11	AA	2421	OMU	2	0
11	AA	817	A2M	2	0
11	AA	2959	OMC	1	0
11	AA	898	OMU	2	0
57	c	1639	OMC	1	0
11	AA	2347	OMU	2	0
11	AA	2948	OMC	3	0
11	AA	2417	OMU	4	0
57	c	541	A2M	4	0
11	AA	645	1MA	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 172 ligands modelled in this entry, 171 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
84	GTP	Aa	901	82	33,34,34	1.20	4 (12%)	50,54,54	1.67	6 (12%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
84	GTP	Aa	901	82	-	3/22/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	Aa	901	GTP	C5-C4	3.01	1.47	1.38
84	Aa	901	GTP	C6-N1	-2.88	1.33	1.38
84	Aa	901	GTP	C5-N7	-2.30	1.34	1.39
84	Aa	901	GTP	C4-N9	-2.07	1.32	1.38

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	Aa	901	GTP	C5-C4-N3	-5.73	119.27	128.39
84	Aa	901	GTP	C2-N3-C4	4.69	120.38	112.30
84	Aa	901	GTP	N9-C4-N3	4.35	134.65	125.95
84	Aa	901	GTP	C6-C5-N7	3.15	136.02	130.29
84	Aa	901	GTP	C3'-C2'-C1'	2.33	105.86	101.46

There are no chirality outliers.

All (3) torsion outliers are listed below:

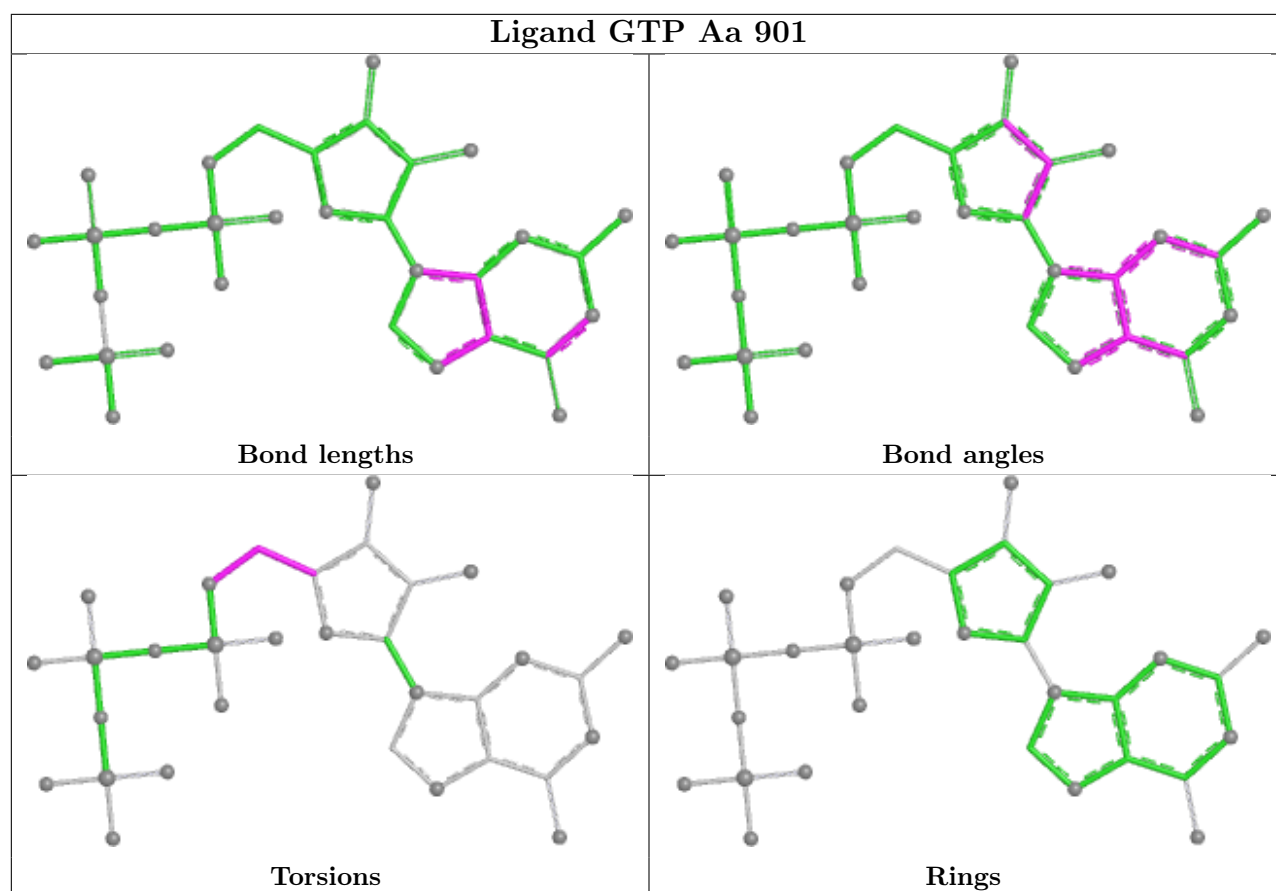
Mol	Chain	Res	Type	Atoms
84	Aa	901	GTP	O4'-C4'-C5'-O5'
84	Aa	901	GTP	C3'-C4'-C5'-O5'
84	Aa	901	GTP	C4'-C5'-O5'-PA

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
84	Aa	901	GTP	7	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

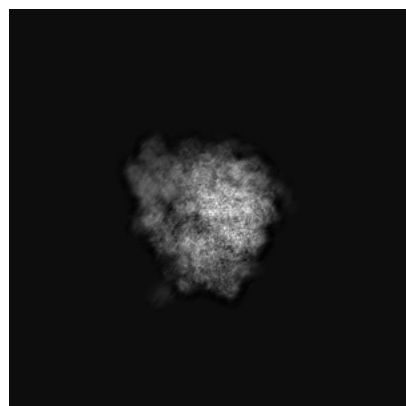
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16729. These allow visual inspection of the internal detail of the map and identification of artifacts.

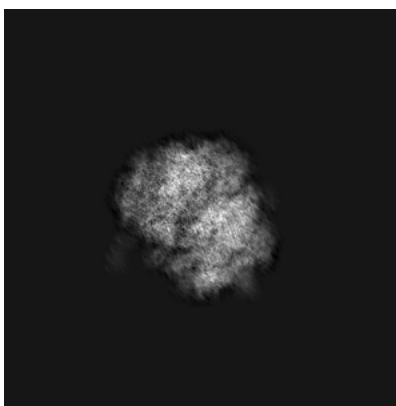
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

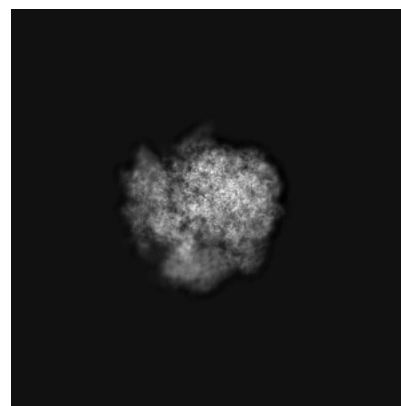
6.1.1 Primary map



X

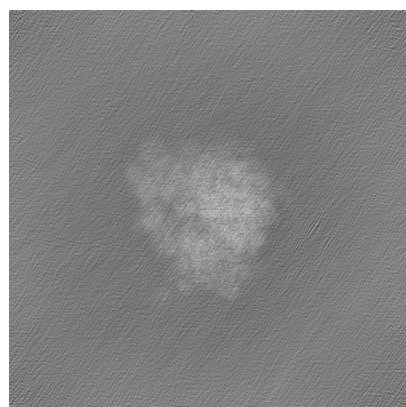


Y

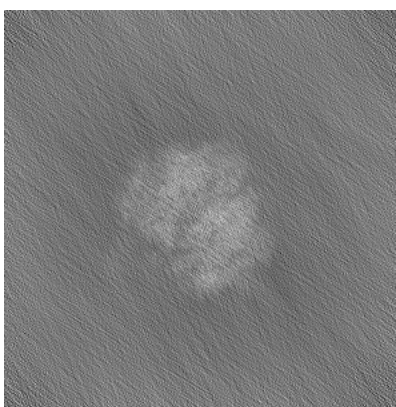


Z

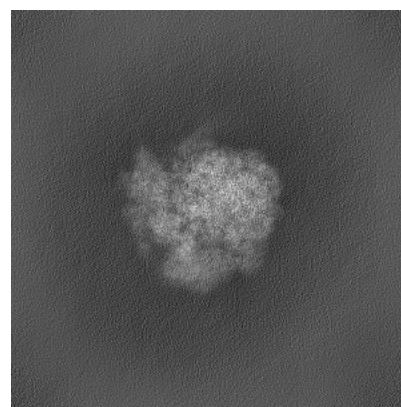
6.1.2 Raw map



X



Y

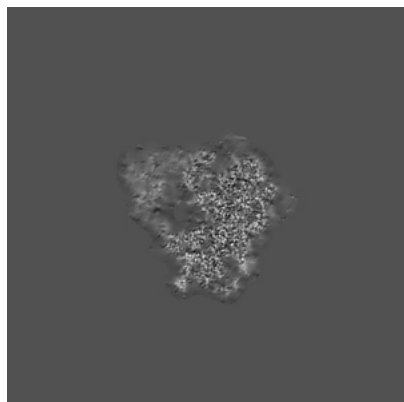


Z

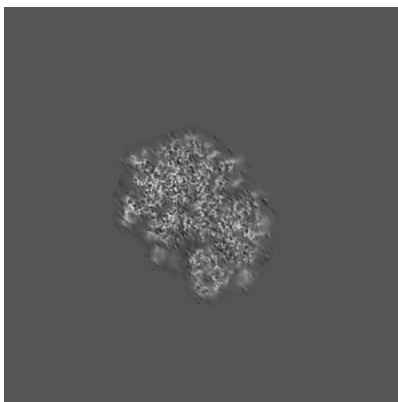
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 220

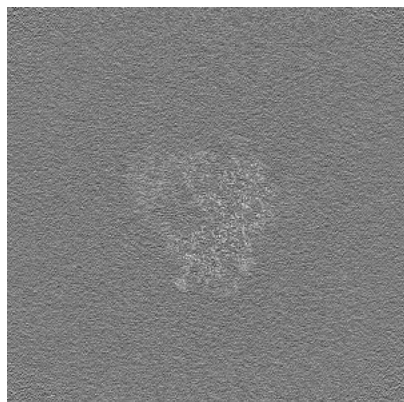


Y Index: 220

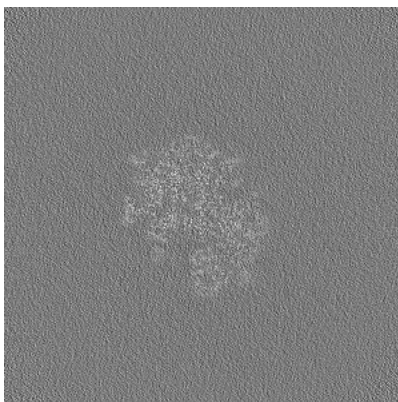


Z Index: 220

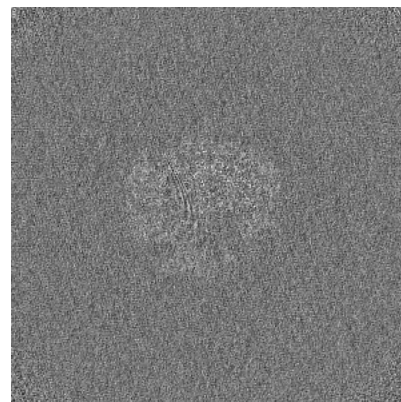
6.2.2 Raw map



X Index: 220



Y Index: 220

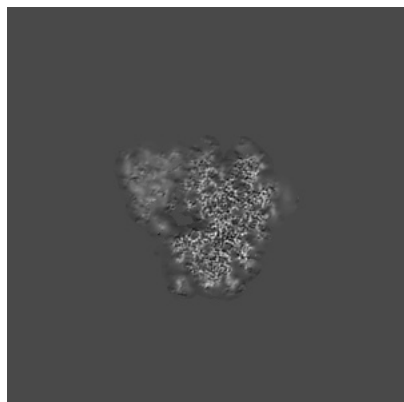


Z Index: 220

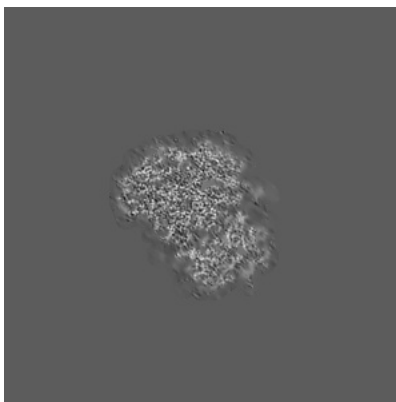
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

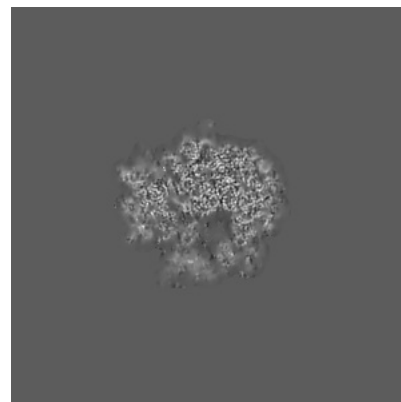
6.3.1 Primary map



X Index: 214

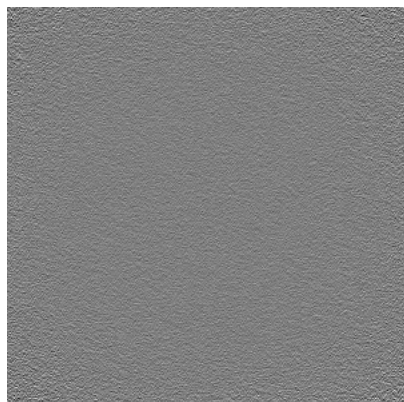


Y Index: 230

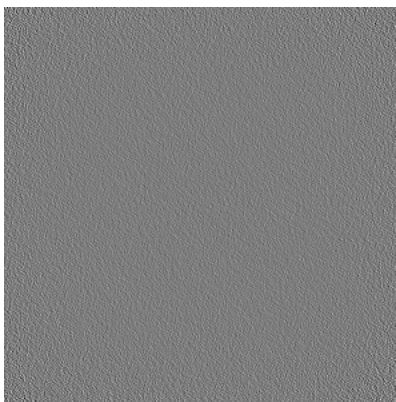


Z Index: 216

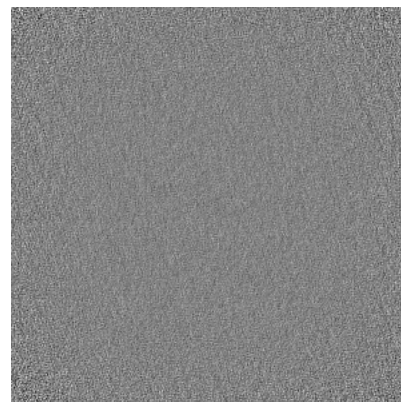
6.3.2 Raw map



X Index: 0



Y Index: 0

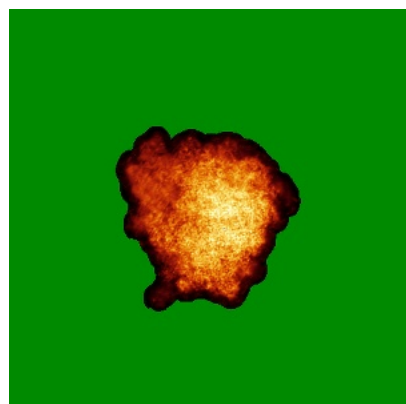


Z Index: 0

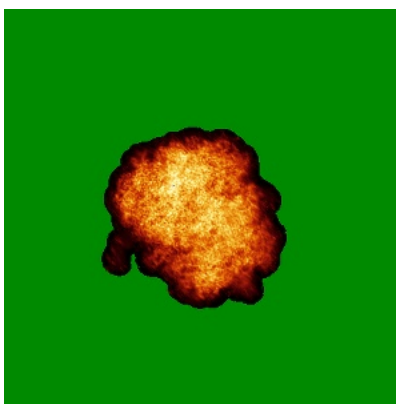
The images above show the largest variance slices of the map in three orthogonal directions.

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

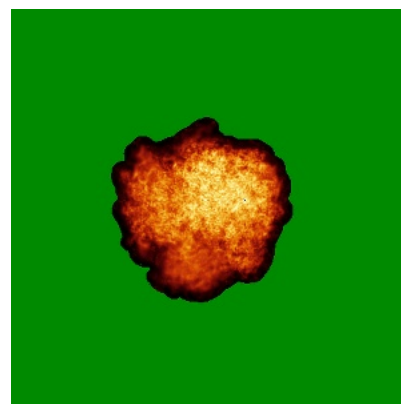
6.4.1 Primary map



X

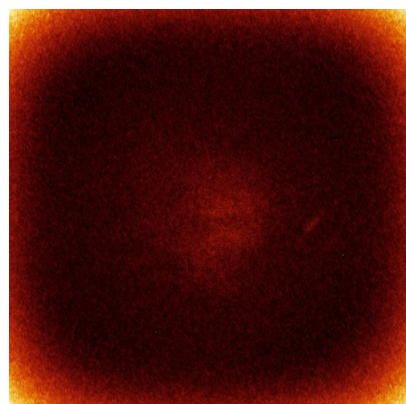


Y

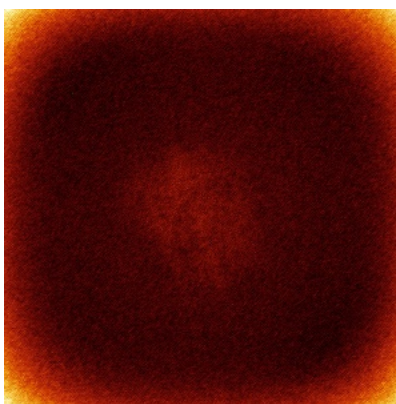


Z

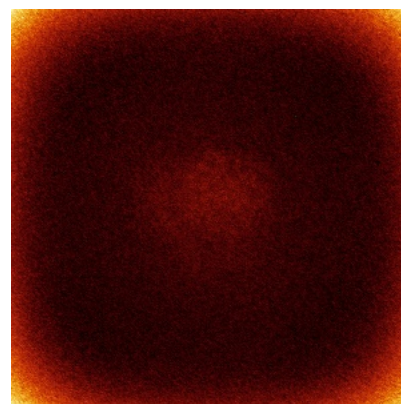
6.4.2 Raw map



X



Y



Z

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

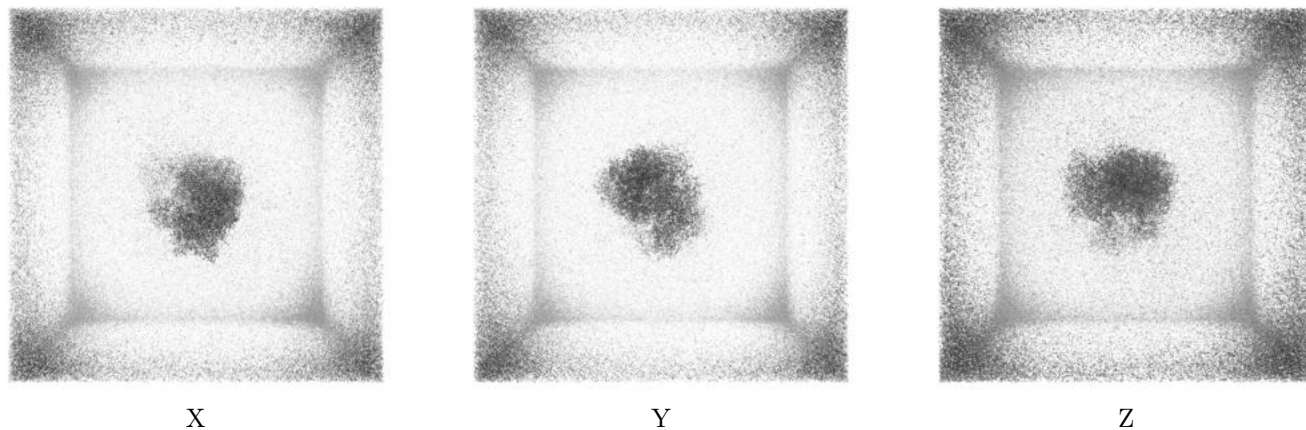
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

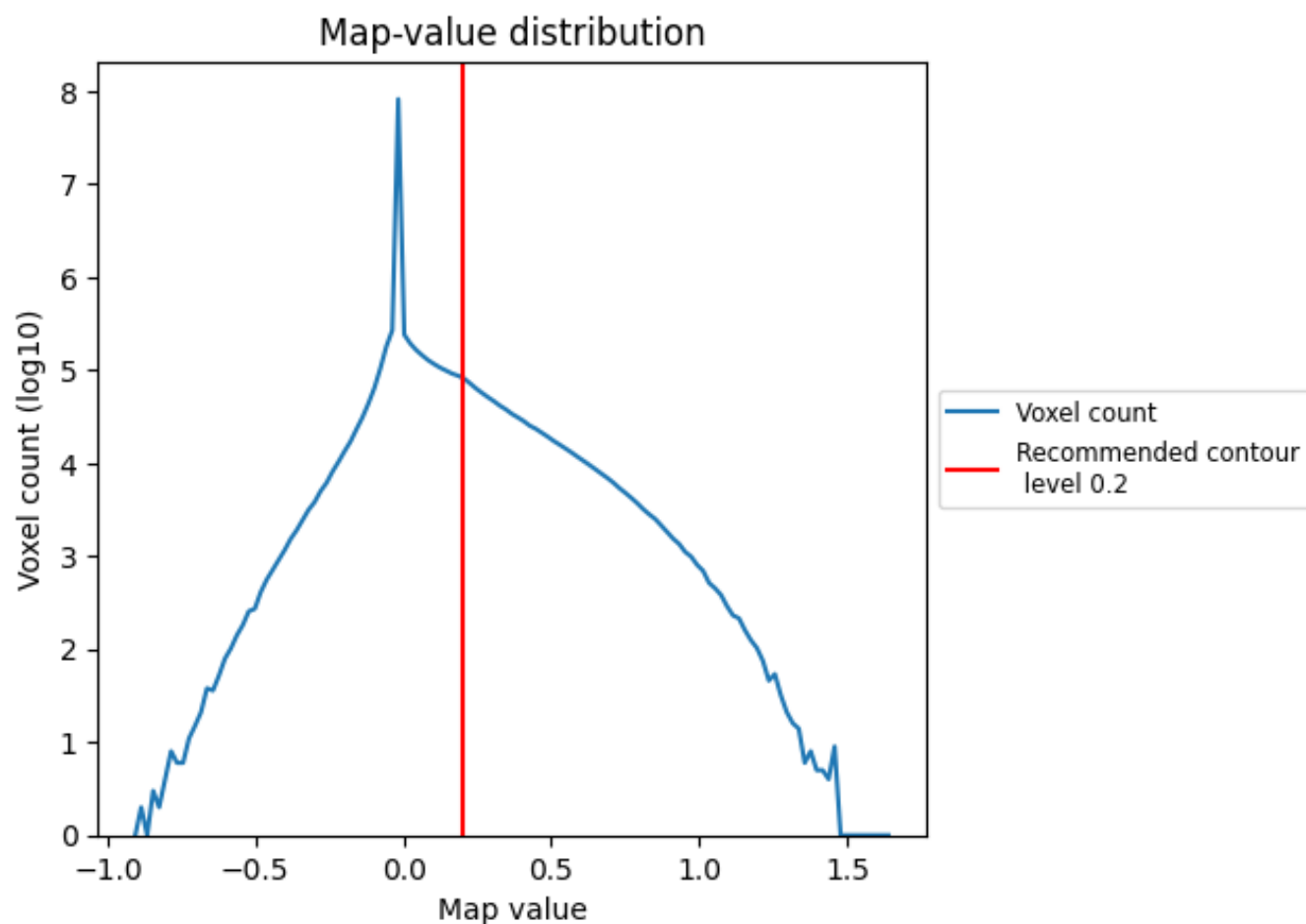
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

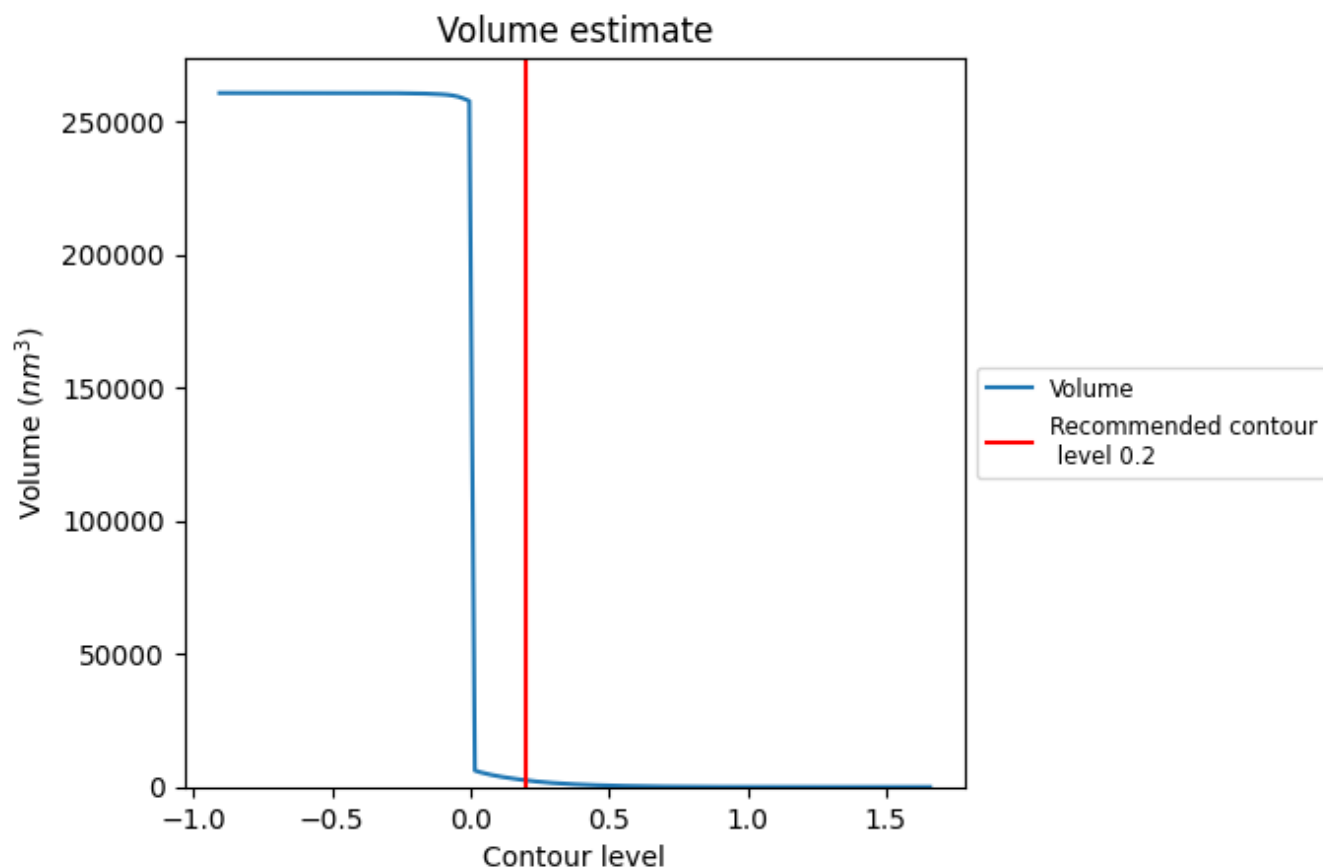
This section contains the results of statistical analysis of the map.

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.

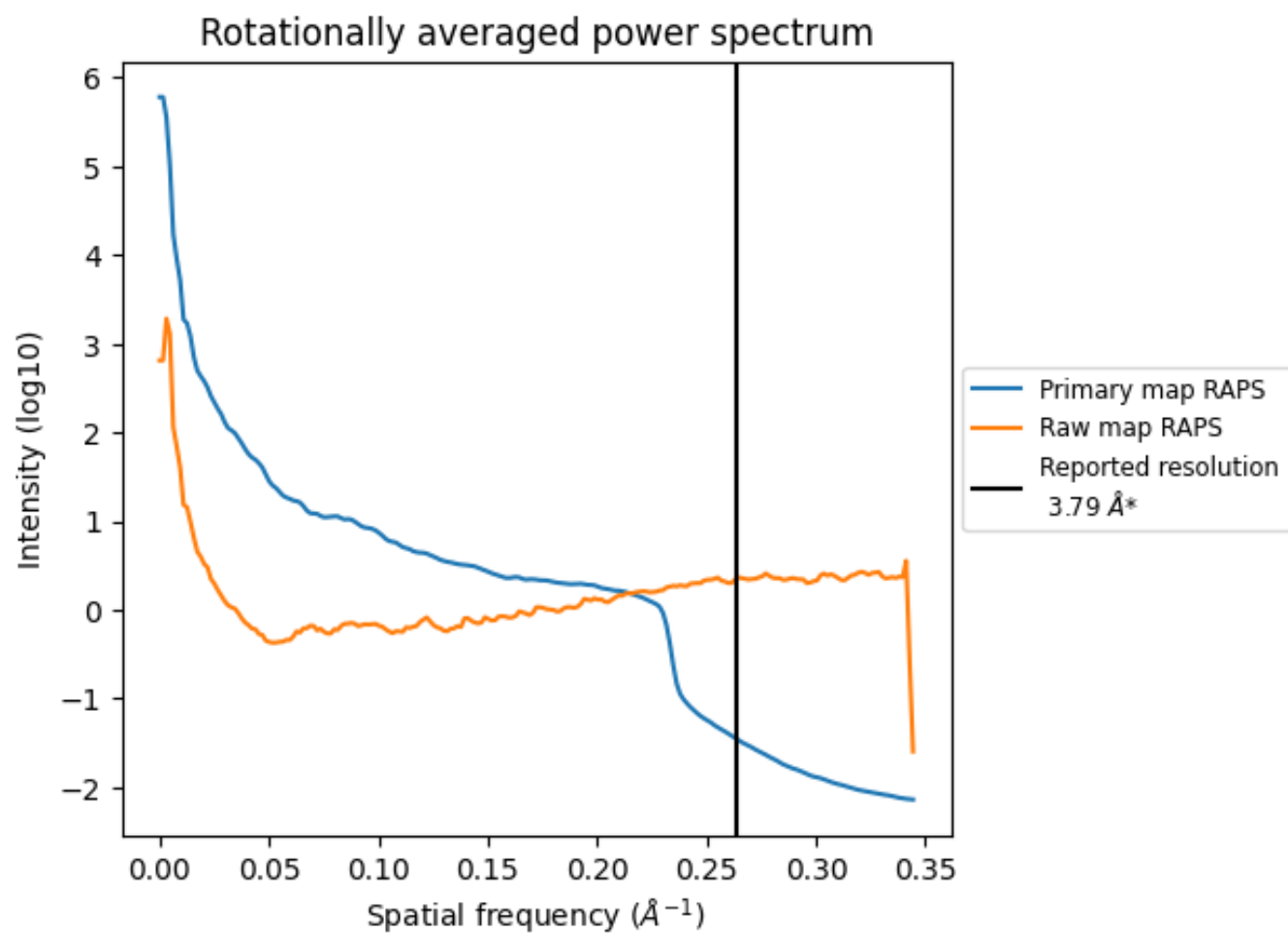
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2503 nm³; this corresponds to an approximate mass of 2261 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 ⓘ

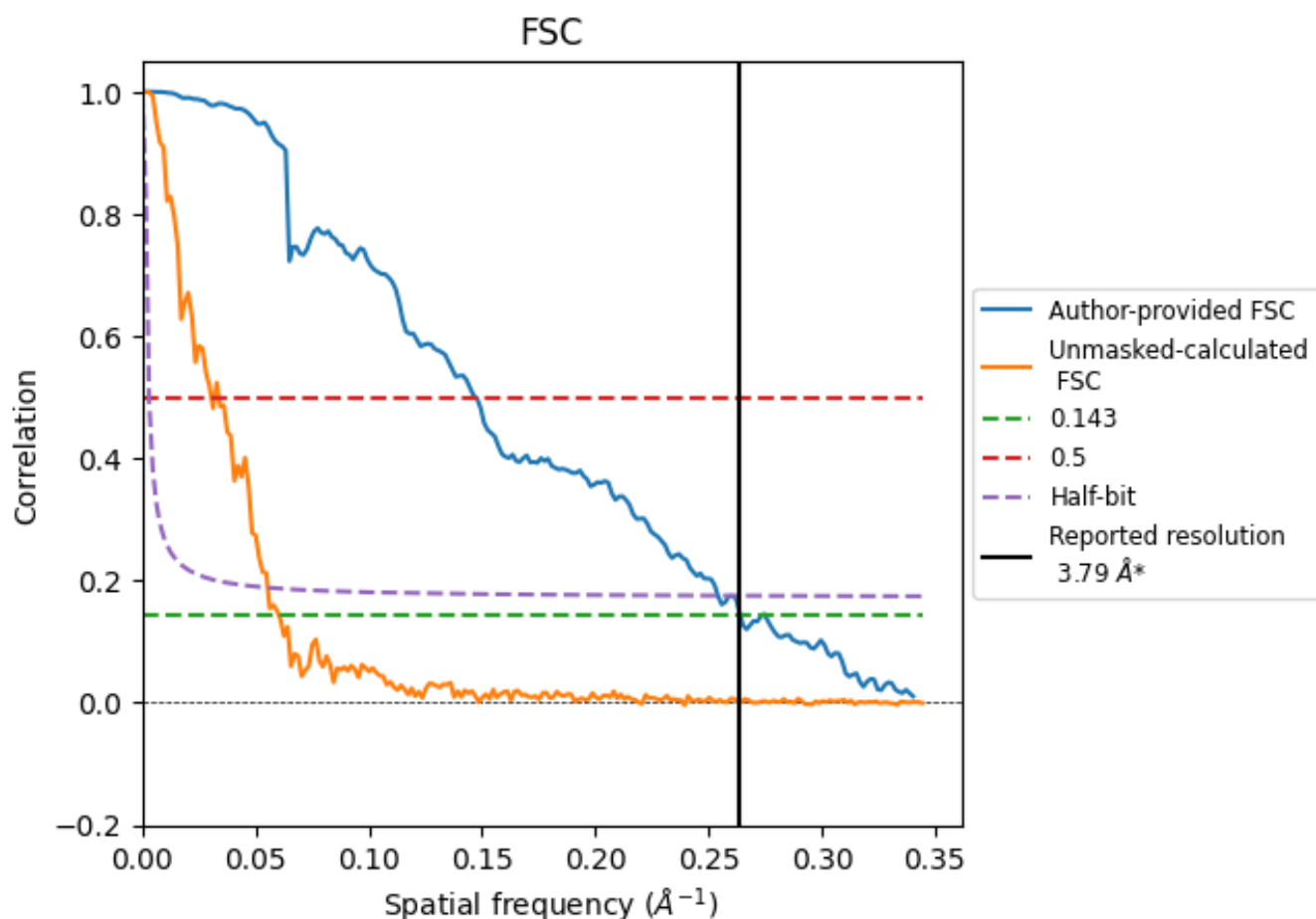


*Reported resolution corresponds to spatial frequency of 0.264 Å⁻¹

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 0.264 Å⁻¹

8.2 Resolution estimates [i](#)

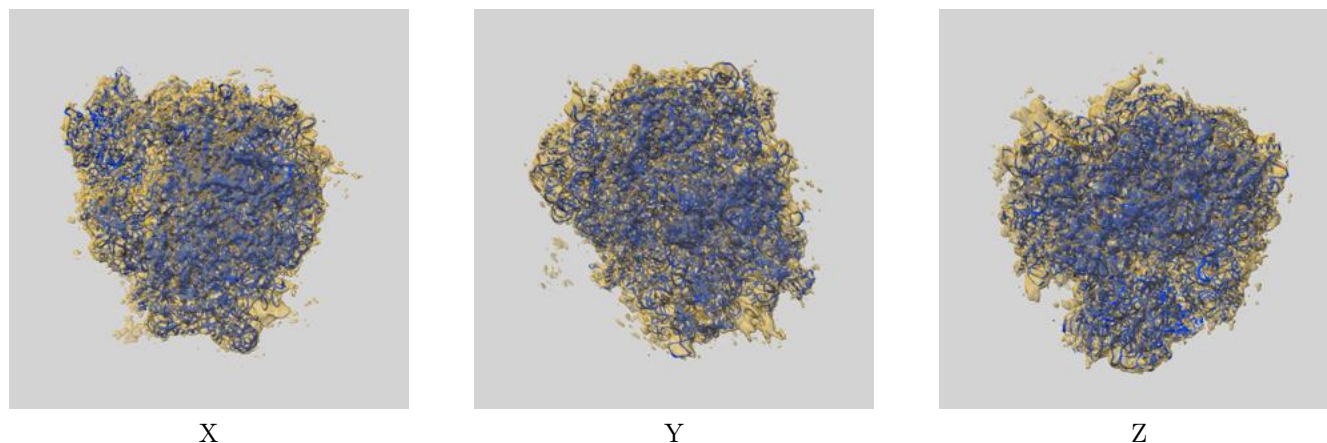
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.79	-	-
Author-provided FSC curve	3.79	6.79	3.93
Unmasked-calculated*	16.58	32.79	18.05

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 16.58 differs from the reported value 3.79 by more than 10 %

9 Map-model fit [i](#)

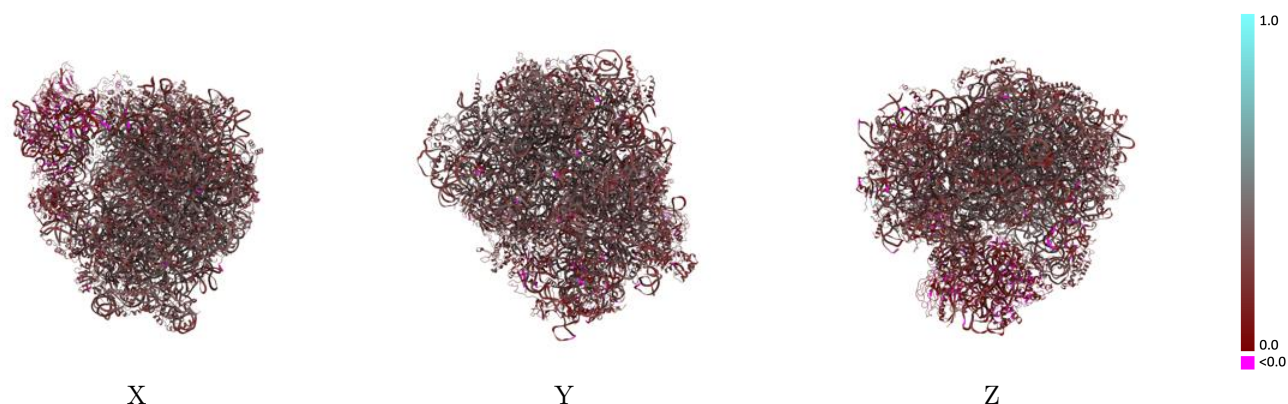
This section contains information regarding the fit between EMDB map EMD-16729 and PDB model 8CMJ. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



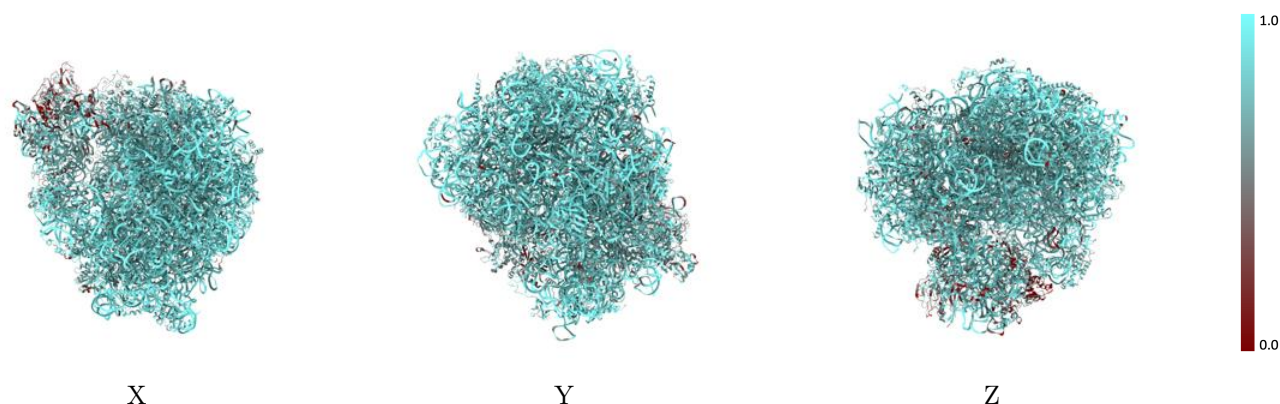
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



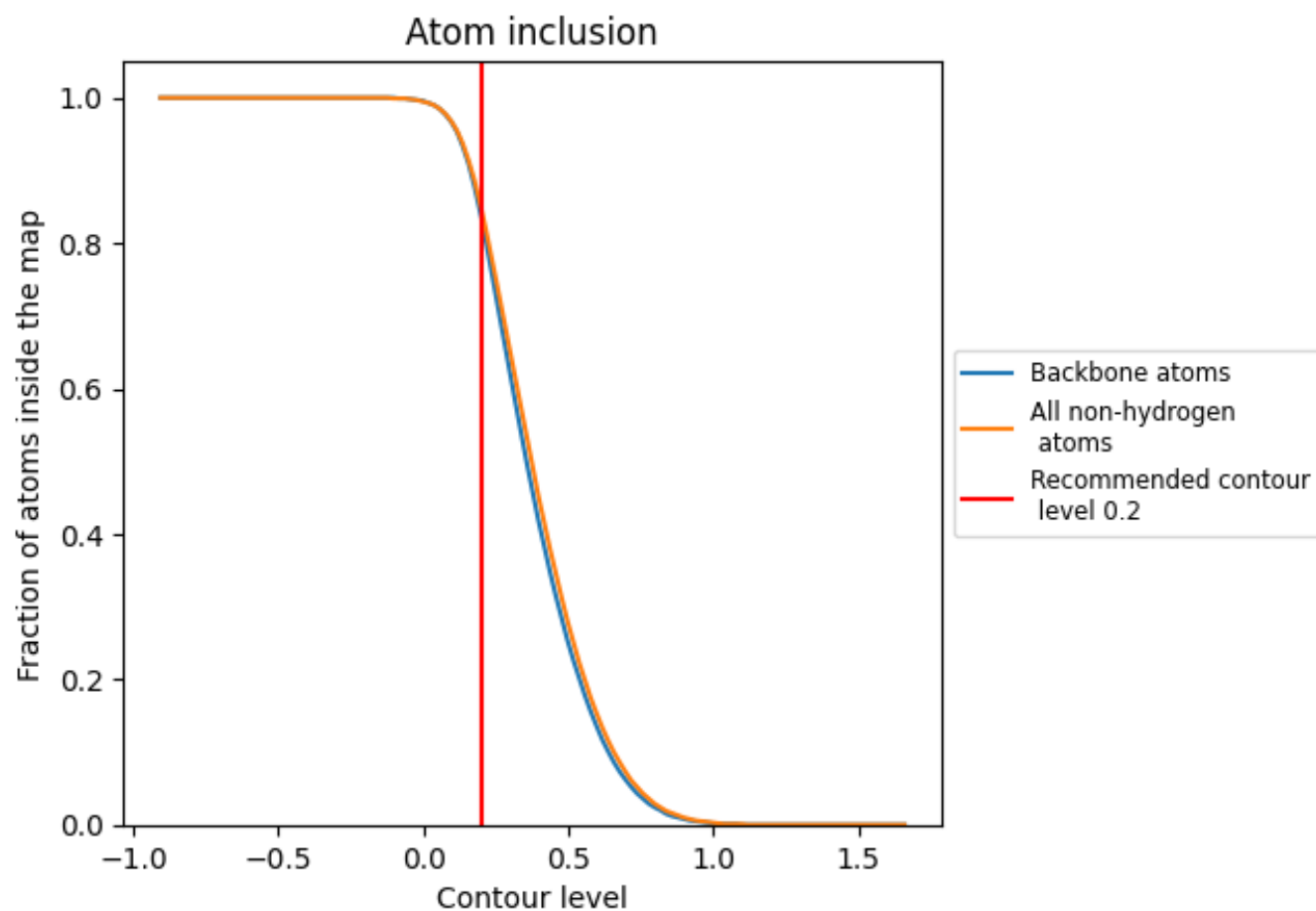
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8480	 0.2900
0	 0.7450	 0.2500
1	 0.0510	 0.0910
2	 0.8390	 0.3270
3	 0.7820	 0.2570
4	 0.5600	 0.1500
5	 0.9150	 0.1740
6	 0.8470	 0.2580
7	 0.4470	 0.1480
8	 0.5110	 0.1560
A	 0.8380	 0.3320
AA	 0.9300	 0.3220
Aa	 0.6130	 0.2200
B	 0.8350	 0.3460
BB	 0.9730	 0.3180
C	 0.8510	 0.3340
CC	 0.9650	 0.3420
D	 0.8250	 0.3270
DD	 0.5870	 0.2330
E	 0.8420	 0.3340
EE	 0.7580	 0.3230
Ee	 0.5350	 0.1950
F	 0.8620	 0.3300
FF	 0.8330	 0.3250
G	 0.8370	 0.2670
GG	 0.8600	 0.3380
H	 0.7560	 0.3570
HH	 0.8040	 0.2650
I	 0.7520	 0.3140
II	 0.8680	 0.3250
J	 0.8470	 0.3380
JJ	 0.8680	 0.3410
K	 0.8570	 0.3280
KK	 0.8380	 0.2840
L	 0.8520	 0.2830



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Chain	Atom inclusion	Q-score
LL	 0.7520	 0.2990
M	 0.8580	 0.3280
MM	 0.8000	 0.3190
N	 0.7850	 0.2990
NN	 0.8190	 0.2470
O	 0.7520	 0.2950
OO	 0.8550	 0.2980
P	 0.8220	 0.3320
PP	 0.8500	 0.3310
Q	 0.8560	 0.3480
QQ	 0.8450	 0.2980
R	 0.8850	 0.3380
S	 0.8780	 0.3460
T	 0.8710	 0.2960
U	 0.8360	 0.2770
V	 0.9090	 0.3420
W	 0.7800	 0.2880
X	 0.8510	 0.3390
Y	 0.7330	 0.2920
Z	 0.6930	 0.2920
a	 0.7760	 0.2710
b	 0.7340	 0.3100
c	 0.9160	 0.2670
d	 0.6900	 0.2470
e	 0.7530	 0.2620
f	 0.8370	 0.3010
g	 0.7630	 0.2070
h	 0.8170	 0.2710
i	 0.5210	 0.1250
j	 0.7570	 0.2060
k	 0.6680	 0.2520
l	 0.6870	 0.2300
m	 0.8620	 0.2960
n	 0.8690	 0.2260
o	 0.7520	 0.2930
p	 0.7770	 0.2830
q	 0.8260	 0.2950
r	 0.5480	 0.1400
s	 0.6360	 0.1740
t	 0.6280	 0.2250
u	 0.5220	 0.1490
v	 0.6450	 0.1410

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Chain	Atom inclusion	Q-score
w	 0.8000	 0.2000
x	 0.8520	 0.3030
y	 0.7520	 0.2820
z	 0.7380	 0.3130