wwPDB EM Validation Summary Report (i)

Mar 20, 2026 – 10:30 AM UTC

PDB ID	:	8CKU / pdb_00008cku
EMDB ID	:	EMD-16702
Title	:	Translocation intermediate 1 (TI-1*) of 80S S. cerevisiae ribosome with ligands and eEF2 in the absence of sordarin
Authors	:	Milicevic, N.; Jenner, L.; Myasnikov, A.; Yusupov, M.; Yusupova, G.
Deposited on	:	2023-02-16
Resolution	:	3.11 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 (i) 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 (i)) were used in the production of this report:

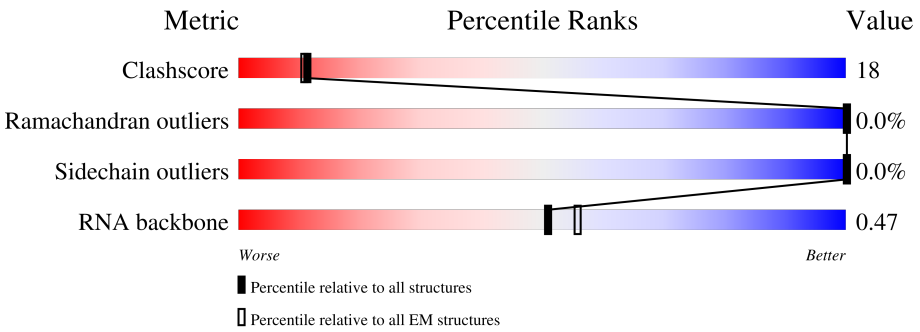
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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

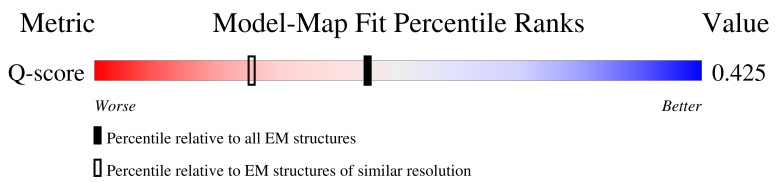
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.11 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	14465 (2.61 - 3.61)

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 <=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	57% 42%
2	1	108	13% 31% 33% 35%
3	2	119	55% 27% 18%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	3	82	61% 38%
5	4	67	6% 63% 30% 6%
6	5	56	57% 38% 5%
7	6	63	5% 52% 30% 16%
8	7	319	8% 52% 48%
9	8	152	21% 76%
10	A	199	64% 35%
11	AA	3396	38% 46% 10% 6%
12	Aa	842	44% 53% 47%
13	B	184	45% 39% 16%
14	BB	121	50% 45% 6%
15	Bb	76	26% 20% 45% 34%
16	C	186	68% 32%
17	CC	158	39% 54% 8%
18	Cc	77	32% 47% 21%
19	D	189	52% 41% 7%
20	DD	312	36% 38% 27% 36%
21	Dd	39	13% 15% 5% 67%
22	E	172	61% 39%
23	EE	254	62% 37%
24	Ee	165	45% 58% 39%
25	F	160	71% 29%
26	FF	387	62% 37%
27	G	121	56% 24% 20%
28	GG	362	73% 27%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	H	137	56% 38% 6%
30	HH	297	63% 37%
31	I	155	20% 21% 59%
32	II	176	65% 23% 12%
33	J	142	54% 31% 15%
34	JJ	244	62% 29% 9%
35	K	127	65% 34%
36	KK	256	62% 29% 9%
37	L	136	67% 32%
38	LL	191	58% 42%
39	M	149	62% 38%
40	MM	221	5% 67% 30%
41	N	59	66% 32%
42	NN	174	50% 47%
43	O	105	58% 34% 8%
44	OO	199	65% 32%
45	P	113	62% 35%
46	PP	138	63% 36%
47	Q	130	74% 24%
48	QQ	204	54% 45%
49	R	107	73% 26%
50	S	121	57% 33% 10%
51	T	120	67% 32%
52	U	100	56% 43%
53	V	88	55% 41% 5%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	W	78	67% 32%
55	X	51	67% 31%
56	Y	128	30% 11% 59%
57	Z	25	56% 44%
58	a	106	58% 37%
59	b	92	64% 35%
60	c	1800	29% 46% 14% 11%
61	d	252	44% 37% 18%
62	e	255	47% 36% 17%
63	f	254	52% 33% 15%
64	g	240	51% 35% 14%
65	h	261	49% 50%
66	i	225	40% 48% 12%
67	j	236	56% 37% 7%
68	k	190	57% 39%
69	l	200	48% 44% 8%
70	m	197	54% 40% 6%
71	n	105	39% 47% 13%
72	o	156	5% 45% 46% 9%
73	p	151	66% 33%
74	q	137	53% 39% 7%
75	r	142	49% 25% 27%
76	s	143	55% 41%
77	t	136	49% 40% 11%
78	u	146	5% 47% 52%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
79	v	144	56% 44%
80	w	121	45% 38% 17%
81	x	87	60% 40%
82	y	130	56% 43%
83	z	145	56% 43%

2 Entry composition (i)

There are 89 unique types of molecules in this entry. The entry contains 207340 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
			Total	C	N	O		
1	0	134	1073	676	208	189	0	0

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	5	53	442	274	92	72	4	0	0

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
11	AA	3190	68285	30524	12313	22258	3190	0	0

- Molecule 12 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	Aa	842	6569	4173	1126	1239	31	0	0

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

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

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

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

- Molecule 15 is a RNA chain called Transfer RNA Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
15	Bb	76	1638	736	294	533	75	0	0

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

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

- Molecule 17 is a RNA chain called 5.8S ribosomal RNA.

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

- Molecule 18 is a RNA chain called Transfer RNA fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
18	Cc	77	1644	732	298	537	77	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cc	18	C	U	conflict	GB 170517292

- Molecule 19 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 20 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	DD	200	1551	994	269	284	4	0	0

- Molecule 21 is a RNA chain called Messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
21	Dd	13	278	125	50	90	13	0	0

- Molecule 22 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 23 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 24 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	Ee	160	1211	759	218	232	2	0	0

- Molecule 25 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 26 is a protein called 60S ribosomal protein L3.

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

- Molecule 27 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 28 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 29 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 30 is a protein called 60S ribosomal protein L5.

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

- Molecule 31 is a protein called 60S ribosomal protein L24-A.

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

- Molecule 32 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 33 is a protein called 60S ribosomal protein L25.

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

- Molecule 34 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 35 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 36 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 37 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 38 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 39 is a protein called 60S ribosomal protein L28.

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

- Molecule 40 is a protein called 60S ribosomal protein L10.

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

- Molecule 41 is a protein called 60S ribosomal protein L29.

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

- Molecule 42 is a protein called 60S ribosomal protein L11-A.

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

- Molecule 43 is a protein called 60S ribosomal protein L30.

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

- Molecule 44 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 45 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 46 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 47 is a protein called 60S ribosomal protein L32.

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

- Molecule 48 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 51 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 52 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 53 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 54 is a protein called 60S ribosomal protein L38.

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

- Molecule 55 is a protein called 60S ribosomal protein L39.

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

- Molecule 56 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 57 is a protein called RPL41A isoform 1.

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

- Molecule 58 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 59 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 60 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
60	c	1604	34236	15322	6079	11231	1604	0	0

- Molecule 61 is a protein called 40S ribosomal protein S0-A.

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

- Molecule 62 is a protein called 40S ribosomal protein S1-A.

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

- Molecule 63 is a protein called 40S ribosomal protein S2.

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

- Molecule 64 is a protein called RPS3 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	g	206	1601	1014	294	287	6	0	0

- Molecule 65 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 66 is a protein called 40S ribosomal protein S5.

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

- Molecule 67 is a protein called 40S ribosomal protein S6-A.

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

- Molecule 68 is a protein called 40S ribosomal protein S7-A.

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

- Molecule 69 is a protein called 40S ribosomal protein S8-A.

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

- Molecule 70 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 71 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	n	91	772	503	123	144	2	0	0

- Molecule 72 is a protein called 40S ribosomal protein S11-A.

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

- Molecule 73 is a protein called 40S ribosomal protein S13.

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

- Molecule 74 is a protein called 40S ribosomal protein S14-A.

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

- Molecule 75 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	r	104	837	533	155	143	6	0	0

- Molecule 76 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
76	s	137	1080	692	199	189	0	0

- Molecule 77 is a protein called 40S ribosomal protein S17-A.

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

- Molecule 78 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 79 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 80 is a protein called 40S ribosomal protein S20.

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

- Molecule 81 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 82 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 83 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 84 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
84	2	1	1	1	0
84	5	1	1	1	0
84	8	1	1	1	0
84	S	1	1	1	0
84	V	1	1	1	0
84	Y	1	1	1	0
84	a	1	1	1	0
84	b	1	1	1	0

- Molecule 85 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
85	AA	157	157	157	0
85	Aa	1	1	1	0
85	B	1	1	1	0
85	BB	3	3	3	0
85	Bb	1	1	1	0
85	CC	2	2	2	0
85	D	1	1	1	0
85	EE	1	1	1	0
85	F	1	1	1	0

Continued on next page...

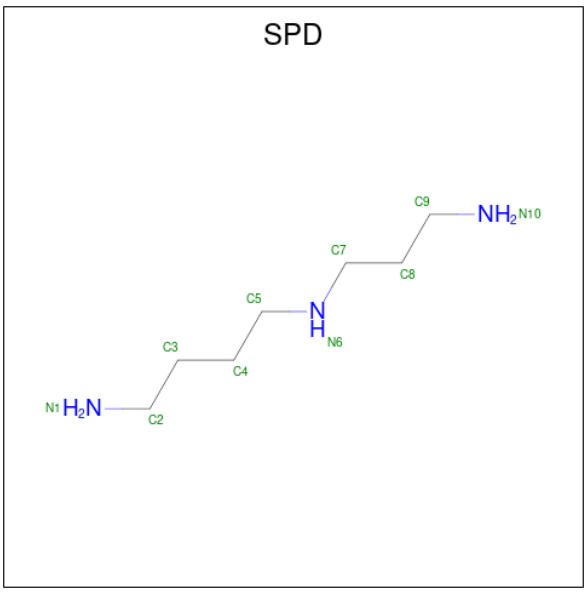
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
85	FF	1	1	1	0
			Total	Mg	
85	H	1	1	1	0
			Total	Mg	
85	c	35	35	35	0

- Molecule 86 is POTASSIUM ION (CCD ID: K) (formula: K).

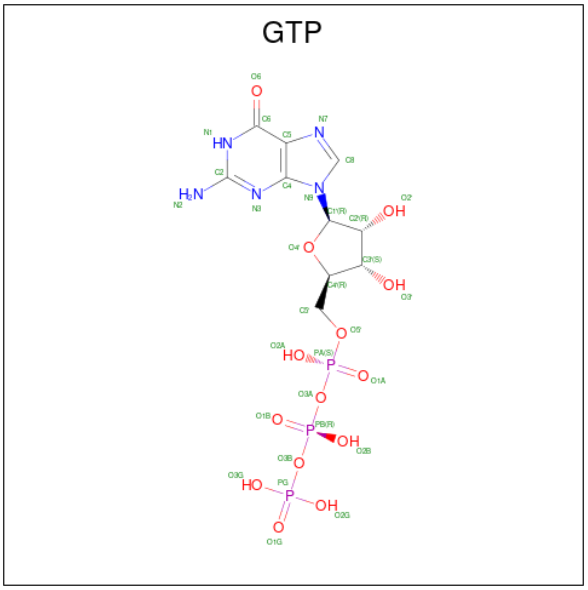
Mol	Chain	Residues	Atoms		AltConf
			Total	K	
86	AA	10	10	10	0
			Total	K	
86	BB	1	1	1	0
			Total	K	
86	Dd	1	1	1	0
			Total	K	
86	EE	1	1	1	0
			Total	K	
86	MM	1	1	1	0
			Total	K	
86	Q	1	1	1	0
			Total	K	
86	c	1	1	1	0

- Molecule 87 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$).



Mol	Chain	Residues	Atoms			AltConf
			Total	C	N	
87	AA	1	10	7	3	0
			Total	C	N	
87	AA	1	10	7	3	0
			Total	C	N	
87	c	1	10	7	3	0

- Molecule 88 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

- Molecule 89 is water.

Mol	Chain	Residues	Atoms		AltConf
			Total	O	
89	2	1	1	1	0
			Total	O	
89	AA	258	258	258	0
			Total	O	
89	Aa	1	1	1	0
			Total	O	
89	B	2	2	2	0
			Total	O	
89	BB	4	4	4	0
			Total	O	
89	CC	3	3	3	0

Continued on next page...

Continued from previous page...

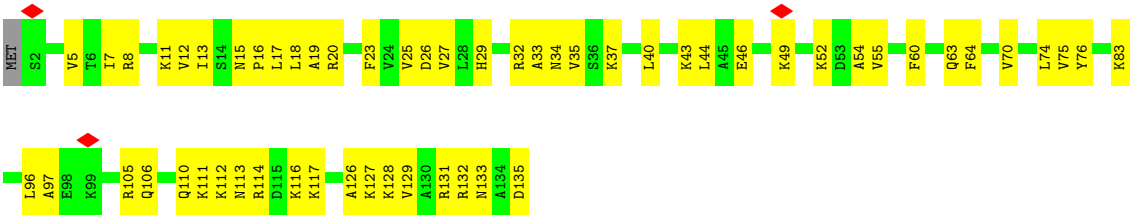
Mol	Chain	Residues	Atoms		AltConf
			Total	O	
89	Cc	1	1	1	0
			Total	O	
89	F	4	4	4	0
			Total	O	
89	FF	3	3	3	0
			Total	O	
89	GG	1	1	1	0
			Total	O	
89	M	1	1	1	0
			Total	O	
89	Q	2	2	2	0
			Total	O	
89	QQ	1	1	1	0
			Total	O	
89	S	1	1	1	0
			Total	O	
89	V	2	2	2	0
			Total	O	
89	a	1	1	1	0
			Total	O	
89	c	53	53	53	0
			Total	O	
89	p	1	1	1	0
			Total	O	
89	q	2	2	2	0

3 Residue-property plots (i)

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

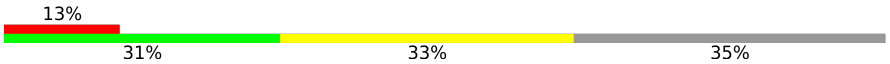
- Molecule 1: 40S ribosomal protein S24-A

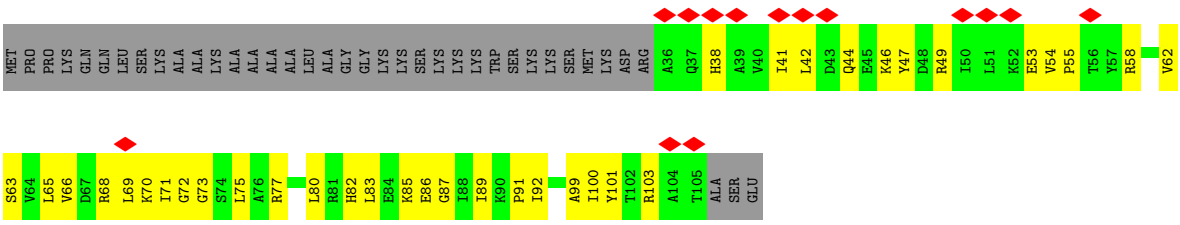
Chain 0:



- Molecule 2: 40S ribosomal protein S25-A

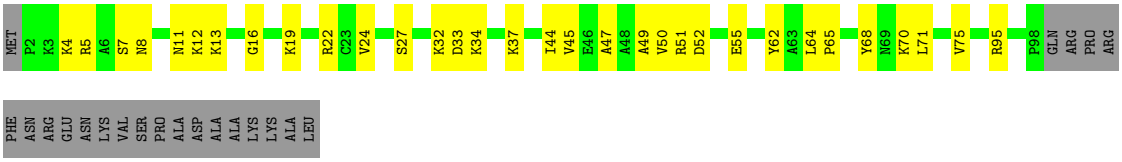
Chain 1:





- Molecule 3: 40S ribosomal protein S26

Chain 2:

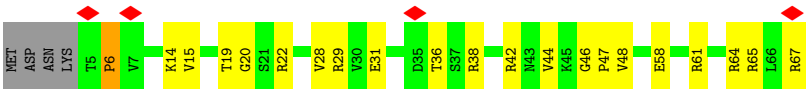


- Molecule 4: 40S ribosomal protein S27-A

Chain 3:

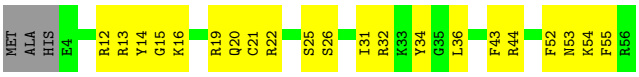
• Molecule 5: 40S ribosomal protein S28-A

Chain 4:



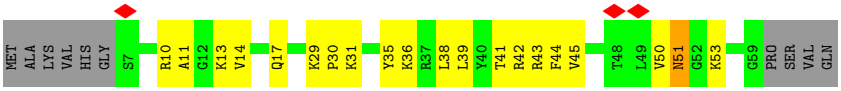
• Molecule 6: HLJ1_G0030400.mRNA.1.CDS.1

Chain 5:



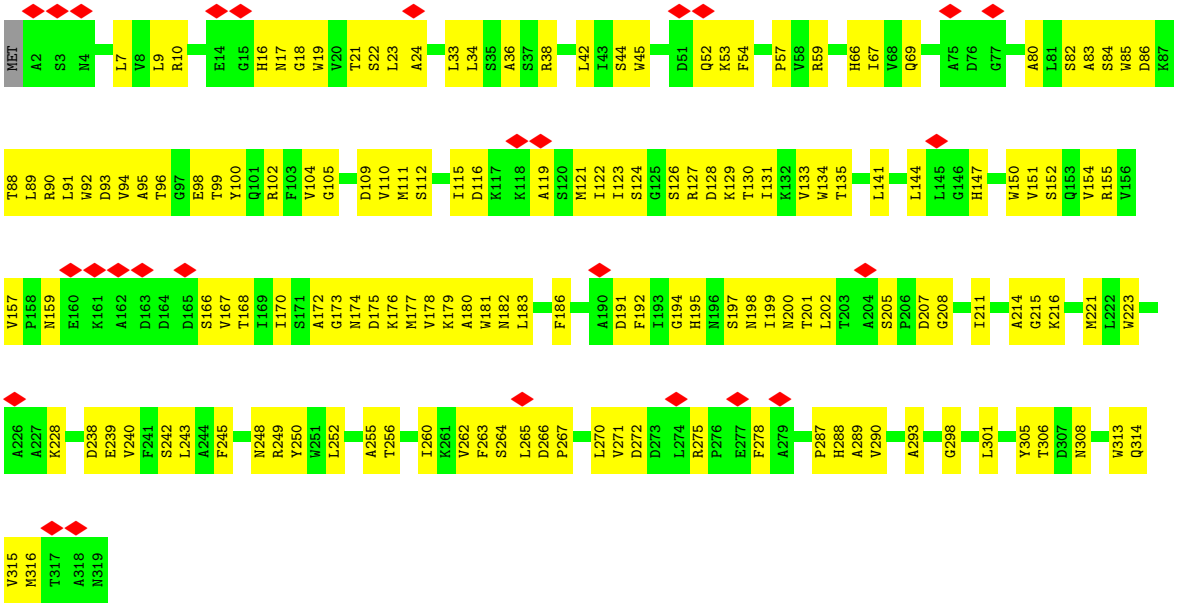
• Molecule 7: 40S ribosomal protein S30-A

Chain 6:



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

Chain 7:



• Molecule 9: Ubiquitin-40S ribosomal protein S31

Chain 8: 21% 76%

MET GLN ILE PHE VAL LYS THR LEU THR GLY LYS THR ILE THR LEU GLU VAL GLU SER SER ASP THR ILE ASP ASN VAL LYS SER LYS ILE GLN ASP LYS GLU GLY ILE PRO PRO ASP GLN GLN ARG LEU ILE PHE ALA GLY LYS GLN LEU GLU ASP GLY ARG THR LEU SER ASP TYR ASN

ILE GLN LYS GLU SER THR LEU HIS LEU VAL LEU ARG LEU ARG GLY GLY GLY LYS LYS ARG LYS LYS LYS VAL TYR THR THR PRO LYS LYS ILE LYS HIS K94 H95 K96 K99 L100 L103 SER TYR TYR LYS VAL ASP ALA GLU GLY LYS VAL THR LYS LEU ARG R119 N123 P124

T125 N134 D137 R138 C144 HIS SER VAL TYR LYS VAL ASN ALA

- Molecule 10: 60S ribosomal protein L16-A

Chain A: 64% 35%

MET SER V3 I9 K12 G13 H14 L15 V16 G17 R18 L19 A20 S21 V22 V23 A24 K25 Q26 L27 L28 V35 V36 R37 A38 E39 E40 E46 F47 N50 Y54 K60 A61 T62 N65 R68 G69 F73 R74 A75 P76 S77 R78 I79 F80 A83 L84 R85

V88 A97 A98 L99 E100 R101 E106 G107 I108 P109 P110 P111 Y112 D113 K114 R117 V120 R125 L129 K130 R133 T136 T137 L138 T143 S144 V145 G146 W147 E150 D151 L156 E157 R160 K161 R172 T175 V178 D189 V190 L194 L197

G198 Y199

- Molecule 11: 25S ribosomal RNA

Chain AA: 38% 46% 10% 6%

G U U3 U4 G5 A6 C7 C8 U9 C10 A11 A12 A13 G17 G18 U19 A20 G21 A26 C27 C28 C29 G30 C31 U32 G33 A34 A35 C36 U37 U38 A39 A40 A43 U46 C47 A48 A49 U50 A51 A52 G53 C54 A57 G58 G59 A60 A61 A62 A63 G64 A65 A66 A67 C68

C69 C72 C73 G74 G75 G76 A77 U78 A85 G86 U87 A88 G92 C93 G94 A95 G98 A99 A100 G101 C102 G103 G104 A107 G110 C111 U112 C113 A114 A115 A116 U117 U118 U119 G120 A121 A122 A123 U126 U129 A130 C135 G136 G137 U138 G139 C140 C141 C142 G143 A144

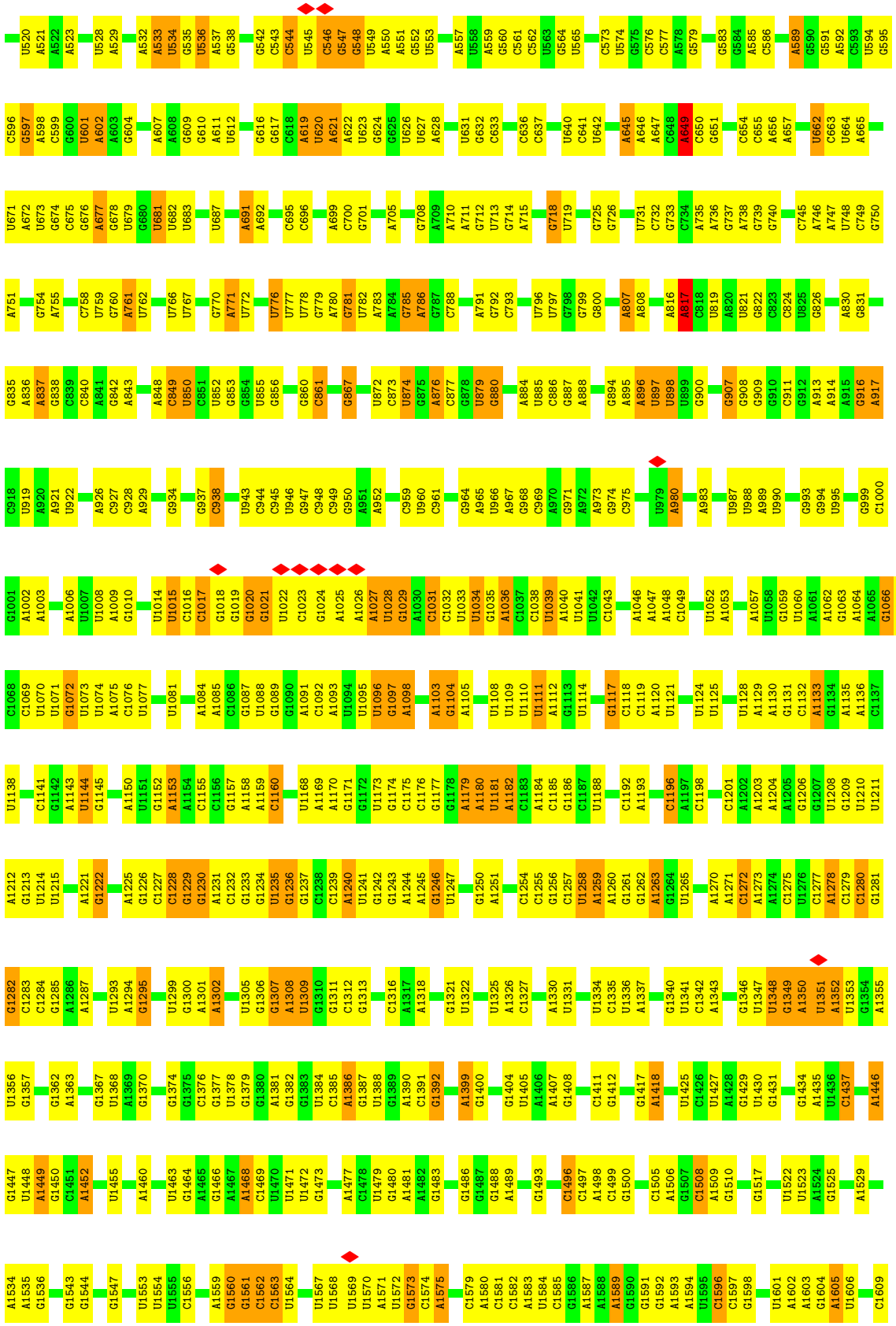
G145 U146 U147 G148 U149 A150 A151 U152 G156 A157 G158 A159 G160 G161 G162 C163 A164 A165 C166 G170 G171 G172 G173 C174 C175 G176 U177 U178 C179 C180 U181 U184 C185 U186 A187 U188 G189 U190 U191 C192 C193 U194 U195 G196 G197 A198 A199 C200 U207 C208 A209 U210 A211 G212 A213 G214

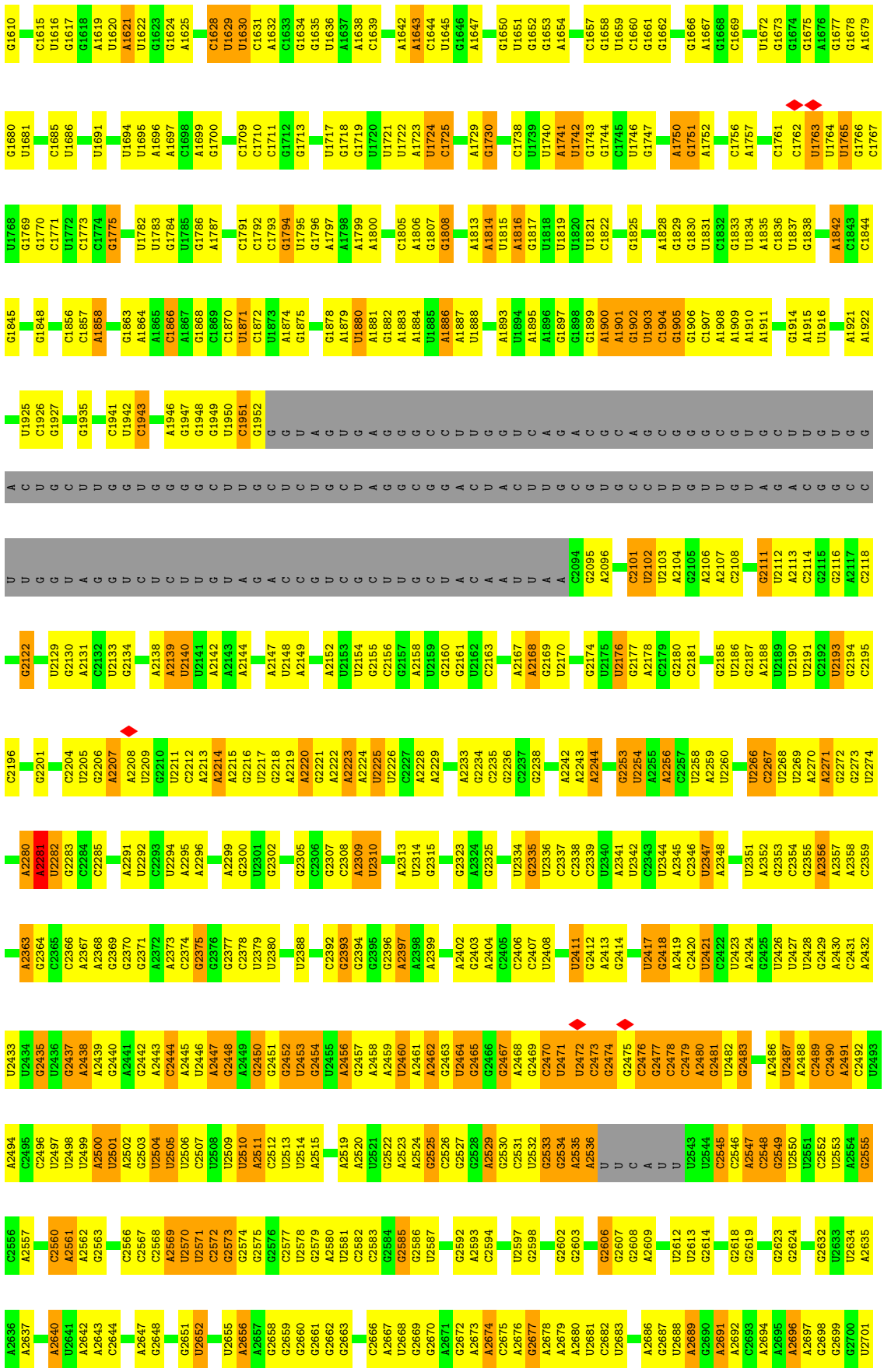
G215 G216 U217 G218 A219 G220 A221 A222 U223 U228 G229 U230 G231 G232 A235 G236 G237 A238 G239 U240 G241 C242 G243 G244 U245 U246 C247 U248 U249 U252 A253 A254 C263 G264 A265 A266 G267 A268 G269 U270 C271 G272 A273 G274 U275 U276 G277 U278 U279 U280 G281 G282 G283 A284 A285 U286

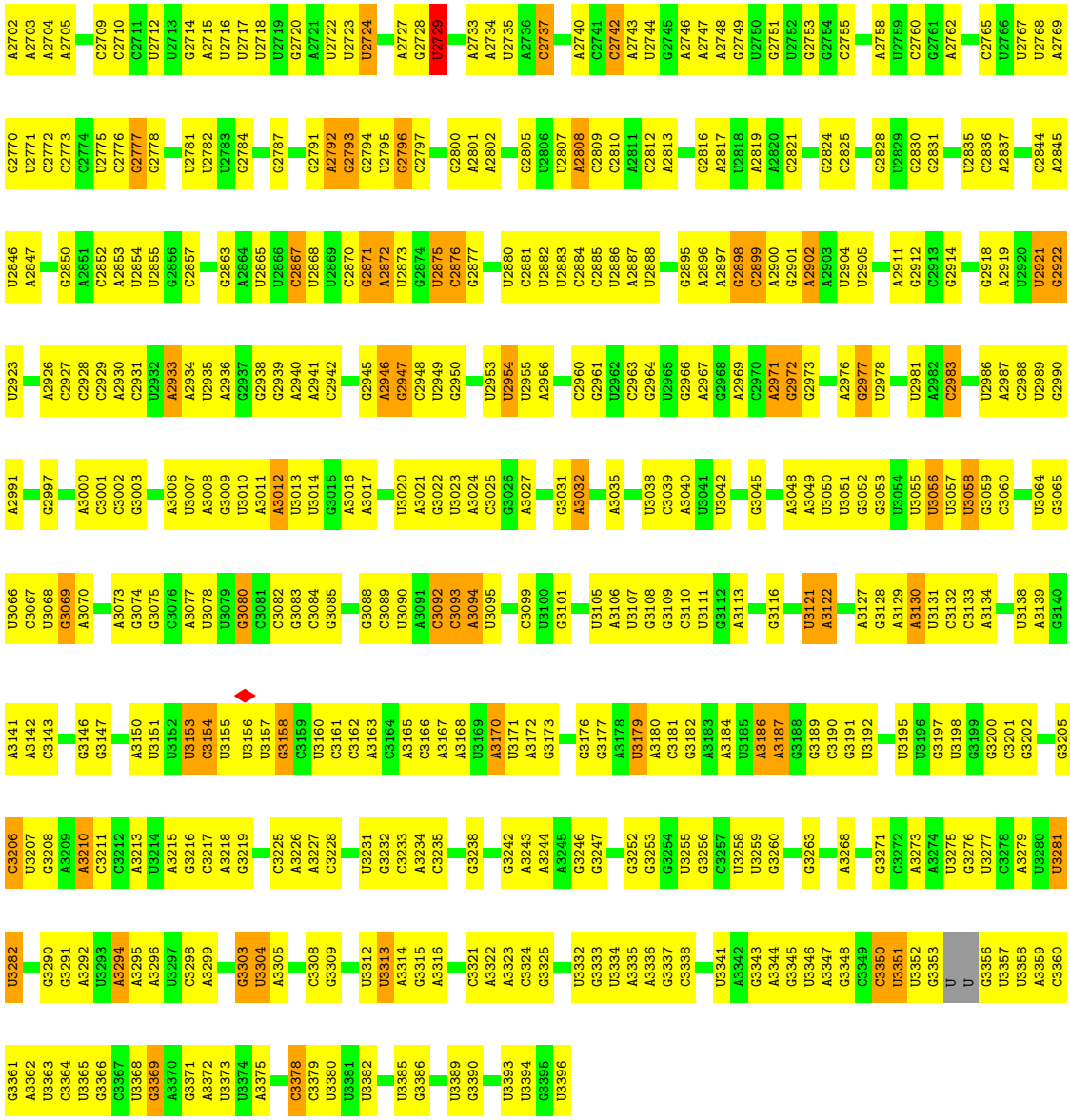
G287 C288 A289 G290 C291 U292 C293 U294 A295 A296 G297 U298 G299 G300 G301 A307 A308 U309 A313 U314 C315 U316 A324 A325 U329 G335 G341 G345 C346 G347 A348 A349 C350 A351 A352 G353 G358 U359 G360 A361 U362 G363 G364 A367 G368 A369 U370 G376 A377

G383 A384 A385 A386 A387 G388 A389 G392 U393 G394 A397 A398 A399 G400 U401 A402 C403 G404 U405 G406 A407 A408 U411 G412 U413 U414 G415 A416 A417 A418 G419 G420 G421 A422 A428 U429 U430 U431 G432 A436 G437 A438 C A U G G U G U U U U G

G C C C U C U G C U C C C U U G U G G G U A G G G G A A U C U C G C A U U U C A C U G G494 G499 C500 A501 U502 C503 A504 G505 U506 U507 U508 U509 G514 C515 A516 G517

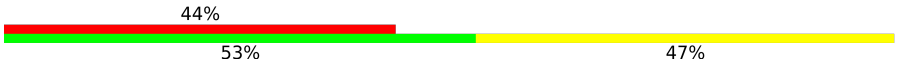

U520 A521 A522 A523 U528 A529 A532 A533 U534 G535 U536 A537 G538 G542 G543 C544 U545 C546 G547 G548 U549 A550 A551 G552 U553 A557 U558 A559 G560 C561 C562 U563 G564 U565 C573 U574 G575 C576 C577 A578 G579 G583 G584 A585 C586 A589 G590 G591 A592 C593 U594 G595
C596 G597 A598 C599 G600 U601 A602 A603 G604 A607 A608 G609 G610 A611 U612 G616 G617 C618 A619 U620 A621 A622 U623 G624 G625 U626 U627 A628 U631 G632 C633 C636 C637 U640 C641 U642 A645 A646 A647 C648 A649 C650 G651 C654 C655 A656 A657 U662 C663 U664 A665
U671 A672 U673 G674 C675 G676 A677 G678 U679 G680 U681 U682 U683 U687 A691 A692 C695 C696 A699 C700 G701 A705 G708 A709 A710 A711 G712 U713 G714 A715 G718 U719 G725 G726 U731 C732 G733 C734 A735 A736 G737 A738 G739 G740 C745 A746 A747 U748 C749 G750
A751 G754 A755 C758 U759 G760 A761 U762 U766 U767 G770 A771 U772 U776 U777 U778 G779 A780 G781 U782 A783 A784 G785 A786 G787 C788 A791 G792 C793 U796 U797 G798 G799 G800 A807 A808 A816 A817 C818 U819 A820 U821 G822 C823 C824 U825 G826 A830 G831
G835 A836 A837 G838 C839 C840 A841 G842 A843 A848 C849 U850 C851 U852 G853 G854 U855 G856 G860 C861 G867 U872 C873 U874 G875 A876 C877 G878 U879 G880 A884 U885 C886 G887 A888 G894 A895 A896 U897 U898 U899 G900 G907 G908 G909 G910 C911 G912 A913 A914 A915 G916 A917
C918 U919 A920 A921 U922 A926 C927 C928 A929 G934 G937 C938 U943 C944 C945 U946 G947 C948 G949 G950 A951 A952 C959 U960 C961 G964 A965 U966 A967 G968 C969 A970 G971 A972 A973 G974 C975 U979 A980 A983 U987 U988 A989 U990 G993 G994 U995 G999 C1000
G1001 A1002 A1003 A1006 U1007 U1008 A1009 G1010 U1014 U1015 C1016 C1017 G1018 G1019 G1020 G1021 U1022 C1023 G1024 A1025 A1026 A1027 U1028 G1029 A1030 C1031 C1032 U1033 U1034 G1035 A1036 C1037 C1038 U1039 A1040 U1041 U1042 C1043 A1046 A1047 A1048 C1049 U1052 A1053 A1057 U1058 G1059 U1060 A1061 A1062 G1063 A1064 A1065 G1066 U1067
C1068 C1069 U1070 U1071 G1072 U1073 U1074 A1075 C1076 U1077 U1081 A1084 A1085 C1086 G1087 U1088 G1089 G1090 A1091 C1092 A1093 U1094 U1095 U1096 G1097 A1098 A1103 G1104 A1105 U1108 U1109 U1110 U1111 A1112 G1113 U1114 G1117 C1118 C1119 A1120 U1121 U1124 U1125 U1128 A1129 A1130 G1131 C1132 A1133 G1134 A1135 A1136 C1137
U1138 C1141 G1142 A1143 U1144 G1145 A1150 U1151 G1152 A1153 A1154 C1155 C1156 G1157 A1158 A1159 C1160 U1168 A1169 A1170 G1171 G1172 U1173 G1174 C1175 C1176 G1177 G1178 A1179 A1180 U1181 A1182 C1183 A1184 C1185 G1186 C1187 U1188 C1192 A1193 C1196 A1197 C1198 C1201 A1202 A1203 A1204 A1205 G1206 G1207 U1208 G1209 U1210 U1211
A1212 G1213 U1214 U1215 A1221 G1222 A1225 G1226 C1227 C1228 G1229 G1230 A1231 C1232 G1233 G1234 U1235 G1236 G1237 C1238 C1239 A1240 U1241 G1242 G1243 A1244 A1245 G1246 U1247 G1250 A1251 C1254 C1255 G1256 C1257 U1258 A1259 A1260 G1261 G1262 A1263 G1264 U1265 A1270 A1271 C1272 A1273 A1274 C1275 U1276 C1277 A1278 C1279 C1280 G1281
G1282 C1283 C1284 G1285 A1286 A1287 U1293 A1294 G1295 U1299 G1300 A1301 A1302 U1305 G1306 G1307 A1308 U1309 G1310 C1311 C1312 G1313 C1316 A1317 A1318 G1321 U1322 U1325 A1326 C1327 A1330 U1331 U1334 C1335 U1336 A1337 G1340 U1341 C1342 A1343 G1346 U1347 U1348 G1349 A1350 U1351 A1352 U1353 G1354 A1355
U1356 G1357 G1362 A1363 G1367 U1368 A1369 G1370 G1374 G1375 C1376 G1377 U1378 G1379 G1380 A1381 G1382 G1383 U1384 C1385 A1386 G1387 U1388 G1389 A1390 C1391 G1392 A1399 G1400 G1404 U1405 A1406 A1407 G1408 C1411 G1412 G1417 A1418 U1425 C1426 U1427 A1428 G1429 U1430 G1431 G1434 A1435 U1436 C1437 A1446
G1447 U1448 A1449 G1450 C1451 A1452 U1455 A1460 U1463 G1464 A1465 G1466 A1467 A1468 C1469 U1470 U1471 U1472 G1473 A1477 C1478 U1479 G1480 A1481 A1482 G1483 G1486 G1487 G1488 A1489 G1493 C1496 C1497 A1498 C1499 G1500 C1505 A1506 G1507 C1508 A1509 G1510 G1517 U1522 U1523 A1524 G1525 A1529
A1534 A1535 G1536 G1543 G1544 G1547 U1553 U1554 U1555 C1556 A1559 G1560 G1561 C1562 C1563 U1564 U1567 U1568 U1569 U1570 A1571 U1572 G1573 C1574 A1575 C1579 A1580 C1581 C1582 A1583 U1584 C1585 G1586 A1587 A1588 A1589 G1590 G1591 G1592 A1593 A1594 U1595 C1596 C1597 G1598 U1601 A1602 A1603 G1604 A1605 U1606 C1609

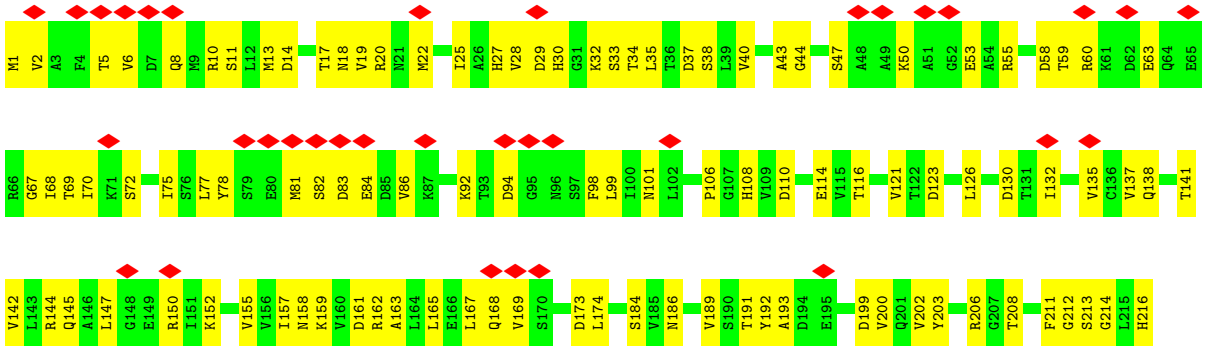

G1610 C1615 U1616 G1617 G1618 A1619 U1620 A1621 U1622 G1623 G1624 A1625 C1628 U1629 U1630 C1631 A1632 C1633 G1634 G1635 U1636 A1637 A1638 C1639 A1642 A1643 C1644 U1645 G1646 A1647 G1650 U1651 G1652 G1653 A1654 C1657 G1658 U1659 C1660 G1661 G1662 G1666 A1667 G1668 C1669 U1672 G1673 G1674 G1675 A1676 G1677 G1678 A1679
G1680 U1681 C1685 U1686 U1691 U1694 U1695 A1696 A1697 C1698 A1699 G1700 C1709 C1710 C1711 G1712 G1713 U1717 G1718 G1719 U1720 U1721 U1722 A1723 U1724 C1725 A1729 G1730 C1738 U1739 U1740 A1741 U1742 G1743 G1744 C1745 U1746 G1747 A1750 G1751 A1752 C1756 A1757 C1761 C1762 U1763 U1764 U1765 G1766 C1767
U1768 G1769 G1770 C1771 U1772 C1773 C1774 G1775 U1782 U1783 G1784 U1785 G1786 A1787 C1791 C1792 C1793 G1794 U1795 G1796 A1797 A1798 A1799 A1800 C1805 A1806 G1807 G1808 A1813 A1814 U1815 A1816 G1817 U1818 U1819 U1820 U1821 C1822 G1825 A1828 G1829 G1830 U1831 C1832 G1833 U1834 A1835 C1836 U1837 G1838 A1842 C1843 C1844
G1845 G1848 C1856 C1857 A1858 G1863 A1864 A1865 C1866 A1867 G1868 C1869 C1870 U1871 C1872 U1873 A1874 G1875 G1878 A1879 U1880 A1881 G1882 A1883 A1884 U1885 A1886 A1887 U1888 A1893 U1894 A1895 A1896 G1897 G1898 G1899 A1900 A1901 G1902 U1903 C1904 G1905 G1906 C1907 A1908 A1909 A1910 A1911 G1914 A1915 U1916 A1921 A1922
U1925 C1926 G1927 G1935 C1941 U1942 C1943 A1946 G1947 G1948 G1949 U1950 C1951 G1952 G G G U A G U G A A G G C C G G C C U U C C U U G G C C A A G G U U C C A A G G U U C C A A G G U U

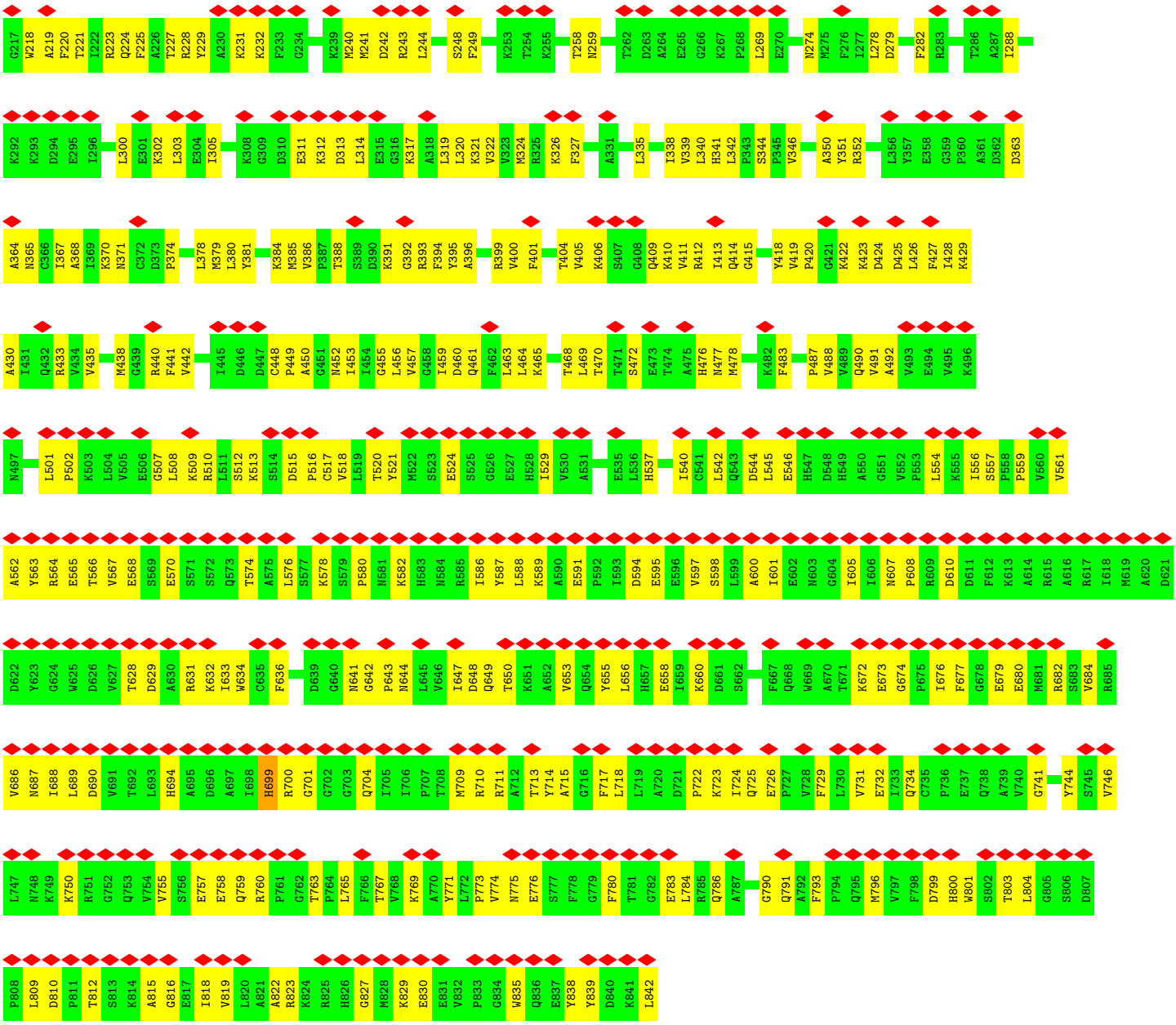


• Molecule 12: Elongation factor 2

Chain Aa:

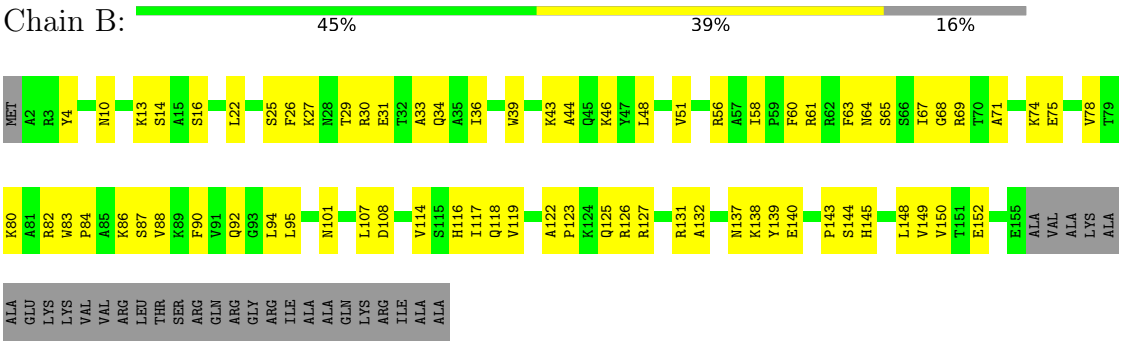






- Molecule 13: 60S ribosomal protein L17-A

Chain B:



- Molecule 14: 5S ribosomal RNA

Chain BB: 50% 45% 6%

G1 U4 G5 C6 G7 G8 C9 C10 A11 U12 A13 U14 C18 A22 A23 A24 G25 C26 A27 C28 C29 U33 G37 U38 C39 C40 G41 C44 A45 A46 C47 U50 U54 A55 G60 G61 A64 G65 G71 A72 C73 C74 G77 U81 G82 U83 A84

G85 C94 A95 U96 A97 C98 G99 C100 G101 A102 C107 A108 G112 C113 U114 G115 A118 U119 C120 U121

- Molecule 15: Transfer RNA Phe

Chain Bb: 26% 20% 45% 34%

G1 C2 G3 G4 A5 U6 U7 U8 A9 G10 A14 G15 U16 U17 G18 G19 G20 A21 G22 A23 G24 G25 G26 C27 C28 A29 G30 A31 C32 U33 A36 G37 A38 G42 G43 A44 G45 G46 U47 C48 C49 U50 G51 U52 G53 U54 U55 A58 U59 C60 C61 A62 C63 A64 G65 A66

A67 U68 U69 C70 G71 C72 A73 C74 C75 A76

- Molecule 16: 60S ribosomal protein L18-A

Chain C: 68% 32%

MET G2 K8 R12 H15 K20 N23 V24 K27 L28 L29 L36 A37 R38 R39 T40 F44 V47 K50 A51 L52 F53 L54 S55 N58 R59 I67 A70 L71 K72 Q73 V81 T88 D89 D90 A91 R92 I93 F94 T99 L104 T107

A110 R111 A112 K113 I114 V115 K116 I122 T123 L124 D125 Q126 R130 R144 E148 R151 H152 M155 G156 P157 H158 K161 A162 L166 G177 K182 K185 V186

- Molecule 17: 5.8S ribosomal RNA

Chain CC: 39% 54% 8%

A1 A2 A3 U6 U7 C8 A9 A10 C11 A12 A13 C14 G15 G16 A17 U18 C19 U20 C21 U22 U23 U26 U27 C28 U29 U34 C35 G36 A37 U38 G39 A40 A41 G42 A43 A44 C47 G51 A59 U60 A61 C62 G63 U64 A65 A66 U67 G68 U69 G70 A71 A72 G75

C76 A79 U82 C83 C84 G85 U86 G87 C91 A92 U93 C94 G95 A96 A97 G103 A104 A105 C106 A109 U113 G114 U121 U122 U123 G124 U125 A126 U127 U128 C129 C130 A131 G132 G133 G134 G135 A138 U139 G140 C141 C142 U143 G144 U145 U146 A149 G150 C151 G152 U153

C154 A155 U156 U157 U158

- Molecule 18: Transfer RNA fMet

Chain Cc: 32% 47% 21%

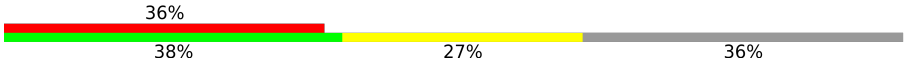
C1 G2 U8 G9 G10 A14 G15 C16 C17 C18 G19 G20 U21 A22 G23 C24 U25 C29 G30 G31 U34 C35 A36 U37 A38 A39 C40 C41 C42 G43 A44 A45 G46 G47 U48 C49 G50 G53 G54 U55 U56 C57 A58 A59 A60 U61 C62 C63 C66 C67 C68 C69 C70 G71

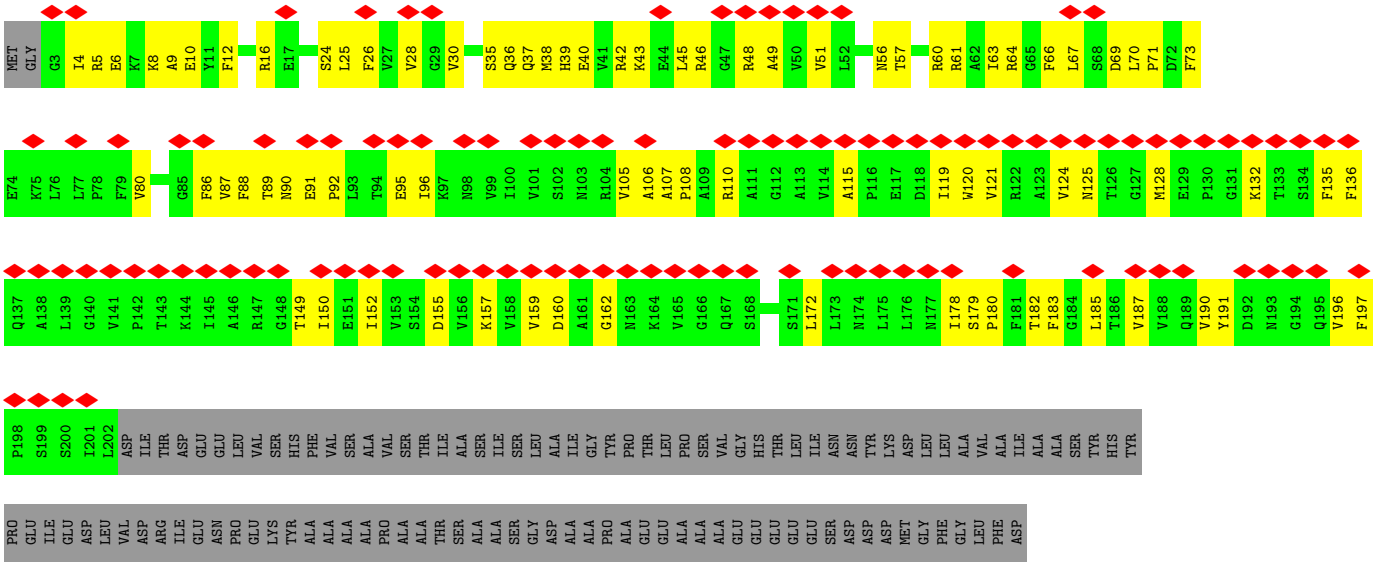
• Molecule 19: 60S ribosomal protein L19-A

Chain D:

• Molecule 20: 60S acidic ribosomal protein P0

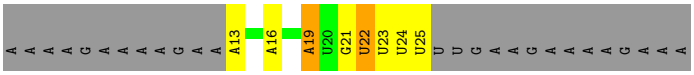
Chain DD:





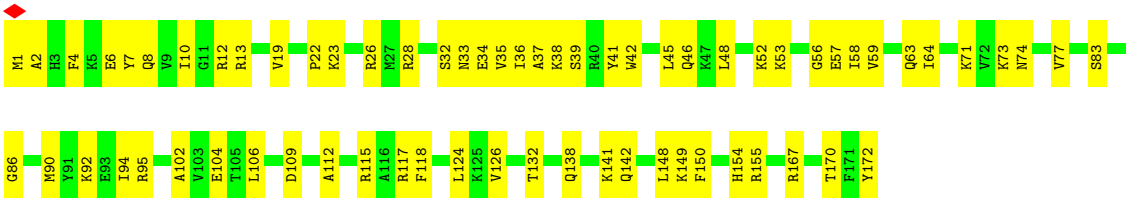
• Molecule 21: Messenger RNA

Chain Dd:



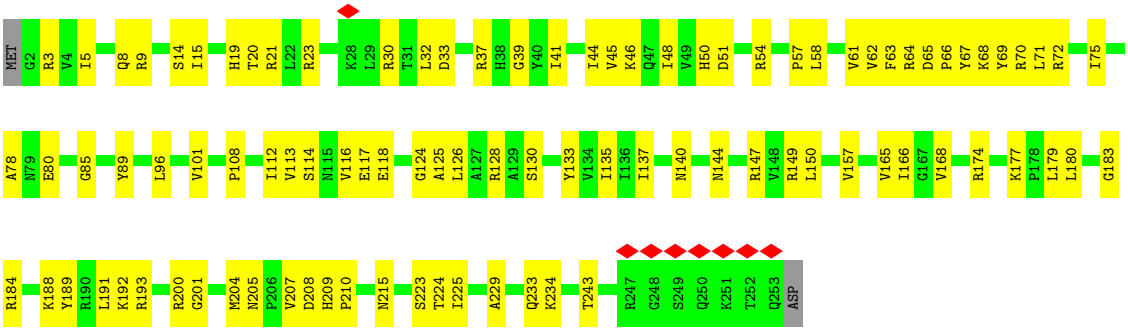
• Molecule 22: 60S ribosomal protein L20-A

Chain E:



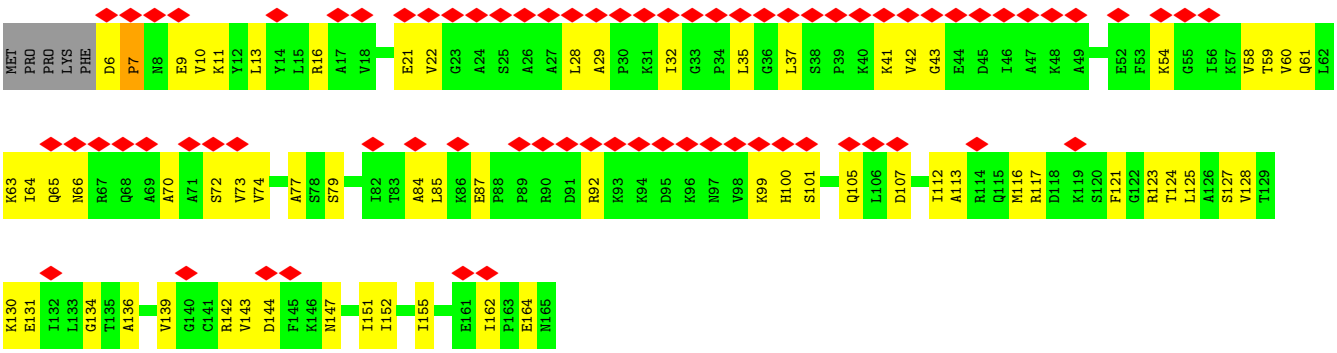
- Molecule 23: 60S ribosomal protein L2-A

Chain EE:



- Molecule 24: 60S ribosomal protein L12-A

Chain Ee:

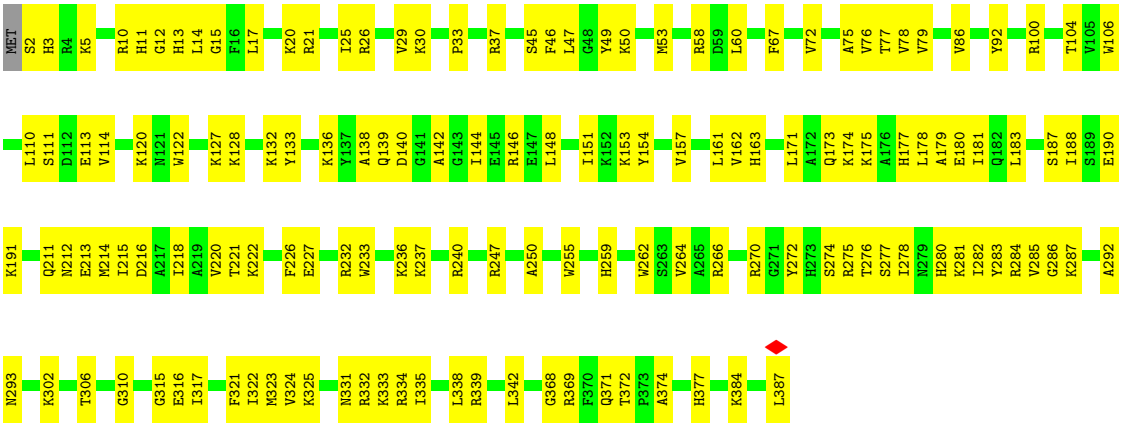


- Molecule 25: 60S ribosomal protein L21-A

Chain F:

- Molecule 26: 60S ribosomal protein L3

Chain FF:

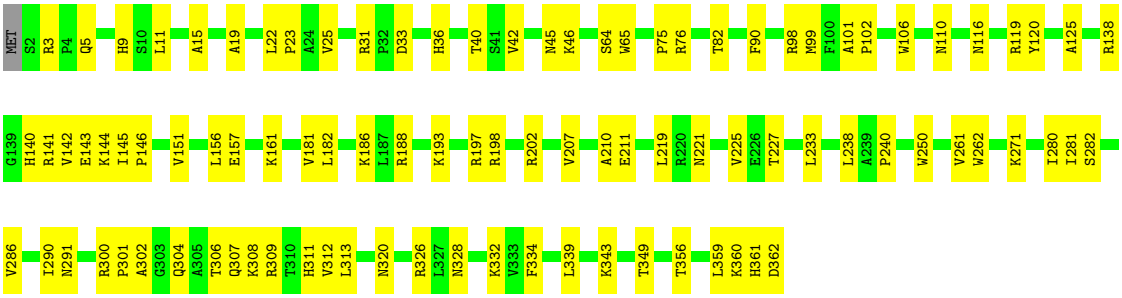


- Molecule 27: 60S ribosomal protein L22-A

Chain G:

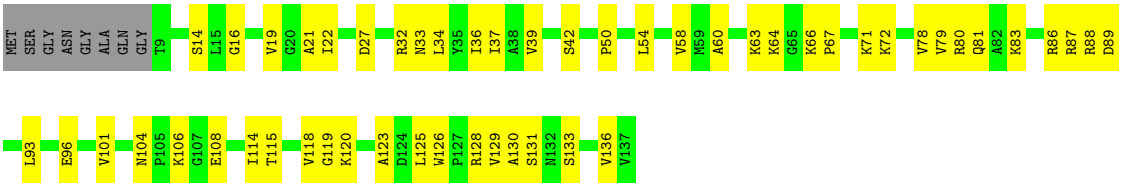
- Molecule 28: 60S ribosomal protein L4-A

Chain GG:



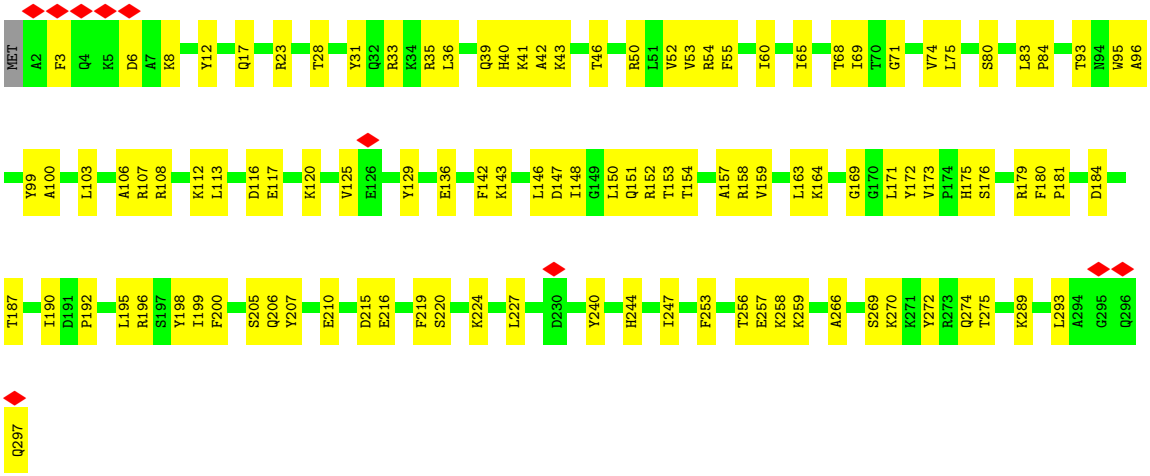
- Molecule 29: 60S ribosomal protein L23-A

Chain H:



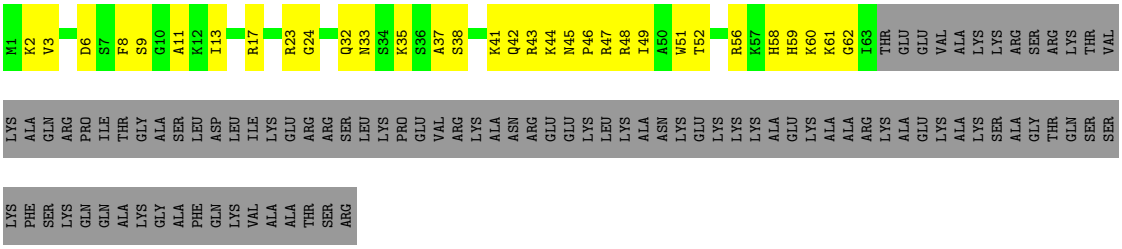
- Molecule 30: 60S ribosomal protein L5

Chain HH:



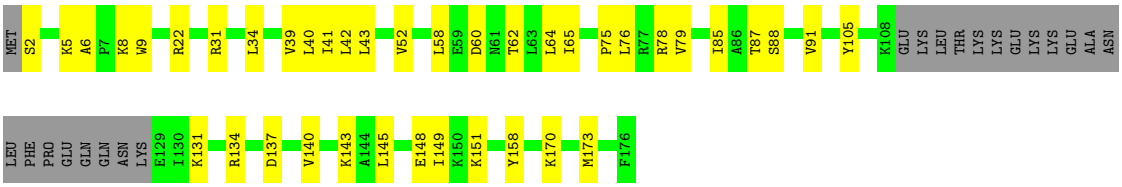
- Molecule 31: 60S ribosomal protein L24-A

Chain I:



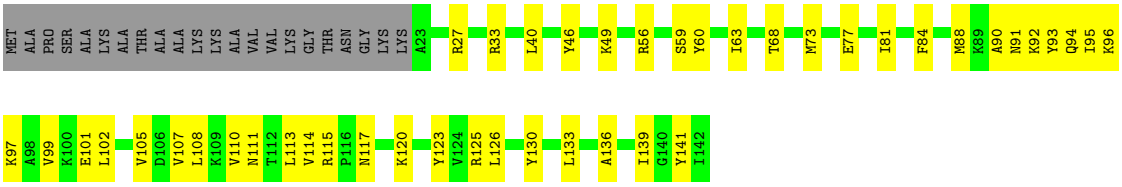
- Molecule 32: 60S ribosomal protein L6-A

Chain II:



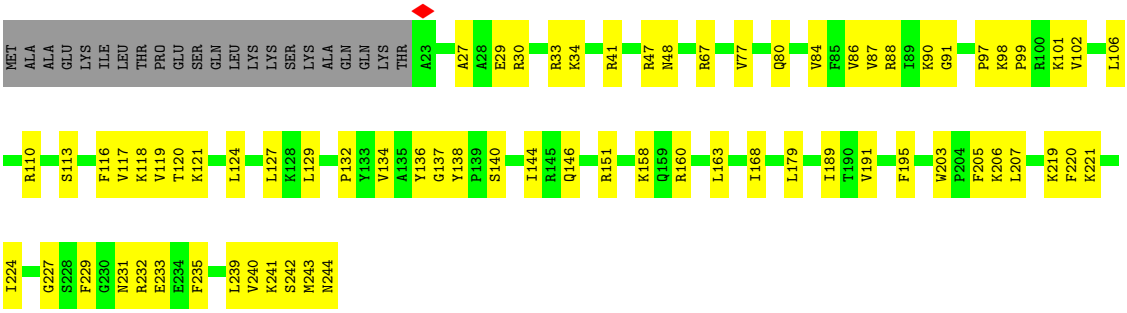
- Molecule 33: 60S ribosomal protein L25

Chain J:



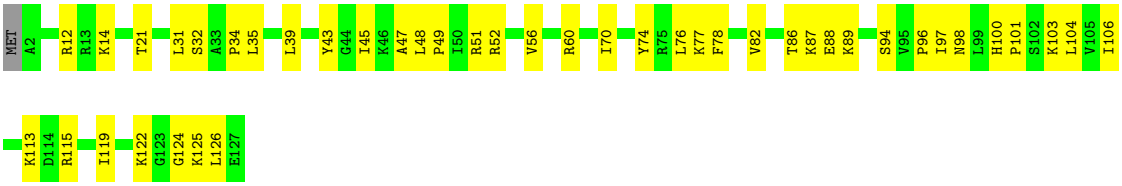
- Molecule 34: 60S ribosomal protein L7-A

Chain JJ:



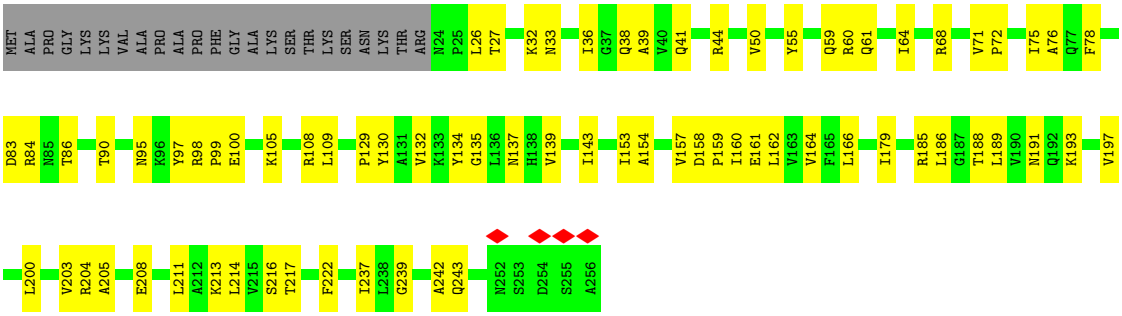
- Molecule 35: 60S ribosomal protein L26-A

Chain K:



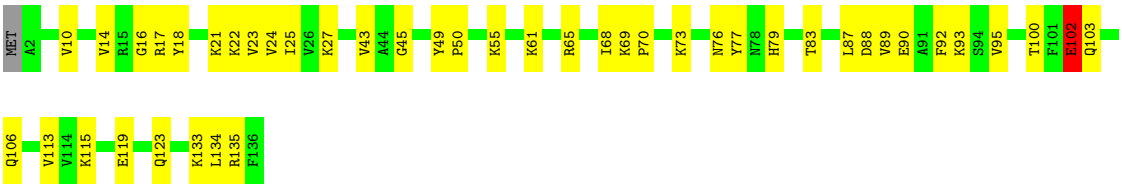
- Molecule 36: 60S ribosomal protein L8-A

Chain KK:



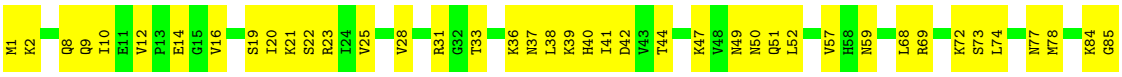
- Molecule 37: 60S ribosomal protein L27-A

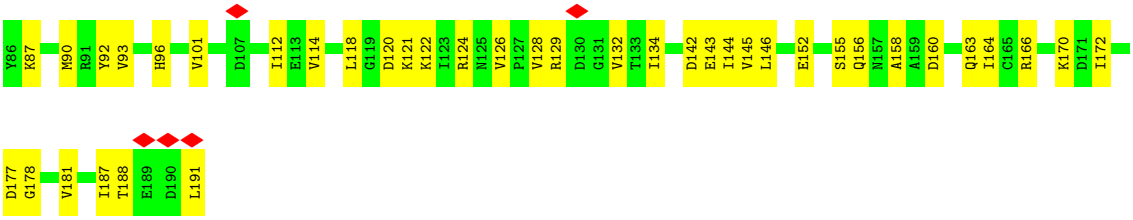
Chain L:



- Molecule 38: 60S ribosomal protein L9-A

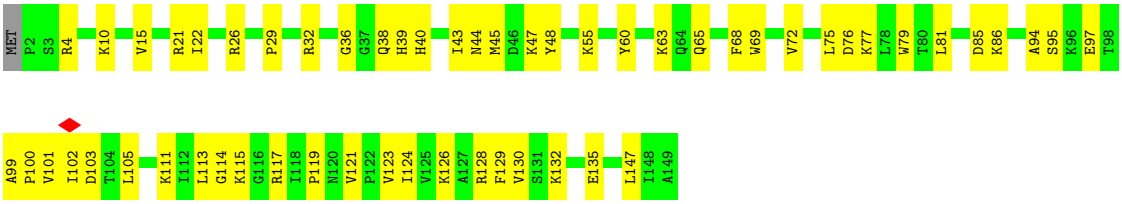
Chain LL:





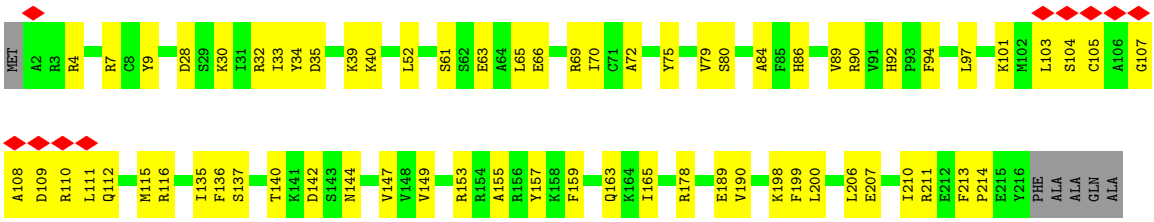
- Molecule 39: 60S ribosomal protein L28

Chain M:



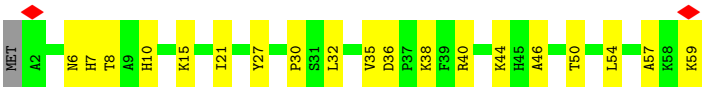
- Molecule 40: 60S ribosomal protein L10

Chain MM:



- Molecule 41: 60S ribosomal protein L29

Chain N:

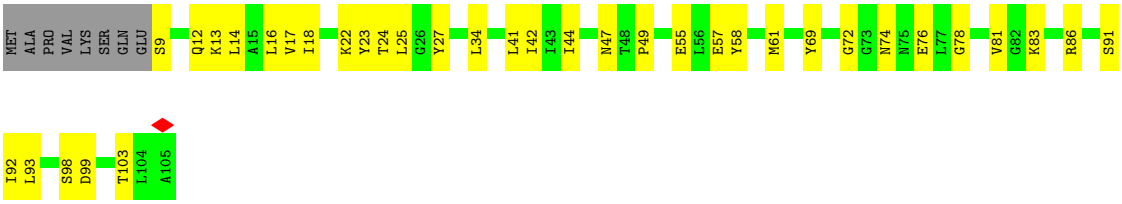


- Molecule 42: 60S ribosomal protein L11-A

Chain NN:

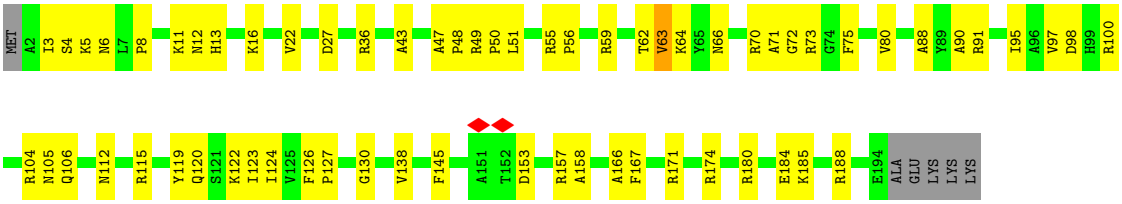
- Molecule 43: 60S ribosomal protein L30

Chain O:



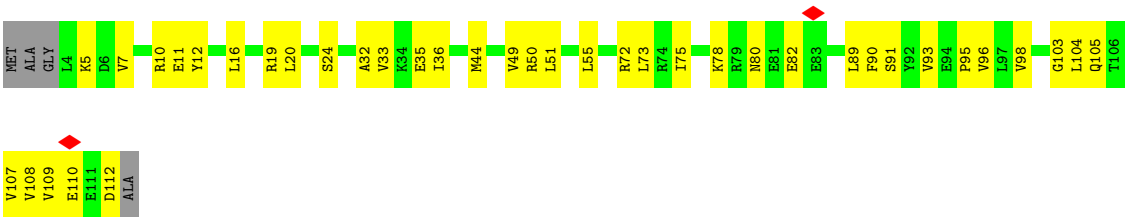
- Molecule 44: 60S ribosomal protein L13-A

Chain OO:



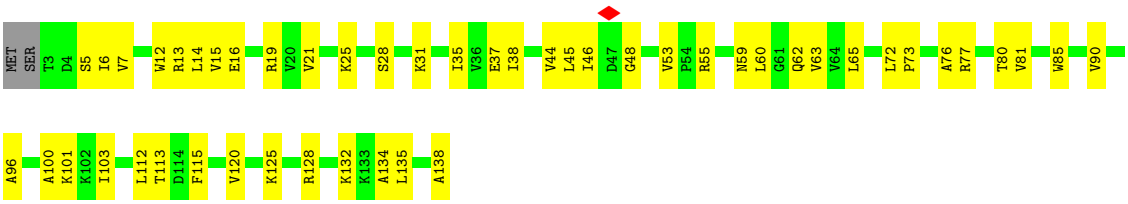
- Molecule 45: 60S ribosomal protein L31-A

Chain P:



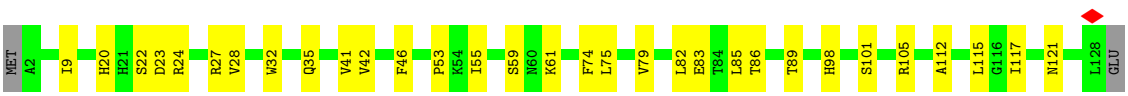
- Molecule 46: 60S ribosomal protein L14-A

Chain PP:



- Molecule 47: 60S ribosomal protein L32

Chain Q:



ALA

- Molecule 48: 60S ribosomal protein L15-A

Chain QQ: 54% 45%

MET G2 K5 Y6 L7 E8 Q11 R12 K13 K14 Q15 S16 L19 R20 Q23 R24 Y25 R26 V27 Y30 R31 Q32 K33 N34 V35 R38 D46 K47 A48 R49 R50 L51 G52 Y53 K56 V60 I61 Y62 R63 V64 R65 V66 R67 R68 G69 N70 R73 P74 V75 P76

K77 K83 Q87 G88 V89 N90 E91 L92 K93 Y94 Q95 R96 S97 L98 R99 A100 T101 A102 E103 E104 R105 V106 G107 R108 R109 L113 R114 V115 L116 N117 S118 Y119 W120 V121 N122 Q123 D124 S125 T126 Y127 K128 Y129 F130 E131 V132 I133 L134 R144 D145 Y148 K157 E160 A161

L164 T165 G168 K169 K170 N181 N182 T183 R187 R188 K189 T190 W191 K192 R193 Q194 N195 T196 L197 R203 K204

- Molecule 49: 60S ribosomal protein L33-A

Chain R: 73% 26%

MET A2 R6 L7 Y8 Y16 Q17 R18 S19 K20 R21 V22 N23 V35 A41 L45 G46 K47 R48 Y53 R54 R65 V71 T72 R73 T74 H75 V80 L89 P90 A91 K92 T93 R99 N106 I107

- Molecule 50: 60S ribosomal protein L34-A

Chain S: 57% 33% 10%

MET A2 Q3 R4 V5 T6 F7 R8 R9 R10 N11 N18 K19 I20 T25 I29 L30 H34 V35 K36 K37 T40 Q52 T56 L57 R58 Q61 T64 S73 R74 S79 R80 C81 A82 V85 K86 E87 R88 I89 I90 R91 A92 F93 L94 I95 E96 K103

K106 E110 ALA ALA ALA LYS LYS SER GLU LYS LYS ALA LYS LYS

- Molecule 51: 60S ribosomal protein L35-A

Chain T: 67% 32%

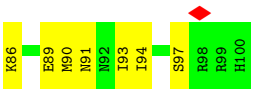
MET A2 R10 Q20 L24 K25 L28 A29 V33 L41 R48 K49 S50 I51 V54 L55 T56 V57 I58 Q61 E64 Y70 K74 Y75 Q76 P77 K78 R81 T85 R86 A87 L88 R89 L92 T93 K94 F95 E96 A97 S98 E102 R105

R114 K115 I118 K119 A120

- Molecule 52: 60S ribosomal protein L36-A

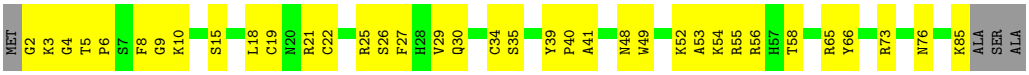
Chain U: 56% 43%

MET T2 V3 K4 T5 G6 I7 L11 N12 K13 G14 M20 K25 I26 K29 K30 S34 N35 R36 T37 L43 E46 I47 L50 S51 E54 R55 R56 L57 I58 D59 L60 I61 R62 N63 S64 G65 E66 R70 K71 V72 R76 F80 T81 R82 A83 K84 A85



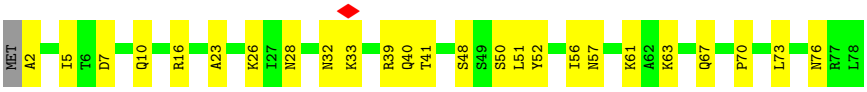
• Molecule 53: 60S ribosomal protein L37-A

Chain V:



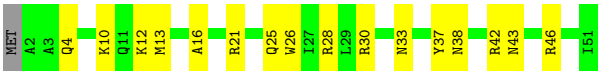
• Molecule 54: 60S ribosomal protein L38

Chain W:



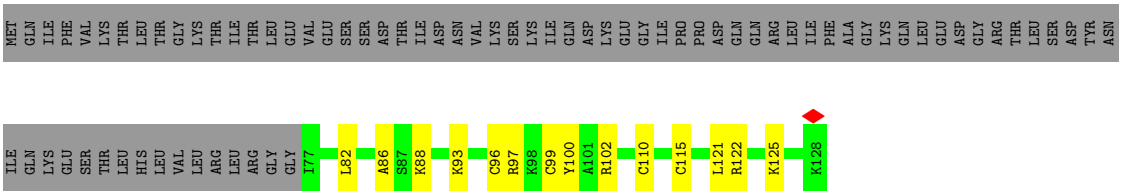
• Molecule 55: 60S ribosomal protein L39

Chain X:



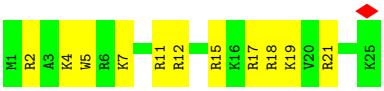
• Molecule 56: Ubiquitin-60S ribosomal protein L40

Chain Y:



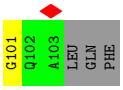
• Molecule 57: RPL41A isoform 1

Chain Z:



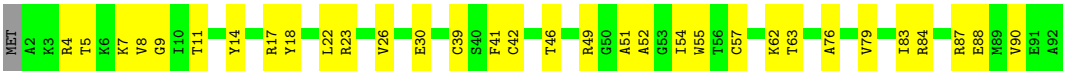
• Molecule 58: 60S ribosomal protein L42-A

Chain a:



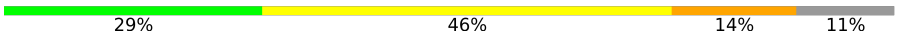
- Molecule 59: 60S ribosomal protein L43-A

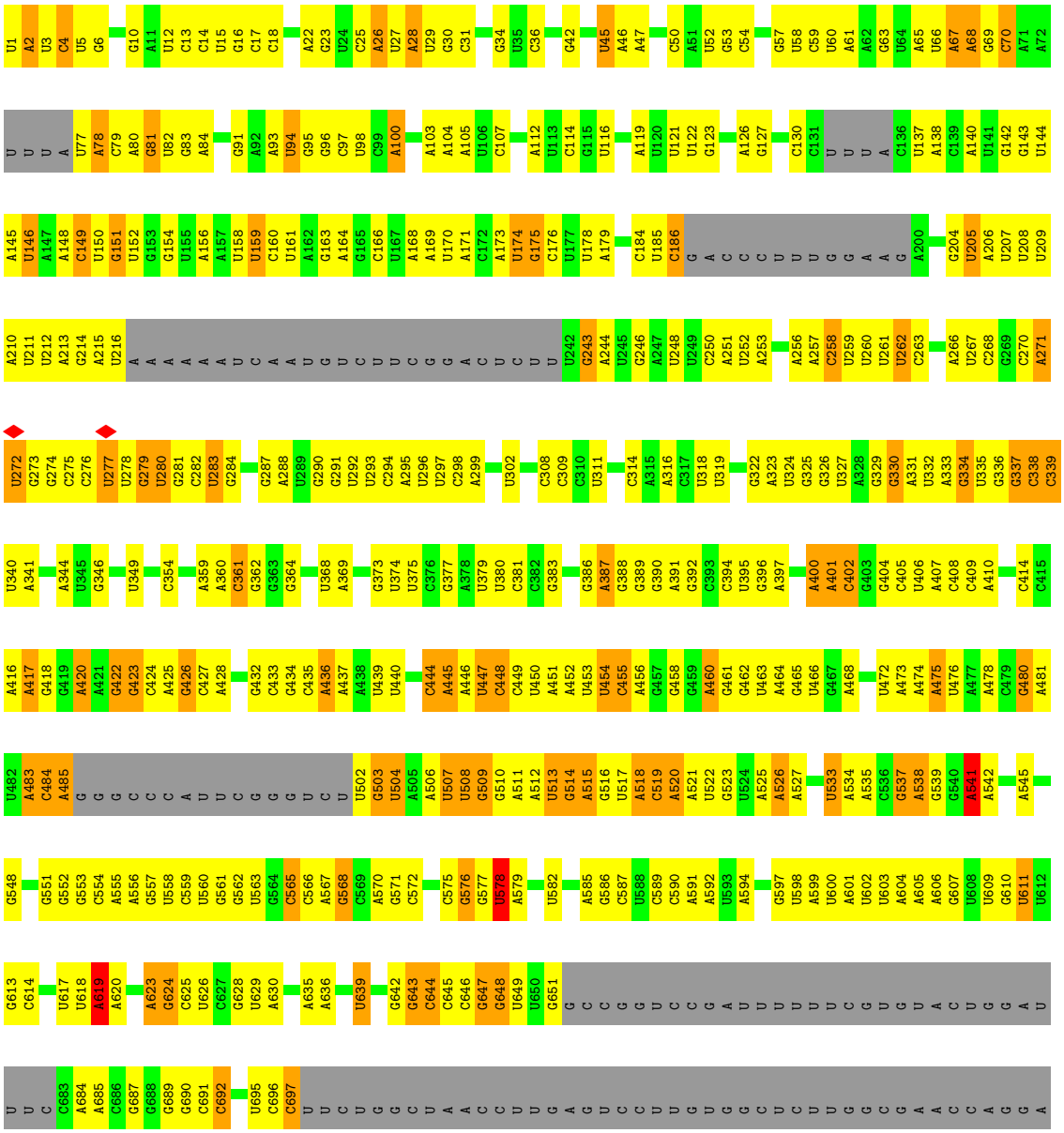
Chain b:



- Molecule 60: 18S ribosomal RNA

Chain c:

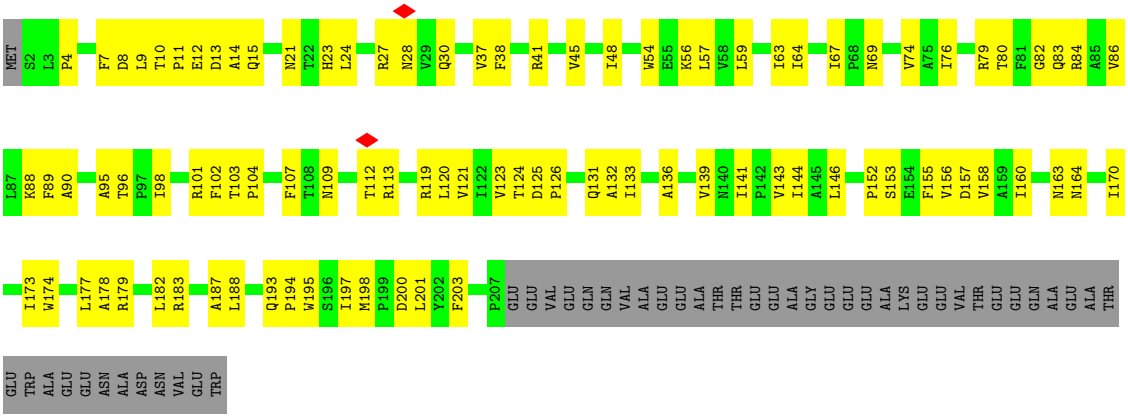




A1722 U1723 U1724 U1725 G1726 G1727
A1730
C1733 U1734 U1735 G1736 G1737 U1738 C1739 A1740 U1741 U1742 U1743
A1746
C1751 U1752
A1755 A1756
G1760 U1761 A1762
A1765 A1766
U1769
C1772 N1773 G1774 U1775 A1776
G1780 A1781 A1782 C1783 C1784 U1785 G1786 C1787 G1788 G1789 A1790 A1791 G1792 G1793 A1794 U1795
U1661 G1662 G1663 C1664 U1665
U1669 G1670 A1671 G1672 G1673 C1674 C1675 U1676 C1677 A1678 G1679 G1680 A1681 U1682 C1683 U1684 G1685 C U U A G A G A A G G G C A C C A U U C U C A U G A G A G C1716 G1717 G1718 A1719 G1720 A1721
C1591 A1592 A1593 G1594 U1595 C1596 A1597
A1600 G1601 C1602 U1603
C1606 G1607 U1608 U1609 G1610 A1611 U1612 U1613 A1614 C1615 G1616 U1617 C1618 C1619 C1620 U1621 G1622 C1623 C1624 C1625 U1626 U1627
A1631 C1632 A1633 C1634 A1635 C1636
C1639 C1640 C1641 G1642
U1647 A1648 G1649 U1650 A1651 C1652 C1653 G1654 A1655 U1656 U1657 G1658
G1531 U1532 C1533 G1534 U1535 G1536 C1537 U1538 G1539 G1540 G1541 G1542 A1543 U1544 A1545 G1546 A1547 G1548 C1549 A1550 U1551 U1552 C1553 G1554 A1555 A1556 U1557 U1558 A1559 U1560 U1561 G1562 C1563 U1564 C1565 U1566 U1567 C1568 A1569 A1570 C1571 G1572 A1573 G1574 G1575 A1576 A1577 U1578 U1579 C1580 C1581 U1582 A1583 G1584 U1585 A1586 A1587 G1588 C1589 G1590
C1467 U1468 A1469 C1470 A1471 C1472 U1473 G1474 A1475 C1476 G1477 G1478 A1479 C1482 A1483 G1484 C1485 G1486 A1487 G1488 U1489 C1490 U1491 A1492 A1493 U1496 U1497 G1498 G1499 C1500 C1501 G1502 A1503 G1504 A1505 U1508 C1509 U1510 U1511 G1512 G1513 U1514 A1515 A1516 U1517 C1518 G1521 U1522 G1523 A1524 A1525 A1526 C1527 U1528 C1529 C1530
G1395 U1396 U1397 U1398 C1399 A1400 A1401 G1402 C1403 C1404 G1405 A1406 U1407 G1408 G1409 A1410 A1411 G1412 U1413 U1414 U1415 G1416 A1425 C1426 A1427 G1428 C1431 G1435 A1436 U1437 C1441 U1442 U1443 A1444 G1445 A1446 C1447 G1448 U1449 U1450 C1451 U1452 G1453 G1454 G1455 C1456 C1457 G1458 C1459 A1460 C1461 G1462 C1463 G1464 C1465 G1466
A1331 C1332 C1333 U1334 U1335 A1336 A1337 C1338 C1339 U1340 A1341 A1344 A1345 A1346 U1347 A1348 G1349 U1350 G1351 G1352 U1353 G1354 C1355 U1356 A1357 G1358 C1359 A1360 U1361 U1362 U1363 G1364 C1365 U1366 G1367 G1368 U1369 U1370 A1371 U1372 C1373 C1374 A1375 C1376 U1377 U1378 A1382 G1383 A1384 G1387 A1388 C1389 U1390 A1391 U1392 C1393 G1394
U1250 U1251 C1252 U1253 U1254 G1255 A1256 U1257 U1258 U1259 U1260 G1261 U1262 G1263 U1269 G1270 G1271 A1275 U1276 C1279 N1280 G1281 C1284 U1285 U1286 G1294 G1297 U1298 G1299 A1300 U1301 U1302 U1303 G1308 C1309 U1314 U1315 G1316 C1317 G1318 A1319 U1320 A1321 A1322 C1323 G1324 A1325 A1326 C1327 G1328 A1329 G1330
A1183 A1184 U1185 U1186 C1190 B8N1191 A1194 C1195 A1196 G1199 G1200 G1201 A1202 A1203 A1204 C1205 U1206 C1207 A1208 C1209 C1210 A1211 G1212 G1213 C1216 A1217 G1218 A1219 C1220 A1221 C1222 A1223 A1224 U1225 A1226 A1227 G1228 G1229 A1230 U1231 C1235 A1236 G1237 A1238 G1241 A1242 G1243 A1244 G1245 C1246 U1247 C1248 U1249
U1106 G1107 G1108 G1109 A1113 A1116 U1117 G1118 G1119 U1120 C1121 A1125 G1126 G1127 A1132 A1133 C1134 U1135 U1136 A1137 A1138 A1142 A1143 U1144 U1145 G1146 A1147 C1148 G1149 G1150 A1151 C1156 A1157 C1158 C1159 A1160 C1161 C1162 A1163 G1164 G1165 A1166 G1169 G1170 A1171 G1172 C1173 C1174 U1175 G1176 C1177 G1178 G1179
U1024 A1025 A1026 A1027 C1028 U1029 A1030 U1031 G1032 A1039 G1040 G1041 G1042 A1043 G1047 G1048 U1052 G1053 U1054 U1058 U1059 U1060 A1061 G1064 A1065 C1066 C1067 C1068 A1069 C1072 G1073 C1077 C1078 U1079 U1080 A1081 C1082 C1090 A1091 A1092 A1093 G1094 U1095 C1096 U1097 U1098 U1099 G1100 G1101 G1102 U1103
A941 G942 C943 A944 U945 U946 U947 G948 C949 C950 A951 A952 G953 G954 A955 C956 G957 U958 U959 U960 U961 C962 A963 A966 A967 U968 A971 G972 A973 A974 G980 G987 A988 U989 C990 G991 A992 A993 U996 G997 A998 U999 C1000 A1001 G1002 A1003 U1004 A1005 C1006 C1007 C1010 G1011 U1012
C870 G871 G872 U873 C874 G875 G876 G877 G878 G879 U882 C883 A884 G885 U886 A887 U888 U889 C890 A891 U894 G895 U896 C897 A898 G899 A900 G901 G902 U903 A906 U912 G913 G914 A915 U918 A919 U920 U921 G922 A923 A924 G925 A926 C927 U928 A929 U932 A933 C934 U935 A939 A940
G810 A811 A812 U813 A814 G815 G816 A817 C818 G819 U820 U821 U822 G G G U U U C U A U U U U G U U U G G U U U C U A G G A C C A850 U851 C852 G853 U854 A855 A856 U857 G858 A859 U860 U861 A862 A863 U864 A865 G866 G867 G868 A869
C U U743 U744 U745 U749 U750 G751 A752 A753 U759 A760 G761 A762 G763 U764 G765 U766 U767 C768 A769 A770 A771 G772 C773 A774 G775 G776 C777 G778 U779 A780 U781 U782 G783 C784 U785 C786 G787 A788 A789 U790 A791 U792 A793 U794 U795 A796 A799 U800 G801 A804 U805 U808 A809

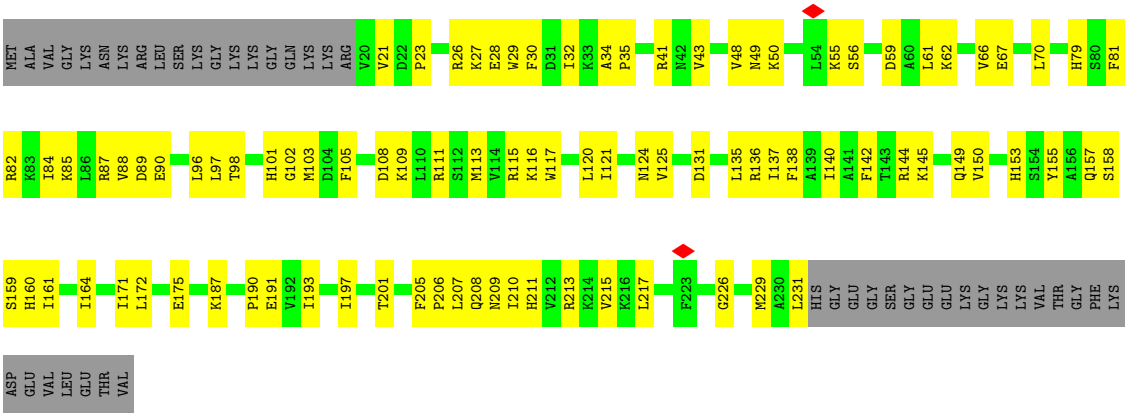
• Molecule 61: 40S ribosomal protein S0-A

Chain d:



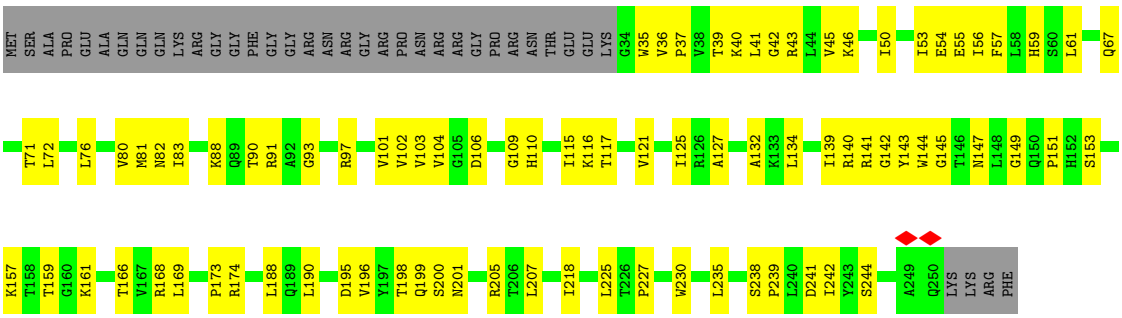
• Molecule 62: 40S ribosomal protein S1-A

Chain e:



• Molecule 63: 40S ribosomal protein S2

Chain f:



- Molecule 64: RPS3 isoform 1

Chain g: 51% 35% 14%

MET VAL ALA LEU I5 S6 K7 K8 R9 K10 L11 V12 V16 L21 N22 E23 F24 F25 T26 R27 E28 L29 E32 G33 Y34 V37 E38 V39 R40 V41 K45 T46 E47 V48 I49 I50 R51 A52 V58 R65 I66 N67 E68 L69 T70 L71 L72 R76 F77 K78 Y79 A80

T83 I84 V85 L86 E89 R90 V91 Q92 D93 R94 G95 A98 Q101 M105 K106 I115 V122 Y125 G133 V136 G140 K141 L142 R143 A144 A147 M150 K151 F152 G155 F156 L157 S160 G161 Q162 P163 V164 N165 I168 D169 R173 H174 V175

L182 K185 M189 S195 R196 T197 P203 D204 I208 I209 E210 PRO LYS GLU GLU GLU PRO ILE LEU ALA PRO SER VAL LYS ASP TYR ARG PRO ALA GLU GLU THR GLU ALA GLN ALA GLU PRO VAL GLU ALA

- Molecule 65: 40S ribosomal protein S4-A

Chain h: 49% 50%

MET A2 R3 K7 H8 L9 K10 R11 W18 L19 L20 Y27 A28 P29 R30 P31 P35 H36 K37 E40 S41 L42 P43 L44 I45 V46 R49 N50 R51 L56 N57 G58 R59 E60 V61 K62 A63 I64 L65 M66 Q67 R68 H69 V70 D73 V76 R77 T78 D79 Y82

P83 F86 M87 D88 L92 D93 A94 T95 N96 R100 L101 D104 V105 K106 G107 R108 F109 A110 V111 H112 R113 I114 T115 D116 E117 E118 A119 S120 Y121 K122 L123 G124 K125 V126 V129 K133 V136 V139 V140 T141 H142 D143 G144 R145 T146 I147 R148 Y149 P150 I154 K155

D158 K161 I162 D163 L164 I169 T170 D171 F172 I173 K174 F175 D176 A177 G178 K179 L180 V183 R187 R191 I192 I195 E199 R200 H201 D202 G203 H209 I210 K211 D215 N216 T217 F218 V219 L222 V225 F226 V227 I228 G229 E230 Q231 G232 K233 S237 L238

P239 K240 G241 K242 K245 I248 E251 R252 D253 R254 R255 Q259 GLY LEU

- Molecule 66: 40S ribosomal protein S5

Chain i: 40% 48% 12%

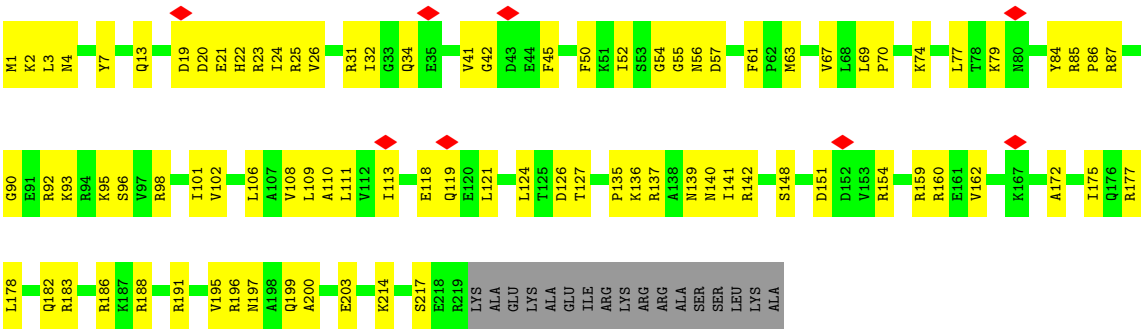
MET SER ASP THR GLU ALA PRO VAL GLU VAL GLN GLU ASP PHE GLU VAL VAL GLU GLU F20 T21 P22 V23 V24 L25 E31 E32 V33 Q34 Q35 A36 Q37 T38 E39 I40 K41 L42 F43 N44 K45 W46 S47 E50 K54 S57 L58 V61 V62 Q63 V64 R65 Q66 P67 I68 F69

V70 A71 H72 T73 A74 G75 R76 N79 K80 R81 F82 P88 I89 R92 L93 T94 N95 S96 L97 M98 M99 R102 N103 N104 K107 L108 K109 A110 V111 R112 I113 I114 K115 H116 T117 I120 I121 N122 V123 L124 T125 D126 Q127 N128 P129 I130 Q131 V134 D135 A136 I137 T138

T147 R148 V149 GLY GLY GLY GLY ALA ALA ARG R157 D161 V162 S163 P164 L165 R166 R167 V168 N169 Q170 A171 I172 A173 L174 R180 I187 K188 T189 I190 A191 E192 T193 L194 A195 E196 E197 L198 I199 N200 A201 A202 K203 Y209 A210 I211 K212 K213 K214 D215 E216 L217 V220 A221 K222

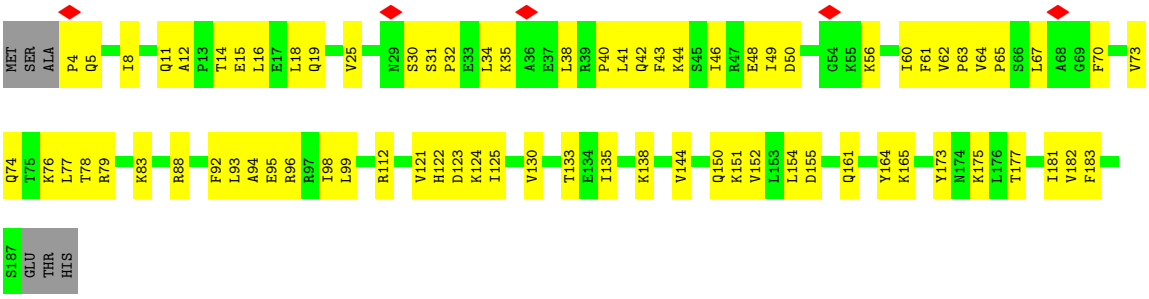
R225

Chain j: 56% 37% 7%



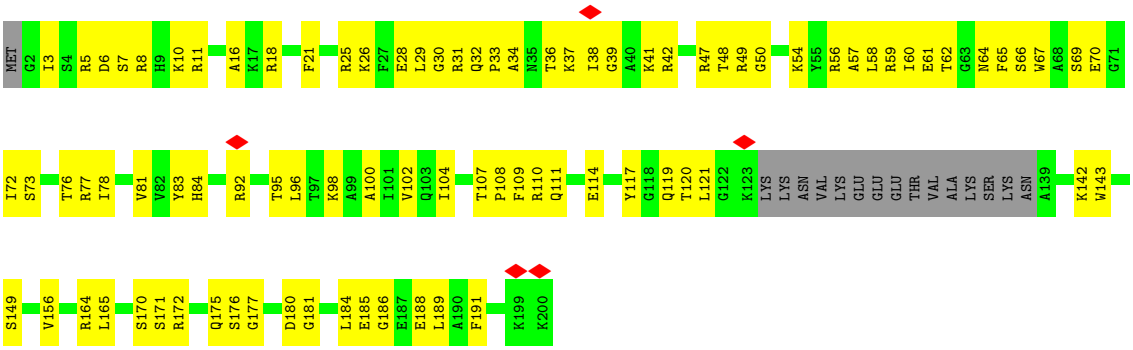
- Molecule 68: 40S ribosomal protein S7-A

Chain k: 57% 39%



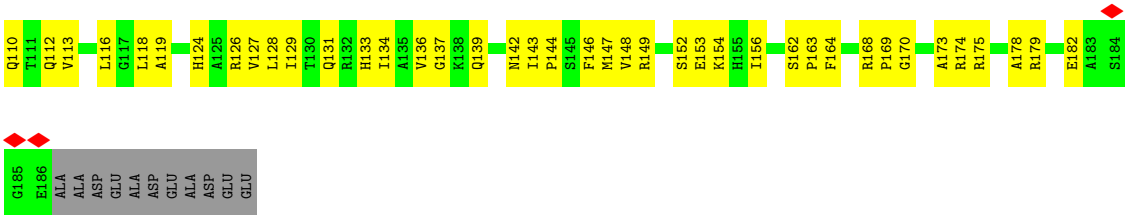
- Molecule 69: 40S ribosomal protein S8-A

Chain l: 48% 44% 8%



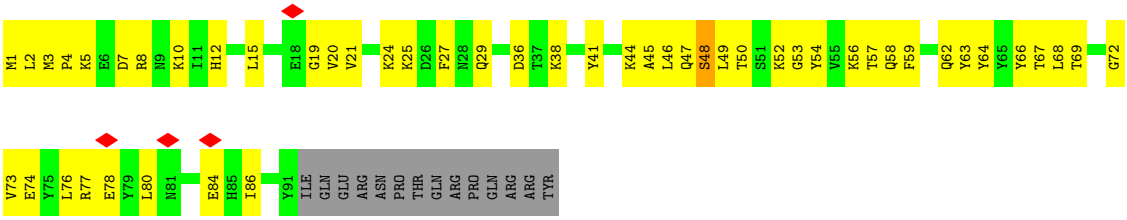
- Molecule 70: 40S ribosomal protein S9-A

Chain m: 54% 40% 6%



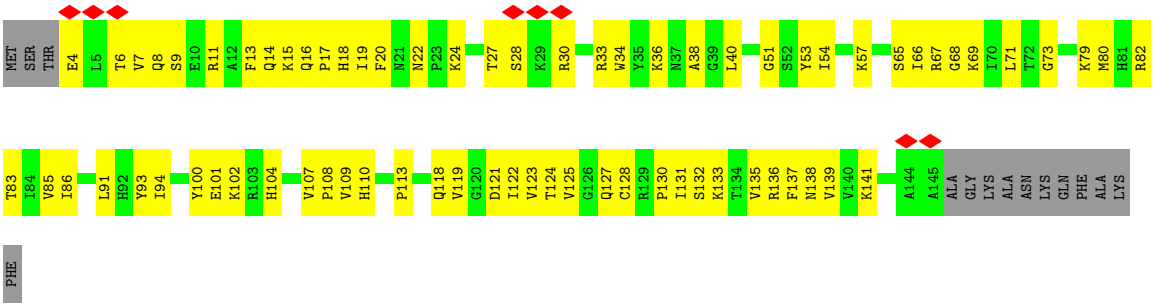
• Molecule 71: 40S ribosomal protein S10-A

Chain n:



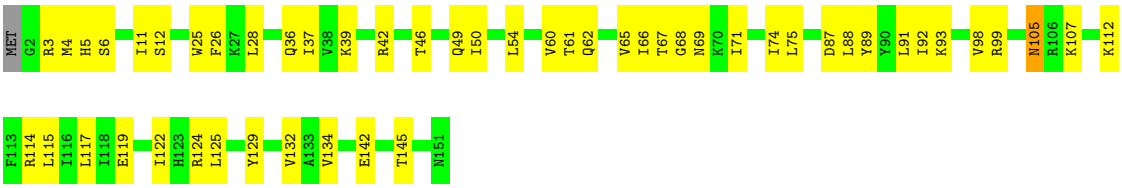
• Molecule 72: 40S ribosomal protein S11-A

Chain o:



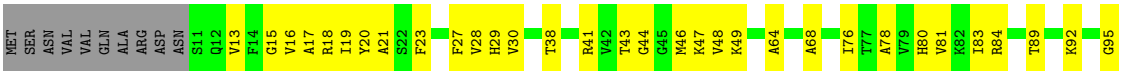
• Molecule 73: 40S ribosomal protein S13

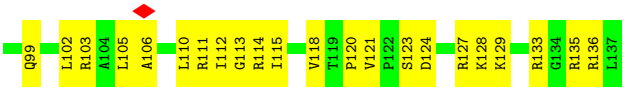
Chain p:



• Molecule 74: 40S ribosomal protein S14-A

Chain q:



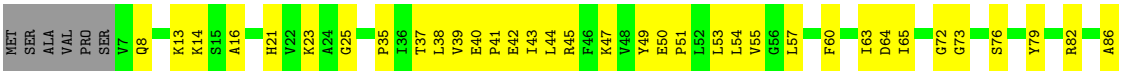


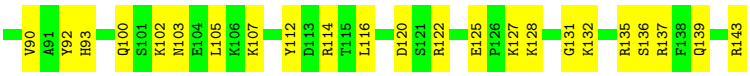
• Molecule 75: 40S ribosomal protein S15

Chain r:

• Molecule 76: 40S ribosomal protein S16-A

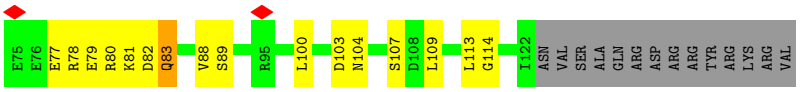
Chain s:





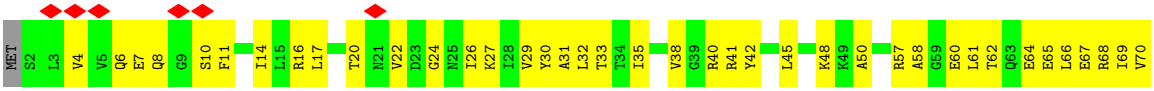
• Molecule 77: 40S ribosomal protein S17-A

Chain t:



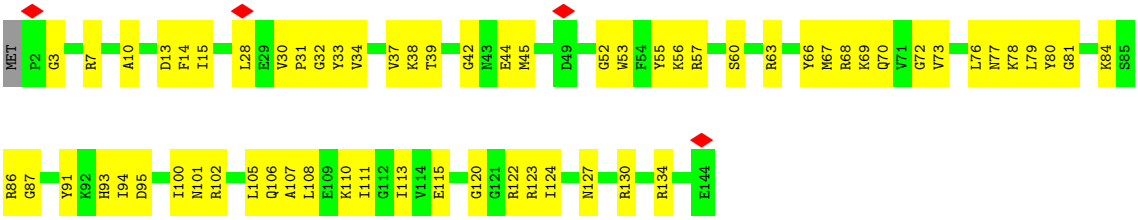
• Molecule 78: 40S ribosomal protein S18-A

Chain u:



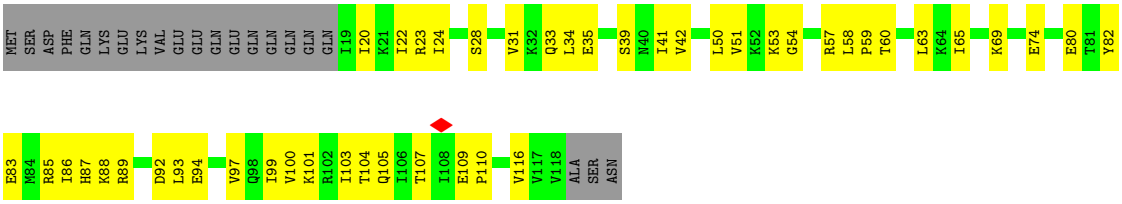
• Molecule 79: 40S ribosomal protein S19-A

Chain v:



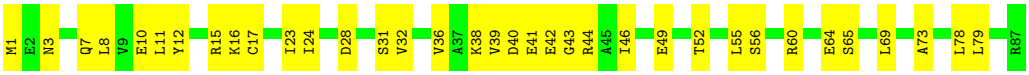
- Molecule 80: 40S ribosomal protein S20

Chain w:



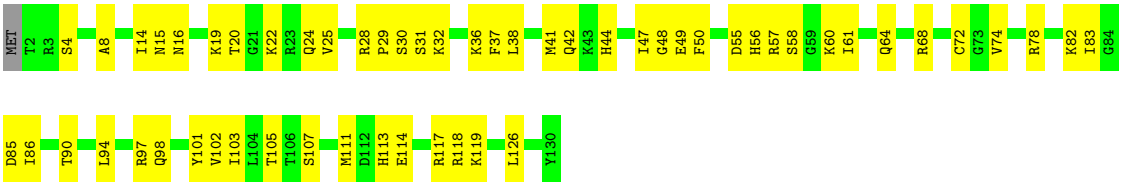
- Molecule 81: 40S ribosomal protein S21-A

Chain x:



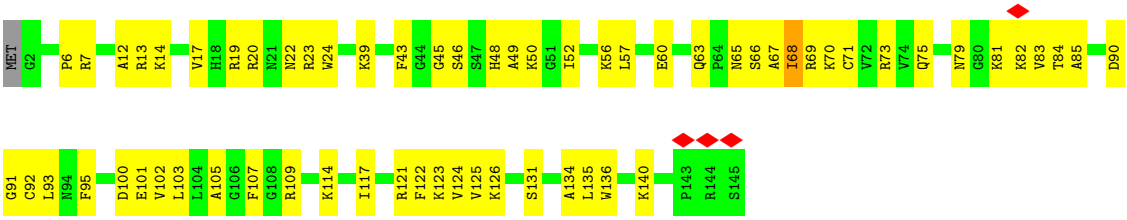
- Molecule 82: 40S ribosomal protein S22-A

Chain y:



- Molecule 83: 40S ribosomal protein S23-A

Chain z:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	22551	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 ($e^-/Å^2$)	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	1.734	Depositor
Minimum map value	-0.933	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.050	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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, G7M, MA6, OMU, 5MC, OMG, YYG, SPD, 4AC, UR3, ZN, 1MA, MG, A2M, OMC, DDE, K, B8N

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	0.19	0/1087	0.45	0/1449
2	1	0.22	0/571	0.62	0/768
3	2	0.25	0/782	0.43	0/1047
4	3	0.23	0/620	0.42	0/838
5	4	0.24	0/499	0.53	1/670 (0.1%)
6	5	0.21	0/452	0.42	0/600
7	6	0.20	0/433	0.47	0/575
8	7	0.21	0/2489	0.51	0/3389
9	8	0.15	0/279	0.50	0/369
10	A	0.30	0/1585	0.42	0/2128
11	AA	0.28	1/75384 (0.0%)	0.33	2/117530 (0.0%)
12	Aa	0.18	0/6673	0.42	0/9032
13	B	0.30	0/1245	0.42	0/1676
14	BB	0.23	0/2883	0.28	0/4491
15	Bb	0.17	0/1788	0.38	0/2786
16	C	0.26	0/1465	0.40	0/1965
17	CC	0.27	0/3746	0.36	2/5832 (0.0%)
18	Cc	0.20	0/1836	0.49	4/2859 (0.1%)
19	D	0.26	0/1440	0.49	0/1921
20	DD	0.15	0/1578	0.40	0/2134
21	Dd	0.25	0/311	0.42	0/482
22	E	0.29	0/1481	0.52	0/1990
23	EE	0.28	0/1948	0.40	0/2617
24	Ee	0.16	0/1226	0.38	0/1650
25	F	0.27	0/1300	0.45	0/1743
26	FF	0.27	0/3146	0.43	0/4228
27	G	0.21	0/786	0.40	0/1065
28	GG	0.26	0/2800	0.39	0/3790
29	H	0.27	0/978	0.42	0/1316
30	HH	0.20	0/2425	0.38	0/3271
31	I	0.29	0/533	0.49	0/707

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	II	0.25	0/1251	0.39	0/1682
33	J	0.27	0/974	0.44	0/1314
34	JJ	0.29	0/1821	0.37	0/2451
35	K	0.25	0/1004	0.45	0/1341
36	KK	0.22	0/1836	0.37	0/2481
37	L	0.24	0/1118	0.41	0/1497
38	LL	0.27	0/1539	0.47	0/2073
39	M	0.27	0/1204	0.44	0/1612
40	MM	0.26	0/1779	0.46	0/2386
41	N	0.23	0/473	0.44	0/629
42	NN	0.23	0/1374	0.45	0/1842
43	O	0.24	0/750	0.37	0/1008
44	OO	0.23	0/1568	0.41	0/2106
45	P	0.26	0/897	0.47	0/1205
46	PP	0.25	0/1068	0.37	0/1438
47	Q	0.27	0/1041	0.38	0/1394
48	QQ	0.28	0/1757	0.43	0/2354
49	R	0.32	0/868	0.38	0/1168
50	S	0.28	0/871	0.48	0/1164
51	T	0.25	0/978	0.45	0/1301
52	U	0.23	0/778	0.48	0/1034
53	V	0.26	0/680	0.41	0/901
54	W	0.24	0/618	0.48	0/826
55	X	0.27	0/443	0.45	0/588
56	Y	0.24	0/423	0.39	0/562
57	Z	0.25	0/234	0.52	0/300
58	a	0.25	0/831	0.49	0/1097
59	b	0.23	0/701	0.41	0/934
60	c	0.43	10/37665 (0.0%)	0.37	12/58663 (0.0%)
61	d	0.23	0/1623	0.47	0/2222
62	e	0.26	0/1714	0.46	0/2308
63	f	0.26	0/1665	0.49	0/2263
64	g	0.21	0/1622	0.42	0/2180
65	h	0.21	0/2097	0.45	0/2823
66	i	0.24	0/1591	0.52	0/2151
67	j	0.20	0/1790	0.48	0/2393
68	k	0.23	0/1506	0.49	0/2028
69	l	0.24	0/1482	0.50	0/1980
70	m	0.22	0/1519	0.43	0/2035
71	n	0.23	0/792	0.52	0/1071
72	o	0.22	0/1172	0.43	0/1580
73	p	0.28	0/1215	0.41	0/1638
74	q	0.27	0/901	0.51	0/1217

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
75	r	0.23	0/853	0.45	0/1145
76	s	0.23	0/1099	0.54	0/1473
77	t	0.23	0/971	0.60	0/1303
78	u	0.24	0/1211	0.53	0/1628
79	v	0.20	0/1130	0.46	0/1517
80	w	0.24	0/810	0.53	0/1095
81	x	0.25	0/693	0.50	0/935
82	y	0.26	0/1038	0.46	0/1395
83	z	0.24	0/1139	0.53	0/1518
All	All	0.29	11/219946 (0.0%)	0.39	21/322167 (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
24	Ee	0	1
34	JJ	0	1
37	L	0	1
66	i	0	2
73	p	0	1
76	s	0	1
77	t	0	1
78	u	0	1
83	z	0	1
All	All	0	10

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	c	483	A	C1'-N9	37.73	2.04	1.48
60	c	507	U	C2-N3	23.93	1.85	1.37
60	c	507	U	N3-C4	23.42	1.85	1.38
60	c	507	U	N1-C2	22.82	1.84	1.38
60	c	507	U	C4-C5	21.74	1.87	1.43

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
60	c	483	A	C8-N9-C4	-12.74	67.58	105.80
60	c	483	A	N9-C1'-C2'	12.61	130.91	112.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
60	c	483	A	N7-C8-N9	11.43	148.09	113.80
60	c	780	A	OP2-P-O3'	-9.59	79.23	108.00
17	CC	79	A	OP1-P-O3'	-9.32	80.03	108.00

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
24	Ee	7	PRO	Peptide
34	JJ	232	ARG	Peptide
37	L	102	GLU	Peptide
66	i	220	VAL	Peptide
66	i	65	ARG	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	0	1073	0	1132	55	0
2	1	563	0	603	38	0
3	2	769	0	814	33	0
4	3	610	0	633	26	0
5	4	497	0	535	16	0
6	5	442	0	429	20	0
7	6	427	0	476	20	0
8	7	2436	0	2386	127	0
9	8	276	0	287	4	0
10	A	1555	0	1659	60	0
11	AA	68285	0	34372	1680	0
12	Aa	6569	0	6640	331	0
13	B	1222	0	1231	64	0
14	BB	2579	0	1303	60	0
15	Bb	1638	0	836	56	0
16	C	1441	0	1543	50	0
17	CC	3353	0	1695	92	0
18	Cc	1644	0	837	57	0
19	D	1423	0	1510	72	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	DD	1551	0	1596	62	0
21	Dd	278	0	138	11	0
22	E	1445	0	1487	64	0
23	EE	1914	0	1981	88	0
24	Ee	1211	0	1268	58	0
25	F	1276	0	1323	47	0
26	FF	3075	0	3142	128	0
27	G	770	0	780	22	0
28	GG	2748	0	2859	84	0
29	H	963	0	1014	48	0
30	HH	2375	0	2325	95	0
31	I	521	0	551	32	0
32	II	1230	0	1320	30	0
33	J	959	0	1023	50	0
34	JJ	1784	0	1862	65	0
35	K	993	0	1081	37	0
36	KK	1804	0	1877	64	0
37	L	1092	0	1155	37	0
38	LL	1518	0	1587	82	0
39	M	1173	0	1215	61	0
40	MM	1743	0	1785	54	0
41	N	462	0	491	16	0
42	NN	1353	0	1383	82	0
43	O	742	0	797	23	0
44	OO	1543	0	1608	61	0
45	P	883	0	918	35	0
46	PP	1053	0	1149	44	0
47	Q	1020	0	1090	25	0
48	QQ	1720	0	1779	90	0
49	R	850	0	880	22	0
50	S	861	0	918	52	0
51	T	969	0	1078	37	0
52	U	771	0	849	41	0
53	V	665	0	668	29	0
54	W	612	0	682	17	0
55	X	436	0	475	17	0
56	Y	417	0	455	15	0
57	Z	233	0	282	15	0
58	a	819	0	886	38	0
59	b	694	0	734	30	0
60	c	34236	0	17248	1233	0
61	d	1583	0	1578	79	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	e	1689	0	1763	82	0
63	f	1635	0	1723	77	0
64	g	1601	0	1682	73	0
65	h	2056	0	2140	119	0
66	i	1572	0	1639	112	0
67	j	1766	0	1859	87	0
68	k	1481	0	1572	61	0
69	l	1457	0	1488	88	0
70	m	1494	0	1573	72	0
71	n	772	0	760	44	0
72	o	1146	0	1213	70	0
73	p	1192	0	1255	42	0
74	q	891	0	883	55	0
75	r	837	0	868	33	0
76	s	1080	0	1140	57	0
77	t	961	0	999	73	0
78	u	1192	0	1222	70	0
79	v	1112	0	1124	69	0
80	w	800	0	869	44	0
81	x	684	0	672	38	0
82	y	1021	0	1060	48	0
83	z	1121	0	1196	60	0
84	2	1	0	0	0	0
84	5	1	0	0	0	0
84	8	1	0	0	0	0
84	S	1	0	0	0	0
84	V	1	0	0	0	0
84	Y	1	0	0	0	0
84	a	1	0	0	0	0
84	b	1	0	0	0	0
85	AA	157	0	0	0	0
85	Aa	1	0	0	0	0
85	B	1	0	0	0	0
85	BB	3	0	0	0	0
85	Bb	1	0	0	0	0
85	CC	2	0	0	0	0
85	D	1	0	0	0	0
85	EE	1	0	0	0	0
85	F	1	0	0	0	0
85	FF	1	0	0	0	0
85	H	1	0	0	0	0
85	c	35	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	AA	10	0	0	0	0
86	BB	1	0	0	0	0
86	Dd	1	0	0	0	0
86	EE	1	0	0	0	0
86	MM	1	0	0	0	0
86	Q	1	0	0	0	0
86	c	1	0	0	0	0
87	AA	20	0	38	1	0
87	c	10	0	19	1	0
88	Aa	32	0	12	7	0
89	2	1	0	0	0	0
89	AA	258	0	0	5	0
89	Aa	1	0	0	0	0
89	B	2	0	0	0	0
89	BB	4	0	0	1	0
89	CC	3	0	0	0	0
89	Cc	1	0	0	0	0
89	F	4	0	0	0	0
89	FF	3	0	0	0	0
89	GG	1	0	0	0	0
89	M	1	0	0	0	0
89	Q	2	0	0	0	0
89	QQ	1	0	0	1	0
89	S	1	0	0	0	0
89	V	2	0	0	0	0
89	a	1	0	0	0	0
89	c	53	0	0	1	0
89	p	1	0	0	0	0
89	q	2	0	0	0	0
All	All	207340	0	155007	6390	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 18.

The worst 5 of 6390 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)
60:c:507:U:C5	60:c:507:U:C4	1.87	1.60
60:c:507:U:N1	60:c:507:U:C6	1.77	1.51
60:c:507:U:N1	60:c:507:U:C2	1.84	1.44
60:c:507:U:C4	60:c:507:U:N3	1.85	1.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:c:507:U:C2	60:c:507:U:N3	1.85	1.42

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%)	130 (98%)	2 (2%)	0	100	100
2	1	68/108 (63%)	65 (96%)	3 (4%)	0	100	100
3	2	95/119 (80%)	90 (95%)	5 (5%)	0	100	100
4	3	79/82 (96%)	74 (94%)	5 (6%)	0	100	100
5	4	61/67 (91%)	60 (98%)	1 (2%)	0	100	100
6	5	51/56 (91%)	51 (100%)	0	0	100	100
7	6	51/63 (81%)	48 (94%)	3 (6%)	0	100	100
8	7	316/319 (99%)	301 (95%)	15 (5%)	0	100	100
9	8	32/152 (21%)	26 (81%)	6 (19%)	0	100	100
10	A	195/199 (98%)	193 (99%)	2 (1%)	0	100	100
12	Aa	839/842 (100%)	808 (96%)	31 (4%)	0	100	100
13	B	152/184 (83%)	150 (99%)	2 (1%)	0	100	100
16	C	183/186 (98%)	182 (100%)	1 (0%)	0	100	100
19	D	174/189 (92%)	170 (98%)	4 (2%)	0	100	100
20	DD	198/312 (64%)	193 (98%)	5 (2%)	0	100	100
22	E	170/172 (99%)	163 (96%)	7 (4%)	0	100	100
23	EE	250/254 (98%)	246 (98%)	4 (2%)	0	100	100
24	Ee	158/165 (96%)	155 (98%)	3 (2%)	0	100	100
25	F	157/160 (98%)	153 (98%)	4 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	FF	384/387 (99%)	375 (98%)	9 (2%)	0	100	100
27	G	95/121 (78%)	95 (100%)	0	0	100	100
28	GG	359/362 (99%)	350 (98%)	9 (2%)	0	100	100
29	H	127/137 (93%)	126 (99%)	1 (1%)	0	100	100
30	HH	294/297 (99%)	288 (98%)	6 (2%)	0	100	100
31	I	61/155 (39%)	61 (100%)	0	0	100	100
32	II	151/176 (86%)	149 (99%)	2 (1%)	0	100	100
33	J	118/142 (83%)	115 (98%)	3 (2%)	0	100	100
34	JJ	220/244 (90%)	219 (100%)	1 (0%)	0	100	100
35	K	124/127 (98%)	121 (98%)	3 (2%)	0	100	100
36	KK	231/256 (90%)	226 (98%)	5 (2%)	0	100	100
37	L	133/136 (98%)	128 (96%)	4 (3%)	1 (1%)	16	45
38	LL	189/191 (99%)	181 (96%)	8 (4%)	0	100	100
39	M	146/149 (98%)	142 (97%)	4 (3%)	0	100	100
40	MM	213/221 (96%)	206 (97%)	7 (3%)	0	100	100
41	N	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
42	NN	167/174 (96%)	160 (96%)	7 (4%)	0	100	100
43	O	95/105 (90%)	95 (100%)	0	0	100	100
44	OO	191/199 (96%)	178 (93%)	12 (6%)	1 (0%)	24	55
45	P	107/113 (95%)	103 (96%)	4 (4%)	0	100	100
46	PP	134/138 (97%)	133 (99%)	1 (1%)	0	100	100
47	Q	125/130 (96%)	125 (100%)	0	0	100	100
48	QQ	201/204 (98%)	194 (96%)	7 (4%)	0	100	100
49	R	104/107 (97%)	103 (99%)	1 (1%)	0	100	100
50	S	107/121 (88%)	107 (100%)	0	0	100	100
51	T	117/120 (98%)	115 (98%)	2 (2%)	0	100	100
52	U	97/100 (97%)	89 (92%)	8 (8%)	0	100	100
53	V	82/88 (93%)	81 (99%)	1 (1%)	0	100	100
54	W	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
55	X	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
56	Y	50/128 (39%)	50 (100%)	0	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	Z	23/25 (92%)	23 (100%)	0	0	100	100
58	a	100/106 (94%)	95 (95%)	5 (5%)	0	100	100
59	b	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
61	d	204/252 (81%)	193 (95%)	11 (5%)	0	100	100
62	e	210/255 (82%)	200 (95%)	10 (5%)	0	100	100
63	f	215/254 (85%)	205 (95%)	10 (5%)	0	100	100
64	g	204/240 (85%)	198 (97%)	6 (3%)	0	100	100
65	h	256/261 (98%)	248 (97%)	8 (3%)	0	100	100
66	i	195/225 (87%)	182 (93%)	13 (7%)	0	100	100
67	j	217/236 (92%)	209 (96%)	8 (4%)	0	100	100
68	k	182/190 (96%)	175 (96%)	7 (4%)	0	100	100
69	l	180/200 (90%)	170 (94%)	10 (6%)	0	100	100
70	m	183/197 (93%)	177 (97%)	6 (3%)	0	100	100
71	n	89/105 (85%)	84 (94%)	3 (3%)	2 (2%)	5	22
72	o	140/156 (90%)	134 (96%)	6 (4%)	0	100	100
73	p	148/151 (98%)	145 (98%)	3 (2%)	0	100	100
74	q	125/137 (91%)	120 (96%)	5 (4%)	0	100	100
75	r	100/142 (70%)	96 (96%)	4 (4%)	0	100	100
76	s	135/143 (94%)	129 (96%)	6 (4%)	0	100	100
77	t	119/136 (88%)	108 (91%)	11 (9%)	0	100	100
78	u	143/146 (98%)	134 (94%)	9 (6%)	0	100	100
79	v	141/144 (98%)	138 (98%)	3 (2%)	0	100	100
80	w	98/121 (81%)	98 (100%)	0	0	100	100
81	x	85/87 (98%)	82 (96%)	3 (4%)	0	100	100
82	y	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
83	z	142/145 (98%)	131 (92%)	11 (8%)	0	100	100
All	All	11812/13056 (90%)	11426 (97%)	382 (3%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
71	n	49	LEU
71	n	48	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
37	L	102	GLU
44	OO	63	VAL

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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	47/49 (96%)	47 (100%)	0	100	100
7	6	46/54 (85%)	45 (98%)	1 (2%)	45	68
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%)	160 (100%)	0	100	100
12	Aa	714/714 (100%)	714 (100%)	0	100	100
13	B	125/146 (86%)	125 (100%)	0	100	100
16	C	150/151 (99%)	150 (100%)	0	100	100
19	D	143/154 (93%)	143 (100%)	0	100	100
20	DD	169/254 (66%)	169 (100%)	0	100	100
22	E	156/156 (100%)	156 (100%)	0	100	100
23	EE	193/196 (98%)	193 (100%)	0	100	100
24	Ee	131/136 (96%)	131 (100%)	0	100	100
25	F	136/137 (99%)	136 (100%)	0	100	100
26	FF	318/323 (98%)	317 (100%)	1 (0%)	86	86
27	G	84/107 (78%)	84 (100%)	0	100	100
28	GG	288/289 (100%)	288 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	H	101/105 (96%)	101 (100%)	0	100	100
30	HH	244/245 (100%)	244 (100%)	0	100	100
31	I	55/129 (43%)	55 (100%)	0	100	100
32	II	133/153 (87%)	133 (100%)	0	100	100
33	J	104/118 (88%)	104 (100%)	0	100	100
34	JJ	186/205 (91%)	186 (100%)	0	100	100
35	K	109/110 (99%)	109 (100%)	0	100	100
36	KK	187/208 (90%)	187 (100%)	0	100	100
37	L	115/116 (99%)	115 (100%)	0	100	100
38	LL	171/171 (100%)	171 (100%)	0	100	100
39	M	118/119 (99%)	118 (100%)	0	100	100
40	MM	184/187 (98%)	184 (100%)	0	100	100
41	N	46/47 (98%)	46 (100%)	0	100	100
42	NN	147/150 (98%)	147 (100%)	0	100	100
43	O	81/88 (92%)	81 (100%)	0	100	100
44	OO	154/159 (97%)	153 (99%)	1 (1%)	78	81
45	P	94/97 (97%)	94 (100%)	0	100	100
46	PP	107/109 (98%)	107 (100%)	0	100	100
47	Q	109/111 (98%)	109 (100%)	0	100	100
48	QQ	175/176 (99%)	175 (100%)	0	100	100
49	R	90/91 (99%)	90 (100%)	0	100	100
50	S	94/103 (91%)	94 (100%)	0	100	100
51	T	104/105 (99%)	104 (100%)	0	100	100
52	U	81/82 (99%)	81 (100%)	0	100	100
53	V	69/71 (97%)	69 (100%)	0	100	100
54	W	68/69 (99%)	68 (100%)	0	100	100
55	X	45/46 (98%)	45 (100%)	0	100	100
56	Y	47/116 (40%)	47 (100%)	0	100	100
57	Z	23/23 (100%)	23 (100%)	0	100	100
58	a	87/91 (96%)	86 (99%)	1 (1%)	65	76
59	b	71/72 (99%)	71 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
61	d	165/210 (79%)	165 (100%)	0	100	100
62	e	189/224 (84%)	189 (100%)	0	100	100
63	f	176/205 (86%)	176 (100%)	0	100	100
64	g	167/195 (86%)	167 (100%)	0	100	100
65	h	220/222 (99%)	220 (100%)	0	100	100
66	i	172/191 (90%)	172 (100%)	0	100	100
67	j	188/201 (94%)	188 (100%)	0	100	100
68	k	165/170 (97%)	165 (100%)	0	100	100
69	l	146/161 (91%)	146 (100%)	0	100	100
70	m	158/166 (95%)	158 (100%)	0	100	100
71	n	84/98 (86%)	84 (100%)	0	100	100
72	o	127/137 (93%)	127 (100%)	0	100	100
73	p	127/128 (99%)	127 (100%)	0	100	100
74	q	81/105 (77%)	81 (100%)	0	100	100
75	r	89/118 (75%)	89 (100%)	0	100	100
76	s	114/119 (96%)	114 (100%)	0	100	100
77	t	105/124 (85%)	105 (100%)	0	100	100
78	u	128/129 (99%)	128 (100%)	0	100	100
79	v	115/116 (99%)	115 (100%)	0	100	100
80	w	94/114 (82%)	94 (100%)	0	100	100
81	x	74/74 (100%)	74 (100%)	0	100	100
82	y	110/111 (99%)	110 (100%)	0	100	100
83	z	119/120 (99%)	118 (99%)	1 (1%)	73	80
All	All	10043/10969 (92%)	10038 (100%)	5 (0%)	100	100

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	6	51	ASN
26	FF	104	THR
44	OO	120	GLN
58	a	82	GLN
83	z	63	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 125 such sidechains are listed below:

Mol	Chain	Res	Type
31	I	59	HIS
74	q	12	GLN
44	OO	99	HIS
73	p	69	ASN
80	w	47	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	AA	3186/3396 (93%)	592 (18%)	17 (0%)
14	BB	120/121 (99%)	10 (8%)	1 (0%)
15	Bb	75/76 (98%)	36 (48%)	0
17	CC	157/158 (99%)	25 (15%)	0
18	Cc	76/77 (98%)	21 (27%)	0
21	Dd	12/39 (30%)	3 (25%)	0
60	c	1594/1800 (88%)	376 (23%)	0
All	All	5220/5667 (92%)	1063 (20%)	18 (0%)

5 of 1063 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	AA	4	U
11	AA	26	A
11	AA	40	A
11	AA	43	A
11	AA	49	A

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	AA	2792	A
14	BB	72	A
11	AA	3206	C
11	AA	1904	C
11	AA	2500	A

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

68 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	OMG	AA	2791	11	23,26,27	0.49	0	32,38,41	0.52	0
11	OMU	AA	898	11	19,22,23	2.96	8 (42%)	25,31,34	1.91	5 (20%)
11	OMU	AA	2421	11	19,22,23	3.02	8 (42%)	25,31,34	1.88	5 (20%)
60	OMG	c	1271	60	23,26,27	0.45	0	32,38,41	0.48	0
60	A2M	c	619	60,85	22,25,26	3.24	10 (45%)	30,36,39	3.01	11 (36%)
60	MA6	c	1781	60	23,26,27	1.45	4 (17%)	33,38,41	3.32	12 (36%)
11	OMU	AA	2724	11	19,22,23	2.97	8 (42%)	25,31,34	1.88	5 (20%)
60	OMG	c	1428	60,85	23,26,27	0.50	0	32,38,41	0.49	0
11	UR3	AA	2634	11	19,22,23	2.78	7 (36%)	26,32,35	1.65	4 (15%)
60	OMC	c	1007	60	19,22,23	0.60	0	25,31,34	0.64	0
60	G7M	c	1575	60	23,26,27	2.70	7 (30%)	34,39,42	2.48	11 (32%)
15	YYG	Bb	37	85,15	38,42,43	2.42	13 (34%)	45,62,65	2.22	13 (28%)
11	1MA	AA	645	85,11	21,25,26	0.59	0	30,37,40	0.76	1 (3%)
60	A2M	c	796	60	22,25,26	3.26	10 (45%)	30,36,39	2.97	11 (36%)
11	OMC	AA	1437	11	19,22,23	0.65	0	25,31,34	1.34	3 (12%)
11	OMC	AA	2337	11	19,22,23	0.61	0	25,31,34	0.59	0
11	OMU	AA	2417	11	19,22,23	3.05	8 (42%)	25,31,34	1.86	5 (20%)
11	OMG	AA	2793	11	23,26,27	0.53	0	32,38,41	0.52	0
11	OMG	AA	867	11,86	23,26,27	0.51	0	32,38,41	0.47	0
60	A2M	c	541	60	22,25,26	3.17	9 (40%)	30,36,39	2.96	12 (40%)
11	OMU	AA	1888	11	19,22,23	3.01	8 (42%)	25,31,34	1.93	5 (20%)
60	A2M	c	436	60	22,25,26	3.28	9 (40%)	30,36,39	3.03	11 (36%)
11	A2M	AA	2220	11	22,25,26	3.26	10 (45%)	30,36,39	2.88	12 (40%)
11	OMU	AA	2347	11	19,22,23	2.98	8 (42%)	25,31,34	1.84	5 (20%)
11	A2M	AA	2256	11	22,25,26	3.20	10 (45%)	30,36,39	2.99	12 (40%)
11	OMC	AA	650	85,11	19,22,23	0.61	0	25,31,34	0.72	0
11	A2M	AA	649	11	22,25,26	3.22	10 (45%)	30,36,39	2.98	10 (33%)
11	A2M	AA	2281	11	22,25,26	3.26	10 (45%)	30,36,39	3.12	14 (46%)
60	OMC	c	1639	60,85	19,22,23	0.58	0	25,31,34	0.55	0
11	OMG	AA	805	11	23,26,27	0.52	0	32,38,41	0.55	0
12	DDE	Aa	699	12	18,20,21	1.00	1 (5%)	17,28,30	0.86	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
11	A2M	AA	2280	11	22,25,26	3.27	10 (45%)	30,36,39	2.88	11 (36%)
11	A2M	AA	1449	85,11	22,25,26	3.24	10 (45%)	30,36,39	3.04	12 (40%)
60	OMU	c	1269	60	19,22,23	3.07	8 (42%)	25,31,34	1.82	5 (20%)
11	OMG	AA	908	11	23,26,27	0.50	0	32,38,41	0.51	0
60	OMG	c	1572	60	23,26,27	0.53	0	32,38,41	0.50	0
11	OMG	AA	2922	11	23,26,27	0.55	0	32,38,41	0.49	0
11	5MC	AA	2870	11,86	19,22,23	0.79	0	26,32,35	0.63	0
11	A2M	AA	807	11	22,25,26	3.25	10 (45%)	30,36,39	3.10	15 (50%)
11	A2M	AA	817	85,11	22,25,26	3.30	10 (45%)	30,36,39	3.10	12 (40%)
11	5MC	AA	2278	11	19,22,23	0.64	0	26,32,35	0.71	0
11	OMG	AA	1450	11	23,26,27	0.50	0	32,38,41	0.46	0
11	A2M	AA	1133	11	22,25,26	3.27	10 (45%)	30,36,39	3.00	12 (40%)
60	OMU	c	578	60	19,22,23	3.06	8 (42%)	25,31,34	1.76	5 (20%)
11	OMG	AA	2619	11	23,26,27	0.52	0	32,38,41	0.51	0
11	OMG	AA	2288	11	23,26,27	0.52	0	32,38,41	0.47	0
11	OMU	AA	2921	11	19,22,23	2.94	8 (42%)	25,31,34	1.90	5 (20%)
60	A2M	c	420	60	22,25,26	3.21	9 (40%)	30,36,39	2.87	10 (33%)
11	1MA	AA	2142	85,11	21,25,26	0.59	0	30,37,40	0.84	1 (3%)
60	OMG	c	562	60	23,26,27	0.52	0	32,38,41	0.43	0
11	OMC	AA	2197	11,86	19,22,23	0.56	0	25,31,34	0.60	0
60	A2M	c	974	60	22,25,26	3.26	10 (45%)	30,36,39	2.93	10 (33%)
60	OMG	c	1126	60	23,26,27	0.55	0	32,38,41	0.49	0
60	A2M	c	100	60	22,25,26	3.22	10 (45%)	30,36,39	3.04	11 (36%)
11	OMG	AA	2815	11	23,26,27	0.51	0	32,38,41	0.46	0
11	A2M	AA	876	11	22,25,26	3.25	10 (45%)	30,36,39	2.98	10 (33%)
60	OMC	c	414	60	19,22,23	0.54	0	25,31,34	0.69	0
60	B8N	c	1191	60	25,29,30	5.05	10 (40%)	28,42,45	2.37	11 (39%)
60	4AC	c	1280	60	21,24,25	3.51	10 (47%)	28,34,37	1.78	6 (21%)
11	A2M	AA	2946	85,11	22,25,26	3.22	10 (45%)	30,36,39	3.02	11 (36%)
11	OMC	AA	663	11	19,22,23	0.63	0	25,31,34	0.62	0
60	4AC	c	1773	60	21,24,25	3.37	10 (47%)	28,34,37	1.74	6 (21%)
11	A2M	AA	2640	11	22,25,26	3.27	9 (40%)	30,36,39	2.92	12 (40%)
11	OMC	AA	2948	11	19,22,23	0.58	0	25,31,34	0.68	0
11	OMC	AA	2959	11	19,22,23	0.61	0	25,31,34	0.64	0
60	A2M	c	28	60	22,25,26	3.23	10 (45%)	30,36,39	3.01	11 (36%)
11	OMU	AA	2729	11	19,22,23	3.05	8 (42%)	25,31,34	1.75	4 (16%)
60	MA6	c	1782	60	23,26,27	1.46	4 (17%)	33,38,41	3.28	12 (36%)

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	OMG	AA	2791	11	-	2/9/27/28	0/3/3/3
11	OMU	AA	898	11	-	0/9/27/28	0/2/2/2
11	OMU	AA	2421	11	-	1/9/27/28	0/2/2/2
60	OMG	c	1271	60	-	1/9/27/28	0/3/3/3
60	A2M	c	619	60,85	-	3/9/27/28	0/3/3/3
60	MA6	c	1781	60	-	0/11/29/30	0/3/3/3
11	OMU	AA	2724	11	-	1/9/27/28	0/2/2/2
60	OMG	c	1428	60,85	-	0/9/27/28	0/3/3/3
11	UR3	AA	2634	11	-	0/7/25/26	0/2/2/2
60	OMC	c	1007	60	-	1/9/27/28	0/2/2/2
60	G7M	c	1575	60	-	2/7/25/26	0/3/3/3
15	YYG	Bb	37	85,15	-	11/24/42/43	0/4/4/4
11	1MA	AA	645	85,11	-	2/7/25/26	0/3/3/3
60	A2M	c	796	60	-	0/9/27/28	0/3/3/3
11	OMC	AA	1437	11	-	3/9/27/28	0/2/2/2
11	OMC	AA	2337	11	-	1/9/27/28	0/2/2/2
11	OMU	AA	2417	11	-	1/9/27/28	0/2/2/2
11	OMG	AA	2793	11	-	2/9/27/28	0/3/3/3
11	OMG	AA	867	11,86	-	2/9/27/28	0/3/3/3
60	A2M	c	541	60	-	4/9/27/28	0/3/3/3
11	OMU	AA	1888	11	-	1/9/27/28	0/2/2/2
60	A2M	c	436	60	-	1/9/27/28	0/3/3/3
11	A2M	AA	2220	11	-	1/9/27/28	0/3/3/3
11	OMU	AA	2347	11	-	1/9/27/28	0/2/2/2
11	A2M	AA	2256	11	-	1/9/27/28	0/3/3/3
11	OMC	AA	650	85,11	-	0/9/27/28	0/2/2/2
11	A2M	AA	649	11	-	2/9/27/28	0/3/3/3
11	A2M	AA	2281	11	-	3/9/27/28	0/3/3/3
60	OMC	c	1639	60,85	-	1/9/27/28	0/2/2/2
11	OMG	AA	805	11	-	0/9/27/28	0/3/3/3
12	DDE	Aa	699	12	-	9/20/21/23	0/1/1/1
11	A2M	AA	2280	11	-	3/9/27/28	0/3/3/3
11	A2M	AA	1449	85,11	-	0/9/27/28	0/3/3/3
60	OMU	c	1269	60	-	0/9/27/28	0/2/2/2
11	OMG	AA	908	11	-	2/9/27/28	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	OMG	c	1572	60	-	4/9/27/28	0/3/3/3
11	OMG	AA	2922	11	-	1/9/27/28	0/3/3/3
11	5MC	AA	2870	11,86	-	4/7/25/26	0/2/2/2
11	A2M	AA	807	11	-	2/9/27/28	0/3/3/3
11	A2M	AA	817	85,11	-	1/9/27/28	0/3/3/3
11	5MC	AA	2278	11	-	0/7/25/26	0/2/2/2
11	OMG	AA	1450	11	-	3/9/27/28	0/3/3/3
11	A2M	AA	1133	11	-	0/9/27/28	0/3/3/3
60	OMU	c	578	60	-	1/9/27/28	0/2/2/2
11	OMG	AA	2619	11	-	0/9/27/28	0/3/3/3
11	OMG	AA	2288	11	-	0/9/27/28	0/3/3/3
11	OMU	AA	2921	11	-	0/9/27/28	0/2/2/2
60	A2M	c	420	60	-	1/9/27/28	0/3/3/3
11	1MA	AA	2142	85,11	-	1/7/25/26	0/3/3/3
60	OMG	c	562	60	-	1/9/27/28	0/3/3/3
11	OMC	AA	2197	11,86	-	4/9/27/28	0/2/2/2
60	A2M	c	974	60	-	1/9/27/28	0/3/3/3
60	OMG	c	1126	60	-	2/9/27/28	0/3/3/3
60	A2M	c	100	60	-	2/9/27/28	0/3/3/3
11	OMG	AA	2815	11	-	0/9/27/28	0/3/3/3
11	A2M	AA	876	11	-	1/9/27/28	0/3/3/3
60	OMC	c	414	60	-	2/9/27/28	0/2/2/2
60	B8N	c	1191	60	-	5/16/34/35	0/2/2/2
60	4AC	c	1280	60	-	2/11/29/30	0/2/2/2
11	A2M	AA	2946	85,11	-	0/9/27/28	0/3/3/3
11	OMC	AA	663	11	-	1/9/27/28	0/2/2/2
60	4AC	c	1773	60	-	2/11/29/30	0/2/2/2
11	A2M	AA	2640	11	-	1/9/27/28	0/3/3/3
11	OMC	AA	2948	11	-	0/9/27/28	0/2/2/2
11	OMC	AA	2959	11	-	0/9/27/28	0/2/2/2
60	A2M	c	28	60	-	3/9/27/28	0/3/3/3
11	OMU	AA	2729	11	-	3/9/27/28	0/2/2/2
60	MA6	c	1782	60	-	3/11/29/30	0/3/3/3

The worst 5 of 342 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	c	1191	B8N	C2'-C1'	-17.09	1.30	1.53
11	AA	807	A2M	C3'-C4'	-9.16	1.29	1.53

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	c	619	A2M	C3'-C4'	-9.08	1.30	1.53
11	AA	817	A2M	C3'-C4'	-9.04	1.30	1.53
60	c	28	A2M	C3'-C4'	-9.04	1.30	1.53

The worst 5 of 360 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
60	c	1781	MA6	N1-C6-N6	-12.21	101.98	116.86
60	c	1782	MA6	N1-C6-N6	-11.96	102.29	116.86
60	c	1781	MA6	C5-C6-N6	8.12	138.18	125.33
60	c	1782	MA6	C5-C6-N6	7.87	137.78	125.33
15	Bb	37	YYG	C5-C4-N3	-7.21	118.14	123.99

There are no chirality outliers.

5 of 113 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	867	OMG	O4'-C4'-C5'-O5'
11	AA	867	OMG	C3'-C4'-C5'-O5'
11	AA	876	A2M	C1'-C2'-O2'-CM'

There are no ring outliers.

48 monomers are involved in 82 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	AA	898	OMU	1	0
11	AA	2421	OMU	1	0
60	c	1271	OMG	1	0
60	c	619	A2M	1	0
60	c	1781	MA6	2	0
11	AA	2724	OMU	4	0
60	c	1007	OMC	2	0
60	c	1575	G7M	6	0
15	Bb	37	YYG	4	0
11	AA	645	1MA	1	0
11	AA	2337	OMC	1	0
11	AA	2417	OMU	1	0
11	AA	2793	OMG	1	0
11	AA	867	OMG	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	c	541	A2M	3	0
60	c	436	A2M	1	0
11	AA	2220	A2M	1	0
11	AA	2347	OMU	1	0
11	AA	2256	A2M	2	0
11	AA	650	OMC	1	0
11	AA	649	A2M	2	0
11	AA	2281	A2M	1	0
60	c	1639	OMC	2	0
12	Aa	699	DDE	2	0
11	AA	1449	A2M	2	0
60	c	1269	OMU	1	0
60	c	1572	OMG	1	0
11	AA	2922	OMG	3	0
11	AA	2870	5MC	1	0
11	AA	807	A2M	3	0
11	AA	817	A2M	1	0
11	AA	1133	A2M	1	0
60	c	578	OMU	1	0
11	AA	2619	OMG	2	0
11	AA	2921	OMU	1	0
60	c	420	A2M	2	0
60	c	562	OMG	2	0
60	c	974	A2M	3	0
60	c	1126	OMG	2	0
11	AA	876	A2M	1	0
60	c	1280	4AC	2	0
11	AA	2946	A2M	1	0
11	AA	663	OMC	2	0
60	c	1773	4AC	3	0
11	AA	2640	A2M	3	0
11	AA	2948	OMC	1	0
60	c	28	A2M	2	0
11	AA	2729	OMU	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 233 ligands modelled in this entry, 229 are monoatomic - leaving 4 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	$\#\|Z\| > 2$
87	SPD	c	1937	-	9,9,9	0.31	0	8,8,8	0.92	0
87	SPD	AA	3567	-	9,9,9	0.31	0	8,8,8	0.68	0
88	GTP	Aa	1001	85	33,34,34	0.97	3 (9%)	50,54,54	1.63	10 (20%)
87	SPD	AA	3566	-	9,9,9	0.31	0	8,8,8	0.80	0

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
87	SPD	c	1937	-	-	3/7/7/7	-
87	SPD	AA	3567	-	-	3/7/7/7	-
88	GTP	Aa	1001	85	-	2/22/38/38	0/3/3/3
87	SPD	AA	3566	-	-	4/7/7/7	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
88	Aa	1001	GTP	PA-O3A	2.08	1.61	1.59
88	Aa	1001	GTP	C2-N3	2.06	1.38	1.33
88	Aa	1001	GTP	PB-O3A	2.05	1.61	1.59

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
88	Aa	1001	GTP	C5-C4-N3	-4.97	120.48	128.39
88	Aa	1001	GTP	C2-N3-C4	4.59	120.21	112.30
88	Aa	1001	GTP	N9-C4-N3	3.40	132.74	125.95
88	Aa	1001	GTP	C2-N1-C6	-2.84	119.96	125.11

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
88	Aa	1001	GTP	N9-C8-N7	-2.72	108.35	113.40

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

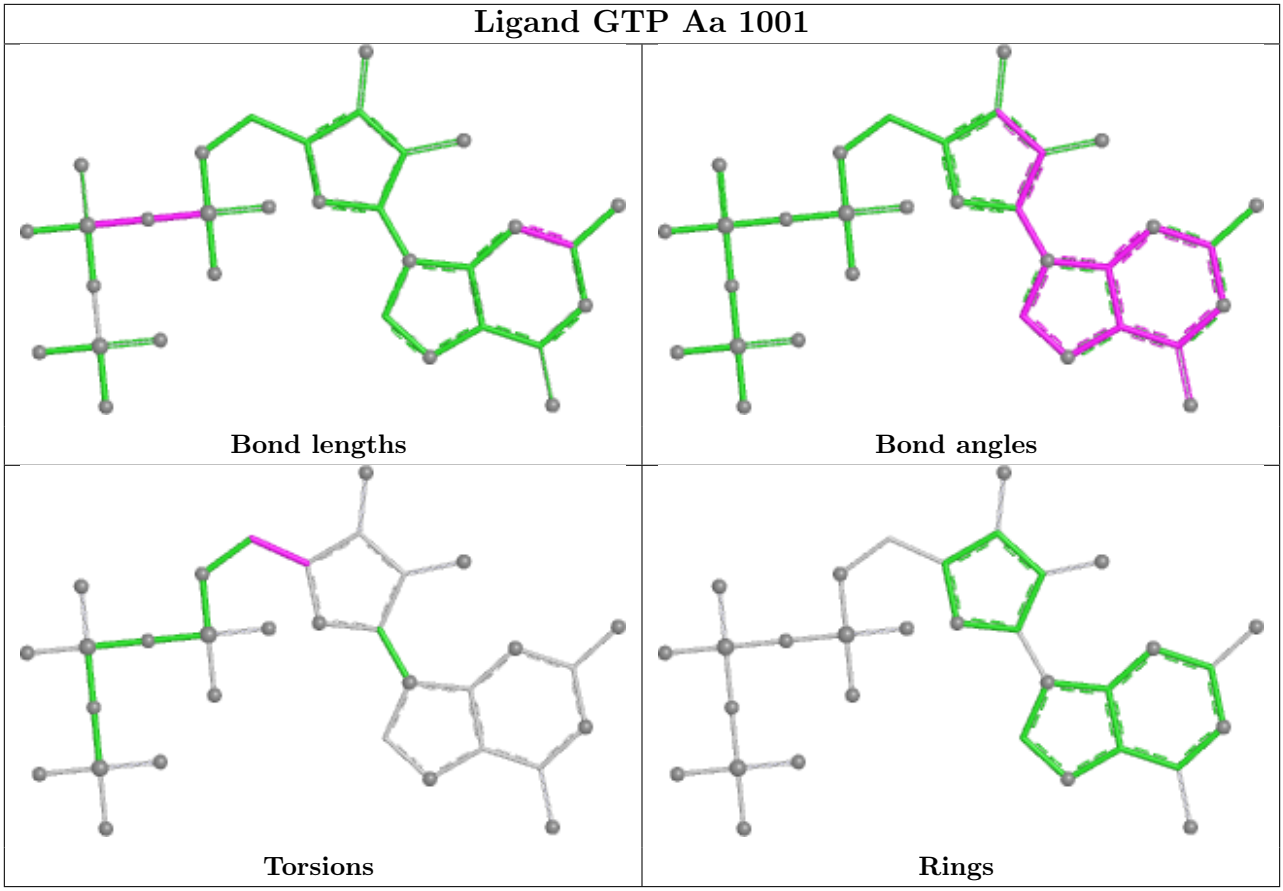
Mol	Chain	Res	Type	Atoms
87	AA	3566	SPD	N6-C7-C8-C9
87	AA	3567	SPD	C3-C4-C5-N6
88	Aa	1001	GTP	O4'-C4'-C5'-O5'
88	Aa	1001	GTP	C3'-C4'-C5'-O5'
87	AA	3567	SPD	C8-C7-N6-C5

There are no ring outliers.

3 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	c	1937	SPD	1	0
87	AA	3567	SPD	1	0
88	Aa	1001	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 then 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.

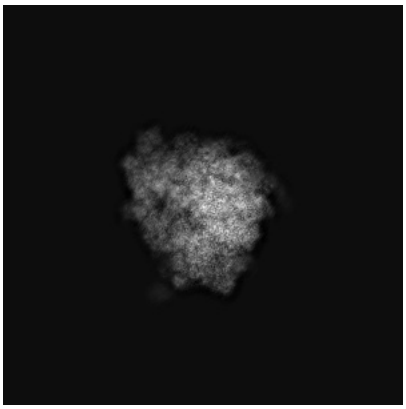
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-16702. These allow visual inspection of the internal detail of the map and identification of artifacts.

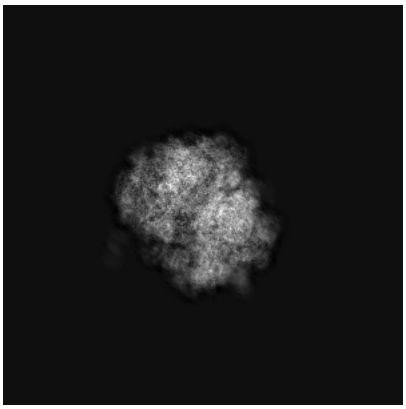
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

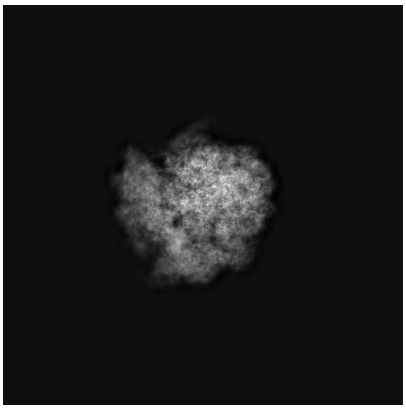
6.1.1 Primary map



X

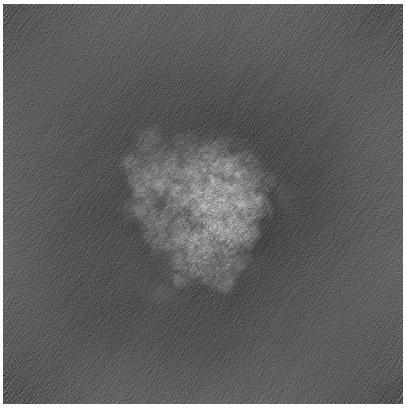


Y

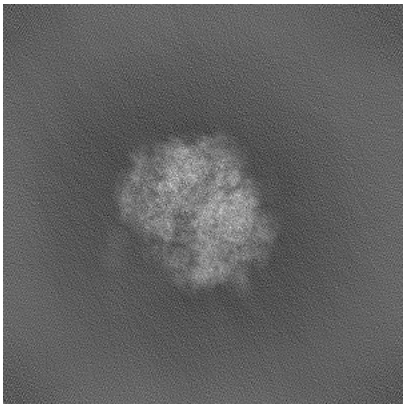


Z

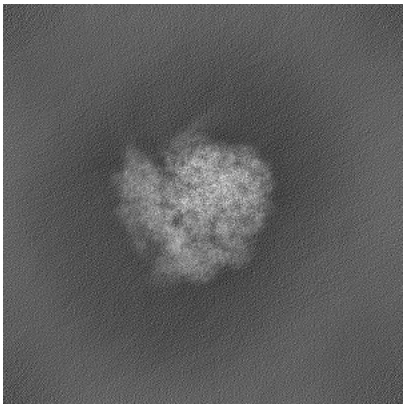
6.1.2 Raw map



X



Y

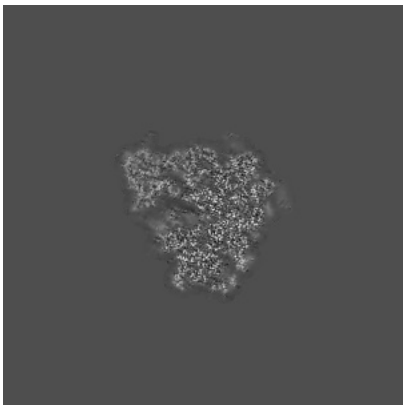


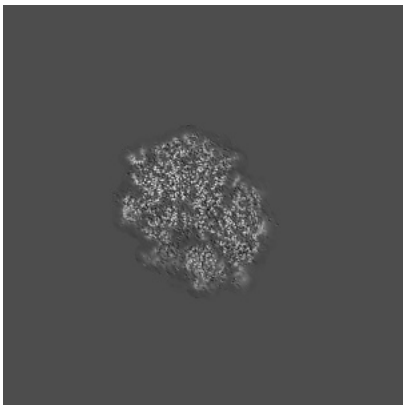
Z

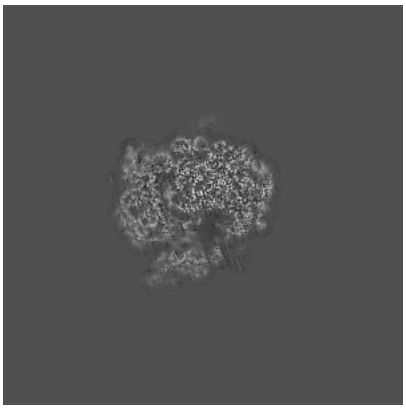
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

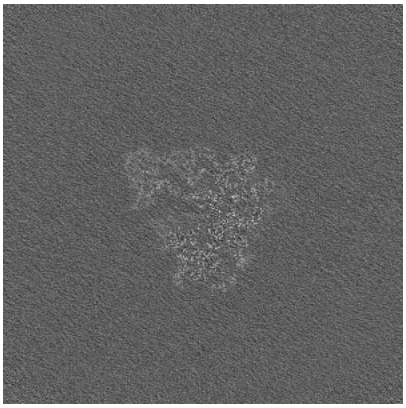
6.2.1 Primary map

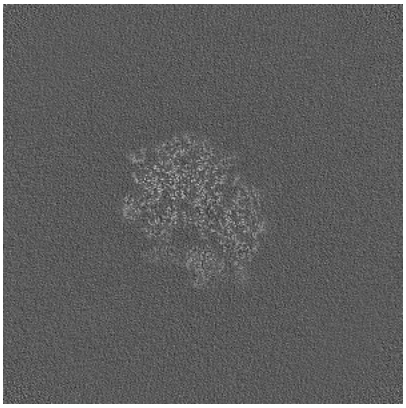

X Index: 220

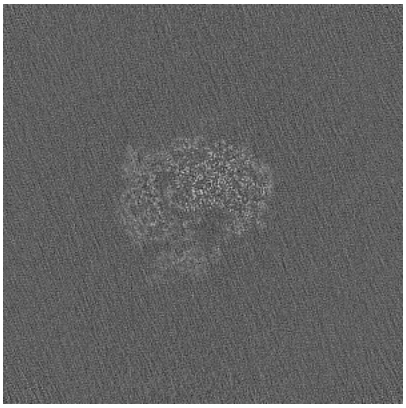

Y Index: 220


Z Index: 220

6.2.2 Raw map


X Index: 220

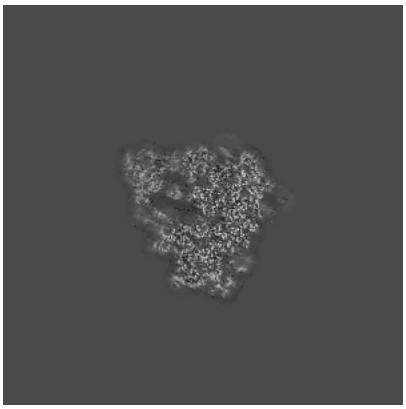

Y Index: 220


Z Index: 220

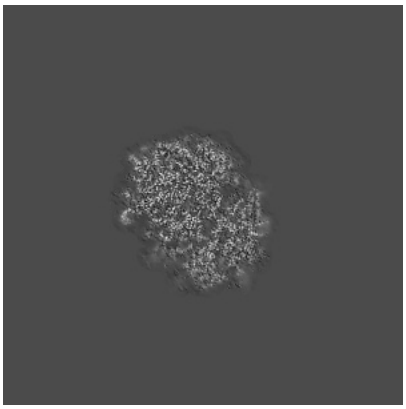
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

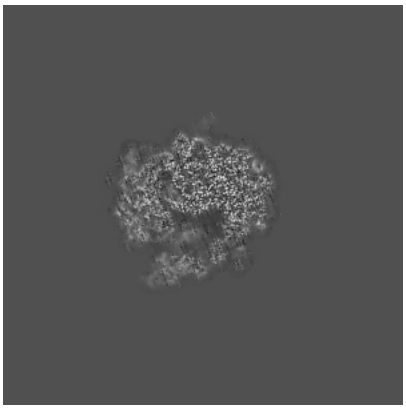
6.3.1 Primary map



X Index: 225

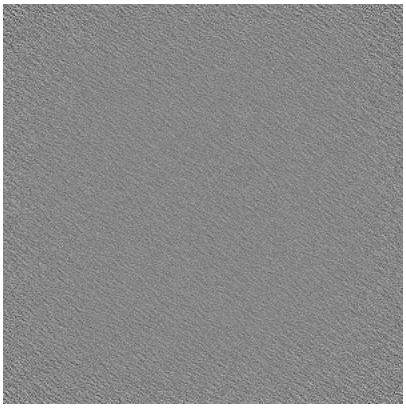


Y Index: 224

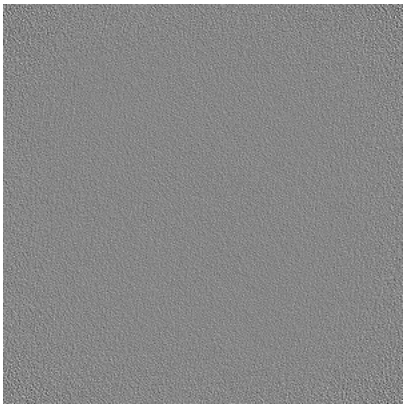


Z Index: 217

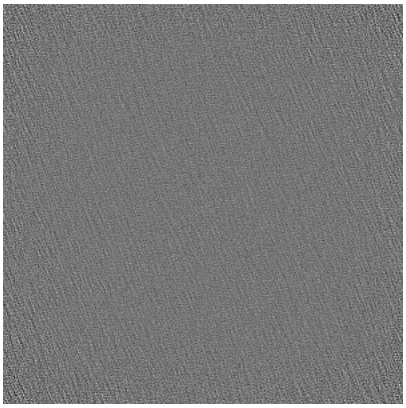
6.3.2 Raw map



X Index: 0



Y Index: 0

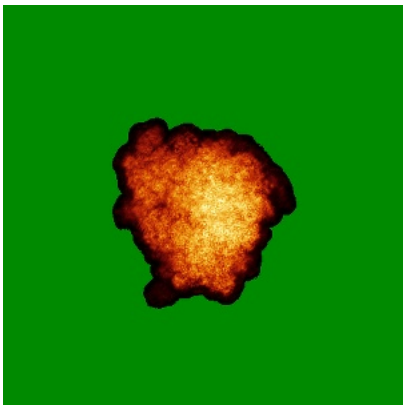


Z Index: 0

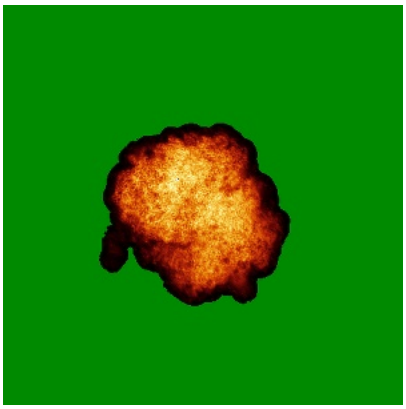
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

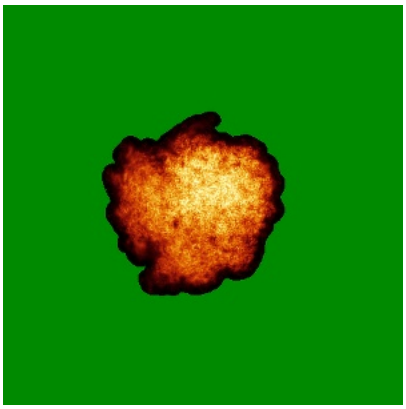
6.4.1 Primary map



X

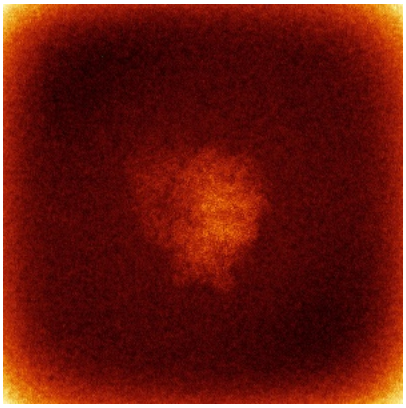


Y

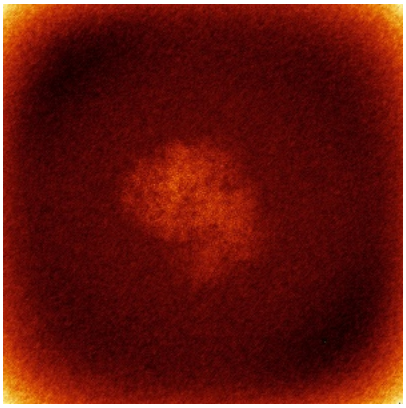


Z

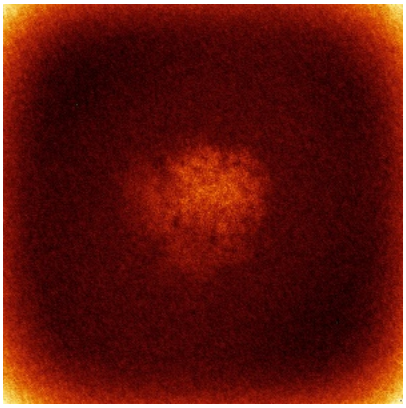
6.4.2 Raw map



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.

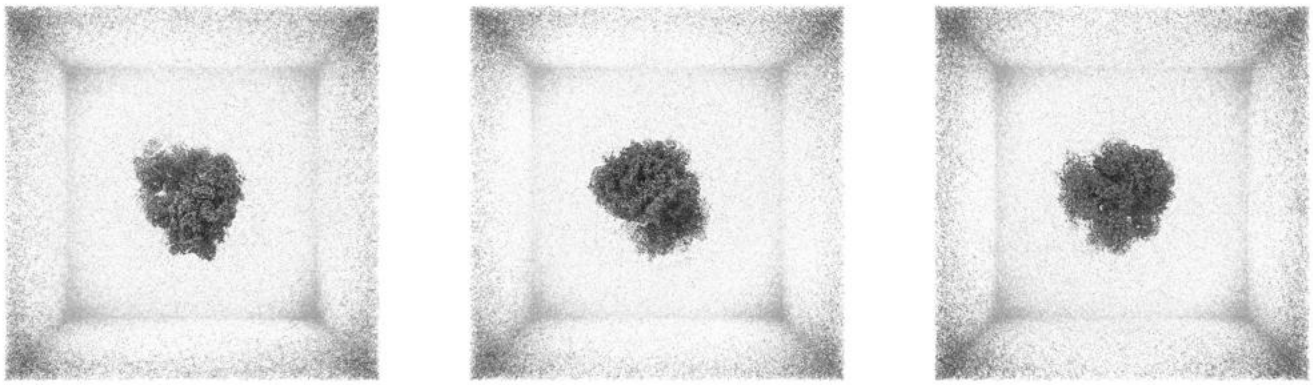
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

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



X Y Z

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.

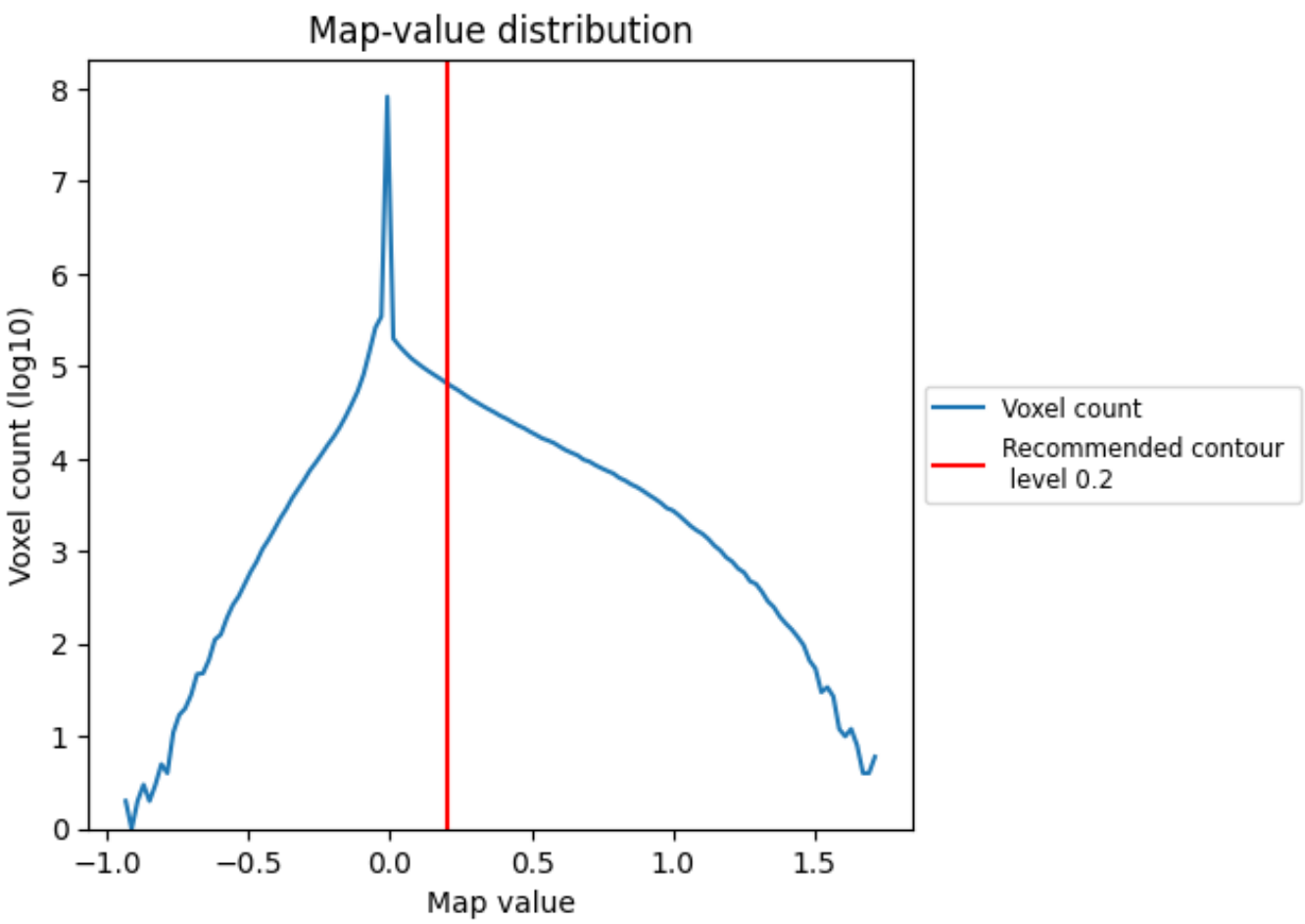
6.6 Mask visualisation (i)

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

7 Map analysis (i)

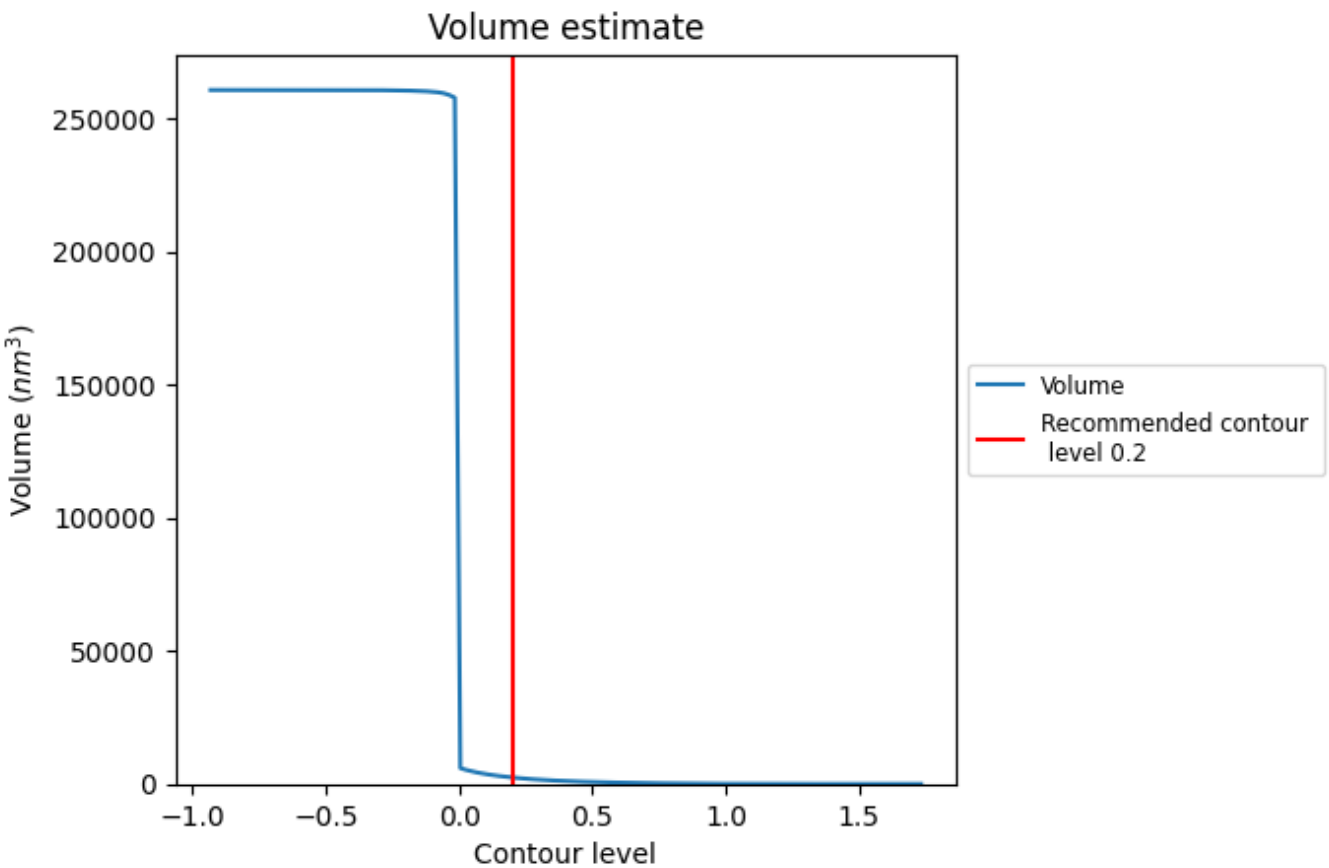
This section contains the results of statistical analysis of the map.

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.

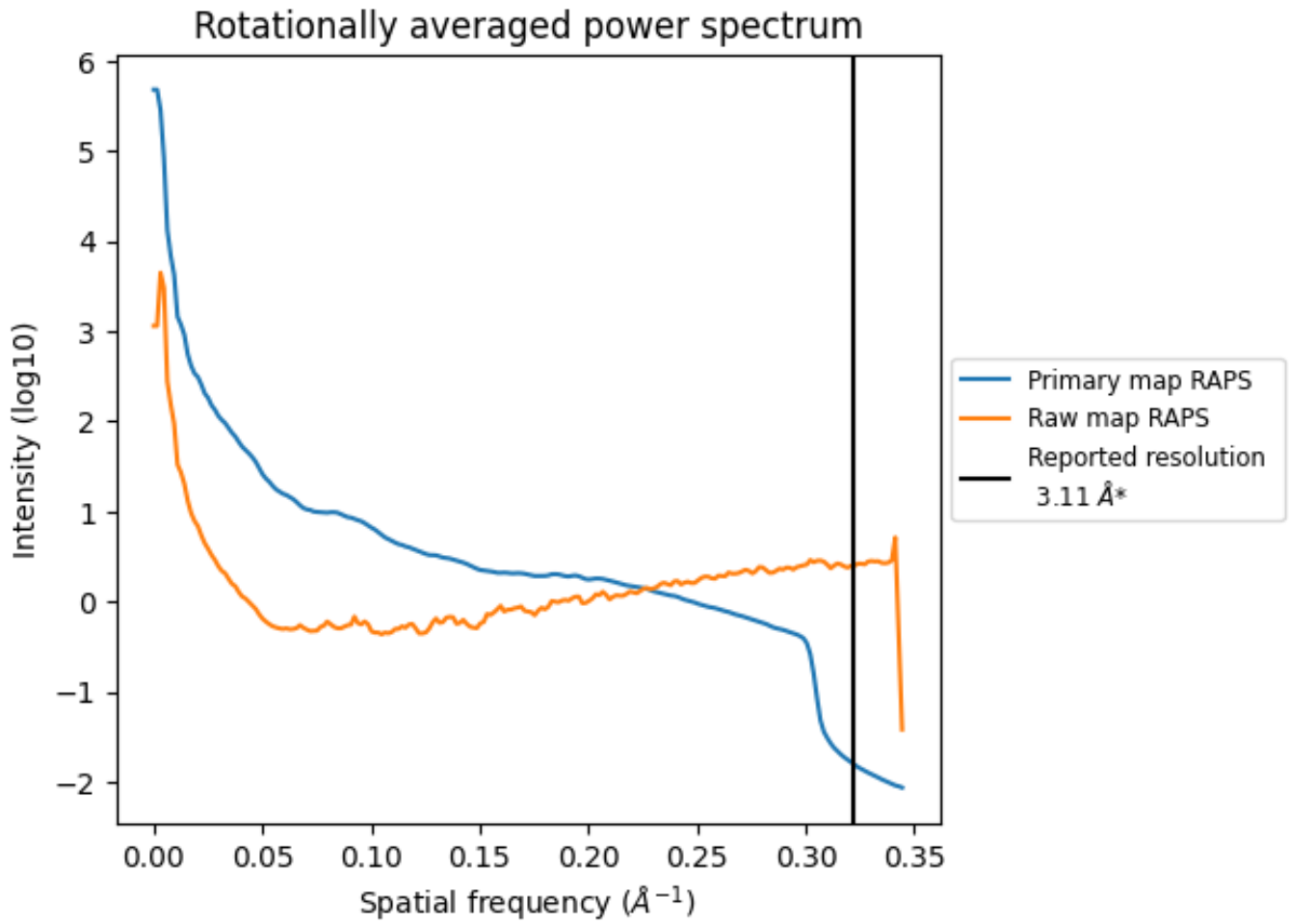
7.2 Volume estimate (i)



The volume at the recommended contour level is 2429 nm^3; this corresponds to an approximate mass of 2194 kDa.

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

7.3 Rotationally averaged power spectrum (i)

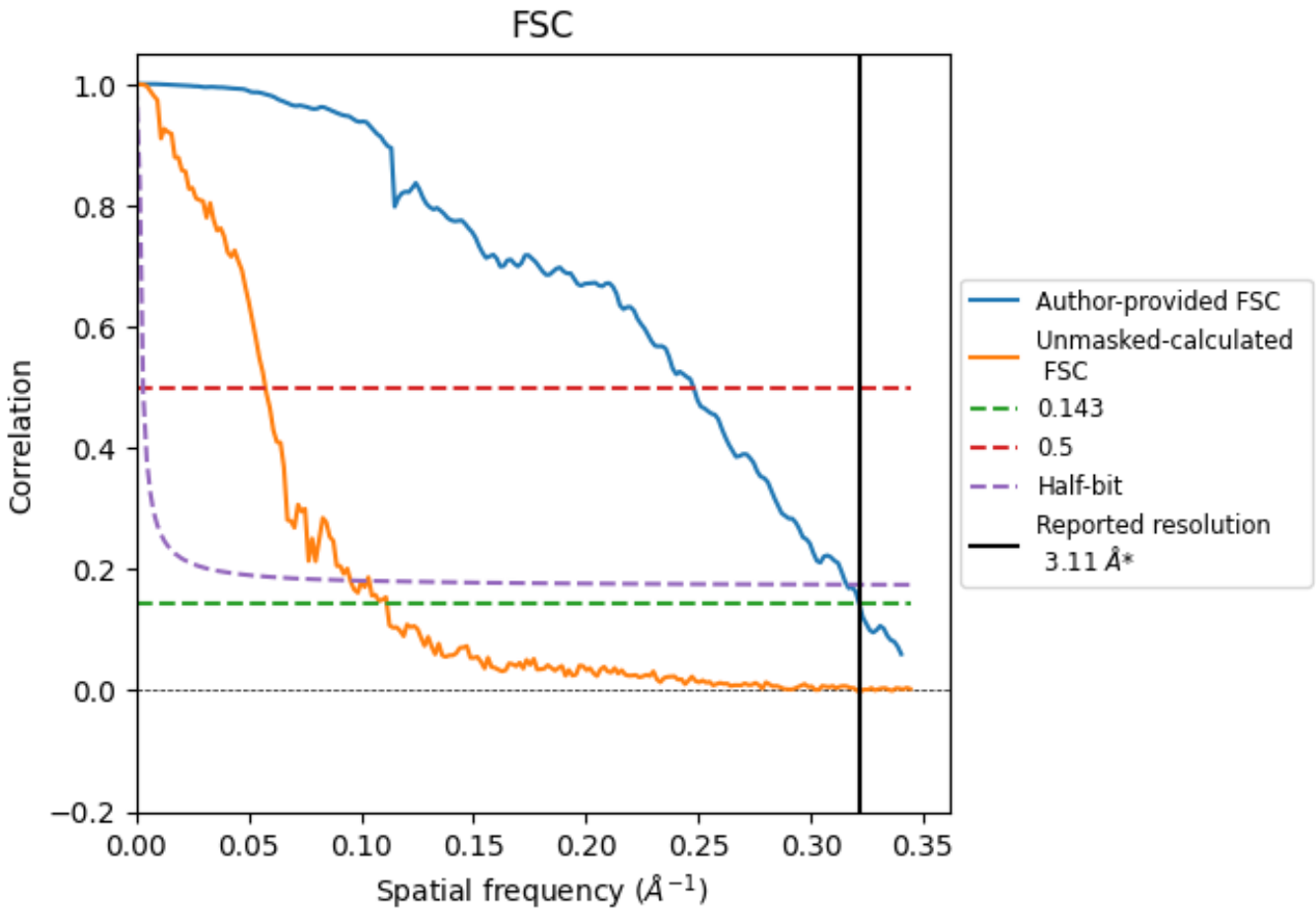


*Reported resolution corresponds to spatial frequency of 0.322 Å^{-1}

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 0.322 Å^{-1}

8.2 Resolution estimates (i)

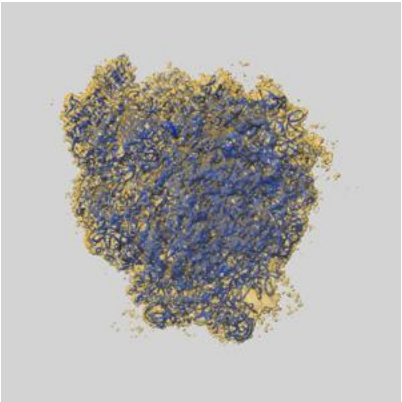
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.11	-	-
Author-provided FSC curve	3.11	4.03	3.16
Unmasked-calculated*	8.97	17.39	10.49

*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 8.97 differs from the reported value 3.11 by more than 10 %

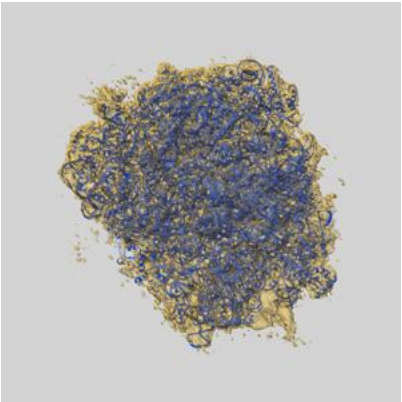
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-16702 and PDB model 8CKU. Per-residue inclusion information can be found in section 3 on page 23.

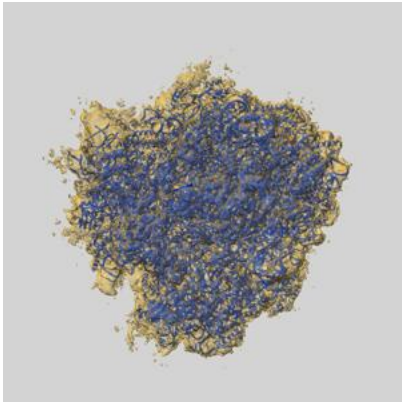
9.1 Map-model overlay (i)



X



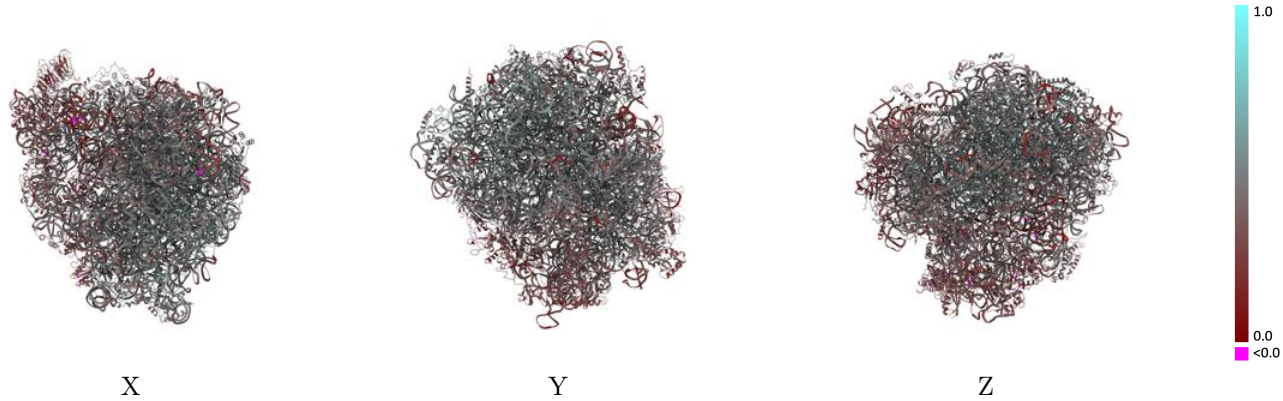
Y



Z

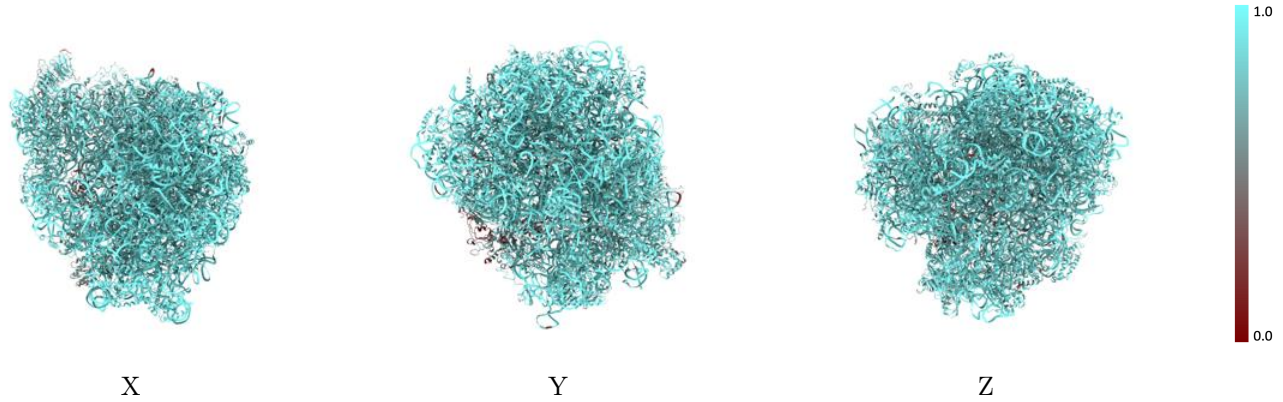
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



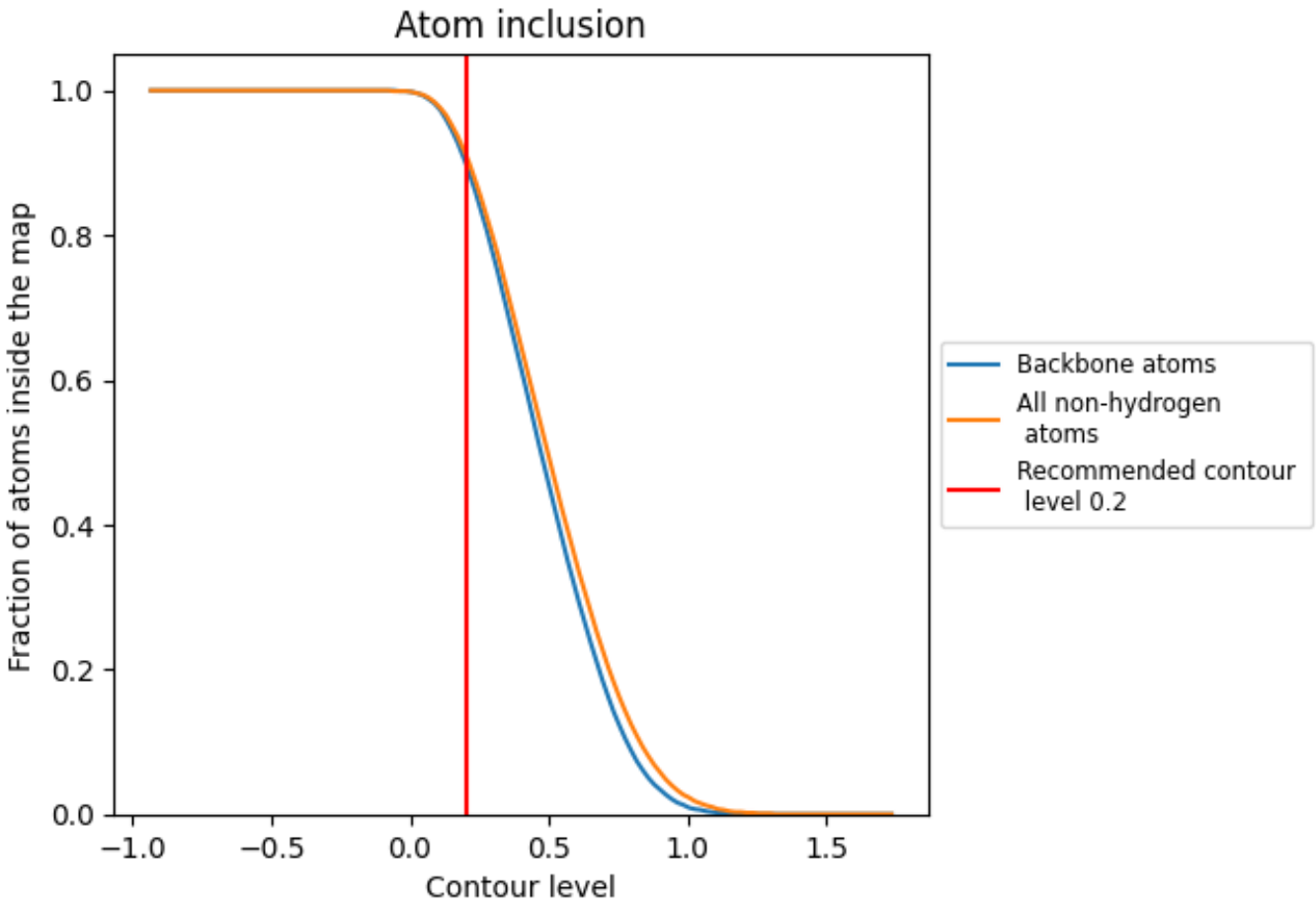
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 90% of all backbone atoms, 91% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

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	0.9120	0.4250
0	0.8810	0.3570
1	0.6860	0.2440
2	0.9350	0.4700
3	0.9080	0.4140
4	0.7880	0.3680
5	0.9360	0.4430
6	0.8740	0.3800
7	0.8120	0.2840
8	0.6430	0.2460
A	0.9420	0.4840
AA	0.9720	0.4590
Aa	0.4630	0.2570
B	0.9440	0.5090
BB	0.9870	0.4560
Bb	0.5740	0.2400
C	0.9390	0.4880
CC	0.9820	0.4750
Cc	0.9010	0.3240
D	0.9210	0.4580
DD	0.3890	0.1920
Dd	0.8600	0.3680
E	0.9230	0.4820
EE	0.8930	0.4990
Ee	0.4300	0.1810
F	0.9150	0.4720
FF	0.9310	0.4730
G	0.9100	0.4110
GG	0.9450	0.4910
H	0.8980	0.4890
HH	0.8830	0.3970
I	0.9250	0.4540
II	0.9540	0.4770
J	0.9310	0.4840
JJ	0.9440	0.4880

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
K	0.9390	0.4900
KK	0.9100	0.4180
L	0.9450	0.4530
LL	0.8860	0.4540
M	0.9290	0.4680
MM	0.8910	0.4770
N	0.8870	0.4320
NN	0.8880	0.3820
O	0.8880	0.4560
OO	0.9200	0.4400
P	0.9070	0.4580
PP	0.9370	0.4770
Q	0.9540	0.5140
QQ	0.9400	0.4840
R	0.9660	0.5320
S	0.9320	0.4880
T	0.9410	0.4470
U	0.9270	0.4110
V	0.9690	0.5250
W	0.8550	0.4170
X	0.9400	0.4860
Y	0.8860	0.4820
Z	0.8110	0.4290
a	0.9000	0.4580
b	0.9150	0.4960
c	0.9660	0.4080
d	0.8870	0.4080
e	0.8840	0.4230
f	0.9150	0.4500
g	0.8980	0.3770
h	0.8790	0.3700
i	0.8100	0.3430
j	0.8410	0.3070
k	0.8220	0.3680
l	0.8530	0.3610
m	0.8900	0.3760
n	0.8320	0.3310
o	0.8580	0.4230
p	0.8910	0.4350
q	0.9150	0.4340
r	0.8820	0.3610
s	0.8800	0.3550

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
t	0.8670	0.3690
u	0.8560	0.3330
v	0.8770	0.3340
w	0.8620	0.3610
x	0.9050	0.4300
y	0.9210	0.4650
z	0.8460	0.4140