



wwPDB EM Validation Summary Report ⓘ

Jun 23, 2026 – 11:25 AM EDT

PDB ID : 6OLI / pdb_00006oli
EMDB ID : EMD-0526
Title : Structure of human ribosome nascent chain complex selectively stalled by a drug-like small molecule (USO1-RNC)
Authors : Li, W.; Cate, J.H.D.
Deposited on : 2019-04-16
Resolution : 3.50 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:

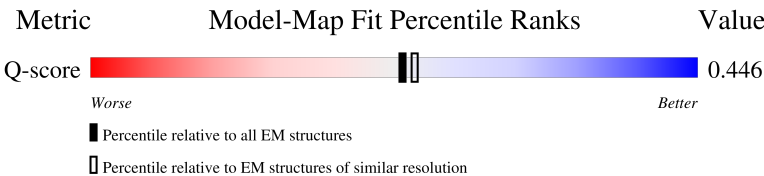
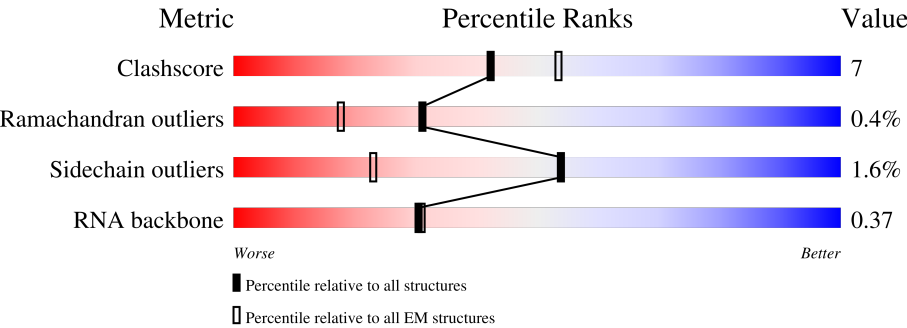
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.50 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	13950 (3.00 - 4.00)

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

Mol	Chain	Length	Quality of chain
1	S2	1714	12% 55% 36% 9%
2	SA	221	28% 74% 25% .
3	SB	214	21% 73% 26% .

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Mol	Chain	Length	Quality of chain
4	SD	226	
5	SE	259	
6	SF	189	
7	SH	189	
8	SI	204	
9	SK	98	
10	SL	153	
11	SP	127	
12	SQ	146	
13	SR	134	
14	SS	145	
15	ST	143	
16	SU	104	
17	SV	82	
18	SX	141	
19	Sa	102	
20	Sc	64	
21	Sd	55	
22	Sg	312	
23	SC	220	
24	SG	237	
25	SJ	185	
26	SM	118	
27	SN	150	
28	SO	137	

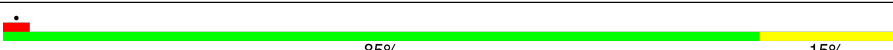
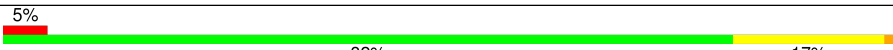
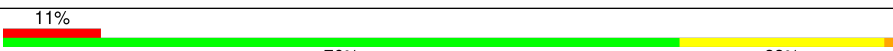
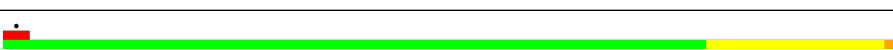
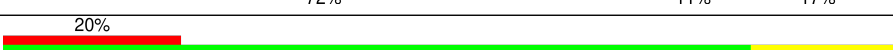
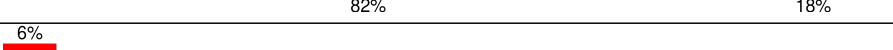
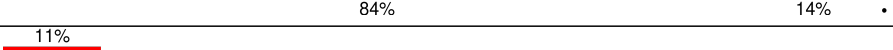
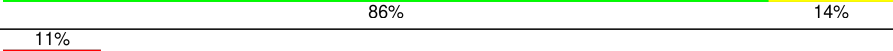
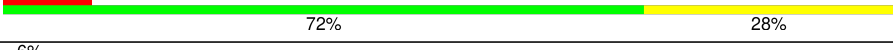
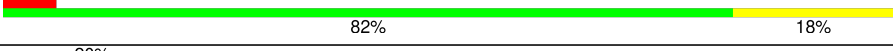
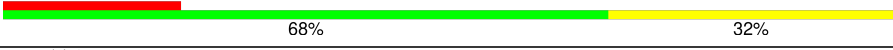
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Mol	Chain	Length	Quality of chain
29	SW	129	
30	SY	131	
31	SZ	73	
32	Sb	82	
33	Se	57	
34	Sf	67	
35	A	252	
36	B	397	
37	C	363	
38	D	157	
39	E	121	
40	F	294	
41	G	247	
42	H	225	
43	I	234	
44	J	191	
45	K	211	
46	L	169	
47	M	205	
48	N	139	
49	O	203	
50	P	195	
51	Q	153	
52	R	187	
53	S	181	

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Mol	Chain	Length	Quality of chain
54	T	175	
55	U	157	
56	V	99	
57	W	129	
58	X	61	
59	Y	117	
60	Z	134	
61	a	134	
62	b	147	
63	c	121	
64	d	103	
65	e	106	
66	f	129	
67	g	109	
68	h	114	
69	i	122	
70	j	97	
71	k	84	
72	l	69	
73	m	50	
74	n	50	
75	o	25	
76	p	105	
77	q	91	
78	r	122	

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Mol	Chain	Length	Quality of chain
79	t	3607	9% 64% 30% 6%
80	u	76	63% 54% 43%
81	v	76	24% 51% 32% 17%
82	w	10	80% 10% 10%
83	y	36	92% 97%

2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 214867 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 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	S2	1714	Total	C	N	O	P	0	0
			36501	16306	6533	11949	1713		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SA	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		

- Molecule 3 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 4 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SD	226	Total	C	N	O	S	0	0
			1757	1120	316	314	7		

- Molecule 5 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SE	259	Total	C	N	O	S	0	0
			2059	1316	383	352	8		

- Molecule 6 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SF	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 7 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SH	186	Total	C	N	O	S	0	0
			1497	956	274	266	1		

- Molecule 8 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SI	204	Total	C	N	O	S	0	0
			1673	1050	329	289	5		

- Molecule 9 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 10 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SL	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 11 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SP	127	Total	C	N	O	S	0	0
			1045	663	198	177	7		

- Molecule 12 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SQ	146	Total	C	N	O	S	0	0
			1158	736	218	200	4		

- Molecule 13 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SR	134	Total	C	N	O	S	0	0
			1082	680	201	197	4		

- Molecule 14 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SS	145	Total	C	N	O	S	0	0
			1198	751	242	203	2		

- Molecule 15 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	ST	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 16 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 17 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SV	82	Total	C	N	O	S	0	0
			625	384	116	120	5		

- Molecule 18 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 19 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Sa	102	Total	C	N	O	S	0	0
			821	512	171	133	5		

- Molecule 20 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 21 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Sd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 22 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Sg	312	Total	C	N	O	S	0	0
			2429	1531	423	463	12		

- Molecule 23 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SC	220	Total	C	N	O	S	1	0
			1715	1109	296	300	10		

- Molecule 24 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 25 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SJ	185	Total	C	N	O	S	1	0
			1533	974	309	248	2		

- Molecule 26 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SM	118	Total	C	N	O	S	0	0
			912	571	161	173	7		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SM	52	GLN	LEU	conflict	UNP P25398
SM	69	LEU	CYS	conflict	UNP P25398
SM	99	ASN	LYS	conflict	UNP P25398

- Molecule 27 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 28 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SO	137	Total	C	N	O	S	0	0
			1024	627	200	191	6		

- Molecule 29 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 30 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	SY	131	Total	C	N	O	S	1	0
			1073	678	212	178	5		

- Molecule 31 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	SZ	73	Total	C	N	O	S	0	0
			579	372	106	100	1		

- Molecule 32 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Sb	82	Total	C	N	O	S	0	0
			640	402	118	113	7		

- Molecule 33 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Se	57	Total	C	N	O	S	0	0
			452	281	99	71	1		

- Molecule 34 is a protein called 40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Sf	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 35 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	A	252	Total	C	N	O	S	0	0
			1930	1209	395	320	6		

- Molecule 36 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	B	397	Total	C	N	O	S	0	0
			3202	2039	602	547	14		

- Molecule 37 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	C	363	Total	C	N	O	S	0	0
			2888	1817	577	480	14		

- Molecule 38 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	D	157	Total	C	N	O	P	0	0
			3337	1489	587	1104	157		

- Molecule 39 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	E	119	Total	C	N	O	P	0	0
			2541	1132	454	836	119		

- Molecule 40 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	F	294	Total	C	N	O	S	0	0
			2392	1510	436	432	14		

- Molecule 41 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	G	236	Total	C	N	O	S	0	0
			1904	1222	361	317	4		

- Molecule 42 is a protein called 60S ribosomal protein L7.

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

- Molecule 43 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	I	234	Total	C	N	O	S	0	0
			1880	1197	362	317	4		

- Molecule 44 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	J	191	Total	C	N	O	S	0	0
			1526	960	285	275	6		

- Molecule 45 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	K	208	Total	C	N	O	S	0	0
			1692	1074	327	278	13		

- Molecule 46 is a protein called 60S ribosomal protein L11.

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

- Molecule 47 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	M	205	Total	C	N	O	S	0	0
			1657	1036	344	273	4		

- Molecule 48 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	N	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

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

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

- Molecule 50 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	P	195	Total	C	N	O	S	0	0
			1606	1034	315	252	5		

- Molecule 51 is a protein called 60S ribosomal protein L17.

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

- Molecule 52 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	R	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 53 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	S	181	Total	C	N	O	S	0	0
			1517	938	329	241	9		

- Molecule 54 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	T	175	Total	C	N	O	S	0	0
			1449	921	283	234	11		

- Molecule 55 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	U	157	Total	C	N	O	S	0	0
			1284	815	250	214	5		

- Molecule 56 is a protein called 60S ribosomal protein L22.

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

- Molecule 57 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	W	129	Total	C	N	O	S	0	0
			969	613	182	169	5		

- Molecule 58 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	X	61	Total	C	N	O	S	0	0
			511	327	100	82	2		

- Molecule 59 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Y	117	Total	C	N	O	S	0	0
			958	612	180	165	1		

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

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

- Molecule 61 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	a	134	Total	C	N	O	S	0	0
			1103	712	207	181	3		

- Molecule 62 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	b	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 63 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	c	100	Total	C	N	O	S	0	0
			814	506	179	125	4		

- Molecule 64 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	d	103	Total	C	N	O	S	0	0
			801	508	141	145	7		

- Molecule 65 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	e	106	Total	C	N	O	S	0	0
			879	555	170	152	2		

- Molecule 66 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	f	129	Total	C	N	O	S	0	0
			1064	673	220	166	5		

- Molecule 67 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	g	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 68 is a protein called 60S ribosomal protein L34.

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

- Molecule 69 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	i	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 70 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	j	97	Total	C	N	O	S	0	0
			794	497	168	124	5		

- Molecule 71 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	k	84	Total	C	N	O	S	0	0
			689	423	152	109	5		

- Molecule 72 is a protein called 60S ribosomal protein L38.

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

- Molecule 73 is a protein called 60S ribosomal protein L39.

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

- Molecule 74 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	n	50	Total	C	N	O	S	0	0
			411	254	87	64	6		

- Molecule 75 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	o	25	Total	C	N	O	S	0	0
			240	145	64	28	3		

- Molecule 76 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	p	105	Total	C	N	O	S	0	0
			863	542	175	140	6		

- Molecule 77 is a protein called 60S ribosomal protein L37a.

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

- Molecule 78 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	r	122	Total	C	N	O	S	0	0
			980	607	204	165	4		

- Molecule 79 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	t	3607	Total	C	N	O	P	0	0
			77332	34436	14150	25139	3607		

- Molecule 80 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	u	76	Total	C	N	O	P	0	0
			1613	720	283	535	75		

- Molecule 81 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	v	76	Total	C	N	O	P	0	0
			1618	721	287	534	76		

- Molecule 82 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	w	10	Total	C	N	O	P	0	0
			213	95	37	72	9		

- Molecule 83 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
83	y	36	Total	C	N	O	0	0
			178	106	36	36		

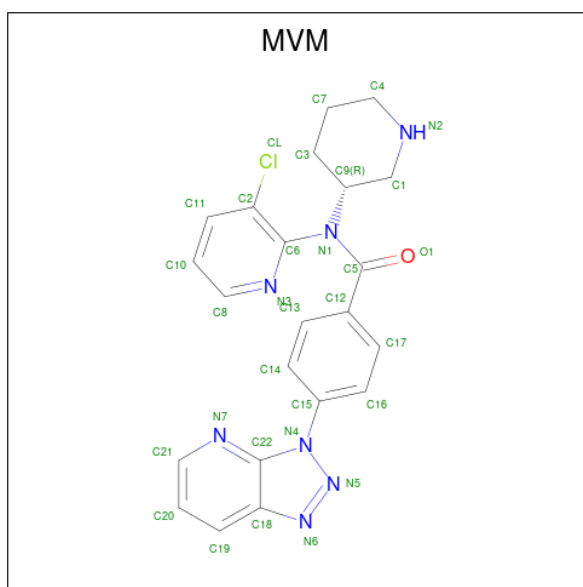
- Molecule 84 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
84	S2	2	Total	Mg	0
			2	2	
84	B	1	Total	Mg	0
			1	1	
84	D	7	Total	Mg	0
			7	7	
84	E	9	Total	Mg	0
			9	9	
84	O	1	Total	Mg	0
			1	1	
84	b	1	Total	Mg	0
			1	1	
84	o	1	Total	Mg	0
			1	1	
84	t	9	Total	Mg	0
			9	9	

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

Mol	Chain	Residues	Atoms		AltConf
85	S2	1	Total	Zn	0
			1	1	
85	Sa	1	Total	Zn	0
			1	1	
85	Sf	1	Total	Zn	0
			1	1	
85	k	1	Total	Zn	0
			1	1	
85	p	1	Total	Zn	0
			1	1	
85	q	1	Total	Zn	0
			1	1	

- Molecule 86 is N-(3-chloropyridin-2-yl)-N-[(3R)-piperidin-3-yl]-4-(3H-[1,2,3]triazolo[4,5-b]pyridin-3-yl)benzamide (CCD ID: MVM) (formula: C₂₂H₂₀ClN₇O).



Mol	Chain	Residues	Atoms					AltConf
86	t	1	Total	C	Cl	N	O	0
			31	22	1	7	1	

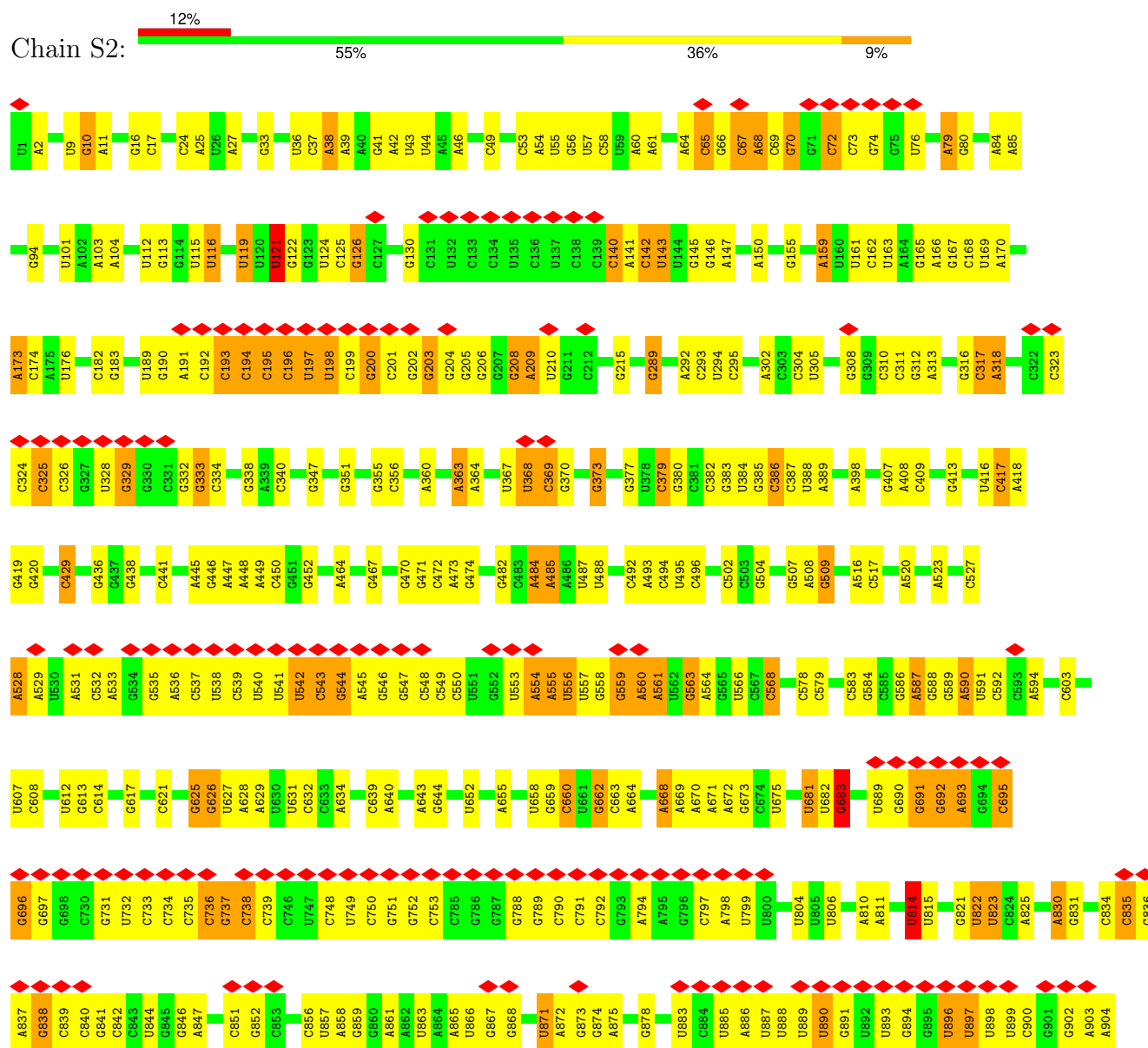
- Molecule 87 is water.

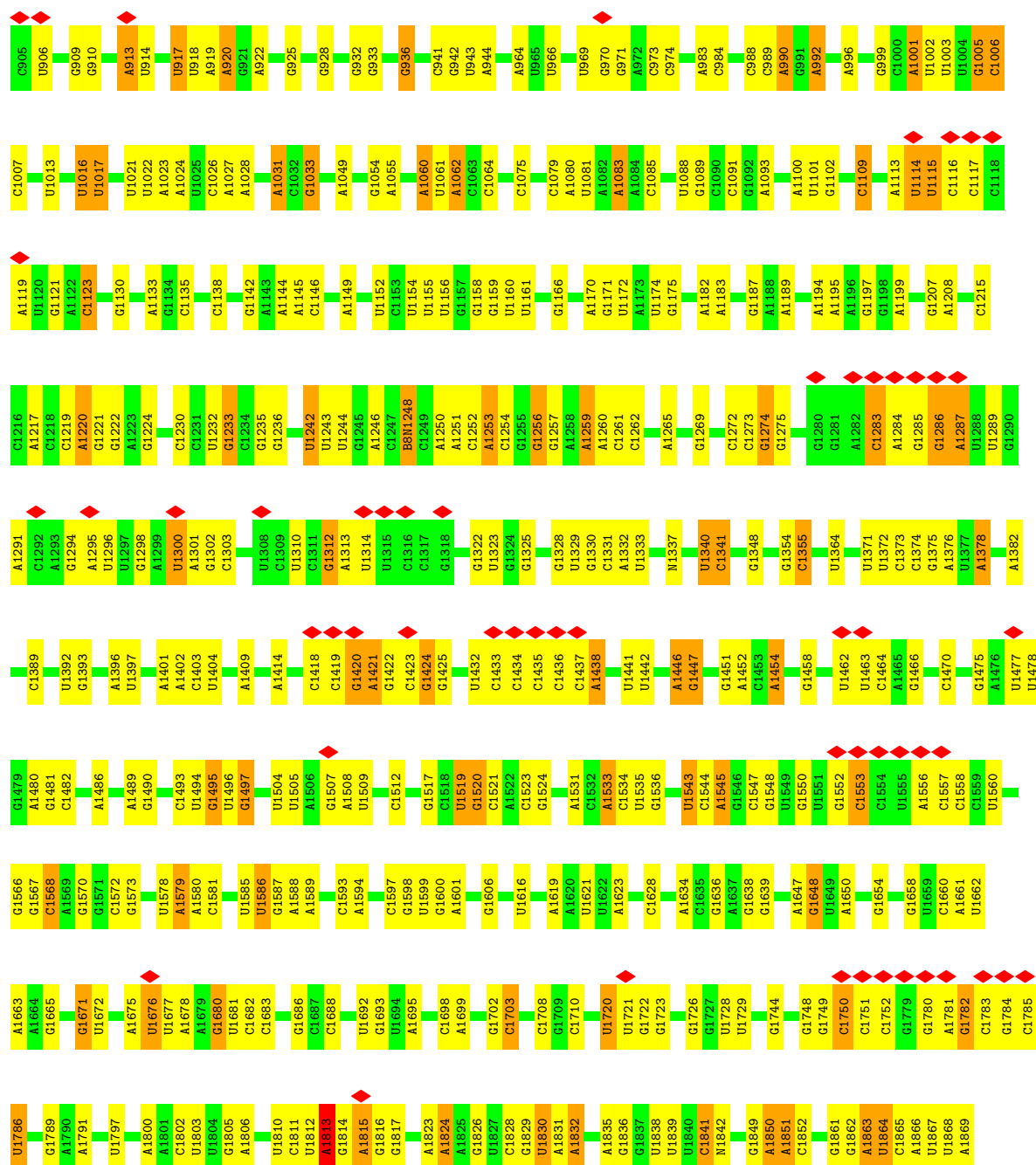
Mol	Chain	Residues	Atoms		AltConf
87	S2	5	Total	O	0
			5	5	
87	SP	1	Total	O	0
			1	1	
87	SQ	1	Total	O	0
			1	1	
87	SR	1	Total	O	0
			1	1	
87	SS	1	Total	O	0
			1	1	
87	SC	1	Total	O	0
			1	1	
87	SJ	1	Total	O	0
			1	1	
87	Sb	1	Total	O	0
			1	1	
87	Sf	1	Total	O	0
			1	1	
87	u	1	Total	O	0
			1	1	

3 Residue-property plots

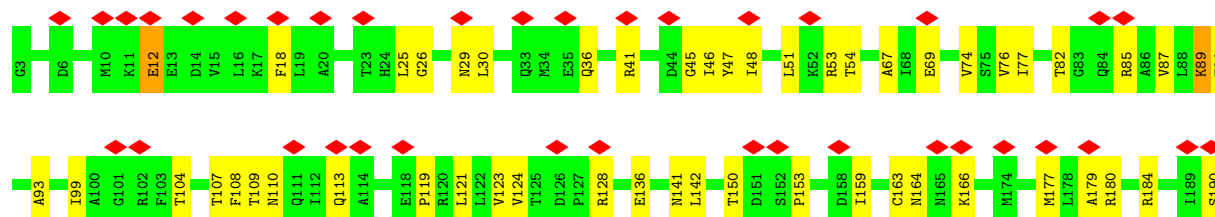
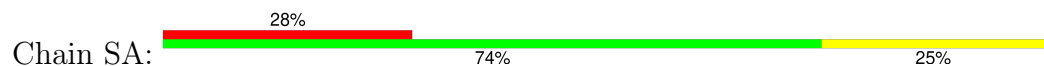
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

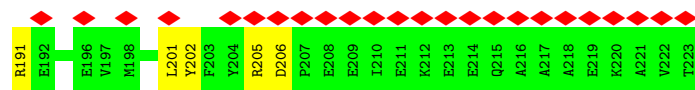
• Molecule 1: 18S ribosomal RNA



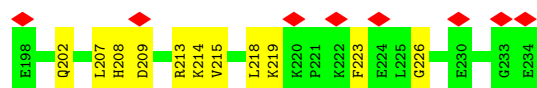
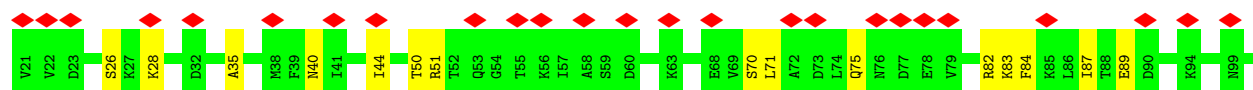
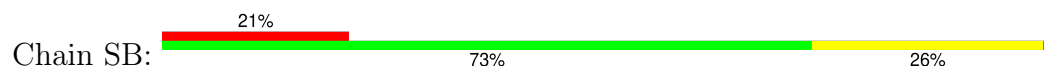


• Molecule 2: 40S ribosomal protein SA

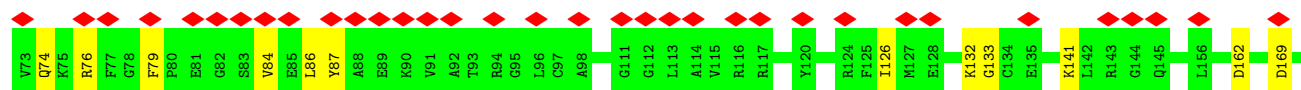
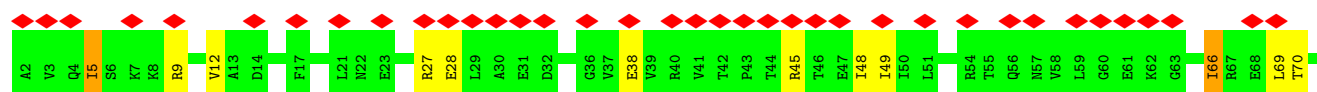
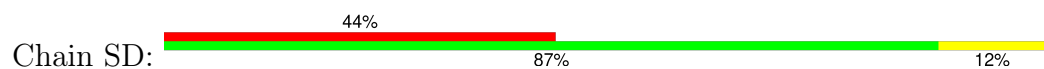




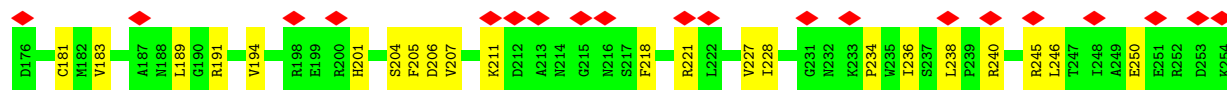
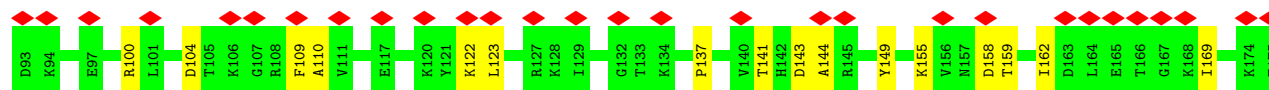
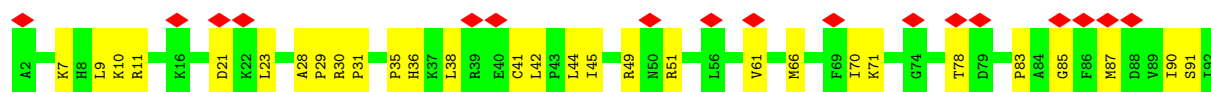
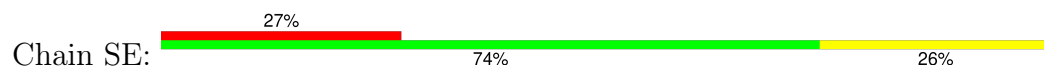
• Molecule 3: 40S ribosomal protein S3a

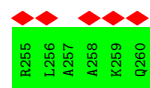


• Molecule 4: 40S ribosomal protein S3

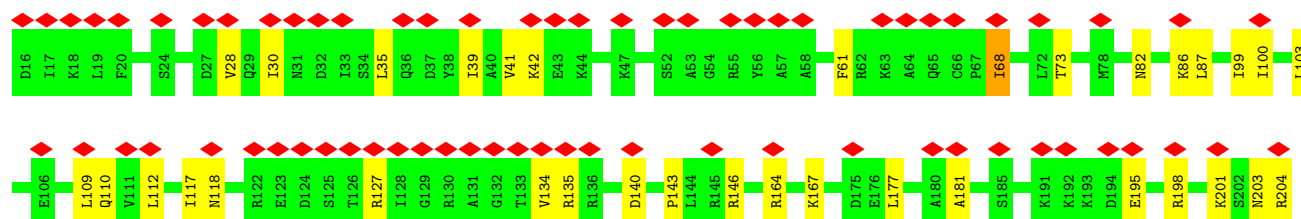
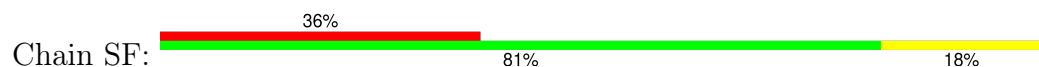


• Molecule 5: 40S ribosomal protein S4, X isoform

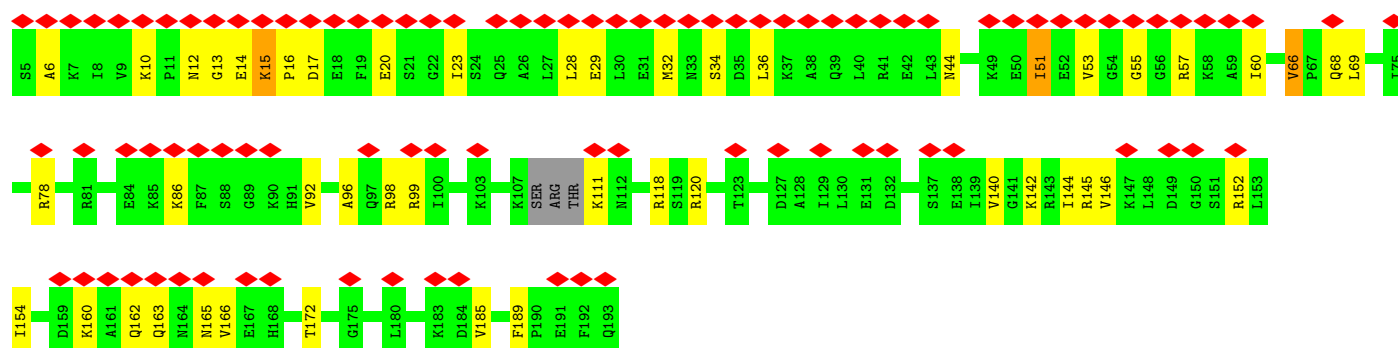
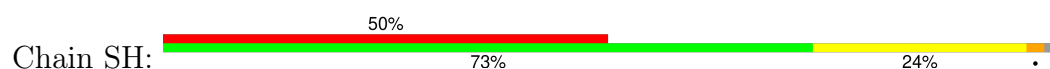




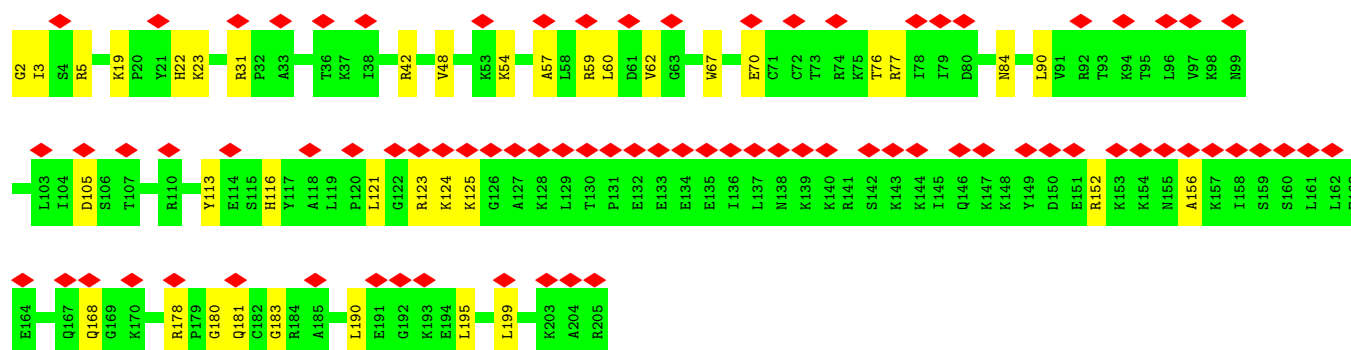
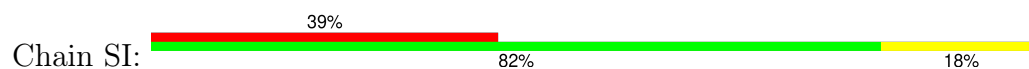
• Molecule 6: 40S ribosomal protein S5



• Molecule 7: 40S ribosomal protein S7

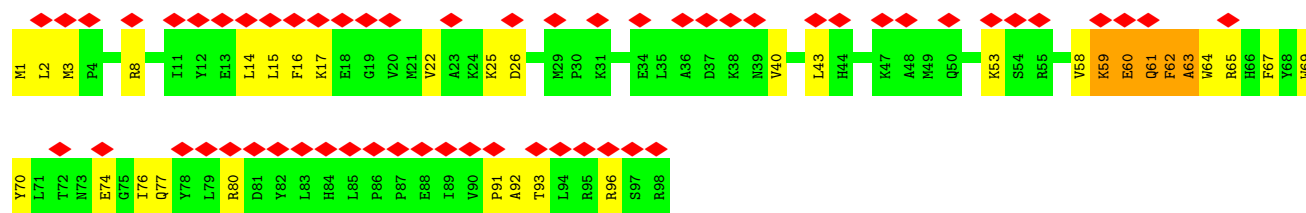


• Molecule 8: 40S ribosomal protein S8

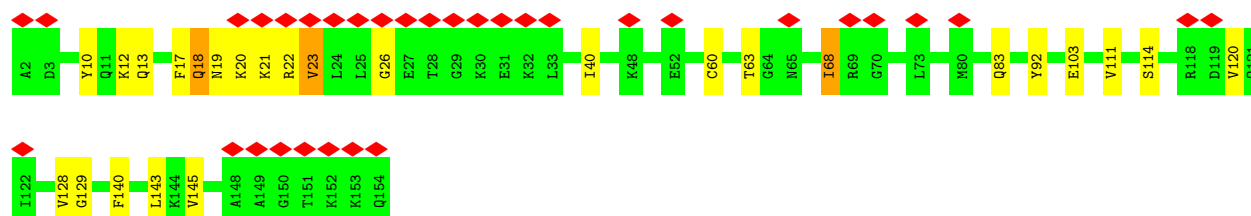
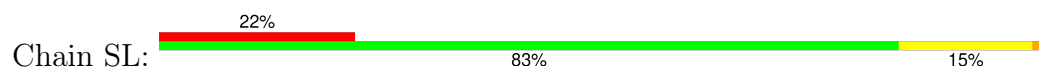


• Molecule 9: 40S ribosomal protein S10

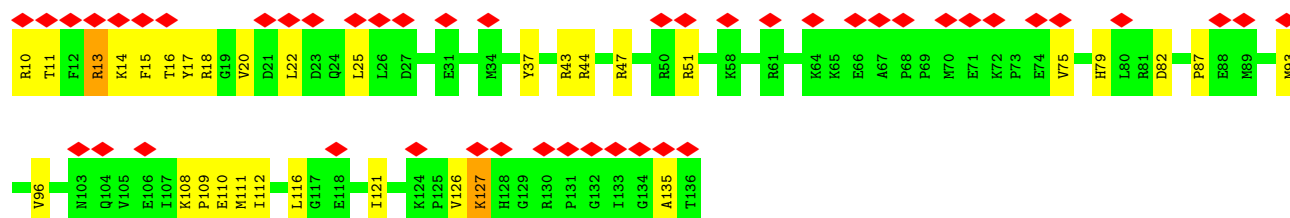
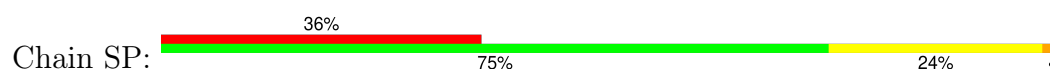




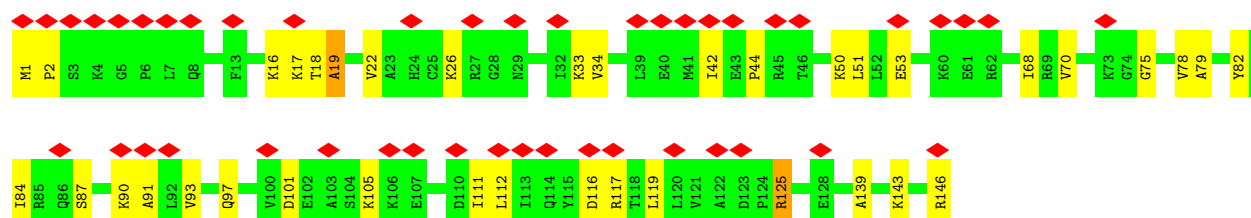
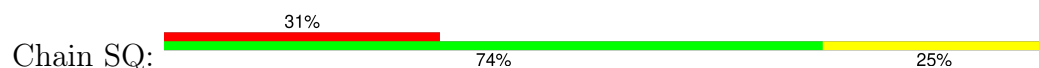
• Molecule 10: 40S ribosomal protein S11



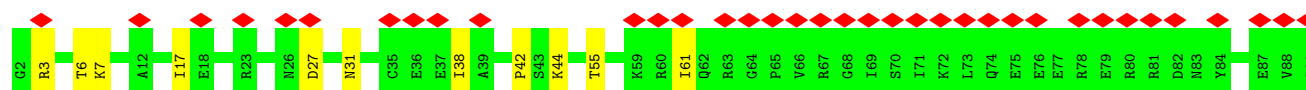
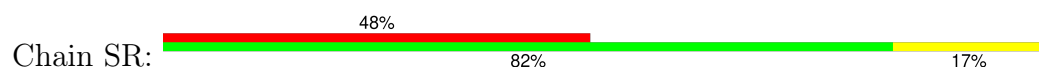
• Molecule 11: 40S ribosomal protein S15

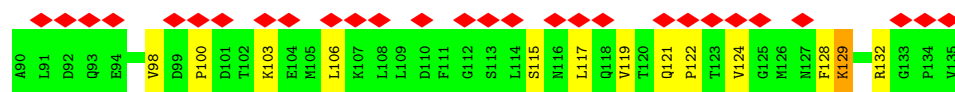


• Molecule 12: 40S ribosomal protein S16

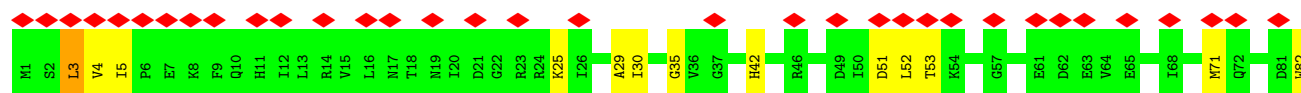
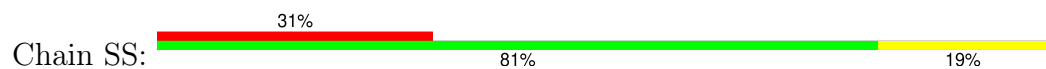


• Molecule 13: 40S ribosomal protein S17

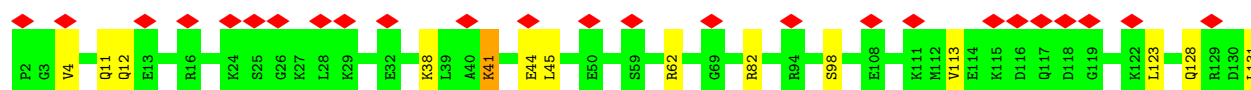
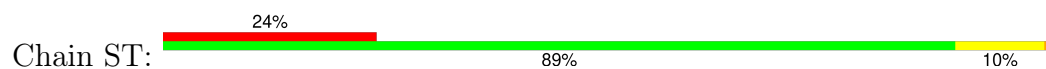




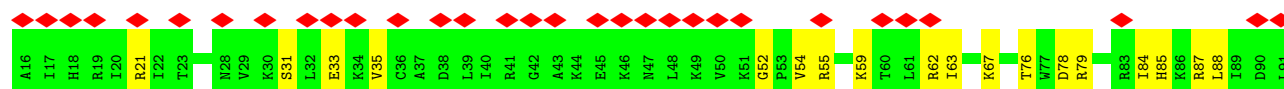
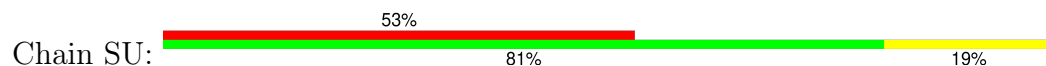
- Molecule 14: 40S ribosomal protein S18



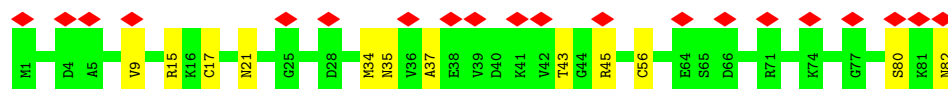
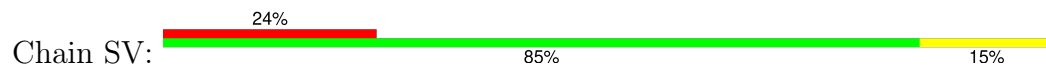
- Molecule 15: 40S ribosomal protein S19



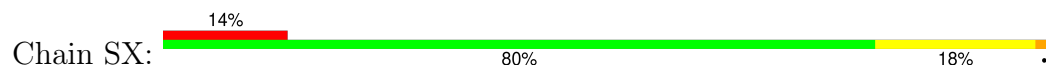
- Molecule 16: 40S ribosomal protein S20

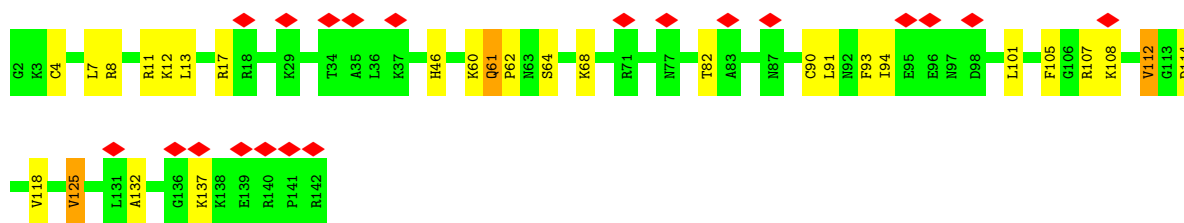


- Molecule 17: 40S ribosomal protein S21

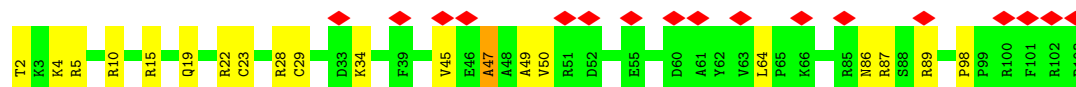
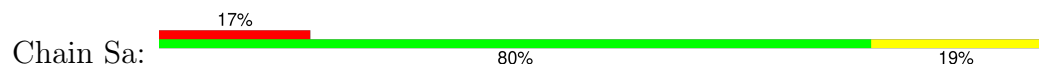


- Molecule 18: 40S ribosomal protein S23

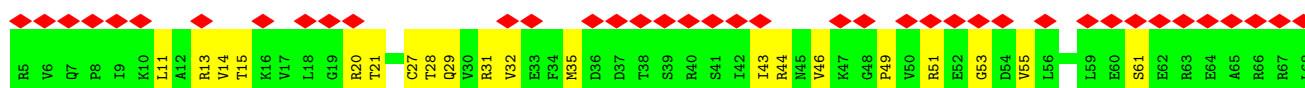




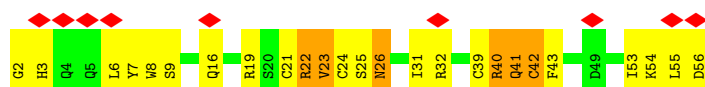
- Molecule 19: 40S ribosomal protein S26



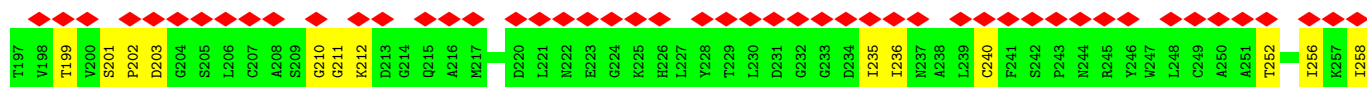
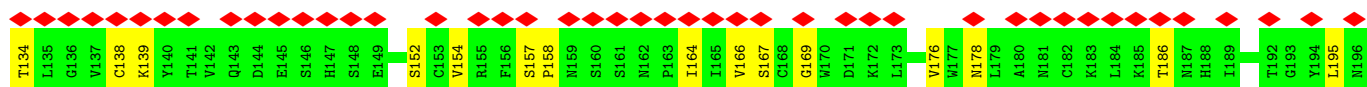
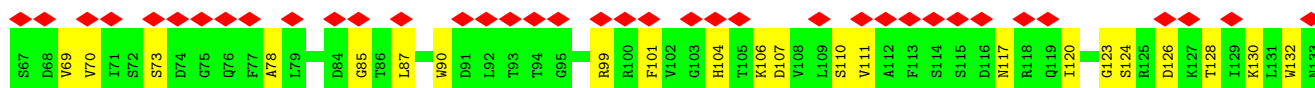
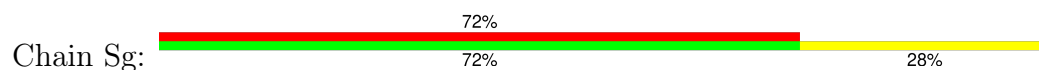
- Molecule 20: 40S ribosomal protein S28

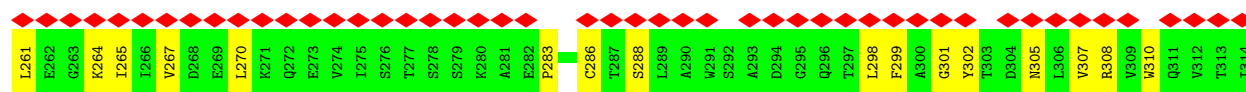


- Molecule 21: 40S ribosomal protein S29

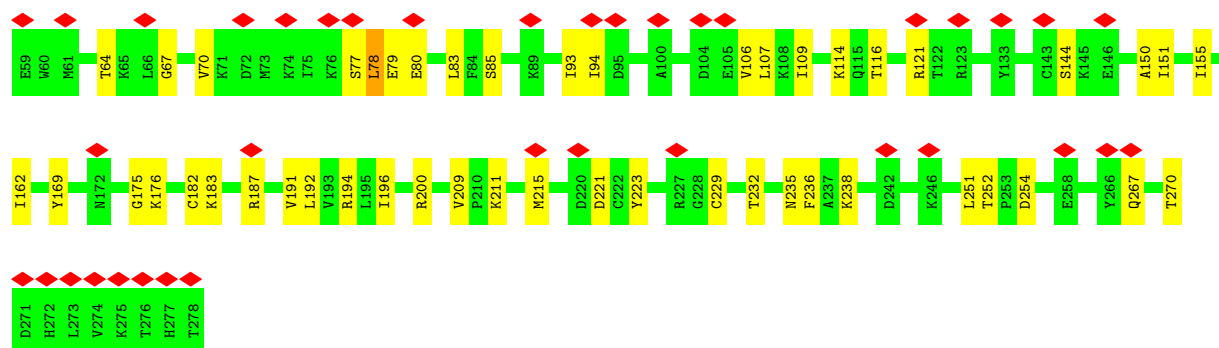
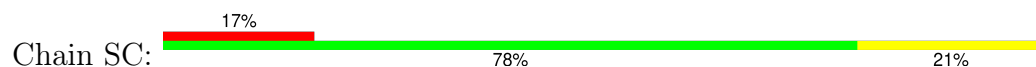


- Molecule 22: Receptor of activated protein C kinase 1

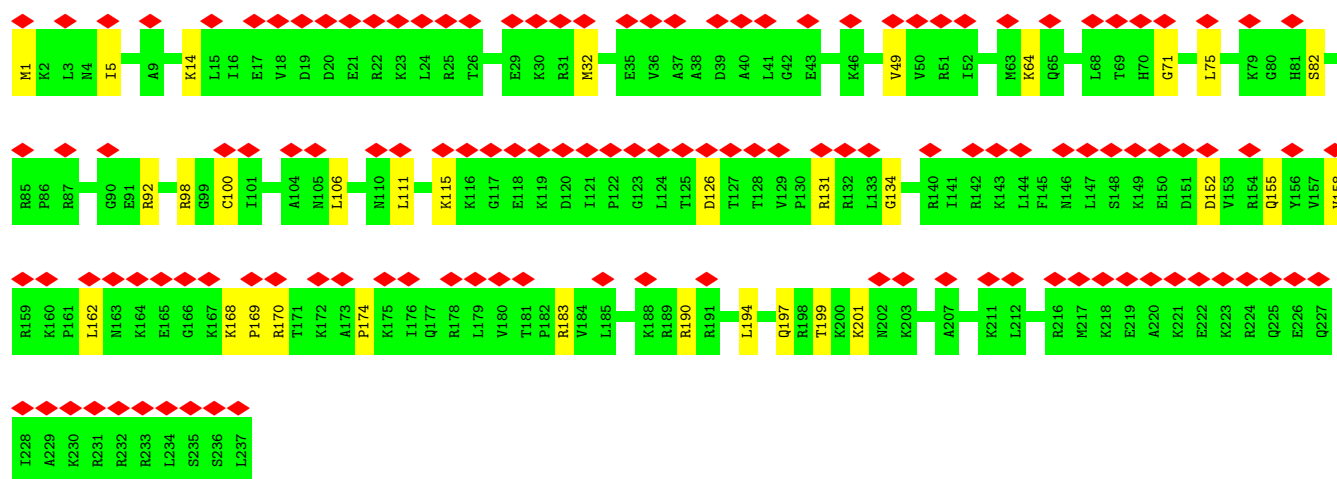
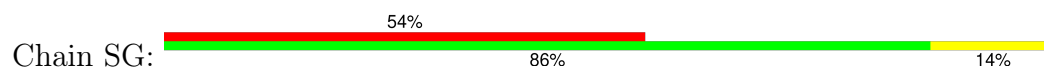




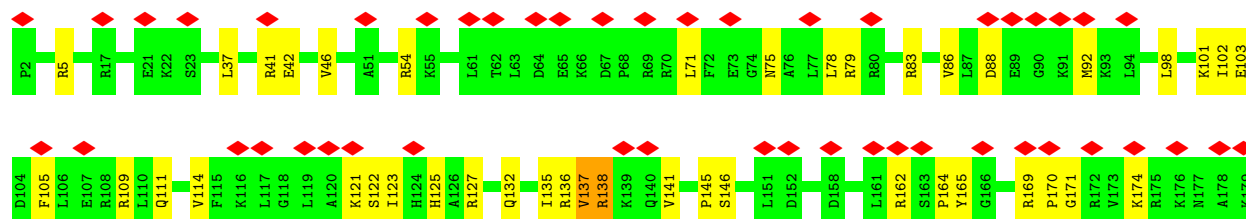
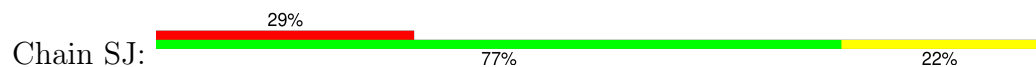
• Molecule 23: 40S ribosomal protein S2

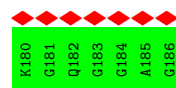


• Molecule 24: 40S ribosomal protein S6

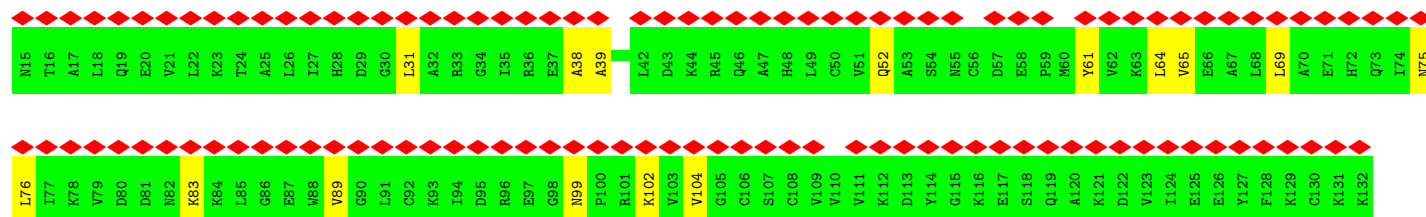
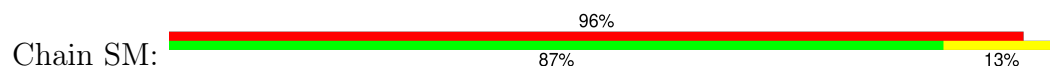


• Molecule 25: 40S ribosomal protein S9

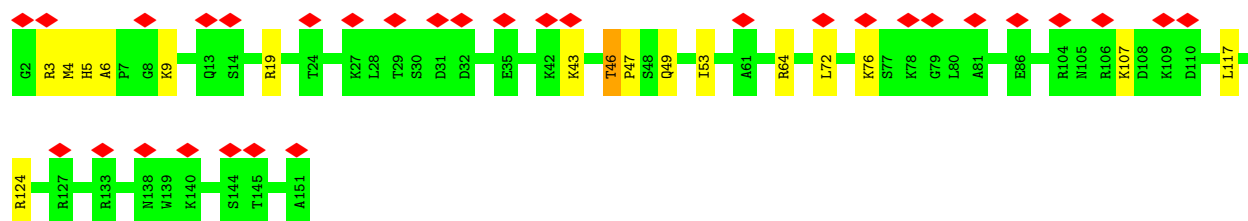
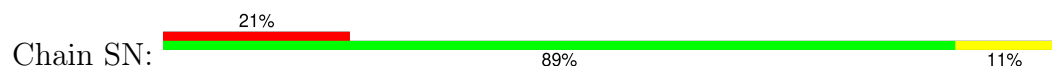




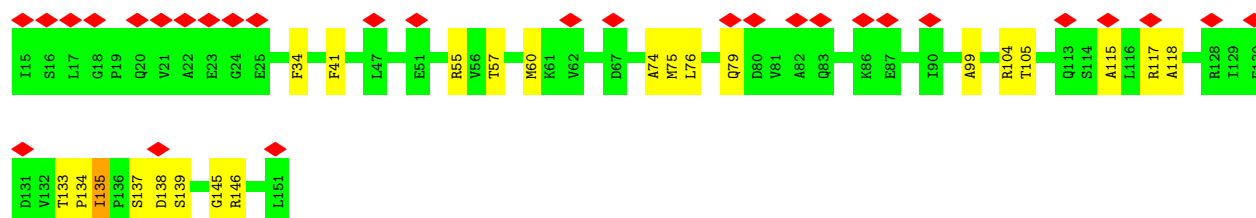
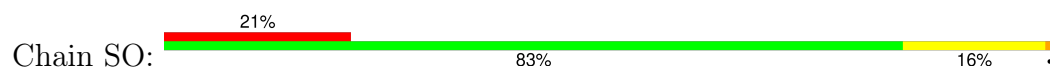
- Molecule 26: 40S ribosomal protein S12



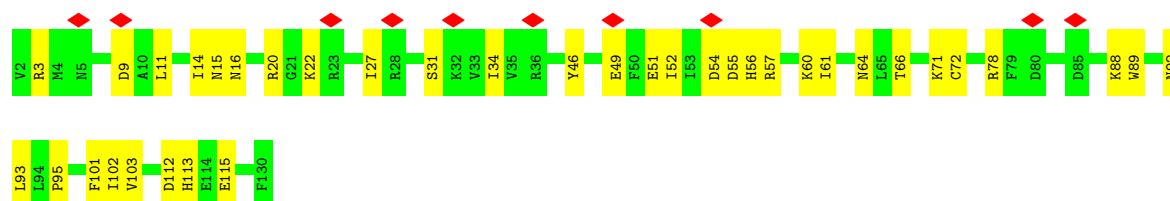
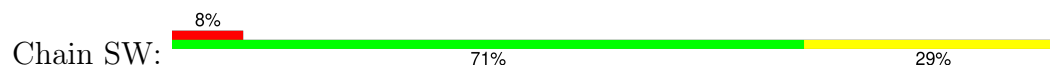
- Molecule 27: 40S ribosomal protein S13



- Molecule 28: 40S ribosomal protein S14

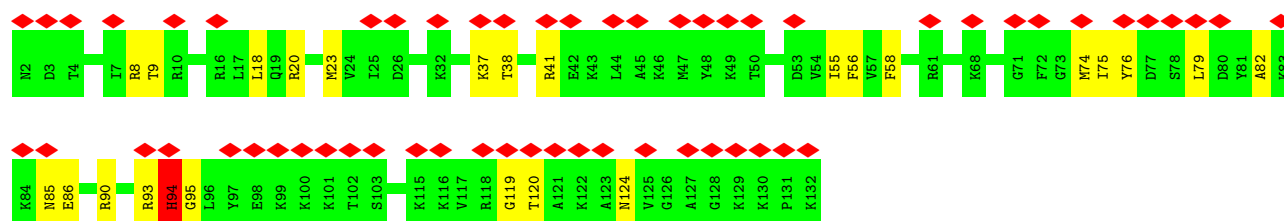


- Molecule 29: 40S ribosomal protein S15a



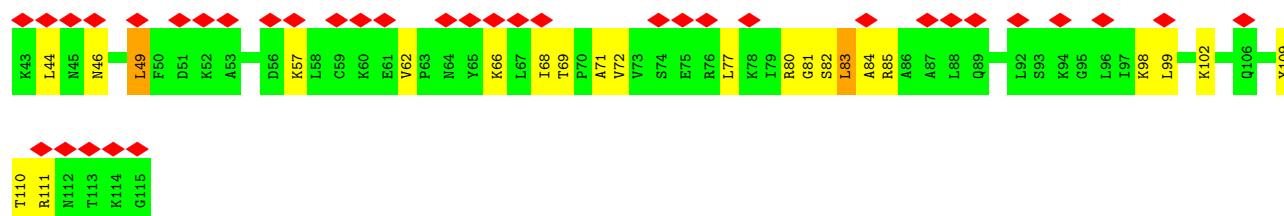
- Molecule 30: 40S ribosomal protein S24

Chain SY: 



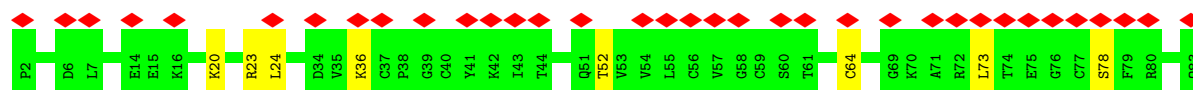
- Molecule 31: 40S ribosomal protein S25

Chain SZ: 

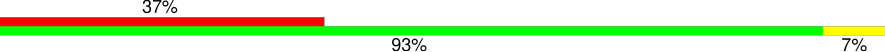


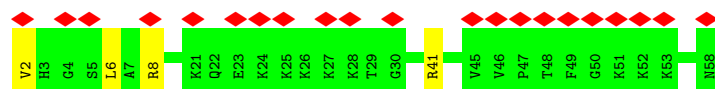
- Molecule 32: 40S ribosomal protein S27

Chain Sb: 



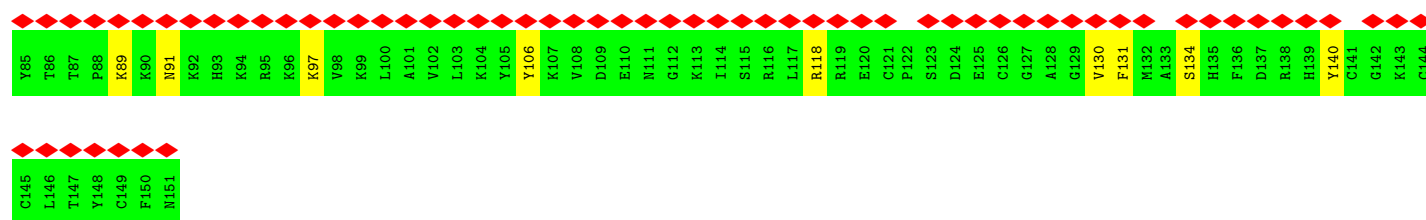
- Molecule 33: 40S ribosomal protein S30

Chain Se: 



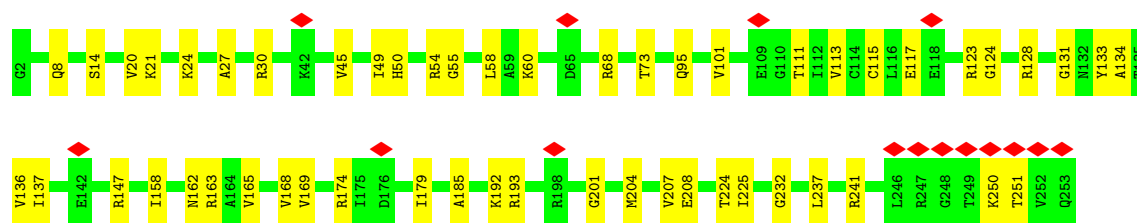
- Molecule 34: 40S ribosomal protein S27a

Chain Sf: 

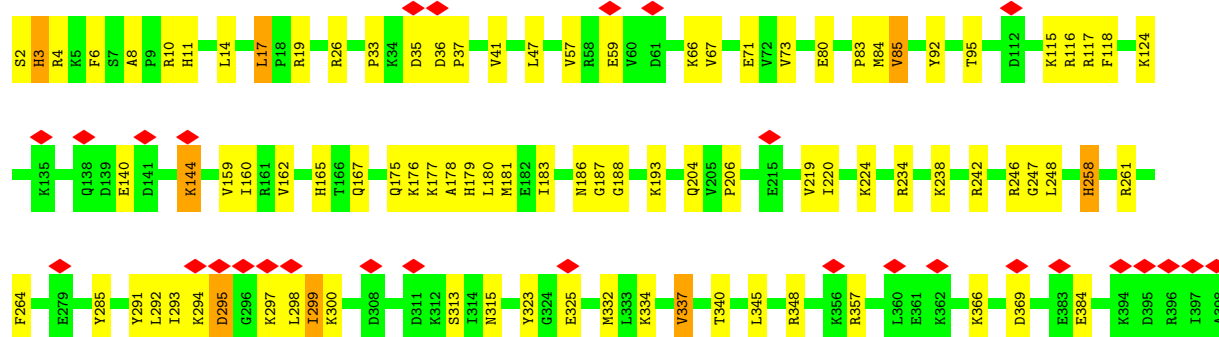
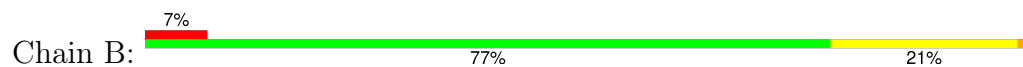


- Molecule 35: 60S ribosomal protein L8

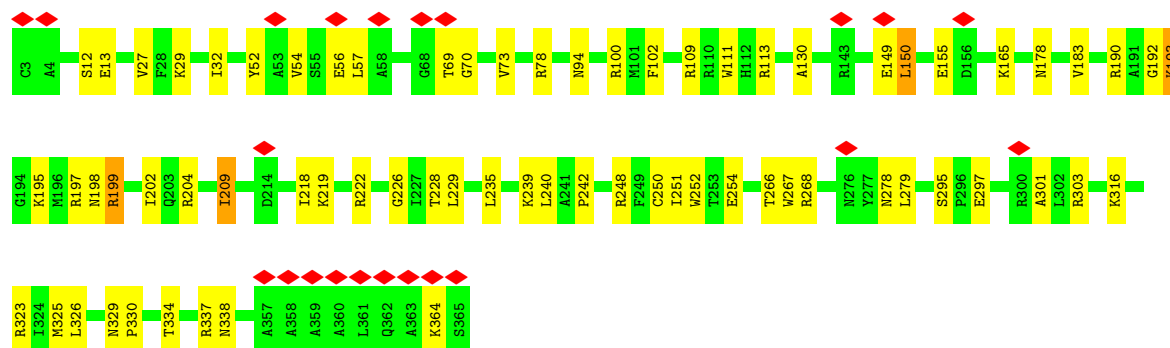
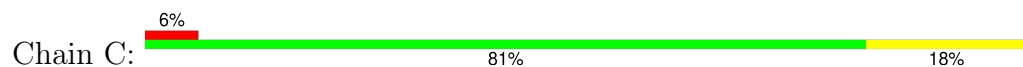
Chain A: 



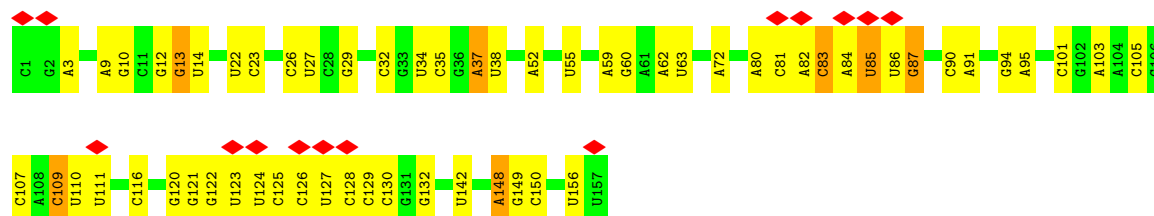
• Molecule 36: 60S ribosomal protein L3



• Molecule 37: 60S ribosomal protein L4



• Molecule 38: 5.8S ribosomal RNA



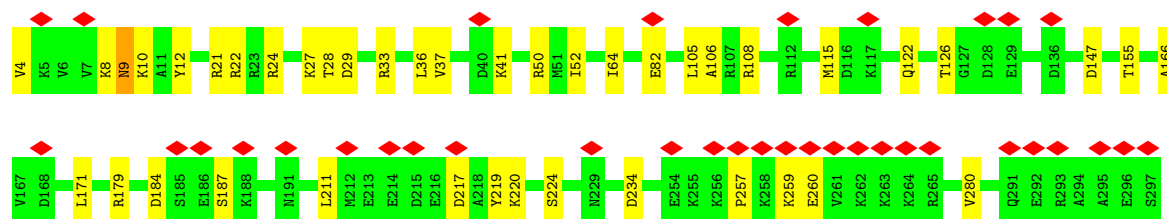
• Molecule 39: 5S ribosomal RNA

Chain E: 



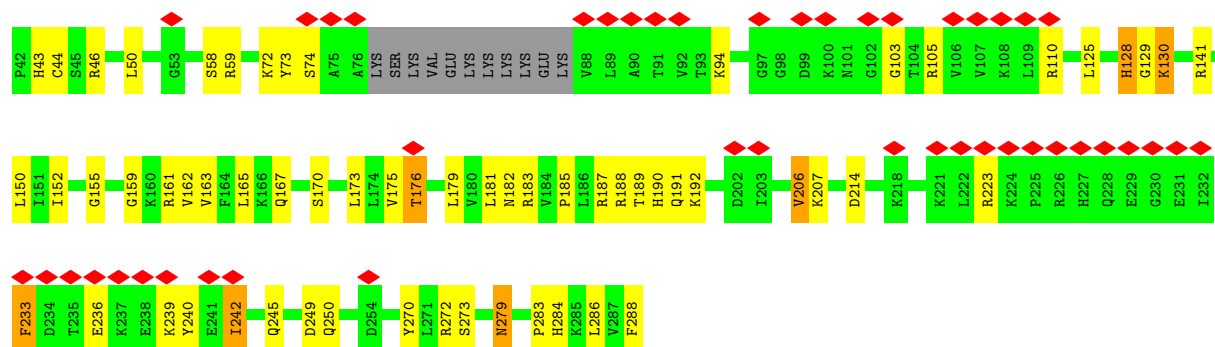
- Molecule 40: 60S ribosomal protein L5

Chain F: 



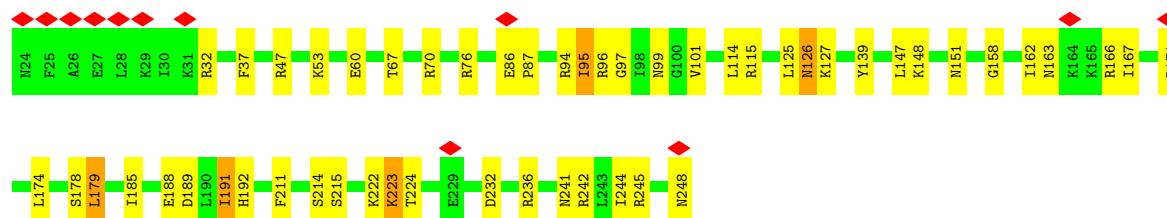
- Molecule 41: 60S ribosomal protein L6

Chain G: 



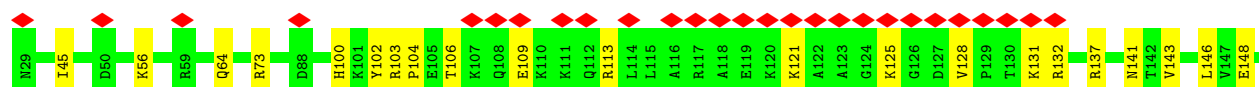
- Molecule 42: 60S ribosomal protein L7

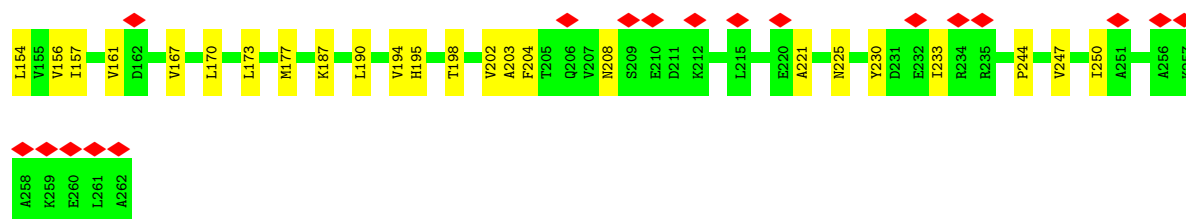
Chain H: 



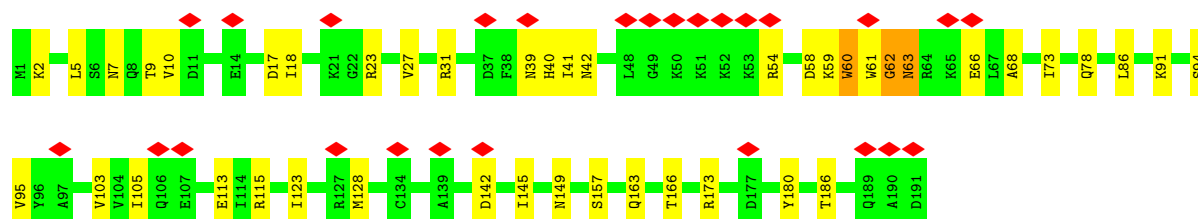
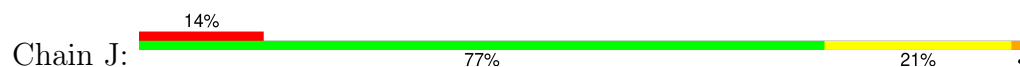
- Molecule 43: 60S ribosomal protein L7a

Chain I: 

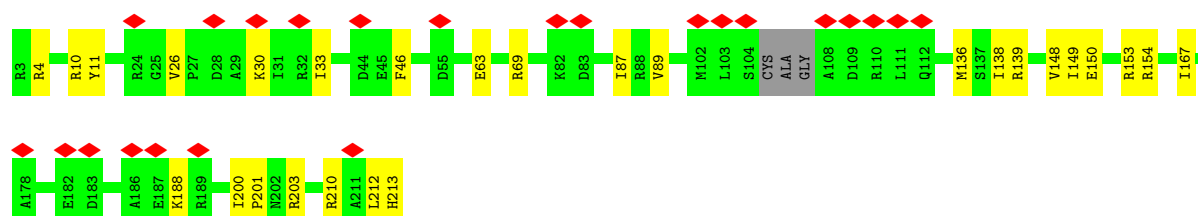
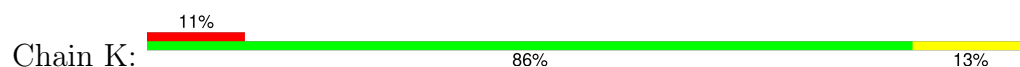




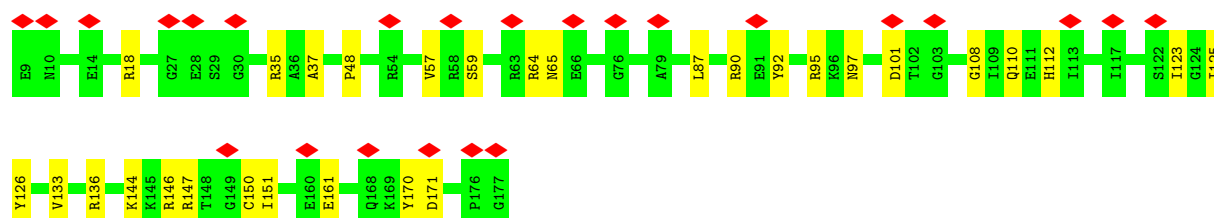
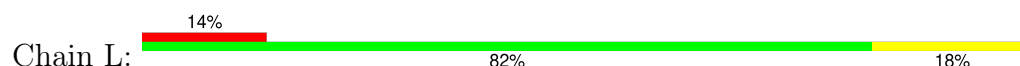
- Molecule 44: 60S ribosomal protein L9



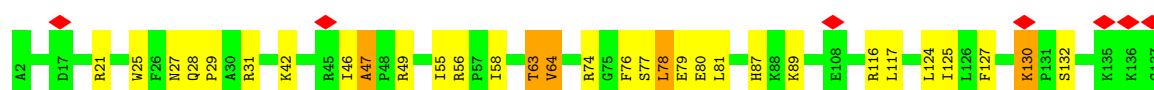
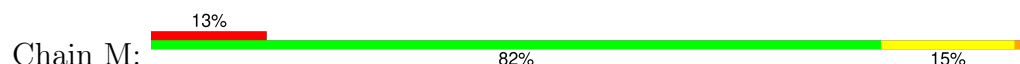
- Molecule 45: 60S ribosomal protein L10

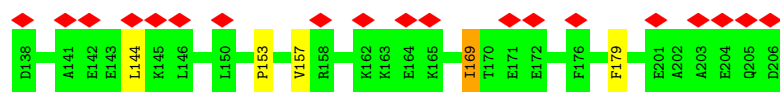


- Molecule 46: 60S ribosomal protein L11

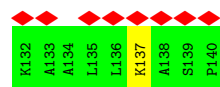
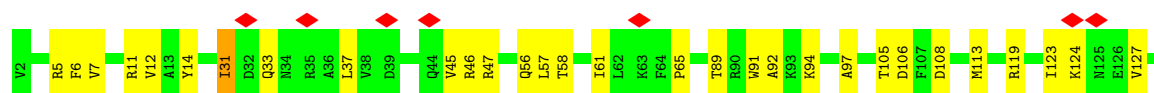
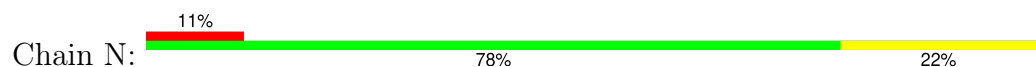


- Molecule 47: 60S ribosomal protein L13

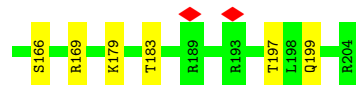
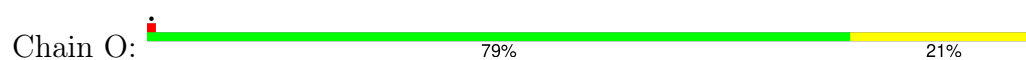




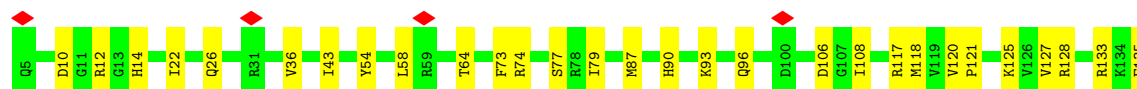
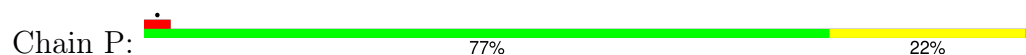
- Molecule 48: 60S ribosomal protein L14



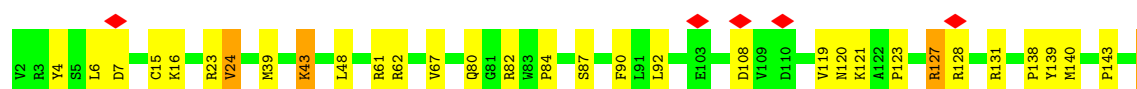
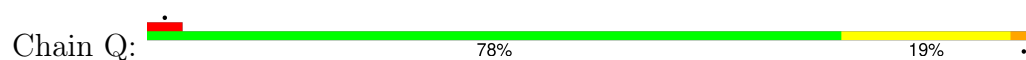
- Molecule 49: 60S ribosomal protein L15



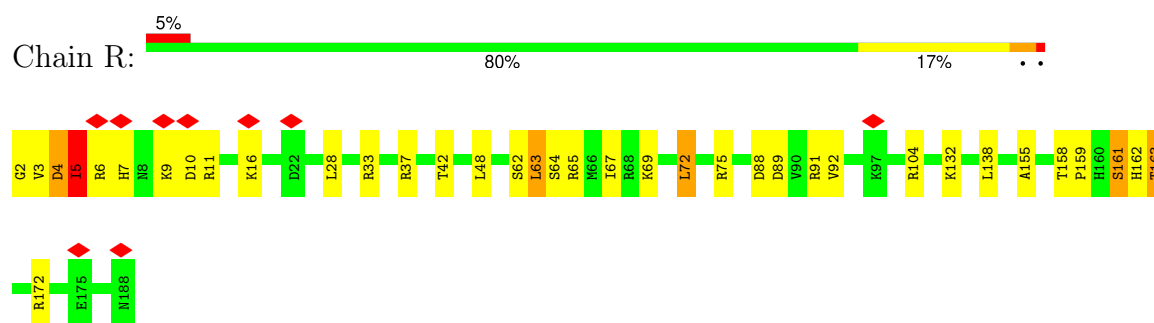
- Molecule 50: 60S ribosomal protein L13a



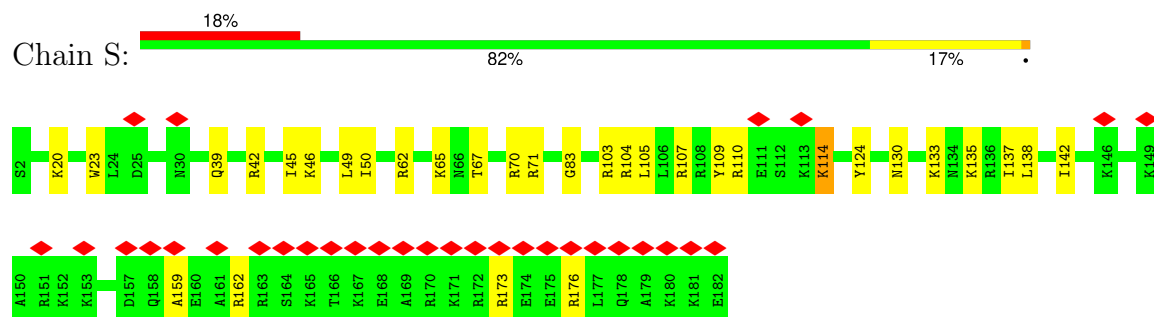
- Molecule 51: 60S ribosomal protein L17



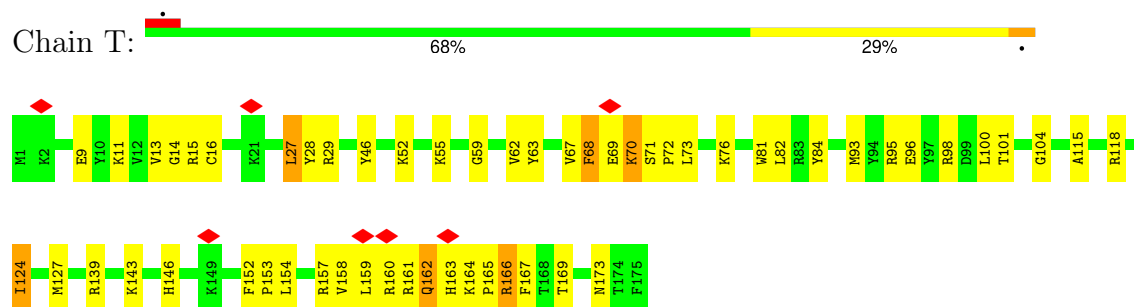
- Molecule 52: 60S ribosomal protein L18



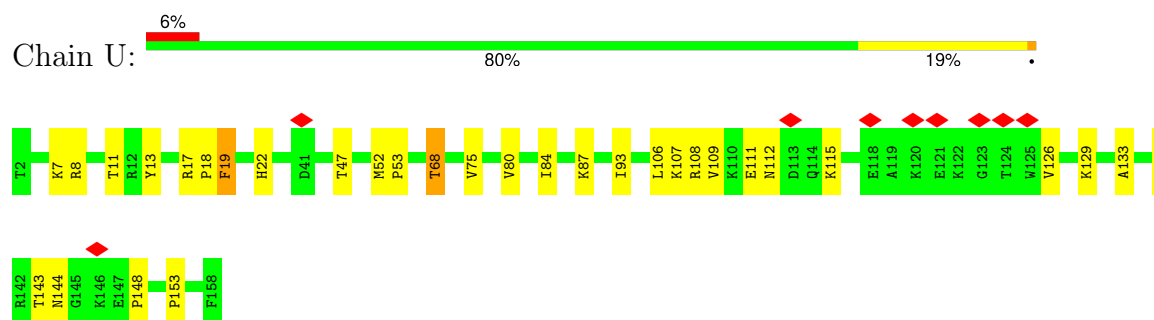
- Molecule 53: 60S ribosomal protein L19



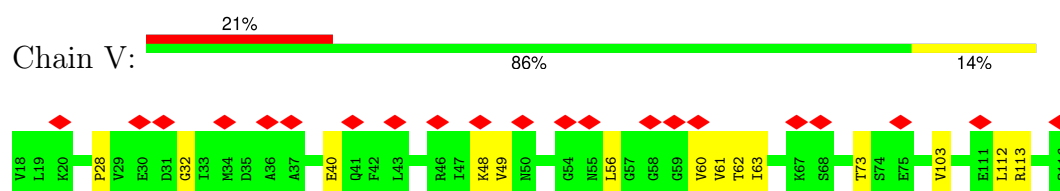
- Molecule 54: 60S ribosomal protein L18a



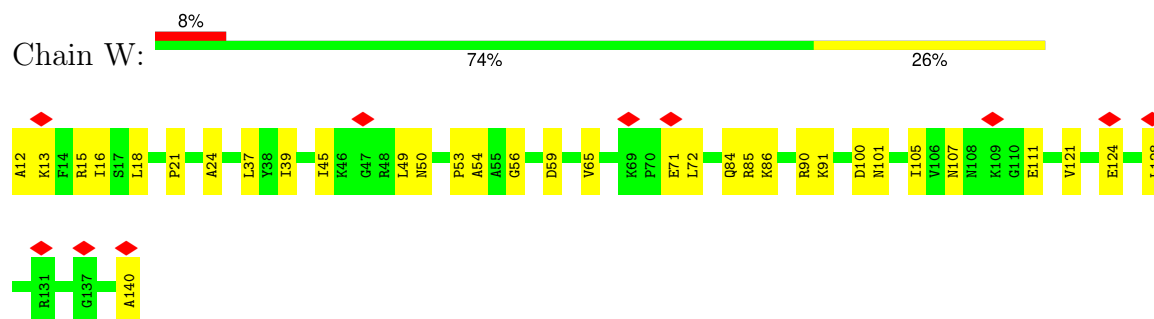
- Molecule 55: 60S ribosomal protein L21



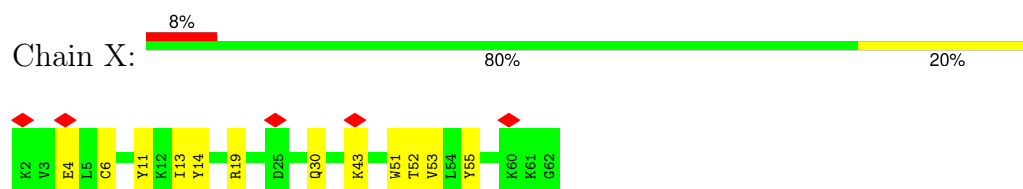
- Molecule 56: 60S ribosomal protein L22



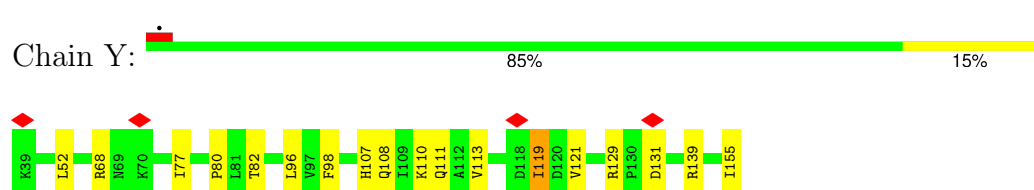
- Molecule 57: 60S ribosomal protein L23



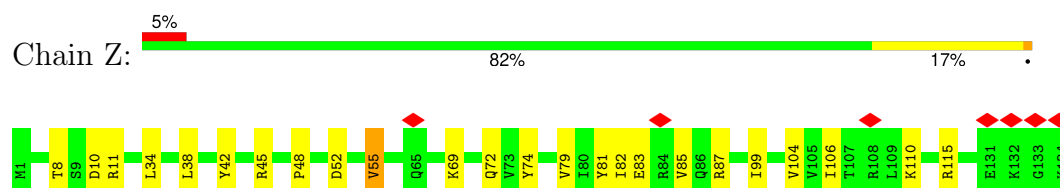
- Molecule 58: 60S ribosomal protein L24



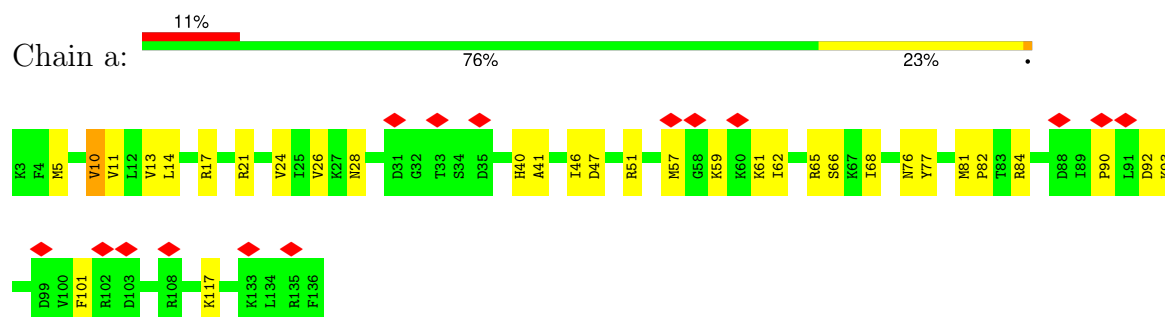
- Molecule 59: 60S ribosomal protein L23a



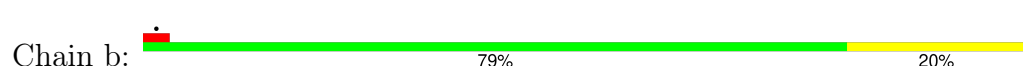
- Molecule 60: 60S ribosomal protein L26

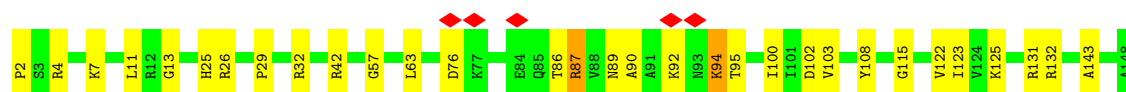


- Molecule 61: 60S ribosomal protein L27

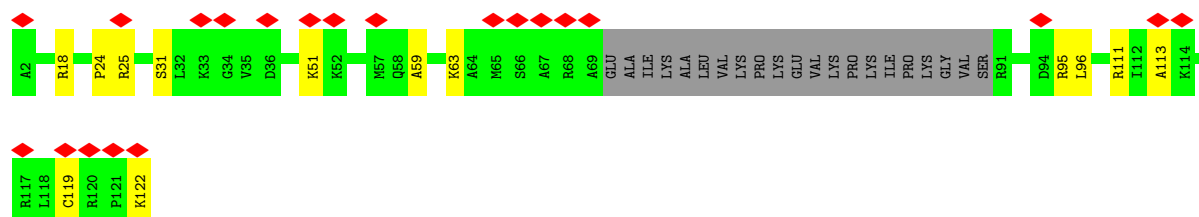


- Molecule 62: 60S ribosomal protein L27a

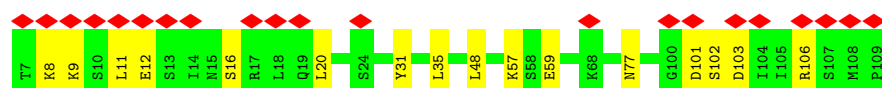
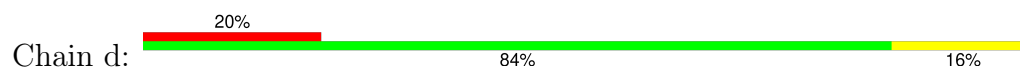




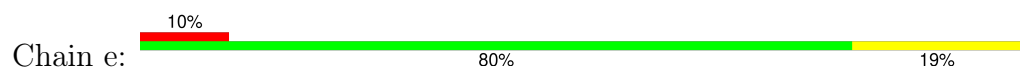
- Molecule 63: 60S ribosomal protein L29



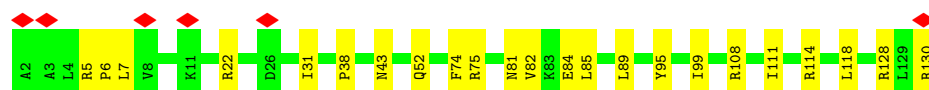
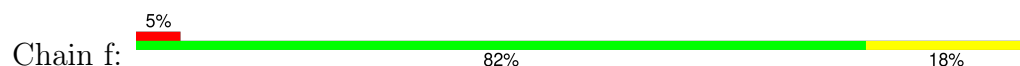
- Molecule 64: 60S ribosomal protein L30



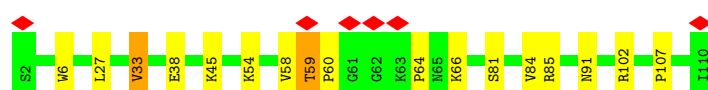
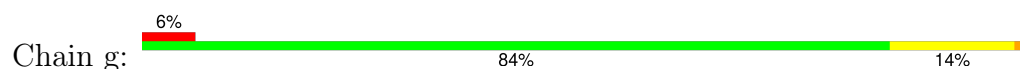
- Molecule 65: 60S ribosomal protein L31



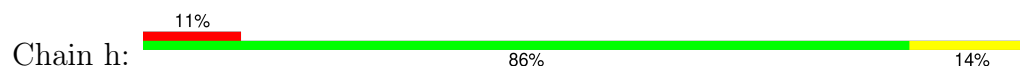
- Molecule 66: 60S ribosomal protein L32



- Molecule 67: 60S ribosomal protein L35a

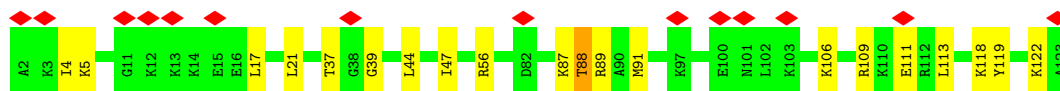
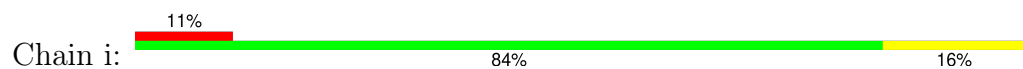


- Molecule 68: 60S ribosomal protein L34

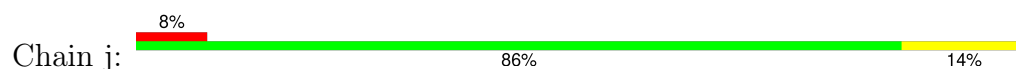




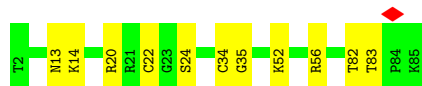
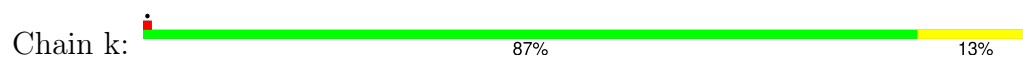
- Molecule 69: 60S ribosomal protein L35



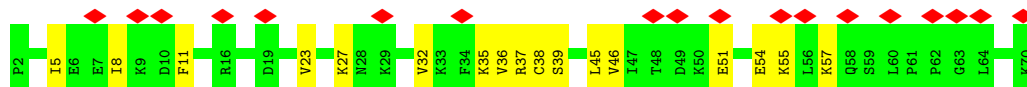
- Molecule 70: 60S ribosomal protein L36



- Molecule 71: 60S ribosomal protein L37



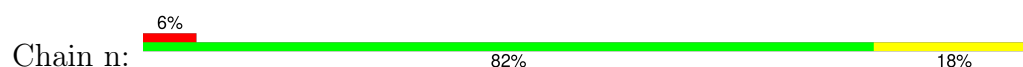
- Molecule 72: 60S ribosomal protein L38



- Molecule 73: 60S ribosomal protein L39



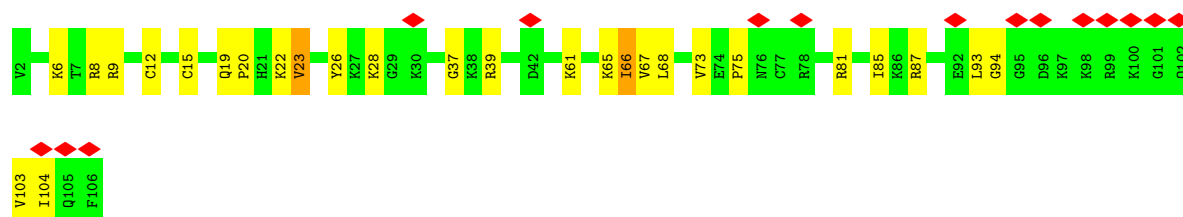
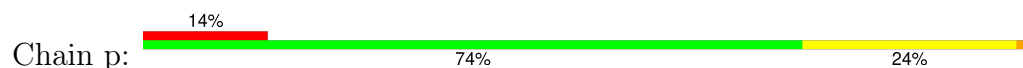
- Molecule 74: 60S ribosomal protein L40



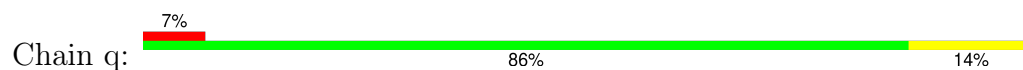
- Molecule 75: 60S ribosomal protein L41



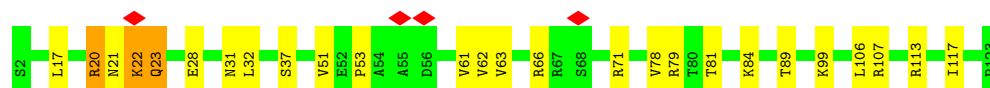
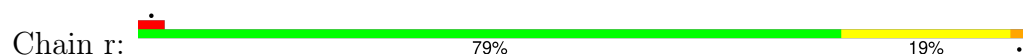
- Molecule 76: 60S ribosomal protein L36a



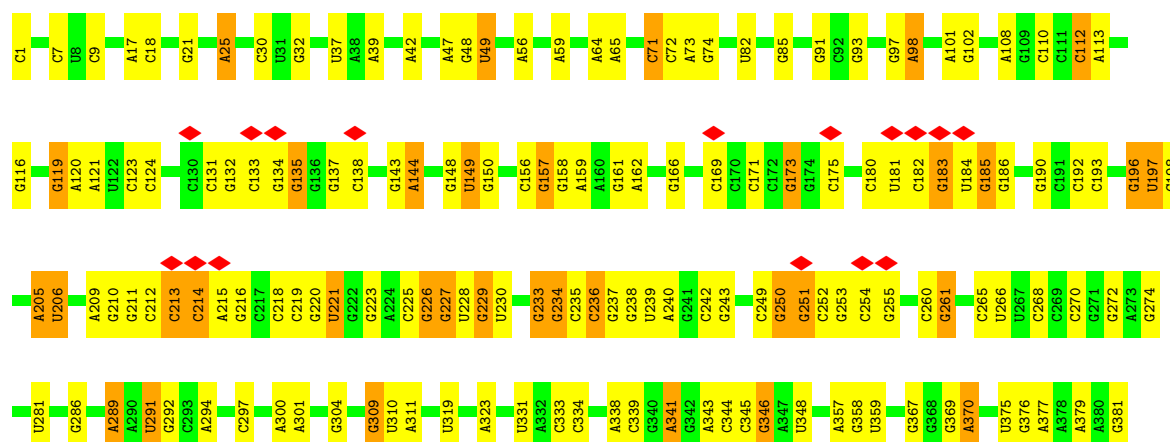
- Molecule 77: 60S ribosomal protein L37a

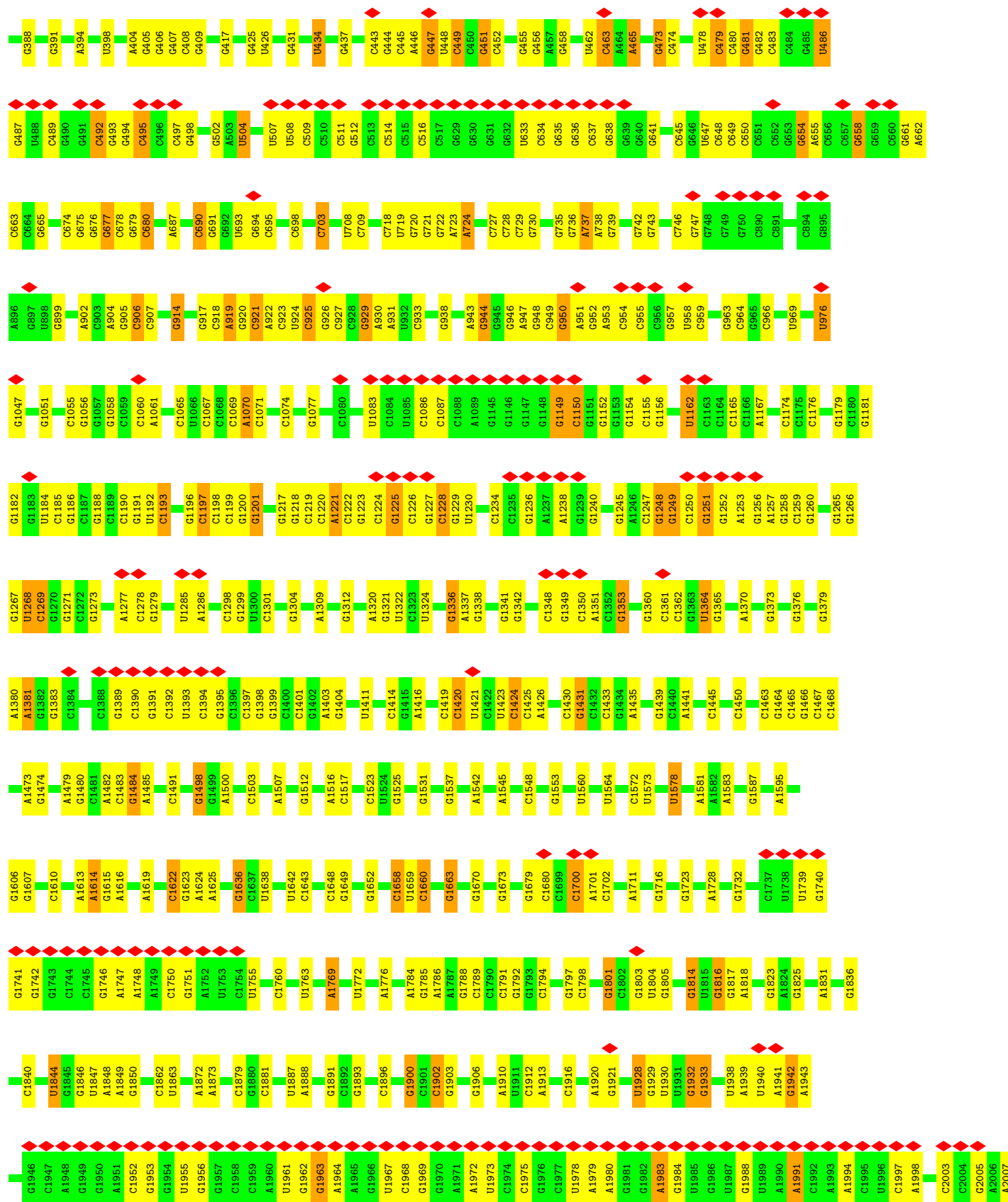


- Molecule 78: 60S ribosomal protein L28

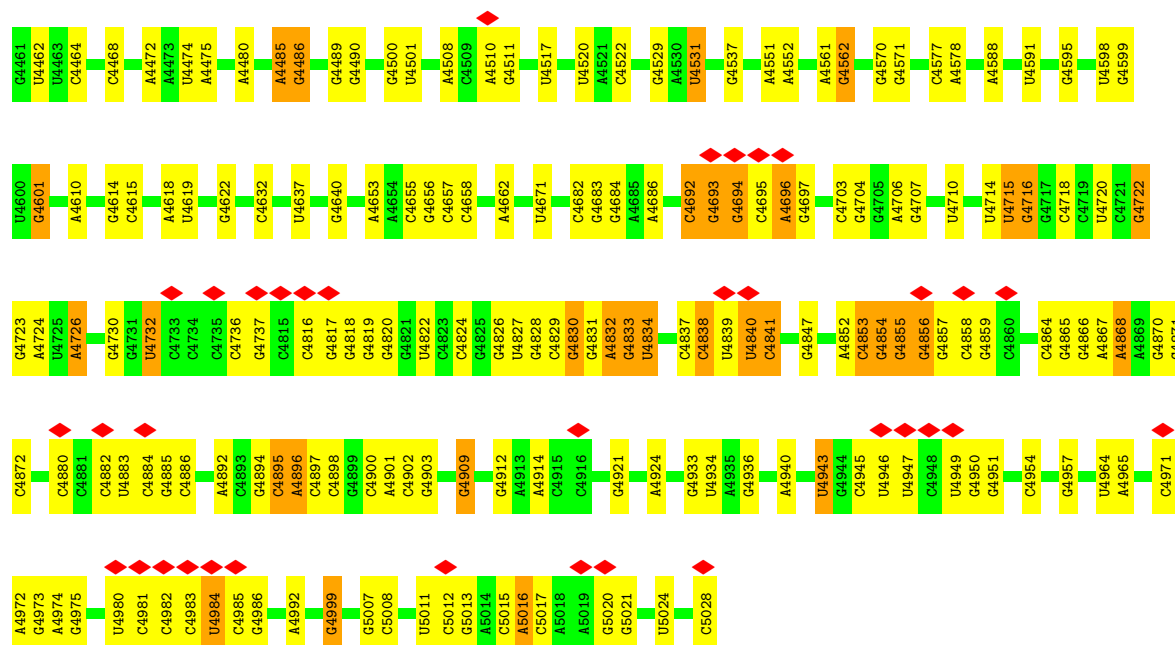


- Molecule 79: 28S ribosomal RNA

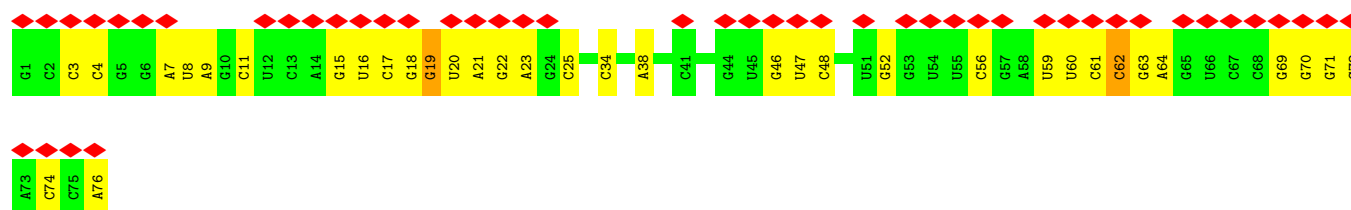




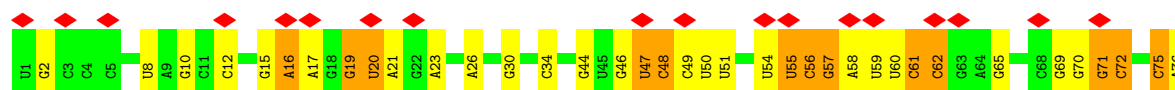




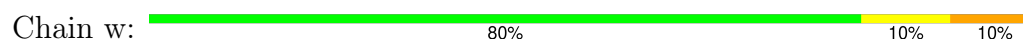
• Molecule 80: tRNA



• Molecule 81: tRNA



• Molecule 82: mRNA



• Molecule 83: Nascent chain



X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17	X18	X19	X20	X21	X22	X23	X24	X25	X26	X27	X28	X29	X30	X31	X32	X33	X34	X35	X36	X37	X38	X39
----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	38314	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	55	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.106	Depositor
Minimum map value	-0.052	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.021	Depositor
Map size ($\text{\AA}$)	460.0, 460.0, 460.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.15, 1.15, 1.15	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MA6, A2M, B8N, MG, M7A, OMC, OMG, 4AC, B8Q, 6MZ, PSU, 5MC, OMU, E3C, UR3, 5MU, MVM

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	S2	0.38	0/39959	0.46	3/62253 (0.0%)
2	SA	0.41	0/1778	0.76	0/2416
3	SB	0.39	0/1765	0.71	3/2362 (0.1%)
4	SD	0.37	0/1785	0.73	0/2404
5	SE	0.36	0/2101	0.69	0/2828
6	SF	0.38	0/1516	0.71	0/2037
7	SH	0.42	1/1519 (0.1%)	0.76	1/2033 (0.0%)
8	SI	0.36	0/1702	0.71	0/2271
9	SK	0.44	0/851	0.78	3/1147 (0.3%)
10	SL	0.37	0/1268	0.70	1/1696 (0.1%)
11	SP	0.39	0/1065	0.70	0/1423
12	SQ	0.38	0/1177	0.84	1/1575 (0.1%)
13	SR	0.34	0/1097	0.81	2/1474 (0.1%)
14	SS	0.38	0/1216	0.68	1/1628 (0.1%)
15	ST	0.38	0/1131	0.71	0/1515
16	SU	0.36	0/831	0.77	0/1115
17	SV	0.39	0/631	0.72	0/844
18	SX	0.40	0/1116	0.78	0/1490
19	Sa	0.45	0/836	0.77	0/1121
20	Sc	0.34	0/508	0.76	0/680
21	Sd	0.42	0/470	1.04	4/623 (0.6%)
22	Sg	0.36	1/2486 (0.0%)	0.75	0/3384
23	SC	0.44	0/1755	0.78	3/2371 (0.1%)
24	SG	0.30	0/1946	0.68	0/2590
25	SJ	0.37	0/1561	0.81	1/2083 (0.0%)
26	SM	0.29	0/922	0.66	0/1238
27	SN	0.40	0/1232	0.62	0/1656
28	SO	0.40	0/1037	0.75	0/1391
29	SW	0.47	0/1051	0.70	0/1406
30	SY	0.34	0/1094	0.68	1/1452 (0.1%)
31	SZ	0.37	0/585	0.94	4/785 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Sb	0.36	0/653	0.69	0/876
33	Se	0.32	0/458	0.78	0/604
34	Sf	0.37	0/560	0.90	2/745 (0.3%)
35	A	0.53	0/1968	0.75	2/2639 (0.1%)
36	B	0.49	0/3270	0.82	2/4377 (0.0%)
37	C	0.56	0/2942	0.83	3/3951 (0.1%)
38	D	0.48	0/3726	0.47	0/5804
39	E	0.44	0/2839	0.42	0/4425
40	F	0.45	0/2437	0.75	4/3262 (0.1%)
41	G	0.47	0/1942	0.94	8/2606 (0.3%)
42	H	0.57	0/1905	0.79	0/2539
43	I	0.47	0/1913	0.73	0/2576
44	J	0.43	0/1545	0.72	2/2077 (0.1%)
45	K	0.45	0/1730	0.73	1/2311 (0.0%)
46	L	0.39	0/1376	0.73	2/1841 (0.1%)
47	M	0.49	0/1688	0.87	3/2260 (0.1%)
48	N	0.47	0/1161	0.75	1/1554 (0.1%)
49	O	0.56	0/1746	0.84	0/2338
50	P	0.49	0/1638	0.73	0/2191
51	Q	0.52	0/1268	0.74	1/1701 (0.1%)
52	R	0.54	0/1537	0.86	4/2052 (0.2%)
53	S	0.47	0/1533	0.75	1/2025 (0.0%)
54	T	0.50	0/1488	0.75	2/1997 (0.1%)
55	U	0.49	0/1312	0.77	1/1753 (0.1%)
56	V	0.38	0/822	0.68	0/1103
57	W	0.50	0/983	0.65	0/1319
58	X	0.49	0/524	0.68	0/698
59	Y	0.46	0/975	0.70	0/1312
60	Z	0.49	0/1132	0.73	2/1504 (0.1%)
61	a	0.45	0/1126	0.77	2/1502 (0.1%)
62	b	0.55	1/1191 (0.1%)	0.85	0/1591
63	c	0.43	0/826	0.80	0/1088
64	d	0.46	0/812	0.75	0/1089
65	e	0.47	0/894	0.79	2/1204 (0.2%)
66	f	0.53	0/1082	0.77	0/1443
67	g	0.57	0/895	0.82	0/1198
68	h	0.47	0/916	0.85	0/1220
69	i	0.47	0/1023	0.79	2/1351 (0.1%)
70	j	0.43	0/805	0.80	0/1065
71	k	0.51	0/703	0.73	0/929
72	l	0.43	0/575	0.67	0/761
73	m	0.52	0/454	0.80	0/599
74	n	0.41	0/417	0.78	0/553

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	o	0.41	0/241	0.84	0/305
76	p	0.50	0/877	0.82	2/1156 (0.2%)
77	q	0.51	0/718	0.72	0/953
78	r	0.57	0/995	0.94	3/1334 (0.2%)
79	t	0.46	0/86502	0.48	2/134927 (0.0%)
80	u	0.27	0/1799	0.50	0/2800
81	v	0.32	0/1802	0.49	1/2797 (0.0%)
82	w	0.39	0/235	0.68	0/365
All	All	0.44	3/229950 (0.0%)	0.60	83/337961 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
25	SJ	0	1
40	F	0	1
47	M	0	1
76	p	0	1
All	All	0	4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	SH	66	VAL	CA-CB	7.13	1.58	1.53
22	Sg	283	PRO	CA-C	-5.94	1.48	1.52
62	b	132	ARG	NE-CZ	-5.22	1.27	1.33

The worst 5 of 83 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	G	129	GLY	N-CA-C	10.27	125.05	112.73
52	R	5	ILE	N-CA-C	-9.33	96.53	108.84
21	Sd	23	VAL	N-CA-C	9.10	119.91	110.72
41	G	128	HIS	N-CA-C	9.04	121.22	111.36
31	SZ	84	ALA	N-CA-C	-8.31	102.22	111.28

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
40	F	257	PRO	Peptide
47	M	130	LYS	Peptide
25	SJ	137	VAL	Peptide
76	p	103	VAL	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	S2	36501	0	18404	325	0
2	SA	1741	0	1746	39	0
3	SB	1738	0	1809	61	0
4	SD	1757	0	1853	24	0
5	SE	2059	0	2164	38	0
6	SF	1495	0	1549	25	0
7	SH	1497	0	1587	39	0
8	SI	1673	0	1756	24	0
9	SK	827	0	852	65	0
10	SL	1247	0	1323	28	0
11	SP	1045	0	1095	44	0
12	SQ	1158	0	1232	59	0
13	SR	1082	0	1137	36	0
14	SS	1198	0	1261	18	0
15	ST	1112	0	1146	11	0
16	SU	821	0	883	14	0
17	SV	625	0	628	8	0
18	SX	1098	0	1167	32	0
19	Sa	821	0	870	17	0
20	Sc	506	0	536	15	0
21	Sd	459	0	448	46	0
22	Sg	2429	0	2386	55	0
23	SC	1715	0	1804	32	0
24	SG	1923	0	2089	23	0
25	SJ	1533	0	1653	26	0
26	SM	912	0	930	10	0
27	SN	1208	0	1294	13	0
28	SO	1024	0	1050	16	0
29	SW	1034	0	1080	27	0
30	SY	1073	0	1155	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	SZ	579	0	639	17	0
32	Sb	640	0	665	5	0
33	Se	452	0	498	2	0
34	Sf	548	0	552	9	0
35	A	1930	0	2030	29	0
36	B	3202	0	3343	98	0
37	C	2888	0	3064	50	0
38	D	3337	0	1692	26	0
39	E	2541	0	1285	12	0
40	F	2392	0	2425	26	0
41	G	1904	0	2055	78	0
42	H	1870	0	1996	40	0
43	I	1880	0	2018	28	0
44	J	1526	0	1605	52	0
45	K	1692	0	1744	14	0
46	L	1353	0	1386	16	0
47	M	1657	0	1764	24	0
48	N	1138	0	1204	32	0
49	O	1701	0	1749	32	0
50	P	1606	0	1745	33	0
51	Q	1242	0	1269	26	0
52	R	1513	0	1628	51	0
53	S	1517	0	1670	27	0
54	T	1449	0	1492	86	0
55	U	1284	0	1352	33	0
56	V	808	0	831	13	0
57	W	969	0	1031	22	0
58	X	511	0	521	8	0
59	Y	958	0	1029	10	0
60	Z	1115	0	1205	13	0
61	a	1103	0	1179	17	0
62	b	1162	0	1213	26	0
63	c	814	0	880	12	0
64	d	801	0	845	14	0
65	e	879	0	924	15	0
66	f	1064	0	1160	19	0
67	g	876	0	912	9	0
68	h	906	0	1002	13	0
69	i	1015	0	1148	14	0
70	j	794	0	870	10	0
71	k	689	0	717	8	0
72	l	569	0	637	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
73	m	444	0	483	11	0
74	n	411	0	443	8	0
75	o	240	0	289	6	0
76	p	863	0	931	19	0
77	q	708	0	757	9	0
78	r	980	0	1041	15	0
79	t	77332	0	39076	499	0
80	u	1613	0	822	6	0
81	v	1618	0	826	13	0
82	w	213	0	109	1	0
83	y	178	0	36	1	0
84	B	1	0	0	0	0
84	D	7	0	0	0	0
84	E	9	0	0	0	0
84	O	1	0	0	0	0
84	S2	2	0	0	0	0
84	b	1	0	0	0	0
84	o	1	0	0	0	0
84	t	9	0	0	0	0
85	S2	1	0	0	0	0
85	Sa	1	0	0	0	0
85	Sf	1	0	0	0	0
85	k	1	0	0	0	0
85	p	1	0	0	0	0
85	q	1	0	0	0	0
86	t	31	0	0	0	0
87	S2	5	0	0	1	0
87	SC	1	0	0	0	0
87	SJ	1	0	0	0	0
87	SP	1	0	0	0	0
87	SQ	1	0	0	0	0
87	SR	1	0	0	0	0
87	SS	1	0	0	0	0
87	Sb	1	0	0	0	0
87	Sf	1	0	0	0	0
87	u	1	0	0	1	0
All	All	214867	0	158674	2272	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 7.

The worst 5 of 2272 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)
41:G:165:LEU:HD11	41:G:176:THR:CG2	1.16	1.61
52:R:7:HIS:CE1	79:t:1648:C:H5''	1.09	1.61
1:S2:814:5MU:C4	1:S2:814:5MU:C5	1.81	1.61
41:G:165:LEU:CG	41:G:176:THR:HG22	1.12	1.56
52:R:7:HIS:HE1	79:t:1648:C:C5'	1.12	1.55

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	SA	219/221 (99%)	192 (88%)	26 (12%)	1 (0%)	24	57
3	SB	212/214 (99%)	191 (90%)	21 (10%)	0	100	100
4	SD	224/226 (99%)	194 (87%)	30 (13%)	0	100	100
5	SE	257/259 (99%)	241 (94%)	16 (6%)	0	100	100
6	SF	187/189 (99%)	171 (91%)	16 (9%)	0	100	100
7	SH	182/189 (96%)	163 (90%)	19 (10%)	0	100	100
8	SI	202/204 (99%)	182 (90%)	20 (10%)	0	100	100
9	SK	96/98 (98%)	83 (86%)	12 (12%)	1 (1%)	12	44
10	SL	151/153 (99%)	135 (89%)	15 (10%)	1 (1%)	18	51
11	SP	125/127 (98%)	111 (89%)	14 (11%)	0	100	100
12	SQ	144/146 (99%)	127 (88%)	15 (10%)	2 (1%)	9	38
13	SR	132/134 (98%)	119 (90%)	12 (9%)	1 (1%)	16	49
14	SS	143/145 (99%)	127 (89%)	16 (11%)	0	100	100
15	ST	141/143 (99%)	130 (92%)	10 (7%)	1 (1%)	18	51
16	SU	102/104 (98%)	93 (91%)	9 (9%)	0	100	100
17	SV	80/82 (98%)	72 (90%)	8 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	SX	139/141 (99%)	126 (91%)	13 (9%)	0	100	100
19	Sa	100/102 (98%)	88 (88%)	11 (11%)	1 (1%)	12	44
20	Sc	62/64 (97%)	51 (82%)	11 (18%)	0	100	100
21	Sd	53/55 (96%)	44 (83%)	9 (17%)	0	100	100
22	Sg	310/312 (99%)	255 (82%)	55 (18%)	0	100	100
23	SC	219/220 (100%)	201 (92%)	17 (8%)	1 (0%)	24	57
24	SG	235/237 (99%)	212 (90%)	23 (10%)	0	100	100
25	SJ	184/185 (100%)	168 (91%)	15 (8%)	1 (0%)	24	57
26	SM	116/118 (98%)	102 (88%)	14 (12%)	0	100	100
27	SN	148/150 (99%)	145 (98%)	3 (2%)	0	100	100
28	SO	135/137 (98%)	117 (87%)	18 (13%)	0	100	100
29	SW	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
30	SY	130/131 (99%)	119 (92%)	10 (8%)	1 (1%)	16	49
31	SZ	71/73 (97%)	58 (82%)	13 (18%)	0	100	100
32	Sb	80/82 (98%)	67 (84%)	13 (16%)	0	100	100
33	Se	55/57 (96%)	48 (87%)	7 (13%)	0	100	100
34	Sf	65/67 (97%)	52 (80%)	13 (20%)	0	100	100
35	A	250/252 (99%)	222 (89%)	27 (11%)	1 (0%)	30	62
36	B	395/397 (100%)	355 (90%)	37 (9%)	3 (1%)	16	49
37	C	361/363 (99%)	326 (90%)	31 (9%)	4 (1%)	11	43
40	F	292/294 (99%)	257 (88%)	32 (11%)	3 (1%)	12	44
41	G	232/247 (94%)	194 (84%)	38 (16%)	0	100	100
42	H	223/225 (99%)	209 (94%)	13 (6%)	1 (0%)	30	62
43	I	232/234 (99%)	212 (91%)	20 (9%)	0	100	100
44	J	189/191 (99%)	170 (90%)	19 (10%)	0	100	100
45	K	204/211 (97%)	179 (88%)	24 (12%)	1 (0%)	24	57
46	L	167/169 (99%)	150 (90%)	16 (10%)	1 (1%)	21	54
47	M	203/205 (99%)	168 (83%)	31 (15%)	4 (2%)	6	32
48	N	137/139 (99%)	126 (92%)	11 (8%)	0	100	100
49	O	201/203 (99%)	181 (90%)	20 (10%)	0	100	100
50	P	193/195 (99%)	186 (96%)	6 (3%)	1 (0%)	24	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	Q	151/153 (99%)	144 (95%)	7 (5%)	0	100	100
52	R	185/187 (99%)	171 (92%)	14 (8%)	0	100	100
53	S	179/181 (99%)	171 (96%)	8 (4%)	0	100	100
54	T	173/175 (99%)	158 (91%)	15 (9%)	0	100	100
55	U	155/157 (99%)	136 (88%)	17 (11%)	2 (1%)	9	39
56	V	97/99 (98%)	89 (92%)	8 (8%)	0	100	100
57	W	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
58	X	59/61 (97%)	55 (93%)	4 (7%)	0	100	100
59	Y	115/117 (98%)	107 (93%)	8 (7%)	0	100	100
60	Z	132/134 (98%)	125 (95%)	7 (5%)	0	100	100
61	a	132/134 (98%)	118 (89%)	14 (11%)	0	100	100
62	b	145/147 (99%)	125 (86%)	19 (13%)	1 (1%)	18	51
63	c	94/121 (78%)	83 (88%)	11 (12%)	0	100	100
64	d	101/103 (98%)	86 (85%)	15 (15%)	0	100	100
65	e	104/106 (98%)	99 (95%)	5 (5%)	0	100	100
66	f	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	16	49
67	g	107/109 (98%)	98 (92%)	9 (8%)	0	100	100
68	h	112/114 (98%)	101 (90%)	10 (9%)	1 (1%)	14	47
69	i	120/122 (98%)	111 (92%)	8 (7%)	1 (1%)	16	49
70	j	95/97 (98%)	88 (93%)	6 (6%)	1 (1%)	11	43
71	k	82/84 (98%)	75 (92%)	7 (8%)	0	100	100
72	l	67/69 (97%)	62 (92%)	5 (8%)	0	100	100
73	m	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
74	n	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
75	o	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
76	p	103/105 (98%)	93 (90%)	9 (9%)	1 (1%)	12	44
77	q	89/91 (98%)	83 (93%)	6 (7%)	0	100	100
78	r	120/122 (98%)	105 (88%)	12 (10%)	3 (2%)	4	28
All	All	11195/11390 (98%)	10073 (90%)	1081 (10%)	41 (0%)	31	62

5 of 41 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	SK	63	ALA
10	SL	23	VAL
13	SR	129	LYS
15	ST	41	LYS
23	SC	78	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	SA	183/183 (100%)	180 (98%)	3 (2%)	55	70
3	SB	195/195 (100%)	191 (98%)	4 (2%)	47	66
4	SD	189/189 (100%)	185 (98%)	4 (2%)	47	66
5	SE	222/222 (100%)	219 (99%)	3 (1%)	59	71
6	SF	159/159 (100%)	157 (99%)	2 (1%)	61	72
7	SH	166/169 (98%)	164 (99%)	2 (1%)	63	73
8	SI	177/177 (100%)	176 (99%)	1 (1%)	78	79
9	SK	89/89 (100%)	84 (94%)	5 (6%)	19	46
10	SL	137/137 (100%)	135 (98%)	2 (2%)	57	71
11	SP	113/113 (100%)	108 (96%)	5 (4%)	25	51
12	SQ	121/121 (100%)	118 (98%)	3 (2%)	42	63
13	SR	121/121 (100%)	120 (99%)	1 (1%)	73	77
14	SS	126/126 (100%)	125 (99%)	1 (1%)	73	77
15	ST	113/113 (100%)	111 (98%)	2 (2%)	51	69
16	SU	94/94 (100%)	94 (100%)	0	100	100
17	SV	66/66 (100%)	64 (97%)	2 (3%)	36	60
18	SX	113/113 (100%)	110 (97%)	3 (3%)	39	62
19	Sa	89/89 (100%)	89 (100%)	0	100	100
20	Sc	57/57 (100%)	57 (100%)	0	100	100
21	Sd	48/48 (100%)	43 (90%)	5 (10%)	7	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	Sg	271/271 (100%)	271 (100%)	0	100	100
23	SC	187/186 (100%)	186 (100%)	1 (0%)	81	80
24	SG	207/207 (100%)	206 (100%)	1 (0%)	81	80
25	SJ	162/161 (101%)	160 (99%)	2 (1%)	63	73
26	SM	98/100 (98%)	98 (100%)	0	100	100
27	SN	130/130 (100%)	128 (98%)	2 (2%)	57	71
28	SO	107/107 (100%)	105 (98%)	2 (2%)	50	68
29	SW	112/112 (100%)	111 (99%)	1 (1%)	70	76
30	SY	114/113 (101%)	113 (99%)	1 (1%)	70	76
31	SZ	64/64 (100%)	62 (97%)	2 (3%)	35	59
32	Sb	74/74 (100%)	73 (99%)	1 (1%)	59	71
33	Se	46/46 (100%)	45 (98%)	1 (2%)	45	65
34	Sf	60/60 (100%)	60 (100%)	0	100	100
35	A	194/194 (100%)	190 (98%)	4 (2%)	47	66
36	B	345/345 (100%)	339 (98%)	6 (2%)	53	70
37	C	302/302 (100%)	297 (98%)	5 (2%)	53	70
40	F	248/248 (100%)	248 (100%)	0	100	100
41	G	209/220 (95%)	205 (98%)	4 (2%)	50	68
42	H	194/194 (100%)	188 (97%)	6 (3%)	35	59
43	I	199/199 (100%)	197 (99%)	2 (1%)	68	75
44	J	170/170 (100%)	166 (98%)	4 (2%)	43	64
45	K	178/179 (99%)	175 (98%)	3 (2%)	53	70
46	L	142/142 (100%)	142 (100%)	0	100	100
47	M	171/171 (100%)	167 (98%)	4 (2%)	44	64
48	N	118/118 (100%)	116 (98%)	2 (2%)	53	70
49	O	171/171 (100%)	166 (97%)	5 (3%)	37	60
50	P	168/168 (100%)	166 (99%)	2 (1%)	63	73
51	Q	134/134 (100%)	130 (97%)	4 (3%)	36	60
52	R	164/164 (100%)	156 (95%)	8 (5%)	22	48
53	S	160/160 (100%)	160 (100%)	0	100	100
54	T	156/156 (100%)	151 (97%)	5 (3%)	34	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	U	138/138 (100%)	135 (98%)	3 (2%)	45	65
56	V	89/89 (100%)	88 (99%)	1 (1%)	65	74
57	W	100/100 (100%)	99 (99%)	1 (1%)	68	75
58	X	53/53 (100%)	52 (98%)	1 (2%)	50	68
59	Y	105/105 (100%)	102 (97%)	3 (3%)	37	60
60	Z	124/124 (100%)	120 (97%)	4 (3%)	34	59
61	a	117/117 (100%)	115 (98%)	2 (2%)	53	70
62	b	120/120 (100%)	116 (97%)	4 (3%)	33	58
63	c	82/101 (81%)	82 (100%)	0	100	100
64	d	88/88 (100%)	86 (98%)	2 (2%)	44	64
65	e	97/97 (100%)	95 (98%)	2 (2%)	47	66
66	f	115/115 (100%)	114 (99%)	1 (1%)	70	76
67	g	88/88 (100%)	85 (97%)	3 (3%)	32	57
68	h	98/98 (100%)	98 (100%)	0	100	100
69	i	109/109 (100%)	109 (100%)	0	100	100
70	j	83/83 (100%)	83 (100%)	0	100	100
71	k	71/71 (100%)	71 (100%)	0	100	100
72	l	64/64 (100%)	63 (98%)	1 (2%)	55	70
73	m	47/47 (100%)	47 (100%)	0	100	100
74	n	46/46 (100%)	46 (100%)	0	100	100
75	o	24/24 (100%)	24 (100%)	0	100	100
76	p	93/93 (100%)	90 (97%)	3 (3%)	34	59
77	q	74/74 (100%)	73 (99%)	1 (1%)	59	71
78	r	106/106 (100%)	104 (98%)	2 (2%)	50	68
All	All	9764/9797 (100%)	9604 (98%)	160 (2%)	54	70

5 of 160 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
52	R	28	LEU
62	b	94	LYS
52	R	138	LEU
57	W	65	VAL
67	g	33	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 175 such sidechains are listed below:

Mol	Chain	Res	Type
45	K	130	HIS
54	T	163	HIS
46	L	71	HIS
50	P	14	HIS
59	Y	111	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	S2	1698/1714 (99%)	568 (33%)	31 (1%)
38	D	156/157 (99%)	38 (24%)	0
39	E	118/121 (97%)	19 (16%)	0
79	t	3593/3607 (99%)	880 (24%)	0
80	u	74/76 (97%)	28 (37%)	0
81	v	72/76 (94%)	28 (38%)	0
82	w	9/10 (90%)	2 (22%)	0
All	All	5720/5761 (99%)	1563 (27%)	31 (0%)

5 of 1563 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	S2	2	A
1	S2	9	U
1	S2	10	G
1	S2	11	A
1	S2	16	G

5 of 31 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	S2	563	G
1	S2	1813	A
1	S2	872	A
1	S2	1815	A
1	S2	1661	A

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

34 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
1	PSU	S2	1243	1	18,21,22	4.39	7 (38%)	21,30,33	1.96	4 (19%)
1	A2M	S2	1678	1	22,25,26	4.21	9 (40%)	30,36,39	2.83	13 (43%)
1	A2M	S2	159	1	22,25,26	4.12	9 (40%)	30,36,39	3.12	17 (56%)
1	MA6	S2	1851	1	23,26,27	1.56	5 (21%)	33,38,41	3.66	14 (42%)
1	OMG	S2	683	1	23,26,27	2.38	8 (34%)	32,38,41	2.14	10 (31%)
1	PSU	S2	612	1	18,21,22	4.25	8 (44%)	21,30,33	2.22	6 (28%)
1	PSU	S2	1081	1	18,21,22	4.30	8 (44%)	21,30,33	1.95	4 (19%)
1	MA6	S2	1850	1	23,26,27	1.53	5 (21%)	33,38,41	3.73	13 (39%)
1	OMG	S2	644	1	23,26,27	2.40	9 (39%)	32,38,41	2.23	10 (31%)
1	A2M	S2	166	1	22,25,26	4.12	9 (40%)	30,36,39	3.02	14 (46%)
1	5MU	S2	814	1	19,22,23	7.59	8 (42%)	27,32,35	3.61	11 (40%)
1	4AC	S2	1337	1	21,24,25	3.28	9 (42%)	28,34,37	1.25	3 (10%)
1	OMG	S2	509	1	23,26,27	2.38	7 (30%)	32,38,41	2.16	10 (31%)
1	OMC	S2	174	1	19,22,23	3.53	8 (42%)	25,31,34	0.92	1 (4%)
1	UR3	S2	1830	1	19,22,23	2.79	7 (36%)	26,32,35	3.04	9 (34%)
1	B8Q	S2	1219	1	18,22,23	4.74	7 (38%)	21,32,35	1.90	5 (23%)
1	6MZ	S2	1832	1	22,25,26	2.60	5 (22%)	29,36,39	2.39	9 (31%)
1	OMU	S2	116	1	19,22,23	3.16	6 (31%)	25,31,34	1.81	4 (16%)
1	OMU	S2	121	1	19,22,23	3.08	7 (36%)	25,31,34	2.00	6 (24%)
1	PSU	S2	822	1	18,21,22	4.38	8 (44%)	21,30,33	1.92	4 (19%)
1	A2M	S2	27	1	22,25,26	4.09	9 (40%)	30,36,39	3.04	14 (46%)
1	B8N	S2	1248	1	25,29,30	3.15	7 (28%)	28,42,45	2.12	7 (25%)
1	M7A	S2	1806	1	19,25,26	1.67	2 (10%)	25,37,40	3.74	8 (32%)
1	OMC	S2	1703	1	19,22,23	3.48	8 (42%)	25,31,34	0.61	0
1	A2M	S2	668	1	22,25,26	4.09	10 (45%)	30,36,39	3.14	14 (46%)
1	4AC	S2	1842	1	21,24,25	3.23	9 (42%)	28,34,37	1.12	3 (10%)
1	OMC	S2	1710	1	19,22,23	3.58	8 (42%)	25,31,34	0.65	0
1	5MC	S2	1374	1	19,22,23	3.64	8 (42%)	26,32,35	1.05	2 (7%)
1	A2M	S2	484	1	22,25,26	4.11	9 (40%)	30,36,39	3.01	12 (40%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	S2	823	1	18,21,22	4.49	8 (44%)	21,30,33	2.18	4 (19%)
1	PSU	S2	119	1	18,21,22	4.45	7 (38%)	21,30,33	2.10	5 (23%)
1	E3C	S2	568	1	19,23,24	3.59	7 (36%)	21,33,36	2.64	6 (28%)
1	OMC	S2	517	1	19,22,23	3.39	8 (42%)	25,31,34	0.86	1 (4%)
1	A2M	S2	1031	1	22,25,26	4.13	9 (40%)	30,36,39	3.05	15 (50%)

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
1	PSU	S2	1243	1	-	2/7/25/26	0/2/2/2
1	A2M	S2	1678	1	-	0/9/27/28	0/3/3/3
1	A2M	S2	159	1	-	3/9/27/28	0/3/3/3
1	MA6	S2	1851	1	-	4/11/29/30	0/3/3/3
1	OMG	S2	683	1	-	2/9/27/28	0/3/3/3
1	PSU	S2	612	1	-	2/7/25/26	0/2/2/2
1	PSU	S2	1081	1	-	2/7/25/26	0/2/2/2
1	MA6	S2	1850	1	-	5/11/29/30	0/3/3/3
1	OMG	S2	644	1	-	1/9/27/28	0/3/3/3
1	A2M	S2	166	1	-	0/9/27/28	0/3/3/3
1	5MU	S2	814	1	-	0/7/25/26	0/2/2/2
1	4AC	S2	1337	1	-	0/11/29/30	0/2/2/2
1	OMG	S2	509	1	-	1/9/27/28	0/3/3/3
1	OMC	S2	174	1	-	1/9/27/28	0/2/2/2
1	UR3	S2	1830	1	-	4/7/25/26	0/2/2/2
1	B8Q	S2	1219	1	-	0/7/42/43	0/2/2/2
1	6MZ	S2	1832	1	-	2/9/27/28	0/3/3/3
1	OMU	S2	116	1	-	2/9/27/28	0/2/2/2
1	OMU	S2	121	1	-	3/9/27/28	0/2/2/2
1	PSU	S2	822	1	-	4/7/25/26	0/2/2/2
1	A2M	S2	27	1	-	1/9/27/28	0/3/3/3
1	B8N	S2	1248	1	-	4/16/34/35	0/2/2/2
1	M7A	S2	1806	1	-	3/7/37/38	0/3/3/3
1	OMC	S2	1703	1	-	2/9/27/28	0/2/2/2
1	A2M	S2	668	1	-	3/9/27/28	0/3/3/3
1	4AC	S2	1842	1	-	0/11/29/30	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMC	S2	1710	1	-	0/9/27/28	0/2/2/2
1	5MC	S2	1374	1	-	0/7/25/26	0/2/2/2
1	A2M	S2	484	1	-	0/9/27/28	0/3/3/3
1	PSU	S2	823	1	-	3/7/25/26	0/2/2/2
1	PSU	S2	119	1	-	2/7/25/26	0/2/2/2
1	E3C	S2	568	1	-	4/9/44/45	0/2/2/2
1	OMC	S2	517	1	-	0/9/27/28	0/2/2/2
1	A2M	S2	1031	1	-	1/9/27/28	0/3/3/3

The worst 5 of 258 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	S2	814	5MU	C4-C5	22.49	1.81	1.44
1	S2	814	5MU	C6-N1	16.54	1.66	1.38
1	S2	823	PSU	C6-C5	11.93	1.48	1.35
1	S2	814	5MU	C6-C5	-11.89	1.15	1.34
1	S2	1243	PSU	C6-C5	11.78	1.48	1.35

The worst 5 of 258 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S2	1851	MA6	N1-C6-N6	-13.26	100.69	116.86
1	S2	1850	MA6	N1-C6-N6	-12.61	101.50	116.86
1	S2	1806	M7A	C5-C6-N6	11.08	142.57	123.75
1	S2	814	5MU	C5-C4-N3	9.88	123.91	115.32
1	S2	1806	M7A	N6-C6-N1	-9.59	97.03	118.38

There are no chirality outliers.

5 of 61 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	S2	27	A2M	C1'-C2'-O2'-CM'
1	S2	116	OMU	O4'-C4'-C5'-O5'
1	S2	121	OMU	C3'-C4'-C5'-O5'
1	S2	121	OMU	O4'-C4'-C5'-O5'
1	S2	159	A2M	O4'-C4'-C5'-O5'

There are no ring outliers.

7 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	S2	683	OMG	1	0
1	S2	814	5MU	1	0
1	S2	509	OMG	2	0
1	S2	1832	6MZ	1	0
1	S2	121	OMU	2	0
1	S2	484	A2M	1	0
1	S2	1031	A2M	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 38 ligands modelled in this entry, 37 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	$\# Z > 2$
86	MVM	t	5110	-	35,35,35	1.82	6 (17%)	44,49,49	3.14	15 (34%)

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
86	MVM	t	5110	-	-	3/20/28/28	0/5/5/5

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	t	5110	MVM	N4-N5	-6.18	1.31	1.38
86	t	5110	MVM	C5-N1	5.94	1.45	1.37
86	t	5110	MVM	C6-N1	2.40	1.45	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	t	5110	MVM	C12-C5	2.26	1.53	1.50
86	t	5110	MVM	C7-C3	-2.01	1.48	1.53

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	t	5110	MVM	C15-N4-N5	10.16	128.40	119.25
86	t	5110	MVM	C15-N4-C22	-9.80	121.84	130.55
86	t	5110	MVM	N7-C22-N4	8.01	134.88	125.88
86	t	5110	MVM	C18-C22-N7	-5.04	120.25	127.18
86	t	5110	MVM	C6-N1-C5	-4.82	117.17	122.94

There are no chirality outliers.

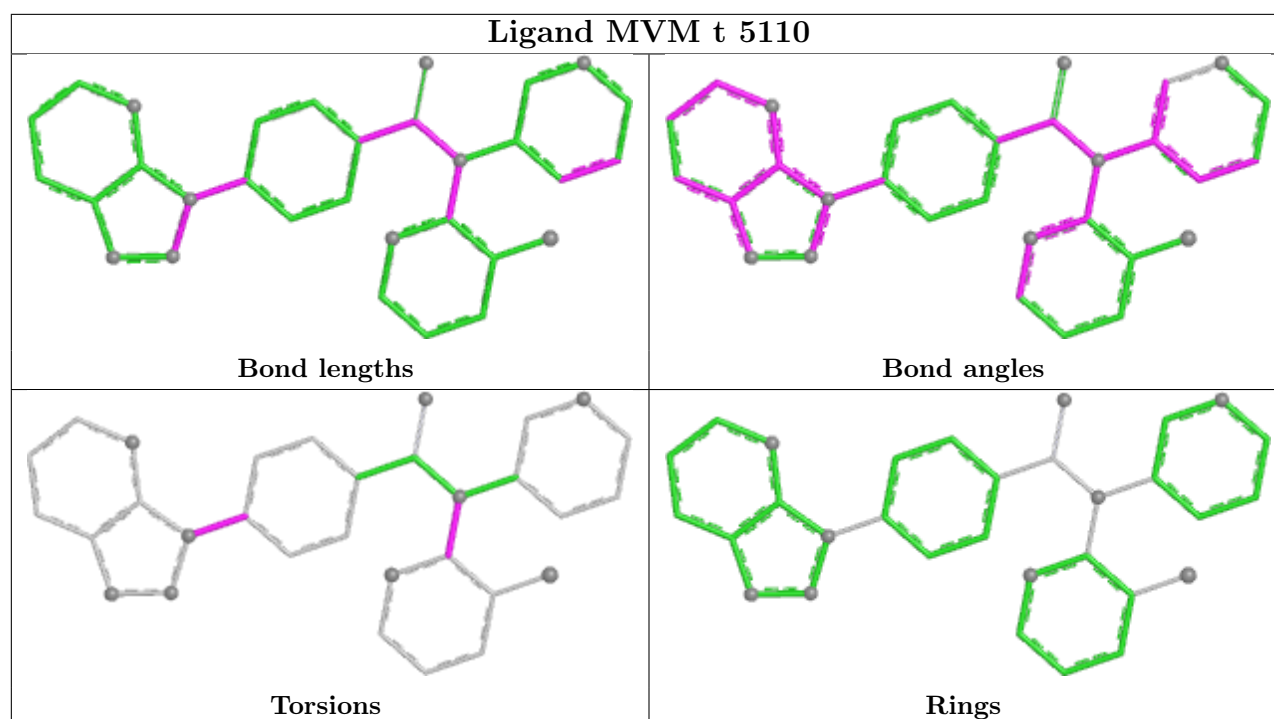
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
86	t	5110	MVM	C16-C15-N4-C22
86	t	5110	MVM	C2-C6-N1-C5
86	t	5110	MVM	C14-C15-N4-C22

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 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
79	t	16
1	S2	5
81	v	4
63	c	1
80	u	1

The worst 5 of 27 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	S2	753:C	O3'	785:C	P	25.98
1	t	750:G	O3'	890:C	P	20.40
1	t	3919:C	O3'	4035:G	P	18.39
1	t	517:C	O3'	629:G	P	17.30
1	t	1680:C	O3'	1699:C	P	16.29

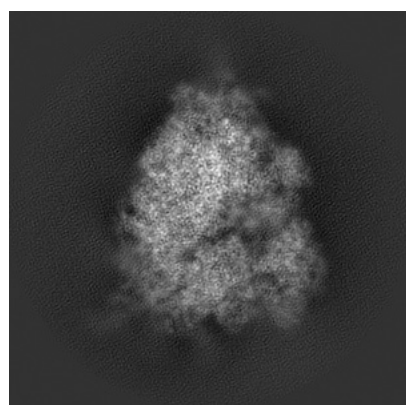
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0526. These allow visual inspection of the internal detail of the map and identification of artifacts.

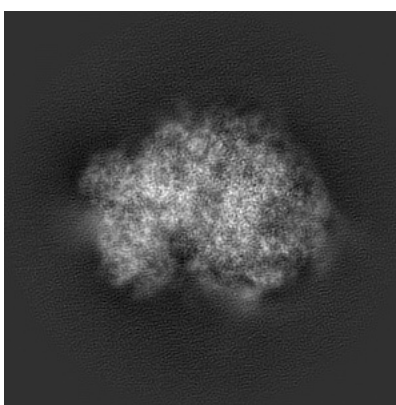
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

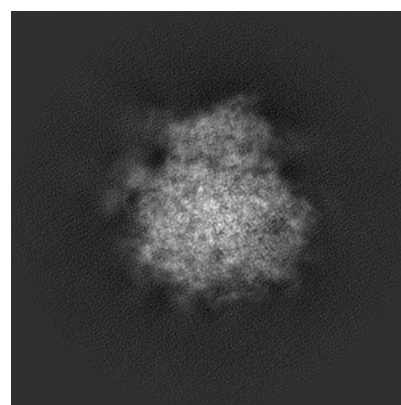
6.1.1 Primary map



X



Y

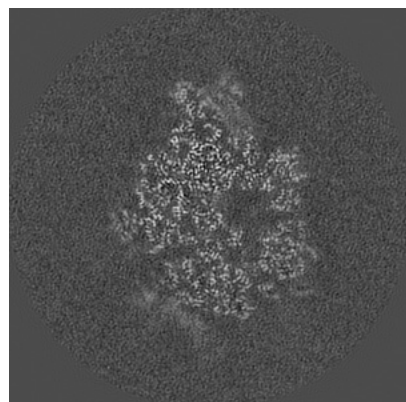


Z

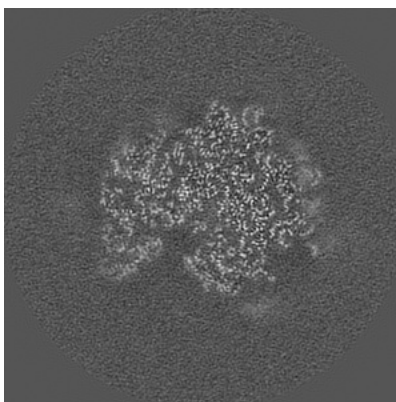
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

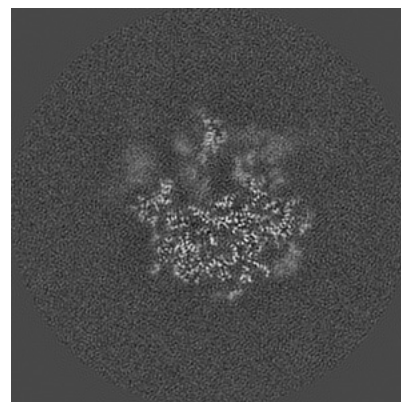
6.2.1 Primary map



X Index: 200



Y Index: 200

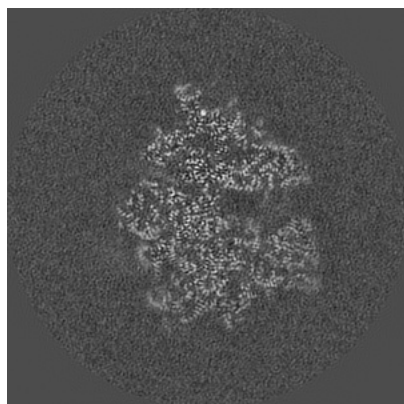


Z Index: 200

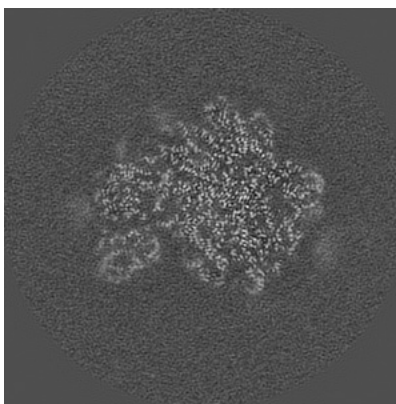
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

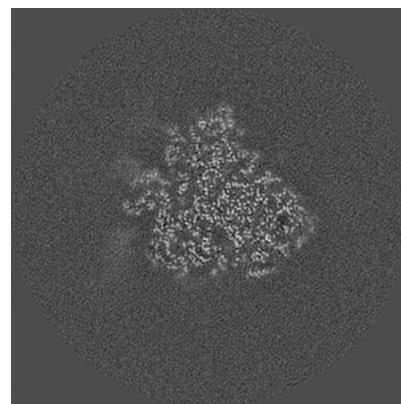
6.3.1 Primary map



X Index: 216



Y Index: 192

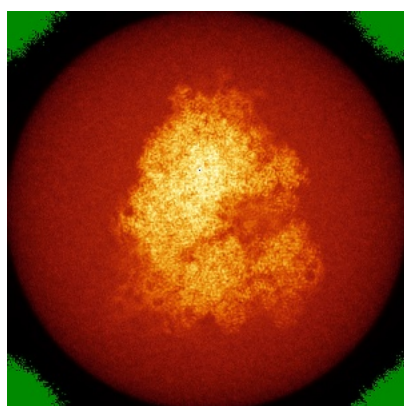


Z Index: 230

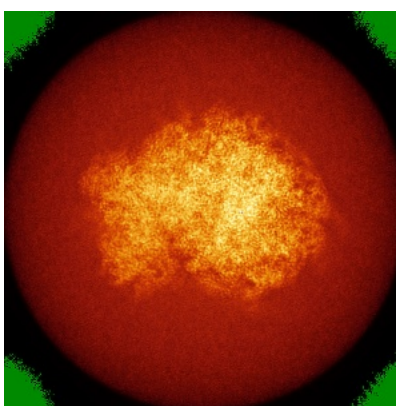
The images above show the largest variance slices of the map in three orthogonal directions.

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

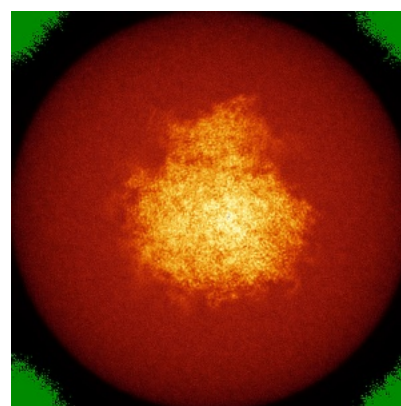
6.4.1 Primary map



X



Y

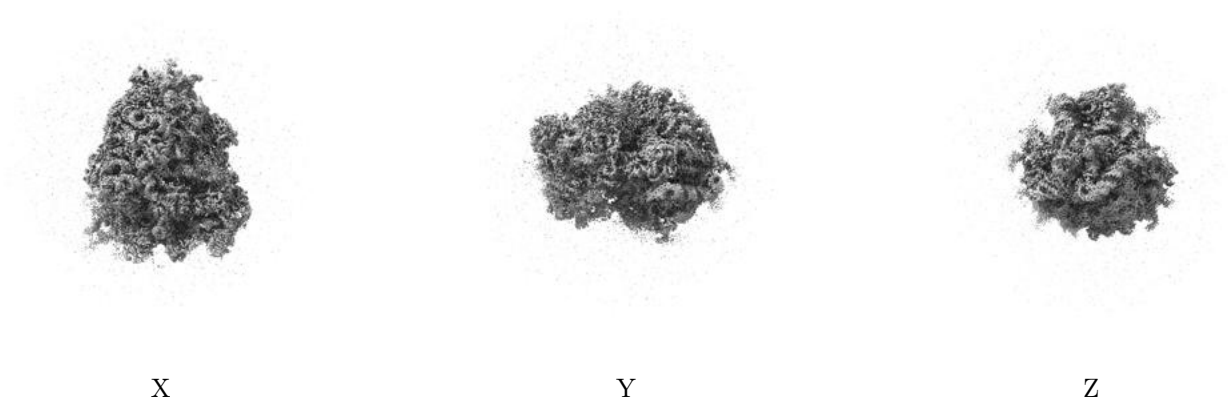


Z

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 0.021. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

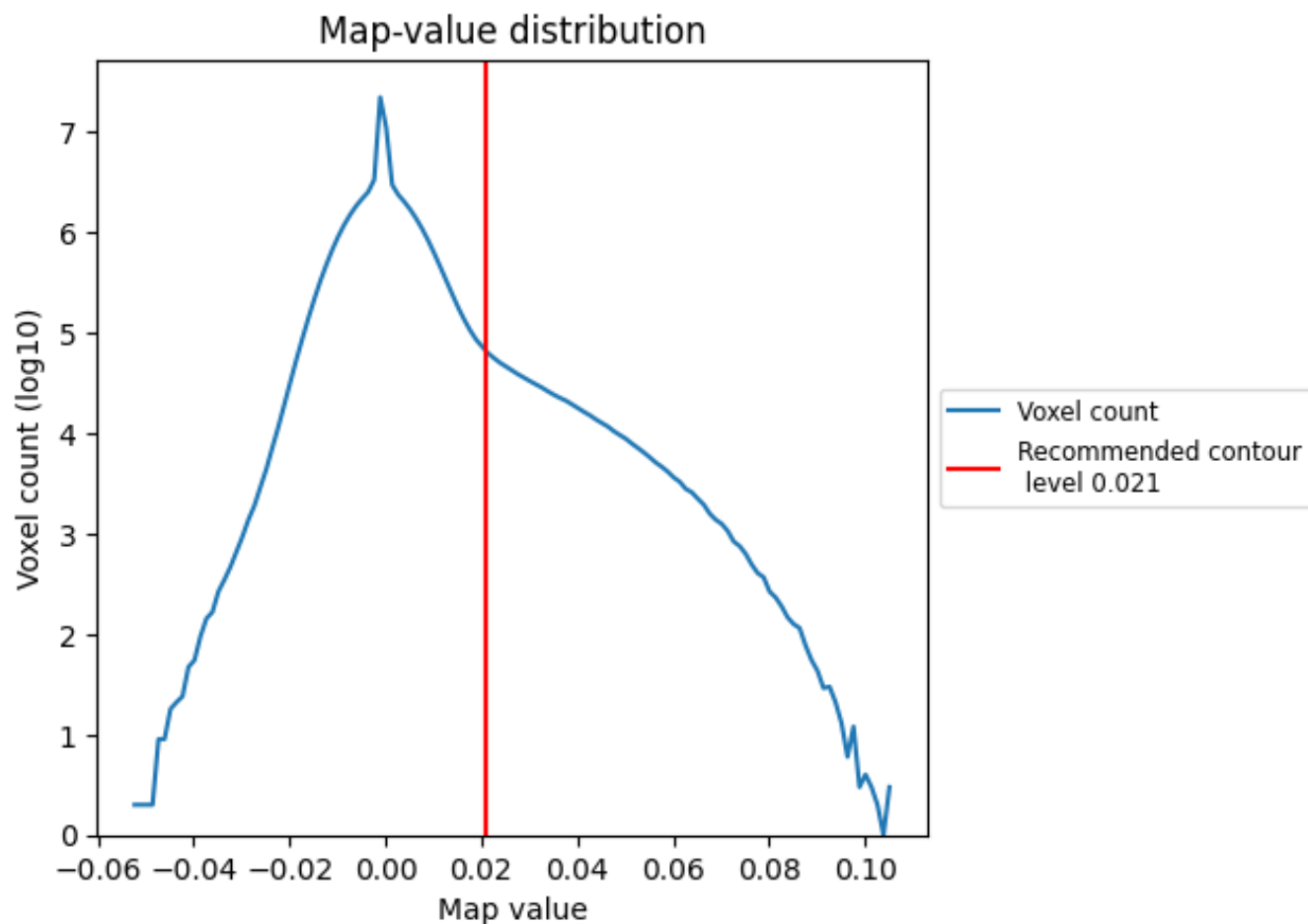
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

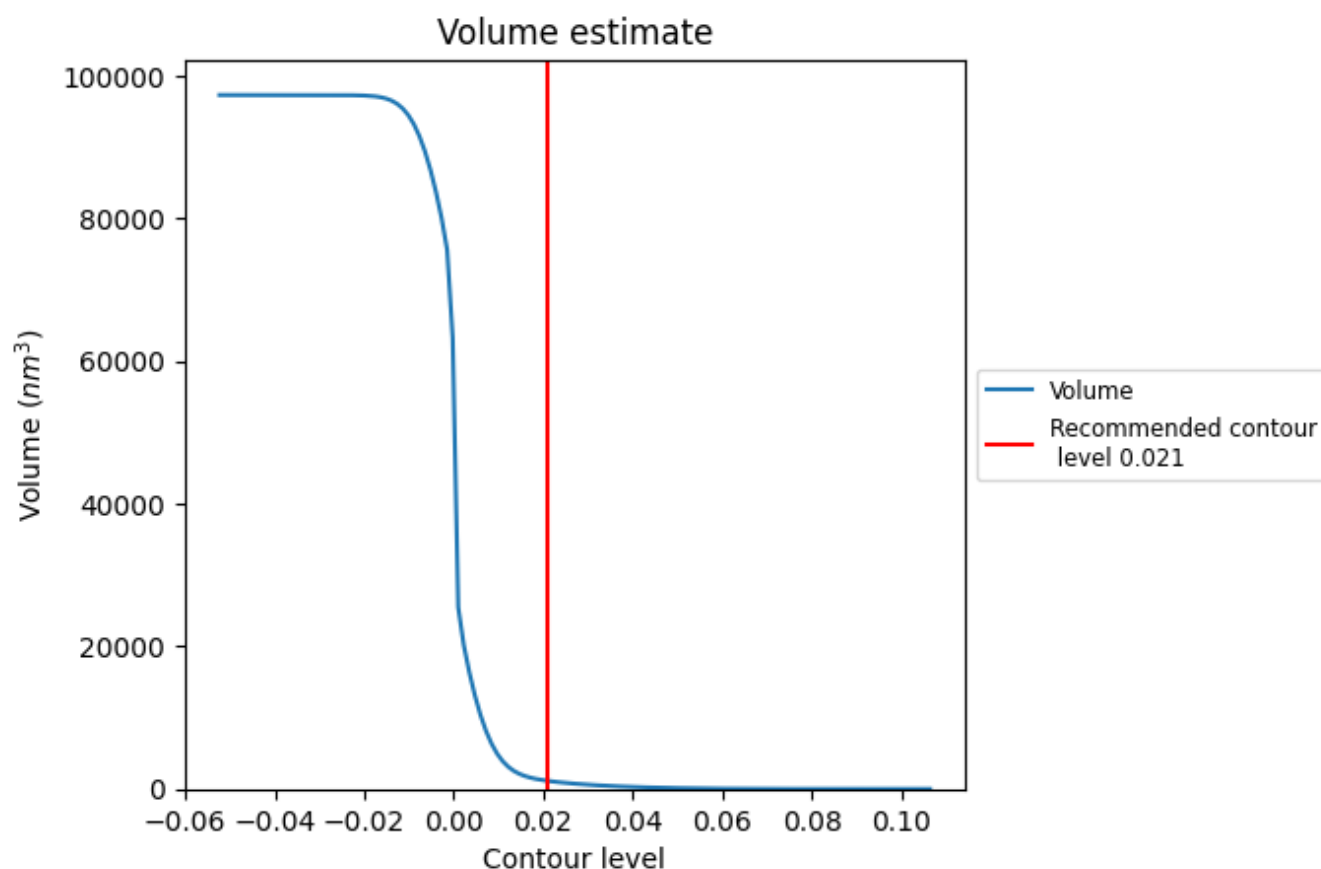
This section contains the results of statistical analysis of the map.

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.

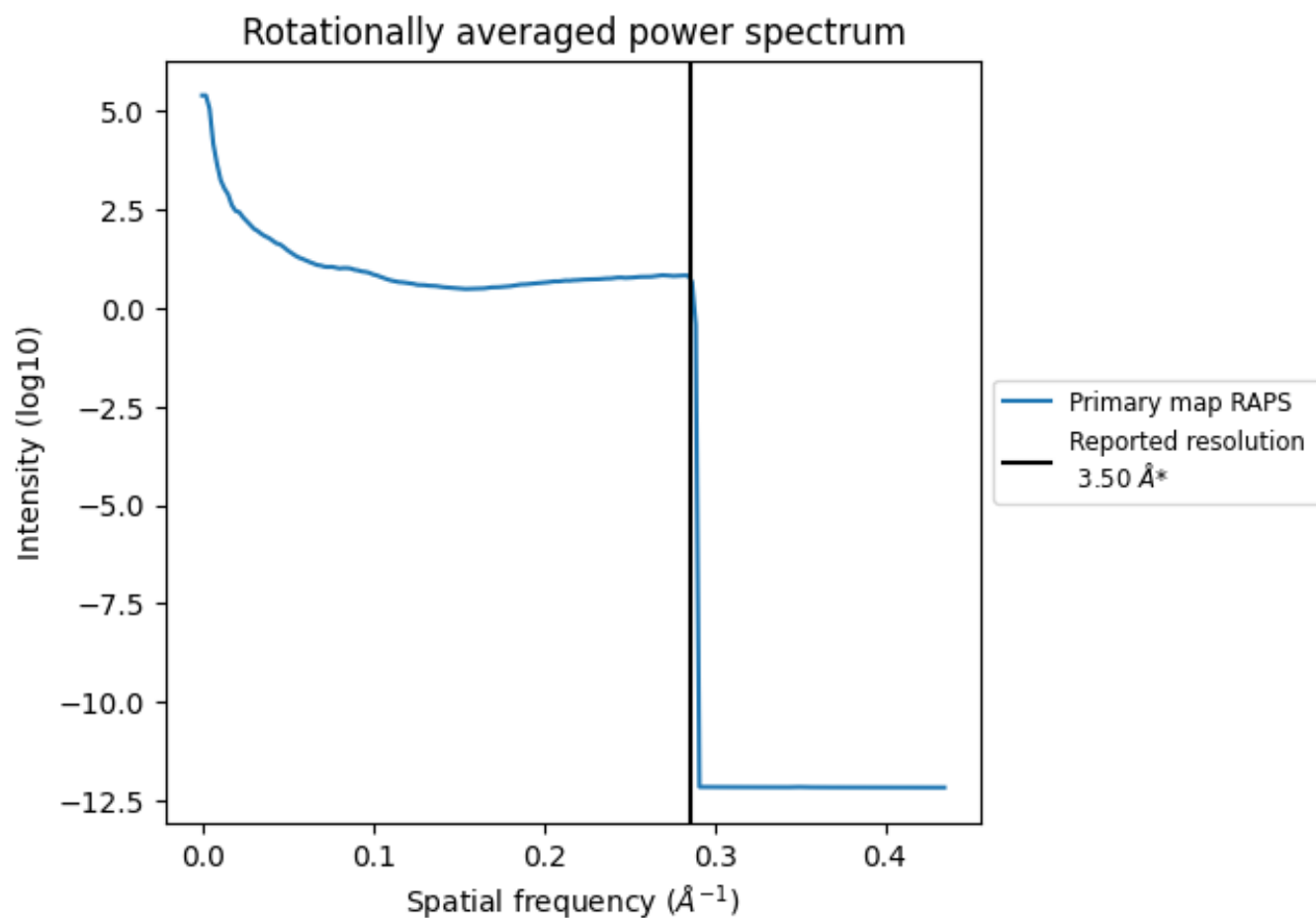
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1131 nm^3 ; this corresponds to an approximate mass of 1022 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 ⓘ

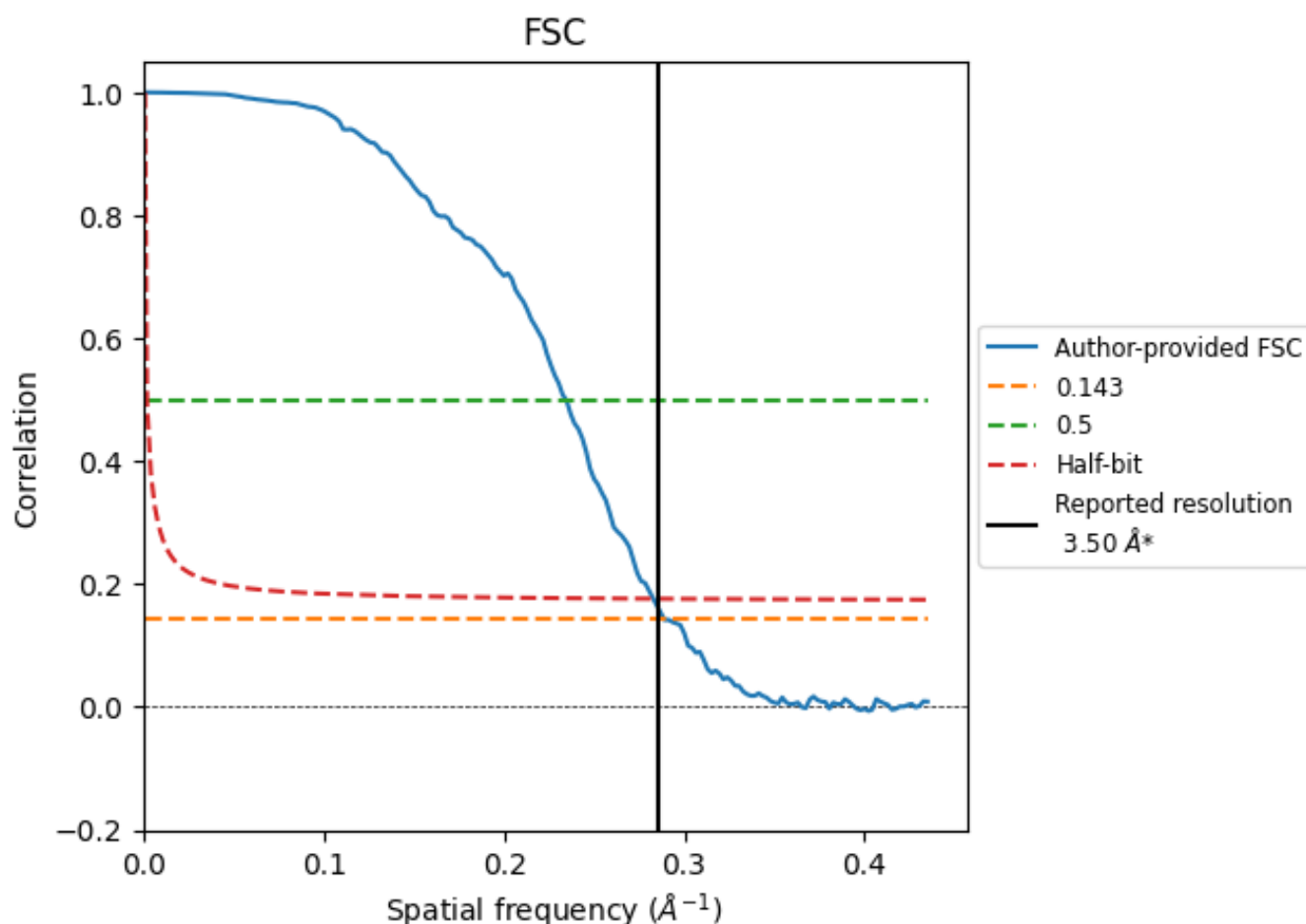


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

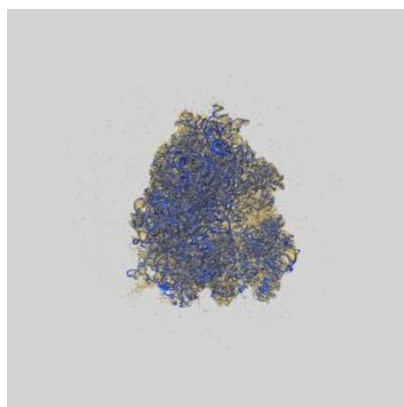
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.46	4.27	3.54
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

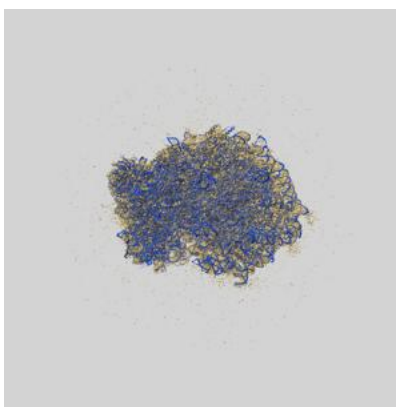
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0526 and PDB model 6OLI. Per-residue inclusion information can be found in [section 3](#) on [page 21](#).

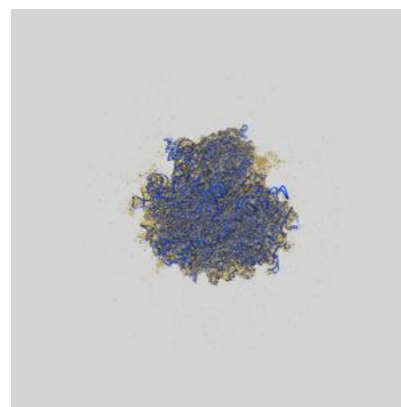
9.1 Map-model overlay [i](#)



X



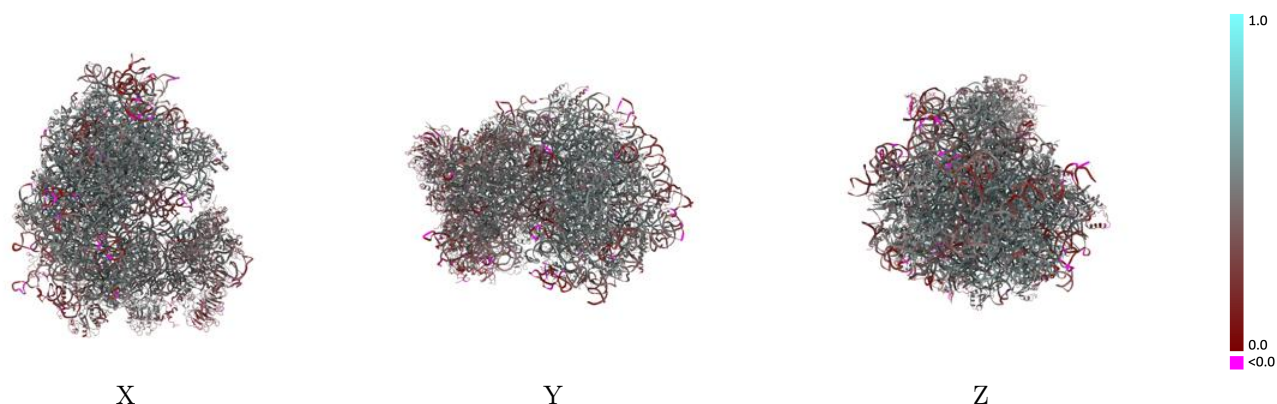
Y



Z

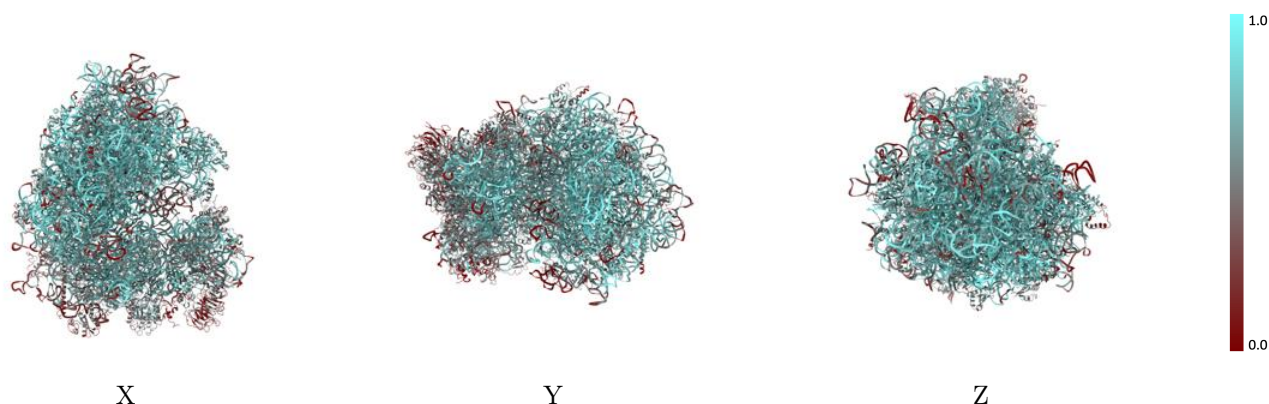
The images above show the 3D surface view of the map at the recommended contour level 0.021 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



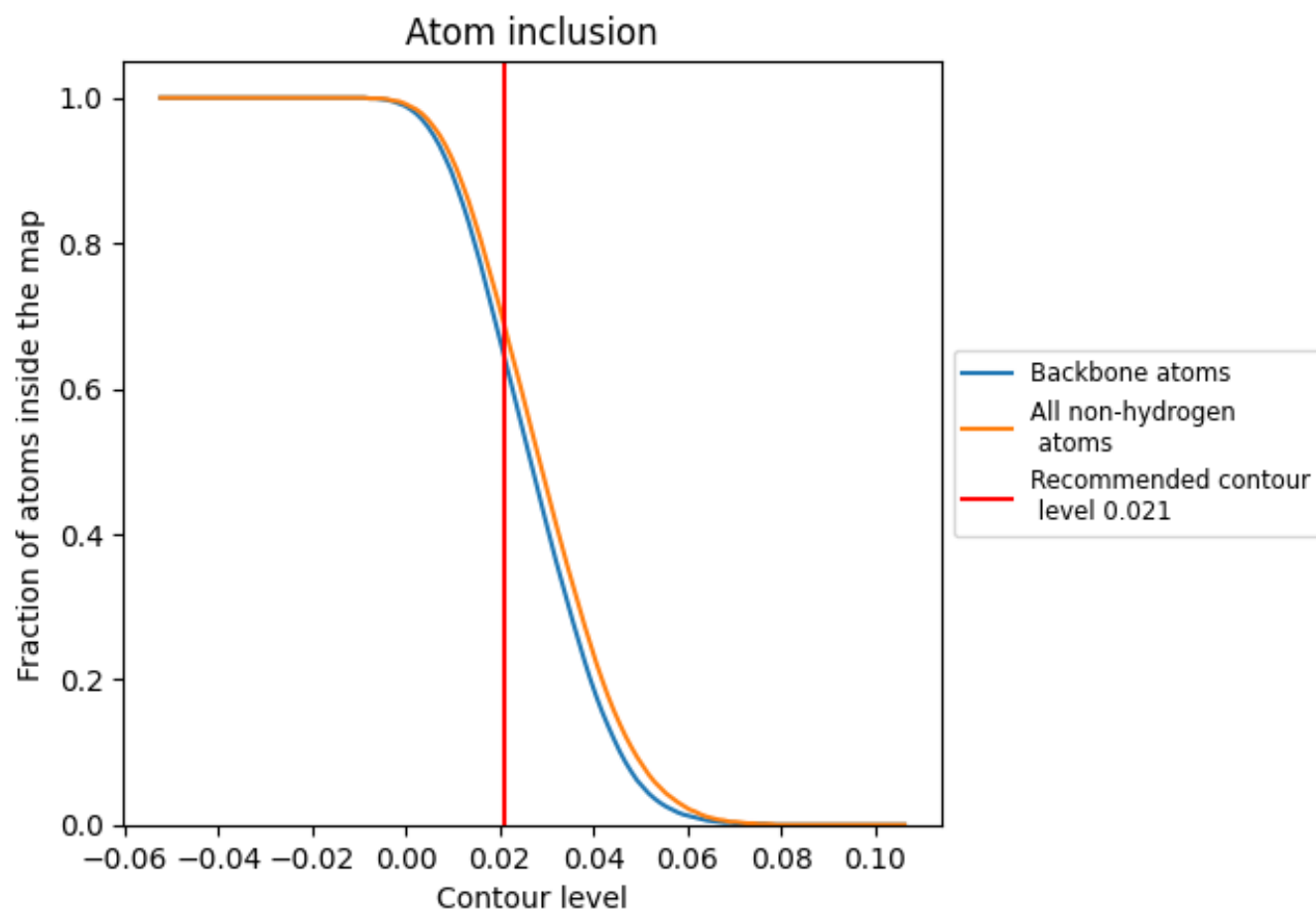
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.021).

9.4 Atom inclusion [i](#)



At the recommended contour level, 64% of all backbone atoms, 69% 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 (0.021) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6870	 0.4460
A	 0.7050	 0.5190
B	 0.6990	 0.4940
C	 0.7380	 0.5140
D	 0.8160	 0.4720
E	 0.9000	 0.5080
F	 0.6510	 0.4550
G	 0.6160	 0.4300
H	 0.7230	 0.5050
I	 0.5910	 0.4390
J	 0.6140	 0.4570
K	 0.6690	 0.4830
L	 0.6210	 0.4500
M	 0.6650	 0.4670
N	 0.6720	 0.4870
O	 0.7600	 0.5300
P	 0.7080	 0.5010
Q	 0.7410	 0.5120
R	 0.7090	 0.5040
S	 0.6140	 0.4470
S2	 0.7340	 0.4290
SA	 0.4960	 0.4220
SB	 0.5460	 0.4450
SC	 0.5710	 0.4530
SD	 0.4250	 0.3930
SE	 0.4950	 0.4090
SF	 0.4650	 0.3900
SG	 0.3580	 0.3210
SH	 0.3740	 0.3560
SI	 0.4570	 0.3860
SJ	 0.5280	 0.3850
SK	 0.3960	 0.3550
SL	 0.5350	 0.4160
SM	 0.0890	 0.1970
SN	 0.5730	 0.4500



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Chain	Atom inclusion	Q-score
SO	 0.5630	 0.4530
SP	 0.5110	 0.4060
SQ	 0.4940	 0.4080
SR	 0.4050	 0.3720
SS	 0.5230	 0.3960
ST	 0.5300	 0.4170
SU	 0.3940	 0.3650
SV	 0.5250	 0.4280
SW	 0.6190	 0.4930
SX	 0.5890	 0.4600
SY	 0.4350	 0.3420
SZ	 0.4130	 0.3530
Sa	 0.6050	 0.4510
Sb	 0.4820	 0.4200
Sc	 0.3480	 0.3440
Sd	 0.6050	 0.4310
Se	 0.4530	 0.3850
Sf	 0.0810	 0.2030
Sg	 0.2720	 0.2970
T	 0.7280	 0.5090
U	 0.6790	 0.4890
V	 0.5590	 0.4190
W	 0.6740	 0.5070
X	 0.6970	 0.4850
Y	 0.6930	 0.5050
Z	 0.6960	 0.4900
a	 0.6450	 0.4660
b	 0.7440	 0.5230
c	 0.6150	 0.4490
d	 0.5820	 0.4390
e	 0.6950	 0.4720
f	 0.7520	 0.5240
g	 0.7540	 0.5210
h	 0.6810	 0.4820
i	 0.6800	 0.4830
j	 0.6500	 0.4650
k	 0.8050	 0.5360
l	 0.5460	 0.4340
m	 0.7230	 0.5010
n	 0.6930	 0.4800
o	 0.5640	 0.4820
p	 0.6660	 0.4870

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Chain	Atom inclusion	Q-score
q	 0.6820	 0.4990
r	 0.7620	 0.5120
t	 0.7940	 0.4590
u	 0.3360	 0.2860
v	 0.5480	 0.3300
w	 0.7650	 0.4830
y	 0.1290	 0.3260