



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2025 – 04:43 PM EDT

PDB ID : 9B0Q
EMDB ID : EMD-44050
Title : In situ human top-back di-ribosome structure (Composite map)
Authors : Wei, Z.; Yong, Z.
Deposited on : 2024-03-12
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev117
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

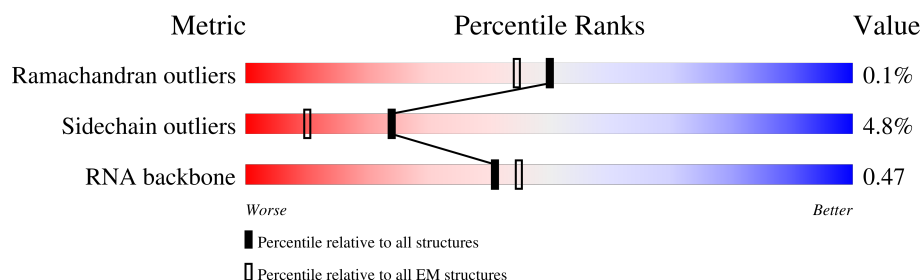
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



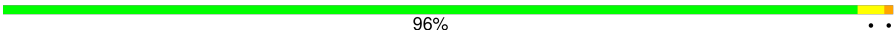
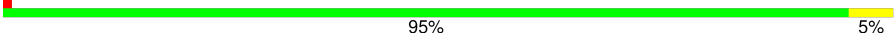
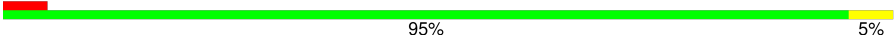
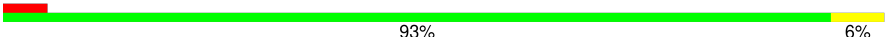
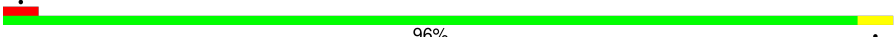





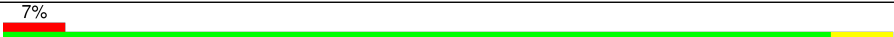


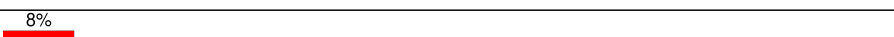
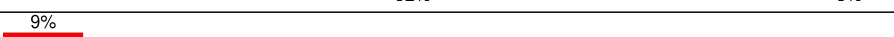
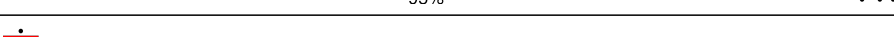
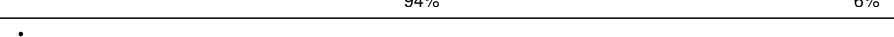

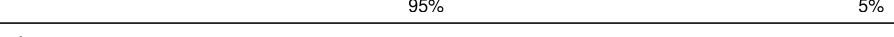
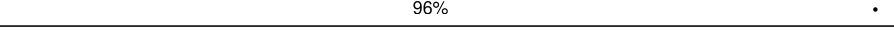
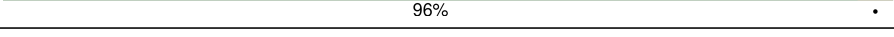
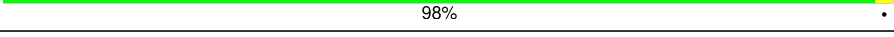
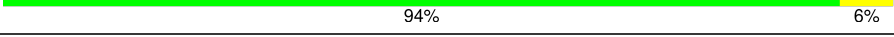
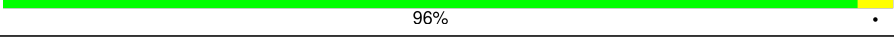
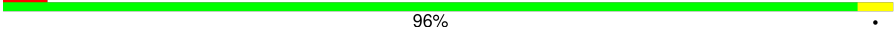
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	
1	cH	125	
2	SE	262	
2	sE	262	
3	SI	206	
3	sI	206	
4	SL	153	
4	sL	153	

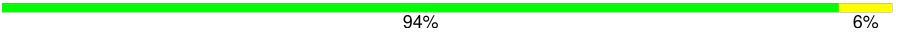
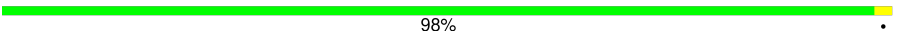
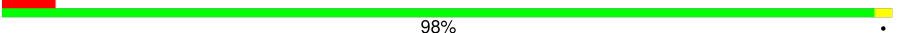












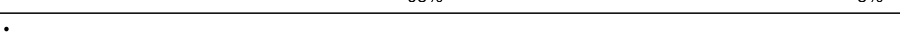
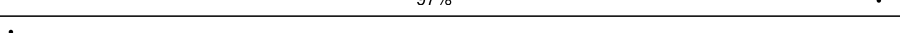

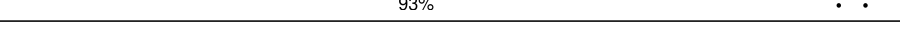
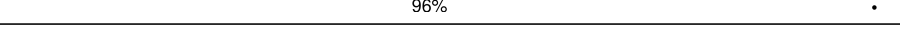
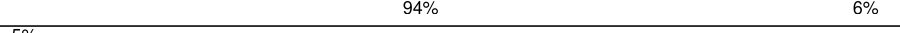
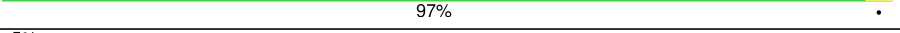
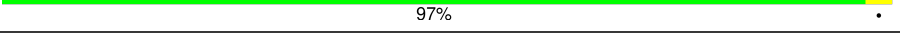
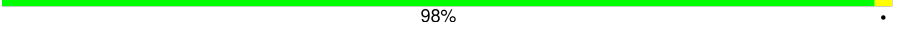
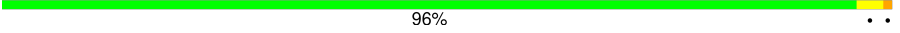
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	SX	141	 96%
5	sX	141	 95%5%
6	SG	237	 95%5%
6	sG	237	 93%6%
7	SJ	185	 96%
7	sJ	185	 97%
8	SY	131	 91%9%
8	sY	131	 93%7%
9	se	58	 16%98%
10	SA	221	 7%96%
10	sA	221	 7%93%7%
11	SB	214	 97%
11	sB	214	 95%5%
12	SH	189	 8%92%6% ..
12	sH	189	 9%95% ..
13	SV	83	 94%6%
13	sV	83	 88%12%
14	Sa	102	 95%5%
14	sa	102	 96%
15	SC	222	 96%
15	sC	222	 98%
16	SN	150	 94%6%
16	sN	150	 96%
17	SO	140	 5%96%
17	sO	140	 5%96%



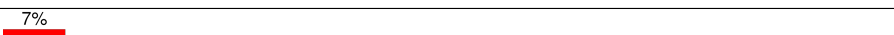
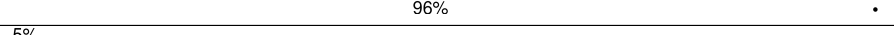
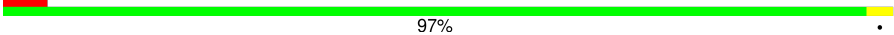

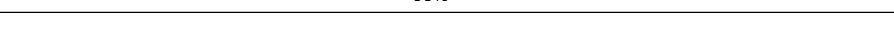
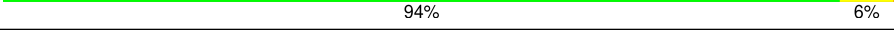


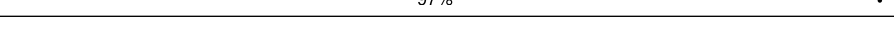
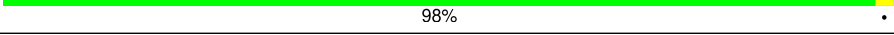
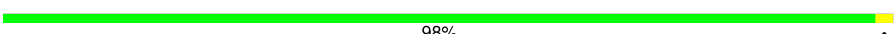
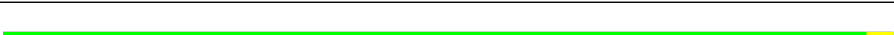
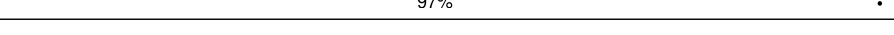
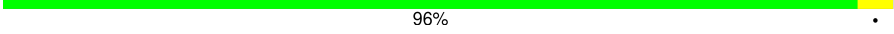
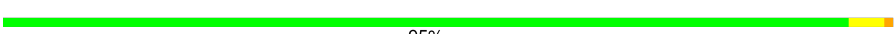

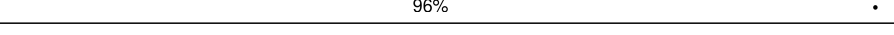
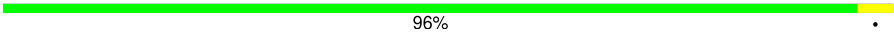

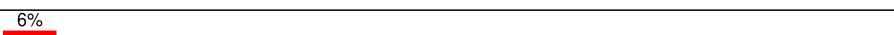
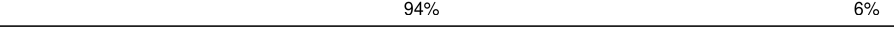
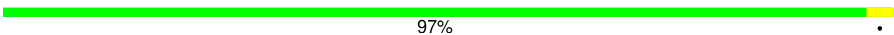

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
18	SW	129	 94% 6%
18	sW	129	 98% .
19	Sb	83	 98% .
19	sb	83	 93% 7%
20	L7	120	 88% 12%
20	l7	120	 87% 13%
21	L8	156	 82% 18%
21	l8	156	 77% 23%
22	LA	248	 97% .
22	lA	248	 96% .
23	LB	402	 98% .
23	lB	402	 97% .
24	LC	368	 96% .
24	lC	368	 95% 5%
25	LD	293	 95% 5%
25	lD	293	 97% .
26	LE	247	 92% . .
26	lE	247	 93% . .
27	LF	225	 96% .
27	lF	225	 94% 6%
28	LG	241	 97% .
28	lG	241	 97% .
29	LH	190	 98% .
29	lH	190	 96% . .
30	LI	213	 91% . 5%

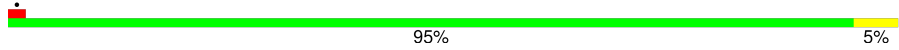
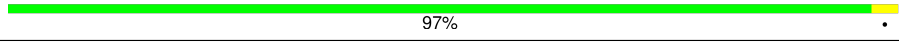
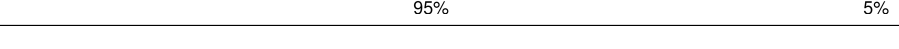
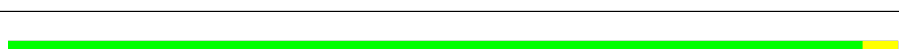
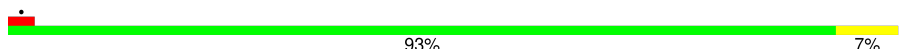
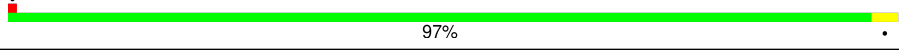
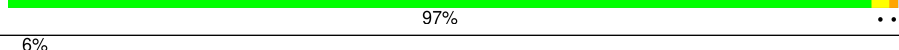
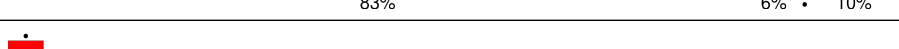

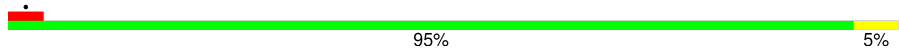
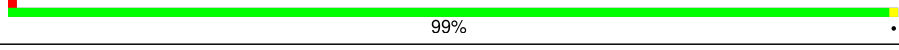
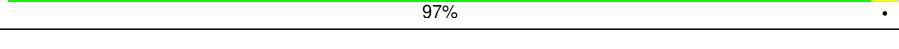
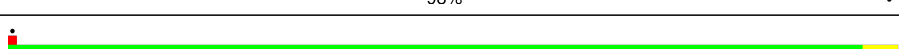
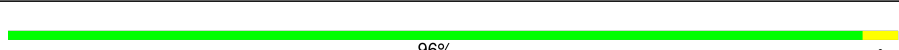
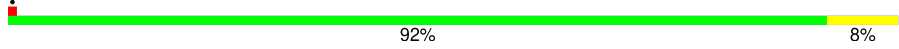
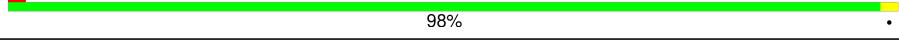
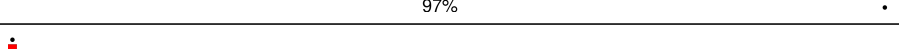


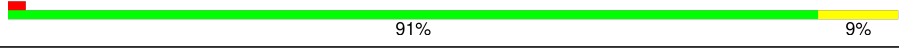
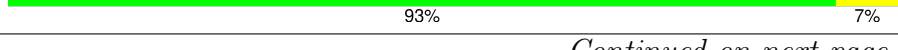



Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
30	II	213	 90% 5% 5%
31	LJ	176	 5% 95% 5%
31	IJ	176	 7% 96% 5%
32	LL	210	 5% 97% 5%
32	IL	210	 5% 96% 5%
33	LM	139	 94% 6%
33	IM	139	 92% 7%
34	LN	203	 97%
34	IN	203	 98%
35	LO	201	 98%
35	IO	201	 97%
36	LP	153	 96%
36	IP	153	 95%
37	LQ	187	 96%
37	IQ	187	 96%
38	LR	187	 5% 93% 7%
38	IR	187	 6% 94% 6%
39	LS	175	 97%
39	IS	175	 94% 6%
40	LT	159	 96%
40	IT	159	 96%
41	LU	101	 88% 12%
41	IU	101	 90% 10%
42	LV	131	 98%
42	IV	131	 97%

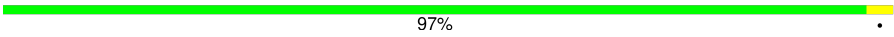
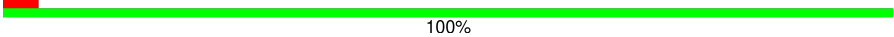
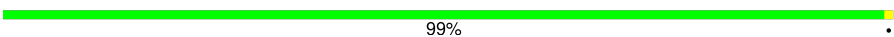
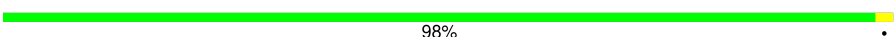

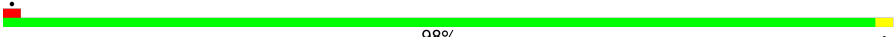
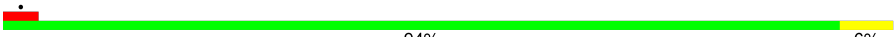



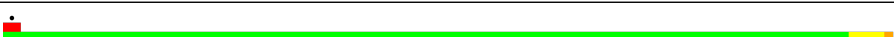


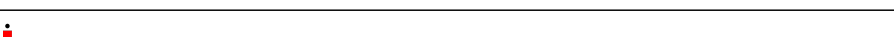
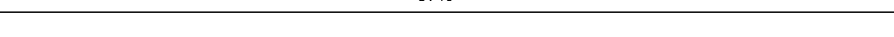
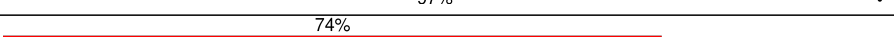
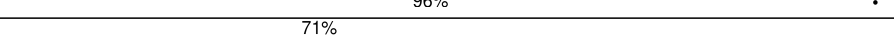

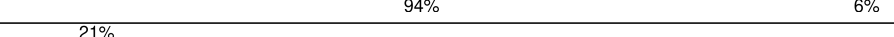
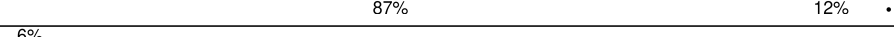
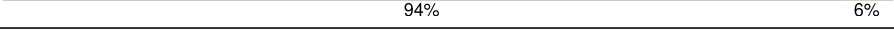
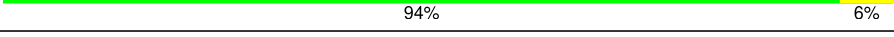
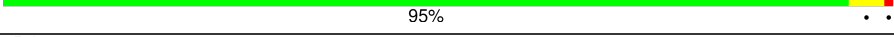
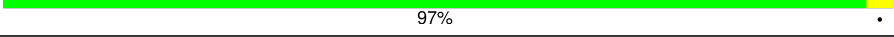

Continued on next page...

Continued from previous page...

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

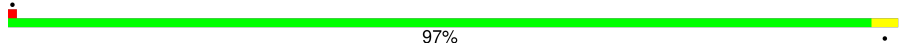
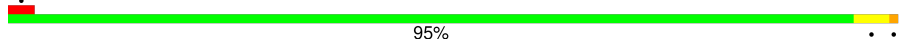
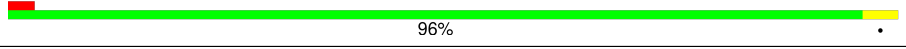

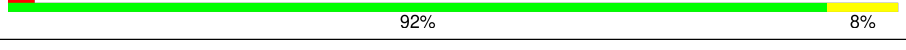
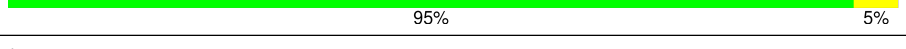
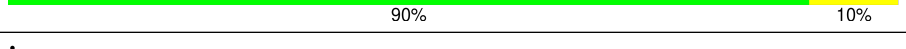
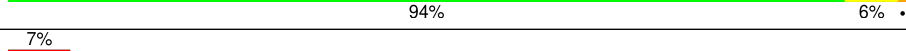
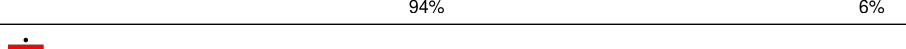
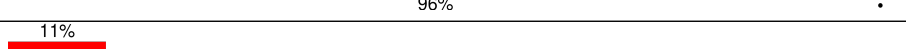
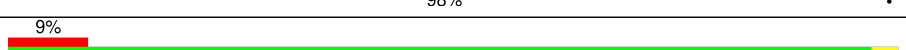
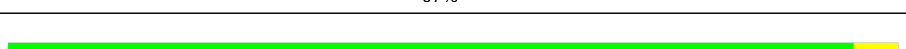
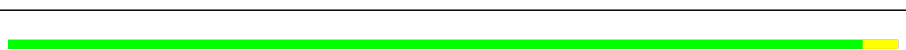
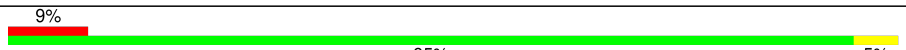
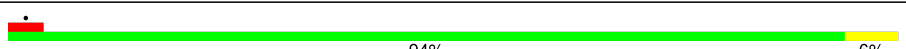
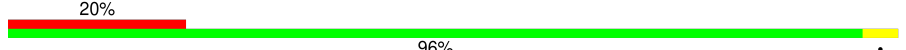


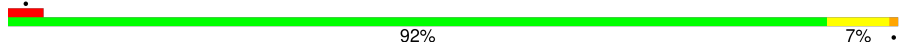
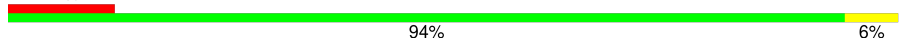
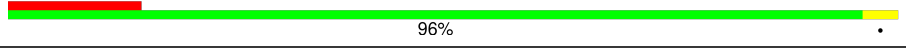
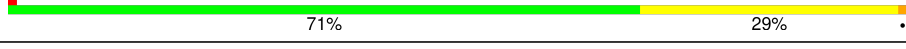

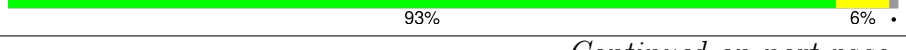

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
55	lj	86	 97%
56	Lk	69	 100%
56	lk	69	 99%
57	Ll	50	 98%
57	ll	50	 90% 10%
58	Lm	52	 98%
58	lm	52	 94% 6%
59	Ln	24	 100%
59	ln	24	 92% 8%
60	Lo	105	 95% 5%
60	lo	105	 95% 5%
61	Lp	91	 98%
61	lp	91	 97%
62	Lr	125	 97%
62	lr	125	 97%
63	Lz	217	 74% 96%
63	lz	217	 71% 90% 10%
64	SR	135	 7% 94% 6%
64	sR	135	 21% 87% 12%
65	SD	227	 6% 94% 6%
65	sD	227	 94% 6%
66	SF	189	 95% 5%
66	sF	189	 97%
67	SK	98	 84% 16%
67	sK	98	 92% 8%

Continued on next page...

Continued from previous page...

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	856	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
80	cB	856	
81	AP	73	
81	aP	73	
82	PE	76	
82	pE	76	
83	Ls	196	
83	ls	196	
84	Lt	141	
84	lt	141	
85	L5	3740	
85	l5	3740	
86	Se	47	
87	LW	124	
87	IW	124	

2 Entry composition

There are 89 unique types of molecules in this entry. The entry contains 459641 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		
1	cH	125	Total	C	N	O	0	0
			968	595	189	184		

There are 8 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
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		
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		

- 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 RNA (120-MER)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		
20	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 21 is a RNA chain called RNA (156-MER)5.8S rRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
21	18	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	1A	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	1B	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	1C	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	1D	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
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		
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		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
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		
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		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
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		
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		

Continued on next page...

Continued from previous page...

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

- 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		
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	PE	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	3708	Total	C	N	O	P	0	0
			79496	35401	14553	25835	3707		
85	L5	3708	Total	C	N	O	P	0	0
			79496	35401	14553	25835	3707		

- Molecule 86 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	Se	47	Total	C	N	O	S	0	0
			378	234	84	59	1		

- Molecule 87 is a protein called Ribosomal protein L24.

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

- Molecule 88 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
88	sa	1	Total	Zn	0
			1	1	
88	lg	1	Total	Zn	0
			1	1	
88	lj	1	Total	Zn	0
			1	1	
88	lm	1	Total	Zn	0
			1	1	
88	lo	1	Total	Zn	0
			1	1	
88	lp	1	Total	Zn	0
			1	1	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
88	Sa	1	Total 1	Zn 1	0
88	Lg	1	Total 1	Zn 1	0
88	Lj	1	Total 1	Zn 1	0
88	Lm	1	Total 1	Zn 1	0
88	Lo	1	Total 1	Zn 1	0
88	Lp	1	Total 1	Zn 1	0

- Molecule 89 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
89	l7	3	Total 3	Mg 3	0
89	l8	5	Total 5	Mg 5	0
89	lA	1	Total 1	Mg 1	0
89	lB	1	Total 1	Mg 1	0
89	le	2	Total 2	Mg 2	0
89	lg	1	Total 1	Mg 1	0
89	lj	1	Total 1	Mg 1	0
89	s2	29	Total 29	Mg 29	0
89	l5	212	Total 212	Mg 212	0
89	L5	213	Total 213	Mg 213	0
89	L7	3	Total 3	Mg 3	0
89	L8	5	Total 5	Mg 5	0
89	LA	1	Total 1	Mg 1	0

Continued on next page...

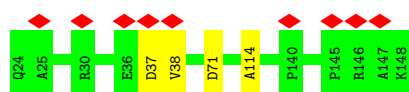
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
89	LP	1	Total 1	Mg 1	0
89	LV	1	Total 1	Mg 1	0
89	Le	1	Total 1	Mg 1	0
89	Lj	1	Total 1	Mg 1	0
89	S2	29	Total 29	Mg 29	0

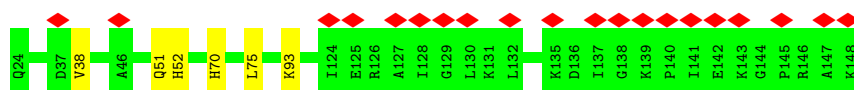
3 Residue-property plots

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.

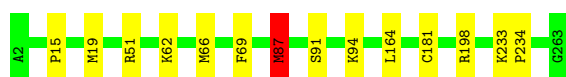
- Molecule 1: Endothelial differentiation-related factor 1



- Molecule 1: Endothelial differentiation-related factor 1



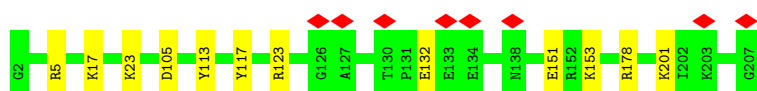
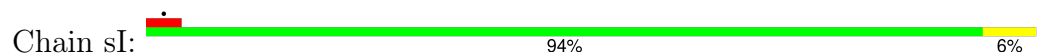
- Molecule 2: Small ribosomal subunit protein eS4, X isoform



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

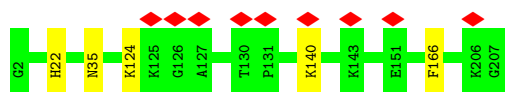


- Molecule 3: 40S ribosomal protein S8



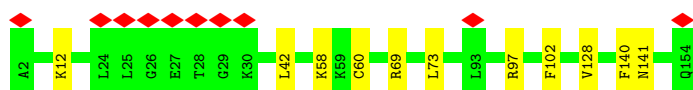
- Molecule 3: 40S ribosomal protein S8

Chain SI:  98%



- Molecule 4: 40S ribosomal protein S11

Chain sL:  7% 93% 7%



- Molecule 4: 40S ribosomal protein S11

Chain SL:  5% 96%



- Molecule 5: 40S ribosomal protein S23

Chain sX:  95% 5%



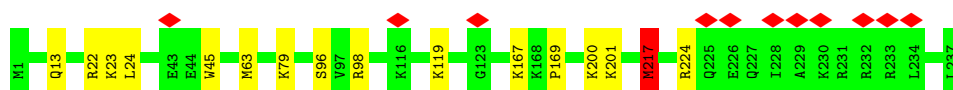
- Molecule 5: 40S ribosomal protein S23

Chain SX:  96%



- Molecule 6: 40S ribosomal protein S6

Chain sG:  5% 93% 6%

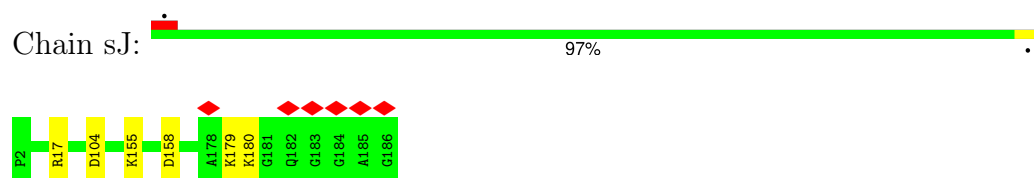


- Molecule 6: 40S ribosomal protein S6

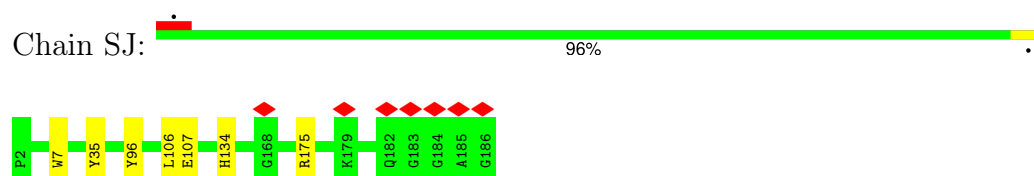
Chain SG:  5% 95% 5%



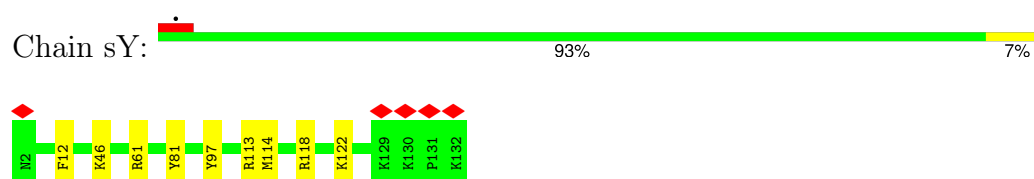
- Molecule 7: 40S ribosomal protein S9



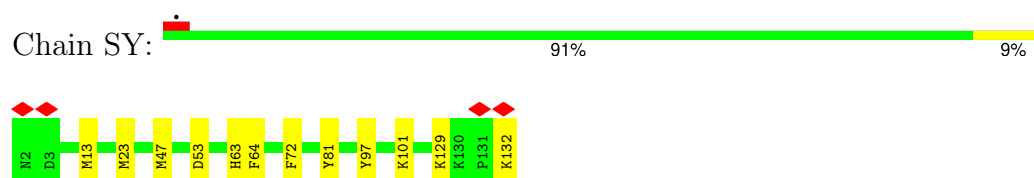
- Molecule 7: 40S ribosomal protein S9



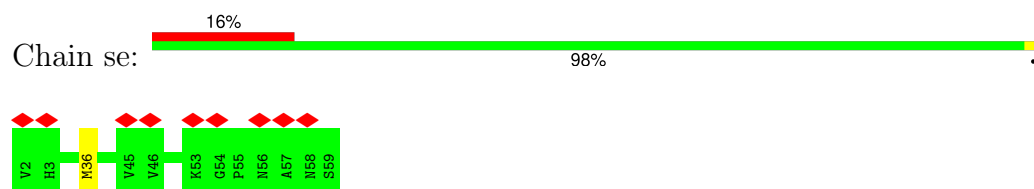
- Molecule 8: 40S ribosomal protein S24



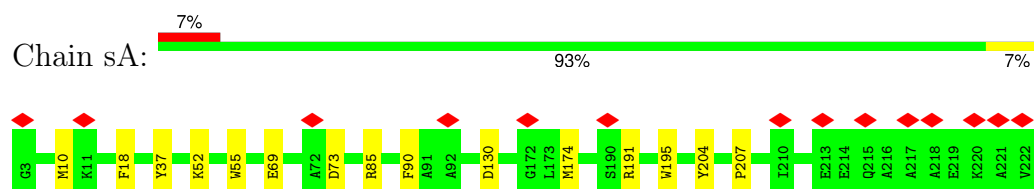
- Molecule 8: 40S ribosomal protein S24



- Molecule 9: Small ribosomal subunit protein eS30

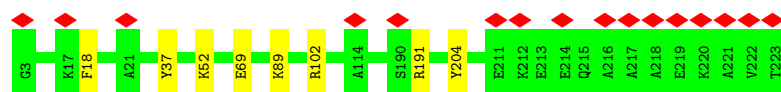


- Molecule 10: 40S ribosomal protein SA



- Molecule 10: 40S ribosomal protein SA

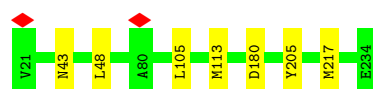




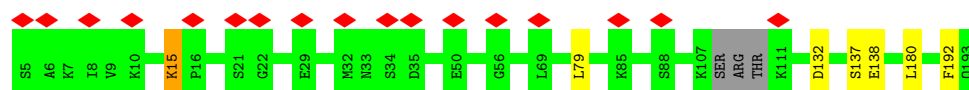
- Molecule 11: 40S ribosomal protein S3a



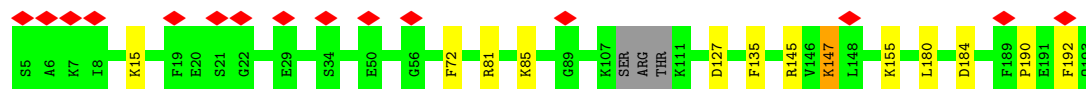
- Molecule 11: 40S ribosomal protein S3a



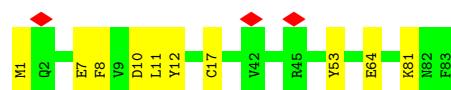
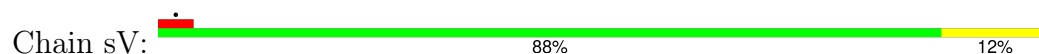
- Molecule 12: Small ribosomal subunit protein eS7



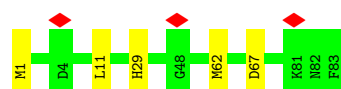
- Molecule 12: Small ribosomal subunit protein eS7



- Molecule 13: 40S ribosomal protein S21



- Molecule 13: 40S ribosomal protein S21



- Molecule 14: 40S ribosomal protein S26

Chain sa:  96%



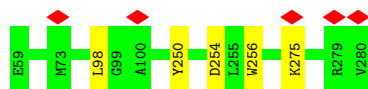
- Molecule 14: 40S ribosomal protein S26

Chain Sa:  95%



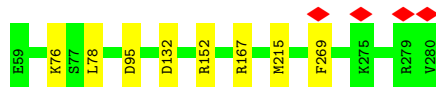
- Molecule 15: 40S ribosomal protein S2

Chain sC:  98%



- Molecule 15: 40S ribosomal protein S2

Chain SC:  96%



- Molecule 16: 40S ribosomal protein S13

Chain sN:  96%



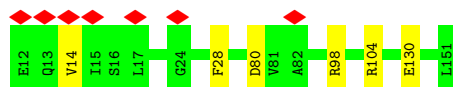
- Molecule 16: 40S ribosomal protein S13

Chain SN:  94%



- Molecule 17: Small ribosomal subunit protein uS11

Chain sO:  96%



- Molecule 17: Small ribosomal subunit protein uS11



- Molecule 18: 40S ribosomal protein S15a



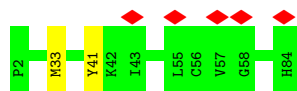
- Molecule 18: 40S ribosomal protein S15a



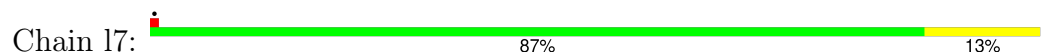
- Molecule 19: Small ribosomal subunit protein eS27



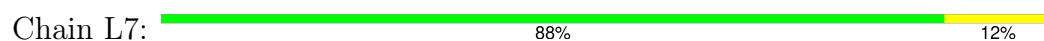
- Molecule 19: Small ribosomal subunit protein eS27



- Molecule 20: RNA (120-MER)5S rRNA [Homo sapiens]

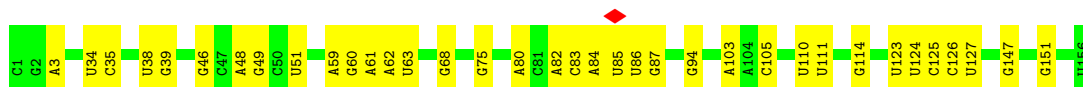
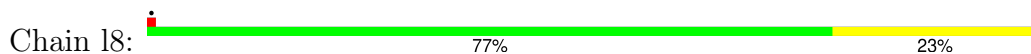


- Molecule 20: RNA (120-MER)5S rRNA [Homo sapiens]

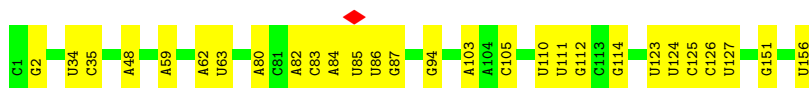
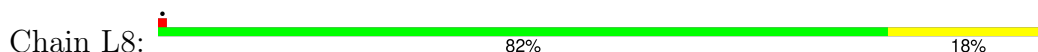




- Molecule 21: RNA (156-MER) 5.8S rRNA [Homo sapiens]



- Molecule 21: RNA (156-MER) 5.8S rRNA [Homo sapiens]



- Molecule 22: 60S ribosomal protein L8



- Molecule 22: 60S ribosomal protein L8



- Molecule 23: Large ribosomal subunit protein uL3



- Molecule 23: Large ribosomal subunit protein uL3



- Molecule 24: 60S ribosomal protein L4

M1	A2	Q50	W67	R78	M95	M101	K157	K175	D179	R188	M189	R190	N223	H245	F257	R291	K325	L326	K348	K353	A359	A360	L361	Q362	A363	K364	S365	D366	E367	R369
----	----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

-
- | Author | Number of Publications |
|--------|------------------------|
| M1 | 1 |
| A2 | 2 |
| V10 | 3 |
| K14 | 4 |
| N38 | 5 |
| Q50 | 6 |
| F102 | 7 |
| M196 | 8 |
| K234 | 9 |
| F249 | 10 |
| F257 | 11 |
| R258 | 12 |
| K259 | 13 |
| L273 | 14 |
| M325 | 15 |
| Y331 | 16 |
| M335 | 17 |
| A360 | 18 |
| A363 | 19 |
| K364 | 20 |
| S365 | 21 |
| D366 | 22 |
| E367 | 23 |
| K368 | 24 |

-

-
- | Category | Count |
|----------|-------|
| G2 | 1 |
| K5 | 1 |
| K41 | 1 |
| R68 | 1 |
| N94 | 1 |
| C100 | 1 |
| N111 | 1 |
| G127 | 1 |
| D128 | 1 |
| L146 | 1 |
| M208 | 1 |
| D217 | 1 |
| A218 | 1 |
| Y219 | 1 |
| N229 | 1 |
| M235 | 1 |
| M236 | 1 |
| M239 | 1 |
| K258 | 1 |
| Q291 | 1 |
| A294 | 1 |

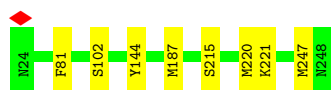
-
- A horizontal bar chart showing the distribution of amino acid types across different protein regions. The x-axis represents the count of amino acids, ranging from 0 to 142. The y-axis lists amino acid types: P42, R59, A76, LYS, SER, LYS, VAL, GLU, LYS, LYS, LYS, LYS, LYS, LYS, LYS, LYS, V88, R114, K130, F164, K224, P225, R226, H227, Q228, E231, I232, F233, E238, N279, Y282, and F288. The bars are color-coded: yellow for P42, R59, A76, R114, K130, F164, N279, Y282, and F288; grey for LYS, SER, VAL, GLU, and V88; and green for K224, P225, R226, H227, Q228, E231, I232, F233, E238. Red diamond markers are placed above the bars for K224, P225, R226, H227, Q228, E231, I232, F233, and E238.

-

-
- | Letter | Count |
|--------|-------|
| M | 24 |
| R | 34 |
| R | 43 |
| K | 44 |
| M | 64 |
| E | 68 |
| K | 88 |
| Y | 144 |
| C | 186 |
| D | 189 |
| M | 220 |
| D | 232 |
| D | 238 |
| M | 247 |
| M | 248 |

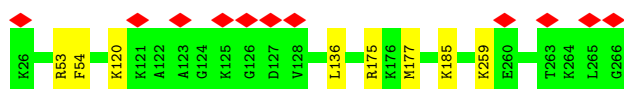
- Molecule 27: 60S ribosomal protein L7

Chain LF:  96%



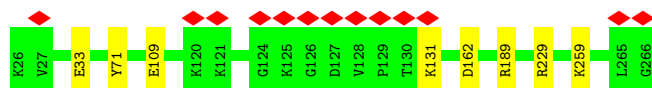
- Molecule 28: 60S ribosomal protein L7a

Chain IG:  97%



- Molecule 28: 60S ribosomal protein L7a

Chain LG:  97%



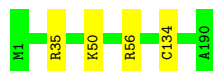
- Molecule 29: 60S ribosomal protein L9

Chain IH:  96%



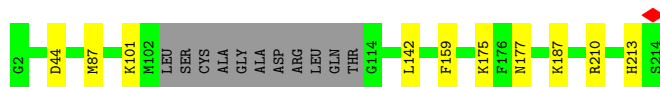
- Molecule 29: 60S ribosomal protein L9

Chain LH:  98%



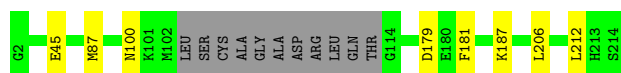
- Molecule 30: Ribosomal protein uL16-like

Chain II:  90% 5% 5%

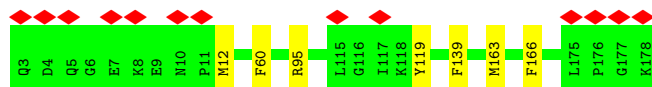


- Molecule 30: Ribosomal protein uL16-like

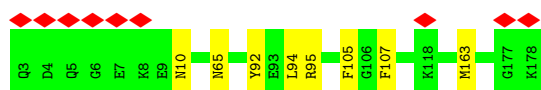
Chain LI:  91%



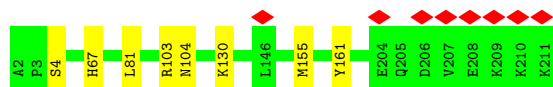
- Molecule 31: 60S ribosomal protein L11



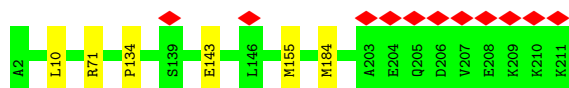
- Molecule 31: 60S ribosomal protein L11



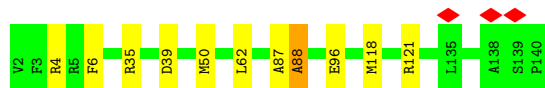
- Molecule 32: Large ribosomal subunit protein eL13



- Molecule 32: Large ribosomal subunit protein eL13



- Molecule 33: 60S ribosomal protein L14



- Molecule 33: 60S ribosomal protein L14



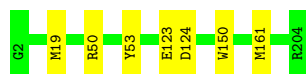
- Molecule 34: 60S ribosomal protein L15

Chain IN:  98% .



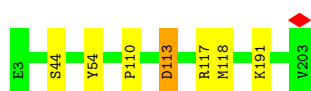
- Molecule 34: 60S ribosomal protein L15

Chain LN:  97% .



- Molecule 35: 60S ribosomal protein L13a

Chain LO:  97% .



- Molecule 35: 60S ribosomal protein L13a

Chain LO:  98% .



- Molecule 36: 60S ribosomal protein L17

Chain IP:  95% . .



- Molecule 36: 60S ribosomal protein L17

Chain LP:  96% .



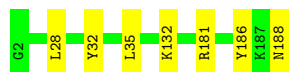
- Molecule 37: 60S ribosomal protein L18

Chain IQ:  96% .



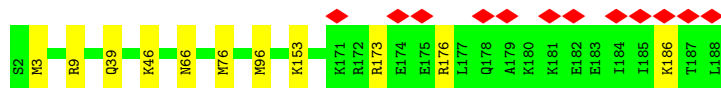
- Molecule 37: 60S ribosomal protein L18

Chain LQ:  96%



- Molecule 38: 60S ribosomal protein L19

Chain IR:  6% 94% 6%



- Molecule 38: 60S ribosomal protein L19

Chain LR:  5% 93% 7%



- Molecule 39: 60S ribosomal protein L18a

Chain IS:  94% 6%



- Molecule 39: 60S ribosomal protein L18a

Chain LS:  97%



- Molecule 40: 60S ribosomal protein L21

Chain IT:  96%



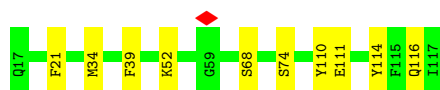
- Molecule 40: 60S ribosomal protein L21

Chain LT:  96%




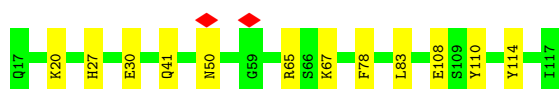
- Molecule 41: Heparin-binding protein HBp15

Chain IU:  90% 10%



- Molecule 41: Heparin-binding protein HBp15

Chain LU:  88% 12%



- 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%



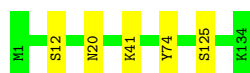
- Molecule 43: 60S ribosomal protein L23a

Chain LX:  95% 5%



- Molecule 44: 60S ribosomal protein L26

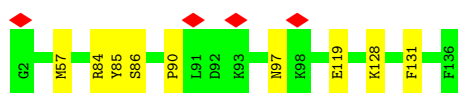
Chain IY:  96%



- Molecule 44: 60S ribosomal protein L26



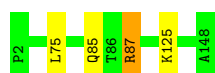
- Molecule 45: 60S ribosomal protein L27



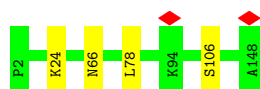
- Molecule 45: 60S ribosomal protein L27



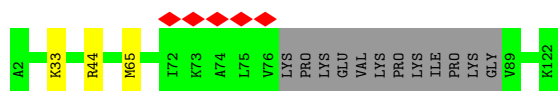
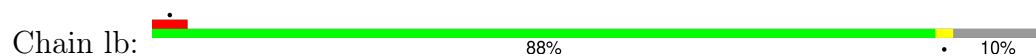
- Molecule 46: 60S ribosomal protein L27a



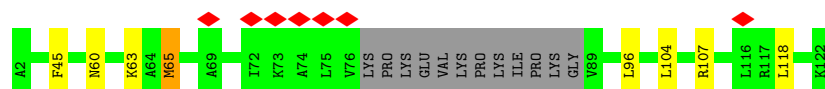
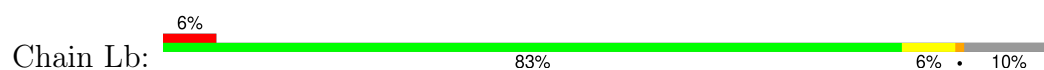
- Molecule 46: 60S ribosomal protein L27a



- Molecule 47: Large ribosomal subunit protein eL29



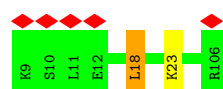
- Molecule 47: Large ribosomal subunit protein eL29



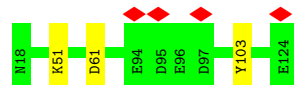
- Molecule 48: 60S ribosomal protein L30



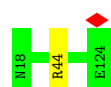
- Molecule 48: 60S ribosomal protein L30



- Molecule 49: 60S ribosomal protein L31



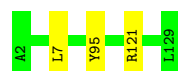
- Molecule 49: 60S ribosomal protein L31



- Molecule 50: 60S ribosomal protein L32



- Molecule 50: 60S ribosomal protein L32



- Molecule 51: 60S ribosomal protein L35a

Chain lf:  92% 8%



- Molecule 51: 60S ribosomal protein L35a

Chain Lf:  96% .



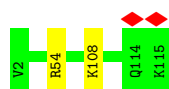
- Molecule 52: 60S ribosomal protein L34

Chain lg:  97% .



- Molecule 52: 60S ribosomal protein L34

Chain Lg:  98% .



- Molecule 53: 60S ribosomal protein L35

Chain lh:  97% .



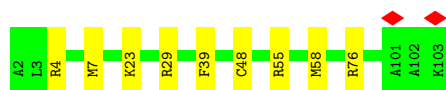
- Molecule 53: 60S ribosomal protein L35

Chain Lh:  94% 6%

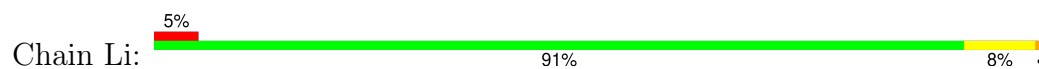


- Molecule 54: 60S ribosomal protein L36

Chain li:  91% 9%



- Molecule 54: 60S ribosomal protein L36



- Molecule 55: 60S ribosomal protein L37



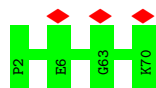
- Molecule 55: 60S ribosomal protein L37



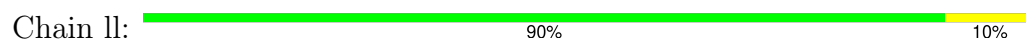
- Molecule 56: 60S ribosomal protein L38



- Molecule 56: 60S ribosomal protein L38



- Molecule 57: 60S ribosomal protein L39

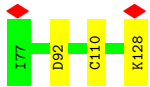


- Molecule 57: 60S ribosomal protein L39

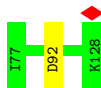




- Molecule 58: Large ribosomal subunit protein eL40



- Molecule 58: Large ribosomal subunit protein eL40



- Molecule 59: 60S ribosomal protein L41

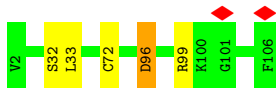


- Molecule 59: 60S ribosomal protein L41



There are no outlier residues recorded for this chain.

- Molecule 60: 60S ribosomal protein L36a



- Molecule 60: 60S ribosomal protein L36a



- Molecule 61: 60S ribosomal protein L37a





- Molecule 61: 60S ribosomal protein L37a

Chain Lp: 98%



- Molecule 62: 60S ribosomal protein L28

Chain lr: 97%



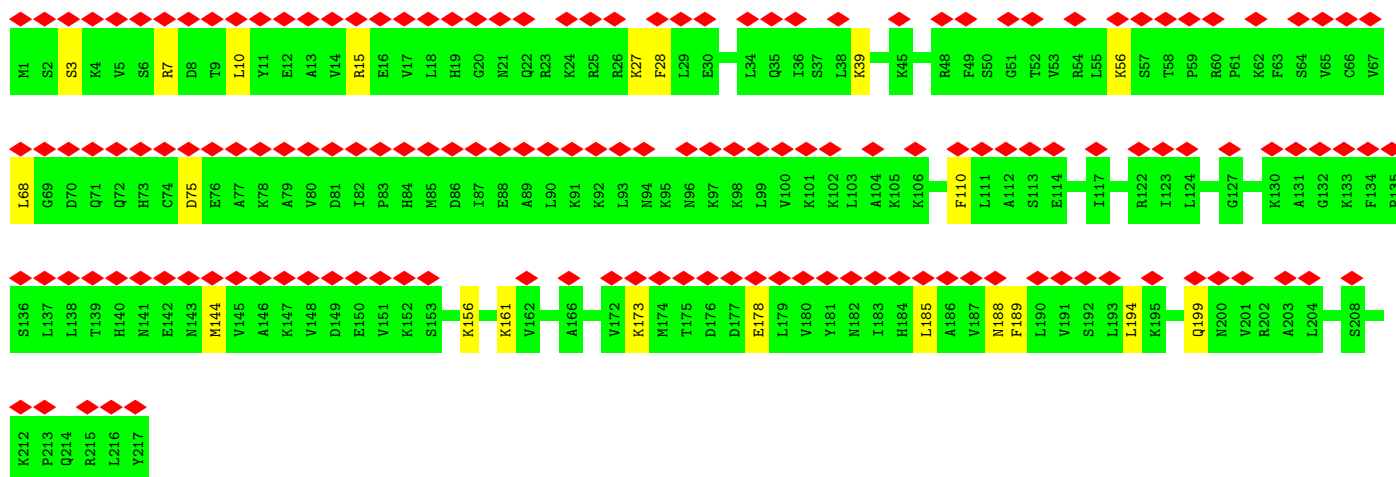
- Molecule 62: 60S ribosomal protein L28

Chain Lr: 97%



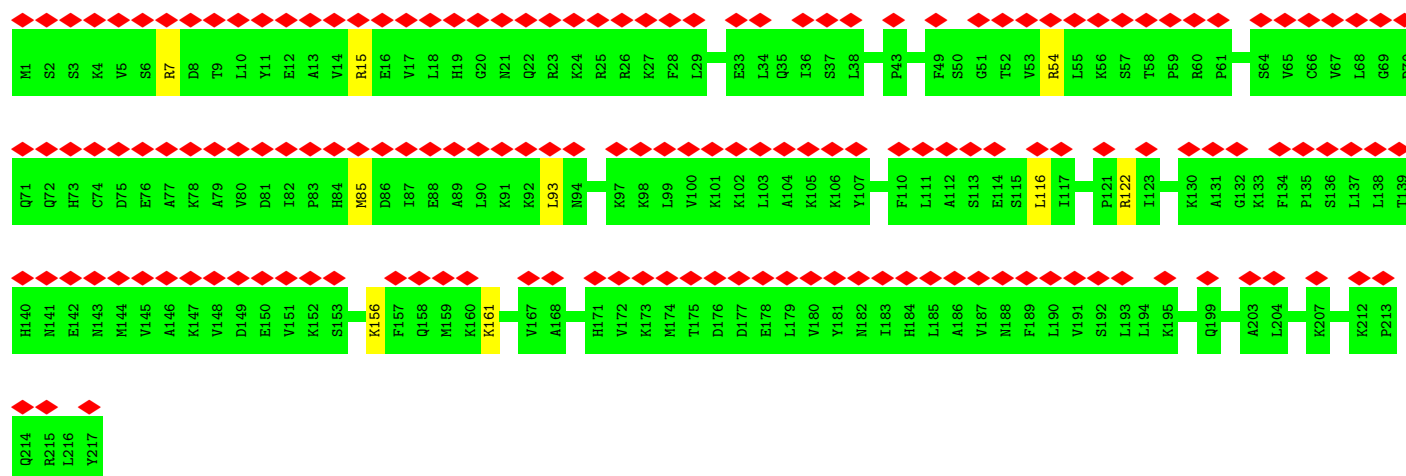
- Molecule 63: 60S ribosomal protein L10a

Chain lz: 71% 90% 10%

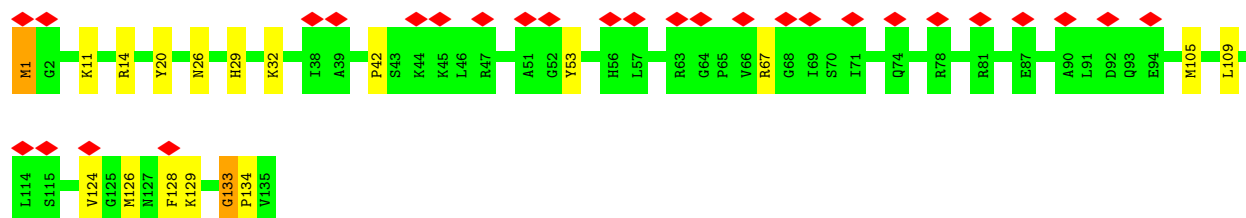
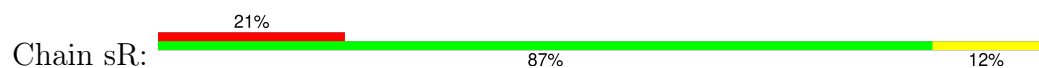


- Molecule 63: 60S ribosomal protein L10a

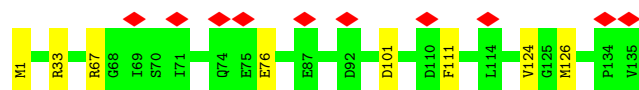
Chain Lz: 74% 96%



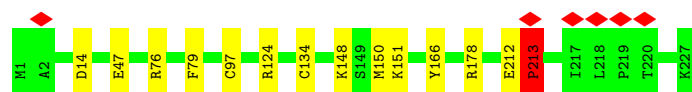
- Molecule 64: 40S ribosomal protein S17



- Molecule 64: 40S ribosomal protein S17



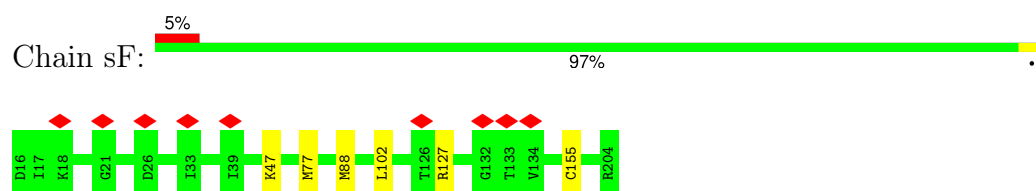
- Molecule 65: Small ribosomal subunit protein uS3



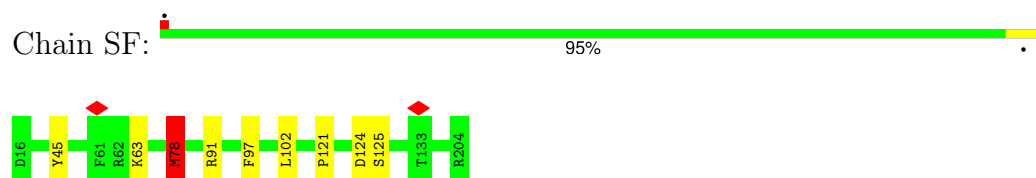
- Molecule 65: Small ribosomal subunit protein uS3



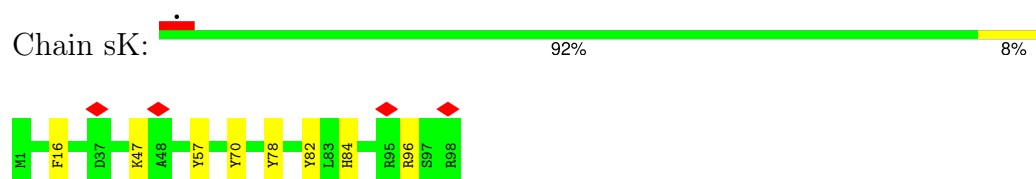
- Molecule 66: 40S ribosomal protein S5



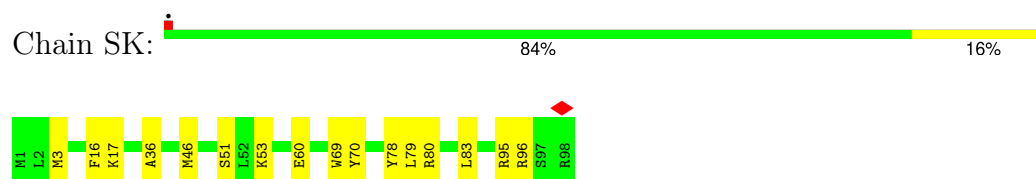
- Molecule 66: 40S ribosomal protein S5



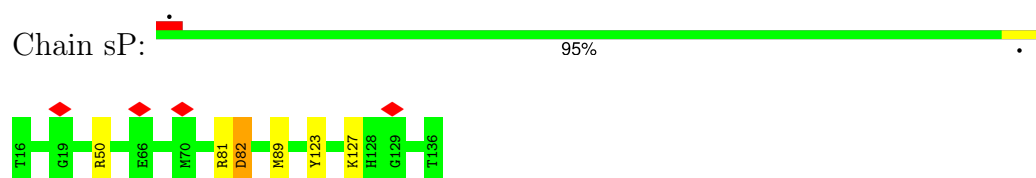
- Molecule 67: 40S ribosomal protein S10



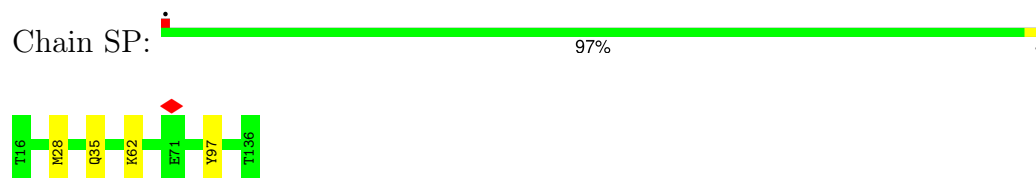
- Molecule 67: 40S ribosomal protein S10



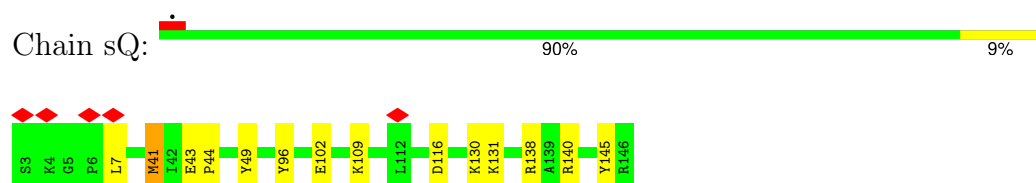
- Molecule 68: Small ribosomal subunit protein uS19



- Molecule 68: Small ribosomal subunit protein uS19

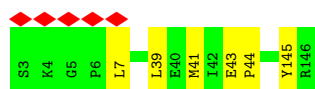


- Molecule 69: Small ribosomal subunit protein uS9



- Molecule 69: Small ribosomal subunit protein uS9

Chain SQ:  96%



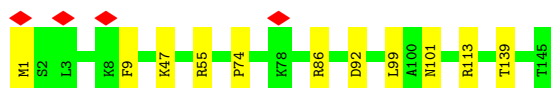
- Molecule 70: 40S ribosomal protein S18

Chain sS:  95%



- Molecule 70: 40S ribosomal protein S18

Chain SS:  92%




- Molecule 71: 40S ribosomal protein S19

Chain sT:  94%



- Molecule 71: 40S ribosomal protein S19

Chain ST:  90%



- Molecule 72: 40S ribosomal protein S20

Chain sU:  96%

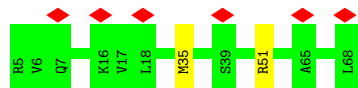


- Molecule 72: 40S ribosomal protein S20

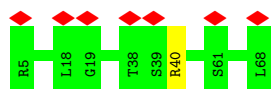
Chain SU:  94%



- Molecule 73: 40S ribosomal protein S28



- Molecule 73: 40S ribosomal protein S28



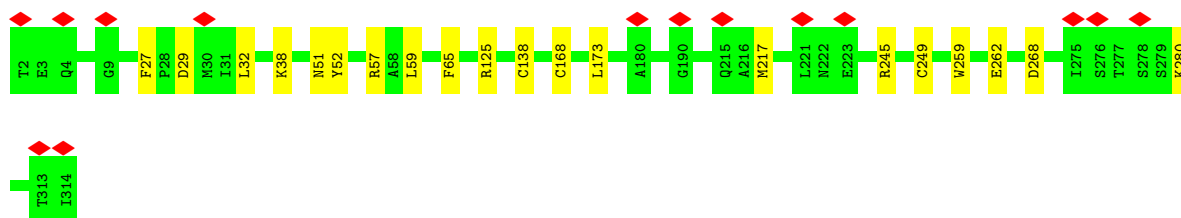
- Molecule 74: 40S ribosomal protein S29



- Molecule 74: 40S ribosomal protein S29

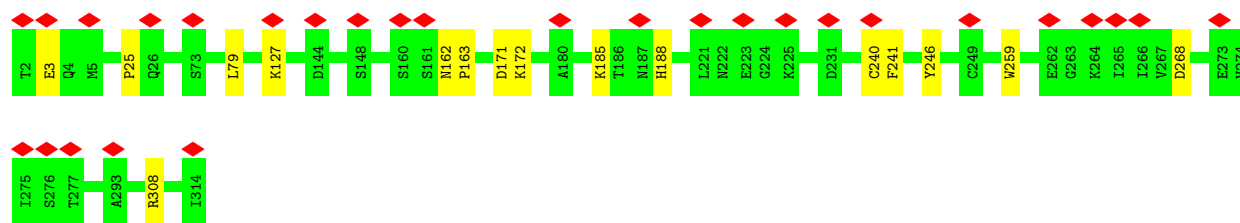


- Molecule 75: Receptor of activated protein C kinase 1

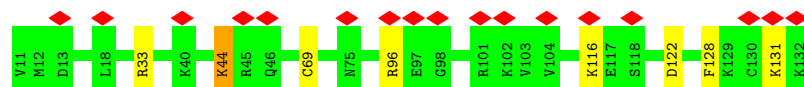


- Molecule 75: Receptor of activated protein C kinase 1

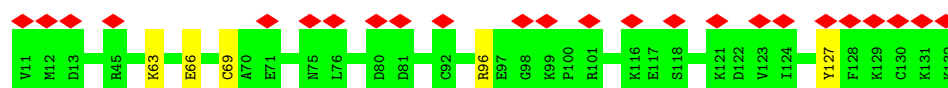




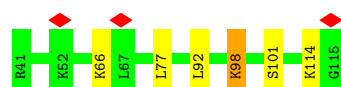
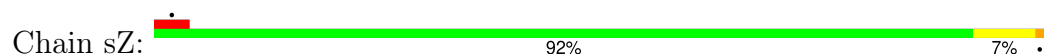
- Molecule 76: Small ribosomal subunit protein eS12



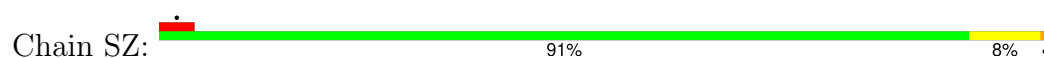
- Molecule 76: Small ribosomal subunit protein eS12



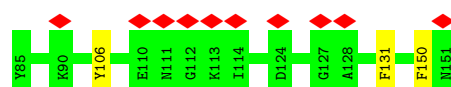
- Molecule 77: Small ribosomal subunit protein eS25



- Molecule 77: Small ribosomal subunit protein eS25

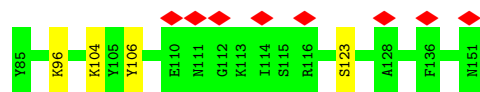


- Molecule 78: Ubiquitin-40S ribosomal protein S27a



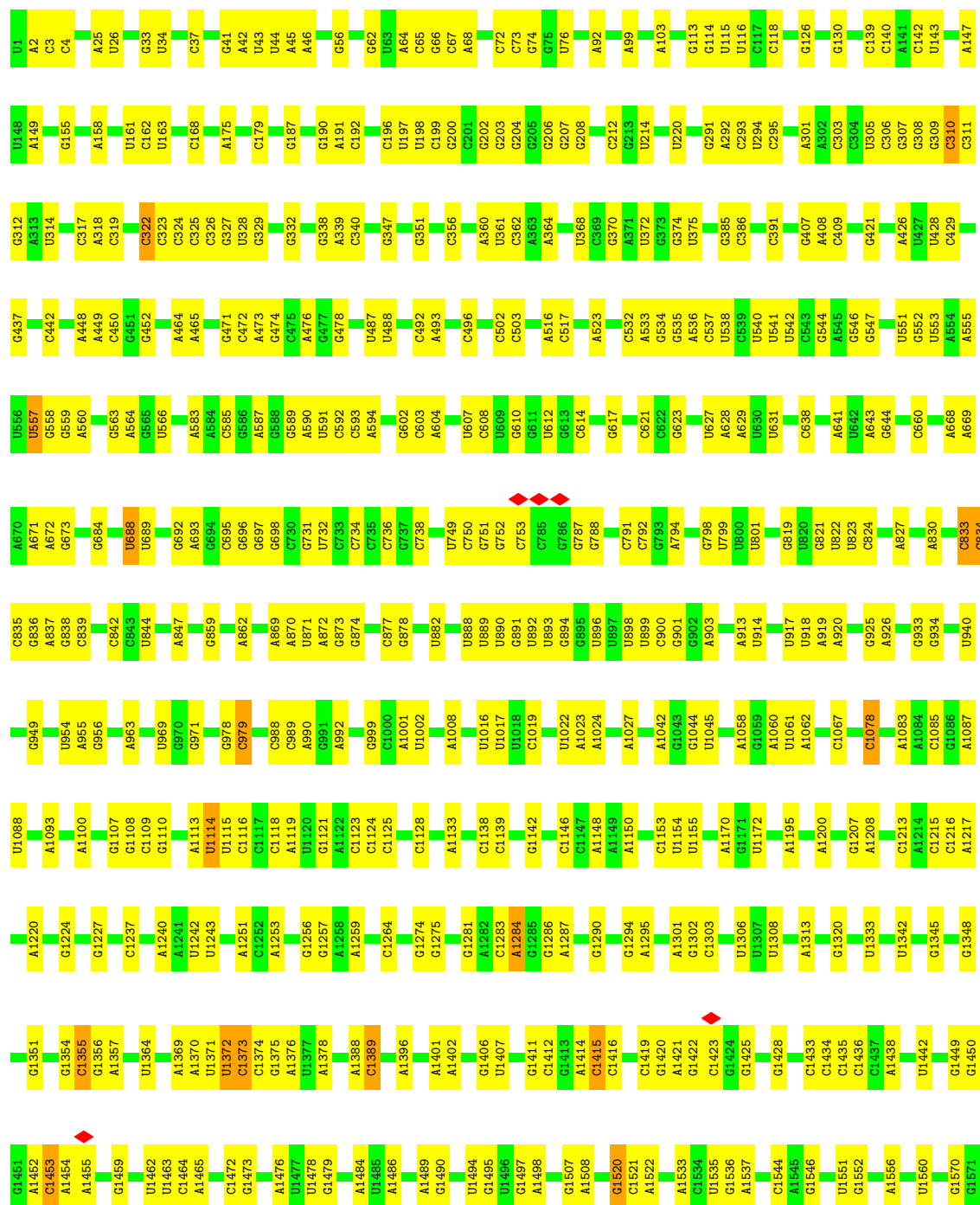
- Molecule 78: Ubiquitin-40S ribosomal protein S27a

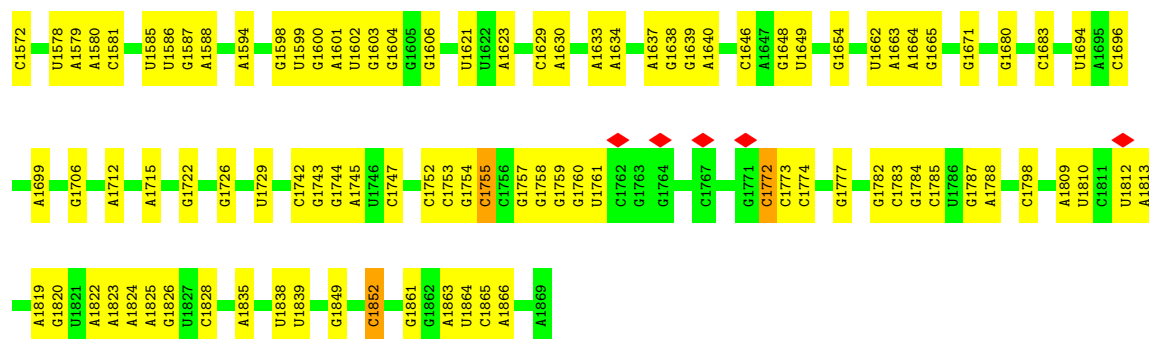




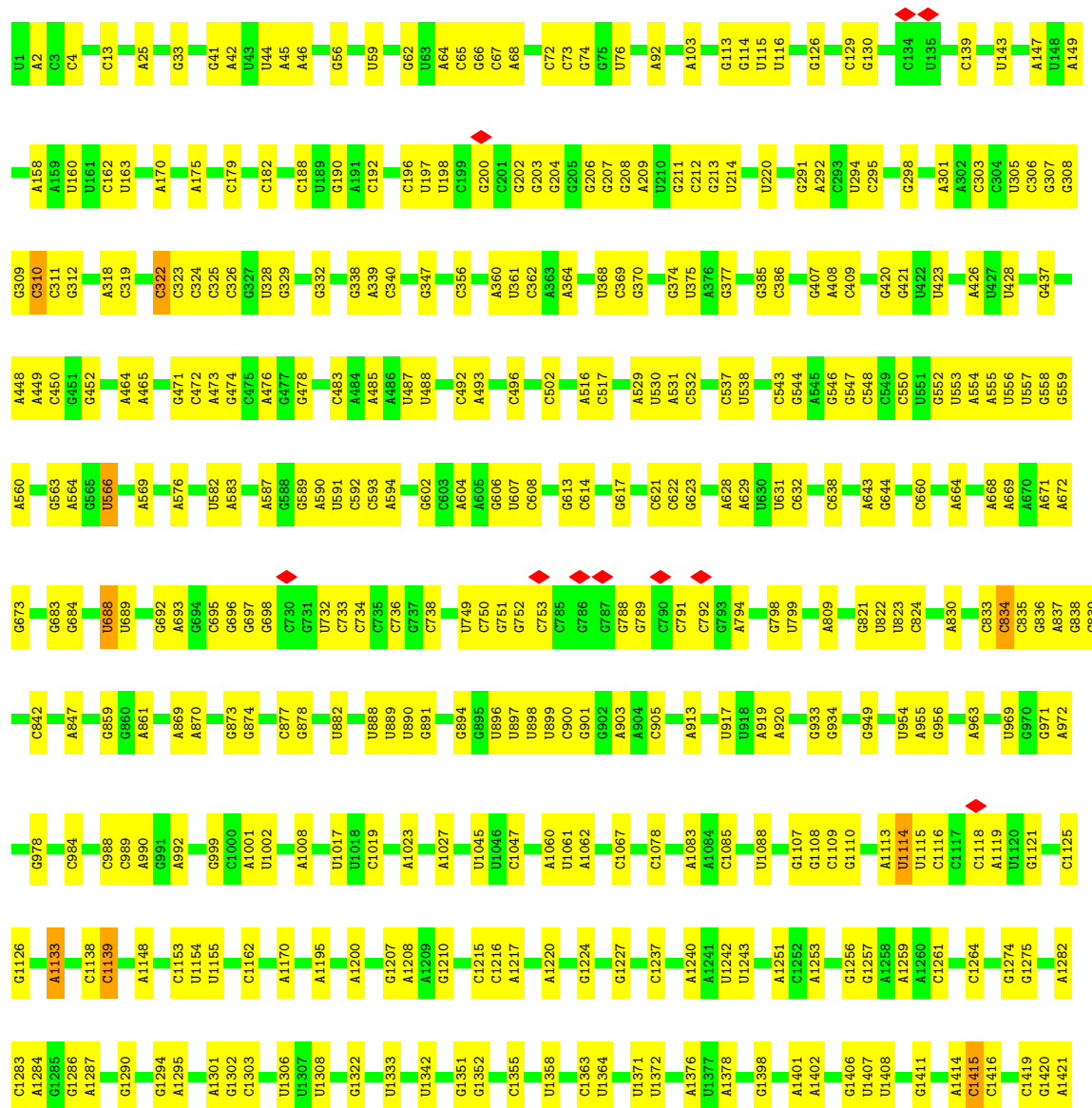
• Molecule 79: 18S rRNA [Homo sapiens]

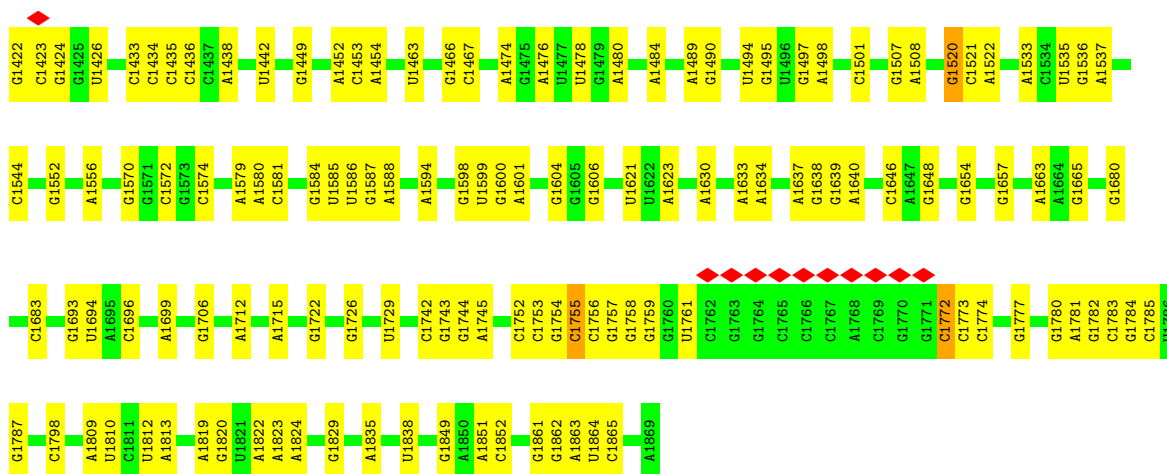
Chain s2: 68% 31%



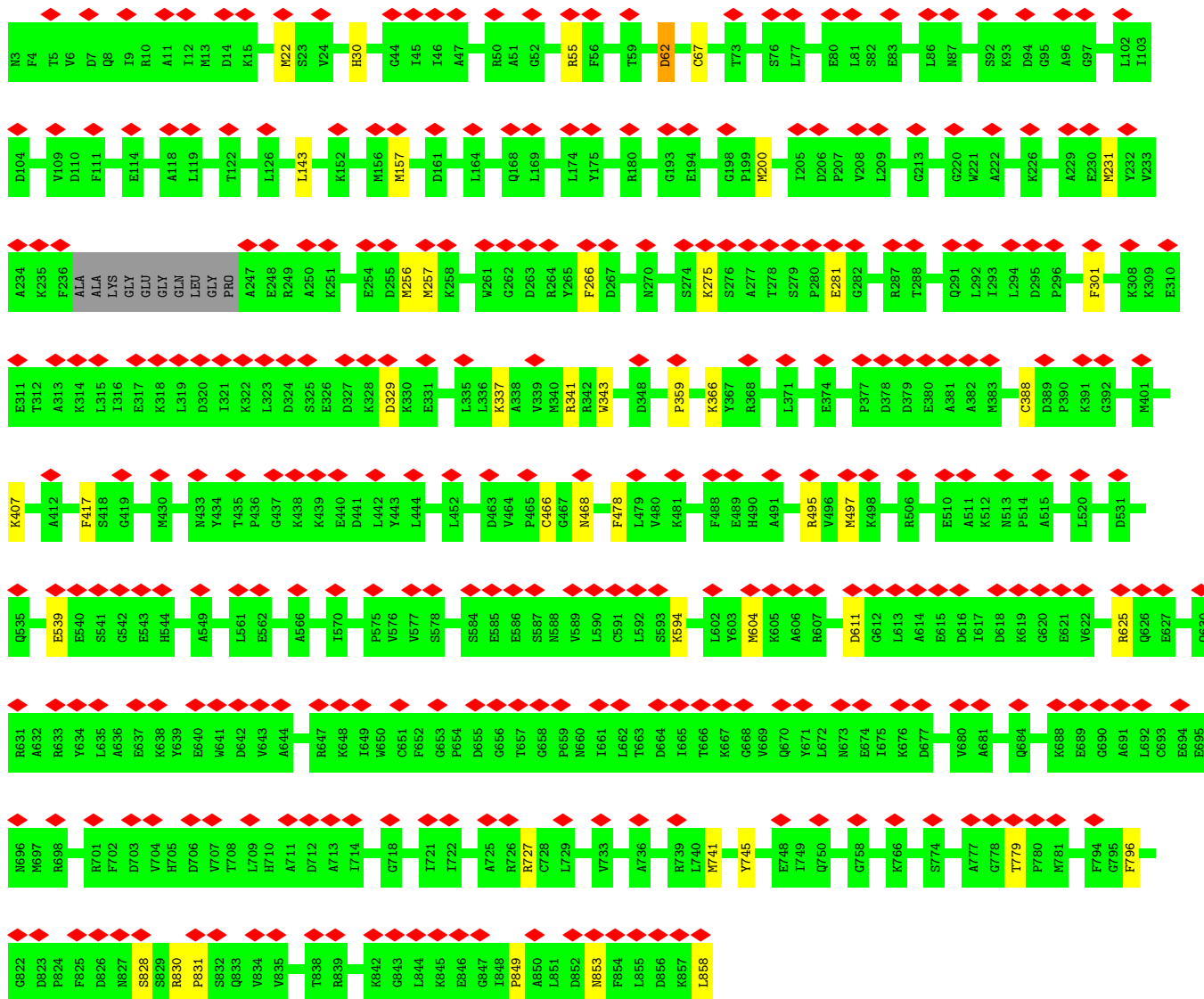


• Molecule 79: 18S rRNA [Homo sapiens]





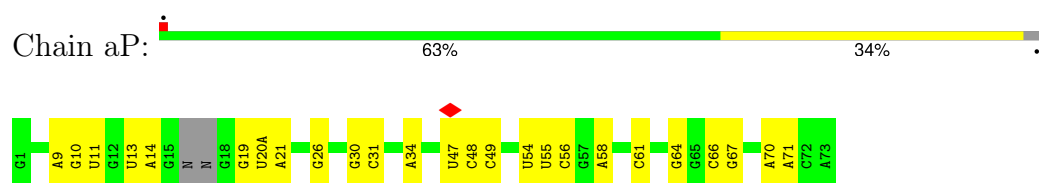
• Molecule 80: Elongation factor 2



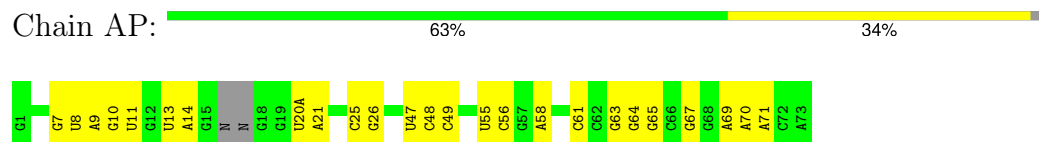
- Molecule 80: Elongation factor 2



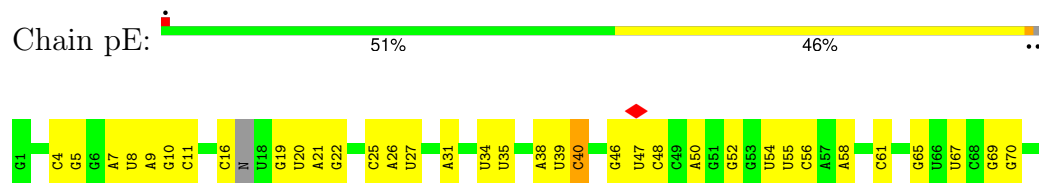
- Molecule 81: A/P site tRNA [Homo sapiens]



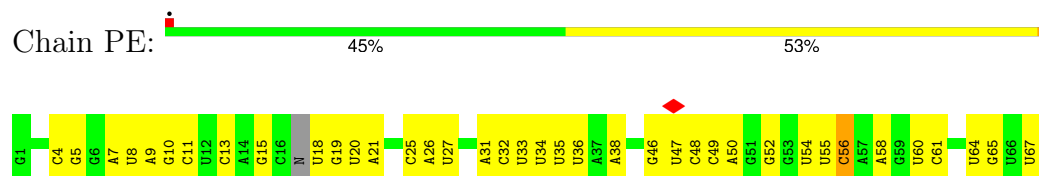
- Molecule 81: A/P site tRNA [Homo sapiens]



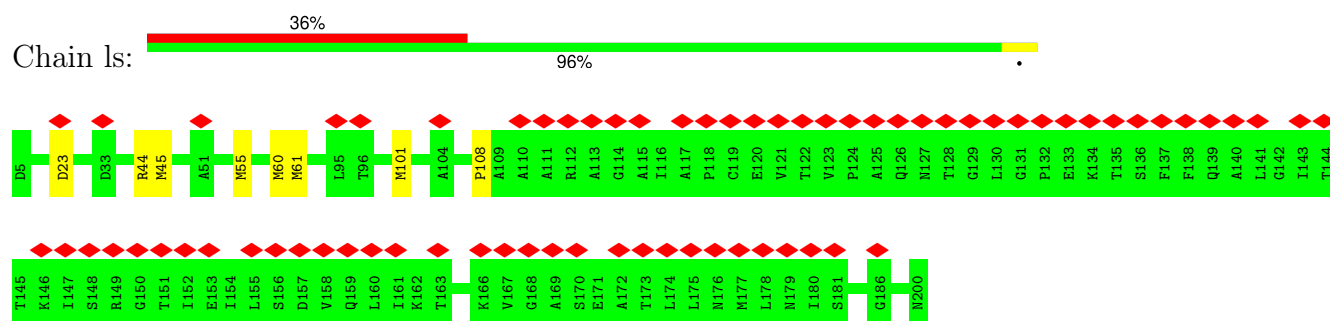
- Molecule 82: P/E site tRNA [Homo sapiens]



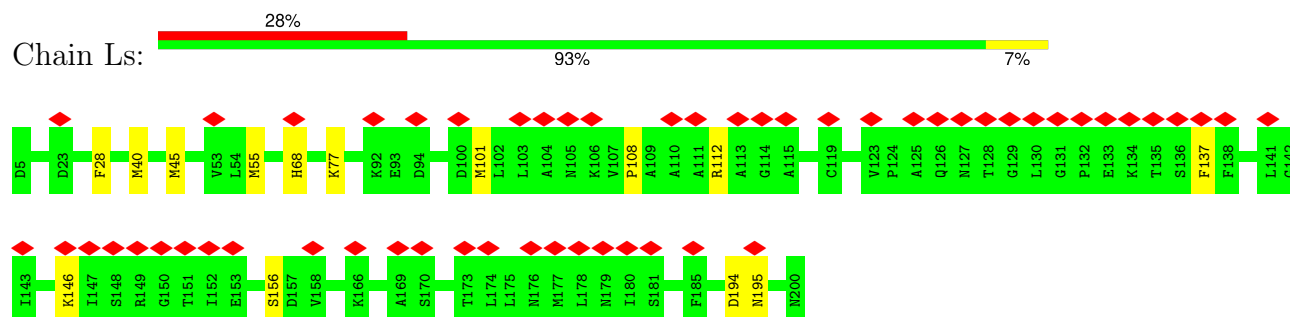
- Molecule 82: P/E site tRNA [Homo sapiens]



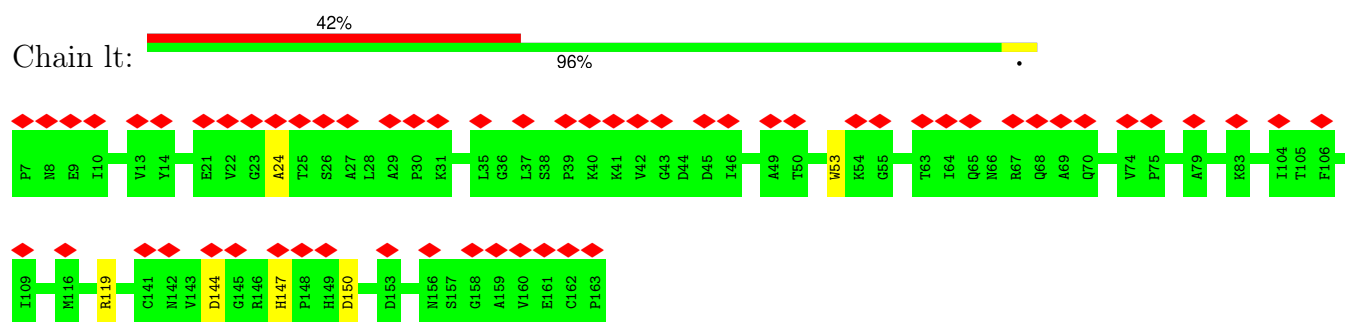
- Molecule 83: 60S acidic ribosomal protein P0



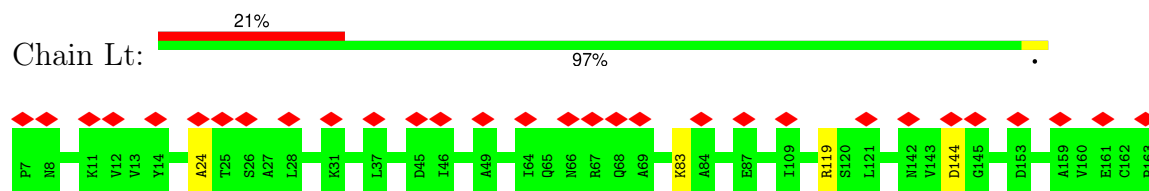
- Molecule 83: 60S acidic ribosomal protein P0



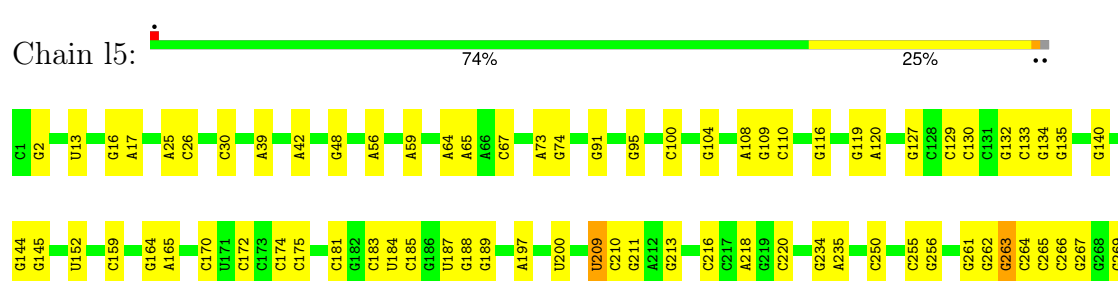
- Molecule 84: 60S ribosomal protein L12 [Homo sapiens]

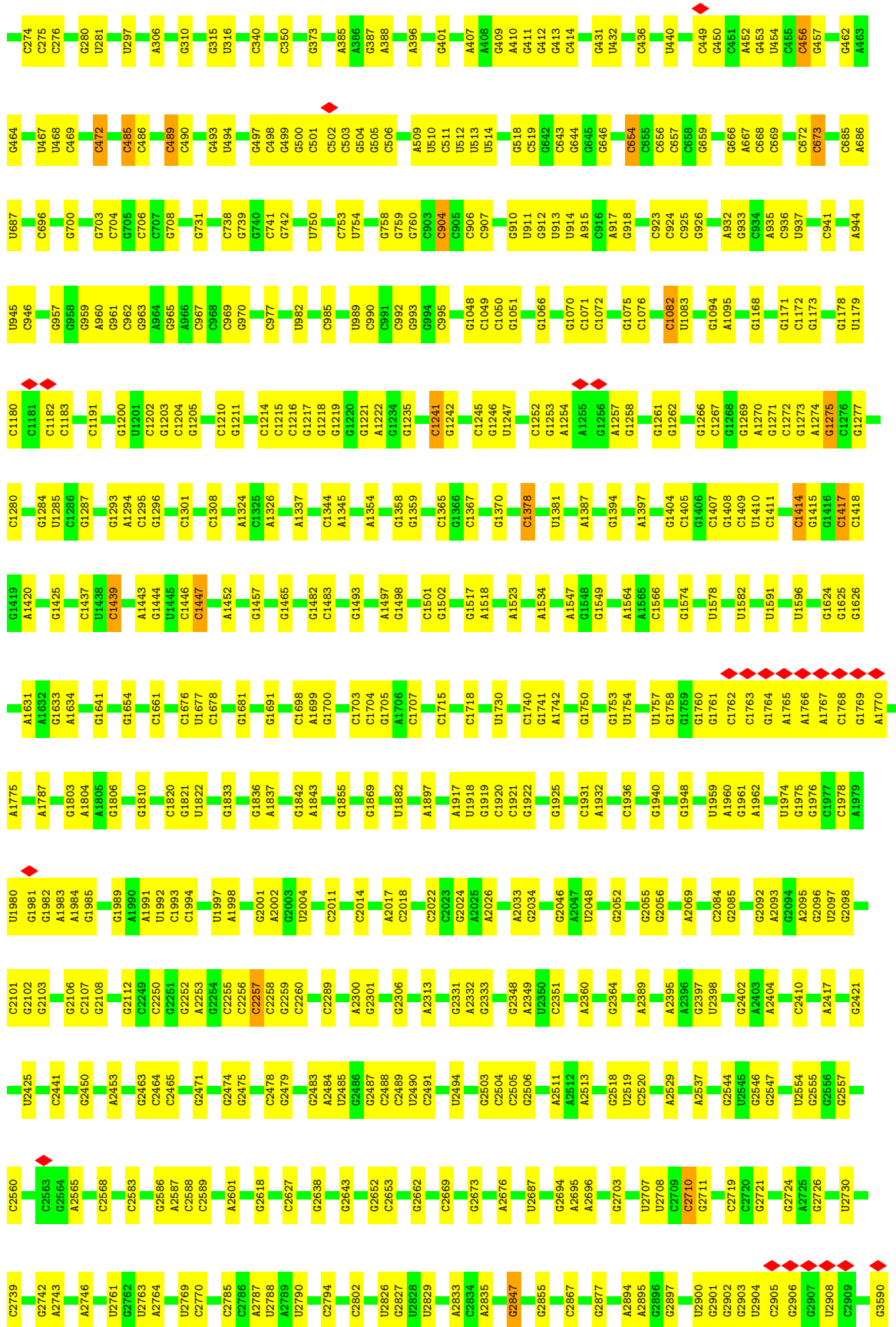


- Molecule 84: 60S ribosomal protein L12 [Homo sapiens]



- Molecule 85: 28S rRNA [Homo sapiens]

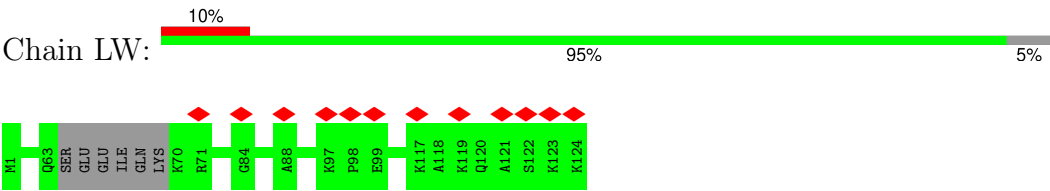








● Molecule 87: Ribosomal protein L24



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45867	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	0.580	Depositor
Minimum map value	-0.081	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.032	Depositor
Recommended contour level	0.096	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: MG, ZN

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	0.34	0/977	0.67	1/1306 (0.1%)
1	cH	0.32	0/977	0.66	0/1306
2	SE	0.33	1/2118 (0.0%)	0.62	4/2849 (0.1%)
2	sE	0.39	0/2118	0.68	5/2849 (0.2%)
3	SI	0.30	0/1715	0.60	0/2287
3	sI	0.32	0/1715	0.59	0/2287
4	SL	0.31	0/1268	0.59	1/1696 (0.1%)
4	sL	0.44	0/1268	0.69	3/1696 (0.2%)
5	SX	0.32	0/1116	0.59	0/1490
5	sX	0.40	0/1116	0.66	1/1490 (0.1%)
6	SG	0.30	0/1946	0.63	1/2590 (0.0%)
6	sG	0.32	0/1946	0.66	3/2590 (0.1%)
7	SJ	0.29	0/1550	0.65	0/2069
7	sJ	0.31	0/1550	0.62	0/2069
8	SY	0.29	0/1083	0.60	0/1438
8	sY	0.33	0/1083	0.64	0/1438
9	se	0.30	0/465	0.67	0/612
10	SA	0.33	0/1778	0.63	0/2416
10	sA	0.56	3/1778 (0.2%)	0.85	5/2416 (0.2%)
11	SB	0.30	0/1765	0.58	0/2362
11	sB	0.47	2/1765 (0.1%)	0.65	1/2362 (0.0%)
12	SH	0.32	0/1519	0.62	1/2033 (0.0%)
12	sH	0.31	0/1519	0.62	0/2033
13	SV	0.31	0/643	0.59	0/860
13	sV	0.43	0/643	0.77	1/860 (0.1%)
14	Sa	0.39	1/836 (0.1%)	0.76	2/1121 (0.2%)
14	sa	0.37	0/836	0.66	0/1121
15	SC	0.36	0/1762	0.65	1/2381 (0.0%)
15	sC	0.38	0/1762	0.64	1/2381 (0.0%)
16	SN	0.30	0/1232	0.62	1/1656 (0.1%)
16	sN	0.37	0/1232	0.66	0/1656
17	SO	0.33	0/1062	0.67	1/1425 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	sO	0.33	0/1062	0.69	2/1425 (0.1%)
18	SW	0.35	0/1051	0.68	1/1406 (0.1%)
18	sW	0.38	0/1051	0.65	0/1406
19	Sb	0.30	0/665	0.60	0/891
19	sb	0.56	3/665 (0.5%)	0.95	3/891 (0.3%)
20	L7	0.38	0/2861	0.78	0/4459
20	l7	0.53	0/2861	0.81	0/4459
21	L8	0.39	0/3701	0.80	0/5766
21	l8	0.51	0/3701	0.81	1/5766 (0.0%)
22	LA	0.37	0/1936	0.69	3/2596 (0.1%)
22	lA	0.41	0/1936	0.67	2/2596 (0.1%)
23	LB	0.31	0/3306	0.58	1/4424 (0.0%)
23	lB	0.36	0/3306	0.61	1/4424 (0.0%)
24	LC	0.50	6/2981 (0.2%)	0.76	6/4002 (0.1%)
24	lC	0.35	0/2981	0.63	3/4002 (0.1%)
25	LD	0.33	0/2428	0.64	2/3252 (0.1%)
25	lD	0.35	0/2428	0.59	0/3252
26	LE	0.29	0/1942	0.57	0/2606
26	lE	0.38	0/1942	0.61	0/2606
27	LF	0.33	0/1905	0.60	0/2539
27	lF	0.37	0/1905	0.63	1/2539 (0.0%)
28	LG	0.29	0/1960	0.57	1/2637 (0.0%)
28	lG	0.34	0/1960	0.61	0/2637
29	LH	0.28	0/1537	0.58	0/2066
29	lH	0.41	1/1537 (0.1%)	0.63	0/2066
30	LI	0.32	0/1673	0.61	0/2233
30	lI	0.36	0/1673	0.61	0/2233
31	LJ	0.33	0/1433	0.65	0/1915
31	lJ	0.36	0/1433	0.67	1/1915 (0.1%)
32	LL	0.30	0/1732	0.60	0/2315
32	lL	0.33	0/1732	0.62	0/2315
33	LM	0.36	1/1161 (0.1%)	0.62	0/1554
33	lM	0.46	1/1161 (0.1%)	0.79	2/1554 (0.1%)
34	LN	0.31	0/1746	0.60	0/2338
34	lN	0.40	0/1746	0.63	0/2338
35	LO	0.31	0/1682	0.60	1/2250 (0.0%)
35	lO	0.41	0/1682	0.65	1/2250 (0.0%)
36	LP	0.31	0/1268	0.57	0/1701
36	lP	0.38	0/1268	0.66	2/1701 (0.1%)
37	LQ	0.33	0/1537	0.68	1/2052 (0.0%)
37	lQ	0.36	0/1537	0.66	2/2052 (0.1%)
38	LR	0.27	0/1582	0.61	0/2091
38	lR	0.33	0/1582	0.66	1/2091 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
39	LS	0.31	0/1493	0.59	0/2003
39	IS	0.37	0/1493	0.64	0/2003
40	LT	0.33	0/1326	0.63	0/1770
40	IT	0.37	0/1326	0.64	1/1770 (0.1%)
41	LU	0.31	0/839	0.64	0/1126
41	IU	0.41	0/839	0.66	0/1126
42	LV	0.30	0/993	0.53	0/1332
42	IV	0.37	0/993	0.63	1/1332 (0.1%)
43	LX	0.31	0/1002	0.63	0/1345
43	IX	0.37	0/1002	0.62	0/1345
44	LY	0.30	0/1132	0.59	0/1504
44	IY	0.32	0/1132	0.59	0/1504
45	LZ	0.33	0/1130	0.59	0/1507
45	IZ	0.45	0/1130	0.72	1/1507 (0.1%)
46	La	0.32	0/1191	0.60	0/1591
46	la	0.38	0/1191	0.62	1/1591 (0.1%)
47	Lb	0.30	0/889	0.68	1/1175 (0.1%)
47	lb	0.33	0/889	0.66	0/1175
48	Lc	0.32	0/774	0.68	1/1038 (0.1%)
48	lc	0.37	0/774	0.63	0/1038
49	Ld	0.30	0/903	0.63	0/1216
49	ld	0.35	0/903	0.62	0/1216
50	Le	0.32	0/1071	0.68	1/1429 (0.1%)
50	le	0.38	0/1071	0.62	0/1429
51	Lf	0.29	0/895	0.60	0/1198
51	lf	0.38	0/895	0.67	1/1198 (0.1%)
52	Lg	0.30	0/916	0.60	0/1220
52	lg	0.37	0/916	0.71	0/1220
53	Lh	0.34	0/1023	0.66	0/1351
53	lh	0.42	1/1023 (0.1%)	0.61	0/1351
54	Li	0.43	0/843	0.84	5/1115 (0.4%)
54	li	0.33	0/843	0.67	0/1115
55	Lj	0.34	0/720	0.74	2/952 (0.2%)
55	lj	0.46	0/720	0.69	0/952
56	Lk	0.32	0/575	0.60	0/761
56	lk	0.36	0/575	0.63	0/761
57	Ll	0.27	0/454	0.58	0/599
57	ll	0.36	0/454	0.84	2/599 (0.3%)
58	Lm	0.29	0/435	0.61	0/575
58	lm	0.33	0/435	0.63	0/575
59	Ln	0.29	0/231	0.83	0/294
59	ln	0.31	0/231	0.84	0/294
60	Lo	0.29	0/876	0.62	0/1156

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
60	lo	0.39	0/876	0.68	2/1156 (0.2%)
61	Lp	0.31	0/718	0.62	1/953 (0.1%)
61	lp	0.40	0/718	0.63	0/953
62	Lr	0.31	0/1017	0.68	2/1364 (0.1%)
62	lr	0.44	0/1017	0.67	1/1364 (0.1%)
63	Lz	0.26	0/1769	0.60	1/2371 (0.0%)
63	lz	0.26	0/1769	0.57	1/2371 (0.0%)
64	SR	0.37	0/1105	0.78	2/1484 (0.1%)
64	sR	0.73	2/1105 (0.2%)	1.14	7/1484 (0.5%)
65	SD	0.33	0/1793	0.63	2/2414 (0.1%)
65	sD	0.86	6/1793 (0.3%)	0.97	7/2414 (0.3%)
66	SF	0.33	0/1516	0.64	1/2037 (0.0%)
66	sF	0.41	1/1516 (0.1%)	0.70	2/2037 (0.1%)
67	SK	0.35	0/851	0.72	1/1147 (0.1%)
67	sK	0.41	0/851	0.70	0/1147
68	SP	0.30	0/1003	0.66	0/1342
68	sP	0.37	0/1003	0.72	2/1342 (0.1%)
69	SQ	0.35	0/1160	0.78	2/1553 (0.1%)
69	sQ	0.38	0/1160	0.75	1/1553 (0.1%)
70	SS	0.30	0/1216	0.67	1/1628 (0.1%)
70	sS	0.34	0/1216	0.71	1/1628 (0.1%)
71	ST	0.33	0/1131	0.67	1/1515 (0.1%)
71	sT	0.38	0/1131	0.66	1/1515 (0.1%)
72	SU	0.30	0/831	0.64	0/1115
72	sU	0.34	0/831	0.69	1/1115 (0.1%)
73	Sc	0.28	0/508	0.66	0/680
73	sc	0.39	0/508	0.77	0/680
74	Sd	0.31	0/470	0.66	0/623
74	sd	0.37	0/470	0.60	0/623
75	Sg	0.46	2/2493 (0.1%)	0.84	5/3394 (0.1%)
75	sg	0.33	0/2493	0.61	1/3394 (0.0%)
76	SM	0.35	0/950	0.61	0/1275
76	sM	0.38	0/950	0.67	1/1275 (0.1%)
77	SZ	0.39	0/604	0.79	2/810 (0.2%)
77	sZ	0.37	0/604	0.76	1/810 (0.1%)
78	Sf	0.29	0/560	0.59	0/745
78	sf	0.31	0/560	0.63	0/745
79	S2	0.38	0/41243	0.85	44/64259 (0.1%)
79	s2	0.49	2/41241 (0.0%)	0.90	68/64251 (0.1%)
80	CB	0.32	0/6734	0.59	4/9094 (0.0%)
80	cB	0.63	4/6734 (0.1%)	0.78	15/9094 (0.2%)
81	AP	0.29	0/1692	0.82	0/2634
81	aP	0.33	0/1692	0.83	0/2634

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
82	PE	0.34	0/1778	0.94	1/2767 (0.0%)
82	pE	0.41	0/1778	0.95	2/2767 (0.1%)
83	Ls	0.29	0/1519	0.59	1/2052 (0.0%)
83	ls	0.33	0/1519	0.70	2/2052 (0.1%)
84	Lt	0.28	0/1058	0.58	0/1430
84	lt	0.27	0/1058	0.60	0/1430
85	L5	0.68	29/88929 (0.0%)	1.08	184/138727 (0.1%)
85	l5	0.52	0/88929	0.88	74/138727 (0.1%)
86	Se	0.30	0/382	0.62	0/504
87	LW	0.29	0/979	0.58	0/1295
87	IW	0.39	0/979	0.62	0/1295
All	All	0.48	66/492435 (0.0%)	0.84	533/721182 (0.1%)

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
23	LB	0	2
23	lB	0	2
31	LJ	0	1
33	LM	0	2
33	lM	0	2
35	LO	0	1
35	lO	0	1
46	la	0	1
51	Lf	0	1
51	lf	0	1
55	Lj	0	1
55	lj	0	1
64	sR	0	4
66	SF	0	1
68	sP	0	1
69	SQ	0	1
69	sQ	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
71	ST	0	1
71	sT	0	1
All	All	0	32

The worst 5 of 66 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	L5	4102	C	N1-C6	69.44	1.78	1.37
85	L5	4102	C	N3-C4	65.95	1.80	1.33
85	L5	4105	A	N9-C4	59.75	1.73	1.37
85	L5	4102	C	C2-N3	57.78	1.81	1.35
85	L5	4102	C	C4-C5	50.94	1.83	1.43

The worst 5 of 533 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	L5	4105	A	C8-N9-C4	-169.83	37.87	105.80
85	L5	4105	A	C5-N7-C8	-93.32	57.24	103.90
85	L5	4101	C	C6-N1-C2	-59.99	96.30	120.30
85	L5	4105	A	N7-C8-N9	51.78	139.69	113.80
85	L5	4101	C	C5-C6-N1	37.79	139.90	121.00

There are no chirality outliers.

5 of 32 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	cH	51	GLN	Peptide
22	lA	13	GLY	Peptide
23	lB	17	LEU	Peptide
12	sH	15	LYS	Peptide
5	sX	126	ALA	Peptide

5.2 Too-close contacts

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%)	109 (89%)	12 (10%)	2 (2%)	8	37
1	cH	123/125 (98%)	106 (86%)	16 (13%)	1 (1%)	16	51
2	SE	260/262 (99%)	246 (95%)	14 (5%)	0	100	100
2	sE	260/262 (99%)	243 (94%)	16 (6%)	1 (0%)	30	64
3	SI	204/206 (99%)	191 (94%)	13 (6%)	0	100	100
3	sI	204/206 (99%)	191 (94%)	13 (6%)	0	100	100
4	SL	151/153 (99%)	137 (91%)	14 (9%)	0	100	100
4	sL	151/153 (99%)	136 (90%)	15 (10%)	0	100	100
5	SX	139/141 (99%)	124 (89%)	14 (10%)	1 (1%)	19	54
5	sX	139/141 (99%)	121 (87%)	17 (12%)	1 (1%)	19	54
6	SG	235/237 (99%)	219 (93%)	16 (7%)	0	100	100
6	sG	235/237 (99%)	220 (94%)	14 (6%)	1 (0%)	30	64
7	SJ	183/185 (99%)	168 (92%)	15 (8%)	0	100	100
7	sJ	183/185 (99%)	171 (93%)	12 (7%)	0	100	100
8	SY	129/131 (98%)	116 (90%)	13 (10%)	0	100	100
8	sY	129/131 (98%)	117 (91%)	12 (9%)	0	100	100
9	se	56/58 (97%)	47 (84%)	9 (16%)	0	100	100
10	SA	219/221 (99%)	201 (92%)	18 (8%)	0	100	100
10	sA	219/221 (99%)	196 (90%)	23 (10%)	0	100	100
11	SB	212/214 (99%)	204 (96%)	8 (4%)	0	100	100
11	sB	212/214 (99%)	199 (94%)	13 (6%)	0	100	100
12	SH	182/189 (96%)	159 (87%)	23 (13%)	0	100	100
12	sH	182/189 (96%)	156 (86%)	26 (14%)	0	100	100
13	SV	81/83 (98%)	74 (91%)	7 (9%)	0	100	100
13	sV	81/83 (98%)	70 (86%)	11 (14%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	Sa	100/102 (98%)	81 (81%)	18 (18%)	1 (1%)	13	47
14	sa	100/102 (98%)	90 (90%)	10 (10%)	0	100	100
15	SC	220/222 (99%)	202 (92%)	18 (8%)	0	100	100
15	sC	220/222 (99%)	203 (92%)	17 (8%)	0	100	100
16	SN	148/150 (99%)	142 (96%)	6 (4%)	0	100	100
16	sN	148/150 (99%)	143 (97%)	5 (3%)	0	100	100
17	SO	138/140 (99%)	125 (91%)	13 (9%)	0	100	100
17	sO	138/140 (99%)	124 (90%)	14 (10%)	0	100	100
18	SW	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
18	sW	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
19	Sb	81/83 (98%)	70 (86%)	11 (14%)	0	100	100
19	sb	81/83 (98%)	69 (85%)	12 (15%)	0	100	100
22	LA	246/248 (99%)	219 (89%)	27 (11%)	0	100	100
22	lA	246/248 (99%)	225 (92%)	21 (8%)	0	100	100
23	LB	400/402 (100%)	364 (91%)	36 (9%)	0	100	100
23	lB	400/402 (100%)	371 (93%)	29 (7%)	0	100	100
24	LC	366/368 (100%)	347 (95%)	19 (5%)	0	100	100
24	lC	366/368 (100%)	340 (93%)	26 (7%)	0	100	100
25	LD	291/293 (99%)	279 (96%)	12 (4%)	0	100	100
25	lD	291/293 (99%)	271 (93%)	20 (7%)	0	100	100
26	LE	232/247 (94%)	212 (91%)	20 (9%)	0	100	100
26	lE	232/247 (94%)	210 (90%)	22 (10%)	0	100	100
27	LF	223/225 (99%)	211 (95%)	12 (5%)	0	100	100
27	lF	223/225 (99%)	211 (95%)	12 (5%)	0	100	100
28	LG	239/241 (99%)	224 (94%)	15 (6%)	0	100	100
28	lG	239/241 (99%)	224 (94%)	15 (6%)	0	100	100
29	LH	188/190 (99%)	174 (93%)	14 (7%)	0	100	100
29	lH	188/190 (99%)	173 (92%)	15 (8%)	0	100	100
30	LI	198/213 (93%)	183 (92%)	15 (8%)	0	100	100
30	lI	198/213 (93%)	188 (95%)	10 (5%)	0	100	100
31	LJ	174/176 (99%)	158 (91%)	16 (9%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	IJ	174/176 (99%)	155 (89%)	19 (11%)	0	100	100
32	LL	208/210 (99%)	190 (91%)	18 (9%)	0	100	100
32	IL	208/210 (99%)	191 (92%)	17 (8%)	0	100	100
33	LM	137/139 (99%)	127 (93%)	9 (7%)	1 (1%)	19	54
33	IM	137/139 (99%)	126 (92%)	10 (7%)	1 (1%)	19	54
34	LN	201/203 (99%)	184 (92%)	16 (8%)	1 (0%)	25	60
34	IN	201/203 (99%)	190 (94%)	10 (5%)	1 (0%)	25	60
35	LO	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
35	IO	199/201 (99%)	190 (96%)	9 (4%)	0	100	100
36	LP	151/153 (99%)	140 (93%)	11 (7%)	0	100	100
36	IP	151/153 (99%)	138 (91%)	13 (9%)	0	100	100
37	LQ	185/187 (99%)	175 (95%)	10 (5%)	0	100	100
37	IQ	185/187 (99%)	175 (95%)	10 (5%)	0	100	100
38	LR	185/187 (99%)	179 (97%)	6 (3%)	0	100	100
38	IR	185/187 (99%)	175 (95%)	10 (5%)	0	100	100
39	LS	173/175 (99%)	160 (92%)	13 (8%)	0	100	100
39	IS	173/175 (99%)	159 (92%)	14 (8%)	0	100	100
40	LT	157/159 (99%)	149 (95%)	8 (5%)	0	100	100
40	IT	157/159 (99%)	143 (91%)	14 (9%)	0	100	100
41	LU	99/101 (98%)	84 (85%)	15 (15%)	0	100	100
41	IU	99/101 (98%)	81 (82%)	18 (18%)	0	100	100
42	LV	129/131 (98%)	121 (94%)	8 (6%)	0	100	100
42	IV	129/131 (98%)	119 (92%)	10 (8%)	0	100	100
43	LX	118/120 (98%)	114 (97%)	4 (3%)	0	100	100
43	IX	118/120 (98%)	113 (96%)	5 (4%)	0	100	100
44	LY	132/134 (98%)	130 (98%)	2 (2%)	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%)	120 (90%)	13 (10%)	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

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	Lb	105/121 (87%)	95 (90%)	10 (10%)	0	100	100
47	lb	105/121 (87%)	94 (90%)	11 (10%)	0	100	100
48	Lc	96/98 (98%)	89 (93%)	7 (7%)	0	100	100
48	lc	96/98 (98%)	90 (94%)	6 (6%)	0	100	100
49	Ld	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
49	ld	105/107 (98%)	101 (96%)	4 (4%)	0	100	100
50	Le	126/128 (98%)	119 (94%)	7 (6%)	0	100	100
50	le	126/128 (98%)	116 (92%)	10 (8%)	0	100	100
51	Lf	107/109 (98%)	97 (91%)	10 (9%)	0	100	100
51	lf	107/109 (98%)	97 (91%)	10 (9%)	0	100	100
52	Lg	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
52	lg	112/114 (98%)	100 (89%)	12 (11%)	0	100	100
53	Lh	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
53	lh	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
54	Li	100/102 (98%)	96 (96%)	4 (4%)	0	100	100
54	li	100/102 (98%)	97 (97%)	3 (3%)	0	100	100
55	Lj	84/86 (98%)	76 (90%)	8 (10%)	0	100	100
55	lj	84/86 (98%)	73 (87%)	11 (13%)	0	100	100
56	Lk	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
56	lk	67/69 (97%)	64 (96%)	3 (4%)	0	100	100
57	Ll	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
57	ll	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
58	Lm	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
58	lm	50/52 (96%)	48 (96%)	2 (4%)	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%)	94 (91%)	9 (9%)	0	100	100
60	lo	103/105 (98%)	99 (96%)	4 (4%)	0	100	100
61	Lp	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
61	lp	89/91 (98%)	82 (92%)	7 (8%)	0	100	100
62	Lr	123/125 (98%)	116 (94%)	7 (6%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	lr	123/125 (98%)	110 (89%)	13 (11%)	0	100	100
63	Lz	215/217 (99%)	166 (77%)	49 (23%)	0	100	100
63	lz	215/217 (99%)	172 (80%)	43 (20%)	0	100	100
64	SR	133/135 (98%)	114 (86%)	18 (14%)	1 (1%)	16	51
64	sR	133/135 (98%)	106 (80%)	25 (19%)	2 (2%)	8	38
65	SD	225/227 (99%)	208 (92%)	17 (8%)	0	100	100
65	sD	225/227 (99%)	205 (91%)	19 (8%)	1 (0%)	30	64
66	SF	187/189 (99%)	159 (85%)	28 (15%)	0	100	100
66	sF	187/189 (99%)	165 (88%)	22 (12%)	0	100	100
67	SK	96/98 (98%)	85 (88%)	9 (9%)	2 (2%)	5	31
67	sK	96/98 (98%)	85 (88%)	10 (10%)	1 (1%)	13	47
68	SP	119/121 (98%)	112 (94%)	7 (6%)	0	100	100
68	sP	119/121 (98%)	109 (92%)	10 (8%)	0	100	100
69	SQ	142/144 (99%)	121 (85%)	20 (14%)	1 (1%)	19	54
69	sQ	142/144 (99%)	122 (86%)	19 (13%)	1 (1%)	19	54
70	SS	143/145 (99%)	132 (92%)	11 (8%)	0	100	100
70	sS	143/145 (99%)	131 (92%)	12 (8%)	0	100	100
71	ST	141/143 (99%)	127 (90%)	13 (9%)	1 (1%)	19	54
71	sT	141/143 (99%)	128 (91%)	12 (8%)	1 (1%)	19	54
72	SU	102/104 (98%)	91 (89%)	11 (11%)	0	100	100
72	sU	102/104 (98%)	93 (91%)	9 (9%)	0	100	100
73	Sc	62/64 (97%)	51 (82%)	11 (18%)	0	100	100
73	sc	62/64 (97%)	50 (81%)	12 (19%)	0	100	100
74	Sd	53/55 (96%)	49 (92%)	4 (8%)	0	100	100
74	sd	53/55 (96%)	48 (91%)	5 (9%)	0	100	100
75	Sg	311/313 (99%)	275 (88%)	36 (12%)	0	100	100
75	sg	311/313 (99%)	274 (88%)	37 (12%)	0	100	100
76	SM	120/122 (98%)	101 (84%)	18 (15%)	1 (1%)	16	51
76	sM	120/122 (98%)	109 (91%)	10 (8%)	1 (1%)	16	51
77	SZ	73/75 (97%)	58 (80%)	15 (20%)	0	100	100
77	sZ	73/75 (97%)	62 (85%)	11 (15%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
78	Sf	65/67 (97%)	55 (85%)	10 (15%)	0	100	100
78	sf	65/67 (97%)	55 (85%)	10 (15%)	0	100	100
80	CB	842/856 (98%)	782 (93%)	57 (7%)	3 (0%)	30	64
80	cB	842/856 (98%)	782 (93%)	57 (7%)	3 (0%)	30	64
83	Ls	194/196 (99%)	184 (95%)	10 (5%)	0	100	100
83	ls	194/196 (99%)	176 (91%)	18 (9%)	0	100	100
84	Lt	137/141 (97%)	103 (75%)	32 (23%)	2 (2%)	8	38
84	lt	137/141 (97%)	104 (76%)	31 (23%)	2 (2%)	8	38
86	Se	45/47 (96%)	43 (96%)	2 (4%)	0	100	100
87	LW	114/124 (92%)	109 (96%)	5 (4%)	0	100	100
87	IW	114/124 (92%)	112 (98%)	2 (2%)	0	100	100
All	All	25645/26099 (98%)	23469 (92%)	2141 (8%)	35 (0%)	50	80

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	sG	217	MET
67	sK	96	ARG
80	cB	779	THR
80	CB	407	LYS
80	CB	779	THR

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%)	99 (99%)	1 (1%)	73	87
1	cH	100/100 (100%)	96 (96%)	4 (4%)	27	59
2	SE	224/224 (100%)	215 (96%)	9 (4%)	27	59
2	sE	224/224 (100%)	214 (96%)	10 (4%)	23	56
3	SI	178/178 (100%)	173 (97%)	5 (3%)	38	68

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	sI	178/178 (100%)	166 (93%)	12 (7%)	13	44
4	SL	137/137 (100%)	132 (96%)	5 (4%)	30	62
4	sL	137/137 (100%)	128 (93%)	9 (7%)	14	45
5	SX	113/113 (100%)	109 (96%)	4 (4%)	31	63
5	sX	113/113 (100%)	109 (96%)	4 (4%)	31	63
6	SG	207/207 (100%)	195 (94%)	12 (6%)	17	49
6	sG	207/207 (100%)	193 (93%)	14 (7%)	13	43
7	SJ	161/161 (100%)	154 (96%)	7 (4%)	25	57
7	sJ	161/161 (100%)	155 (96%)	6 (4%)	29	62
8	SY	113/113 (100%)	101 (89%)	12 (11%)	5	24
8	sY	113/113 (100%)	104 (92%)	9 (8%)	10	37
9	se	47/47 (100%)	46 (98%)	1 (2%)	48	74
10	SA	183/183 (100%)	175 (96%)	8 (4%)	24	57
10	sA	183/183 (100%)	172 (94%)	11 (6%)	16	48
11	SB	195/195 (100%)	188 (96%)	7 (4%)	30	62
11	sB	195/195 (100%)	187 (96%)	8 (4%)	26	59
12	SH	166/169 (98%)	154 (93%)	12 (7%)	12	41
12	sH	166/169 (98%)	159 (96%)	7 (4%)	25	58
13	SV	67/67 (100%)	62 (92%)	5 (8%)	11	40
13	sV	67/67 (100%)	58 (87%)	9 (13%)	3	15
14	Sa	89/89 (100%)	86 (97%)	3 (3%)	32	63
14	sa	89/89 (100%)	85 (96%)	4 (4%)	23	56
15	SC	188/188 (100%)	181 (96%)	7 (4%)	29	62
15	sC	188/188 (100%)	184 (98%)	4 (2%)	48	74
16	SN	130/130 (100%)	122 (94%)	8 (6%)	15	47
16	sN	130/130 (100%)	124 (95%)	6 (5%)	23	56
17	SO	110/110 (100%)	105 (96%)	5 (4%)	23	56
17	sO	110/110 (100%)	106 (96%)	4 (4%)	30	62
18	SW	112/112 (100%)	105 (94%)	7 (6%)	15	46
18	sW	112/112 (100%)	109 (97%)	3 (3%)	40	69
19	Sb	75/75 (100%)	73 (97%)	2 (3%)	40	69

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	sb	75/75 (100%)	71 (95%)	4 (5%)	19	52
22	LA	190/190 (100%)	185 (97%)	5 (3%)	41	70
22	lA	190/190 (100%)	181 (95%)	9 (5%)	22	55
23	LB	348/348 (100%)	340 (98%)	8 (2%)	45	72
23	lB	348/348 (100%)	335 (96%)	13 (4%)	29	62
24	LC	306/306 (100%)	295 (96%)	11 (4%)	30	62
24	lC	306/306 (100%)	289 (94%)	17 (6%)	17	50
25	LD	246/247 (100%)	232 (94%)	14 (6%)	17	50
25	lD	246/247 (100%)	237 (96%)	9 (4%)	29	62
26	LE	209/220 (95%)	201 (96%)	8 (4%)	28	60
26	lE	209/220 (95%)	203 (97%)	6 (3%)	37	67
27	LF	194/194 (100%)	186 (96%)	8 (4%)	26	59
27	lF	194/194 (100%)	182 (94%)	12 (6%)	15	47
28	LG	203/205 (99%)	196 (97%)	7 (3%)	32	63
28	lG	203/205 (99%)	195 (96%)	8 (4%)	27	60
29	LH	169/169 (100%)	165 (98%)	4 (2%)	44	71
29	lH	169/169 (100%)	162 (96%)	7 (4%)	26	59
30	LI	172/180 (96%)	164 (95%)	8 (5%)	22	55
30	lI	172/180 (96%)	162 (94%)	10 (6%)	17	49
31	LJ	148/148 (100%)	141 (95%)	7 (5%)	22	55
31	lJ	148/148 (100%)	142 (96%)	6 (4%)	26	59
32	LL	176/176 (100%)	170 (97%)	6 (3%)	32	63
32	lL	176/176 (100%)	168 (96%)	8 (4%)	23	56
33	LM	118/118 (100%)	112 (95%)	6 (5%)	20	53
33	lM	118/118 (100%)	111 (94%)	7 (6%)	16	48
34	LN	171/171 (100%)	165 (96%)	6 (4%)	31	63
34	lN	171/171 (100%)	167 (98%)	4 (2%)	45	72
35	LO	173/173 (100%)	170 (98%)	3 (2%)	56	78
35	lO	173/173 (100%)	167 (96%)	6 (4%)	31	63
36	LP	134/134 (100%)	128 (96%)	6 (4%)	23	56
36	lP	134/134 (100%)	126 (94%)	8 (6%)	16	48

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	LQ	164/164 (100%)	158 (96%)	6 (4%)	29	62
37	lQ	164/164 (100%)	158 (96%)	6 (4%)	29	62
38	LR	166/166 (100%)	152 (92%)	14 (8%)	9	34
38	lR	166/166 (100%)	156 (94%)	10 (6%)	16	48
39	LS	156/156 (100%)	150 (96%)	6 (4%)	28	60
39	lS	156/156 (100%)	146 (94%)	10 (6%)	14	46
40	LT	139/139 (100%)	133 (96%)	6 (4%)	25	57
40	lT	139/139 (100%)	134 (96%)	5 (4%)	30	62
41	LU	91/91 (100%)	79 (87%)	12 (13%)	3	16
41	lU	91/91 (100%)	81 (89%)	10 (11%)	5	23
42	LV	101/101 (100%)	99 (98%)	2 (2%)	50	75
42	lV	101/101 (100%)	98 (97%)	3 (3%)	36	66
43	LX	108/108 (100%)	102 (94%)	6 (6%)	17	50
43	lX	108/108 (100%)	104 (96%)	4 (4%)	29	62
44	LY	124/124 (100%)	117 (94%)	7 (6%)	17	50
44	lY	124/124 (100%)	119 (96%)	5 (4%)	27	59
45	LZ	117/117 (100%)	112 (96%)	5 (4%)	25	57
45	lZ	117/117 (100%)	109 (93%)	8 (7%)	13	43
46	La	120/120 (100%)	116 (97%)	4 (3%)	33	64
46	la	120/120 (100%)	117 (98%)	3 (2%)	42	71
47	Lb	88/101 (87%)	80 (91%)	8 (9%)	7	29
47	lb	88/101 (87%)	85 (97%)	3 (3%)	32	63
48	Lc	83/83 (100%)	81 (98%)	2 (2%)	44	71
48	lc	83/83 (100%)	78 (94%)	5 (6%)	16	48
49	Ld	98/98 (100%)	97 (99%)	1 (1%)	73	87
49	ld	98/98 (100%)	95 (97%)	3 (3%)	35	66
50	Le	114/114 (100%)	112 (98%)	2 (2%)	54	77
50	le	114/114 (100%)	109 (96%)	5 (4%)	24	57
51	Lf	88/88 (100%)	85 (97%)	3 (3%)	32	63
51	lf	88/88 (100%)	81 (92%)	7 (8%)	10	37
52	Lg	98/98 (100%)	96 (98%)	2 (2%)	50	75

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	lg	98/98 (100%)	95 (97%)	3 (3%)	35	66
53	Lh	109/109 (100%)	102 (94%)	7 (6%)	14	46
53	lh	109/109 (100%)	106 (97%)	3 (3%)	38	68
54	Li	86/86 (100%)	80 (93%)	6 (7%)	12	42
54	li	86/86 (100%)	77 (90%)	9 (10%)	5	24
55	Lj	73/73 (100%)	69 (94%)	4 (6%)	18	51
55	lj	73/73 (100%)	71 (97%)	2 (3%)	40	69
56	Lk	64/64 (100%)	64 (100%)	0	100	100
56	lk	64/64 (100%)	63 (98%)	1 (2%)	58	79
57	Ll	47/47 (100%)	46 (98%)	1 (2%)	48	74
57	ll	47/47 (100%)	43 (92%)	4 (8%)	8	34
58	Lm	48/48 (100%)	47 (98%)	1 (2%)	48	74
58	lm	48/48 (100%)	45 (94%)	3 (6%)	15	46
59	Ln	23/23 (100%)	23 (100%)	0	100	100
59	ln	23/23 (100%)	21 (91%)	2 (9%)	8	32
60	Lo	93/93 (100%)	88 (95%)	5 (5%)	18	51
60	lo	93/93 (100%)	89 (96%)	4 (4%)	25	57
61	Lp	74/74 (100%)	73 (99%)	1 (1%)	62	82
61	lp	74/74 (100%)	71 (96%)	3 (4%)	26	59
62	Lr	109/109 (100%)	106 (97%)	3 (3%)	38	68
62	lr	109/109 (100%)	106 (97%)	3 (3%)	38	68
63	Lz	195/196 (100%)	187 (96%)	8 (4%)	26	59
63	lz	195/196 (100%)	175 (90%)	20 (10%)	6	25
64	SR	122/122 (100%)	117 (96%)	5 (4%)	26	59
64	sR	122/122 (100%)	111 (91%)	11 (9%)	8	30
65	SD	190/190 (100%)	176 (93%)	14 (7%)	11	40
65	sD	190/190 (100%)	179 (94%)	11 (6%)	17	49
66	SF	159/159 (100%)	150 (94%)	9 (6%)	17	50
66	sF	159/159 (100%)	156 (98%)	3 (2%)	52	76
67	SK	89/89 (100%)	76 (85%)	13 (15%)	2	13
67	sK	89/89 (100%)	82 (92%)	7 (8%)	10	38

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	SP	107/107 (100%)	103 (96%)	4 (4%)	29	62
68	sP	107/107 (100%)	103 (96%)	4 (4%)	29	62
69	SQ	119/119 (100%)	116 (98%)	3 (2%)	42	71
69	sQ	119/119 (100%)	107 (90%)	12 (10%)	6	26
70	SS	126/126 (100%)	116 (92%)	10 (8%)	10	38
70	sS	126/126 (100%)	120 (95%)	6 (5%)	21	55
71	ST	113/113 (100%)	102 (90%)	11 (10%)	6	27
71	sT	113/113 (100%)	106 (94%)	7 (6%)	15	47
72	SU	94/94 (100%)	88 (94%)	6 (6%)	14	46
72	sU	94/94 (100%)	91 (97%)	3 (3%)	34	65
73	Sc	57/57 (100%)	56 (98%)	1 (2%)	54	77
73	sc	57/57 (100%)	55 (96%)	2 (4%)	31	63
74	Sd	48/48 (100%)	45 (94%)	3 (6%)	15	46
74	sd	48/48 (100%)	46 (96%)	2 (4%)	25	58
75	Sg	272/272 (100%)	258 (95%)	14 (5%)	20	53
75	sg	272/272 (100%)	253 (93%)	19 (7%)	12	42
76	SM	102/104 (98%)	98 (96%)	4 (4%)	27	60
76	sM	102/104 (98%)	95 (93%)	7 (7%)	13	43
77	SZ	66/66 (100%)	60 (91%)	6 (9%)	7	29
77	sZ	66/66 (100%)	60 (91%)	6 (9%)	7	29
78	Sf	60/60 (100%)	56 (93%)	4 (7%)	13	44
78	sf	60/60 (100%)	57 (95%)	3 (5%)	20	54
80	CB	722/728 (99%)	672 (93%)	50 (7%)	13	43
80	cB	722/728 (99%)	688 (95%)	34 (5%)	22	55
83	Ls	162/164 (99%)	149 (92%)	13 (8%)	10	37
83	ls	162/164 (99%)	155 (96%)	7 (4%)	25	57
84	Lt	112/115 (97%)	110 (98%)	2 (2%)	54	77
84	lt	112/115 (97%)	108 (96%)	4 (4%)	30	62
86	Se	39/39 (100%)	36 (92%)	3 (8%)	10	39
87	LW	97/103 (94%)	97 (100%)	0	100	100
87	IW	97/103 (94%)	95 (98%)	2 (2%)	48	74

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	22282/22398 (100%)	21206 (95%)	1076 (5%)	24 55

5 of 1076 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
54	Li	35	LYS
64	SR	67	ARG
54	Li	29	ARG
75	Sg	241	PHE
63	lz	27	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 141 such sidechains are listed below:

Mol	Chain	Res	Type
35	LO	63	ASN
39	LS	117	HIS
66	SF	149	GLN
43	IX	93	ASN
42	IV	135	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
20	L7	119/120 (99%)	15 (12%)	0
20	l7	119/120 (99%)	16 (13%)	0
21	L8	155/156 (99%)	28 (18%)	0
21	l8	155/156 (99%)	35 (22%)	0
79	S2	1716/1740 (98%)	496 (28%)	12 (0%)
79	s2	1714/1740 (98%)	547 (31%)	0
81	AP	69/73 (94%)	25 (36%)	1 (1%)
81	aP	69/73 (94%)	25 (36%)	0
82	PE	74/76 (97%)	40 (54%)	3 (4%)
82	pE	73/76 (96%)	35 (47%)	0
85	L5	3696/3740 (98%)	969 (26%)	34 (0%)
85	l5	3696/3740 (98%)	929 (25%)	0
All	All	11655/11810 (98%)	3160 (27%)	50 (0%)

5 of 3160 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
20	17	2	U
20	17	7	G
20	17	22	A
20	17	24	C
20	17	33	U

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
85	L5	4111	U
79	S2	307	G
82	PE	34	U
85	L5	4112	C
85	L5	4699	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
85	L5	10
85	l5	10
79	s2	7
79	S2	5
84	Lt	1
84	lt	1

The worst 5 of 34 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	27.80
1	s2	753:C	O3'	785:C	P	27.36
1	L5	2910:G	O3'	3584:C	P	20.89
1	l5	2910:G	O3'	3584:C	P	20.75
1	l5	760:G	O3'	903:C	P	17.11

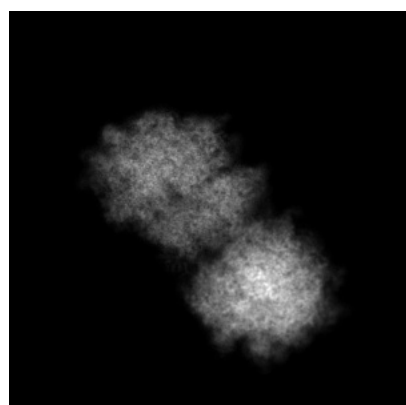
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44050. These allow visual inspection of the internal detail of the map and identification of artifacts.

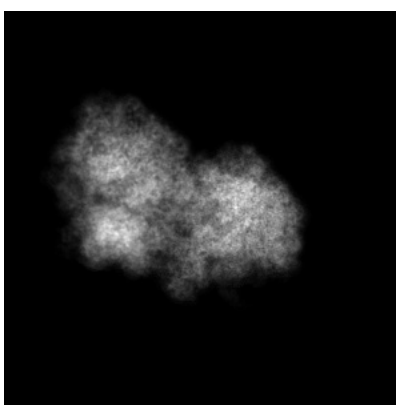
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

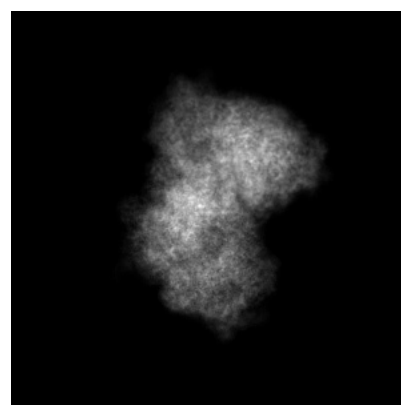
6.1.1 Primary map



X



Y

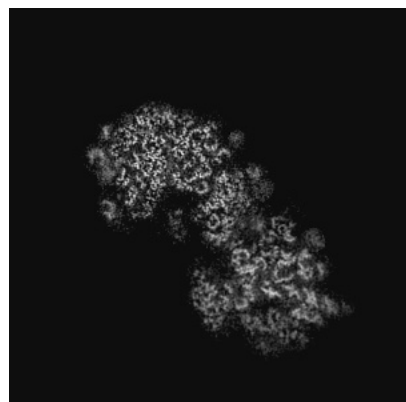


Z

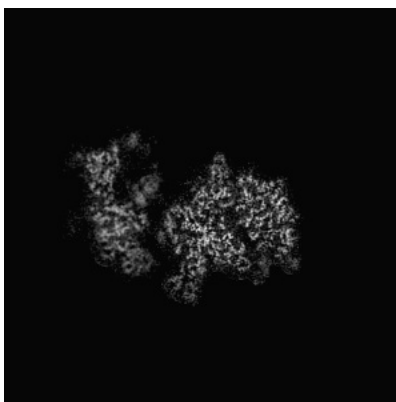
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

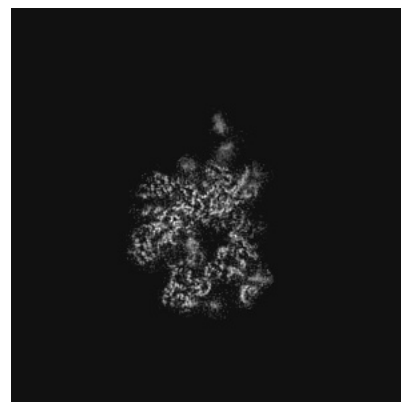
6.2.1 Primary map



X Index: 300



Y Index: 300

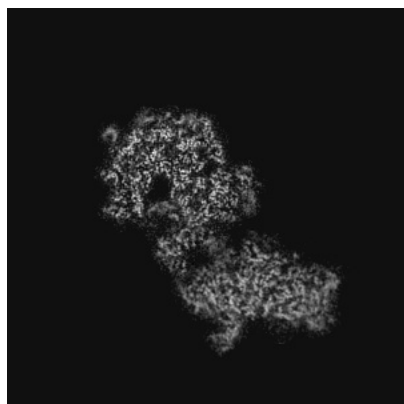


Z Index: 300

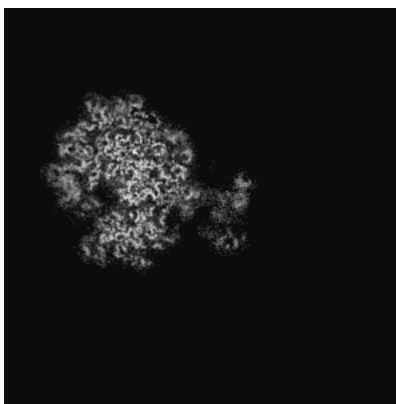
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

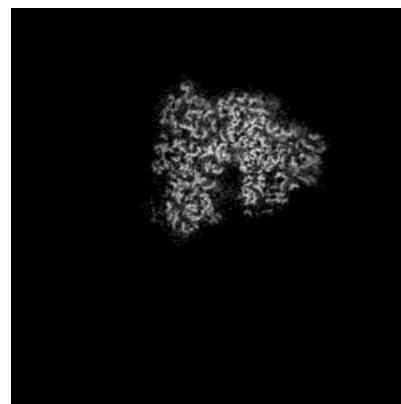
6.3.1 Primary map



X Index: 266



Y Index: 375

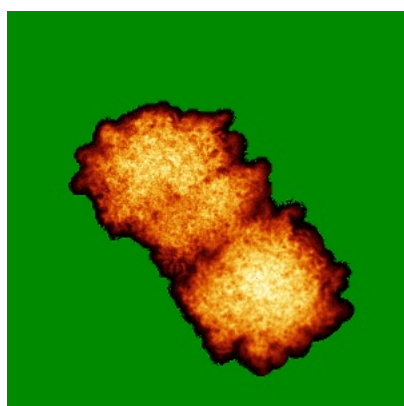


Z Index: 176

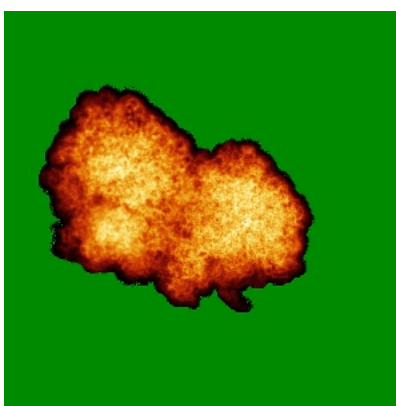
The images above show the largest variance slices of the map in three orthogonal directions.

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

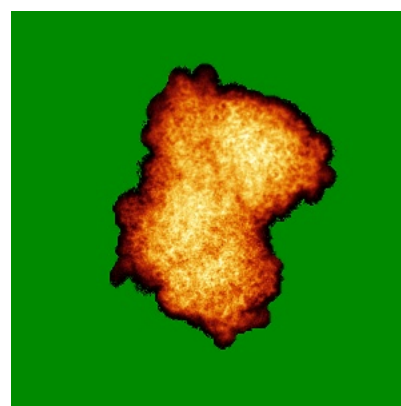
6.4.1 Primary map



X



Y

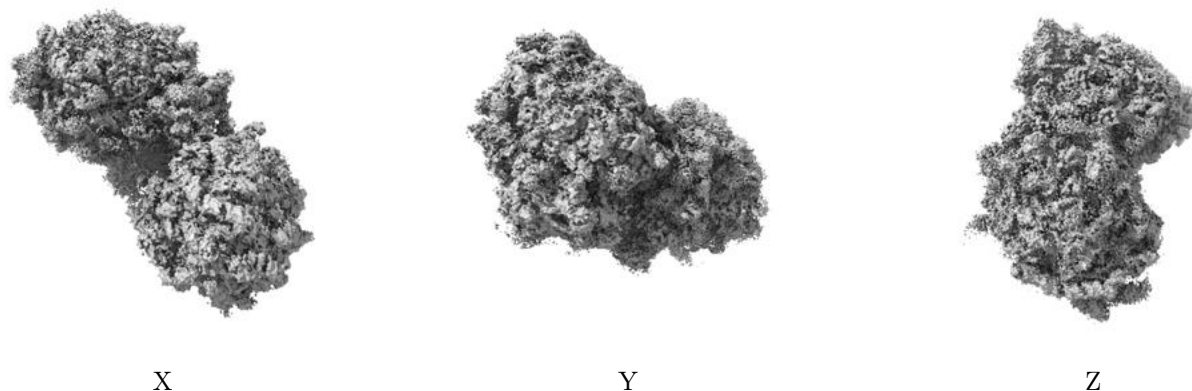


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.096. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

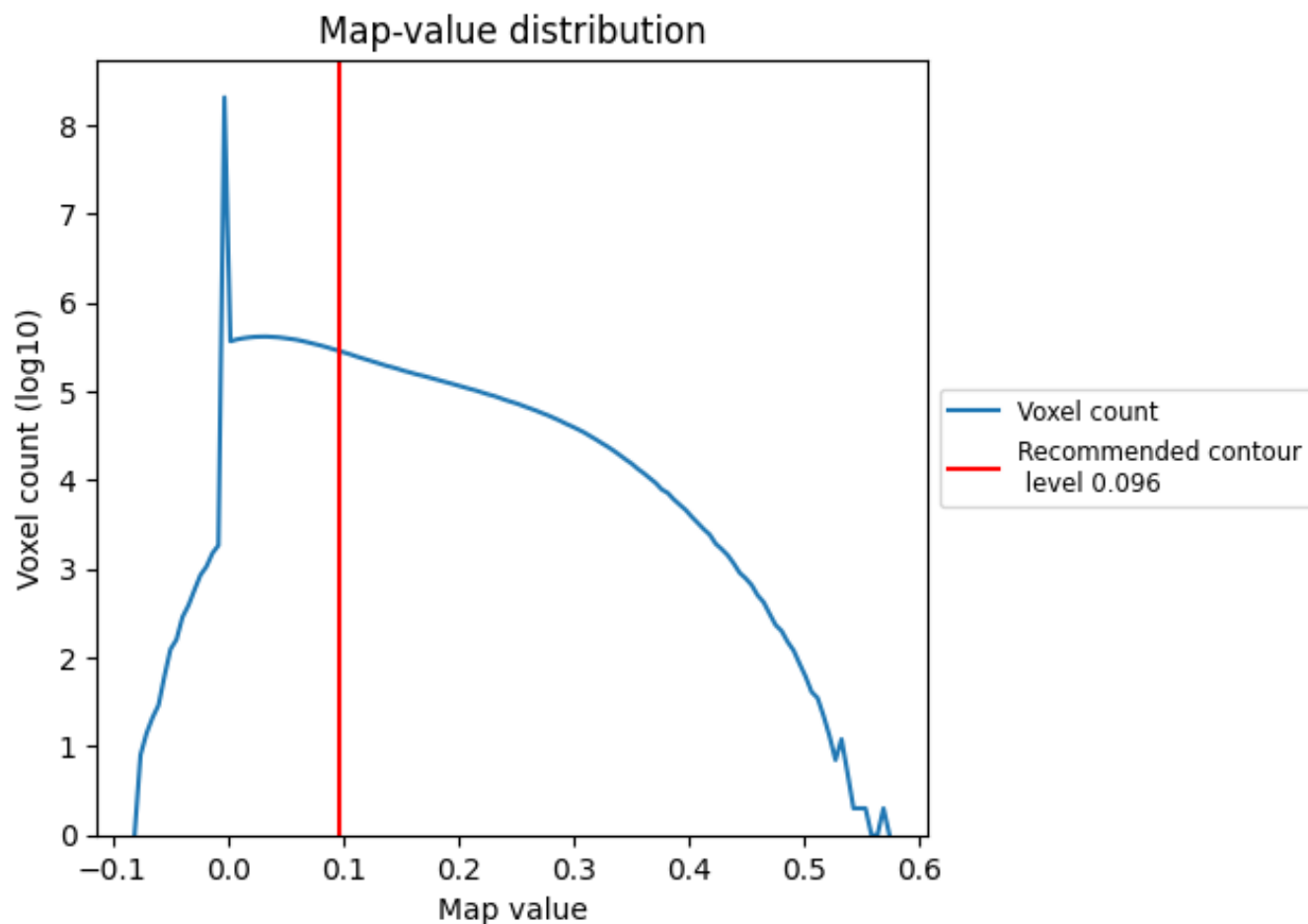
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

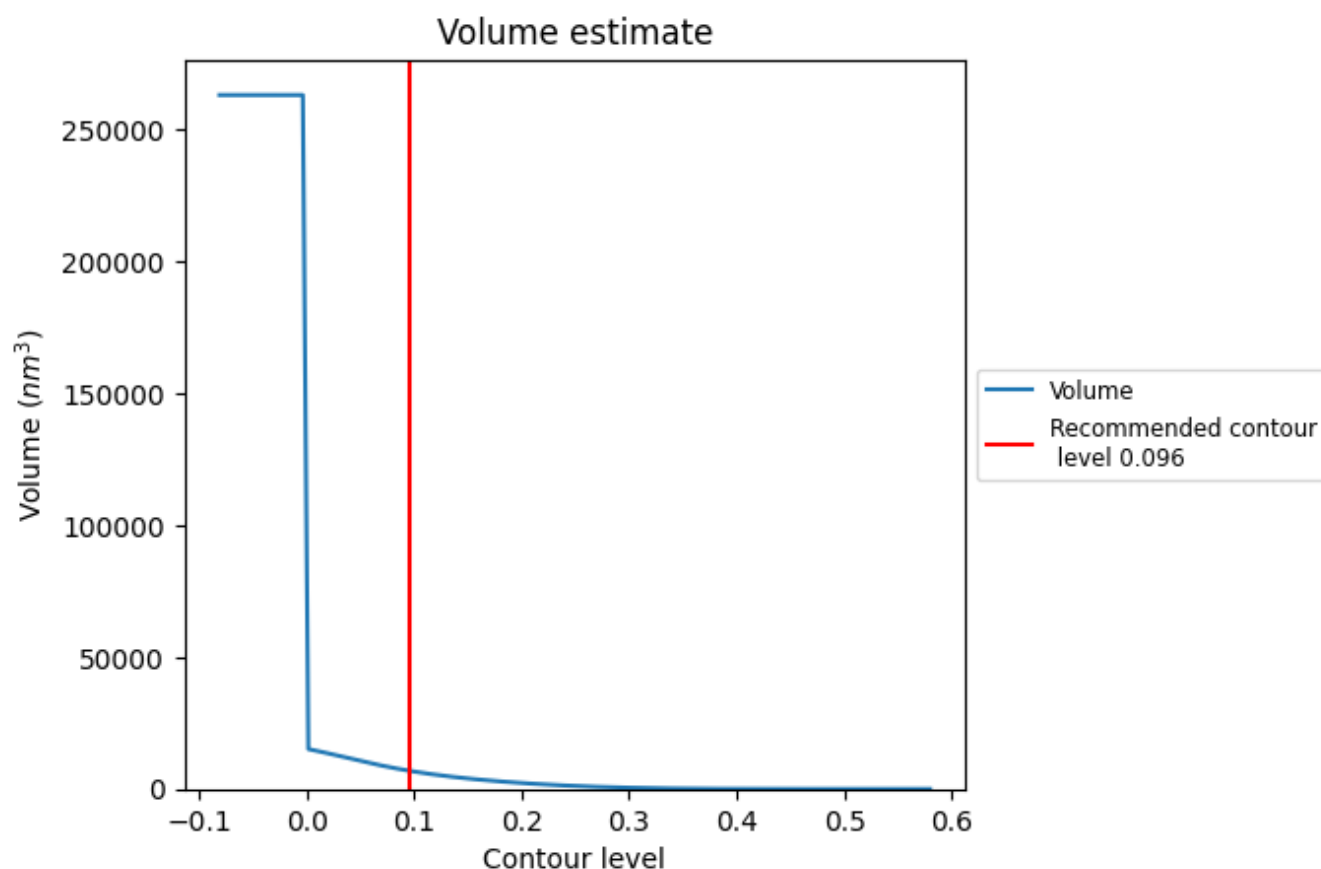
This section contains the results of statistical analysis of the map.

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.

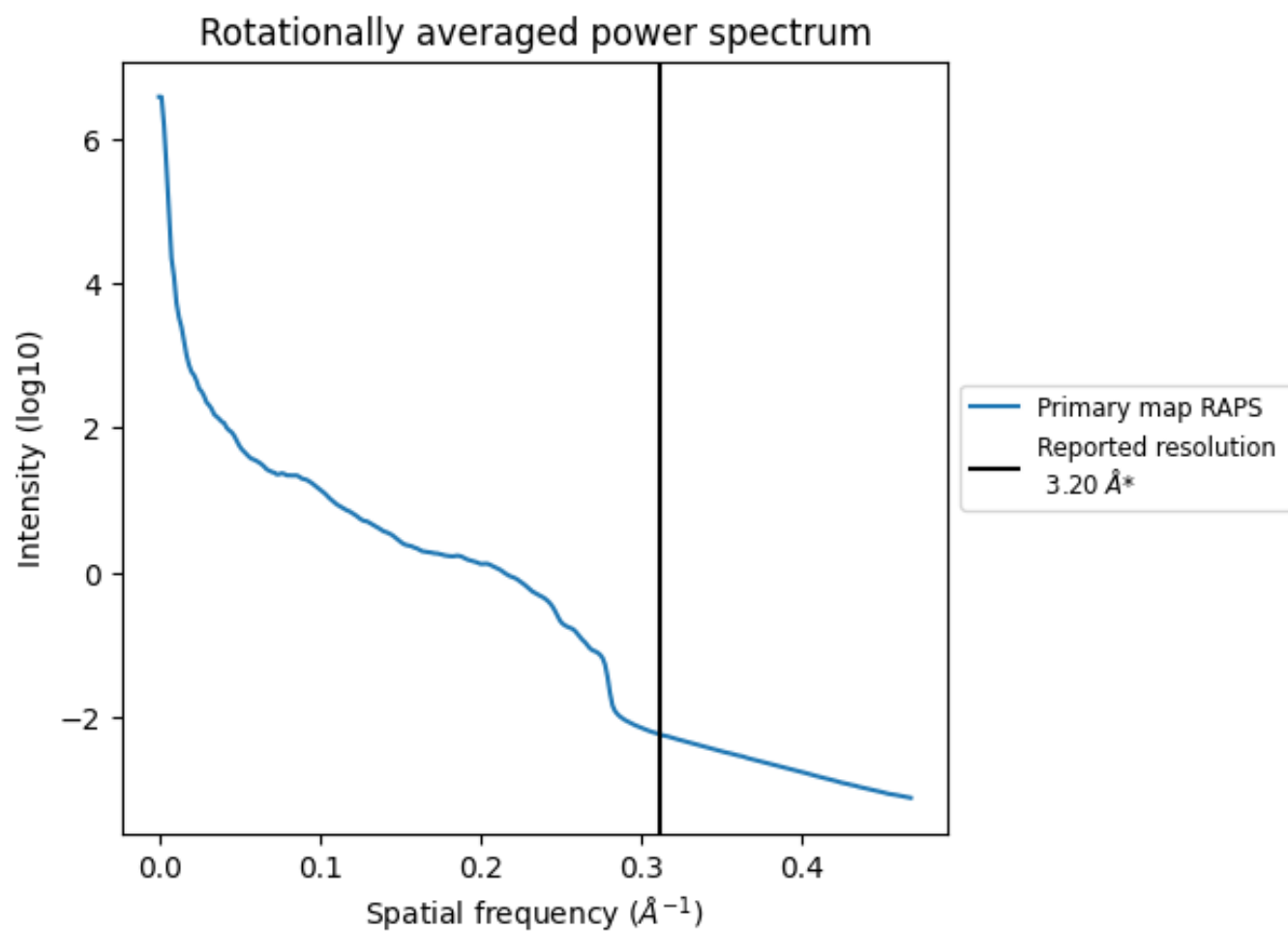
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6868 nm^3 ; this corresponds to an approximate mass of 6204 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

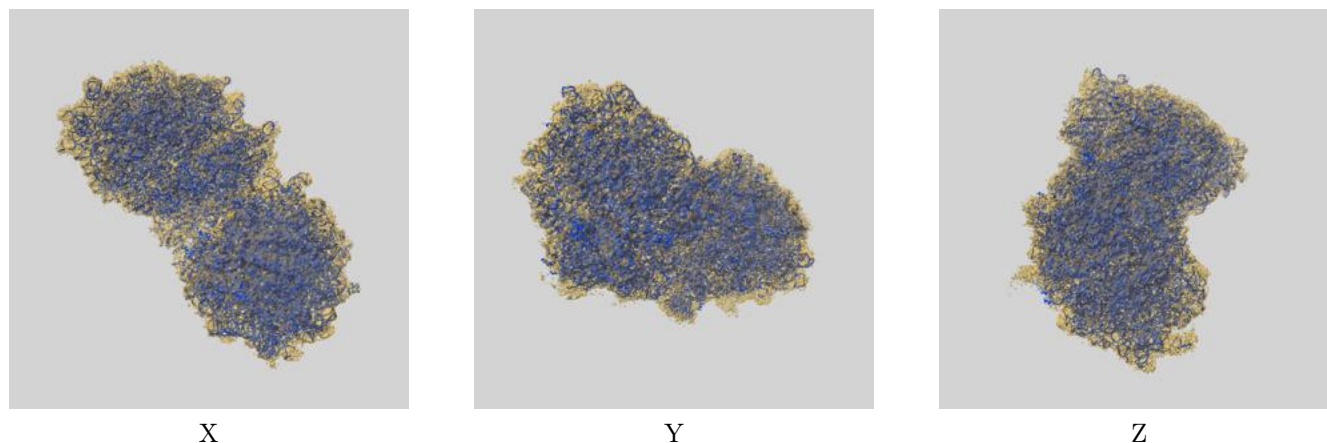
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

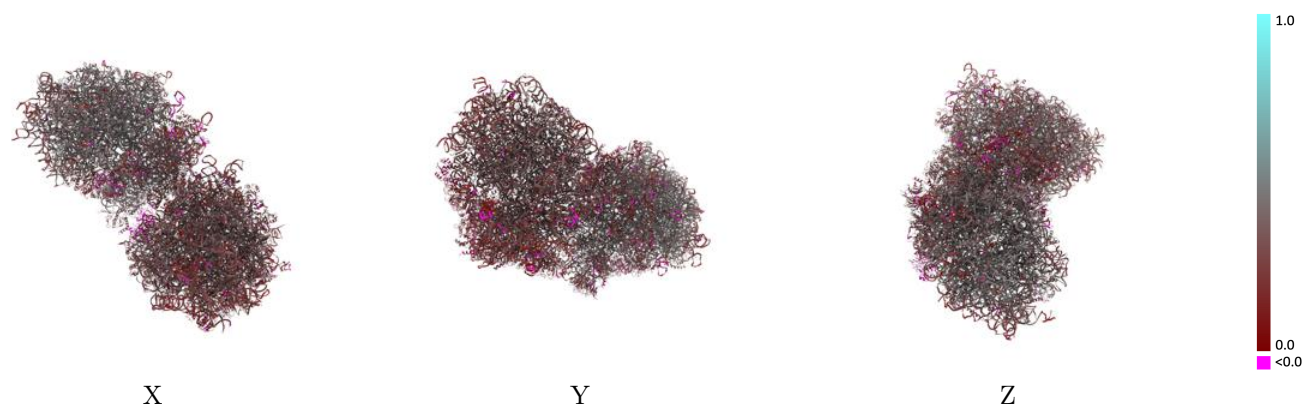
This section contains information regarding the fit between EMDB map EMD-44050 and PDB model 9B0Q. Per-residue inclusion information can be found in [section 3](#) on [page 29](#).

9.1 Map-model overlay [i](#)



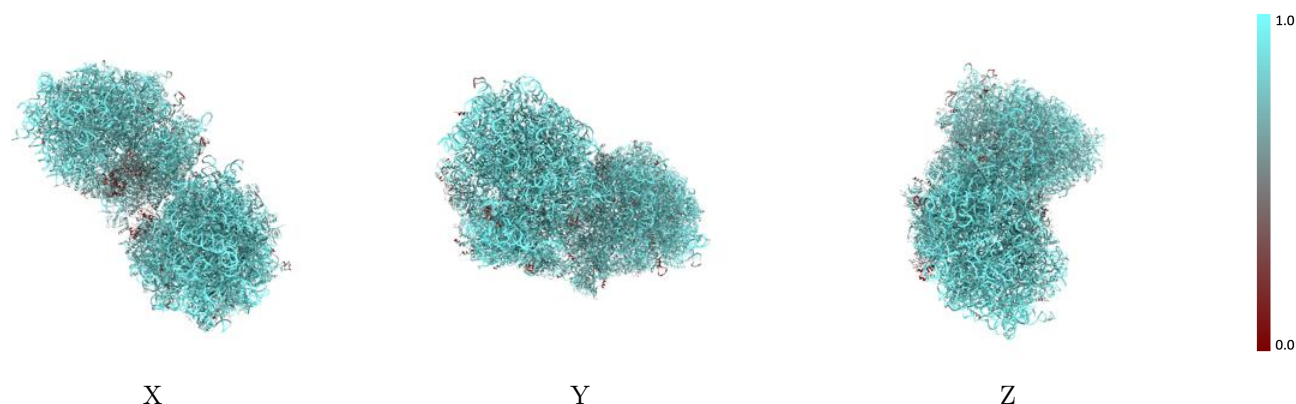
The images above show the 3D surface view of the map at the recommended contour level 0.096 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



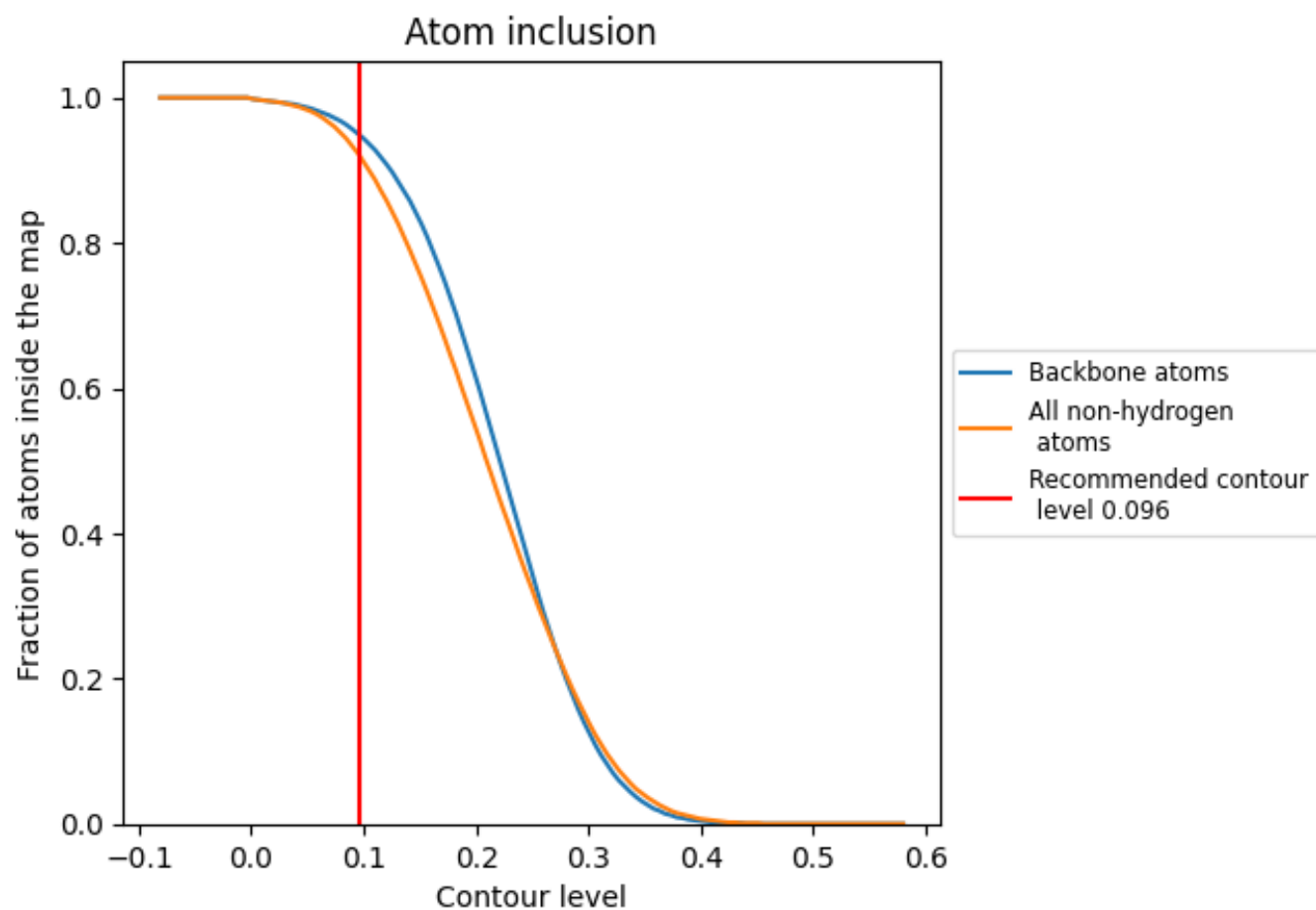
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.096).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 92% 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 (0.096) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9210	 0.3380
AP	 0.9890	 0.2490
CB	 0.7800	 0.2340
CH	 0.8100	 0.2630
L5	 0.9770	 0.3260
L7	 0.9940	 0.3480
L8	 0.9890	 0.3380
LA	 0.9430	 0.3620
LB	 0.9500	 0.3260
LC	 0.9170	 0.3350
LD	 0.8620	 0.3050
LE	 0.8910	 0.2770
LF	 0.9420	 0.3060
LG	 0.8550	 0.3020
LH	 0.9460	 0.2980
LI	 0.9600	 0.3440
LJ	 0.8400	 0.2860
LL	 0.8590	 0.3240
LM	 0.9390	 0.2950
LN	 0.9520	 0.3440
LO	 0.9490	 0.3060
LP	 0.9710	 0.3410
LQ	 0.9360	 0.3500
LR	 0.8780	 0.2920
LS	 0.9630	 0.3360
LT	 0.9420	 0.3450
LU	 0.8790	 0.2710
LV	 0.9800	 0.3660
LW	 0.8630	 0.2550
LX	 0.9060	 0.3360
LY	 0.9390	 0.3400
LZ	 0.8370	 0.3300
La	 0.9270	 0.3560
Lb	 0.8700	 0.3000
Lc	 0.8180	 0.3150























































































Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Ld	 0.9580	 0.3460
Le	 0.9750	 0.3560
Lf	 0.9830	 0.3420
Lg	 0.9210	 0.3380
Lh	 0.8980	 0.3140
Li	 0.8760	 0.3220
Lj	 0.9760	 0.3360
Lk	 0.8350	 0.3020
Ll	 0.9860	 0.3620
Lm	 0.9660	 0.3330
Ln	 1.0000	 0.3110
Lo	 0.9250	 0.3720
Lp	 0.9450	 0.3520
Lr	 0.9200	 0.3330
Ls	 0.6150	 0.1490
Lt	 0.6780	 0.1520
Lz	 0.2280	 0.0230
PE	 0.9750	 0.2490
S2	 0.9770	 0.3130
SA	 0.7830	 0.2940
SB	 0.8680	 0.3190
SC	 0.8790	 0.3120
SD	 0.8310	 0.2850
SE	 0.9030	 0.2810
SF	 0.8540	 0.2690
SG	 0.8750	 0.2410
SH	 0.7460	 0.2620
SI	 0.8770	 0.2800
SJ	 0.8770	 0.2650
SK	 0.8680	 0.2670
SL	 0.8780	 0.3170
SM	 0.6840	 0.2260
SN	 0.8540	 0.3050
SO	 0.8680	 0.3130
SP	 0.9020	 0.2970
SQ	 0.8740	 0.2650
SR	 0.7730	 0.2640
SS	 0.8410	 0.2900
ST	 0.8760	 0.2640
SU	 0.8450	 0.2660
SV	 0.8390	 0.2970
SW	 0.9210	 0.3140





















































































Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
SX	 0.9570	 0.3270
SY	 0.8950	 0.2280
SZ	 0.7920	 0.2820
Sa	 0.9240	 0.3510
Sb	 0.7920	 0.3030
Sc	 0.7690	 0.2130
Sd	 0.9910	 0.2900
Se	 0.9280	 0.2890
Sf	 0.7800	 0.2520
Sg	 0.7610	 0.2190
aP	 0.9410	 0.2670
cB	 0.4910	 0.2650
cH	 0.7590	 0.2850
l5	 0.9720	 0.3850
l7	 0.9900	 0.4140
l8	 0.9840	 0.3920
lA	 0.9490	 0.4410
lB	 0.9010	 0.4250
lC	 0.9370	 0.4300
lD	 0.9060	 0.3910
lE	 0.8760	 0.3780
lF	 0.9490	 0.4230
lG	 0.8750	 0.3660
lH	 0.8760	 0.4080
lI	 0.9190	 0.4380
lJ	 0.8060	 0.3410
lL	 0.9140	 0.4000
lM	 0.9010	 0.4050
lN	 0.9620	 0.4360
lO	 0.9270	 0.4220
lP	 0.9510	 0.4590
lQ	 0.9600	 0.4480
lR	 0.8850	 0.3770
lS	 0.9360	 0.4390
lT	 0.9530	 0.4330
lU	 0.8650	 0.3410
lV	 0.9000	 0.4350
lW	 0.8700	 0.3470
lX	 0.9200	 0.4110
lY	 0.9520	 0.4120
lZ	 0.8750	 0.3880
la	 0.9630	 0.4400

























Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
lb	 0.9070	 0.3700
lc	 0.8720	 0.3740
ld	 0.9290	 0.4230
le	 0.9600	 0.4530
lf	 0.9570	 0.4440
lg	 0.9400	 0.4310
lh	 0.9380	 0.3960
li	 0.9010	 0.3950
lj	 0.9910	 0.4490
lk	 0.8740	 0.3870
ll	 0.9740	 0.4330
lm	 0.9210	 0.4170
ln	 0.9670	 0.4230
lo	 0.9200	 0.4420
lp	 0.9300	 0.4150
lr	 0.9490	 0.4310
ls	 0.5370	 0.1750
lt	 0.4830	 0.1610
lz	 0.2500	 0.0520
pE	 0.9460	 0.2340
s2	 0.9720	 0.3540
sA	 0.8050	 0.3430
sB	 0.8870	 0.3690
sC	 0.8850	 0.3830
sD	 0.8530	 0.3680
sE	 0.9170	 0.3530
sF	 0.8590	 0.3310
sG	 0.8450	 0.2910
sH	 0.7730	 0.3100
sI	 0.8830	 0.3390
sJ	 0.8870	 0.3260
sK	 0.8550	 0.3460
sL	 0.8900	 0.3770
sM	 0.6750	 0.2310
sN	 0.9180	 0.3770
sO	 0.8750	 0.3800
sP	 0.8440	 0.3730
sQ	 0.8870	 0.3290
sR	 0.6810	 0.1450
sS	 0.8760	 0.3500
sT	 0.8650	 0.3330
sU	 0.8590	 0.3370

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
sV	 0.8180	 0.3410
sW	 0.9360	 0.4060
sX	 0.8980	 0.3890
sY	 0.8750	 0.2830
sZ	 0.8340	 0.3240
sa	 0.9020	 0.3880
sb	 0.8700	 0.3570
sc	 0.7570	 0.2720
sd	 0.9410	 0.3860
se	 0.7370	 0.2490
sf	 0.7320	 0.2540
sg	 0.7940	 0.2850