



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:16 AM UTC

PDB ID : 8CG8 / pdb_00008cg8
EMDB ID : EMD-16634
Title : Translocation intermediate 3 (TI-3) of 80S *S. cerevisiae* ribosome with ligands and eEF2 in the presence of sordarin
Authors : Milicevic, N.; Jenner, L.; Myasnikov, A.; Yusupov, M.; Yusupova, G.
Deposited on : 2023-02-03
Resolution : 2.57 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

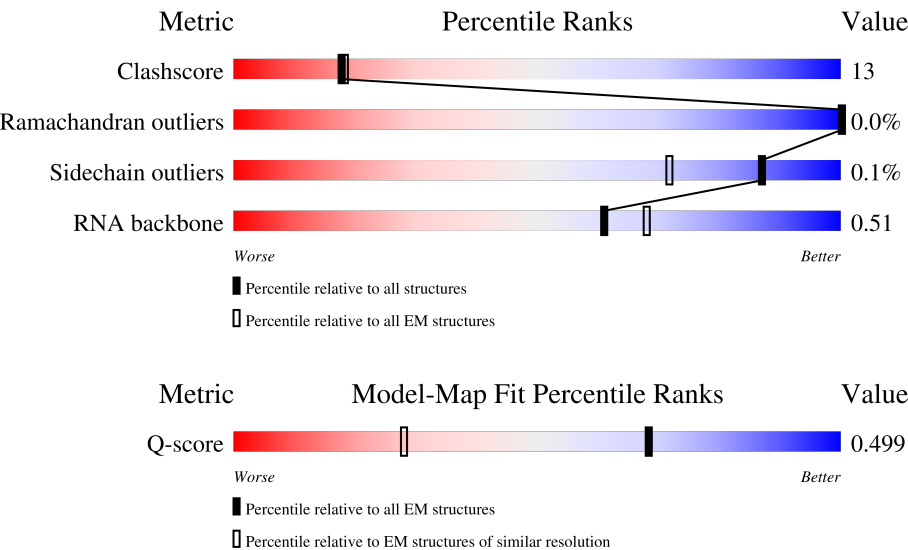
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.57 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.



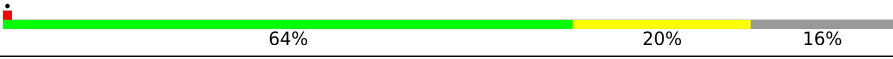
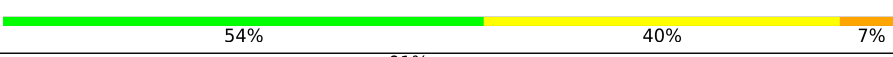
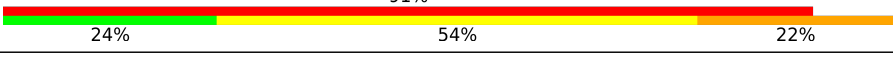
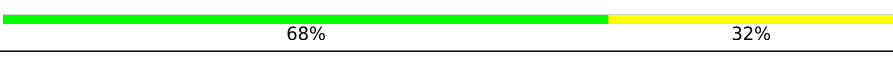
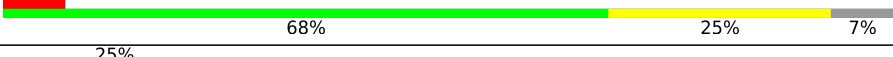
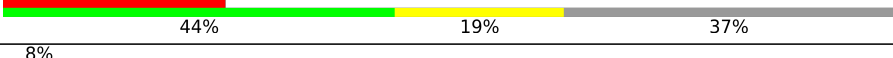
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7615 (2.07 - 3.07)

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

Mol	Chain	Length	Quality of chain
1	0	135	44% 67% 32% .
2	1	108	58% 40% 25% 35%
3	2	119	9% 54% 28% 18%

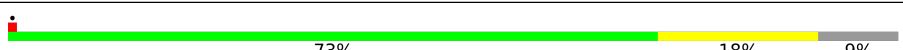
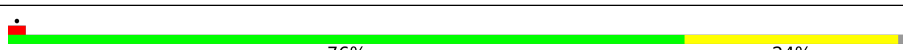
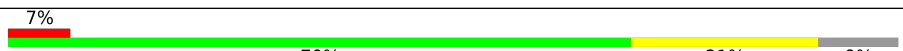
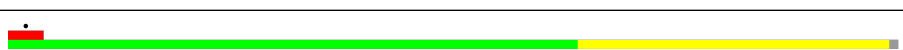
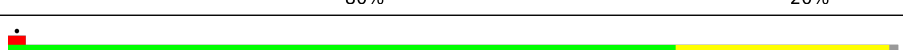
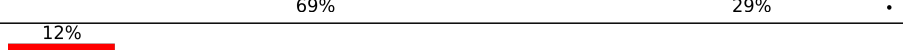
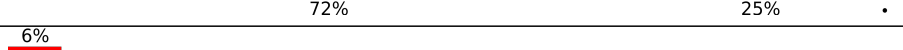
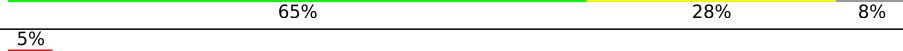
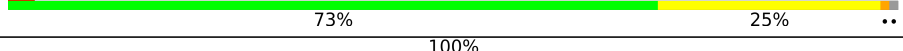
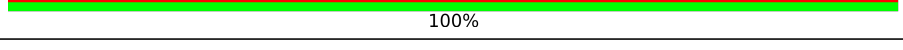
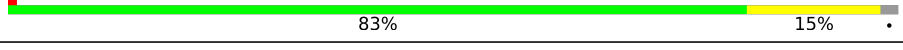
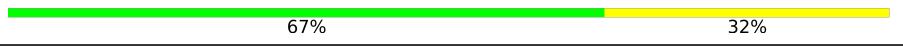
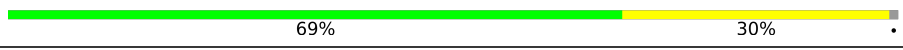
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Mol	Chain	Length	Quality of chain
4	3	82	
5	4	67	
6	5	56	
7	6	63	
8	7	319	
9	8	152	
10	A	199	
11	AA	3396	
12	Aa	842	
13	B	184	
14	BB	121	
15	Bb	76	
16	C	186	
17	CC	158	
18	Cc	77	
19	D	189	
20	DD	312	
21	Dd	39	
22	E	172	
23	EE	254	
24	Ee	165	
25	F	160	
26	FF	387	
27	G	121	
28	GG	362	

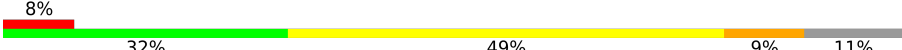
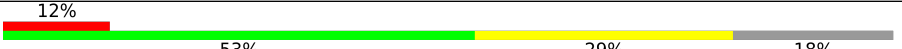
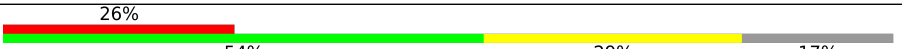
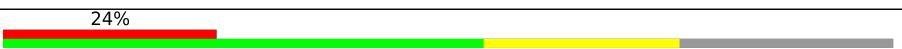
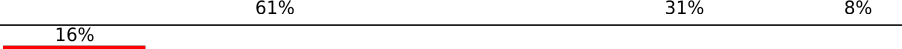
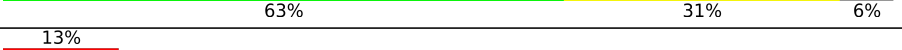
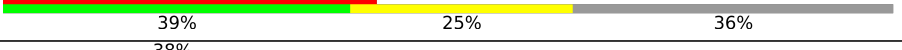
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Mol	Chain	Length	Quality of chain
29	H	137	
30	HH	297	
31	I	155	
32	II	176	
33	J	142	
34	JJ	244	
35	K	127	
36	KK	256	
37	L	136	
38	LL	191	
39	M	149	
40	MM	221	
41	N	59	
42	NN	174	
43	O	105	
44	OO	199	
45	P	113	
46	PP	138	
47	Pp	2	
48	Q	130	
49	QQ	204	
50	R	107	
51	S	121	
52	T	120	
53	U	100	

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Mol	Chain	Length	Quality of chain
54	V	88	
55	W	78	
56	X	51	
57	Y	128	
58	Z	25	
59	a	106	
60	b	92	
61	c	1800	
62	d	252	
63	e	255	
64	f	254	
65	g	240	
66	h	261	
67	i	225	
68	j	236	
69	k	190	
70	l	200	
71	m	197	
72	n	105	
73	o	156	
74	p	151	
75	q	137	
76	r	142	
77	s	143	
78	t	136	

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Mol	Chain	Length	Quality of chain
79	u	146	
80	v	144	
81	w	121	
82	x	87	
83	y	130	
84	z	145	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
85	ZN	a	201	-	-	X	-

2 Entry composition

There are 91 unique types of molecules in this entry. The entry contains 207325 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 12 is a protein called Elongation factor 2.

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

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

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

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

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

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

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

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

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

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

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

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

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

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
19	D	176	Total	C	N	O	0	0
			1423	875	308	240		

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

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

- Molecule 21 is a RNA chain called Messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Dd	6	Total	C	N	O	P	0	0
			125	56	18	45	6		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 38 is a protein called RPL9A isoform 1.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 47 is a protein called Polypeptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Pp	2	Total	C	N	O	S	0	0
			19	14	2	2	1		

- Molecule 48 is a protein called 60S ribosomal protein L32.

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

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

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

- Molecule 50 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 51 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 52 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 53 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 54 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 55 is a protein called 60S ribosomal protein L38.

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

- Molecule 56 is a protein called 60S ribosomal protein L39.

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

- Molecule 57 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 58 is a protein called 60S ribosomal protein L41.

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

- Molecule 59 is a protein called 60S ribosomal protein L42-A.

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

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

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

- Molecule 61 is a RNA chain called 18S ribosomal RNA.

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

- Molecule 62 is a protein called 40S ribosomal protein S0-A.

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

- Molecule 63 is a protein called 40S ribosomal protein S1-A.

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

- Molecule 64 is a protein called 40S ribosomal protein S2.

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

- Molecule 65 is a protein called RPS3 isoform 1.

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

- Molecule 66 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 67 is a protein called 40S ribosomal protein S5.

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

- Molecule 68 is a protein called 40S ribosomal protein S6-A.

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

- Molecule 69 is a protein called 40S ribosomal protein S7-A.

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

- Molecule 70 is a protein called 40S ribosomal protein S8-B.

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

- Molecule 71 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 72 is a protein called 40S ribosomal protein S10-A.

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

- Molecule 73 is a protein called 40S ribosomal protein S11-A.

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

- Molecule 74 is a protein called 40S ribosomal protein S13.

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

- Molecule 75 is a protein called 40S ribosomal protein S14-A.

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

- Molecule 76 is a protein called 40S ribosomal protein S15.

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

- Molecule 77 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 78 is a protein called 40S ribosomal protein S17-A.

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

- Molecule 79 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 80 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 81 is a protein called 40S ribosomal protein S20.

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

- Molecule 82 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 83 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 84 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
85	2	1	Total	Zn	0
			1	1	
85	5	1	Total	Zn	0
			1	1	
85	8	1	Total	Zn	0
			1	1	
85	S	1	Total	Zn	0
			1	1	
85	V	1	Total	Zn	0
			1	1	
85	Y	1	Total	Zn	0
			1	1	
85	a	1	Total	Zn	0
			1	1	
85	b	1	Total	Zn	0
			1	1	

- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

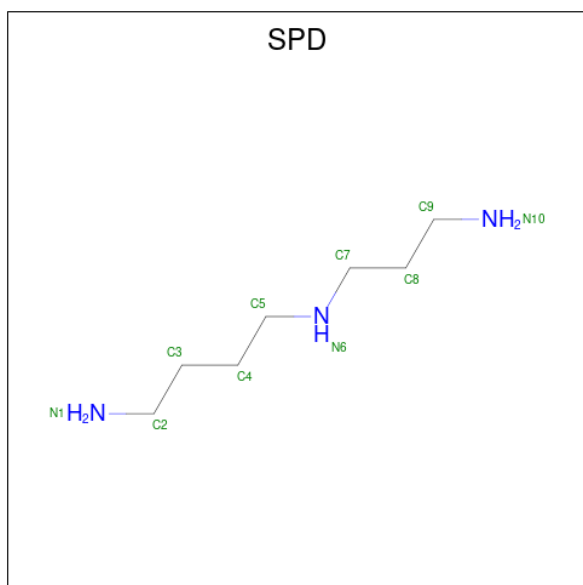
Mol	Chain	Residues	Atoms		AltConf
86	AA	188	Total	Mg	0
			188	188	
86	Aa	1	Total	Mg	0
			1	1	
86	BB	5	Total	Mg	0
			5	5	
86	CC	3	Total	Mg	0
			3	3	
86	FF	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
86	H	1	Total	Mg	0
			1	1	
86	c	42	Total	Mg	0
			42	42	

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

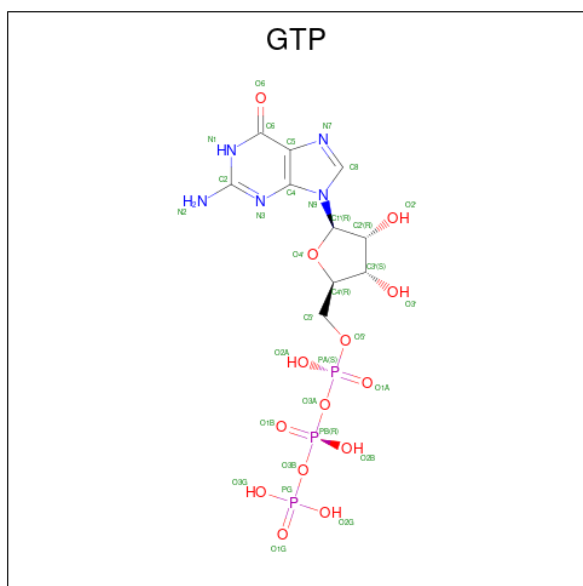


Mol	Chain	Residues	Atoms			AltConf
87	AA	1	Total	C	N	0
			10	7	3	
87	AA	1	Total	C	N	0
			10	7	3	
87	AA	1	Total	C	N	0
			10	7	3	
87	AA	1	Total	C	N	0
			10	7	3	
87	AA	1	Total	C	N	0
			10	7	3	
87	QQ	1	Total	C	N	0
			10	7	3	
87	c	1	Total	C	N	0
			10	7	3	

- Molecule 88 is POTASSIUM ION (CCD ID: K) (formula: K).

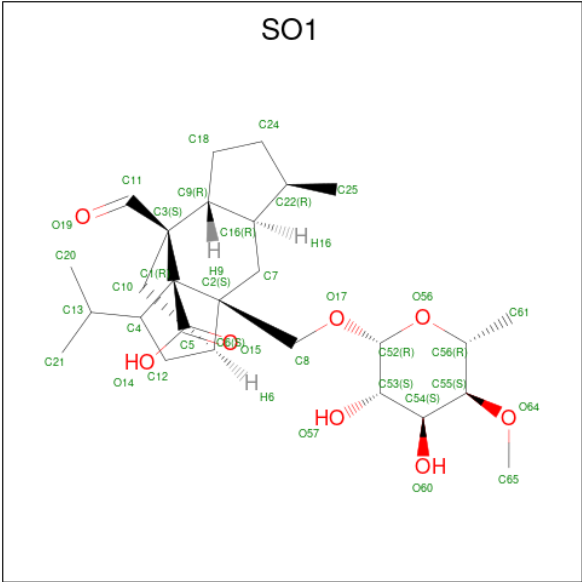
Mol	Chain	Residues	Atoms		AltConf
88	AA	12	Total	K	0
			12	12	
88	CC	1	Total	K	0
			1	1	
88	EE	1	Total	K	0
			1	1	
88	MM	1	Total	K	0
			1	1	
88	Q	1	Total	K	0
			1	1	
88	a	1	Total	K	0
			1	1	
88	c	2	Total	K	0
			2	2	

- Molecule 89 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 90 is [1R-(1.ALPHA.,3A.BETA.,4.BETA.,4A.BETA.,7.BETA.,7A.ALPHA.,8A.BETA.)]8A-[(6-DEOXY-4-O-METHYL-BETA-D-ALTROPYRANOSYLOXY)METHYL]-4-FORMYL-4,4A,5,6,7,7A,8,8A-OCTAHYDRO-7-METHYL-3-(1-METHYLETHYL)-1,4-METHANO-S-INDACENE-3A(1H)-CARBOXYLIC ACID (CCD ID: SO1) (formula: C₂₇H₄₂O₈) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
90	Aa	1	Total	C	O	0
			35	27	8	

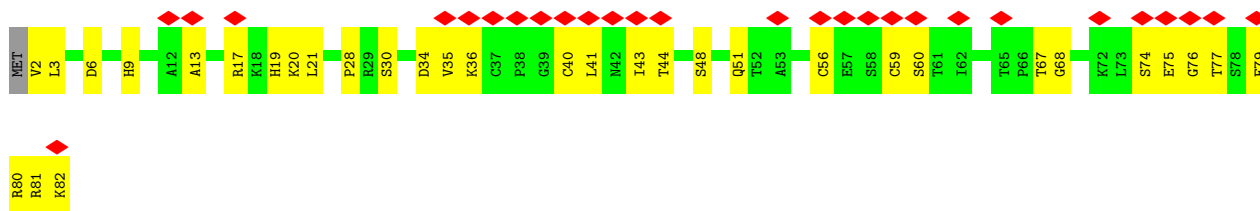
• Molecule 91 is water.

Mol	Chain	Residues	Atoms		AltConf
91	2	1	Total	O	0
			1	1	
91	A	2	Total	O	0
			2	2	
91	AA	764	Total	O	0
			764	764	
91	B	1	Total	O	0
			1	1	
91	BB	20	Total	O	0
			20	20	
91	CC	13	Total	O	0
			13	13	
91	Cc	1	Total	O	0
			1	1	
91	D	4	Total	O	0
			4	4	
91	EE	5	Total	O	0
			5	5	
91	F	4	Total	O	0
			4	4	
91	FF	4	Total	O	0
			4	4	

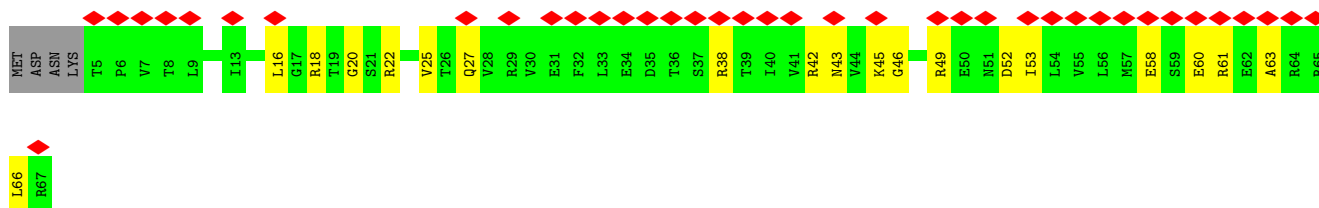
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Mol	Chain	Residues	Atoms		AltConf
91	GG	2	Total 2	O 2	0
91	H	2	Total 2	O 2	0
91	HH	1	Total 1	O 1	0
91	J	2	Total 2	O 2	0
91	JJ	1	Total 1	O 1	0
91	LL	1	Total 1	O 1	0
91	M	4	Total 4	O 4	0
91	MM	2	Total 2	O 2	0
91	N	1	Total 1	O 1	0
91	NN	2	Total 2	O 2	0
91	OO	1	Total 1	O 1	0
91	Q	5	Total 5	O 5	0
91	QQ	1	Total 1	O 1	0
91	S	1	Total 1	O 1	0
91	V	4	Total 4	O 4	0
91	a	3	Total 3	O 3	0
91	c	89	Total 89	O 89	0
91	h	1	Total 1	O 1	0
91	o	2	Total 2	O 2	0
91	p	3	Total 3	O 3	0



- Molecule 5: 40S ribosomal protein S28-A



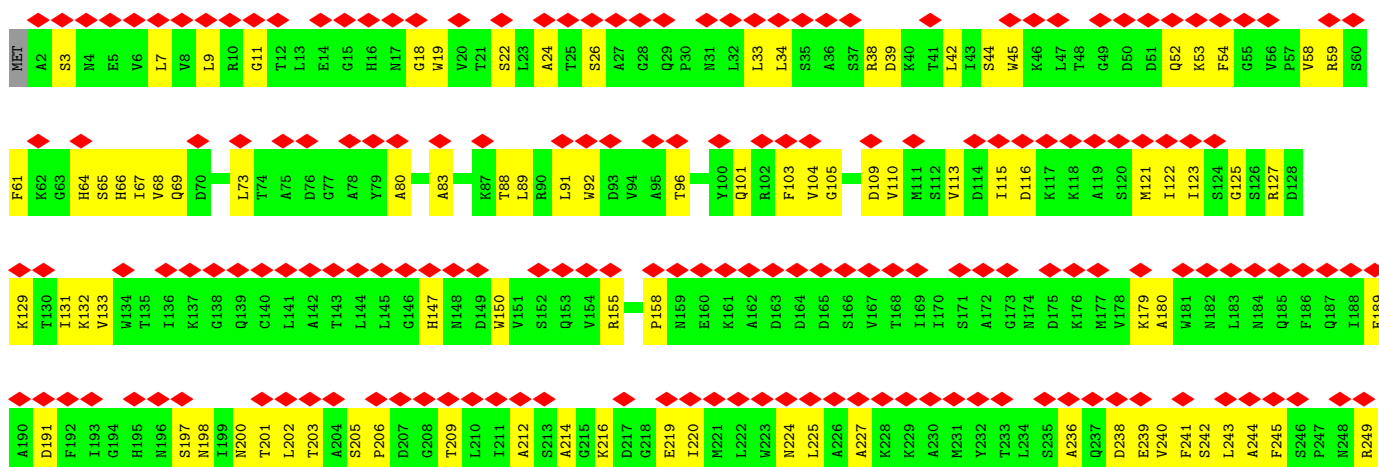
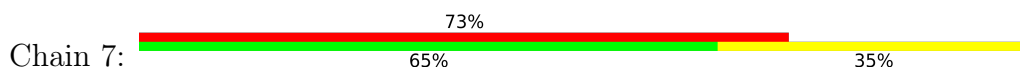
- Molecule 6: HLJ1_G0030400.mRNA.1.CDS.1



- Molecule 7: 40S ribosomal protein S30-A



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

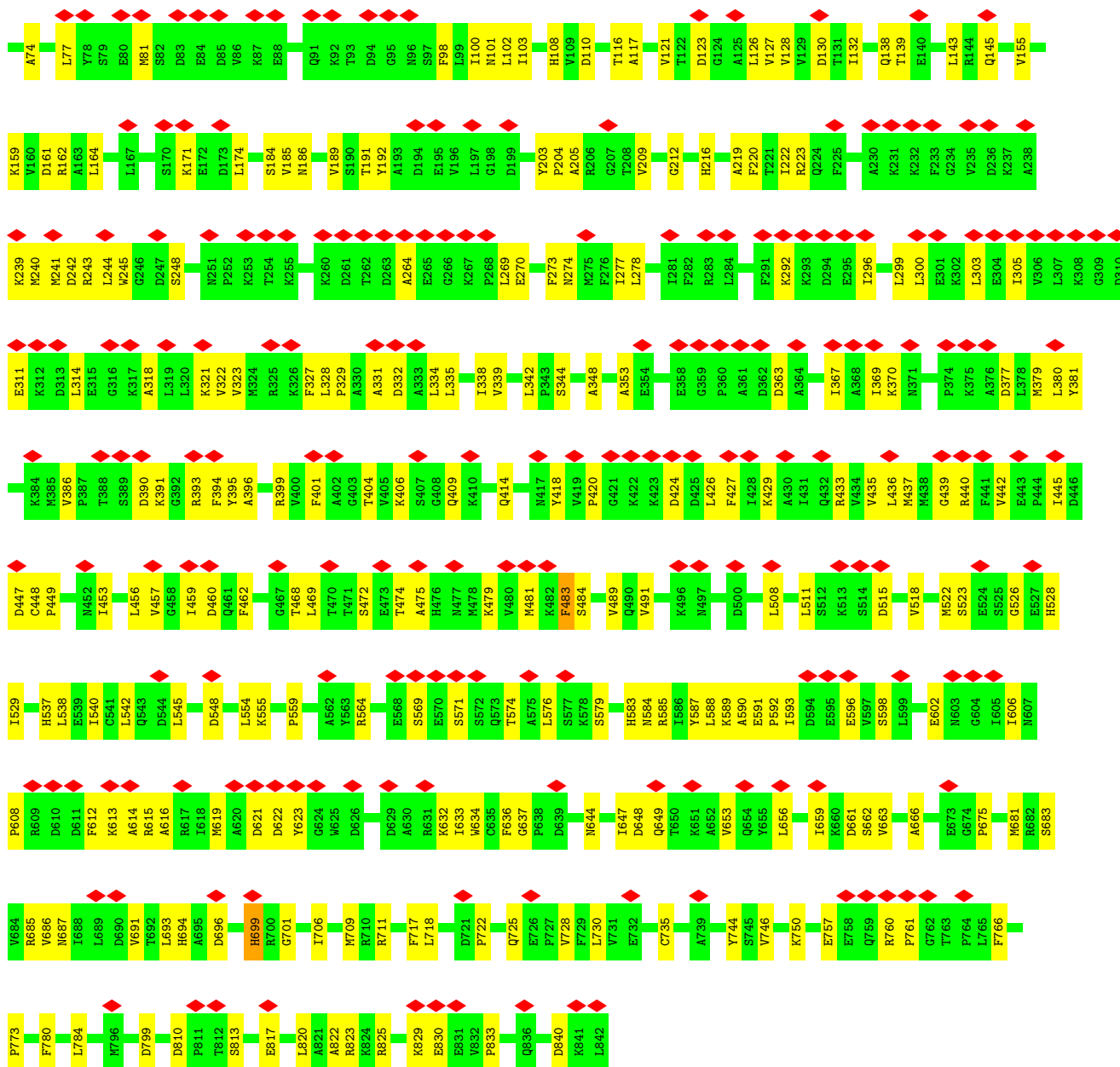




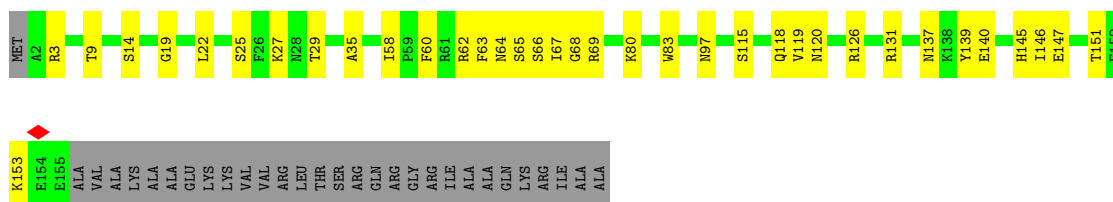
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U2464	A2403	A2324	U2225	G2150	C	G	A1883	A1800	G1725	G1646	G1573	A1477	A1394
G2465	A2404	G2324	C2227	U2154	A	A	U1884	U1801	A1729	A1647	C1574	U1479	C1397
G2466	C2405	G2328	A2228	G2155	C	C	U1886	C1802	G1730	G1650	A1575	G1480	U1398
G2467	C2406	C2329	A2229	G2156	A	U	A1887	A1803	U1737	U1651	G1576	A1481	A1399
A2468	C2407	C2330	A2230	G2157	A	A	U1888	C1805	U1738	G1652	G1577	G1482	G1400
G2469	U2408	C2331	A2232	A2158	U	C	U1889	A1806	G1738	G1653	C1578	G1483	A1401
C2470	U2411	A2332	C2232	U2159	U	C	A1893	G1807	A1741	C1657	G1579	U1484	G1404
C2471	C2333	C2333	C2235	G2160	A	A	U1894	G1808	U1742	G1658	A1580	G1485	A1407
C2472	C2334	G2161	G2151	G2162	C	G	A1895	A1809	G1743	G1659	C1581	G1486	
U2473	G2335	U2162	U2163	U2163	C	A	A1896	A1810	G1744	C1660	G1582	U1487	
C2474	U2336	A2164	A2164	A2164	U	G	G1897	G1811	C1745	G1661	C1579	G1488	
G2475	C2337				C	C	G1898	G1812	U1746	G1662	U1584	U1489	
U2476	C2338	A2167	G2249	A2167	C	A	G1899	A1813	U1747	G1663	G1585	G1490	
C2477	C2339	A2168	G2250	A2168	C	A	U1900	A1814	G1748	G1664	C1586	U1491	
G2478	U2344	G2169	A2251	G2169	U	C	G1906	U1815	A1749	G1665	A1587	G1492	
C2479	A2418	U2170	A2252	U2170	C	G	C1907	A1816	U1750	G1666	A1588	G1493	
U2480	A2345	U2171	U2171	U2171	U	G	A1908	G1817	G1751	A1667	A1589	U1501	
G2481	G2346	U2176	A2254	U2176	C	G	A1909	U1821	G1754	G1668	G1592	U1502	
C2482	U2347	G2177	A2255	G2177	U	C	A1910	A1822	C1755	C1669	C1596	G1507	
U2483	A2348	G2178	A2256	G2178	C	G	A1911	A1823	U1756	G1670	G1597	U1508	
G2484	U2349	G2179	A2257	G2179	U	A	G1914	U1824	A1757	C1671	C1598	C1420	
C2485	U2350	G2180	A2258	G2180	C	C	C1917	G1825	G1675	G1676	U1523	U1427	
A2486	U2351	C2181	U2264	C2181	A	C	U1920	A1826	G1677	A1524	G1525	G1431	
U2487	A2352	U2186	C2265	U2186	C	U	A1921	A1827	C1678	G1679	U1601	G1434	
C2488	U2353	G2187	U2266	G2187	G	G	U1922	A1828	U1763	A1679	C1531	U1435	
U2489	A2354	A2188	C2267	A2188	C	U	A1923	G1830	U1764	G1680	U1532	U1436	
G2490	U2355	U2189	U2268	U2189	C	C	C1924	U1831	U1765	U1681	U1533	U1437	
C2491	U2356	G2192	G2272	C2192	U	C	U1925	G1832	G1766	U1686	A1612	U1439	
U2492	A2357	U2193	G2273	U2193	U	C	C1926	A1833	U1687	U1688	C1615	G1443	
C2493	U2358	G2194	U2274	G2194	C	C	G1927	U1834	U1688	U1689	U1616	G1444	
U2494	A2359	C2195	G2280	C2195	U	G	U1928	C1836	C1770	G1617	G1618	U1445	
G2495	U2360	U2201	A2281	G2201	A	U	A1930	U1837	U1772	U1771	A1619	G1446	
C2496	U2361	C2202	U2282	C2202	C	U	U1931	G1838	C1773	U1694	G1620	G1447	
U2497	A2362	U2203	G2283	U2203	G	G	A1932	A1839	G1778	U1695	A1621	U1448	
C2498	U2363	G2204	C2284	G2204	C	C	G1935	U1841	G1779	A1699	G1622	A1449	
U2499	A2364	C2205	U2285	U2205	U	C	G1940	A1842	C1780	G1700	G1623	G1450	
A2500	U2365	G2206	A2286	G2206	C	C	C1941	C1843	C1781	C1701	G1624	A1461	
C2501	U2366	A2207	U2287	A2207	U	G	U1942	G1852	U1782	G1702	A1625	U1462	
U2502	A2367	U2208	G2288	U2208	C	C	G1949	U1853	U1783			G1464	
C2503	U2368	G2209	C2289	G2209	A	U	U1952	C1856	G1784	C1709	U1629	A1465	
U2504	A2369	U2210	U2290	U2210	G	C	G	A1858	G1785	C1710	U1630	G1560	
G2505	U2370	C2212	A2291	C2212	A	C	U	U1862	G1786	G1711	C1631	C1562	
C2506	U2371	A2213	U2292	A2213	C	C	U	G1863	G1788	G1712	A1632	U1467	
U2507	A2372	U2214	U2293	U2214	C	C	U	A	G1789	G1717	U1635	A1468	
C2508	U2373	G2215	A2294	G2215	C	C	U	C1872	G1790	G1718	A1637	G1565	
U2509	A2374	U2216	U2295	U2216	U	C	U	G1878	C1792	G1719	C1639	A1566	
C2510	U2375	C2217	A2296	C2217	C	C	U	A1879	G1794	U1720	G1640	U1567	
U2511	A2376	U2218	U2297	U2218	A	G	U	U1880	U1795	U1721	U1641	U1568	
C2512	U2377	A2219	A2298	A2219	C	C	U	A1881	G1796	U1722	A1642	A1473	
U2513	U2378	G2220	U2299	G2220	C	C	U		A1797	A1723	U1570	A1475	
C2514	A2379	U2221	A2300	U2221	U	U	U						
A2515	U2380	C2222	U2301	C2222	C	C	U						
U2516	A2381	U2223	A2302	U2223	A	C	U						
C2517	U2382	U2224	U2303	U2224	C	C	U						
U2518	A2383	A2225	A2304	A2225	C	C	U						
C2519	U2384	U2226	G2305	U2226	C	C	U						
U2520	A2385	U2227	U2306	U2227	C	C	U						
C2521	U2386	A2228	G2307	U2228	C	C	U						
U2522	A2387	U2229	C2308	U2229	C	C	U						
C2523	U2388	U2230	A2309	U2230	C	C	U						
U2524	A2389	G2231	U2310	G2231	C	C	U						
A2525	U2390	U2232	A2311	U2232	A	C	U						
C2526	U2391	U2233	U2312	U2233	C	C	U						



M1	V2	A3	F4	T5	V6	D7	Q8	M9	R10	S11	L12	M13	D14	R20	N21	M22	S23	V24	I25	A26	H27	V28	D29	H30	G31	K32	S33	T34	S38	L39	V40	Q41	R42	A43	O44	I45	I46	S47	A48	A49	K50	A51	G52	F53	A54	R55	D58	K61	D62	E65	I68	T69	L70
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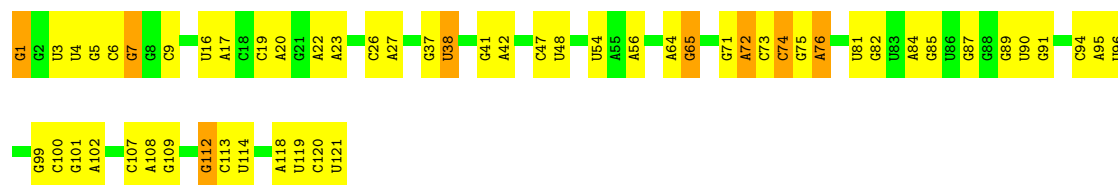


• Molecule 13: 60S ribosomal protein L17-A

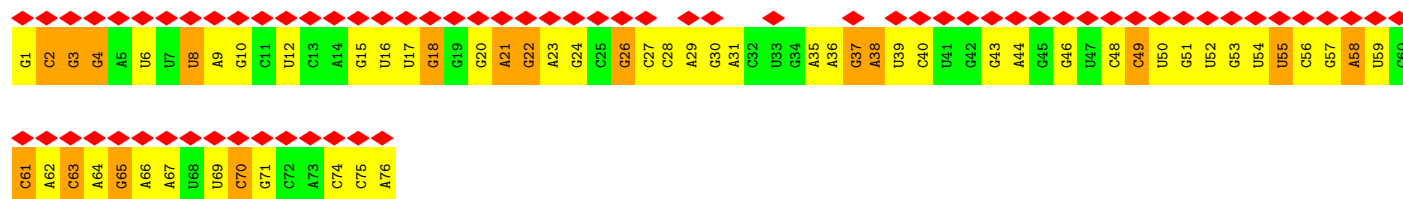


• Molecule 14: 5S ribosomal RNA

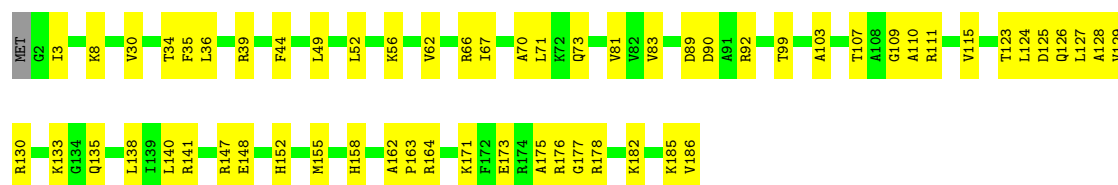




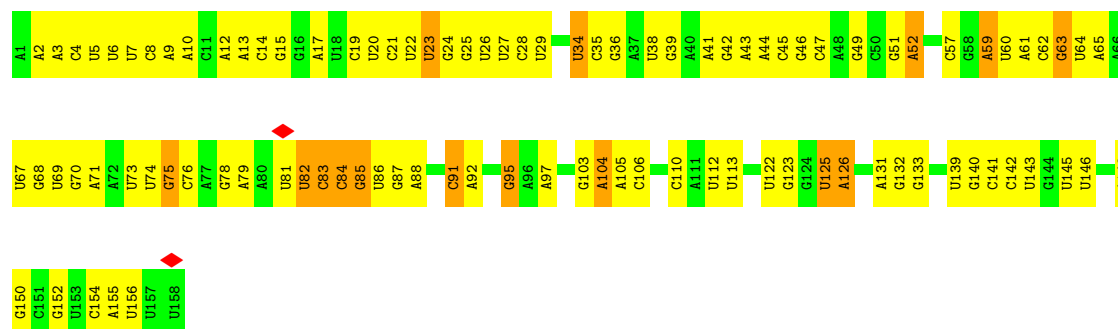
• Molecule 15: Transfer RNA Phe



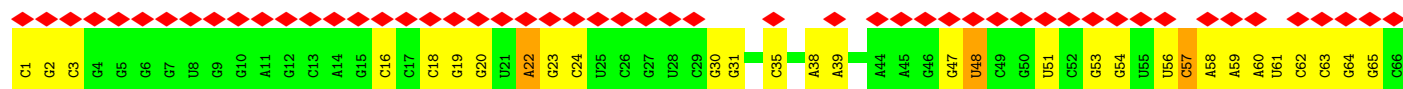
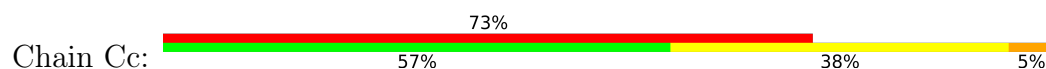
• Molecule 16: 60S ribosomal protein L18-A

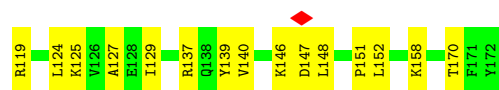


• Molecule 17: 5.8S ribosomal RNA



• Molecule 18: Transfer RNA fMet





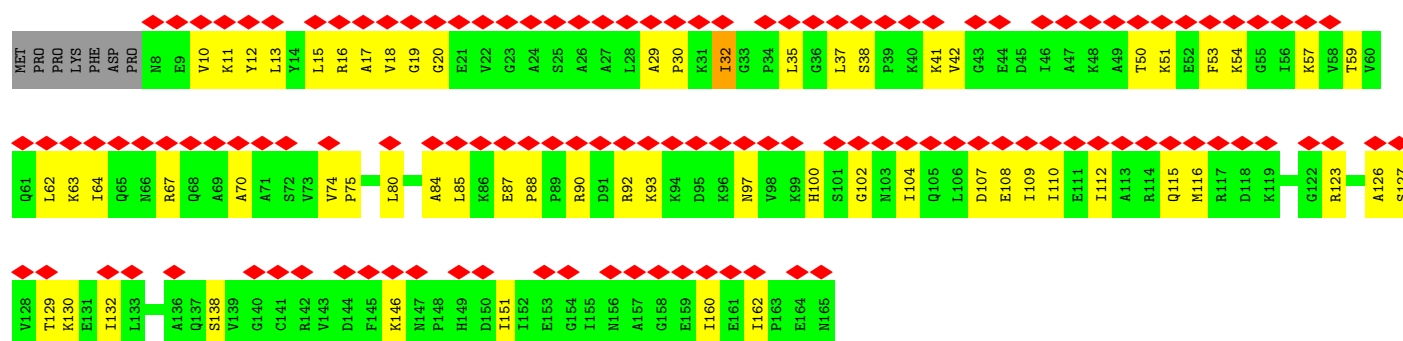
- Molecule 23: 60S ribosomal protein L2-A

Chain EE: 70% 29%



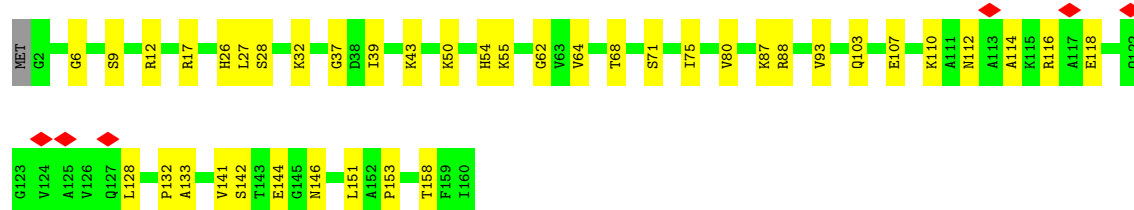
- Molecule 24: 60S ribosomal protein L12-A

Chain Ee: 76% 59% 36%



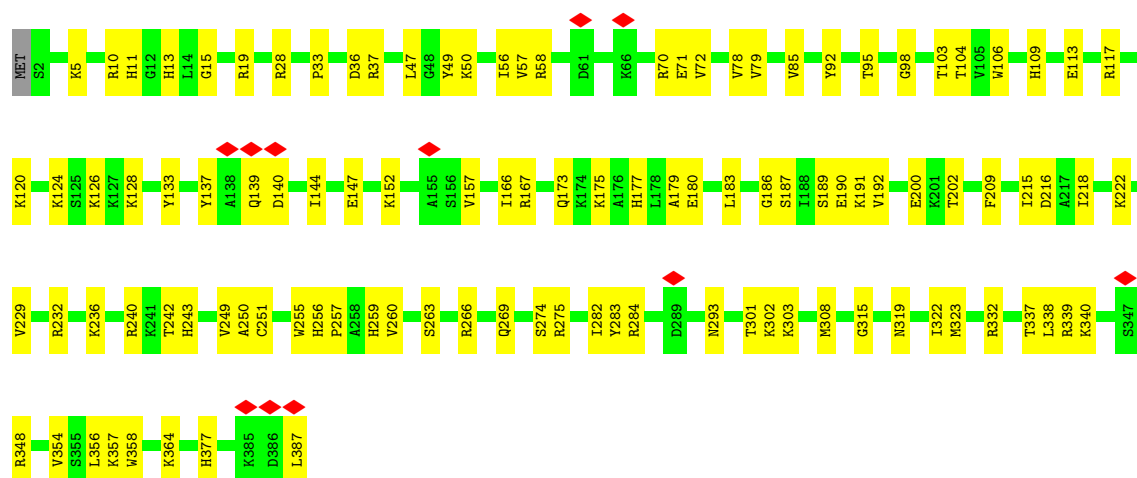
- Molecule 25: 60S ribosomal protein L21-A

Chain F: 74% 25%

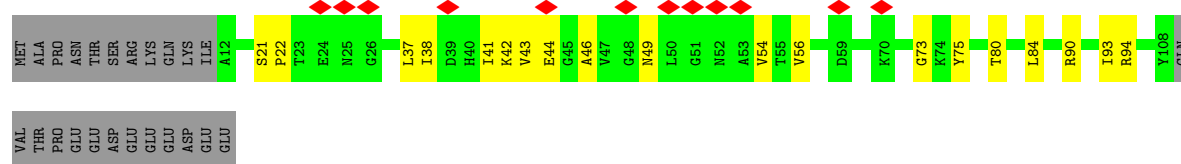


- Molecule 26: 60S ribosomal protein L3

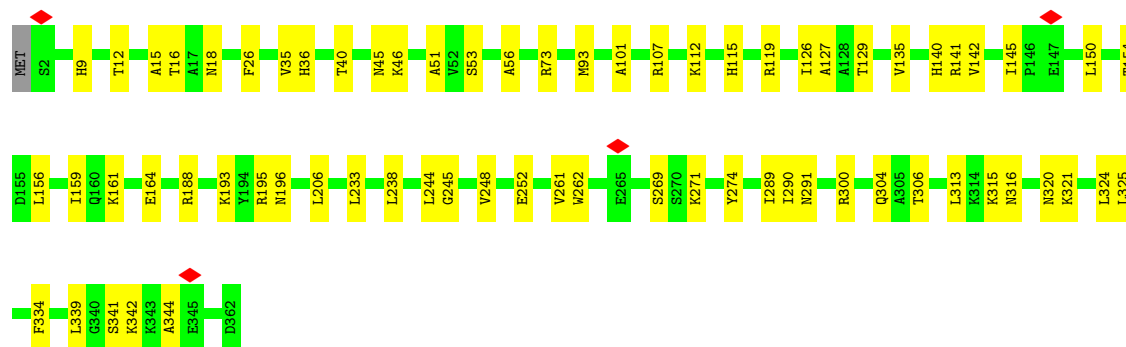
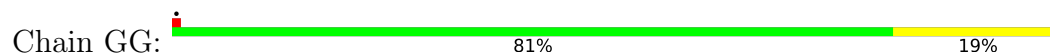
Chain FF: 72% 28%



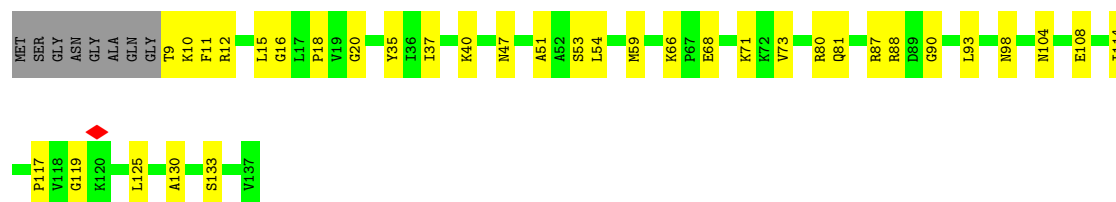
- Molecule 27: 60S ribosomal protein L22-A



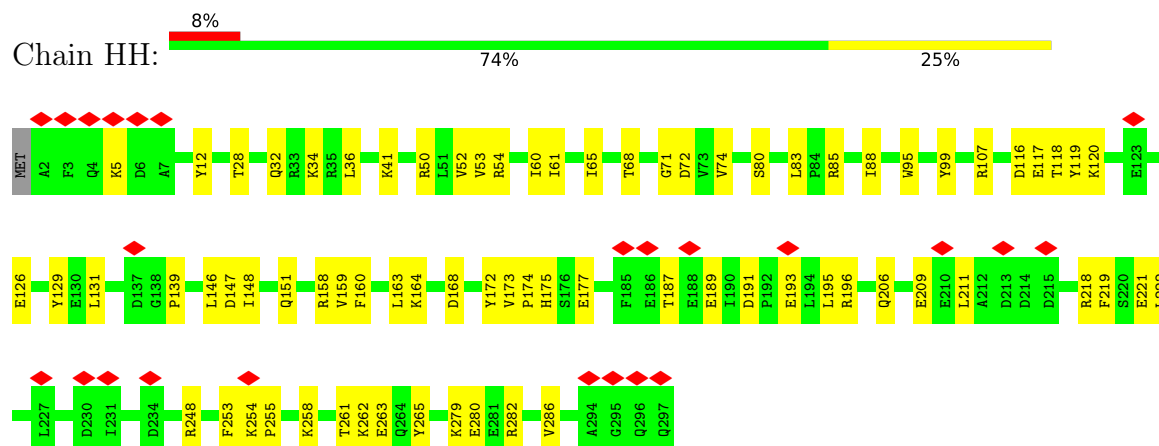
- Molecule 28: 60S ribosomal protein L4-A



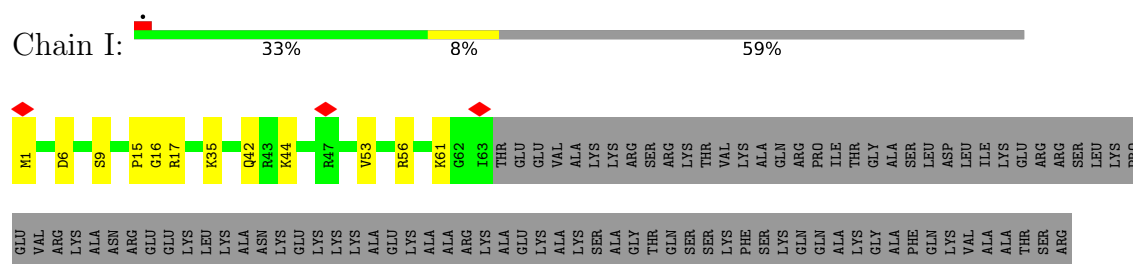
- Molecule 29: 60S ribosomal protein L23-A



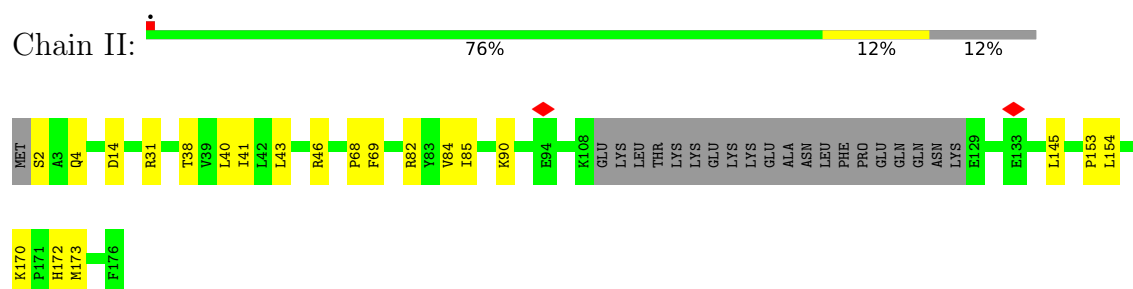
- Molecule 30: 60S ribosomal protein L5



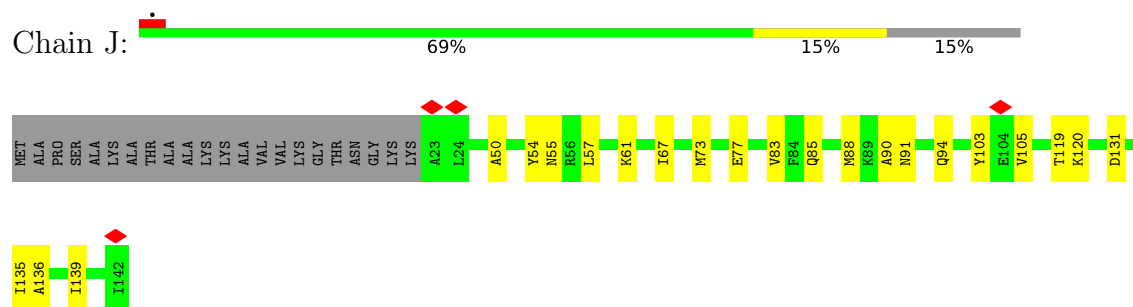
- Molecule 31: 60S ribosomal protein L24-A



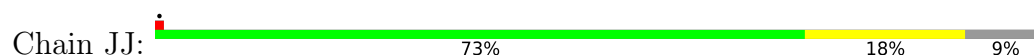
- Molecule 32: 60S ribosomal protein L6-A

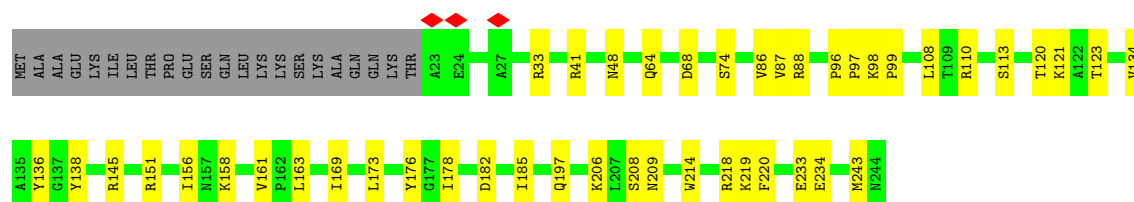


- Molecule 33: 60S ribosomal protein L25

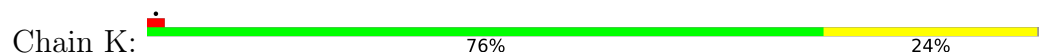


- Molecule 34: 60S ribosomal protein L7-A

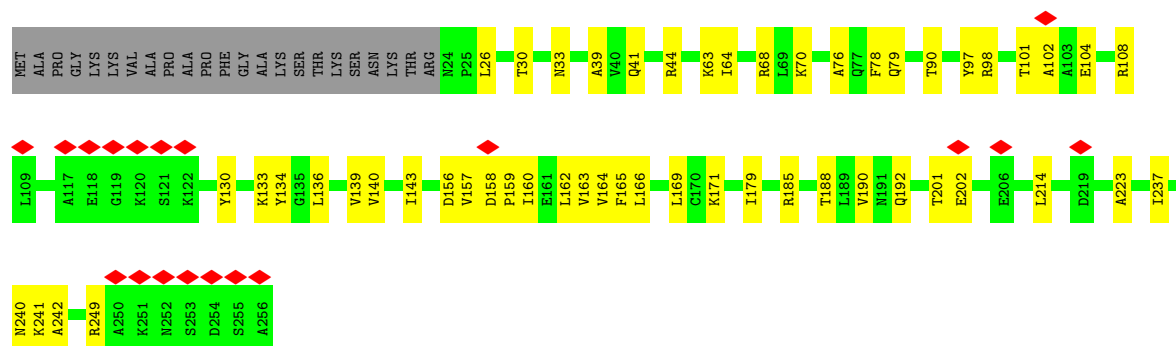
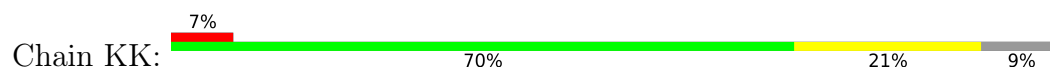




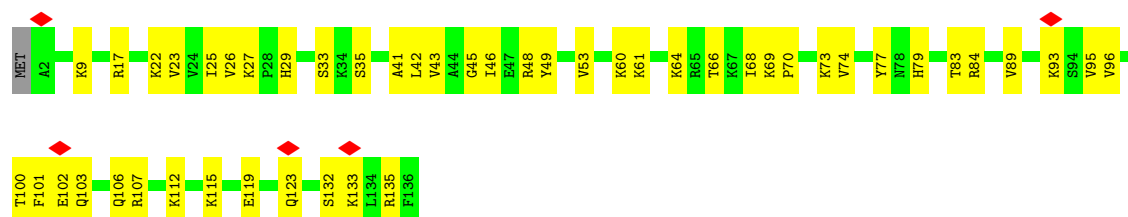
- Molecule 35: 60S ribosomal protein L26-A



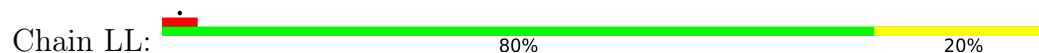
- Molecule 36: 60S ribosomal protein L8-A

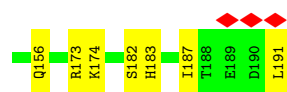


- Molecule 37: 60S ribosomal protein L27-A



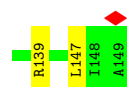
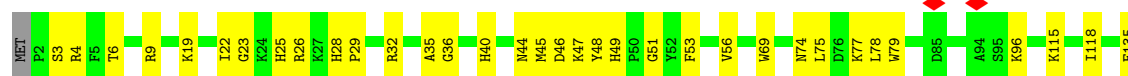
- Molecule 38: RPL9A isoform 1





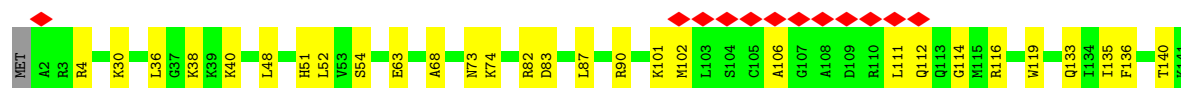
- Molecule 39: 60S ribosomal protein L28

Chain M: 75% 24%



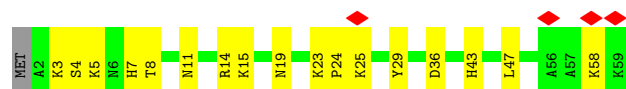
- Molecule 40: 60S ribosomal protein L10

Chain MM: 6% 76% 21%



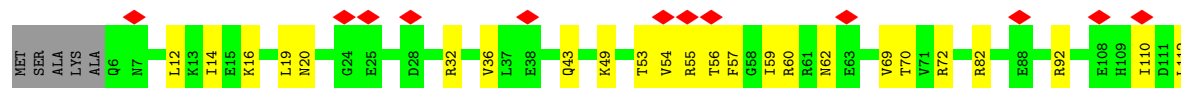
- Molecule 41: 60S ribosomal protein L29

Chain N: 7% 69% 29%



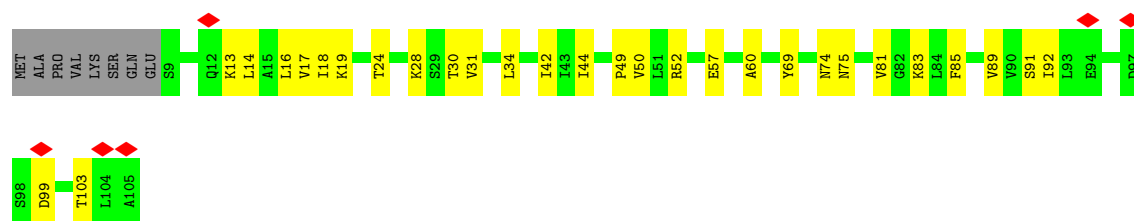
- Molecule 42: 60S ribosomal protein L11-A

Chain NN: 12% 72% 25%

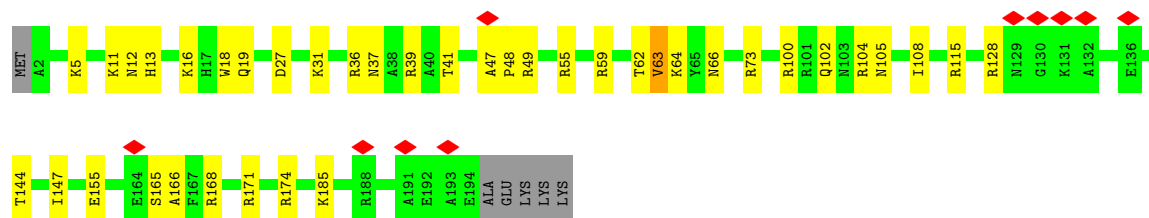
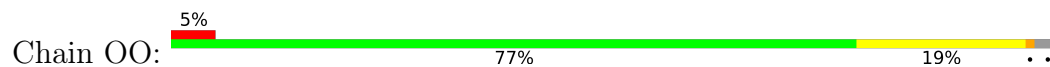


- Molecule 43: 60S ribosomal protein L30

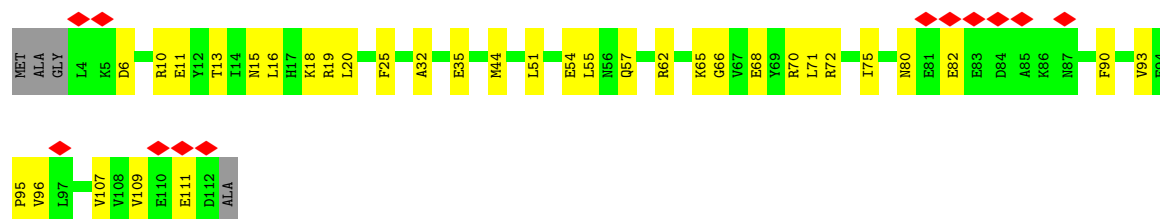
Chain O: 6% 65% 28% 8%



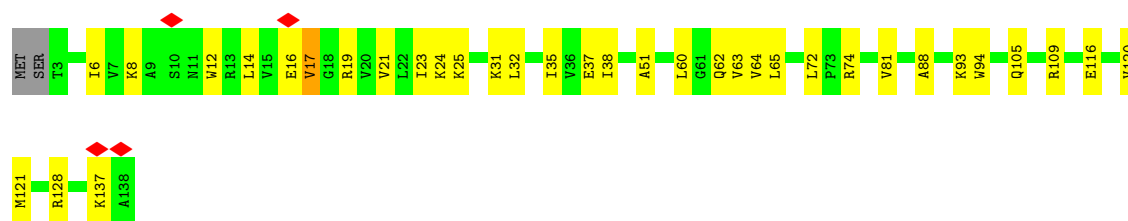
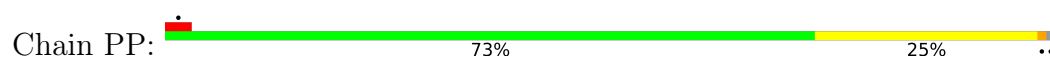
- Molecule 44: 60S ribosomal protein L13-A



- Molecule 45: 60S ribosomal protein L31-A



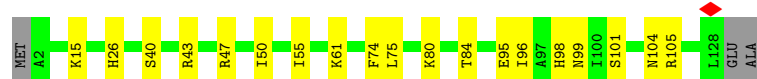
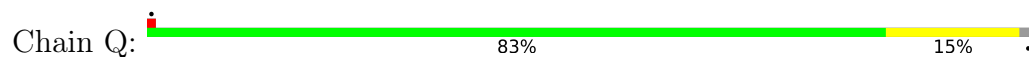
- Molecule 46: 60S ribosomal protein L14-A



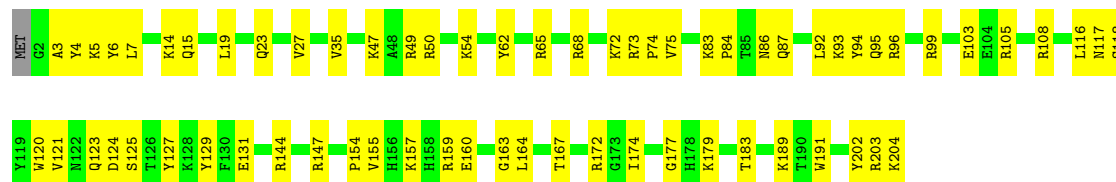
- Molecule 47: Polypeptide



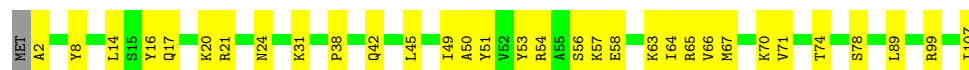
- Molecule 48: 60S ribosomal protein L32



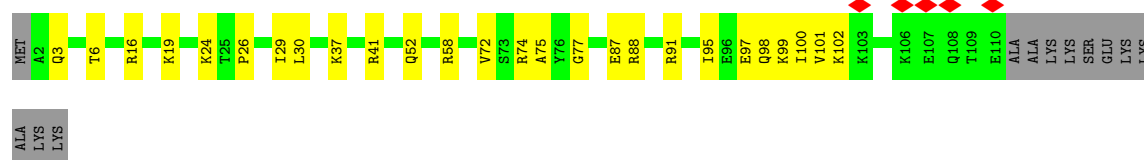
- Molecule 49: 60S ribosomal protein L15-A



- Molecule 50: 60S ribosomal protein L33-A



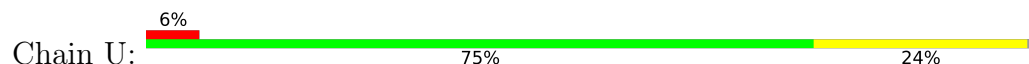
- Molecule 51: 60S ribosomal protein L34-A



- Molecule 52: 60S ribosomal protein L35-A

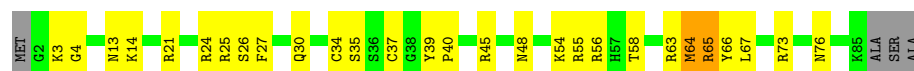


- Molecule 53: 60S ribosomal protein L36-A





- Molecule 54: 60S ribosomal protein L37-A



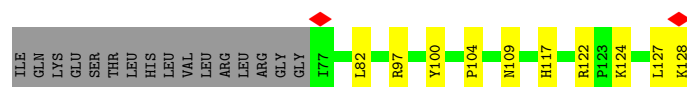
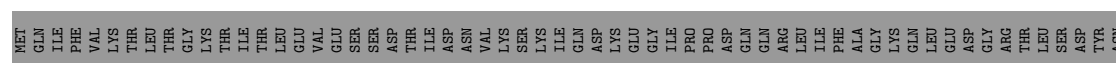
- Molecule 55: 60S ribosomal protein L38



- Molecule 56: 60S ribosomal protein L39



- Molecule 57: Ubiquitin-60S ribosomal protein L40

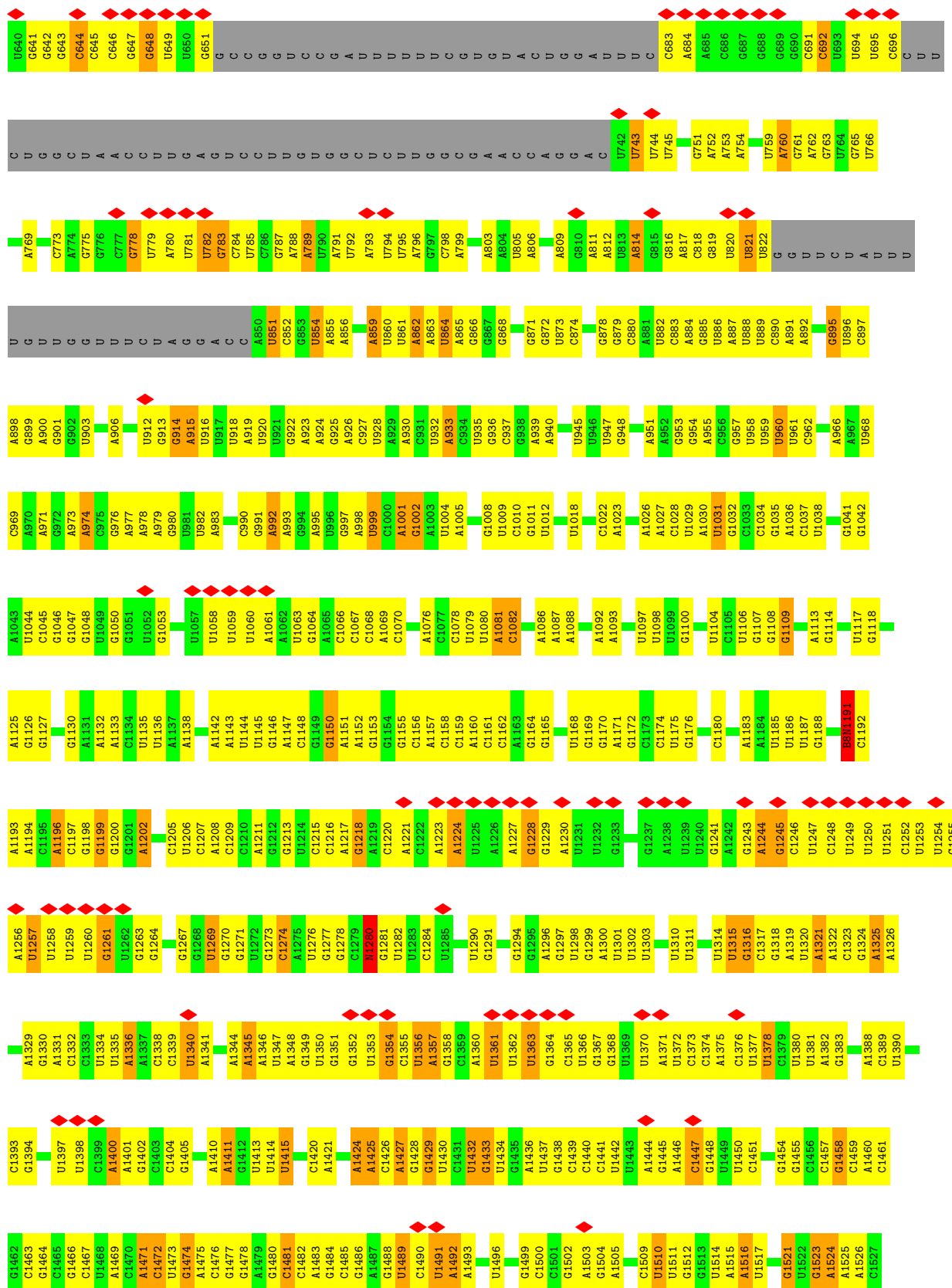


- Molecule 58: 60S ribosomal protein L41

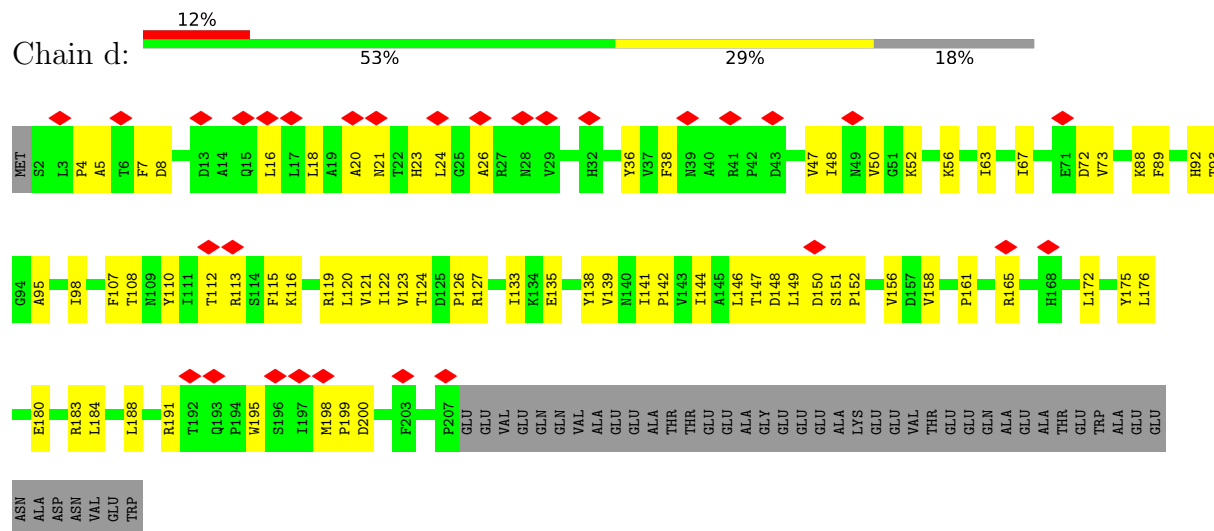


- Molecule 59: 60S ribosomal protein L42-A

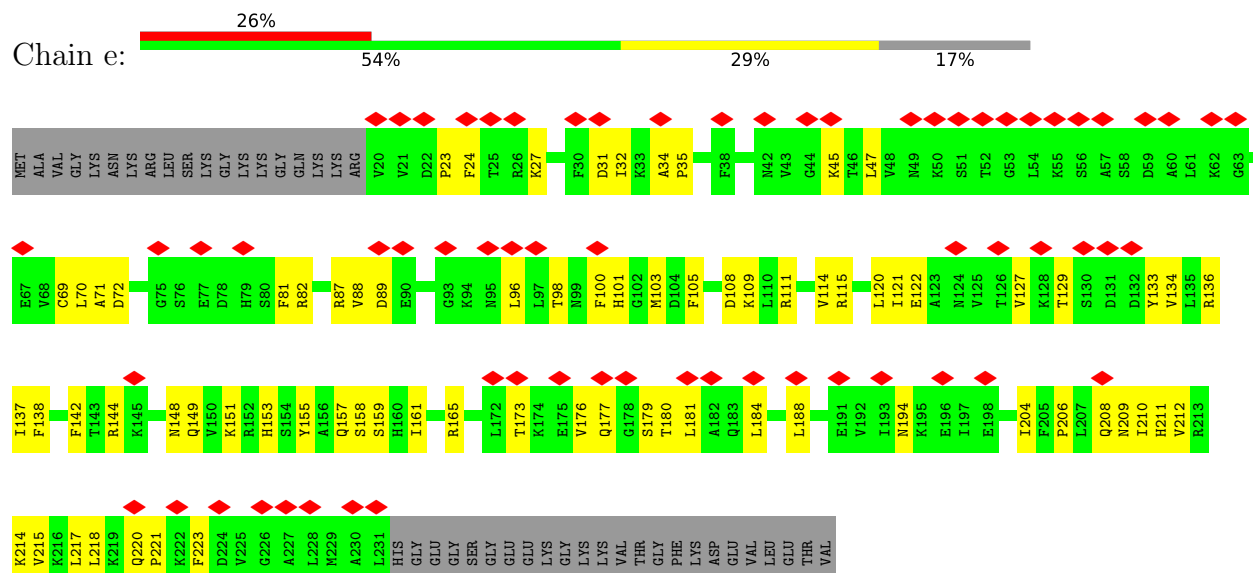




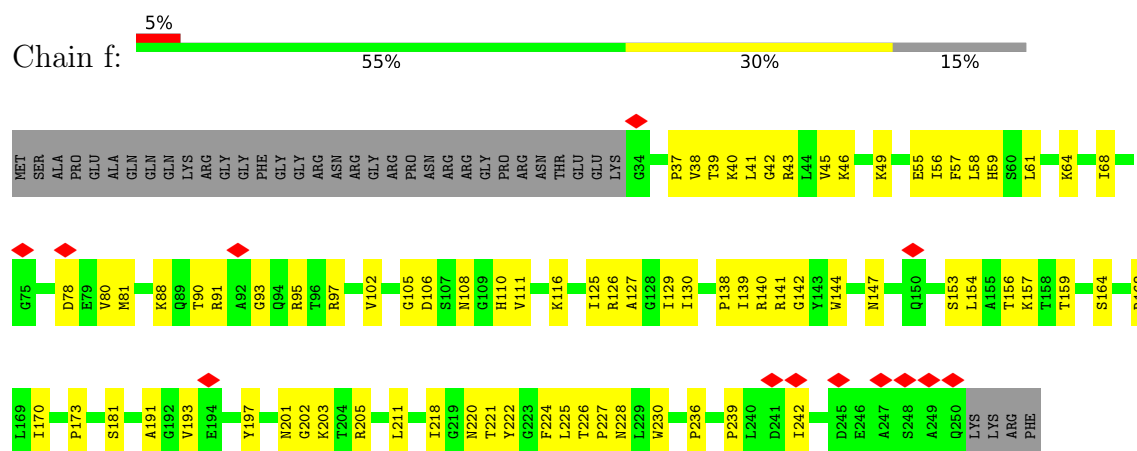
- Molecule 62: 40S ribosomal protein S0-A



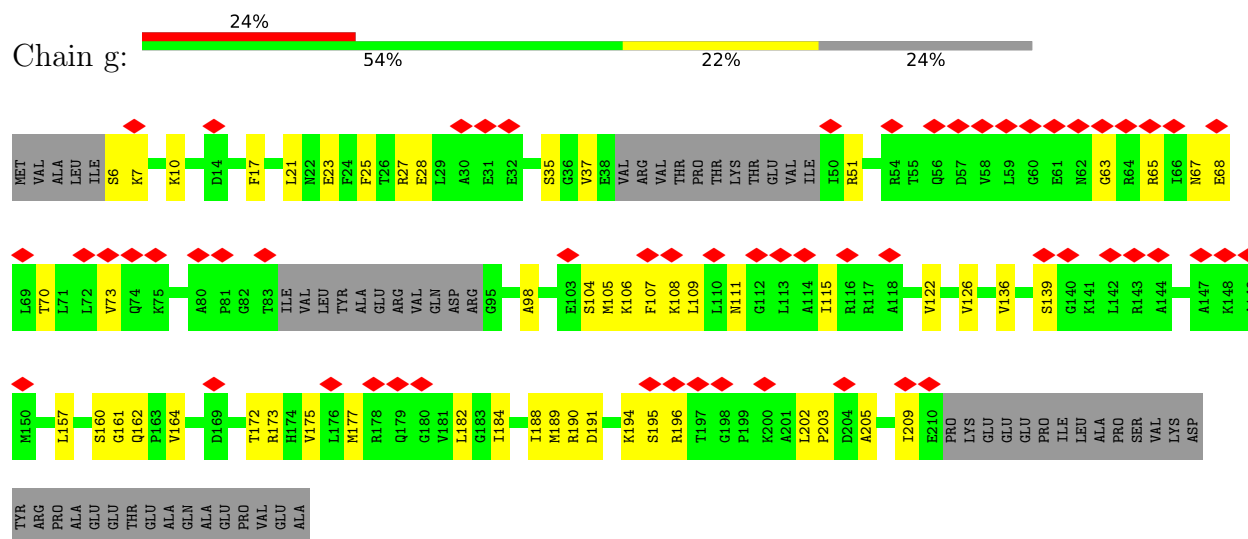
- Molecule 63: 40S ribosomal protein S1-A



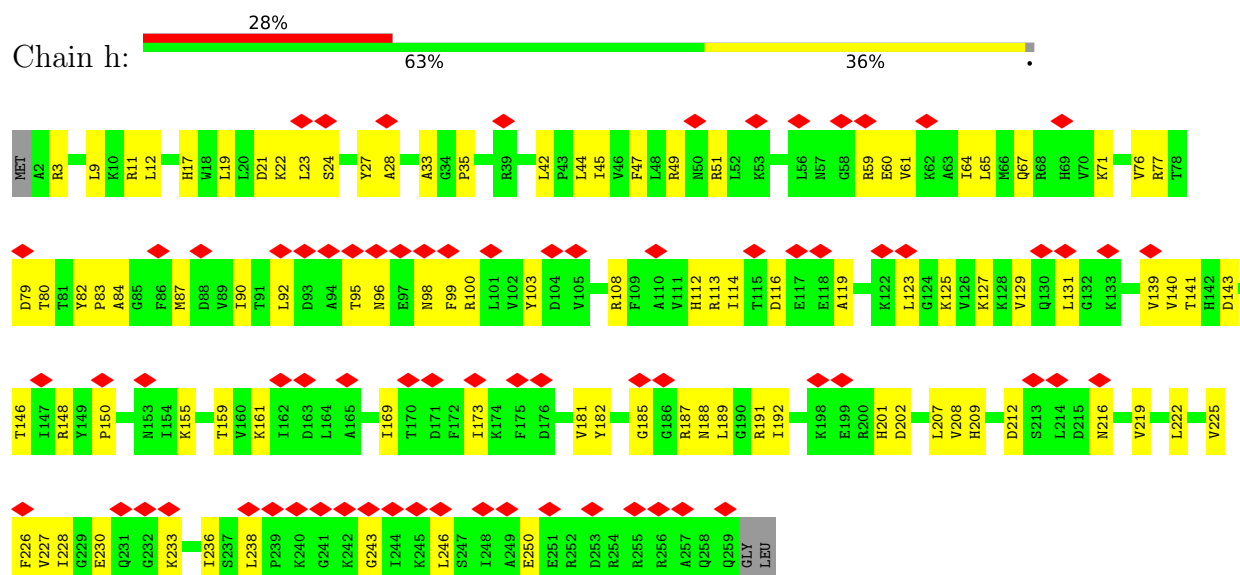
- Molecule 64: 40S ribosomal protein S2

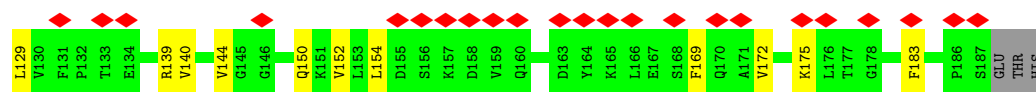


- Molecule 65: RPS3 isoform 1

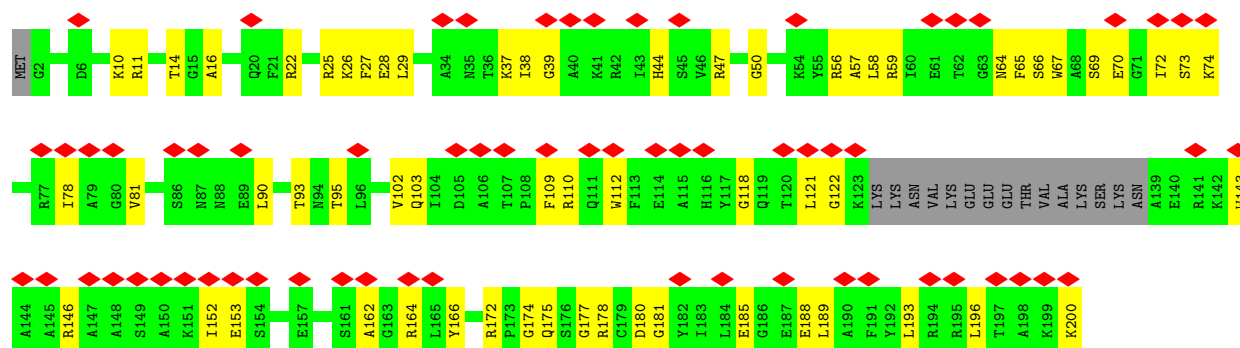


- Molecule 66: 40S ribosomal protein S4-A

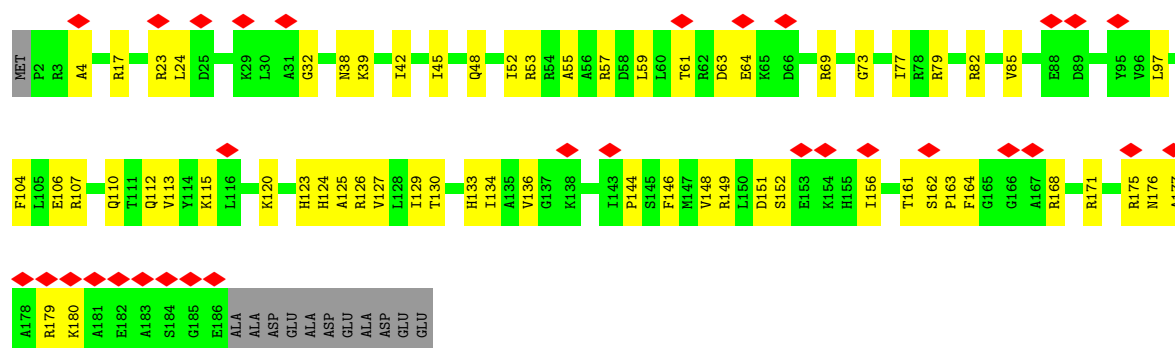




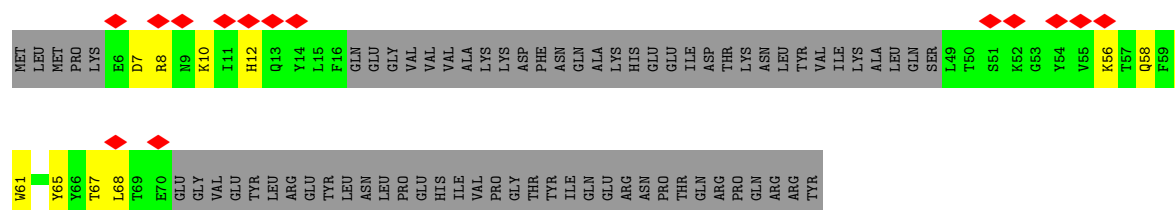
• Molecule 70: 40S ribosomal protein S8-B



• Molecule 71: 40S ribosomal protein S9-A

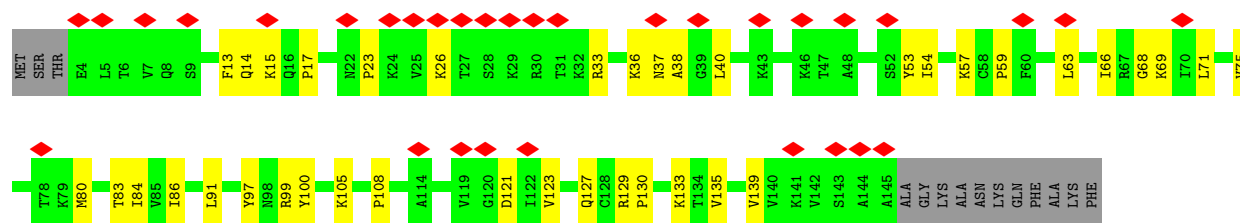


• Molecule 72: 40S ribosomal protein S10-A

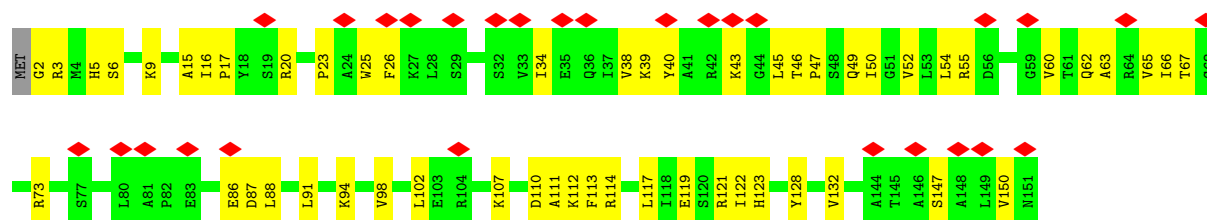


• Molecule 73: 40S ribosomal protein S11-A

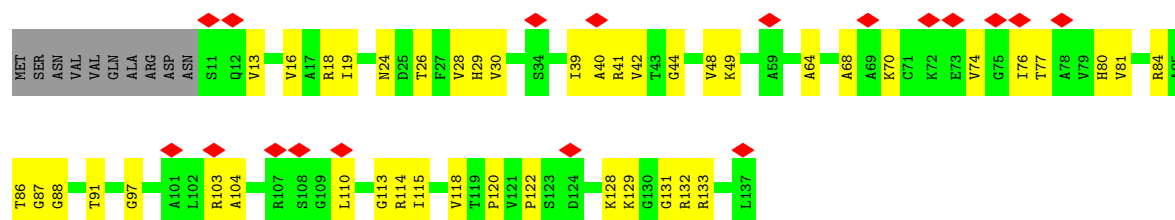




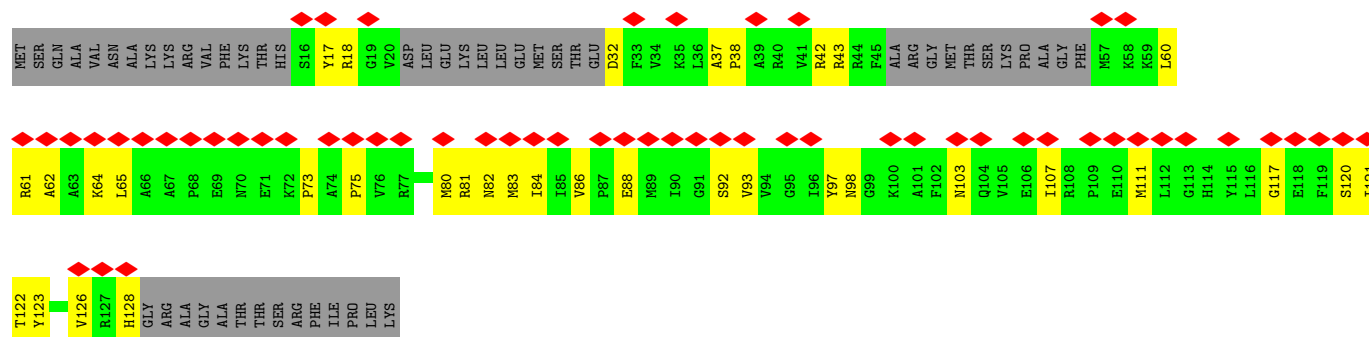
• Molecule 74: 40S ribosomal protein S13



• Molecule 75: 40S ribosomal protein S14-A

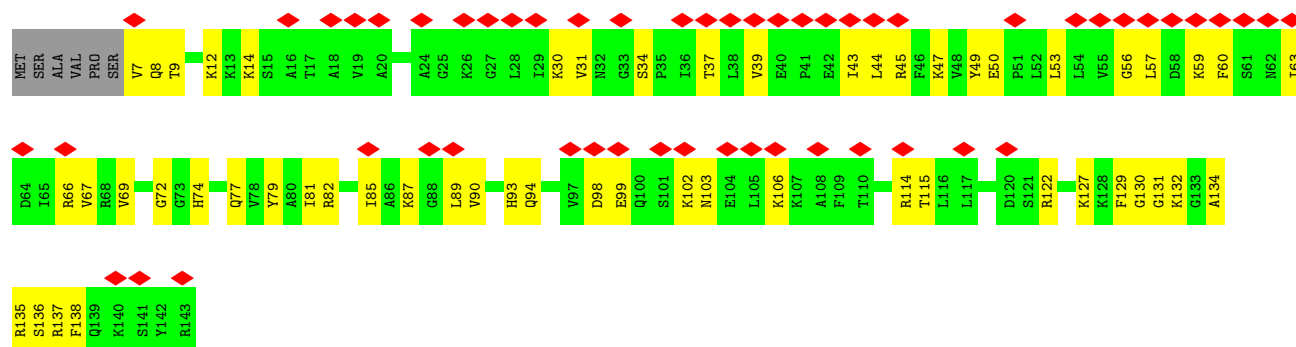


• Molecule 76: 40S ribosomal protein S15

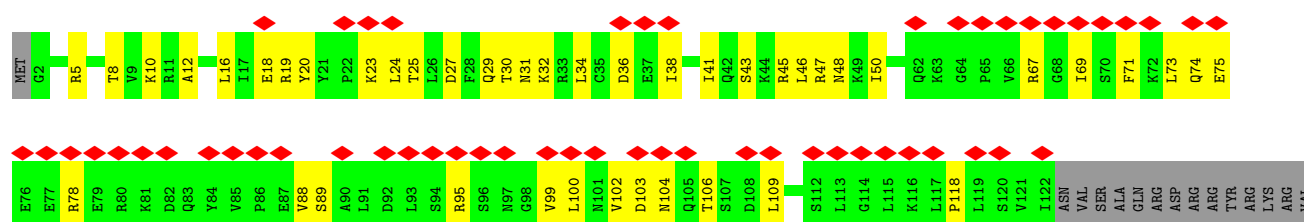
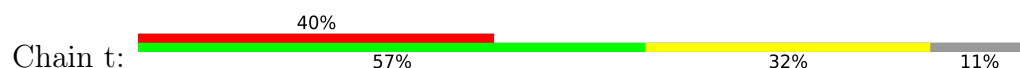


• Molecule 77: 40S ribosomal protein S16-A

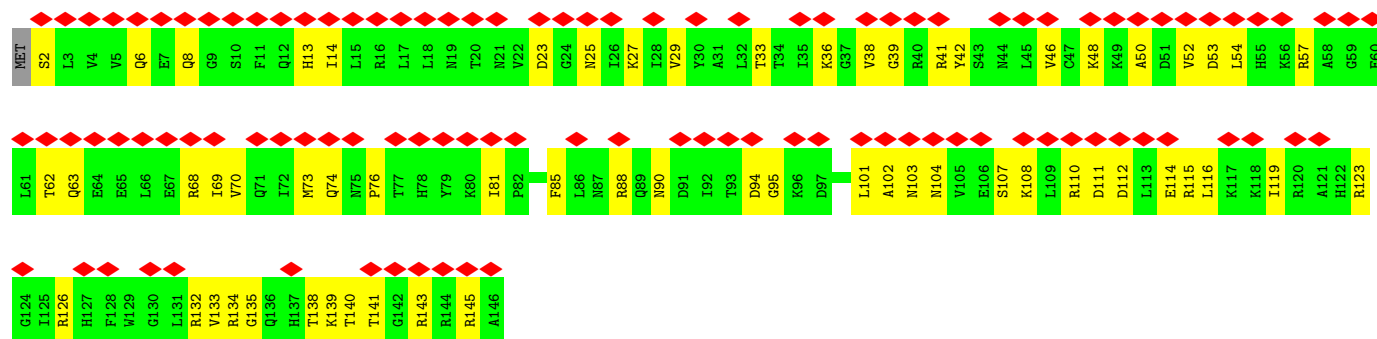




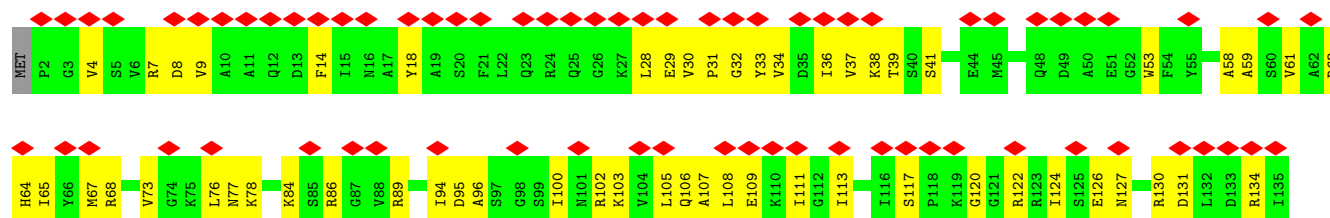
• Molecule 78: 40S ribosomal protein S17-A

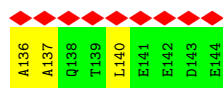


• Molecule 79: 40S ribosomal protein S18-A

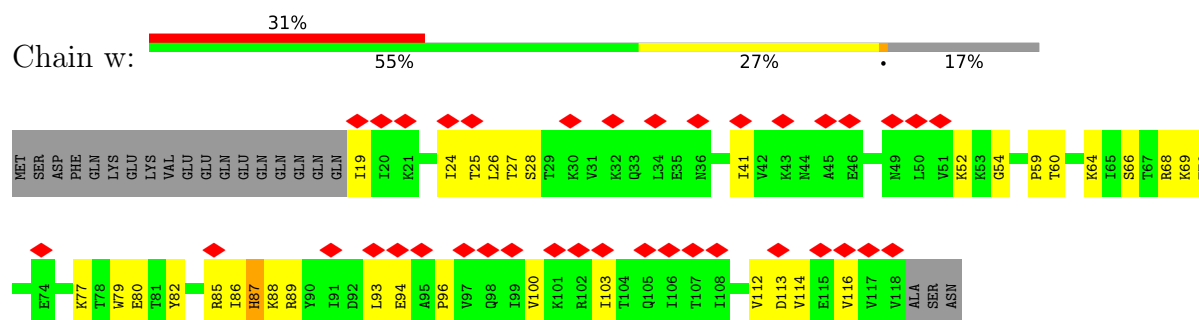


• Molecule 80: 40S ribosomal protein S19-A

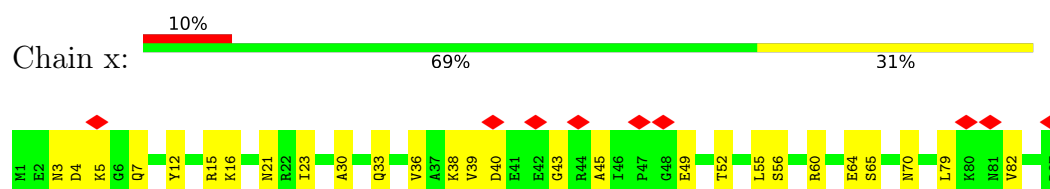




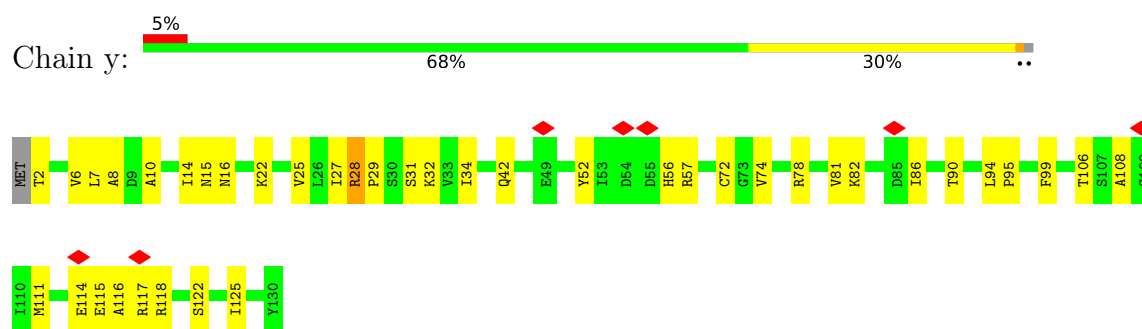
- Molecule 81: 40S ribosomal protein S20



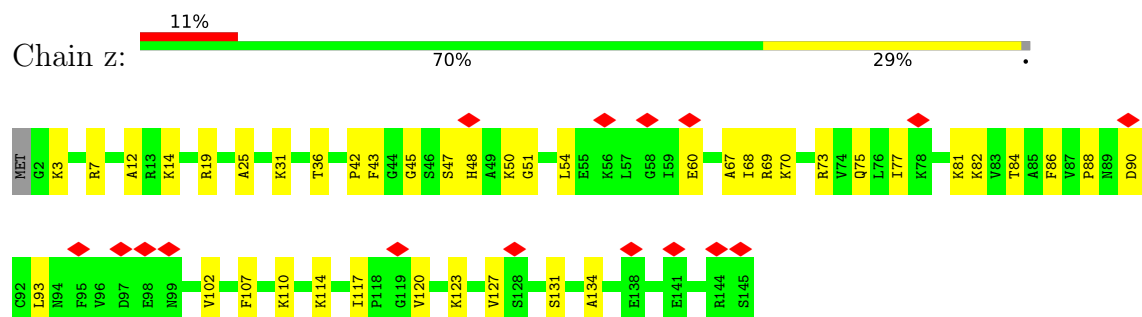
- Molecule 82: 40S ribosomal protein S21-A



- Molecule 83: 40S ribosomal protein S22-A



- Molecule 84: 40S ribosomal protein S23-A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	73086	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	1000	Depositor
Magnification	270000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.223	Depositor
Minimum map value	-0.545	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.045	Depositor
Recommended contour level	0.18	Depositor
Map size (Å)	540.0, 540.0, 540.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.9, 0.9, 0.9	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMC, 1MA, SO1, B8N, UR3, A2M, MA6, 4AC, MG, K, G7M, SPD, 5MC, YYG, DDE, OMU, OMG, ZN, GTP

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	0.11	0/1087	0.32	0/1449
2	1	0.15	0/571	0.59	2/768 (0.3%)
3	2	0.12	0/782	0.35	0/1047
4	3	0.13	0/620	0.46	0/838
5	4	0.15	0/499	0.42	0/670
6	5	0.17	0/412	0.42	1/544 (0.2%)
7	6	0.14	0/433	0.43	0/575
8	7	0.13	0/2489	0.41	0/3389
9	8	0.11	0/279	0.36	0/369
10	A	0.14	0/1585	0.35	0/2128
11	AA	0.12	1/75545 (0.0%)	0.26	0/117782
12	Aa	0.13	0/6673	0.36	2/9032 (0.0%)
13	B	0.10	0/1245	0.29	0/1676
14	BB	0.08	0/2883	0.20	0/4491
15	Bb	0.10	0/1788	0.27	0/2786
16	C	0.09	0/1465	0.30	0/1965
17	CC	0.09	0/3746	0.25	0/5832
18	Cc	0.08	0/1836	0.19	0/2859
19	D	0.10	0/1440	0.29	0/1921
20	DD	0.14	0/1558	0.36	0/2107
21	Dd	0.13	0/138	0.37	0/212
22	E	0.12	0/1481	0.34	0/1990
23	EE	0.11	0/1948	0.31	0/2617
24	Ee	0.15	0/1210	0.50	1/1627 (0.1%)
25	F	0.13	0/1300	0.35	0/1743
26	FF	0.11	0/3146	0.31	0/4228
27	G	0.13	0/786	0.41	0/1065
28	GG	0.09	0/2800	0.30	0/3790
29	H	0.10	0/978	0.33	0/1316
30	HH	0.10	0/2425	0.29	0/3271
31	I	0.10	0/533	0.29	0/707

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	II	0.09	0/1251	0.27	0/1682
33	J	0.11	0/974	0.31	0/1314
34	JJ	0.09	0/1821	0.27	0/2451
35	K	0.12	0/1004	0.32	0/1341
36	KK	0.10	0/1836	0.29	0/2481
37	L	0.14	0/1118	0.38	0/1497
38	LL	0.12	0/1539	0.32	0/2073
39	M	0.11	0/1204	0.35	0/1612
40	MM	0.08	0/1779	0.27	0/2386
41	N	0.15	0/473	0.35	0/629
42	NN	0.11	0/1374	0.34	0/1842
43	O	0.10	0/750	0.27	0/1008
44	OO	0.11	0/1568	0.34	0/2106
45	P	0.10	0/897	0.29	0/1205
46	PP	0.11	0/1068	0.33	0/1438
47	Pp	0.06	0/19	0.12	0/23
48	Q	0.09	0/1041	0.26	0/1394
49	QQ	0.10	0/1757	0.31	0/2354
50	R	0.12	0/868	0.34	0/1168
51	S	0.10	0/871	0.29	0/1164
52	T	0.11	0/978	0.31	0/1301
53	U	0.12	0/778	0.36	0/1034
54	V	0.11	0/680	0.39	0/901
55	W	0.12	0/618	0.32	0/826
56	X	0.13	0/443	0.36	0/588
57	Y	0.12	0/423	0.26	0/562
58	Z	0.11	0/234	0.24	0/300
59	a	0.12	0/831	0.38	0/1097
60	b	0.12	0/701	0.35	0/934
61	c	0.13	1/37760 (0.0%)	0.26	0/58811
62	d	0.13	0/1623	0.37	0/2222
63	e	0.14	0/1714	0.40	0/2308
64	f	0.15	0/1665	0.41	0/2263
65	g	0.15	0/1429	0.41	0/1913
66	h	0.11	0/2097	0.34	0/2823
67	i	0.15	0/1591	0.41	0/2151
68	j	0.18	0/1790	0.46	1/2393 (0.0%)
69	k	0.16	0/1506	0.48	0/2028
70	l	0.19	0/1482	0.44	0/1980
71	m	0.12	0/1519	0.34	0/2035
72	n	0.11	0/309	0.37	0/416
73	o	0.11	0/1172	0.31	0/1580
74	p	0.14	0/1215	0.35	0/1638

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	q	0.11	0/901	0.36	0/1217
76	r	0.13	0/747	0.40	0/1002
77	s	0.14	0/1099	0.46	0/1473
78	t	0.15	0/971	0.42	0/1303
79	u	0.14	0/1211	0.40	0/1628
80	v	0.12	0/1130	0.37	0/1517
81	w	0.17	0/810	0.49	0/1095
82	x	0.14	0/693	0.43	0/935
83	y	0.13	0/1038	0.43	1/1395 (0.1%)
84	z	0.11	0/1139	0.39	0/1518
All	All	0.12	2/219190 (0.0%)	0.30	8/321149 (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
37	L	0	1
46	PP	0	1
54	V	0	1
59	a	0	1
67	i	0	1
69	k	0	1
All	All	0	6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	c	1269	OMU	O3'-P	5.16	1.61	1.56
11	AA	2946	A2M	O3'-P	5.02	1.61	1.56

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	j	173	PRO	CA-N-CD	-9.39	98.86	112.00
83	y	28	ARG	C-N-CD	-6.08	107.23	120.60
12	Aa	459	ILE	CA-C-N	5.88	136.54	125.66
12	Aa	459	ILE	C-N-CA	5.88	136.54	125.66
2	1	53	GLU	CA-C-N	5.60	123.77	120.24

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
37	L	102	GLU	Peptide
46	PP	17	VAL	Peptide
54	V	64	MET	Peptide
59	a	7	THR	Peptide
67	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	34	0
2	1	563	0	603	22	0
3	2	769	0	814	30	0
4	3	610	0	633	28	0
5	4	497	0	535	17	0
6	5	404	0	397	16	0
7	6	427	0	475	15	0
8	7	2436	0	2386	79	0
9	8	276	0	289	5	0
10	A	1555	0	1659	48	0
11	AA	68429	0	34442	1651	0
12	Aa	6569	0	6639	191	0
13	B	1222	0	1231	29	0
14	BB	2579	0	1304	48	0
15	Bb	1638	0	835	29	0
16	C	1441	0	1543	49	0
17	CC	3353	0	1695	90	0
18	Cc	1644	0	837	17	0
19	D	1423	0	1510	38	0
20	DD	1531	0	1571	39	0
21	Dd	125	0	63	4	0
22	E	1445	0	1487	40	0
23	EE	1914	0	1981	62	0
24	Ee	1196	0	1257	42	0
25	F	1276	0	1323	36	0
26	FF	3075	0	3142	85	0
27	G	770	0	780	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	GG	2748	0	2859	54	0
29	H	963	0	1015	30	0
30	HH	2375	0	2325	58	0
31	I	521	0	551	9	0
32	II	1230	0	1320	17	0
33	J	959	0	1023	14	0
34	JJ	1784	0	1862	35	0
35	K	993	0	1081	23	0
36	KK	1804	0	1877	40	0
37	L	1092	0	1155	40	0
38	LL	1518	0	1587	29	0
39	M	1173	0	1215	39	0
40	MM	1743	0	1785	39	0
41	N	462	0	491	15	0
42	NN	1353	0	1383	29	0
43	O	742	0	797	18	0
44	OO	1543	0	1608	42	0
45	P	883	0	918	30	0
46	PP	1053	0	1149	27	0
47	Pp	19	0	20	0	0
48	Q	1020	0	1090	19	0
49	QQ	1720	0	1779	62	0
50	R	850	0	880	28	0
51	S	861	0	918	23	0
52	T	969	0	1078	37	0
53	U	771	0	849	18	0
54	V	665	0	668	25	0
55	W	612	0	682	22	0
56	X	436	0	475	19	0
57	Y	417	0	456	7	0
58	Z	233	0	284	7	0
59	a	819	0	889	34	0
60	b	694	0	735	18	0
61	c	34321	0	17286	899	0
62	d	1583	0	1578	59	0
63	e	1689	0	1763	65	0
64	f	1635	0	1723	61	0
65	g	1412	0	1473	37	0
66	h	2056	0	2140	84	0
67	i	1572	0	1639	82	0
68	j	1766	0	1859	61	0
69	k	1481	0	1572	53	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	l	1457	0	1488	57	0
71	m	1494	0	1573	65	0
72	n	300	0	279	9	0
73	o	1146	0	1213	31	0
74	p	1192	0	1255	44	0
75	q	891	0	883	37	0
76	r	732	0	760	32	0
77	s	1080	0	1140	48	0
78	t	961	0	999	39	0
79	u	1192	0	1222	58	0
80	v	1112	0	1124	48	0
81	w	800	0	869	23	0
82	x	684	0	672	27	0
83	y	1021	0	1060	34	0
84	z	1121	0	1196	33	0
85	2	1	0	0	0	0
85	5	1	0	0	0	0
85	8	1	0	0	0	0
85	S	1	0	0	0	0
85	V	1	0	0	0	0
85	Y	1	0	0	0	0
85	a	1	0	0	2	0
85	b	1	0	0	0	0
86	AA	188	0	0	0	0
86	Aa	1	0	0	0	0
86	BB	5	0	0	1	0
86	CC	3	0	0	0	0
86	FF	1	0	0	0	0
86	H	1	0	0	0	0
86	c	42	0	0	0	0
87	AA	60	0	114	10	0
87	QQ	10	0	19	0	0
87	c	10	0	19	2	0
88	AA	12	0	0	0	0
88	CC	1	0	0	0	0
88	EE	1	0	0	0	0
88	MM	1	0	0	0	0
88	Q	1	0	0	0	0
88	a	1	0	0	0	0
88	c	2	0	0	0	0
89	Aa	32	0	12	3	0
90	Aa	35	0	41	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
91	2	1	0	0	0	0
91	A	2	0	0	0	0
91	AA	764	0	0	30	0
91	B	1	0	0	0	0
91	BB	20	0	0	0	0
91	CC	13	0	0	0	0
91	Cc	1	0	0	1	0
91	D	4	0	0	0	0
91	EE	5	0	0	0	0
91	F	4	0	0	0	0
91	FF	4	0	0	0	0
91	GG	2	0	0	0	0
91	H	2	0	0	0	0
91	HH	1	0	0	1	0
91	J	2	0	0	0	0
91	JJ	1	0	0	0	0
91	LL	1	0	0	0	0
91	M	4	0	0	0	0
91	MM	2	0	0	0	0
91	N	1	0	0	0	0
91	NN	2	0	0	0	0
91	OO	1	0	0	0	0
91	Q	5	0	0	0	0
91	QQ	1	0	0	0	0
91	S	1	0	0	0	0
91	V	4	0	0	0	0
91	a	3	0	0	0	0
91	c	89	0	0	2	0
91	h	1	0	0	0	0
91	o	2	0	0	0	0
91	p	3	0	0	0	0
All	All	207325	0	154338	4753	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 13.

The worst 5 of 4753 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)
66:h:92:LEU:O	66:h:96:ASN:HA	1.49	1.10
30:HH:32:GLN:OE1	91:HH:301:HOH:O	1.65	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AA:1018:G:OP1	11:AA:1035:G:N2	1.93	1.01
11:AA:1531:C:OP2	91:AA:3703:HOH:O	1.79	1.00
11:AA:640:U:O4	91:AA:3704:HOH:O	1.81	0.99

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%)	129 (98%)	3 (2%)	0	100	100
2	1	68/108 (63%)	58 (85%)	10 (15%)	0	100	100
3	2	95/119 (80%)	89 (94%)	6 (6%)	0	100	100
4	3	79/82 (96%)	74 (94%)	5 (6%)	0	100	100
5	4	61/67 (91%)	59 (97%)	2 (3%)	0	100	100
6	5	47/56 (84%)	47 (100%)	0	0	100	100
7	6	51/63 (81%)	49 (96%)	2 (4%)	0	100	100
8	7	316/319 (99%)	301 (95%)	15 (5%)	0	100	100
9	8	32/152 (21%)	23 (72%)	9 (28%)	0	100	100
10	A	195/199 (98%)	193 (99%)	2 (1%)	0	100	100
12	Aa	839/842 (100%)	816 (97%)	23 (3%)	0	100	100
13	B	152/184 (83%)	149 (98%)	3 (2%)	0	100	100
16	C	183/186 (98%)	182 (100%)	1 (0%)	0	100	100
19	D	174/189 (92%)	169 (97%)	5 (3%)	0	100	100
20	DD	195/312 (62%)	191 (98%)	4 (2%)	0	100	100
22	E	170/172 (99%)	163 (96%)	7 (4%)	0	100	100
23	EE	250/254 (98%)	245 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	Ee	156/165 (94%)	148 (95%)	8 (5%)	0	100	100
25	F	157/160 (98%)	153 (98%)	4 (2%)	0	100	100
26	FF	384/387 (99%)	376 (98%)	8 (2%)	0	100	100
27	G	95/121 (78%)	93 (98%)	2 (2%)	0	100	100
28	GG	359/362 (99%)	352 (98%)	7 (2%)	0	100	100
29	H	127/137 (93%)	126 (99%)	1 (1%)	0	100	100
30	HH	294/297 (99%)	289 (98%)	5 (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%)	217 (99%)	3 (1%)	0	100	100
35	K	124/127 (98%)	122 (98%)	2 (2%)	0	100	100
36	KK	231/256 (90%)	228 (99%)	3 (1%)	0	100	100
37	L	133/136 (98%)	129 (97%)	4 (3%)	0	100	100
38	LL	189/191 (99%)	186 (98%)	3 (2%)	0	100	100
39	M	146/149 (98%)	143 (98%)	3 (2%)	0	100	100
40	MM	213/221 (96%)	209 (98%)	4 (2%)	0	100	100
41	N	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
42	NN	167/174 (96%)	158 (95%)	9 (5%)	0	100	100
43	O	95/105 (90%)	95 (100%)	0	0	100	100
44	OO	191/199 (96%)	177 (93%)	13 (7%)	1 (0%)	24	44
45	P	107/113 (95%)	105 (98%)	2 (2%)	0	100	100
46	PP	134/138 (97%)	132 (98%)	2 (2%)	0	100	100
48	Q	125/130 (96%)	125 (100%)	0	0	100	100
49	QQ	201/204 (98%)	197 (98%)	4 (2%)	0	100	100
50	R	104/107 (97%)	103 (99%)	1 (1%)	0	100	100
51	S	107/121 (88%)	106 (99%)	1 (1%)	0	100	100
52	T	117/120 (98%)	115 (98%)	2 (2%)	0	100	100
53	U	97/100 (97%)	91 (94%)	6 (6%)	0	100	100
54	V	82/88 (93%)	79 (96%)	2 (2%)	1 (1%)	10	22
55	W	75/78 (96%)	71 (95%)	4 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
56	X	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
57	Y	50/128 (39%)	50 (100%)	0	0	100	100
58	Z	23/25 (92%)	23 (100%)	0	0	100	100
59	a	100/106 (94%)	97 (97%)	3 (3%)	0	100	100
60	b	89/92 (97%)	88 (99%)	1 (1%)	0	100	100
62	d	204/252 (81%)	194 (95%)	10 (5%)	0	100	100
63	e	210/255 (82%)	201 (96%)	9 (4%)	0	100	100
64	f	215/254 (85%)	205 (95%)	10 (5%)	0	100	100
65	g	177/240 (74%)	168 (95%)	9 (5%)	0	100	100
66	h	256/261 (98%)	247 (96%)	9 (4%)	0	100	100
67	i	195/225 (87%)	190 (97%)	5 (3%)	0	100	100
68	j	217/236 (92%)	213 (98%)	4 (2%)	0	100	100
69	k	182/190 (96%)	170 (93%)	12 (7%)	0	100	100
70	l	180/200 (90%)	166 (92%)	14 (8%)	0	100	100
71	m	183/197 (93%)	178 (97%)	5 (3%)	0	100	100
72	n	29/105 (28%)	26 (90%)	3 (10%)	0	100	100
73	o	140/156 (90%)	133 (95%)	7 (5%)	0	100	100
74	p	148/151 (98%)	146 (99%)	2 (1%)	0	100	100
75	q	125/137 (91%)	119 (95%)	6 (5%)	0	100	100
76	r	85/142 (60%)	83 (98%)	2 (2%)	0	100	100
77	s	135/143 (94%)	126 (93%)	9 (7%)	0	100	100
78	t	119/136 (88%)	115 (97%)	4 (3%)	0	100	100
79	u	143/146 (98%)	135 (94%)	8 (6%)	0	100	100
80	v	141/144 (98%)	134 (95%)	7 (5%)	0	100	100
81	w	98/121 (81%)	97 (99%)	1 (1%)	0	100	100
82	x	85/87 (98%)	81 (95%)	4 (5%)	0	100	100
83	y	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
84	z	142/145 (98%)	132 (93%)	10 (7%)	0	100	100
All	All	11701/13056 (90%)	11331 (97%)	368 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
54	V	65	ARG
44	OO	63	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	112/113 (99%)	112 (100%)	0	100	100
2	1	61/89 (68%)	61 (100%)	0	100	100
3	2	83/101 (82%)	83 (100%)	0	100	100
4	3	70/71 (99%)	70 (100%)	0	100	100
5	4	56/60 (93%)	56 (100%)	0	100	100
6	5	43/49 (88%)	43 (100%)	0	100	100
7	6	46/54 (85%)	46 (100%)	0	100	100
8	7	259/262 (99%)	259 (100%)	0	100	100
9	8	30/135 (22%)	30 (100%)	0	100	100
10	A	160/162 (99%)	160 (100%)	0	100	100
12	Aa	714/714 (100%)	713 (100%)	1 (0%)	88	96
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	167/254 (66%)	167 (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	129/136 (95%)	129 (100%)	0	100	100
25	F	136/137 (99%)	136 (100%)	0	100	100
26	FF	319/323 (99%)	317 (99%)	2 (1%)	78	89
27	G	84/107 (78%)	84 (100%)	0	100	100
28	GG	288/289 (100%)	287 (100%)	1 (0%)	86	94

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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%)	154 (100%)	0	100	100
45	P	94/97 (97%)	94 (100%)	0	100	100
46	PP	107/109 (98%)	107 (100%)	0	100	100
47	Pp	2/2 (100%)	2 (100%)	0	100	100
48	Q	109/111 (98%)	109 (100%)	0	100	100
49	QQ	175/176 (99%)	175 (100%)	0	100	100
50	R	90/91 (99%)	90 (100%)	0	100	100
51	S	94/103 (91%)	94 (100%)	0	100	100
52	T	104/105 (99%)	104 (100%)	0	100	100
53	U	81/82 (99%)	81 (100%)	0	100	100
54	V	69/71 (97%)	69 (100%)	0	100	100
55	W	68/69 (99%)	68 (100%)	0	100	100
56	X	45/46 (98%)	45 (100%)	0	100	100
57	Y	47/116 (40%)	47 (100%)	0	100	100
58	Z	23/23 (100%)	23 (100%)	0	100	100
59	a	87/91 (96%)	87 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
60	b	71/72 (99%)	71 (100%)	0	100	100
62	d	165/210 (79%)	165 (100%)	0	100	100
63	e	189/224 (84%)	189 (100%)	0	100	100
64	f	176/205 (86%)	176 (100%)	0	100	100
65	g	145/195 (74%)	145 (100%)	0	100	100
66	h	220/222 (99%)	220 (100%)	0	100	100
67	i	172/191 (90%)	172 (100%)	0	100	100
68	j	188/201 (94%)	188 (100%)	0	100	100
69	k	165/170 (97%)	165 (100%)	0	100	100
70	l	146/161 (91%)	146 (100%)	0	100	100
71	m	158/166 (95%)	158 (100%)	0	100	100
72	n	32/98 (33%)	32 (100%)	0	100	100
73	o	127/137 (93%)	127 (100%)	0	100	100
74	p	127/128 (99%)	127 (100%)	0	100	100
75	q	81/105 (77%)	81 (100%)	0	100	100
76	r	77/118 (65%)	77 (100%)	0	100	100
77	s	114/119 (96%)	114 (100%)	0	100	100
78	t	105/124 (85%)	105 (100%)	0	100	100
79	u	128/129 (99%)	128 (100%)	0	100	100
80	v	115/116 (99%)	115 (100%)	0	100	100
81	w	94/114 (82%)	93 (99%)	1 (1%)	65	83
82	x	74/74 (100%)	74 (100%)	0	100	100
83	y	110/111 (99%)	110 (100%)	0	100	100
84	z	119/120 (99%)	119 (100%)	0	100	100
All	All	9952/10971 (91%)	9947 (100%)	5 (0%)	87	96

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

Mol	Chain	Res	Type
12	Aa	483	PHE
26	FF	104	THR
26	FF	319	ASN
28	GG	12	THR
81	w	87	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 93 such sidechains are listed below:

Mol	Chain	Res	Type
62	d	15	GLN
71	m	74	ASN
63	e	40	ASN
66	h	201	HIS
74	p	5	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	AA	3194/3396 (94%)	480 (15%)	16 (0%)
14	BB	121/121 (100%)	10 (8%)	2 (1%)
15	Bb	75/76 (98%)	38 (50%)	0
17	CC	157/158 (99%)	23 (14%)	0
18	Cc	76/77 (98%)	12 (15%)	0
21	Dd	5/39 (12%)	2 (40%)	0
61	c	1598/1800 (88%)	323 (20%)	0
All	All	5226/5667 (92%)	888 (16%)	18 (0%)

5 of 888 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	AA	6	A
11	AA	14	U
11	AA	26	A
11	AA	40	A
11	AA	43	A

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	AA	3121	U
14	BB	72	A
14	BB	1	G
11	AA	2101	C
11	AA	2971	A

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

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	908	11	23,26,27	0.46	0	32,38,41	0.49	0
11	A2M	AA	817	11,86	22,25,26	3.20	9 (40%)	30,36,39	2.91	10 (33%)
61	MA6	c	1782	61	23,26,27	1.37	4 (17%)	33,38,41	3.25	12 (36%)
11	A2M	AA	2281	11	22,25,26	3.19	10 (45%)	30,36,39	3.08	13 (43%)
11	OMG	AA	1450	11	23,26,27	0.45	0	32,38,41	0.51	0
61	A2M	c	541	61	22,25,26	3.20	9 (40%)	30,36,39	3.01	11 (36%)
11	OMG	AA	2793	11	23,26,27	0.45	0	32,38,41	0.49	0
11	A2M	AA	1133	11,86	22,25,26	3.21	9 (40%)	30,36,39	2.97	11 (36%)
15	YYG	Bb	37	15	38,42,43	1.97	8 (21%)	45,62,65	2.32	12 (26%)
11	OMG	AA	2619	15,11	23,26,27	0.46	0	32,38,41	0.48	0
61	A2M	c	796	61	22,25,26	3.21	9 (40%)	30,36,39	2.97	11 (36%)
61	B8N	c	1191	61	25,29,30	3.41	7 (28%)	28,42,45	2.06	7 (25%)
11	OMU	AA	2729	11	19,22,23	3.12	8 (42%)	25,31,34	1.77	5 (20%)
11	OMC	AA	2337	11	19,22,23	0.48	0	25,31,34	0.70	0
61	OMG	c	1428	61	23,26,27	0.45	0	32,38,41	0.54	0
11	5MC	AA	2278	11,86	19,22,23	0.46	0	26,32,35	0.66	0
61	OMG	c	1572	61	23,26,27	0.52	0	32,38,41	0.58	0
12	DDE	Aa	699	12	18,20,21	1.04	1 (5%)	17,28,30	0.80	1 (5%)
61	MA6	c	1781	61	23,26,27	1.38	4 (17%)	33,38,41	3.20	12 (36%)
11	OMU	AA	1888	11	19,22,23	3.13	8 (42%)	25,31,34	1.82	5 (20%)
11	OMG	AA	2288	11	23,26,27	0.46	0	32,38,41	0.46	0
61	OMG	c	1126	61	23,26,27	0.47	0	32,38,41	0.55	0
11	A2M	AA	2220	11	22,25,26	3.19	9 (40%)	30,36,39	2.90	10 (33%)
61	A2M	c	28	61	22,25,26	3.16	9 (40%)	30,36,39	2.95	10 (33%)
11	UR3	AA	2634	11	19,22,23	2.97	6 (31%)	26,32,35	1.59	3 (11%)
61	A2M	c	100	61,86	22,25,26	3.21	9 (40%)	30,36,39	2.96	11 (36%)
61	A2M	c	420	61	22,25,26	3.20	9 (40%)	30,36,39	2.91	11 (36%)
11	A2M	AA	2280	11	22,25,26	3.19	9 (40%)	30,36,39	2.96	10 (33%)
61	A2M	c	436	61	22,25,26	3.21	9 (40%)	30,36,39	2.86	10 (33%)
11	OMU	AA	2417	11	19,22,23	3.15	8 (42%)	25,31,34	1.78	5 (20%)
11	A2M	AA	2946	11,86	22,25,26	3.19	9 (40%)	30,36,39	2.95	11 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
11	OMC	AA	663	11	19,22,23	0.48	0	25,31,34	0.69	0
11	1MA	AA	2142	11,86	21,25,26	0.42	0	30,37,40	0.79	1 (3%)
61	OMC	c	414	61	19,22,23	0.49	0	25,31,34	0.66	0
61	4AC	c	1773	61	21,24,25	3.56	10 (47%)	28,34,37	1.72	5 (17%)
11	A2M	AA	876	11	22,25,26	3.20	9 (40%)	30,36,39	2.92	10 (33%)
11	OMC	AA	2959	11,86	19,22,23	0.50	0	25,31,34	0.73	0
61	OMU	c	1269	61	19,22,23	3.18	8 (42%)	25,31,34	1.79	5 (20%)
11	OMG	AA	2815	11	23,26,27	0.45	0	32,38,41	0.50	0
61	A2M	c	974	61	22,25,26	3.20	9 (40%)	30,36,39	2.95	11 (36%)
61	4AC	c	1280	61	21,24,25	3.58	10 (47%)	28,34,37	1.70	5 (17%)
61	OMC	c	1639	61,86	19,22,23	0.47	0	25,31,34	0.58	0
11	1MA	AA	645	11,86	21,25,26	1.37	4 (19%)	30,37,40	1.71	6 (20%)
61	A2M	c	619	61,86	22,25,26	3.20	9 (40%)	30,36,39	2.95	10 (33%)
61	OMG	c	1271	61	23,26,27	0.43	0	32,38,41	0.45	0
11	OMC	AA	2948	11	19,22,23	0.52	0	25,31,34	0.94	2 (8%)
11	OMG	AA	805	11	23,26,27	0.46	0	32,38,41	0.58	0
11	OMC	AA	2197	88,11	19,22,23	0.45	0	25,31,34	0.65	0
11	OMU	AA	2724	11	19,22,23	3.13	8 (42%)	25,31,34	1.74	5 (20%)
11	5MC	AA	2870	88,11	19,22,23	0.58	0	26,32,35	0.61	0
11	OMU	AA	2347	11	19,22,23	3.16	8 (42%)	25,31,34	1.77	5 (20%)
61	OMU	c	578	61	19,22,23	3.15	8 (42%)	25,31,34	1.77	5 (20%)
61	G7M	c	1575	61	23,26,27	2.69	8 (34%)	34,39,42	2.34	11 (32%)
11	A2M	AA	2640	11	22,25,26	3.19	9 (40%)	30,36,39	2.91	10 (33%)
11	OMC	AA	650	11	19,22,23	0.47	0	25,31,34	0.69	0
11	OMG	AA	2791	11	23,26,27	0.45	0	32,38,41	0.51	0
11	A2M	AA	649	11	22,25,26	3.18	9 (40%)	30,36,39	2.91	10 (33%)
61	OMC	c	1007	61	19,22,23	0.48	0	25,31,34	0.67	0
11	OMG	AA	867	11	23,26,27	0.46	0	32,38,41	0.51	0
11	A2M	AA	1449	11,86	22,25,26	3.22	9 (40%)	30,36,39	2.92	11 (36%)
11	OMU	AA	2921	11	19,22,23	3.14	8 (42%)	25,31,34	1.77	5 (20%)
11	OMG	AA	2922	11	23,26,27	0.49	0	32,38,41	0.48	0
61	OMG	c	562	61	23,26,27	0.44	0	32,38,41	0.64	0
11	A2M	AA	2256	11	22,25,26	3.19	9 (40%)	30,36,39	3.09	13 (43%)
11	OMC	AA	1437	11,86	19,22,23	0.49	0	25,31,34	0.81	1 (4%)
11	OMU	AA	898	11	19,22,23	3.14	8 (42%)	25,31,34	1.74	4 (16%)
11	A2M	AA	807	11	22,25,26	3.21	9 (40%)	30,36,39	2.97	11 (36%)
11	OMU	AA	2421	11	19,22,23	3.15	8 (42%)	25,31,34	1.77	4 (16%)

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	908	11	-	0/9/27/28	0/3/3/3
11	A2M	AA	817	11,86	-	1/9/27/28	0/3/3/3
61	MA6	c	1782	61	-	2/11/29/30	0/3/3/3
11	A2M	AA	2281	11	-	2/9/27/28	0/3/3/3
11	OMG	AA	1450	11	-	2/9/27/28	0/3/3/3
61	A2M	c	541	61	-	4/9/27/28	0/3/3/3
11	OMG	AA	2793	11	-	0/9/27/28	0/3/3/3
11	A2M	AA	1133	11,86	-	0/9/27/28	0/3/3/3
15	YYG	Bb	37	15	-	14/24/42/43	0/4/4/4
11	OMG	AA	2619	15,11	-	1/9/27/28	0/3/3/3
61	A2M	c	796	61	-	0/9/27/28	0/3/3/3
61	B8N	c	1191	61	-	7/16/34/35	0/2/2/2
11	OMU	AA	2729	11	-	1/9/27/28	0/2/2/2
11	OMC	AA	2337	11	-	1/9/27/28	0/2/2/2
61	OMG	c	1428	61	-	1/9/27/28	0/3/3/3
11	5MC	AA	2278	11,86	-	0/7/25/26	0/2/2/2
61	OMG	c	1572	61	-	4/9/27/28	0/3/3/3
12	DDE	Aa	699	12	-	1/20/21/23	0/1/1/1
61	MA6	c	1781	61	-	1/11/29/30	0/3/3/3
11	OMU	AA	1888	11	-	0/9/27/28	0/2/2/2
11	OMG	AA	2288	11	-	0/9/27/28	0/3/3/3
61	OMG	c	1126	61	-	0/9/27/28	0/3/3/3
11	A2M	AA	2220	11	-	1/9/27/28	0/3/3/3
61	A2M	c	28	61	-	2/9/27/28	0/3/3/3
11	UR3	AA	2634	11	-	0/7/25/26	0/2/2/2
61	A2M	c	100	61,86	-	2/9/27/28	0/3/3/3
61	A2M	c	420	61	-	1/9/27/28	0/3/3/3
11	A2M	AA	2280	11	-	2/9/27/28	0/3/3/3
61	A2M	c	436	61	-	1/9/27/28	0/3/3/3
11	OMU	AA	2417	11	-	0/9/27/28	0/2/2/2
11	A2M	AA	2946	11,86	-	1/9/27/28	0/3/3/3
11	OMC	AA	663	11	-	1/9/27/28	0/2/2/2
11	1MA	AA	2142	11,86	-	0/7/25/26	0/3/3/3
61	OMC	c	414	61	-	1/9/27/28	0/2/2/2
61	4AC	c	1773	61	-	2/11/29/30	0/2/2/2
11	A2M	AA	876	11	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	OMC	AA	2959	11,86	-	0/9/27/28	0/2/2/2
61	OMU	c	1269	61	-	5/9/27/28	0/2/2/2
11	OMG	AA	2815	11	-	0/9/27/28	0/3/3/3
61	A2M	c	974	61	-	1/9/27/28	0/3/3/3
61	4AC	c	1280	61	-	5/11/29/30	0/2/2/2
61	OMC	c	1639	61,86	-	0/9/27/28	0/2/2/2
11	1MA	AA	645	11,86	-	2/7/25/26	0/3/3/3
61	A2M	c	619	61,86	-	4/9/27/28	0/3/3/3
61	OMG	c	1271	61	-	1/9/27/28	0/3/3/3
11	OMC	AA	2948	11	-	1/9/27/28	0/2/2/2
11	OMG	AA	805	11	-	0/9/27/28	0/3/3/3
11	OMC	AA	2197	88,11	-	4/9/27/28	0/2/2/2
11	OMU	AA	2724	11	-	1/9/27/28	0/2/2/2
11	5MC	AA	2870	88,11	-	4/7/25/26	0/2/2/2
11	OMU	AA	2347	11	-	1/9/27/28	0/2/2/2
61	OMU	c	578	61	-	2/9/27/28	0/2/2/2
61	G7M	c	1575	61	-	3/7/25/26	0/3/3/3
11	A2M	AA	2640	11	-	1/9/27/28	0/3/3/3
11	OMC	AA	650	11	-	0/9/27/28	0/2/2/2
11	OMG	AA	2791	11	-	0/9/27/28	0/3/3/3
11	A2M	AA	649	11	-	1/9/27/28	0/3/3/3
61	OMC	c	1007	61	-	0/9/27/28	0/2/2/2
11	OMG	AA	867	11	-	0/9/27/28	0/3/3/3
11	A2M	AA	1449	11,86	-	0/9/27/28	0/3/3/3
11	OMU	AA	2921	11	-	0/9/27/28	0/2/2/2
11	OMG	AA	2922	11	-	2/9/27/28	0/3/3/3
61	OMG	c	562	61	-	2/9/27/28	0/3/3/3
11	A2M	AA	2256	11	-	3/9/27/28	0/3/3/3
11	OMC	AA	1437	11,86	-	0/9/27/28	0/2/2/2
11	OMU	AA	898	11	-	1/9/27/28	0/2/2/2
11	A2M	AA	807	11	-	4/9/27/28	0/3/3/3
11	OMU	AA	2421	11	-	1/9/27/28	0/2/2/2

The worst 5 of 323 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	AA	807	A2M	C3'-C4'	-8.97	1.30	1.53
61	c	796	A2M	C3'-C4'	-8.88	1.30	1.53
11	AA	817	A2M	C3'-C4'	-8.88	1.30	1.53
61	c	100	A2M	C3'-C4'	-8.88	1.30	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	c	541	A2M	C3'-C4'	-8.87	1.30	1.53

The worst 5 of 341 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	c	1782	MA6	N1-C6-N6	-11.79	102.49	116.86
61	c	1781	MA6	N1-C6-N6	-11.59	102.74	116.86
15	Bb	37	YYG	C5-C4-N3	-8.35	117.22	123.99
61	c	1782	MA6	C5-C6-N6	7.89	137.82	125.33
61	c	1781	MA6	C5-C6-N6	7.71	137.54	125.33

There are no chirality outliers.

5 of 105 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	898	OMU	C1'-C2'-O2'-CM2
11	AA	1450	OMG	O4'-C4'-C5'-O5'
11	AA	2220	A2M	C1'-C2'-O2'-CM'

There are no ring outliers.

45 monomers are involved in 83 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	AA	908	OMG	1	0
11	AA	817	A2M	1	0
61	c	1782	MA6	1	0
61	c	541	A2M	1	0
11	AA	2793	OMG	1	0
11	AA	1133	A2M	1	0
15	Bb	37	YYG	4	0
11	AA	2619	OMG	1	0
61	c	1191	B8N	1	0
11	AA	2729	OMU	1	0
11	AA	2337	OMC	1	0
12	Aa	699	DDE	1	0
61	c	1781	MA6	2	0
61	c	1126	OMG	1	0
11	AA	2220	A2M	1	0
61	c	28	A2M	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	AA	2634	UR3	1	0
61	c	100	A2M	1	0
61	c	420	A2M	4	0
61	c	436	A2M	3	0
11	AA	2946	A2M	2	0
11	AA	663	OMC	3	0
61	c	414	OMC	2	0
61	c	1773	4AC	2	0
11	AA	2959	OMC	2	0
61	c	1269	OMU	2	0
11	AA	2815	OMG	2	0
61	c	974	A2M	2	0
61	c	1280	4AC	4	0
61	c	1271	OMG	1	0
11	AA	2948	OMC	4	0
11	AA	2724	OMU	6	0
11	AA	2870	5MC	1	0
11	AA	2347	OMU	3	0
61	c	1575	G7M	2	0
11	AA	2640	A2M	2	0
11	AA	650	OMC	2	0
11	AA	649	A2M	3	0
11	AA	867	OMG	1	0
11	AA	1449	A2M	1	0
11	AA	2922	OMG	1	0
11	AA	2256	A2M	1	0
11	AA	1437	OMC	1	0
11	AA	898	OMU	3	0
11	AA	2421	OMU	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 278 ligands modelled in this entry, 268 are monoatomic - leaving 10 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	AA	3406	-	9,9,9	0.32	0	8,8,8	0.80	0
89	GTP	Aa	1001	86	33,34,34	0.96	2 (6%)	50,54,54	1.58	9 (18%)
90	SO1	Aa	1003	-	34,39,39	1.17	3 (8%)	38,64,64	1.10	3 (7%)
87	SPD	AA	3407	-	9,9,9	0.31	0	8,8,8	0.78	0
87	SPD	AA	3405	-	9,9,9	0.32	0	8,8,8	0.80	0
87	SPD	QQ	301	-	9,9,9	0.33	0	8,8,8	0.81	0
87	SPD	c	1901	-	9,9,9	0.32	0	8,8,8	0.85	0
87	SPD	AA	3402	-	9,9,9	0.33	0	8,8,8	0.84	0
87	SPD	AA	3403	-	9,9,9	0.31	0	8,8,8	0.91	0
87	SPD	AA	3404	-	9,9,9	0.33	0	8,8,8	0.78	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	AA	3406	-	-	3/7/7/7	-
89	GTP	Aa	1001	86	-	3/22/38/38	0/3/3/3
90	SO1	Aa	1003	-	-	10/21/104/104	0/7/5/5
87	SPD	AA	3407	-	-	2/7/7/7	-
87	SPD	AA	3405	-	-	4/7/7/7	-
87	SPD	QQ	301	-	-	3/7/7/7	-
87	SPD	c	1901	-	-	2/7/7/7	-
87	SPD	AA	3402	-	-	5/7/7/7	-
87	SPD	AA	3403	-	-	0/7/7/7	-
87	SPD	AA	3404	-	-	2/7/7/7	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
90	Aa	1003	SO1	C2-C6	-3.96	1.49	1.55
90	Aa	1003	SO1	C16-C22	-2.35	1.51	1.54
89	Aa	1001	GTP	C2-N3	2.18	1.38	1.33
89	Aa	1001	GTP	PA-O3A	2.07	1.61	1.59
90	Aa	1003	SO1	C3-C9	-2.07	1.51	1.56

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
89	Aa	1001	GTP	C5-C4-N3	-5.03	120.39	128.39
89	Aa	1001	GTP	C2-N3-C4	4.62	120.25	112.30
89	Aa	1001	GTP	N9-C4-N3	3.19	132.33	125.95
89	Aa	1001	GTP	C2-N1-C6	-2.87	119.91	125.11
90	Aa	1003	SO1	C12-C6-C10	-2.78	105.75	107.92

There are no chirality outliers.

5 of 34 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
89	Aa	1001	GTP	PB-O3A-PA-O5'
90	Aa	1003	SO1	C2-C1-C5-O14
90	Aa	1003	SO1	C2-C1-C5-O15
90	Aa	1003	SO1	C20-C13-C4-C1
90	Aa	1003	SO1	C21-C13-C4-C1

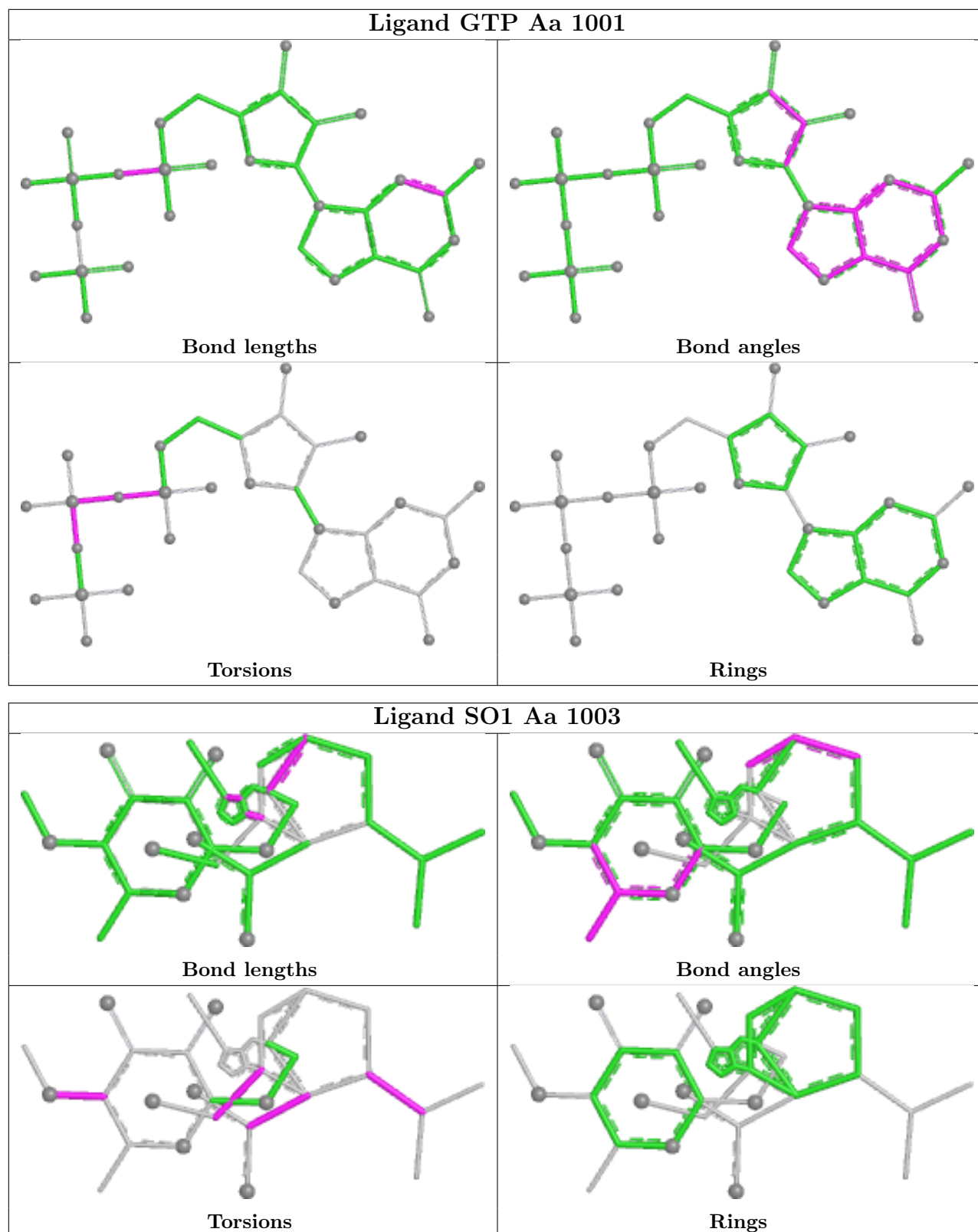
There are no ring outliers.

9 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	AA	3406	SPD	2	0
89	Aa	1001	GTP	3	0
90	Aa	1003	SO1	2	0
87	AA	3407	SPD	3	0
87	AA	3405	SPD	2	0
87	c	1901	SPD	2	0
87	AA	3402	SPD	1	0
87	AA	3403	SPD	1	0
87	AA	3404	SPD	1	0

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

equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

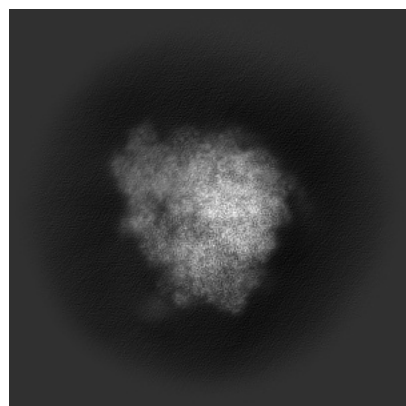
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16634. These allow visual inspection of the internal detail of the map and identification of artifacts.

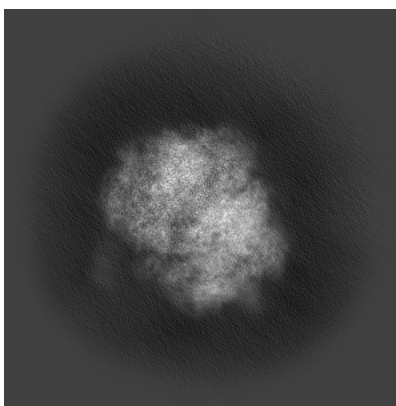
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

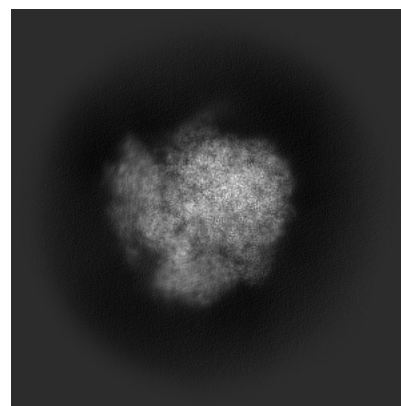
6.1.1 Primary map



X

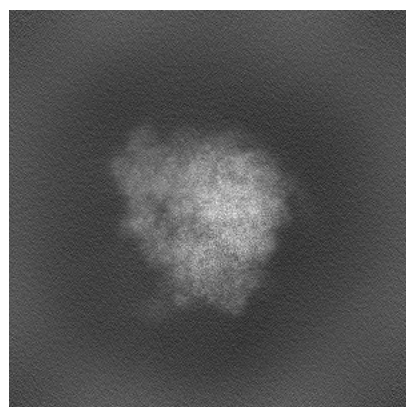


Y

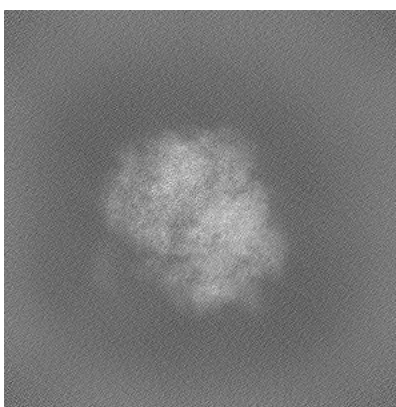


Z

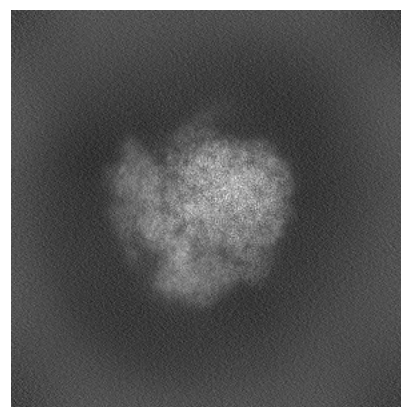
6.1.2 Raw map



X



Y

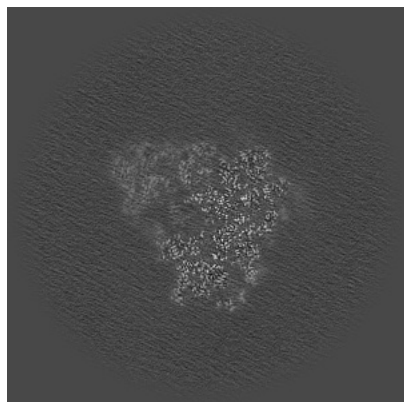


Z

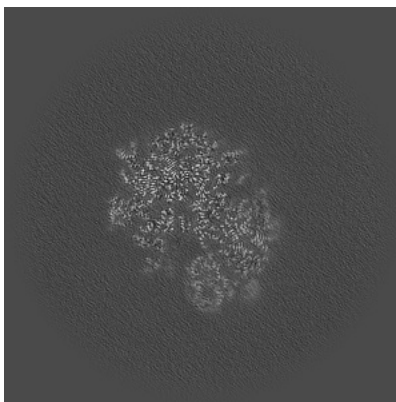
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

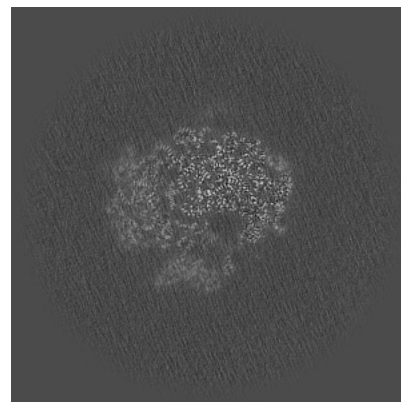
6.2.1 Primary map



X Index: 300

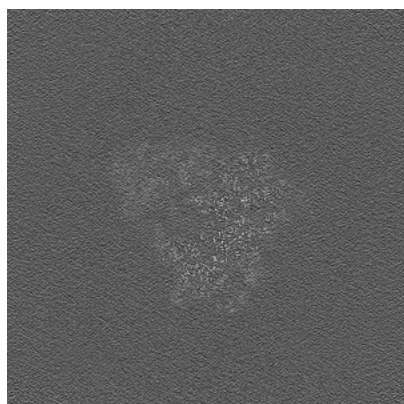


Y Index: 300

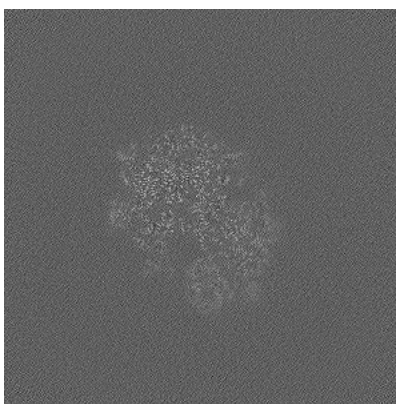


Z Index: 300

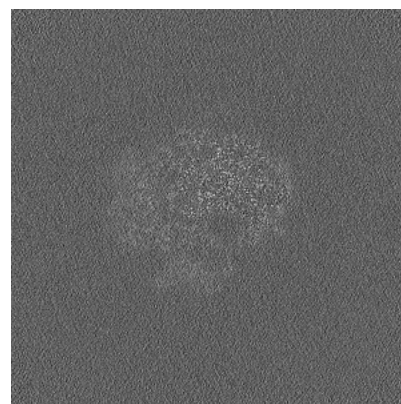
6.2.2 Raw map



X Index: 300



Y Index: 300

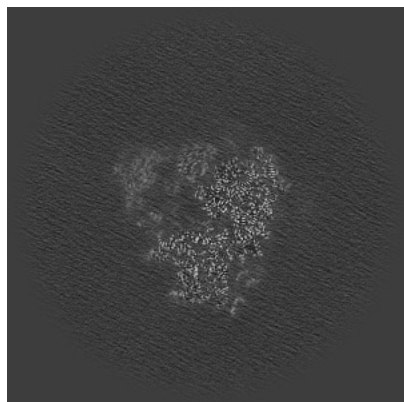


Z Index: 300

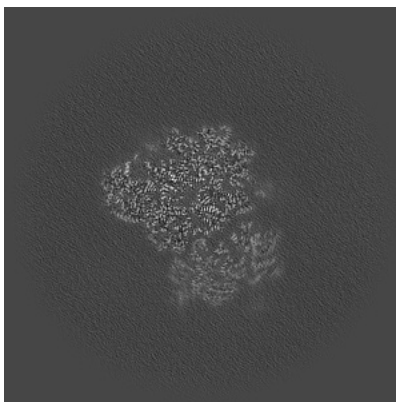
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

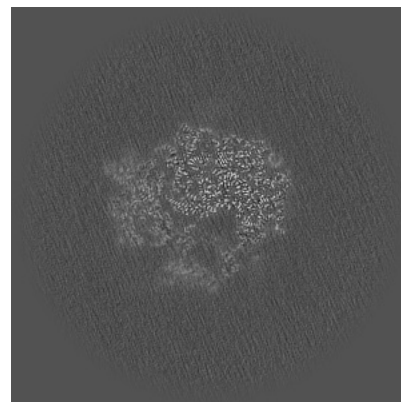
6.3.1 Primary map



X Index: 310

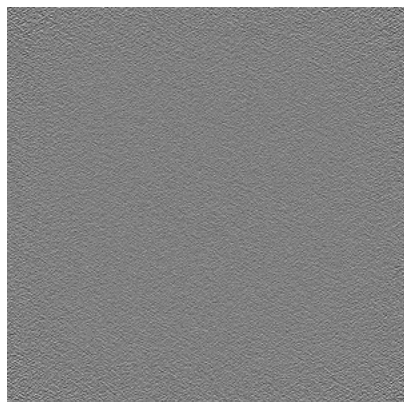


Y Index: 324

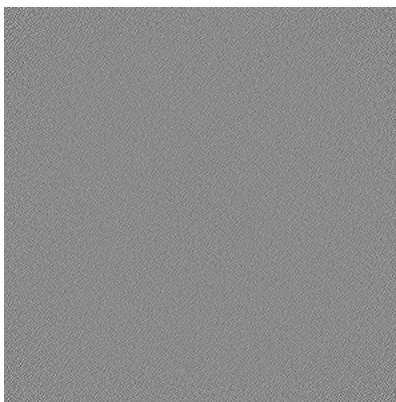


Z Index: 295

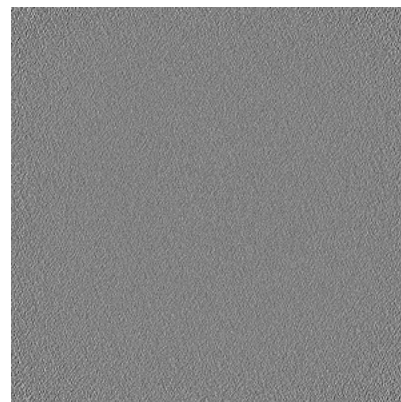
6.3.2 Raw map



X Index: 0



Y Index: 0

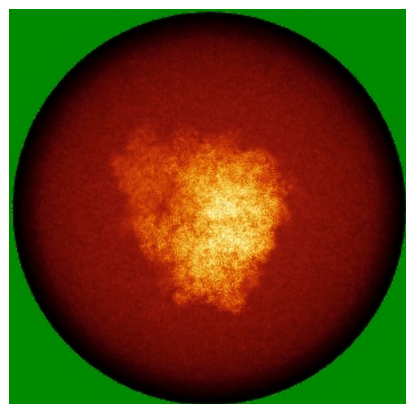


Z Index: 0

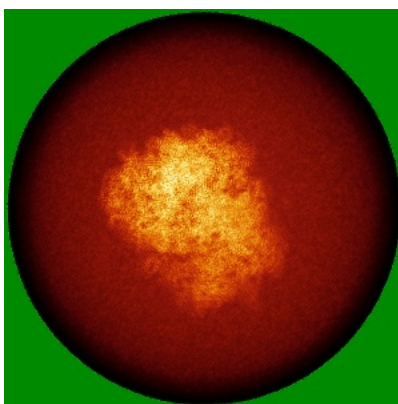
The images above show the largest variance slices of the map in three orthogonal directions.

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

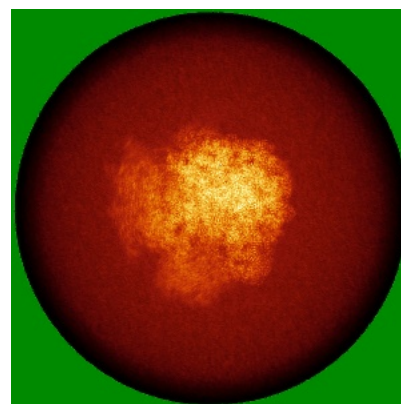
6.4.1 Primary map



X

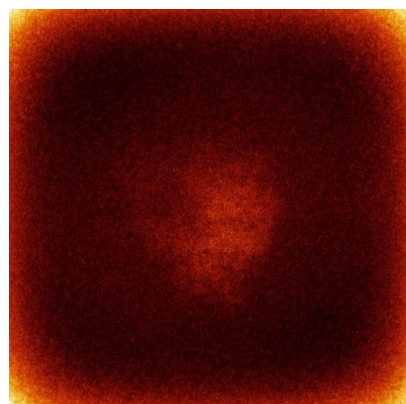


Y

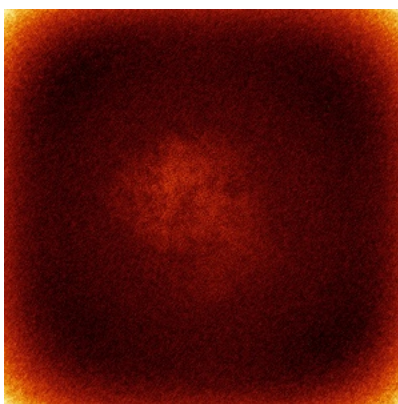


Z

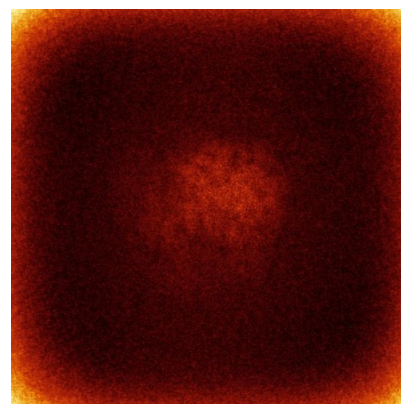
6.4.2 Raw map



X



Y

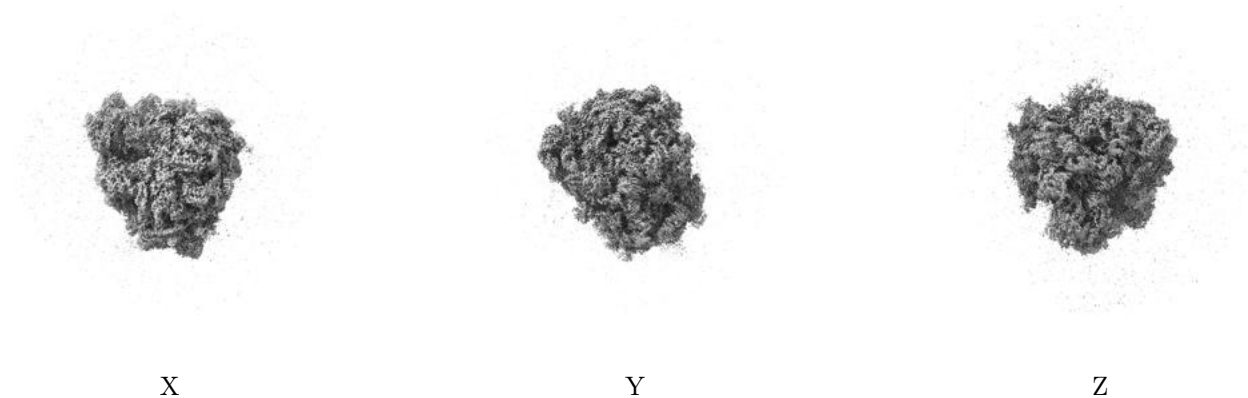


Z

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

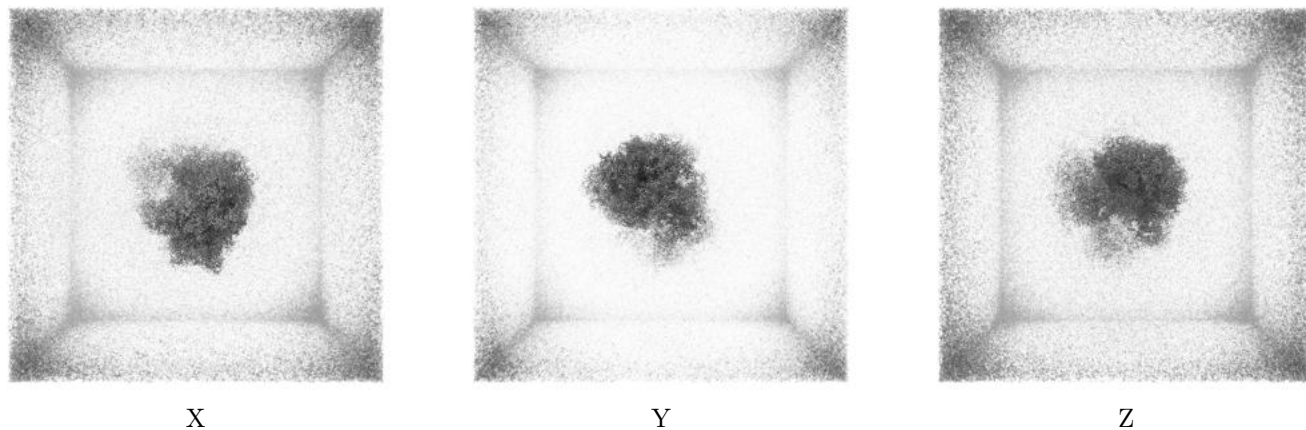
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.18. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

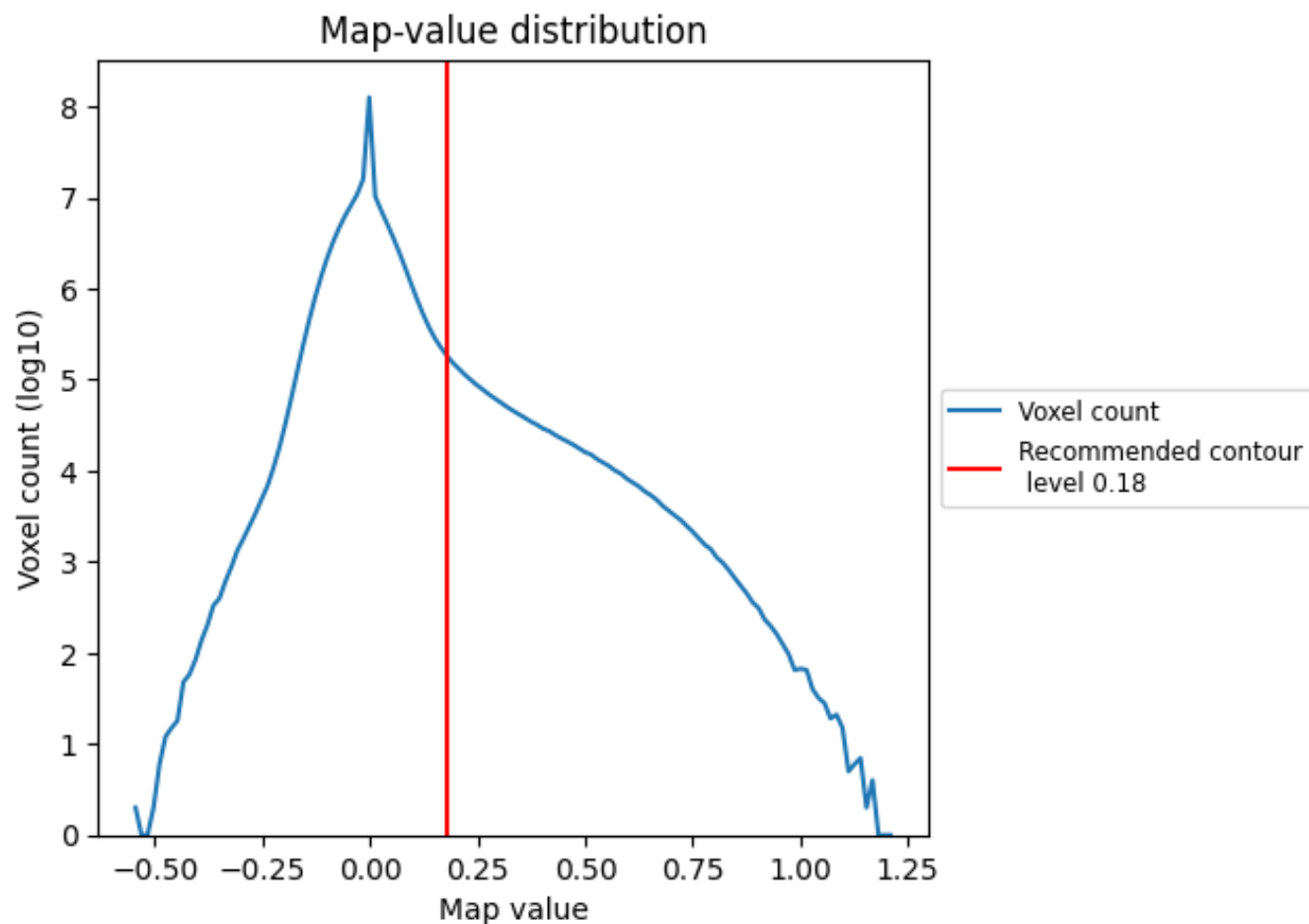
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

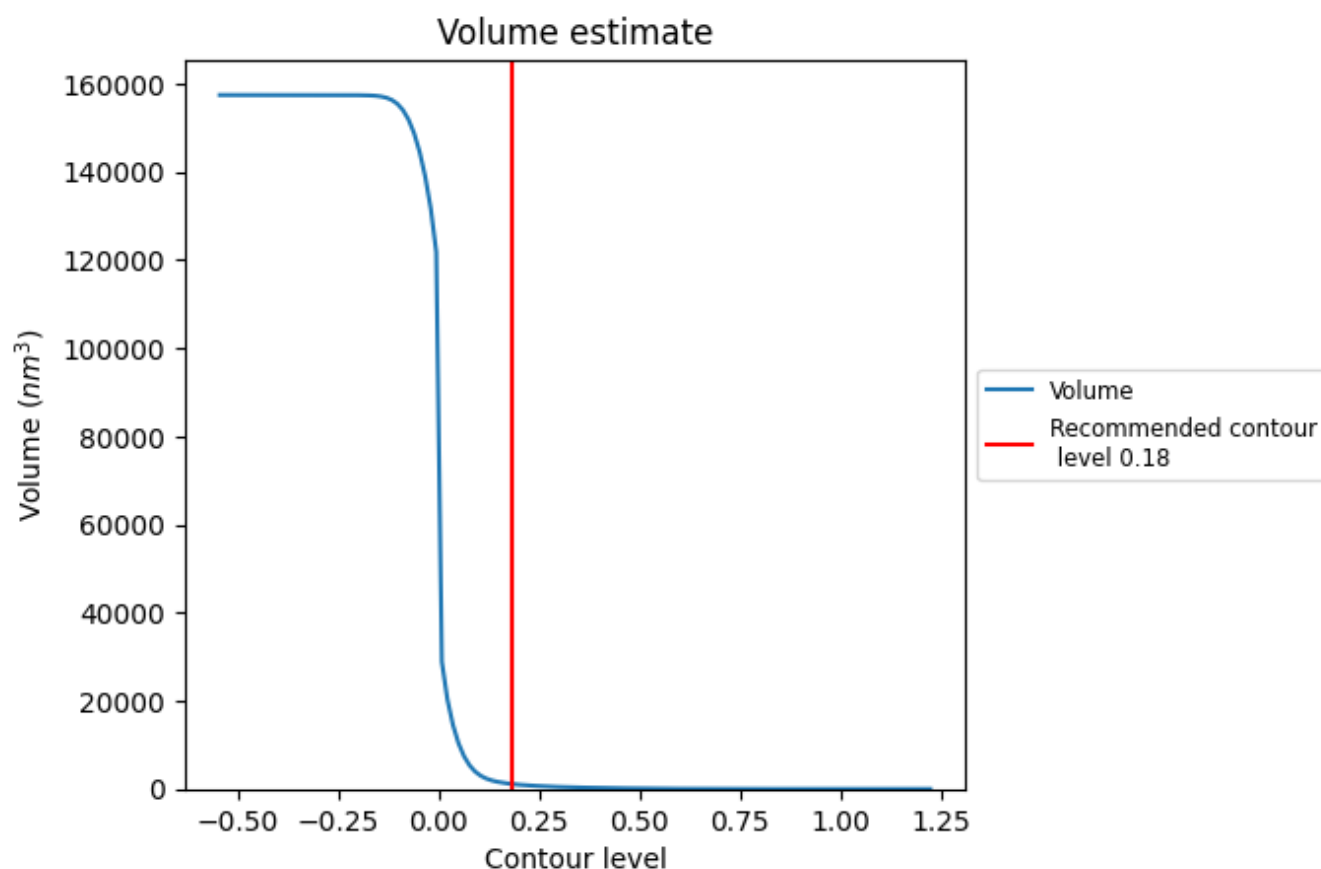
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

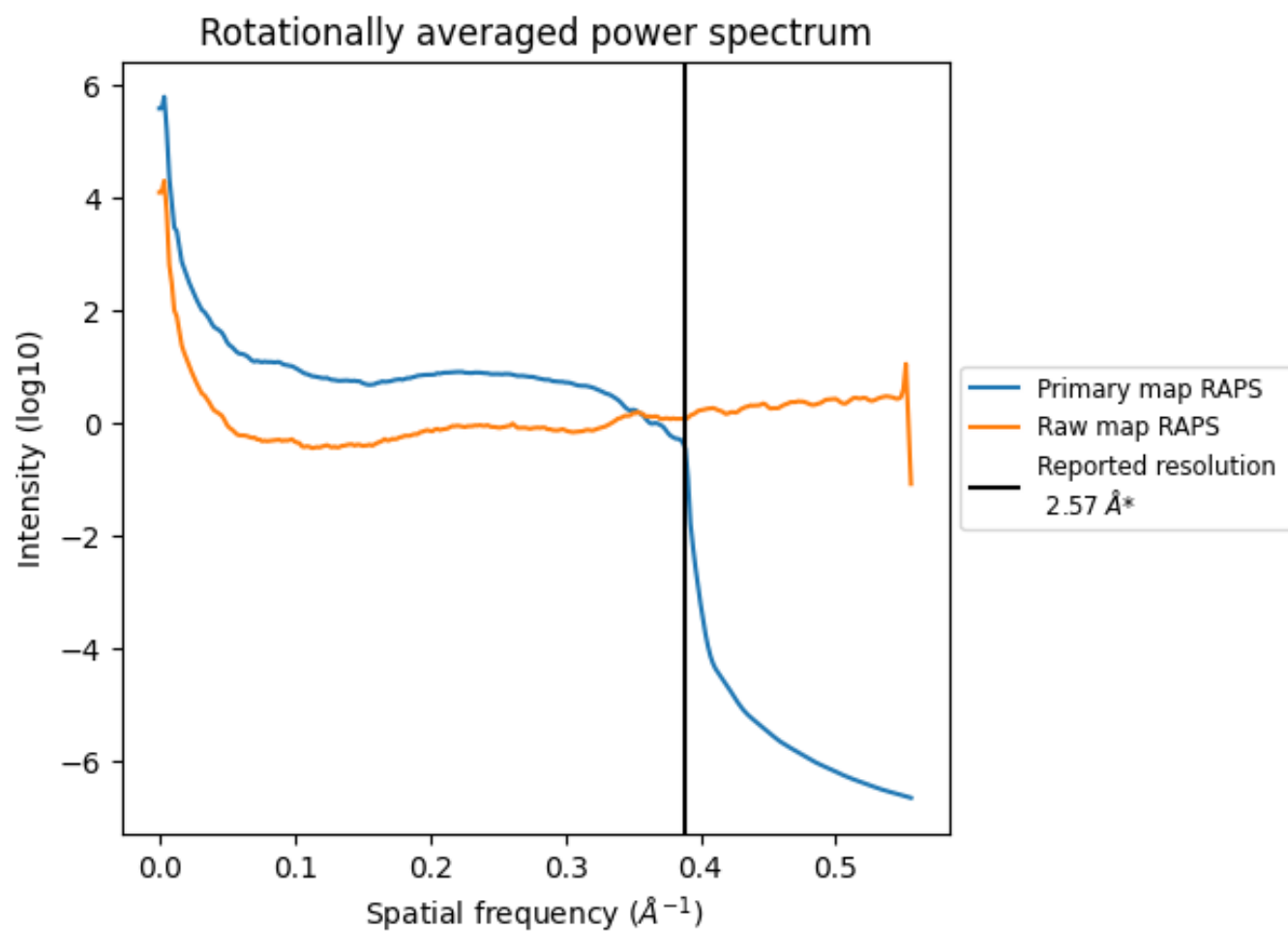
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1149 nm³; this corresponds to an approximate mass of 1038 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

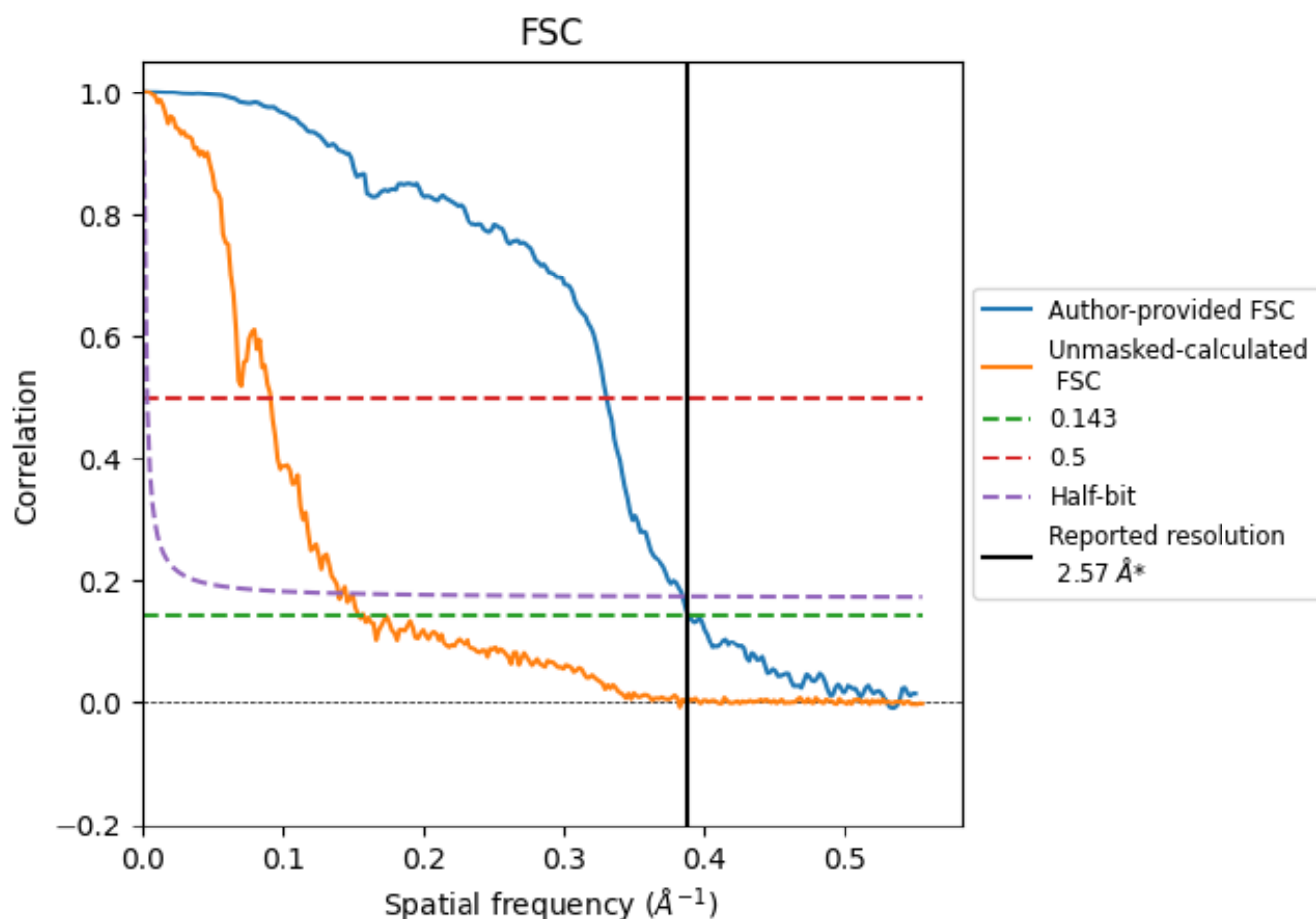


*Reported resolution corresponds to spatial frequency of 0.389 Å⁻¹

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 0.389 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

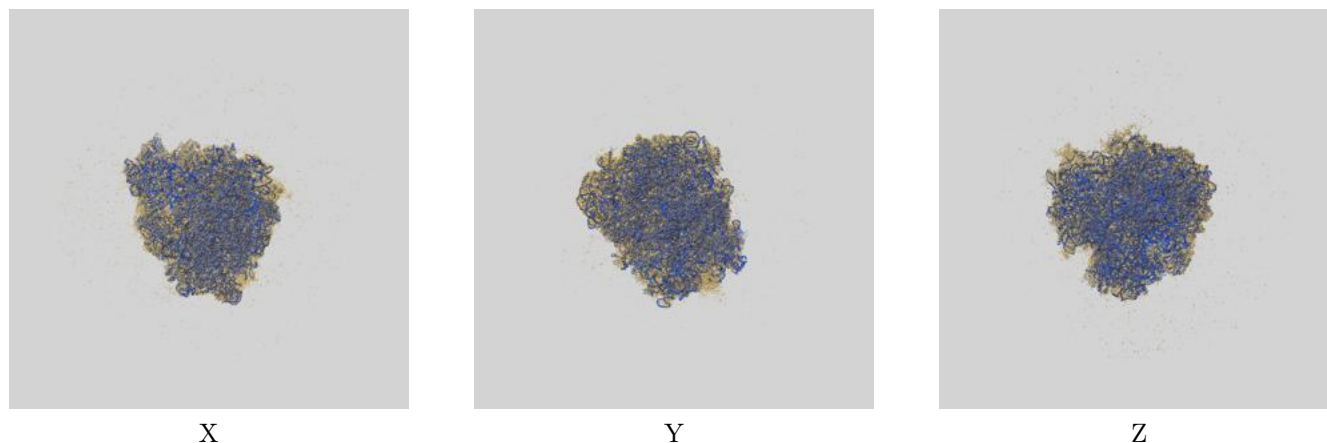
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.57	-	-
Author-provided FSC curve	2.57	3.03	2.60
Unmasked-calculated*	6.47	10.98	7.14

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.47 differs from the reported value 2.57 by more than 10 %

9 Map-model fit [i](#)

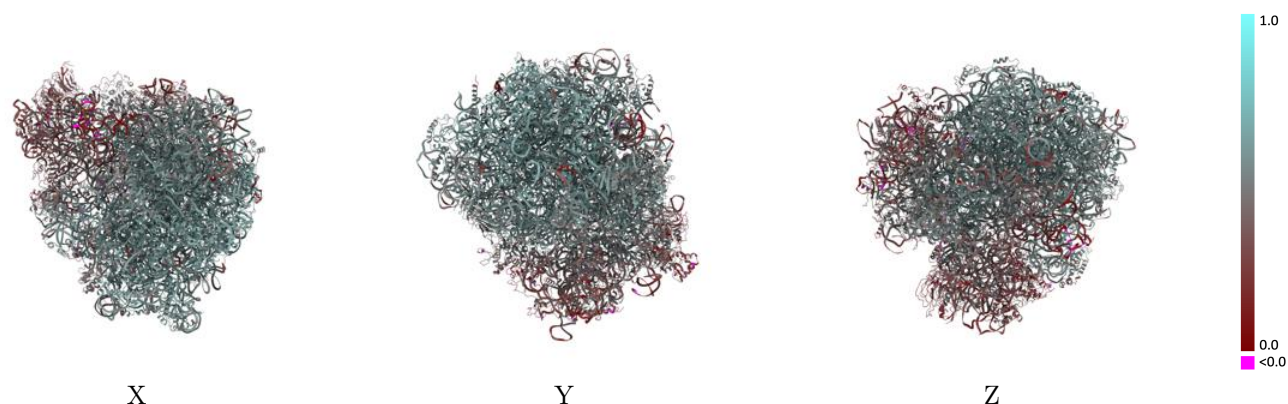
This section contains information regarding the fit between EMDB map EMD-16634 and PDB model 8CG8. Per-residue inclusion information can be found in [section 3](#) on [page 24](#).

9.1 Map-model overlay [i](#)



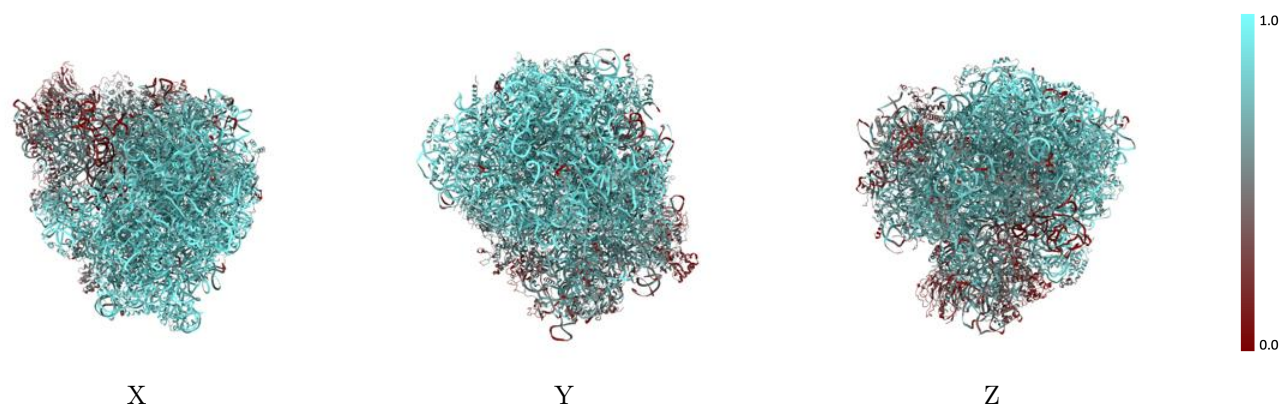
The images above show the 3D surface view of the map at the recommended contour level 0.18 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



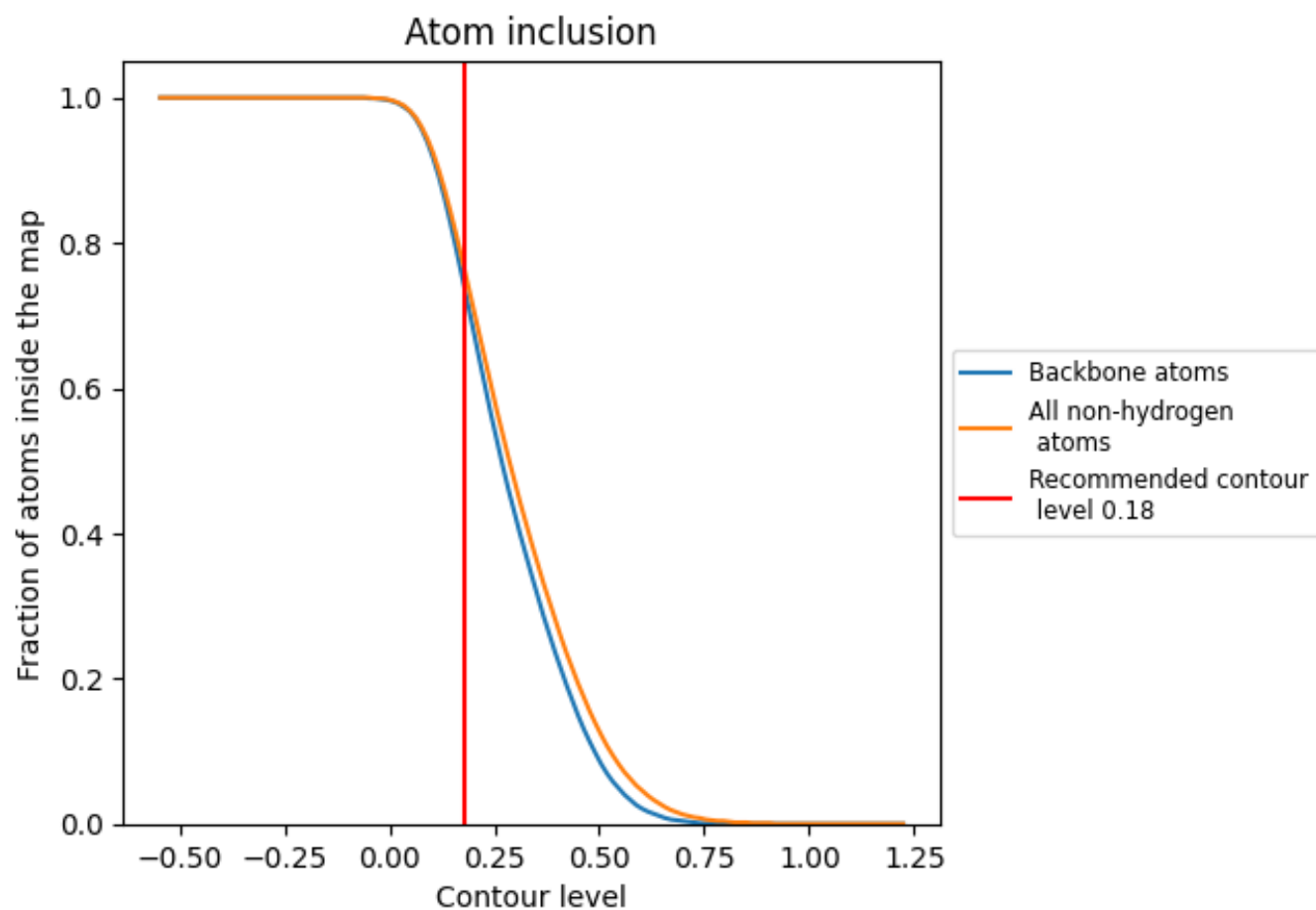
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.18).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 76% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.18) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7610	 0.4990
0	 0.4330	 0.3550
1	 0.1220	 0.2380
2	 0.7430	 0.5060
3	 0.5320	 0.3970
4	 0.3420	 0.3430
5	 0.7470	 0.4350
6	 0.5180	 0.4150
7	 0.2820	 0.2990
8	 0.1510	 0.2250
A	 0.8770	 0.5780
AA	 0.8940	 0.5530
Aa	 0.5450	 0.4560
B	 0.9060	 0.6040
BB	 0.9350	 0.5610
Bb	 0.1860	 0.3440
C	 0.8860	 0.5840
CC	 0.9410	 0.5800
Cc	 0.2720	 0.3330
D	 0.7860	 0.5390
DD	 0.4710	 0.4380
Dd	 0.4560	 0.5040
E	 0.8660	 0.5770
EE	 0.8860	 0.6060
Ee	 0.2300	 0.3270
F	 0.8680	 0.5720
FF	 0.8470	 0.5580
G	 0.7040	 0.4900
GG	 0.8860	 0.5950
H	 0.8460	 0.5850
HH	 0.7420	 0.4960
I	 0.8080	 0.5450
II	 0.8330	 0.5620
J	 0.8460	 0.5800
JJ	 0.8960	 0.5960



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Chain	Atom inclusion	Q-score
K	 0.8730	 0.5900
KK	 0.7400	 0.5130
L	 0.7810	 0.5310
LL	 0.7800	 0.5300
M	 0.8780	 0.5680
MM	 0.8130	 0.5680
N	 0.8230	 0.5380
NN	 0.6740	 0.4800
O	 0.7850	 0.5540
OO	 0.8180	 0.5330
P	 0.7810	 0.5480
PP	 0.8280	 0.5550
Pp	 0.1050	 0.4110
Q	 0.9190	 0.6230
QQ	 0.9110	 0.5890
R	 0.9270	 0.6110
S	 0.8560	 0.5790
T	 0.8560	 0.5670
U	 0.7500	 0.4830
V	 0.9420	 0.6070
W	 0.7080	 0.5060
X	 0.9180	 0.5870
Y	 0.8290	 0.5760
Z	 0.7880	 0.5720
a	 0.8030	 0.5640
b	 0.8210	 0.5810
c	 0.7550	 0.4360
d	 0.6370	 0.4750
e	 0.5420	 0.4150
f	 0.7540	 0.5030
g	 0.5080	 0.3770
h	 0.5530	 0.4090
i	 0.3360	 0.3260
j	 0.3590	 0.3230
k	 0.3330	 0.3210
l	 0.5240	 0.3780
m	 0.6270	 0.4330
n	 0.4570	 0.3030
o	 0.5950	 0.4290
p	 0.6550	 0.4510
q	 0.6700	 0.4740
r	 0.3390	 0.3160

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Chain	Atom inclusion	Q-score
s	 0.4920	 0.3780
t	 0.4670	 0.3680
u	 0.2910	 0.3140
v	 0.4070	 0.3160
w	 0.4900	 0.3590
x	 0.6900	 0.4860
y	 0.7340	 0.5010
z	 0.6790	 0.4950