



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 09:25 PM UTC

PDB ID : 9GGR / pdb_00009ggr
EMDB ID : EMD-51340
Title : Structure of the HrpA-bound E. coli disome, Class II
Authors : Esser, H.F.; Berninghausen, O.; Becker, T.; Beckmann, R.
Deposited on : 2024-08-14
Resolution : 3.20 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

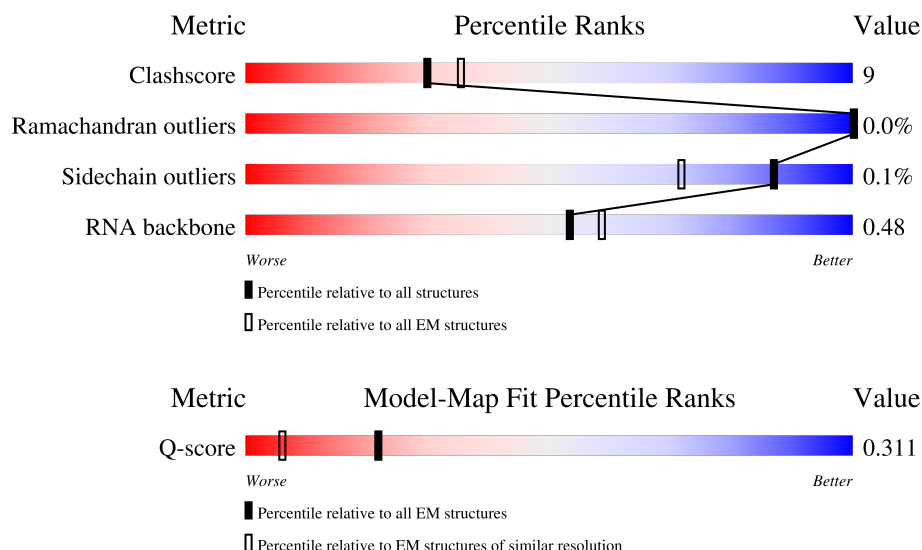
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	0	1542	
1	AA	1542	
2	1	241	

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Mol	Chain	Length	Quality of chain
2	AB	241	
3	2	233	
3	AC	233	
4	3	206	
4	AD	206	
5	4	167	
5	AE	167	
6	5	135	
6	AF	135	
7	6	179	
7	AG	179	
8	7	130	
8	AH	130	
9	8	130	
9	AI	130	
10	9	103	
10	AJ	103	
11	A	76	
12	A1	71	
12	v	71	
13	A2	1300	
14	A3	77	
15	AK	234	
15	C	234	
16	AL	118	

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Mol	Chain	Length	Quality of chain
16	F	118	
17	AM	101	
17	G	101	
18	AN	89	
18	H	89	
19	AO	82	
19	I	82	
20	AP	84	
20	J	84	
21	AQ	75	
21	K	75	
22	AR	92	
22	t	92	
23	AS	87	
23	u	87	
24	AT	70	
24	L	70	
25	AU	76	
26	AV	2903	
26	N	2903	
27	AW	120	
27	O	120	
28	AX	273	
28	P	273	
29	AY	209	

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Mol	Chain	Length	Quality of chain
29	Q	209	
30	AZ	201	
30	R	201	
31	Aa	179	
31	S	179	
32	Ab	177	
32	T	177	
33	Ac	149	
33	U	149	
34	Ad	142	
34	V	142	
35	Ae	142	
35	W	142	
36	Af	123	
36	X	123	
37	Ag	144	
37	Y	144	
38	Ah	136	
38	Z	136	
39	Ai	127	
39	a	127	
40	Aj	117	
40	b	117	
41	Ak	115	
41	c	115	

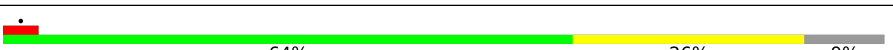
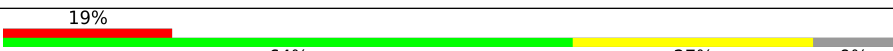
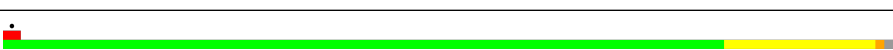
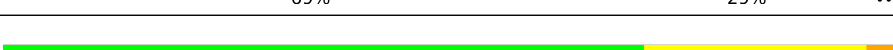
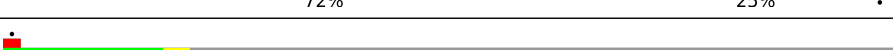
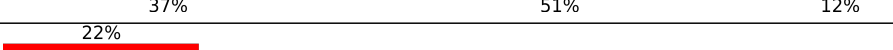
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Mol	Chain	Length	Quality of chain
42	Al	118	
42	d	118	
43	Am	103	
43	e	103	
44	An	110	
44	f	110	
45	Ao	100	
45	g	100	
46	Ap	104	
46	h	104	
47	Aq	94	
47	i	94	
48	Ar	85	
48	j	85	
49	As	78	
49	k	78	
50	At	63	
50	l	63	
51	Au	59	
51	m	59	
52	Av	57	
52	n	57	
53	Aw	55	
53	o	55	
54	Ax	46	

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Mol	Chain	Length	Quality of chain
54	p	46	
55	Ay	65	
55	q	65	
56	Az	38	
56	r	38	
57	B	1326	
58	D	129	
58	y	129	
59	E	124	
59	z	124	
60	M	75	
61	s	179	
62	w	57	
63	x	165	

2 Entry composition [i](#)

There are 63 unique types of molecules in this entry. The entry contains 309783 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	1533	Total	C	N	O	P	0	0
			32895	14671	6036	10655	1533		
1	AA	1539	Total	C	N	O	P	0	0
			33015	14725	6052	10699	1539		

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		
2	AB	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 3 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		
3	AC	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 4 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		
4	AD	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 5 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		
5	AE	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

- Molecule 6 is a protein called Small ribosomal subunit protein bS6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	100	Total	C	N	O	S	0	0
			817	515	148	148	6		
6	AF	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 7 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		
7	AG	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 8 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	129	Total	C	N	O	S	0	0
			979	616	173	184	6		
8	AH	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 9 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	8	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		
9	AI	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 10 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	9	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 11 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A	76	Total	C	N	O	P	0	0
			1622	723	290	533	76		

- Molecule 12 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	A1	66	Total	C	N	O	S	0	0
			551	340	118	92	1		
12	v	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 13 is a protein called ATP-dependent RNA helicase HrpA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	A2	290	Total	C	N	O	S	0	0
			2340	1494	413	424	9		

- Molecule 14 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	A3	77	Total	C	N	O	P	0	0
			1638	732	291	538	77		

- Molecule 15 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AK	134	Total	C	N	O	S	0	0
			1026	645	186	193	2		
15	C	134	Total	C	N	O	S	0	0
			1026	645	186	193	2		

- Molecule 16 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AL	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
16	F	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 17 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AM	96	Total	C	N	O	S	0	0
			774	483	160	128	3		
17	G	98	Total	C	N	O	S	0	0
			791	490	161	137	3		

- Molecule 18 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AN	88	Total	C	N	O	S	0	0
			710	437	143	129	1		
18	H	87	Total	C	N	O	S	0	0
			702	433	140	128	1		

- Molecule 19 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AO	82	Total	C	N	O	S	0	0
			649	406	128	114	1		
19	I	82	Total	C	N	O	S	0	0
			648	406	128	113	1		

- Molecule 20 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AP	80	Total	C	N	O	S	0	0
			648	411	121	113	3		
20	J	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 21 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AQ	66	Total	C	N	O	S	0	0
			544	345	102	96	1		
21	K	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 22 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AR	79	Total	C	N	O	S	0	0
			637	408	120	107	2		
22	t	77	Total	C	N	O	S	0	0
			620	399	115	104	2		

- Molecule 23 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AS	85	Total	C	N	O	S	0	0
			665	411	137	114	3		
23	u	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 24 is a protein called Large ribosomal subunit protein bL31A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AT	64	Total	C	N	O	S	0	0
			511	317	97	91	6		
24	L	62	Total	C	N	O	S	0	0
			499	309	95	89	6		

- Molecule 25 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AU	76	Total	C	N	O	P	0	0
			1625	724	293	532	76		

- Molecule 26 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AV	2897	Total	C	N	O	P	0	0
			62195	27745	11446	20107	2897		
26	N	2897	Total	C	N	O	P	0	0
			62195	27745	11446	20107	2897		

- Molecule 27 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AW	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

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Mol	Chain	Residues	Atoms					AltConf	Trace
27	O	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 28 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AX	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		
28	P	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 29 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AY	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		
29	Q	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 30 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AZ	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		
30	R	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 31 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Aa	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		
31	S	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 32 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ab	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		
32	T	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 33 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ac	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		
33	U	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 34 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ad	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		
34	V	134	Total	C	N	O	S	0	0
			979	619	169	185	6		

- Molecule 35 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ae	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		
35	W	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 36 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Af	122	Total	C	N	O	S	0	0
			938	587	180	165	6		
36	X	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 37 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ag	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		
37	Y	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 38 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ah	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		
38	Z	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 39 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Ai	118	Total	C	N	O	S	0	0
			945	585	194	161	5		
39	a	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 40 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Aj	116	Total	C	N	O		0	0
			892	552	178	162			
40	b	116	Total	C	N	O		0	0
			892	552	178	162			

- Molecule 41 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Ak	114	Total	C	N	O	S	0	0
			917	574	179	163	1		
41	c	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 42 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Al	117	Total	C	N	O		0	0
			947	604	192	151			
42	d	117	Total	C	N	O		0	0
			947	604	192	151			

- Molecule 43 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Am	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
43	e	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 44 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	An	110	Total	C	N	O	S	0	0
			857	532	166	156	3		
44	f	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 45 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Ao	93	Total	C	N	O	S	0	0
			738	466	139	131	2		
45	g	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 46 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ap	102	Total	C	N	O		0	0
			779	492	146	141			
46	h	102	Total	C	N	O		0	0
			779	492	146	141			

- Molecule 47 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Aq	94	Total	C	N	O	S	0	0
			753	479	137	134	3		
47	i	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 48 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Ar	75	Total	C	N	O	S	0	0
			569	353	113	102	1		
48	j	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 49 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	As	77	Total	C	N	O	S	0	0
			625	388	129	106	2		
49	k	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 50 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	At	63	Total	C	N	O	S	0	0
			509	313	99	95	2		
50	l	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 51 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Au	56	Total	C	N	O	S	0	0
			435	272	84	77	2		
51	m	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 52 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Av	56	Total	C	N	O	S	0	0
			444	269	94	80	1		
52	n	54	Total	C	N	O	S	0	0
			429	260	91	77	1		

- Molecule 53 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	Aw	50	Total	C	N	O	0	0
			409	263	75	71		
53	o	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 54 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Ax	46	Total	C	N	O	S	0	0
			377	228	90	57	2		
54	p	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 55 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Ay	64	Total	C	N	O	S	0	0
			504	323	105	74	2		
55	q	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 56 is a protein called Large ribosomal subunit protein bL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Az	38	Total	C	N	O	S	0	0
			302	185	65	48	4		
56	r	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 57 is a protein called ATP-dependent RNA helicase HrpA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	B	1295	Total	C	N	O	S	0	0
			10462	6619	1887	1924	32		

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-25	MET	-	initiating methionine	UNP P43329
B	-24	GLY	-	expression tag	UNP P43329
B	-23	HIS	-	expression tag	UNP P43329
B	-22	HIS	-	expression tag	UNP P43329
B	-21	HIS	-	expression tag	UNP P43329
B	-20	HIS	-	expression tag	UNP P43329
B	-19	HIS	-	expression tag	UNP P43329
B	-18	HIS	-	expression tag	UNP P43329
B	-17	HIS	-	expression tag	UNP P43329
B	-16	HIS	-	expression tag	UNP P43329
B	-15	ASP	-	expression tag	UNP P43329
B	-14	TYR	-	expression tag	UNP P43329
B	-13	ASP	-	expression tag	UNP P43329

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	ILE	-	expression tag	UNP P43329
B	-11	PRO	-	expression tag	UNP P43329
B	-10	THR	-	expression tag	UNP P43329
B	-9	THR	-	expression tag	UNP P43329
B	-8	LEU	-	expression tag	UNP P43329
B	-7	GLU	-	expression tag	UNP P43329
B	-6	VAL	-	expression tag	UNP P43329
B	-5	LEU	-	expression tag	UNP P43329
B	-4	PHE	-	expression tag	UNP P43329
B	-3	GLN	-	expression tag	UNP P43329
B	-2	GLY	-	expression tag	UNP P43329
B	-1	PRO	-	expression tag	UNP P43329
B	0	GLY	-	expression tag	UNP P43329
B	1	THR	-	expression tag	UNP P43329

- Molecule 58 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	D	117	Total	C	N	O	S	0	0
			877	540	174	160	3		
58	y	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 59 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	E	123	Total	C	N	O	S	0	0
			955	590	196	165	4		
59	z	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 60 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	M	75	Total	C	N	O	P	0	0
			1593	711	281	526	75		

- Molecule 61 is a protein called VemP nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	s	37	Total	C	N	O	S	0	0
			316	198	58	58	2		

- Molecule 62 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	w	57	Total	C	N	O	P	0	0
			1175	527	165	426	57		

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
w	556	U	-	expression tag	GB 1895674257
w	557	U	-	expression tag	GB 1895674257
w	558	U	-	expression tag	GB 1895674257
w	559	U	-	expression tag	GB 1895674257
w	560	U	-	expression tag	GB 1895674257
w	561	U	-	expression tag	GB 1895674257
w	562	U	-	expression tag	GB 1895674257
w	563	U	-	expression tag	GB 1895674257
w	564	U	-	expression tag	GB 1895674257
w	565	U	-	expression tag	GB 1895674257
w	566	U	-	expression tag	GB 1895674257
w	567	U	-	expression tag	GB 1895674257
w	568	U	-	expression tag	GB 1895674257
w	569	U	-	expression tag	GB 1895674257
w	570	U	-	expression tag	GB 1895674257
w	571	U	-	expression tag	GB 1895674257
w	572	U	-	expression tag	GB 1895674257
w	573	U	-	expression tag	GB 1895674257
w	574	U	-	expression tag	GB 1895674257
w	575	U	-	expression tag	GB 1895674257
w	576	U	-	expression tag	GB 1895674257
w	577	U	-	expression tag	GB 1895674257

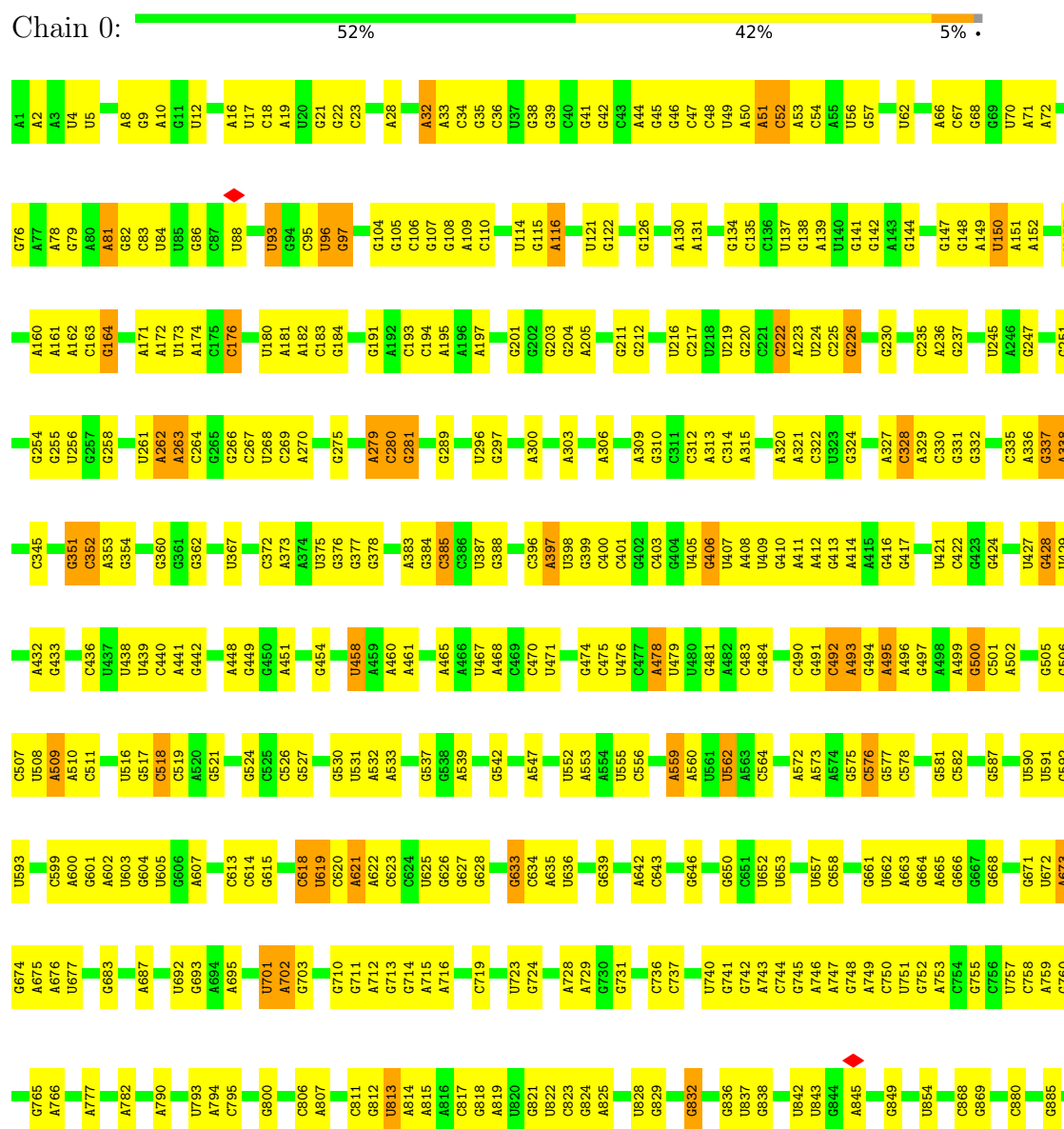
- Molecule 63 is a protein called Large ribosomal subunit protein uL10.

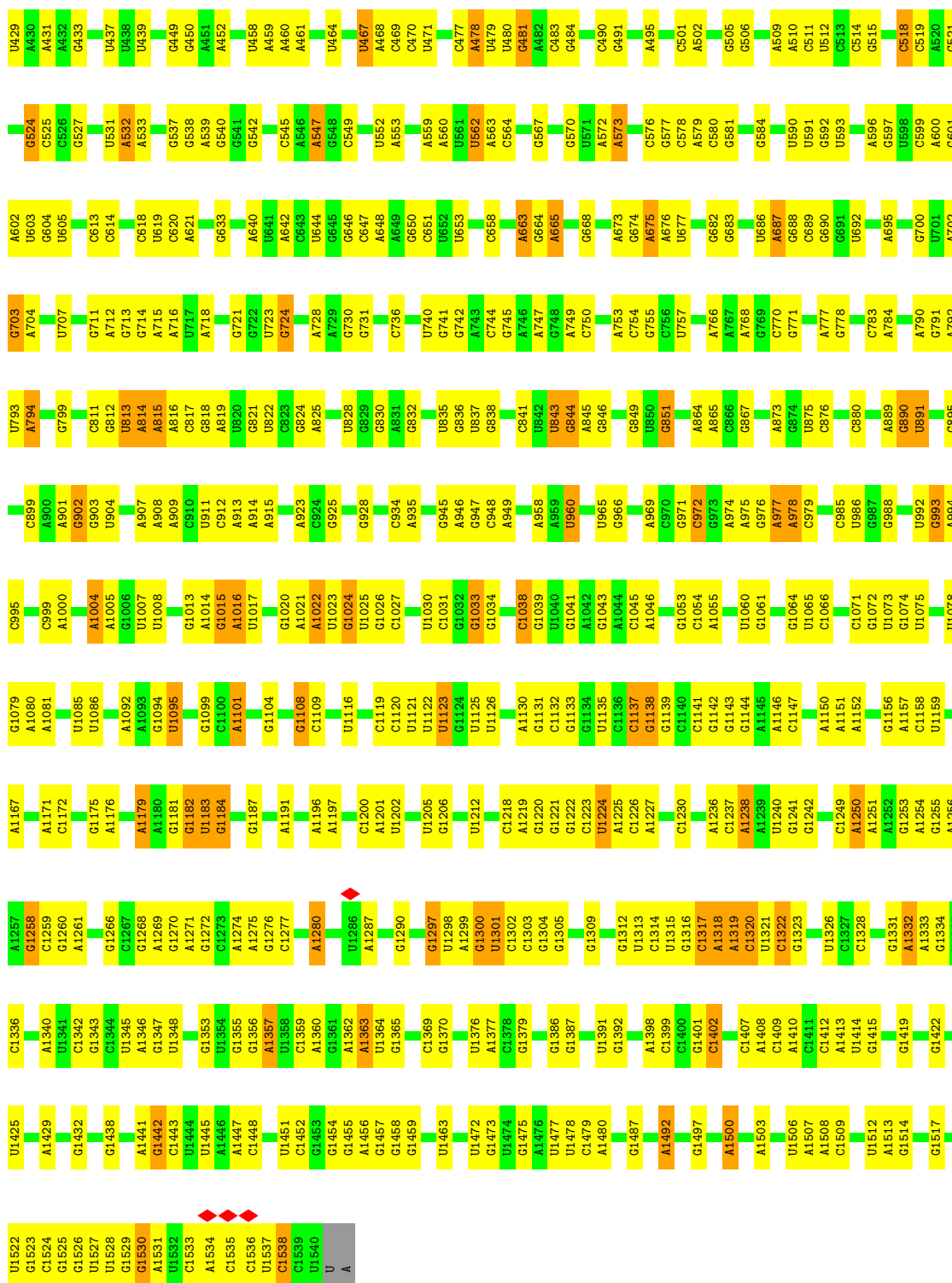
Mol	Chain	Residues	Atoms					AltConf	Trace
63	x	127	Total	C	N	O	S	0	0
			958	605	171	178	4		

3 Residue-property plots

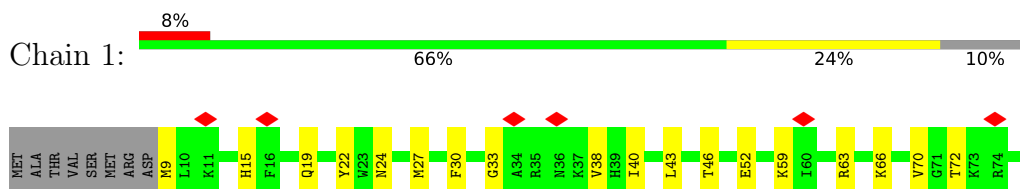
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

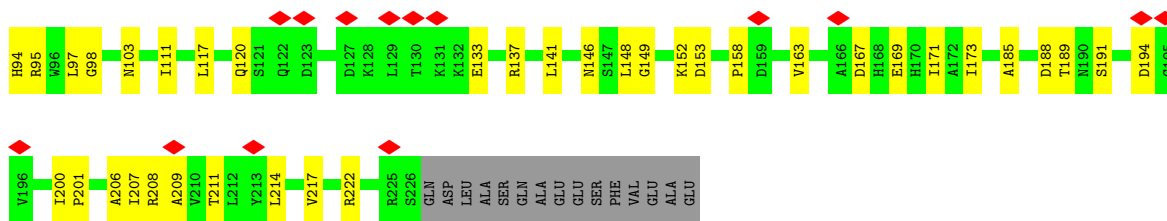
• Molecule 1: 16S ribosomal RNA



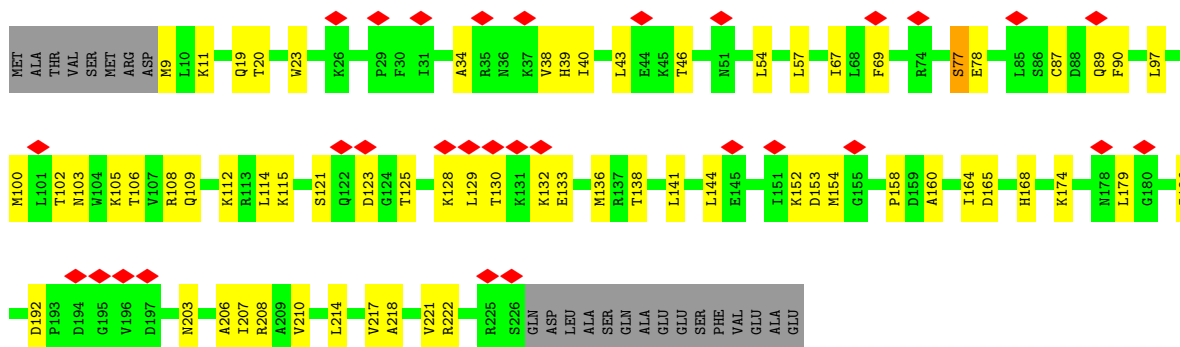


• Molecule 2: Small ribosomal subunit protein uS2

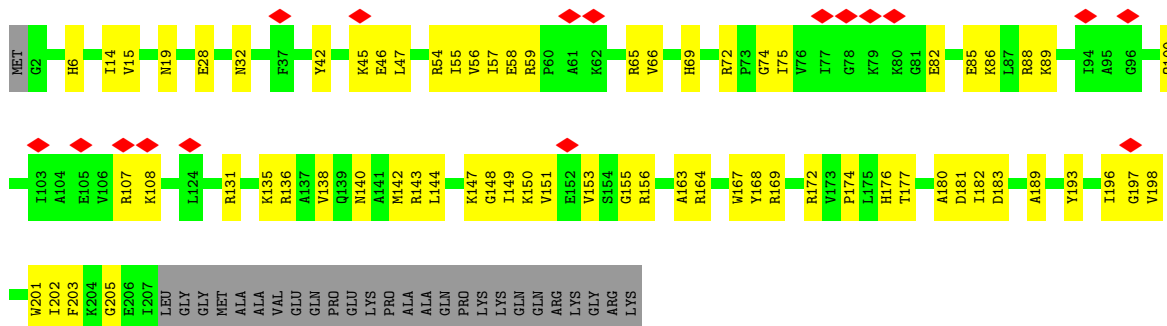




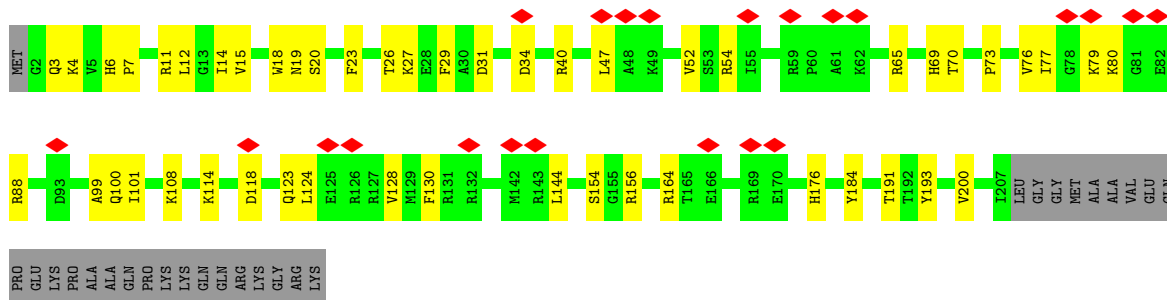
• Molecule 2: Small ribosomal subunit protein uS2



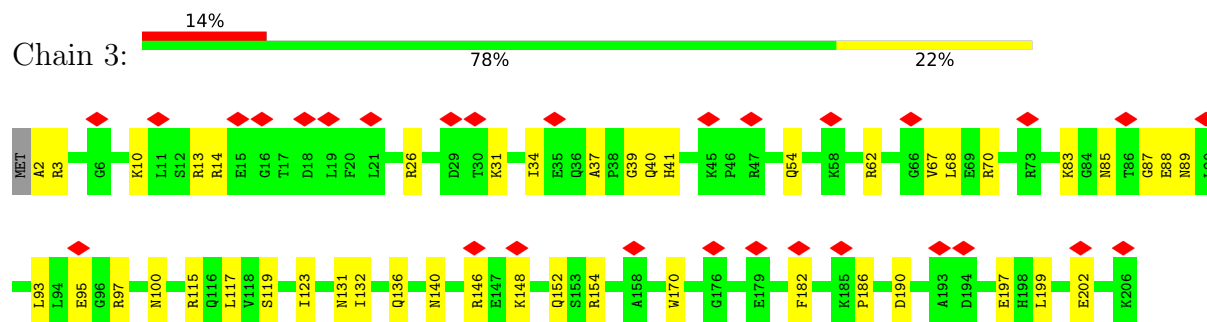
• Molecule 3: Small ribosomal subunit protein uS3



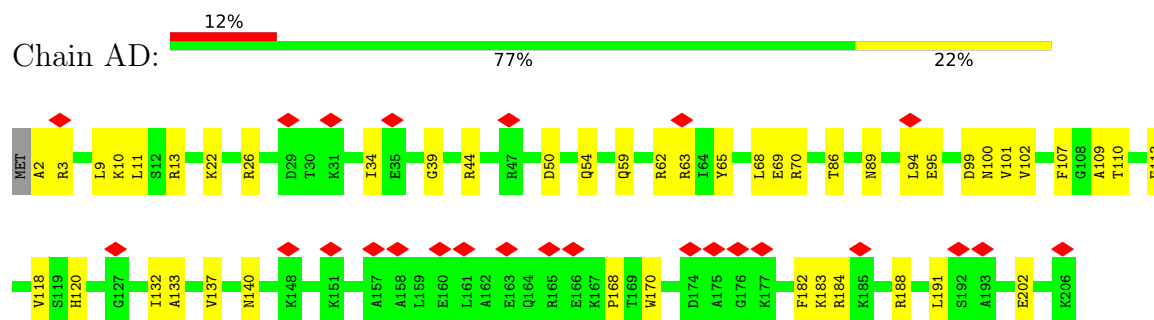
• Molecule 3: Small ribosomal subunit protein uS3



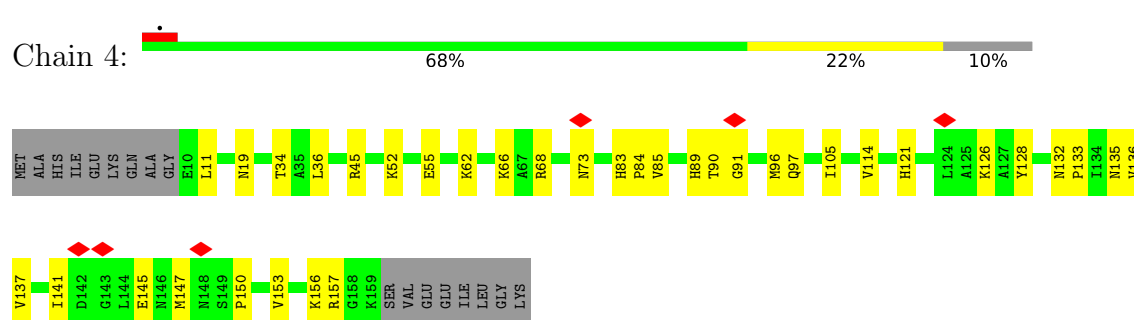
- Molecule 4: Small ribosomal subunit protein uS4



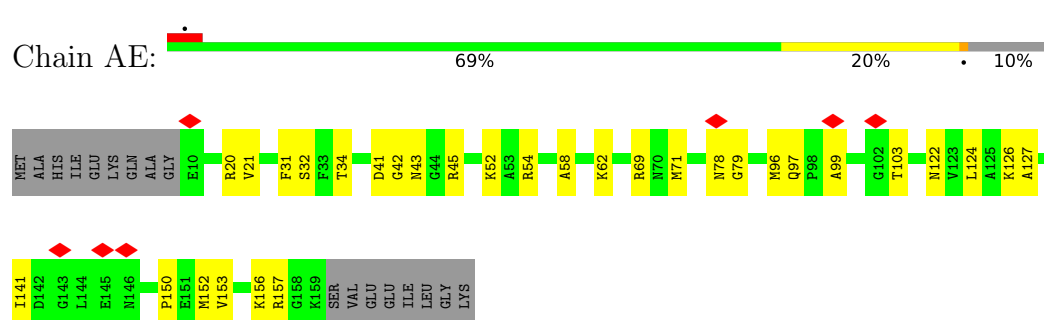
- Molecule 4: Small ribosomal subunit protein uS4



- Molecule 5: Small ribosomal subunit protein uS5

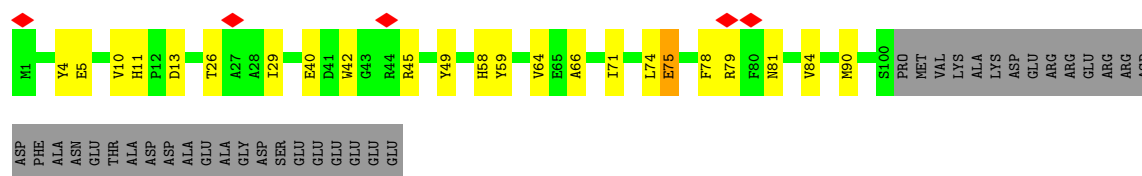


- Molecule 5: Small ribosomal subunit protein uS5

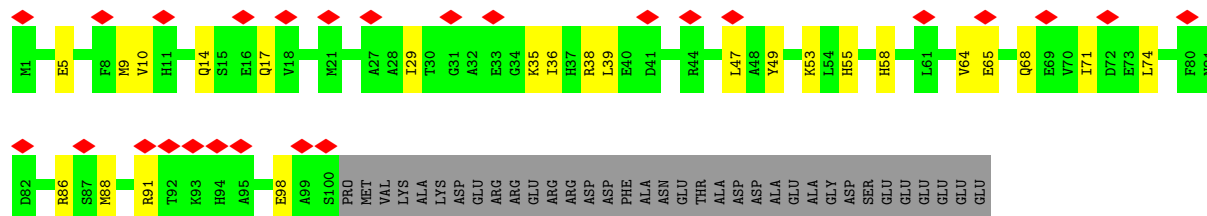


- Molecule 6: Small ribosomal subunit protein bS6, fully modified isoform

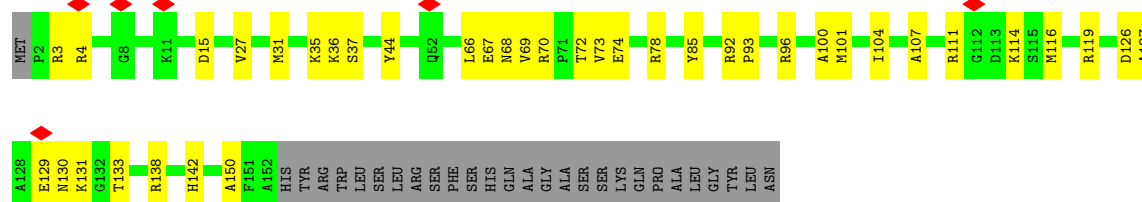




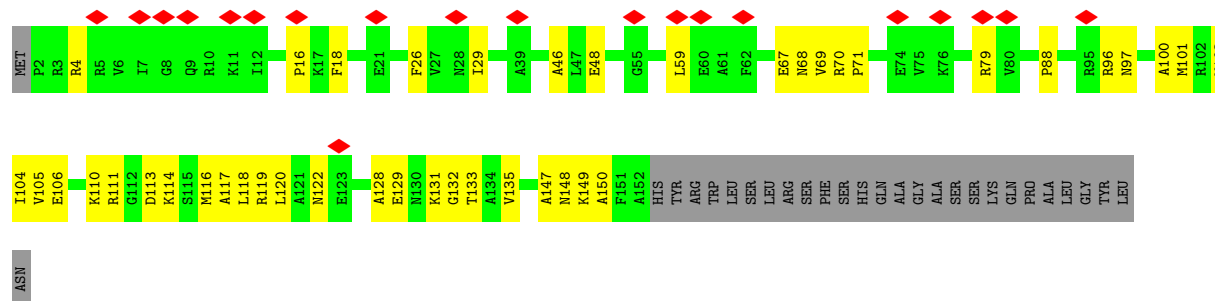
- Molecule 6: Small ribosomal subunit protein bS6, fully modified isoform



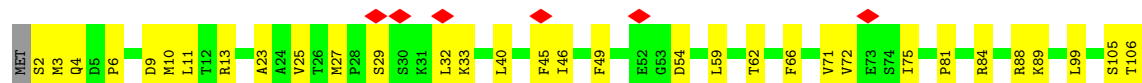
- Molecule 7: Small ribosomal subunit protein uS7



- Molecule 7: Small ribosomal subunit protein uS7



- Molecule 8: Small ribosomal subunit protein uS8

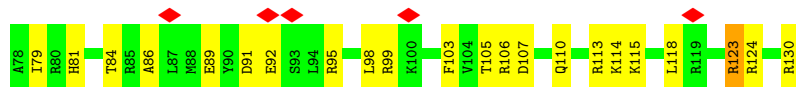
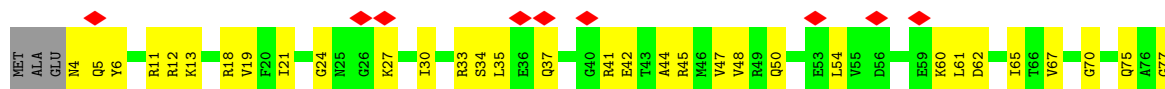




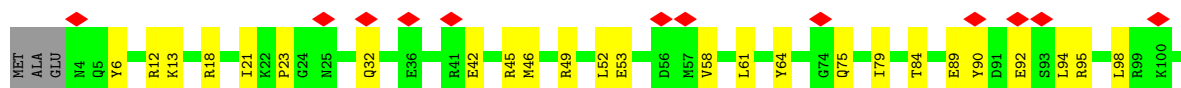
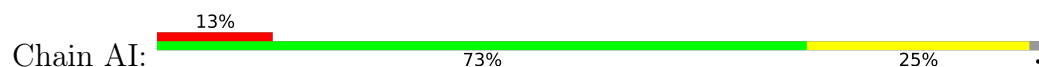
- Molecule 8: Small ribosomal subunit protein uS8



- Molecule 9: Small ribosomal subunit protein uS9



- Molecule 9: Small ribosomal subunit protein uS9



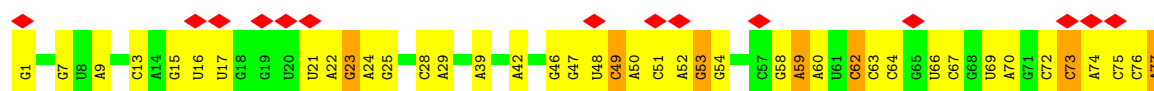
- Molecule 10: Small ribosomal subunit protein uS10



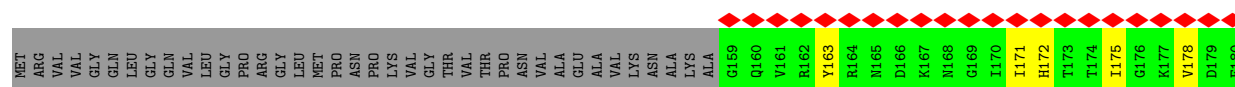
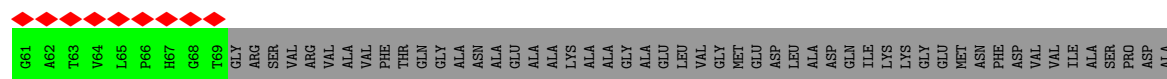
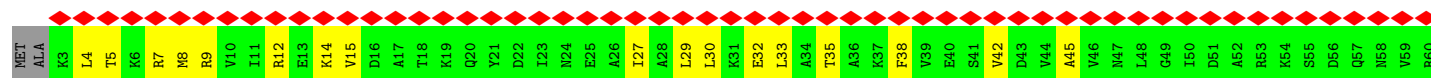
- Molecule 10: Small ribosomal subunit protein uS10

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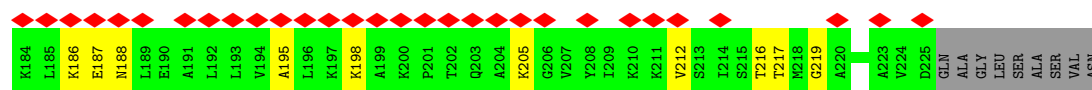
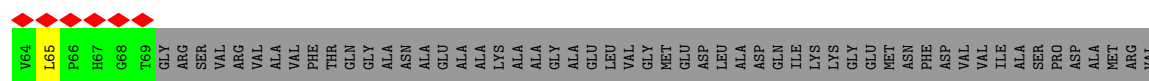
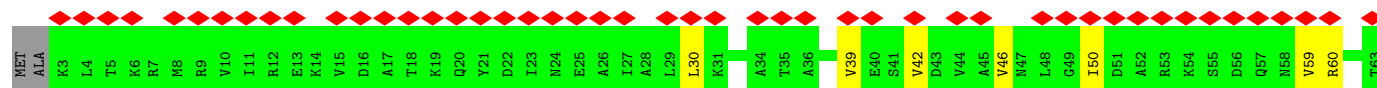
- Molecule 14: A-site tRNA



• Molecule 15: Large ribosomal subunit protein uL1

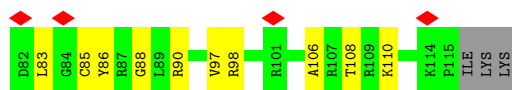


• Molecule 15: Large ribosomal subunit protein uL1

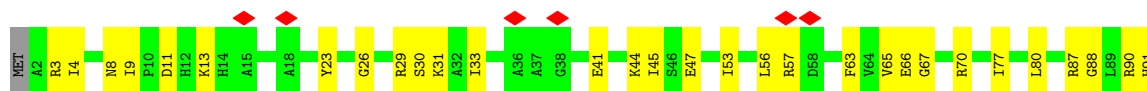


• Molecule 16: Small ribosomal subunit protein uS13

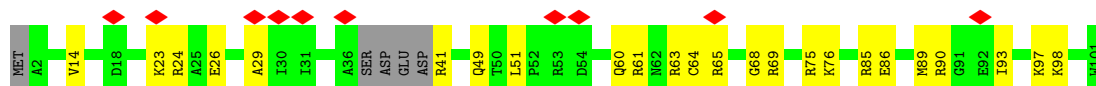
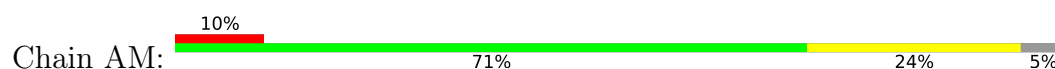




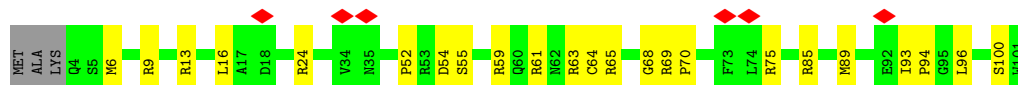
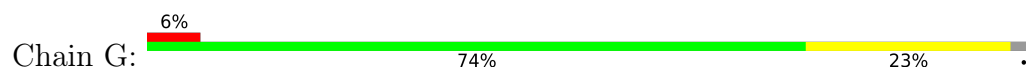
- Molecule 16: Small ribosomal subunit protein uS13



- Molecule 17: Small ribosomal subunit protein uS14



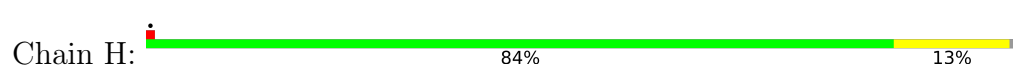
- Molecule 17: Small ribosomal subunit protein uS14



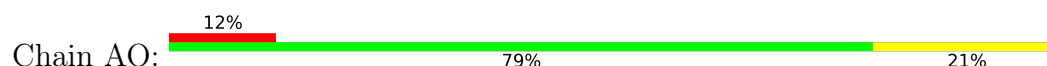
- Molecule 18: Small ribosomal subunit protein uS15



- Molecule 18: Small ribosomal subunit protein uS15

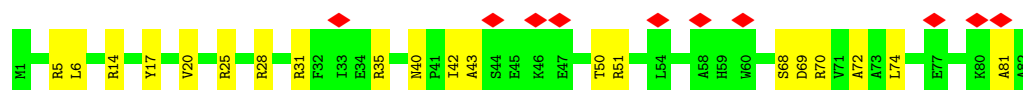
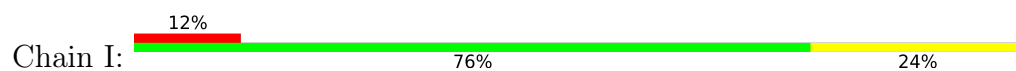


- Molecule 19: Small ribosomal subunit protein bS16

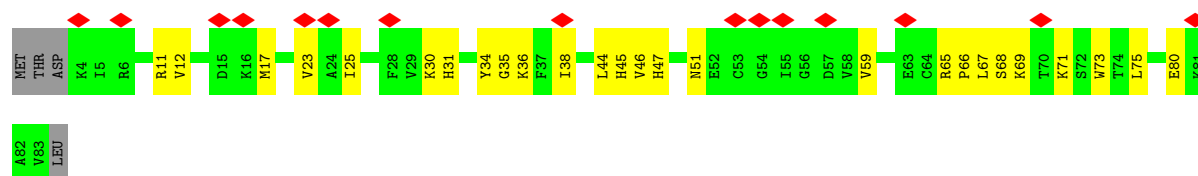




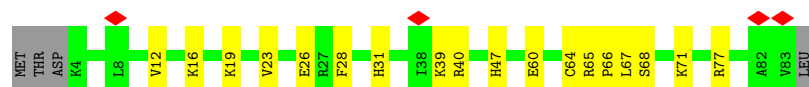
- Molecule 19: Small ribosomal subunit protein bS16



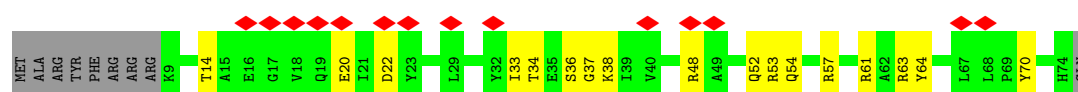
- Molecule 20: Small ribosomal subunit protein uS17



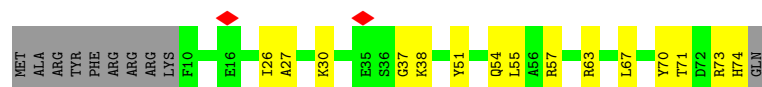
- Molecule 20: Small ribosomal subunit protein uS17



- Molecule 21: Small ribosomal subunit protein bS18

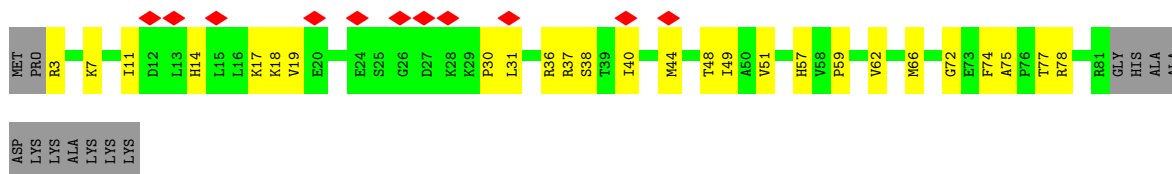


- Molecule 21: Small ribosomal subunit protein bS18

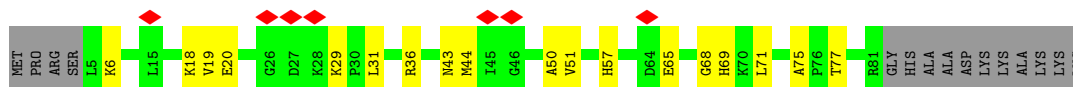


- Molecule 22: Small ribosomal subunit protein uS19

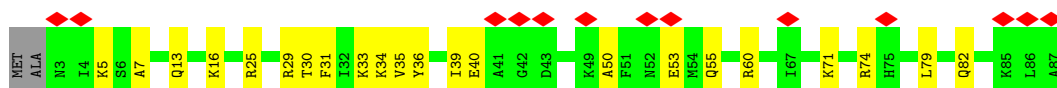
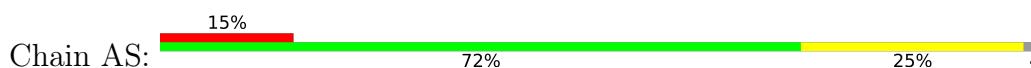




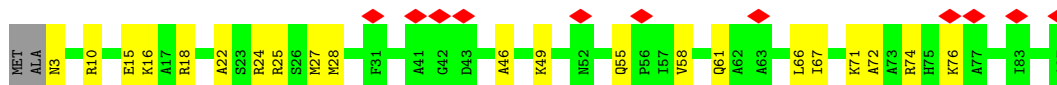
- Molecule 22: Small ribosomal subunit protein uS19



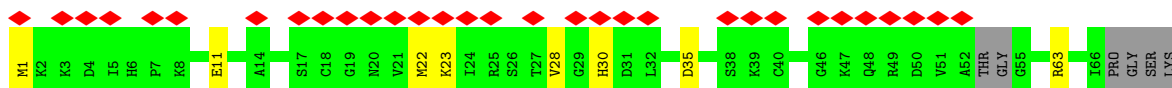
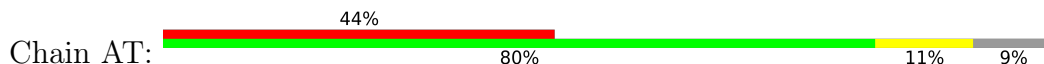
- Molecule 23: Small ribosomal subunit protein bS20



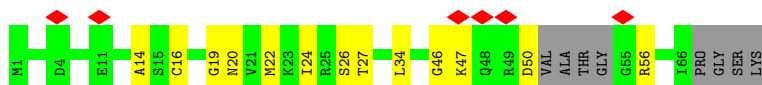
- Molecule 23: Small ribosomal subunit protein bS20



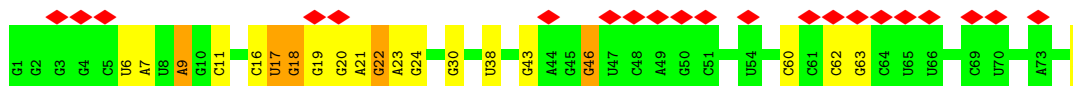
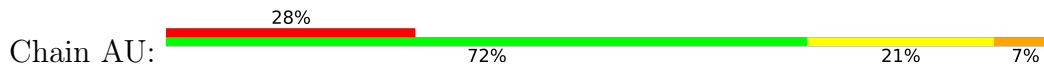
- Molecule 24: Large ribosomal subunit protein bL31A



- Molecule 24: Large ribosomal subunit protein bL31A



- Molecule 25: P-site tRNA



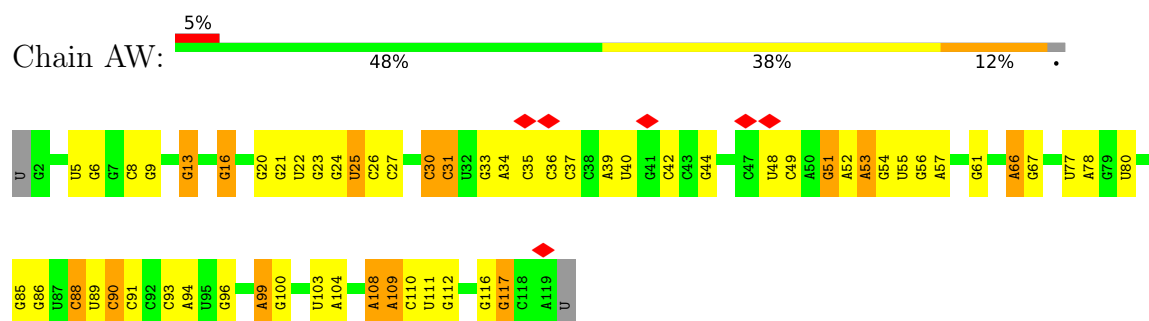
Chain AV:



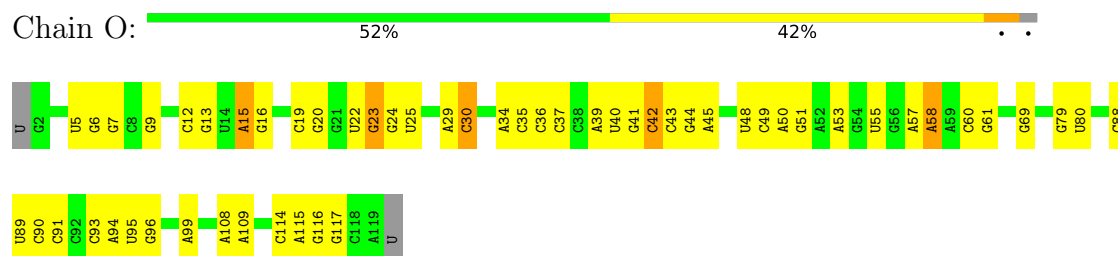
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A2158	U2098	C1997	G1884	C1804	A1608	C1531	U1443	G1355	A1269	U1174	A1096
G2159	U2099	A1998	A1885	A1805	G1715	A1532	G1444	C1357	C1270	A1175	U1097
C2160	G2100	C1999	A1889	G1806	A1717	C1533	U1534	G1358	G1271	U1176	C1100
C2161	A2101	A1890	A1890	G1807	G1631	U1535	C1447	A1359	A1272	G1177	U1101
G2162	G2102	A2019	A1899	A1808	U1729	A1536	U1535	C1363	U1273	U1180	C1102
A2163	C2103	U2022	A1899	A1910	C1730	U1537	G1450	C1364	A1274	U1181	A1103
C2164	G2104	C2023	A1900	G1811	G1733	G1537	G1451	A1365	A1275	U1182	C1104
C2165	C2105	C2025	A1901	U1812	G1734	A1637	G1452	A1366	C1278	U1183	U1105
U2166	U2106	G1906	G1906	G1813	G1738	C1540	C1454	G1368	G1279	G1186	G1106
U2167	G2107	G2029	A1913	C1816	A1738	C1541	C1454	G1371	G1283	U1187	U1107
G2168	A2108	U2030	A1913	G1817	G1743	U1542	U1460	G1371	U1188	U1188	U1108
A2169	U2109	A2031	A1918	U1818	A1744	G1543	U1544	A1286	A1287	U1189	G1109
C2170	G2110	G2032	A1918	A1819	A1745	A1546	C1463	G1377	A1287	U1190	G1110
A2171	U2111	A2033	A1919	A1919	G1745	C1547	G1464	A1378	A1111	U1191	U1111
U2172	G2112	G2034	C1920	U1825	C1752	A1548	G1465	U1379	G1292	G1112	U1113
C2173	U2113	G2035	G1920	G1826	G1752	A1549	A1469	C1293	C1293	A1204	U1116
A2174	G2114	C2036	A1927	A1829	G1753	A1549	A1469	G1381	G1296	A1205	G1116
C2175	U2115	A1926	A1926	C1830	A1754	A1550	A1470	G1206	G1297	G1206	U1119
G2176	G2116	G2037	G1929	G1831	G1755	C1550	G1471	A1385	C1297	U1209	C1123
C2177	U2117	U2038	G1930	G1832	G1756	A1551	G1471	A1386	C1298	U1209	G1124
A2178	G2118	G2040	G1930	C1832	A1757	A1551	G1471	A1387	C1299	U1209	G1124
C2179	U2119	G2043	G1935	C1833	A1759	C1556	G1475	A1301	G1300	A1212	U1129
U2180	G2120	C2043	A1936	C1837	G1759	C1558	G1478	A1302	A1301	A1213	U1130
G2181	U2121	C2047	A1937	C1838	A1762	U1559	G1479	A1302	A1302	A1214	G1131
U2182	G2122	G2048	A1938	G1839	G1763	C1560	G1480	C1306	C1306	U1217	U1132
A2183	U2123	G2048	U1939	C1839	C1764	A1566	U1481	A1307	A1307	G1223	A1133
C2184	G2124	A2052	C1947	C1844	G1769	G1567	G1482	U1402	G1308	U1224	A1134
U2185	U2125	C2055	G1948	G1845	U1770	A1569	G1483	U1405	G1309	G1225	C1135
U2188	G2126	G2056	U1955	G1846	C1771	A1570	G1491	U1406	G1310	A1226	G1136
U2189	C2127	G1964	C1958	A1847	A1772	A1571	G1492	G1410	G1311	G1227	U1139
G2190	A2128	U1964	C1958	G1850	A1773	A1572	A1494	U1411	U1412	G1235	U1141
A2198	U2129	C1967	C1962	U1851	U1777	G1573	U1497	U1412	U1316	G1236	A1142
A2199	G2130	G1968	U1963	U1852	U1778	C1574	U1497	C1414	G1317	A1237	A1143
U2203	U2131	A1969	G1964	A1853	U1779	U1575	G1501	G1415	U1318	G1238	C1146
G2204	U2132	A1970	U1971	A1854	U1780	U1578	A1502	G1416	G1319	U1248	A1147
C2208	C2133	U2076	G1972	G1863	U1781	A1579	A1503	C1417	A1321	G1251	G1153
G2209	A2134	G1975	G1975	G1869	U1782	C1592	A1504	G1418	U1326	G1252	G1154
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A2211	G2136	G2083	U1982	C1870	A1784	U1584	A1505	A1420	A1327	G1254	A1156
C2212	U2137	G1983	U1983	A1871	A1785	C1586	A1508	G1422	C1330	U1255	G1157
G2213	G2138	A2088	A1987	A1872	U1786	G1587	G1510	G1423	G1331	G1266	C1158
U2214	U2139	C2089	A1987	A1876	C1788	U1594	A1515	G1424	G1332	C1267	C1161
C2215	G2140	G1988	U1991	A1876	U1796	A1593	G1516	G1425	U1339	U1258	G1162
G2216	U2141	C2091	U1991	A1877	G1797	U1594	G1521	G1426	G1340	G1259	G1166
C2217	G2142	U2092	U1991	A1877	U1798	A1596	A1522	A1431	U1340	U1263	A1169
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C2226	C2146										
G2230	A2147										
U2233	G2148										
	U2149										
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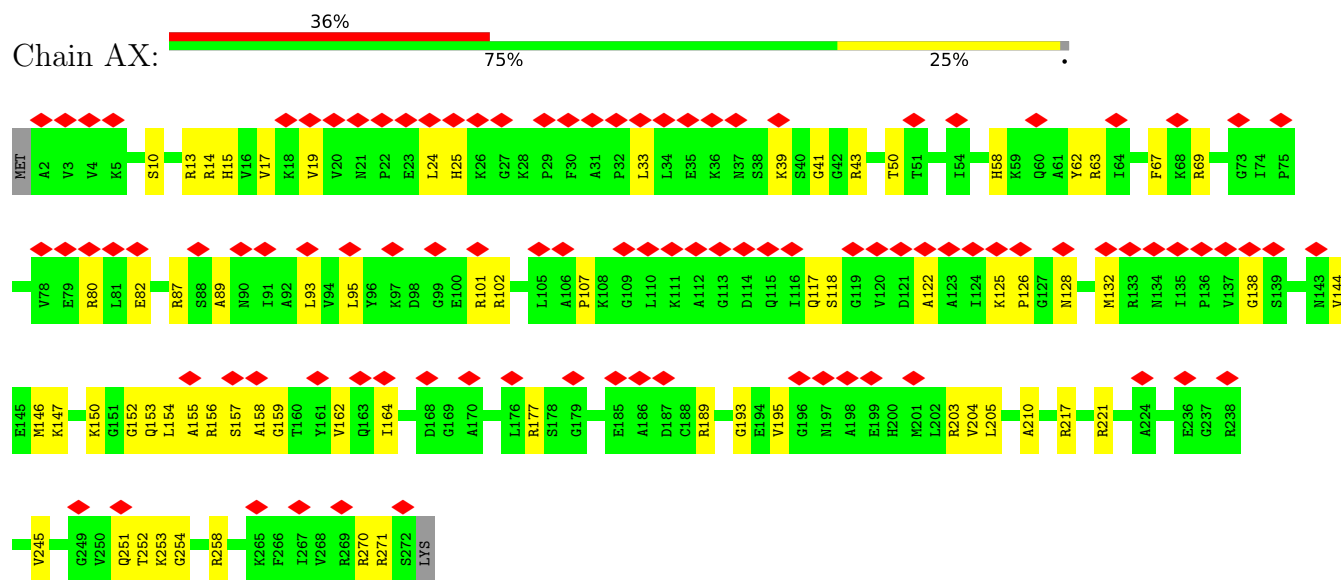
- Molecule 27: 5S ribosomal RNA



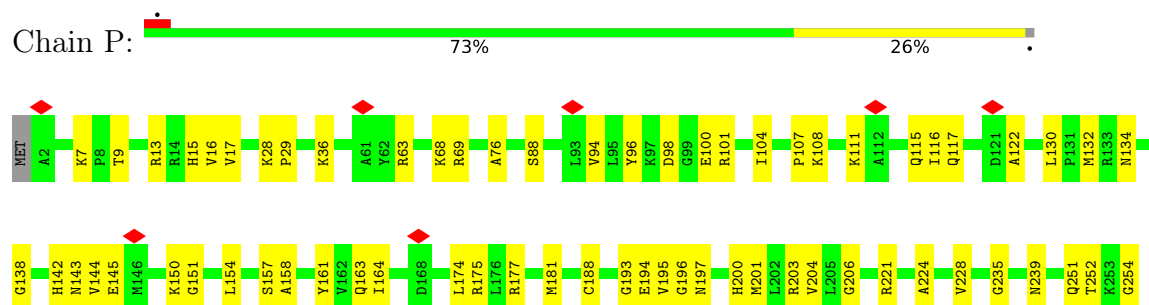
- Molecule 27: 5S ribosomal RNA

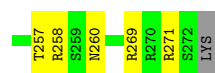


- Molecule 28: Large ribosomal subunit protein uL2

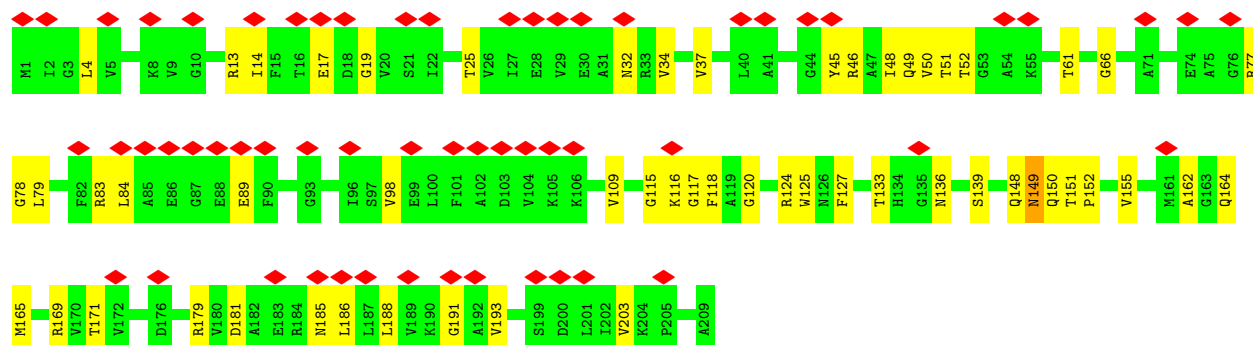
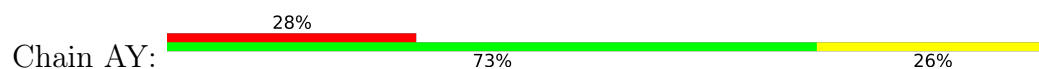


- Molecule 28: Large ribosomal subunit protein uL2

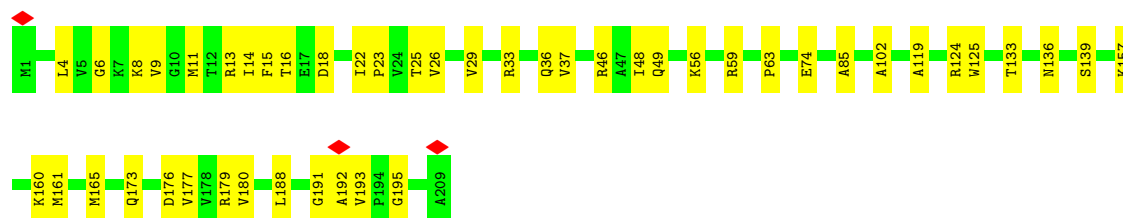
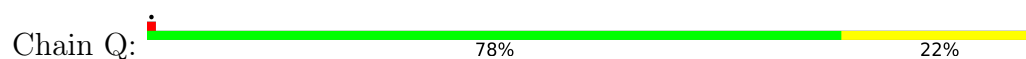




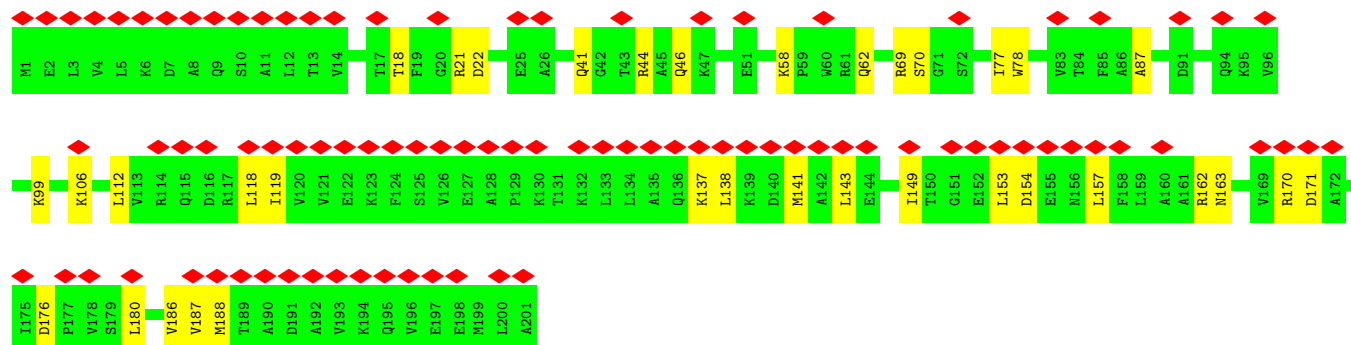
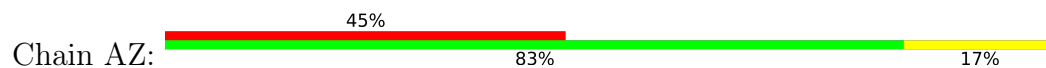
- Molecule 29: 50S ribosomal protein L3



- Molecule 29: 50S ribosomal protein L3

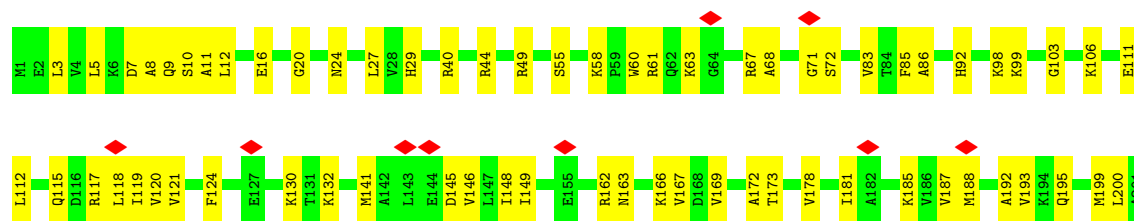


- Molecule 30: Large ribosomal subunit protein uL4

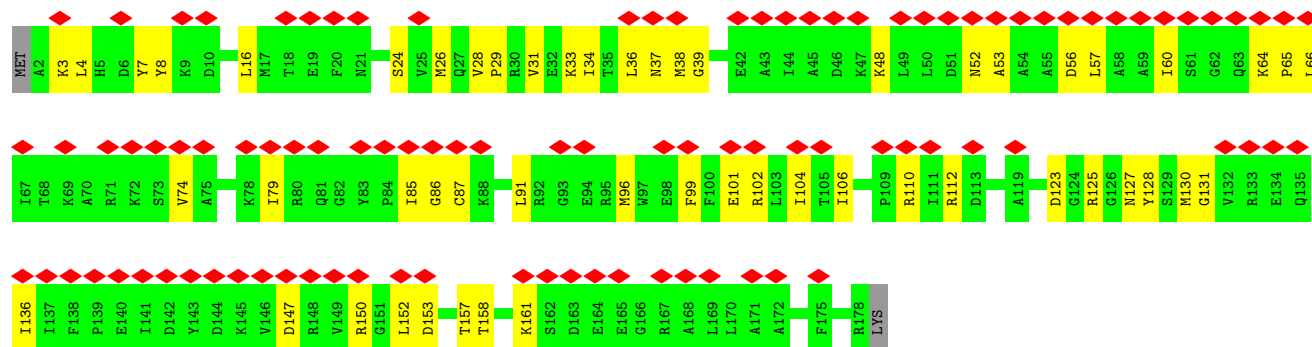


- Molecule 30: Large ribosomal subunit protein uL4

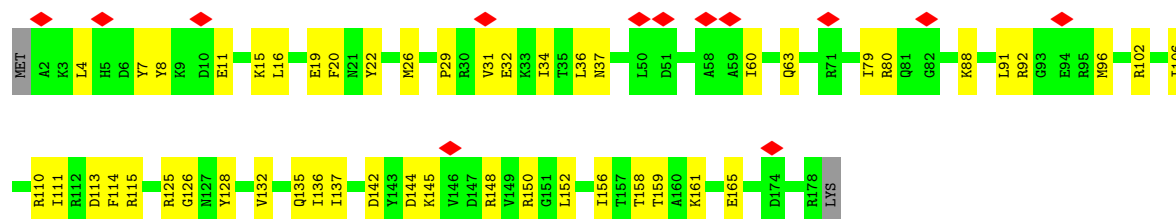
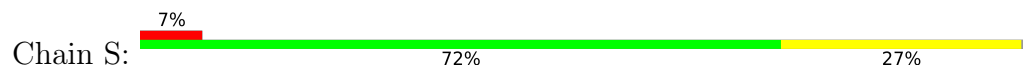




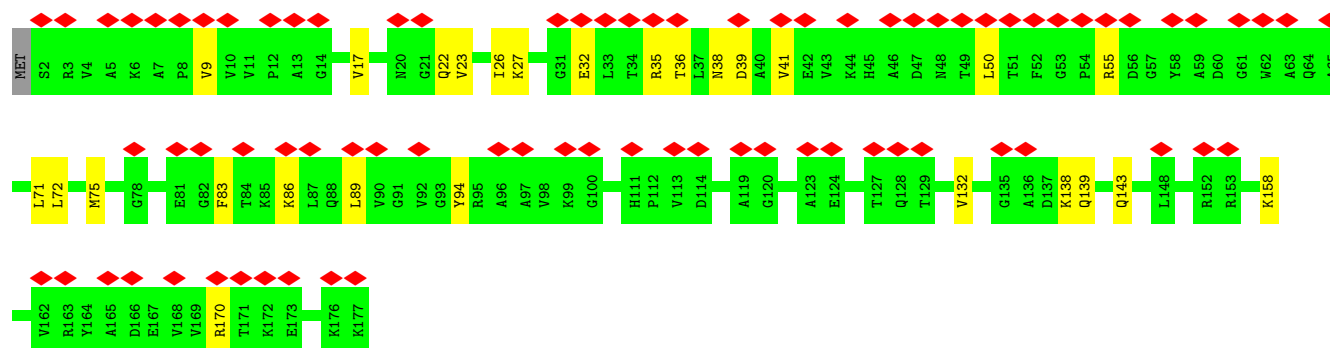
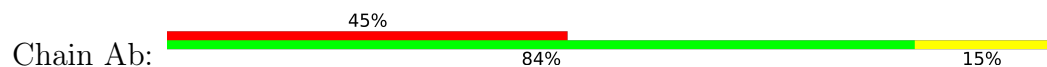
• Molecule 31: Large ribosomal subunit protein uL5



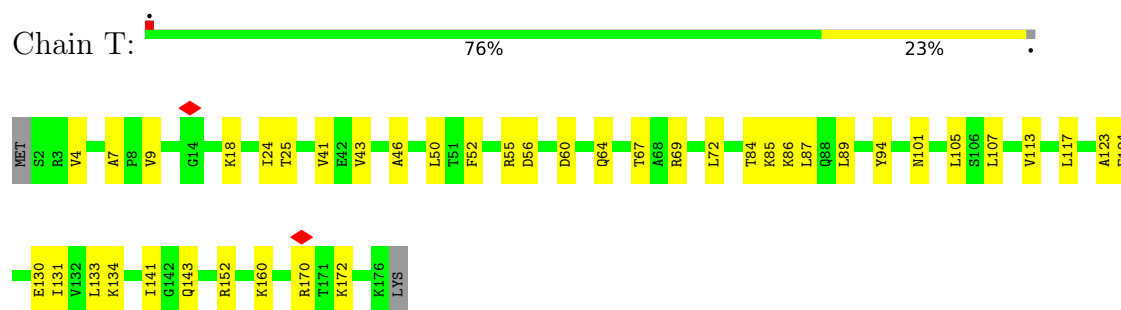
• Molecule 31: Large ribosomal subunit protein uL5



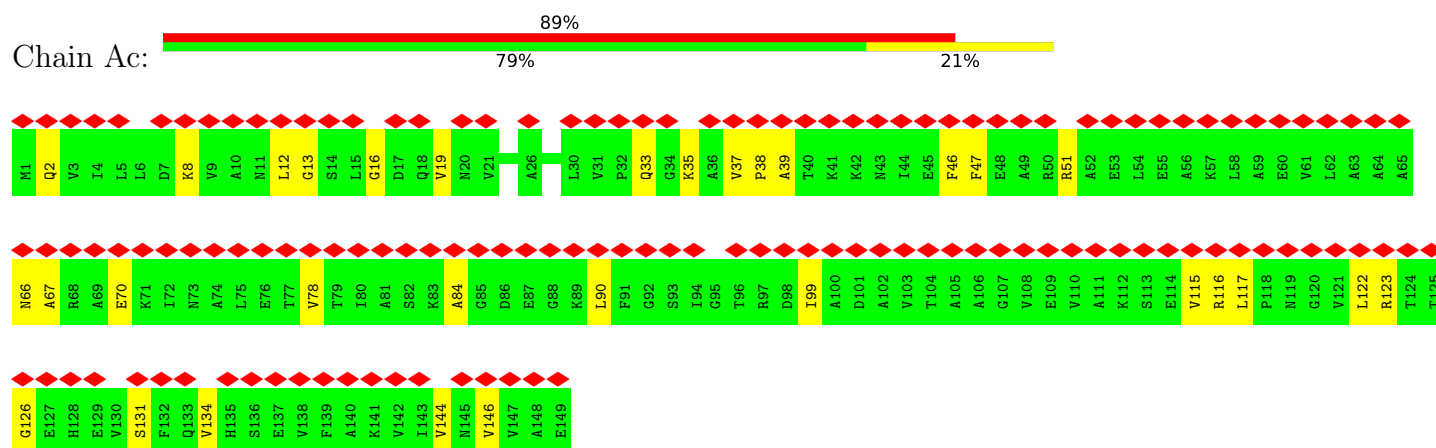
• Molecule 32: Large ribosomal subunit protein uL6



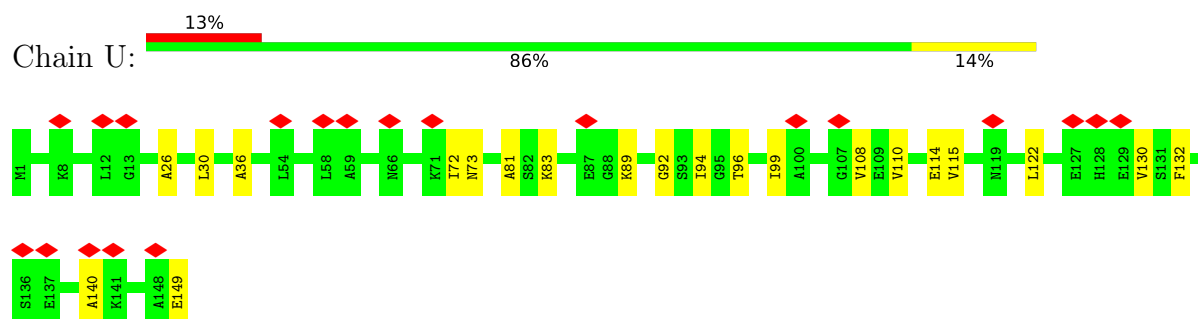
• Molecule 32: Large ribosomal subunit protein uL6



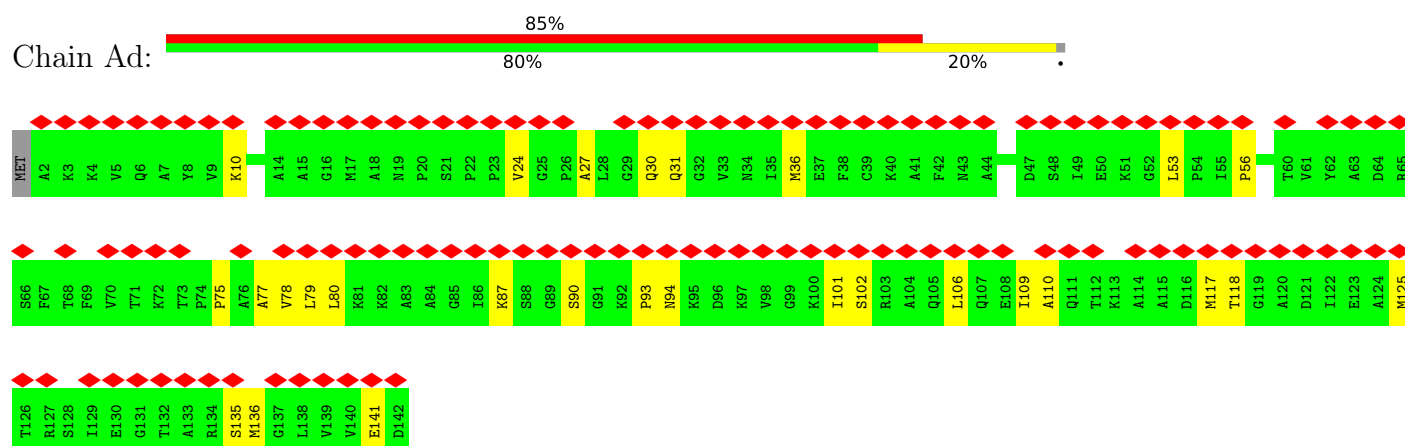
- Molecule 33: Large ribosomal subunit protein bL9



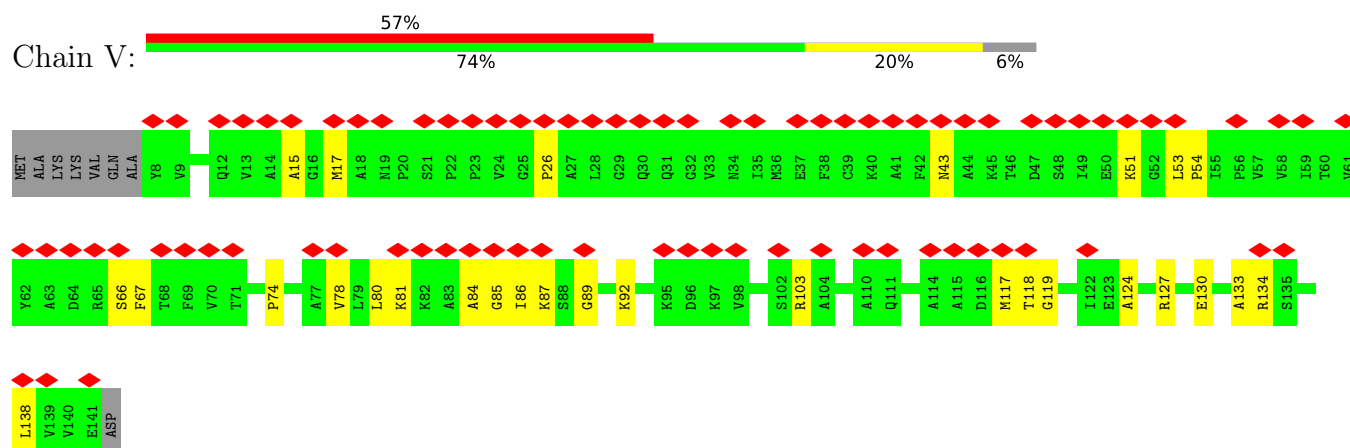
- Molecule 33: Large ribosomal subunit protein bL9



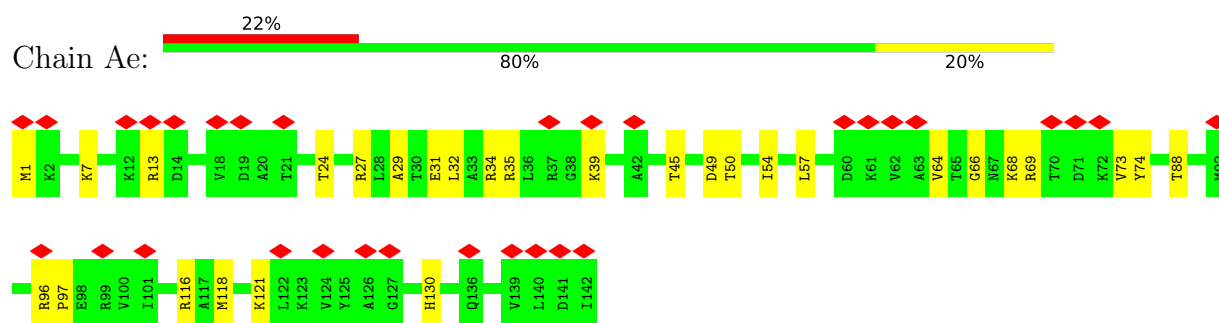
- Molecule 34: 50S ribosomal protein L11



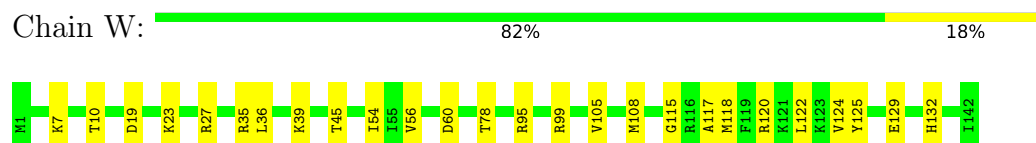
- Molecule 34: 50S ribosomal protein L11



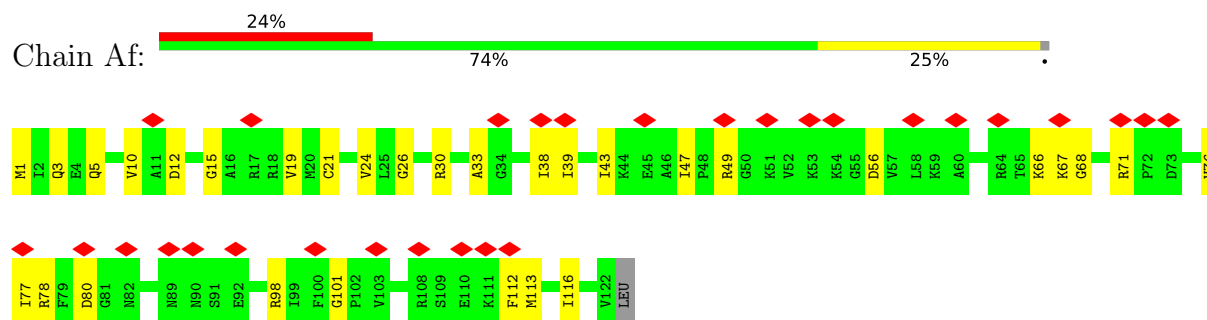
- Molecule 35: Large ribosomal subunit protein uL13



- Molecule 35: Large ribosomal subunit protein uL13

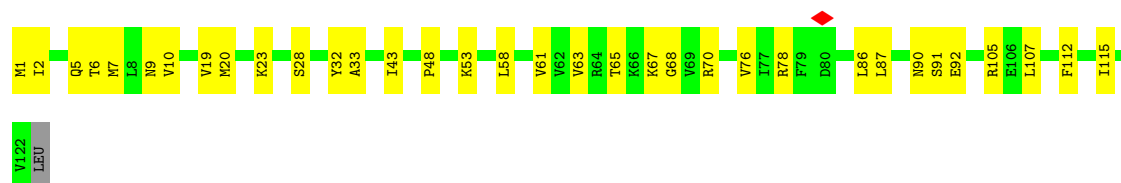


- Molecule 36: Large ribosomal subunit protein uL14

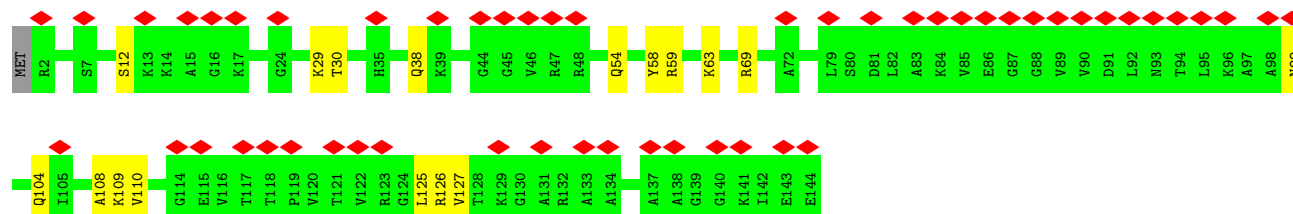
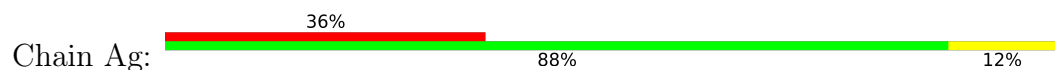


- Molecule 36: Large ribosomal subunit protein uL14

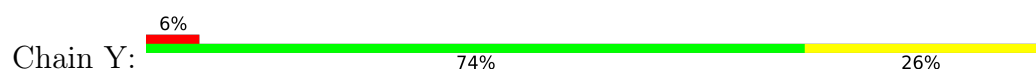




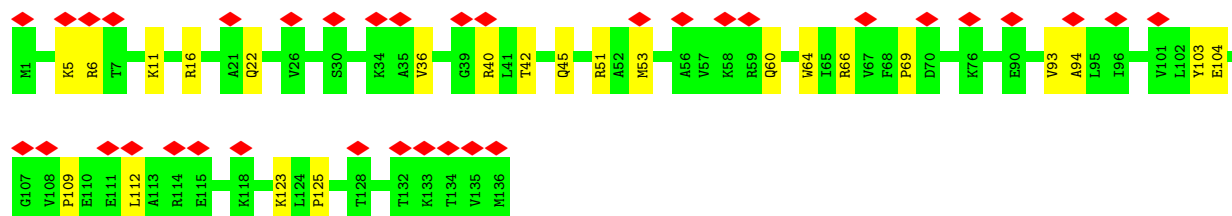
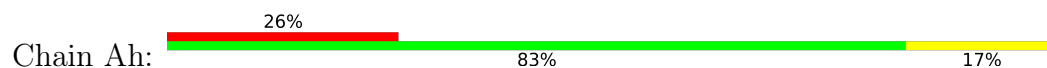
- Molecule 37: Large ribosomal subunit protein uL15



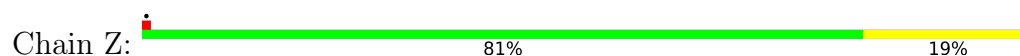
- Molecule 37: Large ribosomal subunit protein uL15



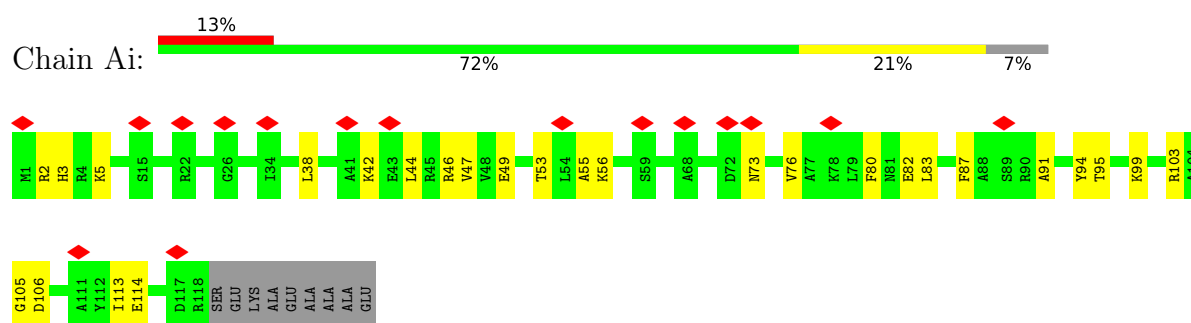
- Molecule 38: 50S ribosomal protein L16



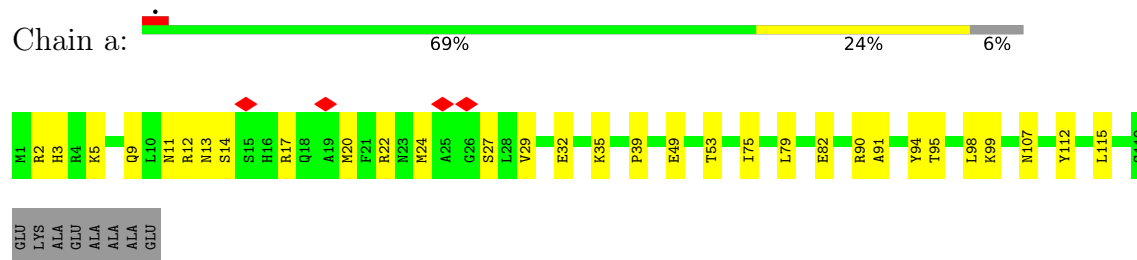
- Molecule 38: 50S ribosomal protein L16



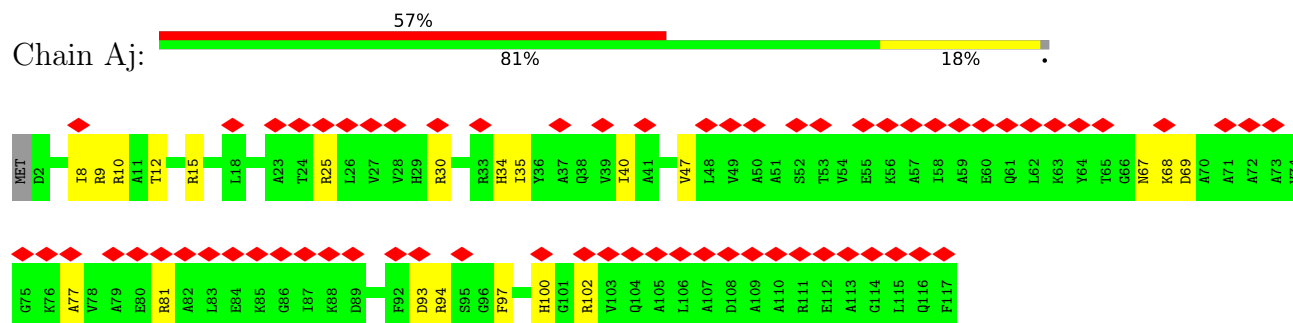
- Molecule 39: Large ribosomal subunit protein bL17



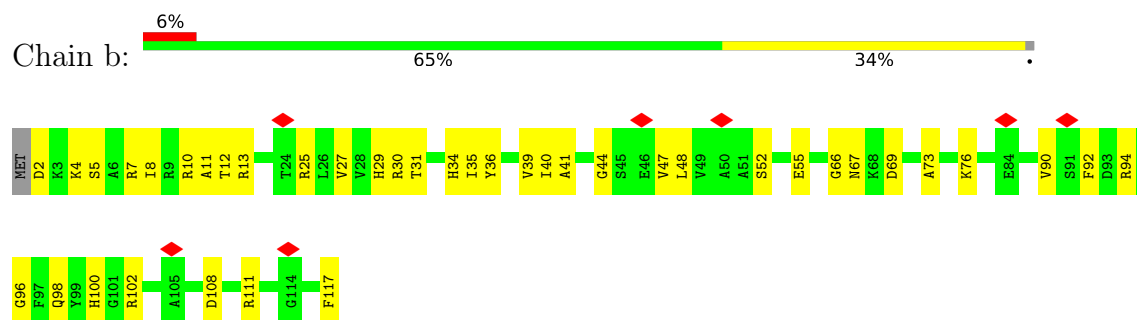
- Molecule 39: Large ribosomal subunit protein bL17



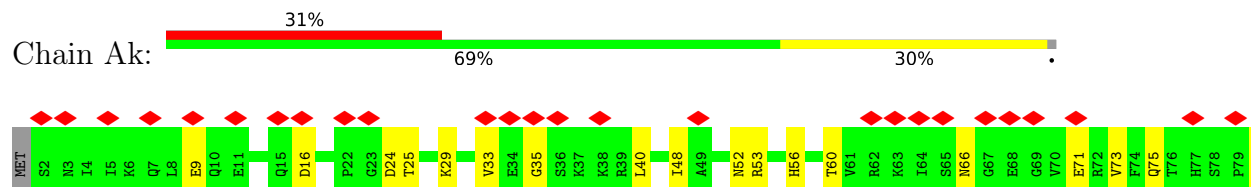
- Molecule 40: Large ribosomal subunit protein uL18

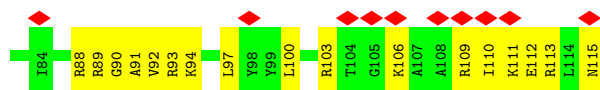


- Molecule 40: Large ribosomal subunit protein uL18

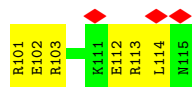


- Molecule 41: Large ribosomal subunit protein bL19

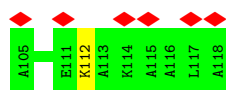
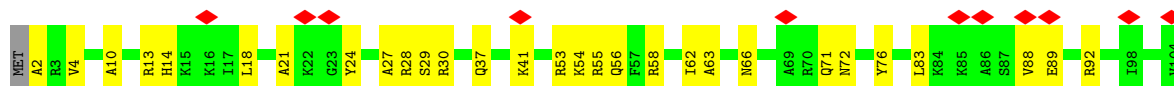
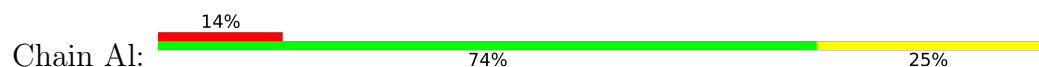




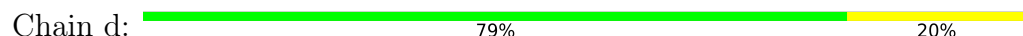
- Molecule 41: Large ribosomal subunit protein bL19



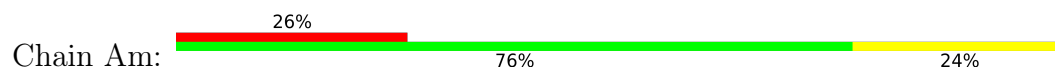
- Molecule 42: Large ribosomal subunit protein bL20



- Molecule 42: Large ribosomal subunit protein bL20



- Molecule 43: Large ribosomal subunit protein bL21

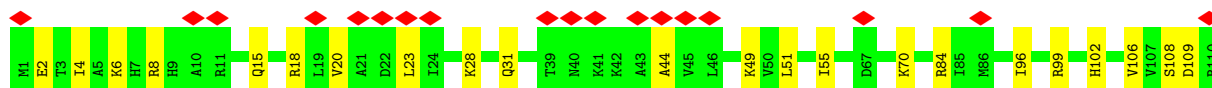
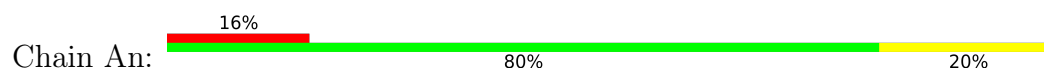


- Molecule 43: Large ribosomal subunit protein bL21





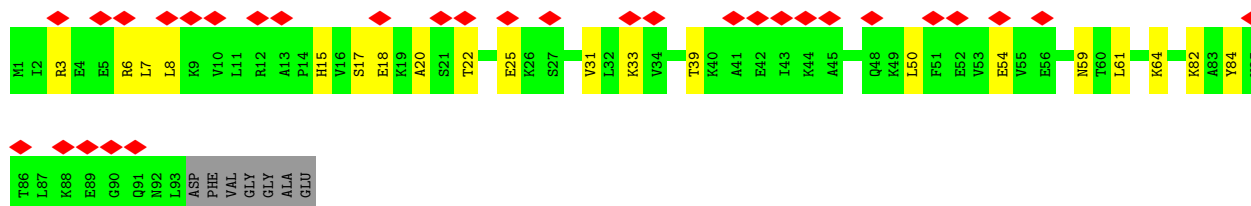
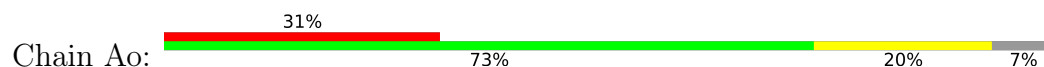
- Molecule 44: Large ribosomal subunit protein uL22



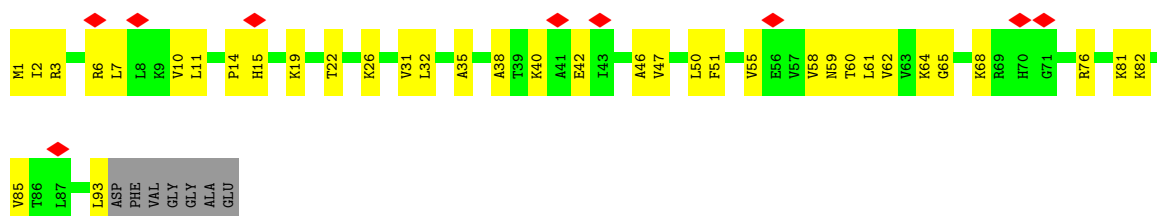
- Molecule 44: Large ribosomal subunit protein uL22



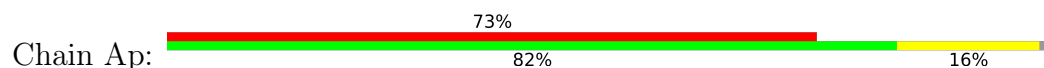
- Molecule 45: Large ribosomal subunit protein uL23



- Molecule 45: Large ribosomal subunit protein uL23

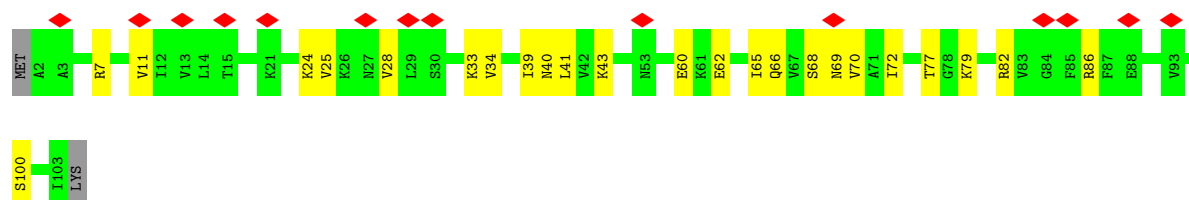
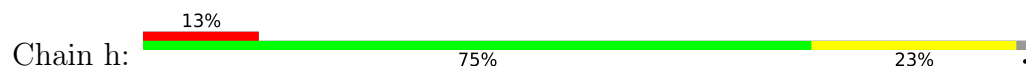


- Molecule 46: Large ribosomal subunit protein uL24

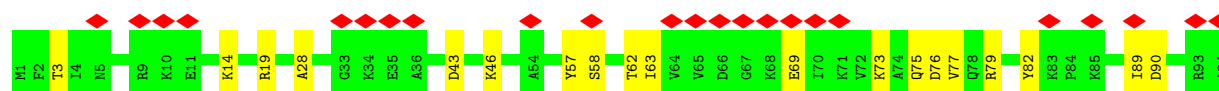
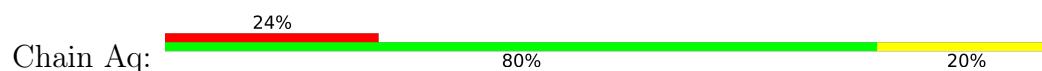




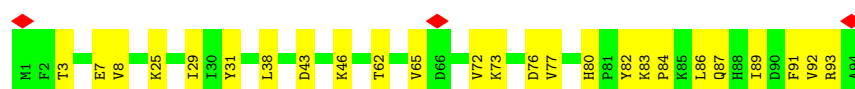
- Molecule 46: Large ribosomal subunit protein uL24



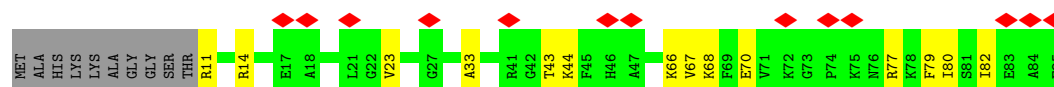
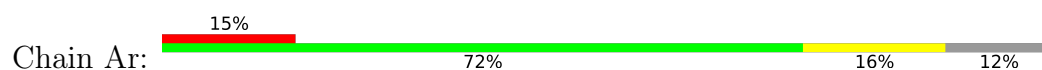
- Molecule 47: Large ribosomal subunit protein bL25



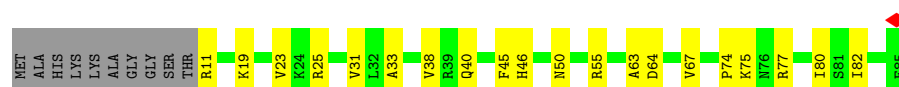
- Molecule 47: Large ribosomal subunit protein bL25



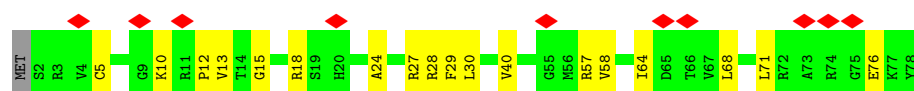
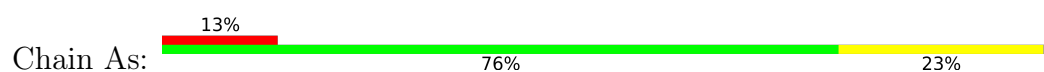
- Molecule 48: Large ribosomal subunit protein bL27



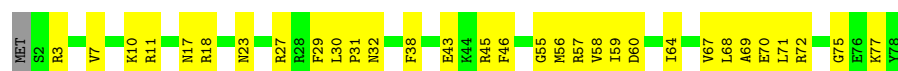
- Molecule 48: Large ribosomal subunit protein bL27



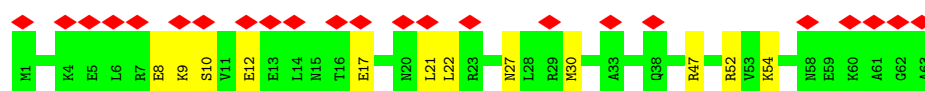
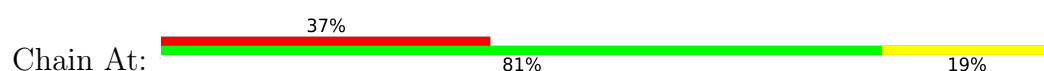
- Molecule 49: Large ribosomal subunit protein bL28



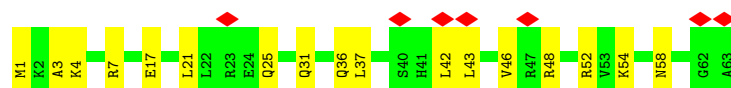
- Molecule 49: Large ribosomal subunit protein bL28



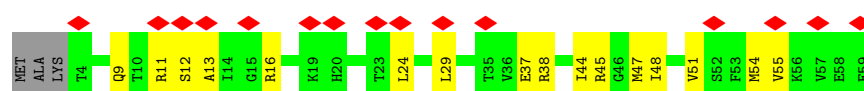
- Molecule 50: Large ribosomal subunit protein uL29



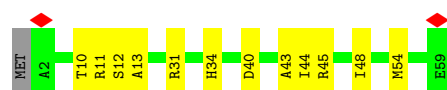
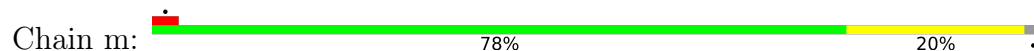
- Molecule 50: Large ribosomal subunit protein uL29



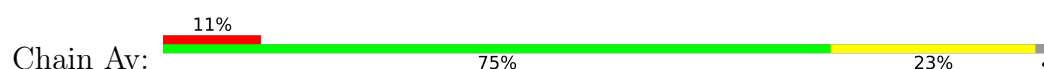
- Molecule 51: Large ribosomal subunit protein uL30



- Molecule 51: Large ribosomal subunit protein uL30



- Molecule 52: Large ribosomal subunit protein bL32



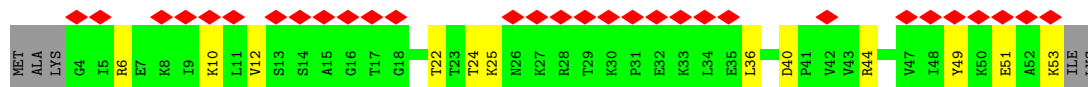
- Molecule 52: Large ribosomal subunit protein bL32

Chain n: 



- Molecule 53: Large ribosomal subunit protein bL33

Chain Aw: 



- Molecule 53: Large ribosomal subunit protein bL33

Chain o: 



- Molecule 54: Large ribosomal subunit protein bL34

Chain Ax: 



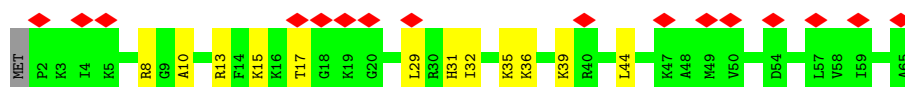
- Molecule 54: Large ribosomal subunit protein bL34

Chain p: 



- Molecule 55: Large ribosomal subunit protein bL35

Chain Ay: 

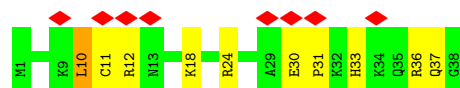
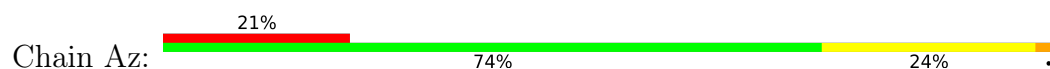


- Molecule 55: Large ribosomal subunit protein bL35

Chain q: 



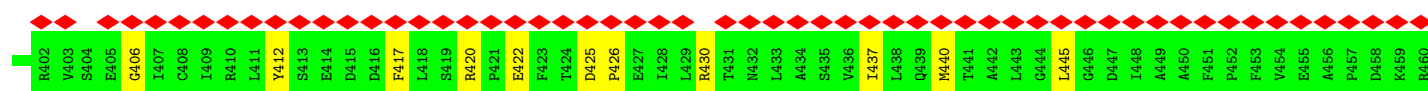
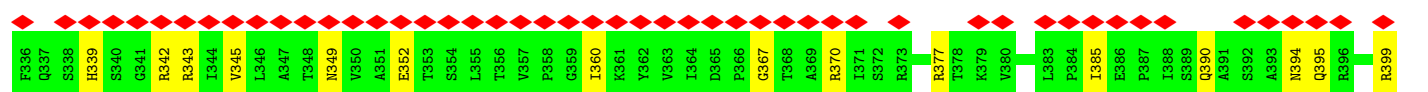
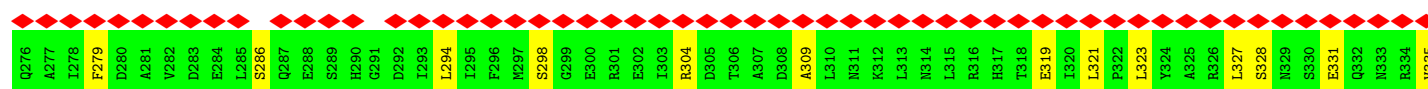
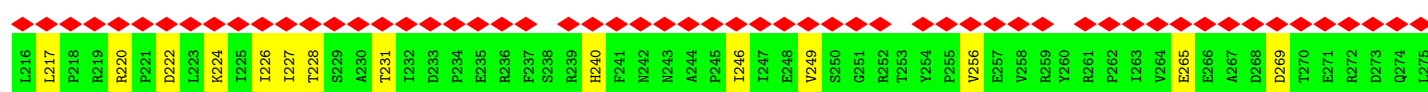
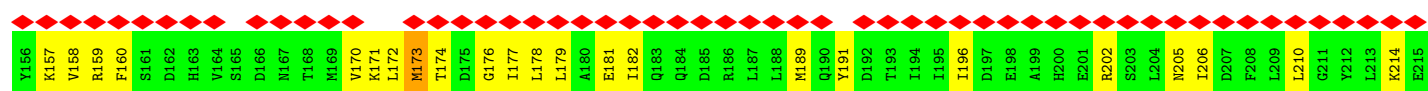
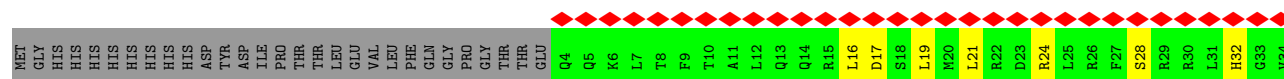
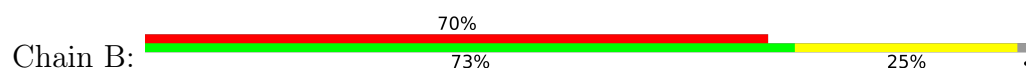
- Molecule 56: Large ribosomal subunit protein bL36A

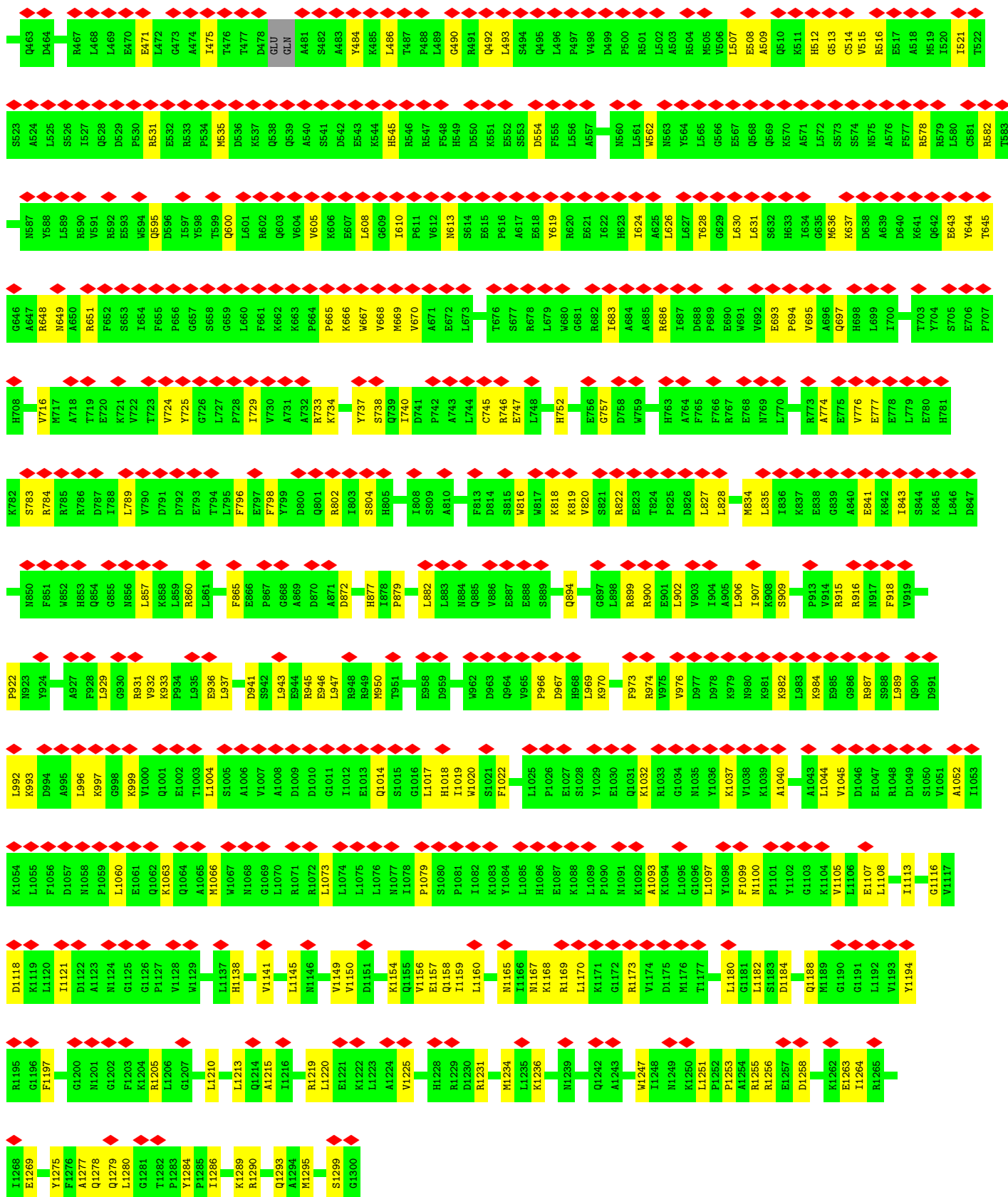


- Molecule 56: Large ribosomal subunit protein bL36A



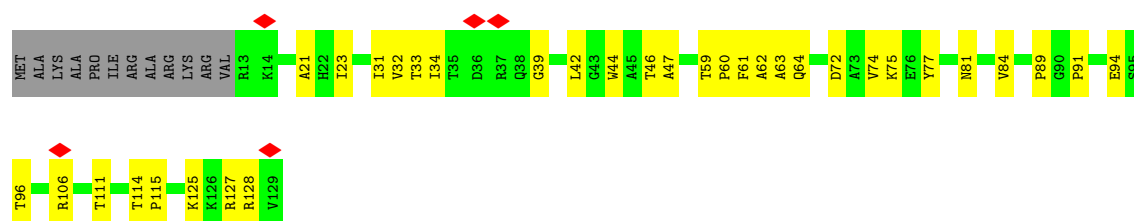
- Molecule 57: ATP-dependent RNA helicase HrpA





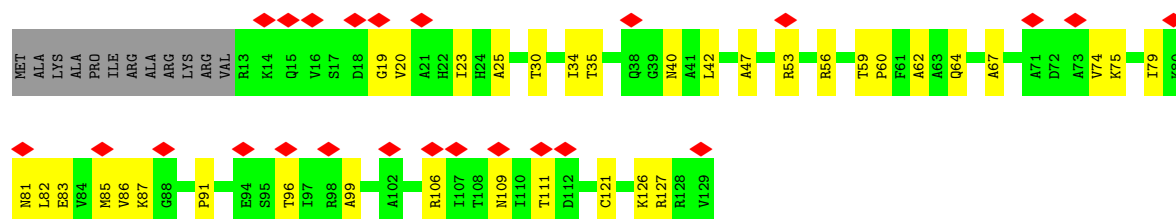
• Molecule 58: Small ribosomal subunit protein uS11

Chain D: 



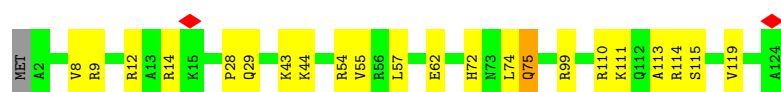
- Molecule 58: Small ribosomal subunit protein uS11

Chain y: 



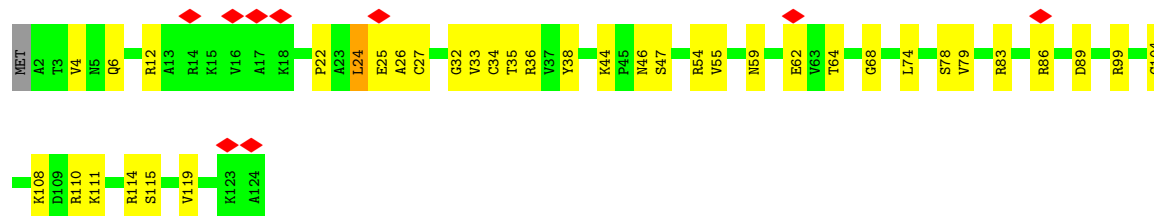
- Molecule 59: Small ribosomal subunit protein uS12

Chain E: 



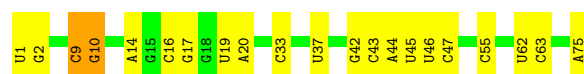
- Molecule 59: Small ribosomal subunit protein uS12

Chain z: 



- Molecule 60: P-site tRNA

Chain M: 



- Molecule 61: VemP nascent chain

Chain s: 

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	17805	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	2.044	Depositor
Minimum map value	-0.926	Depositor
Average map value	0.011	Depositor
Map value standard deviation	0.118	Depositor
Recommended contour level	0.32	Depositor
Map size (Å)	508.9, 508.9, 508.9	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.454, 1.454, 1.454	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	0	0.21	0/36834	0.36	0/57462
1	AA	0.19	0/36966	0.36	0/57666
2	1	0.30	0/1735	0.79	2/2338 (0.1%)
2	AB	0.29	0/1735	0.75	2/2338 (0.1%)
3	2	0.28	0/1651	0.72	0/2225
3	AC	0.26	0/1651	0.70	0/2225
4	3	0.24	0/1665	0.67	2/2227 (0.1%)
4	AD	0.25	0/1665	0.71	0/2227
5	4	0.29	0/1118	0.75	0/1504
5	AE	0.30	0/1118	0.83	2/1504 (0.1%)
6	5	0.30	0/835	0.78	1/1128 (0.1%)
6	AF	0.28	0/835	0.80	1/1128 (0.1%)
7	6	0.28	0/1195	0.73	0/1602
7	AG	0.30	0/1195	0.85	2/1602 (0.1%)
8	7	0.27	0/989	0.68	0/1326
8	AH	0.27	0/989	0.71	0/1326
9	8	0.29	0/1034	0.83	2/1375 (0.1%)
9	AI	0.27	0/1034	0.84	0/1375
10	9	0.27	0/796	0.78	1/1077 (0.1%)
10	AJ	0.33	0/796	0.84	0/1077
11	A	0.19	0/1812	0.43	0/2823
12	A1	0.24	0/557	0.67	0/738
12	v	0.25	0/597	0.71	0/792
13	A2	0.24	0/2387	0.63	1/3221 (0.0%)
14	A3	0.18	0/1830	0.47	0/2849
15	AK	0.20	0/1033	0.56	0/1387
15	C	0.17	0/1033	0.53	0/1387
16	AL	0.25	0/892	0.81	1/1193 (0.1%)
16	F	0.28	0/892	0.78	0/1193
17	AM	0.28	0/785	0.77	0/1043
17	G	0.25	0/803	0.67	0/1070
18	AN	0.32	0/718	0.90	1/959 (0.1%)
18	H	0.46	0/710	0.96	0/950
19	AO	0.30	0/659	0.75	0/884

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
19	I	0.27	0/658	0.82	2/884 (0.2%)
20	AP	0.37	0/657	0.96	0/881
20	J	0.25	0/657	0.70	0/881
21	AQ	0.28	0/553	0.76	0/742
21	K	0.28	0/544	0.71	0/731
22	AR	0.25	0/652	0.64	0/877
22	t	0.25	0/635	0.64	0/855
23	AS	0.26	0/671	0.72	1/888 (0.1%)
23	u	0.30	0/671	0.82	1/888 (0.1%)
24	AT	0.22	0/519	0.66	0/691
24	L	0.27	0/507	0.67	0/674
25	AU	0.17	0/1816	0.38	0/2830
26	AV	0.16	0/69659	0.34	1/108672 (0.0%)
26	N	0.21	0/69659	0.36	0/108672
27	AW	0.15	0/2828	0.34	0/4410
27	O	0.18	0/2828	0.35	0/4410
28	AX	0.24	0/2121	0.69	0/2852
28	P	0.27	0/2121	0.70	0/2852
29	AY	0.25	0/1586	0.65	1/2134 (0.0%)
29	Q	0.24	0/1586	0.61	0/2134
30	AZ	0.19	0/1571	0.57	0/2113
30	R	0.24	0/1571	0.66	0/2113
31	Aa	0.24	0/1434	0.72	0/1926
31	S	0.29	0/1434	0.68	0/1926
32	Ab	0.22	0/1343	0.62	0/1816
32	T	0.23	0/1333	0.64	2/1805 (0.1%)
33	Ac	0.23	0/1122	0.67	0/1515
33	U	0.26	0/1122	0.69	0/1515
34	Ad	0.25	0/1046	0.65	1/1410 (0.1%)
34	V	0.30	0/993	0.65	0/1341
35	Ae	0.21	0/1152	0.59	0/1551
35	W	0.23	0/1152	0.58	0/1551
36	Af	0.23	0/947	0.70	0/1268
36	X	0.29	0/947	0.71	0/1268
37	Ag	0.23	0/1054	0.69	0/1403
37	Y	0.28	0/1054	0.69	0/1403
38	Ah	0.25	0/1093	0.65	0/1460
38	Z	0.27	0/1093	0.68	0/1460
39	Ai	0.26	0/958	0.83	2/1281 (0.2%)
39	a	0.29	0/964	0.80	0/1289
40	Aj	0.20	0/902	0.58	0/1209
40	b	0.27	0/902	0.80	0/1209
41	Ak	0.25	0/929	0.73	0/1242

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
41	c	0.29	0/929	0.75	0/1242
42	Al	0.24	0/960	0.64	0/1278
42	d	0.27	0/960	0.68	0/1278
43	Am	0.25	0/829	0.72	0/1107
43	e	0.28	0/829	0.76	2/1107 (0.2%)
44	An	0.22	0/864	0.65	0/1156
44	f	0.28	0/864	0.75	0/1156
45	Ao	0.22	0/744	0.64	0/994
45	g	0.26	0/744	0.72	0/994
46	Ap	0.18	0/787	0.61	0/1051
46	h	0.25	0/787	0.65	0/1051
47	Aq	0.24	0/766	0.64	0/1025
47	i	0.24	0/766	0.63	0/1025
48	Ar	0.20	0/576	0.62	0/762
48	j	0.24	0/582	0.65	0/769
49	As	0.21	0/635	0.67	0/848
49	k	0.30	0/635	0.76	0/848
50	At	0.20	0/510	0.63	0/677
50	l	0.29	0/510	0.77	0/677
51	Au	0.27	0/439	0.74	0/587
51	m	0.27	0/453	0.75	0/605
52	Av	0.20	0/450	0.64	0/599
52	n	0.23	0/435	0.67	0/581
53	Aw	0.19	0/416	0.57	0/554
53	o	0.26	0/416	0.78	1/554 (0.2%)
54	Ax	0.23	0/380	0.72	0/498
54	p	0.26	0/380	0.74	0/498
55	Ay	0.22	0/513	0.60	0/676
55	q	0.31	0/513	0.74	0/676
56	Az	0.22	0/303	0.76	2/397 (0.5%)
56	r	0.30	0/303	0.80	0/397
57	B	0.24	0/10668	0.64	3/14419 (0.0%)
58	D	0.25	0/893	0.61	0/1205
58	y	0.27	0/893	0.76	0/1205
59	E	0.31	0/969	0.70	1/1300 (0.1%)
59	z	0.28	0/969	0.78	2/1300 (0.2%)
60	M	0.19	0/1778	0.34	0/2768
61	s	0.24	0/326	0.53	0/441
62	w	0.20	0/1302	0.47	0/2018
63	x	0.23	0/970	0.65	0/1307
All	All	0.21	0/335634	0.48	40/499883 (0.0%)

There are no bond length outliers.

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	e	51	VAL	N-CA-C	-11.28	96.56	108.96
18	AN	59	MET	CB-CG-SD	6.93	133.49	112.70
2	1	52	GLU	N-CA-CB	6.60	120.47	110.30
7	AG	48	GLU	N-CA-CB	6.53	120.36	110.30
2	AB	77	SER	CA-C-N	6.38	133.73	121.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	32895	0	16553	459	0
1	AA	33015	0	16617	438	0
2	1	1704	0	1732	40	0
2	AB	1704	0	1732	48	0
3	2	1624	0	1696	52	0
3	AC	1624	0	1696	35	0
4	3	1643	0	1707	31	0
4	AD	1643	0	1707	34	0
5	4	1105	0	1148	30	0
5	AE	1105	0	1148	25	0
6	5	817	0	808	18	0
6	AF	817	0	808	16	0
7	6	1181	0	1238	28	0
7	AG	1181	0	1238	33	0
8	7	979	0	1031	31	0
8	AH	979	0	1031	31	0
9	8	1022	0	1070	38	0
9	AI	1022	0	1070	23	0
10	9	786	0	828	20	0
10	AJ	786	0	828	23	0
11	A	1622	0	821	17	0
12	A1	551	0	588	10	0
12	v	589	0	629	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	A2	2340	0	2379	46	0
14	A3	1638	0	830	18	0
15	AK	1026	0	1092	22	0
15	C	1026	0	1092	14	0
16	AL	883	0	941	26	0
16	F	883	0	941	29	0
17	AM	774	0	824	24	0
17	G	791	0	826	17	0
18	AN	710	0	728	19	0
18	H	702	0	721	9	0
19	AO	649	0	666	17	0
19	I	648	0	666	17	0
20	AP	648	0	691	19	0
20	J	648	0	691	17	0
21	AQ	544	0	565	13	0
21	K	535	0	552	13	0
22	AR	637	0	665	19	0
22	t	620	0	647	17	0
23	AS	665	0	714	16	0
23	u	665	0	714	19	0
24	AT	511	0	513	6	0
24	L	499	0	499	15	0
25	AU	1625	0	822	12	0
26	AV	62195	0	31280	794	0
26	N	62195	0	31280	882	0
27	AW	2529	0	1281	41	0
27	O	2529	0	1281	36	0
28	AX	2082	0	2154	51	0
28	P	2082	0	2154	52	0
29	AY	1565	0	1616	45	0
29	Q	1565	0	1616	34	0
30	AZ	1552	0	1619	27	0
30	R	1552	0	1619	51	0
31	Aa	1410	0	1444	36	0
31	S	1410	0	1444	35	0
32	Ab	1323	0	1371	21	0
32	T	1313	0	1358	29	0
33	Ac	1111	0	1148	17	0
33	U	1111	0	1148	14	0
34	Ad	1032	0	1085	19	0
34	V	979	0	1028	23	0
35	Ae	1129	0	1162	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	W	1129	0	1162	22	0
36	Af	938	0	1012	21	0
36	X	938	0	1012	27	0
37	Ag	1045	0	1117	15	0
37	Y	1045	0	1117	29	0
38	Ah	1074	0	1157	18	0
38	Z	1074	0	1157	22	0
39	Ai	945	0	989	17	0
39	a	951	0	994	28	0
40	Aj	892	0	923	15	0
40	b	892	0	923	30	0
41	Ak	917	0	962	27	0
41	c	917	0	962	32	0
42	Al	947	0	1019	26	0
42	d	947	0	1019	18	0
43	Am	816	0	839	19	0
43	e	816	0	839	18	0
44	An	857	0	922	16	0
44	f	857	0	922	24	0
45	Ao	738	0	807	22	0
45	g	738	0	807	25	0
46	Ap	779	0	831	12	0
46	h	779	0	831	19	0
47	Aq	753	0	780	13	0
47	i	753	0	780	16	0
48	Ar	569	0	581	9	0
48	j	575	0	592	16	0
49	As	625	0	652	12	0
49	k	625	0	652	24	0
50	At	509	0	543	9	0
50	l	509	0	543	13	0
51	Au	435	0	470	11	0
51	m	449	0	488	8	0
52	Av	444	0	458	10	0
52	n	429	0	440	8	0
53	Aw	409	0	440	10	0
53	o	409	0	440	10	0
54	Ax	377	0	418	9	0
54	p	377	0	418	11	0
55	Ay	504	0	572	10	0
55	q	504	0	572	15	0
56	Az	302	0	343	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	r	302	0	343	12	0
57	B	10462	0	10585	212	0
58	D	877	0	887	25	0
58	y	877	0	887	28	0
59	E	955	0	1016	18	0
59	z	955	0	1016	36	0
60	M	1593	0	810	6	0
61	s	316	0	283	3	0
62	w	1175	0	594	12	0
63	x	958	0	988	23	0
All	All	309783	0	213505	4516	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 4516 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)
26:N:408:G:H1	26:N:419:U:H3	1.07	1.01
26:N:1215:G:H1	26:N:1234:U:H3	1.11	0.99
1:AA:1116:U:H3	1:AA:1184:G:H1	1.10	0.98
1:0:76:G:H1	1:0:93:U:H3	1.01	0.98
1:0:1006:G:N1	1:0:1022:A:C2	2.33	0.97

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	1	216/241 (90%)	203 (94%)	13 (6%)	0	100	100
2	AB	216/241 (90%)	204 (94%)	12 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	2	204/233 (88%)	197 (97%)	7 (3%)	0	100	100
3	AC	204/233 (88%)	197 (97%)	7 (3%)	0	100	100
4	3	203/206 (98%)	194 (96%)	9 (4%)	0	100	100
4	AD	203/206 (98%)	196 (97%)	7 (3%)	0	100	100
5	4	148/167 (89%)	140 (95%)	8 (5%)	0	100	100
5	AE	148/167 (89%)	137 (93%)	11 (7%)	0	100	100
6	5	98/135 (73%)	94 (96%)	4 (4%)	0	100	100
6	AF	98/135 (73%)	91 (93%)	7 (7%)	0	100	100
7	6	149/179 (83%)	145 (97%)	4 (3%)	0	100	100
7	AG	149/179 (83%)	143 (96%)	6 (4%)	0	100	100
8	7	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
8	AH	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
9	8	125/130 (96%)	114 (91%)	11 (9%)	0	100	100
9	AI	125/130 (96%)	118 (94%)	7 (6%)	0	100	100
10	9	96/103 (93%)	89 (93%)	7 (7%)	0	100	100
10	AJ	96/103 (93%)	84 (88%)	11 (12%)	1 (1%)	12	45
12	A1	64/71 (90%)	63 (98%)	1 (2%)	0	100	100
12	v	68/71 (96%)	68 (100%)	0	0	100	100
13	A2	288/1300 (22%)	280 (97%)	8 (3%)	0	100	100
15	AK	130/234 (56%)	124 (95%)	6 (5%)	0	100	100
15	C	130/234 (56%)	128 (98%)	2 (2%)	0	100	100
16	AL	112/118 (95%)	105 (94%)	7 (6%)	0	100	100
16	F	112/118 (95%)	106 (95%)	6 (5%)	0	100	100
17	AM	92/101 (91%)	80 (87%)	12 (13%)	0	100	100
17	G	96/101 (95%)	94 (98%)	2 (2%)	0	100	100
18	AN	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
18	H	85/89 (96%)	83 (98%)	2 (2%)	0	100	100
19	AO	80/82 (98%)	73 (91%)	7 (9%)	0	100	100
19	I	80/82 (98%)	73 (91%)	7 (9%)	0	100	100
20	AP	78/84 (93%)	69 (88%)	9 (12%)	0	100	100
20	J	78/84 (93%)	71 (91%)	7 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	AQ	64/75 (85%)	59 (92%)	5 (8%)	0	100	100
21	K	63/75 (84%)	62 (98%)	1 (2%)	0	100	100
22	AR	77/92 (84%)	73 (95%)	4 (5%)	0	100	100
22	t	75/92 (82%)	71 (95%)	4 (5%)	0	100	100
23	AS	83/87 (95%)	83 (100%)	0	0	100	100
23	u	83/87 (95%)	82 (99%)	1 (1%)	0	100	100
24	AT	60/70 (86%)	56 (93%)	4 (7%)	0	100	100
24	L	58/70 (83%)	54 (93%)	4 (7%)	0	100	100
28	AX	269/273 (98%)	257 (96%)	12 (4%)	0	100	100
28	P	269/273 (98%)	252 (94%)	17 (6%)	0	100	100
29	AY	207/209 (99%)	197 (95%)	10 (5%)	0	100	100
29	Q	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
30	AZ	199/201 (99%)	195 (98%)	4 (2%)	0	100	100
30	R	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
31	Aa	175/179 (98%)	168 (96%)	7 (4%)	0	100	100
31	S	175/179 (98%)	166 (95%)	9 (5%)	0	100	100
32	Ab	174/177 (98%)	163 (94%)	11 (6%)	0	100	100
32	T	173/177 (98%)	169 (98%)	4 (2%)	0	100	100
33	Ac	147/149 (99%)	137 (93%)	10 (7%)	0	100	100
33	U	147/149 (99%)	141 (96%)	6 (4%)	0	100	100
34	Ad	139/142 (98%)	122 (88%)	17 (12%)	0	100	100
34	V	132/142 (93%)	121 (92%)	11 (8%)	0	100	100
35	Ae	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
35	W	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
36	Af	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
36	X	120/123 (98%)	115 (96%)	5 (4%)	0	100	100
37	Ag	141/144 (98%)	134 (95%)	7 (5%)	0	100	100
37	Y	141/144 (98%)	135 (96%)	6 (4%)	0	100	100
38	Ah	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
38	Z	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
39	Ai	116/127 (91%)	111 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	a	117/127 (92%)	110 (94%)	7 (6%)	0	100	100
40	Aj	114/117 (97%)	111 (97%)	3 (3%)	0	100	100
40	b	114/117 (97%)	107 (94%)	7 (6%)	0	100	100
41	Ak	112/115 (97%)	106 (95%)	6 (5%)	0	100	100
41	c	112/115 (97%)	102 (91%)	10 (9%)	0	100	100
42	Al	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
42	d	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
43	Am	101/103 (98%)	91 (90%)	10 (10%)	0	100	100
43	e	101/103 (98%)	96 (95%)	5 (5%)	0	100	100
44	An	108/110 (98%)	103 (95%)	5 (5%)	0	100	100
44	f	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
45	Ao	91/100 (91%)	86 (94%)	5 (6%)	0	100	100
45	g	91/100 (91%)	81 (89%)	10 (11%)	0	100	100
46	Ap	100/104 (96%)	93 (93%)	7 (7%)	0	100	100
46	h	100/104 (96%)	90 (90%)	10 (10%)	0	100	100
47	Aq	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
47	i	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
48	Ar	73/85 (86%)	71 (97%)	2 (3%)	0	100	100
48	j	73/85 (86%)	68 (93%)	5 (7%)	0	100	100
49	As	75/78 (96%)	75 (100%)	0	0	100	100
49	k	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
50	At	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
50	l	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
51	Au	54/59 (92%)	53 (98%)	1 (2%)	0	100	100
51	m	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
52	Av	54/57 (95%)	50 (93%)	4 (7%)	0	100	100
52	n	52/57 (91%)	49 (94%)	3 (6%)	0	100	100
53	Aw	48/55 (87%)	47 (98%)	1 (2%)	0	100	100
53	o	48/55 (87%)	46 (96%)	2 (4%)	0	100	100
54	Ax	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
54	p	44/46 (96%)	43 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
55	Ay	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
55	q	62/65 (95%)	57 (92%)	5 (8%)	0	100	100
56	Az	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
56	r	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
57	B	1291/1326 (97%)	1235 (96%)	56 (4%)	0	100	100
58	D	115/129 (89%)	110 (96%)	5 (4%)	0	100	100
58	y	115/129 (89%)	105 (91%)	10 (9%)	0	100	100
59	E	121/124 (98%)	111 (92%)	10 (8%)	0	100	100
59	z	121/124 (98%)	113 (93%)	7 (6%)	1 (1%)	16	50
61	s	35/179 (20%)	33 (94%)	2 (6%)	0	100	100
63	x	125/165 (76%)	119 (95%)	6 (5%)	0	100	100
All	All	13392/15548 (86%)	12714 (95%)	676 (5%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
59	z	25	GLU
10	AJ	89	ARG

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	1	180/199 (90%)	180 (100%)	0	100	100
2	AB	180/199 (90%)	180 (100%)	0	100	100
3	2	170/190 (90%)	170 (100%)	0	100	100
3	AC	170/190 (90%)	170 (100%)	0	100	100
4	3	172/173 (99%)	172 (100%)	0	100	100
4	AD	172/173 (99%)	172 (100%)	0	100	100
5	4	113/126 (90%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	AE	113/126 (90%)	112 (99%)	1 (1%)	70	81
6	5	87/116 (75%)	87 (100%)	0	100	100
6	AF	87/116 (75%)	87 (100%)	0	100	100
7	6	124/147 (84%)	124 (100%)	0	100	100
7	AG	124/147 (84%)	124 (100%)	0	100	100
8	7	104/105 (99%)	104 (100%)	0	100	100
8	AH	104/105 (99%)	104 (100%)	0	100	100
9	8	105/107 (98%)	104 (99%)	1 (1%)	68	80
9	AI	105/107 (98%)	105 (100%)	0	100	100
10	9	86/90 (96%)	86 (100%)	0	100	100
10	AJ	86/90 (96%)	86 (100%)	0	100	100
12	A1	56/61 (92%)	56 (100%)	0	100	100
12	v	60/61 (98%)	60 (100%)	0	100	100
13	A2	249/1135 (22%)	249 (100%)	0	100	100
15	AK	110/181 (61%)	110 (100%)	0	100	100
15	C	110/181 (61%)	110 (100%)	0	100	100
16	AL	92/96 (96%)	92 (100%)	0	100	100
16	F	92/96 (96%)	92 (100%)	0	100	100
17	AM	79/84 (94%)	79 (100%)	0	100	100
17	G	82/84 (98%)	82 (100%)	0	100	100
18	AN	75/77 (97%)	75 (100%)	0	100	100
18	H	75/77 (97%)	75 (100%)	0	100	100
19	AO	65/65 (100%)	65 (100%)	0	100	100
19	I	65/65 (100%)	65 (100%)	0	100	100
20	AP	74/78 (95%)	74 (100%)	0	100	100
20	J	74/78 (95%)	74 (100%)	0	100	100
21	AQ	57/65 (88%)	56 (98%)	1 (2%)	51	74
21	K	56/65 (86%)	56 (100%)	0	100	100
22	AR	70/79 (89%)	70 (100%)	0	100	100
22	t	68/79 (86%)	68 (100%)	0	100	100
23	AS	65/66 (98%)	65 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	u	65/66 (98%)	65 (100%)	0	100	100
24	AT	58/62 (94%)	58 (100%)	0	100	100
24	L	57/62 (92%)	57 (100%)	0	100	100
28	AX	216/218 (99%)	216 (100%)	0	100	100
28	P	216/218 (99%)	216 (100%)	0	100	100
29	AY	164/164 (100%)	164 (100%)	0	100	100
29	Q	164/164 (100%)	164 (100%)	0	100	100
30	AZ	165/165 (100%)	165 (100%)	0	100	100
30	R	165/165 (100%)	165 (100%)	0	100	100
31	Aa	148/150 (99%)	148 (100%)	0	100	100
31	S	148/150 (99%)	148 (100%)	0	100	100
32	Ab	137/138 (99%)	137 (100%)	0	100	100
32	T	136/138 (99%)	136 (100%)	0	100	100
33	Ac	114/114 (100%)	114 (100%)	0	100	100
33	U	114/114 (100%)	114 (100%)	0	100	100
34	Ad	109/110 (99%)	109 (100%)	0	100	100
34	V	104/110 (94%)	104 (100%)	0	100	100
35	Ae	116/116 (100%)	116 (100%)	0	100	100
35	W	116/116 (100%)	116 (100%)	0	100	100
36	Af	103/104 (99%)	103 (100%)	0	100	100
36	X	103/104 (99%)	103 (100%)	0	100	100
37	Ag	102/103 (99%)	102 (100%)	0	100	100
37	Y	102/103 (99%)	102 (100%)	0	100	100
38	Ah	109/109 (100%)	109 (100%)	0	100	100
38	Z	109/109 (100%)	109 (100%)	0	100	100
39	Ai	98/103 (95%)	98 (100%)	0	100	100
39	a	99/103 (96%)	98 (99%)	1 (1%)	68	80
40	Aj	86/87 (99%)	86 (100%)	0	100	100
40	b	86/87 (99%)	86 (100%)	0	100	100
41	Ak	99/100 (99%)	99 (100%)	0	100	100
41	c	99/100 (99%)	98 (99%)	1 (1%)	68	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	Al	89/90 (99%)	89 (100%)	0	100	100
42	d	89/90 (99%)	89 (100%)	0	100	100
43	Am	84/84 (100%)	83 (99%)	1 (1%)	63	79
43	e	84/84 (100%)	83 (99%)	1 (1%)	63	79
44	An	93/93 (100%)	93 (100%)	0	100	100
44	f	93/93 (100%)	93 (100%)	0	100	100
45	Ao	80/84 (95%)	80 (100%)	0	100	100
45	g	80/84 (95%)	80 (100%)	0	100	100
46	Ap	83/85 (98%)	83 (100%)	0	100	100
46	h	83/85 (98%)	83 (100%)	0	100	100
47	Aq	78/78 (100%)	78 (100%)	0	100	100
47	i	78/78 (100%)	78 (100%)	0	100	100
48	Ar	56/63 (89%)	56 (100%)	0	100	100
48	j	57/63 (90%)	57 (100%)	0	100	100
49	As	67/68 (98%)	67 (100%)	0	100	100
49	k	67/68 (98%)	66 (98%)	1 (2%)	57	76
50	At	55/55 (100%)	55 (100%)	0	100	100
50	l	55/55 (100%)	55 (100%)	0	100	100
51	Au	47/49 (96%)	47 (100%)	0	100	100
51	m	48/49 (98%)	48 (100%)	0	100	100
52	Av	47/48 (98%)	47 (100%)	0	100	100
52	n	46/48 (96%)	46 (100%)	0	100	100
53	Aw	45/49 (92%)	45 (100%)	0	100	100
53	o	45/49 (92%)	45 (100%)	0	100	100
54	Ax	38/38 (100%)	38 (100%)	0	100	100
54	p	38/38 (100%)	38 (100%)	0	100	100
55	Ay	51/52 (98%)	51 (100%)	0	100	100
55	q	51/52 (98%)	51 (100%)	0	100	100
56	Az	34/34 (100%)	34 (100%)	0	100	100
56	r	34/34 (100%)	34 (100%)	0	100	100
57	B	1130/1158 (98%)	1128 (100%)	2 (0%)	87	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	D	90/99 (91%)	90 (100%)	0	100	100
58	y	90/99 (91%)	90 (100%)	0	100	100
59	E	103/104 (99%)	102 (99%)	1 (1%)	68	80
59	z	103/104 (99%)	102 (99%)	1 (1%)	68	80
61	s	34/158 (22%)	34 (100%)	0	100	100
63	x	96/123 (78%)	96 (100%)	0	100	100
All	All	11204/12816 (87%)	11192 (100%)	12 (0%)	87	91

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	a	107	ASN
41	c	3	ASN
59	z	24	LEU
43	e	51	VAL
43	Am	66	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 107 such sidechains are listed below:

Mol	Chain	Res	Type
50	At	38	GLN
57	B	1165	ASN
50	l	39	GLN
50	At	58	ASN
57	B	439	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	1532/1542 (99%)	276 (18%)	14 (0%)
1	AA	1538/1542 (99%)	276 (17%)	14 (0%)
11	A	75/76 (98%)	20 (26%)	4 (5%)
14	A3	76/77 (98%)	29 (38%)	5 (6%)
25	AU	75/76 (98%)	12 (16%)	0
26	AV	2895/2903 (99%)	509 (17%)	20 (0%)
26	N	2895/2903 (99%)	539 (18%)	14 (0%)
27	AW	117/120 (97%)	23 (19%)	0
27	O	117/120 (97%)	22 (18%)	2 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
60	M	74/75 (98%)	14 (18%)	1 (1%)
62	w	56/57 (98%)	32 (57%)	0
All	All	9450/9491 (99%)	1752 (18%)	74 (0%)

5 of 1752 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	4	U
1	0	5	U
1	0	9	G
1	0	32	A
1	0	39	G

5 of 74 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
60	M	44	A
26	N	2832	U
26	N	277	G
26	N	1134	A
1	AA	115	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 ⓘ

There are no chain breaks in this entry.

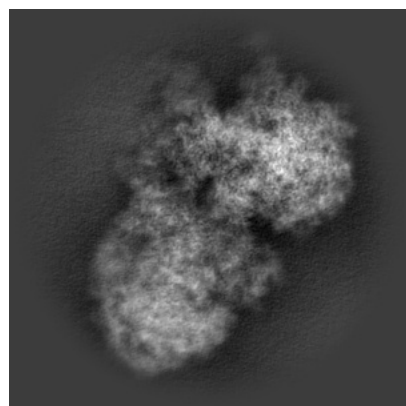
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51340. These allow visual inspection of the internal detail of the map and identification of artifacts.

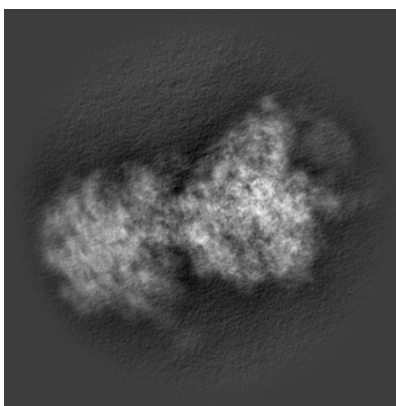
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

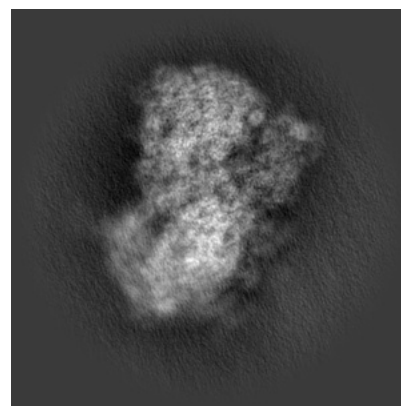
6.1.1 Primary map



X

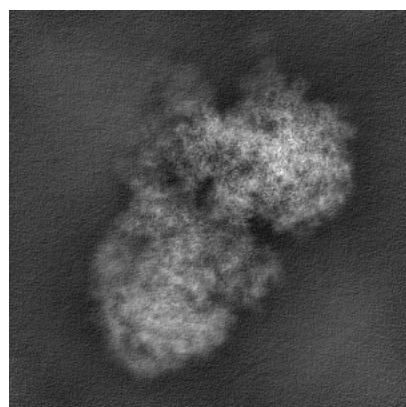


Y

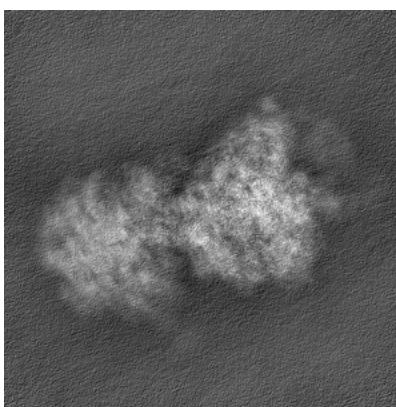


Z

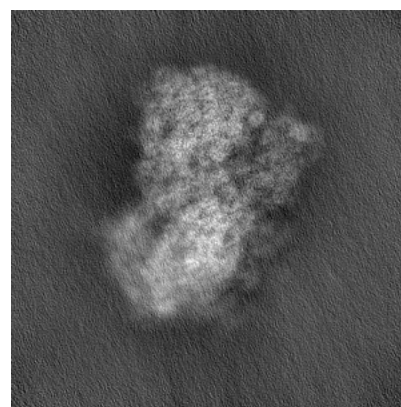
6.1.2 Raw map



X



Y

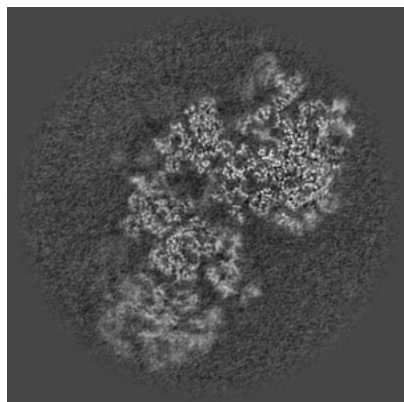


Z

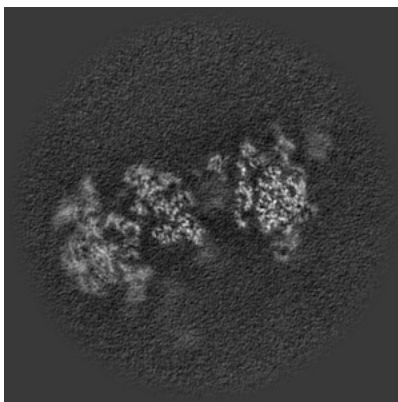
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

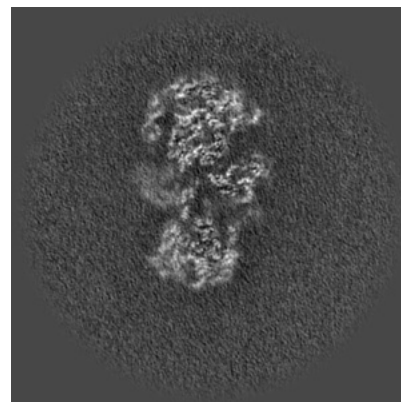
6.2.1 Primary map



X Index: 175

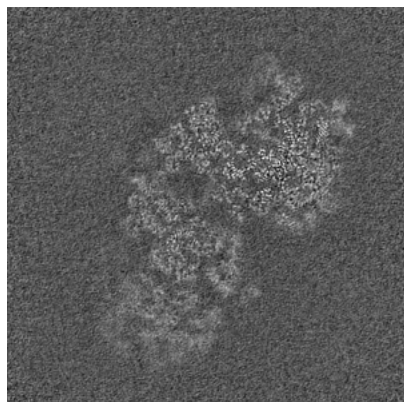


Y Index: 175

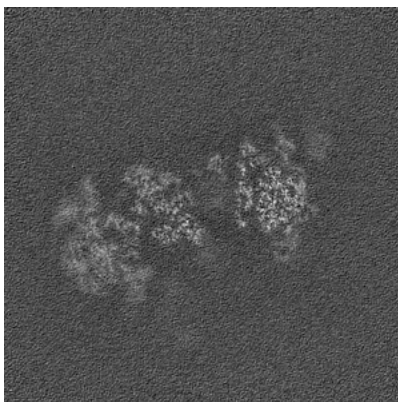


Z Index: 175

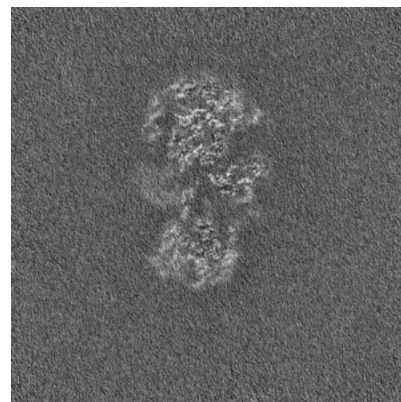
6.2.2 Raw map



X Index: 175



Y Index: 175

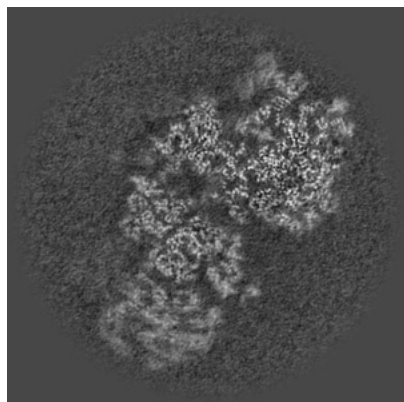


Z Index: 175

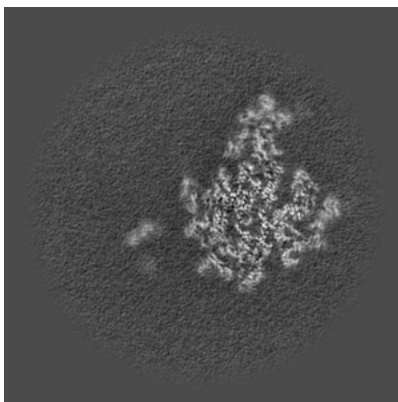
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

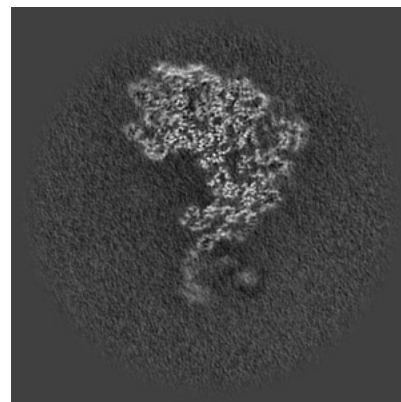
6.3.1 Primary map



X Index: 176

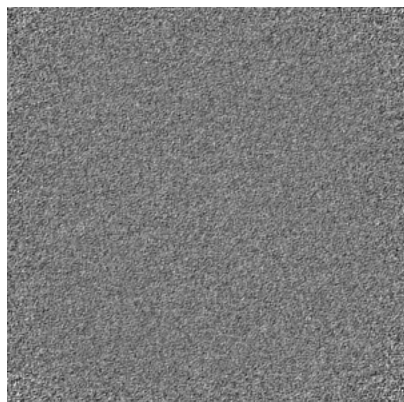


Y Index: 236

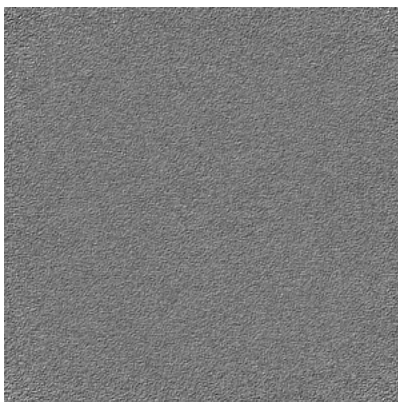


Z Index: 211

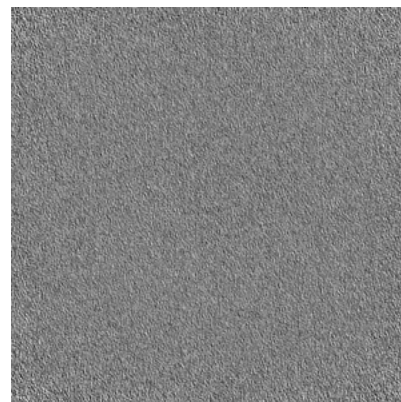
6.3.2 Raw map



X Index: 0



Y Index: 0

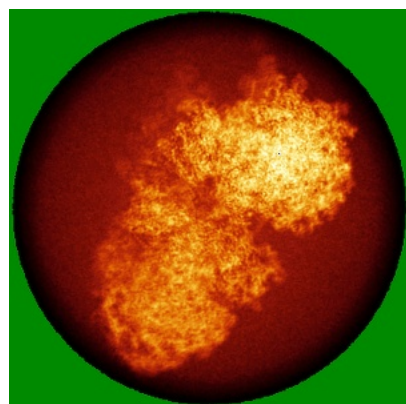


Z Index: 0

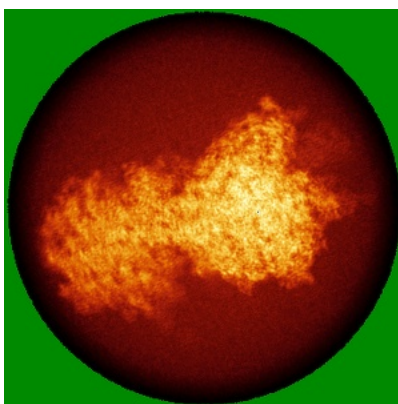
The images above show the largest variance slices of the map in three orthogonal directions.

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

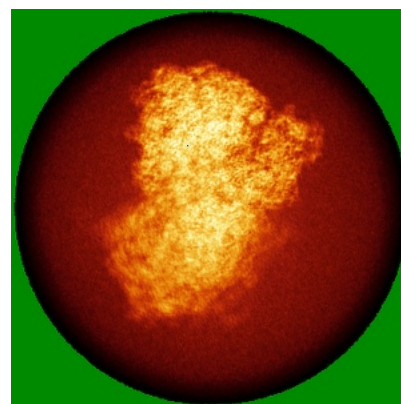
6.4.1 Primary map



X

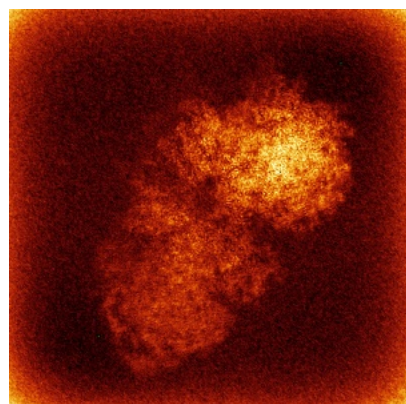


Y

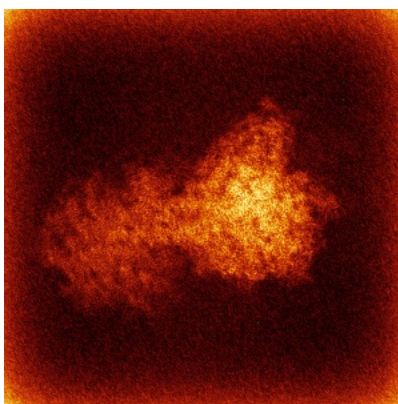


Z

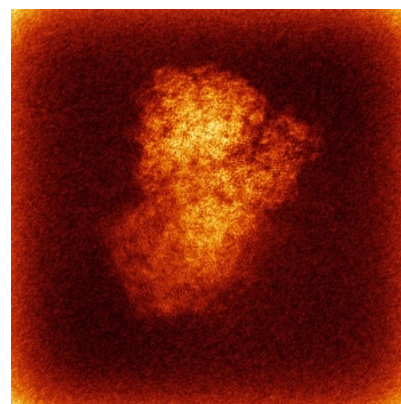
6.4.2 Raw map



X



Y

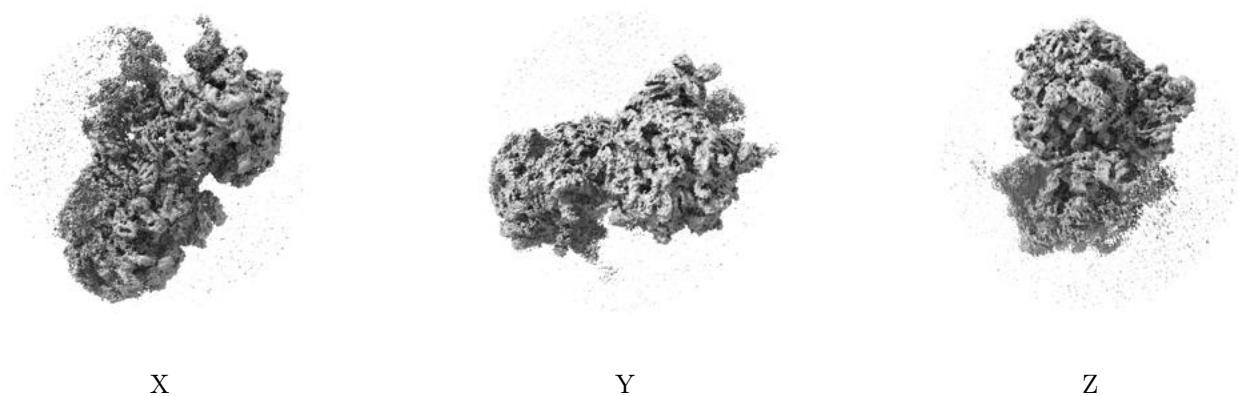


Z

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

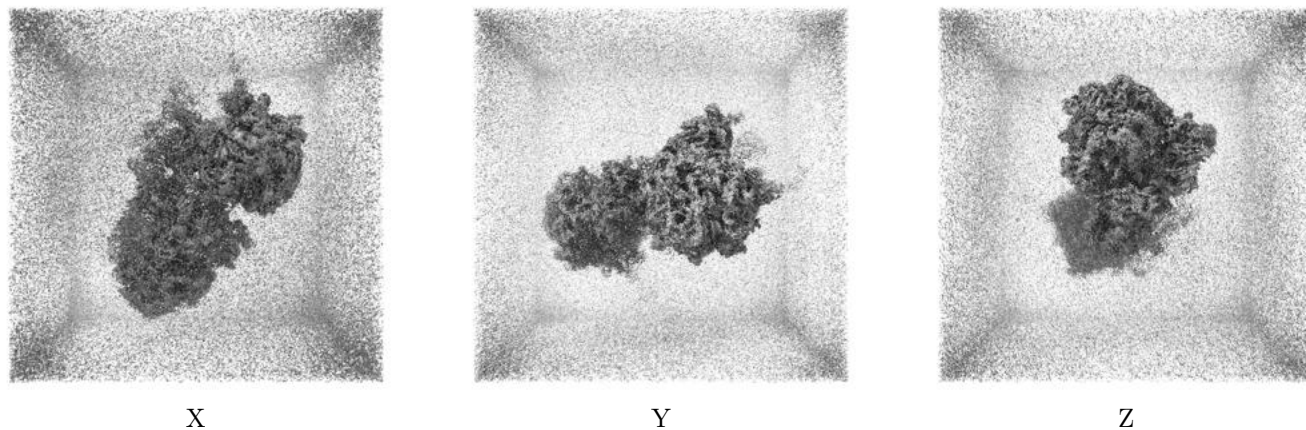
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.32. 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.

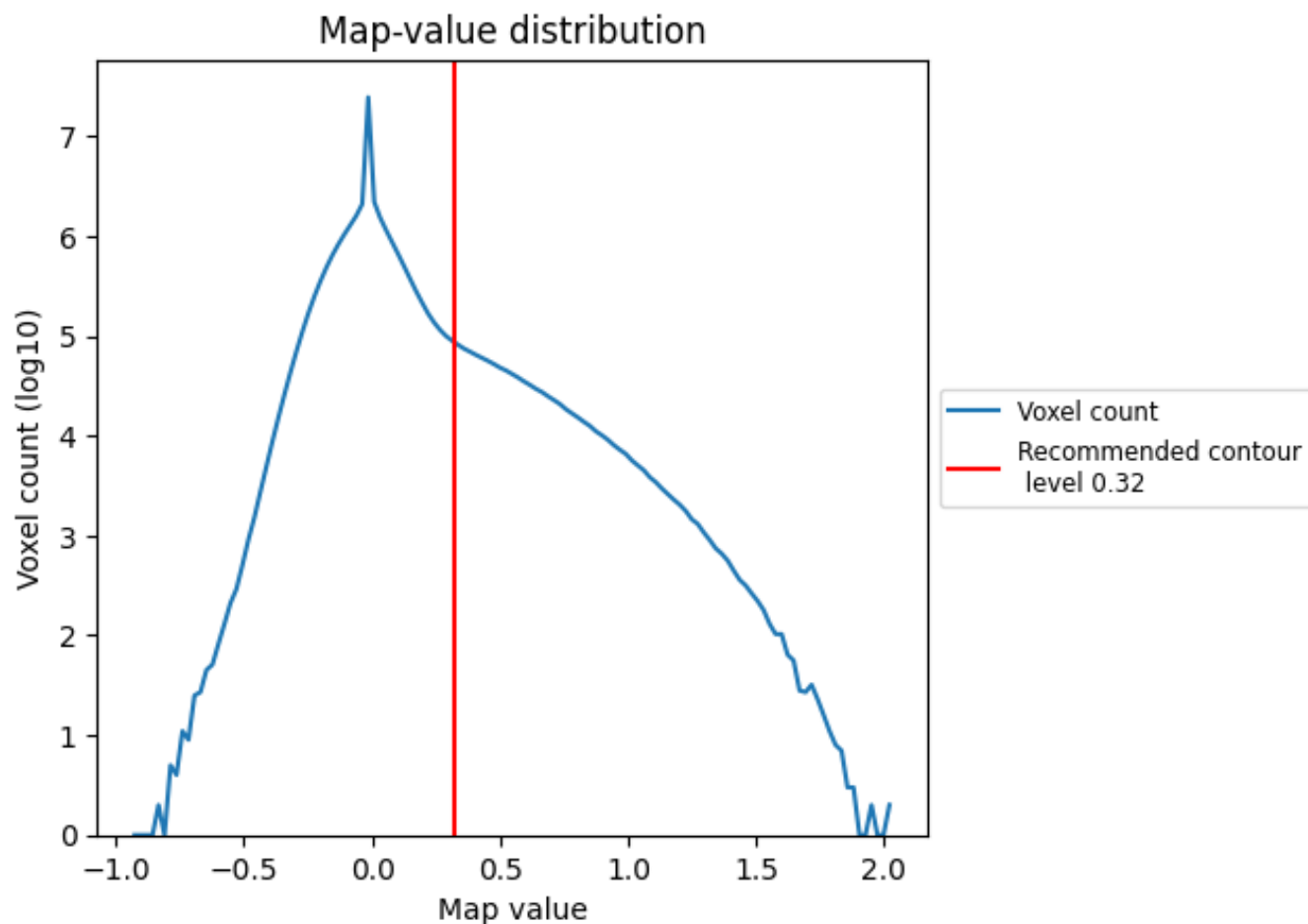
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

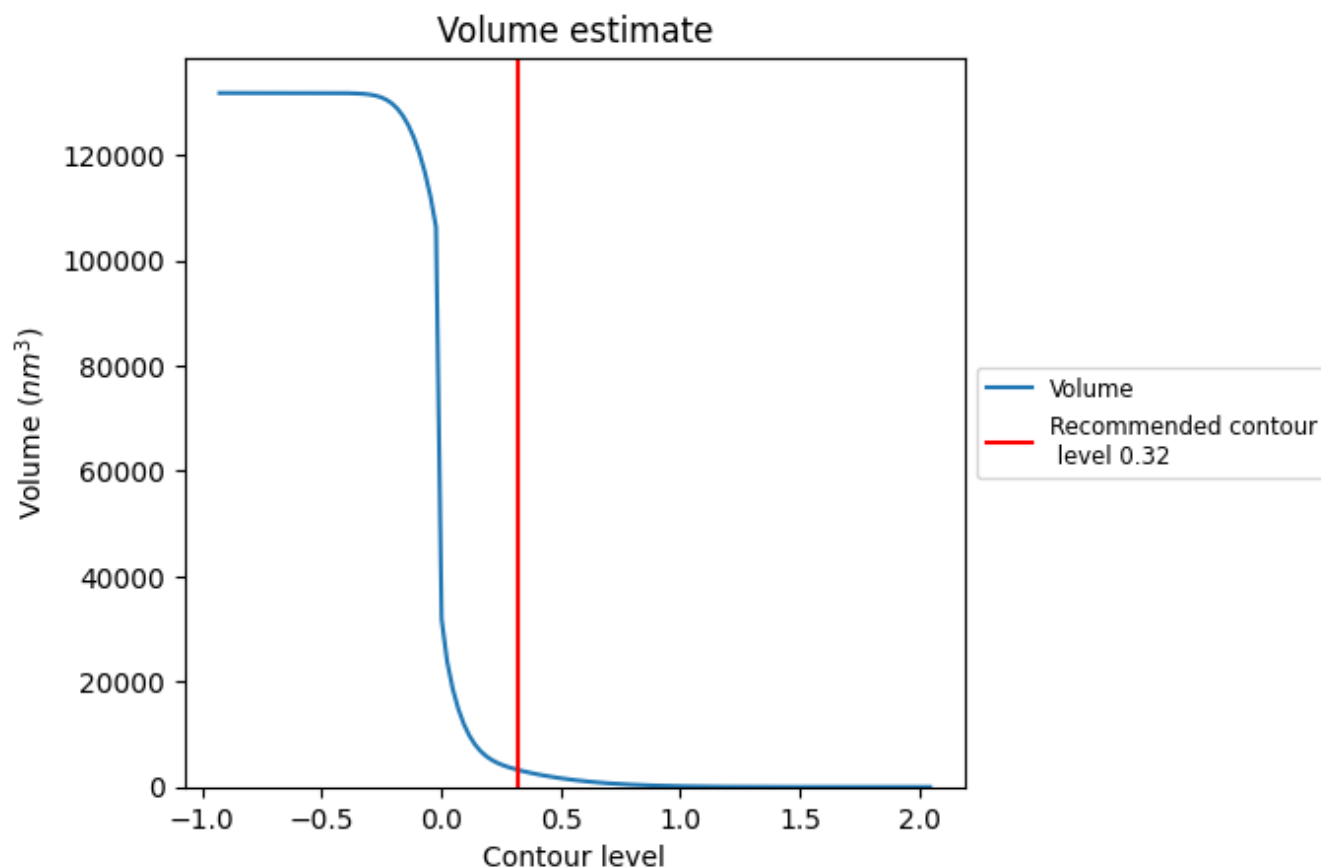
This section contains the results of statistical analysis of the map.

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.

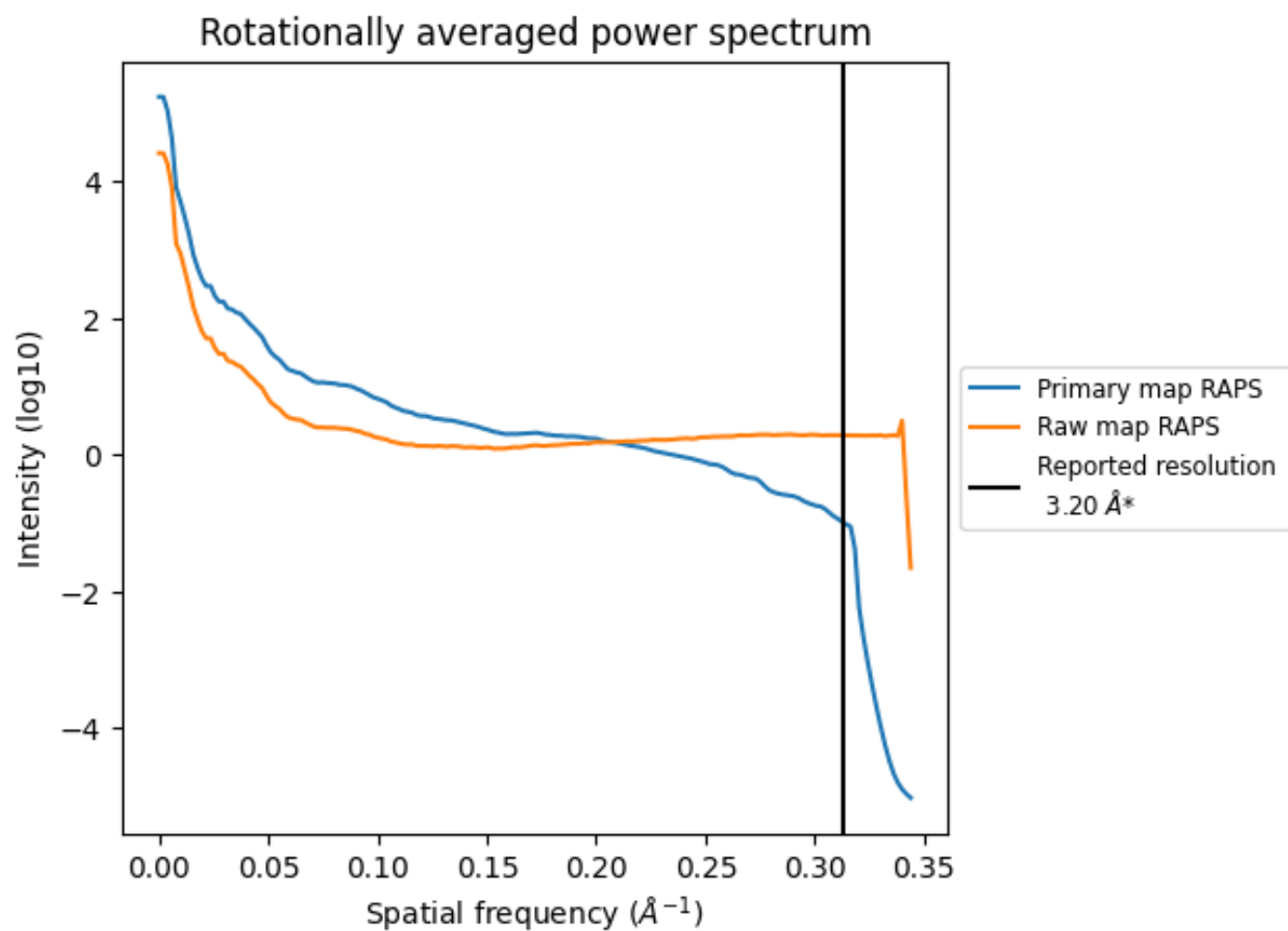
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3255 nm³; this corresponds to an approximate mass of 2940 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 ⓘ

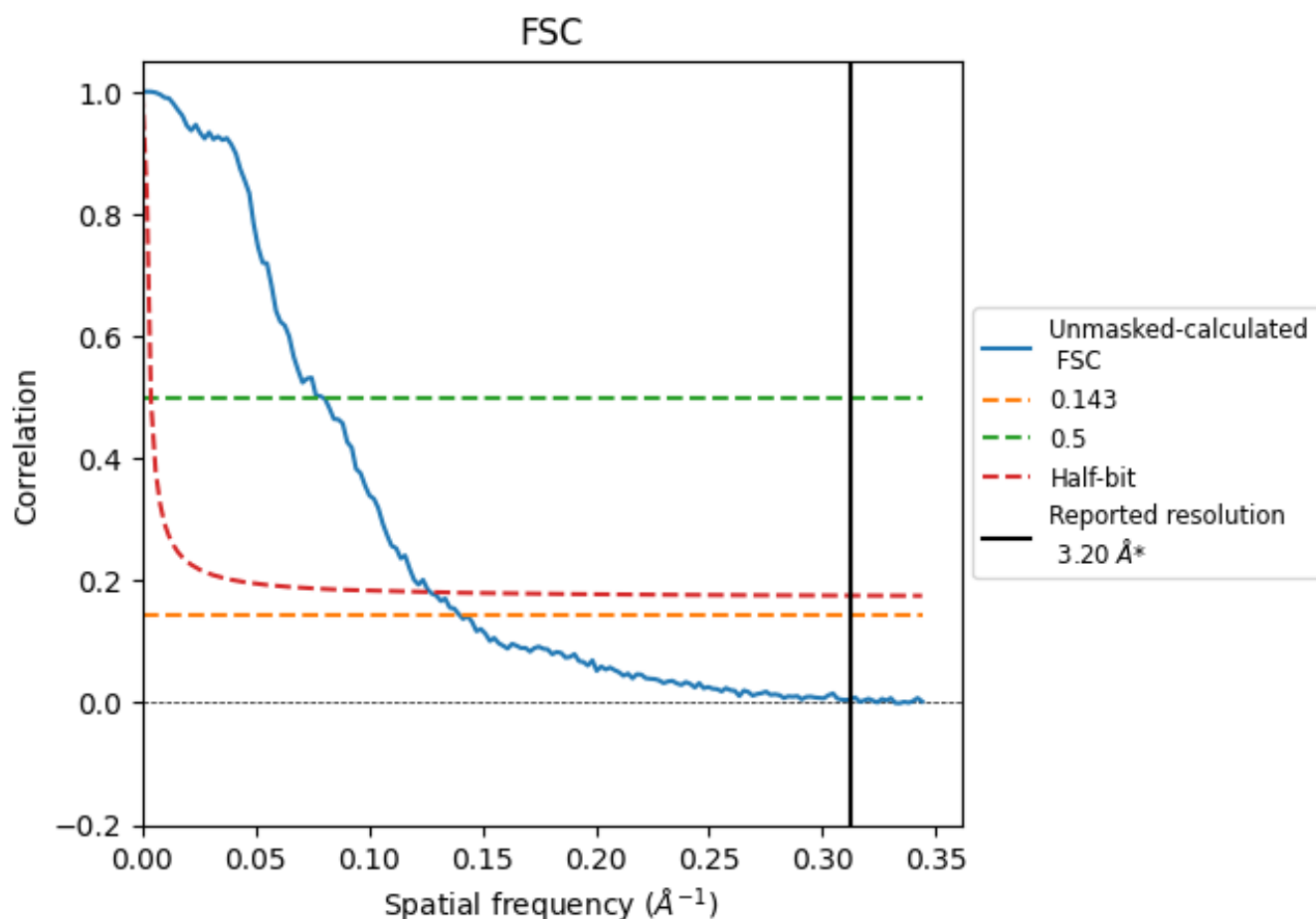


*Reported resolution corresponds to spatial frequency of 0.312 $\text{\AA}^{-1}$

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

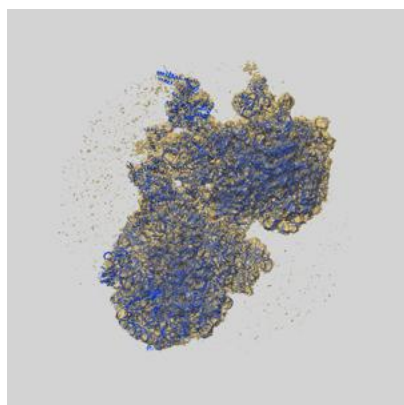
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.14	12.61	7.87

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.14 differs from the reported value 3.2 by more than 10 %

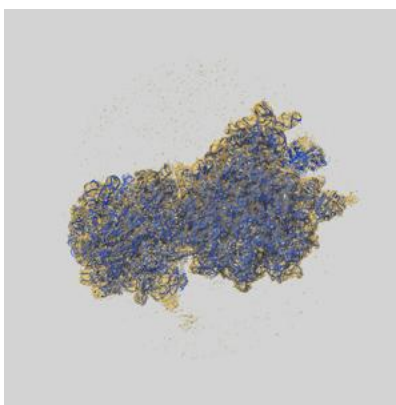
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51340 and PDB model 9GGR. Per-residue inclusion information can be found in section [3](#) on page [21](#).

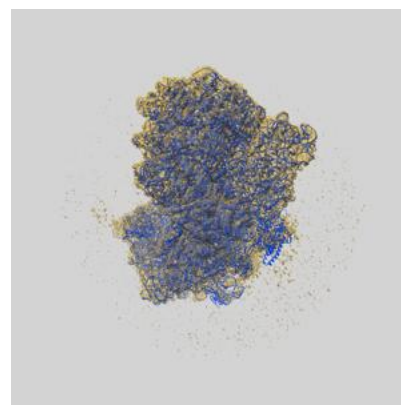
9.1 Map-model overlay [i](#)



X



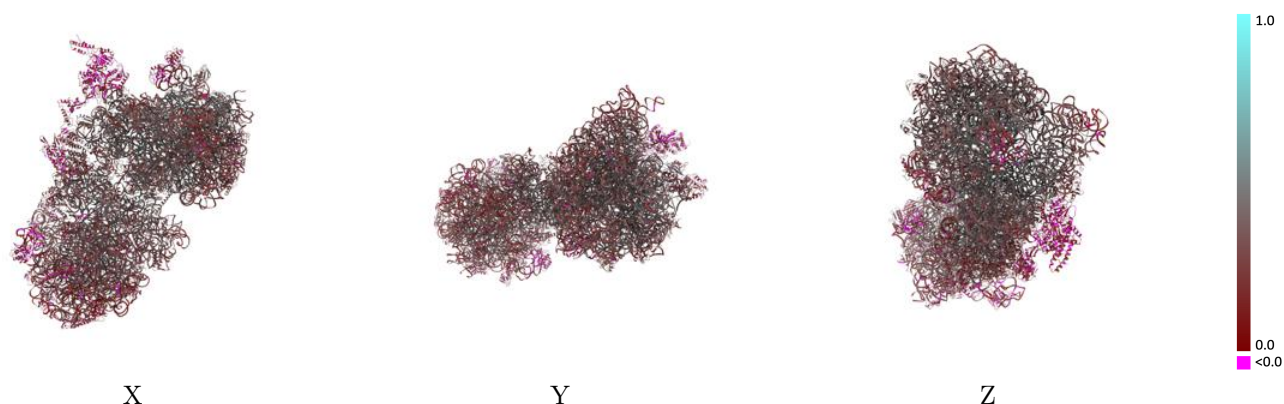
Y



Z

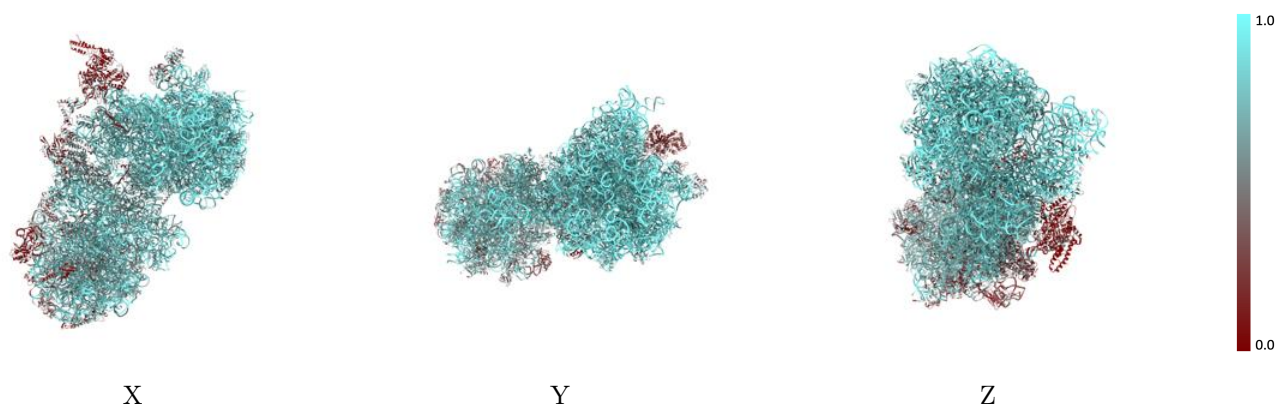
The images above show the 3D surface view of the map at the recommended contour level 0.32 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



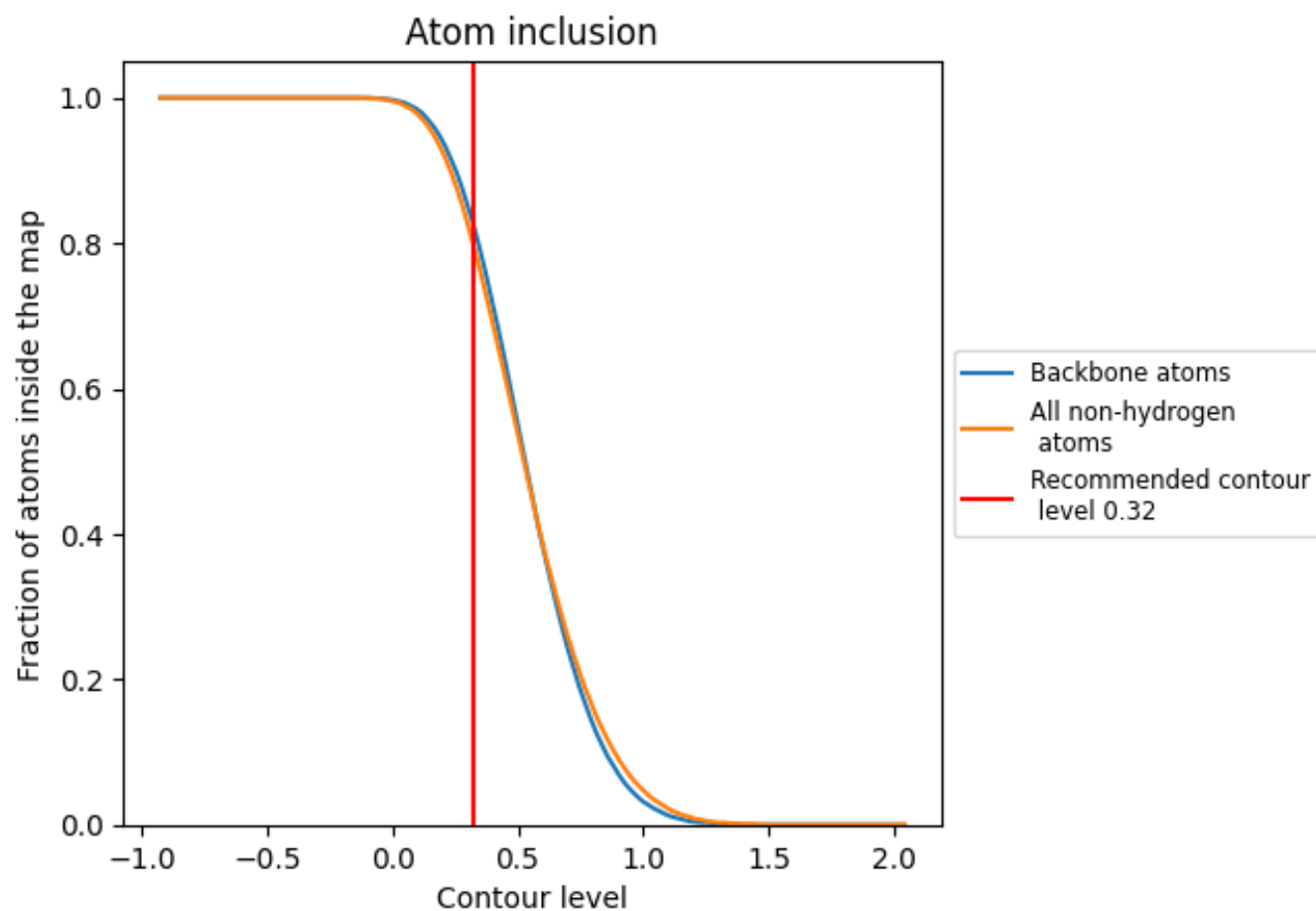
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.32).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 80% 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 (0.32) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8020	 0.3110
0	 0.9510	 0.3720
1	 0.6820	 0.3260
2	 0.6850	 0.3590
3	 0.6880	 0.3110
4	 0.7500	 0.3820
5	 0.7390	 0.3720
6	 0.7290	 0.3850
7	 0.7490	 0.3500
8	 0.7130	 0.3610
9	 0.6060	 0.3570
A	 0.9240	 0.3910
A1	 0.5590	 0.2950
A2	 0.4000	 0.2130
A3	 0.6820	 0.2620
AA	 0.9350	 0.3460
AB	 0.6460	 0.3140
AC	 0.6560	 0.3730
AD	 0.6500	 0.3880
AE	 0.7020	 0.3890
AF	 0.6220	 0.2620
AG	 0.6440	 0.2980
AH	 0.6500	 0.3050
AI	 0.6680	 0.3000
AJ	 0.6690	 0.3560
AK	 0.0200	 0.1160
AL	 0.6320	 0.2510
AM	 0.6880	 0.3160
AN	 0.6910	 0.2400
AO	 0.7000	 0.3260
AP	 0.6580	 0.2750
AQ	 0.6370	 0.2720
AR	 0.6990	 0.2710
AS	 0.7050	 0.2320
AT	 0.4440	 0.2180



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Chain	Atom inclusion	Q-score
AU	 0.5880	 0.2780
AV	 0.8350	 0.2520
AW	 0.7900	 0.1910
AX	 0.5120	 0.2560
AY	 0.5760	 0.2580
AZ	 0.4250	 0.2030
Aa	 0.3940	 0.2120
Ab	 0.4630	 0.1890
Ac	 0.1300	 0.1490
Ad	 0.1590	 0.0850
Ae	 0.6720	 0.2260
Af	 0.5510	 0.3320
Ag	 0.5470	 0.2600
Ah	 0.5830	 0.2730
Ai	 0.7090	 0.2300
Aj	 0.3910	 0.1750
Ak	 0.5330	 0.2650
Al	 0.7000	 0.2100
Am	 0.6260	 0.1960
An	 0.6720	 0.2650
Ao	 0.5420	 0.1850
Ap	 0.2360	 0.1650
Aq	 0.6270	 0.1770
Ar	 0.7050	 0.2260
As	 0.6340	 0.2540
At	 0.5110	 0.1510
Au	 0.6150	 0.2230
Av	 0.7500	 0.2490
Aw	 0.3740	 0.2300
Ax	 0.7010	 0.2720
Ay	 0.6640	 0.2690
Az	 0.6370	 0.2730
B	 0.2610	 0.1590
C	 0.1960	 0.1290
D	 0.7330	 0.4350
E	 0.8180	 0.4410
F	 0.7720	 0.3150
G	 0.7530	 0.3510
H	 0.7930	 0.3290
I	 0.7200	 0.3080
J	 0.7480	 0.3100
K	 0.7350	 0.4030

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Chain	Atom inclusion	Q-score
L	 0.7480	 0.2670
M	 0.9480	 0.4000
N	 0.9420	 0.3650
O	 0.9610	 0.3170
P	 0.7950	 0.4250
Q	 0.8560	 0.4130
R	 0.7850	 0.3250
S	 0.7530	 0.3120
T	 0.8350	 0.3670
U	 0.6810	 0.3270
V	 0.3590	 0.1110
W	 0.8930	 0.4000
X	 0.8010	 0.4370
Y	 0.7850	 0.3660
Z	 0.8530	 0.4490
a	 0.8380	 0.3170
b	 0.7680	 0.2700
c	 0.7520	 0.3440
d	 0.8500	 0.3680
e	 0.8420	 0.3720
f	 0.7790	 0.3360
g	 0.7370	 0.2950
h	 0.6940	 0.2710
i	 0.8420	 0.3390
j	 0.8680	 0.4060
k	 0.8270	 0.4170
l	 0.7560	 0.2720
m	 0.8600	 0.3640
n	 0.8790	 0.3330
o	 0.7560	 0.3650
p	 0.7940	 0.3690
q	 0.7820	 0.4010
r	 0.8600	 0.4480
s	 0.8020	 0.4170
t	 0.8070	 0.3610
u	 0.7190	 0.2470
v	 0.6350	 0.3610
w	 0.4820	 0.2710
x	 0.5730	 0.1820
y	 0.6060	 0.2700
z	 0.7290	 0.4200