



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:20 AM UTC

PDB ID : 6FTJ / pdb_00006ftj
EMDB ID : EMD-4317
Title : Cryo-EM Structure of the Mammalian Oligosaccharyltransferase Bound to Sec61 and the Non-programmed 80S Ribosome
Authors : Braunger, K.; Becker, T.; Beckmann, R.
Deposited on : 2018-02-22
Resolution : 4.70 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

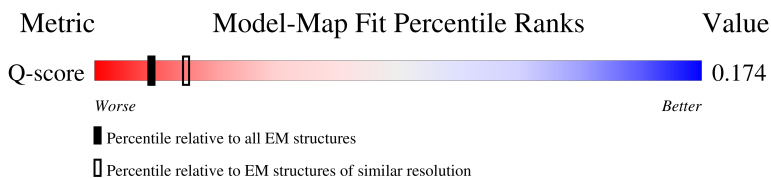
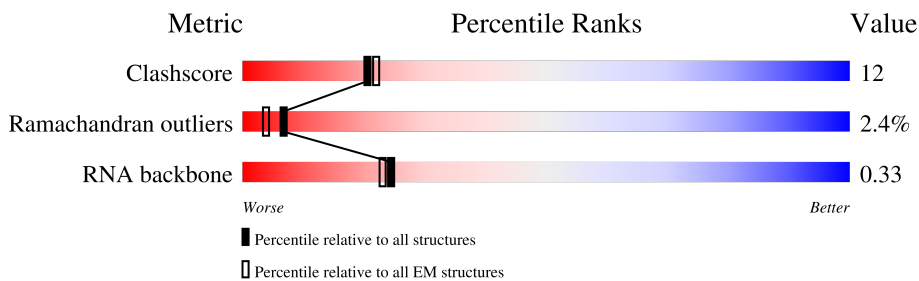
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.70 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	1989 (4.20 - 5.20)

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	A	244	<p>57% (Poor fit), 81% (0 outliers), 18% (1 outlier), . (2+ outliers)</p>
2	B	394	<p>55% (Poor fit), 82% (0 outliers), 16% (1 outlier), . (2+ outliers)</p>
3	C	362	<p>61% (Poor fit), 80% (0 outliers), 20% (1 outlier)</p>
4	D	292	<p>58% (Poor fit), 86% (0 outliers), 14% (1 outlier)</p>

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Mol	Chain	Length	Quality of chain
5	E	248	69% 68% 24% 5%
6	F	225	77% 85% 14%
7	G	241	76% 88% 12%
8	H	190	79% 86% 13%
9	I	213	62% 77% 16%
10	J	169	54% 89% 11%
11	L	210	61% 80% 20%
12	M	138	68% 87% 13%
13	N	203	57% 87% 13%
14	O	199	75% 83% 16%
15	P	153	30% 89% 11%
16	Q	187	61% 87% 12%
17	R	180	49% 82% 17%
18	S	175	74% 86% 13%
19	T	159	76% 87% 13%
20	U	99	46% 85% 13%
21	V	131	62% 92% 8%
22	W	63	52% 90% 10%
23	X	119	48% 86% 13%
24	Y	134	49% 90% 10%
25	Z	135	58% 79% 18%
26	a	147	69% 82% 16%
27	b	75	63% 89% 9%
28	c	94	59% 88% 12%
29	d	107	43% 88% 12%

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Mol	Chain	Length	Quality of chain
30	e	128	72% 77% 22% .
31	f	109	83% 69% 27% 5%
32	g	114	68% 83% 17%
33	h	122	42% 87% 11% .
34	i	102	64% 92% 8%
35	j	86	24% 79% 15% 6%
36	k	69	67% 83% 14% .
37	l	50	20% 84% 16%
38	m	52	69% 85% 15%
39	n	23	57% 91% 9%
40	o	104	46% 82% 16% .
41	p	91	60% 90% 9% .
42	r	136	61% 65% 31% .
43	s	198	84% 88% 11% .
44	t	163	86% 75% 23% .
45	u	3662	20% 44% 39% 14% .
46	v	120	8% 63% 31% 6%
47	w	156	11% 42% 46% 12% .
48	x	426	26% 62% 36% .
49	y	62	26% 73% 27%
50	z	29	69% 38% 52% 10%
51	1	162	28% 93% 7%
52	2	60	15% 92% 7% .
53	3	120	31% 72% 26% .
54	4	34	9% 79% 21%

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Mol	Chain	Length	Quality of chain
55	5	696	
56	6	97	
57	7	25	
58	8	80	
59	K	8	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
61	ZN	o	201	-	-	X	-
62	9UB	5	809	-	-	X	-

2 Entry composition [i](#)

There are 62 unique types of molecules in this entry. The entry contains 152111 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 uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	244	1868	1171	382	309	6	0	0

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	394	3148	2007	591	537	13	0	0

- Molecule 3 is a protein called Ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	362	2884	1814	578	478	14	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	362	LYS	SER	conflict	UNP G1SVW5
C	363	SER	ASP	conflict	UNP G1SVW5

- Molecule 4 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	292	2386	1509	437	426	14	0	0

- Molecule 5 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	236	1898	1215	362	318	3	0	0

- Molecule 6 is a protein called U130.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	225	1870	1202	358	301	9	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	175	ALA	THR	conflict	UNP G1SV32
F	185	GLY	ASN	conflict	UNP G1SV32
F	202	ARG	HIS	conflict	UNP G1SV32
F	233	GLU	GLY	conflict	UNP G1SV32

- Molecule 7 is a protein called uL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	241	1934	1233	371	326	4	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	191	GLY	CYS	conflict	UNP G1STW0

- Molecule 8 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	190	1516	954	284	272	6	0	0

- Molecule 9 is a protein called Ribosomal protein L10 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	204	1655	1051	319	272	13	0	0

- Molecule 10 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	169	1353	855	252	240	6	0	0

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	L	210	1703	1065	354	280	4	0	0

- Molecule 12 is a protein called Ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	M	138	1137	727	221	182	7	0	0

- Molecule 13 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	N	203	1701	1072	359	266	4	0	0

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	O	199	1638	1056	321	256	5	0	0

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	P	153	1242	776	241	216	9	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	54	GLN	LYS	conflict	UNP G1TVT6

- Molecule 16 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	Q	187	1506	941	311	249	5	0	0

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	R	180	1508	933	328	238	9	0	0

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	S	175	1454	925	284	235	10	0	0

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	T	159	1298	823	252	217	6	0	0

- Molecule 20 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	U	99	808	518	141	147	2	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	32	GLY	ARG	conflict	UNP G1TSG1
U	36	ALA	GLU	conflict	UNP G1TSG1
U	39	PHE	SER	conflict	UNP G1TSG1
U	54	GLY	ARG	conflict	UNP G1TSG1
U	60	VAL	ALA	conflict	UNP G1TSG1
U	97	ARG	HIS	conflict	UNP G1TSG1

- Molecule 21 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	V	131	979	618	184	172	5	0	0

- Molecule 22 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	W	63	528	337	103	85	3	0	0

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	X	119	976	624	183	168	1	0	0

- Molecule 24 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	Y	134	1115	700	226	186	3	0	0

- Molecule 25 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	Z	135	1107	714	208	182	3	0	0

- Molecule 26 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	a	147	1162	734	239	185	4	0	0

- Molecule 27 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	b	75	609	378	130	98	3	0	0

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	c	94	732	465	130	131	6	0	0

- Molecule 29 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	d	107	888	560	171	155	2	0	0

- Molecule 30 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 32 is a protein called eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 33 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 34 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 35 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 36 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 39 is a protein called 60s ribosomal protein l41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 41 is a protein called Ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 42 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	136	Total	C	N	O	S	0	0
			1094	676	229	183	6		

- Molecule 43 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	198	Total	C	N	O	S	0	0
			1523	969	265	280	9		

- Molecule 44 is a protein called Ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	163	Total	C	N	O	S	0	0
			1238	773	230	230	5		

- Molecule 45 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	u	3662	Total	C	N	O	P	0	0
			78486	34947	14363	25515	3661		

- Molecule 46 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	v	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 47 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	w	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 48 is a protein called Protein transport protein Sec61 subunit alpha isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	x	426	Total	C	N	O	S	0	0
			3313	2181	535	576	21		

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	?	-	THR	deletion	UNP P38377
x	?	-	GLY	deletion	UNP P38377
x	?	-	MET	deletion	UNP P38377
x	?	-	TYR	deletion	UNP P38377
x	?	-	GLY	deletion	UNP P38377
x	?	-	ASP	deletion	UNP P38377
x	?	-	PRO	deletion	UNP P38377
x	?	-	SER	deletion	UNP P38377
x	?	-	GLU	deletion	UNP P38377
x	?	-	MET	deletion	UNP P38377
x	?	-	GLY	deletion	UNP P38377
x	145	SER	ALA	conflict	UNP P38377
x	?	-	SER	deletion	UNP P38377

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Chain	Residue	Modelled	Actual	Comment	Reference
x	?	-	GLY	deletion	UNP P38377
x	?	-	ASN	deletion	UNP P38377
x	?	-	LEU	deletion	UNP P38377
x	?	-	LEU	deletion	UNP P38377
x	?	-	VAL	deletion	UNP P38377
x	?	-	SER	deletion	UNP P38377
x	?	-	LEU	deletion	UNP P38377
x	?	-	LEU	deletion	UNP P38377
x	?	-	GLY	deletion	UNP P38377
x	?	-	THR	deletion	UNP P38377
x	?	-	TRP	deletion	UNP P38377
x	?	-	SER	deletion	UNP P38377
x	?	-	ASP	deletion	UNP P38377
x	?	-	THR	deletion	UNP P38377
x	?	-	SER	deletion	UNP P38377
x	?	-	SER	deletion	UNP P38377
x	?	-	GLY	deletion	UNP P38377
x	?	-	GLY	deletion	UNP P38377
x	?	-	PRO	deletion	UNP P38377
x	?	-	ALA	deletion	UNP P38377
x	?	-	ARG	deletion	UNP P38377
x	?	-	ALA	deletion	UNP P38377
x	?	-	TYR	deletion	UNP P38377

- Molecule 49 is a protein called Protein transport protein Sec61 subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	y	62	Total	C	N	O	S	0	0
			494	326	86	79	3		

- Molecule 50 is a protein called Protein transport protein Sec61 subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	z	29	Total	C	N	O	S	0	0
			229	157	36	34	2		

- Molecule 51 is a protein called Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1,RPN1.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	1	162	Total	C	N	O	0	0
			882	550	165	167		

- Molecule 52 is a protein called TMEM258.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
52	2	60	300	180	60	60	0	0

- Molecule 53 is a protein called Oligosaccharyltransferase complex subunit OSTC.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	3	120	802	529	130	136	7	0	0

- Molecule 54 is a protein called OST4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	4	34	268	180	41	45	2	0	0

- Molecule 55 is a protein called Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	5	644	5090	3331	819	904	36	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	88	LEU	ILE	conflict	UNP F1PJP5

- Molecule 56 is a protein called DAD1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
56	6	97	485	291	97	97	0	0

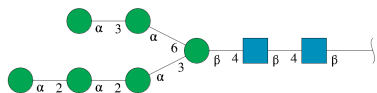
- Molecule 57 is a protein called OST48.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
57	7	25	125	75	25	25	0	0

- Molecule 58 is a protein called RPN2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
58	8	80	400	240	80	80	0	0

- Molecule 59 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
59	K	8	94	52	2	40	0	0

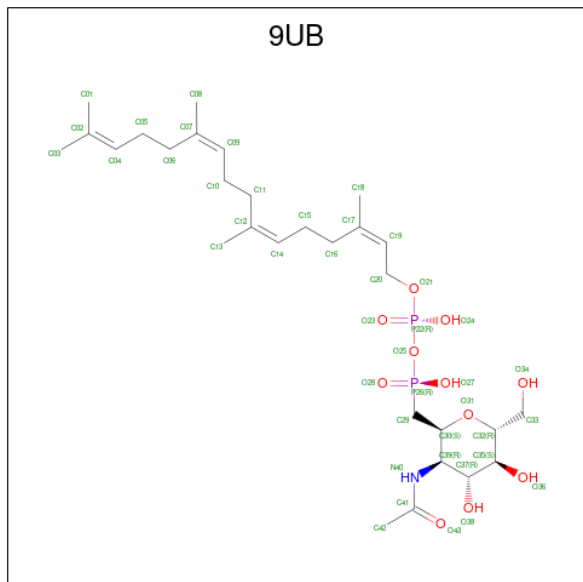
- Molecule 60 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
60	B	1	Total	Mg	0
			1	1	
60	I	1	Total	Mg	0
			1	1	
60	P	1	Total	Mg	0
			1	1	
60	V	1	Total	Mg	0
			1	1	
60	a	1	Total	Mg	0
			1	1	
60	e	1	Total	Mg	0
			1	1	
60	g	1	Total	Mg	0
			1	1	
60	u	145	Total	Mg	0
			145	145	
60	v	5	Total	Mg	0
			5	5	
60	w	2	Total	Mg	0
			2	2	

- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
61	g	1	Total	Zn	0
			1	1	
61	j	1	Total	Zn	0
			1	1	
61	m	1	Total	Zn	0
			1	1	
61	o	1	Total	Zn	0
			1	1	
61	p	1	Total	Zn	0
			1	1	

- Molecule 62 is [(2 {S},3 {R},4 {R},5 {S},6 {R})-3-acetamido-6-(hydroxymethyl)-4,5-bis(oxidanyl)oxan-2-yl]methyl-[oxidanyl-[(2 {Z},6 {Z},10 {Z})-3,7,11,15-tetramethylhexadeca-2,6,10,14-tetraenoxy]phosphoryl]oxy-phosphinic acid (CCD ID: 9UB) (formula: C₂₉H₅₁NO₁₁P₂).

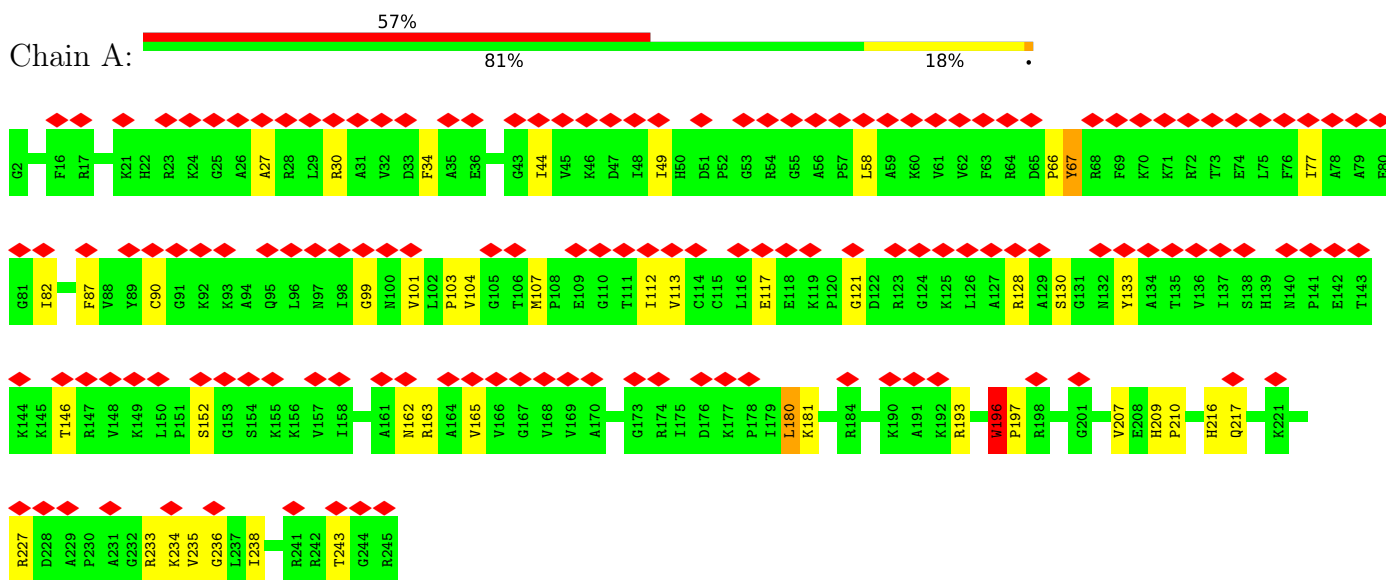


Mol	Chain	Residues	Atoms					AltConf
62	5	1	Total	C	N	O	P	0
			43	29	1	11	2	

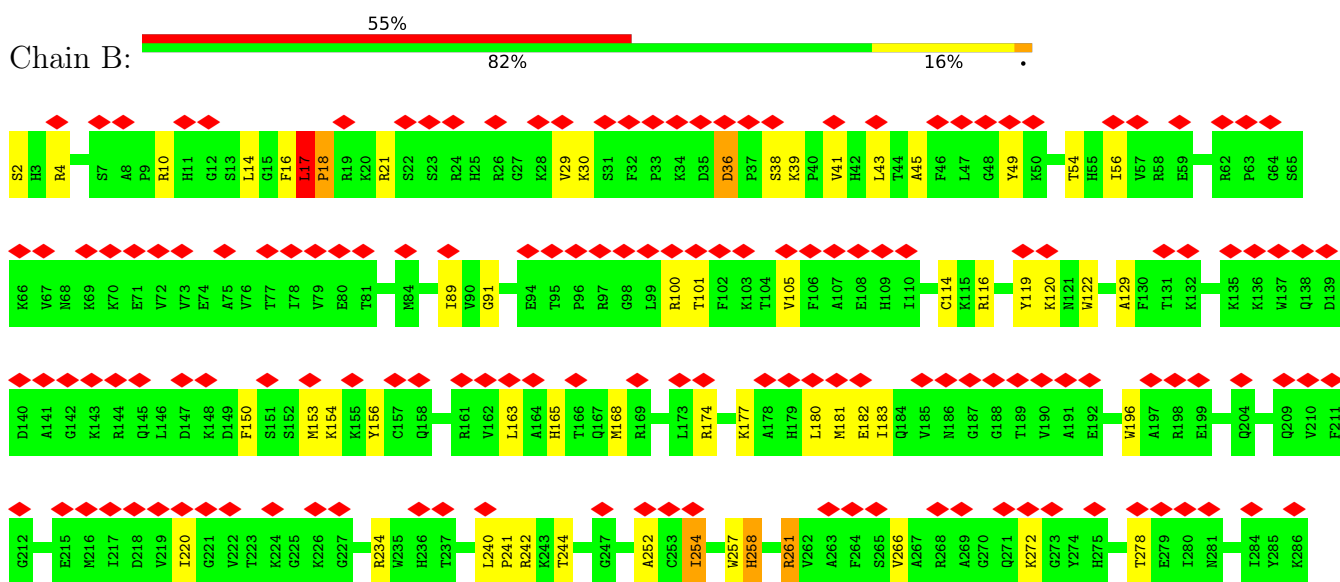
3 Residue-property plots [i](#)

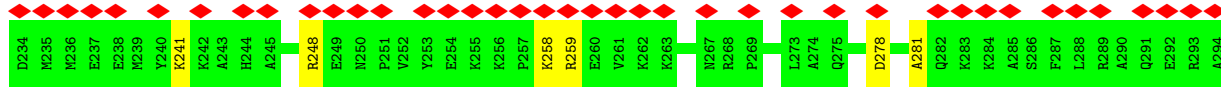
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: uL2

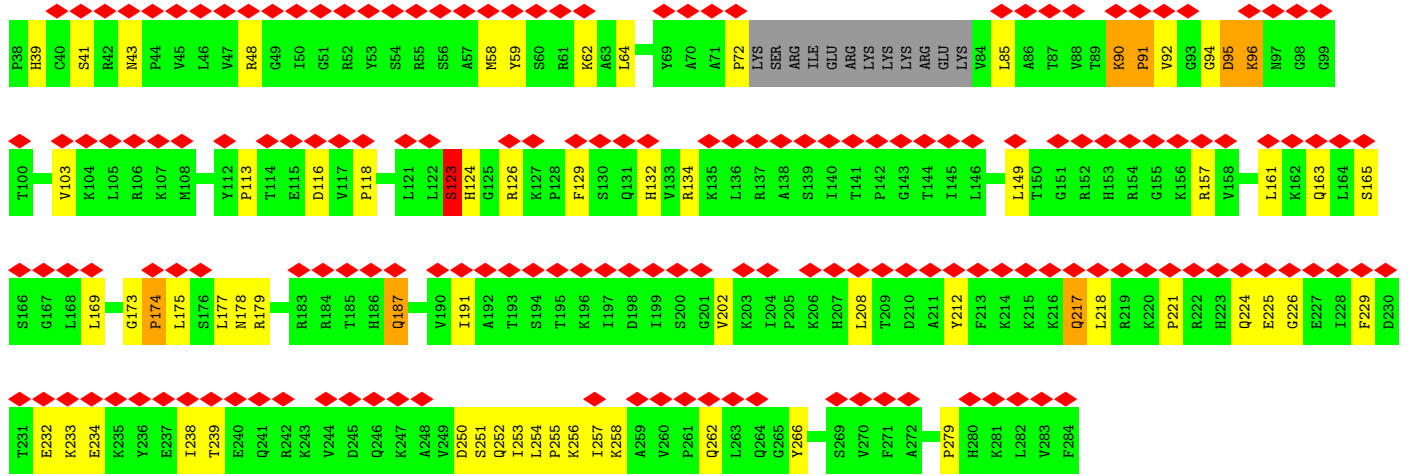


- Molecule 2: uL3

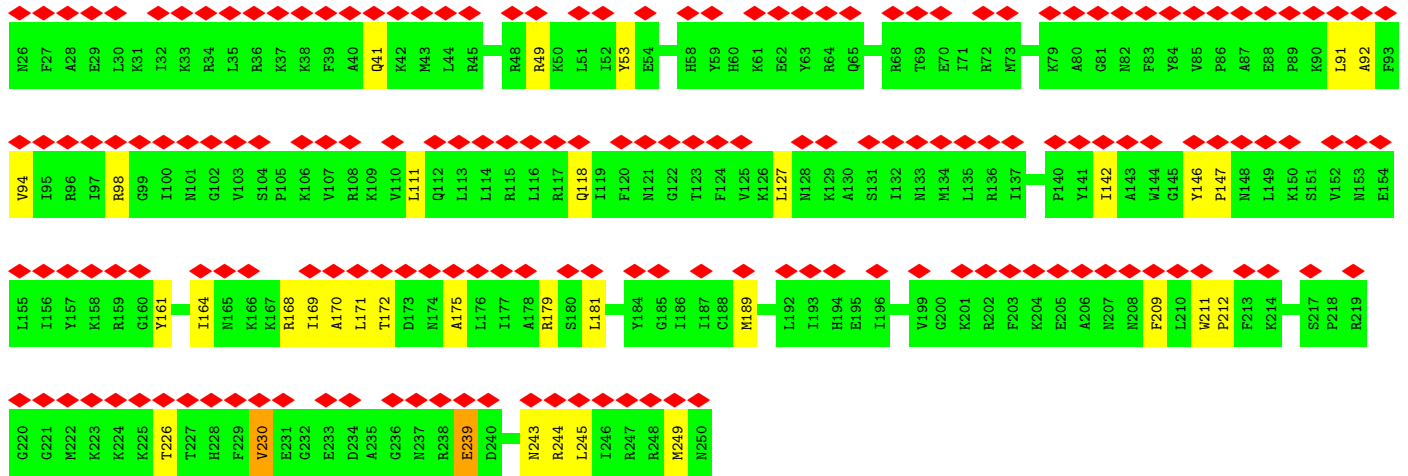
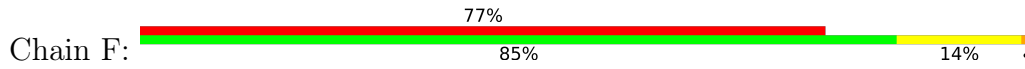




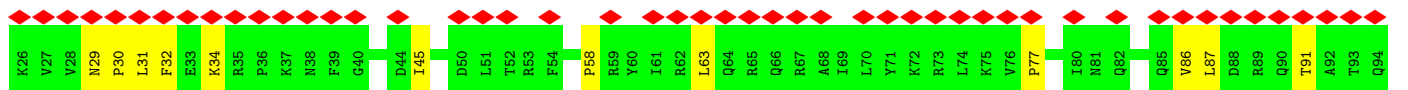
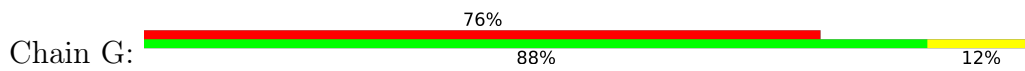
• Molecule 5: 60S ribosomal protein L6

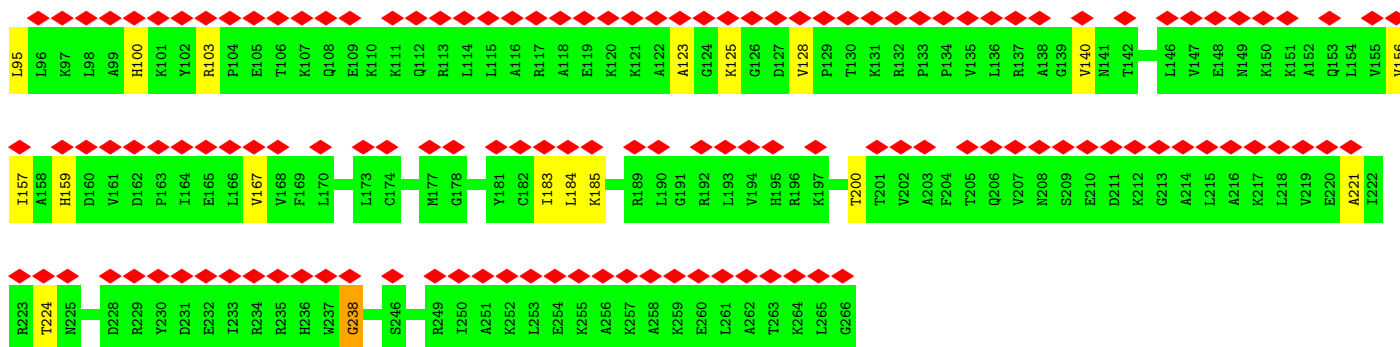


• Molecule 6: Ul30

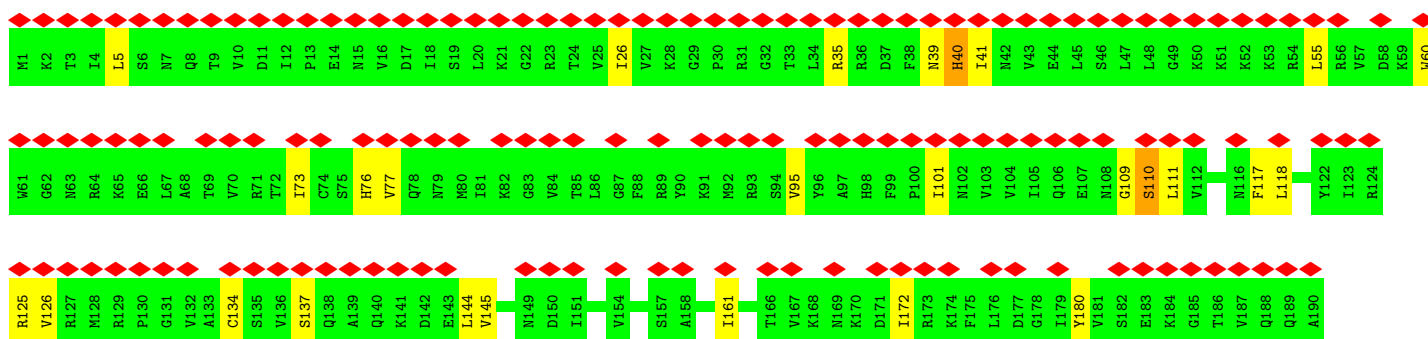
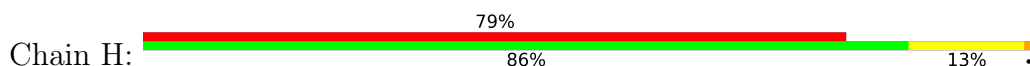


• Molecule 7: uL8

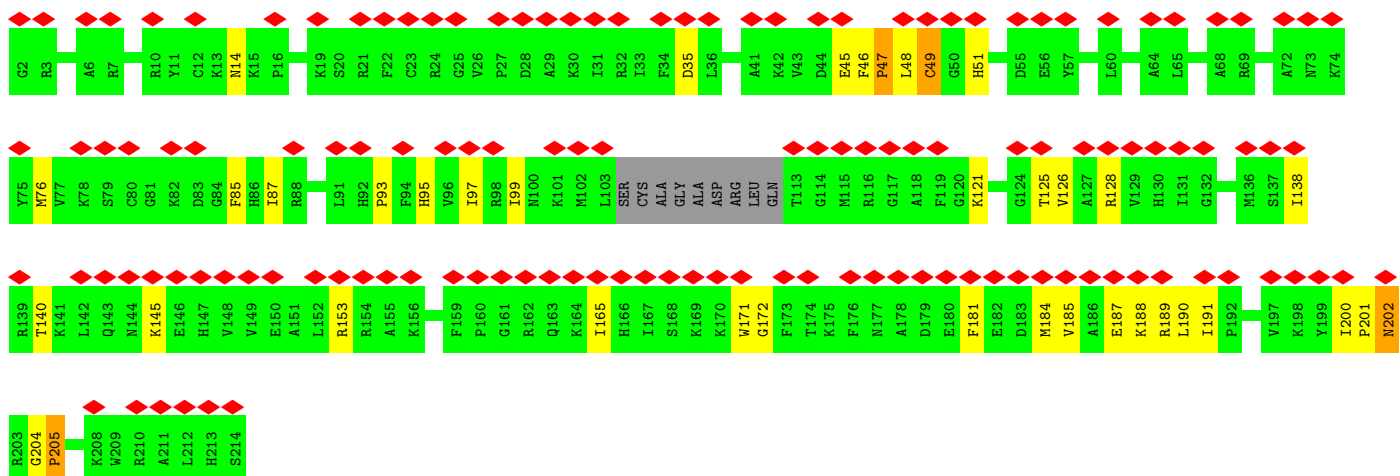
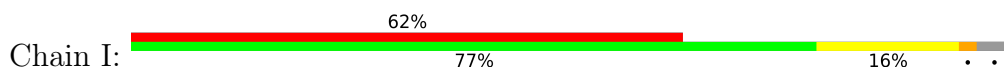




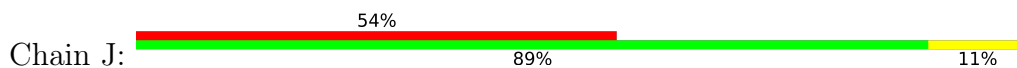
• Molecule 8: uL6

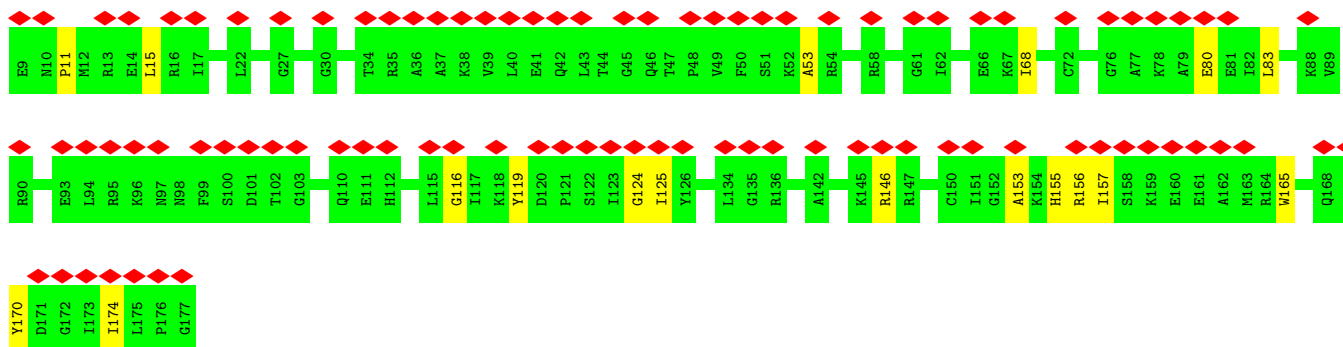


• Molecule 9: Ribosomal protein L10 (Predicted)

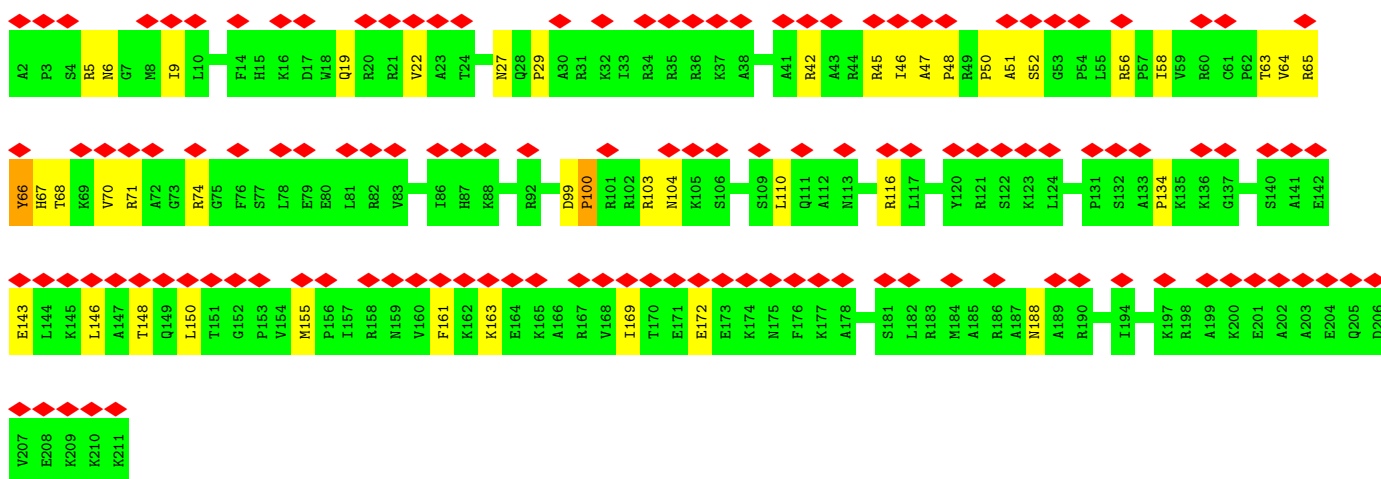
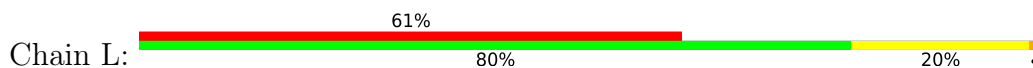


• Molecule 10: Ribosomal protein L11

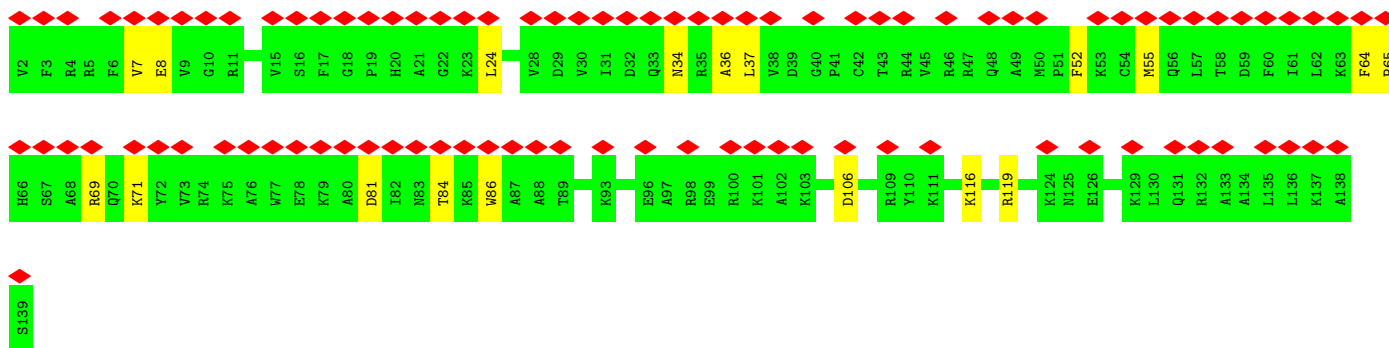
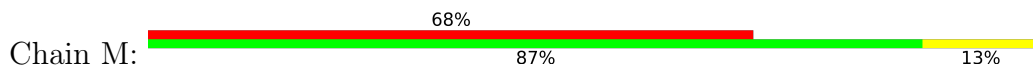




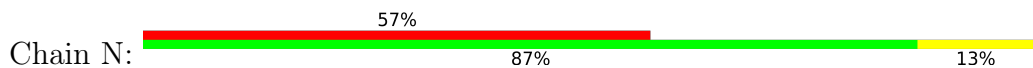
• Molecule 11: eL13

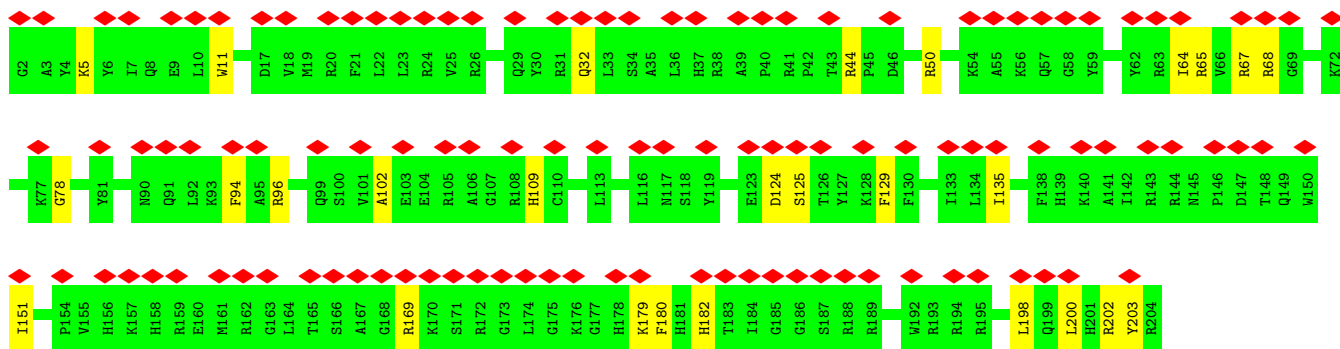


• Molecule 12: Ribosomal protein L14

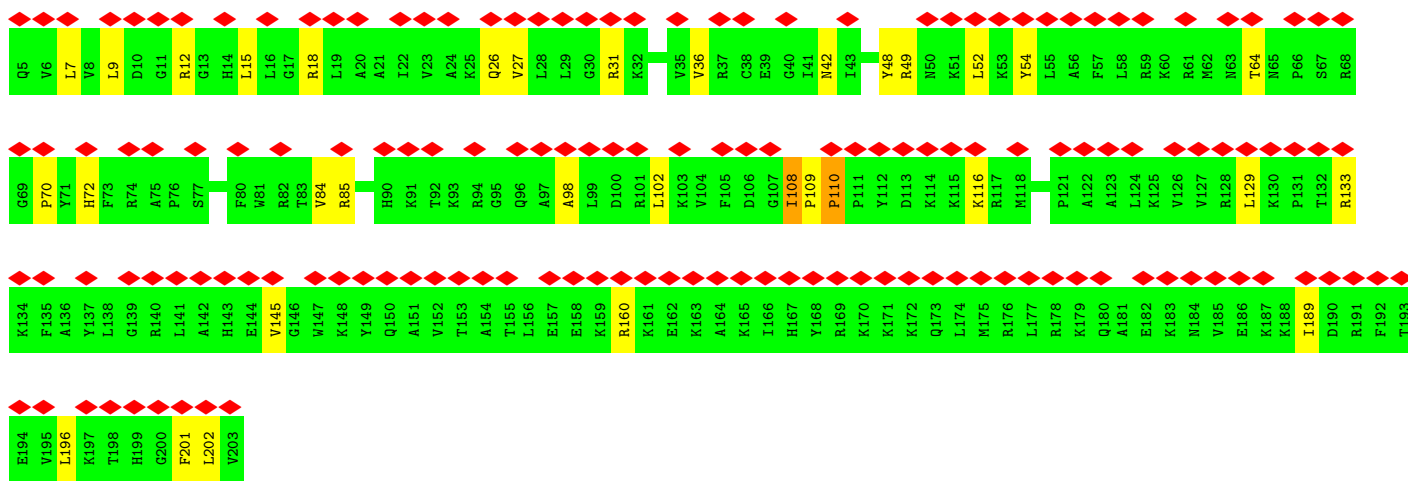
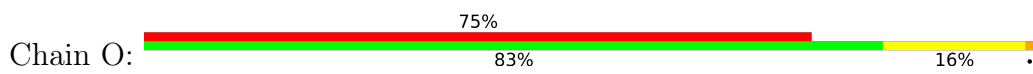


• Molecule 13: Ribosomal protein L15

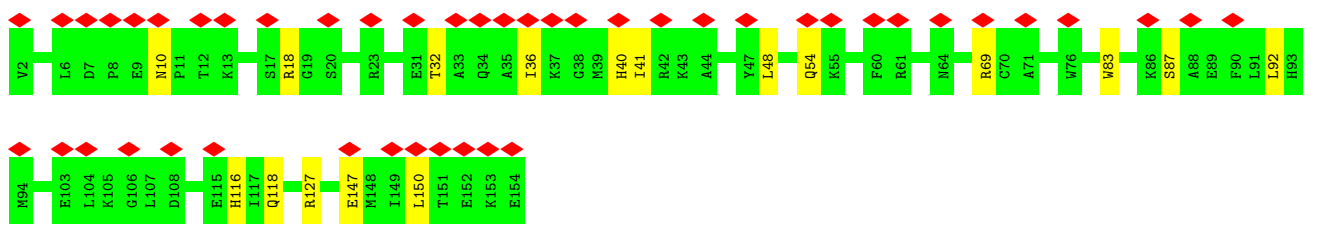
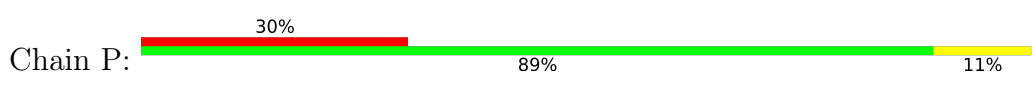




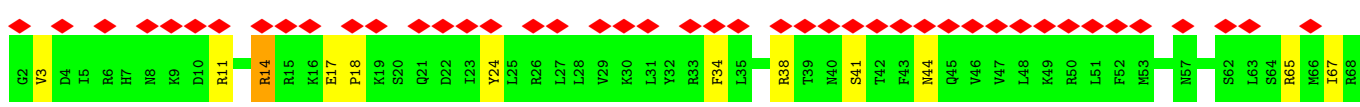
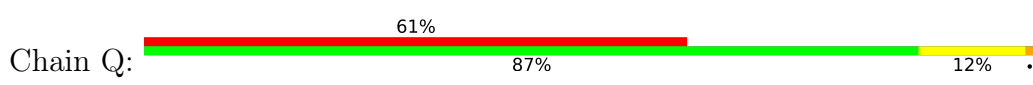
• Molecule 14: uL13

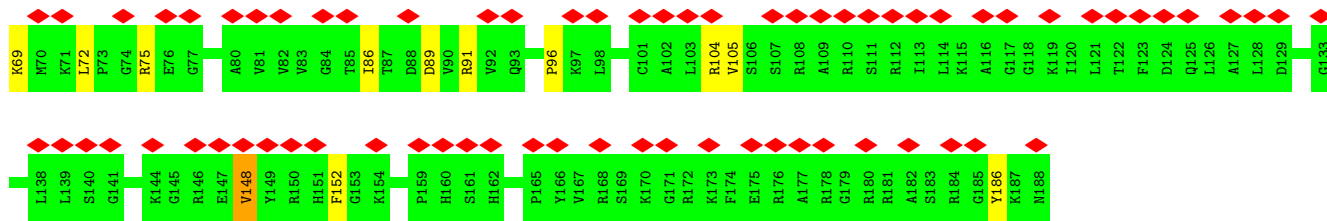


• Molecule 15: uL22

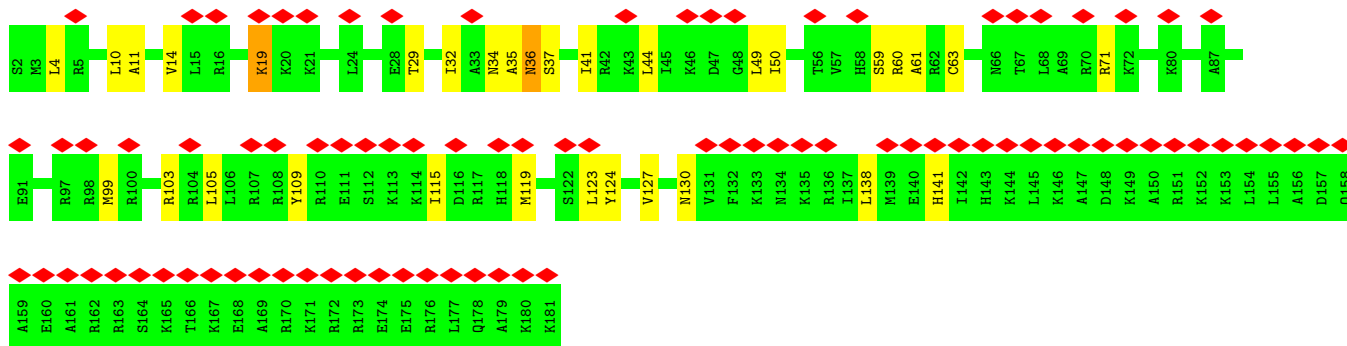
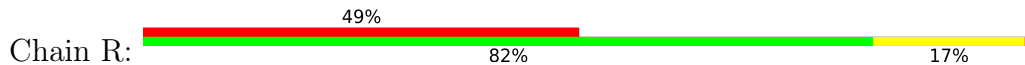


• Molecule 16: uL14

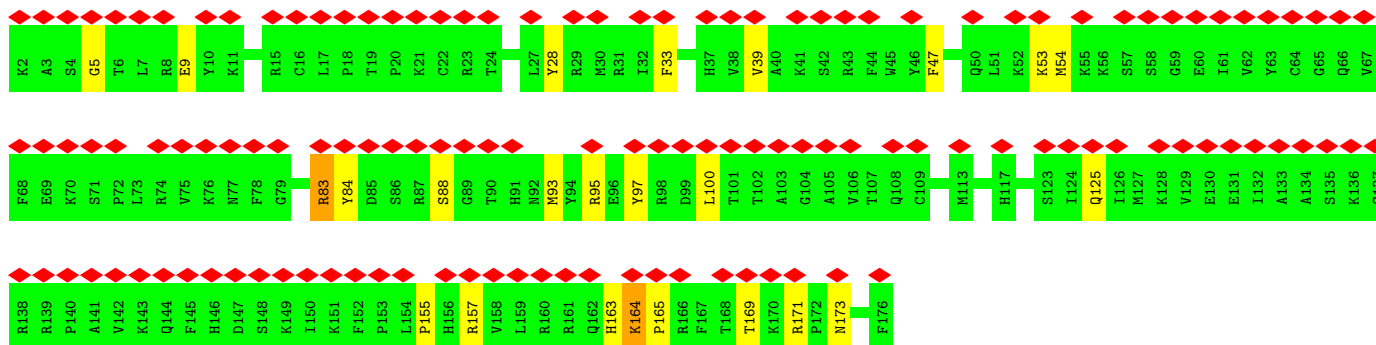
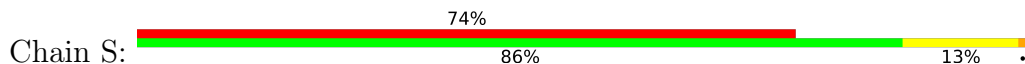




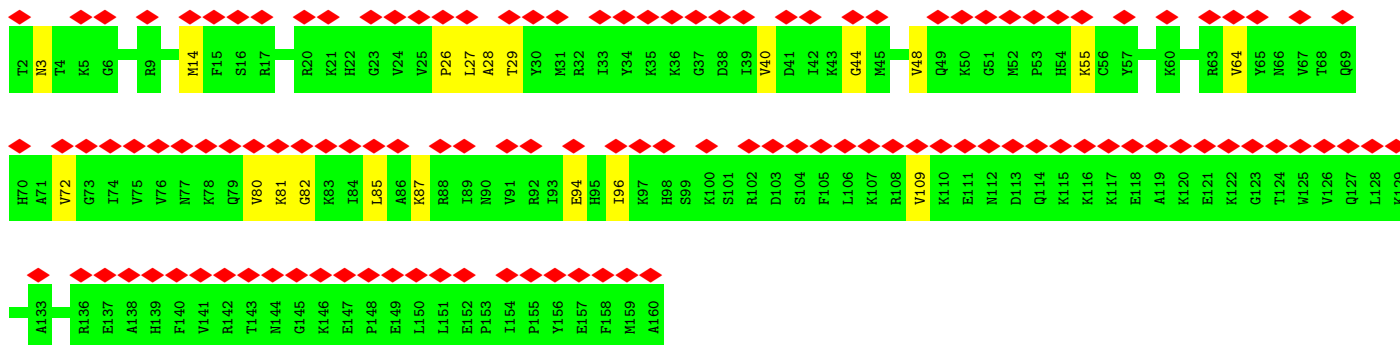
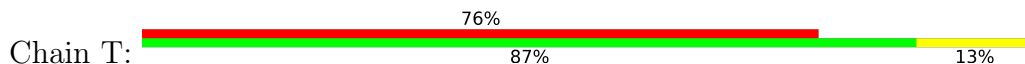
• Molecule 17: eL19



• Molecule 18: eL20

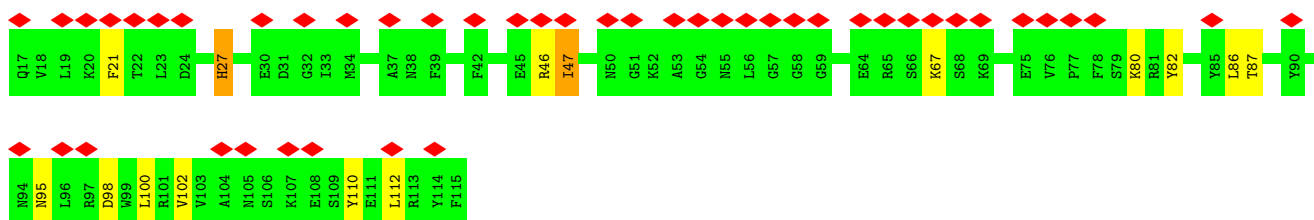


• Molecule 19: eL21



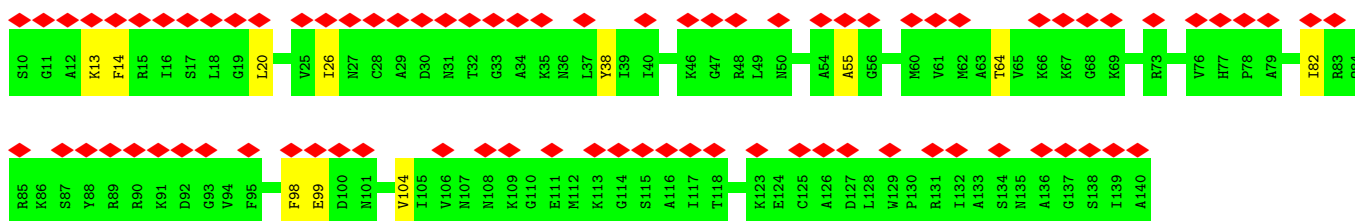
- Molecule 20: Ribosomal protein L22

Chain U: .



- Molecule 21: uL14

Chain V: .



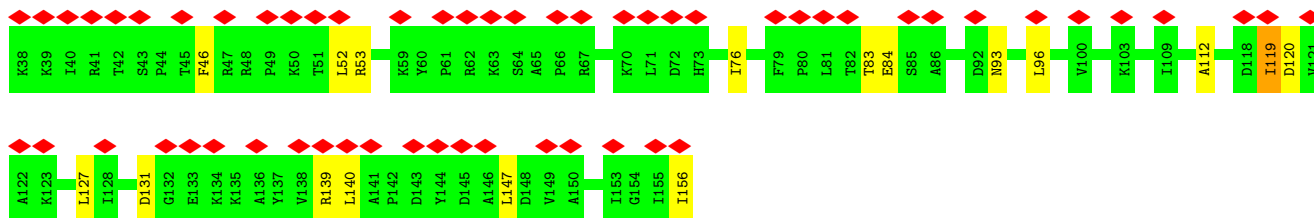
- Molecule 22: Ribosomal protein L24

Chain W: .



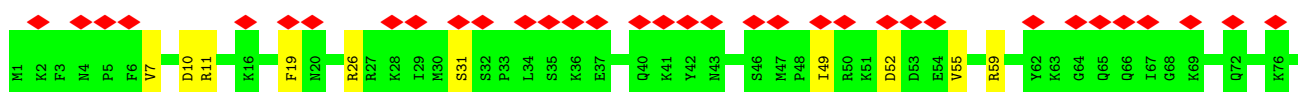
- Molecule 23: uL23

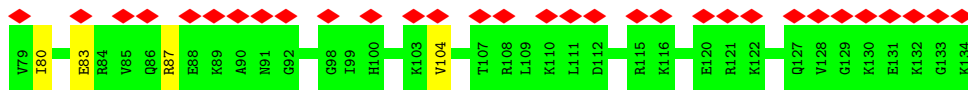
Chain X: .



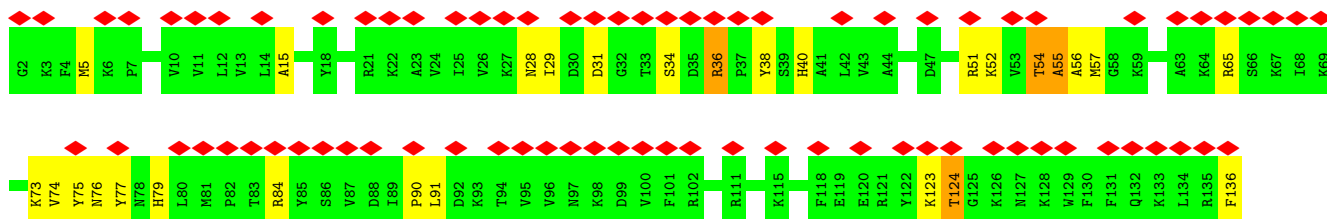
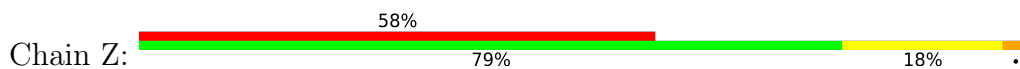
- Molecule 24: Ribosomal protein L26

Chain Y: .

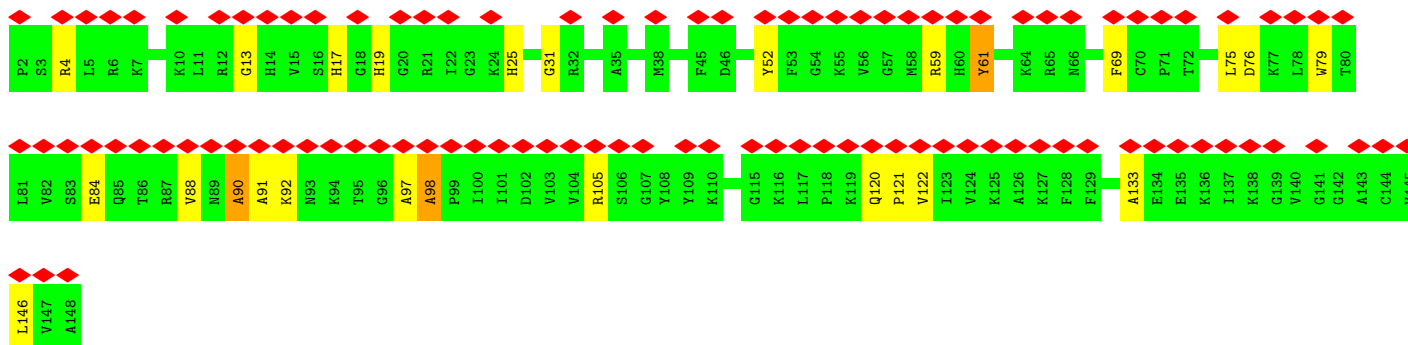
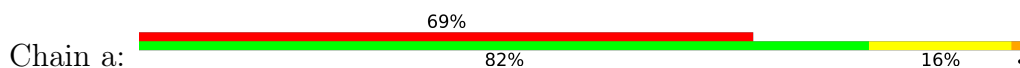




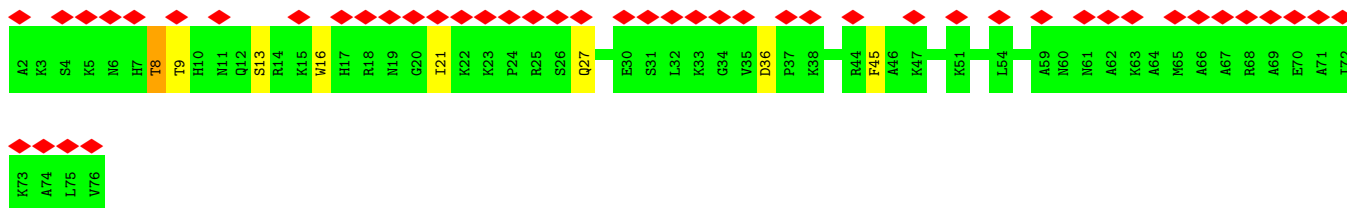
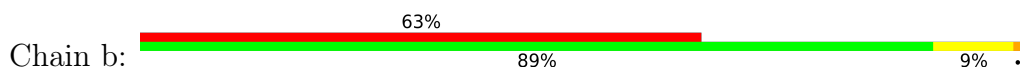
• Molecule 25: 60S ribosomal protein L27



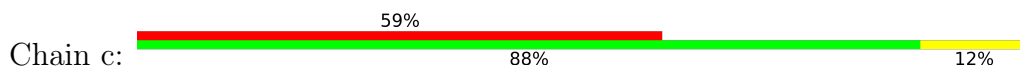
• Molecule 26: uL15

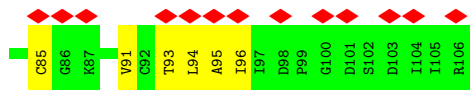


• Molecule 27: 60S ribosomal protein L29

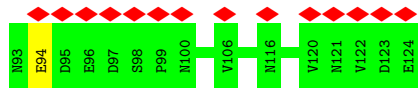
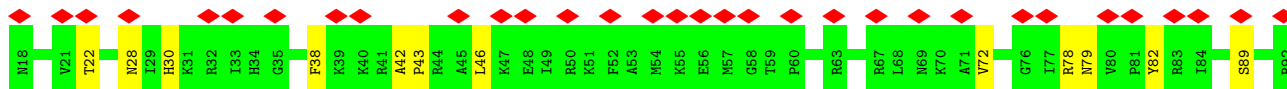
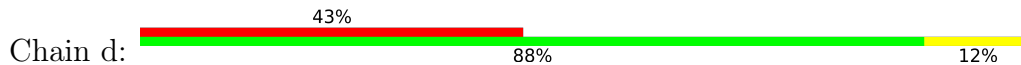


• Molecule 28: eL30

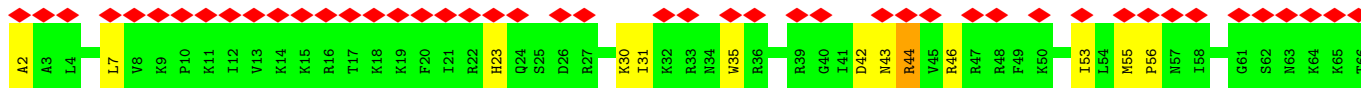
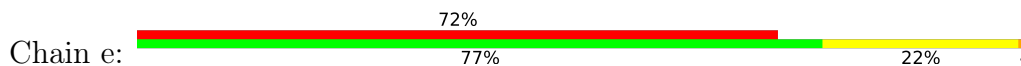




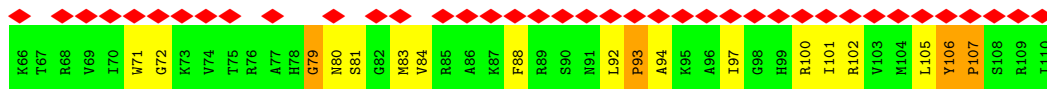
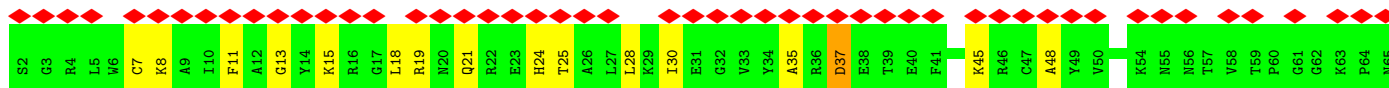
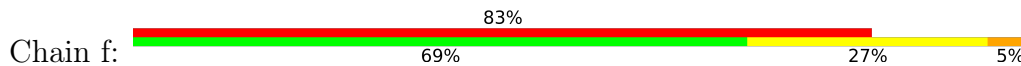
• Molecule 29: eL31



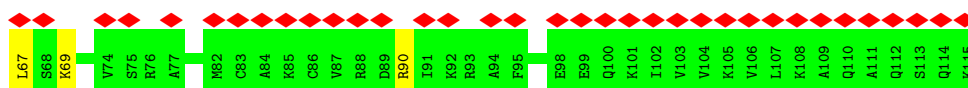
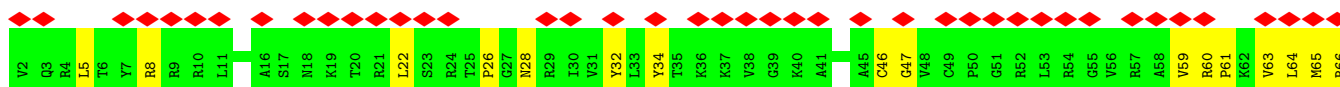
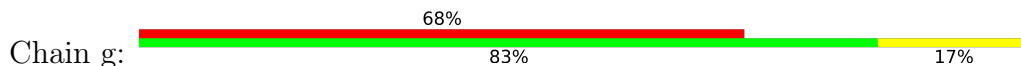
• Molecule 30: eL32



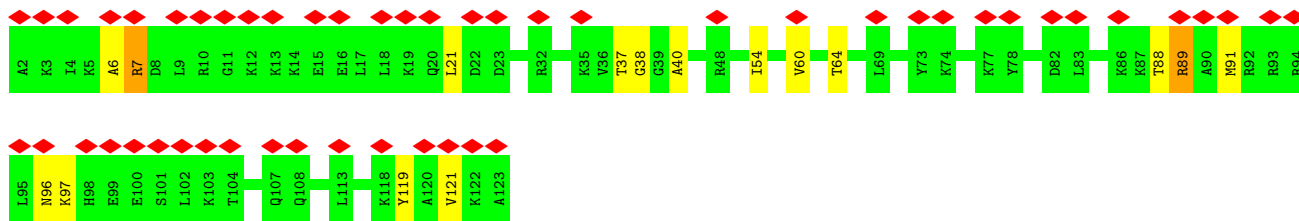
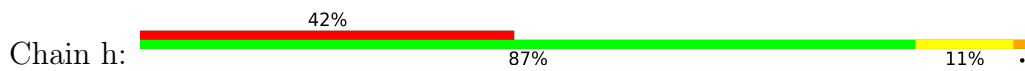
• Molecule 31: eL33



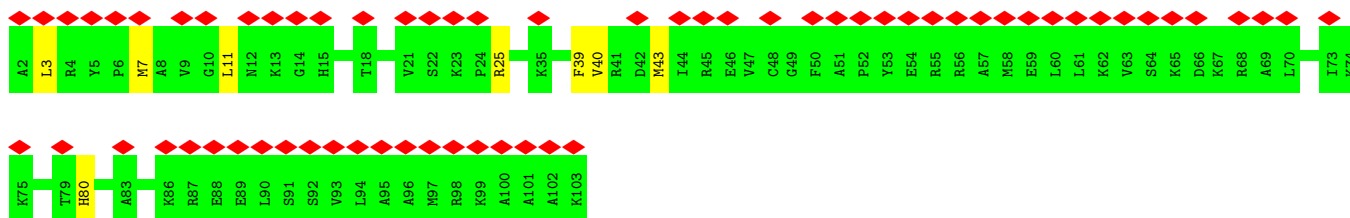
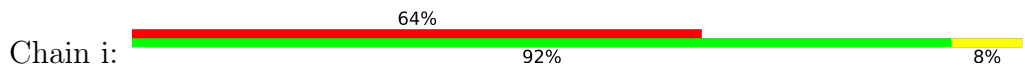
• Molecule 32: eL34



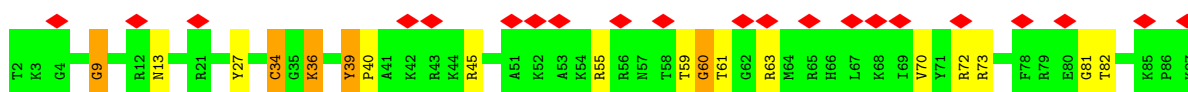
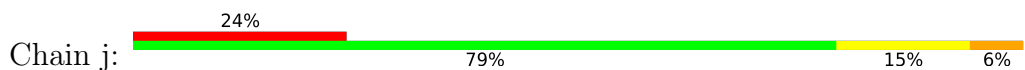
• Molecule 33: uL29



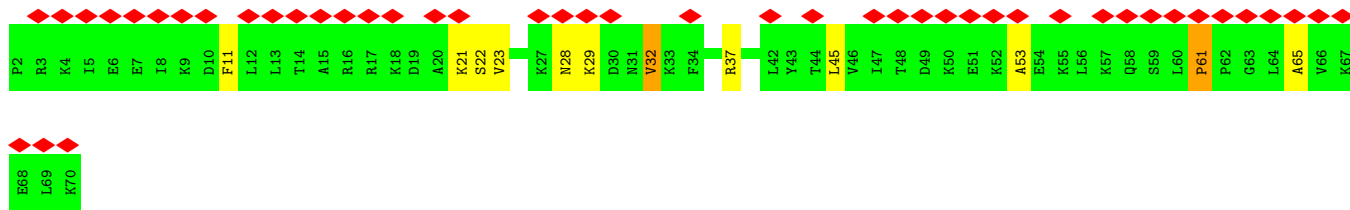
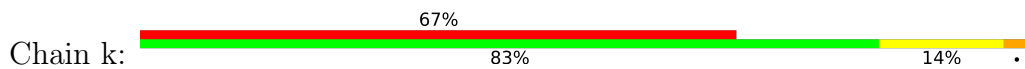
• Molecule 34: 60S ribosomal protein L36



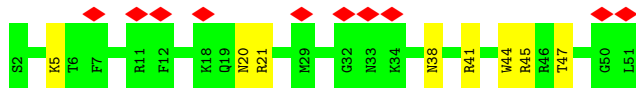
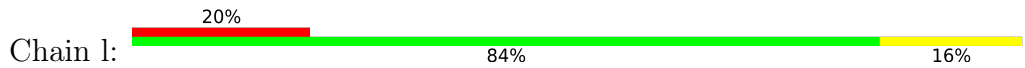
• Molecule 35: Ribosomal protein L37



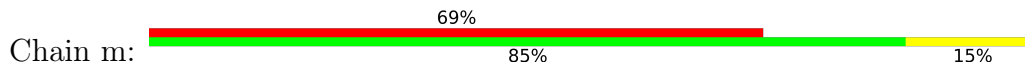
• Molecule 36: eL38

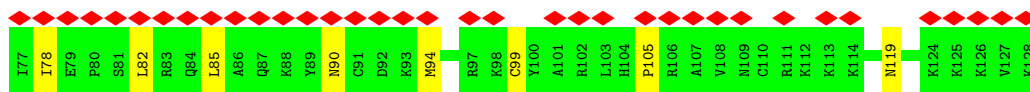


• Molecule 37: eL39

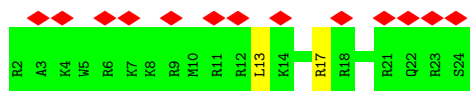
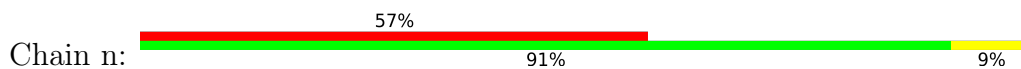


• Molecule 38: eL40

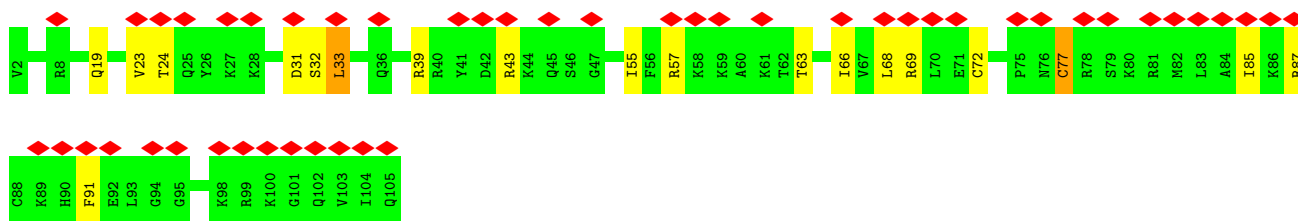
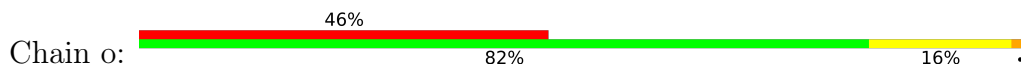




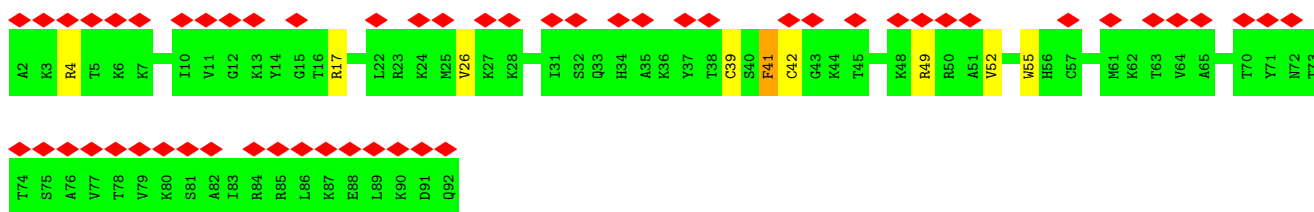
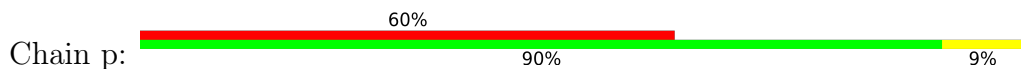
- Molecule 39: 60s ribosomal protein l41



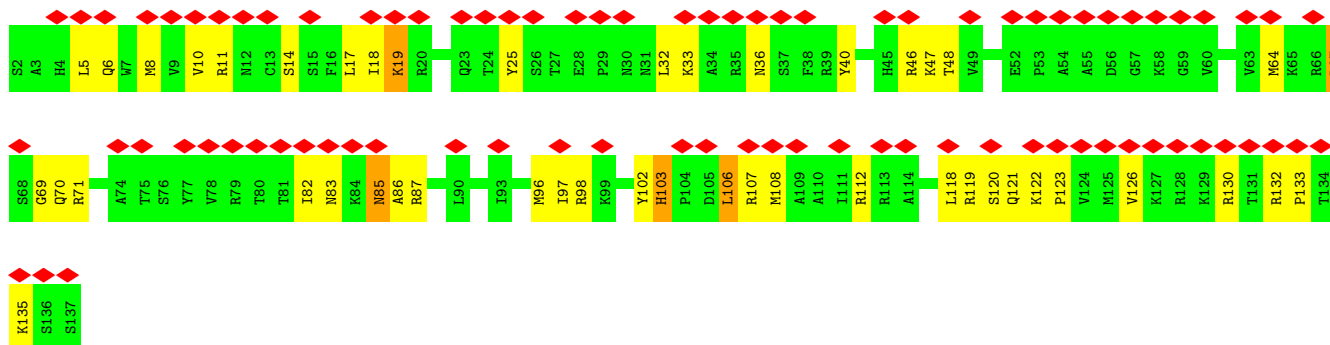
- Molecule 40: eL42



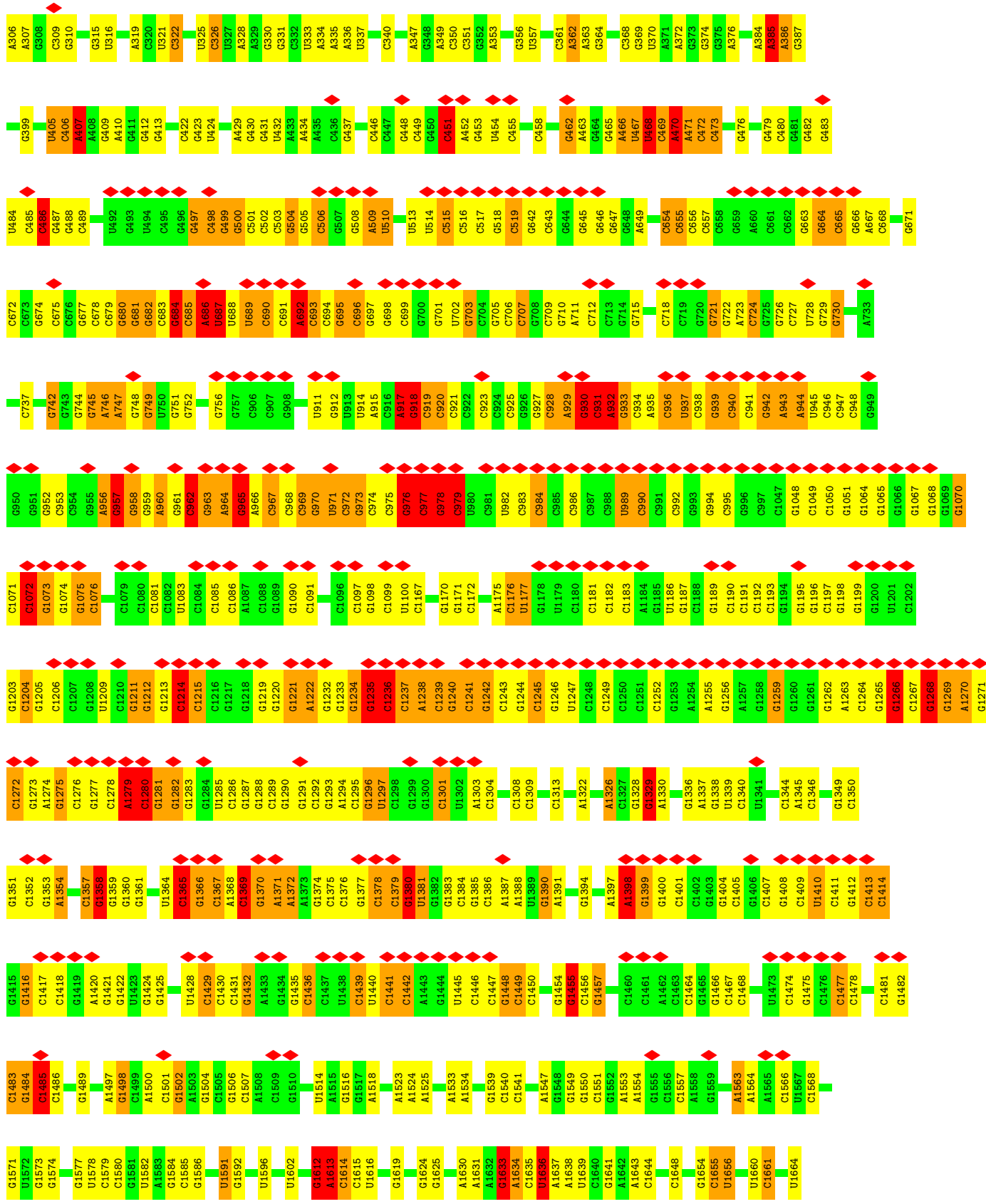
- Molecule 41: Ribosomal protein L37a

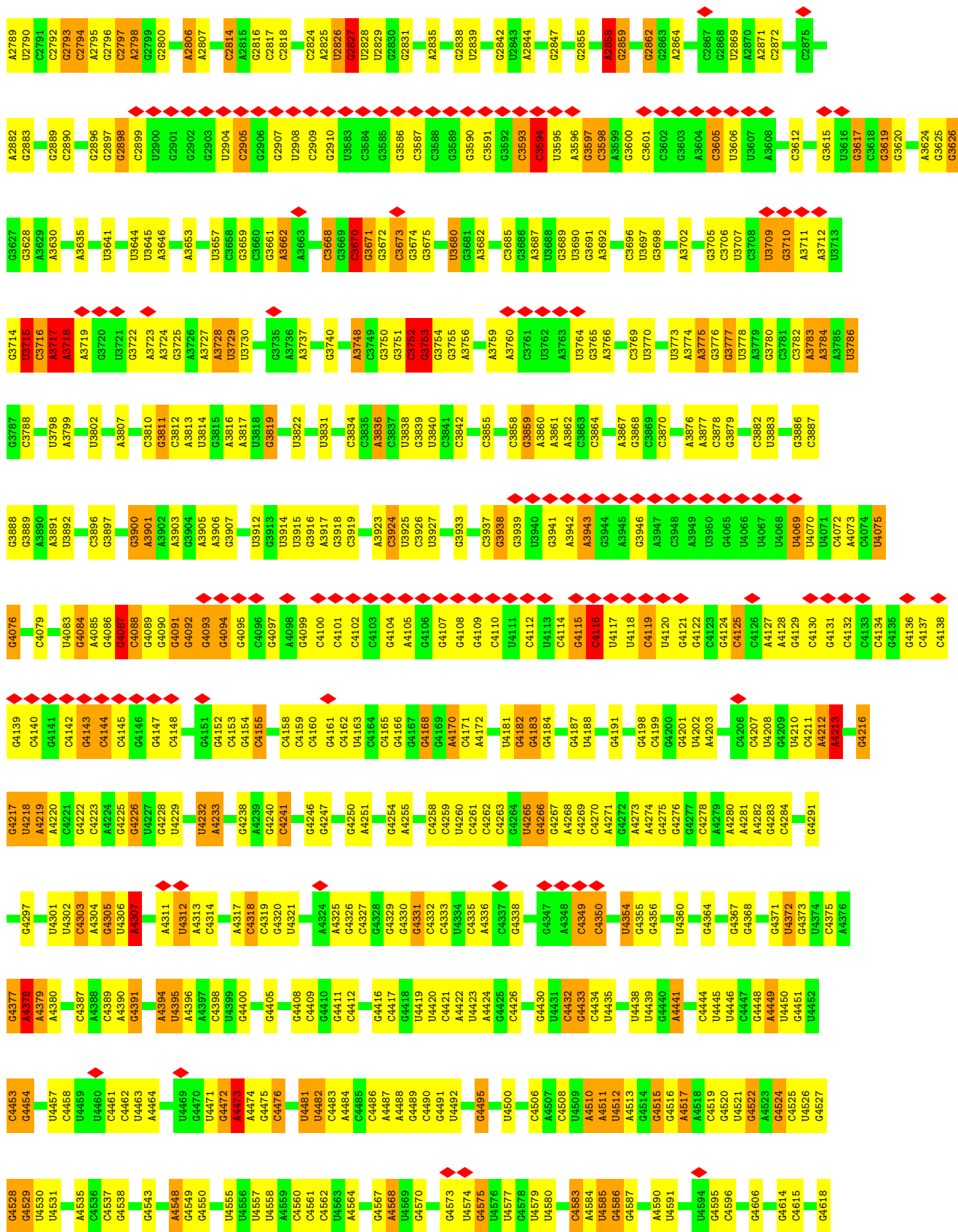


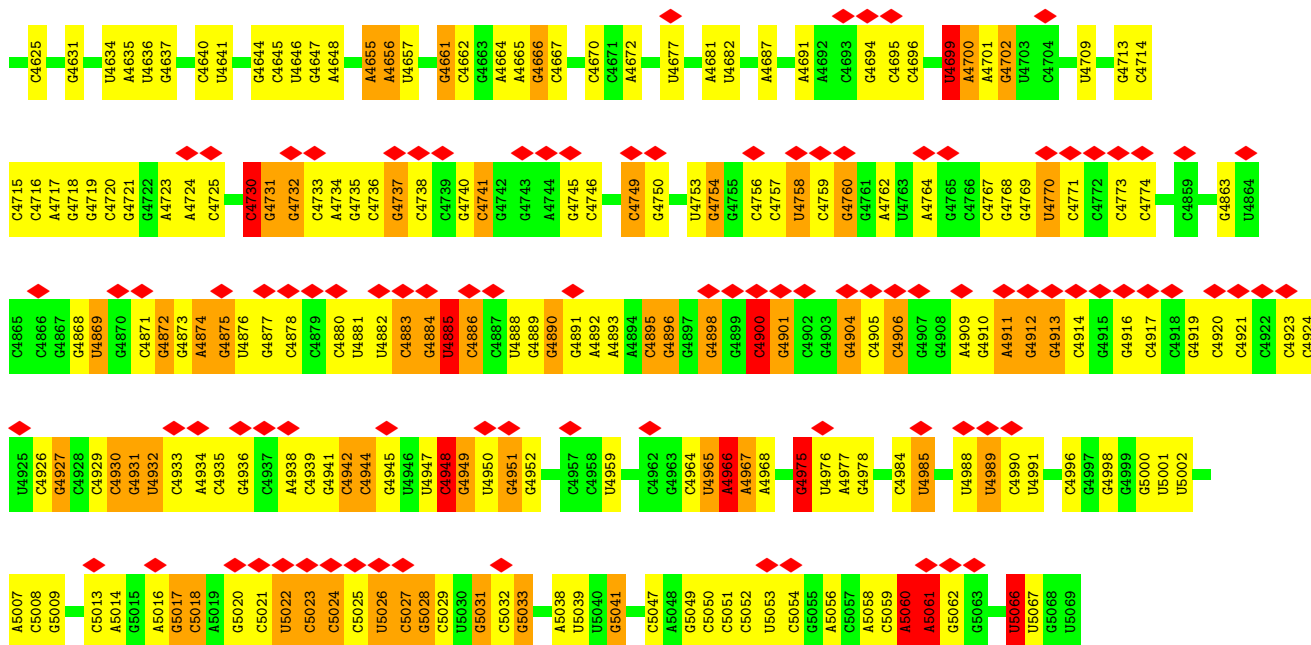
- Molecule 42: eL28



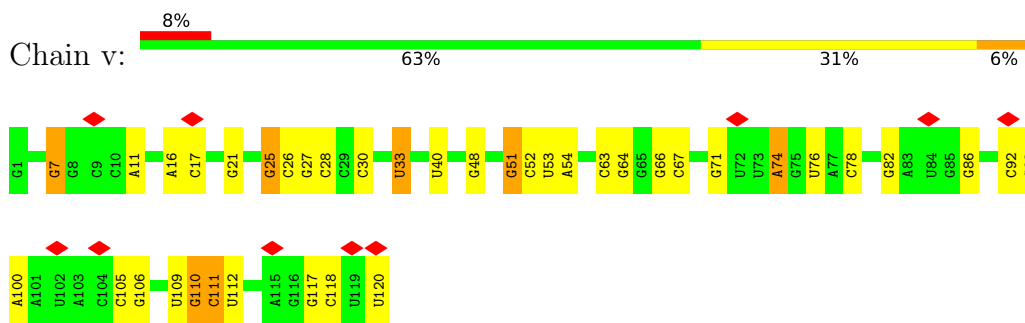
- Molecule 43: 60S acidic ribosomal protein P0



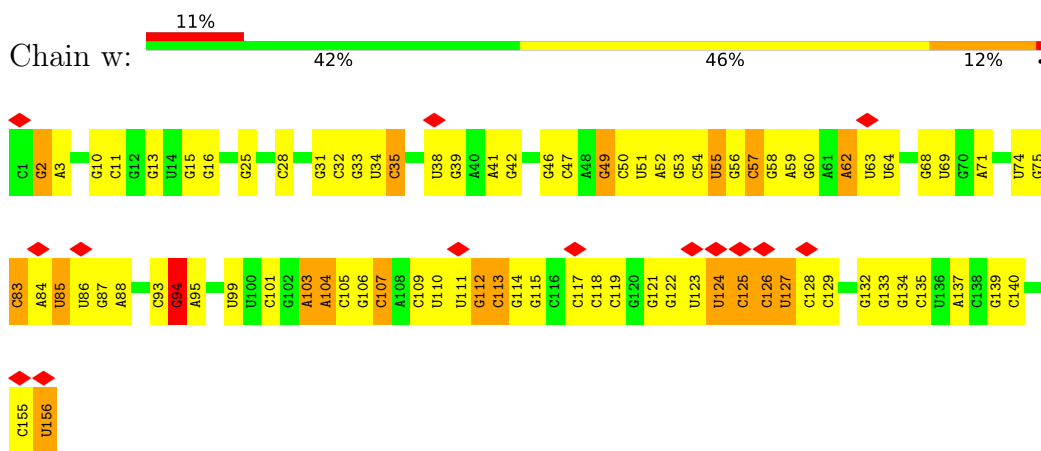




• Molecule 46: 5S ribosomal RNA



• Molecule 47: 5.8S ribosomal RNA

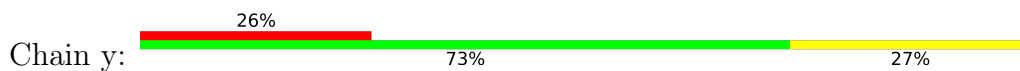


• Molecule 48: Protein transport protein Sec61 subunit alpha isoform 1

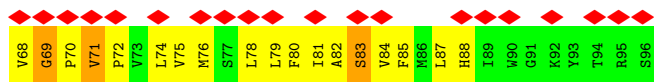
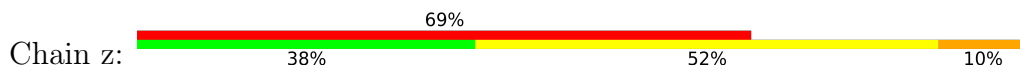




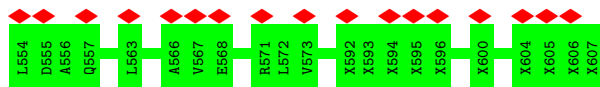
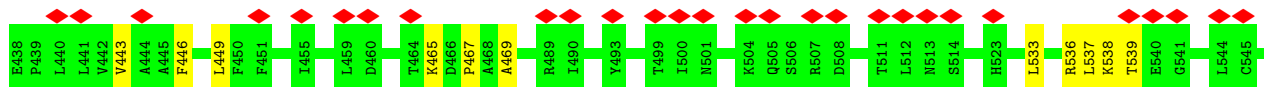
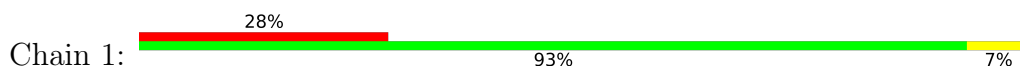
• Molecule 49: Protein transport protein Sec61 subunit gamma



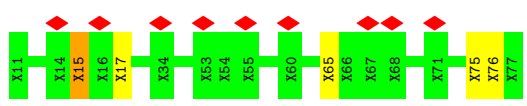
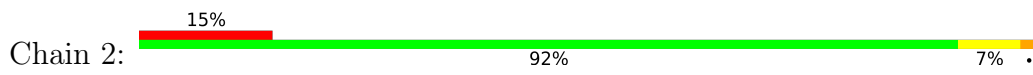
• Molecule 50: Protein transport protein Sec61 subunit beta



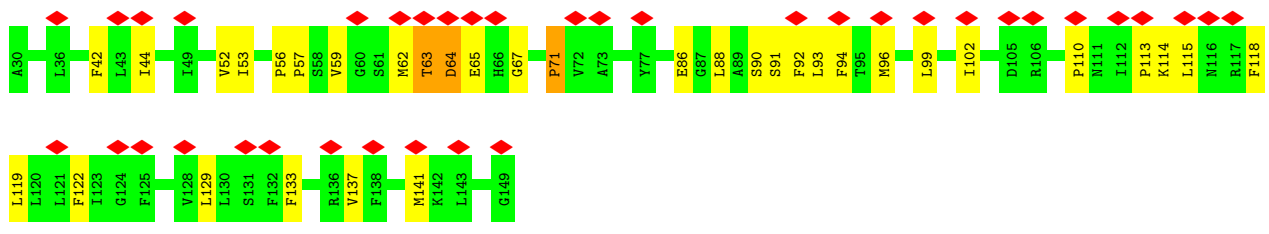
• Molecule 51: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1,RPN1



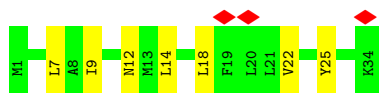
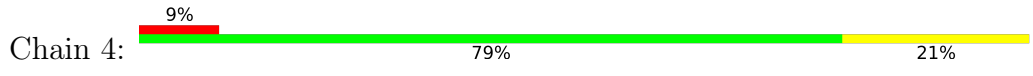
• Molecule 52: TMEM258



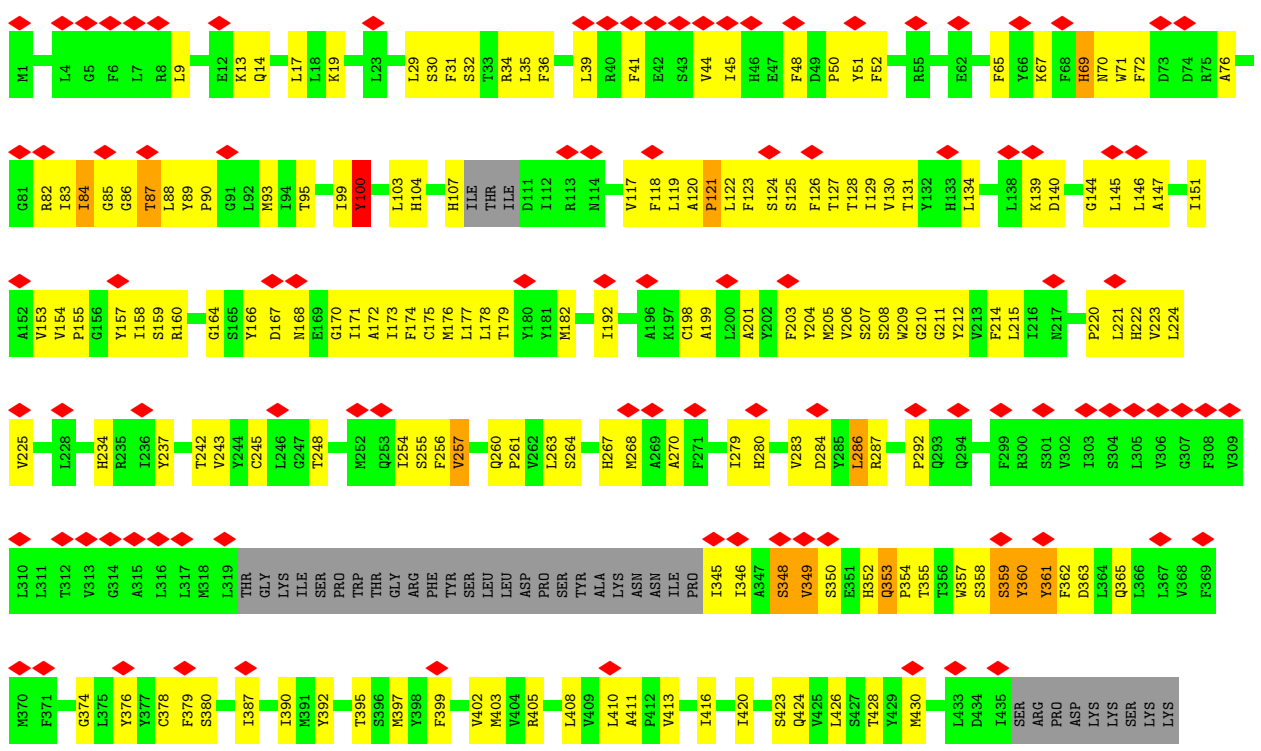
• Molecule 53: Oligosaccharyltransferase complex subunit OSTC

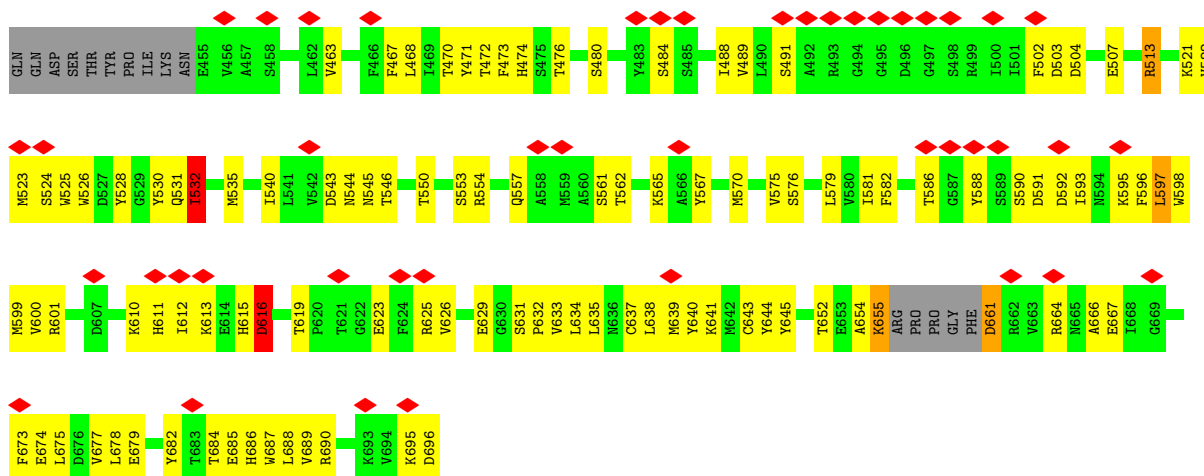


• Molecule 54: OST4

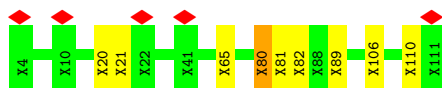


• Molecule 55: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A

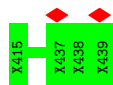




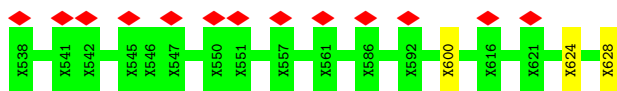
- Molecule 56: DAD1



- Molecule 57: OST48



- Molecule 58: RPN2



- Molecule 59: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	90895	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 ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.291	Depositor
Minimum map value	-0.169	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	596.2, 596.2, 596.2	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1924, 1.1924, 1.1924	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: MAN, 9UB, ZN, BMA, NAG, 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	A	0.63	3/1906 (0.2%)	0.92	2/2556 (0.1%)
2	B	0.53	0/3216	0.93	13/4311 (0.3%)
3	C	0.56	2/2938 (0.1%)	0.96	3/3946 (0.1%)
4	D	0.48	0/2432	0.86	0/3257
5	E	0.65	3/1936 (0.2%)	1.00	7/2600 (0.3%)
6	F	0.51	0/1905	0.87	0/2539
7	G	0.54	0/1967	0.94	2/2647 (0.1%)
8	H	0.52	1/1535 (0.1%)	0.82	2/2063 (0.1%)
9	I	0.56	1/1693 (0.1%)	0.87	3/2260 (0.1%)
10	J	0.48	0/1376	0.85	0/1841
11	L	0.55	1/1734 (0.1%)	0.92	1/2317 (0.0%)
12	M	0.49	0/1158	0.94	1/1547 (0.1%)
13	N	0.58	1/1746 (0.1%)	0.96	3/2338 (0.1%)
14	O	0.54	0/1671	0.95	3/2234 (0.1%)
15	P	0.59	3/1268 (0.2%)	0.91	4/1701 (0.2%)
16	Q	0.54	0/1530	0.89	0/2041
17	R	0.58	2/1524 (0.1%)	0.95	2/2013 (0.1%)
18	S	0.52	0/1493	0.95	2/2002 (0.1%)
19	T	0.55	1/1326 (0.1%)	0.84	1/1770 (0.1%)
20	U	0.52	1/822 (0.1%)	0.77	0/1103
21	V	0.55	0/993	0.88	1/1332 (0.1%)
22	W	0.58	0/541	0.94	2/720 (0.3%)
23	X	0.55	1/993 (0.1%)	0.90	0/1334
24	Y	0.48	0/1132	0.91	1/1504 (0.1%)
25	Z	0.51	0/1130	0.90	3/1507 (0.2%)
26	a	0.52	0/1191	0.97	4/1590 (0.3%)
27	b	0.57	1/619 (0.2%)	0.96	1/818 (0.1%)
28	c	0.49	0/742	0.93	0/996
29	d	0.51	0/903	0.87	0/1216
30	e	0.62	1/1071 (0.1%)	0.98	1/1429 (0.1%)
31	f	0.70	3/895 (0.3%)	1.02	7/1198 (0.6%)
32	g	0.55	1/916 (0.1%)	0.89	1/1220 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.49	0/1021	0.93	1/1348 (0.1%)
34	i	0.57	1/841 (0.1%)	0.94	2/1112 (0.2%)
35	j	0.61	0/720	1.03	1/952 (0.1%)
36	k	0.55	0/575	0.90	1/761 (0.1%)
37	l	0.67	0/454	0.92	0/599
38	m	0.51	0/435	0.90	0/575
39	n	0.55	0/223	0.88	0/284
40	o	0.52	0/864	0.86	0/1140
41	p	0.57	0/718	0.94	1/953 (0.1%)
42	r	0.62	2/1110 (0.2%)	0.98	2/1484 (0.1%)
43	s	0.59	0/1547	0.81	3/2088 (0.1%)
44	t	0.64	0/1257	0.97	3/1697 (0.2%)
45	u	0.44	7/87790 (0.0%)	0.90	299/136937 (0.2%)
46	v	0.38	0/2858	0.77	1/4455 (0.0%)
47	w	0.40	0/3701	0.82	3/5766 (0.1%)
48	x	0.52	0/3383	0.96	9/4584 (0.2%)
49	y	0.47	0/504	0.93	0/673
50	z	0.53	0/236	1.50	5/321 (1.6%)
51	1	0.45	0/757	0.74	1/1052 (0.1%)
53	3	0.53	0/815	1.16	10/1107 (0.9%)
54	4	0.43	0/273	0.68	0/371
55	5	0.80	4/5224 (0.1%)	1.11	28/7093 (0.4%)
All	All	0.50	40/161608 (0.0%)	0.91	440/237302 (0.2%)

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
1	A	0	1
2	B	0	4
3	C	0	2
4	D	0	1
5	E	0	1
7	G	0	1
9	I	0	2
11	L	0	3
17	R	0	1
18	S	0	2
19	T	0	1
20	U	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
24	Y	0	1
31	f	0	1
42	r	0	2
45	u	0	1
48	x	0	2
52	2	0	1
53	3	0	2
55	5	0	6
56	6	0	5
All	All	0	41

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	5	545	ASN	C-N	-29.89	0.91	1.33
55	5	550	THR	C-N	-28.48	0.96	1.34
45	u	680	G	O3'-P	-26.91	1.20	1.61
45	u	692	A	O3'-P	26.39	2.00	1.61
45	u	1965	G	O3'-P	-18.43	1.33	1.61

The worst 5 of 440 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	5	545	ASN	CA-C-N	-22.05	79.43	121.54
55	5	545	ASN	C-N-CA	-22.05	79.43	121.54
55	5	545	ASN	O-C-N	20.82	146.53	122.79
45	u	680	G	O3'-P-O5'	18.20	131.31	104.00
55	5	550	THR	O-C-N	-14.62	106.30	122.09

There are no chirality outliers.

5 of 41 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	196	TRP	Peptide
2	B	17	LEU	Peptide
2	B	257	TRP	Peptide
2	B	258	HIS	Peptide
2	B	351	LEU	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1868	0	1959	31	0
2	B	3148	0	3267	63	0
3	C	2884	0	3062	46	0
4	D	2386	0	2419	34	0
5	E	1898	0	2035	93	0
6	F	1870	0	1994	27	0
7	G	1934	0	2087	31	0
8	H	1516	0	1597	18	0
9	I	1655	0	1704	42	0
10	J	1353	0	1386	11	0
11	L	1703	0	1820	27	0
12	M	1137	0	1211	18	0
13	N	1701	0	1749	20	0
14	O	1638	0	1777	31	0
15	P	1242	0	1269	13	0
16	Q	1506	0	1623	17	0
17	R	1508	0	1664	19	0
18	S	1454	0	1496	15	0
19	T	1298	0	1366	11	0
20	U	808	0	831	7	0
21	V	979	0	1039	5	0
22	W	528	0	541	5	0
23	X	976	0	1052	37	0
24	Y	1115	0	1205	8	0
25	Z	1107	0	1182	16	0
26	a	1162	0	1209	19	0
27	b	609	0	650	5	0
28	c	732	0	769	7	0
29	d	888	0	930	9	0
30	e	1053	0	1147	29	0
31	f	876	0	912	19	0
32	g	906	0	999	12	0
33	h	1013	0	1147	25	0
34	i	830	0	916	4	0
35	j	705	0	738	16	0
36	k	569	0	637	6	0
37	l	444	0	482	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	m	429	0	466	9	0
39	n	222	0	264	1	0
40	o	851	0	921	12	0
41	p	708	0	756	7	0
42	r	1094	0	1168	125	0
43	s	1523	0	1577	27	0
44	t	1238	0	1295	10	0
45	u	78486	0	39663	1531	0
46	v	2558	0	1296	27	0
47	w	3314	0	1683	54	0
48	x	3313	0	3433	351	0
49	y	494	0	527	27	0
50	z	229	0	245	62	0
51	1	882	0	485	18	0
52	2	300	0	64	5	0
53	3	802	0	705	79	0
54	4	268	0	285	6	0
55	5	5090	0	4915	427	0
56	6	485	0	104	3	0
57	7	125	0	27	0	0
58	8	400	0	86	2	0
59	K	94	0	79	0	0
60	B	1	0	0	0	0
60	I	1	0	0	0	0
60	P	1	0	0	0	0
60	V	1	0	0	0	0
60	a	1	0	0	0	0
60	e	1	0	0	0	0
60	g	1	0	0	0	0
60	u	145	0	0	0	0
60	v	5	0	0	0	0
60	w	2	0	0	0	0
61	g	1	0	0	0	0
61	j	1	0	0	0	0
61	m	1	0	0	1	0
61	o	1	0	0	2	0
61	p	1	0	0	0	0
62	5	43	0	0	24	0
All	All	152111	0	111915	3173	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 12.

The worst 5 of 3173 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)
48:x:29:LYS:HG3	53:3:118:PHE:CE2	1.26	1.68
48:x:157:VAL:CG1	50:z:80:PHE:CD2	1.76	1.65
48:x:66:ARG:HH22	48:x:70:ALA:CA	1.06	1.64
48:x:157:VAL:HB	50:z:80:PHE:CZ	1.28	1.64
53:3:92:PHE:CE1	53:3:96:MET:CE	1.78	1.64

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	A	242/244 (99%)	209 (86%)	28 (12%)	5 (2%)	5	29
2	B	392/394 (100%)	345 (88%)	42 (11%)	5 (1%)	9	41
3	C	360/362 (99%)	322 (89%)	27 (8%)	11 (3%)	3	21
4	D	290/292 (99%)	262 (90%)	25 (9%)	3 (1%)	12	47
5	E	232/248 (94%)	179 (77%)	36 (16%)	17 (7%)	1	11
6	F	223/225 (99%)	204 (92%)	17 (8%)	2 (1%)	14	49
7	G	239/241 (99%)	203 (85%)	31 (13%)	5 (2%)	5	29
8	H	188/190 (99%)	166 (88%)	19 (10%)	3 (2%)	7	37
9	I	200/213 (94%)	181 (90%)	15 (8%)	4 (2%)	6	31
10	J	167/169 (99%)	147 (88%)	13 (8%)	7 (4%)	2	17
11	L	208/210 (99%)	180 (86%)	16 (8%)	12 (6%)	1	14
12	M	136/138 (99%)	123 (90%)	12 (9%)	1 (1%)	18	55
13	N	201/203 (99%)	181 (90%)	20 (10%)	0	100	100
14	O	197/199 (99%)	184 (93%)	12 (6%)	1 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	P	151/153 (99%)	135 (89%)	16 (11%)	0	100	100
16	Q	185/187 (99%)	169 (91%)	14 (8%)	2 (1%)	11	45
17	R	178/180 (99%)	166 (93%)	9 (5%)	3 (2%)	7	35
18	S	173/175 (99%)	157 (91%)	12 (7%)	4 (2%)	5	28
19	T	157/159 (99%)	139 (88%)	15 (10%)	3 (2%)	6	32
20	U	97/99 (98%)	82 (84%)	11 (11%)	4 (4%)	2	18
21	V	129/131 (98%)	115 (89%)	13 (10%)	1 (1%)	16	53
22	W	61/63 (97%)	56 (92%)	4 (7%)	1 (2%)	7	37
23	X	117/119 (98%)	109 (93%)	6 (5%)	2 (2%)	7	35
24	Y	132/134 (98%)	114 (86%)	17 (13%)	1 (1%)	16	53
25	Z	133/135 (98%)	113 (85%)	13 (10%)	7 (5%)	1	15
26	a	145/147 (99%)	122 (84%)	19 (13%)	4 (3%)	4	24
27	b	73/75 (97%)	67 (92%)	5 (7%)	1 (1%)	9	39
28	c	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
29	d	105/107 (98%)	91 (87%)	13 (12%)	1 (1%)	12	47
30	e	126/128 (98%)	115 (91%)	6 (5%)	5 (4%)	2	18
31	f	107/109 (98%)	94 (88%)	8 (8%)	5 (5%)	2	16
32	g	112/114 (98%)	103 (92%)	8 (7%)	1 (1%)	14	49
33	h	120/122 (98%)	106 (88%)	10 (8%)	4 (3%)	3	21
34	i	100/102 (98%)	92 (92%)	6 (6%)	2 (2%)	6	31
35	j	84/86 (98%)	71 (84%)	8 (10%)	5 (6%)	1	13
36	k	67/69 (97%)	56 (84%)	7 (10%)	4 (6%)	1	13
37	l	48/50 (96%)	40 (83%)	7 (15%)	1 (2%)	5	29
38	m	50/52 (96%)	44 (88%)	6 (12%)	0	100	100
39	n	21/23 (91%)	21 (100%)	0	0	100	100
40	o	102/104 (98%)	92 (90%)	7 (7%)	3 (3%)	3	23
41	p	89/91 (98%)	80 (90%)	8 (9%)	1 (1%)	11	45
42	r	132/136 (97%)	113 (86%)	12 (9%)	7 (5%)	1	15
43	s	196/198 (99%)	164 (84%)	22 (11%)	10 (5%)	1	15
44	t	161/163 (99%)	102 (63%)	33 (20%)	26 (16%)	0	3
48	x	420/426 (99%)	373 (89%)	46 (11%)	1 (0%)	43	78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	y	60/62 (97%)	52 (87%)	8 (13%)	0	100	100
50	z	27/29 (93%)	25 (93%)	1 (4%)	1 (4%)	2	19
51	1	134/162 (83%)	129 (96%)	5 (4%)	0	100	100
53	3	118/120 (98%)	99 (84%)	18 (15%)	1 (1%)	16	53
54	4	32/34 (94%)	31 (97%)	1 (3%)	0	100	100
55	5	632/696 (91%)	538 (85%)	88 (14%)	6 (1%)	14	49
All	All	8141/8362 (97%)	7150 (88%)	798 (10%)	193 (2%)	7	27

5 of 193 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	196	TRP
3	C	273	LEU
5	E	91	PRO
5	E	95	ASP
5	E	118	PRO

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	u	3647/3662 (99%)	1211 (33%)	0
46	v	119/120 (99%)	20 (16%)	0
47	w	155/156 (99%)	52 (33%)	0
All	All	3921/3938 (99%)	1283 (32%)	0

5 of 1283 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	u	2	G
45	u	8	U
45	u	9	C
45	u	10	A
45	u	12	A

There are no RNA pucker outliers to report.

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](#)

8 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
59	NAG	K	1	59,55	14,14,15	0.47	0	17,19,21	0.64	0
59	NAG	K	2	59	14,14,15	0.25	0	17,19,21	0.55	0
59	BMA	K	3	59	11,11,12	0.65	0	15,15,17	0.86	1 (6%)
59	MAN	K	4	59	11,11,12	0.82	0	15,15,17	1.62	2 (13%)
59	MAN	K	5	59	11,11,12	0.70	0	15,15,17	1.21	2 (13%)
59	MAN	K	6	59	11,11,12	0.89	1 (9%)	15,15,17	0.96	2 (13%)
59	MAN	K	7	59	11,11,12	1.24	1 (9%)	15,15,17	1.25	2 (13%)
59	MAN	K	8	59	11,11,12	0.67	0	15,15,17	1.02	2 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	NAG	K	1	59,55	-	2/6/23/26	0/1/1/1
59	NAG	K	2	59	-	1/6/23/26	0/1/1/1
59	BMA	K	3	59	-	2/2/19/22	0/1/1/1
59	MAN	K	4	59	-	0/2/19/22	0/1/1/1
59	MAN	K	5	59	-	1/2/19/22	0/1/1/1
59	MAN	K	6	59	-	0/2/19/22	0/1/1/1
59	MAN	K	7	59	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	MAN	K	8	59	-	2/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	K	7	MAN	C2-C3	2.43	1.56	1.52
59	K	6	MAN	O5-C1	-2.00	1.40	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	K	4	MAN	C1-O5-C5	4.45	118.15	112.19
59	K	4	MAN	O2-C2-C3	-3.64	102.62	110.15
59	K	7	MAN	C1-O5-C5	3.25	116.55	112.19
59	K	5	MAN	C1-O5-C5	3.04	116.27	112.19
59	K	5	MAN	O2-C2-C3	-2.96	104.02	110.15

There are no chirality outliers.

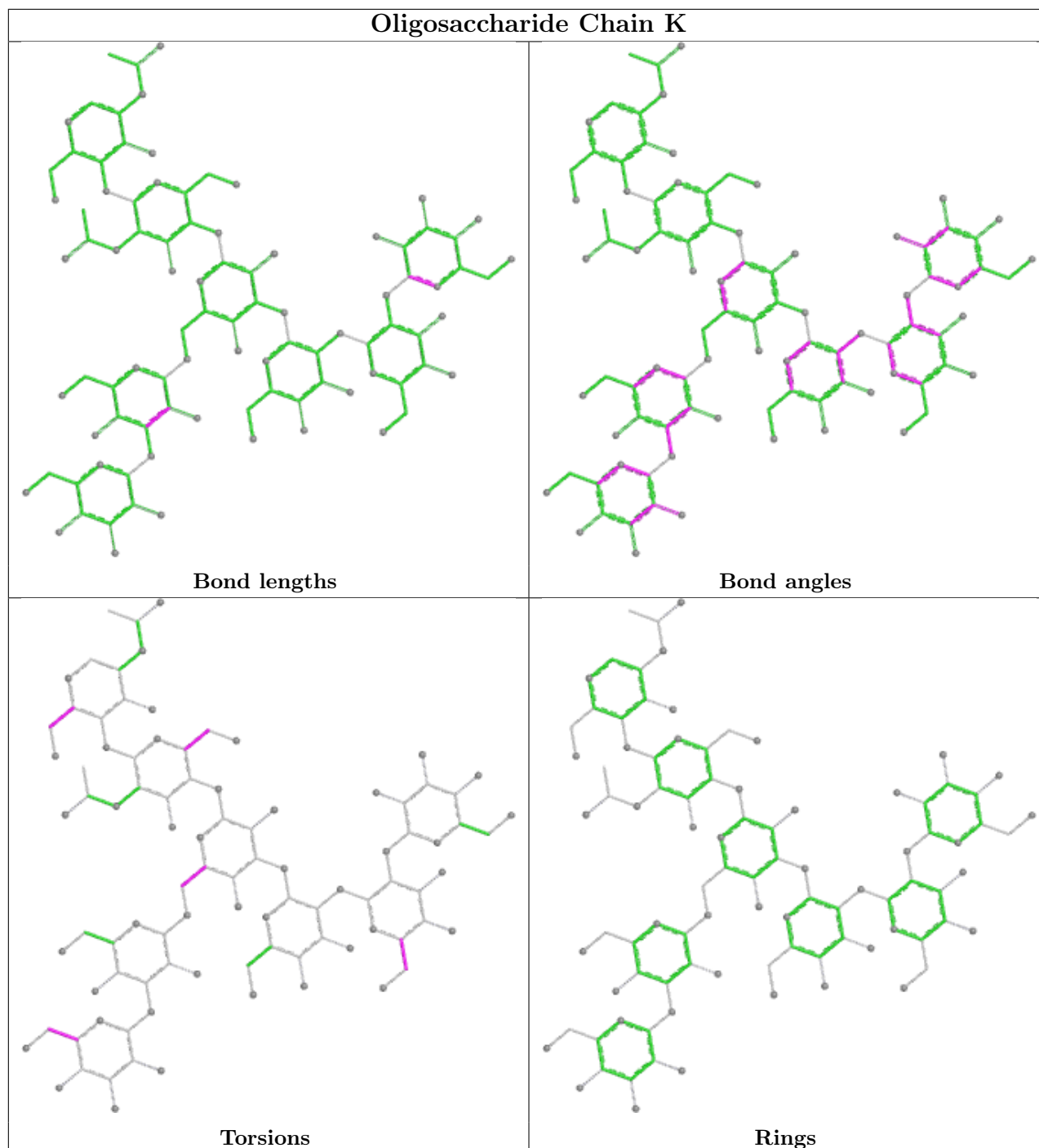
5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	K	3	BMA	C4-C5-C6-O6
59	K	3	BMA	O5-C5-C6-O6
59	K	8	MAN	O5-C5-C6-O6
59	K	8	MAN	C4-C5-C6-O6
59	K	1	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



5.6 Ligand geometry [i](#)

Of 165 ligands modelled in this entry, 164 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
62	9UB	5	809	-	43,43,43	2.55	10 (23%)	48,59,59	1.64	13 (27%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
62	9UB	5	809	-	-	3/39/62/62	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	5	809	9UB	P26-O25	8.09	1.67	1.58
62	5	809	9UB	P22-O25	7.82	1.67	1.59
62	5	809	9UB	P26-C29	6.76	1.91	1.80
62	5	809	9UB	C37-C39	-3.75	1.46	1.53
62	5	809	9UB	C41-N40	3.56	1.45	1.34

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	5	809	9UB	C18-C17-C16	4.13	122.39	115.23
62	5	809	9UB	C20-C19-C17	-3.78	120.01	126.20
62	5	809	9UB	C39-N40-C41	-2.68	116.83	123.11
62	5	809	9UB	C01-C02-C03	2.62	120.61	114.59
62	5	809	9UB	C32-O31-C30	2.59	117.72	113.19

There are no chirality outliers.

All (3) torsion outliers are listed below:

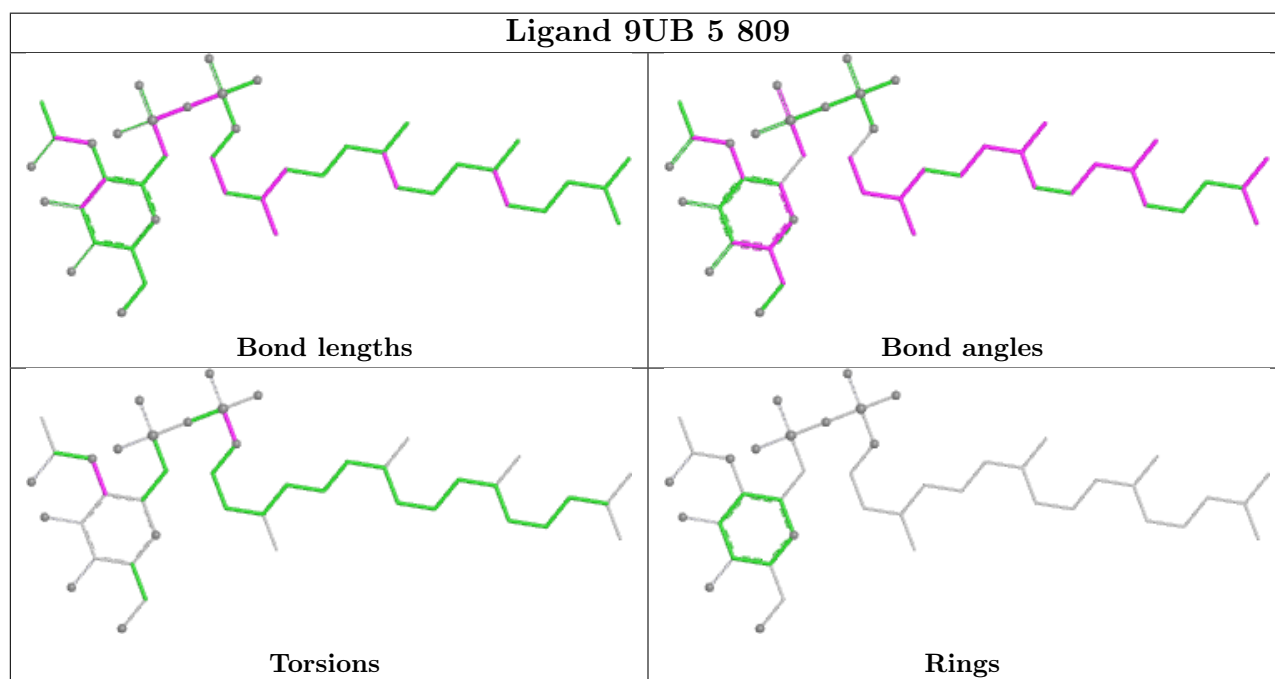
Mol	Chain	Res	Type	Atoms
62	5	809	9UB	C20-O21-P22-O25
62	5	809	9UB	C20-O21-P22-O23
62	5	809	9UB	C30-C39-N40-C41

There are no ring outliers.

1 monomer is involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
62	5	809	9UB	24	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
45	u	21

Continued on next page...

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Mol	Chain	Number of breaks
55	5	4
58	8	2
56	6	2
48	x	2
51	1	1
52	2	1
42	r	1

The worst 5 of 34 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	u	4776:G	O3'	4859:C	P	17.95
1	u	757:G	O3'	906:C	P	17.49
1	u	519:C	O3'	642:G	P	16.73
1	u	2910:G	O3'	3583:U	P	16.46
1	8	566:UNK	C	577:UNK	N	15.56

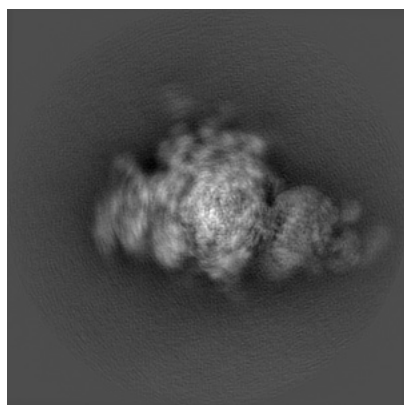
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4317. These allow visual inspection of the internal detail of the map and identification of artifacts.

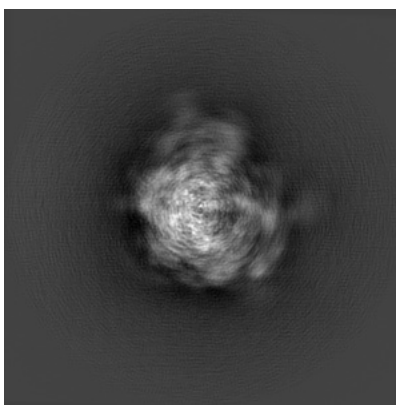
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

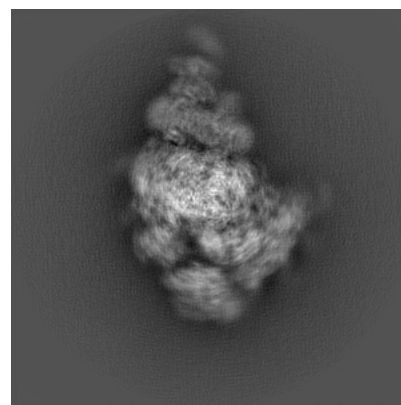
6.1.1 Primary map



X



Y

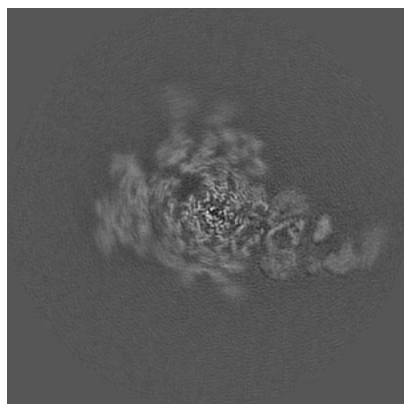


Z

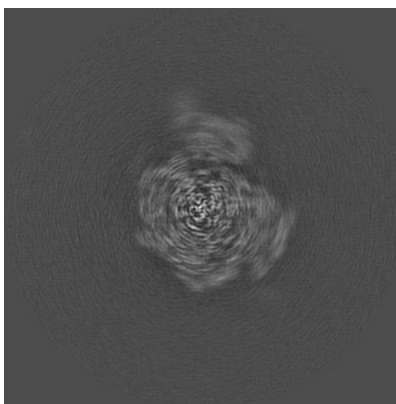
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

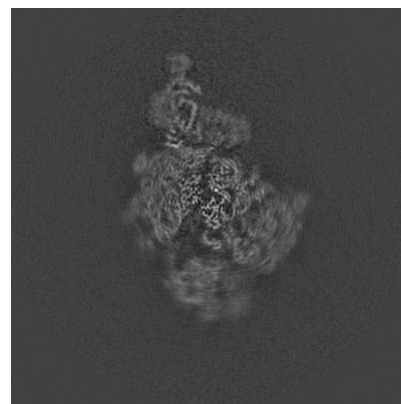
6.2.1 Primary map



X Index: 250



Y Index: 250

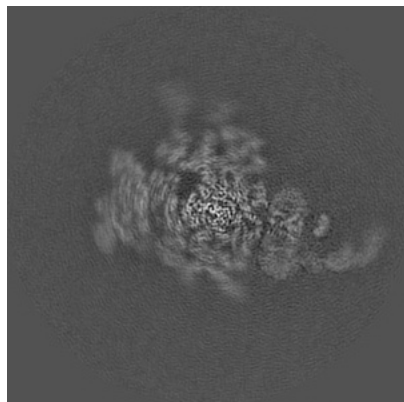


Z Index: 250

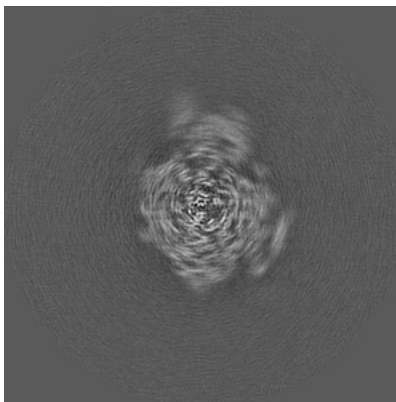
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [\(i\)](#)

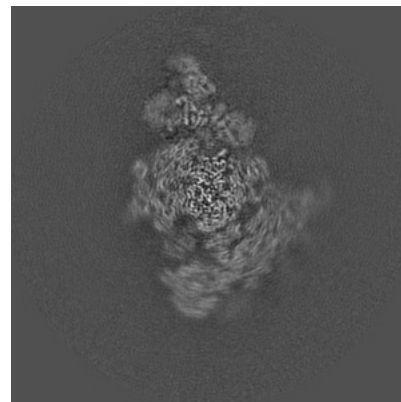
6.3.1 Primary map



X Index: 253



Y Index: 245

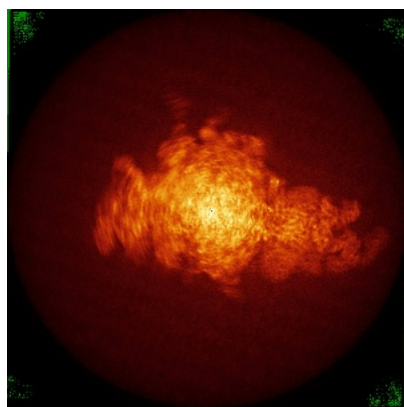


Z Index: 235

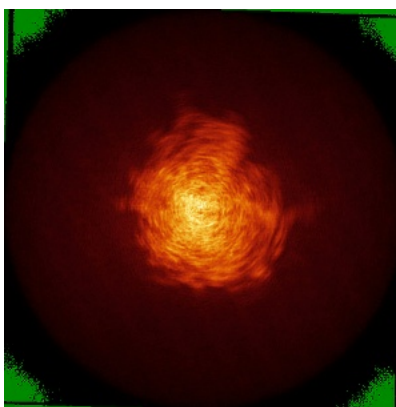
The images above show the largest variance slices of the map in three orthogonal directions.

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

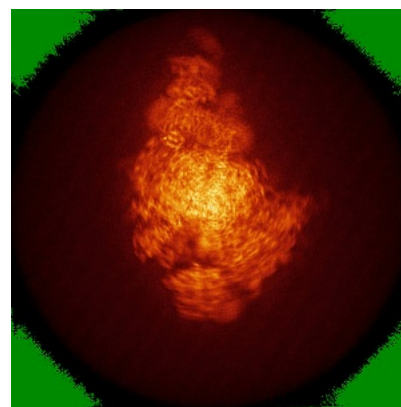
6.4.1 Primary map



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



The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

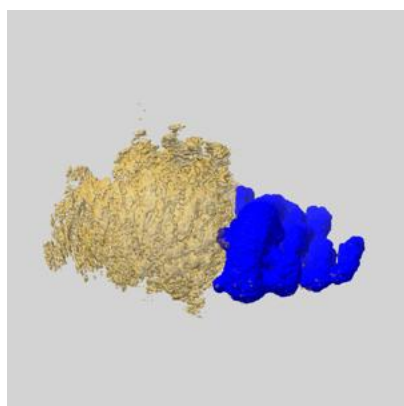
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

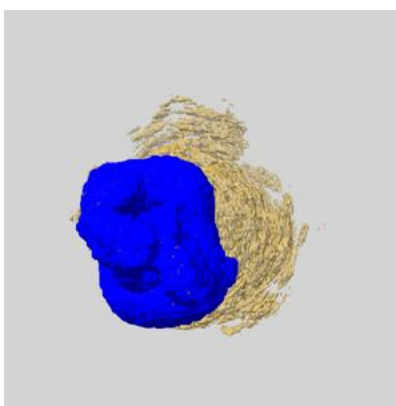
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

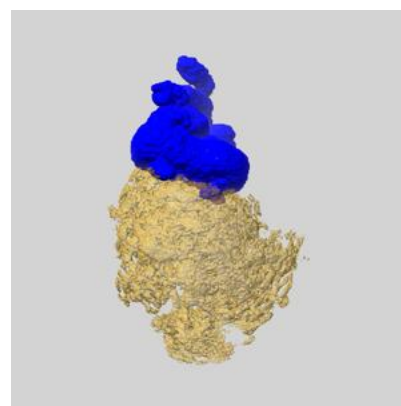
6.6.1 emd_4317_msk_1.map [i](#)



X



Y

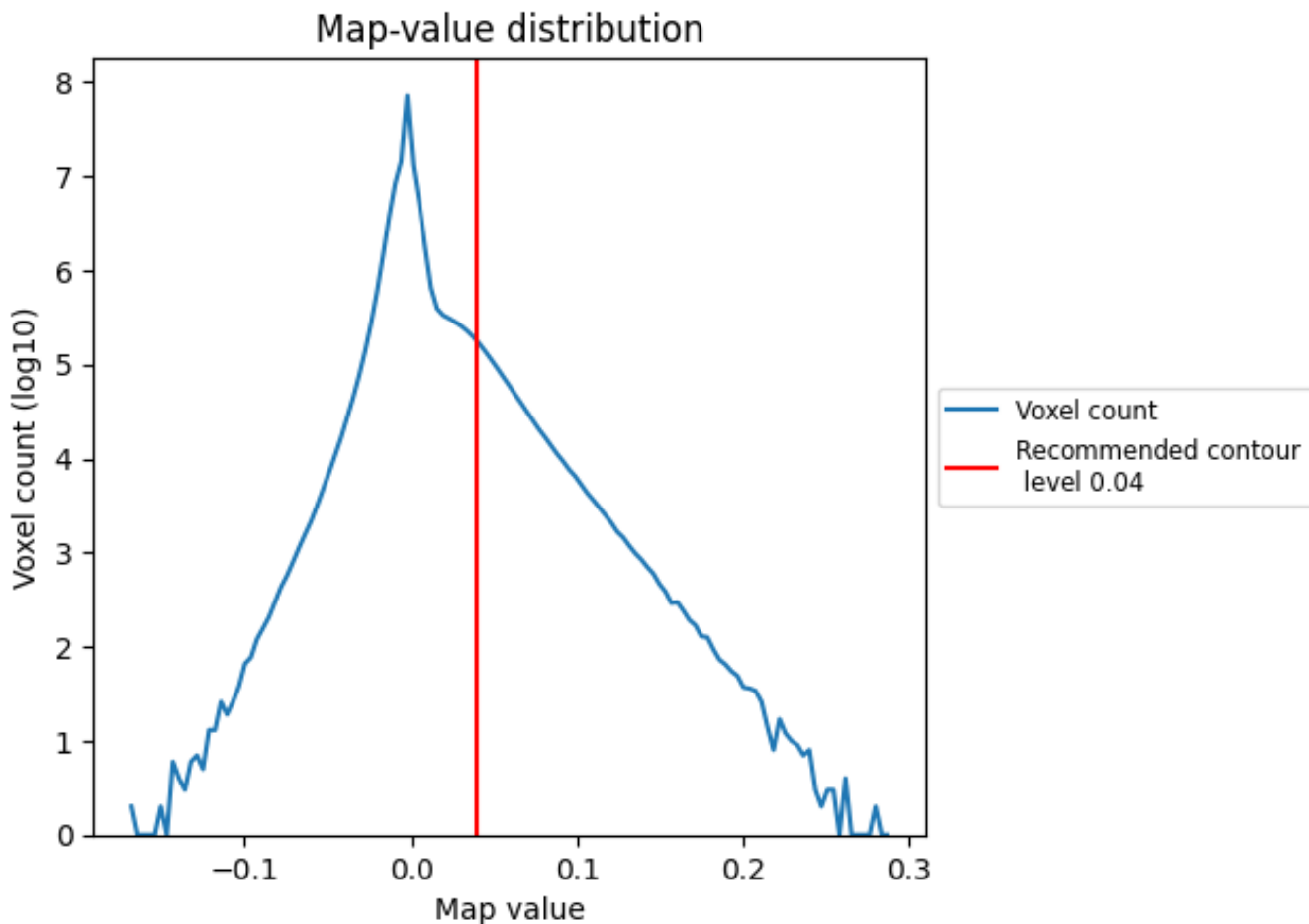


Z

7 Map analysis [i](#)

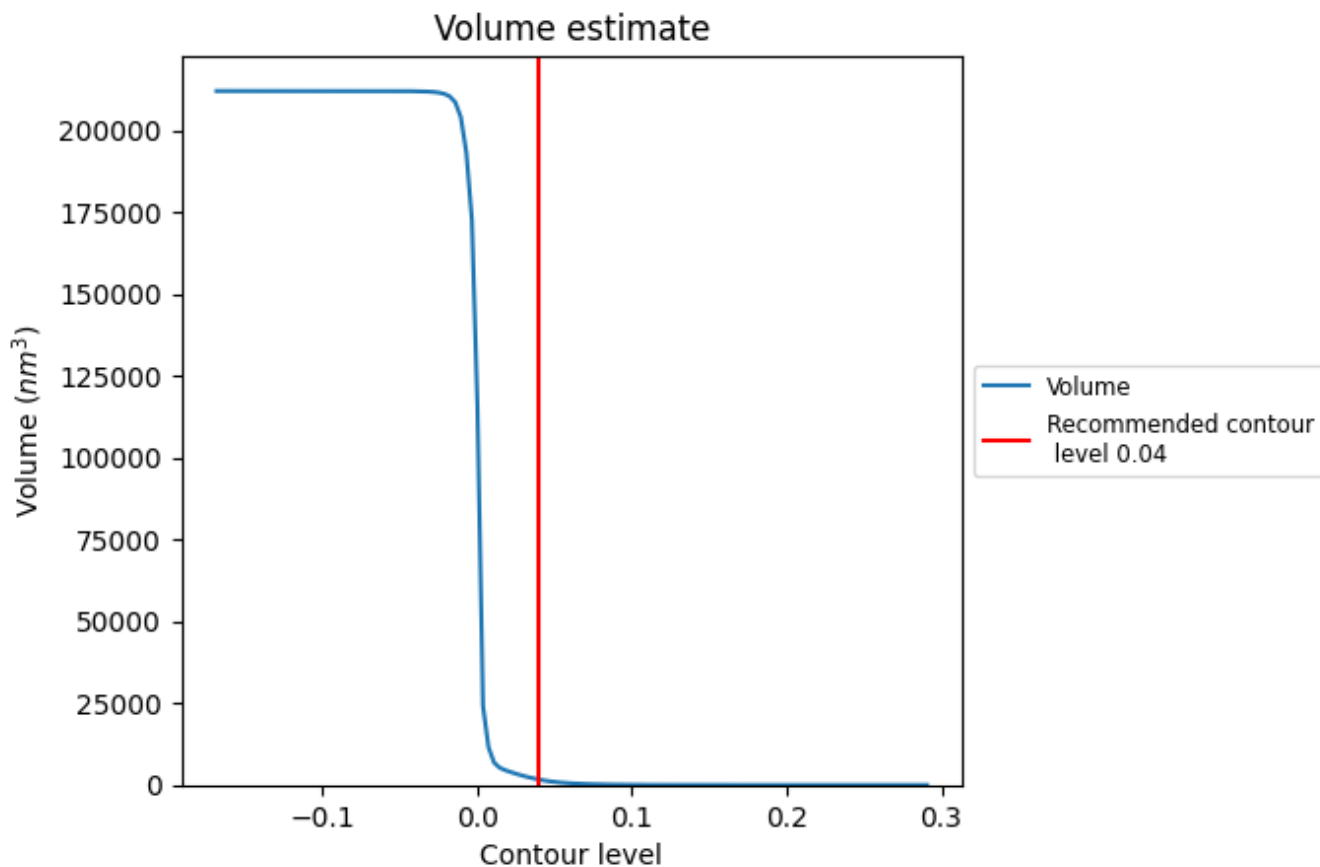
This section contains the results of statistical analysis of the map.

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.

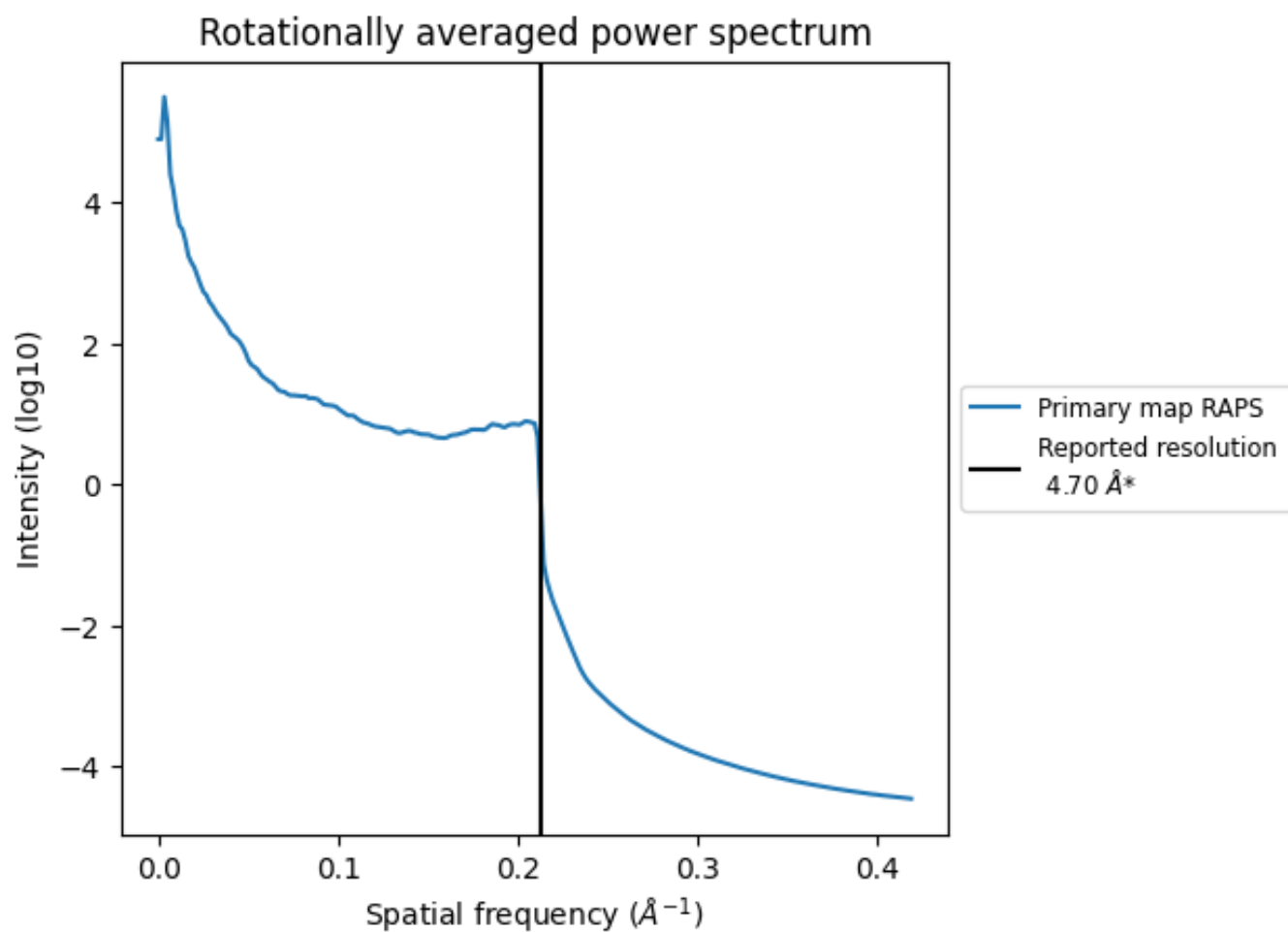
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1641 nm^3 ; this corresponds to an approximate mass of 1482 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 0.213 Å⁻¹

8 Fourier-Shell correlation

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

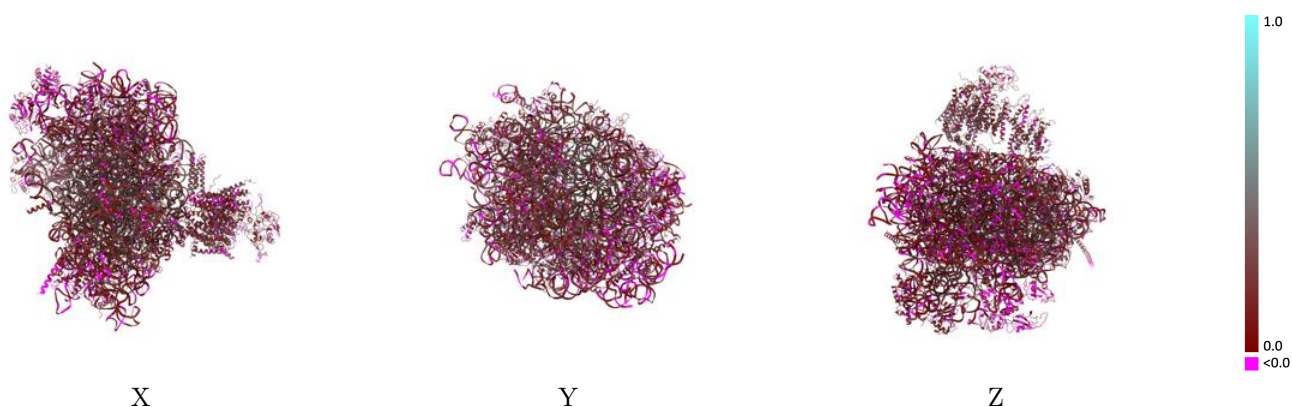
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4317 and PDB model 6FTJ. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)

This section was not generated.

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

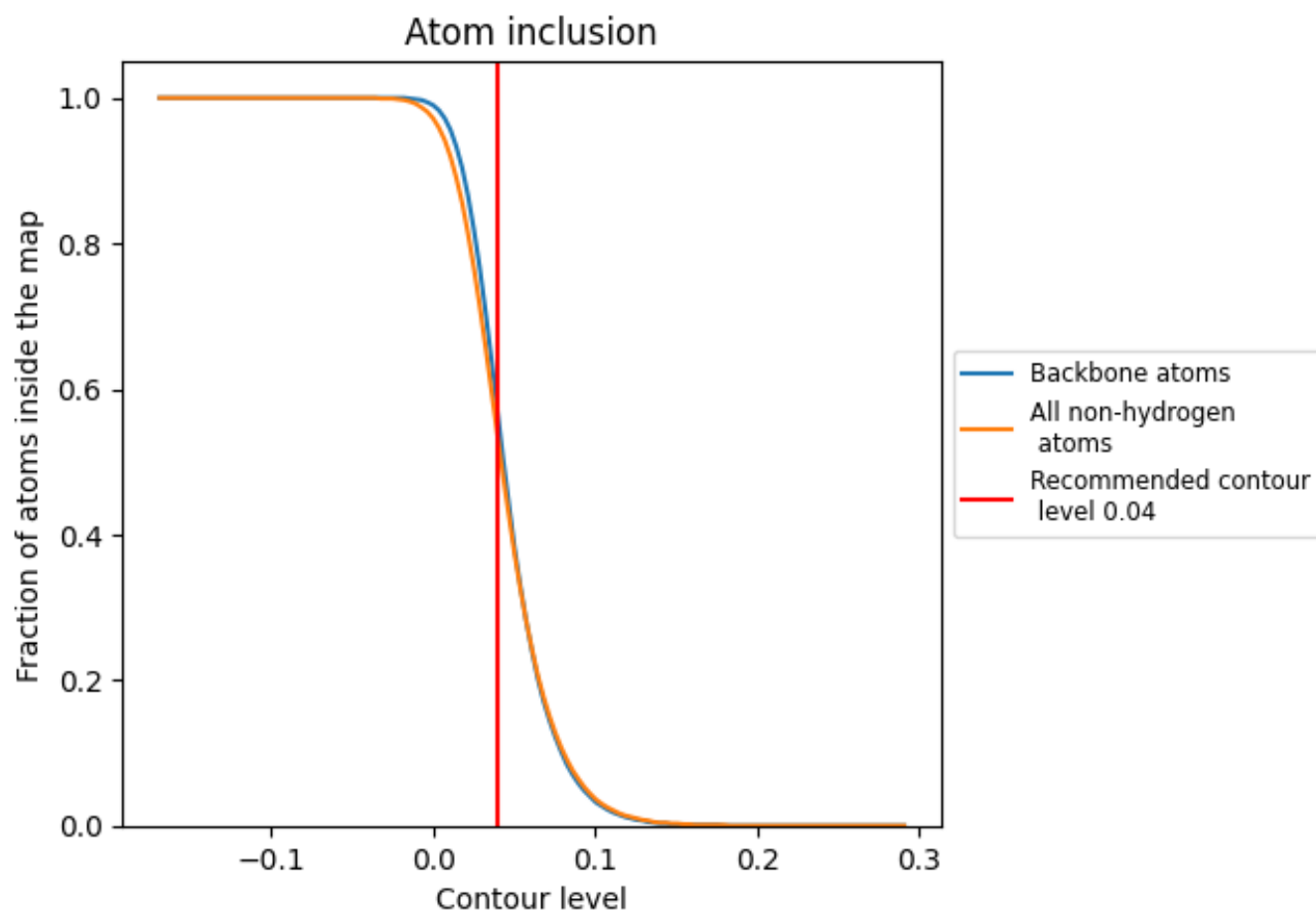


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 57% of all backbone atoms, 53% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5340	 0.1740
1	 0.6550	 0.1980
2	 0.7600	 0.2210
3	 0.5740	 0.1750
4	 0.6090	 0.2080
5	 0.5850	 0.1790
6	 0.8470	 0.2550
7	 0.8160	 0.2140
8	 0.7770	 0.2330
A	 0.3640	 0.1920
B	 0.3700	 0.1570
C	 0.3320	 0.1680
D	 0.3630	 0.1080
E	 0.2450	 0.0940
F	 0.2580	 0.1230
G	 0.2180	 0.1030
H	 0.2080	 0.0760
I	 0.3290	 0.1670
J	 0.3870	 0.1220
K	 0.5210	 0.1490
L	 0.3220	 0.1430
M	 0.2970	 0.1060
N	 0.3930	 0.1800
O	 0.2380	 0.1060
P	 0.5140	 0.2280
Q	 0.3310	 0.1600
R	 0.3910	 0.1490
S	 0.2490	 0.1080
T	 0.2310	 0.1230
U	 0.4110	 0.1380
V	 0.3350	 0.1830
W	 0.3930	 0.1850
X	 0.4090	 0.1880
Y	 0.4170	 0.1650
Z	 0.3620	 0.1310



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Chain	Atom inclusion	Q-score
a	 0.3010	 0.1530
b	 0.3340	 0.1360
c	 0.3160	 0.1520
d	 0.4640	 0.2090
e	 0.2440	 0.1380
f	 0.1830	 0.0770
g	 0.3030	 0.1600
h	 0.4390	 0.1690
i	 0.3370	 0.1660
j	 0.5720	 0.2520
k	 0.3000	 0.1370
l	 0.5580	 0.2660
m	 0.2520	 0.0870
n	 0.4530	 0.1880
o	 0.4210	 0.1890
p	 0.3220	 0.1620
r	 0.3350	 0.1260
s	 0.1440	 0.0380
t	 0.1180	 0.0100
u	 0.6530	 0.1930
v	 0.7110	 0.1640
w	 0.7430	 0.2300
x	 0.5500	 0.1930
y	 0.5620	 0.1960
z	 0.2620	 0.0520