



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 07:51 AM UTC

PDB ID : 7NRD / pdb_00007nrd
EMDB ID : EMD-12535
Title : Structure of the yeast Gcn1 bound to a colliding stalled 80S ribosome with MBF1, A/P-tRNA and P/E-tRNA
Authors : Pochopien, A.A.; Beckert, B.; Wilson, D.N.
Deposited on : 2021-03-03
Resolution : 4.36 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

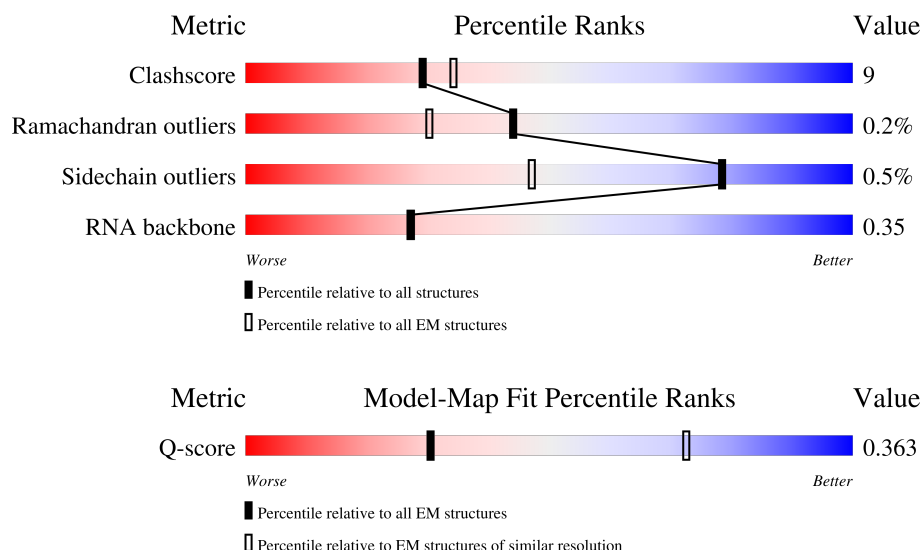
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.36 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	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	3737 (3.87 - 4.86)

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	S2	1800	
2	SA	223	
3	SB	206	

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Mol	Chain	Length	Quality of chain
4	SC	92	
5	SD	124	
6	SE	119	
7	SF	141	
8	SG	125	
9	SH	145	
10	SI	143	
11	SJ	101	
12	SK	69	
13	SL	63	
14	SM	53	
15	SN	73	
16	SO	313	
17	SP	206	
18	SQ	216	
19	SR	217	
20	SS	260	
21	ST	218	
22	SU	185	
23	SV	188	
24	SW	185	
25	SX	146	
26	SY	150	
27	SZ	128	
28	Sa	87	

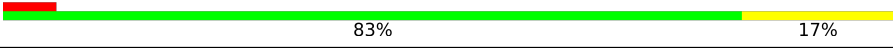
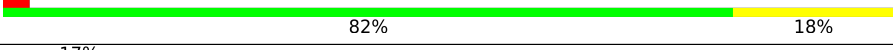
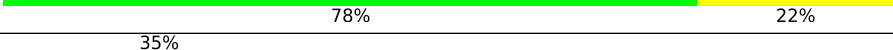
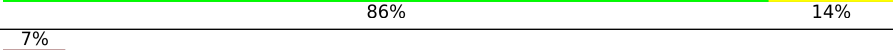
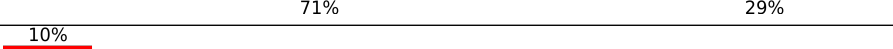
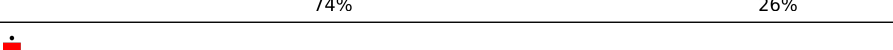
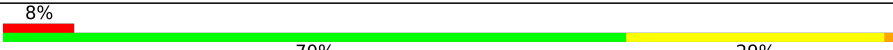
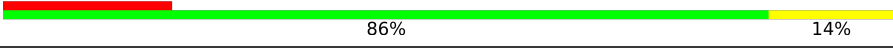
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Mol	Chain	Length	Quality of chain
29	Sb	129	
30	Sc	144	
31	Sd	134	
32	Se	97	
33	Sf	81	
34	Sg	44	
35	Sh	120	
36	S3	32	
37	Sn	75	
38	Sm	77	
39	LA	3394	
40	LB	121	
41	LC	158	
42	LD	251	
43	LE	386	
44	LF	361	
45	LG	294	
46	LH	167	
47	LI	222	
48	LJ	233	
49	LK	191	
50	LL	218	
51	LM	169	
52	LN	193	
53	LO	136	

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Mol	Chain	Length	Quality of chain
54	LP	203	
55	LQ	197	
56	LR	183	
57	LS	185	
58	LT	188	
59	LU	171	
60	LV	159	
61	LW	100	
62	LX	136	
63	LY	61	
64	LZ	121	
65	La	125	
66	Lb	135	
67	Lc	148	
68	Ld	58	
69	Le	96	
70	Lf	109	
71	Lg	127	
72	Lh	106	
73	Li	112	
74	Lj	119	
75	Lk	99	
76	Ll	81	
77	Lm	77	
78	Ln	50	

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Mol	Chain	Length	Quality of chain
79	Lo	52	21% 71% 29%
80	Lp	25	8% 72% 12% 16%
81	Lq	103	15% 71% 29%
82	Lr	91	79% 19%

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 204032 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called TPA_inf: Saccharomyces cerevisiae S288C chromosome XII, complete sequence.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There are 11 discrepancies between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There are 8 discrepancies between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

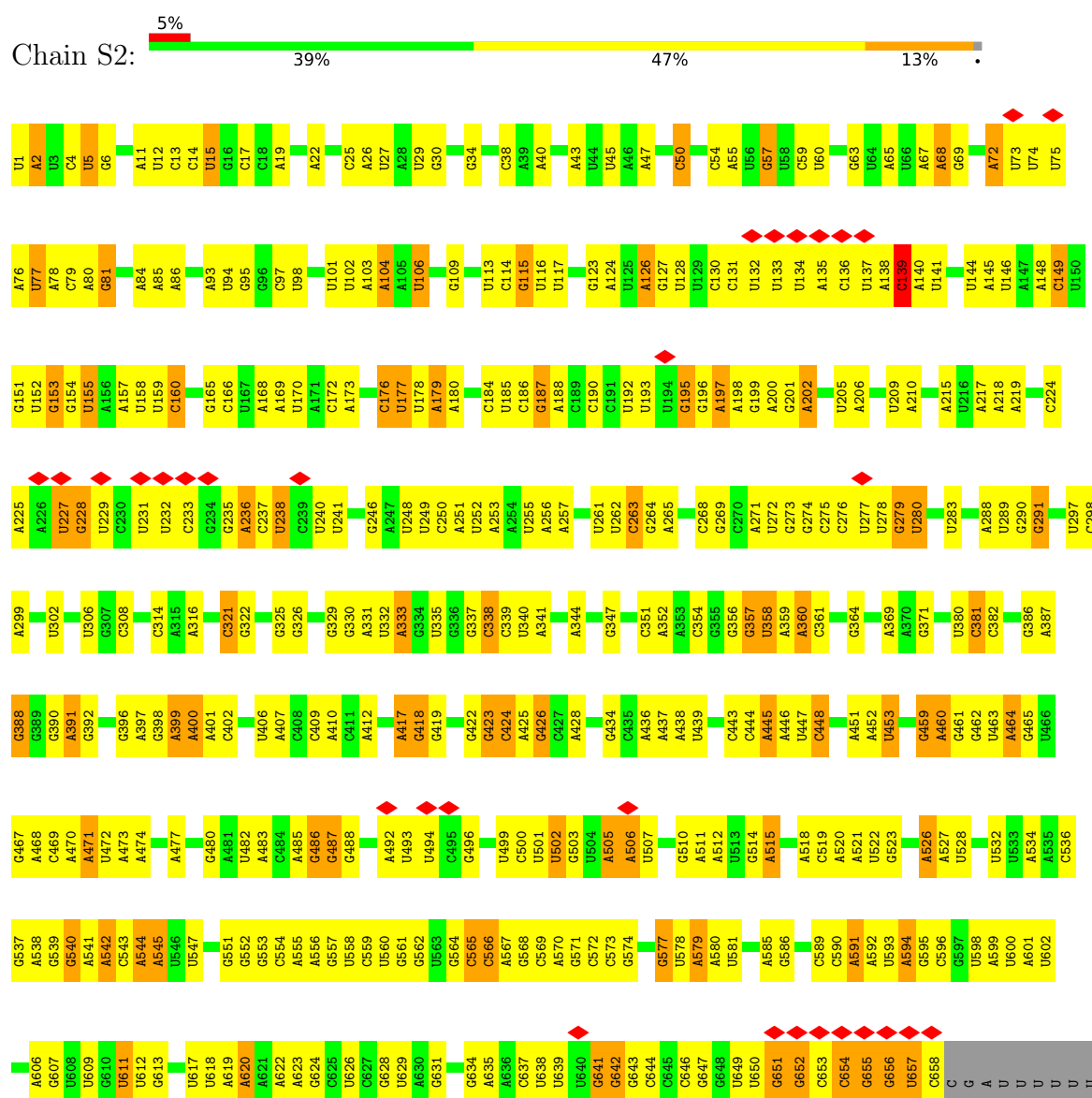
- Molecule 82 is a protein called 60S ribosomal protein L43-A.

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

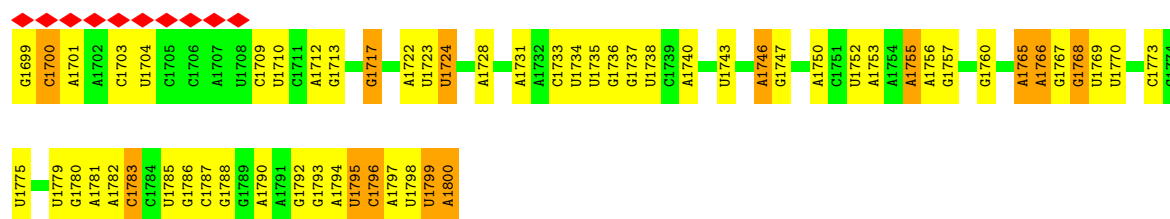
3 Residue-property plots

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

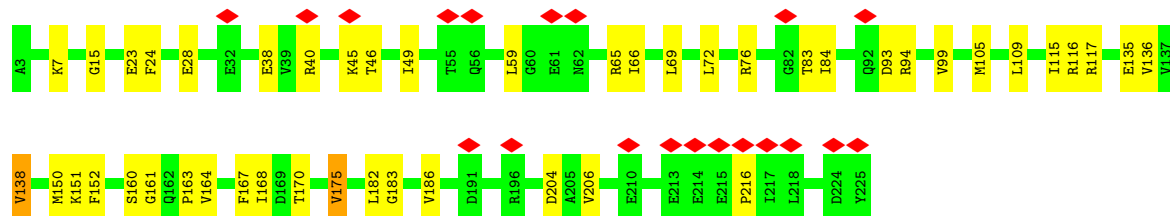
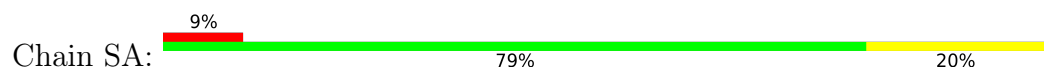
- Molecule 1: TPA_inf: *Saccharomyces cerevisiae* S288C chromosome XII, complete sequence



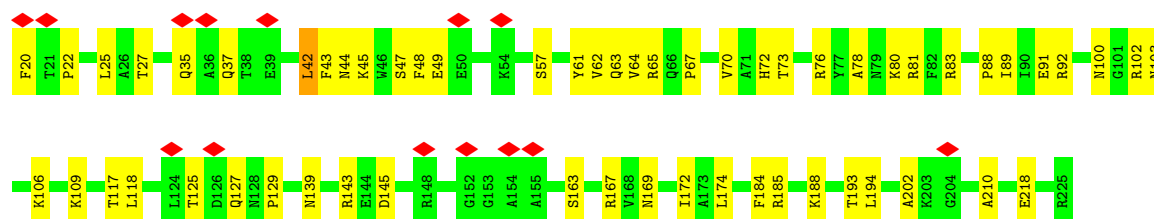
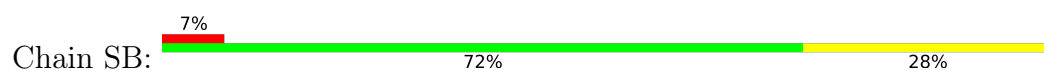
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U728	G729	G730	G731	G732	A733	A734	C735	C736	A737	G738	G739	A740	C741	U742	U743	G751	A752	A753	A754	A755	A756	A762	G765	U766	U767	C768	G769	A770	C773	A774	G775	G776	C777	G778	U779	A780	U781	U782	G783	C784	U785	C786	A787	A788	A789	U792	A793	U794	A795	A796	G797	C798	A799	U800						
G801	G802	A803	A806	A809	G810	A811	A812	U813	A814	G815	G816	A817	C818	G819	U820	U821	U822	G823	G824	U825	U826	C827	U828	A829	U830	U831	U832	U833	U834	U835	U836	G837	G838	U841	C842	U843	A844	G845	G846	C849	A850	U854	A855	A856	U860	U861	A862	A863	U864	C870	G871	A872	G873	U874	U875	U876	U877	U878	U879	U880
U873	C874	G875	G876	G877	G878	G879	C883	A884	G885	U886	U887	U888	U894	G895	A898	G899	A900	G901	G902	U911	U912	G913	G914	U915	U916	U917	U918	A919	U920	U921	G922	A923	A924	G925	A926	U927	U928	A929	A930	C931	U932	A933	C934	U935	G936	G942	C943	A944	U945	A951	A952	A955								
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G1042	A1043	U1044	C1045	U1046	G1047	U1048	U1049	G1050	U1051	U1052	G1053	U1054	U1055	U1056	U1057	U1058	U1059	A1060	A1061	A1062	U1063	G1064	A1065	C1066	C1067	C1072	U1073	G1074	A1081	C1082	G1083	A1084	G1085	A1086	A1087	A1088	A1092	A1093	U1095	C1096	U1097	U1098	U1099	G1100	G1101	U1104	C1105	U1106	U1107	G1108	G1109	G1110	G1111	G1112						
A1113	G1114	U1117	U1118	G1119	U1120	G1121	G1122	C1123	A1124	U1125	G1126	G1127	G1130	A1131	A1132	A1133	C1134	U1135	A1138	A1139	G1140	G1141	A1142	A1143	U1144	U1145	U1146	A1147	C1148	G1149	G1150	A1151	G1158	C1159	G1164	U1165	A1166	G1167	U1168	G1169	A1170	U1171	G1172	C1173	C1174	U1175	G1176	U1182	U1183	A1184	U1185	A1189								
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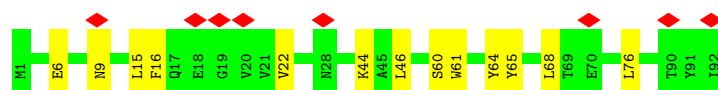
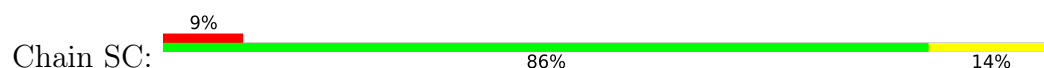
• Molecule 2: 40S ribosomal protein S3



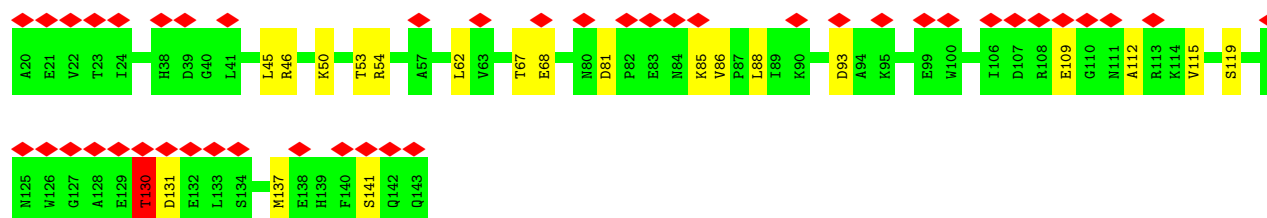
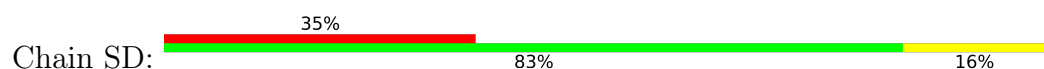
• Molecule 3: 40S ribosomal protein S5



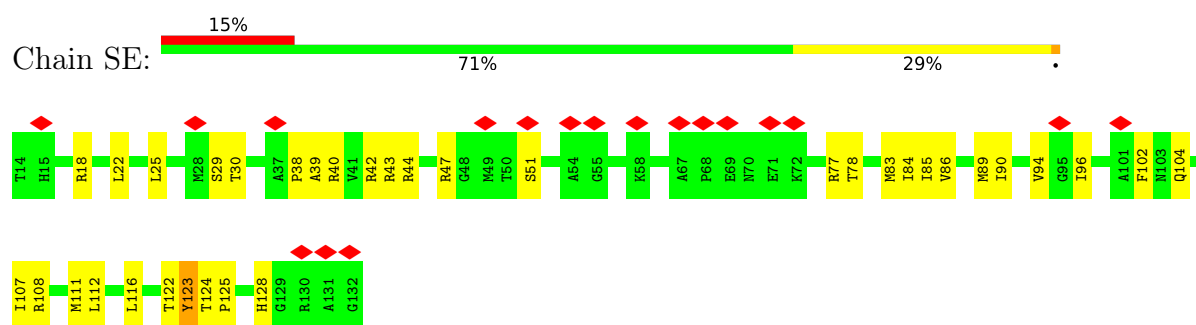
• Molecule 4: 40S ribosomal protein S10-A



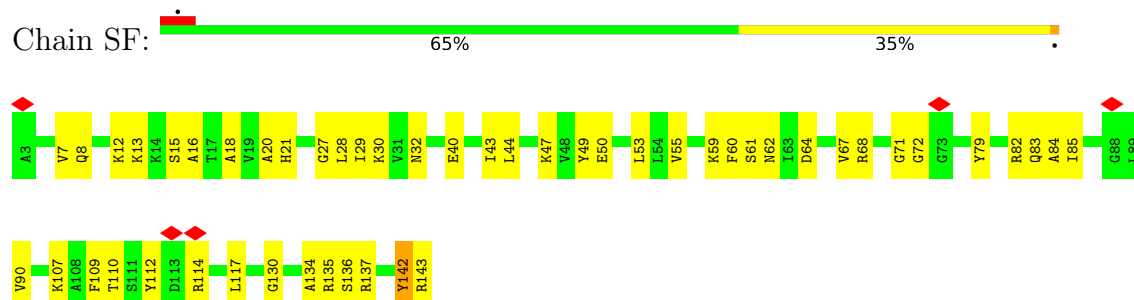
• Molecule 5: 40S ribosomal protein S12



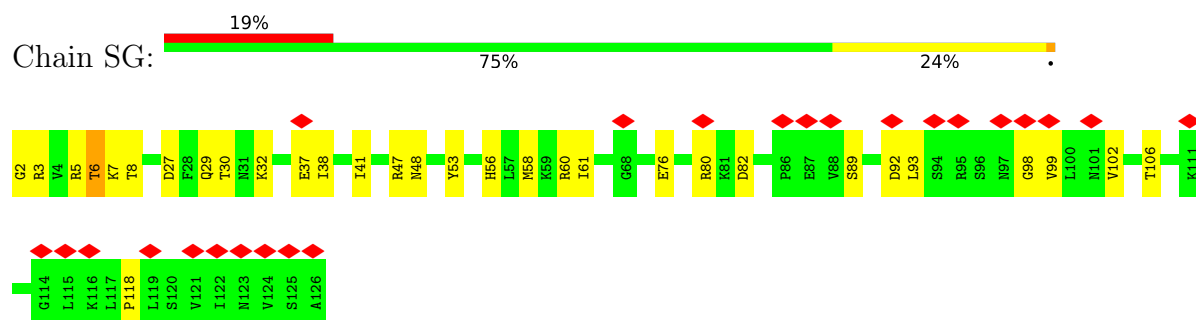
• Molecule 6: 40S ribosomal protein S15



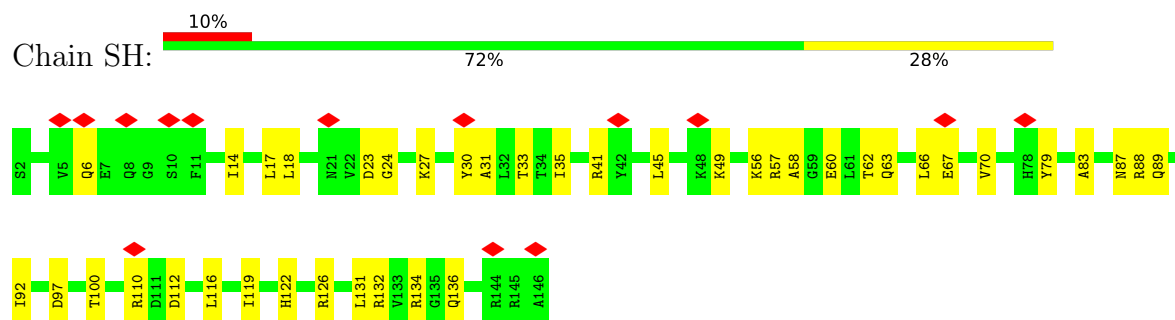
• Molecule 7: 40S ribosomal protein S16-A



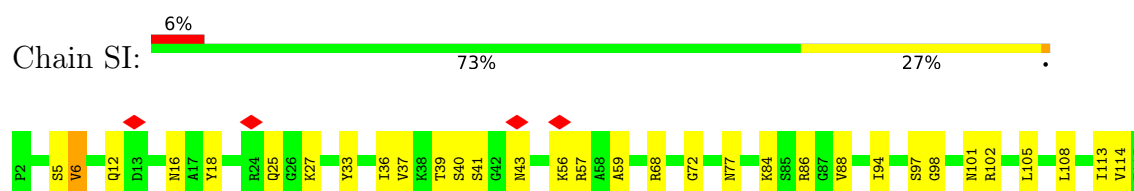
• Molecule 8: 40S ribosomal protein S17-B

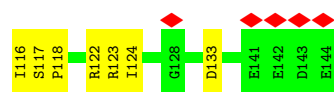


• Molecule 9: 40S ribosomal protein S18-A

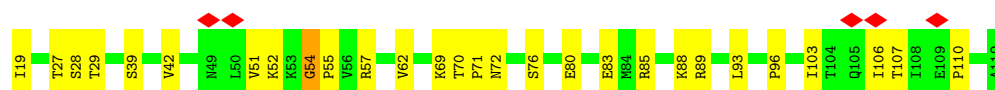
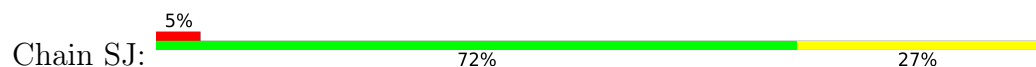


• Molecule 10: 40S ribosomal protein S19-A

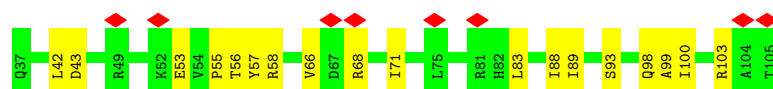
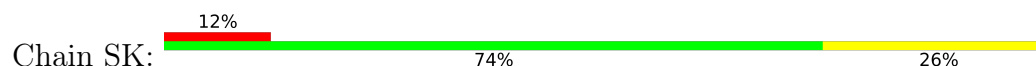




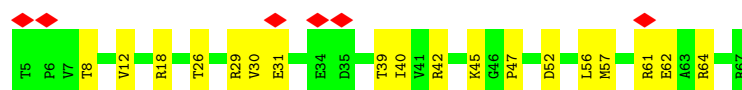
- Molecule 11: 40S ribosomal protein S20



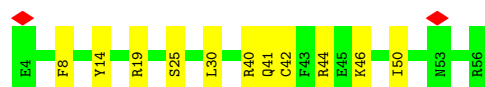
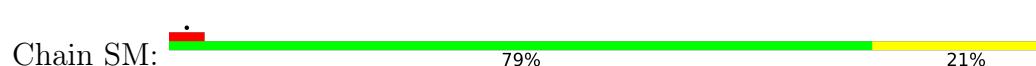
- Molecule 12: 40S ribosomal protein S25-A



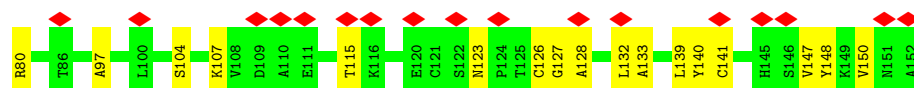
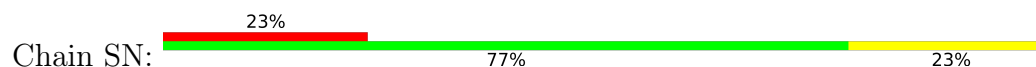
- Molecule 13: 40S ribosomal protein S28-A



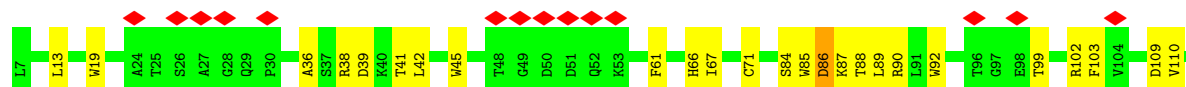
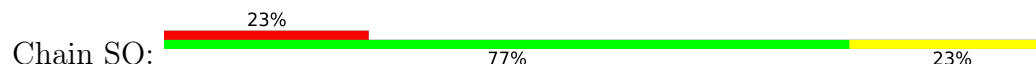
- Molecule 14: 40S ribosomal protein S29-A

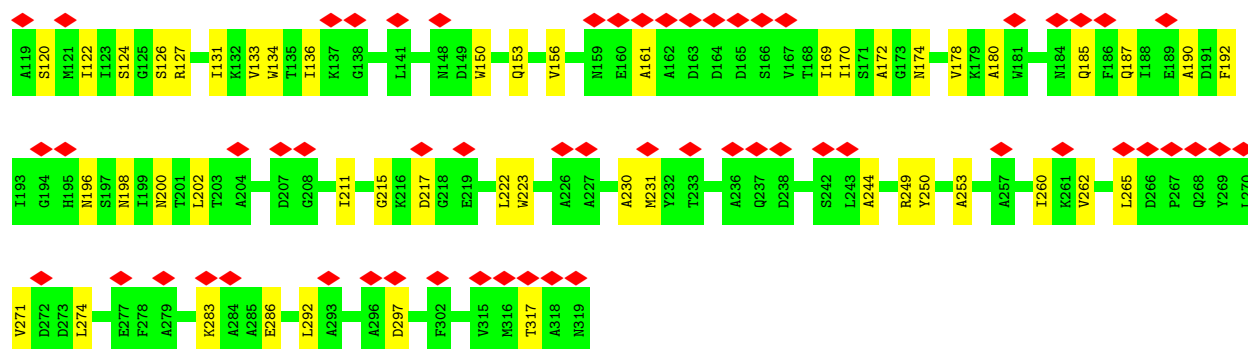


- Molecule 15: Ubiquitin-40S ribosomal protein S31



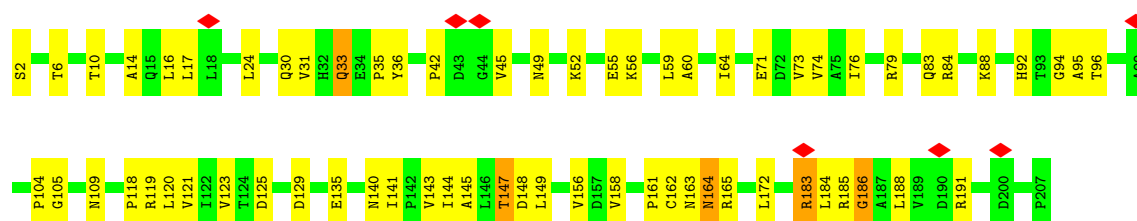
- Molecule 16: Guanine nucleotide-binding protein subunit beta-like protein





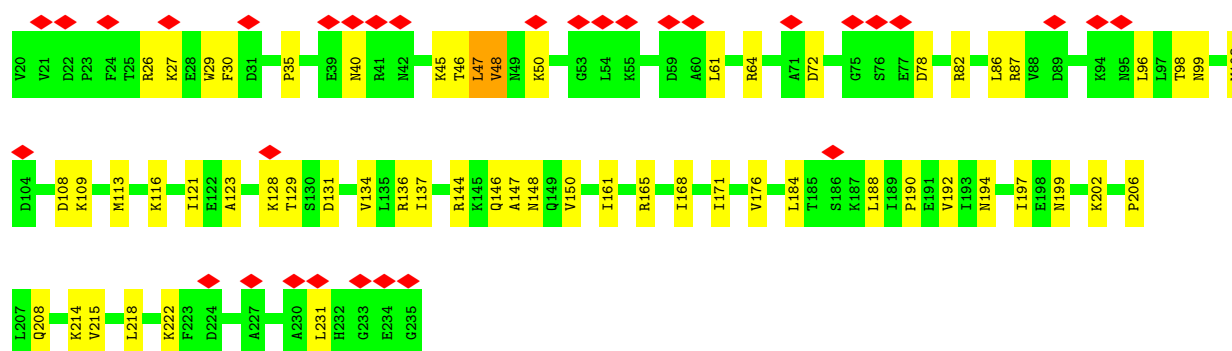
• Molecule 17: 40S ribosomal protein S0-A

Chain SP: 68% 30% .



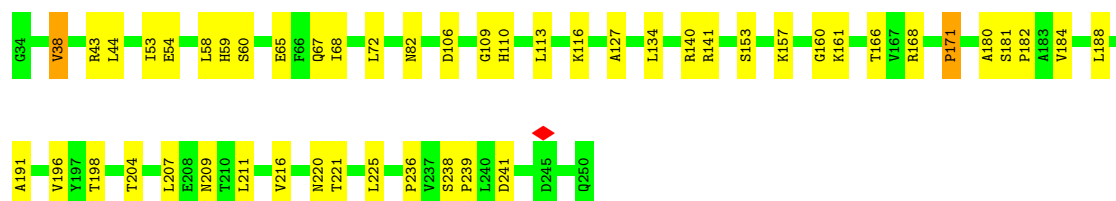
• Molecule 18: 40S ribosomal protein S1-A

Chain SQ: 15% 73% 26% .



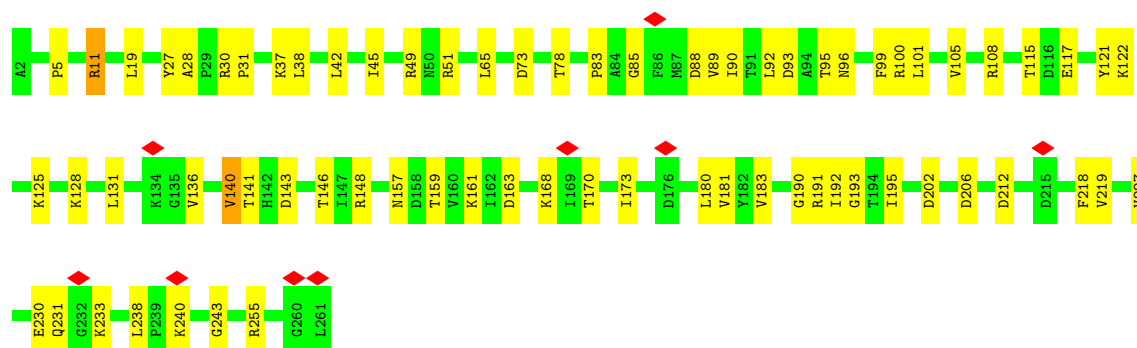
• Molecule 19: 40S ribosomal protein S2

Chain SR: 77% 22% .



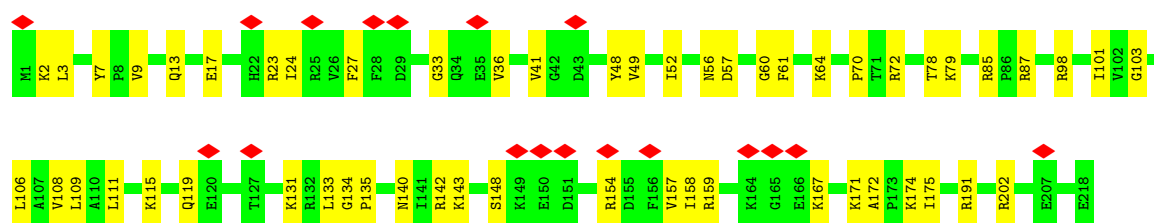
• Molecule 20: 40S ribosomal protein S4-A

Chain SS:  73% 27%



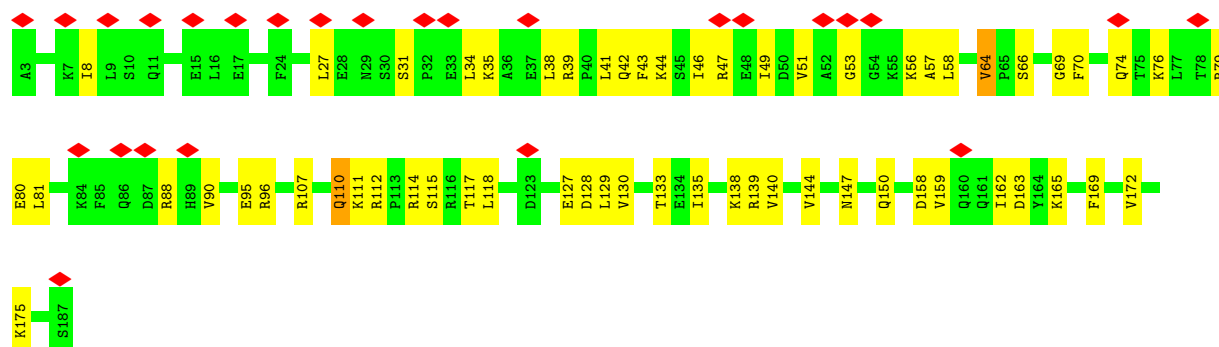
• Molecule 21: 40S ribosomal protein S6-A

Chain ST:  8% 75% 25%



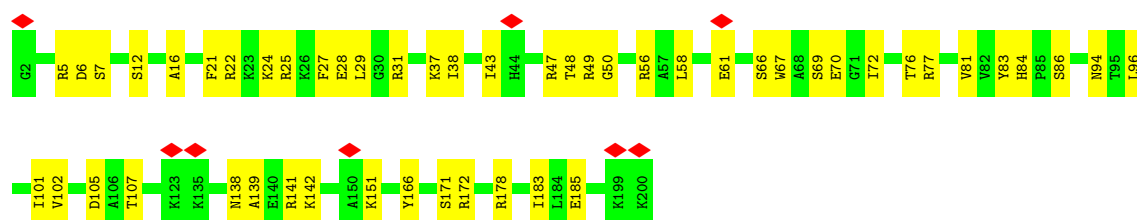
• Molecule 22: 40S ribosomal protein S7-A

Chain SU:  14% 68% 31%



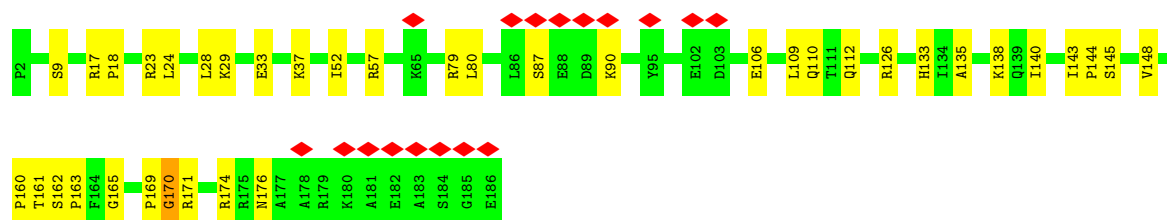
• Molecule 23: 40S ribosomal protein S8-A

Chain SV:  73% 27%



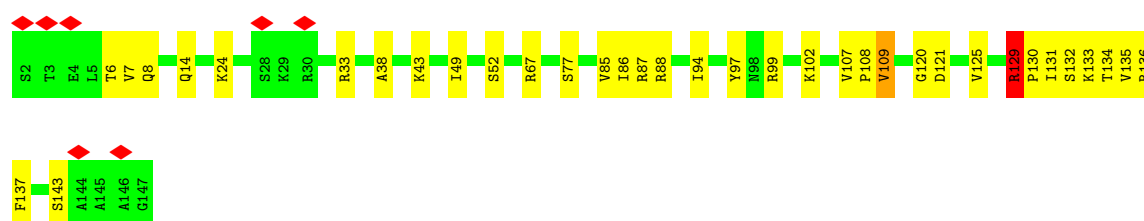
- Molecule 24: 40S ribosomal protein S9-A

Chain SW: 



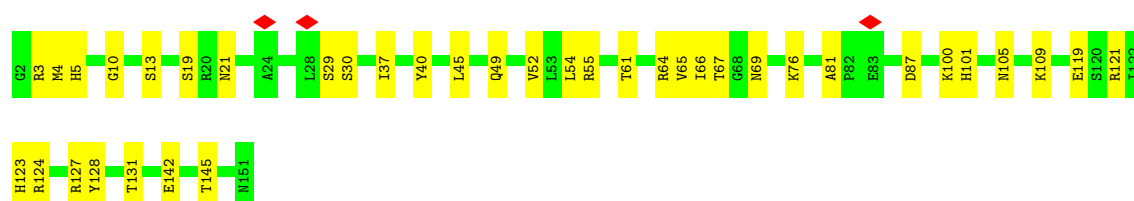
- Molecule 25: 40S ribosomal protein S11-A

Chain SX: 



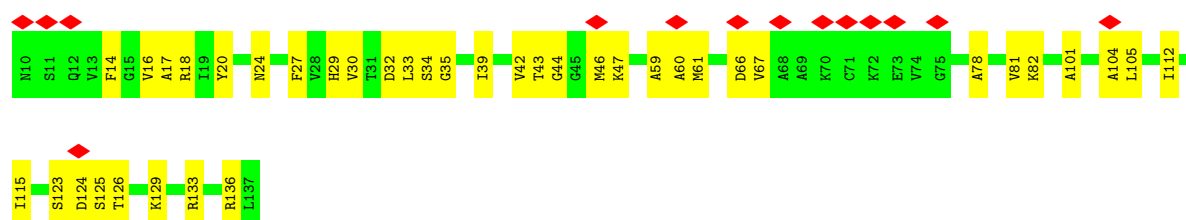
- Molecule 26: 40S ribosomal protein S13

Chain SY: 



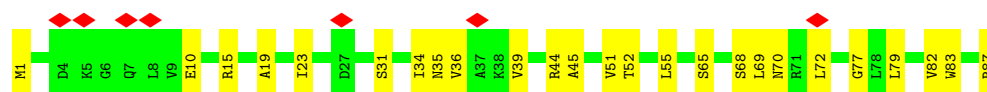
- Molecule 27: 40S ribosomal protein S14-B

Chain SZ: 



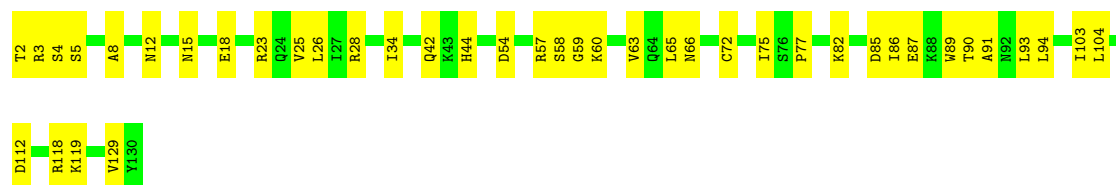
- Molecule 28: 40S ribosomal protein S21-A

Chain Sa: 



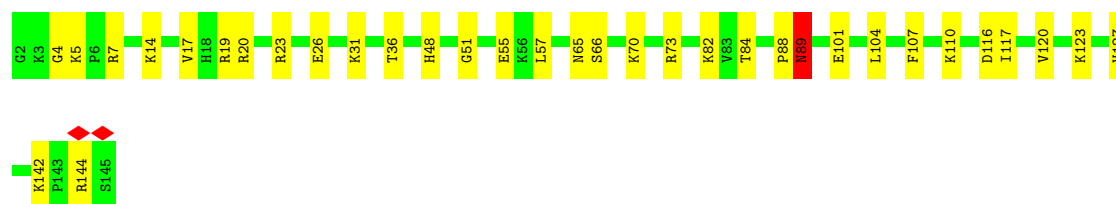
- Molecule 29: 40S ribosomal protein S22-A

Chain Sb:



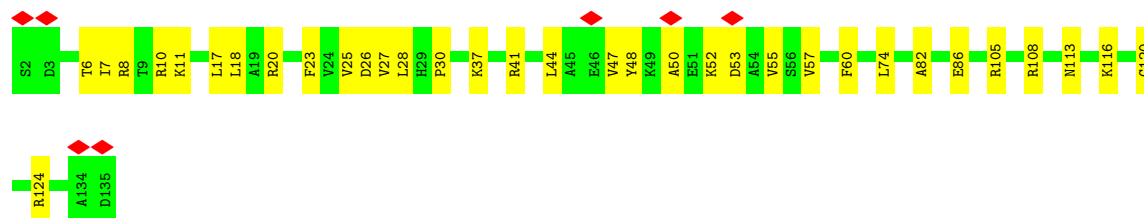
- Molecule 30: 40S ribosomal protein S23-A

Chain Sc:



- Molecule 31: 40S ribosomal protein S24-A

Chain Sd:



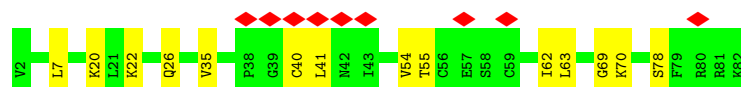
- Molecule 32: 40S ribosomal protein S26-B

Chain Se:

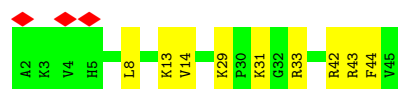
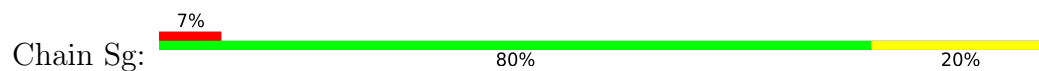


- Molecule 33: 40S ribosomal protein S27-A

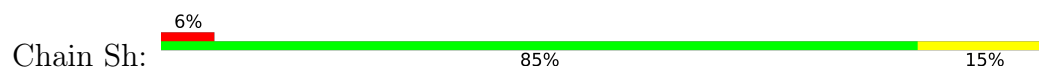
Chain Sf:



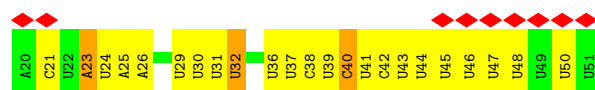
- Molecule 34: 40S ribosomal protein S30-A



- Molecule 35: Multiprotein-bridging factor 1



- Molecule 36: mRNA (32-MER)



- Molecule 37: tRNA (75-MER)

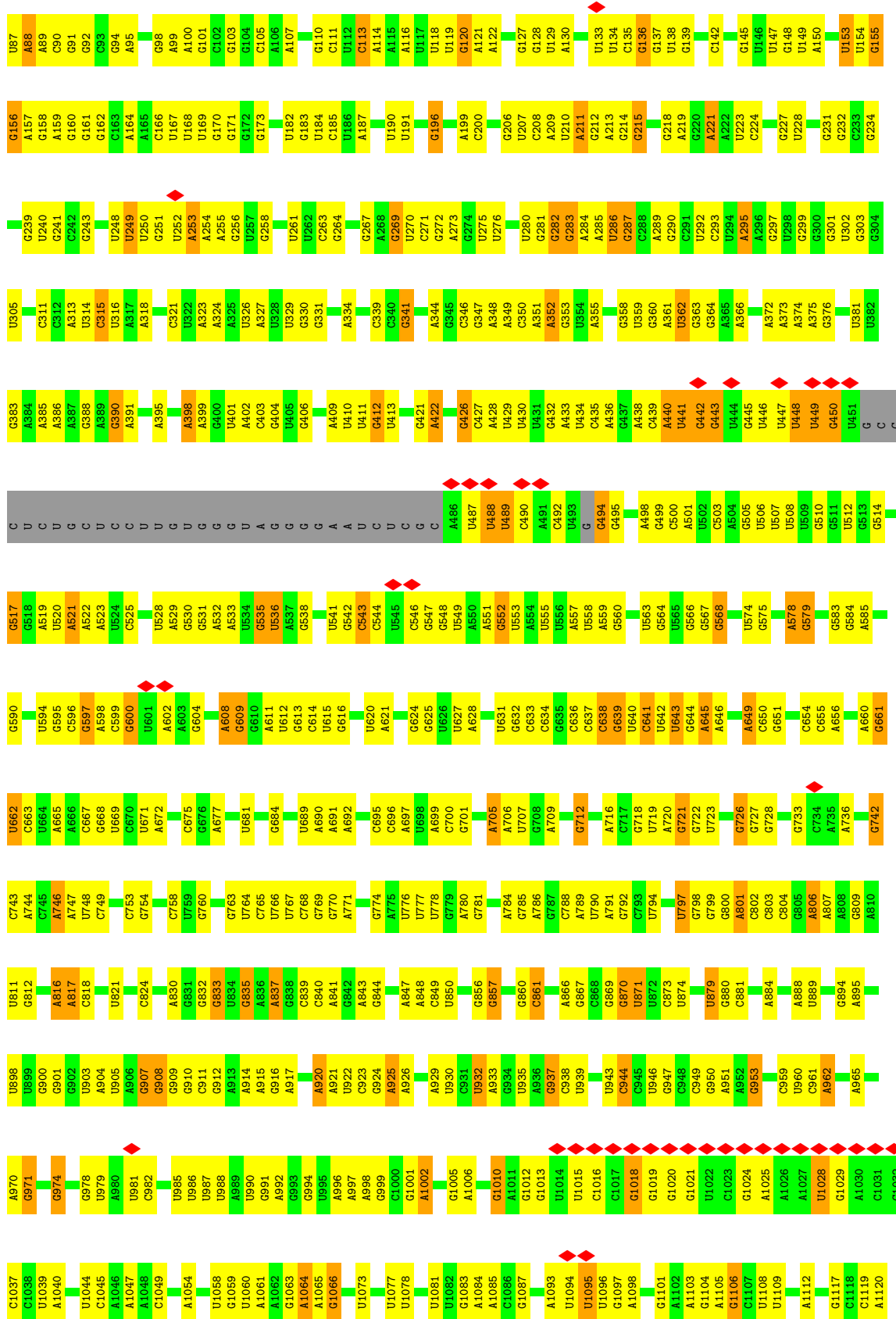


- Molecule 38: tRNA (77-MER)



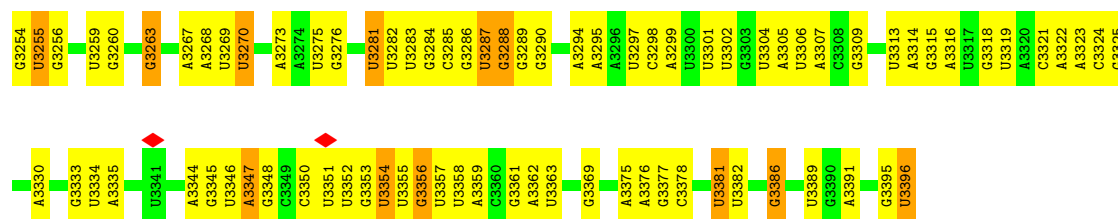
- Molecule 39: 25S rRNA (3184-MER)



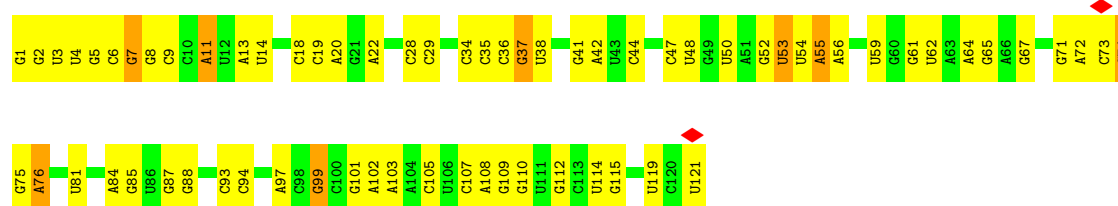




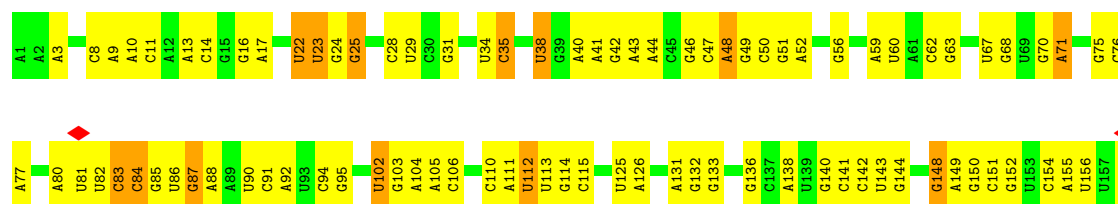




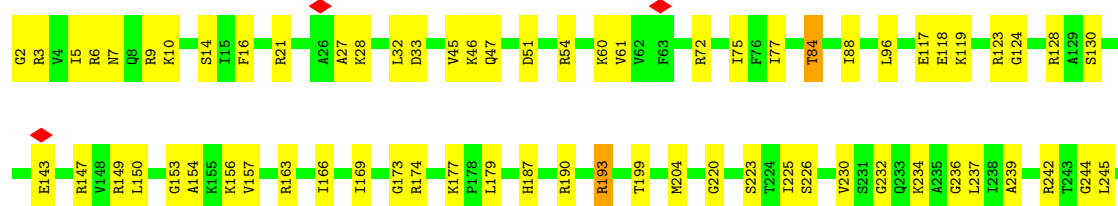
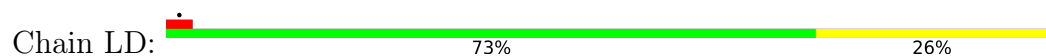
• Molecule 40: 5S rRNA (121-MER)



• Molecule 41: 5.8S rRNA (158-MER)

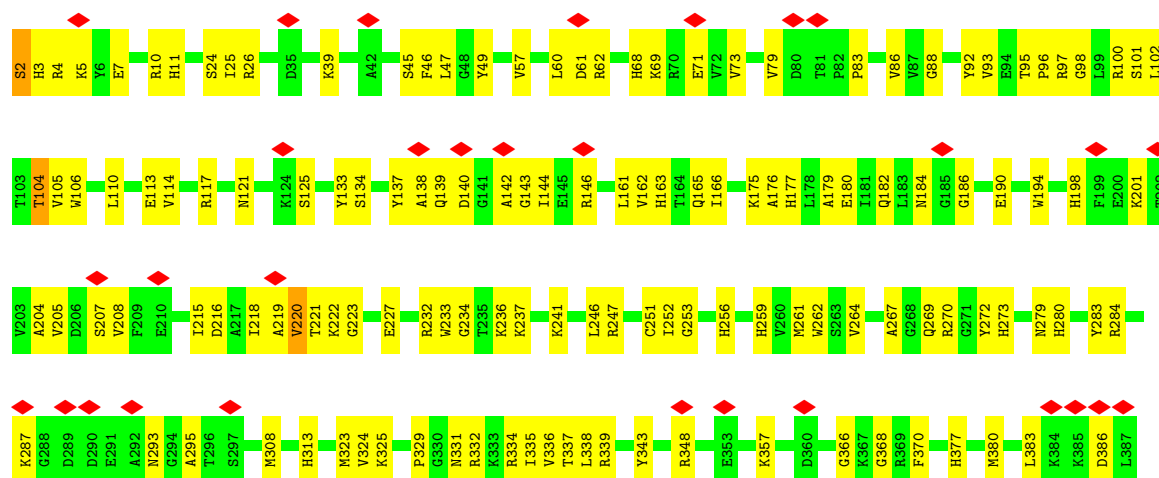


• Molecule 42: 60S ribosomal protein L2-A

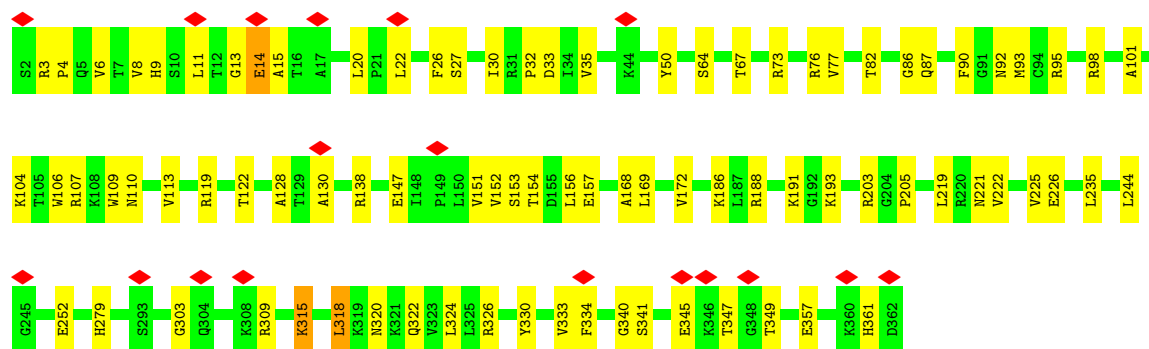
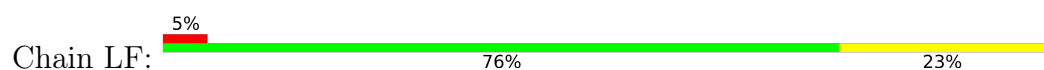


• Molecule 43: 60S ribosomal protein L3

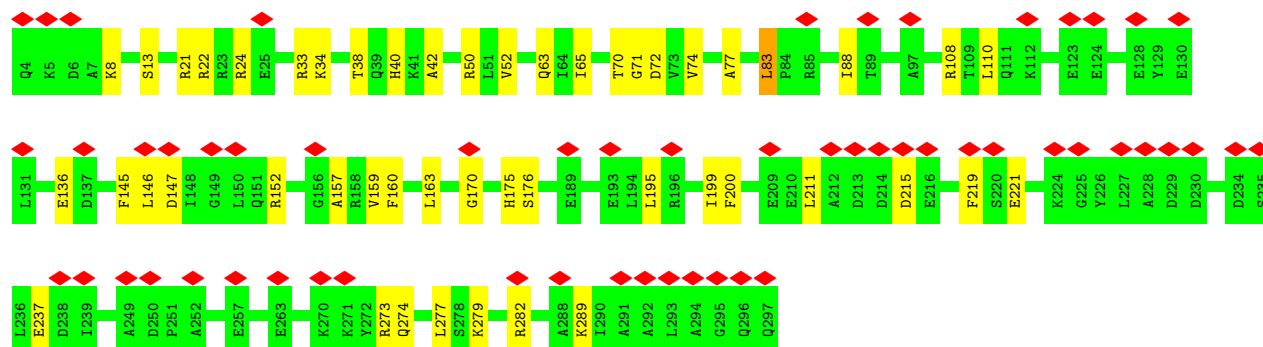
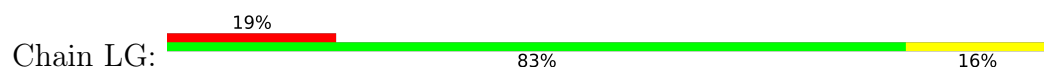




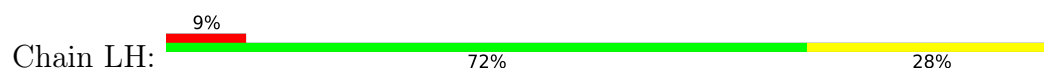
• Molecule 44: 60S ribosomal protein L4-A

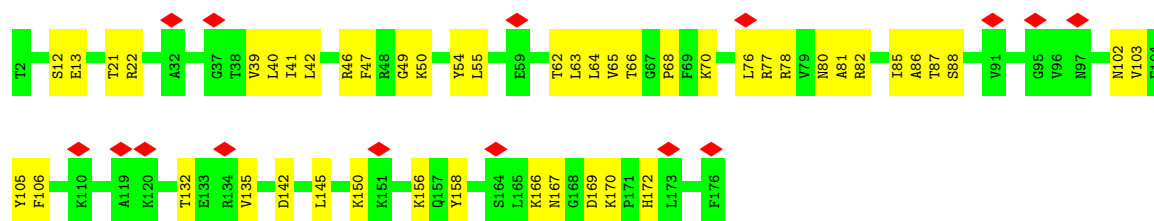


• Molecule 45: 60S ribosomal protein L5

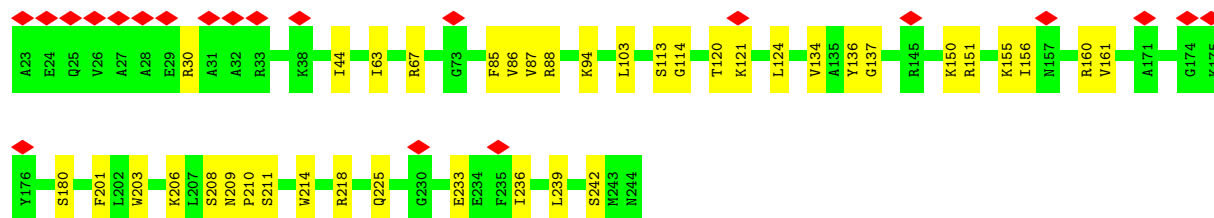
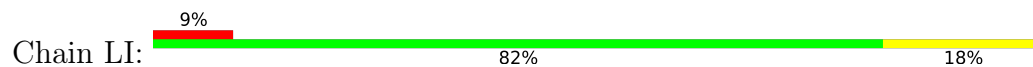


• Molecule 46: 60S ribosomal protein L6-B

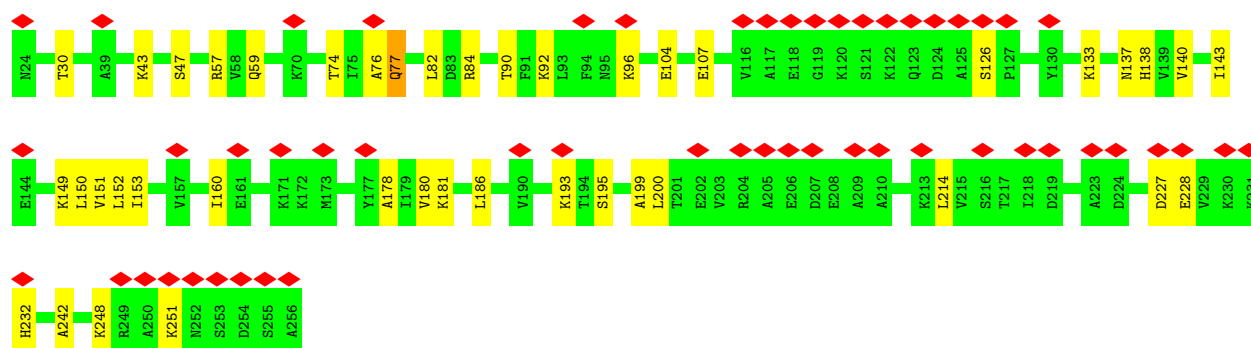
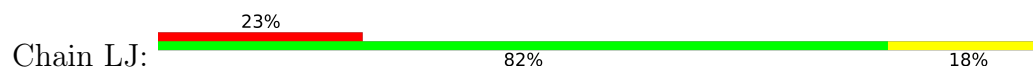




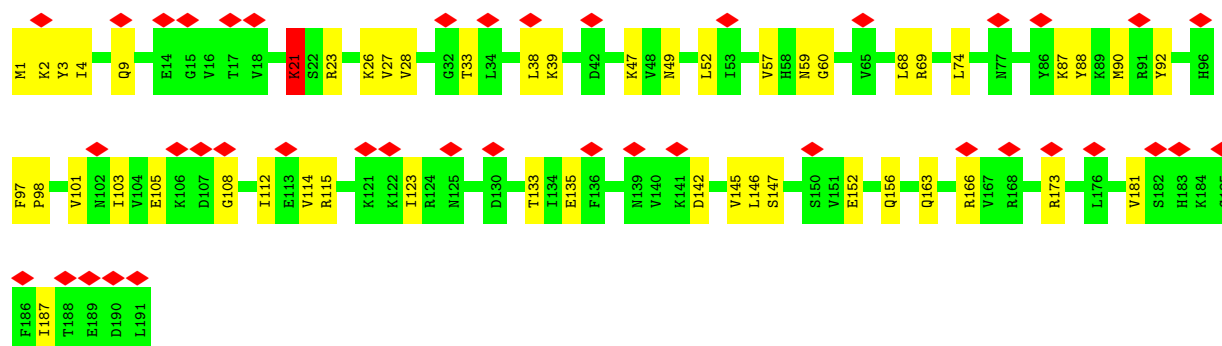
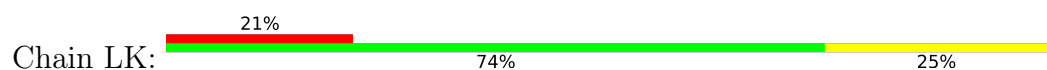
• Molecule 47: 60S ribosomal protein L7-A



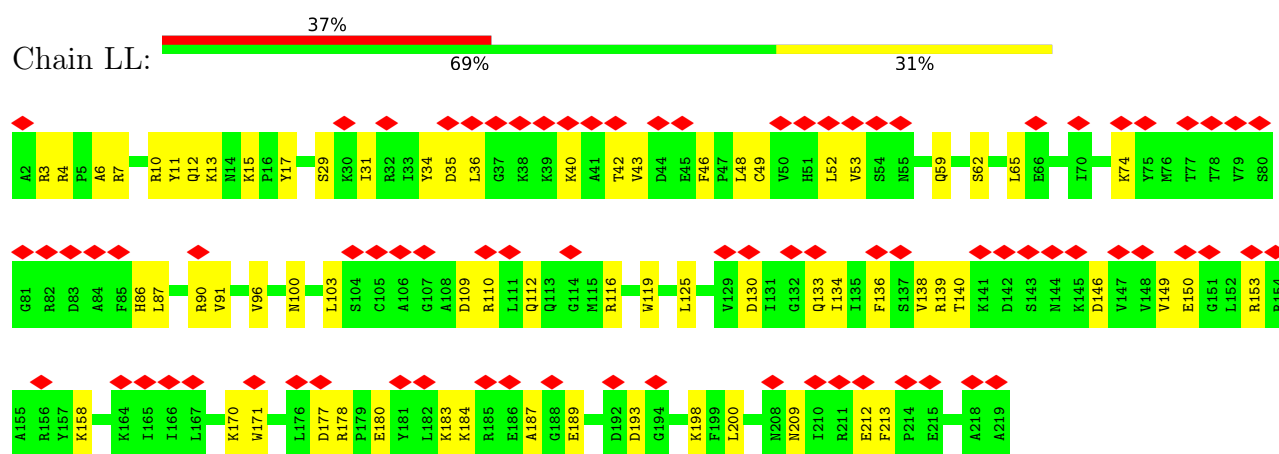
• Molecule 48: 60S ribosomal protein L8-A



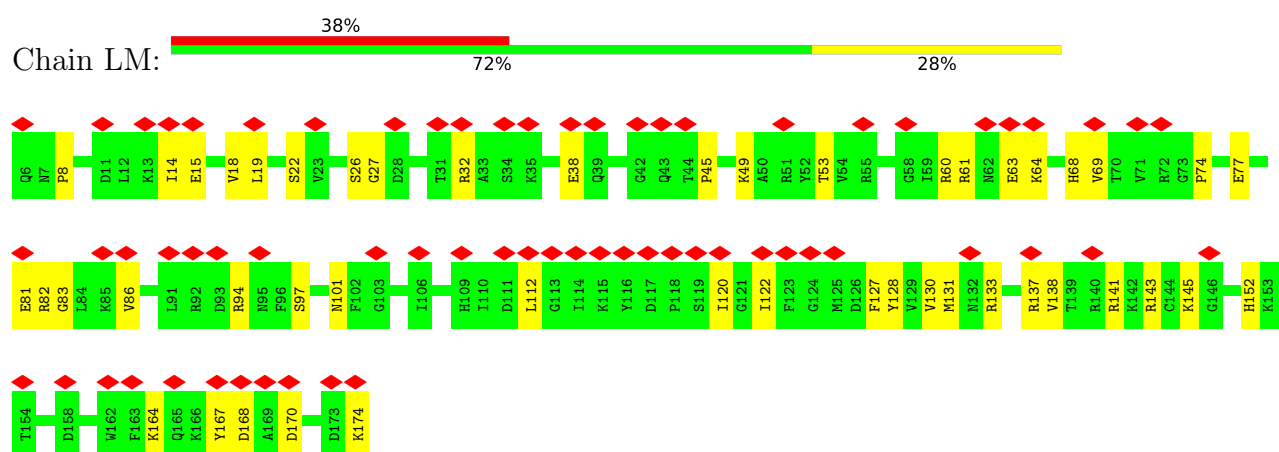
• Molecule 49: 60S ribosomal protein L9-A



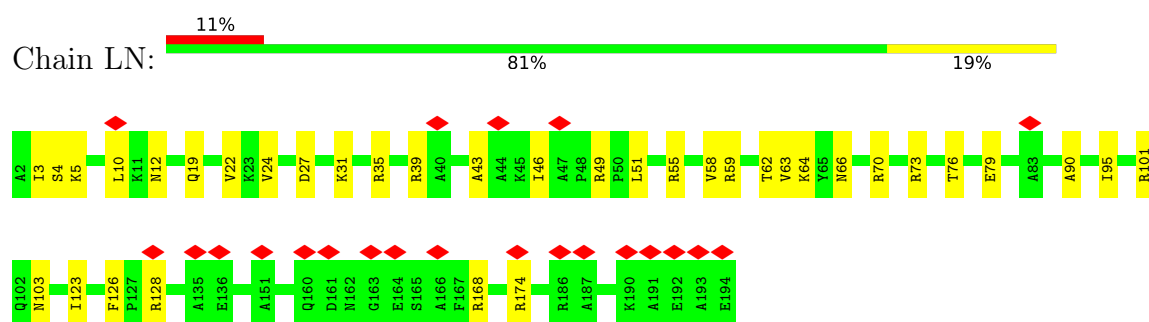
• Molecule 50: 60S ribosomal protein L10



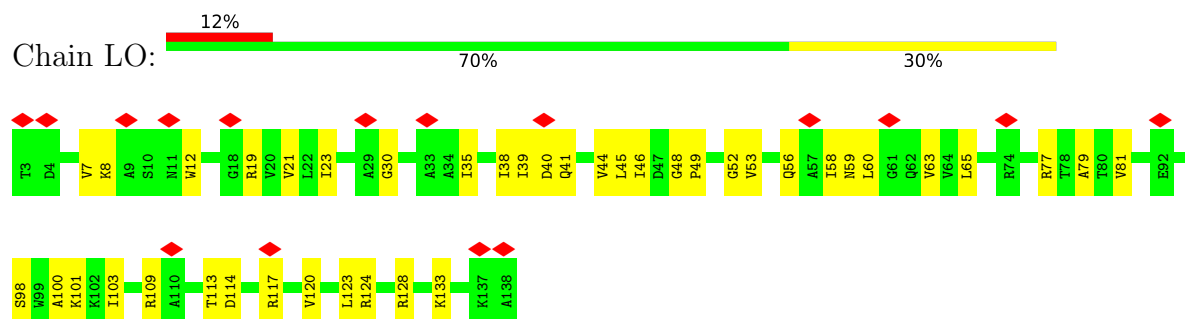
• Molecule 51: 60S ribosomal protein L11-B



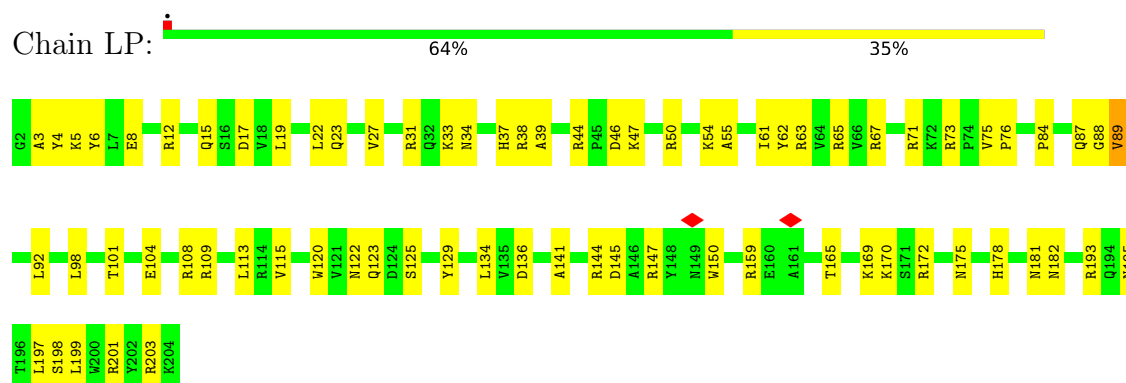
• Molecule 52: 60S ribosomal protein L13-A



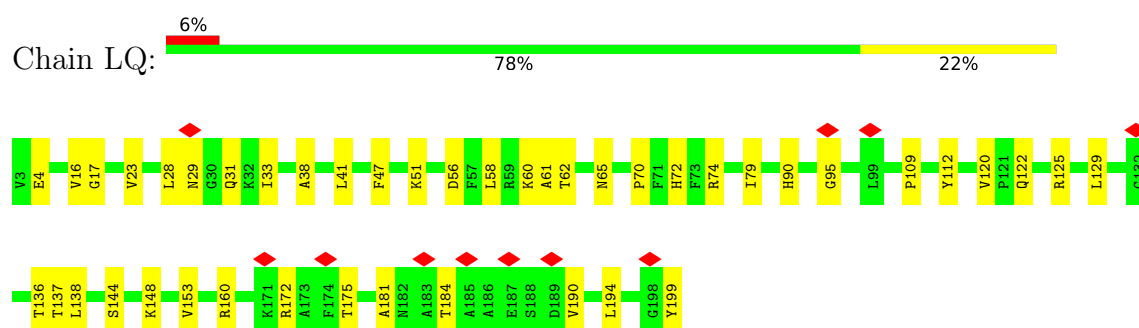
• Molecule 53: 60S ribosomal protein L14-A



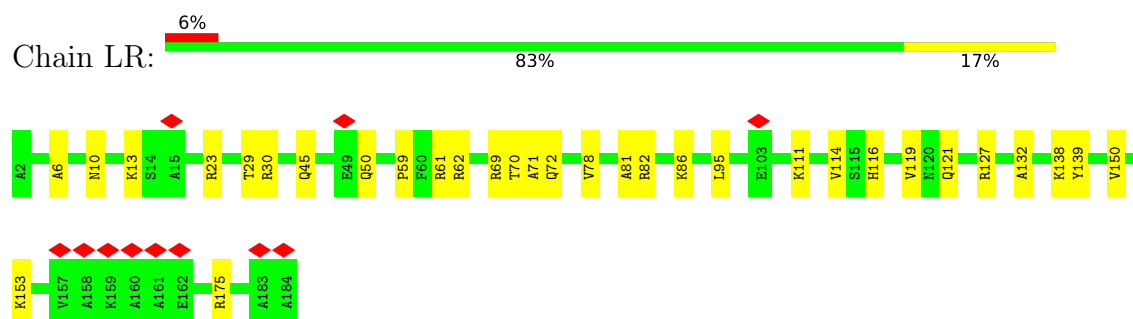
- Molecule 54: 60S ribosomal protein L15-A



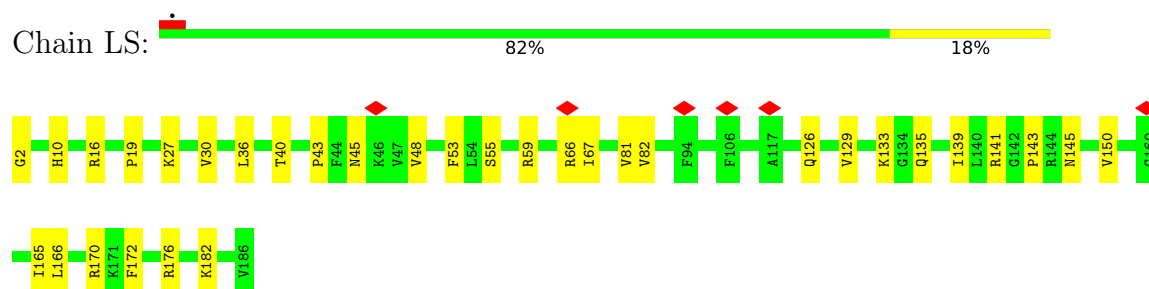
- Molecule 55: 60S ribosomal protein L16-A



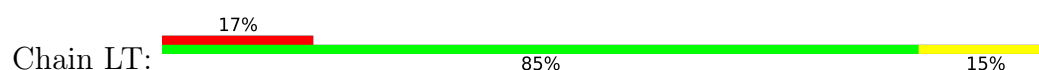
- Molecule 56: 60S ribosomal protein L17-A

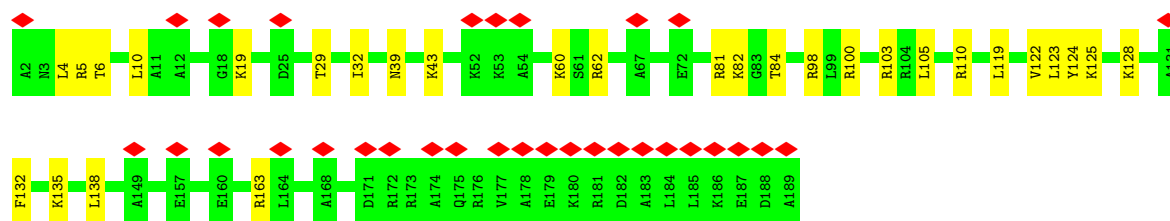


- Molecule 57: 60S ribosomal protein L18-A

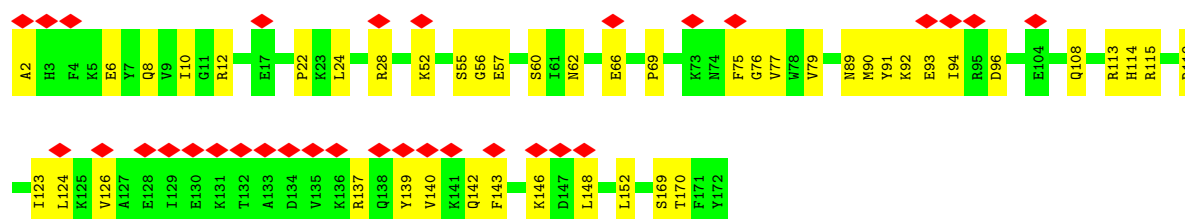
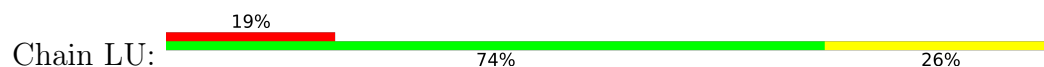


- Molecule 58: 60S ribosomal protein L19-A

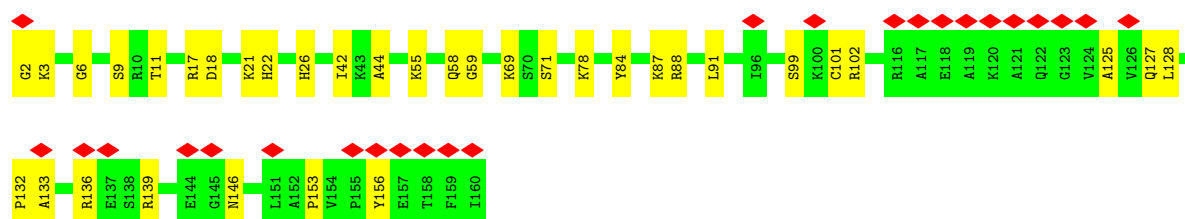
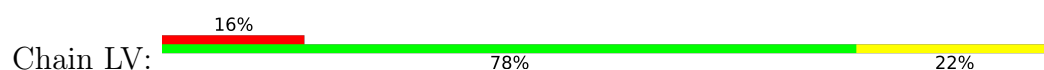




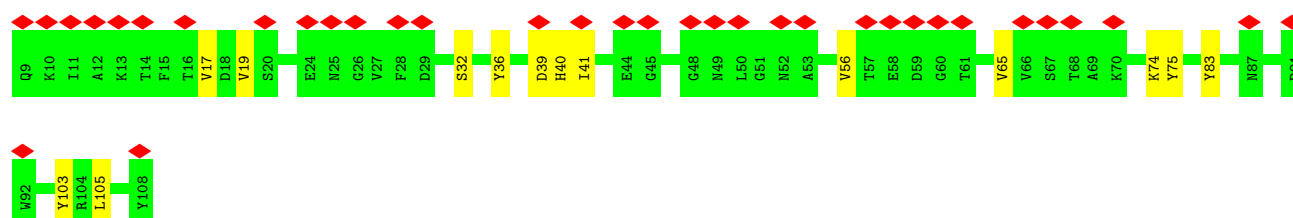
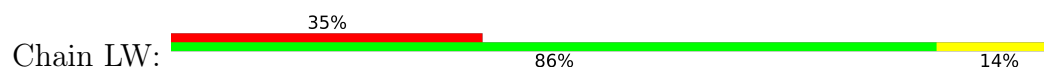
• Molecule 59: 60S ribosomal protein L20-A



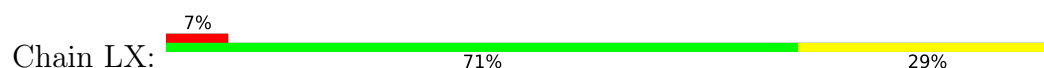
• Molecule 60: 60S ribosomal protein L21-A

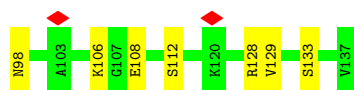


• Molecule 61: 60S ribosomal protein L22-A

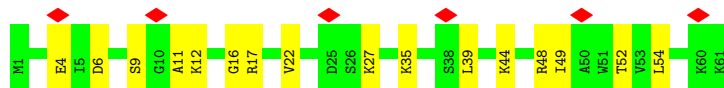
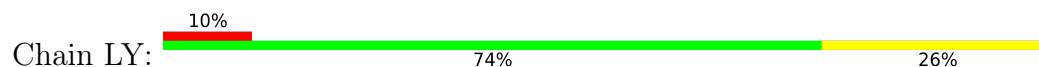


• Molecule 62: 60S ribosomal protein L23-A





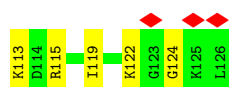
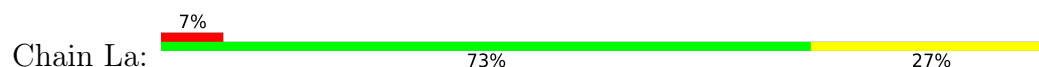
- Molecule 63: 60S ribosomal protein L24-A



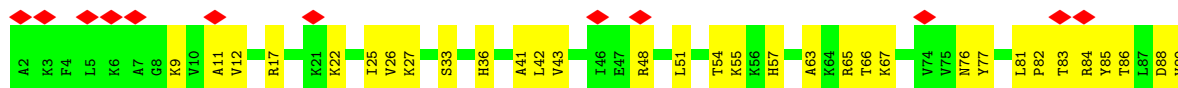
- Molecule 64: 60S ribosomal protein L25



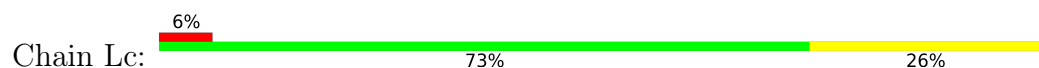
- Molecule 65: 60S ribosomal protein L26-A



- Molecule 66: 60S ribosomal protein L27-A

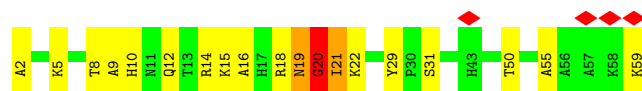


- Molecule 67: 60S ribosomal protein L28

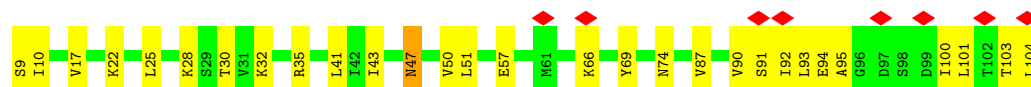




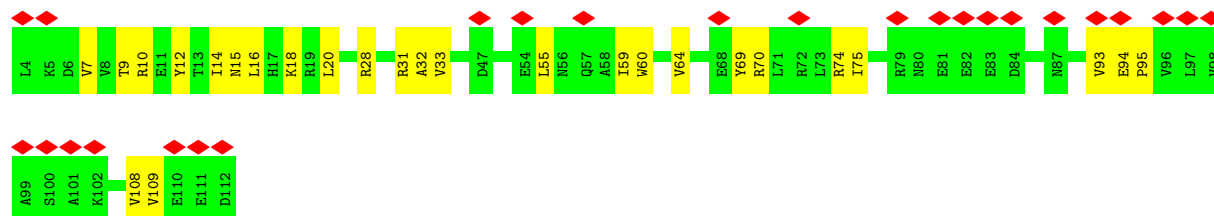
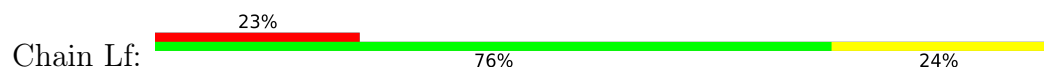
- Molecule 68: 60S ribosomal protein L29



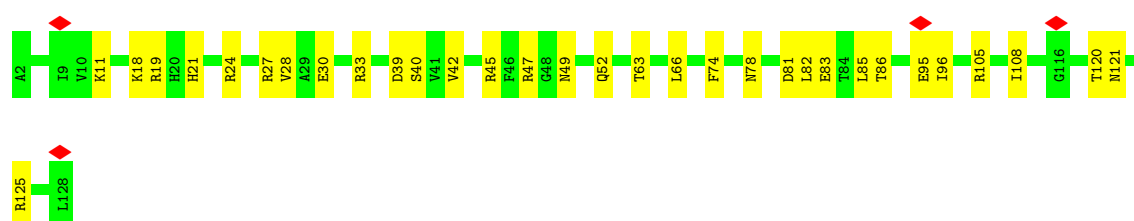
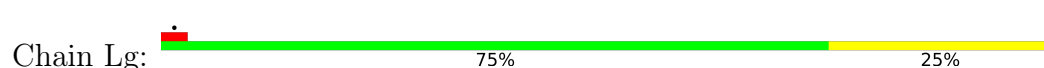
- Molecule 69: 60S ribosomal protein L30



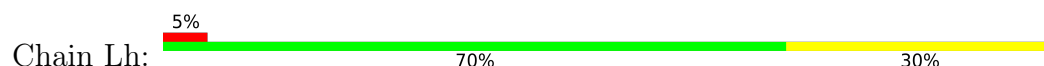
- Molecule 70: 60S ribosomal protein L31-A



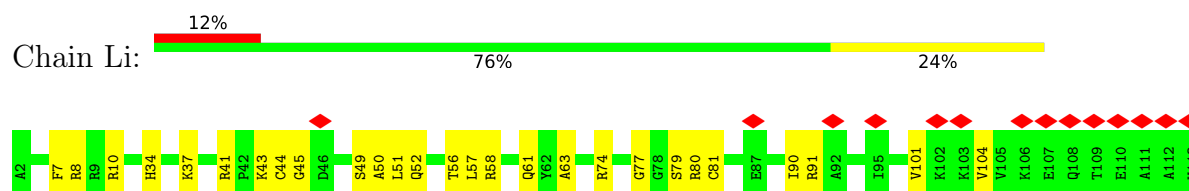
- Molecule 71: 60S ribosomal protein L32



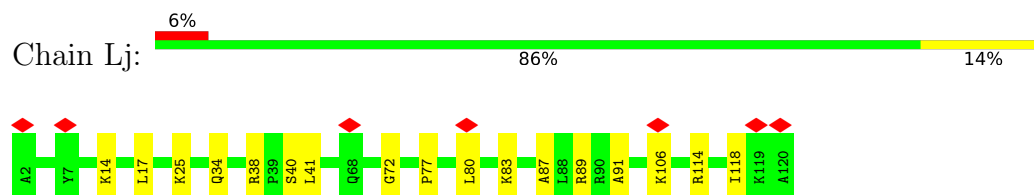
- Molecule 72: 60S ribosomal protein L33-A



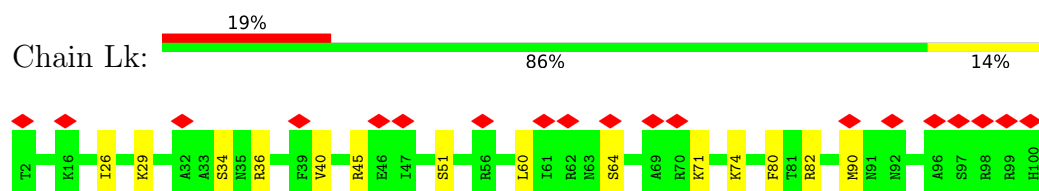
- Molecule 73: 60S ribosomal protein L34-A



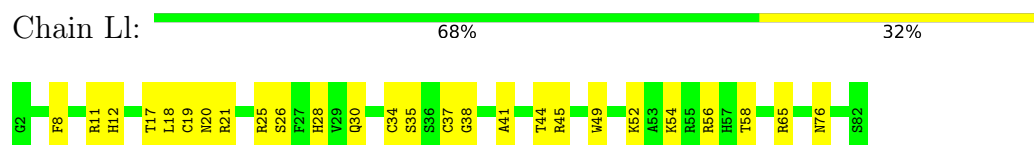
- Molecule 74: 60S ribosomal protein L35-A



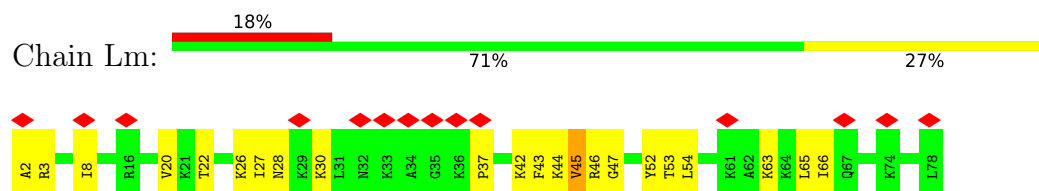
- Molecule 75: 60S ribosomal protein L36-A



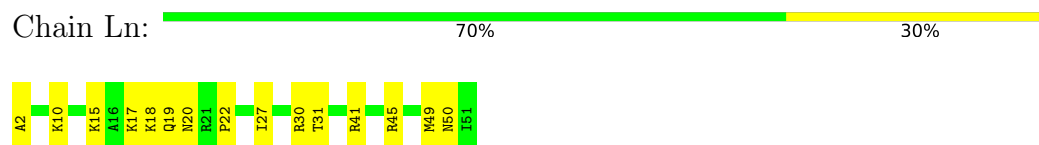
- Molecule 76: 60S ribosomal protein L37-A



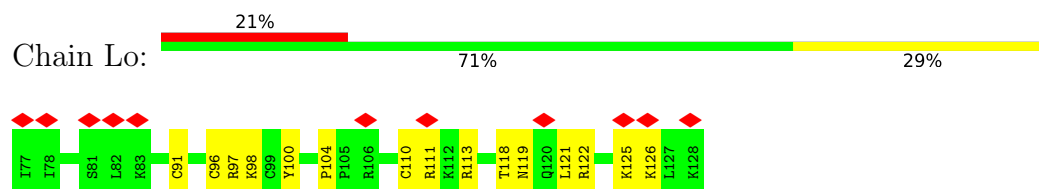
- Molecule 77: 60S ribosomal protein L38



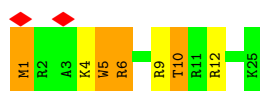
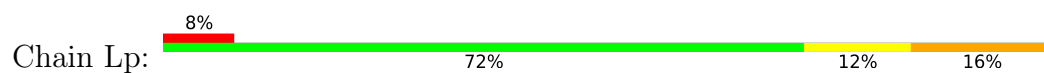
- Molecule 78: 60S ribosomal protein L39



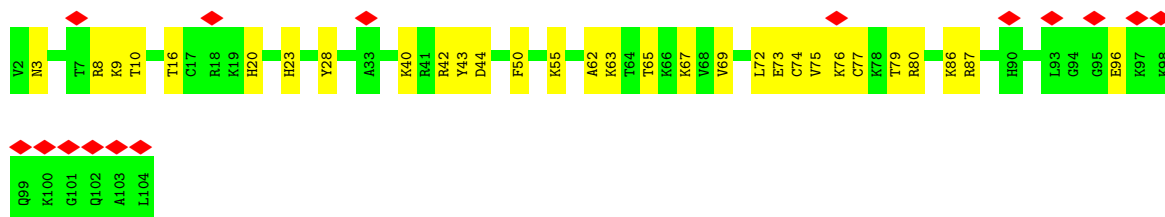
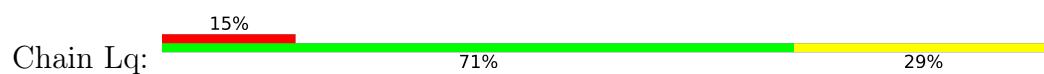
- Molecule 79: Ubiquitin-60S ribosomal protein L40



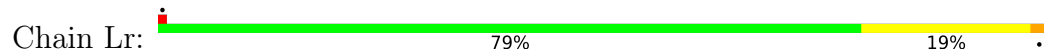
- Molecule 80: 60S ribosomal protein L41-B



- Molecule 81: 60S ribosomal protein L42-A



- Molecule 82: 60S ribosomal protein L43-A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	30016	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.508	Depositor
Minimum map value	-0.313	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	758.8, 758.8, 758.8	wwPDB
Map dimensions	700, 700, 700	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	S2	0.72	0/42491	0.69	8/66211 (0.0%)
2	SA	0.49	0/1759	0.79	0/2368
3	SB	0.43	0/1629	0.82	2/2202 (0.1%)
4	SC	0.42	0/757	0.75	0/1022
5	SD	0.28	0/898	0.75	0/1220
6	SE	0.47	1/959 (0.1%)	0.79	1/1288 (0.1%)
7	SF	0.59	0/1125	1.00	3/1510 (0.2%)
8	SG	0.47	0/1011	0.78	0/1355
9	SH	0.38	0/1211	0.80	0/1628
10	SI	0.43	0/1130	0.79	1/1517 (0.1%)
11	SJ	0.54	0/815	0.99	1/1102 (0.1%)
12	SK	0.36	0/566	0.71	2/761 (0.3%)
13	SL	0.38	0/499	0.87	0/670
14	SM	0.56	0/452	1.00	0/600
15	SN	0.32	0/567	0.90	0/764
16	SO	0.38	0/2456	0.76	3/3343 (0.1%)
17	SP	0.55	0/1623	0.96	4/2222 (0.2%)
18	SQ	0.52	0/1748	0.84	0/2352
19	SR	0.71	1/1665 (0.1%)	0.94	1/2263 (0.0%)
20	SS	0.56	0/2109	0.87	2/2839 (0.1%)
21	ST	0.31	0/1779	0.67	0/2379
22	SU	0.40	0/1511	0.80	0/2036
23	SV	0.53	0/1514	0.84	0/2021
24	SW	0.51	0/1519	0.79	1/2035 (0.0%)
25	SX	0.69	0/1194	0.94	2/1610 (0.1%)
26	SY	0.54	0/1215	0.82	0/1638
27	SZ	0.55	0/960	0.88	1/1290 (0.1%)
28	Sa	0.60	0/693	0.90	0/935
29	Sb	0.89	0/1038	1.01	2/1395 (0.1%)
30	Sc	0.85	1/1139 (0.1%)	1.08	5/1518 (0.3%)
31	Sd	0.47	0/1087	0.86	2/1449 (0.1%)
32	Se	0.74	0/782	1.09	0/1047
33	Sf	0.45	0/620	0.86	0/838
34	Sg	0.55	0/361	0.95	0/478

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Sh	0.40	0/934	0.79	0/1251
36	S3	0.54	0/721	0.79	0/1114
37	Sn	0.34	0/1796	0.56	1/2799 (0.0%)
38	Sm	0.34	0/1814	0.45	0/2824
39	LA	0.55	0/76214	0.59	3/118821 (0.0%)
40	LB	0.33	0/2883	0.46	0/4491
41	LC	0.44	0/3746	0.53	0/5832
42	LD	0.76	0/1933	1.00	7/2598 (0.3%)
43	LE	0.49	0/3146	0.79	2/4228 (0.0%)
44	LF	0.44	0/2800	0.81	5/3790 (0.1%)
45	LG	0.31	1/2400 (0.0%)	0.68	2/3239 (0.1%)
46	LH	0.29	0/1329	0.63	0/1794
47	LI	0.41	0/1821	0.73	0/2451
48	LJ	0.34	0/1836	0.73	0/2481
49	LK	0.33	0/1529	0.71	1/2060 (0.0%)
50	LL	0.32	0/1801	0.69	0/2416
51	LM	0.32	0/1367	0.73	0/1834
52	LN	0.37	0/1568	0.72	0/2106
53	LO	0.30	0/1068	0.65	0/1438
54	LP	0.59	0/1757	0.93	1/2354 (0.0%)
55	LQ	0.50	0/1585	0.81	0/2128
56	LR	0.44	0/1439	0.73	0/1938
57	LS	0.39	0/1465	0.78	0/1965
58	LT	0.40	0/1532	0.70	0/2043
59	LU	0.36	0/1473	0.66	0/1980
60	LV	0.39	0/1296	0.72	0/1739
61	LW	0.28	0/812	0.69	0/1099
62	LX	0.60	0/1018	0.94	2/1369 (0.1%)
63	LY	0.42	0/521	0.78	0/691
64	LZ	0.36	0/979	0.69	0/1321
65	La	0.31	0/995	0.64	0/1329
66	Lb	0.31	0/1106	0.61	0/1485
67	Lc	0.53	0/1200	0.86	0/1607
68	Ld	0.42	0/473	0.88	1/629 (0.2%)
69	Le	0.50	1/745 (0.1%)	0.68	0/1001
70	Lf	0.34	0/890	0.71	0/1196
71	Lg	0.46	0/1038	0.79	0/1390
72	Lh	0.49	0/868	0.83	0/1168
73	Li	0.51	0/890	0.87	1/1189 (0.1%)
74	Lj	0.26	0/978	0.62	0/1301
75	Lk	0.28	0/772	0.65	0/1026
76	Ll	0.67	0/660	0.92	0/875
77	Lm	0.30	0/618	0.66	0/826

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	Ln	0.49	0/443	0.73	0/588
79	Lo	0.33	0/416	0.65	0/553
80	Lp	0.83	0/230	1.36	2/296 (0.7%)
81	Lq	0.42	0/836	0.72	0/1104
82	Lr	0.68	0/701	0.92	0/934
All	All	0.55	5/219324 (0.0%)	0.69	69/322597 (0.0%)

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

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

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

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	Sc	4	GLY	C-N	-9.79	1.20	1.33
69	Le	47	ASN	C-N	-8.37	1.20	1.33
6	SE	123	TYR	C-N	-5.43	1.25	1.33
19	SR	171	PRO	C-N	-5.09	1.24	1.33
45	LG	83	LEU	C-N	5.03	1.39	1.33

The worst 5 of 69 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	Ld	20	GLY	N-CA-C	9.71	119.05	110.21
7	SF	43	ILE	N-CA-C	-7.70	105.65	112.12
62	LX	65	GLY	CA-C-N	7.42	131.26	120.51
62	LX	65	GLY	C-N-CA	7.42	131.26	120.51
27	SZ	133	ARG	N-CA-C	-6.68	106.08	114.56

There are no chirality outliers.

5 of 54 planarity outliers are listed below:

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

5.2 Too-close contacts ⓘ

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	S2	37990	0	19109	568	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	SA	1734	0	1817	32	0
3	SB	1609	0	1675	37	0
4	SC	741	0	691	9	0
5	SD	890	0	887	14	0
6	SE	939	0	968	22	0
7	SF	1105	0	1166	37	0
8	SG	1001	0	1063	21	0
9	SH	1192	0	1222	30	0
10	SI	1112	0	1124	30	0
11	SJ	805	0	874	22	0
12	SK	558	0	598	11	0
13	SL	497	0	535	16	0
14	SM	442	0	432	14	0
15	SN	556	0	552	12	0
16	SO	2403	0	2353	49	0
17	SP	1583	0	1578	40	0
18	SQ	1722	0	1793	39	0
19	SR	1635	0	1723	36	0
20	SS	2068	0	2154	49	0
21	ST	1755	0	1846	39	0
22	SU	1486	0	1576	36	0
23	SV	1489	0	1525	44	0
24	SW	1494	0	1573	31	0
25	SX	1168	0	1233	25	0
26	SY	1192	0	1255	28	0
27	SZ	949	0	985	28	0
28	Sa	684	0	672	23	0
29	Sb	1021	0	1060	25	0
30	Sc	1121	0	1196	25	0
31	Sd	1073	0	1132	23	0
32	Se	769	0	818	25	0
33	Sf	610	0	633	11	0
34	Sg	355	0	398	13	0
35	Sh	928	0	974	12	0
36	S3	652	0	332	6	0
37	Sn	1606	0	816	13	0
38	Sm	1625	0	824	27	0
39	LA	68091	0	34217	1048	0
40	LB	2579	0	1304	51	0
41	LC	3353	0	1695	59	0
42	LD	1899	0	1957	47	0
43	LE	3075	0	3142	96	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	LF	2748	0	2859	66	0
45	LG	2351	0	2294	38	0
46	LH	1307	0	1377	33	0
47	LI	1784	0	1862	30	0
48	LJ	1804	0	1877	29	0
49	LK	1508	0	1572	33	0
50	LL	1764	0	1804	48	0
51	LM	1346	0	1370	35	0
52	LN	1543	0	1608	29	0
53	LO	1053	0	1149	30	0
54	LP	1720	0	1779	64	0
55	LQ	1555	0	1659	29	0
56	LR	1416	0	1433	27	0
57	LS	1441	0	1543	26	0
58	LT	1515	0	1606	31	0
59	LU	1437	0	1475	36	0
60	LV	1272	0	1312	29	0
61	LW	796	0	812	8	0
62	LX	1003	0	1048	27	0
63	LY	509	0	537	15	0
64	LZ	964	0	1025	12	0
65	La	984	0	1075	24	0
66	Lb	1080	0	1122	30	0
67	Lc	1169	0	1211	38	0
68	Ld	462	0	491	18	0
69	Le	737	0	792	17	0
70	Lf	876	0	912	18	0
71	Lg	1017	0	1081	24	0
72	Lh	850	0	880	30	0
73	Li	880	0	945	21	0
74	Lj	969	0	1078	13	0
75	Lk	766	0	844	11	0
76	Ll	645	0	649	24	0
77	Lm	612	0	682	16	0
78	Ln	436	0	475	17	0
79	Lo	410	0	446	10	0
80	Lp	229	0	273	8	0
81	Lq	824	0	892	23	0
82	Lr	694	0	738	13	0
All	All	204032	0	150064	3129	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 9.

The worst 5 of 3129 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)
82:Lr:53:GLY:HA2	82:Lr:66:GLY:O	1.47	1.14
63:LY:4:GLU:O	63:LY:12:LYS:HA	1.53	1.07
38:Sm:15:G:N2	38:Sm:49:C:H42	1.57	1.02
1:S2:1203:A:N1	1:S2:1553:G:N2	2.08	1.00
39:LA:900:G:N2	39:LA:1589:A:C8	2.31	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	
2	SA	221/223 (99%)	199 (90%)	22 (10%)	0	100	100
3	SB	204/206 (99%)	184 (90%)	20 (10%)	0	100	100
4	SC	90/92 (98%)	83 (92%)	7 (8%)	0	100	100
5	SD	122/124 (98%)	105 (86%)	14 (12%)	3 (2%)	4	26
6	SE	117/119 (98%)	100 (86%)	17 (14%)	0	100	100
7	SF	139/141 (99%)	122 (88%)	17 (12%)	0	100	100
8	SG	123/125 (98%)	108 (88%)	14 (11%)	1 (1%)	16	52
9	SH	143/145 (99%)	126 (88%)	17 (12%)	0	100	100
10	SI	141/143 (99%)	126 (89%)	15 (11%)	0	100	100
11	SJ	99/101 (98%)	86 (87%)	13 (13%)	0	100	100
12	SK	67/69 (97%)	59 (88%)	8 (12%)	0	100	100
13	SL	61/63 (97%)	51 (84%)	10 (16%)	0	100	100
14	SM	51/53 (96%)	43 (84%)	8 (16%)	0	100	100
15	SN	71/73 (97%)	51 (72%)	20 (28%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	SO	311/313 (99%)	278 (89%)	33 (11%)	0	100	100
17	SP	204/206 (99%)	171 (84%)	30 (15%)	3 (2%)	8	38
18	SQ	214/216 (99%)	185 (86%)	28 (13%)	1 (0%)	24	62
19	SR	215/217 (99%)	193 (90%)	22 (10%)	0	100	100
20	SS	258/260 (99%)	214 (83%)	43 (17%)	1 (0%)	30	66
21	ST	216/218 (99%)	196 (91%)	20 (9%)	0	100	100
22	SU	183/185 (99%)	159 (87%)	23 (13%)	1 (0%)	24	62
23	SV	184/188 (98%)	167 (91%)	17 (9%)	0	100	100
24	SW	183/185 (99%)	161 (88%)	22 (12%)	0	100	100
25	SX	144/146 (99%)	118 (82%)	24 (17%)	2 (1%)	9	39
26	SY	148/150 (99%)	132 (89%)	16 (11%)	0	100	100
27	SZ	126/128 (98%)	105 (83%)	21 (17%)	0	100	100
28	Sa	85/87 (98%)	76 (89%)	9 (11%)	0	100	100
29	Sb	127/129 (98%)	112 (88%)	15 (12%)	0	100	100
30	Sc	142/144 (99%)	114 (80%)	28 (20%)	0	100	100
31	Sd	132/134 (98%)	114 (86%)	17 (13%)	1 (1%)	16	52
32	Se	95/97 (98%)	80 (84%)	14 (15%)	1 (1%)	11	45
33	Sf	79/81 (98%)	68 (86%)	11 (14%)	0	100	100
34	Sg	42/44 (96%)	35 (83%)	7 (17%)	0	100	100
35	Sh	118/120 (98%)	106 (90%)	12 (10%)	0	100	100
42	LD	249/251 (99%)	213 (86%)	36 (14%)	0	100	100
43	LE	384/386 (100%)	344 (90%)	40 (10%)	0	100	100
44	LF	359/361 (99%)	325 (90%)	33 (9%)	1 (0%)	36	71
45	LG	292/294 (99%)	261 (89%)	31 (11%)	0	100	100
46	LH	163/167 (98%)	147 (90%)	16 (10%)	0	100	100
47	LI	220/222 (99%)	206 (94%)	14 (6%)	0	100	100
48	LJ	231/233 (99%)	211 (91%)	20 (9%)	0	100	100
49	LK	189/191 (99%)	173 (92%)	16 (8%)	0	100	100
50	LL	216/218 (99%)	197 (91%)	19 (9%)	0	100	100
51	LM	167/169 (99%)	147 (88%)	20 (12%)	0	100	100
52	LN	191/193 (99%)	170 (89%)	21 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	LO	134/136 (98%)	125 (93%)	9 (7%)	0	100	100
54	LP	201/203 (99%)	178 (89%)	22 (11%)	1 (0%)	24	62
55	LQ	195/197 (99%)	182 (93%)	13 (7%)	0	100	100
56	LR	181/183 (99%)	164 (91%)	17 (9%)	0	100	100
57	LS	183/185 (99%)	167 (91%)	16 (9%)	0	100	100
58	LT	186/188 (99%)	179 (96%)	7 (4%)	0	100	100
59	LU	169/171 (99%)	160 (95%)	9 (5%)	0	100	100
60	LV	157/159 (99%)	140 (89%)	17 (11%)	0	100	100
61	LW	98/100 (98%)	91 (93%)	7 (7%)	0	100	100
62	LX	134/136 (98%)	120 (90%)	14 (10%)	0	100	100
63	LY	59/61 (97%)	54 (92%)	5 (8%)	0	100	100
64	LZ	119/121 (98%)	111 (93%)	8 (7%)	0	100	100
65	La	123/125 (98%)	114 (93%)	9 (7%)	0	100	100
66	Lb	133/135 (98%)	118 (89%)	15 (11%)	0	100	100
67	Lc	146/148 (99%)	126 (86%)	19 (13%)	1 (1%)	18	55
68	Ld	56/58 (97%)	46 (82%)	9 (16%)	1 (2%)	6	33
69	Le	94/96 (98%)	92 (98%)	2 (2%)	0	100	100
70	Lf	107/109 (98%)	96 (90%)	11 (10%)	0	100	100
71	Lg	125/127 (98%)	113 (90%)	12 (10%)	0	100	100
72	Lh	104/106 (98%)	98 (94%)	6 (6%)	0	100	100
73	Li	110/112 (98%)	100 (91%)	10 (9%)	0	100	100
74	Lj	117/119 (98%)	113 (97%)	4 (3%)	0	100	100
75	Lk	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
76	Ll	79/81 (98%)	71 (90%)	8 (10%)	0	100	100
77	Lm	75/77 (97%)	73 (97%)	2 (3%)	0	100	100
78	Ln	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
79	Lo	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
80	Lp	23/25 (92%)	23 (100%)	0	0	100	100
81	Lq	101/103 (98%)	91 (90%)	10 (10%)	0	100	100
82	Lr	89/91 (98%)	81 (91%)	8 (9%)	0	100	100
All	All	11009/11163 (99%)	9830 (89%)	1161 (10%)	18 (0%)	44	77

5 of 18 Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	SA	182/182 (100%)	177 (97%)	5 (3%)	39	59
3	SB	173/173 (100%)	173 (100%)	0	100	100
4	SC	73/85 (86%)	73 (100%)	0	100	100
5	SD	88/100 (88%)	87 (99%)	1 (1%)	65	74
6	SE	98/98 (100%)	98 (100%)	0	100	100
7	SF	117/117 (100%)	116 (99%)	1 (1%)	70	76
8	SG	113/113 (100%)	112 (99%)	1 (1%)	70	76
9	SH	128/128 (100%)	128 (100%)	0	100	100
10	SI	115/115 (100%)	114 (99%)	1 (1%)	70	76
11	SJ	94/94 (100%)	93 (99%)	1 (1%)	65	74
12	SK	61/61 (100%)	61 (100%)	0	100	100
13	SL	56/56 (100%)	56 (100%)	0	100	100
14	SM	47/47 (100%)	47 (100%)	0	100	100
15	SN	56/63 (89%)	56 (100%)	0	100	100
16	SO	255/256 (100%)	254 (100%)	1 (0%)	84	82
17	SP	165/173 (95%)	163 (99%)	2 (1%)	63	73
18	SQ	192/192 (100%)	190 (99%)	2 (1%)	68	76
19	SR	176/176 (100%)	175 (99%)	1 (1%)	78	80
20	SS	221/221 (100%)	218 (99%)	3 (1%)	59	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	ST	187/187 (100%)	185 (99%)	2 (1%)	65	74
22	SU	165/165 (100%)	165 (100%)	0	100	100
23	SV	150/150 (100%)	149 (99%)	1 (1%)	76	79
24	SW	158/158 (100%)	158 (100%)	0	100	100
25	SX	129/129 (100%)	124 (96%)	5 (4%)	28	49
26	SY	127/127 (100%)	126 (99%)	1 (1%)	73	77
27	SZ	97/97 (100%)	97 (100%)	0	100	100
28	Sa	74/74 (100%)	74 (100%)	0	100	100
29	Sb	110/110 (100%)	109 (99%)	1 (1%)	70	76
30	Sc	119/119 (100%)	119 (100%)	0	100	100
31	Sd	112/112 (100%)	112 (100%)	0	100	100
32	Se	83/83 (100%)	82 (99%)	1 (1%)	63	73
33	Sf	70/70 (100%)	70 (100%)	0	100	100
34	Sg	37/37 (100%)	37 (100%)	0	100	100
35	Sh	101/101 (100%)	101 (100%)	0	100	100
42	LD	190/193 (98%)	186 (98%)	4 (2%)	47	65
43	LE	318/322 (99%)	316 (99%)	2 (1%)	78	80
44	LF	288/288 (100%)	287 (100%)	1 (0%)	86	84
45	LG	241/243 (99%)	240 (100%)	1 (0%)	84	82
46	LH	139/146 (95%)	139 (100%)	0	100	100
47	LI	186/186 (100%)	186 (100%)	0	100	100
48	LJ	187/191 (98%)	187 (100%)	0	100	100
49	LK	168/171 (98%)	168 (100%)	0	100	100
50	LL	185/185 (100%)	185 (100%)	0	100	100
51	LM	145/147 (99%)	145 (100%)	0	100	100
52	LN	154/154 (100%)	153 (99%)	1 (1%)	78	80
53	LO	107/107 (100%)	107 (100%)	0	100	100
54	LP	175/175 (100%)	173 (99%)	2 (1%)	65	74
55	LQ	160/160 (100%)	160 (100%)	0	100	100
56	LR	138/145 (95%)	138 (100%)	0	100	100
57	LS	150/150 (100%)	150 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	LT	152/153 (99%)	152 (100%)	0	100	100
59	LU	155/155 (100%)	155 (100%)	0	100	100
60	LV	135/136 (99%)	135 (100%)	0	100	100
61	LW	87/87 (100%)	87 (100%)	0	100	100
62	LX	104/104 (100%)	103 (99%)	1 (1%)	68	76
63	LY	54/54 (100%)	54 (100%)	0	100	100
64	LZ	104/105 (99%)	104 (100%)	0	100	100
65	La	108/108 (100%)	108 (100%)	0	100	100
66	Lb	112/115 (97%)	112 (100%)	0	100	100
67	Lc	117/118 (99%)	117 (100%)	0	100	100
68	Ld	46/46 (100%)	45 (98%)	1 (2%)	45	64
69	Le	81/81 (100%)	81 (100%)	0	100	100
70	Lf	92/96 (96%)	92 (100%)	0	100	100
71	Lg	108/109 (99%)	108 (100%)	0	100	100
72	Lh	90/90 (100%)	90 (100%)	0	100	100
73	Li	95/95 (100%)	95 (100%)	0	100	100
74	Lj	104/104 (100%)	104 (100%)	0	100	100
75	Lk	80/81 (99%)	80 (100%)	0	100	100
76	Ll	67/67 (100%)	67 (100%)	0	100	100
77	Lm	68/68 (100%)	67 (98%)	1 (2%)	57	70
78	Ln	45/45 (100%)	45 (100%)	0	100	100
79	Lo	45/47 (96%)	45 (100%)	0	100	100
80	Lp	22/23 (96%)	21 (96%)	1 (4%)	24	46
81	Lq	87/88 (99%)	87 (100%)	0	100	100
82	Lr	71/71 (100%)	70 (99%)	1 (1%)	59	71
All	All	9289/9378 (99%)	9243 (100%)	46 (0%)	78	81

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	Sb	34	ILE
43	LE	220	VAL
32	Se	84	VAL

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Mol	Chain	Res	Type
42	LD	193	ARG
45	LG	159	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 161 such sidechains are listed below:

Mol	Chain	Res	Type
56	LR	28	ASN
68	Ld	43	HIS
58	LT	144	GLN
62	LX	81	GLN
73	Li	52	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	S2	1781/1800 (98%)	648 (36%)	40 (2%)
36	S3	31/32 (96%)	21 (67%)	2 (6%)
37	Sn	74/75 (98%)	27 (36%)	0
38	Sm	75/77 (97%)	15 (20%)	0
39	LA	3180/3394 (93%)	919 (28%)	33 (1%)
40	LB	120/121 (99%)	20 (16%)	1 (0%)
41	LC	157/158 (99%)	41 (26%)	2 (1%)
All	All	5418/5657 (95%)	1691 (31%)	78 (1%)

5 of 1691 RNA backbone outliers are listed below:

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

5 of 78 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
39	LA	2138	A
39	LA	3228	C
39	LA	2445	A
39	LA	2801	A

Continued on next page...

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Mol	Chain	Res	Type
40	LB	52	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

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

All chain breaks are listed below:

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

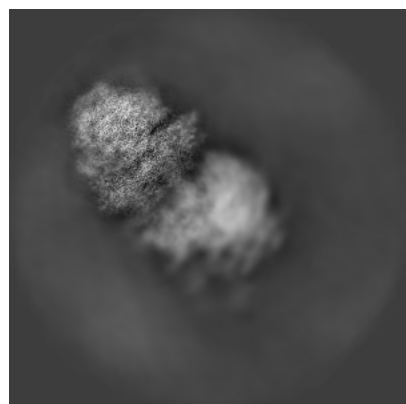
6 Map visualisation [i](#)

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

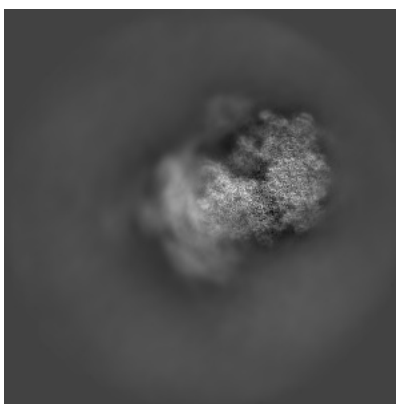
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

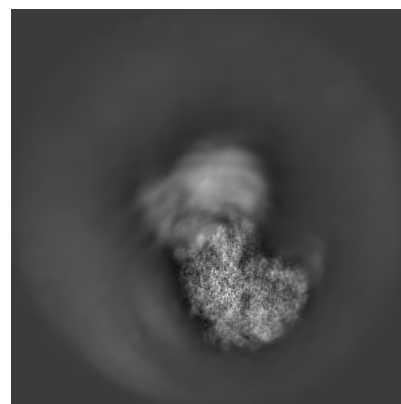
6.1.1 Primary map



X

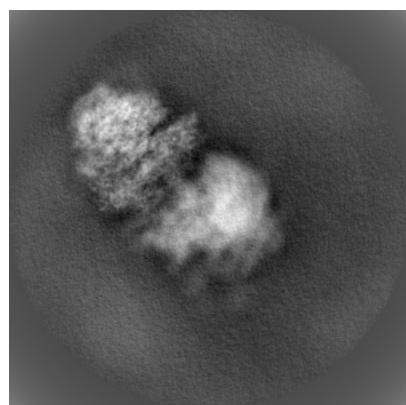


Y

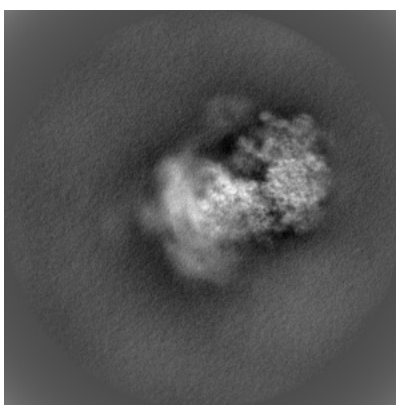


Z

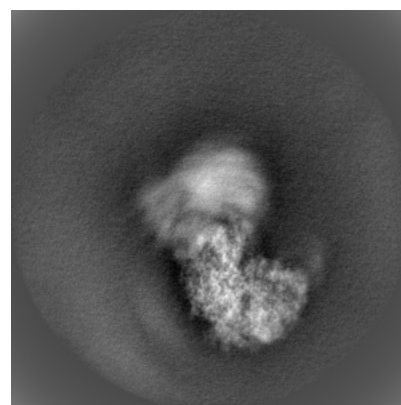
6.1.2 Raw map



X



Y

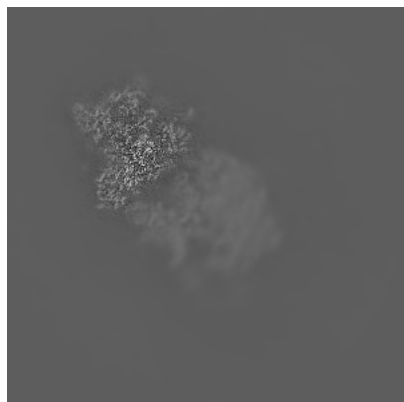


Z

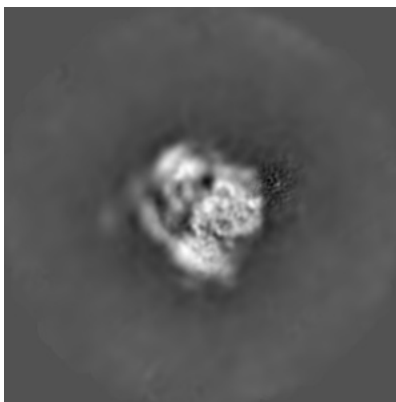
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

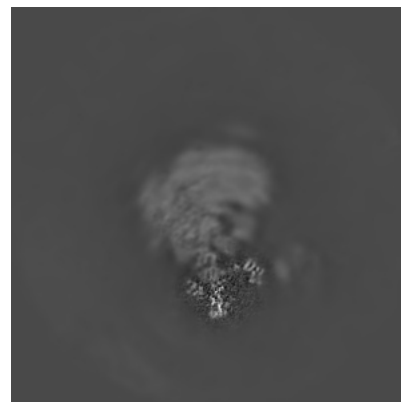
6.2.1 Primary map



X Index: 350

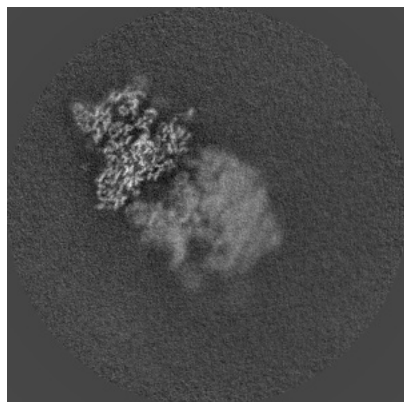


Y Index: 350

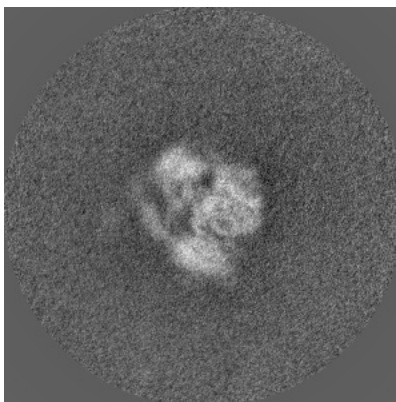


Z Index: 350

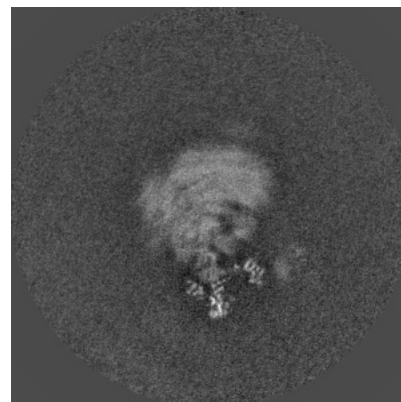
6.2.2 Raw map



X Index: 350



Y Index: 350

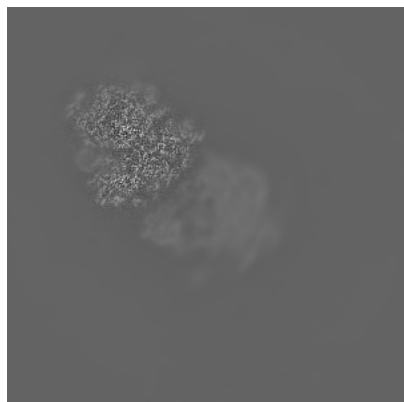


Z Index: 350

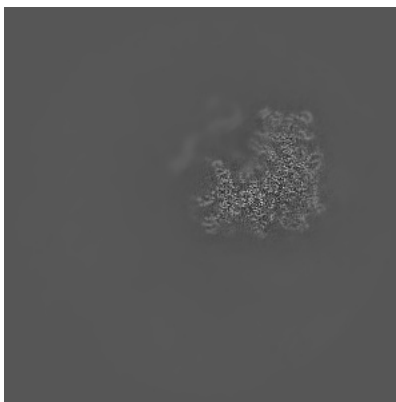
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

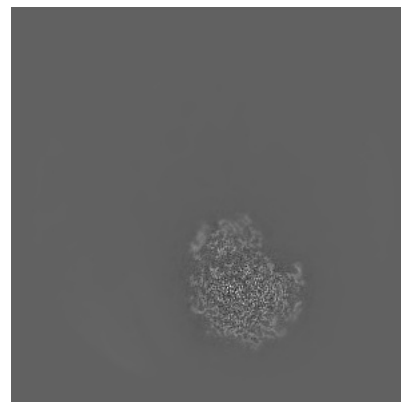
6.3.1 Primary map



X Index: 383

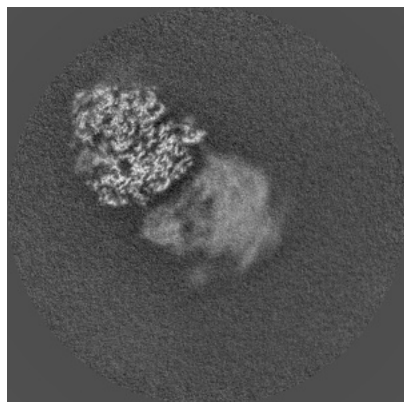


Y Index: 212

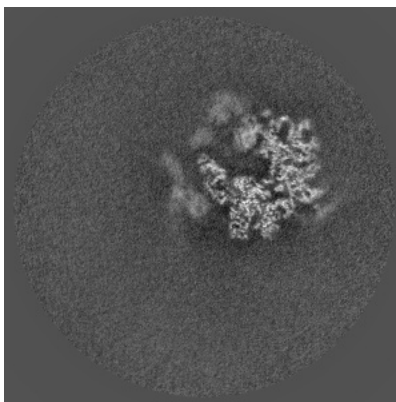


Z Index: 489

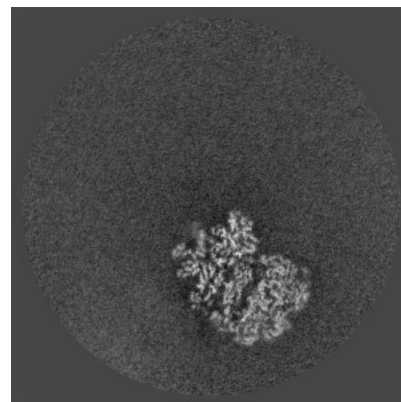
6.3.2 Raw map



X Index: 388



Y Index: 239

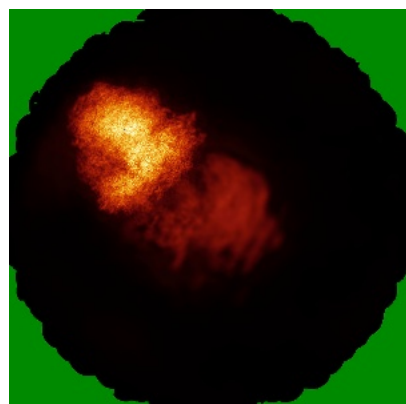


Z Index: 466

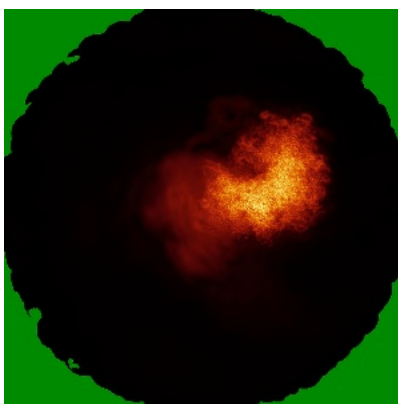
The images above show the largest variance slices of the map in three orthogonal directions.

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

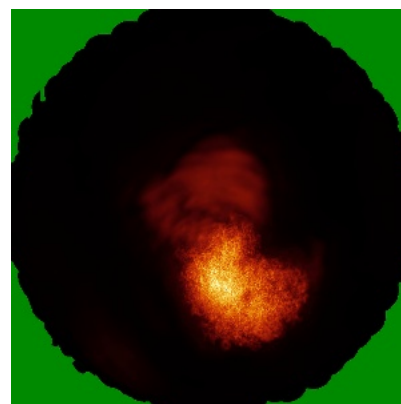
6.4.1 Primary map



X

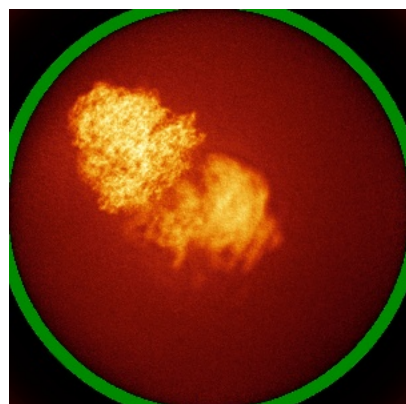


Y

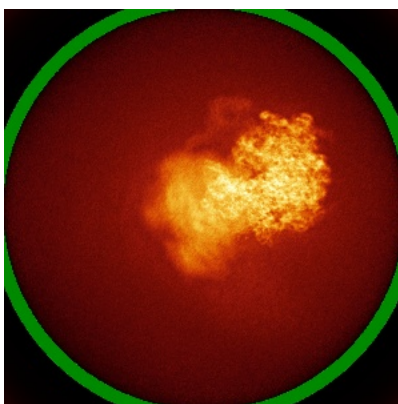


Z

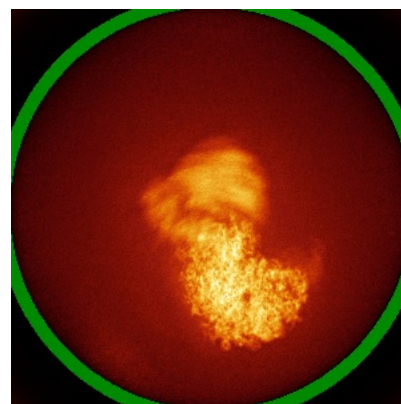
6.4.2 Raw map



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.

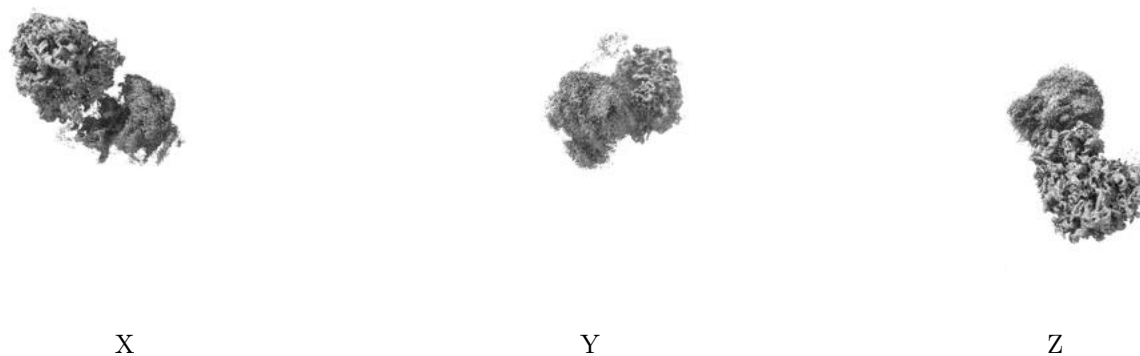
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. 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.

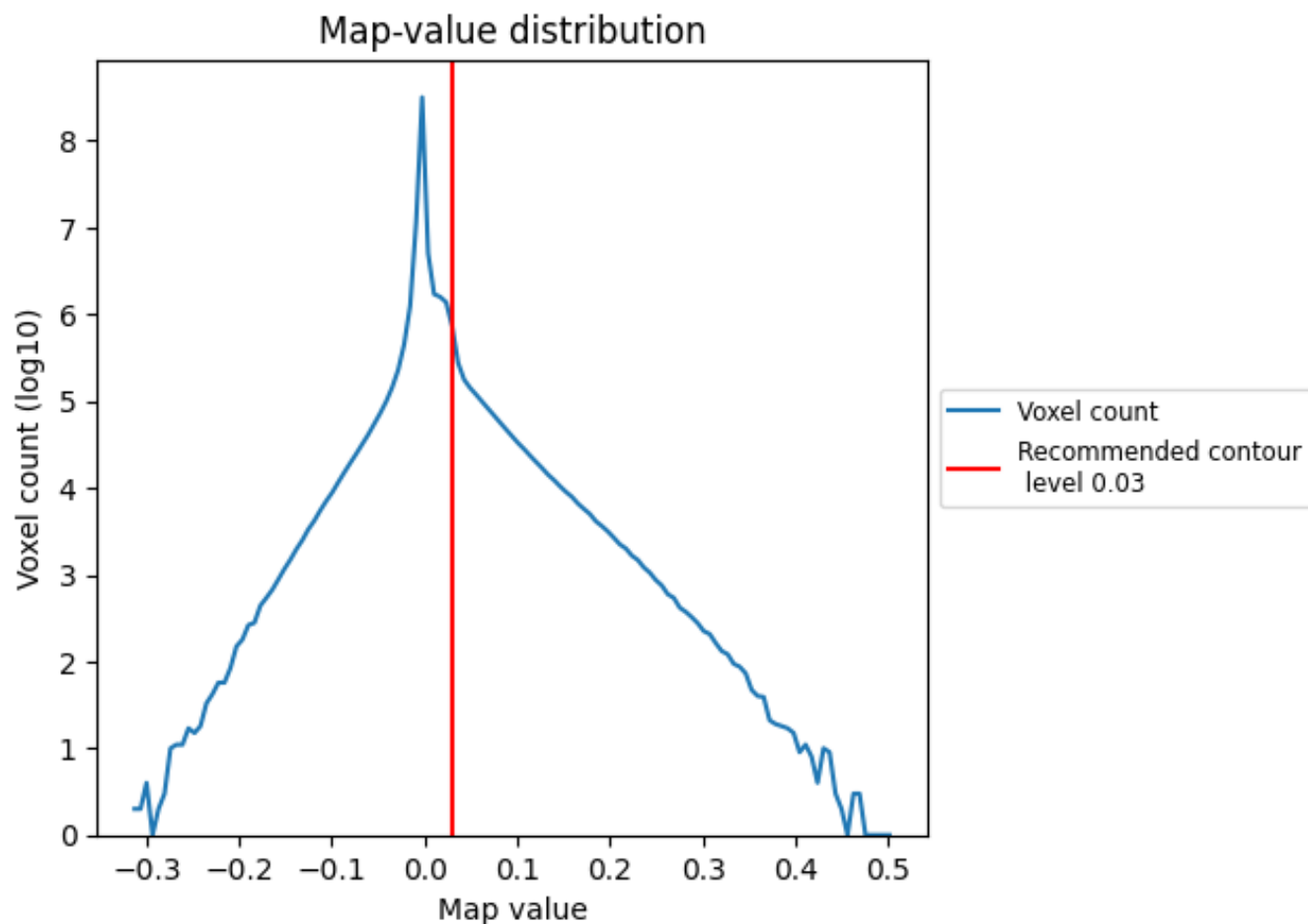
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

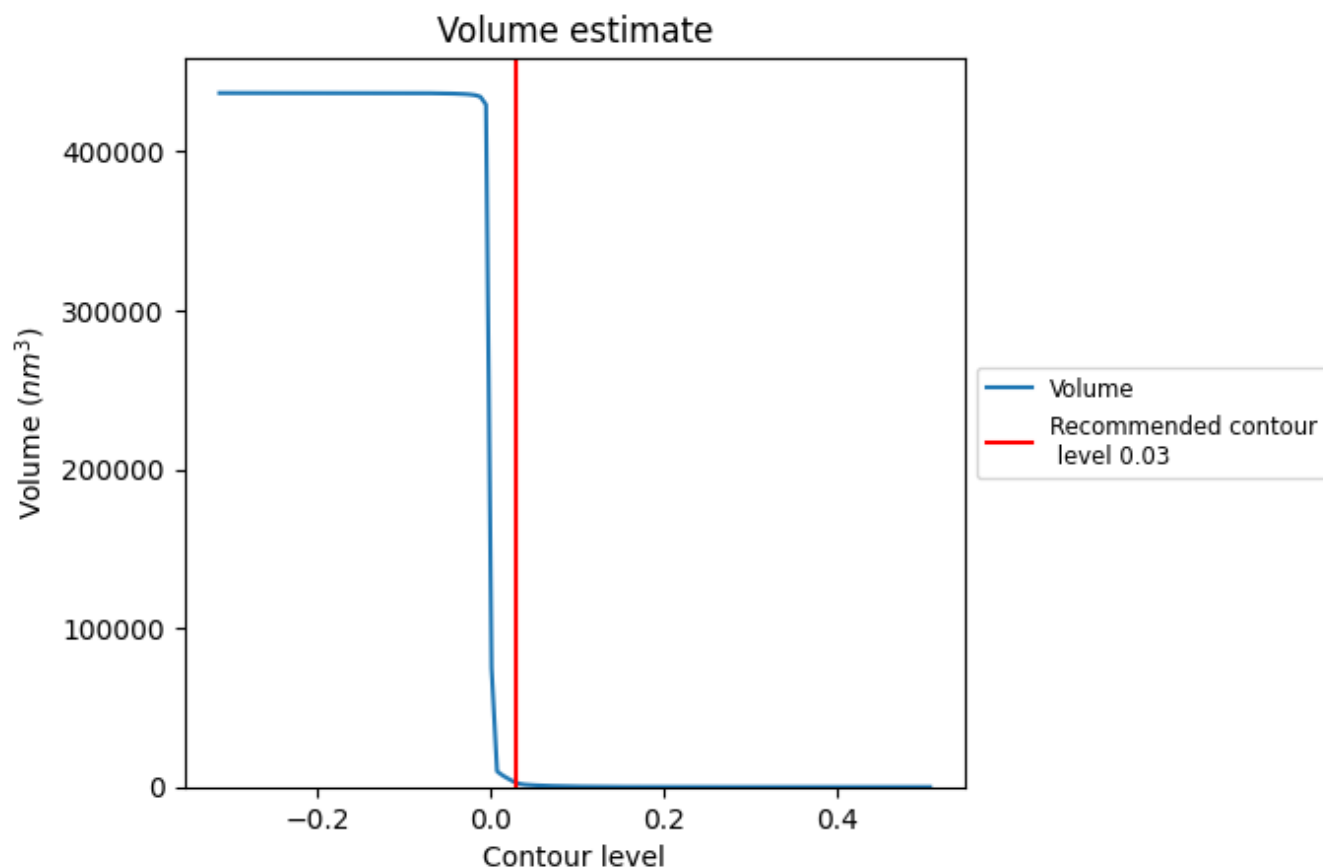
This section contains the results of statistical analysis of the map.

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.

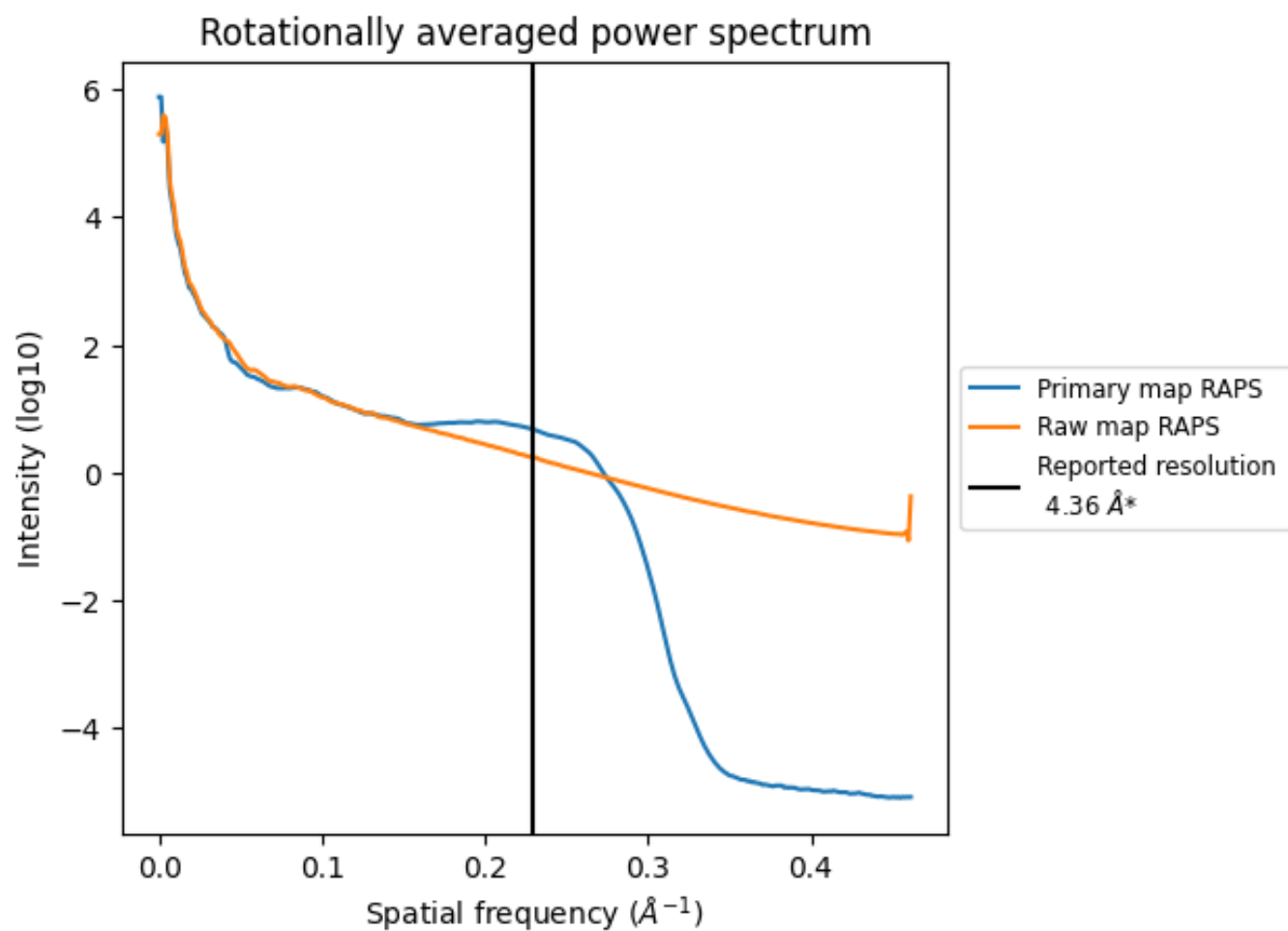
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2684 nm^3 ; this corresponds to an approximate mass of 2425 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

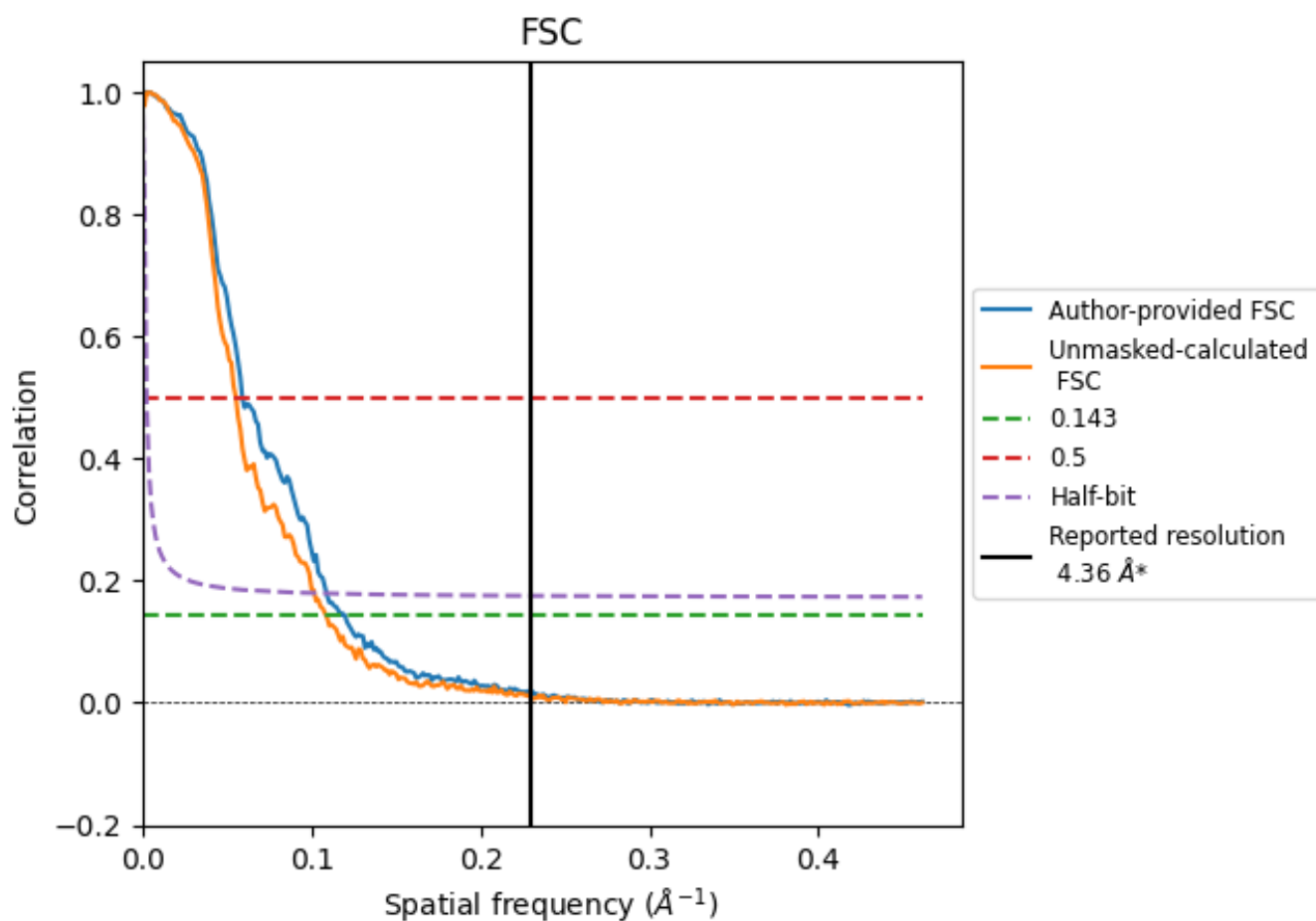


*Reported resolution corresponds to spatial frequency of 0.229 Å⁻¹

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 0.229 Å⁻¹

8.2 Resolution estimates

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.36	-	-
Author-provided FSC curve	8.35	16.89	9.17
Unmasked-calculated*	9.21	18.08	9.82

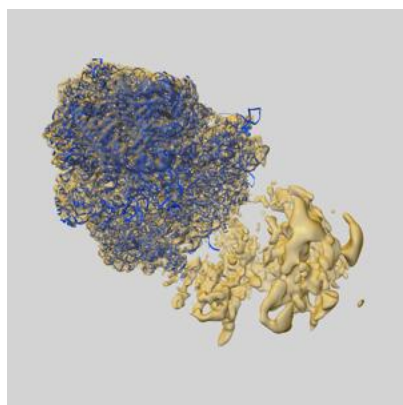
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 8.35 differs from the reported value 4.36 by more than 10 %

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

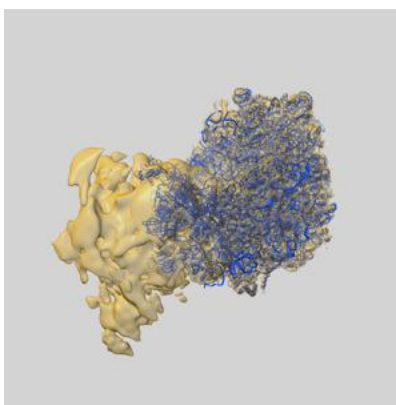
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12535 and PDB model 7NRD. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

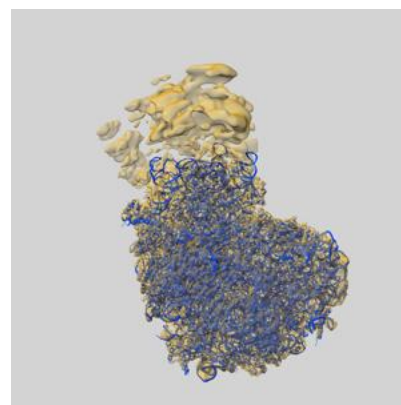
9.1 Map-model overlay [i](#)



X



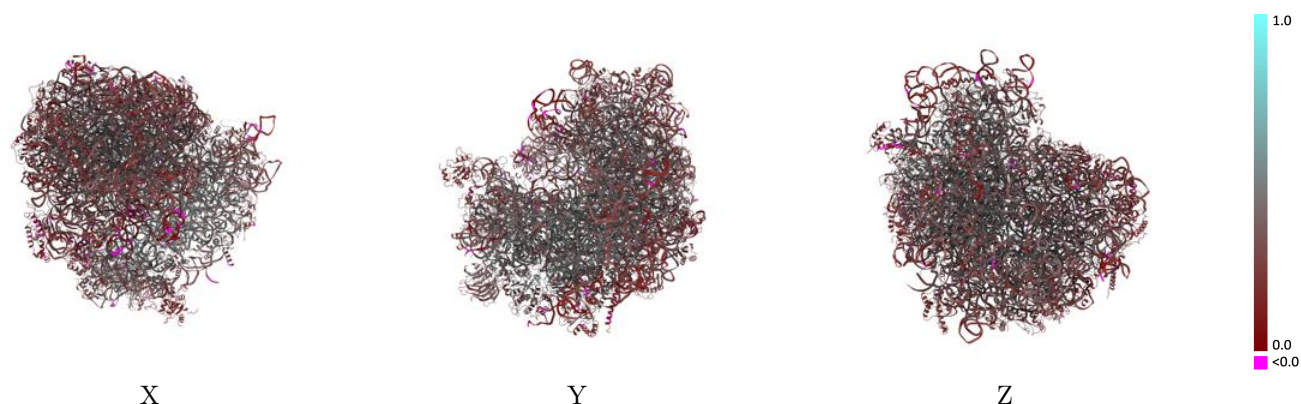
Y



Z

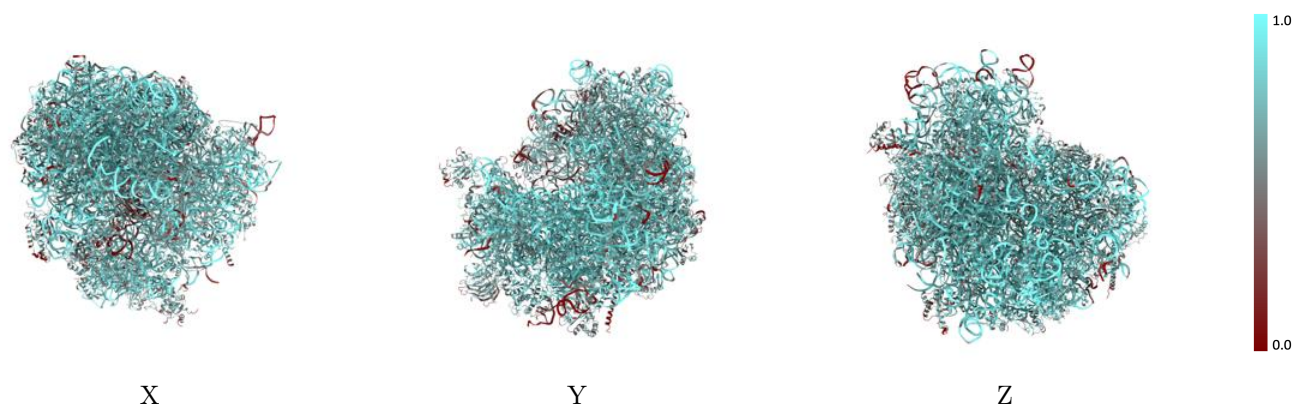
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



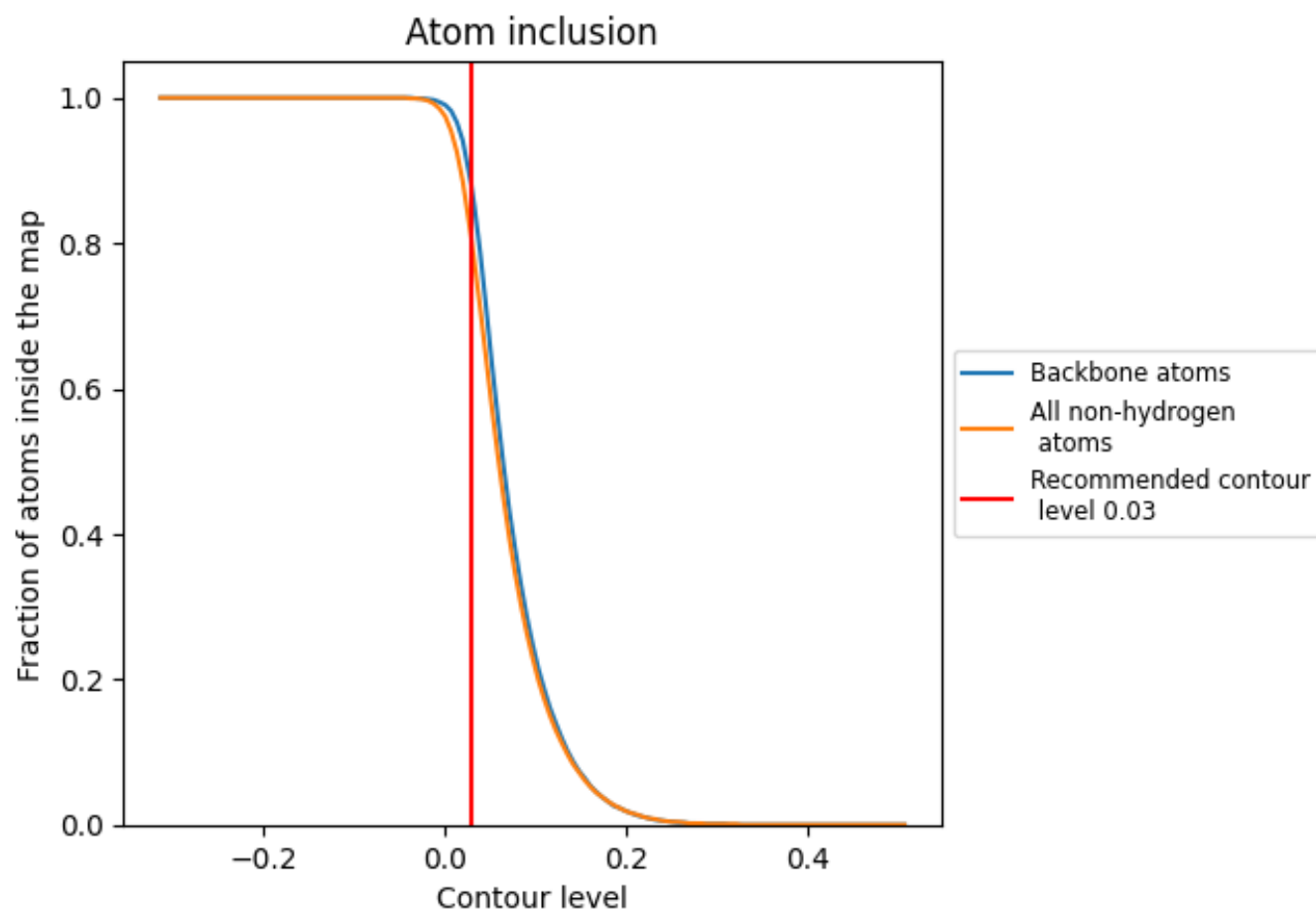
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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

9.4 Atom inclusion [i](#)



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

9.5 Map-model fit summary ⓘ

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

Chain	Atom inclusion	Q-score
All	 0.8070	 0.3630
LA	 0.8840	 0.3670
LB	 0.9120	 0.3100
LC	 0.9120	 0.3670
LD	 0.8290	 0.4600
LE	 0.7140	 0.3550
LF	 0.7750	 0.3420
LG	 0.6330	 0.2290
LH	 0.7000	 0.2580
LI	 0.6860	 0.3250
LJ	 0.5580	 0.2920
LK	 0.5780	 0.2820
LL	 0.5100	 0.2650
LM	 0.4880	 0.1750
LN	 0.7120	 0.3320
LO	 0.7000	 0.2610
LP	 0.8020	 0.4030
LQ	 0.7340	 0.3460
LR	 0.7530	 0.3640
LS	 0.7730	 0.3450
LT	 0.6830	 0.3360
LU	 0.6290	 0.3130
LV	 0.6930	 0.3350
LW	 0.5100	 0.2420
LX	 0.7540	 0.4220
LY	 0.7120	 0.3670
LZ	 0.7670	 0.3670
La	 0.7620	 0.3100
Lb	 0.5810	 0.2800
Lc	 0.7910	 0.3760
Ld	 0.7680	 0.3590
Le	 0.6650	 0.3510
Lf	 0.5790	 0.3070
Lg	 0.7850	 0.3760
Lh	 0.7670	 0.3600



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Chain	Atom inclusion	Q-score
Li	 0.7160	 0.3860
Lj	 0.7090	 0.3040
Lk	 0.6310	 0.2990
Ll	 0.8920	 0.4450
Lm	 0.6290	 0.2560
Ln	 0.8120	 0.4160
Lo	 0.5710	 0.3260
Lp	 0.7070	 0.3810
Lq	 0.6600	 0.3450
Lr	 0.8190	 0.4470
S2	 0.8900	 0.4030
S3	 0.5840	 0.3100
SA	 0.7050	 0.3950
SB	 0.7100	 0.3340
SC	 0.6920	 0.3470
SD	 0.4760	 0.2010
SE	 0.6860	 0.3390
SF	 0.7630	 0.3710
SG	 0.6430	 0.3380
SH	 0.7020	 0.3370
SI	 0.7610	 0.3450
SJ	 0.7460	 0.3730
SK	 0.6480	 0.2720
SL	 0.6750	 0.3650
SM	 0.8200	 0.4310
SN	 0.6080	 0.2430
SO	 0.5920	 0.3060
SP	 0.7690	 0.3990
SQ	 0.6770	 0.3940
SR	 0.8340	 0.4640
SS	 0.7830	 0.4150
ST	 0.6950	 0.3130
SU	 0.6420	 0.3160
SV	 0.7920	 0.3750
SW	 0.7200	 0.3970
SX	 0.8100	 0.4430
SY	 0.8230	 0.4240
SZ	 0.7230	 0.4050
Sa	 0.7590	 0.4110
Sb	 0.8970	 0.4820
Sc	 0.8810	 0.4840
Sd	 0.7270	 0.3560

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Chain	Atom inclusion	Q-score
Se	 0.8230	 0.4590
Sf	 0.7340	 0.3990
Sg	 0.8050	 0.4270
Sh	 0.7120	 0.3420
Sm	 0.8060	 0.3000
Sn	 0.4830	 0.1880