wwPDB EM Validation Summary Report

Sep 5, 2026 – 02:12 PM EDT

PDB ID	:	9YXB / pdb_00009yxb
EMDB ID	:	EMD-73602
Title	:	Babesia divergens ribosome structure by single-particle cryo-EM (3D class1, A-, P-, and E-site tRNAs and mRNA)
Authors	:	Gutierrez-Vargas, C.; Izhaki-Tavor, L.S.; Leger-Abraham, M.
Deposited on	:	2025-10-27
Resolution	:	3.10 Å(reported)
Based on initial models	:	., 9YGM

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

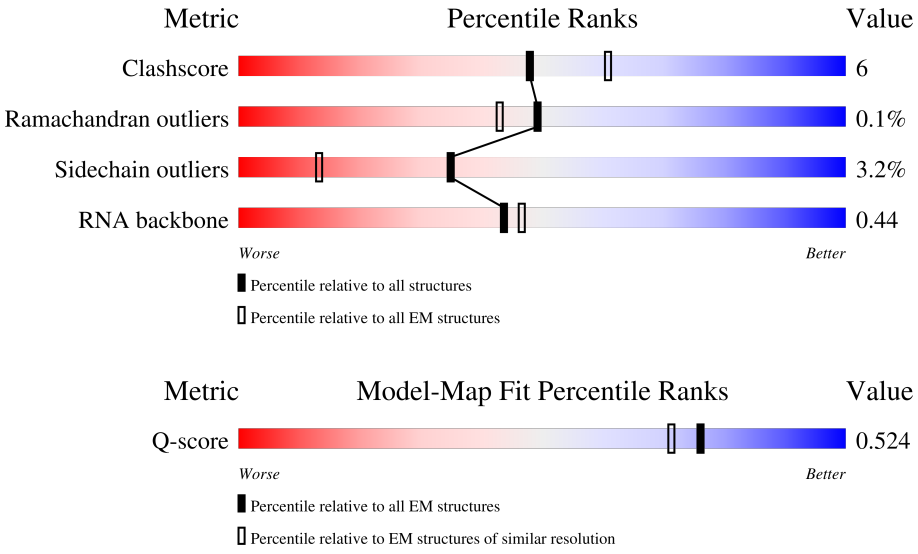
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.10 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	14724 (2.60 - 3.60)

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

Mol	Chain	Length	Quality of chain
1	SP	145	76% 9% 15%
2	SX	174	85% 10%
3	SU	156	89% 7%

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Mol	Chain	Length	Quality of chain
4	SL	149	79% 13% 7%
5	SR	154	75% 16% 8%
6	SH	192	88% 9%
7	ST	151	85% 11%
8	SA	264	69% 9% 21%
9	SN	113	73% 12% 15%
10	SJ	130	80% 14%
11	SI	194	59% 5% 35%
12	SK	192	75% 16% 9%
13	SG	239	70% 8% 22%
14	SM	120	65% 14% 20%
15	Se	61	51% 10% 38%
16	SS	66	65% 9% 24%
17	Sd	67	69% 12% 19%
18	SC	223	70% 14% 16%
19	SW	149	68% 28%
20	SB	274	45% 15% 40%
21	SF	196	63% 14% 22%
22	Sb	115	59% 12% 29%
23	SV	134	51% 44%
24	SO	157	52% 10% 38%
25	SZ	135	40% 10% 49%
26	Sa	104	62% 6% 32%
27	SQ	135	48% 15% 36%
28	SD	184	51% 7% 41%

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Mol	Chain	Length	Quality of chain
29	Sf	77	65% 32%
30	Sc	82	67% 5% 27%
31	S1	1728	52% 28% 9% 11%
32	LM	147	89% 8%
33	LS	188	8% 91% 5%
34	Le	117	83% 16%
35	Lf	132	89% 6% 5%
36	Lj	98	89% 11%
37	LQ	222	76% 7% 17%
38	LB	257	78% 16% 5%
39	LI	202	6% 89% 9%
40	LJ	203	6% 89% 6% 5%
41	LX	137	77% 11% 12%
42	La	123	92% 7%
43	LD	360	19% 79% 12% 9%
44	LP	306	9% 75% 14% 8%
45	LZ	146	8% 87% 7% 6%
46	LU	194	84% 5% 11%
47	LH	285	8% 74% 5% 21%
48	LC	395	85% 9% 5%
49	LL	133	8% 86% 10%
50	LK	139	87% 8%
51	LW	153	74% 24%
52	Li	116	79% 10% 9%
53	Lm	55	5% 78% 13% 9%

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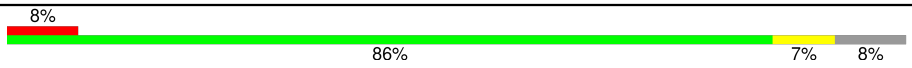
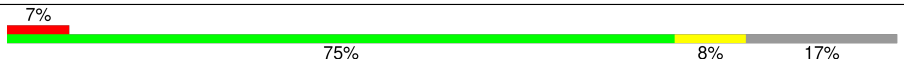
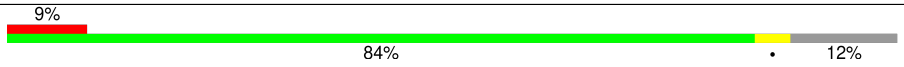
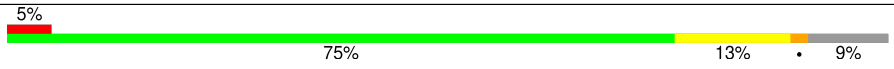
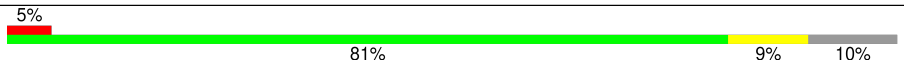
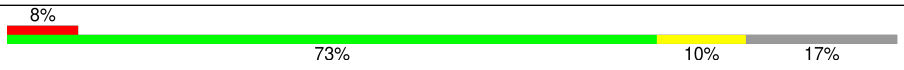
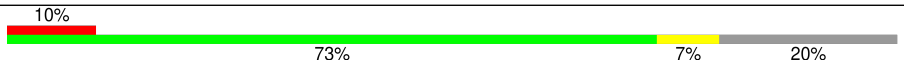
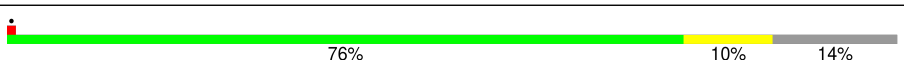
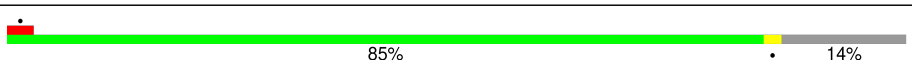
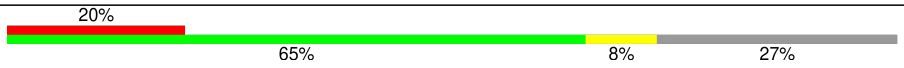
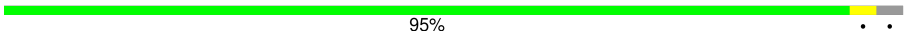
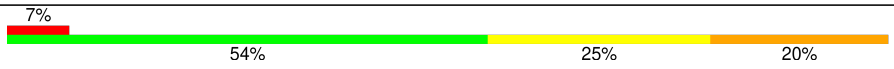
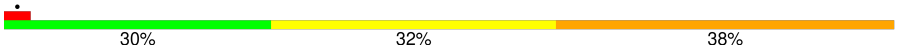
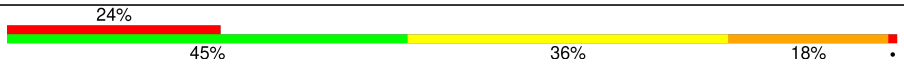
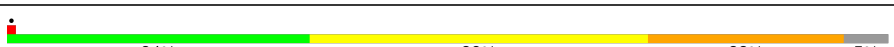
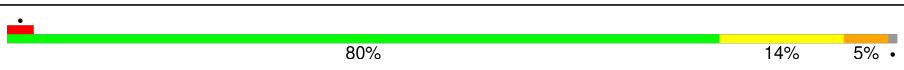
Mol	Chain	Length	Quality of chain
54	LT	160	
55	Lo	105	
56	Ll	59	
57	LR	194	
58	LE	171	
59	LO	227	
60	LN	204	
61	Lg	115	
62	Lc	259	
63	LV	122	
64	Ld	108	
65	Lp	94	
66	Lb	59	
67	Lh	150	
68	LY	156	
69	LG	212	
70	Ln	39	
71	L3	122	
72	L4	159	
73	L5	3326	
74	S7	74	
75	S8	76	
76	S9	76	
77	S6	11	
78	SY	79	

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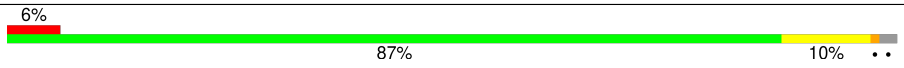
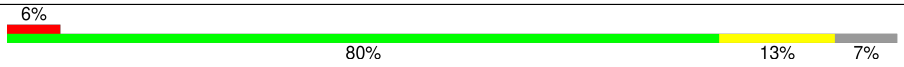
Mol	Chain	Length	Quality of chain
79	SE	266	
80	Sg	323	
81	LF	190	
82	Lk	70	

2 Entry composition (i)

There are 84 unique types of molecules in this entry. The entry contains 186450 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 uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	SP	123	959	605	194	158	2	0	0

- Molecule 2 is a protein called 40S ribosomal protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	SX	167	1365	860	262	237	6	0	0

- Molecule 3 is a protein called 40S ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	SU	151	1237	794	230	203	10	0	0

- Molecule 4 is a protein called 40S ribosomal protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	SL	139	1090	686	215	186	3	0	0

- Molecule 5 is a protein called 40S ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	SR	141	1128	699	221	201	7	0	0

- Molecule 6 is a protein called 40S ribosomal protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	SH	187	1466	918	278	261	9	0	0

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SH	?	-	LYS	deletion	UNP A0AAD9GEF4
SH	?	-	TYR	deletion	UNP A0AAD9GEF4
SH	?	-	ASP	deletion	UNP A0AAD9GEF4
SH	?	-	ASP	deletion	UNP A0AAD9GEF4
SH	?	-	ILE	deletion	UNP A0AAD9GEF4
SH	?	-	ASN	deletion	UNP A0AAD9GEF4
SH	?	-	SER	deletion	UNP A0AAD9GEF4
SH	?	-	SER	deletion	UNP A0AAD9GEF4
SH	?	-	ASN	deletion	UNP A0AAD9GEF4
SH	?	-	GLU	deletion	UNP A0AAD9GEF4
SH	?	-	LEU	deletion	UNP A0AAD9GEF4
SH	?	-	SER	deletion	UNP A0AAD9GEF4
SH	?	-	GLU	deletion	UNP A0AAD9GEF4
SH	?	-	LEU	deletion	UNP A0AAD9GEF4
SH	?	-	CYS	deletion	UNP A0AAD9GEF4
SH	?	-	ASN	deletion	UNP A0AAD9GEF4
SH	?	-	LYS	deletion	UNP A0AAD9GEF4
SH	?	-	PHE	deletion	UNP A0AAD9GEF4
SH	?	-	SER	deletion	UNP A0AAD9GEF4
SH	?	-	PRO	deletion	UNP A0AAD9GEF4
SH	?	-	LEU	deletion	UNP A0AAD9GEF4
SH	?	-	SER	deletion	UNP A0AAD9GEF4
SH	?	-	ASP	deletion	UNP A0AAD9GEF4
SH	?	-	PHE	deletion	UNP A0AAD9GEF4
SH	?	-	ARG	deletion	UNP A0AAD9GEF4
SH	?	-	SER	deletion	UNP A0AAD9GEF4
SH	?	-	ASN	deletion	UNP A0AAD9GEF4
SH	?	-	ALA	deletion	UNP A0AAD9GEF4

- Molecule 7 is a protein called 40S ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	ST	145	Total	C	N	O	S	0	0
			1182	757	221	199	5		

- Molecule 8 is a protein called 40S ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SA	208	Total	C	N	O	S	0	0
			1687	1073	304	297	13		

- Molecule 9 is a protein called 40S ribosomal protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SN	96	Total	C	N	O	S	0	0
			802	528	135	134	5		

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SN	?	-	GLY	deletion	UNP A0AAD9G6F1
SN	?	-	GLU	deletion	UNP A0AAD9G6F1
SN	?	-	LEU	deletion	UNP A0AAD9G6F1
SN	?	-	ARG	deletion	UNP A0AAD9G6F1
SN	?	-	PHE	deletion	UNP A0AAD9G6F1
SN	?	-	MET	deletion	UNP A0AAD9G6F1
SN	?	-	THR	deletion	UNP A0AAD9G6F1
SN	?	-	VAL	deletion	UNP A0AAD9G6F1
SN	?	-	LEU	deletion	UNP A0AAD9G6F1
SN	?	-	THR	deletion	UNP A0AAD9G6F1
SN	?	-	TYR	deletion	UNP A0AAD9G6F1
SN	?	-	TYR	deletion	UNP A0AAD9G6F1
SN	?	-	PHE	deletion	UNP A0AAD9G6F1
SN	?	-	VAL	deletion	UNP A0AAD9G6F1
SN	?	-	GLY	deletion	UNP A0AAD9G6F1
SN	?	-	SER	deletion	UNP A0AAD9G6F1
SN	?	-	LEU	deletion	UNP A0AAD9G6F1
SN	?	-	HIS	deletion	UNP A0AAD9G6F1
SN	?	-	GLY	deletion	UNP A0AAD9G6F1
SN	?	-	ARG	deletion	UNP A0AAD9G6F1
SN	?	-	ALA	deletion	UNP A0AAD9G6F1

- Molecule 10 is a protein called 40S ribosomal protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SJ	126	Total	C	N	O	S	0	0
			1004	641	184	173	6		

- Molecule 11 is a protein called 40S ribosomal protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SI	126	Total	C	N	O	S	0	0
			1038	670	193	174	1		

- Molecule 12 is a protein called 40S ribosomal protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SK	175	Total	C	N	O	S	0	0
			1412	882	277	246	7		

- Molecule 13 is a protein called 40S ribosomal protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SG	186	Total	C	N	O	S	0	0
			1517	955	298	254	10		

- Molecule 14 is a protein called 40S ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SM	96	Total	C	N	O	S	0	0
			761	474	139	142	6		

- Molecule 15 is a protein called 40S ribosomal protein eS30.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	Se	38	Total	C	N	O	0	0
			313	193	71	49		

- Molecule 16 is a protein called 40S ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SS	50	Total	C	N	O	S	0	0
			411	258	84	65	4		

- Molecule 17 is a protein called 40S ribosomal protein eS28.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	Sd	54	Total	C	N	O	0	0
			421	261	86	74		

- Molecule 18 is a protein called 40S ribosomal protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SC	187	Total	C	N	O	S	0	0
			1459	922	273	258	6		

- Molecule 19 is a protein called 40S ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SW	108	Total	C	N	O	S	0	0
			875	564	158	148	5		

- Molecule 20 is a protein called 40S ribosomal protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SB	165	Total	C	N	O	S	0	0
			1289	825	223	231	10		

- Molecule 21 is a protein called 40S ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SF	152	Total	C	N	O	S	0	0
			1141	730	204	200	7		

- Molecule 22 is a protein called 40S ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Sb	82	Total	C	N	O	S	0	0
			661	407	145	103	6		

- Molecule 23 is a protein called 40S ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SV	75	Total	C	N	O	S	0	0
			616	392	121	101	2		

- Molecule 24 is a protein called 40S ribosomal protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SO	98	Total	C	N	O	S	0	0
			739	462	142	131	4		

- Molecule 25 is a protein called 40S ribosomal protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SZ	69	Total	C	N	O	S	0	0
			582	367	120	94	1		

- Molecule 26 is a protein called 40S ribosomal protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Sa	71	Total	C	N	O	S	0	0
			569	361	100	104	4		

- Molecule 27 is a protein called 40S ribosomal protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SQ	87	Total	C	N	O	S	0	0
			660	418	114	123	5		

- Molecule 28 is a protein called 40S ribosomal protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SD	108	Total	C	N	O	S	0	0
			935	594	184	153	4		

- Molecule 29 is a protein called 40S ribosomal protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Sf	52	Total	C	N	O	S	0	0
			407	261	73	68	5		

- Molecule 30 is a protein called 40S ribosomal protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Sc	60	Total	C	N	O	S	0	0
			474	299	89	81	5		

- Molecule 31 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	S1	1535	Total	C	N	O	P	0	0
			32741	14634	5836	10736	1535		

- Molecule 32 is a protein called 60S ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LM	144	Total	C	N	O	S	0	0
			1146	730	228	182	6		

- Molecule 33 is a protein called 60S ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LS	179	Total	C	N	O	S	0	0
			1445	919	274	244	8		

- Molecule 34 is a protein called 60S ribosomal protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Le	98	Total	C	N	O	S	0	0
			818	520	161	134	3		

- Molecule 35 is a protein called 60S ribosomal protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lf	125	Total	C	N	O	S	0	0
			1026	647	212	165	2		

- Molecule 36 is a protein called 60S ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lj	87	Total	C	N	O	S	0	0
			689	419	152	111	7		

- Molecule 37 is a protein called 60S ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LQ	184	Total	C	N	O	S	0	0
			1432	900	282	245	5		

There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LQ	?	-	VAL	deletion	UNP A0AAD9G7R0
LQ	?	-	ASP	deletion	UNP A0AAD9G7R0
LQ	?	-	PHE	deletion	UNP A0AAD9G7R0
LQ	?	-	HIS	deletion	UNP A0AAD9G7R0
LQ	?	-	GLU	deletion	UNP A0AAD9G7R0
LQ	?	-	LYS	deletion	UNP A0AAD9G7R0
LQ	?	-	ASP	deletion	UNP A0AAD9G7R0
LQ	?	-	MET	deletion	UNP A0AAD9G7R0
LQ	?	-	MET	deletion	UNP A0AAD9G7R0
LQ	?	-	MET	deletion	UNP A0AAD9G7R0
LQ	?	-	HIS	deletion	UNP A0AAD9G7R0
LQ	?	-	VAL	deletion	UNP A0AAD9G7R0

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Chain	Residue	Modelled	Actual	Comment	Reference
LQ	?	-	SER	deletion	UNP A0AAD9G7R0
LQ	?	-	THR	deletion	UNP A0AAD9G7R0
LQ	?	-	GLU	deletion	UNP A0AAD9G7R0
LQ	?	-	SER	deletion	UNP A0AAD9G7R0
LQ	?	-	ARG	deletion	UNP A0AAD9G7R0
LQ	?	-	ARG	deletion	UNP A0AAD9G7R0
LQ	?	-	SER	deletion	UNP A0AAD9G7R0
LQ	?	-	SER	deletion	UNP A0AAD9G7R0
LQ	?	-	ASP	deletion	UNP A0AAD9G7R0
LQ	?	-	SER	deletion	UNP A0AAD9G7R0
LQ	?	-	ALA	deletion	UNP A0AAD9G7R0
LQ	?	-	GLY	deletion	UNP A0AAD9G7R0
LQ	?	-	GLU	deletion	UNP A0AAD9G7R0

- Molecule 38 is a protein called 60S ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LB	245	Total	C	N	O	S	0	0
			1868	1165	375	323	5		

- Molecule 39 is a protein called 60S ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LI	198	Total	C	N	O	S	0	0
			1610	1027	314	260	9		

- Molecule 40 is a protein called 60S ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LJ	193	Total	C	N	O	S	0	0
			1522	956	303	253	10		

- Molecule 41 is a protein called 60S ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LX	121	Total	C	N	O	S	0	0
			1003	623	203	173	4		

- Molecule 42 is a protein called 60S ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	La	115	Total	C	N	O	S	0	0
			957	606	190	158	3		

- Molecule 43 is a protein called 60S ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LD	327	Total	C	N	O	S	0	0
			2521	1587	490	433	11		

- Molecule 44 is a protein called 60S ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LP	281	Total	C	N	O	S	0	0
			2293	1447	424	413	9		

- Molecule 45 is a protein called 60S ribosomal protein eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LZ	137	Total	C	N	O	S	0	0
			1114	703	216	189	6		

- Molecule 46 is a protein called 60S ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LU	172	Total	C	N	O	S	0	0
			1392	875	281	231	5		

- Molecule 47 is a protein called 60S ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	LH	224	Total	C	N	O	S	0	0
			1816	1164	336	308	8		

- Molecule 48 is a protein called 60S ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	LC	377	Total	C	N	O	S	0	0
			3009	1918	561	515	15		

- Molecule 49 is a protein called 60S ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	LL	128	Total	C	N	O	S	0	0
			1016	655	183	175	3		

- Molecule 50 is a protein called 60S ribosomal protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	LK	128	Total	C	N	O	S	0	0
			964	616	177	165	6		

- Molecule 51 is a protein called 60S ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	LW	116	Total	C	N	O	S	0	0
			946	600	178	165	3		

- Molecule 52 is a protein called 60S ribosomal protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Li	105	Total	C	N	O	S	0	0
			827	518	162	142	5		

- Molecule 53 is a protein called 60S ribosomal protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Lm	50	Total	C	N	O	S	0	0
			407	252	85	63	7		

- Molecule 54 is a protein called 60S ribosomal protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	LT	148	Total	C	N	O	S	0	0
			1196	757	235	199	5		

- Molecule 55 is a protein called 60S ribosomal protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Lo	96	Total	C	N	O	S	0	0
			776	489	154	127	6		

- Molecule 56 is a protein called 60S ribosomal protein eL39.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	Ll	49	Total 435	C 279	N 93	O 63	0	0

- Molecule 57 is a protein called 60S ribosomal protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LR	170	Total 1387	C 865	N 287	O 224	S 11	0	0

- Molecule 58 is a protein called 60S ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	LE	155	Total 1259	C 794	N 238	O 221	S 6	0	0

- Molecule 59 is a protein called 60S ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	LO	205	Total 1648	C 1061	N 308	O 272	S 7	0	0

- Molecule 60 is a protein called 60S ribosomal protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	LN	197	Total 1656	C 1040	N 349	O 258	S 9	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LN	1	MET	-	insertion	UNP A0AAD9LIN3
LN	2	GLY	-	insertion	UNP A0AAD9LIN3
LN	3	ALA	-	insertion	UNP A0AAD9LIN3
LN	4	TYR	-	insertion	UNP A0AAD9LIN3
LN	5	ARG	-	insertion	UNP A0AAD9LIN3
LN	6	TYR	-	insertion	UNP A0AAD9LIN3

- Molecule 61 is a protein called 60S ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Lg	108	Total 879	C 563	N 167	O 144	S 5	0	0

- Molecule 62 is a protein called 60S ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Lc	214	Total	C	N	O	S	0	0
			1751	1128	331	286	6		

- Molecule 63 is a protein called 60S ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	LV	97	Total	C	N	O	S	0	0
			799	513	141	144	1		

- Molecule 64 is a protein called 60S ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Ld	93	Total	C	N	O	S	0	0
			706	444	126	127	9		

- Molecule 65 is a protein called 60S ribosomal protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Lp	88	Total	C	N	O	S	0	0
			695	434	139	117	5		

- Molecule 66 is a protein called 60S ribosomal protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Lb	51	Total	C	N	O	S	0	0
			417	258	92	64	3		

- Molecule 67 is a protein called 60S ribosomal protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Lh	100	Total	C	N	O	S	0	0
			816	501	181	129	5		

- Molecule 68 is a protein called 60S ribosomal protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	LY	61	Total	C	N	O	S	0	0
			509	331	95	82	1		

There are 43 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LY	?	-	VAL	deletion	UNP A0AAD9LE14
LY	?	-	CYS	deletion	UNP A0AAD9LE14
LY	?	-	PRO	deletion	UNP A0AAD9LE14
LY	?	-	LYS	deletion	UNP A0AAD9LE14
LY	?	-	VAL	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14
LY	?	-	CYS	deletion	UNP A0AAD9LE14
LY	?	-	ASN	deletion	UNP A0AAD9LE14
LY	?	-	ASN	deletion	UNP A0AAD9LE14
LY	?	-	PHE	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14
LY	?	-	GLN	deletion	UNP A0AAD9LE14
LY	?	-	TRP	deletion	UNP A0AAD9LE14
LY	?	-	PRO	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14
LY	?	-	HIS	deletion	UNP A0AAD9LE14
LY	?	-	ASN	deletion	UNP A0AAD9LE14
LY	?	-	ASN	deletion	UNP A0AAD9LE14
LY	?	-	CYS	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14
LY	?	-	ALA	deletion	UNP A0AAD9LE14
LY	?	-	LEU	deletion	UNP A0AAD9LE14
LY	?	-	PHE	deletion	UNP A0AAD9LE14
LY	?	-	VAL	deletion	UNP A0AAD9LE14
LY	?	-	THR	deletion	UNP A0AAD9LE14
LY	?	-	MET	deletion	UNP A0AAD9LE14
LY	?	-	VAL	deletion	UNP A0AAD9LE14
LY	?	-	THR	deletion	UNP A0AAD9LE14
LY	?	-	LEU	deletion	UNP A0AAD9LE14
LY	?	-	THR	deletion	UNP A0AAD9LE14
LY	?	-	LYS	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14
LY	?	-	ASP	deletion	UNP A0AAD9LE14
LY	?	-	ILE	deletion	UNP A0AAD9LE14
LY	?	-	PHE	deletion	UNP A0AAD9LE14
LY	?	-	ILE	deletion	UNP A0AAD9LE14
LY	?	-	ILE	deletion	UNP A0AAD9LE14
LY	?	-	LEU	deletion	UNP A0AAD9LE14
LY	?	-	ALA	deletion	UNP A0AAD9LE14
LY	?	-	PHE	deletion	UNP A0AAD9LE14
LY	?	-	LEU	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14

- Molecule 69 is a protein called 60S ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	LG	155	Total	C	N	O	S	0	0
			1223	791	212	215	5		

- Molecule 70 is a protein called 60S ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Ln	38	Total	C	N	O	S	0	0
			349	213	89	45	2		

- Molecule 71 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	L3	122	Total	C	N	O	P	0	0
			2610	1163	476	849	122		

- Molecule 72 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	L4	145	Total	C	N	O	P	0	0
			3082	1380	552	1005	145		

- Molecule 73 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	L5	2875	Total	C	N	O	P	0	0
			61352	27401	10974	20102	2875		

- Molecule 74 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	S7	74	Total	C	N	O	P	0	0
			1571	702	275	521	73		

- Molecule 75 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	S8	76	Total	C	N	O	P	0	0
			1620	723	295	527	75		

- Molecule 76 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	S9	72	Total	C	N	O	P	0	0
			1532	684	273	504	71		

- Molecule 77 is a RNA chain called mRNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	S6	11	Total	C	N	O	P	0	0
			227	102	31	83	11		

- Molecule 78 is a protein called 40S ribosomal protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SY	78	Total	C	N	O	S	0	0
			600	368	107	121	4		

- Molecule 79 is a protein called 40S ribosomal protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	SE	255	Total	C	N	O	S	0	0
			2034	1291	375	360	8		

- Molecule 80 is a protein called Receptor for activated C kinase 1, RACK1 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sg	315	Total	C	N	O	S	0	0
			2429	1534	418	463	14		

- Molecule 81 is a protein called 60S ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	LF	186	Total	C	N	O	S	0	0
			1469	934	263	266	6		

- Molecule 82 is a protein called 60S ribosomal protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Lk	65	Total	C	N	O	S	0	0
			525	333	99	92	1		

- Molecule 83 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
83	S1	1	Total Mg 1 1	0
83	L3	1	Total Mg 1 1	0
83	L5	122	Total Mg 122 122	0

- Molecule 84 is POTASSIUM ION (CCD ID: K) (formula: K).

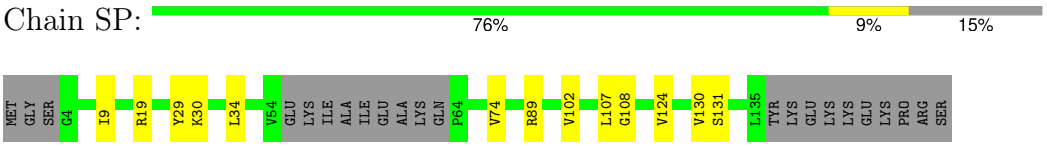
Mol	Chain	Residues	Atoms	AltConf
84	L5	12	Total K 12 12	0

3 Residue-property plots (i)

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

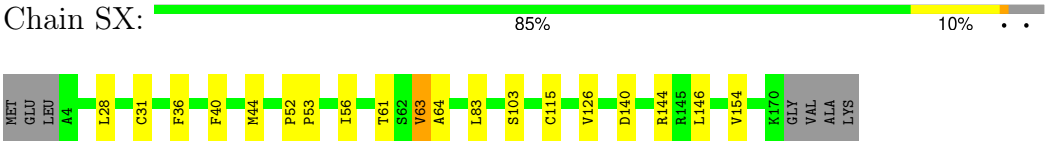
- Molecule 1: 40S ribosomal protein uS12

Chain SP:



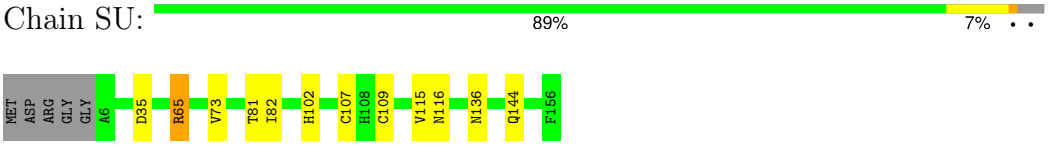
- Molecule 2: 40S ribosomal protein eS19

Chain SX:



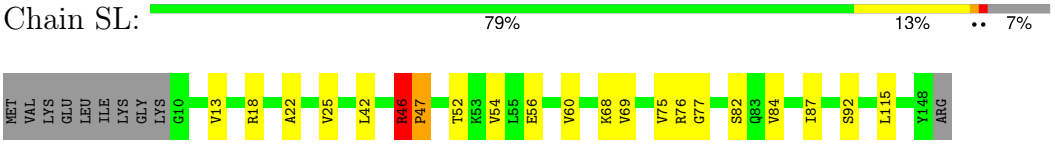
- Molecule 3: 40S ribosomal protein uS17

Chain SU:



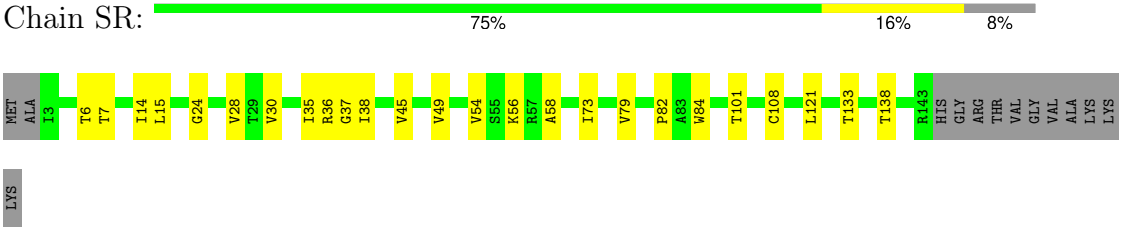
- Molecule 4: 40S ribosomal protein uS9

Chain SL:



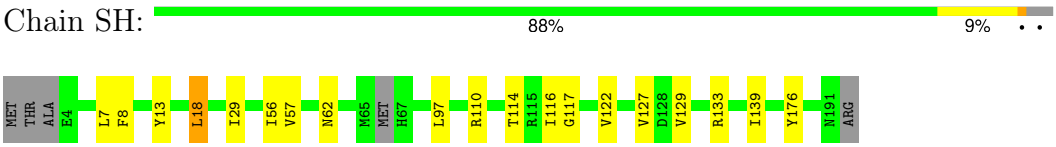
- Molecule 5: 40S ribosomal protein uS13

Chain SR:



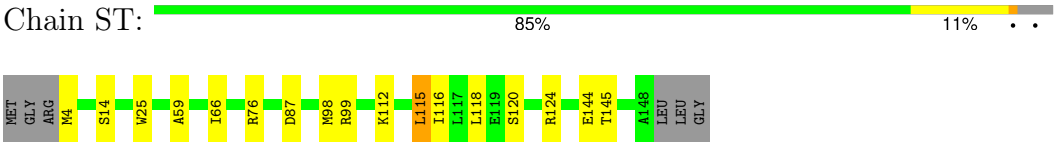
• Molecule 6: 40S ribosomal protein uS7

Chain SH:



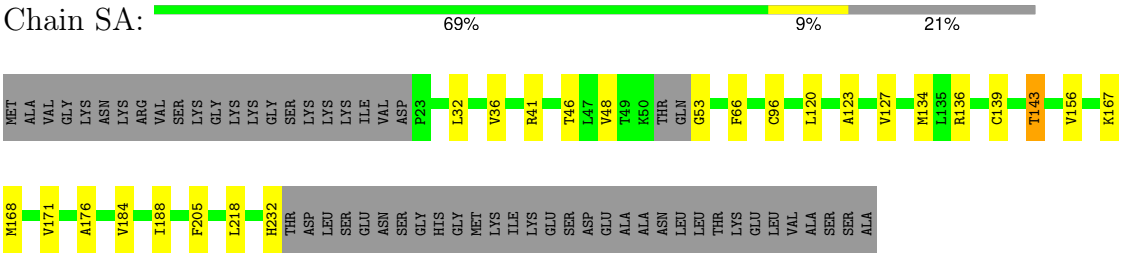
• Molecule 7: 40S ribosomal protein uS15

Chain ST:



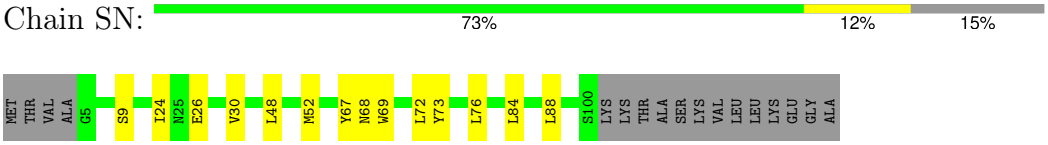
• Molecule 8: 40S ribosomal protein eS1

Chain SA:



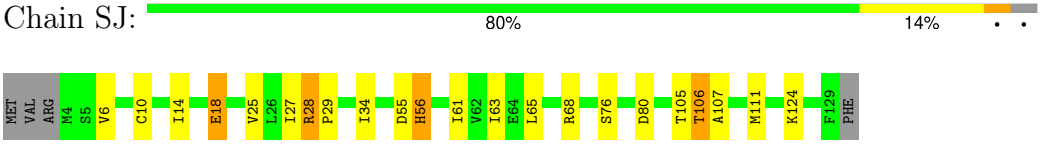
• Molecule 9: 40S ribosomal protein eS10

Chain SN:



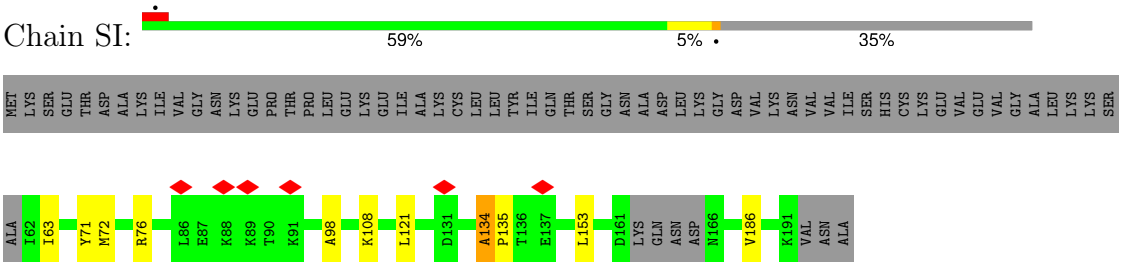
• Molecule 10: 40S ribosomal protein uS8

Chain SJ:



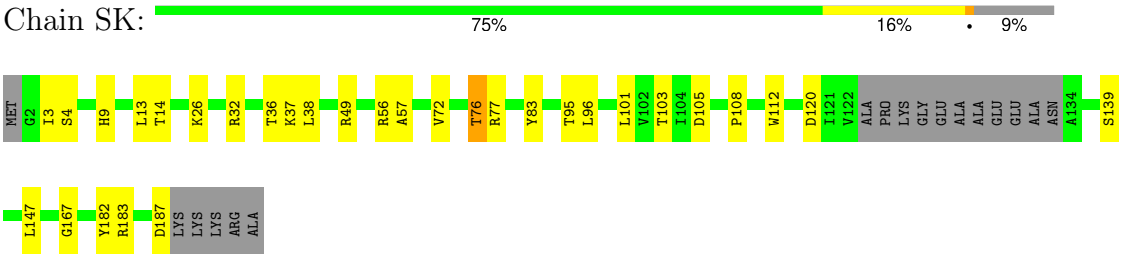
• Molecule 11: 40S ribosomal protein eS7

Chain SI:



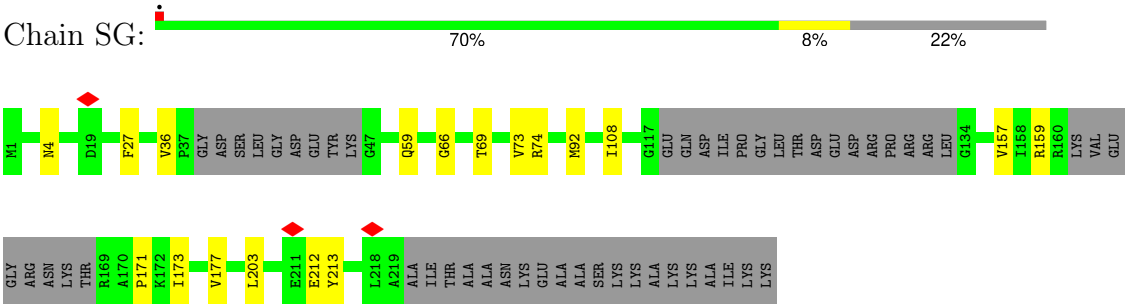
• Molecule 12: 40S ribosomal protein eS8

Chain SK:



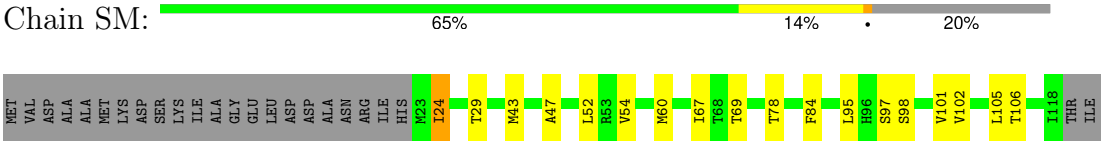
• Molecule 13: 40S ribosomal protein eS6

Chain SG:



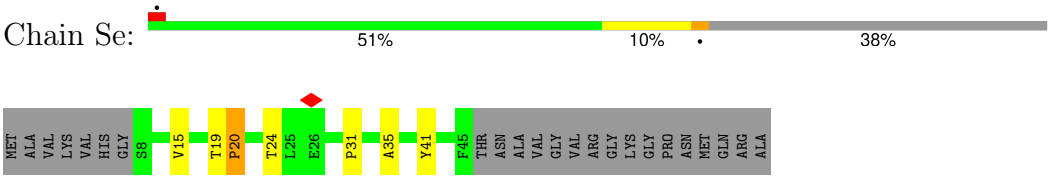
• Molecule 14: 40S ribosomal protein uS10

Chain SM:



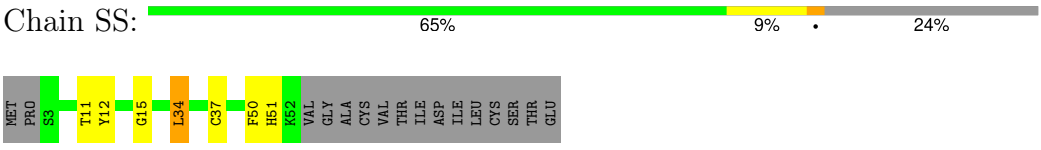
• Molecule 15: 40S ribosomal protein eS30

Chain Se:



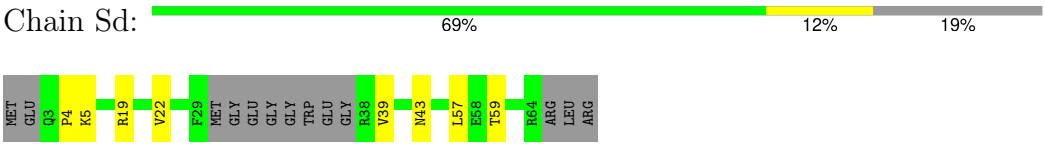
• Molecule 16: 40S ribosomal protein uS14

Chain SS:



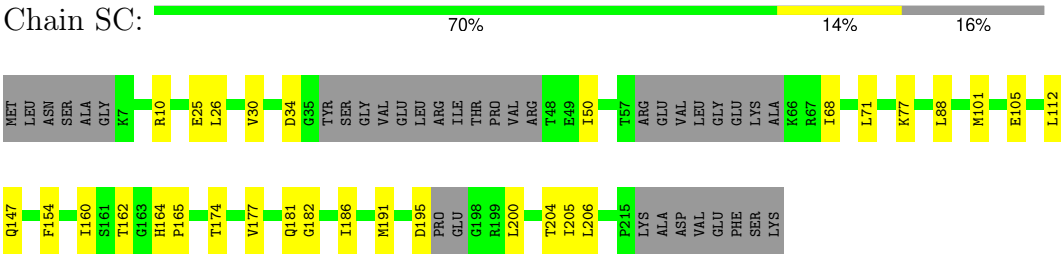
• Molecule 17: 40S ribosomal protein eS28

Chain Sd:



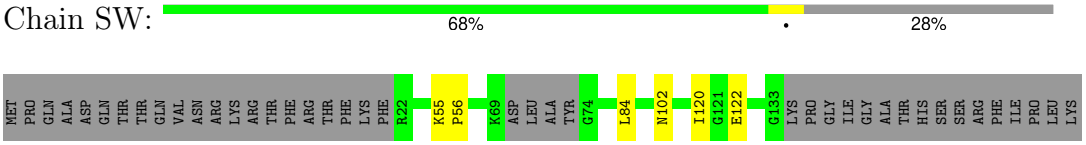
• Molecule 18: 40S ribosomal protein uS3

Chain SC:



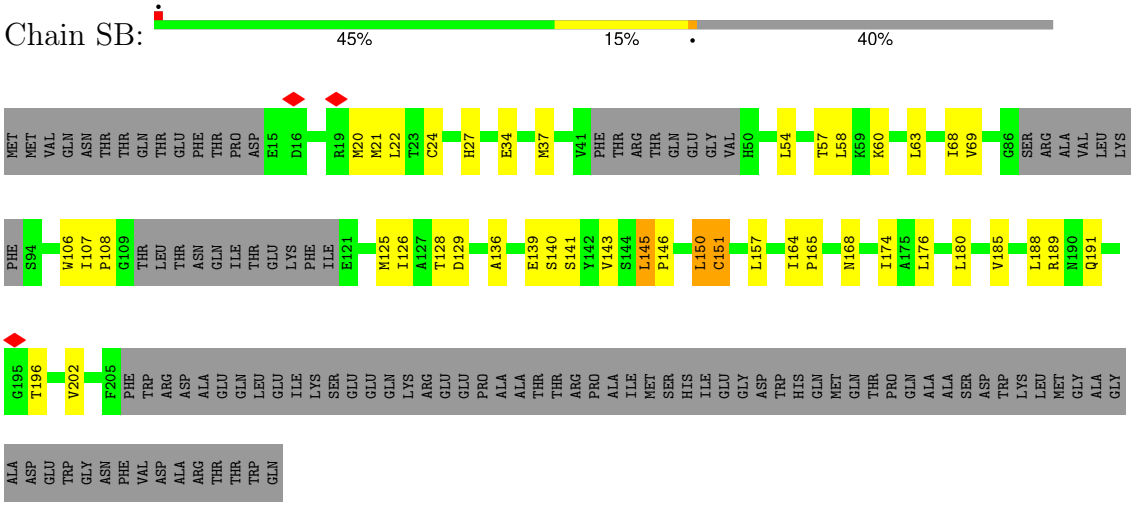
• Molecule 19: 40S ribosomal protein uS19

Chain SW:



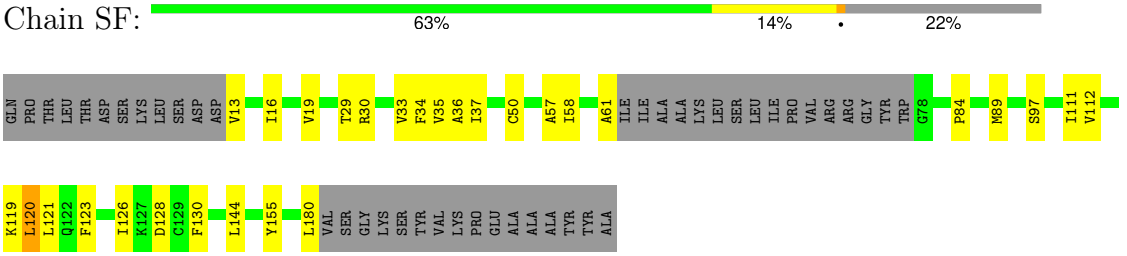
• Molecule 20: 40S ribosomal protein uS2

Chain SB:



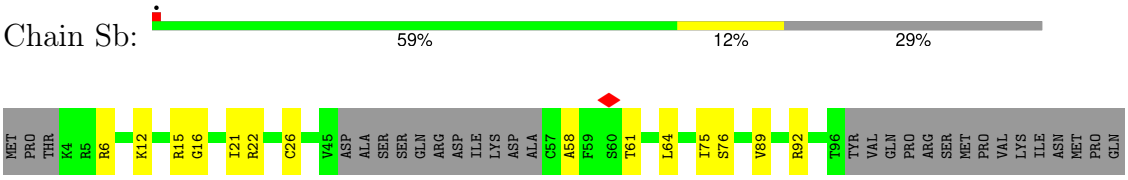
• Molecule 21: 40S ribosomal protein uS5

Chain SF:



• Molecule 22: 40S ribosomal protein eS26

Chain Sb:





• Molecule 23: 40S ribosomal protein eS17

Chain SV:



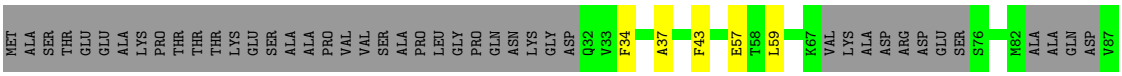




• Molecule 24: 40S ribosomal protein uS11

Chain SO:



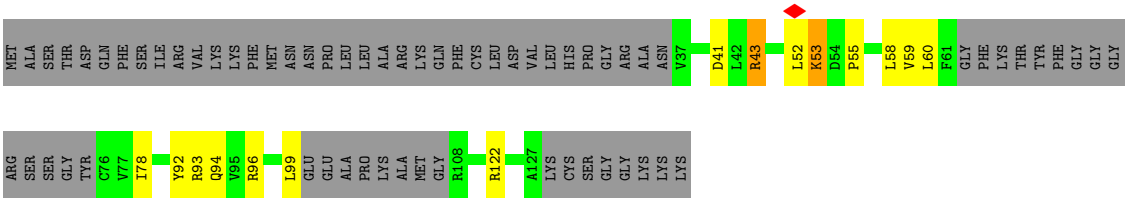




• Molecule 25: 40S ribosomal protein eS24

Chain SZ:





• Molecule 26: 40S ribosomal protein eS25

Chain Sa:

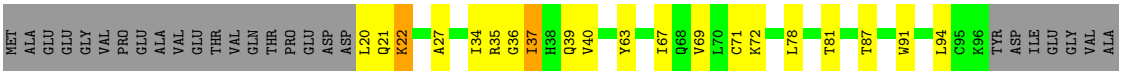




• Molecule 27: 40S ribosomal protein eS12

Chain SQ:

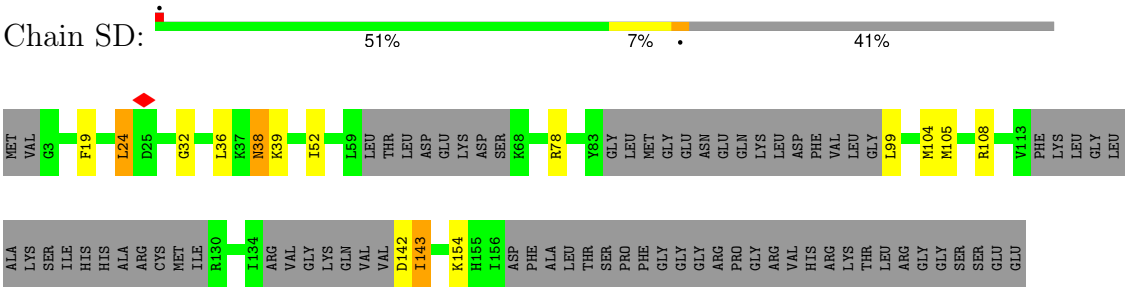






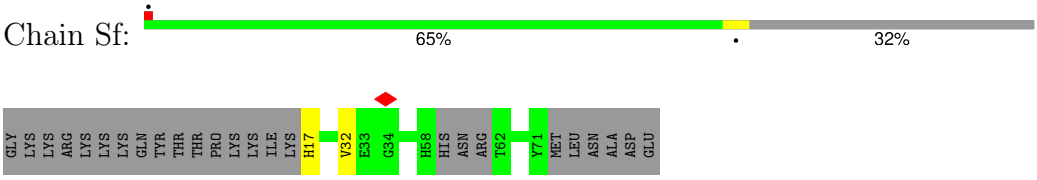
• Molecule 28: 40S ribosomal protein uS4

Chain SD:



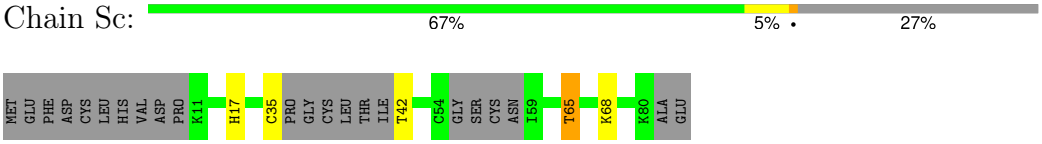
• Molecule 29: 40S ribosomal protein eS31

Chain Sf:



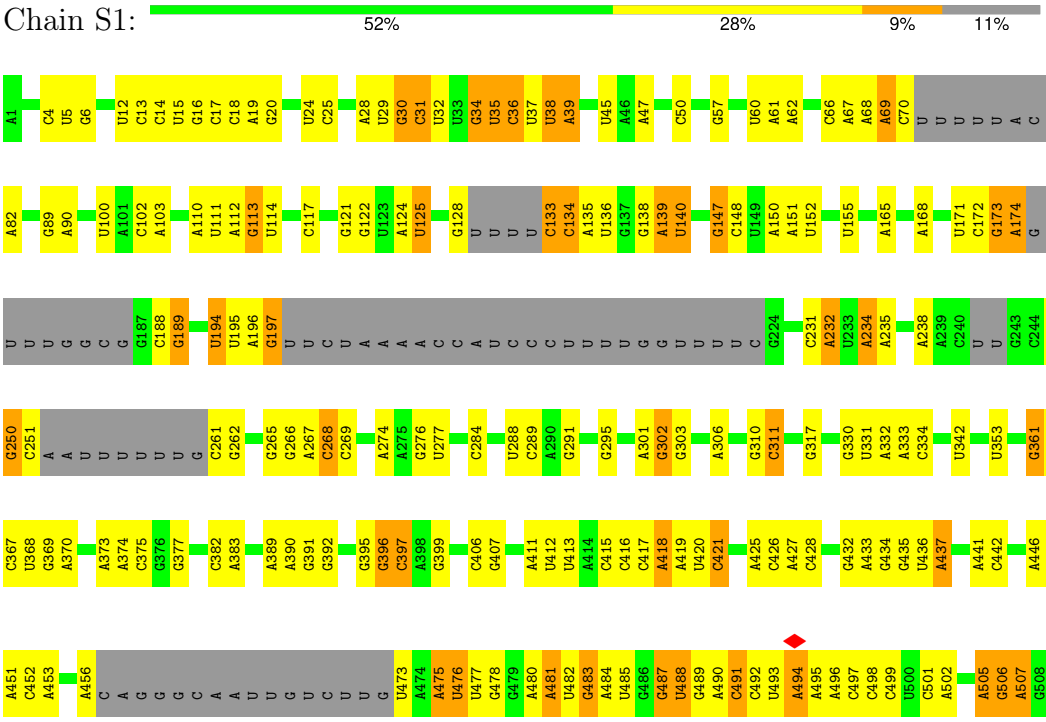
• Molecule 30: 40S ribosomal protein eS27

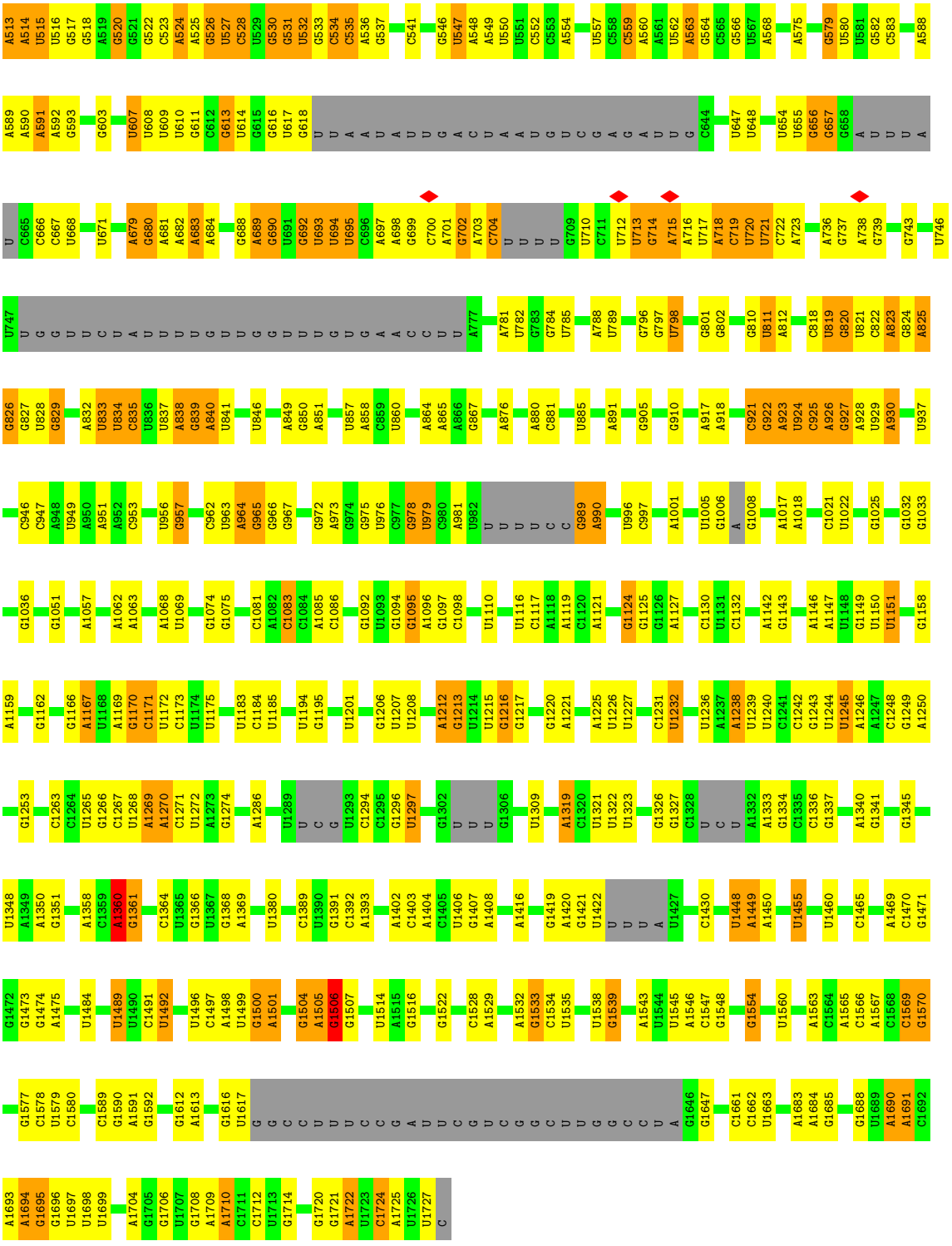
Chain Sc:



• Molecule 31: 18S ribosomal RNA

Chain S1:

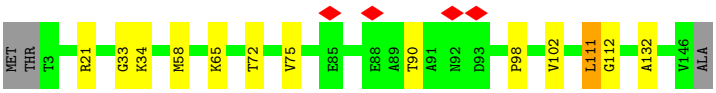




• Molecule 32: 60S ribosomal protein uL15

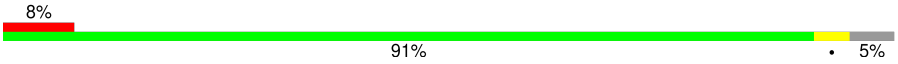
Chain LM:

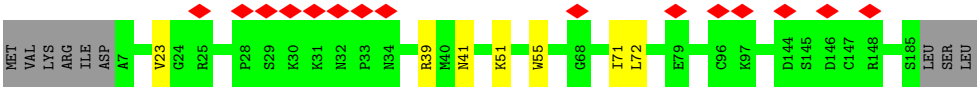




• Molecule 33: 60S ribosomal protein eL20

Chain LS:

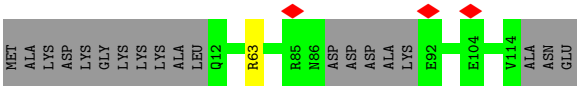




• Molecule 34: 60S ribosomal protein eL31

Chain Le:

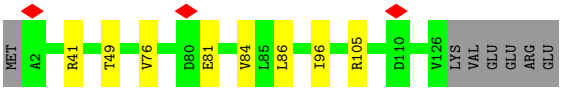




• Molecule 35: 60S ribosomal protein eL32

Chain Lf:





• Molecule 36: 60S ribosomal protein eL37

Chain Lj:

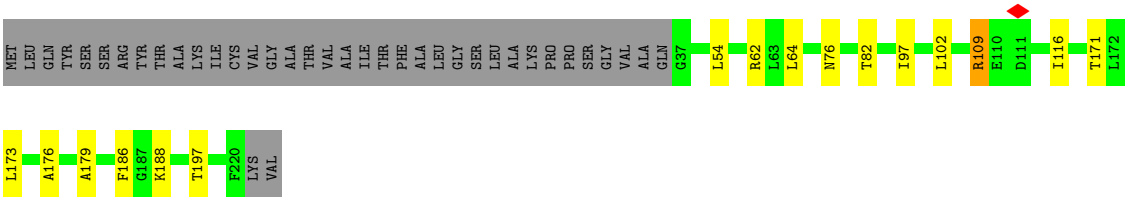




• Molecule 37: 60S ribosomal protein eL18

Chain LQ:





• Molecule 38: 60S ribosomal protein uL2

Chain LB:







• Molecule 39: 60S ribosomal protein uL13

Chain LI:

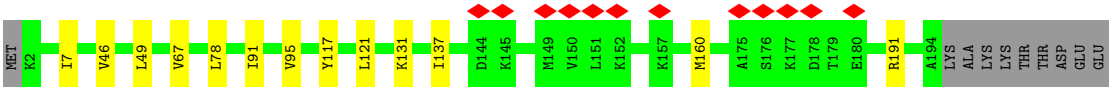




• Molecule 40: 60S ribosomal protein eL13

Chain LJ:





• Molecule 41: 60S ribosomal protein uL24

Chain LX:

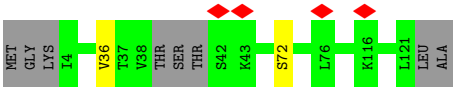




• Molecule 42: 60S ribosomal protein uL29

Chain La:

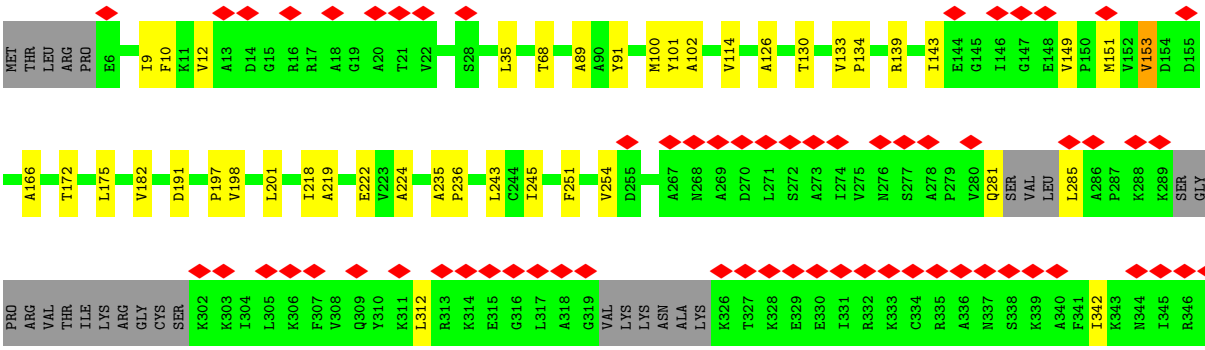


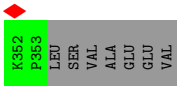


• Molecule 43: 60S ribosomal protein uL4

Chain LD:



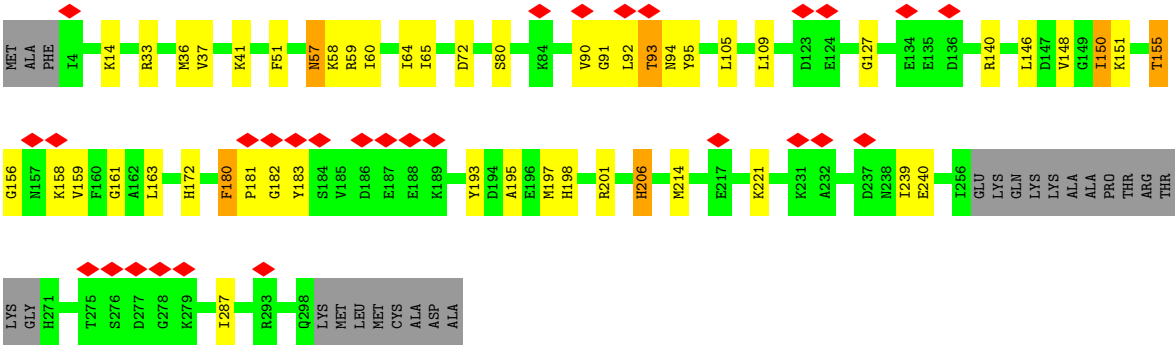




• Molecule 44: 60S ribosomal protein uL18

Chain LP:

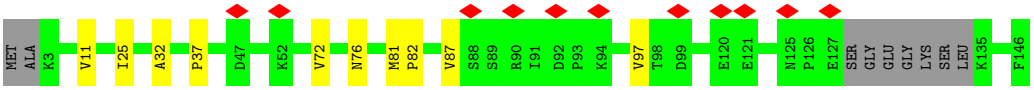




• Molecule 45: 60S ribosomal protein eL27

Chain LZ:

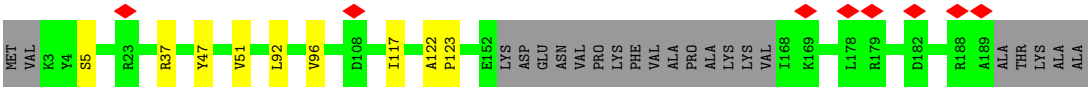




• Molecule 46: 60S ribosomal protein uL22

Chain LU:

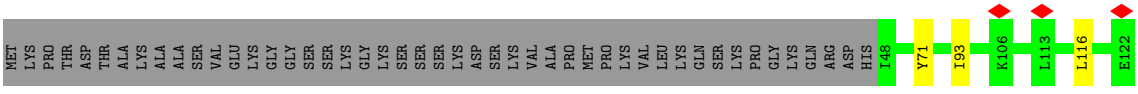


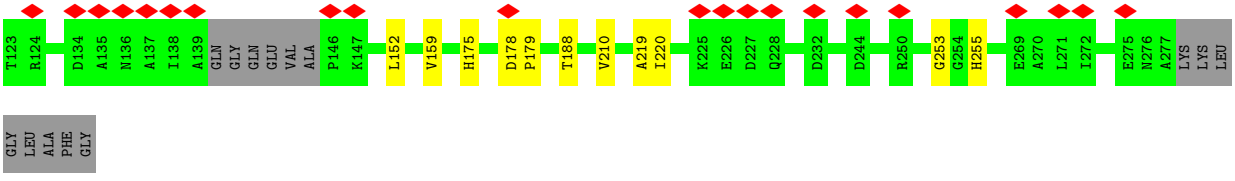


• Molecule 47: 60S ribosomal protein eL8

Chain LH:



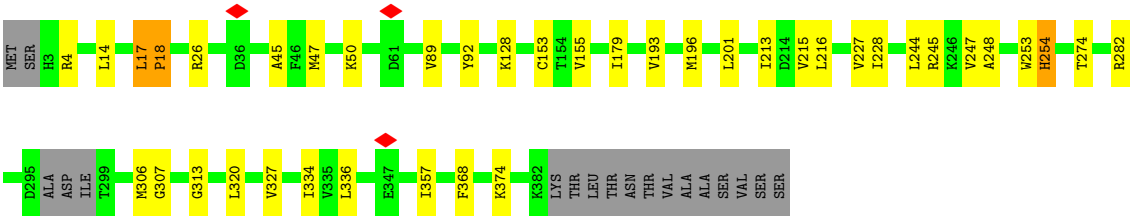




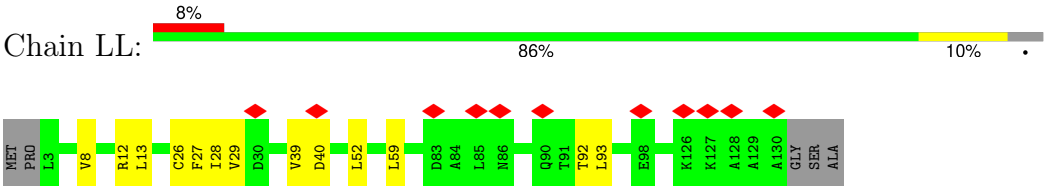
• Molecule 48: 60S ribosomal protein uL3

Chain LC:

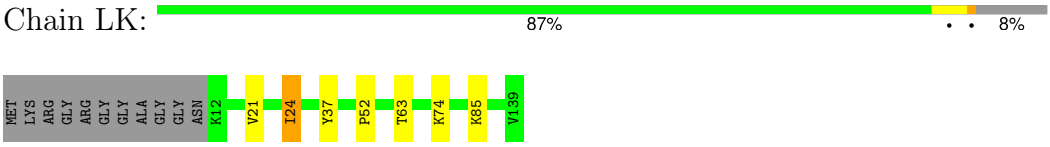




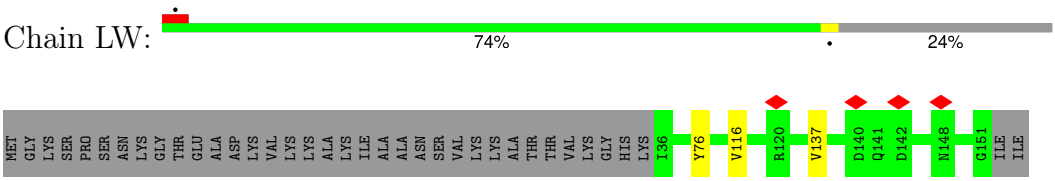
• Molecule 49: 60S ribosomal protein eL14



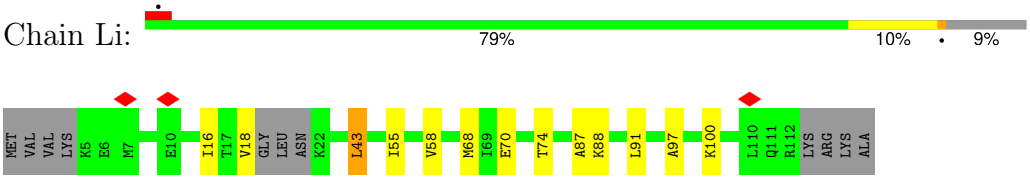
• Molecule 50: 60S ribosomal protein uL14



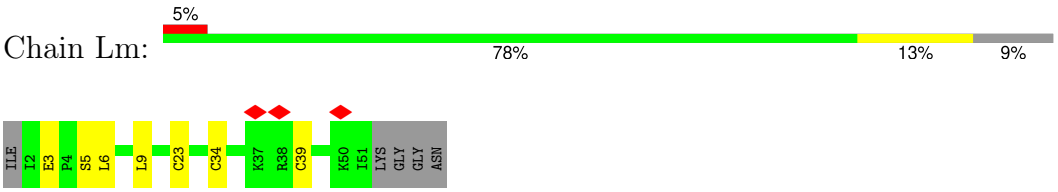
• Molecule 51: 60S ribosomal protein uL23



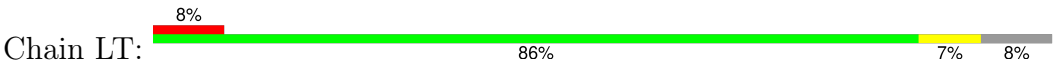
• Molecule 52: 60S ribosomal protein eL36

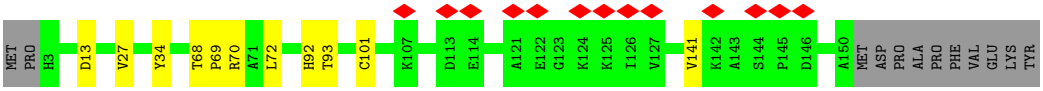


• Molecule 53: 60S ribosomal protein eL40

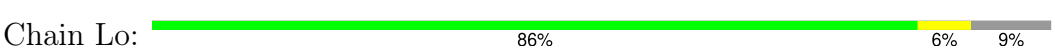


• Molecule 54: 60S ribosomal protein eL21





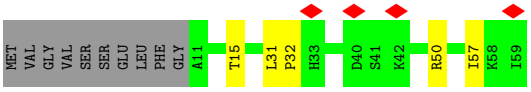
• Molecule 55: 60S ribosomal protein eL42



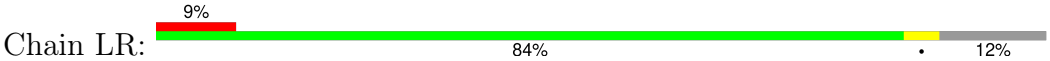


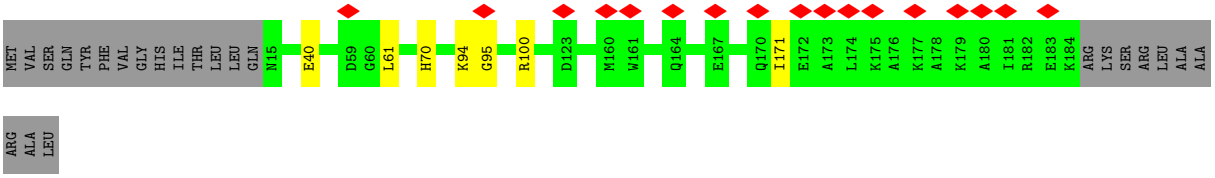
• Molecule 56: 60S ribosomal protein eL39



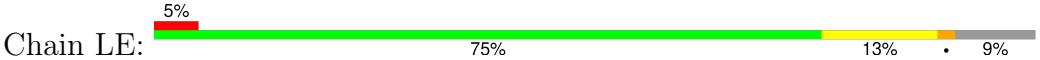


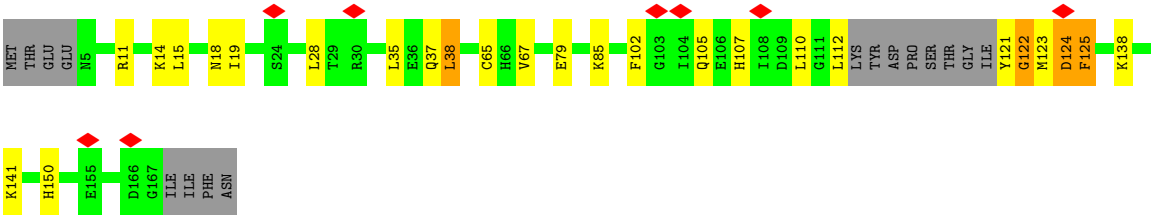
• Molecule 57: 60S ribosomal protein eL19



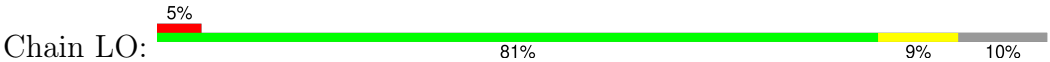


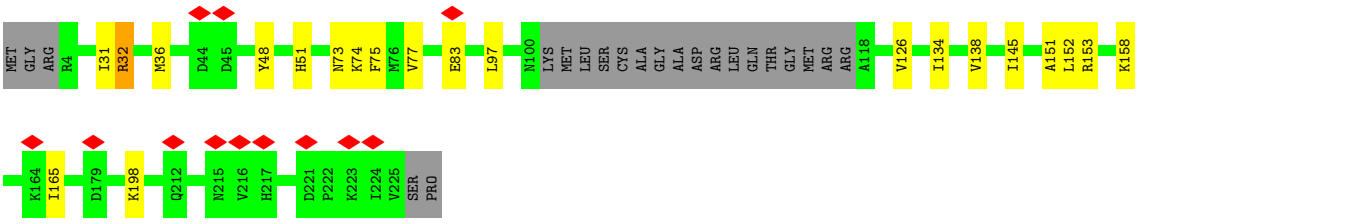
• Molecule 58: 60S ribosomal protein uL5





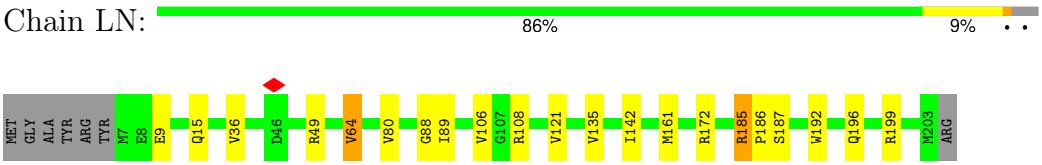
• Molecule 59: 60S ribosomal protein uL16





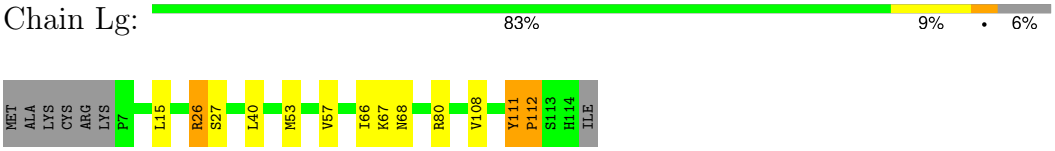
• Molecule 60: 60S ribosomal protein eL15

Chain LN:



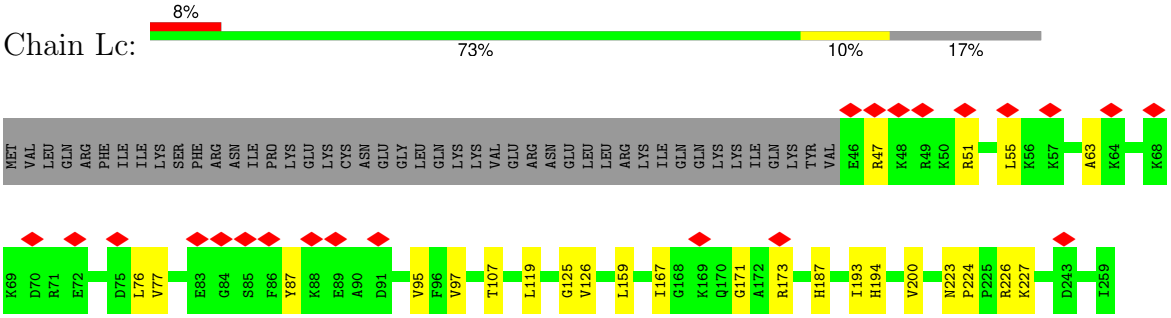
• Molecule 61: 60S ribosomal protein eL33

Chain Lg:



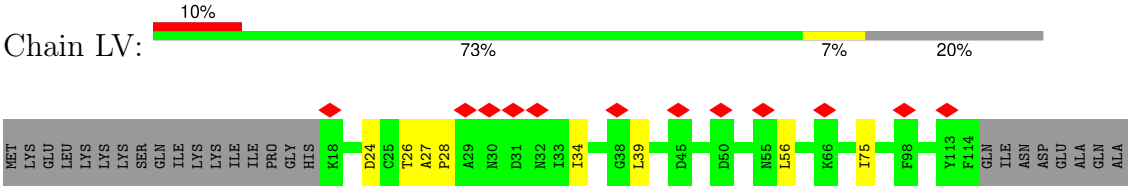
• Molecule 62: 60S ribosomal protein uL30

Chain Lc:



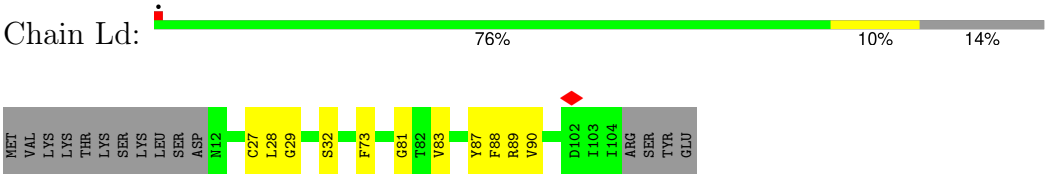
• Molecule 63: 60S ribosomal protein eL22

Chain LV:



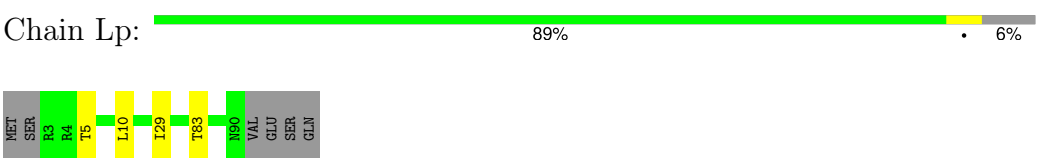
• Molecule 64: 60S ribosomal protein eL30

Chain Ld:



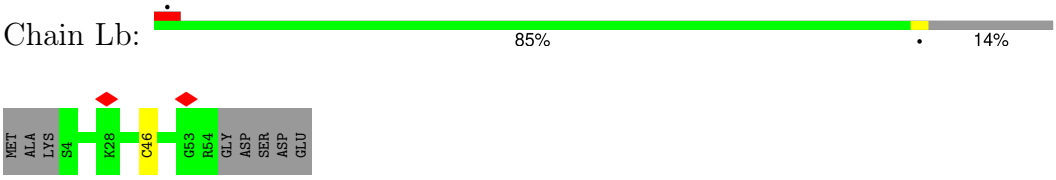
• Molecule 65: 60S ribosomal protein eL43

Chain Lp:



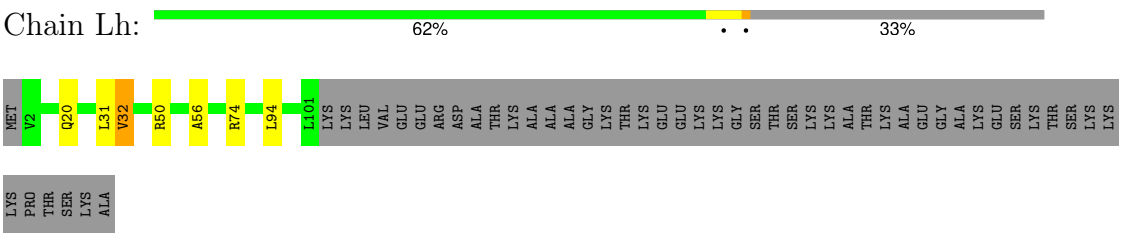
• Molecule 66: 60S ribosomal protein eL29

Chain Lb:



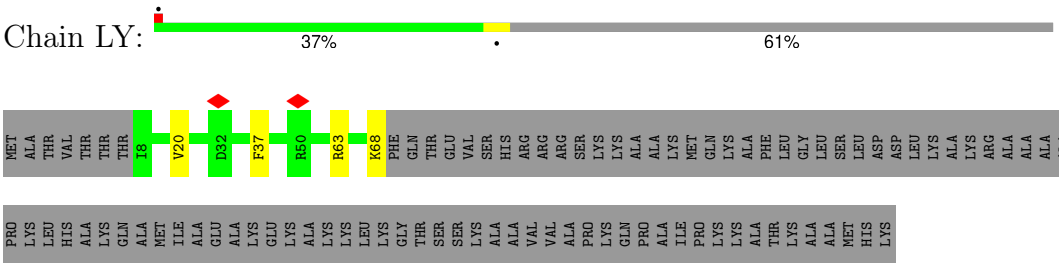
• Molecule 67: 60S ribosomal protein eL34

Chain Lh:



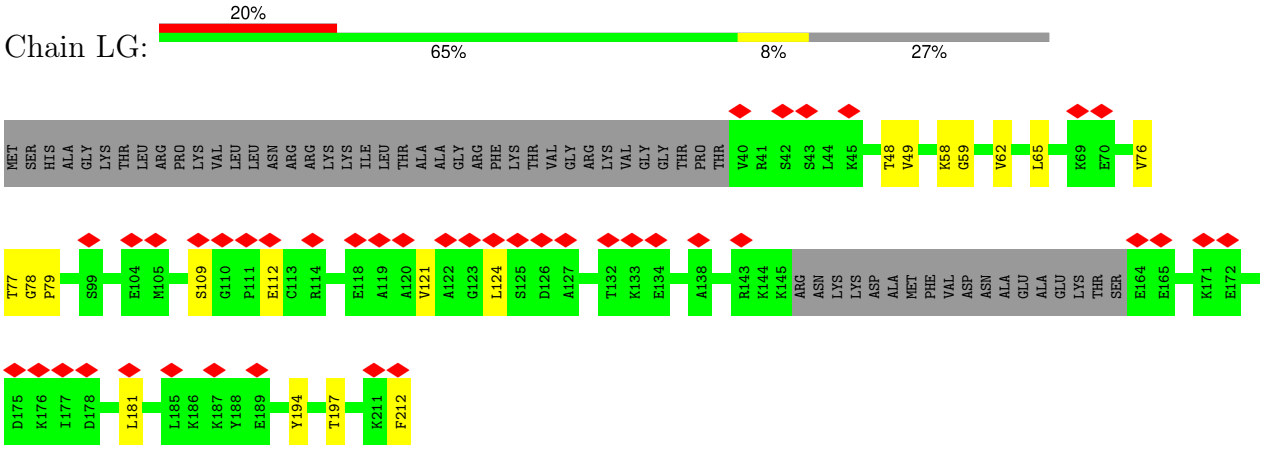
• Molecule 68: 60S ribosomal protein eL24

Chain LY:



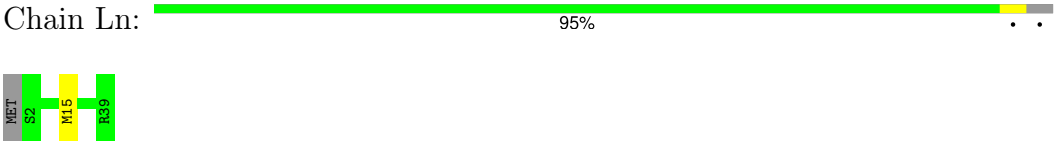
• Molecule 69: 60S ribosomal protein eL6

Chain LG:



• Molecule 70: 60S ribosomal protein eL41

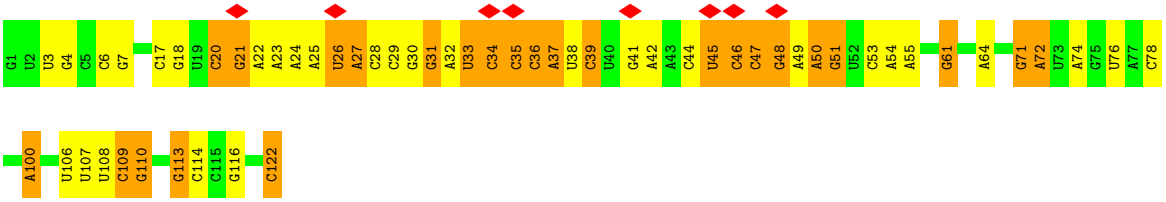
Chain Ln:



• Molecule 71: 5S ribosomal RNA

Chain L3:

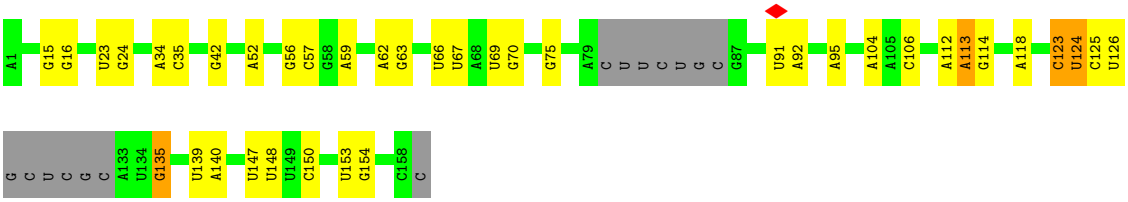




• Molecule 72: 5.8S ribosomal RNA

Chain L4:

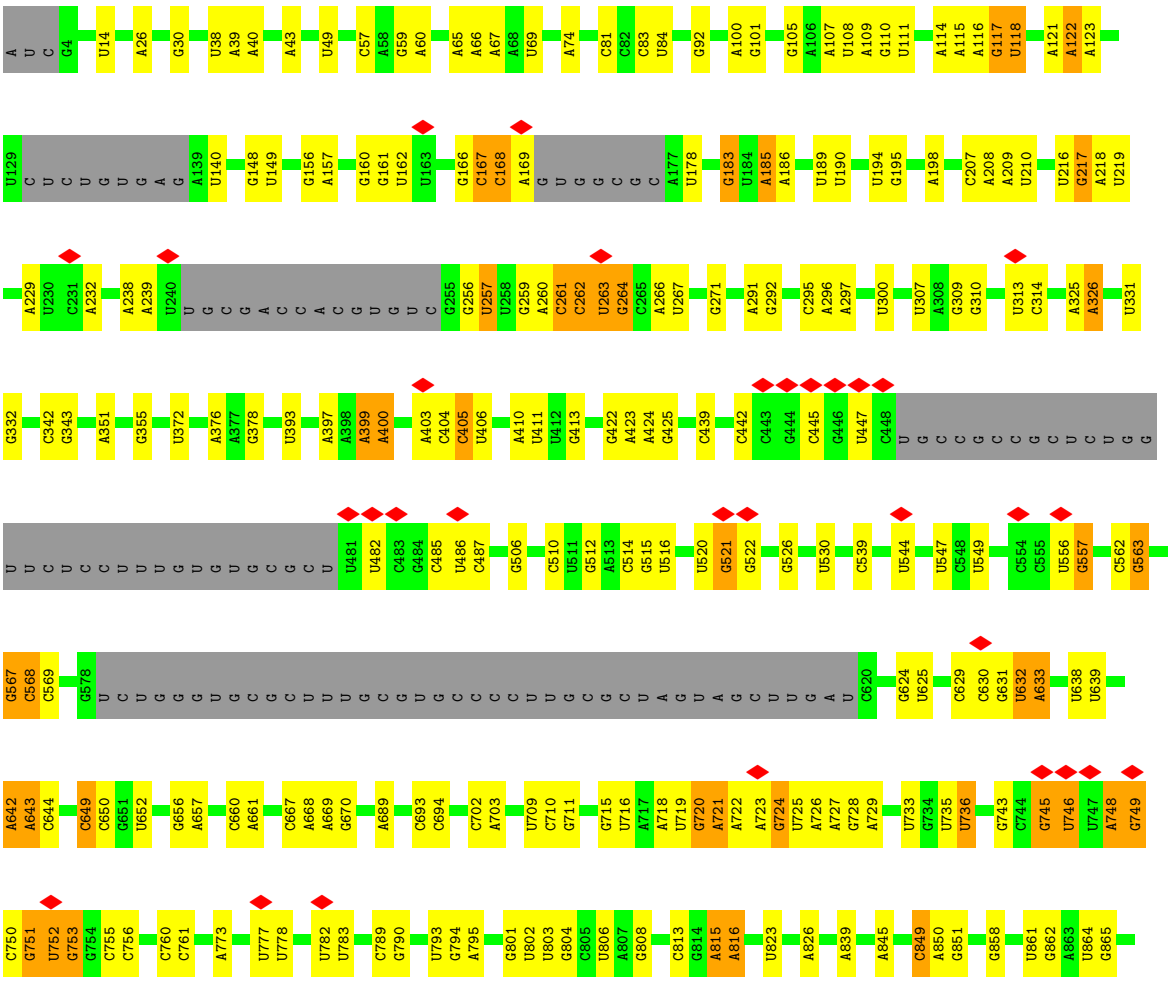


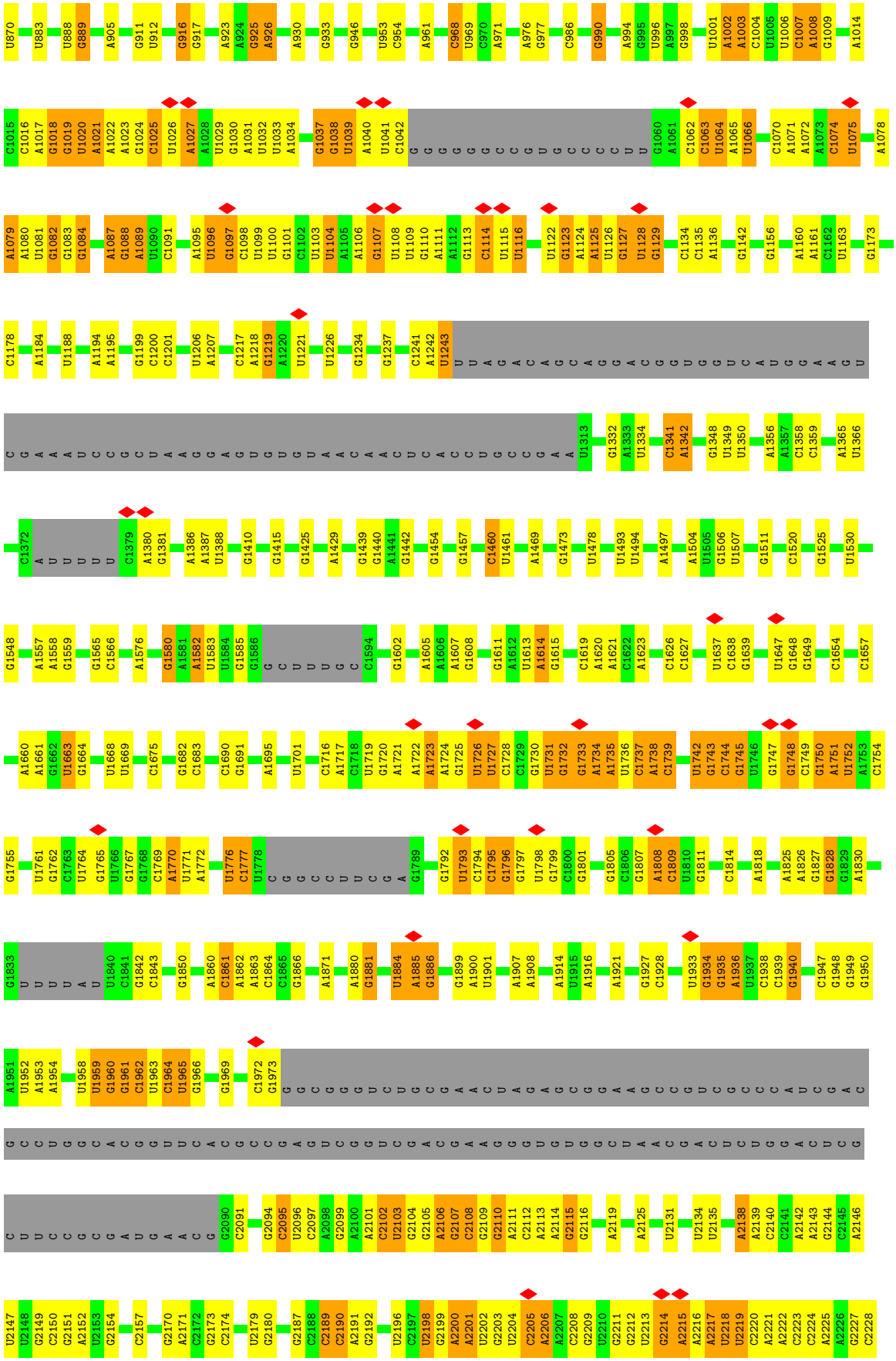


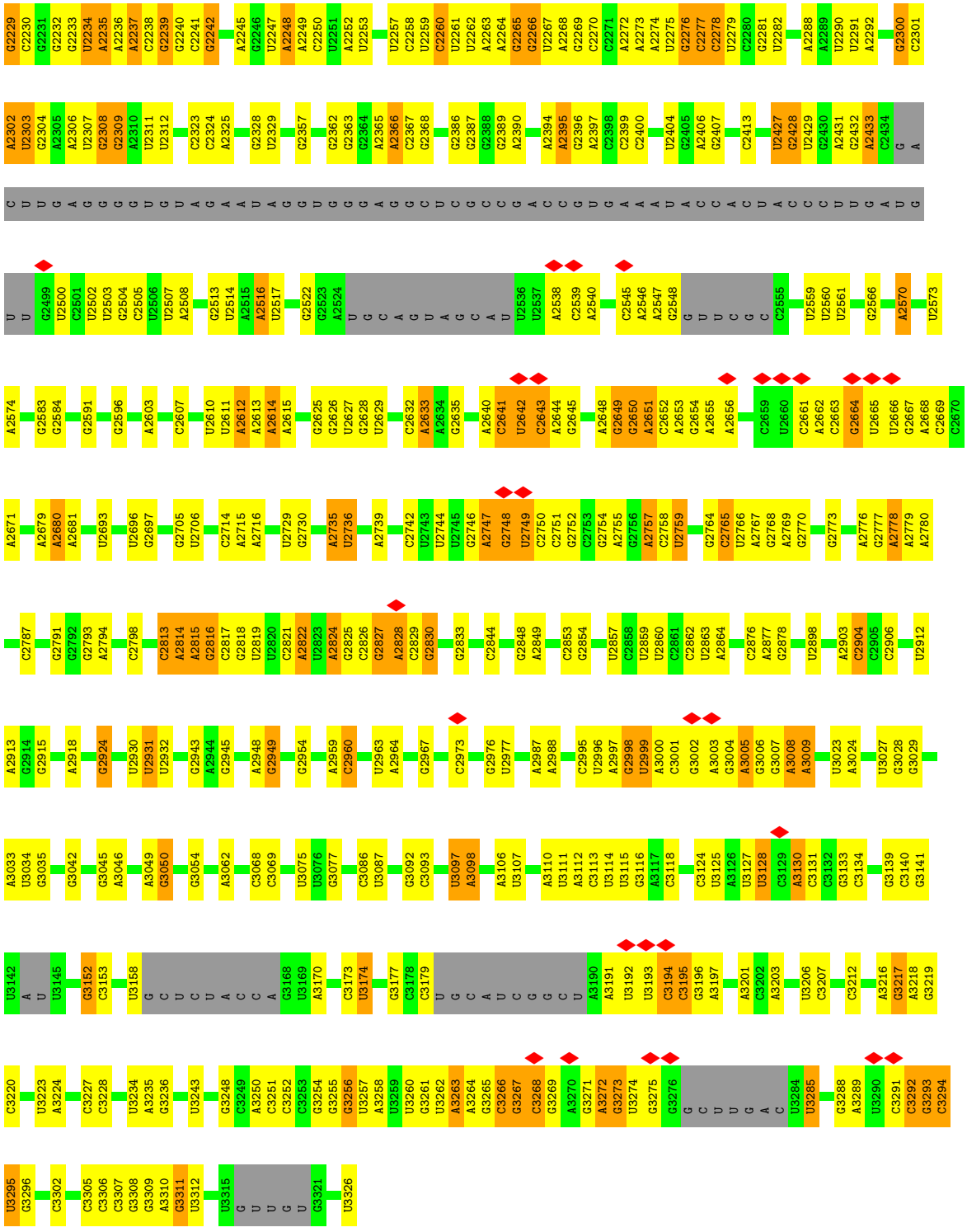
• Molecule 73: 28S ribosomal RNA

Chain L5:



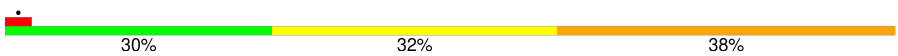


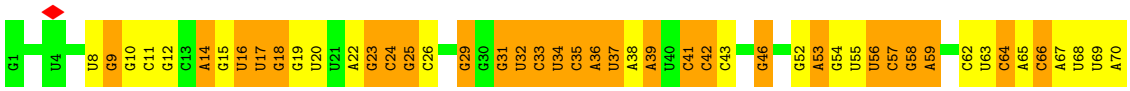




• Molecule 74: E-site tRNA

Chain S7:



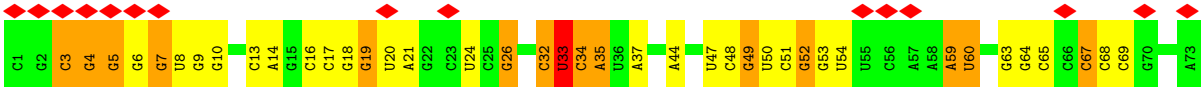




• Molecule 75: P-site tRNA

Chain S8:

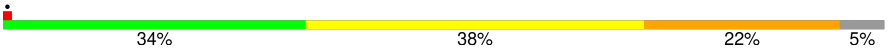


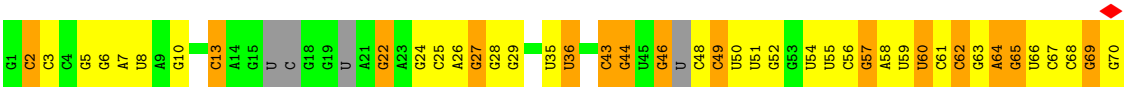




• Molecule 76: A-site tRNA

Chain S9:







• Molecule 77: mRNA fragment

Chain S6:

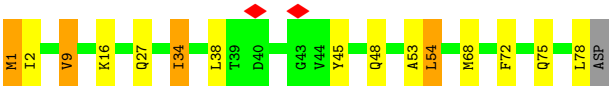




• Molecule 78: 40S ribosomal protein eS21

Chain SY:

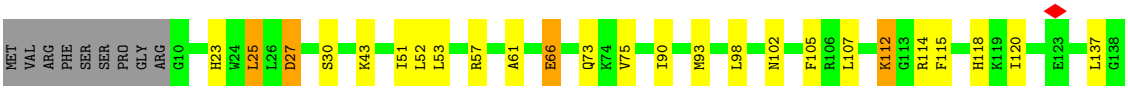


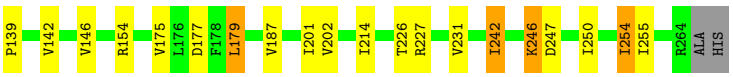


• Molecule 79: 40S ribosomal protein eS4

Chain SE:

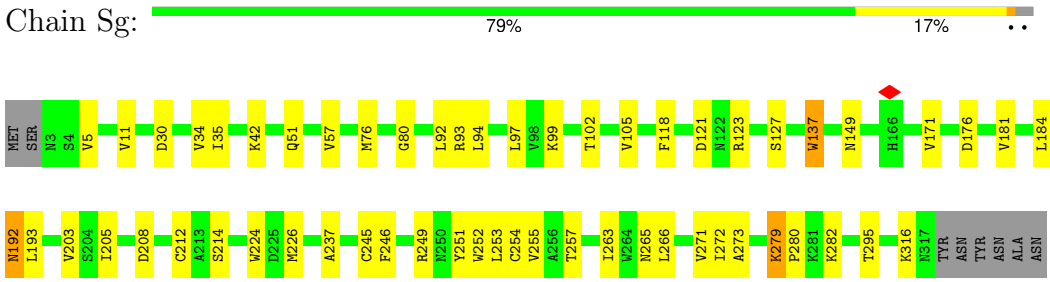






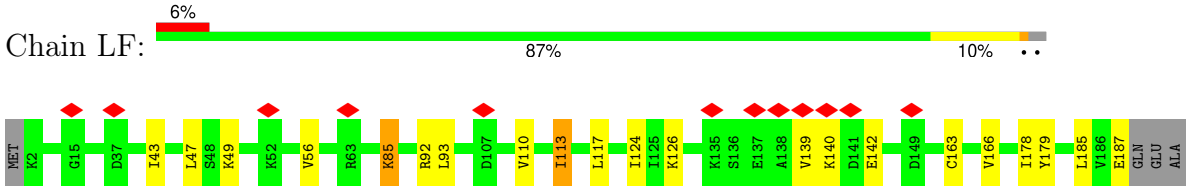
• Molecule 80: Receptor for activated C kinase 1, RACK1 protein

Chain Sg:



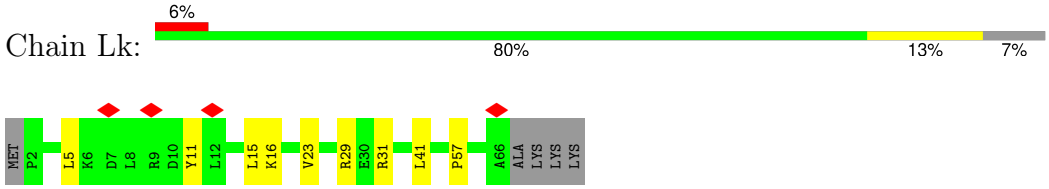
• Molecule 81: 60S ribosomal protein uL6

Chain LF:



• Molecule 82: 60S ribosomal protein eL38

Chain Lk:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	26467	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	42	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	30.107	Depositor
Minimum map value	-2.428	Depositor
Average map value	0.586	Depositor
Map value standard deviation	1.329	Depositor
Recommended contour level	4	Depositor
Map size (Å)	369.6, 369.6, 369.6	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.825, 0.825, 0.825	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: K, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	SP	0.25	0/975	0.30	0/1304
2	SX	0.38	0/1393	0.34	0/1871
3	SU	0.27	0/1263	0.30	0/1689
4	SL	0.41	0/1106	0.38	0/1480
5	SR	0.35	0/1142	0.36	0/1535
6	SH	0.37	0/1486	0.33	0/1997
7	ST	0.25	0/1208	0.29	0/1621
8	SA	0.23	0/1711	0.28	0/2289
9	SN	0.30	0/828	0.32	0/1128
10	SJ	0.28	0/1023	0.36	0/1374
11	SI	0.20	0/1053	0.28	0/1413
12	SK	0.25	0/1436	0.31	0/1919
13	SG	0.20	0/1535	0.28	0/2037
14	SM	0.34	0/772	0.29	0/1040
15	Se	0.22	0/318	0.43	0/422
16	SS	0.41	0/422	0.36	0/564
17	Sd	0.33	0/422	0.32	0/563
18	SC	0.31	0/1475	0.31	0/1973
19	SW	0.33	0/890	0.33	0/1191
20	SB	0.20	0/1313	0.36	0/1780
21	SF	0.28	0/1164	0.34	0/1570
22	Sb	0.25	0/669	0.33	0/889
23	SV	0.35	0/624	0.36	0/829
24	SO	0.25	0/747	0.33	0/999
25	SZ	0.20	0/585	0.40	0/769
26	Sa	0.35	0/576	0.31	0/773
27	SQ	0.20	0/666	0.32	0/898
28	SD	0.22	0/947	0.32	0/1253
29	Sf	0.20	0/413	0.28	0/548
30	Sc	0.24	0/479	0.30	0/634
31	S1	0.36	0/36610	0.38	11/57011 (0.0%)
32	LM	0.23	0/1176	0.28	0/1569

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	LS	0.19	0/1477	0.24	0/1987
34	Le	0.21	0/833	0.25	0/1119
35	Lf	0.21	0/1043	0.27	0/1389
36	Lj	0.24	0/704	0.29	0/933
37	LQ	0.20	0/1453	0.29	0/1941
38	LB	0.22	0/1906	0.29	0/2559
39	LI	0.21	0/1643	0.27	0/2196
40	LJ	0.20	0/1545	0.27	0/2064
41	LX	0.19	0/1018	0.28	0/1353
42	La	0.18	0/964	0.23	0/1278
43	LD	0.19	0/2556	0.28	0/3426
44	LP	0.20	0/2335	0.36	0/3126
45	LZ	0.18	0/1128	0.23	0/1504
46	LU	0.20	0/1416	0.27	0/1895
47	LH	0.18	0/1850	0.25	0/2486
48	LC	0.22	0/3082	0.31	0/4143
49	LL	0.17	0/1030	0.25	0/1381
50	LK	0.21	0/980	0.31	0/1322
51	LW	0.20	0/960	0.26	0/1289
52	Li	0.19	0/836	0.27	0/1112
53	Lm	0.18	0/412	0.35	0/547
54	LT	0.21	0/1221	0.25	0/1637
55	Lo	0.21	0/786	0.25	0/1034
56	Ll	0.21	0/445	0.23	0/591
57	LR	0.20	0/1405	0.27	0/1859
58	LE	0.17	0/1276	0.30	0/1698
59	LO	0.18	0/1691	0.25	0/2276
60	LN	0.24	0/1690	0.29	0/2252
61	Lg	0.23	0/901	0.31	0/1203
62	Lc	0.20	0/1785	0.28	0/2385
63	LV	0.15	0/813	0.26	0/1090
64	Ld	0.20	0/716	0.34	0/961
65	Lp	0.22	0/706	0.32	0/941
66	Lb	0.20	0/424	0.25	0/557
67	Lh	0.22	0/826	0.27	0/1100
68	LY	0.20	0/523	0.29	0/698
69	LG	0.16	0/1243	0.25	0/1665
70	Ln	0.29	0/354	0.34	0/458
71	L3	0.24	0/2918	0.35	0/4549
72	L4	0.25	0/3444	0.36	2/5357 (0.0%)
73	L5	0.25	0/68607	0.35	20/106896 (0.0%)
74	S7	0.16	0/1754	0.29	0/2732
75	S8	0.25	0/1810	0.44	2/2821 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
76	S9	0.20	0/1708	0.35	0/2654
77	S6	0.26	0/251	0.39	0/387
78	SY	0.22	0/607	0.29	0/818
79	SE	0.23	0/2074	0.35	0/2794
80	Sg	0.29	0/2484	0.33	0/3377
81	LF	0.16	0/1488	0.27	0/2005
82	Lk	0.18	0/532	0.27	0/716
All	All	0.27	0/200080	0.34	35/293493 (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
4	SL	0	1
10	SJ	0	1
20	SB	0	1
38	LB	0	1
48	LC	0	2
58	LE	0	1
60	LN	0	1
61	Lg	0	1
All	All	0	9

There are no bond length outliers.

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
31	S1	1506	G	OP2-P-O3'	-11.66	73.02	108.00
73	L5	916	G	OP2-P-O3'	-11.40	73.79	108.00
73	L5	660	C	OP2-P-O3'	-11.28	74.17	108.00
31	S1	1195	G	OP1-P-O3'	-11.07	74.79	108.00
72	L4	42	G	OP1-P-O3'	-11.07	74.80	108.00

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
38	LB	196	TRP	Peptide
48	LC	17	LEU	Peptide

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Mol	Chain	Res	Type	Group
20	SB	150	LEU	Peptide
10	SJ	28	ARG	Peptide
4	SL	46	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	SP	959	0	1019	5	0
2	SX	1365	0	1393	15	0
3	SU	1237	0	1306	5	0
4	SL	1090	0	1158	11	0
5	SR	1128	0	1173	15	0
6	SH	1466	0	1522	14	0
7	ST	1182	0	1250	9	0
8	SA	1687	0	1791	16	0
9	SN	802	0	812	12	0
10	SJ	1004	0	1039	15	0
11	SI	1038	0	1123	6	0
12	SK	1412	0	1448	16	0
13	SG	1517	0	1647	11	0
14	SM	761	0	784	15	0
15	Se	313	0	340	6	0
16	SS	411	0	405	5	0
17	Sd	421	0	456	5	0
18	SC	1459	0	1548	21	0
19	SW	875	0	945	3	0
20	SB	1289	0	1333	31	0
21	SF	1141	0	1184	18	0
22	Sb	661	0	707	8	0
23	SV	616	0	668	3	0
24	SO	739	0	771	7	0
25	SZ	582	0	636	10	0
26	Sa	569	0	596	4	0
27	SQ	660	0	697	10	0
28	SD	935	0	987	12	0
29	Sf	407	0	427	3	0
30	Sc	474	0	499	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	S1	32741	0	16498	399	0
32	LM	1146	0	1180	8	0
33	LS	1445	0	1510	6	0
34	Le	818	0	867	1	0
35	Lf	1026	0	1108	6	0
36	Lj	689	0	702	0	0
37	LQ	1432	0	1554	9	0
38	LB	1868	0	1922	39	0
39	LI	1610	0	1717	13	0
40	LJ	1522	0	1638	9	0
41	LX	1003	0	1066	9	0
42	La	957	0	1079	1	0
43	LD	2521	0	2686	26	0
44	LP	2293	0	2323	89	0
45	LZ	1114	0	1206	6	0
46	LU	1392	0	1457	4	0
47	LH	1816	0	1926	10	0
48	LC	3009	0	3120	29	0
49	LL	1016	0	1099	8	0
50	LK	964	0	1024	3	0
51	LW	946	0	1009	2	0
52	Li	827	0	902	9	0
53	Lm	407	0	445	2	0
54	LT	1196	0	1257	9	0
55	Lo	776	0	852	2	0
56	Ll	435	0	479	4	0
57	LR	1387	0	1494	4	0
58	LE	1259	0	1307	30	0
59	LO	1648	0	1689	15	0
60	LN	1656	0	1754	15	0
61	Lg	879	0	915	8	0
62	Lc	1751	0	1867	14	0
63	LV	799	0	836	5	0
64	Ld	706	0	726	12	0
65	Lp	695	0	730	3	0
66	Lb	417	0	451	2	0
67	Lh	816	0	875	4	0
68	LY	509	0	531	2	0
69	LG	1223	0	1311	10	0
70	Ln	349	0	393	0	0
71	L3	2610	0	1323	93	0
72	L4	3082	0	1565	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
73	L5	61352	0	30940	685	0
74	S7	1571	0	797	38	0
75	S8	1620	0	827	34	0
76	S9	1532	0	782	44	0
77	S6	227	0	114	1	0
78	SY	600	0	590	12	0
79	SE	2034	0	2114	24	0
80	Sg	2429	0	2400	30	0
81	LF	1469	0	1561	9	0
82	Lk	525	0	568	7	0
83	L3	1	0	0	0	0
83	L5	122	0	0	0	0
83	S1	1	0	0	0	0
84	L5	12	0	0	0	0
All	All	186450	0	138750	1897	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 6.

The worst 5 of 1897 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)
31:S1:518:G:N2	31:S1:559:C:C2	2.21	1.07
73:L5:1104:U:O2	73:L5:1106:A:N7	1.92	1.02
73:L5:3000:A:N6	73:L5:3007:G:H21	1.57	1.01
73:L5:1960:G:O6	73:L5:2103:U:O2	1.77	1.00
73:L5:2999:U:O4	73:L5:3008:A:N7	1.93	1.00

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	SP	119/145 (82%)	110 (92%)	9 (8%)	0	100	100
2	SX	165/174 (95%)	152 (92%)	13 (8%)	0	100	100
3	SU	149/156 (96%)	135 (91%)	14 (9%)	0	100	100
4	SL	137/149 (92%)	125 (91%)	10 (7%)	2 (2%)	8	32
5	SR	139/154 (90%)	129 (93%)	9 (6%)	1 (1%)	18	49
6	SH	183/192 (95%)	169 (92%)	14 (8%)	0	100	100
7	ST	143/151 (95%)	142 (99%)	1 (1%)	0	100	100
8	SA	204/264 (77%)	195 (96%)	9 (4%)	0	100	100
9	SN	94/113 (83%)	87 (93%)	7 (7%)	0	100	100
10	SJ	124/130 (95%)	110 (89%)	14 (11%)	0	100	100
11	SI	122/194 (63%)	115 (94%)	6 (5%)	1 (1%)	16	47
12	SK	171/192 (89%)	160 (94%)	11 (6%)	0	100	100
13	SG	178/239 (74%)	170 (96%)	8 (4%)	0	100	100
14	SM	94/120 (78%)	85 (90%)	9 (10%)	0	100	100
15	Se	36/61 (59%)	31 (86%)	4 (11%)	1 (3%)	4	20
16	SS	48/66 (73%)	44 (92%)	4 (8%)	0	100	100
17	Sd	50/67 (75%)	46 (92%)	4 (8%)	0	100	100
18	SC	179/223 (80%)	164 (92%)	15 (8%)	0	100	100
19	SW	104/149 (70%)	95 (91%)	9 (9%)	0	100	100
20	SB	157/274 (57%)	139 (88%)	18 (12%)	0	100	100
21	SF	148/196 (76%)	141 (95%)	7 (5%)	0	100	100
22	Sb	78/115 (68%)	71 (91%)	7 (9%)	0	100	100
23	SV	73/134 (54%)	71 (97%)	2 (3%)	0	100	100
24	SO	90/157 (57%)	78 (87%)	10 (11%)	2 (2%)	5	24
25	SZ	63/135 (47%)	56 (89%)	6 (10%)	1 (2%)	7	30
26	Sa	69/104 (66%)	65 (94%)	4 (6%)	0	100	100
27	SQ	83/135 (62%)	80 (96%)	3 (4%)	0	100	100
28	SD	98/184 (53%)	92 (94%)	6 (6%)	0	100	100
29	Sf	48/77 (62%)	42 (88%)	6 (12%)	0	100	100
30	Sc	54/82 (66%)	48 (89%)	6 (11%)	0	100	100
32	LM	142/147 (97%)	136 (96%)	6 (4%)	0	100	100
33	LS	177/188 (94%)	170 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	Le	94/117 (80%)	93 (99%)	1 (1%)	0	100	100
35	Lf	123/132 (93%)	117 (95%)	6 (5%)	0	100	100
36	Lj	85/98 (87%)	79 (93%)	6 (7%)	0	100	100
37	LQ	182/222 (82%)	168 (92%)	14 (8%)	0	100	100
38	LB	243/257 (95%)	223 (92%)	20 (8%)	0	100	100
39	LI	196/202 (97%)	190 (97%)	6 (3%)	0	100	100
40	LJ	191/203 (94%)	184 (96%)	7 (4%)	0	100	100
41	LX	119/137 (87%)	116 (98%)	3 (2%)	0	100	100
42	La	111/123 (90%)	107 (96%)	4 (4%)	0	100	100
43	LD	319/360 (89%)	295 (92%)	24 (8%)	0	100	100
44	LP	277/306 (90%)	257 (93%)	20 (7%)	0	100	100
45	LZ	133/146 (91%)	127 (96%)	6 (4%)	0	100	100
46	LU	168/194 (87%)	159 (95%)	9 (5%)	0	100	100
47	LH	220/285 (77%)	214 (97%)	6 (3%)	0	100	100
48	LC	373/395 (94%)	349 (94%)	23 (6%)	1 (0%)	36	67
49	LL	126/133 (95%)	119 (94%)	7 (6%)	0	100	100
50	LK	126/139 (91%)	115 (91%)	11 (9%)	0	100	100
51	LW	114/153 (74%)	111 (97%)	3 (3%)	0	100	100
52	Li	101/116 (87%)	98 (97%)	3 (3%)	0	100	100
53	Lm	48/55 (87%)	44 (92%)	4 (8%)	0	100	100
54	LT	146/160 (91%)	135 (92%)	11 (8%)	0	100	100
55	Lo	94/105 (90%)	89 (95%)	5 (5%)	0	100	100
56	Ll	47/59 (80%)	46 (98%)	1 (2%)	0	100	100
57	LR	168/194 (87%)	161 (96%)	7 (4%)	0	100	100
58	LE	151/171 (88%)	137 (91%)	14 (9%)	0	100	100
59	LO	201/227 (88%)	190 (94%)	11 (6%)	0	100	100
60	LN	195/204 (96%)	187 (96%)	8 (4%)	0	100	100
61	Lg	106/115 (92%)	97 (92%)	7 (7%)	2 (2%)	6	27
62	Lc	212/259 (82%)	206 (97%)	6 (3%)	0	100	100
63	LV	95/122 (78%)	90 (95%)	5 (5%)	0	100	100
64	Ld	91/108 (84%)	86 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
65	Lp	86/94 (92%)	77 (90%)	9 (10%)	0	100	100
66	Lb	49/59 (83%)	47 (96%)	2 (4%)	0	100	100
67	Lh	98/150 (65%)	92 (94%)	6 (6%)	0	100	100
68	LY	59/156 (38%)	58 (98%)	1 (2%)	0	100	100
69	LG	151/212 (71%)	143 (95%)	8 (5%)	0	100	100
70	Ln	36/39 (92%)	34 (94%)	2 (6%)	0	100	100
78	SY	76/79 (96%)	70 (92%)	6 (8%)	0	100	100
79	SE	253/266 (95%)	236 (93%)	17 (7%)	0	100	100
80	Sg	313/323 (97%)	289 (92%)	24 (8%)	0	100	100
81	LF	184/190 (97%)	178 (97%)	6 (3%)	0	100	100
82	Lk	63/70 (90%)	61 (97%)	2 (3%)	0	100	100
All	All	9942/12002 (83%)	9327 (94%)	604 (6%)	11 (0%)	49	78

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	SR	36	ARG
11	SI	134	ALA
15	Se	20	PRO
25	SZ	53	LYS
48	LC	18	PRO

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	SP	99/118 (84%)	92 (93%)	7 (7%)	13	41
2	SX	146/151 (97%)	143 (98%)	3 (2%)	47	71
3	SU	137/140 (98%)	131 (96%)	6 (4%)	25	56
4	SL	113/122 (93%)	108 (96%)	5 (4%)	25	56
5	SR	122/131 (93%)	118 (97%)	4 (3%)	33	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
6	SH	158/162 (98%)	156 (99%)	2 (1%)	61 77
7	ST	128/132 (97%)	123 (96%)	5 (4%)	28 60
8	SA	191/237 (81%)	188 (98%)	3 (2%)	55 75
9	SN	92/105 (88%)	92 (100%)	0	100 100
10	SJ	110/114 (96%)	104 (94%)	6 (6%)	19 50
11	SI	115/173 (66%)	113 (98%)	2 (2%)	53 74
12	SK	153/164 (93%)	142 (93%)	11 (7%)	13 40
13	SG	166/208 (80%)	163 (98%)	3 (2%)	51 73
14	SM	89/108 (82%)	85 (96%)	4 (4%)	24 56
15	Se	32/48 (67%)	31 (97%)	1 (3%)	35 64
16	SS	44/58 (76%)	41 (93%)	3 (7%)	14 42
17	Sd	45/54 (83%)	43 (96%)	2 (4%)	25 56
18	SC	156/186 (84%)	150 (96%)	6 (4%)	29 60
19	SW	96/132 (73%)	95 (99%)	1 (1%)	68 79
20	SB	144/238 (60%)	136 (94%)	8 (6%)	19 49
21	SF	121/157 (77%)	113 (93%)	8 (7%)	15 43
22	Sb	73/104 (70%)	67 (92%)	6 (8%)	10 36
23	SV	65/118 (55%)	65 (100%)	0	100 100
24	SO	78/123 (63%)	74 (95%)	4 (5%)	21 52
25	SZ	61/115 (53%)	52 (85%)	9 (15%)	3 13
26	Sa	63/90 (70%)	63 (100%)	0	100 100
27	SQ	76/116 (66%)	67 (88%)	9 (12%)	5 21
28	SD	101/163 (62%)	94 (93%)	7 (7%)	14 41
29	Sf	45/68 (66%)	45 (100%)	0	100 100
30	Sc	54/73 (74%)	51 (94%)	3 (6%)	19 49
32	LM	119/121 (98%)	115 (97%)	4 (3%)	32 63
33	LS	155/164 (94%)	155 (100%)	0	100 100
34	Le	91/105 (87%)	91 (100%)	0	100 100
35	Lf	110/117 (94%)	109 (99%)	1 (1%)	70 80
36	Lj	71/78 (91%)	71 (100%)	0	100 100
37	LQ	155/184 (84%)	152 (98%)	3 (2%)	50 73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
38	LB	187/198 (94%)	183 (98%)	4 (2%)	47 71
39	LI	170/172 (99%)	169 (99%)	1 (1%)	78 83
40	LJ	161/170 (95%)	158 (98%)	3 (2%)	50 73
41	LX	113/128 (88%)	111 (98%)	2 (2%)	51 73
42	La	105/111 (95%)	104 (99%)	1 (1%)	68 79
43	LD	259/288 (90%)	251 (97%)	8 (3%)	35 64
44	LP	242/261 (93%)	233 (96%)	9 (4%)	30 61
45	LZ	123/129 (95%)	122 (99%)	1 (1%)	73 81
46	LU	146/163 (90%)	145 (99%)	1 (1%)	76 82
47	LH	195/243 (80%)	193 (99%)	2 (1%)	68 79
48	LC	330/345 (96%)	327 (99%)	3 (1%)	70 80
49	LL	107/110 (97%)	107 (100%)	0	100 100
50	LK	99/104 (95%)	97 (98%)	2 (2%)	48 72
51	LW	106/135 (78%)	106 (100%)	0	100 100
52	Li	91/100 (91%)	89 (98%)	2 (2%)	45 71
53	Lm	46/49 (94%)	42 (91%)	4 (9%)	9 34
54	LT	128/139 (92%)	127 (99%)	1 (1%)	73 81
55	Lo	85/90 (94%)	82 (96%)	3 (4%)	32 62
56	Ll	46/54 (85%)	46 (100%)	0	100 100
57	LR	144/164 (88%)	142 (99%)	2 (1%)	59 76
58	LE	136/151 (90%)	127 (93%)	9 (7%)	15 43
59	LO	171/188 (91%)	167 (98%)	4 (2%)	44 70
60	LN	171/176 (97%)	167 (98%)	4 (2%)	44 70
61	Lg	93/99 (94%)	91 (98%)	2 (2%)	45 71
62	Lc	184/228 (81%)	180 (98%)	4 (2%)	45 71
63	LV	89/111 (80%)	88 (99%)	1 (1%)	65 78
64	Ld	79/94 (84%)	77 (98%)	2 (2%)	42 69
65	Lp	70/76 (92%)	68 (97%)	2 (3%)	37 66
66	Lb	46/52 (88%)	46 (100%)	0	100 100
67	Lh	86/125 (69%)	84 (98%)	2 (2%)	44 70
68	LY	54/126 (43%)	54 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
69	LG	135/181 (75%)	131 (97%)	4 (3%)	36 65
70	Ln	34/35 (97%)	33 (97%)	1 (3%)	37 66
78	SY	67/68 (98%)	60 (90%)	7 (10%)	7 27
79	SE	226/235 (96%)	205 (91%)	21 (9%)	8 31
80	Sg	274/281 (98%)	252 (92%)	22 (8%)	11 37
81	LF	167/170 (98%)	157 (94%)	10 (6%)	17 47
82	Lk	58/62 (94%)	57 (98%)	1 (2%)	53 74
All	All	8797/10288 (86%)	8516 (97%)	281 (3%)	35 64

5 of 281 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
79	SE	66	GLU
79	SE	146	VAL
80	Sg	184	LEU
24	SO	97	THR
22	Sb	61	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 52 such sidechains are listed below:

Mol	Chain	Res	Type
39	LI	117	GLN
47	LH	81	GLN
67	Lh	33	GLN
41	LX	71	GLN
44	LP	190	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	S1	1517/1728 (87%)	366 (24%)	14 (0%)
71	L3	121/122 (99%)	39 (32%)	4 (3%)
72	L4	142/159 (89%)	23 (16%)	1 (0%)
73	L5	2854/3326 (85%)	635 (22%)	31 (1%)
74	S7	73/74 (98%)	38 (52%)	1 (1%)
75	S8	75/76 (98%)	32 (42%)	3 (4%)
76	S9	68/76 (89%)	27 (39%)	1 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
77	S6	10/11 (90%)	2 (20%)	0
All	All	4860/5572 (87%)	1162 (23%)	55 (1%)

5 of 1162 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
31	S1	4	C
31	S1	17	C
31	S1	25	C
31	S1	30	G
31	S1	31	C

5 of 55 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
73	L5	1088	G
73	L5	2106	A
76	S9	51	U
73	L5	3266	C
73	L5	1735	A

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 136 ligands modelled in this entry, 136 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

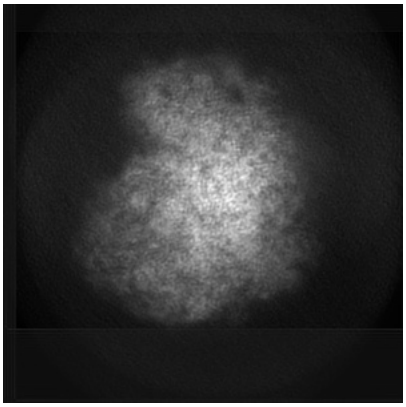
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-73602. These allow visual inspection of the internal detail of the map and identification of artifacts.

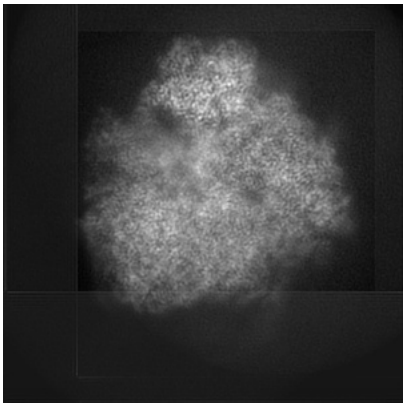
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

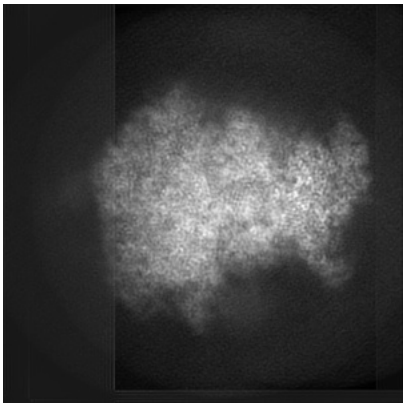
6.1.1 Primary map



X



Y

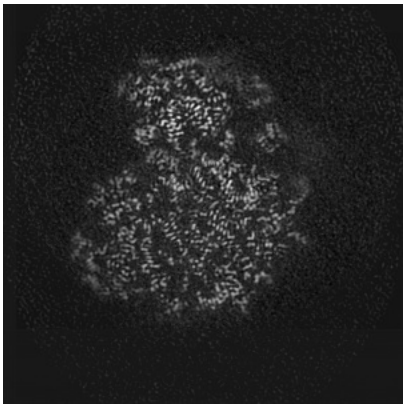


Z

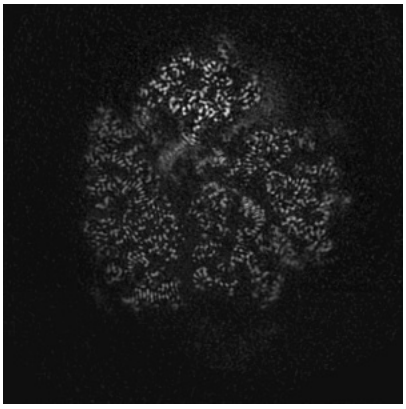
The images above show the map projected in three orthogonal directions.

6.2 Central slices

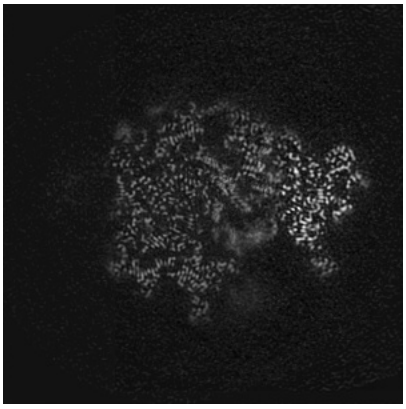
6.2.1 Primary map



X Index: 224



Y Index: 224

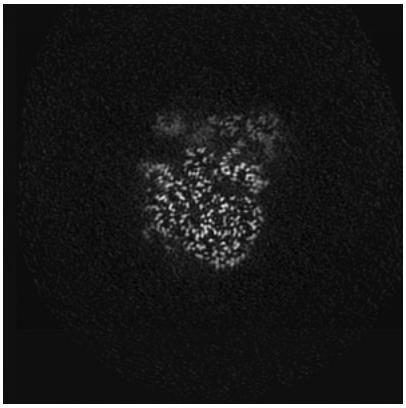


Z Index: 224

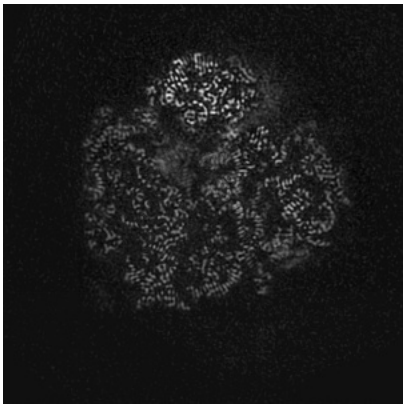
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

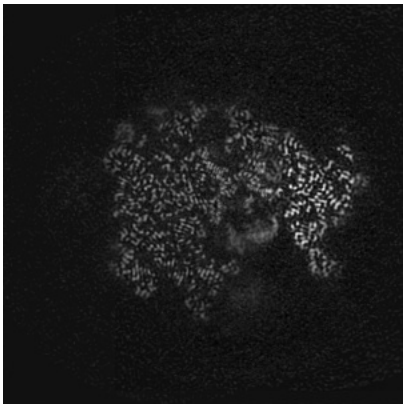
6.3.1 Primary map



X Index: 340



Y Index: 216

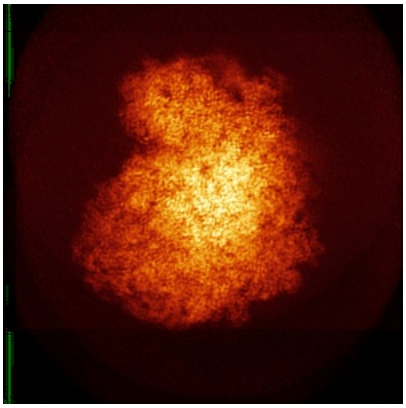


Z Index: 227

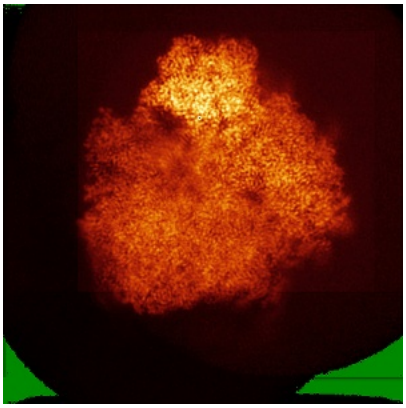
The images above show the largest variance slices of the map in three orthogonal directions.

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

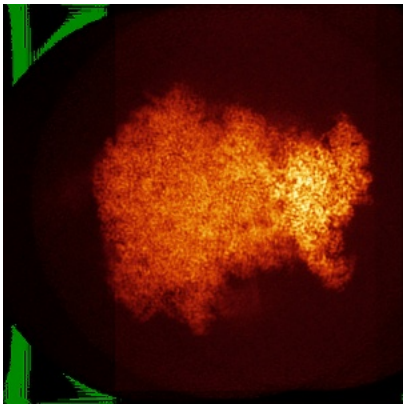
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 4.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

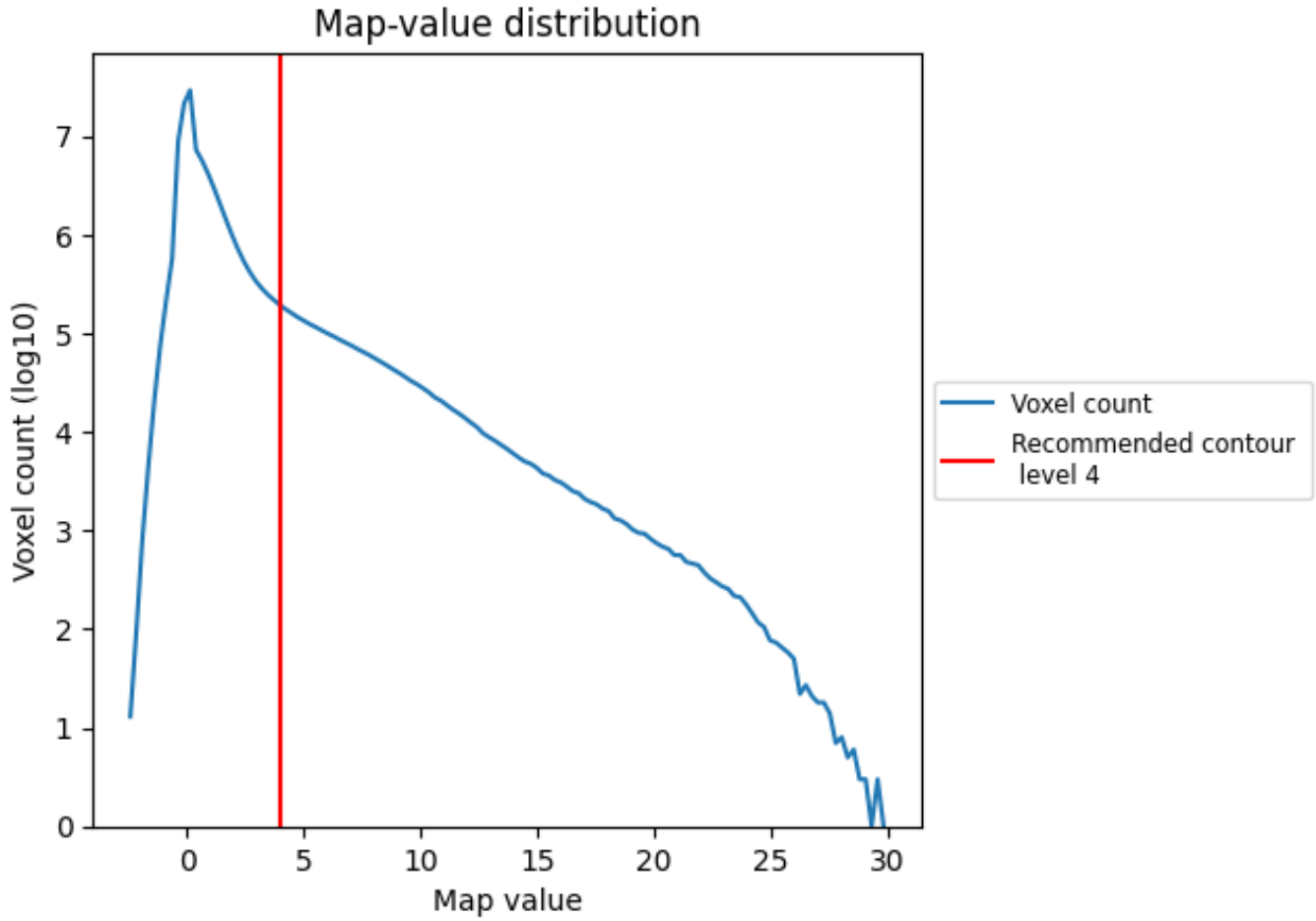
6.6 Mask visualisation (i)

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

7 Map analysis

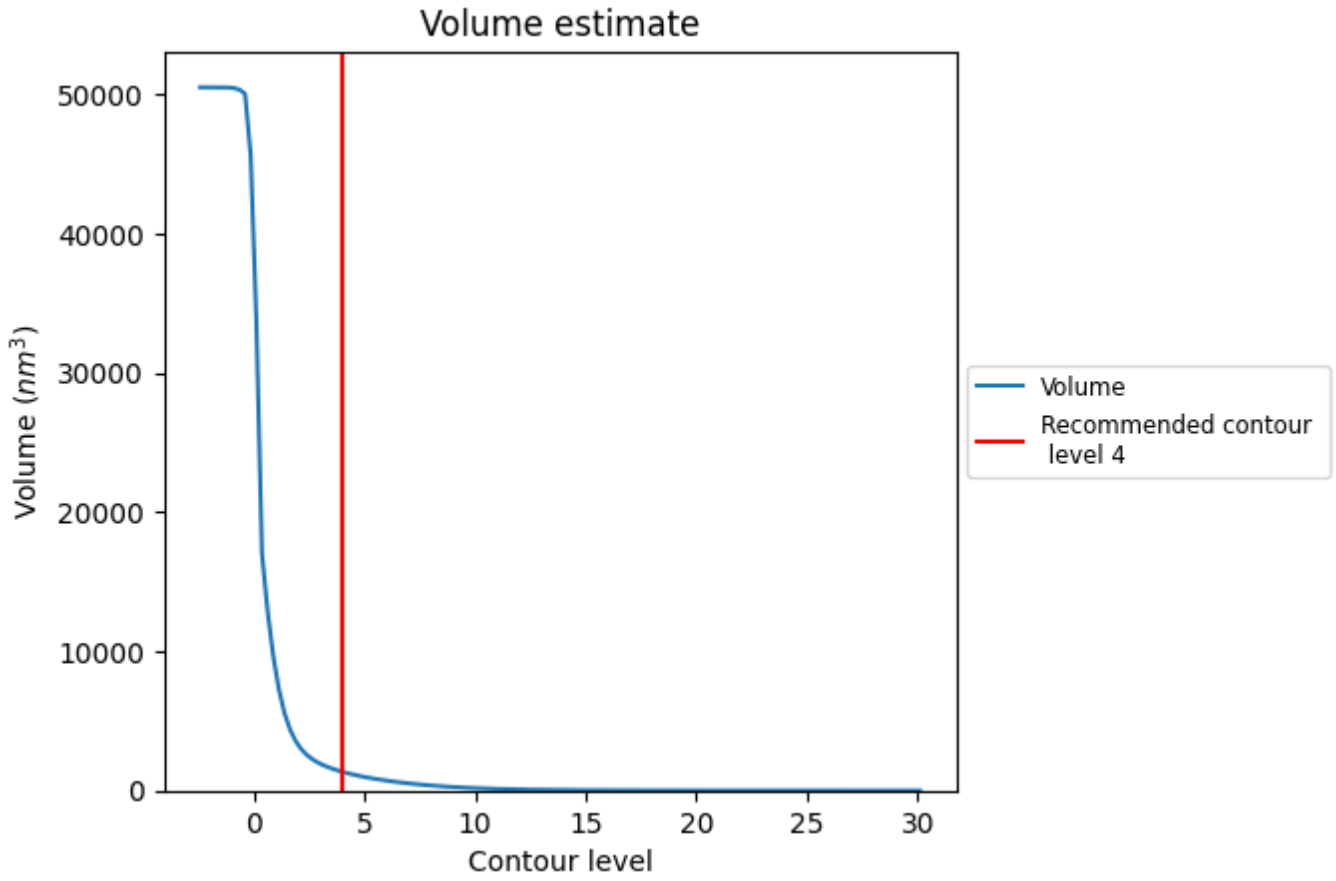
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

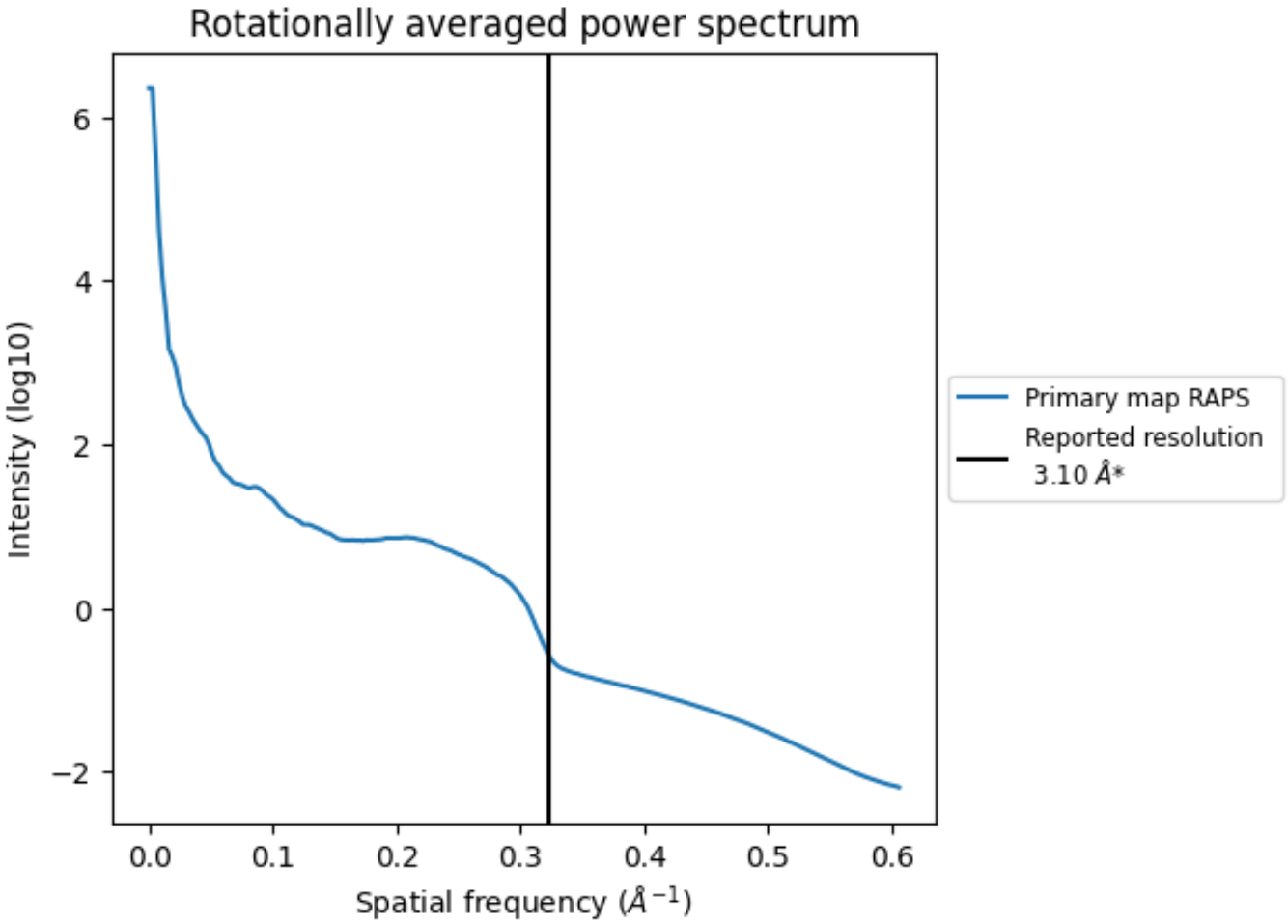
7.2 Volume estimate (i)



The volume at the recommended contour level is 1345 nm^3; this corresponds to an approximate mass of 1215 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.323 Å^{-1}

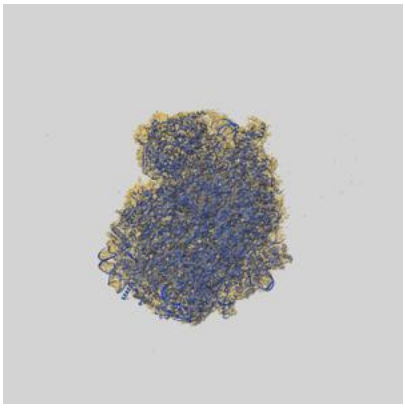
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

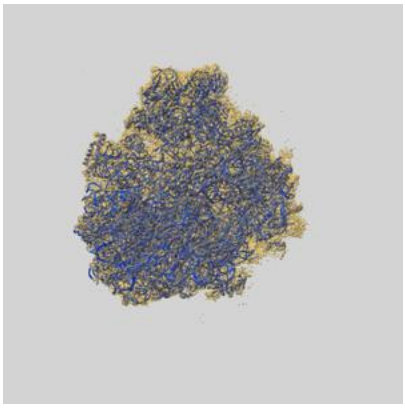
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-73602 and PDB model 9YXB. Per-residue inclusion information can be found in section 3 on page 23.

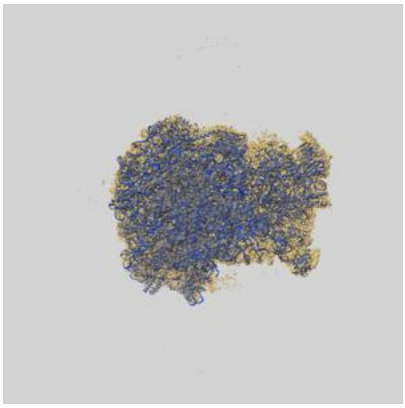
9.1 Map-model overlay



X



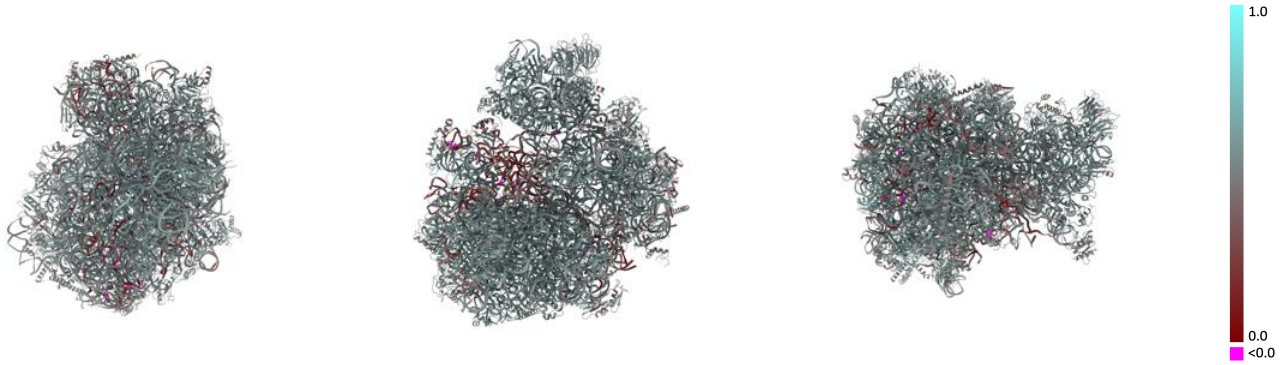
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 4.0 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.

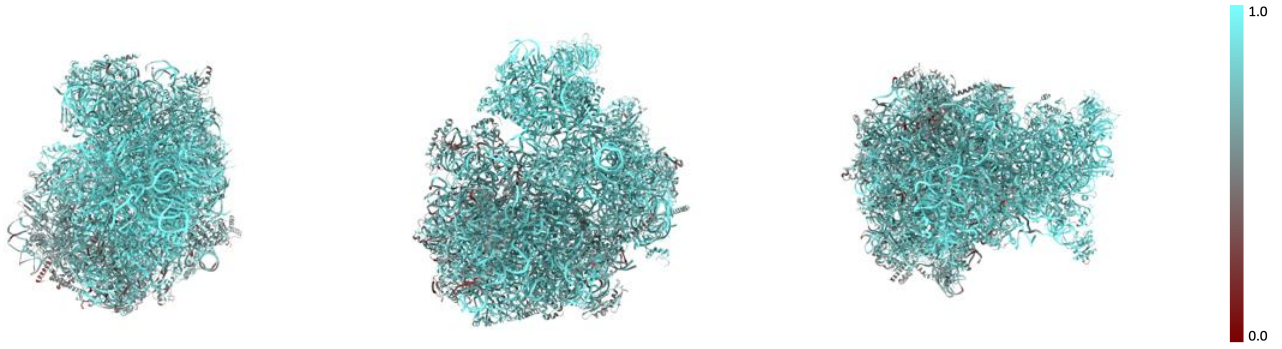
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

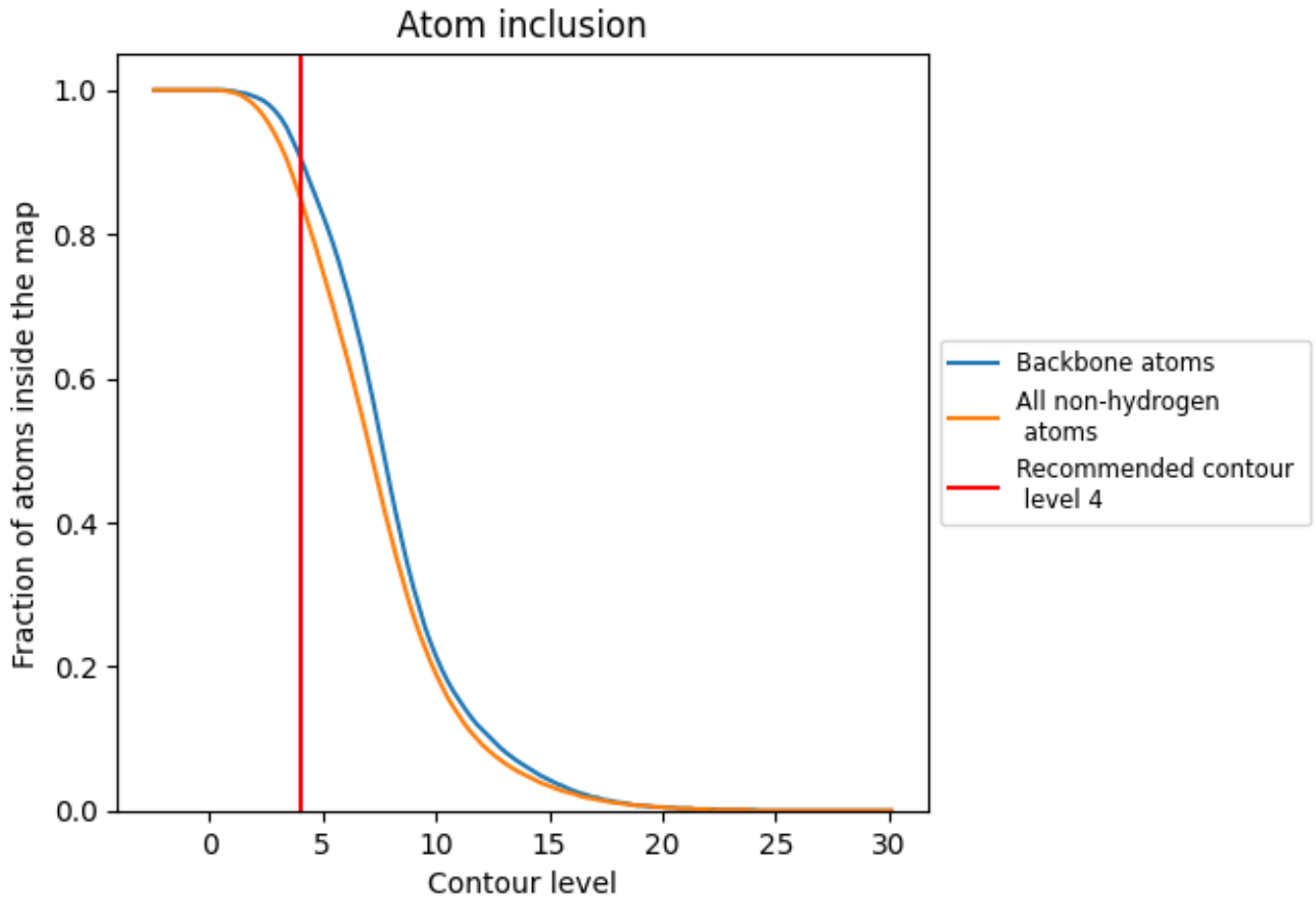
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (4).

9.4 Atom inclusion (i)



At the recommended contour level, 91% of all backbone atoms, 85% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8520	0.5240
L3	0.8390	0.4830
L4	0.9180	0.5610
L5	0.8700	0.5180
LB	0.8420	0.5540
LC	0.8100	0.5730
LD	0.6210	0.5390
LE	0.7170	0.4680
LF	0.6560	0.5330
LG	0.5440	0.5120
LH	0.6590	0.5370
LI	0.7490	0.5600
LJ	0.7490	0.5540
LK	0.8100	0.5310
LL	0.6300	0.5360
LM	0.8090	0.5800
LN	0.8300	0.5830
LO	0.7120	0.5390
LP	0.6650	0.4930
LQ	0.7590	0.5640
LR	0.7350	0.5360
LS	0.6920	0.5500
LT	0.7110	0.5520
LU	0.7490	0.5640
LV	0.6130	0.4900
LW	0.7230	0.5490
LX	0.7640	0.5600
LY	0.8000	0.5430
LZ	0.6390	0.5390
La	0.6850	0.5400
Lb	0.7770	0.5610
Lc	0.7160	0.5530
Ld	0.7440	0.5150
Le	0.7940	0.5700
Lf	0.7590	0.5690



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Chain	Atom inclusion	Q-score
Lg	0.7990	0.5750
Lh	0.7980	0.5760
Li	0.7300	0.5490
Lj	0.8500	0.5810
Lk	0.6690	0.5330
Ll	0.7850	0.5710
Lm	0.6730	0.5380
Ln	0.8910	0.5520
Lo	0.7850	0.5760
Lp	0.8640	0.5370
S1	0.9550	0.5270
S6	1.0000	0.4930
S7	0.8950	0.2840
S8	0.6840	0.2440
S9	0.9120	0.3180
SA	0.8320	0.5280
SB	0.8000	0.4920
SC	0.9420	0.5290
SD	0.8350	0.4890
SE	0.8290	0.5250
SF	0.9260	0.5390
SG	0.7980	0.5080
SH	0.9680	0.5620
SI	0.7200	0.5110
SJ	0.8730	0.5490
SK	0.8850	0.5450
SL	0.9700	0.5700
SM	0.9300	0.5290
SN	0.9570	0.5410
SO	0.8730	0.5310
SP	0.8670	0.5530
SQ	0.8260	0.4760
SR	0.9530	0.5520
SS	0.9920	0.5820
ST	0.8580	0.5430
SU	0.8840	0.5620
SV	0.9310	0.5210
SW	0.9350	0.5500
SX	0.9590	0.5640
SY	0.7910	0.5260
SZ	0.8100	0.4960
Sa	0.9360	0.5490

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Chain	Atom inclusion	Q-score
Sb	0.9400	0.5570
Sc	0.8280	0.5310
Sd	0.9630	0.5740
Se	0.8120	0.4830
Sf	0.8500	0.5060
Sg	0.9100	0.5300