



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2025 – 03:53 PM EDT

PDB ID : 9B0S
EMDB ID : EMD-44052
Title : In situ human top-top di-ribosome structure (Composite map)
Authors : Wei, Z.; Yong, X.
Deposited on : 2024-03-12
Resolution : 3.80 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.dev117
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.4

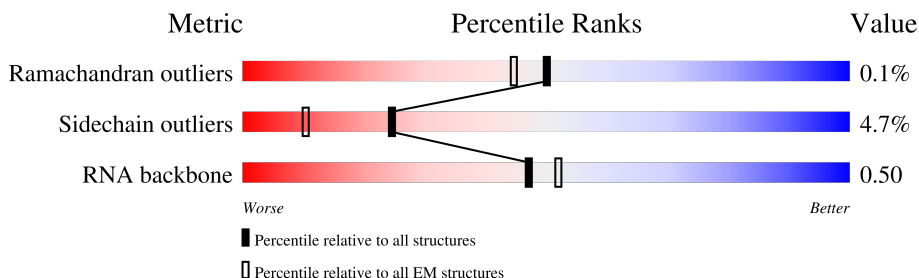
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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.



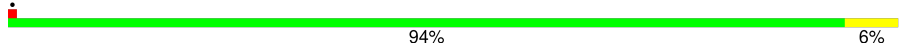
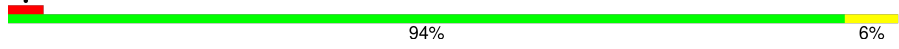
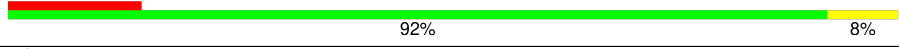
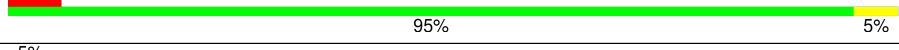
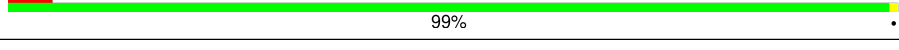
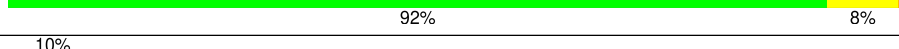
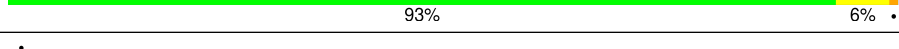
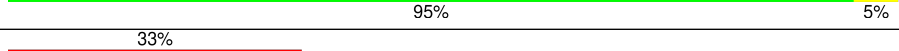
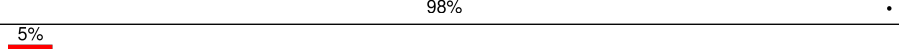
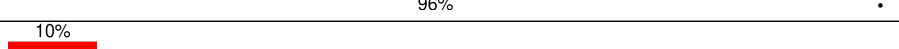
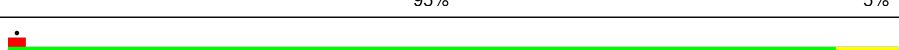
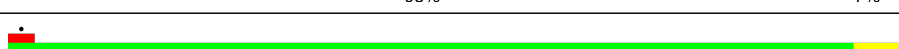
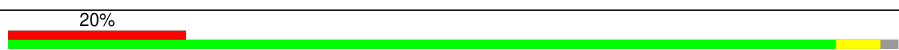
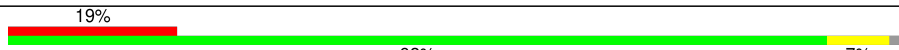
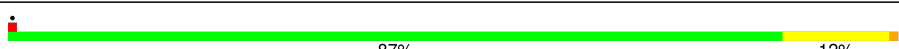

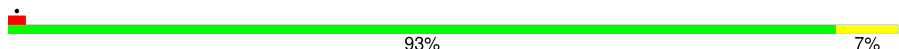
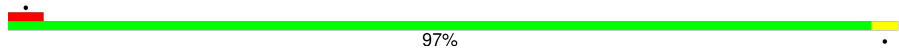
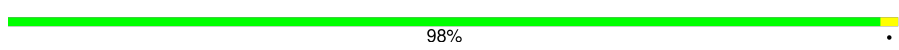
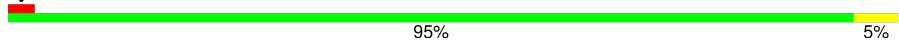
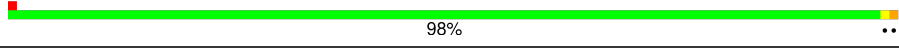
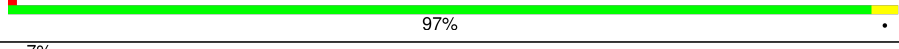
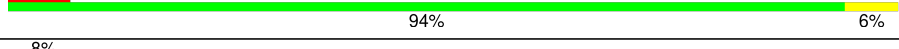
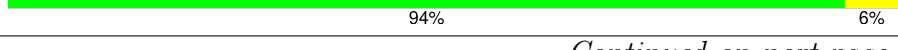

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	cH	125	<div> <div>14%</div> <div>96%</div> <div>.</div> </div>
2	SE	262	<div> <div>.</div> <div>97%</div> <div>.</div> </div>
2	sE	262	<div> <div>.</div> <div>97%</div> <div>.</div> </div>
3	SI	206	<div> <div>8%</div> <div>94%</div> <div>6%</div> </div>
3	sI	206	<div> <div>10%</div> <div>95%</div> <div>5%</div> </div>
4	SL	153	<div> <div>8%</div> <div>95%</div> <div>5%</div> </div>
4	sL	153	<div> <div>10%</div> <div>93%</div> <div>7%</div> </div>
5	SX	141	<div> <div>98%</div> <div>.</div> </div>

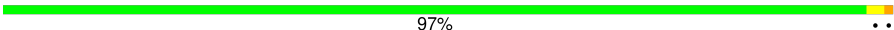
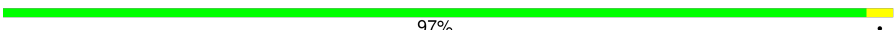

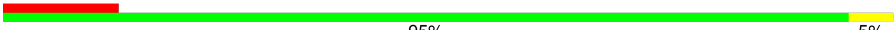






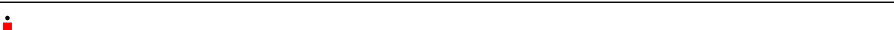

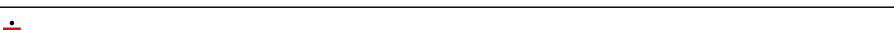
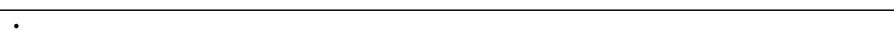
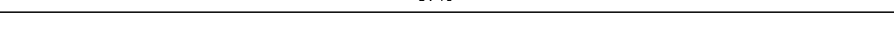
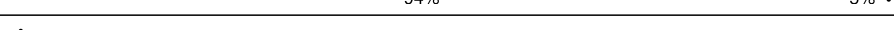
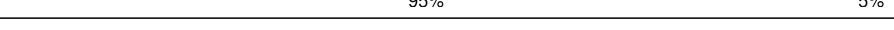


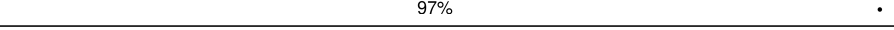
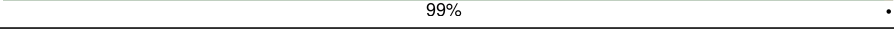
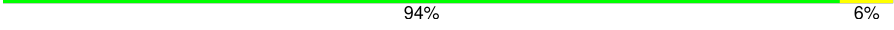
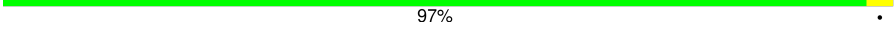
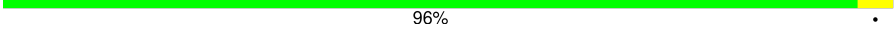
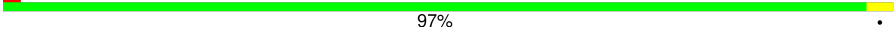
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Mol	Chain	Length	Quality of chain
5	sX	141	
6	SG	237	
6	sG	237	
7	SJ	185	
7	sJ	185	
8	SY	131	
8	sY	131	
9	Se	58	
9	se	58	
10	SA	221	
10	sA	221	
11	SB	214	
11	sB	214	
12	SH	189	
12	sH	189	
13	SV	83	
13	sV	83	
14	Sa	102	
14	sa	102	
15	SC	222	
15	sC	222	
16	SN	150	
16	sN	150	
17	SO	140	
17	sO	140	

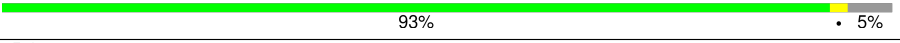
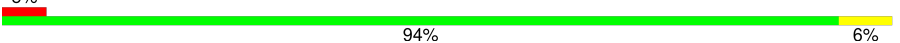

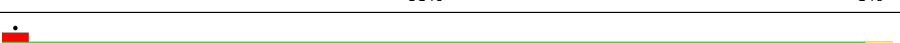
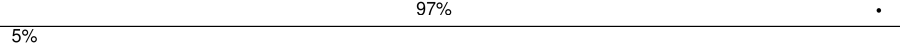
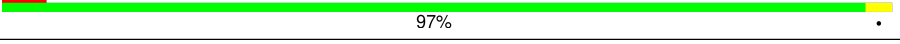
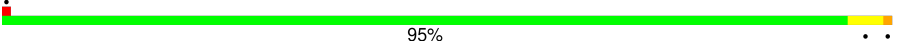

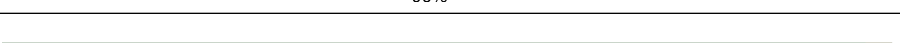
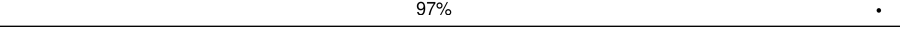
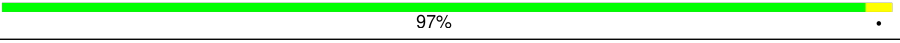
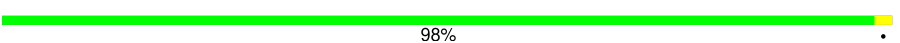

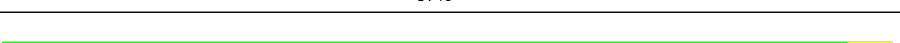
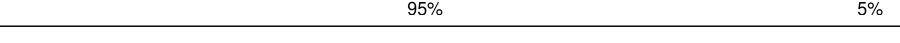
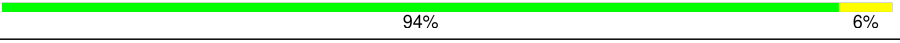
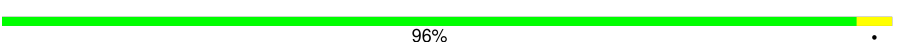

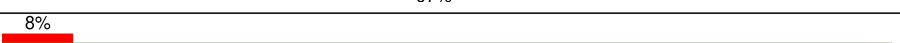
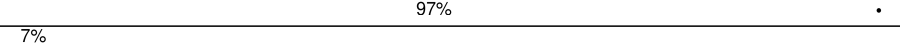
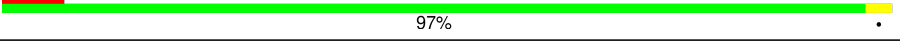
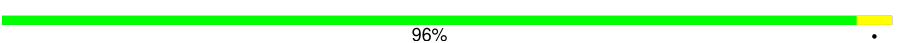

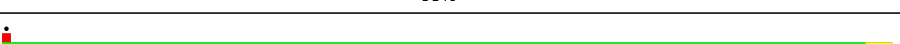
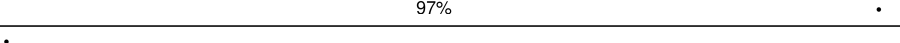
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Mol	Chain	Length	Quality of chain
18	SW	129	 97% ..
18	sW	129	 97% .
19	Sb	83	 7% 90% 10%
19	sb	83	 13% 95% 5%
20	L7	120	 90% 10%
20	l7	120	 88% 12%
21	L8	156	 79% 21%
21	l8	156	 81% 19%
22	LA	248	 96% .
22	lA	248	 95% 5%
23	LB	402	 97% .
23	lB	402	 97% .
24	LC	368	 97% .
24	lC	368	 97% .
25	LD	293	 94% 5% .
25	lD	293	 95% 5%
26	LE	247	 92% . .
26	lE	247	 7% 92% . .
27	LF	225	 97% .
27	lF	225	 99% .
28	LG	241	 5% 94% 6%
28	lG	241	 10% 97% .
29	LH	190	 96% .
29	lH	190	 97% .
30	LI	213	 91% . 5%

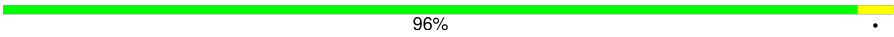
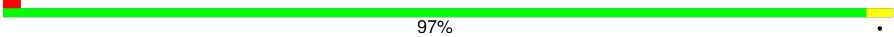
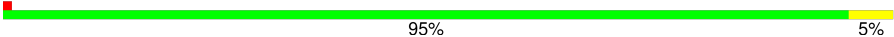
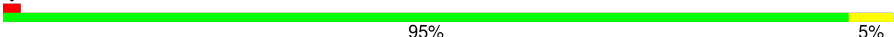
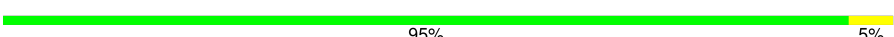
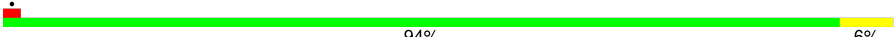




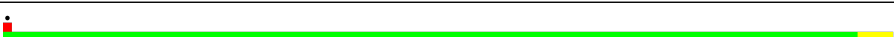


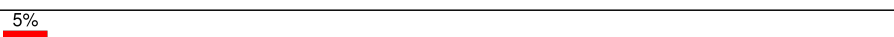
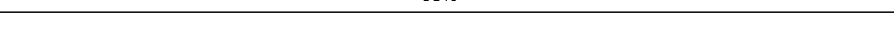
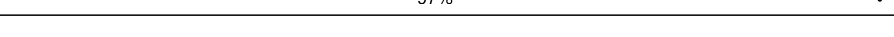
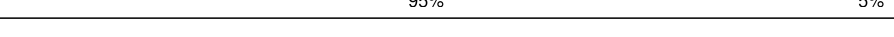
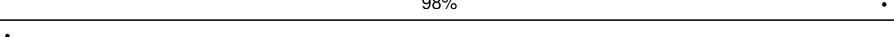
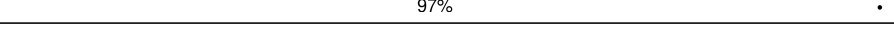
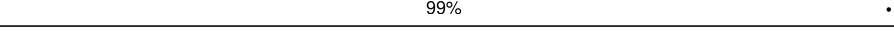
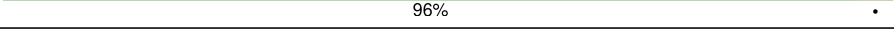
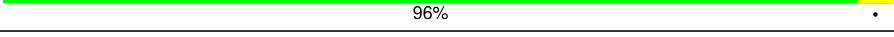
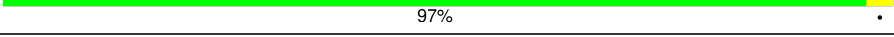
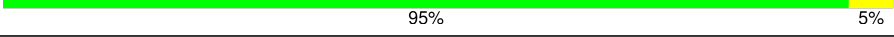
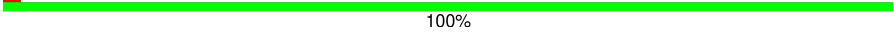
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Mol	Chain	Length	Quality of chain
30	II	213	 93% • 5%
31	LJ	176	 5% 94% 6%
31	IJ	176	 13% 95% 5%
32	LL	210	 97% •
32	IL	210	 5% 97% •
33	LM	139	 95% • •
33	IM	139	 96% • •
34	LN	203	 97% •
34	IN	203	 97% •
35	LO	201	 98% •
35	IO	201	 97% •
36	LP	153	 95% 5%
36	IP	153	 94% 6%
37	LQ	187	 96% •
37	IQ	187	 97% •
38	LR	187	 8% 97% •
38	IR	187	 7% 97% •
39	LS	175	 96% •
39	IS	175	 98% •
40	LT	159	 97% •
40	IT	159	 97% •
41	LU	101	 96% •
41	IU	101	 10% 93% 7%
42	LV	131	 98% •
42	IV	131	 97% •


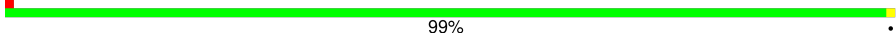
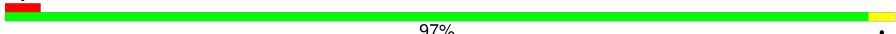
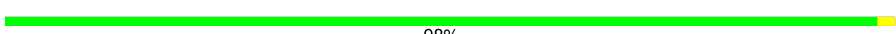


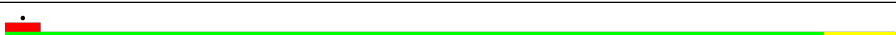
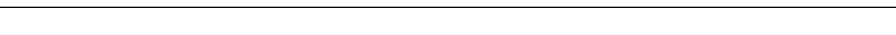
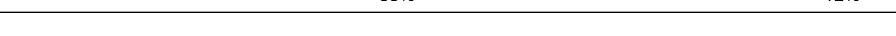
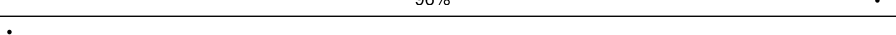
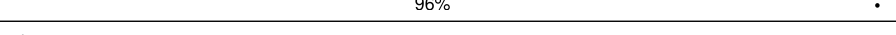
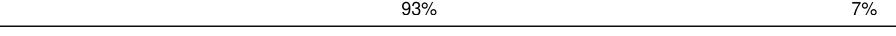
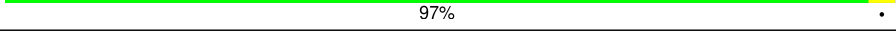
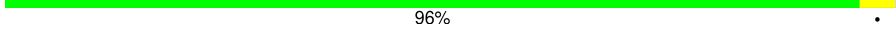
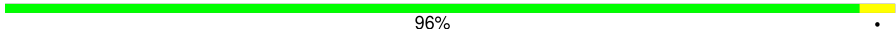
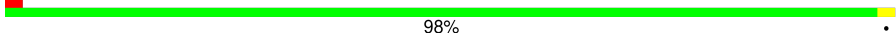







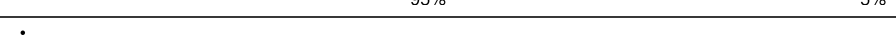
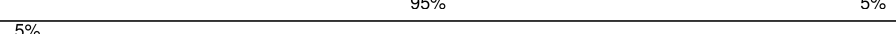

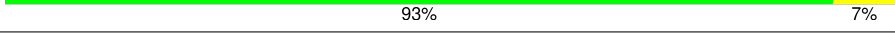



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Mol	Chain	Length	Quality of chain
43	LX	120	 96% .
43	IX	120	 97% .
44	LY	134	 95% 5%
44	IY	134	 95% 5%
45	LZ	135	 95% 5%
45	IZ	135	 94% 6%
46	La	147	 97% .
46	la	147	 97% .
47	Lb	121	 88% . 10%
47	lb	121	 9% 84% 6% 10%
48	Lc	98	 96% .
48	lc	98	 6% 95% 5%
49	Ld	107	 96% .
49	ld	107	 5% 98% .
50	Le	128	 97% .
50	le	128	 95% 5%
51	Lf	109	 98% .
51	lf	109	 97% .
52	Lg	114	 99% .
52	lg	114	 96% .
53	Lh	122	 96% .
53	lh	122	 97% .
54	Li	102	 95% 5%
54	li	102	 100%
55	Lj	86	 95% 5%

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Mol	Chain	Length	Quality of chain
55	lj	86	
56	Lk	69	
56	lk	69	
57	Ll	50	
57	ll	50	
58	Lm	52	
58	lm	52	
59	Ln	24	
59	ln	24	
60	Lo	105	
60	lo	105	
61	Lp	91	
61	lp	91	
62	Lr	125	
62	lr	125	
63	Lz	217	
63	lz	217	
63	lz	217	
64	SR	135	
64	sR	135	
64	sR	135	
65	SD	227	
65	sD	227	
65	sD	227	
66	SF	189	
66	sF	189	
66	sF	189	
67	SK	98	
67	sK	98	
67	sK	98	



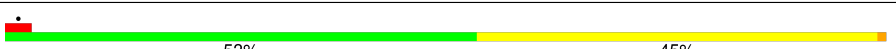
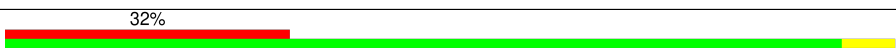
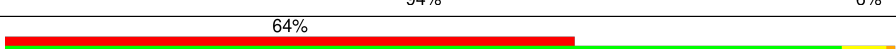
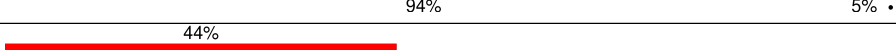
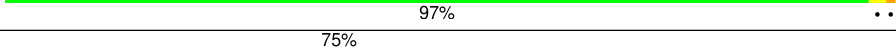
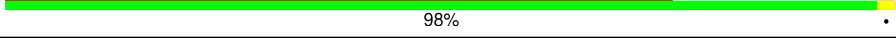
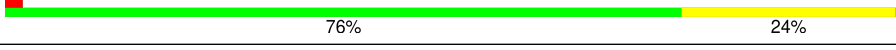



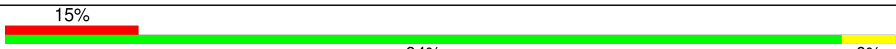
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Mol	Chain	Length	Quality of chain
68	SP	121	
68	sP	121	
69	SQ	144	
69	sQ	144	
70	SS	145	
70	sS	145	
71	ST	143	
71	sT	143	
72	SU	104	
72	sU	104	
73	Sc	64	
73	sc	64	
74	Sd	55	
74	sd	55	
75	Sg	313	
75	sg	313	
76	SM	122	
76	sM	122	
77	SZ	75	
77	sZ	75	
78	Sf	67	
78	sf	67	
79	S2	1740	
79	s2	1740	
80	cB	846	

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Mol	Chain	Length	Quality of chain
81	aP	71	
82	Et	75	
82	pE	75	
83	Ls	196	
83	ls	196	
84	Lt	141	
84	lt	141	
85	L5	3740	
85	l5	3740	
86	LW	124	
87	AT	77	
88	CF	441	
89	Pt	74	

2 Entry composition [i](#)

There are 91 unique types of molecules in this entry. The entry contains 456973 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 Endothelial differentiation-related factor 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	cH	125	Total	C	N	O	0	0
			968	595	189	184		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
cH	30	ARG	GLN	conflict	UNP O60869
cH	32	ALA	ARG	conflict	UNP O60869
cH	33	ALA	-	insertion	UNP O60869
cH	34	ALA	-	insertion	UNP O60869

- Molecule 2 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	sE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		
2	SE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 3 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	sI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		
3	SI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 4 is a protein called 40S ribosomal protein S11.

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

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

- Molecule 5 is a protein called 40S ribosomal protein S23.

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

- Molecule 6 is a protein called 40S ribosomal protein S6.

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

- Molecule 7 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	sJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		
7	SJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 8 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	sY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		
8	SY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 9 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		
9	Se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

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

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

- Molecule 11 is a protein called 40S ribosomal protein S3a.

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

- Molecule 12 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 13 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	sV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		
13	SV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 14 is a protein called 40S ribosomal protein S26.

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

- Molecule 15 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	sC	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		
15	SC	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

- Molecule 16 is a protein called 40S ribosomal protein S13.

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

- Molecule 17 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	sO	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		
17	SO	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		

- Molecule 18 is a protein called 40S ribosomal protein S15a.

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

- Molecule 19 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		
19	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 20 is a RNA chain called 5S rRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
20	17	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

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Mol	Chain	Residues	Atoms					AltConf	Trace
20	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 21 is a RNA chain called 5.8S rRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
21	l8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		
21	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 22 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	lA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		
22	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 23 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	lB	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		
23	LB	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		

- Molecule 24 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	lC	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		
24	LC	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- Molecule 25 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	lD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		
25	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 26 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	lE	236	Total	C	N	O	S	0	0
			1904	1222	361	317	4		
26	LE	236	Total	C	N	O	S	0	0
			1904	1222	361	317	4		

- Molecule 27 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	lF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		
27	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 28 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	lG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		
28	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 29 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	lH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		
29	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 30 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	lI	202	Total	C	N	O	S	0	0
			1634	1037	314	269	14		
30	LI	202	Total	C	N	O	S	0	0
			1634	1037	314	269	14		

- Molecule 31 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	IJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		
31	LJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 32 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	IL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		
32	LL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 33 is a protein called 60S ribosomal protein L14.

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

- Molecule 34 is a protein called 60S ribosomal protein L15.

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

- Molecule 35 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	IO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		
35	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 36 is a protein called 60S ribosomal protein L17.

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

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

- Molecule 37 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	lQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		
37	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 38 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	lR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		
38	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 39 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	lS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		
39	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 40 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	lT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		
40	LT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 41 is a protein called Heparin-binding protein HBp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	lU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		
41	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 42 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	IV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		
42	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 43 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	IX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		
43	LX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

- Molecule 44 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	IY	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		
44	LY	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 45 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	IZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		
45	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 46 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	la	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		
46	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 47 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		
47	Lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- Molecule 48 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		
48	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 49 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		
49	Ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 50 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		
50	Le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 51 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		
51	Lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 52 is a protein called 60S ribosomal protein L34.

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

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

- Molecule 53 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		
53	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 54 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		
54	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 55 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		
55	Lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 56 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	lk	69	Total	C	N	O	S	0	0
			569	366	103	99	1		
56	Lk	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 57 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		
57	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 58 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	lm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		
58	Lm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 59 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		
59	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		
60	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 61 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		
61	Lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 62 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		
62	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 63 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	lz	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		
63	Lz	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 64 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	sR	135	Total	C	N	O	S	0	0
			1090	685	202	198	5		
64	SR	135	Total	C	N	O	S	0	0
			1090	685	202	198	5		

- Molecule 65 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	sD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		
65	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 66 is a protein called 40S ribosomal protein S5.

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

- Molecule 67 is a protein called 40S ribosomal protein S10.

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

- Molecule 68 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	sP	121	Total	C	N	O	S	0	0
			985	623	185	170	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
68	SP	121	Total	C	N	O	S	0	0
			985	623	185	170	7		

- Molecule 69 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	sQ	144	Total	C	N	O	S	0	0
			1142	726	216	197	3		
69	SQ	144	Total	C	N	O	S	0	0
			1142	726	216	197	3		

- Molecule 70 is a protein called 40S ribosomal protein S18.

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

- Molecule 71 is a protein called 40S ribosomal protein S19.

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

- Molecule 72 is a protein called 40S ribosomal protein S20.

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

- Molecule 73 is a protein called 40S ribosomal protein S28.

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

- Molecule 74 is a protein called 40S ribosomal protein S29.

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

- Molecule 75 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		
75	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 76 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	sM	122	Total	C	N	O	S	0	0
			940	590	164	177	9		
76	SM	122	Total	C	N	O	S	0	0
			940	590	164	177	9		

- Molecule 77 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	sZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		
77	SZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 78 is a protein called Ubiquitin-40S ribosomal protein S27a.

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

- Molecule 79 is a RNA chain called 18S rRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
79	s2	1740	Total	C	N	O	P	0	0
			36898	16459	6599	12101	1739		
79	S2	1740	Total	C	N	O	P	0	0
			36898	16459	6599	12101	1739		

- Molecule 80 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	cB	846	Total	C	N	O	S	0	0
			6605	4193	1136	1232	44		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
cB	?	-	ALA	deletion	UNP P13639
cB	?	-	LYS	deletion	UNP P13639
cB	?	-	GLY	deletion	UNP P13639
cB	?	-	GLU	deletion	UNP P13639
cB	?	-	GLY	deletion	UNP P13639
cB	?	-	GLN	deletion	UNP P13639
cB	?	-	LEU	deletion	UNP P13639
cB	?	-	GLY	deletion	UNP P13639
cB	?	-	PRO	deletion	UNP P13639
cB	?	-	ALA	deletion	UNP P13639

- Molecule 81 is a RNA chain called A/P site tRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
81	aP	71	Total	C	N	O	P	0	0
			1514	677	275	492	70		

- Molecule 82 is a RNA chain called P/E site tRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
82	pE	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		
82	Et	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		

- Molecule 83 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	ls	196	Total	C	N	O	S	0	0
			1496	952	259	276	9		
83	Ls	196	Total	C	N	O	S	0	0
			1496	952	259	276	9		

- Molecule 84 is a protein called 60S ribosomal protein L12 [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
84	lt	141	Total	C	N	O	S	0	0
			1046	652	191	199	4		
84	Lt	141	Total	C	N	O	S	0	0
			1046	652	191	199	4		

- Molecule 85 is a RNA chain called 28S rRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
85	l5	3740	Total	C	N	O	P	0	0
			79860	35549	14585	25987	3739		
85	L5	3740	Total	C	N	O	P	0	0
			79860	35549	14585	25987	3739		

- Molecule 86 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	LW	118	Total	C	N	O	S	0	0
			965	604	199	158	4		

- Molecule 87 is a RNA chain called A/T site tRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
87	AT	76	Total	C	N	O	P	0	0
			1616	723	291	527	75		

- Molecule 88 is a protein called Putative elongation factor 1-alpha-like 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	CF	441	Total	C	N	O	P S	0	0
			3383	2148	581	636	1 17		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CF	311	ASN	LYS	conflict	UNP Q5VTE0
CF	365	THR	MET	conflict	UNP Q5VTE0

- Molecule 89 is a RNA chain called P site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	Pt	74	Total	C	N	O	P	0	0
			1576	705	286	512	73		

- Molecule 90 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
90	sa	1	Total	Zn	0
			1	1	
90	lg	1	Total	Zn	0
			1	1	
90	lj	1	Total	Zn	0
			1	1	
90	lm	1	Total	Zn	0
			1	1	
90	lo	1	Total	Zn	0
			1	1	
90	lp	1	Total	Zn	0
			1	1	
90	Sa	1	Total	Zn	0
			1	1	
90	Lg	1	Total	Zn	0
			1	1	
90	Lj	1	Total	Zn	0
			1	1	
90	Lm	1	Total	Zn	0
			1	1	
90	Lo	1	Total	Zn	0
			1	1	
90	Lp	1	Total	Zn	0
			1	1	

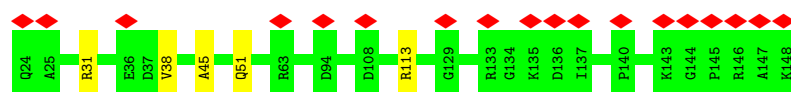
- Molecule 91 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
91	l7	3	Total 3	Mg 3	0
91	l8	3	Total 3	Mg 3	0
91	lA	1	Total 1	Mg 1	0
91	lI	1	Total 1	Mg 1	0
91	lP	1	Total 1	Mg 1	0
91	lV	1	Total 1	Mg 1	0
91	le	1	Total 1	Mg 1	0
91	lj	1	Total 1	Mg 1	0
91	sR	1	Total 1	Mg 1	0
91	s2	28	Total 28	Mg 28	0
91	l5	214	Total 214	Mg 214	0
91	L5	215	Total 215	Mg 215	0
91	L7	3	Total 3	Mg 3	0
91	L8	3	Total 3	Mg 3	0
91	LA	1	Total 1	Mg 1	0
91	LP	1	Total 1	Mg 1	0
91	LV	1	Total 1	Mg 1	0
91	Le	1	Total 1	Mg 1	0
91	Lg	1	Total 1	Mg 1	0
91	S2	29	Total 29	Mg 29	0

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: Endothelial differentiation-related factor 1



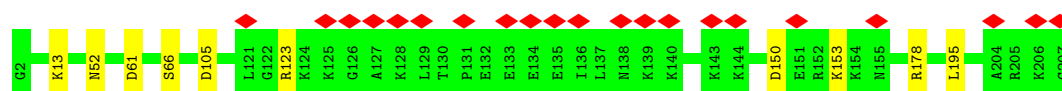
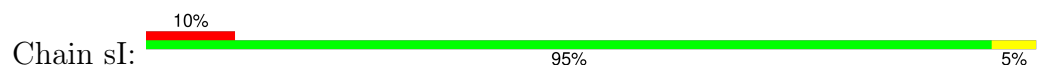
- Molecule 2: Small ribosomal subunit protein eS4, X isoform



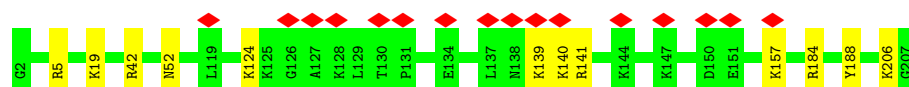
- Molecule 2: Small ribosomal subunit protein eS4, X isoform



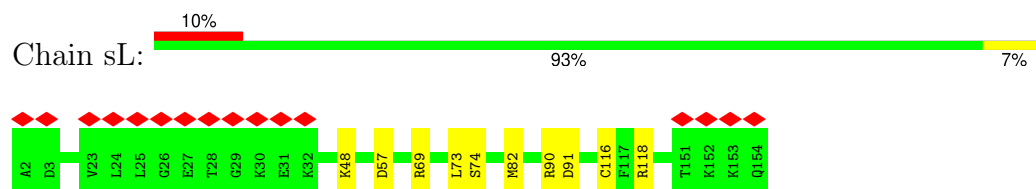
- Molecule 3: 40S ribosomal protein S8



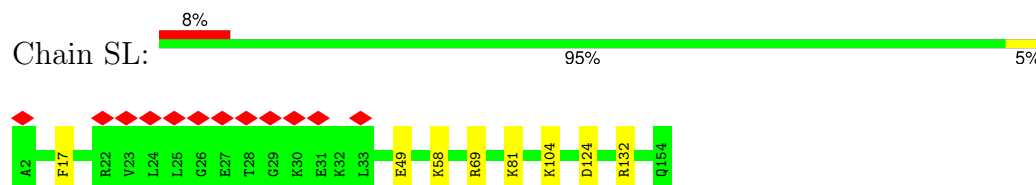
- Molecule 3: 40S ribosomal protein S8



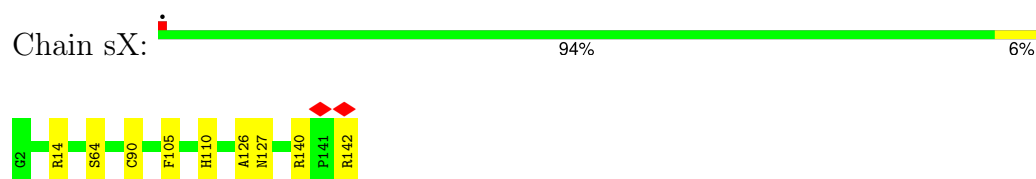
- Molecule 4: 40S ribosomal protein S11



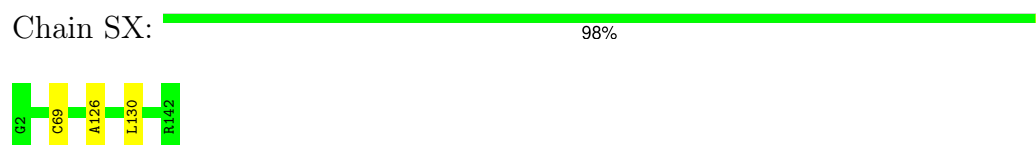
- Molecule 4: 40S ribosomal protein S11



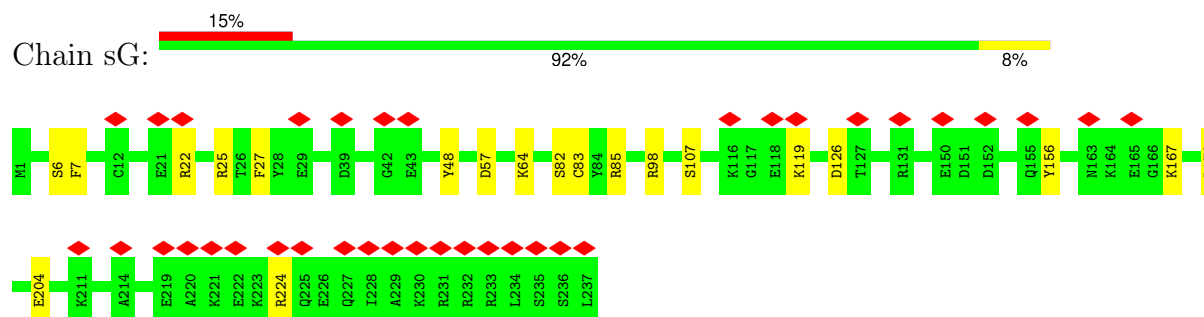
- Molecule 5: 40S ribosomal protein S23



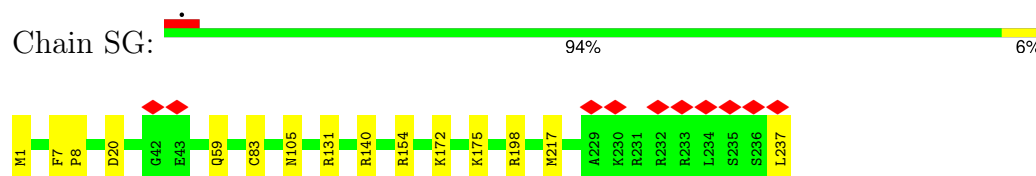
- Molecule 5: 40S ribosomal protein S23



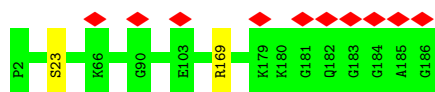
- Molecule 6: 40S ribosomal protein S6



- Molecule 6: 40S ribosomal protein S6



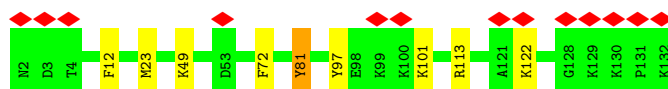
- Molecule 7: 40S ribosomal protein S9



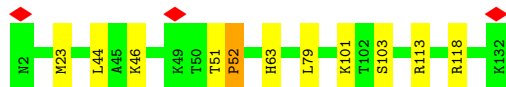
- Molecule 7: 40S ribosomal protein S9



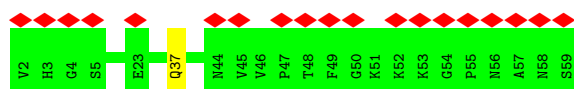
- Molecule 8: 40S ribosomal protein S24



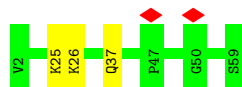
- Molecule 8: 40S ribosomal protein S24



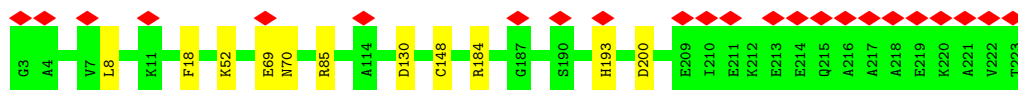
- Molecule 9: Small ribosomal subunit protein eS30



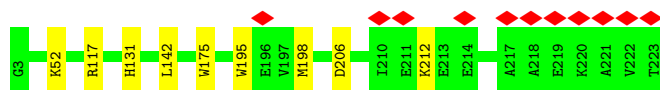
- Molecule 9: Small ribosomal subunit protein eS30



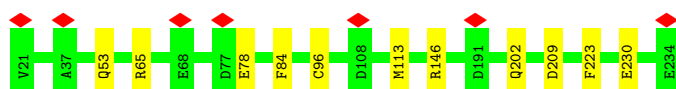
- Molecule 10: 40S ribosomal protein SA



- Molecule 10: 40S ribosomal protein SA



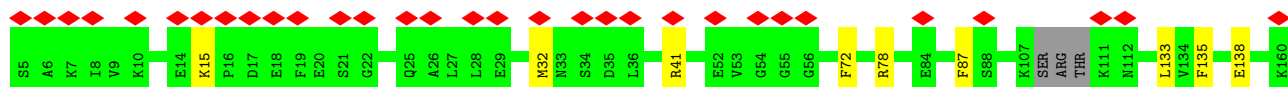
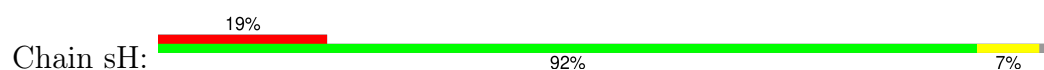
- Molecule 11: 40S ribosomal protein S3a



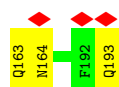
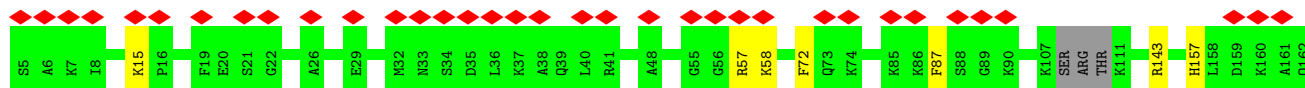
- Molecule 11: 40S ribosomal protein S3a



- Molecule 12: Small ribosomal subunit protein eS7

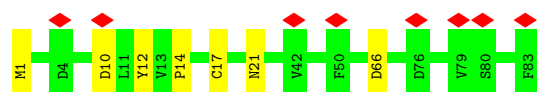


- Molecule 12: Small ribosomal subunit protein eS7

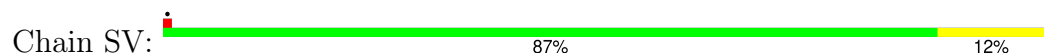


- Molecule 13: 40S ribosomal protein S21

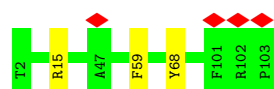




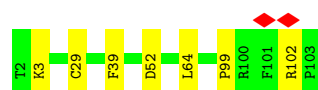
- Molecule 13: 40S ribosomal protein S21



- Molecule 14: 40S ribosomal protein S26



- Molecule 14: 40S ribosomal protein S26



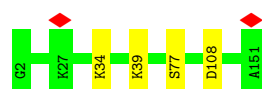
- Molecule 15: 40S ribosomal protein S2



- Molecule 15: 40S ribosomal protein S2

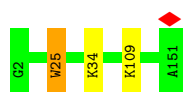


- Molecule 16: 40S ribosomal protein S13



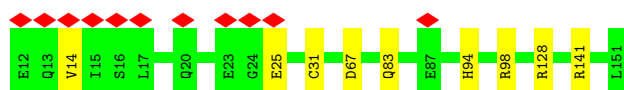
- Molecule 16: 40S ribosomal protein S13

Chain SN:  98% ..



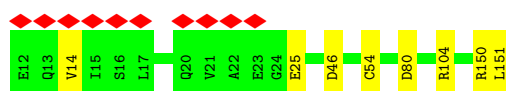
- Molecule 17: Small ribosomal subunit protein uS11

Chain sO:  8% 94% 6%



- Molecule 17: Small ribosomal subunit protein uS11

Chain SO:  7% 94% 6%



- Molecule 18: 40S ribosomal protein S15a

Chain sW:  97% .



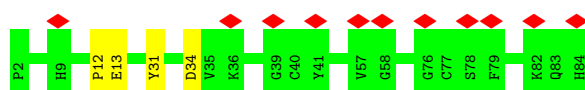
- Molecule 18: 40S ribosomal protein S15a

Chain SW:  97% ..




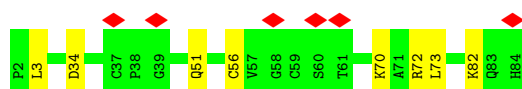
- Molecule 19: Small ribosomal subunit protein eS27

Chain sb:  13% 95% 5%




- Molecule 19: Small ribosomal subunit protein eS27

Chain Sb:  7% 90% 10%

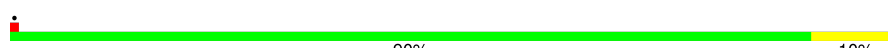


- Molecule 20: 5S rRNA [Homo sapiens]

Chain 17:  88% 12%




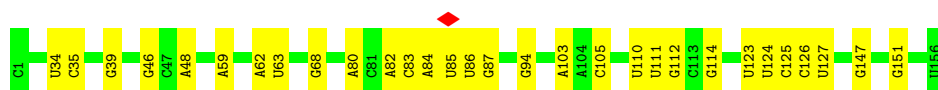
- Molecule 20: 5S rRNA [Homo sapiens]

Chain L7:  90% 10%




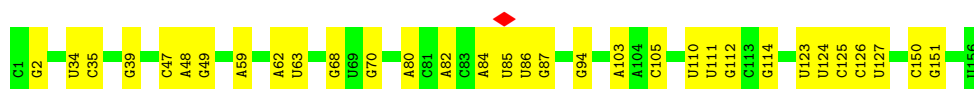
- Molecule 21: 5.8S rRNA [Homo sapiens]

Chain 18:  81% 19%



- Molecule 21: 5.8S rRNA [Homo sapiens]

Chain L8:  79% 21%



- Molecule 22: 60S ribosomal protein L8

Chain 1A:  95% 5%



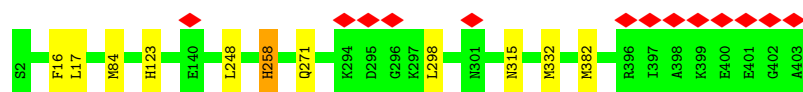
- Molecule 22: 60S ribosomal protein L8

Chain LA:  96%



- Molecule 23: Large ribosomal subunit protein uL3

Chain 1B:  97%



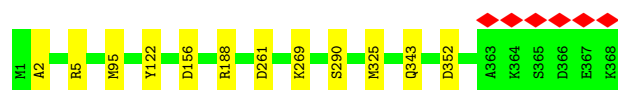
- Molecule 23: Large ribosomal subunit protein uL3



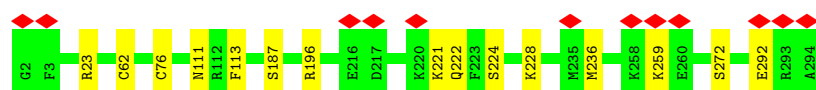
- Molecule 24: 60S ribosomal protein L4



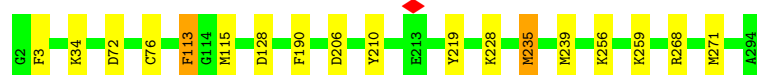
- Molecule 24: 60S ribosomal protein L4



- Molecule 25: Large ribosomal subunit protein uL18



- Molecule 25: Large ribosomal subunit protein uL18

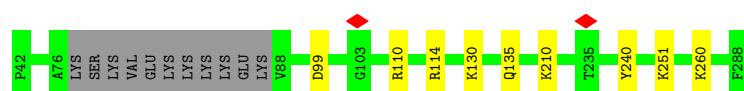


- Molecule 26: Large ribosomal subunit protein eL6



- Molecule 26: Large ribosomal subunit protein eL6

Chain LE:  92%



- Molecule 27: 60S ribosomal protein L7

Chain IF:  99%



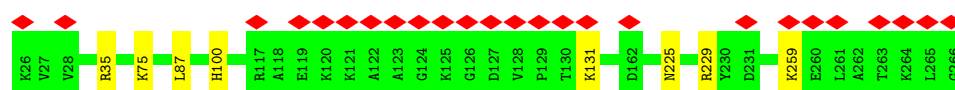
- Molecule 27: 60S ribosomal protein L7

Chain LF:  97%



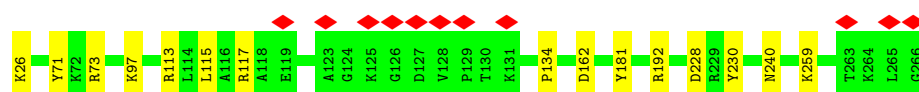
- Molecule 28: 60S ribosomal protein L7a

Chain IG:  10%  97%



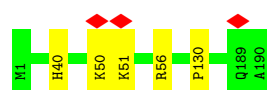
- Molecule 28: 60S ribosomal protein L7a

Chain LG:  5%  94%  6%



- Molecule 29: 60S ribosomal protein L9

Chain IH:  97%



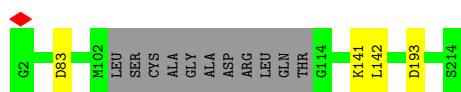
- Molecule 29: 60S ribosomal protein L9

Chain LH:  96%



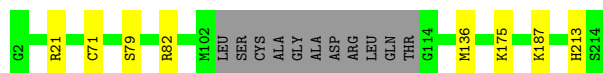
- Molecule 30: Ribosomal protein uL16-like

Chain II:  93% • 5%



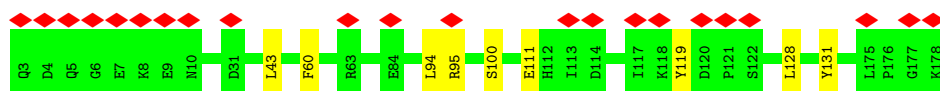
- Molecule 30: Ribosomal protein uL16-like

Chain LI:  91% • 5%



- Molecule 31: 60S ribosomal protein L11

Chain LJ:  13% 95% 5%



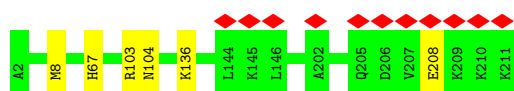
- Molecule 31: 60S ribosomal protein L11

Chain LJ:  5% 94% 6%



- Molecule 32: Large ribosomal subunit protein eL13

Chain IL:  5% 97% •



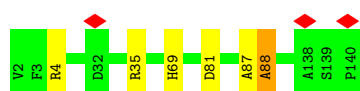
- Molecule 32: Large ribosomal subunit protein eL13

Chain LL:  5% 97% •



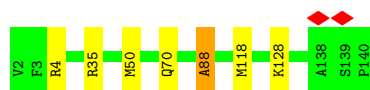
- Molecule 33: 60S ribosomal protein L14

Chain LM:  5% 96% • •



- Molecule 33: 60S ribosomal protein L14

Chain LM:  95%



- Molecule 34: 60S ribosomal protein L15

Chain LN:  97%



- Molecule 34: 60S ribosomal protein L15

Chain LN:  97%



- Molecule 35: 60S ribosomal protein L13a

Chain IO:  97%



- Molecule 35: 60S ribosomal protein L13a

Chain LO:  98%



- Molecule 36: 60S ribosomal protein L17

Chain IP:  94% 6%



- Molecule 36: 60S ribosomal protein L17

Chain LP:  95% 5%



- Molecule 37: 60S ribosomal protein L18

Chain IQ:  97%



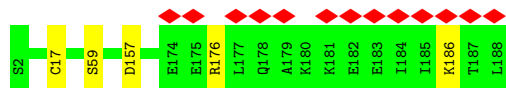
- Molecule 37: 60S ribosomal protein L18

Chain LQ:  96%



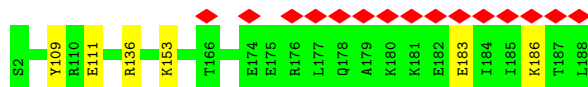
- Molecule 38: 60S ribosomal protein L19

Chain LR:  97%



- Molecule 38: 60S ribosomal protein L19

Chain LR:  97%



- Molecule 39: 60S ribosomal protein L18a

Chain LS:  98%



- Molecule 39: 60S ribosomal protein L18a

Chain LS:  96%



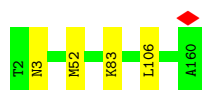
- Molecule 40: 60S ribosomal protein L21

Chain IT:  97%

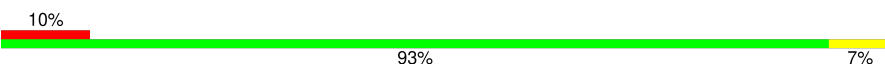


- Molecule 40: 60S ribosomal protein L21

Chain LT:  97%



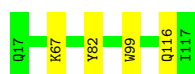
- Molecule 41: Heparin-binding protein HBp15

Chain IU:  93% 7%



- Molecule 41: Heparin-binding protein HBp15

Chain LU:  96%



- Molecule 42: 60S ribosomal protein L23

Chain IV:  97%



- Molecule 42: 60S ribosomal protein L23

Chain LV:  98%



- Molecule 43: 60S ribosomal protein L23a

Chain IX:  97%



- Molecule 43: 60S ribosomal protein L23a

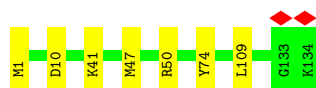
Chain LX:  96%



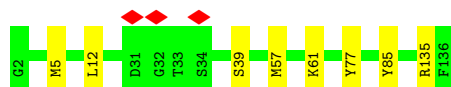
- Molecule 44: 60S ribosomal protein L26



- Molecule 44: 60S ribosomal protein L26



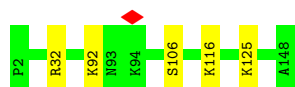
- Molecule 45: 60S ribosomal protein L27



- Molecule 45: 60S ribosomal protein L27



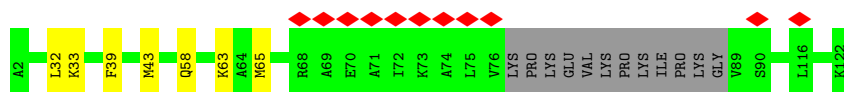
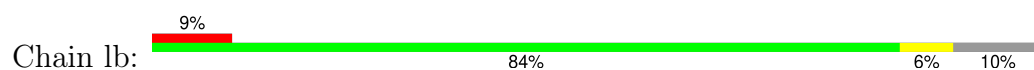
- Molecule 46: 60S ribosomal protein L27a



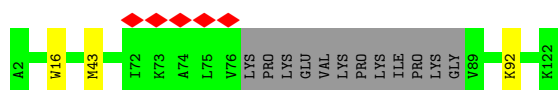
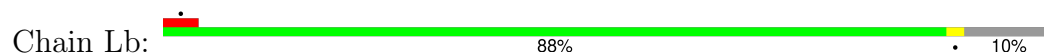
- Molecule 46: 60S ribosomal protein L27a



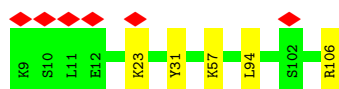
- Molecule 47: Large ribosomal subunit protein eL29



- Molecule 47: Large ribosomal subunit protein eL29



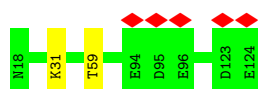
- Molecule 48: 60S ribosomal protein L30



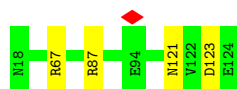
- Molecule 48: 60S ribosomal protein L30



- Molecule 49: 60S ribosomal protein L31



- Molecule 49: 60S ribosomal protein L31

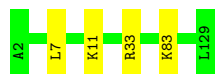


- Molecule 50: 60S ribosomal protein L32



- Molecule 50: 60S ribosomal protein L32

Chain Le:  97%



- Molecule 51: 60S ribosomal protein L35a

Chain lf:  97%



- Molecule 51: 60S ribosomal protein L35a

Chain Lf:  98%



- Molecule 52: 60S ribosomal protein L34

Chain lg:  96%



- Molecule 52: 60S ribosomal protein L34

Chain Lg:  99%



- Molecule 53: 60S ribosomal protein L35

Chain lh:  97%



- Molecule 53: 60S ribosomal protein L35

Chain Lh:  96%



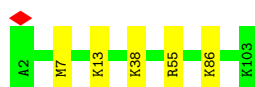
- Molecule 54: 60S ribosomal protein L36

Chain li:  100%




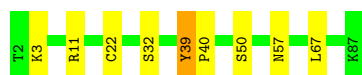
- Molecule 54: 60S ribosomal protein L36

Chain Li:  95% 5%



- Molecule 55: 60S ribosomal protein L37

Chain lj:  90% 9%



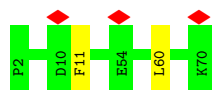
- Molecule 55: 60S ribosomal protein L37

Chain Lj:  95% 5%



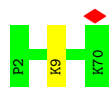
- Molecule 56: 60S ribosomal protein L38

Chain lk:  97%



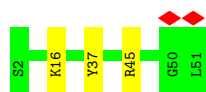
- Molecule 56: 60S ribosomal protein L38

Chain Lk:  99%



- Molecule 57: 60S ribosomal protein L39

Chain ll:  94% 6%



- Molecule 57: 60S ribosomal protein L39

Chain Ll: 98%



- Molecule 58: Large ribosomal subunit protein eL40

Chain lm: 92%



- Molecule 58: Large ribosomal subunit protein eL40

Chain Lm: 100%

There are no outlier residues recorded for this chain.

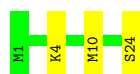
- Molecule 59: 60S ribosomal protein L41

Chain ln: 96%



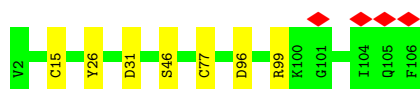
- Molecule 59: 60S ribosomal protein L41

Chain Ln: 88%



- Molecule 60: 60S ribosomal protein L36a

Chain lo: 93%

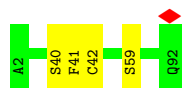


- Molecule 60: 60S ribosomal protein L36a

Chain Lo: 96%



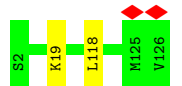
- Molecule 61: 60S ribosomal protein L37a



- Molecule 61: 60S ribosomal protein L37a



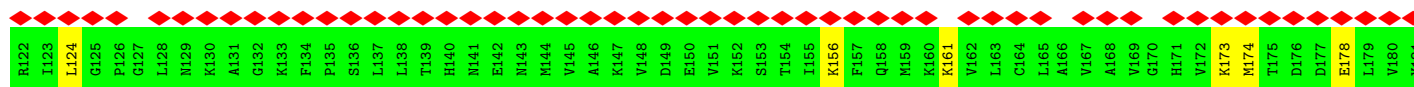
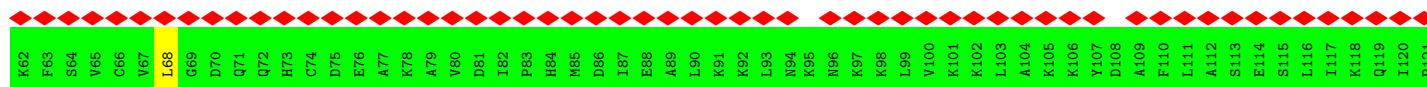
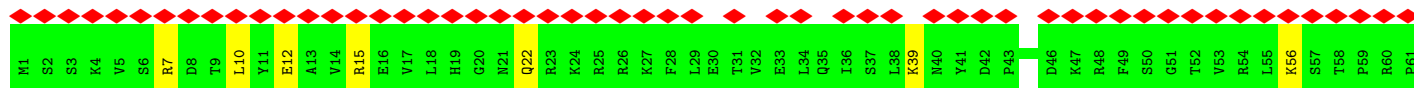
- Molecule 62: 60S ribosomal protein L28

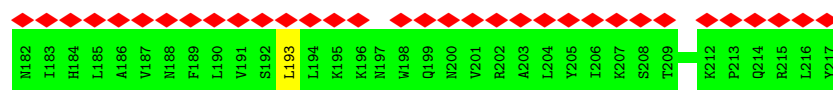


- Molecule 62: 60S ribosomal protein L28

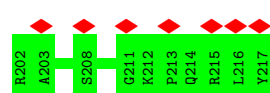
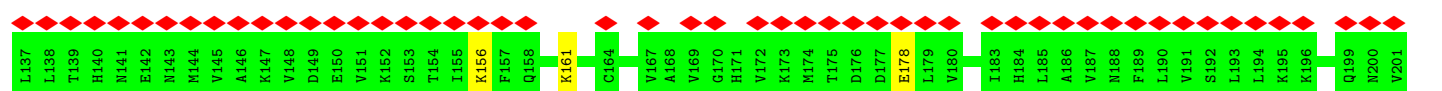
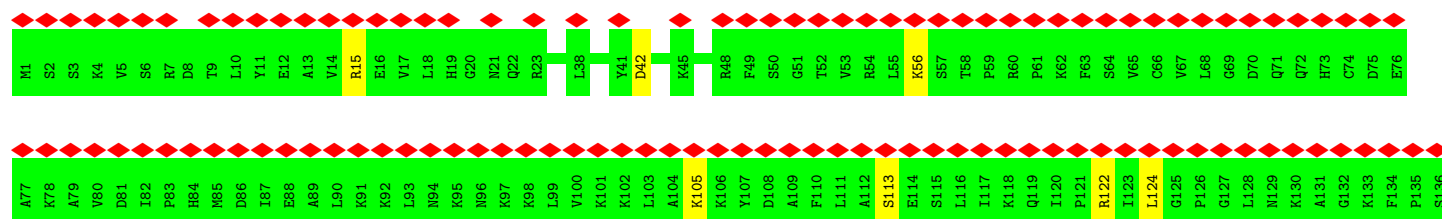
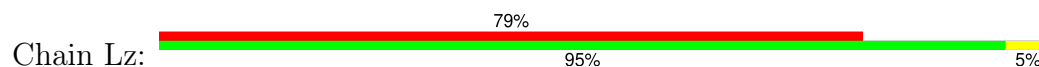


- Molecule 63: 60S ribosomal protein L10a

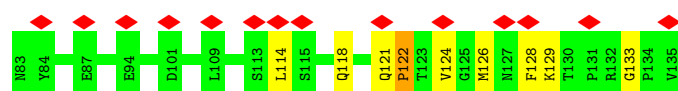
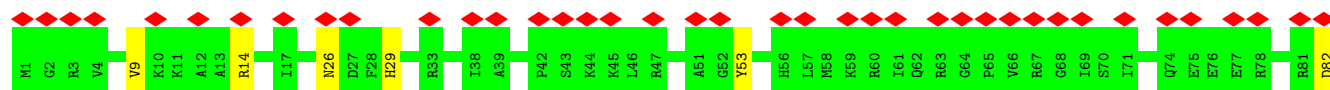
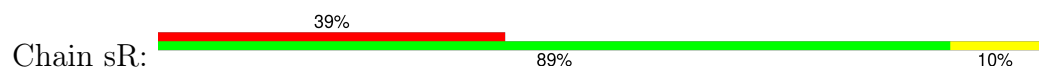




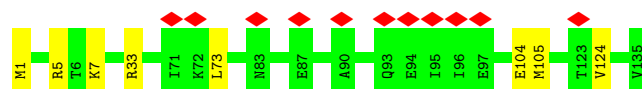
- Molecule 63: 60S ribosomal protein L10a



- Molecule 64: 40S ribosomal protein S17



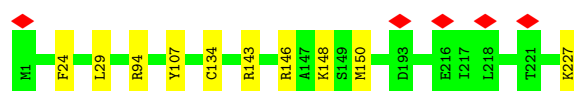
- Molecule 64: 40S ribosomal protein S17



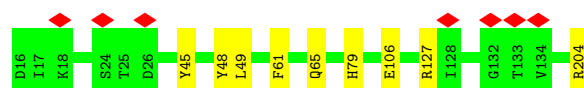
- Molecule 65: Small ribosomal subunit protein uS3



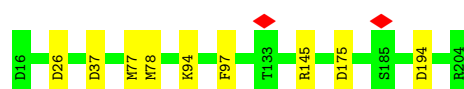
- Molecule 65: Small ribosomal subunit protein uS3



- Molecule 66: 40S ribosomal protein S5



- Molecule 66: 40S ribosomal protein S5



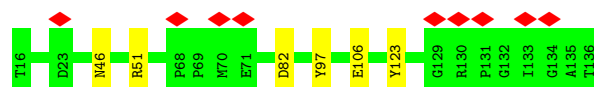
- Molecule 67: 40S ribosomal protein S10



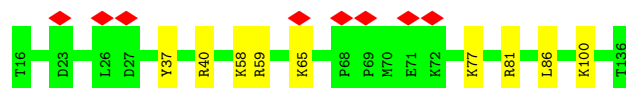
- Molecule 67: 40S ribosomal protein S10



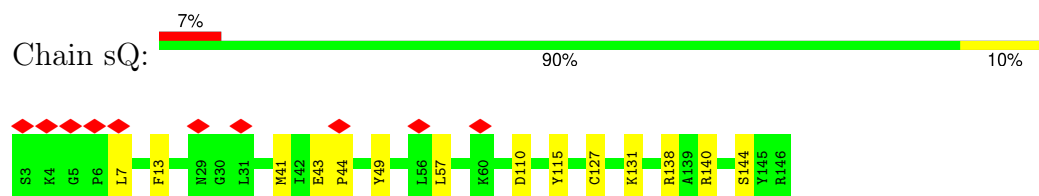
- Molecule 68: Small ribosomal subunit protein uS19



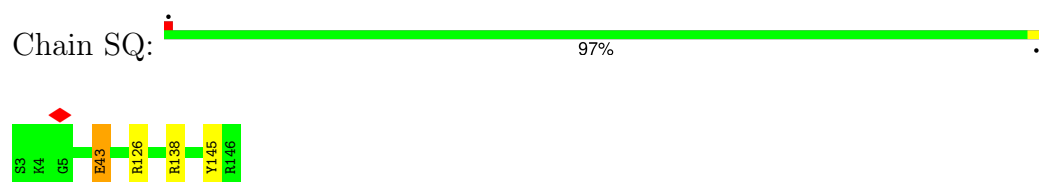
- Molecule 68: Small ribosomal subunit protein uS19



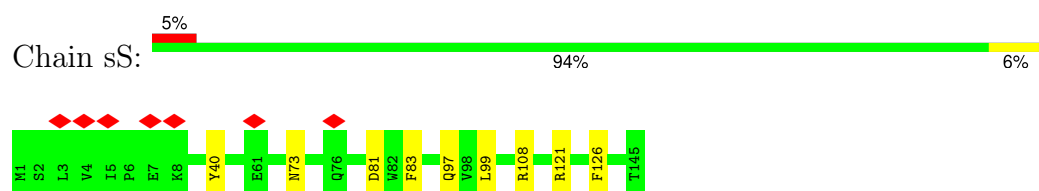
- Molecule 69: Small ribosomal subunit protein uS9



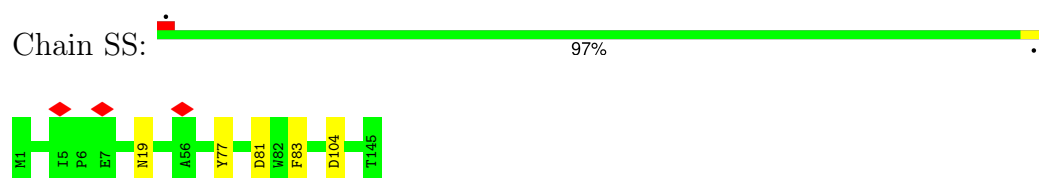
- Molecule 69: Small ribosomal subunit protein uS9



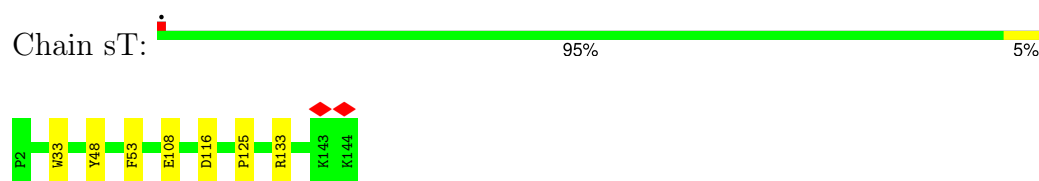
- Molecule 70: 40S ribosomal protein S18



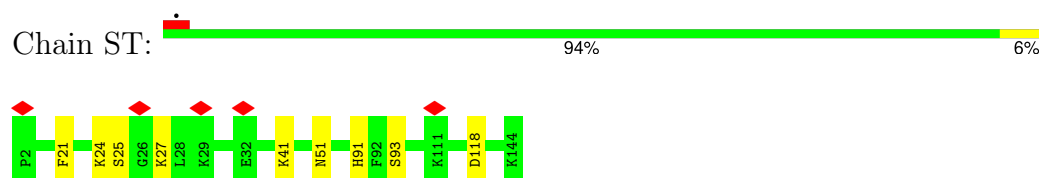
- Molecule 70: 40S ribosomal protein S18



- Molecule 71: 40S ribosomal protein S19



- Molecule 71: 40S ribosomal protein S19



- Molecule 72: 40S ribosomal protein S20

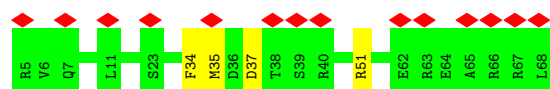




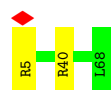
- Molecule 72: 40S ribosomal protein S20



- Molecule 73: 40S ribosomal protein S28



- Molecule 73: 40S ribosomal protein S28



- Molecule 74: 40S ribosomal protein S29

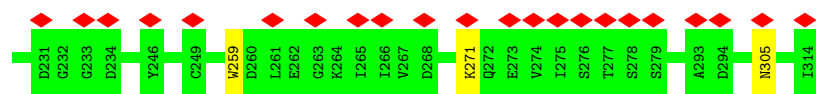


- Molecule 74: 40S ribosomal protein S29

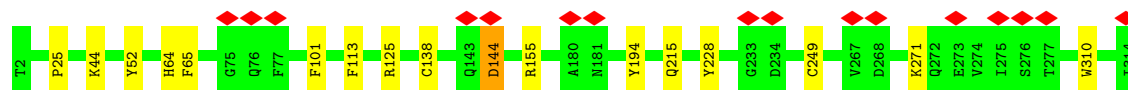


- Molecule 75: Receptor of activated protein C kinase 1

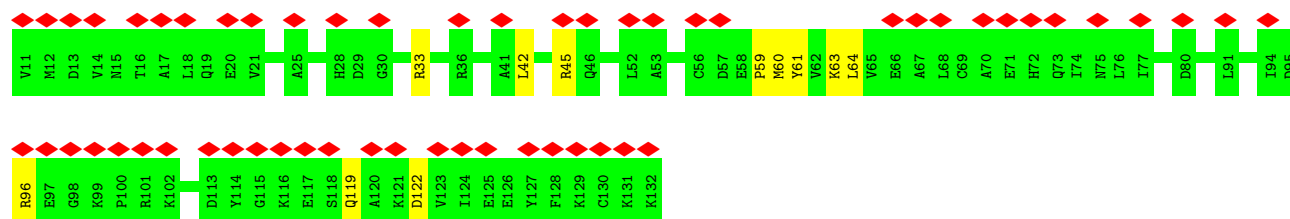




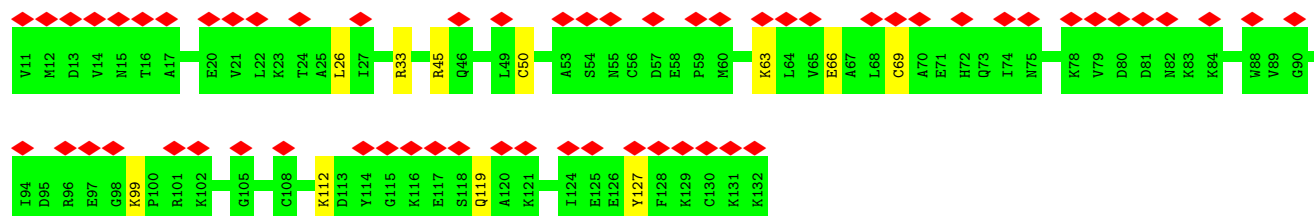
- Molecule 75: Receptor of activated protein C kinase 1



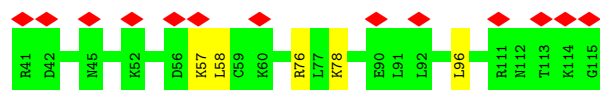
- Molecule 76: Small ribosomal subunit protein eS12



- Molecule 76: Small ribosomal subunit protein eS12



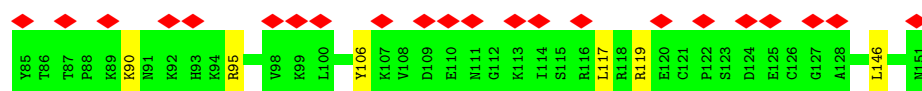
- Molecule 77: Small ribosomal subunit protein eS25



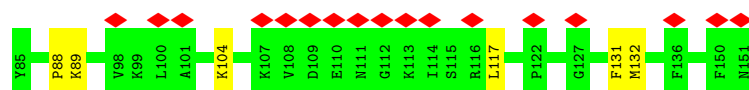
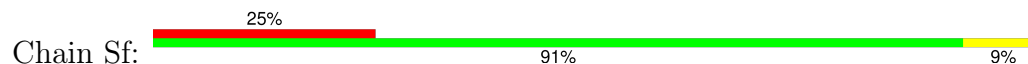
- Molecule 77: Small ribosomal subunit protein eS25



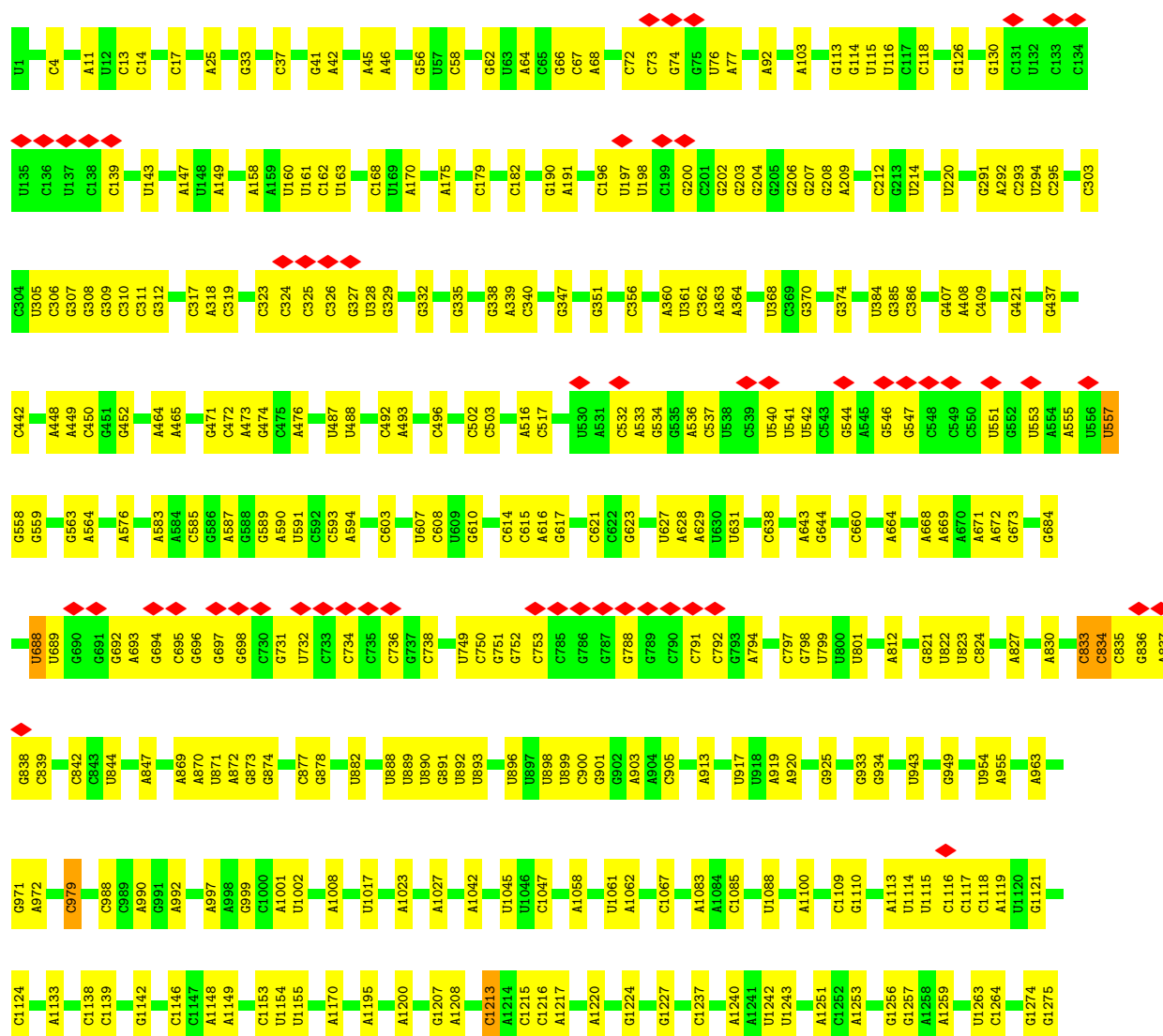
- Molecule 78: Ubiquitin-40S ribosomal protein S27a

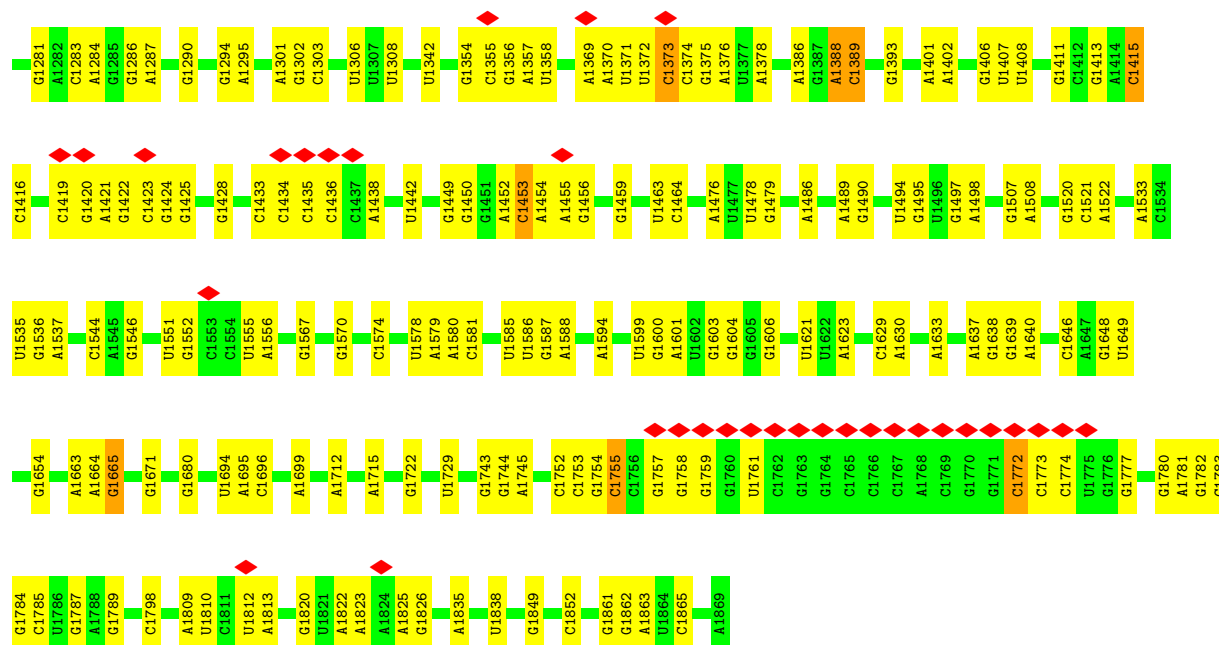


- Molecule 78: Ubiquitin-40S ribosomal protein S27a

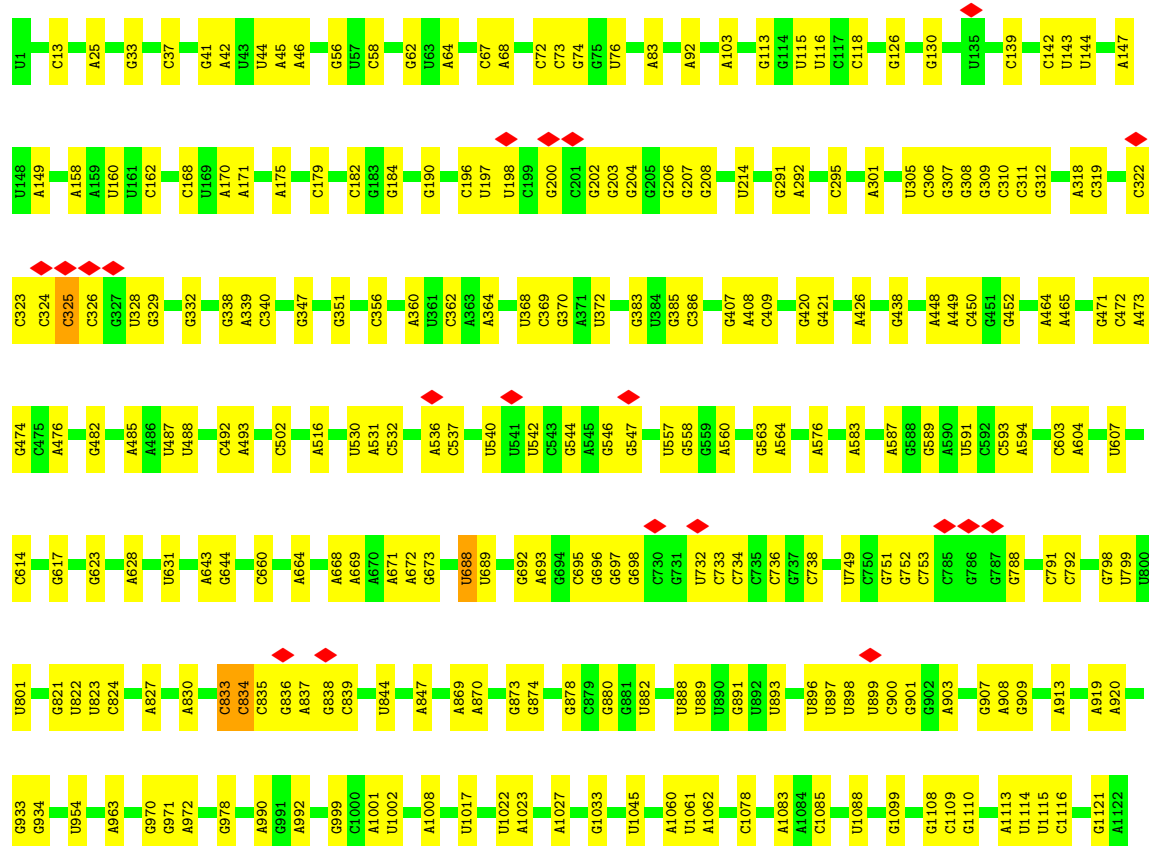
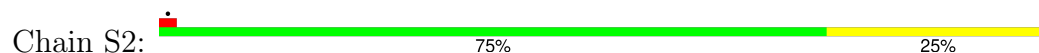


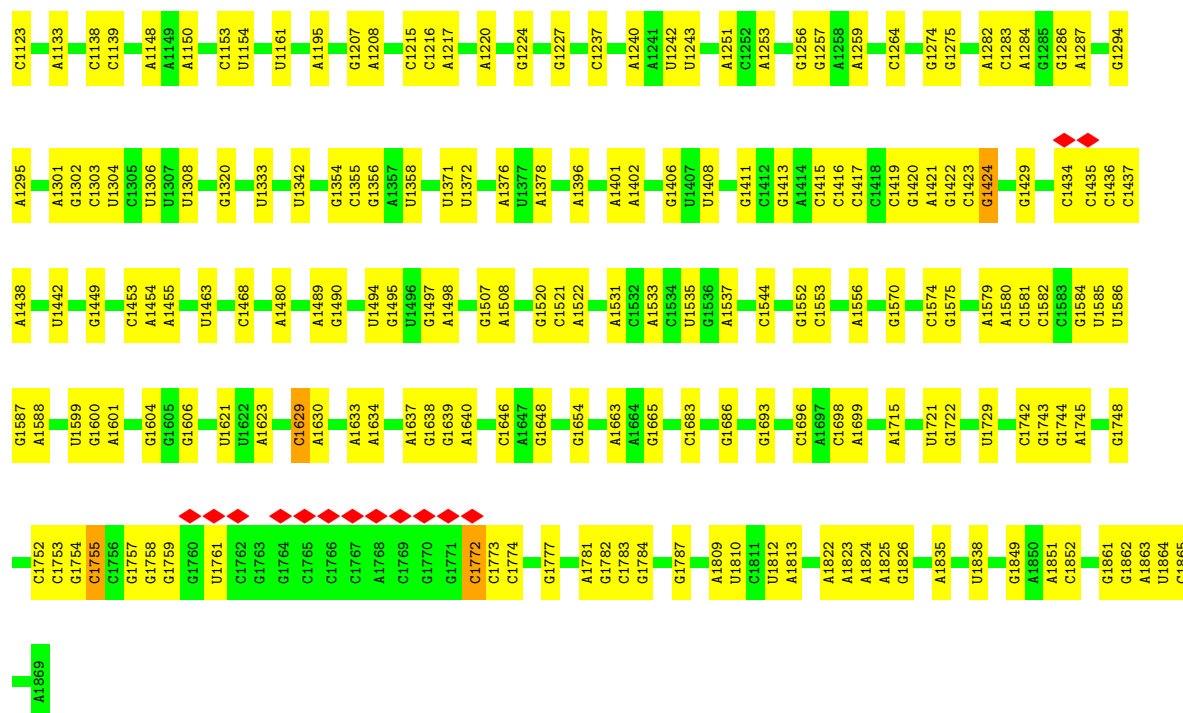
- Molecule 79: 18S rRNA [Homo sapiens]



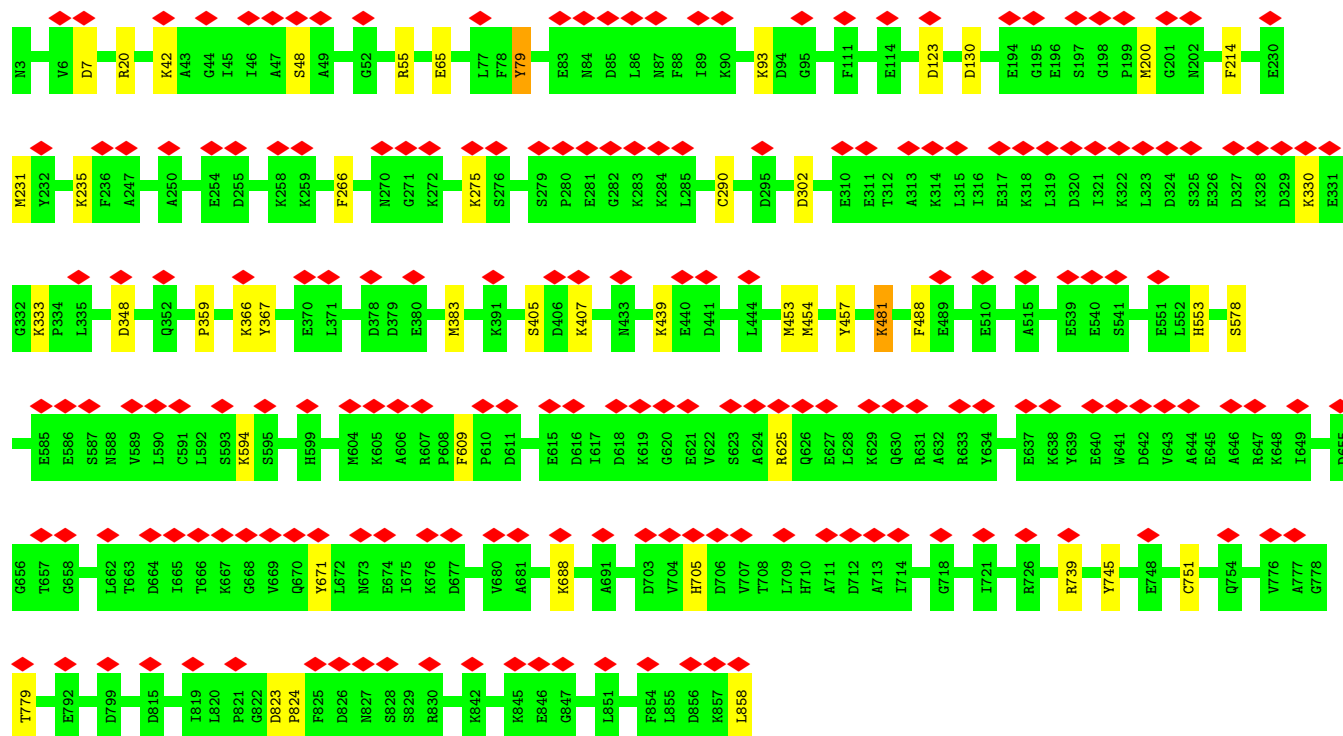


• Molecule 79: 18S rRNA [Homo sapiens]





• Molecule 80: Elongation factor 2

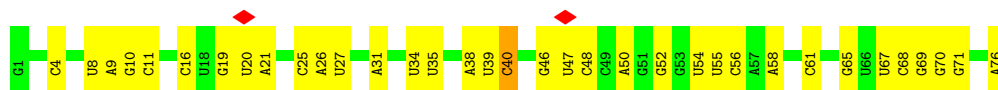


• Molecule 81: A/P site tRNA [Homo sapiens]

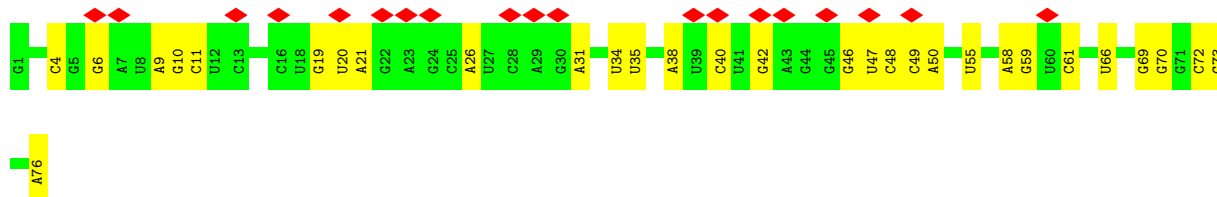




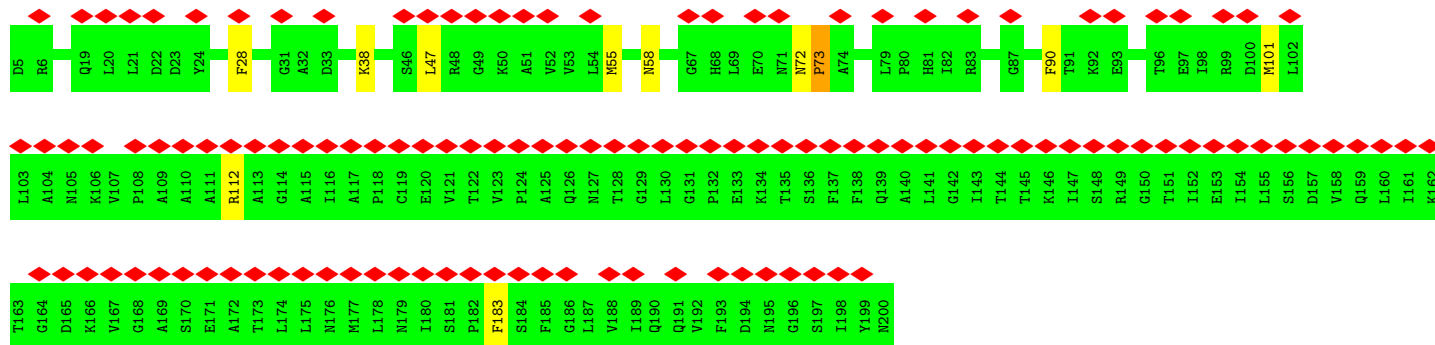
- Molecule 82: P/E site tRNA [Homo sapiens]



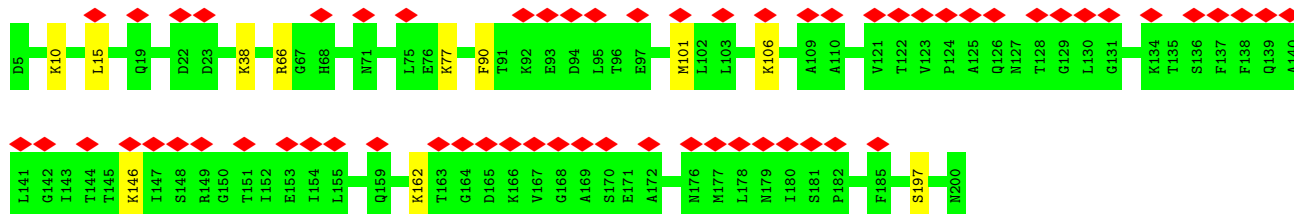
- Molecule 82: P/E site tRNA [Homo sapiens]



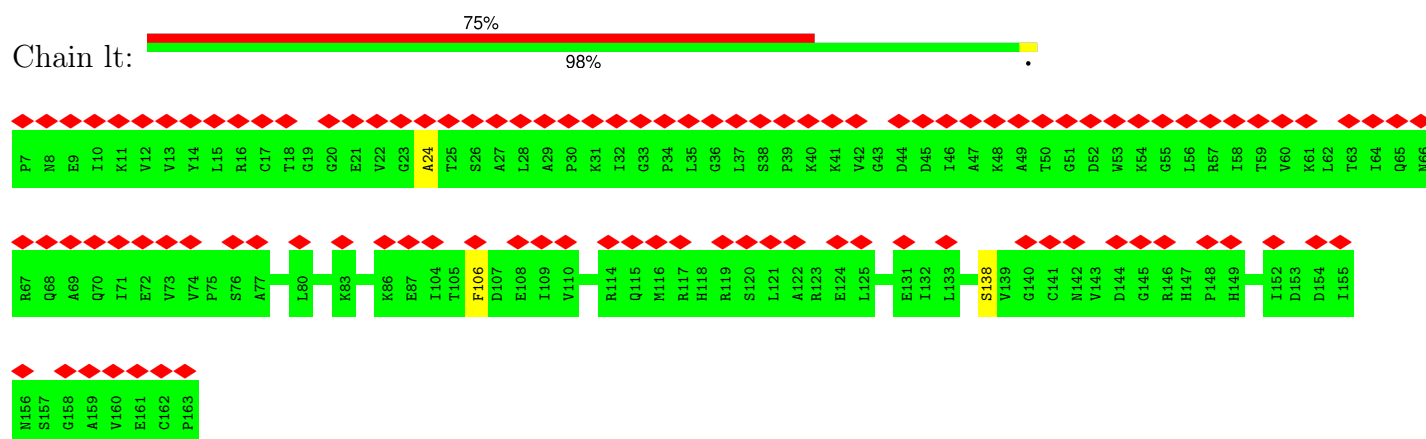
- Molecule 83: 60S acidic ribosomal protein P0



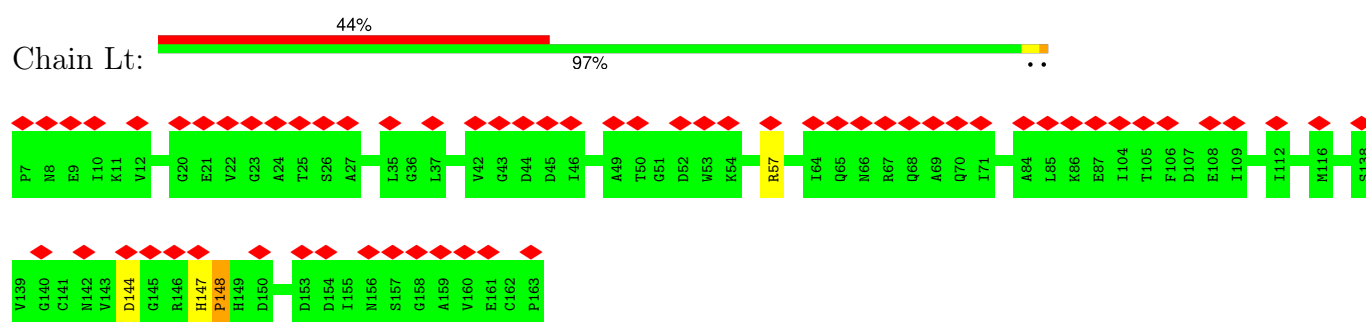
- Molecule 83: 60S acidic ribosomal protein P0



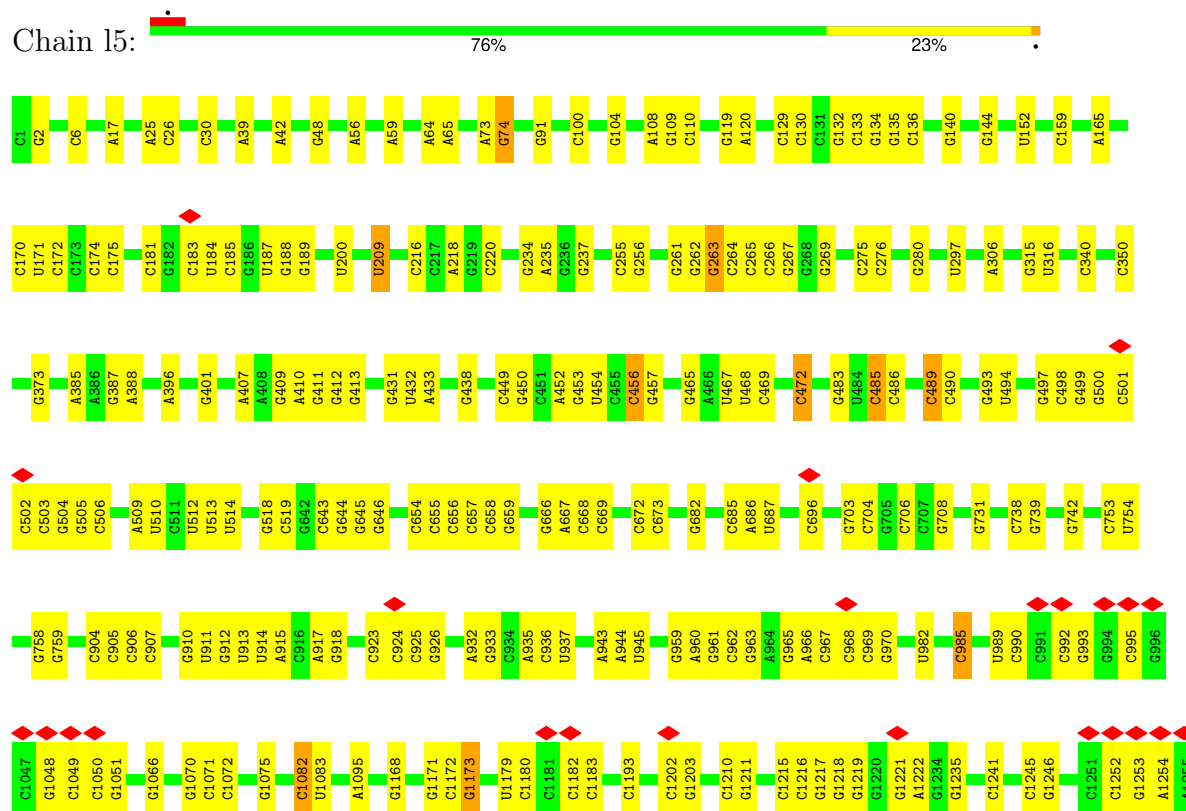
- Molecule 84: 60S ribosomal protein L12 [Homo sapiens]



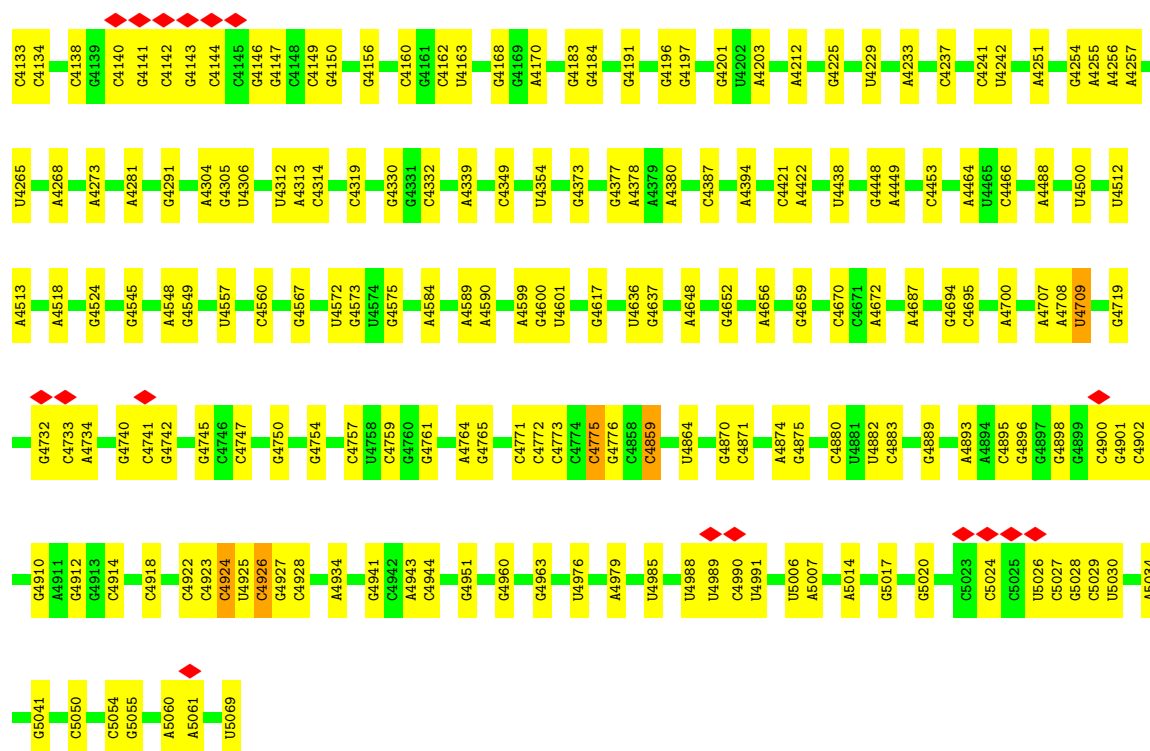
• Molecule 84: 60S ribosomal protein L12 [Homo sapiens]



• Molecule 85: 28S rRNA [Homo sapiens]

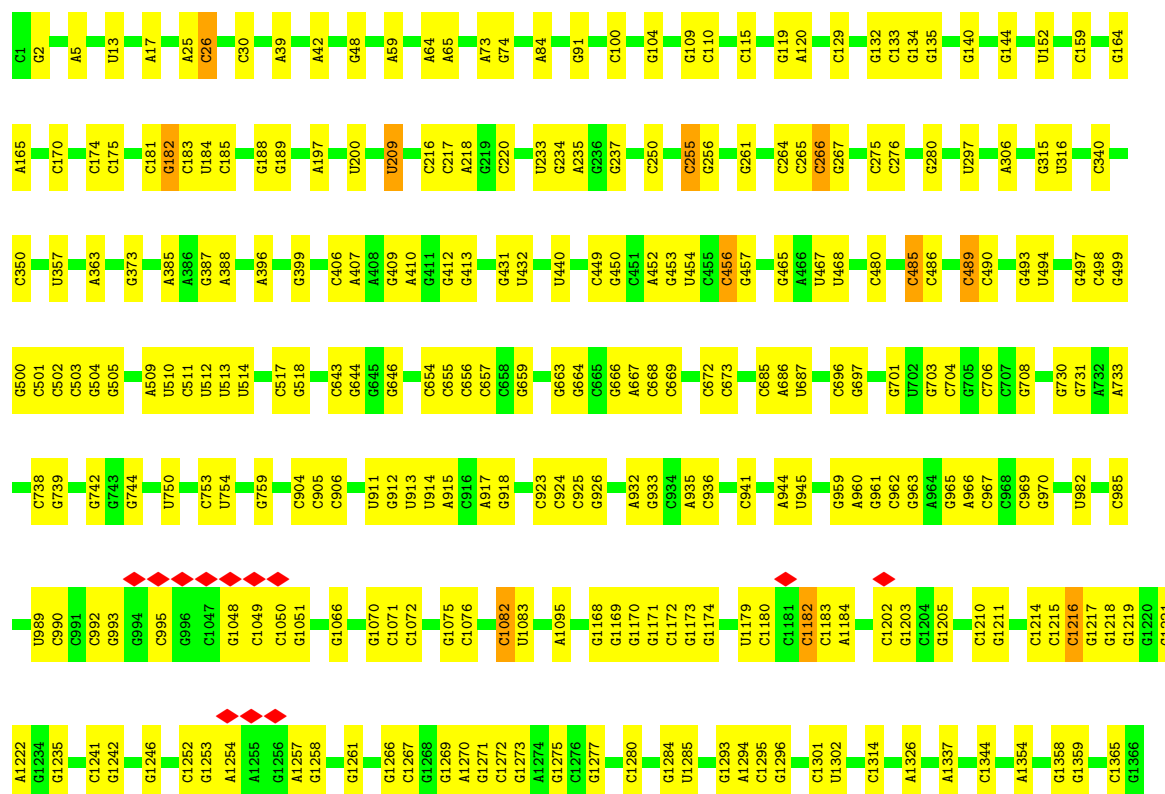


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	G4043	U2900	A3648	U2900	C2665	A2453	C2327	A2065	G1810	G1654	G1425	G1275
	G4044	U2901	A3648	U2901	C2666	A2453	C2328	A2066	G1810	G1654	G1425	G1275
	G4045	U2902	A3648	U2902	C2667	A2453	C2329	A2067	G1810	G1654	G1425	G1275
	G4046	U2903	A3648	U2903	C2668	A2453	C2330	A2068	G1810	G1654	G1425	G1275
		U2904	A3648	U2904	C2669	A2453	C2331	A2069	G1810	G1654	G1425	G1275
		U2905	A3648	U2905	C2670	A2453	C2332	A2070	G1810	G1654	G1425	G1275
		U2906	A3648	U2906	C2671	A2453	C2333	A2071	G1810	G1654	G1425	G1275
		U2907	A3648	U2907	C2672	A2453	C2334	A2072	G1810	G1654	G1425	G1275
		U2908	A3648	U2908	C2673	A2453	C2335	A2073	G1810	G1654	G1425	G1275
		U2909	A3648	U2909	C2674	A2453	C2336	A2074	G1810	G1654	G1425	G1275
		U2910	A3648	U2910	C2675	A2453	C2337	A2075	G1810	G1654	G1425	G1275
		U2911	A3648	U2911	C2676	A2453	C2338	A2076	G1810	G1654	G1425	G1275
		U2912	A3648	U2912	C2677	A2453	C2339	A2077	G1810	G1654	G1425	G1275
		U2913	A3648	U2913	C2678	A2453	C2340	A2078	G1810	G1654	G14	

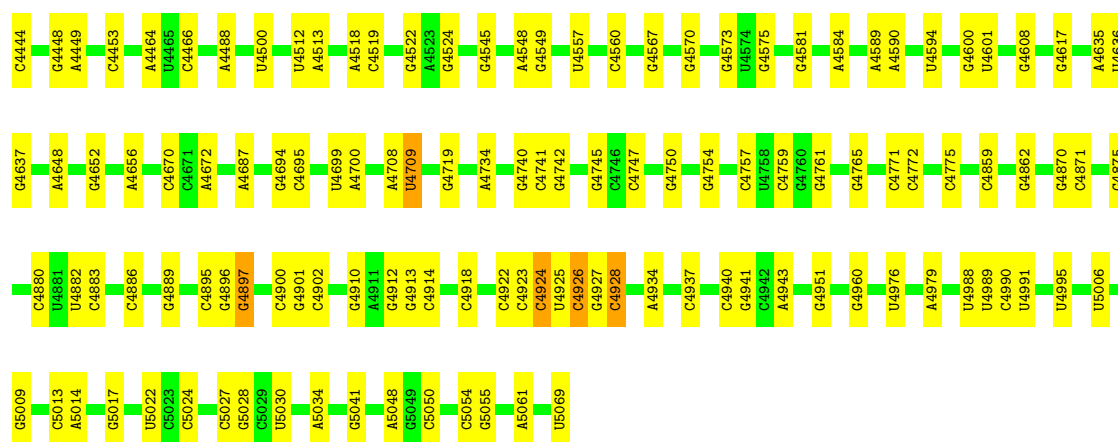


• Molecule 85: 28S rRNA [Homo sapiens]

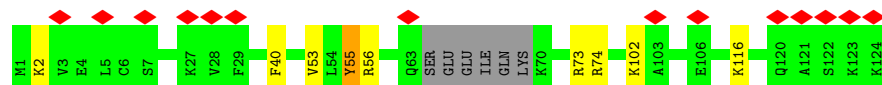
Chain L5: 76% 24% .







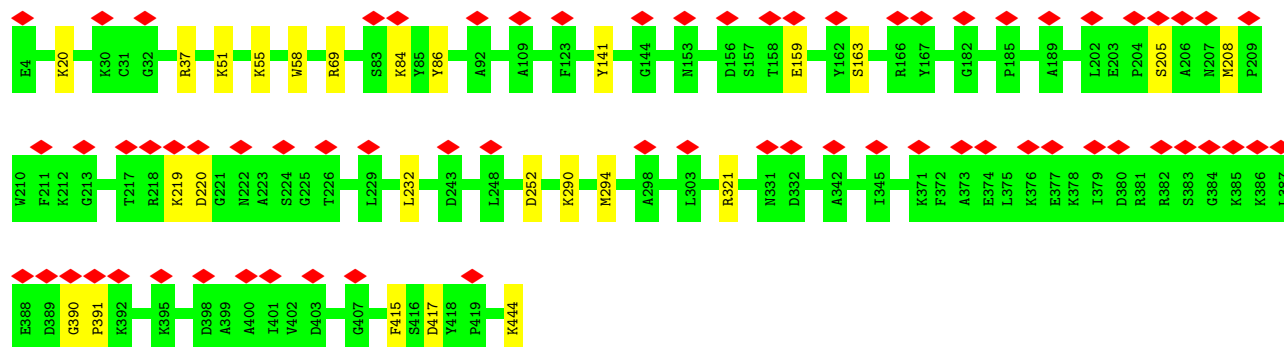
• Molecule 86: Ribosomal protein L24



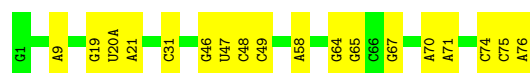
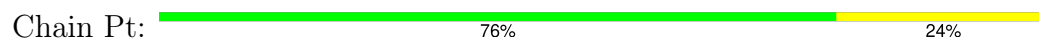
• Molecule 87: A/T site tRNA [Homo sapiens]



• Molecule 88: Putative elongation factor 1-alpha-like 3



• Molecule 89: P site tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	9137	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.691	Depositor
Minimum map value	-0.099	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.033	Depositor
Recommended contour level	0.099	Depositor
Map size (\AA)	640.8, 640.8, 640.8	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.068, 1.068, 1.068	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SEP, ZN, 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	cH	0.28	0/977	0.62	0/1306
2	SE	0.28	0/2118	0.55	0/2849
2	sE	0.28	0/2118	0.57	1/2849 (0.0%)
3	SI	0.27	0/1715	0.59	0/2287
3	sI	0.33	1/1715 (0.1%)	0.60	0/2287
4	SL	0.27	0/1268	0.57	0/1696
4	sL	0.34	0/1268	0.59	0/1696
5	SX	0.26	0/1116	0.54	0/1490
5	sX	0.30	0/1116	0.56	0/1490
6	SG	0.38	2/1946 (0.1%)	0.77	2/2590 (0.1%)
6	sG	0.44	2/1946 (0.1%)	0.59	0/2590
7	SJ	0.29	0/1550	0.59	0/2069
7	sJ	0.28	0/1550	0.59	0/2069
8	SY	0.83	3/1083 (0.3%)	0.97	6/1438 (0.4%)
8	sY	0.56	2/1083 (0.2%)	0.68	0/1438
9	Se	0.27	0/465	0.57	0/612
9	se	0.31	0/465	0.67	0/612
10	SA	0.34	0/1778	0.56	0/2416
10	sA	0.34	0/1778	0.61	1/2416 (0.0%)
11	SB	0.41	2/1765 (0.1%)	0.61	3/2362 (0.1%)
11	sB	0.38	1/1765 (0.1%)	0.58	0/2362
12	SH	0.33	0/1519	0.57	0/2033
12	sH	0.30	0/1519	0.61	1/2033 (0.0%)
13	SV	0.37	0/643	0.73	2/860 (0.2%)
13	sV	0.32	0/643	0.64	0/860
14	Sa	0.35	0/836	0.64	1/1121 (0.1%)
14	sa	0.36	0/836	0.62	0/1121
15	SC	0.31	0/1762	0.54	0/2381
15	sC	0.43	2/1762 (0.1%)	0.59	2/2381 (0.1%)
16	SN	0.46	2/1232 (0.2%)	0.56	0/1656
16	sN	0.32	0/1232	0.55	0/1656
17	SO	0.29	0/1062	0.63	1/1425 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	sO	0.34	0/1062	0.63	1/1425 (0.1%)
18	SW	0.47	2/1051 (0.2%)	0.65	2/1406 (0.1%)
18	sW	0.34	0/1051	0.62	0/1406
19	Sb	0.52	1/665 (0.2%)	0.65	1/891 (0.1%)
19	sb	0.44	1/665 (0.2%)	0.89	3/891 (0.3%)
20	L7	0.38	0/2861	0.78	0/4459
20	l7	0.43	0/2861	0.78	0/4459
21	L8	0.39	0/3701	0.78	0/5766
21	l8	0.43	0/3701	0.77	0/5766
22	LA	0.38	1/1936 (0.1%)	0.62	1/2596 (0.0%)
22	lA	0.35	0/1936	0.62	1/2596 (0.0%)
23	LB	0.30	0/3306	0.55	0/4424
23	lB	0.33	0/3306	0.56	0/4424
24	LC	0.29	0/2981	0.56	1/4002 (0.0%)
24	lC	0.33	1/2981 (0.0%)	0.57	1/4002 (0.0%)
25	LD	0.42	2/2428 (0.1%)	0.65	3/3252 (0.1%)
25	lD	0.39	1/2428 (0.0%)	0.55	0/3252
26	LE	0.29	0/1942	0.57	0/2606
26	lE	0.30	0/1942	0.56	0/2606
27	LF	0.35	0/1905	0.54	0/2539
27	lF	0.33	0/1905	0.53	0/2539
28	LG	0.33	0/1960	0.59	2/2637 (0.1%)
28	lG	0.32	0/1960	0.57	0/2637
29	LH	0.30	0/1537	0.55	0/2066
29	lH	0.34	0/1537	0.58	0/2066
30	LI	0.32	0/1673	0.57	0/2233
30	lI	0.34	0/1673	0.59	1/2233 (0.0%)
31	LJ	0.41	2/1433 (0.1%)	0.65	1/1915 (0.1%)
31	lJ	0.33	0/1433	0.64	0/1915
32	LL	0.30	0/1732	0.60	0/2315
32	lL	0.31	0/1732	0.60	0/2315
33	LM	0.28	0/1161	0.55	0/1554
33	lM	0.31	0/1161	0.56	0/1554
34	LN	0.31	0/1746	0.59	0/2338
34	lN	0.34	0/1746	0.57	0/2338
35	LO	0.29	0/1682	0.53	0/2250
35	lO	0.33	0/1682	0.55	0/2250
36	LP	0.31	0/1268	0.55	0/1701
36	lP	0.33	0/1268	0.57	0/1701
37	LQ	0.33	1/1537 (0.1%)	0.59	0/2052
37	lQ	0.33	0/1537	0.60	0/2052
38	LR	0.28	0/1582	0.59	0/2091
38	lR	0.28	0/1582	0.61	0/2091

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
39	LS	0.33	0/1493	0.58	0/2003
39	IS	0.34	0/1493	0.57	0/2003
40	LT	0.31	0/1326	0.57	0/1770
40	IT	0.33	0/1326	0.56	0/1770
41	LU	0.32	0/839	0.62	0/1126
41	IU	0.36	0/839	0.61	0/1126
42	LV	0.31	0/993	0.56	0/1332
42	IV	0.33	0/993	0.57	0/1332
43	LX	0.36	0/1002	0.60	1/1345 (0.1%)
43	IX	0.31	0/1002	0.58	0/1345
44	LY	0.30	0/1132	0.57	0/1504
44	IY	0.32	0/1132	0.57	0/1504
45	LZ	0.35	0/1130	0.60	0/1507
45	IZ	0.35	0/1130	0.58	0/1507
46	La	0.43	2/1191 (0.2%)	0.57	0/1591
46	la	0.33	0/1191	0.56	0/1591
47	Lb	0.31	0/889	0.55	0/1175
47	lb	0.27	0/889	0.55	0/1175
48	Lc	0.31	0/774	0.60	0/1038
48	lc	0.31	0/774	0.58	0/1038
49	Ld	0.30	0/903	0.58	0/1216
49	ld	0.33	0/903	0.59	0/1216
50	Le	0.30	0/1071	0.59	0/1429
50	le	0.32	0/1071	0.60	1/1429 (0.1%)
51	Lf	0.30	0/895	0.63	1/1198 (0.1%)
51	lf	0.34	0/895	0.58	0/1198
52	Lg	0.30	0/916	0.59	0/1220
52	lg	0.31	0/916	0.60	0/1220
53	Lh	0.29	0/1023	0.56	0/1351
53	lh	0.31	0/1023	0.56	0/1351
54	Li	0.32	0/843	0.65	0/1115
54	li	0.29	0/843	0.60	0/1115
55	Lj	0.31	0/720	0.61	0/952
55	lj	0.51	2/720 (0.3%)	0.92	3/952 (0.3%)
56	Lk	0.32	0/575	0.62	0/761
56	lk	0.30	0/575	0.57	0/761
57	Ll	0.28	0/454	0.59	0/599
57	ll	0.29	0/454	0.58	0/599
58	Lm	0.28	0/435	0.58	0/575
58	lm	0.45	1/435 (0.2%)	0.72	2/575 (0.3%)
59	Ln	0.25	0/231	0.77	0/294
59	ln	0.26	0/231	0.71	0/294
60	Lo	0.31	0/876	0.59	0/1156

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
60	lo	0.32	0/876	0.55	0/1156
61	Lp	0.31	0/718	0.52	0/953
61	lp	0.33	0/718	0.57	0/953
62	Lr	0.29	0/1017	0.58	0/1364
62	lr	0.30	0/1017	0.57	0/1364
63	Lz	0.26	0/1769	0.57	0/2371
63	lz	0.25	0/1769	0.55	1/2371 (0.0%)
64	SR	0.39	1/1105 (0.1%)	0.66	0/1484
64	sR	0.61	4/1105 (0.4%)	1.00	6/1484 (0.4%)
65	SD	0.36	0/1793	0.61	1/2414 (0.0%)
65	sD	0.75	5/1793 (0.3%)	1.01	8/2414 (0.3%)
66	SF	0.27	0/1516	0.55	0/2037
66	sF	0.38	1/1516 (0.1%)	0.64	3/2037 (0.1%)
67	SK	0.64	2/851 (0.2%)	0.74	1/1147 (0.1%)
67	sK	0.48	0/851	0.88	2/1147 (0.2%)
68	SP	0.28	0/1003	0.61	1/1342 (0.1%)
68	sP	0.29	0/1003	0.60	1/1342 (0.1%)
69	SQ	0.27	0/1160	0.60	0/1553
69	sQ	0.39	1/1160 (0.1%)	0.73	2/1553 (0.1%)
70	SS	0.28	0/1216	0.60	0/1628
70	sS	0.29	0/1216	0.62	0/1628
71	ST	0.28	0/1131	0.57	0/1515
71	sT	0.36	1/1131 (0.1%)	0.63	1/1515 (0.1%)
72	SU	0.35	0/831	0.72	2/1115 (0.2%)
72	sU	0.78	4/831 (0.5%)	0.99	5/1115 (0.4%)
73	Sc	0.28	0/508	0.68	0/680
73	sc	0.33	0/508	0.71	0/680
74	Sd	0.33	0/470	0.57	0/623
74	sd	0.32	0/470	0.59	0/623
75	Sg	0.31	0/2493	0.56	1/3394 (0.0%)
75	sg	0.30	0/2493	0.59	1/3394 (0.0%)
76	SM	0.32	0/950	0.53	1/1275 (0.1%)
76	sM	0.28	0/950	0.54	1/1275 (0.1%)
77	SZ	0.58	1/604 (0.2%)	1.11	3/810 (0.4%)
77	sZ	0.32	0/604	0.68	0/810
78	Sf	0.38	0/560	0.74	2/745 (0.3%)
78	sf	0.51	1/560 (0.2%)	0.74	0/745
79	S2	0.30	0/41242	0.83	34/64255 (0.1%)
79	s2	0.39	1/41241 (0.0%)	0.84	44/64251 (0.1%)
80	cB	0.35	3/6734 (0.0%)	0.63	5/9094 (0.1%)
81	aP	0.27	0/1692	0.82	0/2634
82	Et	0.25	0/1778	0.86	0/2767
82	pE	0.34	0/1778	0.94	2/2767 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
83	Ls	0.30	0/1519	0.59	1/2052 (0.0%)
83	ls	0.49	3/1519 (0.2%)	0.73	3/2052 (0.1%)
84	Lt	0.63	1/1058 (0.1%)	0.83	5/1430 (0.3%)
84	lt	0.26	0/1058	0.57	0/1430
85	L5	0.41	0/89312	0.84	72/139287 (0.1%)
85	l5	0.44	0/89313	0.84	74/139291 (0.1%)
86	LW	0.88	5/979 (0.5%)	0.82	1/1295 (0.1%)
87	AT	0.22	0/1805	0.83	1/2809 (0.0%)
88	CF	0.55	5/3442 (0.1%)	0.79	9/4656 (0.2%)
89	Pt	0.27	0/1761	0.83	4/2741 (0.1%)
All	All	0.38	73/489910 (0.0%)	0.76	344/718287 (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
1	cH	0	1
5	SX	0	1
5	sX	0	1
12	SH	0	1
12	sH	0	1
22	LA	0	1
22	lA	0	1
23	LB	0	2
23	lB	0	3
31	LJ	0	1
31	lJ	0	1
33	LM	0	1
33	lM	0	2
35	LO	0	1
35	lO	0	1
51	Lf	0	1
51	lf	0	1
55	Lj	0	1
55	lj	0	1
64	sR	0	2
65	sD	0	1
66	SF	0	1
69	SQ	0	1
69	sQ	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
72	sU	0	1
77	SZ	0	1
All	All	0	31

The worst 5 of 73 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	SY	52	PRO	CG-CD	-20.19	0.84	1.50
88	CF	391	PRO	CG-CD	-18.80	0.88	1.50
84	Lt	148	PRO	CG-CD	-16.99	0.94	1.50
65	sD	194	PRO	CG-CD	-16.78	0.95	1.50
65	sD	194	PRO	N-CD	15.63	1.69	1.47

The worst 5 of 344 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	sD	194	PRO	CA-N-CD	-27.69	72.73	111.50
65	sD	193	ASP	C-N-CD	20.84	172.16	128.40
8	SY	52	PRO	CA-N-CD	-20.49	82.81	111.50
64	sR	122	PRO	CA-N-CD	-20.34	83.02	111.50
77	SZ	70	PRO	CA-N-CD	-20.06	83.42	111.50

There are no chirality outliers.

5 of 31 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	cH	51	GLN	Peptide
22	lA	13	GLY	Peptide
23	lB	16	PHE	Peptide
12	sH	15	LYS	Peptide
5	sX	126	ALA	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
1	cH	123/125 (98%)	106 (86%)	15 (12%)	2 (2%)	8	36
2	SE	260/262 (99%)	246 (95%)	14 (5%)	0	100	100
2	sE	260/262 (99%)	243 (94%)	17 (6%)	0	100	100
3	SI	204/206 (99%)	193 (95%)	11 (5%)	0	100	100
3	sI	204/206 (99%)	196 (96%)	8 (4%)	0	100	100
4	SL	151/153 (99%)	141 (93%)	10 (7%)	0	100	100
4	sL	151/153 (99%)	139 (92%)	12 (8%)	0	100	100
5	SX	139/141 (99%)	126 (91%)	13 (9%)	0	100	100
5	sX	139/141 (99%)	124 (89%)	14 (10%)	1 (1%)	19	52
6	SG	235/237 (99%)	222 (94%)	13 (6%)	0	100	100
6	sG	235/237 (99%)	224 (95%)	11 (5%)	0	100	100
7	SJ	183/185 (99%)	170 (93%)	13 (7%)	0	100	100
7	sJ	183/185 (99%)	175 (96%)	8 (4%)	0	100	100
8	SY	129/131 (98%)	121 (94%)	7 (5%)	1 (1%)	16	49
8	sY	129/131 (98%)	119 (92%)	10 (8%)	0	100	100
9	Se	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
9	se	56/58 (97%)	46 (82%)	10 (18%)	0	100	100
10	SA	219/221 (99%)	200 (91%)	19 (9%)	0	100	100
10	sA	219/221 (99%)	186 (85%)	33 (15%)	0	100	100
11	SB	212/214 (99%)	198 (93%)	14 (7%)	0	100	100
11	sB	212/214 (99%)	200 (94%)	12 (6%)	0	100	100
12	SH	182/189 (96%)	162 (89%)	20 (11%)	0	100	100
12	sH	182/189 (96%)	158 (87%)	24 (13%)	0	100	100
13	SV	81/83 (98%)	73 (90%)	8 (10%)	0	100	100
13	sV	81/83 (98%)	73 (90%)	8 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	Sa	100/102 (98%)	90 (90%)	10 (10%)	0	100	100
14	sa	100/102 (98%)	89 (89%)	11 (11%)	0	100	100
15	SC	220/222 (99%)	207 (94%)	13 (6%)	0	100	100
15	sC	220/222 (99%)	203 (92%)	17 (8%)	0	100	100
16	SN	148/150 (99%)	143 (97%)	5 (3%)	0	100	100
16	sN	148/150 (99%)	143 (97%)	5 (3%)	0	100	100
17	SO	138/140 (99%)	124 (90%)	14 (10%)	0	100	100
17	sO	138/140 (99%)	124 (90%)	14 (10%)	0	100	100
18	SW	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
18	sW	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
19	Sb	81/83 (98%)	69 (85%)	12 (15%)	0	100	100
19	sb	81/83 (98%)	72 (89%)	9 (11%)	0	100	100
22	LA	246/248 (99%)	221 (90%)	25 (10%)	0	100	100
22	lA	246/248 (99%)	222 (90%)	23 (9%)	1 (0%)	30	63
23	LB	400/402 (100%)	372 (93%)	28 (7%)	0	100	100
23	lB	400/402 (100%)	375 (94%)	25 (6%)	0	100	100
24	LC	366/368 (100%)	339 (93%)	27 (7%)	0	100	100
24	lC	366/368 (100%)	343 (94%)	23 (6%)	0	100	100
25	LD	291/293 (99%)	275 (94%)	16 (6%)	0	100	100
25	lD	291/293 (99%)	277 (95%)	14 (5%)	0	100	100
26	LE	232/247 (94%)	213 (92%)	19 (8%)	0	100	100
26	lE	232/247 (94%)	211 (91%)	21 (9%)	0	100	100
27	LF	223/225 (99%)	211 (95%)	12 (5%)	0	100	100
27	lF	223/225 (99%)	213 (96%)	10 (4%)	0	100	100
28	LG	239/241 (99%)	223 (93%)	16 (7%)	0	100	100
28	lG	239/241 (99%)	224 (94%)	15 (6%)	0	100	100
29	LH	188/190 (99%)	175 (93%)	13 (7%)	0	100	100
29	lH	188/190 (99%)	176 (94%)	12 (6%)	0	100	100
30	LI	198/213 (93%)	184 (93%)	14 (7%)	0	100	100
30	lI	198/213 (93%)	187 (94%)	11 (6%)	0	100	100
31	LJ	174/176 (99%)	154 (88%)	20 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	IJ	174/176 (99%)	160 (92%)	14 (8%)	0	100	100
32	LL	208/210 (99%)	192 (92%)	16 (8%)	0	100	100
32	IL	208/210 (99%)	190 (91%)	18 (9%)	0	100	100
33	LM	137/139 (99%)	126 (92%)	10 (7%)	1 (1%)	19	52
33	IM	137/139 (99%)	125 (91%)	11 (8%)	1 (1%)	19	52
34	LN	201/203 (99%)	186 (92%)	14 (7%)	1 (0%)	25	58
34	IN	201/203 (99%)	191 (95%)	9 (4%)	1 (0%)	25	58
35	LO	199/201 (99%)	192 (96%)	7 (4%)	0	100	100
35	IO	199/201 (99%)	192 (96%)	7 (4%)	0	100	100
36	LP	151/153 (99%)	141 (93%)	10 (7%)	0	100	100
36	IP	151/153 (99%)	142 (94%)	9 (6%)	0	100	100
37	LQ	185/187 (99%)	178 (96%)	7 (4%)	0	100	100
37	IQ	185/187 (99%)	178 (96%)	7 (4%)	0	100	100
38	LR	185/187 (99%)	176 (95%)	9 (5%)	0	100	100
38	IR	185/187 (99%)	180 (97%)	5 (3%)	0	100	100
39	LS	173/175 (99%)	164 (95%)	9 (5%)	0	100	100
39	IS	173/175 (99%)	161 (93%)	12 (7%)	0	100	100
40	LT	157/159 (99%)	147 (94%)	10 (6%)	0	100	100
40	IT	157/159 (99%)	148 (94%)	9 (6%)	0	100	100
41	LU	99/101 (98%)	82 (83%)	17 (17%)	0	100	100
41	IU	99/101 (98%)	80 (81%)	19 (19%)	0	100	100
42	LV	129/131 (98%)	125 (97%)	4 (3%)	0	100	100
42	IV	129/131 (98%)	120 (93%)	9 (7%)	0	100	100
43	LX	118/120 (98%)	114 (97%)	4 (3%)	0	100	100
43	IX	118/120 (98%)	117 (99%)	1 (1%)	0	100	100
44	LY	132/134 (98%)	128 (97%)	4 (3%)	0	100	100
44	IY	132/134 (98%)	128 (97%)	4 (3%)	0	100	100
45	LZ	133/135 (98%)	123 (92%)	10 (8%)	0	100	100
45	IZ	133/135 (98%)	121 (91%)	12 (9%)	0	100	100
46	La	145/147 (99%)	137 (94%)	8 (6%)	0	100	100
46	la	145/147 (99%)	137 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	Lb	105/121 (87%)	95 (90%)	10 (10%)	0	100	100
47	lb	105/121 (87%)	96 (91%)	9 (9%)	0	100	100
48	Lc	96/98 (98%)	90 (94%)	6 (6%)	0	100	100
48	lc	96/98 (98%)	87 (91%)	9 (9%)	0	100	100
49	Ld	105/107 (98%)	101 (96%)	4 (4%)	0	100	100
49	ld	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
50	Le	126/128 (98%)	118 (94%)	8 (6%)	0	100	100
50	le	126/128 (98%)	121 (96%)	5 (4%)	0	100	100
51	Lf	107/109 (98%)	98 (92%)	9 (8%)	0	100	100
51	lf	107/109 (98%)	98 (92%)	9 (8%)	0	100	100
52	Lg	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
52	lg	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
53	Lh	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
53	lh	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
54	Li	100/102 (98%)	98 (98%)	2 (2%)	0	100	100
54	li	100/102 (98%)	97 (97%)	3 (3%)	0	100	100
55	Lj	84/86 (98%)	72 (86%)	12 (14%)	0	100	100
55	lj	84/86 (98%)	77 (92%)	7 (8%)	0	100	100
56	Lk	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
56	lk	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
57	Ll	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
57	ll	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
58	Lm	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
58	lm	50/52 (96%)	46 (92%)	4 (8%)	0	100	100
59	Ln	22/24 (92%)	22 (100%)	0	0	100	100
59	ln	22/24 (92%)	22 (100%)	0	0	100	100
60	Lo	103/105 (98%)	100 (97%)	3 (3%)	0	100	100
60	lo	103/105 (98%)	100 (97%)	3 (3%)	0	100	100
61	Lp	89/91 (98%)	83 (93%)	6 (7%)	0	100	100
61	lp	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
62	Lr	123/125 (98%)	114 (93%)	9 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	lr	123/125 (98%)	118 (96%)	5 (4%)	0	100	100
63	Lz	215/217 (99%)	172 (80%)	43 (20%)	0	100	100
63	lz	215/217 (99%)	170 (79%)	45 (21%)	0	100	100
64	SR	133/135 (98%)	120 (90%)	12 (9%)	1 (1%)	16	49
64	sR	133/135 (98%)	104 (78%)	26 (20%)	3 (2%)	5	30
65	SD	225/227 (99%)	205 (91%)	20 (9%)	0	100	100
65	sD	225/227 (99%)	207 (92%)	18 (8%)	0	100	100
66	SF	187/189 (99%)	166 (89%)	21 (11%)	0	100	100
66	sF	187/189 (99%)	166 (89%)	21 (11%)	0	100	100
67	SK	96/98 (98%)	81 (84%)	12 (12%)	3 (3%)	3	25
67	sK	96/98 (98%)	84 (88%)	11 (12%)	1 (1%)	13	44
68	SP	119/121 (98%)	111 (93%)	8 (7%)	0	100	100
68	sP	119/121 (98%)	112 (94%)	7 (6%)	0	100	100
69	SQ	142/144 (99%)	123 (87%)	18 (13%)	1 (1%)	19	52
69	sQ	142/144 (99%)	123 (87%)	18 (13%)	1 (1%)	19	52
70	SS	143/145 (99%)	136 (95%)	7 (5%)	0	100	100
70	sS	143/145 (99%)	132 (92%)	11 (8%)	0	100	100
71	ST	141/143 (99%)	133 (94%)	7 (5%)	1 (1%)	19	52
71	sT	141/143 (99%)	128 (91%)	13 (9%)	0	100	100
72	SU	102/104 (98%)	94 (92%)	8 (8%)	0	100	100
72	sU	102/104 (98%)	95 (93%)	7 (7%)	0	100	100
73	Sc	62/64 (97%)	55 (89%)	7 (11%)	0	100	100
73	sc	62/64 (97%)	52 (84%)	10 (16%)	0	100	100
74	Sd	53/55 (96%)	47 (89%)	6 (11%)	0	100	100
74	sd	53/55 (96%)	48 (91%)	5 (9%)	0	100	100
75	Sg	311/313 (99%)	274 (88%)	37 (12%)	0	100	100
75	sg	311/313 (99%)	270 (87%)	41 (13%)	0	100	100
76	SM	120/122 (98%)	107 (89%)	13 (11%)	0	100	100
76	sM	120/122 (98%)	105 (88%)	14 (12%)	1 (1%)	16	49
77	SZ	73/75 (97%)	61 (84%)	12 (16%)	0	100	100
77	sZ	73/75 (97%)	58 (80%)	15 (20%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
78	Sf	65/67 (97%)	53 (82%)	12 (18%)	0	100	100
78	sf	65/67 (97%)	55 (85%)	10 (15%)	0	100	100
80	cB	842/846 (100%)	790 (94%)	49 (6%)	3 (0%)	30	63
83	Ls	194/196 (99%)	180 (93%)	14 (7%)	0	100	100
83	ls	194/196 (99%)	181 (93%)	12 (6%)	1 (0%)	25	58
84	Lt	137/141 (97%)	102 (74%)	33 (24%)	2 (2%)	8	37
84	lt	137/141 (97%)	108 (79%)	28 (20%)	1 (1%)	19	52
86	LW	114/124 (92%)	102 (90%)	11 (10%)	1 (1%)	14	45
88	CF	438/441 (99%)	420 (96%)	18 (4%)	0	100	100
All	All	25015/25436 (98%)	23064 (92%)	1922 (8%)	29 (0%)	50	79

5 of 29 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
67	sK	96	ARG
80	cB	407	LYS
80	cB	779	THR
83	ls	73	PRO
8	SY	52	PRO

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	
1	cH	100/100 (100%)	98 (98%)	2 (2%)	50	68
2	SE	224/224 (100%)	217 (97%)	7 (3%)	35	56
2	sE	224/224 (100%)	217 (97%)	7 (3%)	35	56
3	SI	178/178 (100%)	166 (93%)	12 (7%)	13	38
3	sI	178/178 (100%)	169 (95%)	9 (5%)	20	45
4	SL	137/137 (100%)	129 (94%)	8 (6%)	17	42
4	sL	137/137 (100%)	127 (93%)	10 (7%)	11	36

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	SX	113/113 (100%)	111 (98%)	2 (2%)	54	71
5	sX	113/113 (100%)	106 (94%)	7 (6%)	15	40
6	SG	207/207 (100%)	194 (94%)	13 (6%)	15	40
6	sG	207/207 (100%)	189 (91%)	18 (9%)	8	30
7	SJ	161/161 (100%)	152 (94%)	9 (6%)	17	43
7	sJ	161/161 (100%)	159 (99%)	2 (1%)	67	77
8	SY	113/113 (100%)	104 (92%)	9 (8%)	10	33
8	sY	113/113 (100%)	104 (92%)	9 (8%)	10	33
9	Se	47/47 (100%)	44 (94%)	3 (6%)	14	39
9	se	47/47 (100%)	46 (98%)	1 (2%)	48	66
10	SA	183/183 (100%)	174 (95%)	9 (5%)	21	45
10	sA	183/183 (100%)	173 (94%)	10 (6%)	18	43
11	SB	195/195 (100%)	183 (94%)	12 (6%)	15	40
11	sB	195/195 (100%)	185 (95%)	10 (5%)	20	45
12	SH	166/169 (98%)	157 (95%)	9 (5%)	18	43
12	sH	166/169 (98%)	155 (93%)	11 (7%)	14	38
13	SV	67/67 (100%)	57 (85%)	10 (15%)	2	15
13	sV	67/67 (100%)	60 (90%)	7 (10%)	5	23
14	Sa	89/89 (100%)	83 (93%)	6 (7%)	13	38
14	sa	89/89 (100%)	86 (97%)	3 (3%)	32	55
15	SC	188/188 (100%)	183 (97%)	5 (3%)	40	60
15	sC	188/188 (100%)	180 (96%)	8 (4%)	25	49
16	SN	130/130 (100%)	127 (98%)	3 (2%)	45	63
16	sN	130/130 (100%)	126 (97%)	4 (3%)	35	56
17	SO	110/110 (100%)	103 (94%)	7 (6%)	14	39
17	sO	110/110 (100%)	102 (93%)	8 (7%)	11	36
18	SW	112/112 (100%)	109 (97%)	3 (3%)	40	60
18	sW	112/112 (100%)	108 (96%)	4 (4%)	30	54
19	Sb	75/75 (100%)	69 (92%)	6 (8%)	10	33
19	sb	75/75 (100%)	72 (96%)	3 (4%)	27	50
22	LA	190/190 (100%)	183 (96%)	7 (4%)	29	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	1A	190/190 (100%)	181 (95%)	9 (5%)	22	46
23	LB	348/348 (100%)	336 (97%)	12 (3%)	32	55
23	1B	348/348 (100%)	339 (97%)	9 (3%)	41	61
24	LC	306/306 (100%)	295 (96%)	11 (4%)	30	54
24	1C	306/306 (100%)	296 (97%)	10 (3%)	33	56
25	LD	246/247 (100%)	229 (93%)	17 (7%)	13	37
25	1D	246/247 (100%)	232 (94%)	14 (6%)	17	43
26	LE	209/220 (95%)	200 (96%)	9 (4%)	25	49
26	1E	209/220 (95%)	200 (96%)	9 (4%)	25	49
27	LF	194/194 (100%)	188 (97%)	6 (3%)	35	56
27	1F	194/194 (100%)	191 (98%)	3 (2%)	60	74
28	LG	203/205 (99%)	189 (93%)	14 (7%)	13	37
28	1G	203/205 (99%)	195 (96%)	8 (4%)	27	51
29	LH	169/169 (100%)	161 (95%)	8 (5%)	22	46
29	1H	169/169 (100%)	164 (97%)	5 (3%)	36	58
30	LI	172/180 (96%)	164 (95%)	8 (5%)	22	46
30	1I	172/180 (96%)	169 (98%)	3 (2%)	56	72
31	LJ	148/148 (100%)	141 (95%)	7 (5%)	22	46
31	1J	148/148 (100%)	140 (95%)	8 (5%)	18	43
32	LL	176/176 (100%)	169 (96%)	7 (4%)	27	50
32	1L	176/176 (100%)	170 (97%)	6 (3%)	32	55
33	LM	118/118 (100%)	112 (95%)	6 (5%)	20	45
33	1M	118/118 (100%)	114 (97%)	4 (3%)	32	55
34	LN	171/171 (100%)	166 (97%)	5 (3%)	37	58
34	1N	171/171 (100%)	165 (96%)	6 (4%)	31	54
35	LO	173/173 (100%)	169 (98%)	4 (2%)	45	63
35	1O	173/173 (100%)	167 (96%)	6 (4%)	31	54
36	LP	134/134 (100%)	127 (95%)	7 (5%)	19	44
36	1P	134/134 (100%)	125 (93%)	9 (7%)	13	38
37	LQ	164/164 (100%)	158 (96%)	6 (4%)	29	53
37	1Q	164/164 (100%)	158 (96%)	6 (4%)	29	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	LR	166/166 (100%)	160 (96%)	6 (4%)	30	54
38	lR	166/166 (100%)	161 (97%)	5 (3%)	36	58
39	LS	156/156 (100%)	149 (96%)	7 (4%)	23	47
39	lS	156/156 (100%)	153 (98%)	3 (2%)	52	69
40	LT	139/139 (100%)	135 (97%)	4 (3%)	37	58
40	lT	139/139 (100%)	134 (96%)	5 (4%)	30	54
41	LU	91/91 (100%)	87 (96%)	4 (4%)	24	48
41	lU	91/91 (100%)	84 (92%)	7 (8%)	10	34
42	LV	101/101 (100%)	99 (98%)	2 (2%)	50	68
42	lV	101/101 (100%)	97 (96%)	4 (4%)	27	50
43	LX	108/108 (100%)	104 (96%)	4 (4%)	29	53
43	lX	108/108 (100%)	104 (96%)	4 (4%)	29	53
44	LY	124/124 (100%)	117 (94%)	7 (6%)	17	43
44	lY	124/124 (100%)	117 (94%)	7 (6%)	17	43
45	LZ	117/117 (100%)	110 (94%)	7 (6%)	16	41
45	lZ	117/117 (100%)	109 (93%)	8 (7%)	13	38
46	La	120/120 (100%)	118 (98%)	2 (2%)	56	72
46	la	120/120 (100%)	115 (96%)	5 (4%)	25	49
47	Lb	88/101 (87%)	85 (97%)	3 (3%)	32	55
47	lb	88/101 (87%)	81 (92%)	7 (8%)	10	33
48	Lc	83/83 (100%)	79 (95%)	4 (5%)	21	46
48	lc	83/83 (100%)	78 (94%)	5 (6%)	16	41
49	Ld	98/98 (100%)	94 (96%)	4 (4%)	26	50
49	ld	98/98 (100%)	96 (98%)	2 (2%)	50	68
50	Le	114/114 (100%)	110 (96%)	4 (4%)	31	54
50	le	114/114 (100%)	108 (95%)	6 (5%)	19	44
51	Lf	88/88 (100%)	88 (100%)	0	100	100
51	lf	88/88 (100%)	86 (98%)	2 (2%)	45	63
52	Lg	98/98 (100%)	97 (99%)	1 (1%)	73	80
52	lg	98/98 (100%)	93 (95%)	5 (5%)	20	45
53	Lh	109/109 (100%)	104 (95%)	5 (5%)	23	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	lh	109/109 (100%)	105 (96%)	4 (4%)	29	53
54	Li	86/86 (100%)	81 (94%)	5 (6%)	17	42
54	li	86/86 (100%)	86 (100%)	0	100	100
55	Lj	73/73 (100%)	70 (96%)	3 (4%)	26	50
55	lj	73/73 (100%)	66 (90%)	7 (10%)	7	26
56	Lk	64/64 (100%)	63 (98%)	1 (2%)	58	73
56	lk	64/64 (100%)	62 (97%)	2 (3%)	35	56
57	Ll	47/47 (100%)	46 (98%)	1 (2%)	48	66
57	ll	47/47 (100%)	44 (94%)	3 (6%)	14	39
58	Lm	48/48 (100%)	48 (100%)	0	100	100
58	lm	48/48 (100%)	45 (94%)	3 (6%)	15	40
59	Ln	23/23 (100%)	20 (87%)	3 (13%)	3	18
59	ln	23/23 (100%)	22 (96%)	1 (4%)	25	49
60	Lo	93/93 (100%)	89 (96%)	4 (4%)	25	49
60	lo	93/93 (100%)	86 (92%)	7 (8%)	11	35
61	Lp	74/74 (100%)	71 (96%)	3 (4%)	26	50
61	lp	74/74 (100%)	70 (95%)	4 (5%)	18	43
62	Lr	109/109 (100%)	104 (95%)	5 (5%)	23	47
62	lr	109/109 (100%)	107 (98%)	2 (2%)	54	71
63	Lz	195/196 (100%)	185 (95%)	10 (5%)	20	45
63	lz	195/196 (100%)	181 (93%)	14 (7%)	12	36
64	SR	122/122 (100%)	116 (95%)	6 (5%)	21	45
64	sR	122/122 (100%)	116 (95%)	6 (5%)	21	45
65	SD	190/190 (100%)	181 (95%)	9 (5%)	22	46
65	sD	190/190 (100%)	179 (94%)	11 (6%)	17	42
66	SF	159/159 (100%)	151 (95%)	8 (5%)	20	45
66	sF	159/159 (100%)	152 (96%)	7 (4%)	24	48
67	SK	89/89 (100%)	82 (92%)	7 (8%)	10	34
67	sK	89/89 (100%)	85 (96%)	4 (4%)	23	47
68	SP	107/107 (100%)	99 (92%)	8 (8%)	11	35
68	sP	107/107 (100%)	102 (95%)	5 (5%)	22	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	SQ	119/119 (100%)	116 (98%)	3 (2%)	42	62
69	sQ	119/119 (100%)	108 (91%)	11 (9%)	7	28
70	SS	126/126 (100%)	121 (96%)	5 (4%)	27	50
70	sS	126/126 (100%)	117 (93%)	9 (7%)	12	36
71	ST	113/113 (100%)	105 (93%)	8 (7%)	12	36
71	sT	113/113 (100%)	108 (96%)	5 (4%)	24	48
72	SU	94/94 (100%)	89 (95%)	5 (5%)	19	44
72	sU	94/94 (100%)	92 (98%)	2 (2%)	48	66
73	Sc	57/57 (100%)	55 (96%)	2 (4%)	31	54
73	sc	57/57 (100%)	53 (93%)	4 (7%)	12	37
74	Sd	48/48 (100%)	44 (92%)	4 (8%)	9	32
74	sd	48/48 (100%)	46 (96%)	2 (4%)	25	49
75	Sg	272/272 (100%)	255 (94%)	17 (6%)	15	40
75	sg	272/272 (100%)	261 (96%)	11 (4%)	27	50
76	SM	102/104 (98%)	92 (90%)	10 (10%)	6	25
76	sM	102/104 (98%)	93 (91%)	9 (9%)	8	30
77	SZ	66/66 (100%)	63 (96%)	3 (4%)	23	47
77	sZ	66/66 (100%)	61 (92%)	5 (8%)	11	34
78	Sf	60/60 (100%)	55 (92%)	5 (8%)	9	32
78	sf	60/60 (100%)	55 (92%)	5 (8%)	9	32
80	cB	722/723 (100%)	679 (94%)	43 (6%)	16	41
83	Ls	162/164 (99%)	152 (94%)	10 (6%)	15	40
83	ls	162/164 (99%)	154 (95%)	8 (5%)	21	45
84	Lt	112/115 (97%)	111 (99%)	1 (1%)	75	82
84	lt	112/115 (97%)	110 (98%)	2 (2%)	54	71
86	LW	97/103 (94%)	89 (92%)	8 (8%)	9	32
88	CF	365/366 (100%)	343 (94%)	22 (6%)	16	41
All	All	21736/21836 (100%)	20710 (95%)	1026 (5%)	24	46

5 of 1026 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
70	SS	81	ASP

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Mol	Chain	Res	Type
75	Sg	101	PHE
70	SS	77	TYR
66	sF	61	PHE
65	sD	76	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 93 such sidechains are listed below:

Mol	Chain	Res	Type
10	SA	111	GLN
31	LJ	155	HIS
10	SA	165	ASN
23	LB	315	ASN
40	LT	131	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
20	L7	119/120 (99%)	12 (10%)	0
20	l7	119/120 (99%)	14 (11%)	0
21	L8	155/156 (99%)	32 (20%)	0
21	l8	155/156 (99%)	30 (19%)	0
79	S2	1715/1740 (98%)	432 (25%)	11 (0%)
79	s2	1714/1740 (98%)	496 (28%)	0
81	aP	69/71 (97%)	22 (31%)	0
82	Et	73/75 (97%)	30 (41%)	0
82	pE	73/75 (97%)	35 (47%)	0
85	L5	3704/3740 (99%)	882 (23%)	25 (0%)
85	l5	3705/3740 (99%)	877 (23%)	0
87	AT	74/77 (96%)	24 (32%)	0
89	Pt	72/74 (97%)	16 (22%)	0
All	All	11747/11884 (98%)	2902 (24%)	36 (0%)

5 of 2902 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
20	l7	2	U
20	l7	7	G
20	l7	22	A
20	l7	24	C
20	l7	33	U

5 of 36 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
79	S2	563	G
79	S2	1781	A
79	S2	688	U
79	S2	1455	A
85	L5	2416	G

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
88	SEP	CF	163	88	8,9,10	1.62	1 (12%)	7,12,14	1.38	1 (14%)

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
88	SEP	CF	163	88	-	6/6/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
88	CF	163	SEP	P-O1P	3.54	1.61	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
88	CF	163	SEP	OG-CB-CA	2.97	111.04	108.14

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
88	CF	163	SEP	N-CA-CB-OG
88	CF	163	SEP	C-CA-CB-OG
88	CF	163	SEP	CA-CB-OG-P
88	CF	163	SEP	CB-OG-P-O1P
88	CF	163	SEP	CB-OG-P-O2P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 522 ligands modelled in this entry, 522 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
85	L5	12
85	l5	11
79	s2	7

Continued on next page...

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Mol	Chain	Number of breaks
79	S2	6
80	cB	1
81	aP	1
84	lt	1
89	Pt	1
84	Lt	1
82	pE	1
82	Et	1

The worst 5 of 43 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	27.56
1	s2	753:C	O3'	785:C	P	27.07
1	L5	2910:G	O3'	3584:C	P	21.08
1	l5	2910:G	O3'	3584:C	P	20.88
1	l5	760:G	O3'	903:C	P	17.26

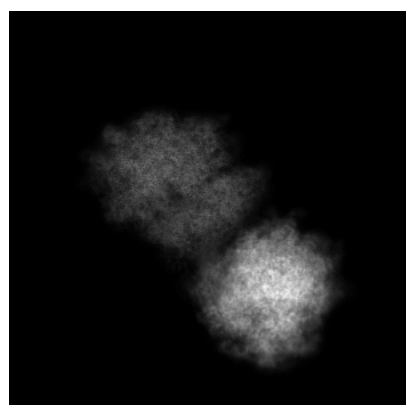
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44052. These allow visual inspection of the internal detail of the map and identification of artifacts.

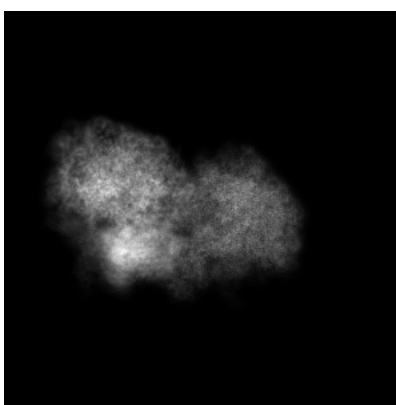
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

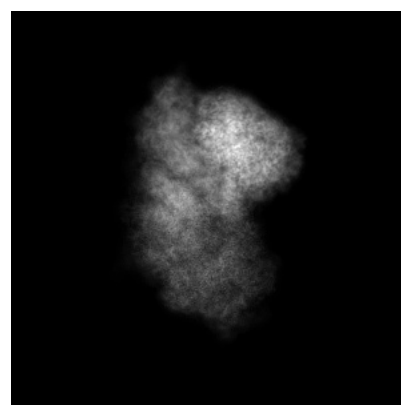
6.1.1 Primary map



X



Y

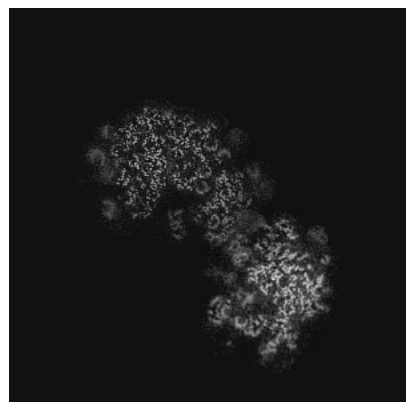


Z

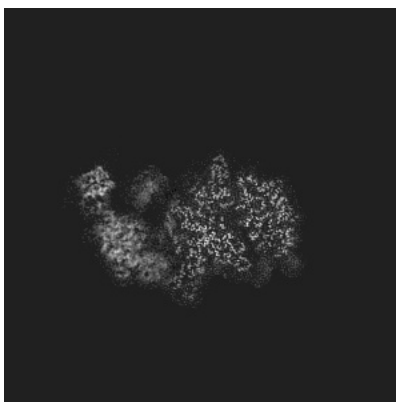
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

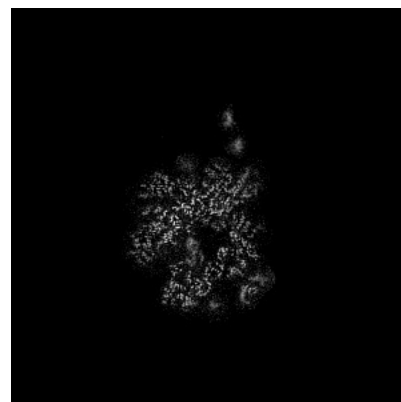
6.2.1 Primary map



X Index: 300



Y Index: 300

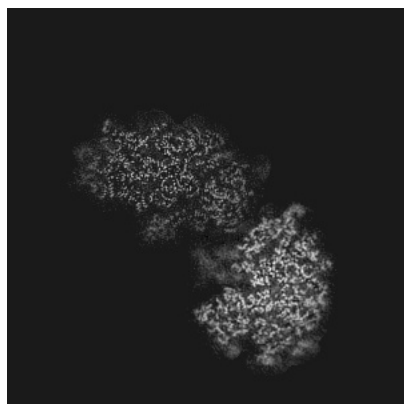


Z Index: 300

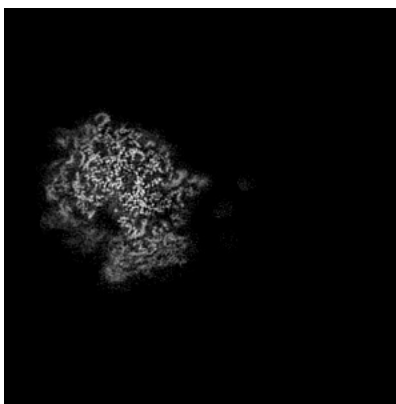
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

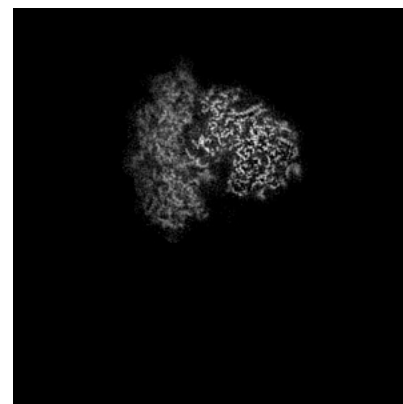
6.3.1 Primary map



X Index: 326



Y Index: 395

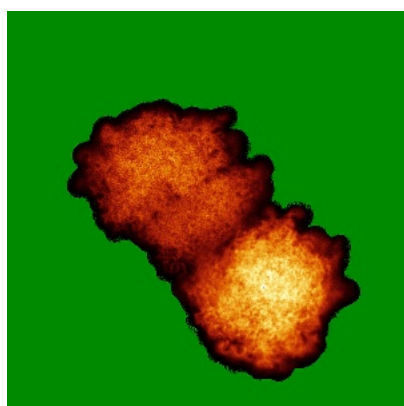


Z Index: 176

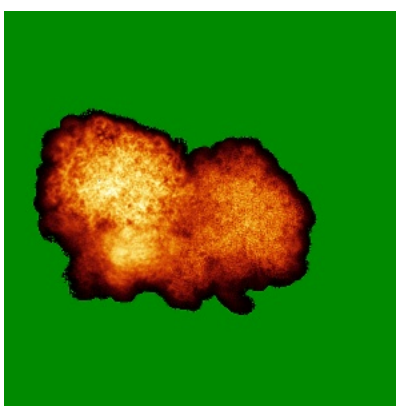
The images above show the largest variance slices of the map in three orthogonal directions.

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

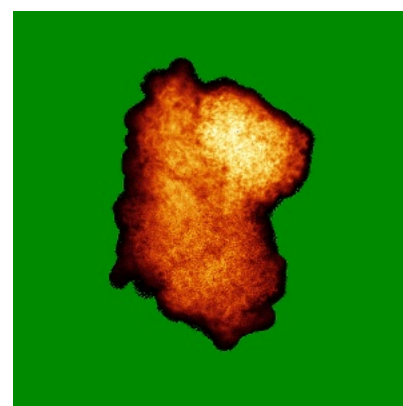
6.4.1 Primary map



X



Y



Z

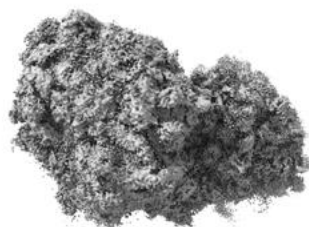
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.099. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

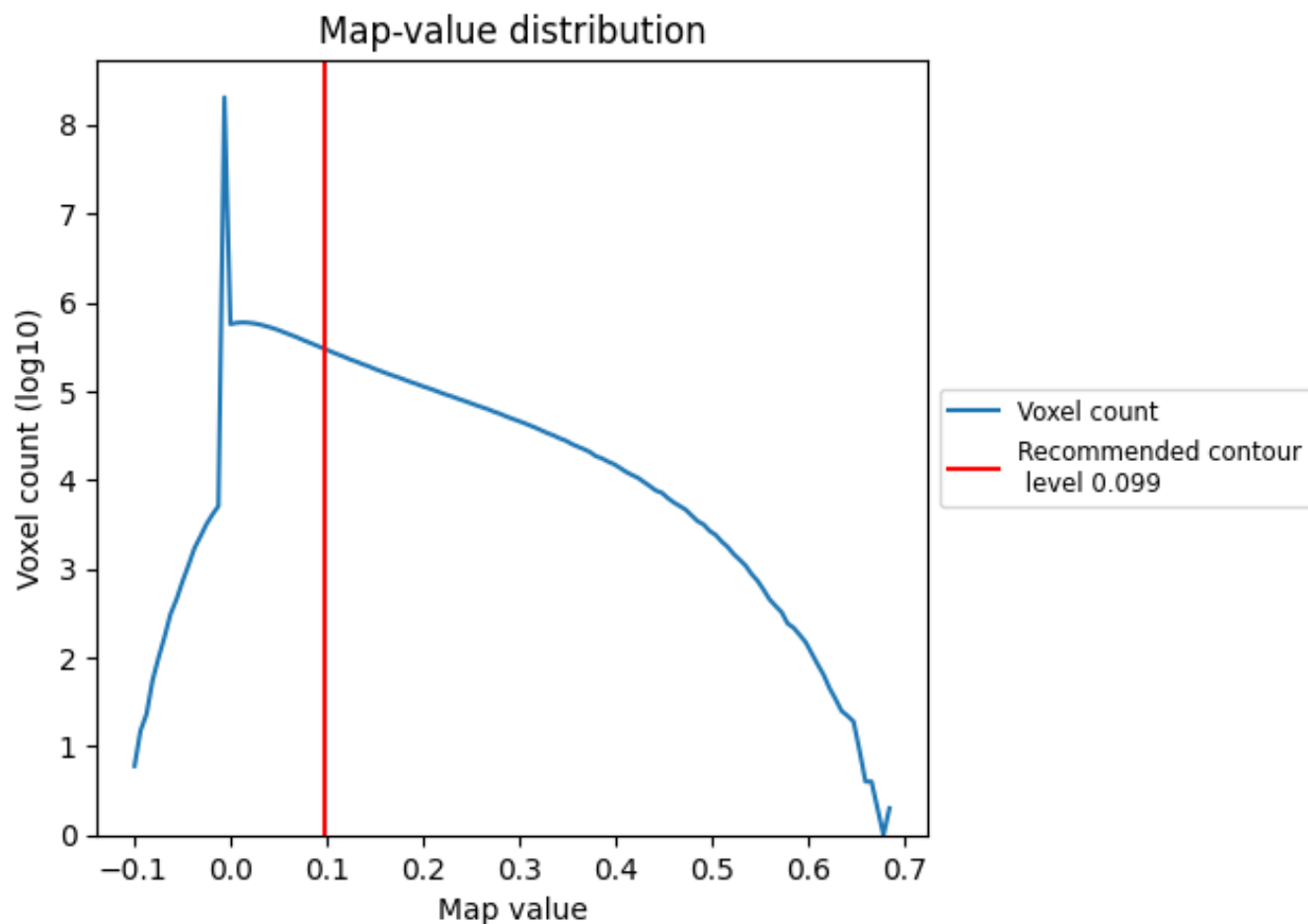
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

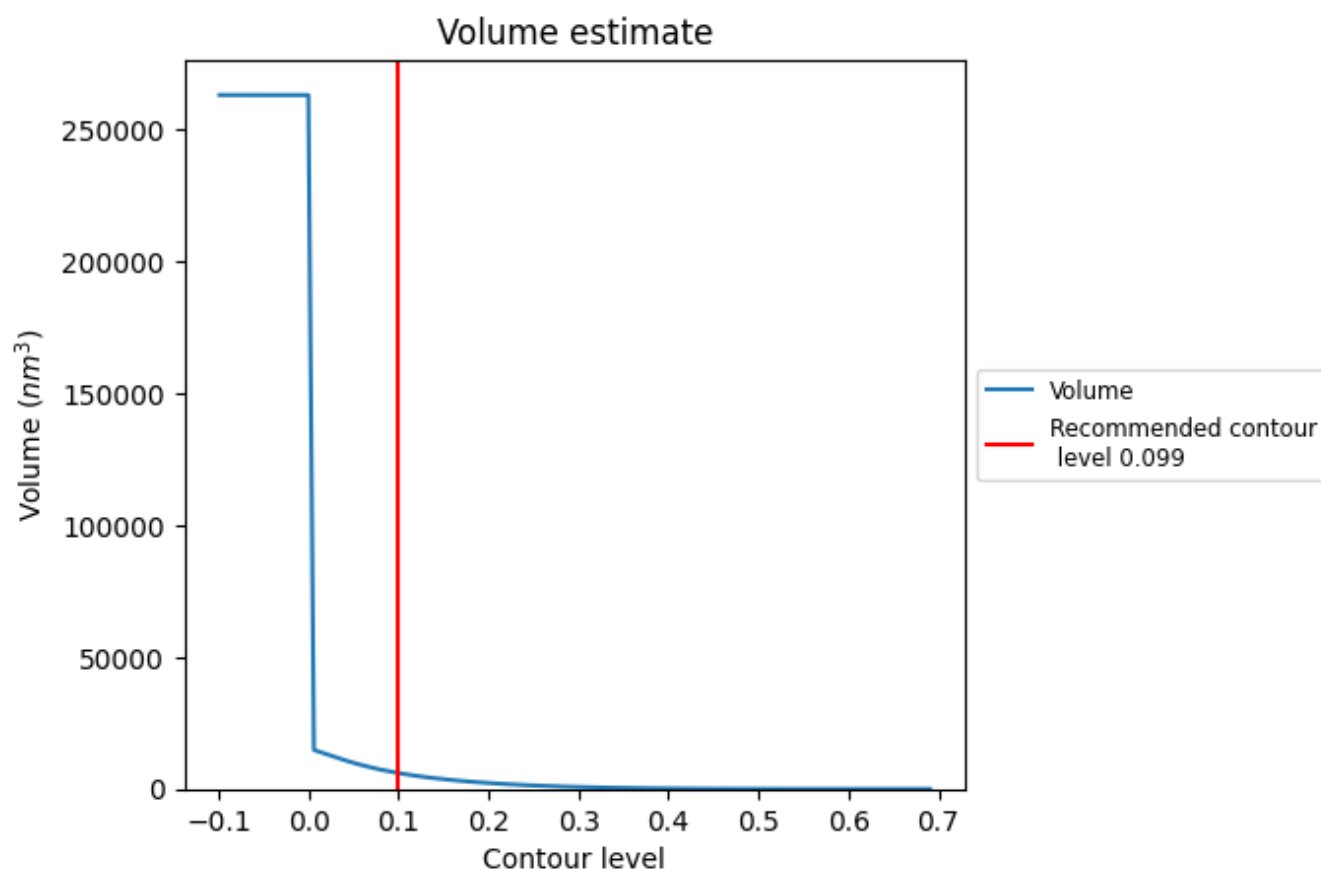
This section contains the results of statistical analysis of the map.

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.

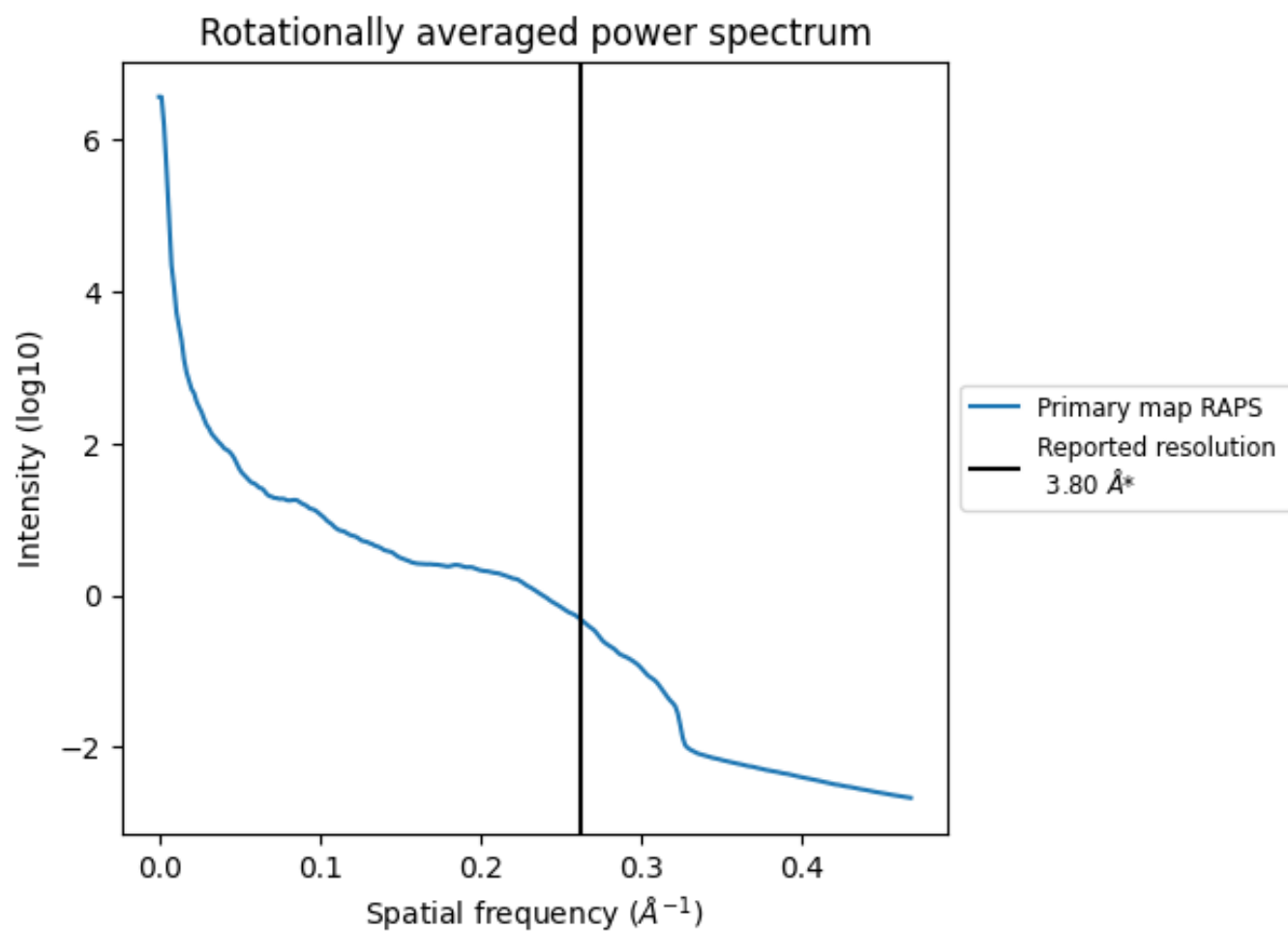
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6084 nm³; this corresponds to an approximate mass of 5496 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 0.263 Å⁻¹

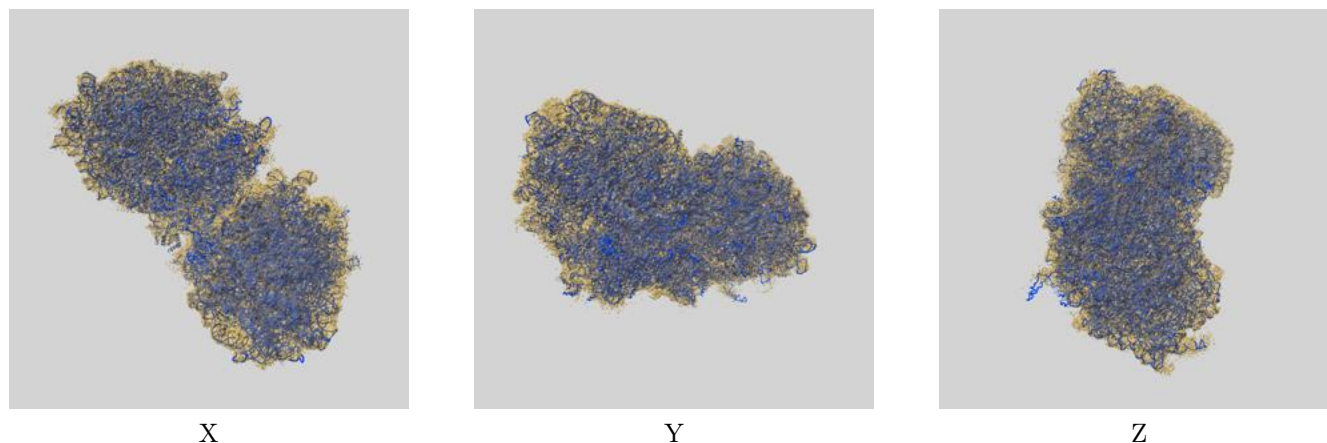
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

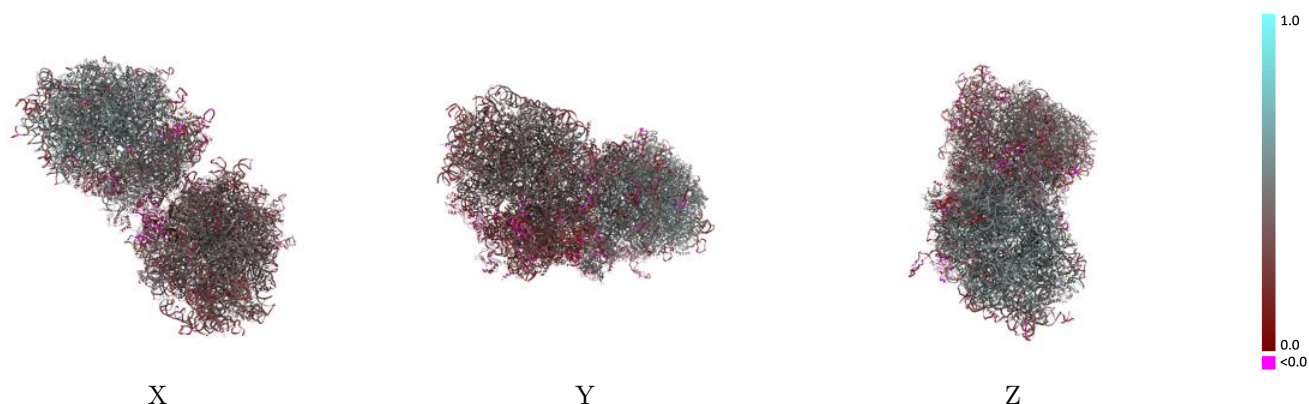
This section contains information regarding the fit between EMDB map EMD-44052 and PDB model 9B0S. Per-residue inclusion information can be found in [section 3](#) on [page 29](#).

9.1 Map-model overlay [i](#)



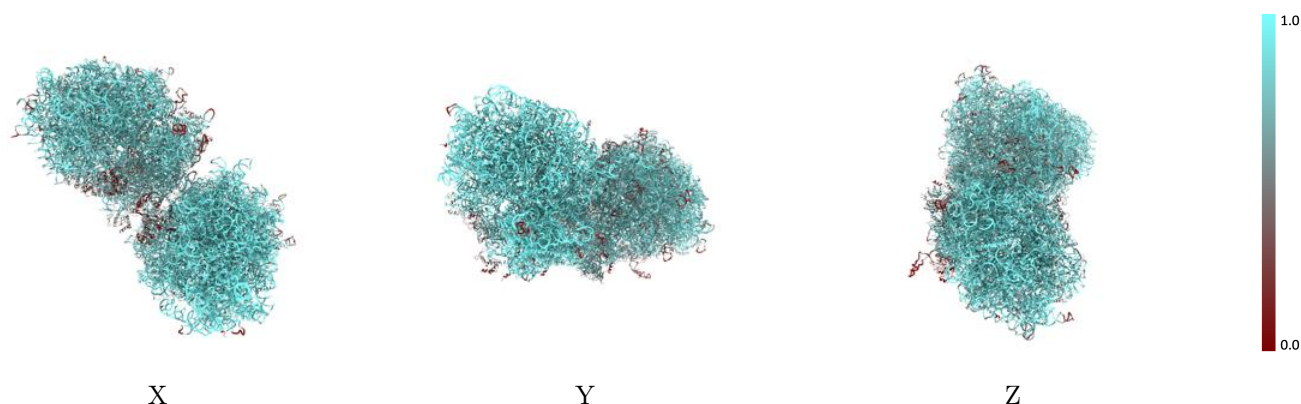
The images above show the 3D surface view of the map at the recommended contour level 0.099 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



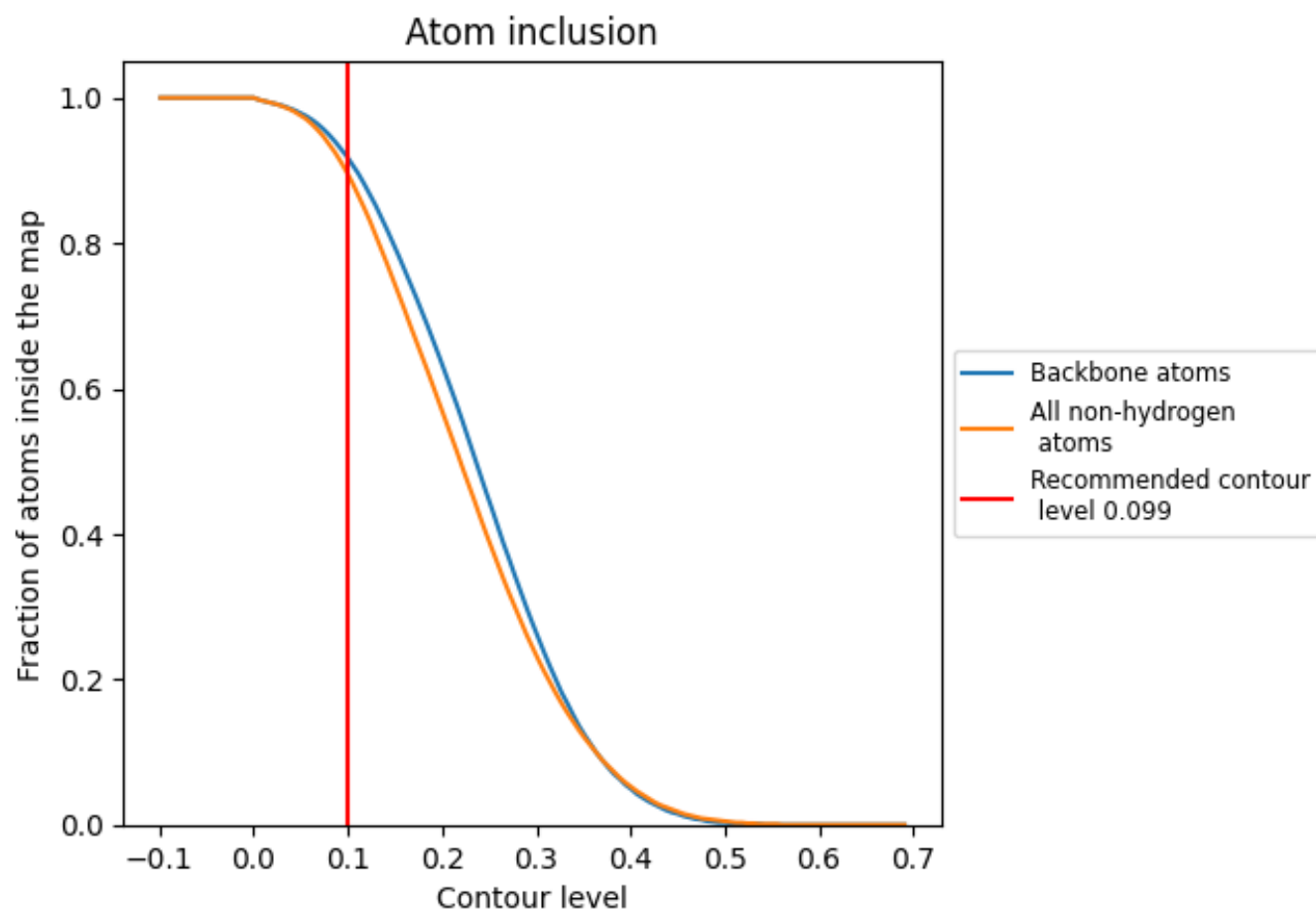
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.099).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 92% of all backbone atoms, 90% 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 (0.099) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8970	 0.3970
AT	 0.9510	 0.1790
CF	 0.7370	 0.2010
Et	 0.6270	 0.1190
L5	 0.9750	 0.3660
L7	 0.9950	 0.3900
L8	 0.9940	 0.3920
LA	 0.9770	 0.4410
LB	 0.9790	 0.4010
LC	 0.9650	 0.4130
LD	 0.9120	 0.3640
LE	 0.9630	 0.3340
LF	 0.9700	 0.3850
LG	 0.8780	 0.3650
LH	 0.9780	 0.3790
LI	 0.9810	 0.4140
LJ	 0.8740	 0.3300
LL	 0.9220	 0.3990
LM	 0.9660	 0.3300
LN	 0.9920	 0.4410
LO	 0.9860	 0.3870
LP	 0.9890	 0.4130
LQ	 0.9720	 0.4270
LR	 0.8930	 0.3520
LS	 0.9870	 0.3990
LT	 0.9820	 0.4240
LU	 0.9730	 0.3680
LV	 0.9950	 0.4300
LW	 0.7980	 0.1800
LX	 0.9780	 0.4180
LY	 0.9690	 0.3970
LZ	 0.9560	 0.4000
La	 0.9750	 0.4330
Lb	 0.9300	 0.3570
Lc	 0.9490	 0.3880























































































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Chain	Atom inclusion	Q-score
Ld	 0.9850	 0.4040
Le	 0.9940	 0.4250
Lf	 0.9950	 0.4060
Lg	 0.9720	 0.4220
Lh	 0.9580	 0.3860
Li	 0.9320	 0.3940
Lj	 0.9990	 0.4420
Lk	 0.9140	 0.3780
Ll	 0.9950	 0.4290
Lm	 0.9980	 0.4000
Ln	 1.0000	 0.3860
Lo	 0.9640	 0.4310
Lp	 0.9700	 0.4230
Lr	 0.9820	 0.4050
Ls	 0.6170	 0.1650
Lt	 0.4990	 0.1400
Lz	 0.1960	 0.0510
Pt	 0.9890	 0.3270
S2	 0.9690	 0.3120
SA	 0.8510	 0.3080
SB	 0.9130	 0.3350
SC	 0.9360	 0.3300
SD	 0.9060	 0.2910
SE	 0.9240	 0.2990
SF	 0.9270	 0.2920
SG	 0.9110	 0.2500
SH	 0.6860	 0.2770
SI	 0.8540	 0.3160
SJ	 0.8910	 0.2760
SK	 0.8830	 0.2780
SL	 0.8710	 0.3300
SM	 0.4590	 0.1850
SN	 0.9260	 0.3540
SO	 0.8820	 0.3540
SP	 0.8830	 0.2790
SQ	 0.9560	 0.2890
SR	 0.8120	 0.2700
SS	 0.9040	 0.3020
ST	 0.9130	 0.2850
SU	 0.8850	 0.2780
SV	 0.9150	 0.3410
SW	 0.9680	 0.3470





















































































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Chain	Atom inclusion	Q-score
SX	 0.9860	 0.3380
SY	 0.9370	 0.2580
SZ	 0.8030	 0.2590
Sa	 0.9570	 0.3590
Sb	 0.8530	 0.3230
Sc	 0.9300	 0.3030
Sd	 0.9860	 0.3200
Se	 0.9170	 0.2750
Sf	 0.7170	 0.2020
Sg	 0.8420	 0.2260
aP	 0.8480	 0.3200
cB	 0.5900	 0.3770
cH	 0.6520	 0.3960
l5	 0.9220	 0.4660
l7	 0.9820	 0.5130
l8	 0.9550	 0.4890
lA	 0.9290	 0.5430
lB	 0.8640	 0.5240
lC	 0.9060	 0.5340
lD	 0.8330	 0.4810
lE	 0.8030	 0.4630
lF	 0.9110	 0.5320
lG	 0.7920	 0.4580
lH	 0.8190	 0.5110
lI	 0.8780	 0.5320
lJ	 0.7490	 0.4290
lL	 0.8740	 0.5010
lM	 0.8630	 0.5030
lN	 0.9670	 0.5600
lO	 0.9060	 0.5330
lP	 0.9240	 0.5490
lQ	 0.9420	 0.5530
lR	 0.8420	 0.4880
lS	 0.9180	 0.5460
lT	 0.9030	 0.5270
lU	 0.7580	 0.4080
lV	 0.8800	 0.5360
lX	 0.9060	 0.5240
lY	 0.8840	 0.5220
lZ	 0.8660	 0.4980
la	 0.9430	 0.5480
lb	 0.8160	 0.4750























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Chain	Atom inclusion	Q-score
lc	 0.8310	 0.4730
ld	 0.8760	 0.5140
le	 0.9450	 0.5510
lf	 0.9390	 0.5570
lg	 0.8770	 0.5170
lh	 0.8800	 0.5120
li	 0.8550	 0.5010
lj	 0.9720	 0.5510
lk	 0.7950	 0.4620
ll	 0.9530	 0.5520
lm	 0.8850	 0.5330
ln	 0.9190	 0.5430
lo	 0.8800	 0.5350
lp	 0.9090	 0.5370
lr	 0.9130	 0.5350
ls	 0.3270	 0.2080
lt	 0.2580	 0.1590
lz	 0.0780	 0.0560
pE	 0.8340	 0.2490
s2	 0.9090	 0.4310
sA	 0.7540	 0.4390
sB	 0.8030	 0.4680
sC	 0.8200	 0.4790
sD	 0.7710	 0.4310
sE	 0.8100	 0.4490
sF	 0.7720	 0.4260
sG	 0.6780	 0.3890
sH	 0.6420	 0.3560
sI	 0.7760	 0.4310
sJ	 0.8070	 0.4280
sK	 0.7950	 0.4340
sL	 0.7950	 0.4580
sM	 0.4130	 0.2500
sN	 0.8450	 0.4930
sO	 0.8010	 0.4670
sP	 0.7810	 0.4520
sQ	 0.7840	 0.4250
sR	 0.4700	 0.1510
sS	 0.7680	 0.4430
sT	 0.8130	 0.4330
sU	 0.7200	 0.3920
sV	 0.7540	 0.4280

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Chain	Atom inclusion	Q-score
sW	 0.8710	 0.4980
sX	 0.8490	 0.4930
sY	 0.7160	 0.3740
sZ	 0.6350	 0.3370
sa	 0.8760	 0.5050
sb	 0.7340	 0.4140
sc	 0.6460	 0.3140
sd	 0.8960	 0.4860
se	 0.5920	 0.3020
sf	 0.5670	 0.2850
sg	 0.6220	 0.3710