



Full wwPDB EM Validation Report ⓘ

Mar 10, 2025 – 04:03 PM EDT

PDB ID : 9B0S
EMDB ID : EMD-44052
Title : In situ human top-top di-ribosome structure (Composite map)
Authors : Wei, Z.; Yong, X.
Deposited on : 2024-03-12
Resolution : 3.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

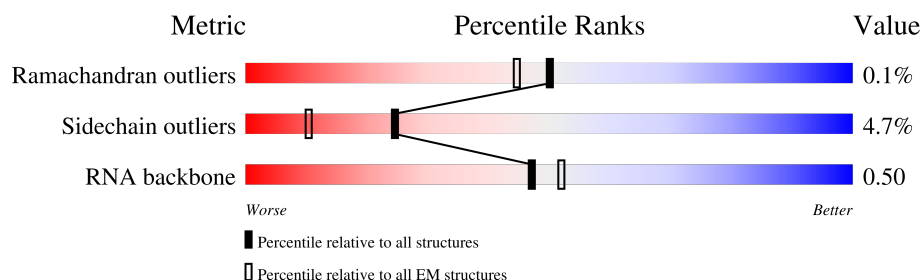
EMDB validation analysis : 0.0.1.dev117
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.4

1 Overall quality at a glance

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

The reported resolution of this entry is 3.80 Å.

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



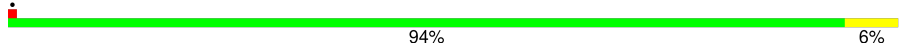
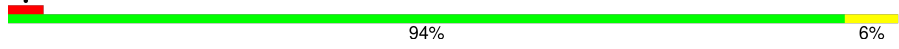
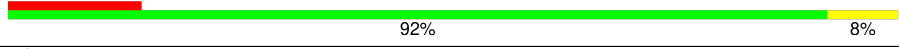
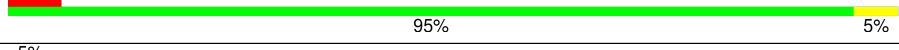
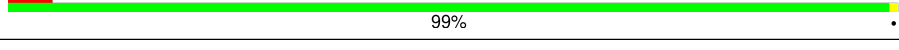
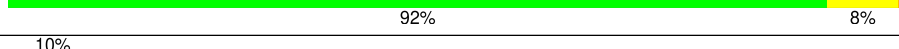
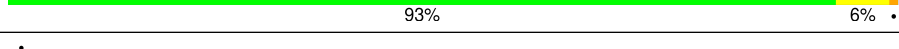
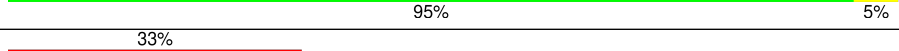
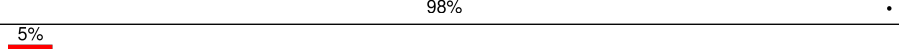
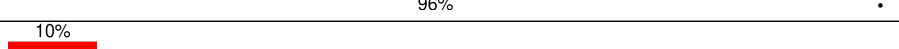
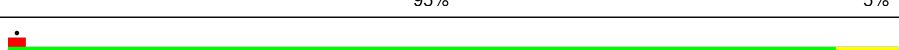
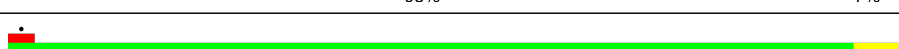
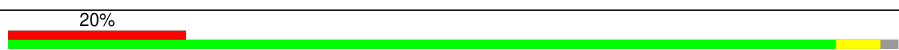
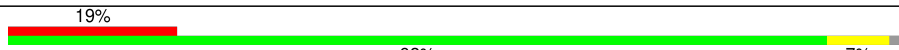
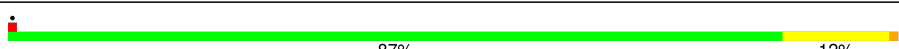

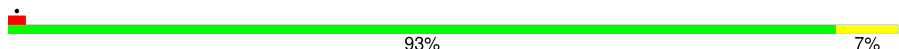
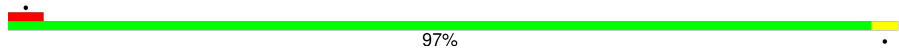
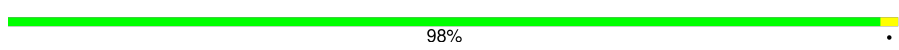
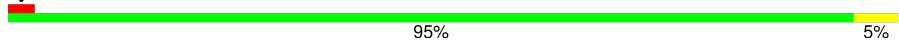
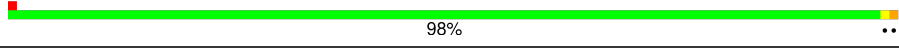
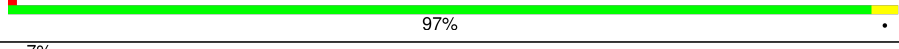
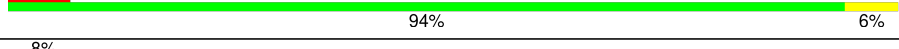
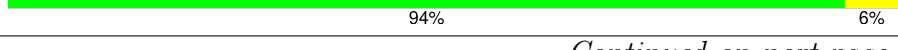

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	cH	125	
2	SE	262	
2	sE	262	
3	SI	206	
3	sI	206	
4	SL	153	
4	sL	153	
5	SX	141	

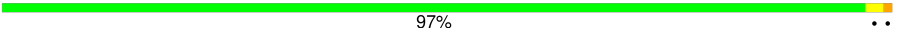
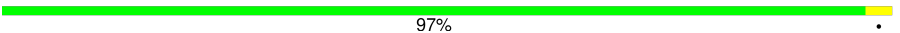

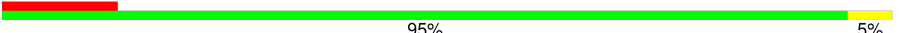











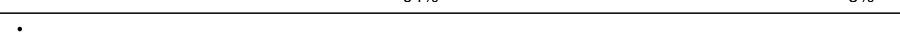
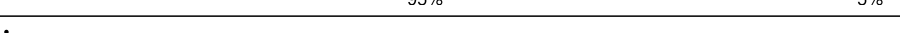


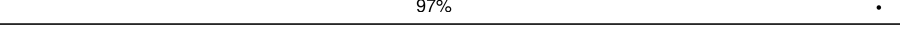
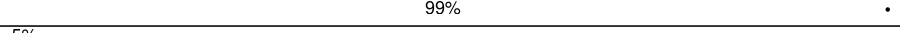
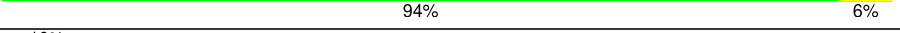
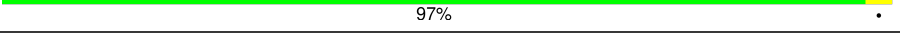
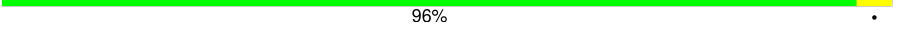
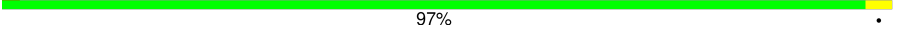
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Mol	Chain	Length	Quality of chain
5	sX	141	
6	SG	237	
6	sG	237	
7	SJ	185	
7	sJ	185	
8	SY	131	
8	sY	131	
9	Se	58	
9	se	58	
10	SA	221	
10	sA	221	
11	SB	214	
11	sB	214	
12	SH	189	
12	sH	189	
13	SV	83	
13	sV	83	
14	Sa	102	
14	sa	102	
15	SC	222	
15	sC	222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



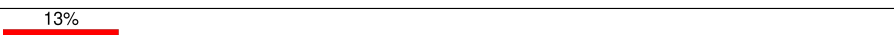
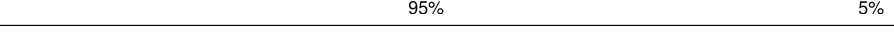
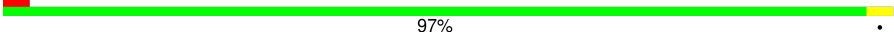

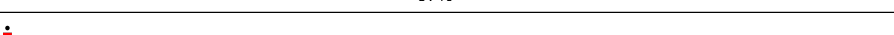
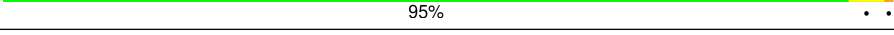
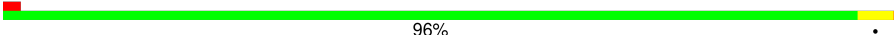

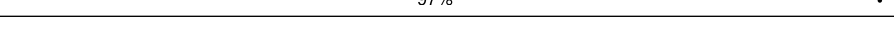
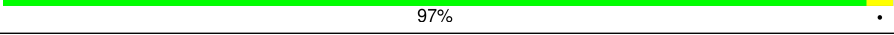
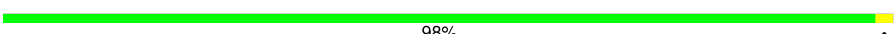
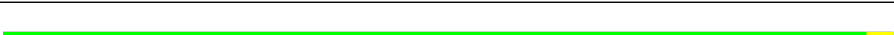
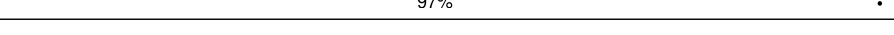
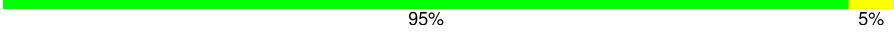


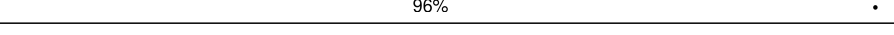
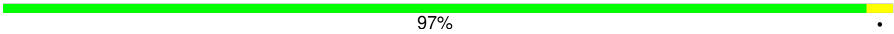

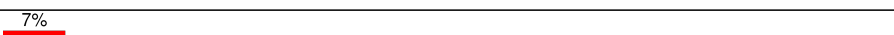
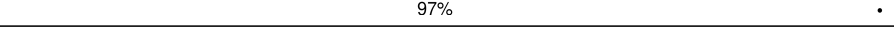
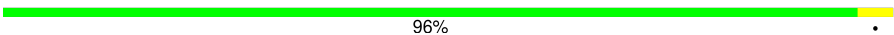

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Mol	Chain	Length	Quality of chain
18	SW	129	 97% ..
18	sW	129	 97% .
19	Sb	83	 7% 90% 10%
19	sb	83	 13% 95% 5%
20	L7	120	 90% 10%
20	l7	120	 88% 12%
21	L8	156	 79% 21%
21	l8	156	 81% 19%
22	LA	248	 96% .
22	lA	248	 95% 5%
23	LB	402	 97% .
23	lB	402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

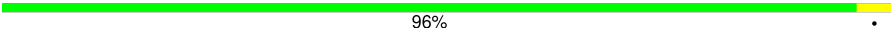
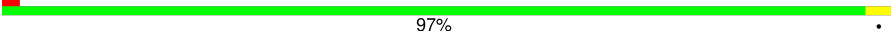
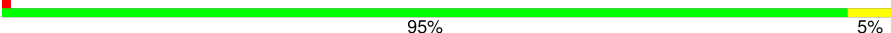
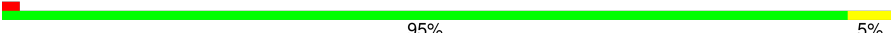

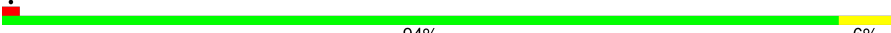









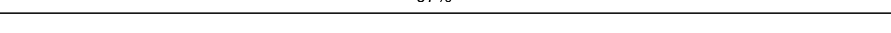
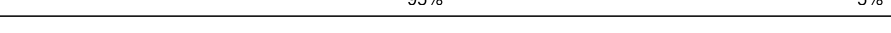
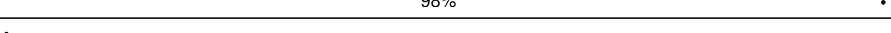
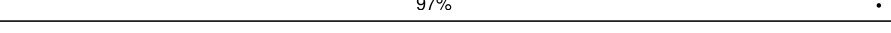
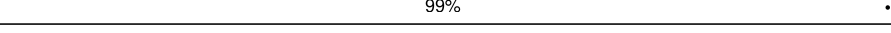
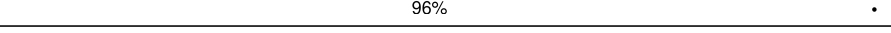
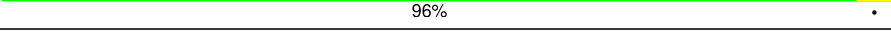
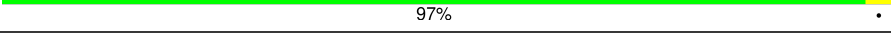
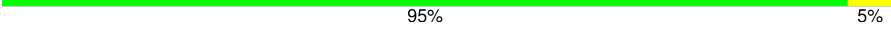
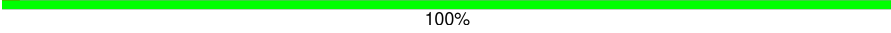
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Mol	Chain	Length	Quality of chain
30	II	213	 93% • 5%
31	LJ	176	 5% 94% 6%
31	IJ	176	 13% 95% 5%
32	LL	210	 • 97% •
32	IL	210	 5% 97% •
33	LM	139	 • 95% • •
33	IM	139	 • 96% • •
34	LN	203	 97% •
34	IN	203	 97% •
35	LO	201	 98% •
35	IO	201	 97% •
36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


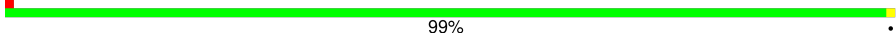
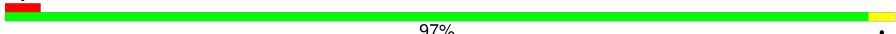
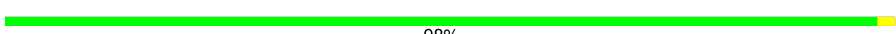


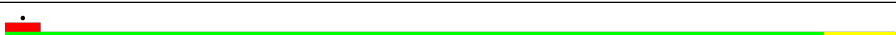
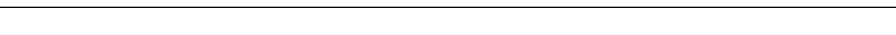
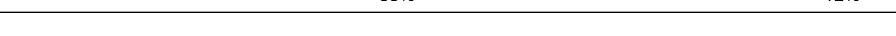
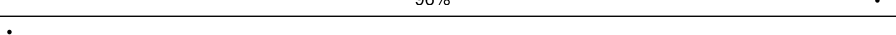
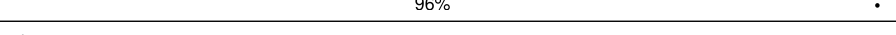
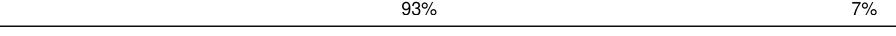
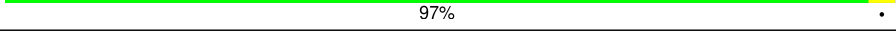
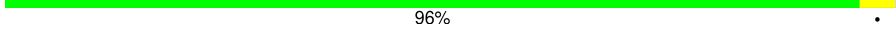
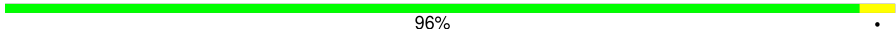
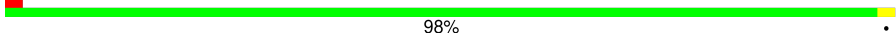







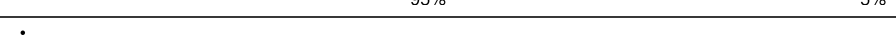
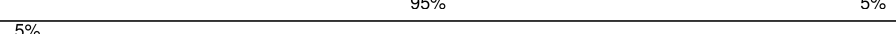

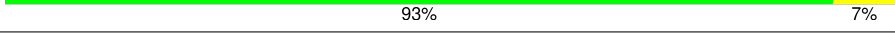


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Mol	Chain	Length	Quality of chain
43	LX	120	 96% .
43	IX	120	 97% .
44	LY	134	 95% 5%
44	IY	134	 95% 5%
45	LZ	135	 95% 5%
45	IZ	135	 94% 6%
46	La	147	 97% .
46	la	147	 97% .
47	Lb	121	 88% . 10%
47	lb	121	 9% 84% 6% 10%
48	Lc	98	 96% .
48	lc	98	 6%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

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



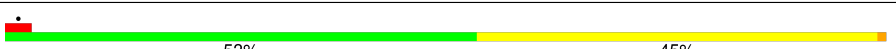
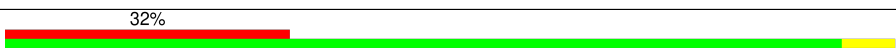
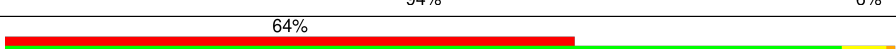
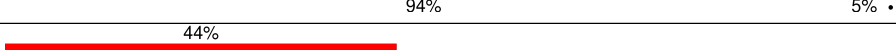
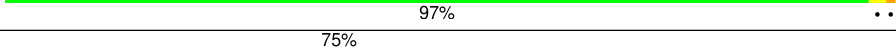
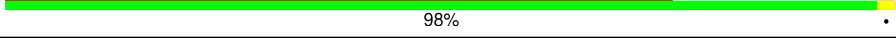
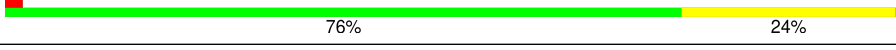



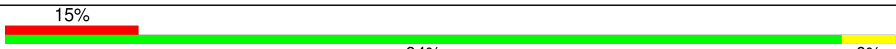
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Mol	Chain	Length	Quality of chain
68	SP	121	
68	sP	121	
69	SQ	144	
69	sQ	144	
70	SS	145	
70	sS	145	
71	ST	143	
71	sT	143	
72	SU	104	
72	sU	104	
73	Sc	64	
73	sc	64	
74	Sd	55	
74	sd	55	
75	Sg	313	
75	sg	313	
76	SM	122	
76	sM	122	
77	SZ	75	
77	sZ	75	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

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

2 Entry composition [i](#)

There are 91 unique types of molecules in this entry. The entry contains 456973 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Endothelial differentiation-related factor 1.

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

There are 4 discrepancies between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 80 is a protein called Elongation factor 2.

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

There are 10 discrepancies between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

- Molecule 86 is a protein called Ribosomal protein L24.

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

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

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

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

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

There are 2 discrepancies between the modelled and reference sequences:

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

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

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

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

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

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

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

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Endothelial differentiation-related factor 1



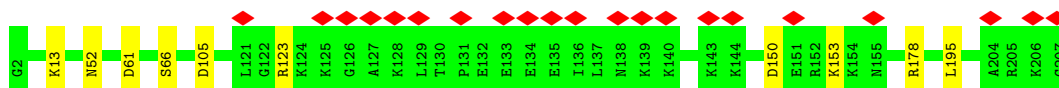
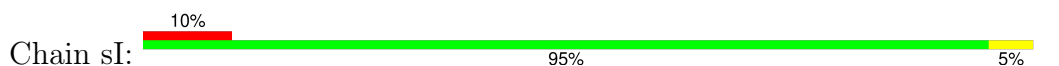
- Molecule 2: Small ribosomal subunit protein eS4, X isoform



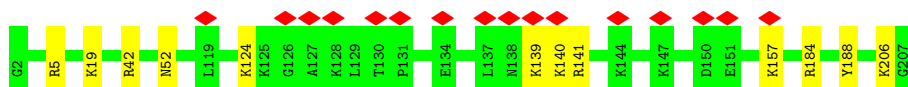
- Molecule 2: Small ribosomal subunit protein eS4, X isoform



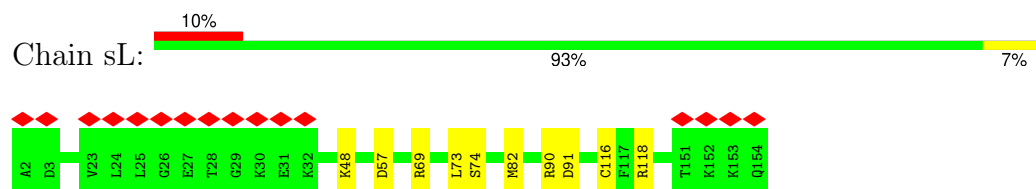
- Molecule 3: 40S ribosomal protein S8



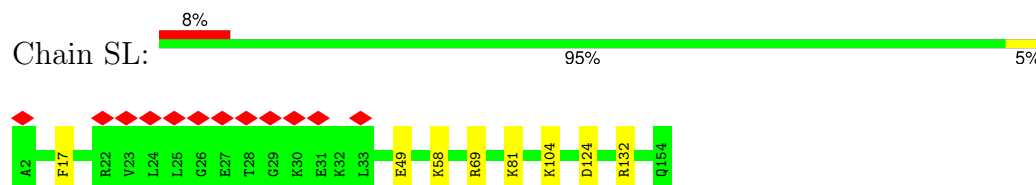
- Molecule 3: 40S ribosomal protein S8



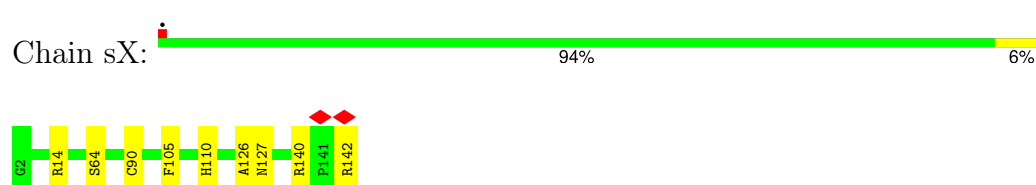
- Molecule 4: 40S ribosomal protein S11



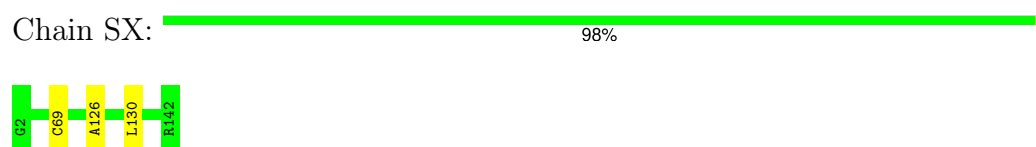
- Molecule 4: 40S ribosomal protein S11



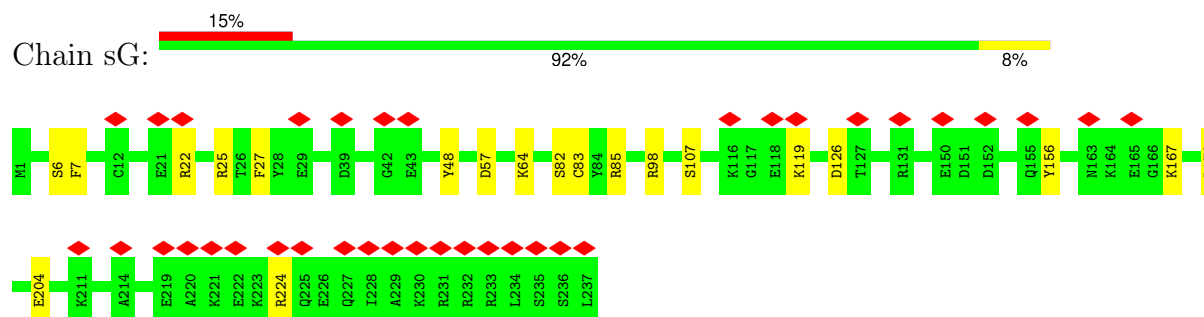
- Molecule 5: 40S ribosomal protein S23



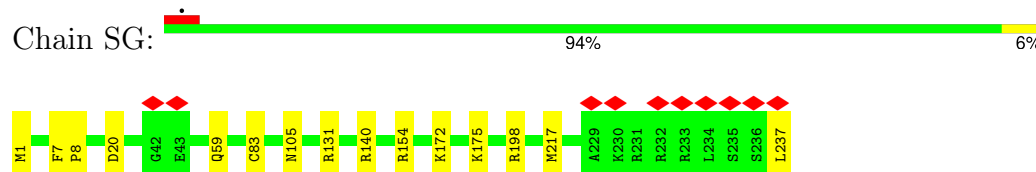
- Molecule 5: 40S ribosomal protein S23



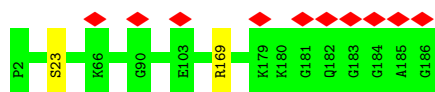
- Molecule 6: 40S ribosomal protein S6



- Molecule 6: 40S ribosomal protein S6



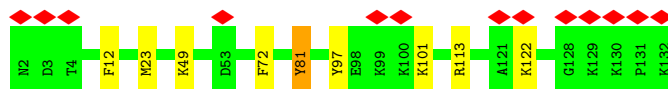
- Molecule 7: 40S ribosomal protein S9



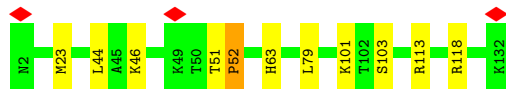
- Molecule 7: 40S ribosomal protein S9



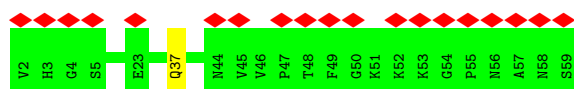
- Molecule 8: 40S ribosomal protein S24



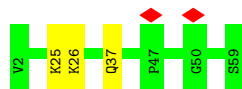
- Molecule 8: 40S ribosomal protein S24



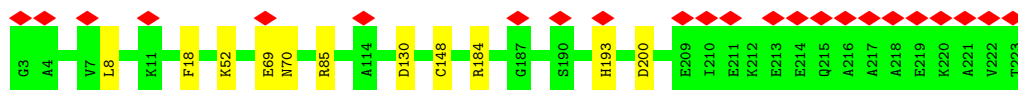
- Molecule 9: Small ribosomal subunit protein eS30



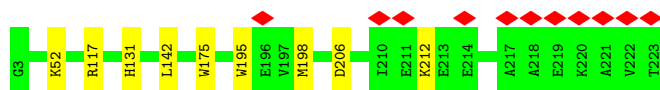
- Molecule 9: Small ribosomal subunit protein eS30



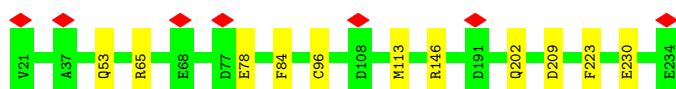
- Molecule 10: 40S ribosomal protein SA



- Molecule 10: 40S ribosomal protein SA



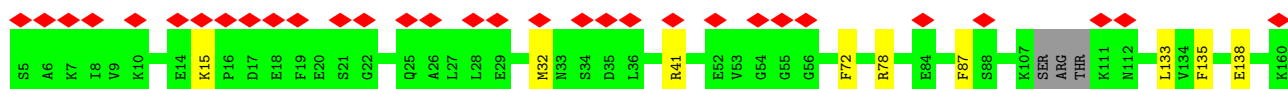
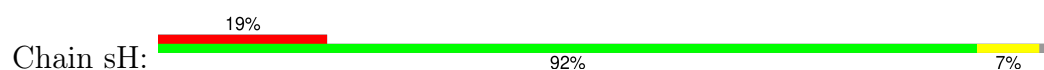
- Molecule 11: 40S ribosomal protein S3a



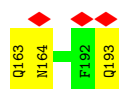
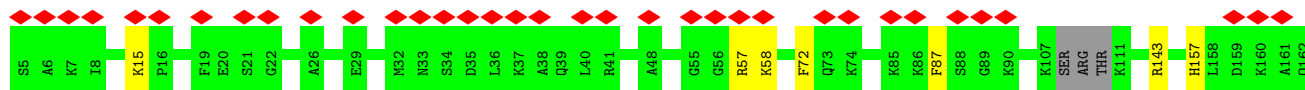
- Molecule 11: 40S ribosomal protein S3a



- Molecule 12: Small ribosomal subunit protein eS7

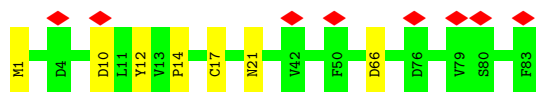


- Molecule 12: Small ribosomal subunit protein eS7

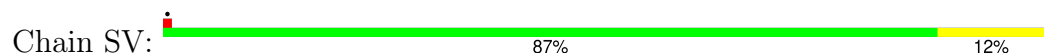


- Molecule 13: 40S ribosomal protein S21

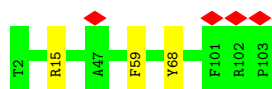




- Molecule 13: 40S ribosomal protein S21



- Molecule 14: 40S ribosomal protein S26



- Molecule 14: 40S ribosomal protein S26



- Molecule 15: 40S ribosomal protein S2



- Molecule 15: 40S ribosomal protein S2

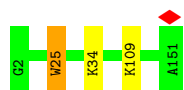


- Molecule 16: 40S ribosomal protein S13



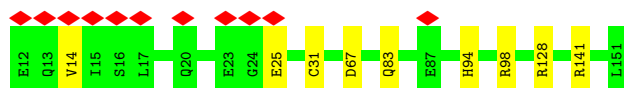
- Molecule 16: 40S ribosomal protein S13

Chain SN:  98% ..



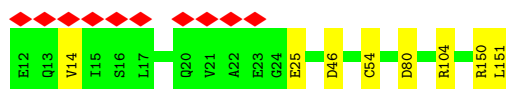
- Molecule 17: Small ribosomal subunit protein uS11

Chain sO:  8% 94% 6%



- Molecule 17: Small ribosomal subunit protein uS11

Chain SO:  7% 94% 6%



- Molecule 18: 40S ribosomal protein S15a

Chain sW:  97% .



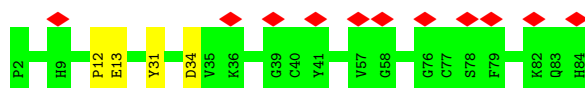
- Molecule 18: 40S ribosomal protein S15a

Chain SW:  97% ..




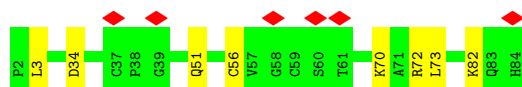
- Molecule 19: Small ribosomal subunit protein eS27

Chain sb:  13% 95% 5%




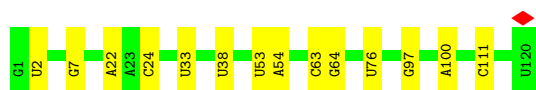
- Molecule 19: Small ribosomal subunit protein eS27

Chain Sb:  7% 90% 10%

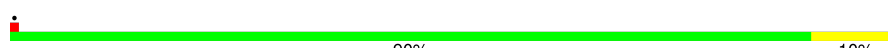


- Molecule 20: 5S rRNA [Homo sapiens]

Chain 17:  88% 12%




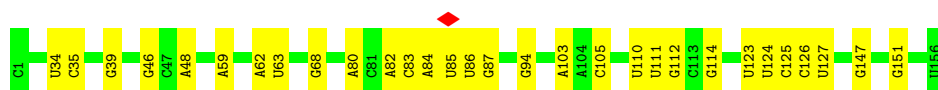
- Molecule 20: 5S rRNA [Homo sapiens]

Chain L7:  90% 10%




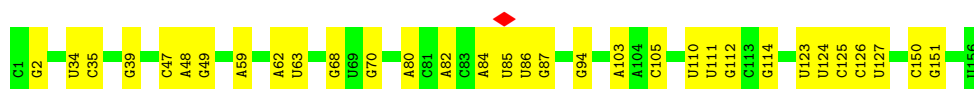
- Molecule 21: 5.8S rRNA [Homo sapiens]

Chain 18:  81% 19%



- Molecule 21: 5.8S rRNA [Homo sapiens]

Chain L8:  79% 21%



- Molecule 22: 60S ribosomal protein L8

Chain 1A:  95% 5%



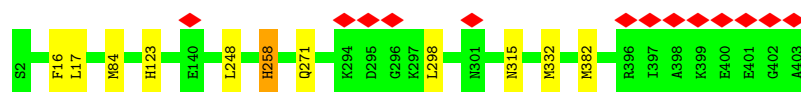
- Molecule 22: 60S ribosomal protein L8

Chain LA:  96%



- Molecule 23: Large ribosomal subunit protein uL3

Chain 1B:  97%



- Molecule 23: Large ribosomal subunit protein uL3



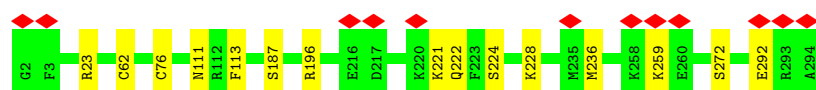
- Molecule 24: 60S ribosomal protein L4



- Molecule 24: 60S ribosomal protein L4



- Molecule 25: Large ribosomal subunit protein uL18



- Molecule 25: Large ribosomal subunit protein uL18

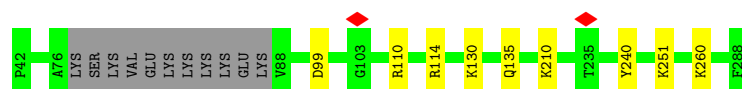


- Molecule 26: Large ribosomal subunit protein eL6



- Molecule 26: Large ribosomal subunit protein eL6

Chain LE:  92%



- Molecule 27: 60S ribosomal protein L7

Chain IF:  99%



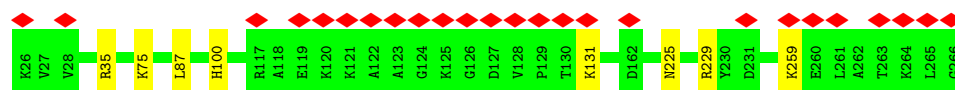
- Molecule 27: 60S ribosomal protein L7

Chain LF:  97%



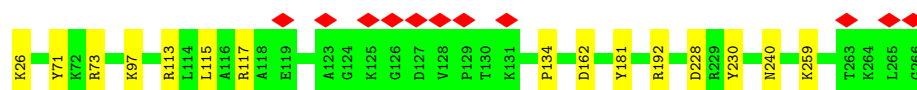
- Molecule 28: 60S ribosomal protein L7a

Chain IG:  10% 97%



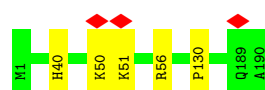
- Molecule 28: 60S ribosomal protein L7a

Chain LG:  5% 94% 6%



- Molecule 29: 60S ribosomal protein L9

Chain IH:  97%



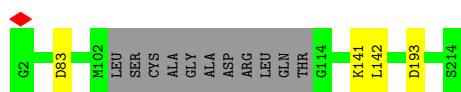
- Molecule 29: 60S ribosomal protein L9

Chain LH:  96%



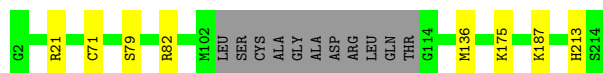
- Molecule 30: Ribosomal protein uL16-like

Chain II:  93% • 5%



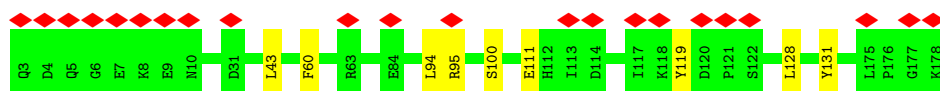
- Molecule 30: Ribosomal protein uL16-like

Chain LI:  91% • 5%



- Molecule 31: 60S ribosomal protein L11

Chain LJ:  13% 95% 5%



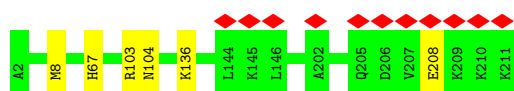
- Molecule 31: 60S ribosomal protein L11

Chain LJ:  5% 94% 6%



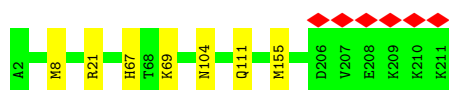
- Molecule 32: Large ribosomal subunit protein eL13

Chain IL:  5% 97% •



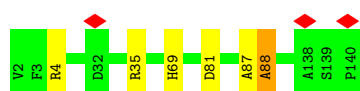
- Molecule 32: Large ribosomal subunit protein eL13

Chain LL:  5% 97% •



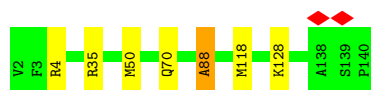
- Molecule 33: 60S ribosomal protein L14

Chain LM:  5% 96% • •



- Molecule 33: 60S ribosomal protein L14

Chain LM:  95%



- Molecule 34: 60S ribosomal protein L15

Chain LN:  97%



- Molecule 34: 60S ribosomal protein L15

Chain LN:  97%



- Molecule 35: 60S ribosomal protein L13a

Chain IO:  97%



- Molecule 35: 60S ribosomal protein L13a

Chain LO:  98%



- Molecule 36: 60S ribosomal protein L17

Chain IP:  94% 6%



- Molecule 36: 60S ribosomal protein L17

Chain LP:  95% 5%



- Molecule 37: 60S ribosomal protein L18

Chain IQ:  97%



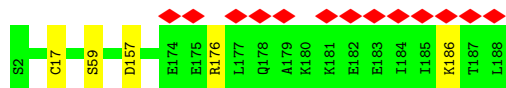
- Molecule 37: 60S ribosomal protein L18

Chain LQ:  96%



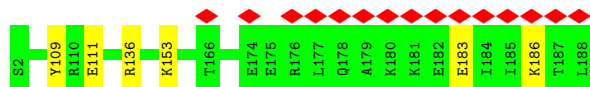
- Molecule 38: 60S ribosomal protein L19

Chain LR:  97%



- Molecule 38: 60S ribosomal protein L19

Chain LR:  97%



- Molecule 39: 60S ribosomal protein L18a

Chain LS:  98%



- Molecule 39: 60S ribosomal protein L18a

Chain LS:  96%



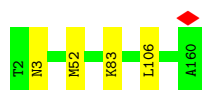
- Molecule 40: 60S ribosomal protein L21

Chain IT:  97%

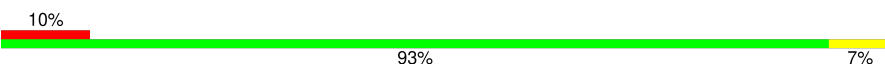


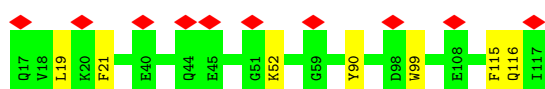
- Molecule 40: 60S ribosomal protein L21

Chain LT:  97%



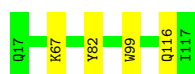
- Molecule 41: Heparin-binding protein HBp15

Chain IU:  93%



- Molecule 41: Heparin-binding protein HBp15

Chain LU:  96%



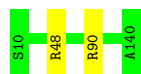
- Molecule 42: 60S ribosomal protein L23

Chain IV:  97%



- Molecule 42: 60S ribosomal protein L23

Chain LV:  98%



- Molecule 43: 60S ribosomal protein L23a

Chain IX:  97%



- Molecule 43: 60S ribosomal protein L23a

Chain LX:  96%



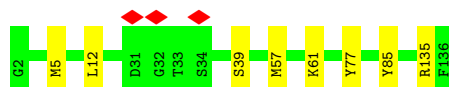
- Molecule 44: 60S ribosomal protein L26



- Molecule 44: 60S ribosomal protein L26



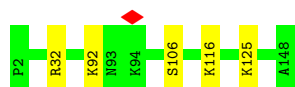
- Molecule 45: 60S ribosomal protein L27



- Molecule 45: 60S ribosomal protein L27



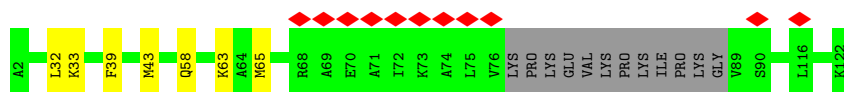
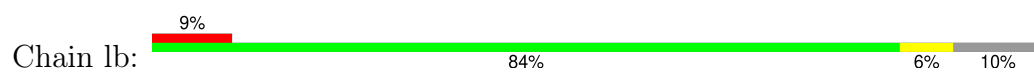
- Molecule 46: 60S ribosomal protein L27a



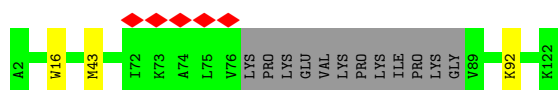
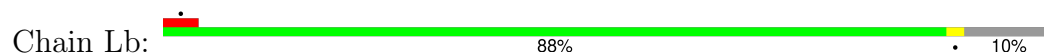
- Molecule 46: 60S ribosomal protein L27a



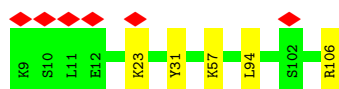
- Molecule 47: Large ribosomal subunit protein eL29



- Molecule 47: Large ribosomal subunit protein eL29



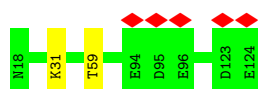
- Molecule 48: 60S ribosomal protein L30



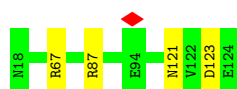
- Molecule 48: 60S ribosomal protein L30



- Molecule 49: 60S ribosomal protein L31



- Molecule 49: 60S ribosomal protein L31

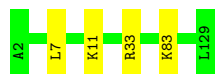


- Molecule 50: 60S ribosomal protein L32



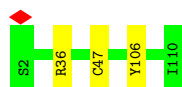
- Molecule 50: 60S ribosomal protein L32

Chain Le:  97%



- Molecule 51: 60S ribosomal protein L35a

Chain lf:  97%



- Molecule 51: 60S ribosomal protein L35a

Chain Lf:  98%



- Molecule 52: 60S ribosomal protein L34

Chain lg:  96%



- Molecule 52: 60S ribosomal protein L34

Chain Lg:  99%



- Molecule 53: 60S ribosomal protein L35

Chain lh:  97%



- Molecule 53: 60S ribosomal protein L35

Chain Lh:  96%



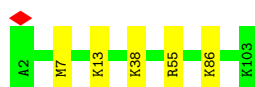
- Molecule 54: 60S ribosomal protein L36

Chain li:  100%




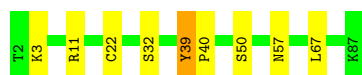
- Molecule 54: 60S ribosomal protein L36

Chain Li:  95% 5%



- Molecule 55: 60S ribosomal protein L37

Chain lj:  90% 9%



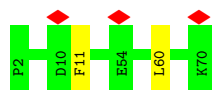
- Molecule 55: 60S ribosomal protein L37

Chain Lj:  95% 5%



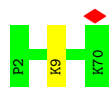
- Molecule 56: 60S ribosomal protein L38

Chain lk:  97%



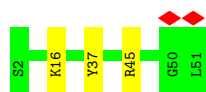
- Molecule 56: 60S ribosomal protein L38

Chain Lk:  99%



- Molecule 57: 60S ribosomal protein L39

Chain ll:  94% 6%



- Molecule 57: 60S ribosomal protein L39

Chain Ll: 98%



- Molecule 58: Large ribosomal subunit protein eL40

Chain lm: 92% 8%



- Molecule 58: Large ribosomal subunit protein eL40

Chain Lm: 100%

There are no outlier residues recorded for this chain.

- Molecule 59: 60S ribosomal protein L41

Chain ln: 96%



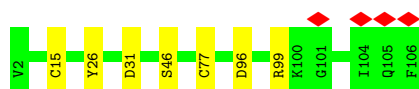
- Molecule 59: 60S ribosomal protein L41

Chain Ln: 88% 12%



- Molecule 60: 60S ribosomal protein L36a

Chain lo: 93% 7%

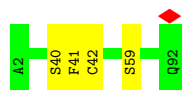


- Molecule 60: 60S ribosomal protein L36a

Chain Lo: 96%



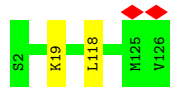
- Molecule 61: 60S ribosomal protein L37a



- Molecule 61: 60S ribosomal protein L37a



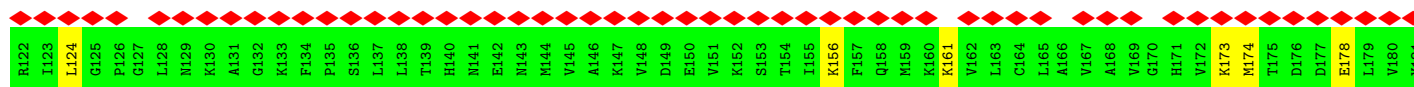
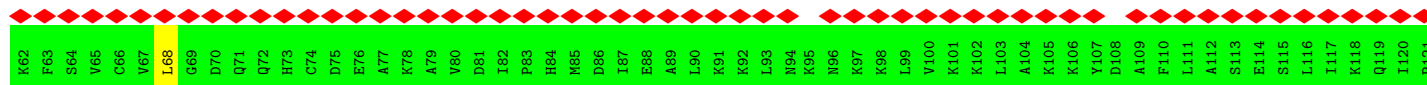
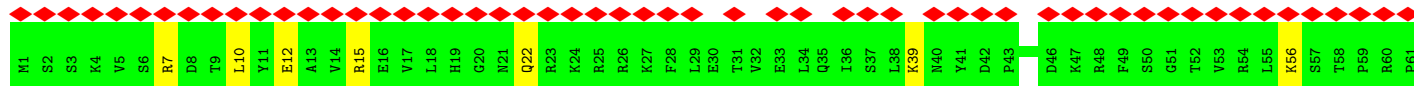
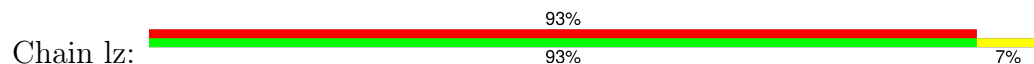
- Molecule 62: 60S ribosomal protein L28

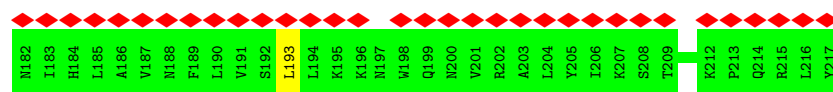


- Molecule 62: 60S ribosomal protein L28

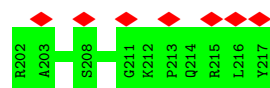
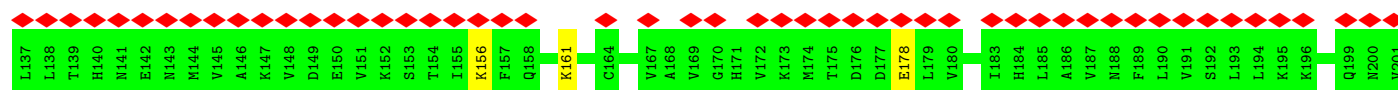
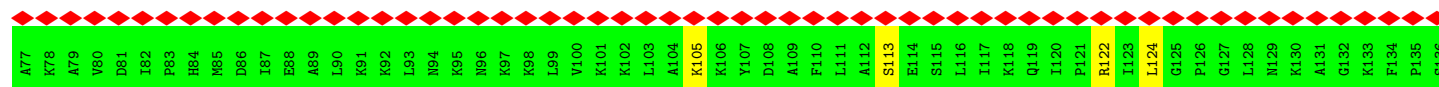
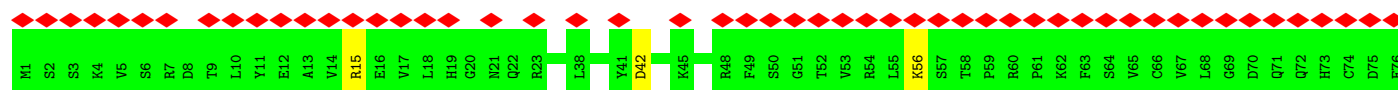
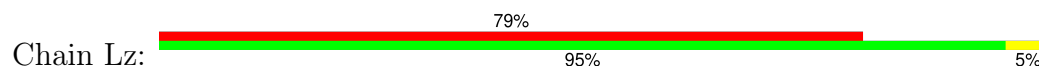


- Molecule 63: 60S ribosomal protein L10a

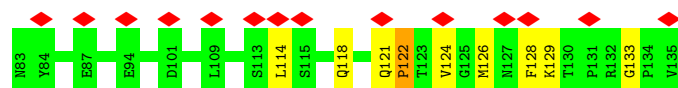
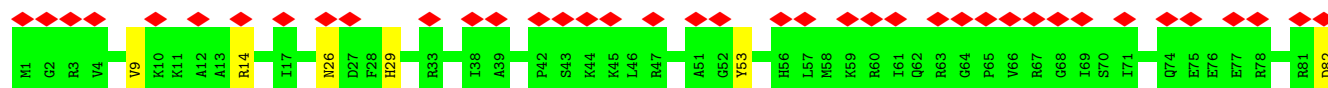
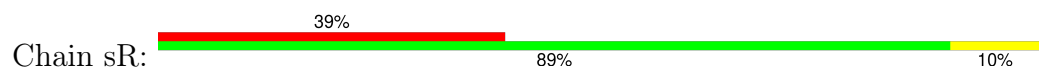




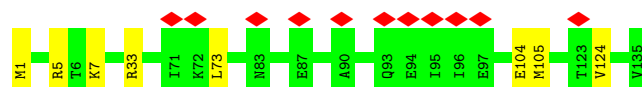
- Molecule 63: 60S ribosomal protein L10a



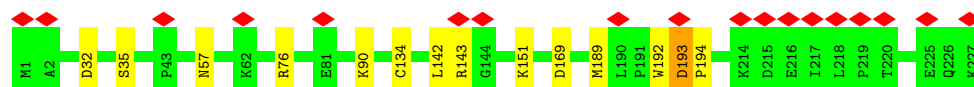
- Molecule 64: 40S ribosomal protein S17



- Molecule 64: 40S ribosomal protein S17



- Molecule 65: Small ribosomal subunit protein uS3



- Molecule 65: Small ribosomal subunit protein uS3

Chain SD:  96%



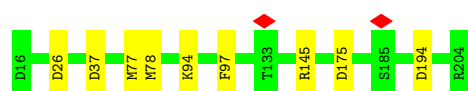
- Molecule 66: 40S ribosomal protein S5

Chain sF:  95% 5%



- Molecule 66: 40S ribosomal protein S5

Chain SF:  95% 5%




- Molecule 67: 40S ribosomal protein S10

Chain sK:  93% 7%



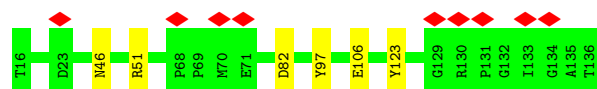
- Molecule 67: 40S ribosomal protein S10

Chain SK:  5% 90% 8%



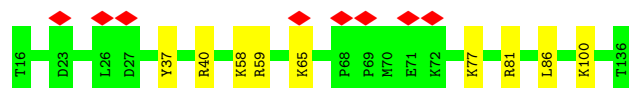
- Molecule 68: Small ribosomal subunit protein uS19

Chain sP:  7% 95% 5%

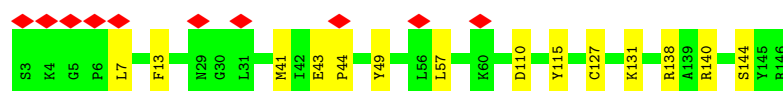
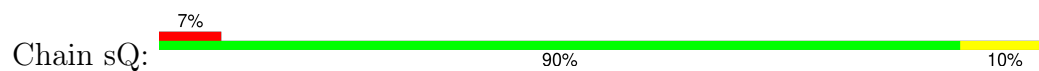


- Molecule 68: Small ribosomal subunit protein uS19

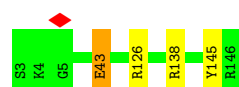
Chain SP:  7% 93% 7%



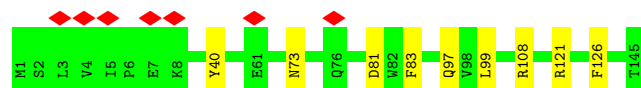
- Molecule 69: Small ribosomal subunit protein uS9



- Molecule 69: Small ribosomal subunit protein uS9



- Molecule 70: 40S ribosomal protein S18



- Molecule 70: 40S ribosomal protein S18



- Molecule 71: 40S ribosomal protein S19



- Molecule 71: 40S ribosomal protein S19

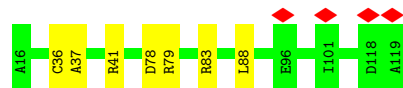


- Molecule 72: 40S ribosomal protein S20

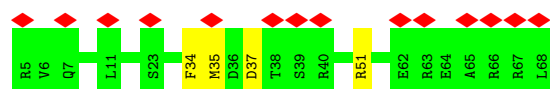




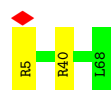
- Molecule 72: 40S ribosomal protein S20



- Molecule 73: 40S ribosomal protein S28



- Molecule 73: 40S ribosomal protein S28



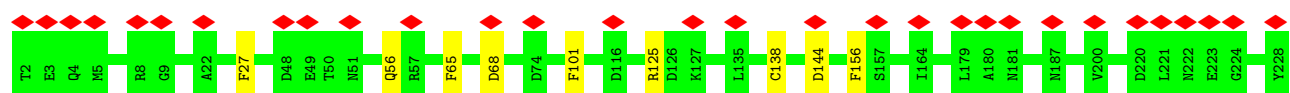
- Molecule 74: 40S ribosomal protein S29

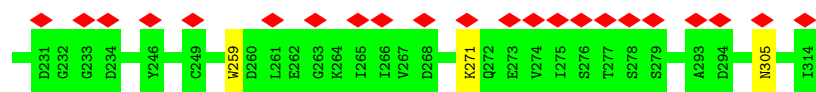


- Molecule 74: 40S ribosomal protein S29

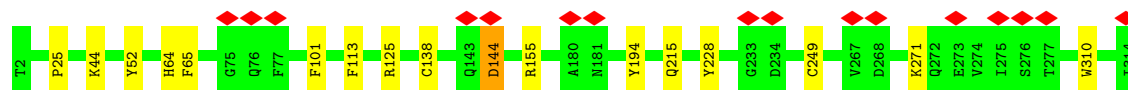


- Molecule 75: Receptor of activated protein C kinase 1

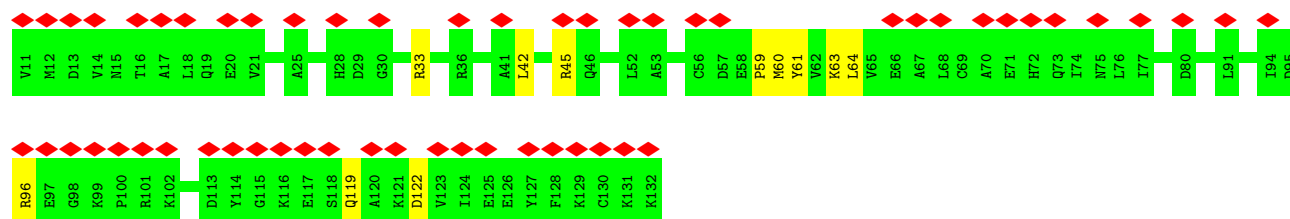




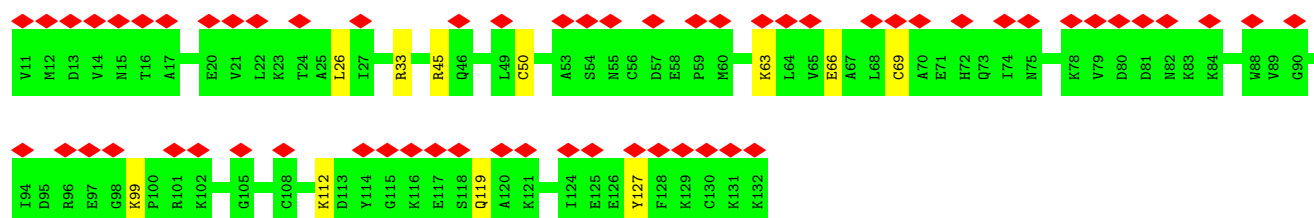
- Molecule 75: Receptor of activated protein C kinase 1



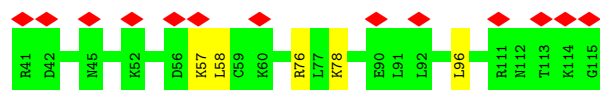
- Molecule 76: Small ribosomal subunit protein eS12



- Molecule 76: Small ribosomal subunit protein eS12



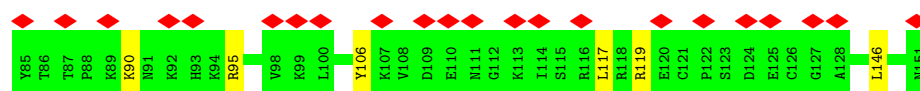
- Molecule 77: Small ribosomal subunit protein eS25



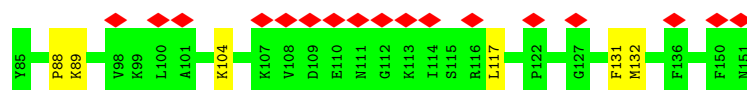
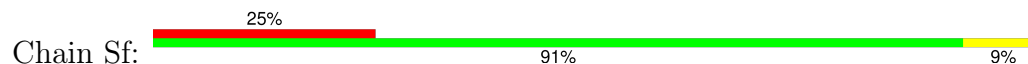
- Molecule 77: Small ribosomal subunit protein eS25



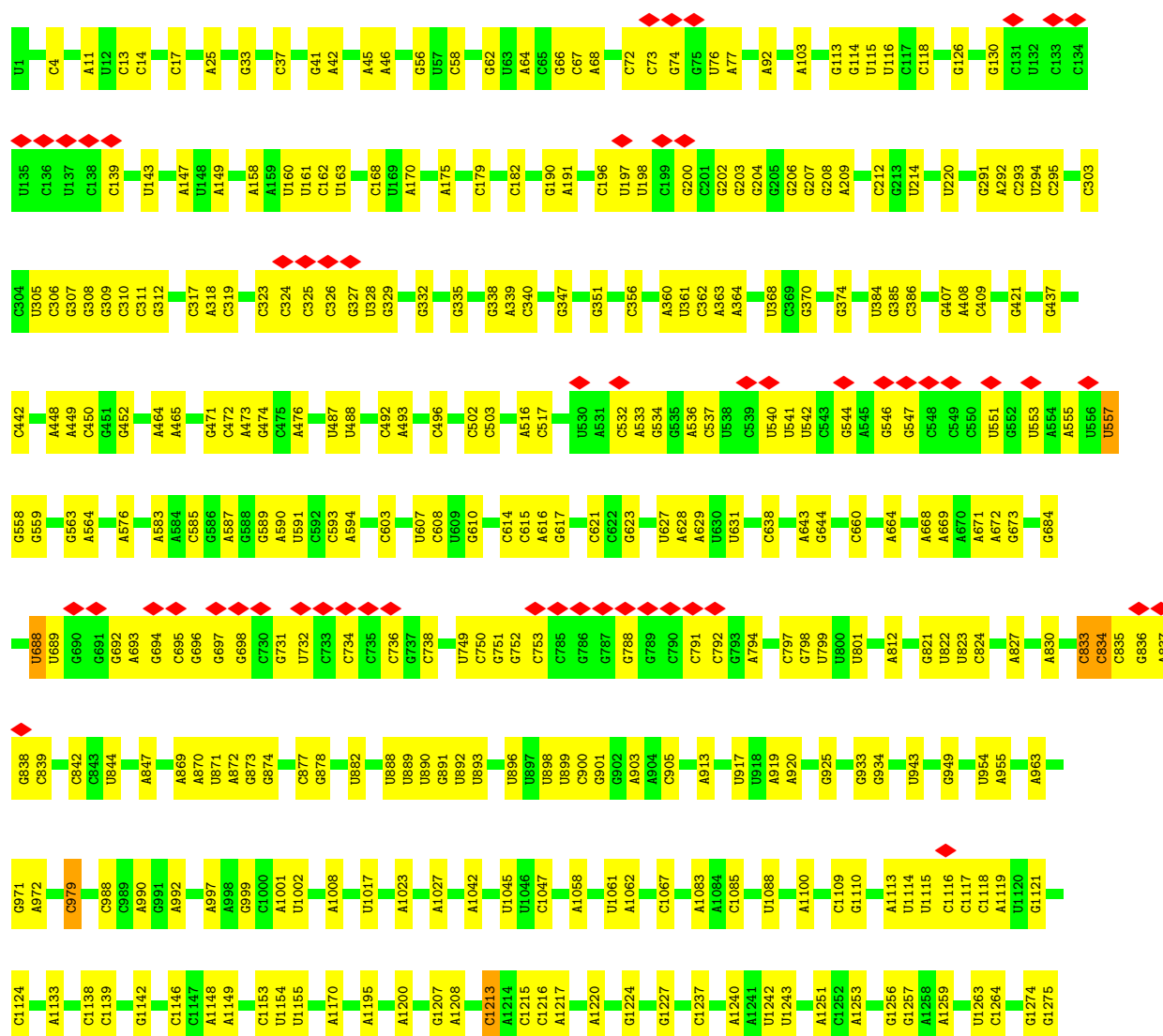
- Molecule 78: Ubiquitin-40S ribosomal protein S27a

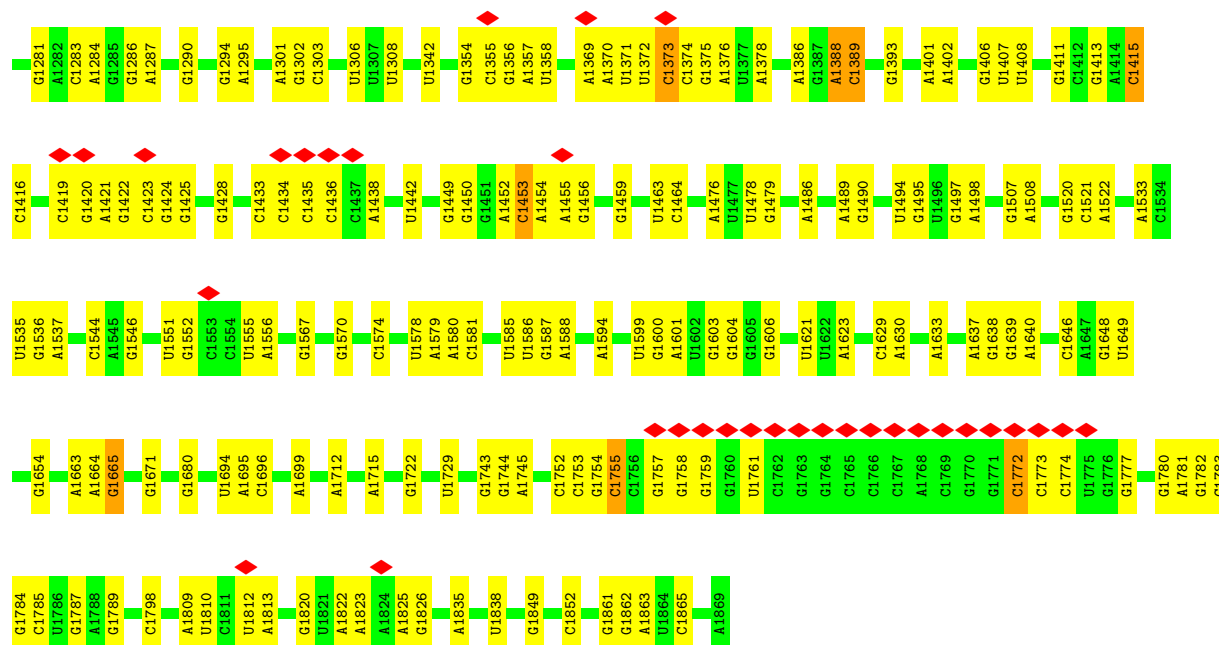


• Molecule 78: Ubiquitin-40S ribosomal protein S27a



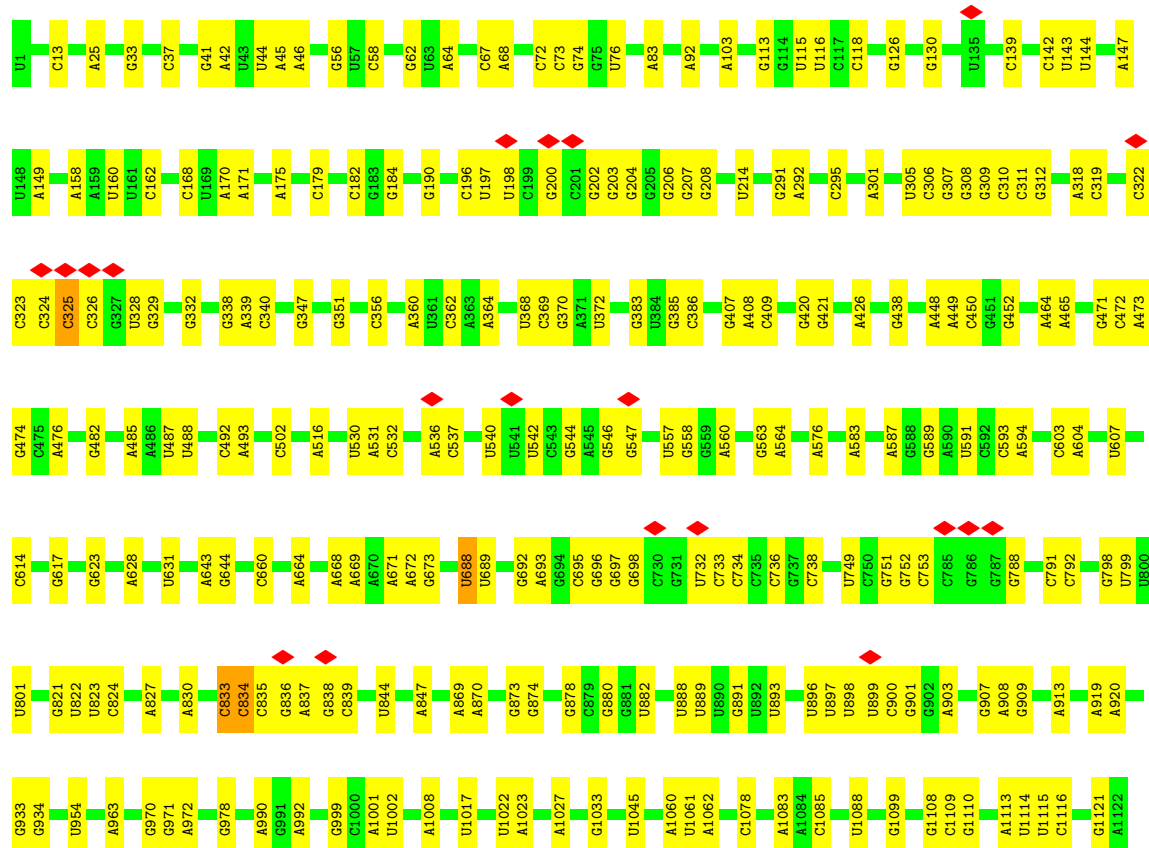
• Molecule 79: 18S rRNA [Homo sapiens]

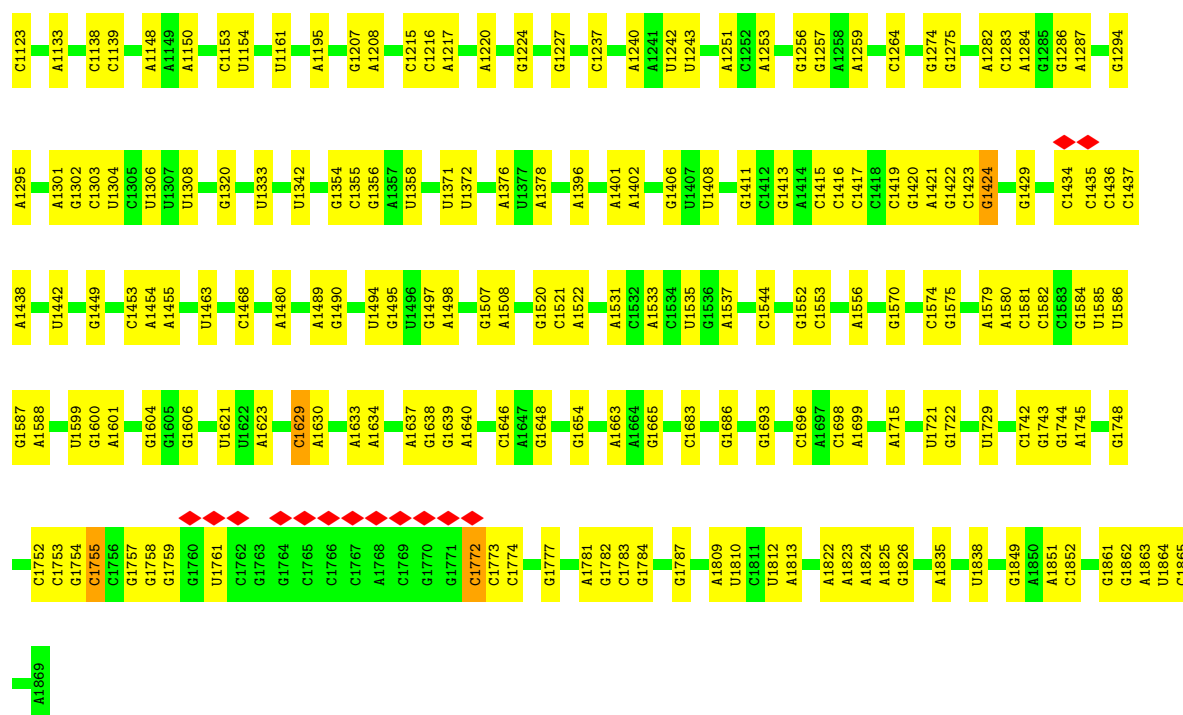




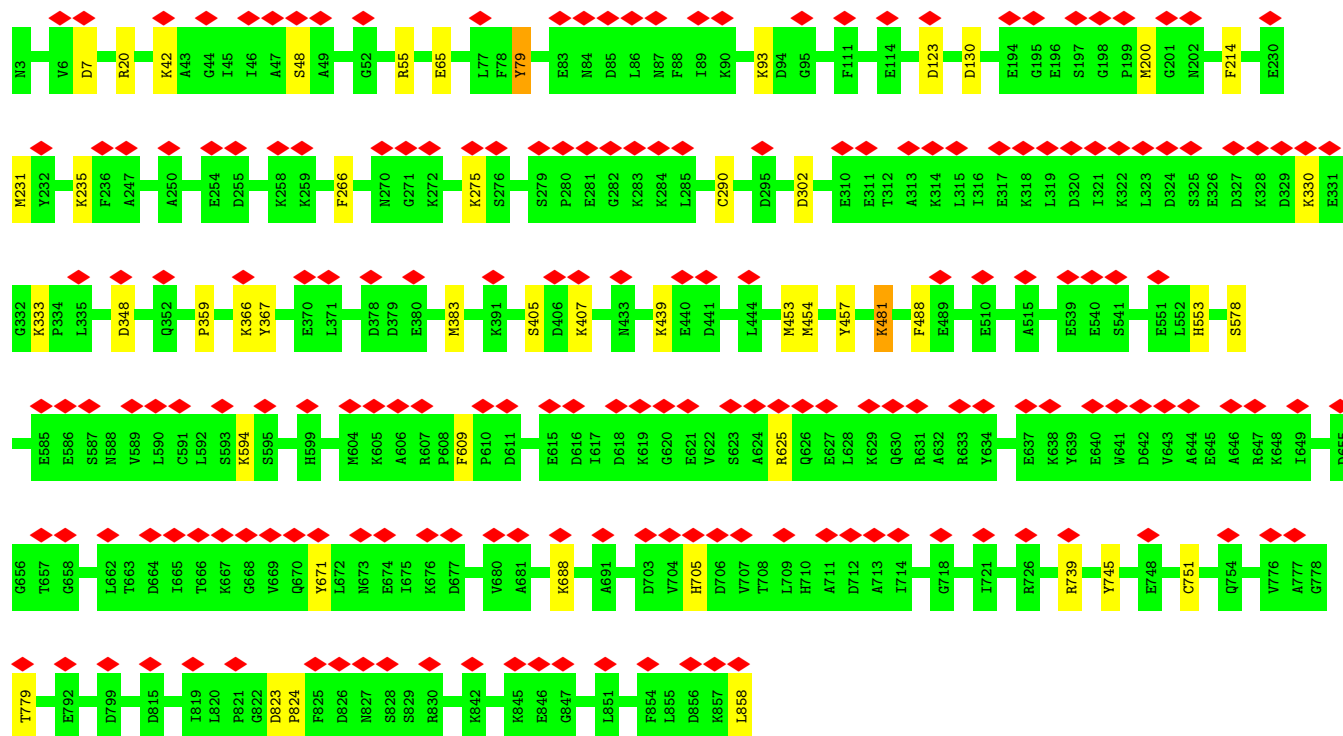
• Molecule 79: 18S rRNA [Homo sapiens]

Chain S2: 75% 25%





• Molecule 80: Elongation factor 2

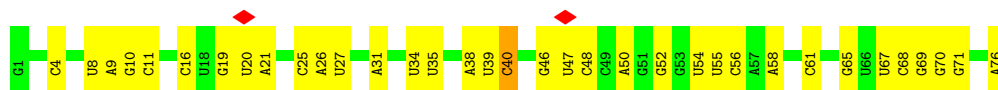


• Molecule 81: A/P site tRNA [Homo sapiens]

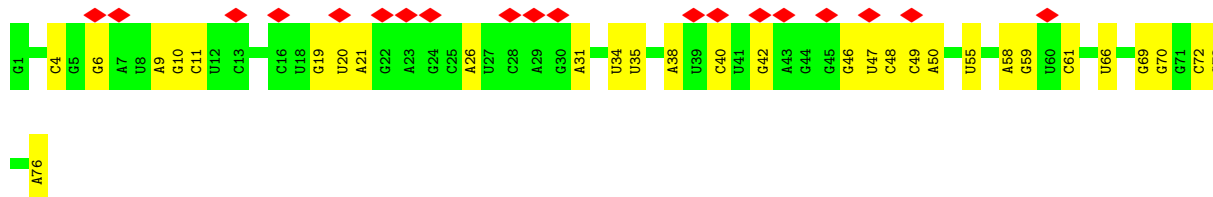




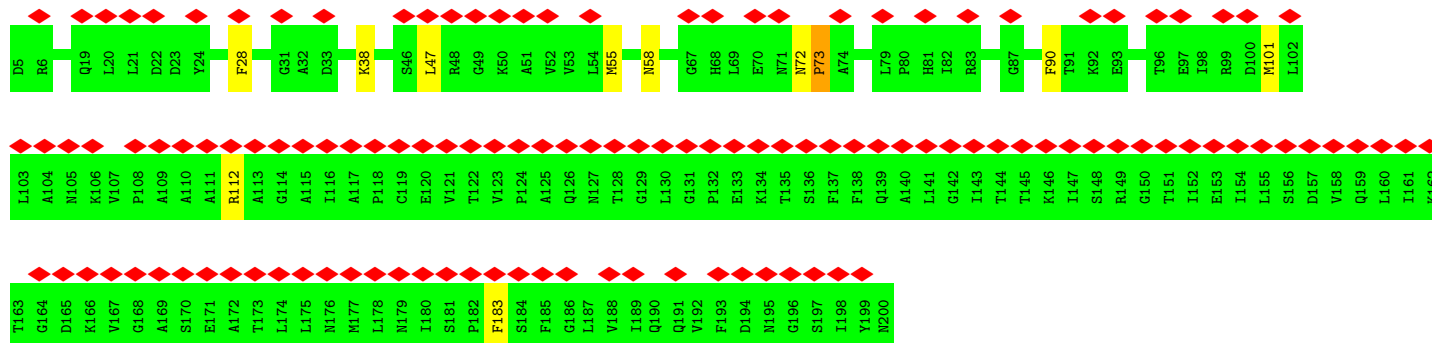
- Molecule 82: P/E site tRNA [Homo sapiens]



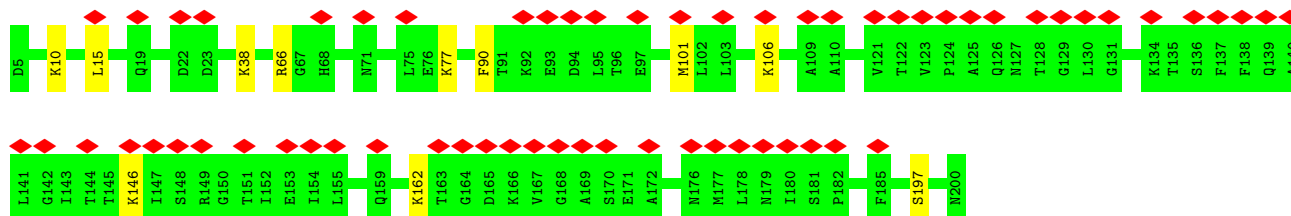
- Molecule 82: P/E site tRNA [Homo sapiens]



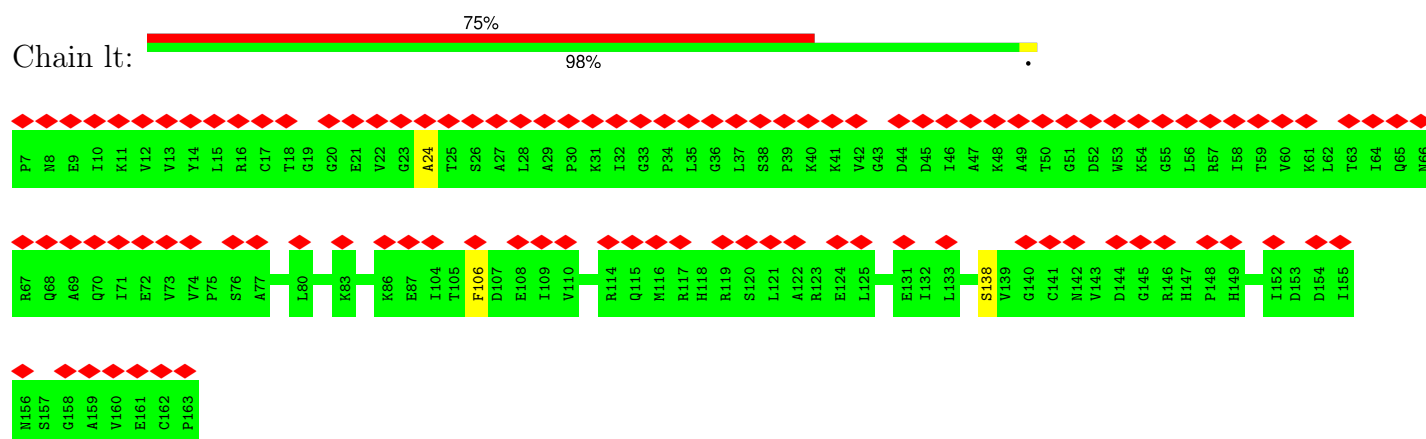
- Molecule 83: 60S acidic ribosomal protein P0



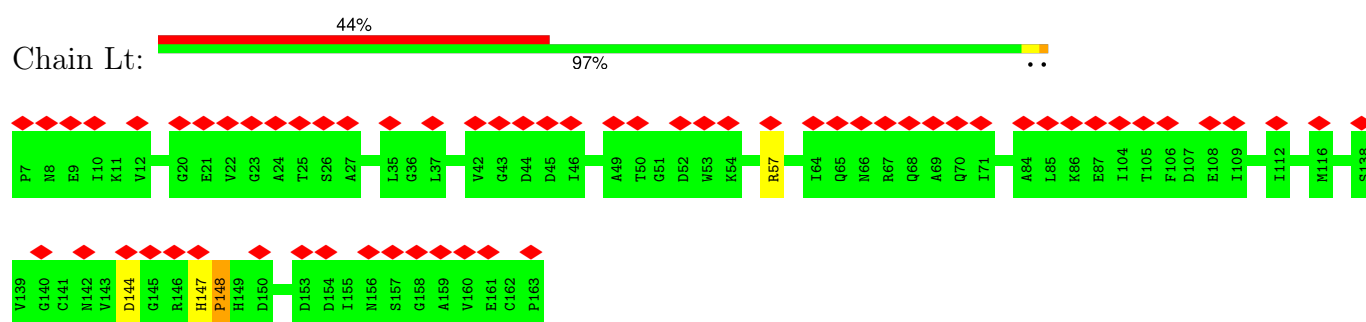
- Molecule 83: 60S acidic ribosomal protein P0



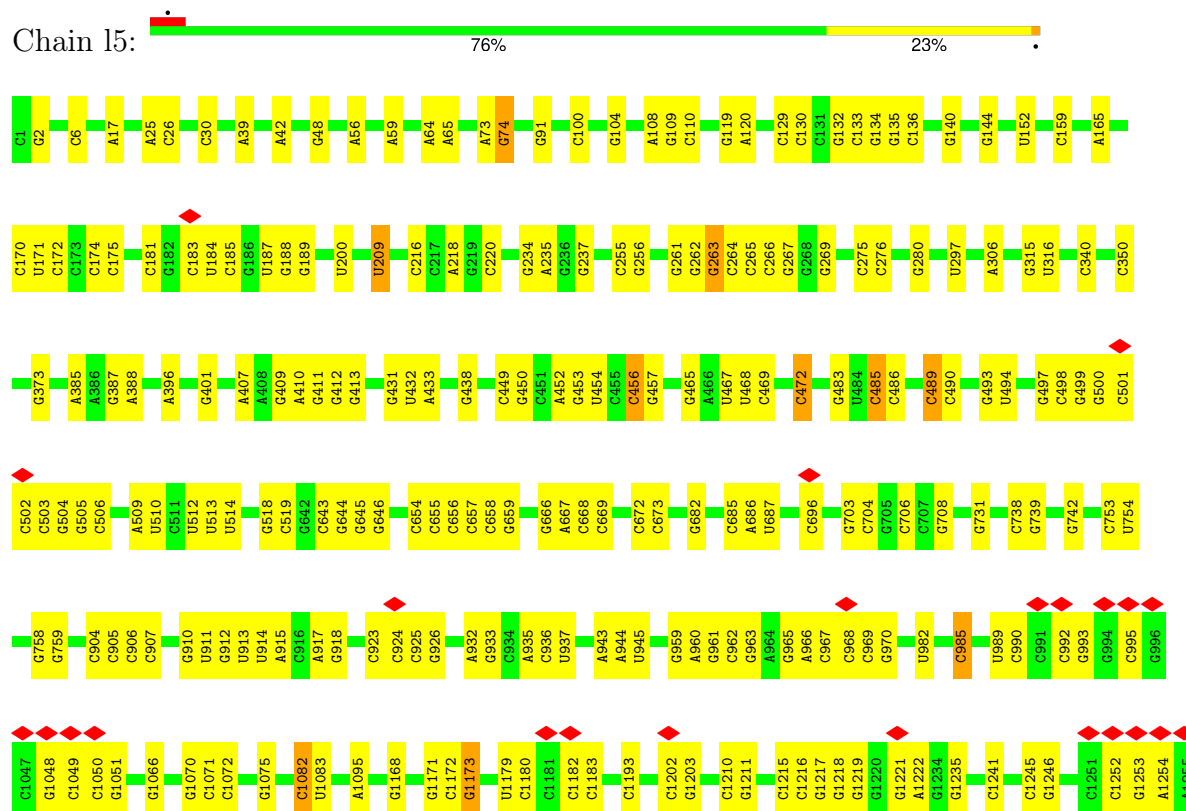
- Molecule 84: 60S ribosomal protein L12 [Homo sapiens]

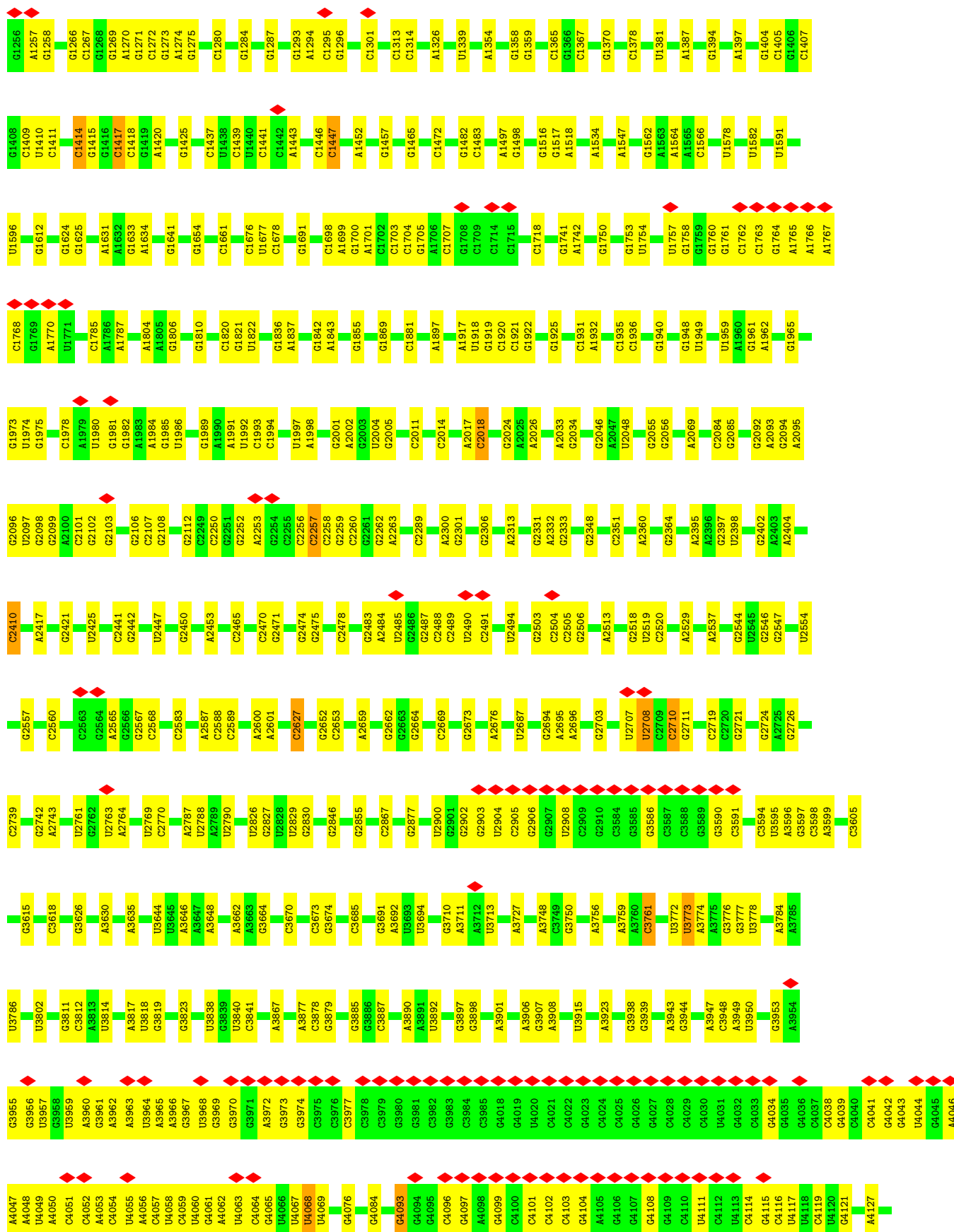


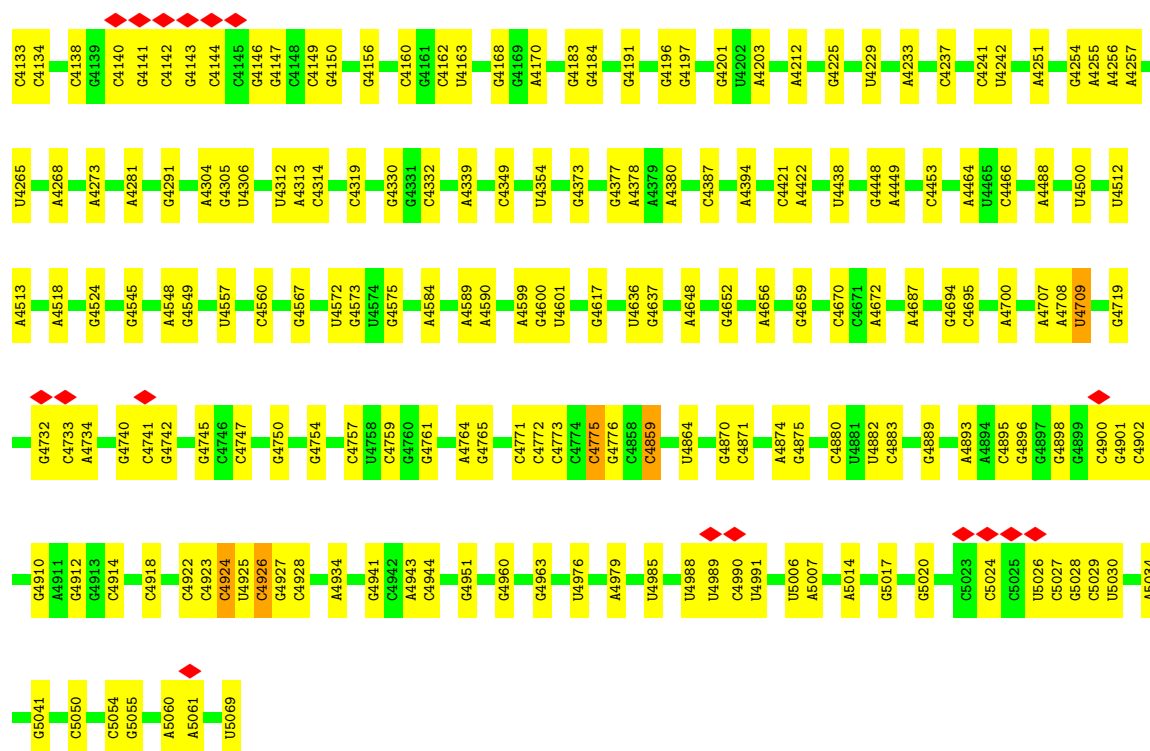
- Molecule 84: 60S ribosomal protein L12 [Homo sapiens]



- Molecule 85: 28S rRNA [Homo sapiens]

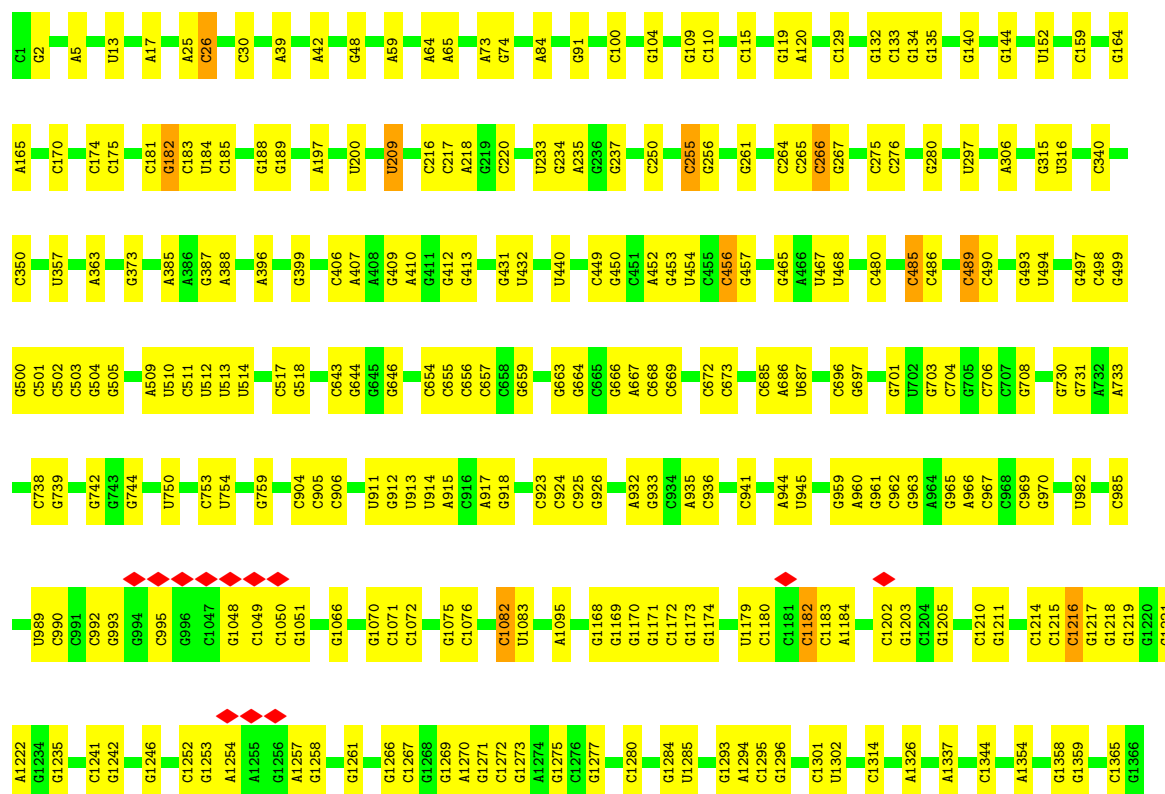




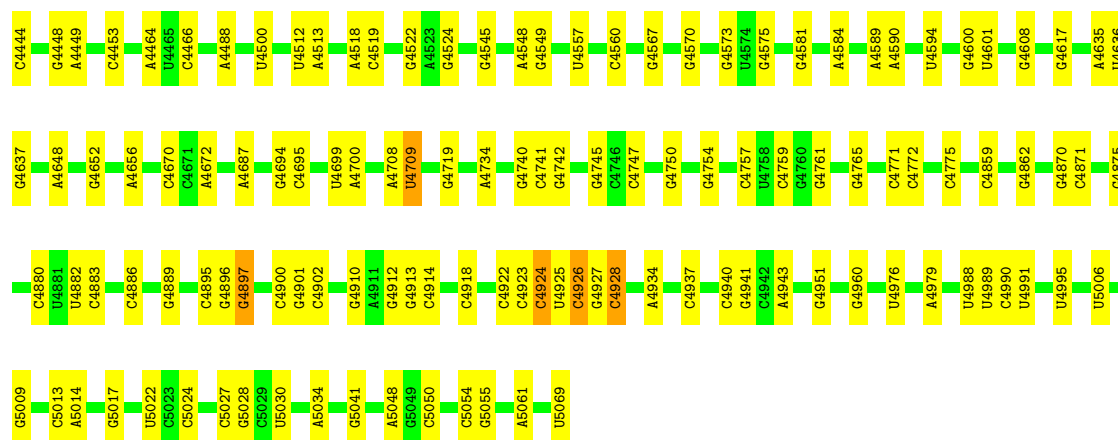


• Molecule 85: 28S rRNA [Homo sapiens]

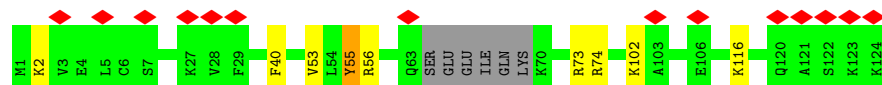
Chain L5: 76% 24%



A4251	G4254	A4255	A4256	A4257	A4258	U4265	A4268	A4273	A4279	A4280	A4281	C4286	G4291	A4304	A4305	A4306	A4313	A4314	A4330	A4331	C4332	A4339	C4349	U4354	G4373	G4377	A4378	A4379	A4380	C4387	G4391	C4392	A4394	C4421	C4422	A4426	U4438																			
A4105	G4108	G4109	A4256	U4111	C4114	C4115	C4116	C4119	A4127	C4133	C4134	C4138	G4139	C4140	C4141	C4142	C4143	C4144	C4145	C4146	C4149	C4160	C4161	C4162	U4163	C4164	A4170	C4183	C4184	C4191	C4196	A4203	A4213	G4222	G4225	U4229	A4233	A4234	C4241																	
G4026	G4027	C4028	C4029	C4030	U4031	C4032	C4033	C4034	G4035	G4036	C4037	C4038	C4039	C4040	C4041	C4042	C4043	U4044	A4045	A4046	A4047	A4048	U4049	A4050	C4051	C4052	A4053	C4054	U4055	A4056	C4057	U4058	C4059	U4060	C4061	C4062	U4063	C4064	U4065	U4066	U4067	U4068	U4069	C4076	C4092	G4093	G4094	C4095	C4096	G4097	A4098	C4099	C4100	C4102	C4103	C4104
G3897	A3901	A3906	A3907	A3908	U3915	G3938	G3939	A3943	G3944	A3947	C3948	A3949	C3953	A3954	G3955	G3956	U3957	G3958	U3959	A3960	A3961	A3962	A3963	U3964	A3965	A3966	G3967	U3968	G3969	A3972	G3973	G3974	C3975	C3976	C3977	C3978	C3979	G3980	C3981	C3982	C3983	C3984	C3985	G4018	G4019	U4020	C4021	C4022	C4023	C4024	C4025					
G3750	G3753	A3756	G3757	U3758	A3759	C3760	C3761	A3766	C3767	U3772	U3773	A3774	A3775	G3776	C3777	U3778	A3784	A3785	U3786	U3802	G3811	C3812	A3813	U3814	A3817	U3818	G3819	G3823	G3839	U3840	C3841	A3867	G3868	C3869	A3876	A3877	C3878	C3879	G3885	G3886	C3887	A3890	A3891	U3892	C3749											
U2900	G2901	G2902	U2903	U2904	C2905	C2906	U2907	U2908	C3588	G3589	G3590	C3591	C3594	U3595	C3596	G3597	C3605	G3614	G3615	U3616	G3626	A3630	A3635	U3644	U3645	A3646	A3647	A3648	A3652	A3662	A3663	G3664	C3673	C3674	A3692	G3698	A3711	A3712	U3713	G3714	A3727	A3748	C3749													
U2707	U2708	C2709	C2710	G2711	C2719	C2720	G2721	G2724	A2725	G2726	C2729	C2739	G2742	A2743	A2746	G2760	U2761	G2762	A2764	U2769	C2770	C2785	C2786	A2787	U2788	A2789	U2790	C2805	U2826	G2827	U2828	U2829	A2835	G2846	G2855	C2867	G2877	A2895	C2899																	
A2511	A2512	A2513	U2519	C2520	A2529	A2537	U2544	U2545	G2546	G2547	U2554	G2555	G2559	C2560	C2563	G2564	A2565	A2573	C2583	A2587	C2588	C2589	A2601	C2627	G2638	G2652	C2653	G2662	C2669	G2673	A2674	A2676	G2686	U2687	G2694	A2695	A2696	G2703																		
G2348	C2351	A2360	A2382	A2395	A2396	G2397	G2402	C2410	C2411	G2416	A2417	G2421	U2425	C2441	G2442	G2450	A2453	G2463	C2464	C2465	C2469	G2474	G2475	C2478	C2479	G2483	A2484	U2485	G2486	C2487	C2488	U2489	C2491	U2494	G2503	C2504	C2506																			
G1753	U1754	C1755	U1756	U1757	G1758	G1759	G1761	C1762	C1763	G1764	A1765	A1766	A1767	C1768	G1769	U1770	A1775	A1776	G1777	C1778	U1787	A1804	A1805	A1806	U1822	G1831	U1834	G1835	A1837	G1842	A1843	G1855	A1917	U1918	G1919	C1920	C1921	G1922	G1925																	
A1547	G1562	A1563	U1564	A1565	C1566	G1574	U1578	C1590	U1591	U1596	G1624	G1625	A1631	A1632	G1633	A1634	G1641	U1649	U1654	G1661	C1676	U1677	C1678	G1681	G1691	C1698	A1699	G1700	C1703	C1704	G1705	A1706	C1707	C1718	A1719	C1731	G1741	A1742	G1750																	
C1931	A1932	C1938	U1939	G1940	A1941	G1948	U1949	G1961	A1962	G1965	G1972	U1973	U1974	G1975	U1976	A1980	G1981	U1982	A1983	A1984	G1985	U1986	A1991	U1992	C1993	U1997	A1998	A1999	G2000	C2001	A2002	C2003	U2004	C2011	A2017	C2018	G2024	A2025	A2026	A2033	G2034	G2046	U2048													
G2052	G2055	A2069	C2084	G2085	G2092	C2094	A2095	U2097	G2098	G2099	A2100	C2101	G2102	G2103	G2104	G2105	G2106	C2107	G2108	G2109	C2110	G2111	G2112	C2249	C2250	G2251	G2252	A2253	G2254	C2255	C2256	C2257	G2258	G2259	C2260	G2261	C2289	A2300	G2301	A2313	G2316	G2322	G2331	G2332	G2333											



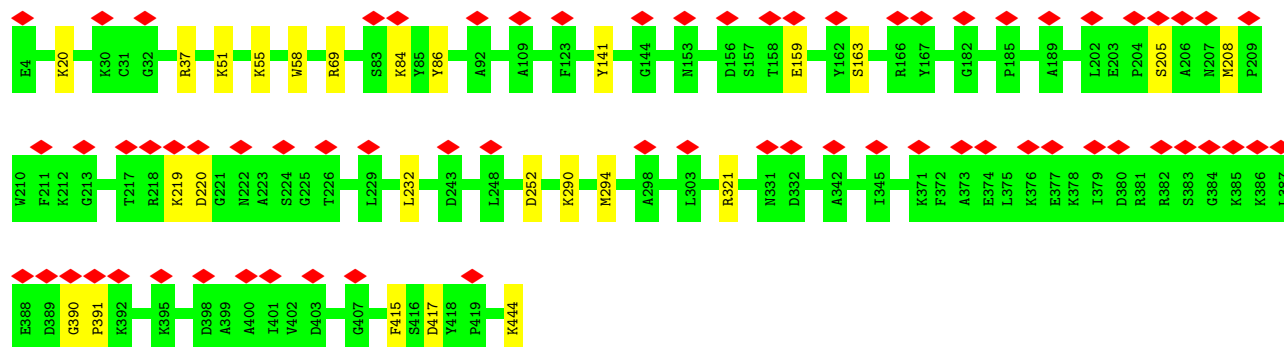
• Molecule 86: Ribosomal protein L24



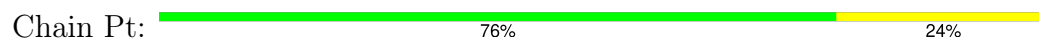
• Molecule 87: A/T site tRNA [Homo sapiens]



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



• Molecule 89: P site tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	9137	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.691	Depositor
Minimum map value	-0.099	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.033	Depositor
Recommended contour level	0.099	Depositor
Map size (\AA)	640.8, 640.8, 640.8	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.068, 1.068, 1.068	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SEP, ZN, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	cH	0.28	0/977	0.62	0/1306
2	SE	0.28	0/2118	0.55	0/2849
2	sE	0.28	0/2118	0.57	1/2849 (0.0%)
3	SI	0.27	0/1715	0.59	0/2287
3	sI	0.33	1/1715 (0.1%)	0.60	0/2287
4	SL	0.27	0/1268	0.57	0/1696
4	sL	0.34	0/1268	0.59	0/1696
5	SX	0.26	0/1116	0.54	0/1490
5	sX	0.30	0/1116	0.56	0/1490
6	SG	0.38	2/1946 (0.1%)	0.77	2/2590 (0.1%)
6	sG	0.44	2/1946 (0.1%)	0.59	0/2590
7	SJ	0.29	0/1550	0.59	0/2069
7	sJ	0.28	0/1550	0.59	0/2069
8	SY	0.83	3/1083 (0.3%)	0.97	6/1438 (0.4%)
8	sY	0.56	2/1083 (0.2%)	0.68	0/1438
9	Se	0.27	0/465	0.57	0/612
9	se	0.31	0/465	0.67	0/612
10	SA	0.34	0/1778	0.56	0/2416
10	sA	0.34	0/1778	0.61	1/2416 (0.0%)
11	SB	0.41	2/1765 (0.1%)	0.61	3/2362 (0.1%)
11	sB	0.38	1/1765 (0.1%)	0.58	0/2362
12	SH	0.33	0/1519	0.57	0/2033
12	sH	0.30	0/1519	0.61	1/2033 (0.0%)
13	SV	0.37	0/643	0.73	2/860 (0.2%)
13	sV	0.32	0/643	0.64	0/860
14	Sa	0.35	0/836	0.64	1/1121 (0.1%)
14	sa	0.36	0/836	0.62	0/1121
15	SC	0.31	0/1762	0.54	0/2381
15	sC	0.43	2/1762 (0.1%)	0.59	2/2381 (0.1%)
16	SN	0.46	2/1232 (0.2%)	0.56	0/1656
16	sN	0.32	0/1232	0.55	0/1656
17	SO	0.29	0/1062	0.63	1/1425 (0.1%)

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

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
83	Ls	0.30	0/1519	0.59	1/2052 (0.0%)
83	ls	0.49	3/1519 (0.2%)	0.73	3/2052 (0.1%)
84	Lt	0.63	1/1058 (0.1%)	0.83	5/1430 (0.3%)
84	lt	0.26	0/1058	0.57	0/1430
85	L5	0.41	0/89312	0.84	72/139287 (0.1%)
85	l5	0.44	0/89313	0.84	74/139291 (0.1%)
86	LW	0.88	5/979 (0.5%)	0.82	1/1295 (0.1%)
87	AT	0.22	0/1805	0.83	1/2809 (0.0%)
88	CF	0.55	5/3442 (0.1%)	0.79	9/4656 (0.2%)
89	Pt	0.27	0/1761	0.83	4/2741 (0.1%)
All	All	0.38	73/489910 (0.0%)	0.76	344/718287 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	cH	0	1
5	SX	0	1
5	sX	0	1
12	SH	0	1
12	sH	0	1
22	LA	0	1
22	lA	0	1
23	LB	0	2
23	lB	0	3
31	LJ	0	1
31	lJ	0	1
33	LM	0	1
33	lM	0	2
35	LO	0	1
35	lO	0	1
51	Lf	0	1
51	lf	0	1
55	Lj	0	1
55	lj	0	1
64	sR	0	2
65	sD	0	1
66	SF	0	1
69	SQ	0	1
69	sQ	0	1

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

All (73) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	SY	52	PRO	CG-CD	-20.19	0.84	1.50
88	CF	391	PRO	CG-CD	-18.80	0.88	1.50
84	Lt	148	PRO	CG-CD	-16.99	0.94	1.50
65	sD	194	PRO	CG-CD	-16.78	0.95	1.50
65	sD	194	PRO	N-CD	15.63	1.69	1.47
88	CF	390	GLY	C-O	14.99	1.47	1.23
86	LW	55	TYR	CE1-CZ	-14.79	1.19	1.38
86	LW	55	TYR	CG-CD1	-14.71	1.20	1.39
8	SY	51	THR	C-N	12.73	1.58	1.34
65	sD	193	ASP	C-O	12.67	1.47	1.23
72	sU	93	SER	CB-OG	-12.09	1.26	1.42
6	sG	64	LYS	CE-NZ	-10.99	1.21	1.49
88	CF	391	PRO	N-CD	10.63	1.62	1.47
72	sU	108	PRO	CG-CD	-10.22	1.17	1.50
8	sY	81	TYR	CE1-CZ	-10.01	1.25	1.38
16	SN	25	TRP	CZ3-CH2	-9.83	1.24	1.40
86	LW	55	TYR	CE2-CZ	-9.78	1.25	1.38
67	SK	25	LYS	CD-CE	-9.73	1.26	1.51
72	sU	107	GLU	C-N	9.17	1.51	1.34
19	Sb	82	LYS	CE-NZ	-9.03	1.26	1.49
77	SZ	70	PRO	CG-CD	-8.95	1.21	1.50
83	ls	73	PRO	CG-CD	-8.54	1.22	1.50
11	SB	30	TRP	CE3-CZ3	-8.48	1.24	1.38
18	SW	50	PHE	CE2-CZ	-8.44	1.21	1.37
15	sC	256	TRP	CZ3-CH2	-8.41	1.26	1.40
80	cB	79	TYR	CE1-CZ	-8.16	1.27	1.38
25	ID	292	GLU	CD-OE1	-8.04	1.16	1.25
25	LD	219	TYR	CE1-CZ	-7.94	1.28	1.38
64	SR	104	GLU	CD-OE2	-7.92	1.17	1.25
65	sD	194	PRO	N-CA	-7.90	1.33	1.47
8	sY	81	TYR	CG-CD1	-7.55	1.29	1.39
64	sR	122	PRO	CG-CD	-7.55	1.25	1.50
86	LW	55	TYR	CD1-CE1	-7.38	1.28	1.39
6	sG	82	SER	CA-CB	7.36	1.64	1.52
78	sf	117	LEU	CG-CD1	-7.32	1.24	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	ls	72	ASN	C-N	7.27	1.48	1.34
64	sR	129	LYS	CD-CE	-7.19	1.33	1.51
65	sD	193	ASP	CA-C	6.96	1.71	1.52
24	lC	13	GLU	CG-CD	-6.63	1.42	1.51
6	SG	8	PRO	N-CD	6.58	1.57	1.47
19	sb	12	PRO	CG-CD	-6.57	1.28	1.50
88	CF	391	PRO	CB-CG	-6.52	1.17	1.50
79	s2	1665	G	C8-N7	-6.48	1.27	1.30
18	SW	50	PHE	CG-CD2	-6.47	1.29	1.38
69	sQ	140	ARG	CZ-NH2	-6.43	1.24	1.33
6	SG	8	PRO	CG-CD	-6.43	1.29	1.50
80	cB	79	TYR	CD1-CE1	-6.42	1.29	1.39
31	LJ	99	PHE	CG-CD2	-6.38	1.29	1.38
64	sR	9	VAL	CB-CG2	-6.36	1.39	1.52
11	SB	30	TRP	CZ2-CH2	-6.25	1.25	1.37
55	lj	40	PRO	CG-CD	-6.15	1.30	1.50
58	lm	106	ARG	CZ-NH2	-6.13	1.25	1.33
22	LA	61	VAL	CB-CG1	-6.03	1.40	1.52
86	LW	55	TYR	CZ-OH	-6.01	1.27	1.37
46	La	120	GLN	CD-NE2	-6.00	1.17	1.32
8	SY	52	PRO	CB-CG	5.95	1.79	1.50
46	La	134	GLU	CD-OE2	-5.91	1.19	1.25
25	LD	113	PHE	CG-CD2	-5.83	1.30	1.38
16	SN	25	TRP	CD2-CE3	-5.79	1.31	1.40
88	CF	390	GLY	C-N	-5.55	1.23	1.34
64	sR	121	GLN	C-O	5.54	1.33	1.23
67	SK	25	LYS	CE-NZ	5.52	1.62	1.49
83	ls	90	PHE	CG-CD1	-5.48	1.30	1.38
80	cB	79	TYR	CG-CD1	-5.40	1.32	1.39
15	sC	256	TRP	CD2-CE3	-5.40	1.32	1.40
3	sI	195	LEU	CG-CD1	-5.14	1.32	1.51
31	LJ	163	MET	CG-SD	-5.10	1.68	1.81
37	LQ	94	GLU	CD-OE2	-5.08	1.20	1.25
72	sU	108	PRO	N-CA	-5.08	1.38	1.47
11	sB	230	GLU	CD-OE2	-5.07	1.20	1.25
55	lj	39	TYR	C-N	-5.07	1.24	1.34
71	sT	108	GLU	CD-OE1	-5.07	1.20	1.25
66	sF	45	TYR	CE1-CZ	-5.06	1.31	1.38

All (344) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	sD	194	PRO	CA-N-CD	-27.69	72.73	111.50
65	sD	193	ASP	C-N-CD	20.84	172.16	128.40
8	SY	52	PRO	CA-N-CD	-20.49	82.81	111.50
64	sR	122	PRO	CA-N-CD	-20.34	83.02	111.50
77	SZ	70	PRO	CA-N-CD	-20.06	83.42	111.50
6	SG	8	PRO	CA-N-CD	-19.61	84.05	111.50
88	CF	391	PRO	CA-N-CD	-19.21	84.61	111.50
88	CF	391	PRO	CB-CG-CD	18.82	179.92	106.50
19	sb	12	PRO	CA-N-CD	-18.57	85.50	111.50
67	sK	86	PRO	CA-N-CD	-18.27	85.93	111.50
88	CF	391	PRO	CA-CB-CG	-17.87	70.04	104.00
55	lj	40	PRO	CA-N-CD	-17.69	86.73	111.50
80	cB	824	PRO	CA-N-CD	-16.98	87.72	111.50
83	ls	73	PRO	CA-N-CD	-16.75	88.05	111.50
72	sU	108	PRO	CA-N-CD	-16.18	88.85	111.50
86	LW	55	TYR	CD1-CE1-CZ	15.18	133.47	119.80
80	cB	79	TYR	CD1-CE1-CZ	15.04	133.34	119.80
88	CF	391	PRO	N-CD-CG	-13.86	82.42	103.20
6	SG	7	PHE	C-N-CD	13.53	156.81	128.40
88	CF	390	GLY	C-N-CD	13.47	156.68	128.40
77	SZ	69	THR	C-N-CD	12.84	155.37	128.40
65	sD	193	ASP	CA-C-O	-12.23	94.42	120.10
8	SY	51	THR	C-N-CD	12.18	153.97	128.40
84	Lt	148	PRO	CA-N-CD	-12.13	94.52	111.50
25	LD	113	PHE	CZ-CE2-CD2	11.16	133.49	120.10
84	Lt	148	PRO	CA-CB-CG	-10.78	83.52	104.00
79	s2	1374	C	C2-N1-C1'	10.61	130.47	118.80
72	sU	94	PRO	CA-N-CD	-10.56	96.72	111.50
72	sU	107	GLU	C-N-CD	10.50	150.46	128.40
8	SY	52	PRO	CA-CB-CG	-10.41	84.21	104.00
88	CF	390	GLY	CA-C-O	-10.02	102.57	120.60
69	sQ	140	ARG	NE-CZ-NH1	9.81	125.20	120.30
84	Lt	148	PRO	N-CD-CG	-9.81	88.49	103.20
85	L5	174	C	N3-C2-O2	-9.77	115.06	121.90
64	sR	121	GLN	C-N-CD	9.71	148.79	128.40
85	l5	485	C	C2-N1-C1'	9.67	129.44	118.80
85	l5	129	C	N3-C2-O2	-9.62	115.17	121.90
85	l5	2710	C	N1-C2-O2	9.60	124.66	118.90
85	L5	485	C	C2-N1-C1'	9.49	129.24	118.80
66	sF	45	TYR	CD1-CE1-CZ	9.41	128.27	119.80
88	CF	391	PRO	N-CA-CB	9.32	114.49	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	S2	1453	C	C2-N1-C1'	9.07	128.78	118.80
67	sK	85	LEU	C-N-CD	9.04	147.38	128.40
72	SU	41	ARG	NE-CZ-NH1	-9.03	115.78	120.30
85	l5	2710	C	C2-N1-C1'	8.95	128.64	118.80
85	l5	174	C	N3-C2-O2	-8.92	115.65	121.90
79	s2	1772	C	N1-C2-O2	8.88	124.23	118.90
79	s2	1772	C	N3-C2-O2	-8.86	115.70	121.90
8	SY	52	PRO	N-CD-CG	-8.66	90.21	103.20
13	SV	14	PRO	CA-N-CD	-8.62	99.43	111.50
58	lm	106	ARG	NE-CZ-NH1	8.55	124.58	120.30
80	cB	7	ASP	CB-CG-OD1	-8.31	110.82	118.30
85	l5	1994	C	N3-C2-O2	-8.28	116.10	121.90
85	L5	2710	C	N1-C2-O2	8.25	123.85	118.90
79	S2	1453	C	N1-C2-O2	8.21	123.82	118.90
67	SK	91	PRO	CA-N-CD	-8.18	100.04	111.50
79	S2	1772	C	N1-C2-O2	8.12	123.78	118.90
79	s2	1374	C	C5-C6-N1	8.11	125.06	121.00
79	S2	1629	C	N3-C2-O2	-8.05	116.26	121.90
64	sR	129	LYS	CG-CD-CE	8.02	135.96	111.90
85	l5	4138	C	N3-C2-O2	-8.01	116.29	121.90
65	sD	193	ASP	CA-C-N	7.99	139.48	117.10
69	sQ	140	ARG	NE-CZ-NH2	-7.96	116.32	120.30
79	S2	1772	C	N3-C2-O2	-7.96	116.33	121.90
85	L5	1082	C	O4'-C1'-N1	7.96	114.56	108.20
85	L5	2710	C	C2-N1-C1'	7.96	127.55	118.80
85	l5	2710	C	N3-C2-O2	-7.88	116.39	121.90
84	Lt	147	HIS	C-N-CD	7.84	144.86	128.40
79	s2	1374	C	C6-N1-C1'	-7.78	111.47	120.80
85	l5	456	C	O4'-C1'-N1	7.69	114.35	108.20
85	l5	1447	C	N3-C2-O2	-7.66	116.54	121.90
85	L5	456	C	N3-C2-O2	-7.63	116.56	121.90
85	l5	485	C	C6-N1-C1'	-7.60	111.68	120.80
8	SY	52	PRO	N-CA-C	7.54	131.70	112.10
79	S2	1022	U	C2-N1-C1'	7.45	126.64	117.70
85	L5	456	C	O4'-C1'-N1	7.41	114.13	108.20
79	s2	607	U	C2-N1-C1'	7.40	126.58	117.70
55	lj	39	TYR	C-N-CD	-7.37	104.40	120.60
79	S2	356	C	C2-N1-C1'	7.35	126.89	118.80
85	l5	456	C	N3-C2-O2	-7.20	116.86	121.90
25	LD	219	TYR	CD1-CE1-CZ	7.17	126.25	119.80
85	L5	485	C	C6-N1-C1'	-7.15	112.22	120.80
85	L5	3773	U	N3-C2-O2	-7.13	117.21	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	l5	130	C	N3-C2-O2	-7.07	116.95	121.90
71	sT	125	PRO	CA-N-CD	-7.06	101.62	111.50
85	l5	209	U	C2-N1-C1'	7.03	126.14	117.70
85	L5	175	C	N3-C2-O2	-7.00	117.00	121.90
85	L5	1252	C	N3-C2-O2	-6.99	117.01	121.90
79	S2	356	C	N1-C2-O2	6.99	123.09	118.90
79	S2	1416	C	N3-C2-O2	-6.97	117.02	121.90
65	SD	29	LEU	CA-CB-CG	6.97	131.33	115.30
85	L5	2785	C	N1-C2-O2	6.94	123.07	118.90
85	l5	1252	C	N3-C2-O2	-6.93	117.05	121.90
85	l5	1082	C	O4'-C1'-N1	6.93	113.74	108.20
15	sC	123	ARG	NE-CZ-NH1	6.91	123.76	120.30
85	l5	490	C	N3-C2-O2	-6.83	117.12	121.90
85	L5	2785	C	N3-C2-O2	-6.83	117.12	121.90
85	l5	4147	G	C5-C6-O6	6.82	132.69	128.60
85	l5	4147	G	N1-C6-O6	-6.81	115.81	119.90
68	sP	123	TYR	C-N-CA	-6.80	104.70	121.70
85	L5	2018	C	C5-C6-N1	6.79	124.40	121.00
85	l5	654	C	N1-C2-O2	6.79	122.97	118.90
85	l5	2257	C	C2-N1-C1'	6.79	126.27	118.80
65	sD	194	PRO	CA-CB-CG	-6.78	91.11	104.00
85	l5	1414	C	N3-C2-O2	-6.76	117.17	121.90
85	l5	175	C	N3-C2-O2	-6.72	117.19	121.90
85	l5	3773	U	N3-C2-O2	-6.71	117.51	122.20
85	L5	2710	C	N3-C2-O2	-6.68	117.22	121.90
65	sD	194	PRO	CB-CG-CD	-6.68	80.46	106.50
85	L5	1414	C	N3-C2-O2	-6.67	117.23	121.90
79	s2	1755	C	N1-C2-O2	6.66	122.90	118.90
80	cB	79	TYR	CG-CD1-CE1	-6.65	115.98	121.30
79	s2	1416	C	N3-C2-O2	-6.64	117.25	121.90
79	s2	557	U	N1-C2-O2	6.62	127.44	122.80
79	s2	834	C	N3-C2-O2	-6.62	117.27	121.90
85	l5	1082	C	N3-C2-O2	-6.61	117.27	121.90
80	cB	823	ASP	C-N-CD	6.59	142.25	128.40
89	Pt	31	C	N1-C2-O2	6.57	122.84	118.90
65	sD	194	PRO	N-CA-CB	6.57	111.18	103.30
79	s2	1374	C	N1-C2-O2	6.57	122.84	118.90
82	pE	40	C	C2-N1-C1'	6.56	126.02	118.80
68	SP	86	LEU	CA-CB-CG	6.56	130.39	115.30
79	s2	557	U	N3-C2-O2	-6.55	117.61	122.20
17	sO	14	VAL	C-N-CA	6.54	138.06	121.70
85	L5	2627	C	N1-C2-O2	6.54	122.82	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	L5	181	C	N1-C2-O2	6.54	122.82	118.90
85	L5	490	C	N3-C2-O2	-6.53	117.33	121.90
85	l5	4924	C	N3-C2-O2	-6.52	117.33	121.90
83	ls	73	PRO	N-CA-C	6.51	129.04	112.10
85	L5	174	C	N1-C2-O2	6.47	122.78	118.90
79	s2	621	C	N3-C2-O2	-6.47	117.37	121.90
85	L5	129	C	N3-C2-O2	-6.45	117.39	121.90
18	SW	50	PHE	CZ-CE2-CD2	6.41	127.79	120.10
85	L5	181	C	C2-N1-C1'	6.39	125.83	118.80
78	Sf	88	PRO	N-CD-CG	-6.36	93.66	103.20
84	Lt	148	PRO	N-CA-C	6.34	128.59	112.10
79	S2	1453	C	C6-N1-C1'	-6.32	113.21	120.80
79	s2	1415	C	N1-C2-O2	6.32	122.69	118.90
79	s2	979	C	C2-N1-C1'	6.31	125.75	118.80
85	L5	1414	C	N1-C2-O2	6.29	122.67	118.90
72	sU	48	LEU	CB-CG-CD1	-6.28	100.33	111.00
79	s2	1453	C	C2-N1-C1'	6.27	125.70	118.80
65	sD	32	ASP	CB-CG-OD1	6.26	123.94	118.30
85	l5	2710	C	C6-N1-C1'	-6.24	113.31	120.80
85	l5	2257	C	N1-C2-O2	6.23	122.64	118.90
85	L5	3773	U	N1-C2-O2	6.21	127.15	122.80
19	Sb	73	LEU	CA-CB-CG	6.21	129.59	115.30
64	sR	9	VAL	CG1-CB-CG2	-6.21	100.97	110.90
43	LX	143	ASP	CB-CG-OD1	-6.20	112.72	118.30
85	l5	4859	C	N3-C2-O2	-6.19	117.57	121.90
85	l5	925	C	N1-C2-O2	6.18	122.61	118.90
85	L5	664	G	C5-C6-O6	6.15	132.29	128.60
79	s2	1374	C	N3-C4-N4	6.14	122.30	118.00
85	L5	1082	C	N3-C2-O2	-6.12	117.61	121.90
85	l5	472	C	C2-N1-C1'	6.12	125.53	118.80
85	l5	4709	U	C2-N1-C1'	6.11	125.04	117.70
79	s2	356	C	C2-N1-C1'	6.11	125.52	118.80
85	l5	209	U	N1-C2-O2	6.11	127.08	122.80
85	l5	1414	C	N1-C2-O2	6.08	122.55	118.90
78	Sf	88	PRO	CA-N-CD	-6.08	103.00	111.50
79	S2	1453	C	N3-C2-O2	-6.07	117.65	121.90
85	l5	2708	U	C2-N1-C1'	6.06	124.97	117.70
12	sH	133	LEU	CA-CB-CG	6.05	129.22	115.30
85	l5	100	C	C2-N1-C1'	6.04	125.44	118.80
85	L5	489	C	N1-C2-O2	6.02	122.51	118.90
79	S2	356	C	N3-C2-O2	-6.01	117.69	121.90
85	L5	255	C	N3-C2-O2	-6.01	117.69	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	L5	3773	U	O4'-C1'-N1	5.99	112.99	108.20
50	le	88	LEU	CA-CB-CG	5.97	129.04	115.30
85	l5	4709	U	C5-C4-O4	-5.97	122.32	125.90
85	L5	100	C	C2-N1-C1'	5.96	125.36	118.80
85	l5	3761	C	C2-N1-C1'	5.96	125.35	118.80
85	L5	925	C	N1-C2-O2	5.95	122.47	118.90
85	L5	209	U	C2-N1-C1'	5.94	124.82	117.70
85	L5	485	C	N1-C2-O2	5.93	122.46	118.90
79	s2	1453	C	N1-C2-O2	5.93	122.46	118.90
85	l5	3773	U	N1-C2-O2	5.92	126.95	122.80
85	l5	925	C	N3-C2-O2	-5.90	117.77	121.90
14	Sa	99	PRO	CA-N-CD	-5.89	103.25	111.50
85	L5	26	C	N1-C2-O2	5.89	122.43	118.90
85	l5	1472	C	C2-N1-C1'	5.86	125.25	118.80
85	l5	485	C	N1-C2-O2	5.85	122.41	118.90
79	s2	1389	C	N1-C2-O2	5.84	122.41	118.90
79	s2	1453	C	N3-C2-O2	-5.82	117.83	121.90
85	L5	2627	C	N3-C2-O2	-5.81	117.83	121.90
79	S2	1424	G	N3-C4-N9	5.80	129.48	126.00
19	sb	12	PRO	N-CD-CG	-5.78	94.53	103.20
85	L5	182	G	N3-C4-N9	-5.78	122.53	126.00
79	s2	1374	C	C6-N1-C2	-5.78	117.99	120.30
79	S2	1453	C	C6-N1-C2	-5.77	117.99	120.30
85	l5	489	C	N1-C2-O2	5.77	122.36	118.90
28	LG	134	PRO	CA-N-CD	-5.76	103.43	111.50
79	s2	1772	C	C2-N1-C1'	5.75	125.13	118.80
79	s2	1389	C	C2-N1-C1'	5.74	125.12	118.80
85	l5	3773	U	C2-N1-C1'	5.74	124.59	117.70
85	L5	4093	G	O4'-C1'-N9	5.73	112.78	108.20
79	S2	834	C	N1-C2-O2	5.73	122.34	118.90
22	lA	96	LEU	CA-CB-CG	5.72	128.47	115.30
51	Lf	43	LEU	CA-CB-CG	5.72	128.46	115.30
85	L5	2018	C	C6-N1-C2	-5.71	118.02	120.30
79	s2	1455	A	O4'-C1'-N9	5.71	112.77	108.20
85	l5	2708	U	N3-C2-O2	-5.71	118.20	122.20
89	Pt	75	C	N3-C2-O2	-5.71	117.91	121.90
89	Pt	31	C	N3-C2-O2	-5.70	117.91	121.90
85	L5	2257	C	C2-N1-C1'	5.68	125.05	118.80
79	S2	1453	C	C5-C6-N1	5.68	123.84	121.00
85	l5	262	G	N1-C6-O6	-5.67	116.50	119.90
18	SW	42	MET	CG-SD-CE	-5.67	91.13	100.20
79	S2	1772	C	C2-N1-C1'	5.65	125.02	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	l5	2710	C	C6-N1-C2	-5.65	118.04	120.30
79	S2	834	C	N3-C2-O2	-5.63	117.96	121.90
79	s2	1146	C	N3-C2-O2	-5.62	117.96	121.90
85	l5	2708	U	N1-C2-O2	5.62	126.73	122.80
85	L5	664	G	N1-C6-O6	-5.61	116.54	119.90
79	s2	607	U	N1-C2-O2	5.60	126.72	122.80
85	L5	1082	C	C2-N1-C1'	-5.60	112.64	118.80
85	l5	4775	C	C2-N1-C1'	5.59	124.95	118.80
24	lC	2	ALA	C-N-CA	5.59	135.68	121.70
79	S2	1078	C	N1-C2-O2	5.58	122.25	118.90
2	sE	19	MET	CA-CB-CG	5.58	122.78	113.30
85	l5	2018	C	C5-C6-N1	5.58	123.79	121.00
85	L5	925	C	N3-C2-O2	-5.57	118.00	121.90
72	sU	108	PRO	CA-CB-CG	-5.56	93.43	104.00
79	S2	118	C	C2-N1-C1'	5.54	124.90	118.80
85	l5	1173	G	N3-C4-N9	-5.54	122.68	126.00
79	s2	356	C	N1-C2-O2	5.54	122.22	118.90
11	SB	30	TRP	CE3-CZ3-CH2	5.53	127.28	121.20
25	LD	235	MET	CA-CB-CG	5.52	122.69	113.30
85	l5	2099	G	C5-C6-O6	5.52	131.91	128.60
85	L5	3761	C	C2-N1-C1'	5.50	124.85	118.80
85	L5	2410	C	C2-N1-C1'	5.49	124.84	118.80
85	l5	1973	G	N1-C2-N2	-5.49	111.26	116.20
85	L5	2627	C	C2-N1-C1'	5.48	124.83	118.80
79	s2	1213	C	C2-N1-C1'	5.48	124.83	118.80
85	l5	4859	C	N1-C2-O2	5.47	122.19	118.90
85	l5	4926	C	C2-N1-C1'	5.46	124.81	118.80
85	L5	701	G	C5-C6-O6	5.46	131.88	128.60
85	L5	2710	C	C6-N1-C1'	-5.46	114.25	120.80
85	L5	1755	C	C2-N1-C1'	5.45	124.80	118.80
85	L5	4709	U	C2-N1-C1'	5.45	124.24	117.70
85	l5	1417	C	C2-N1-C1'	5.45	124.79	118.80
79	S2	834	C	C6-N1-C2	-5.44	118.12	120.30
15	sC	121	ARG	NE-CZ-NH2	-5.42	117.59	120.30
79	s2	1373	C	N3-C2-O2	-5.42	118.11	121.90
79	S2	118	C	N1-C2-O2	5.42	122.15	118.90
8	SY	52	PRO	CB-CG-CD	-5.40	85.46	106.50
79	s2	1772	C	C6-N1-C2	-5.39	118.14	120.30
79	s2	118	C	C2-N1-C1'	5.39	124.73	118.80
13	SV	22	ARG	NE-CZ-NH1	5.39	123.00	120.30
88	CF	390	GLY	CA-C-N	5.39	132.19	117.10
79	S2	325	C	C2-N1-C1'	5.39	124.73	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	s2	1520	G	C4-N9-C1'	5.38	133.49	126.50
85	l5	4068	U	C2-N1-C1'	5.37	124.14	117.70
85	l5	4093	G	O4'-C1'-N9	5.37	112.49	108.20
79	s2	833	C	N1-C2-O2	5.36	122.12	118.90
76	sM	64	LEU	CA-CB-CG	5.35	127.61	115.30
79	s2	1139	C	N1-C2-O2	5.35	122.11	118.90
55	lj	40	PRO	N-CD-CG	-5.35	95.18	103.20
24	LC	2	ALA	C-N-CA	5.35	135.06	121.70
88	CF	391	PRO	N-CA-C	-5.35	98.20	112.10
79	s2	834	C	C6-N1-C2	-5.34	118.17	120.30
83	Ls	90	PHE	CZ-CE2-CD2	5.33	126.50	120.10
30	II	193	ASP	CB-CG-OD2	5.33	123.10	118.30
11	SB	24	PRO	CA-N-CD	-5.33	104.04	111.50
85	l5	2410	C	C2-N1-C1'	5.33	124.66	118.80
85	L5	2805	C	N3-C2-O2	-5.33	118.17	121.90
89	Pt	31	C	C2-N1-C1'	5.32	124.65	118.80
85	l5	129	C	C6-N1-C2	-5.32	118.17	120.30
85	l5	209	U	C6-N1-C1'	-5.31	113.77	121.20
85	L5	3773	U	C2-N1-C1'	5.29	124.05	117.70
85	L5	2710	C	C6-N1-C2	-5.29	118.18	120.30
72	SU	37	ALA	CB-CA-C	5.29	118.04	110.10
79	s2	607	U	C6-N1-C1'	-5.28	113.80	121.20
63	lz	124	LEU	CA-CB-CG	5.27	127.42	115.30
79	s2	834	C	N1-C2-O2	5.27	122.06	118.90
85	l5	74	G	C8-N9-C1'	-5.27	120.15	127.00
66	sF	45	TYR	CG-CD1-CE1	-5.27	117.09	121.30
87	AT	26	C	N1-C2-O2	5.27	122.06	118.90
79	S2	833	C	N1-C2-O2	5.26	122.06	118.90
85	L5	181	C	N3-C2-O2	-5.26	118.22	121.90
85	l5	74	G	C4-N9-C1'	5.26	133.33	126.50
85	L5	4068	U	C2-N1-C1'	5.26	124.01	117.70
31	LJ	83	LEU	CA-CB-CG	5.25	127.39	115.30
85	l5	140	G	C5-C6-O6	5.25	131.75	128.60
85	L5	2257	C	N1-C2-O2	5.25	122.05	118.90
85	l5	4926	C	N1-C2-O2	5.24	122.05	118.90
79	s2	293	C	N1-C2-O2	5.24	122.04	118.90
85	l5	263	G	C5-C6-O6	5.24	131.75	128.60
79	S2	1022	U	C6-N1-C1'	-5.24	113.87	121.20
85	L5	4928	C	N1-C2-O2	5.23	122.04	118.90
85	L5	1082	C	P-O3'-C3'	5.22	125.97	119.70
79	S2	1078	C	N3-C2-O2	-5.22	118.25	121.90
19	sb	12	PRO	CA-CB-CG	-5.20	94.11	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
75	Sg	144	ASP	CB-CG-OD1	5.20	122.98	118.30
79	S2	1139	C	C2-N1-C1'	5.20	124.52	118.80
83	ls	90	PHE	CG-CD1-CE1	5.19	126.51	120.80
76	SM	66	GLU	OE1-CD-OE2	-5.19	117.07	123.30
85	l5	985	C	C2-N1-C1'	5.18	124.50	118.80
85	L5	4924	C	N3-C2-O2	-5.18	118.28	121.90
17	SO	14	VAL	C-N-CA	5.17	134.64	121.70
85	L5	3761	C	N1-C2-O2	5.17	122.00	118.90
85	L5	1216	C	C2-N1-C1'	5.16	124.48	118.80
79	s2	688	U	P-O3'-C3'	5.15	125.88	119.70
85	L5	1082	C	C6-N1-C1'	5.14	126.97	120.80
85	l5	209	U	N3-C2-O2	-5.14	118.60	122.20
85	L5	2107	C	N3-C2-O2	-5.13	118.31	121.90
85	l5	1994	C	N1-C2-O2	5.13	121.98	118.90
58	lm	106	ARG	NE-CZ-NH2	-5.12	117.74	120.30
85	l5	174	C	N1-C2-O2	5.12	121.97	118.90
79	s2	1139	C	C2-N1-C1'	5.12	124.44	118.80
85	l5	262	G	C5-C6-O6	5.12	131.67	128.60
85	L5	4926	C	C2-N1-C1'	5.11	124.42	118.80
79	s2	1142	G	N3-C4-N9	-5.11	122.93	126.00
85	L5	1182	C	N1-C2-O2	5.11	121.97	118.90
22	LA	106	THR	C-N-CA	-5.11	108.92	121.70
64	sR	126	MET	CG-SD-CE	5.11	108.38	100.20
85	L5	266	C	O5'-P-OP1	-5.11	101.10	105.70
85	L5	4709	U	C5-C4-O4	-5.11	122.83	125.90
79	S2	1424	G	C4-N9-C1'	5.10	133.14	126.50
79	S2	356	C	C6-N1-C2	-5.10	118.26	120.30
79	s2	1386	A	N1-C2-N3	5.10	131.85	129.30
85	l5	2627	C	C2-N1-C1'	5.10	124.41	118.80
85	L5	140	G	C5-C6-O6	5.09	131.66	128.60
77	SZ	77	LEU	CA-CB-CG	5.09	127.01	115.30
85	l5	963	G	C4-N9-C1'	5.08	133.10	126.50
28	LG	134	PRO	N-CD-CG	-5.08	95.58	103.20
11	SB	24	PRO	N-CD-CG	-5.07	95.60	103.20
85	L5	963	G	C4-N9-C1'	5.07	133.08	126.50
82	pE	40	C	C6-N1-C1'	-5.06	114.72	120.80
85	L5	115	C	N1-C2-O2	5.06	121.94	118.90
79	S2	1755	C	N1-C2-O2	5.06	121.94	118.90
79	S2	1022	U	N1-C2-O2	5.05	126.34	122.80
75	sg	144	ASP	CB-CG-OD1	5.05	122.84	118.30
79	s2	1388	A	N7-C8-N9	5.04	116.32	113.80
79	S2	688	U	P-O3'-C3'	5.04	125.75	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	L5	4897	G	C5-C6-O6	5.03	131.62	128.60
79	S2	1629	C	C6-N1-C2	-5.03	118.29	120.30
10	sA	8	LEU	CA-CB-CG	5.02	126.86	115.30
85	L5	100	C	N1-C2-O2	5.02	121.91	118.90
79	S2	1123	C	N3-C2-O2	-5.02	118.38	121.90
85	L5	1367	C	C2-N1-C1'	5.02	124.32	118.80
64	sR	122	PRO	CB-CG-CD	-5.02	86.94	106.50
85	l5	2099	G	N1-C6-O6	-5.00	116.90	119.90
66	sF	49	LEU	CA-CB-CG	5.00	126.81	115.30

There are no chirality outliers.

All (31) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
22	LA	13	GLY	Peptide
23	LB	17	LEU	Peptide
23	LB	258	HIS	Peptide
31	LJ	94	LEU	Peptide
33	LM	88	ALA	Peptide
35	LO	110	PRO	Peptide
51	Lf	106	TYR	Peptide
55	Lj	39	TYR	Peptide
66	SF	78	MET	Peptide
12	SH	15	LYS	Peptide
69	SQ	43	GLU	Peptide
5	SX	126	ALA	Peptide
77	SZ	46	ASN	Peptide
1	cH	51	GLN	Peptide
22	lA	13	GLY	Peptide
23	lB	16	PHE	Peptide
23	lB	17	LEU	Peptide
23	lB	258	HIS	Peptide
31	lJ	94	LEU	Peptide
33	lM	87	ALA	Peptide
33	lM	88	ALA	Peptide
35	lO	110	PRO	Peptide
51	lf	106	TYR	Peptide
55	lj	39	TYR	Peptide
65	sD	193	ASP	Peptide
12	sH	15	LYS	Peptide
69	sQ	43	GLU	Peptide
64	sR	133	GLY	Peptide

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Mol	Chain	Res	Type	Group
64	sR	26	ASN	Peptide
72	sU	107	GLU	Peptide
5	sX	126	ALA	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	cH	123/125 (98%)	106 (86%)	15 (12%)	2 (2%)	8	36
2	SE	260/262 (99%)	246 (95%)	14 (5%)	0	100	100
2	sE	260/262 (99%)	243 (94%)	17 (6%)	0	100	100
3	SI	204/206 (99%)	193 (95%)	11 (5%)	0	100	100
3	sI	204/206 (99%)	196 (96%)	8 (4%)	0	100	100
4	SL	151/153 (99%)	141 (93%)	10 (7%)	0	100	100
4	sL	151/153 (99%)	139 (92%)	12 (8%)	0	100	100
5	SX	139/141 (99%)	126 (91%)	13 (9%)	0	100	100
5	sX	139/141 (99%)	124 (89%)	14 (10%)	1 (1%)	19	52
6	SG	235/237 (99%)	222 (94%)	13 (6%)	0	100	100
6	sG	235/237 (99%)	224 (95%)	11 (5%)	0	100	100
7	SJ	183/185 (99%)	170 (93%)	13 (7%)	0	100	100
7	sJ	183/185 (99%)	175 (96%)	8 (4%)	0	100	100
8	SY	129/131 (98%)	121 (94%)	7 (5%)	1 (1%)	16	49
8	sY	129/131 (98%)	119 (92%)	10 (8%)	0	100	100
9	Se	56/58 (97%)	51 (91%)	5 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	se	56/58 (97%)	46 (82%)	10 (18%)	0	100	100
10	SA	219/221 (99%)	200 (91%)	19 (9%)	0	100	100
10	sA	219/221 (99%)	186 (85%)	33 (15%)	0	100	100
11	SB	212/214 (99%)	198 (93%)	14 (7%)	0	100	100
11	sB	212/214 (99%)	200 (94%)	12 (6%)	0	100	100
12	SH	182/189 (96%)	162 (89%)	20 (11%)	0	100	100
12	sH	182/189 (96%)	158 (87%)	24 (13%)	0	100	100
13	SV	81/83 (98%)	73 (90%)	8 (10%)	0	100	100
13	sV	81/83 (98%)	73 (90%)	8 (10%)	0	100	100
14	Sa	100/102 (98%)	90 (90%)	10 (10%)	0	100	100
14	sa	100/102 (98%)	89 (89%)	11 (11%)	0	100	100
15	SC	220/222 (99%)	207 (94%)	13 (6%)	0	100	100
15	sC	220/222 (99%)	203 (92%)	17 (8%)	0	100	100
16	SN	148/150 (99%)	143 (97%)	5 (3%)	0	100	100
16	sN	148/150 (99%)	143 (97%)	5 (3%)	0	100	100
17	SO	138/140 (99%)	124 (90%)	14 (10%)	0	100	100
17	sO	138/140 (99%)	124 (90%)	14 (10%)	0	100	100
18	SW	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
18	sW	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
19	Sb	81/83 (98%)	69 (85%)	12 (15%)	0	100	100
19	sb	81/83 (98%)	72 (89%)	9 (11%)	0	100	100
22	LA	246/248 (99%)	221 (90%)	25 (10%)	0	100	100
22	lA	246/248 (99%)	222 (90%)	23 (9%)	1 (0%)	30	63
23	LB	400/402 (100%)	372 (93%)	28 (7%)	0	100	100
23	lB	400/402 (100%)	375 (94%)	25 (6%)	0	100	100
24	LC	366/368 (100%)	339 (93%)	27 (7%)	0	100	100
24	lC	366/368 (100%)	343 (94%)	23 (6%)	0	100	100
25	LD	291/293 (99%)	275 (94%)	16 (6%)	0	100	100
25	lD	291/293 (99%)	277 (95%)	14 (5%)	0	100	100
26	LE	232/247 (94%)	213 (92%)	19 (8%)	0	100	100
26	lE	232/247 (94%)	211 (91%)	21 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	LF	223/225 (99%)	211 (95%)	12 (5%)	0	100	100
27	IF	223/225 (99%)	213 (96%)	10 (4%)	0	100	100
28	LG	239/241 (99%)	223 (93%)	16 (7%)	0	100	100
28	IG	239/241 (99%)	224 (94%)	15 (6%)	0	100	100
29	LH	188/190 (99%)	175 (93%)	13 (7%)	0	100	100
29	IH	188/190 (99%)	176 (94%)	12 (6%)	0	100	100
30	LI	198/213 (93%)	184 (93%)	14 (7%)	0	100	100
30	II	198/213 (93%)	187 (94%)	11 (6%)	0	100	100
31	LJ	174/176 (99%)	154 (88%)	20 (12%)	0	100	100
31	IJ	174/176 (99%)	160 (92%)	14 (8%)	0	100	100
32	LL	208/210 (99%)	192 (92%)	16 (8%)	0	100	100
32	IL	208/210 (99%)	190 (91%)	18 (9%)	0	100	100
33	LM	137/139 (99%)	126 (92%)	10 (7%)	1 (1%)	19	52
33	IM	137/139 (99%)	125 (91%)	11 (8%)	1 (1%)	19	52
34	LN	201/203 (99%)	186 (92%)	14 (7%)	1 (0%)	25	58
34	IN	201/203 (99%)	191 (95%)	9 (4%)	1 (0%)	25	58
35	LO	199/201 (99%)	192 (96%)	7 (4%)	0	100	100
35	IO	199/201 (99%)	192 (96%)	7 (4%)	0	100	100
36	LP	151/153 (99%)	141 (93%)	10 (7%)	0	100	100
36	IP	151/153 (99%)	142 (94%)	9 (6%)	0	100	100
37	LQ	185/187 (99%)	178 (96%)	7 (4%)	0	100	100
37	IQ	185/187 (99%)	178 (96%)	7 (4%)	0	100	100
38	LR	185/187 (99%)	176 (95%)	9 (5%)	0	100	100
38	IR	185/187 (99%)	180 (97%)	5 (3%)	0	100	100
39	LS	173/175 (99%)	164 (95%)	9 (5%)	0	100	100
39	IS	173/175 (99%)	161 (93%)	12 (7%)	0	100	100
40	LT	157/159 (99%)	147 (94%)	10 (6%)	0	100	100
40	IT	157/159 (99%)	148 (94%)	9 (6%)	0	100	100
41	LU	99/101 (98%)	82 (83%)	17 (17%)	0	100	100
41	IU	99/101 (98%)	80 (81%)	19 (19%)	0	100	100
42	LV	129/131 (98%)	125 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	IV	129/131 (98%)	120 (93%)	9 (7%)	0	100	100
43	LX	118/120 (98%)	114 (97%)	4 (3%)	0	100	100
43	IX	118/120 (98%)	117 (99%)	1 (1%)	0	100	100
44	LY	132/134 (98%)	128 (97%)	4 (3%)	0	100	100
44	IY	132/134 (98%)	128 (97%)	4 (3%)	0	100	100
45	LZ	133/135 (98%)	123 (92%)	10 (8%)	0	100	100
45	IZ	133/135 (98%)	121 (91%)	12 (9%)	0	100	100
46	La	145/147 (99%)	137 (94%)	8 (6%)	0	100	100
46	la	145/147 (99%)	137 (94%)	8 (6%)	0	100	100
47	Lb	105/121 (87%)	95 (90%)	10 (10%)	0	100	100
47	lb	105/121 (87%)	96 (91%)	9 (9%)	0	100	100
48	Lc	96/98 (98%)	90 (94%)	6 (6%)	0	100	100
48	lc	96/98 (98%)	87 (91%)	9 (9%)	0	100	100
49	Ld	105/107 (98%)	101 (96%)	4 (4%)	0	100	100
49	ld	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
50	Le	126/128 (98%)	118 (94%)	8 (6%)	0	100	100
50	le	126/128 (98%)	121 (96%)	5 (4%)	0	100	100
51	Lf	107/109 (98%)	98 (92%)	9 (8%)	0	100	100
51	lf	107/109 (98%)	98 (92%)	9 (8%)	0	100	100
52	Lg	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
52	lg	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
53	Lh	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
53	lh	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
54	Li	100/102 (98%)	98 (98%)	2 (2%)	0	100	100
54	li	100/102 (98%)	97 (97%)	3 (3%)	0	100	100
55	Lj	84/86 (98%)	72 (86%)	12 (14%)	0	100	100
55	lj	84/86 (98%)	77 (92%)	7 (8%)	0	100	100
56	Lk	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
56	lk	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
57	Ll	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
57	ll	48/50 (96%)	46 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
58	Lm	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
58	lm	50/52 (96%)	46 (92%)	4 (8%)	0	100	100
59	Ln	22/24 (92%)	22 (100%)	0	0	100	100
59	ln	22/24 (92%)	22 (100%)	0	0	100	100
60	Lo	103/105 (98%)	100 (97%)	3 (3%)	0	100	100
60	lo	103/105 (98%)	100 (97%)	3 (3%)	0	100	100
61	Lp	89/91 (98%)	83 (93%)	6 (7%)	0	100	100
61	lp	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
62	Lr	123/125 (98%)	114 (93%)	9 (7%)	0	100	100
62	lr	123/125 (98%)	118 (96%)	5 (4%)	0	100	100
63	Lz	215/217 (99%)	172 (80%)	43 (20%)	0	100	100
63	lz	215/217 (99%)	170 (79%)	45 (21%)	0	100	100
64	SR	133/135 (98%)	120 (90%)	12 (9%)	1 (1%)	16	49
64	sR	133/135 (98%)	104 (78%)	26 (20%)	3 (2%)	5	30
65	SD	225/227 (99%)	205 (91%)	20 (9%)	0	100	100
65	sD	225/227 (99%)	207 (92%)	18 (8%)	0	100	100
66	SF	187/189 (99%)	166 (89%)	21 (11%)	0	100	100
66	sF	187/189 (99%)	166 (89%)	21 (11%)	0	100	100
67	SK	96/98 (98%)	81 (84%)	12 (12%)	3 (3%)	3	25
67	sK	96/98 (98%)	84 (88%)	11 (12%)	1 (1%)	13	44
68	SP	119/121 (98%)	111 (93%)	8 (7%)	0	100	100
68	sP	119/121 (98%)	112 (94%)	7 (6%)	0	100	100
69	SQ	142/144 (99%)	123 (87%)	18 (13%)	1 (1%)	19	52
69	sQ	142/144 (99%)	123 (87%)	18 (13%)	1 (1%)	19	52
70	SS	143/145 (99%)	136 (95%)	7 (5%)	0	100	100
70	sS	143/145 (99%)	132 (92%)	11 (8%)	0	100	100
71	ST	141/143 (99%)	133 (94%)	7 (5%)	1 (1%)	19	52
71	sT	141/143 (99%)	128 (91%)	13 (9%)	0	100	100
72	SU	102/104 (98%)	94 (92%)	8 (8%)	0	100	100
72	sU	102/104 (98%)	95 (93%)	7 (7%)	0	100	100
73	Sc	62/64 (97%)	55 (89%)	7 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
73	sc	62/64 (97%)	52 (84%)	10 (16%)	0	100	100
74	Sd	53/55 (96%)	47 (89%)	6 (11%)	0	100	100
74	sd	53/55 (96%)	48 (91%)	5 (9%)	0	100	100
75	Sg	311/313 (99%)	274 (88%)	37 (12%)	0	100	100
75	sg	311/313 (99%)	270 (87%)	41 (13%)	0	100	100
76	SM	120/122 (98%)	107 (89%)	13 (11%)	0	100	100
76	sM	120/122 (98%)	105 (88%)	14 (12%)	1 (1%)	16	49
77	SZ	73/75 (97%)	61 (84%)	12 (16%)	0	100	100
77	sZ	73/75 (97%)	58 (80%)	15 (20%)	0	100	100
78	Sf	65/67 (97%)	53 (82%)	12 (18%)	0	100	100
78	sf	65/67 (97%)	55 (85%)	10 (15%)	0	100	100
80	cB	842/846 (100%)	790 (94%)	49 (6%)	3 (0%)	30	63
83	Ls	194/196 (99%)	180 (93%)	14 (7%)	0	100	100
83	ls	194/196 (99%)	181 (93%)	12 (6%)	1 (0%)	25	58
84	Lt	137/141 (97%)	102 (74%)	33 (24%)	2 (2%)	8	37
84	lt	137/141 (97%)	108 (79%)	28 (20%)	1 (1%)	19	52
86	LW	114/124 (92%)	102 (90%)	11 (10%)	1 (1%)	14	45
88	CF	438/441 (99%)	420 (96%)	18 (4%)	0	100	100
All	All	25015/25436 (98%)	23064 (92%)	1922 (8%)	29 (0%)	50	79

All (29) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
67	sK	96	ARG
80	cB	407	LYS
80	cB	779	THR
83	ls	73	PRO
8	SY	52	PRO
64	SR	124	VAL
1	cH	38	VAL
5	sX	127	ASN
34	lN	124	ASP
64	sR	122	PRO
76	sM	96	ARG
84	lt	24	ALA
34	LN	124	ASP

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Mol	Chain	Res	Type
67	SK	36	ALA
71	ST	41	LYS
84	Lt	144	ASP
84	Lt	148	PRO
33	IM	88	ALA
33	LM	88	ALA
67	SK	96	ARG
64	sR	124	VAL
64	sR	128	PHE
69	sQ	44	PRO
1	cH	45	ALA
80	cB	481	LYS
86	LW	53	VAL
67	SK	91	PRO
22	lA	55	GLY
69	SQ	43	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	cH	100/100 (100%)	98 (98%)	2 (2%)	50	68
2	SE	224/224 (100%)	217 (97%)	7 (3%)	35	56
2	sE	224/224 (100%)	217 (97%)	7 (3%)	35	56
3	SI	178/178 (100%)	166 (93%)	12 (7%)	13	38
3	sI	178/178 (100%)	169 (95%)	9 (5%)	20	45
4	SL	137/137 (100%)	129 (94%)	8 (6%)	17	42
4	sL	137/137 (100%)	127 (93%)	10 (7%)	11	36
5	SX	113/113 (100%)	111 (98%)	2 (2%)	54	71
5	sX	113/113 (100%)	106 (94%)	7 (6%)	15	40
6	SG	207/207 (100%)	194 (94%)	13 (6%)	15	40
6	sG	207/207 (100%)	189 (91%)	18 (9%)	8	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	SJ	161/161 (100%)	152 (94%)	9 (6%)	17	43
7	sJ	161/161 (100%)	159 (99%)	2 (1%)	67	77
8	SY	113/113 (100%)	104 (92%)	9 (8%)	10	33
8	sY	113/113 (100%)	104 (92%)	9 (8%)	10	33
9	Se	47/47 (100%)	44 (94%)	3 (6%)	14	39
9	se	47/47 (100%)	46 (98%)	1 (2%)	48	66
10	SA	183/183 (100%)	174 (95%)	9 (5%)	21	45
10	sA	183/183 (100%)	173 (94%)	10 (6%)	18	43
11	SB	195/195 (100%)	183 (94%)	12 (6%)	15	40
11	sB	195/195 (100%)	185 (95%)	10 (5%)	20	45
12	SH	166/169 (98%)	157 (95%)	9 (5%)	18	43
12	sH	166/169 (98%)	155 (93%)	11 (7%)	14	38
13	SV	67/67 (100%)	57 (85%)	10 (15%)	2	15
13	sV	67/67 (100%)	60 (90%)	7 (10%)	5	23
14	Sa	89/89 (100%)	83 (93%)	6 (7%)	13	38
14	sa	89/89 (100%)	86 (97%)	3 (3%)	32	55
15	SC	188/188 (100%)	183 (97%)	5 (3%)	40	60
15	sC	188/188 (100%)	180 (96%)	8 (4%)	25	49
16	SN	130/130 (100%)	127 (98%)	3 (2%)	45	63
16	sN	130/130 (100%)	126 (97%)	4 (3%)	35	56
17	SO	110/110 (100%)	103 (94%)	7 (6%)	14	39
17	sO	110/110 (100%)	102 (93%)	8 (7%)	11	36
18	SW	112/112 (100%)	109 (97%)	3 (3%)	40	60
18	sW	112/112 (100%)	108 (96%)	4 (4%)	30	54
19	Sb	75/75 (100%)	69 (92%)	6 (8%)	10	33
19	sb	75/75 (100%)	72 (96%)	3 (4%)	27	50
22	LA	190/190 (100%)	183 (96%)	7 (4%)	29	53
22	lA	190/190 (100%)	181 (95%)	9 (5%)	22	46
23	LB	348/348 (100%)	336 (97%)	12 (3%)	32	55
23	lB	348/348 (100%)	339 (97%)	9 (3%)	41	61
24	LC	306/306 (100%)	295 (96%)	11 (4%)	30	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	IC	306/306 (100%)	296 (97%)	10 (3%)	33	56
25	LD	246/247 (100%)	229 (93%)	17 (7%)	13	37
25	ID	246/247 (100%)	232 (94%)	14 (6%)	17	43
26	LE	209/220 (95%)	200 (96%)	9 (4%)	25	49
26	IE	209/220 (95%)	200 (96%)	9 (4%)	25	49
27	LF	194/194 (100%)	188 (97%)	6 (3%)	35	56
27	IF	194/194 (100%)	191 (98%)	3 (2%)	60	74
28	LG	203/205 (99%)	189 (93%)	14 (7%)	13	37
28	IG	203/205 (99%)	195 (96%)	8 (4%)	27	51
29	LH	169/169 (100%)	161 (95%)	8 (5%)	22	46
29	IH	169/169 (100%)	164 (97%)	5 (3%)	36	58
30	LI	172/180 (96%)	164 (95%)	8 (5%)	22	46
30	II	172/180 (96%)	169 (98%)	3 (2%)	56	72
31	LJ	148/148 (100%)	141 (95%)	7 (5%)	22	46
31	IJ	148/148 (100%)	140 (95%)	8 (5%)	18	43
32	LL	176/176 (100%)	169 (96%)	7 (4%)	27	50
32	IL	176/176 (100%)	170 (97%)	6 (3%)	32	55
33	LM	118/118 (100%)	112 (95%)	6 (5%)	20	45
33	IM	118/118 (100%)	114 (97%)	4 (3%)	32	55
34	LN	171/171 (100%)	166 (97%)	5 (3%)	37	58
34	IN	171/171 (100%)	165 (96%)	6 (4%)	31	54
35	LO	173/173 (100%)	169 (98%)	4 (2%)	45	63
35	IO	173/173 (100%)	167 (96%)	6 (4%)	31	54
36	LP	134/134 (100%)	127 (95%)	7 (5%)	19	44
36	IP	134/134 (100%)	125 (93%)	9 (7%)	13	38
37	LQ	164/164 (100%)	158 (96%)	6 (4%)	29	53
37	IQ	164/164 (100%)	158 (96%)	6 (4%)	29	53
38	LR	166/166 (100%)	160 (96%)	6 (4%)	30	54
38	IR	166/166 (100%)	161 (97%)	5 (3%)	36	58
39	LS	156/156 (100%)	149 (96%)	7 (4%)	23	47
39	IS	156/156 (100%)	153 (98%)	3 (2%)	52	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	LT	139/139 (100%)	135 (97%)	4 (3%)	37	58
40	IT	139/139 (100%)	134 (96%)	5 (4%)	30	54
41	LU	91/91 (100%)	87 (96%)	4 (4%)	24	48
41	IU	91/91 (100%)	84 (92%)	7 (8%)	10	34
42	LV	101/101 (100%)	99 (98%)	2 (2%)	50	68
42	IV	101/101 (100%)	97 (96%)	4 (4%)	27	50
43	LX	108/108 (100%)	104 (96%)	4 (4%)	29	53
43	IX	108/108 (100%)	104 (96%)	4 (4%)	29	53
44	LY	124/124 (100%)	117 (94%)	7 (6%)	17	43
44	IY	124/124 (100%)	117 (94%)	7 (6%)	17	43
45	LZ	117/117 (100%)	110 (94%)	7 (6%)	16	41
45	IZ	117/117 (100%)	109 (93%)	8 (7%)	13	38
46	La	120/120 (100%)	118 (98%)	2 (2%)	56	72
46	la	120/120 (100%)	115 (96%)	5 (4%)	25	49
47	Lb	88/101 (87%)	85 (97%)	3 (3%)	32	55
47	lb	88/101 (87%)	81 (92%)	7 (8%)	10	33
48	Lc	83/83 (100%)	79 (95%)	4 (5%)	21	46
48	lc	83/83 (100%)	78 (94%)	5 (6%)	16	41
49	Ld	98/98 (100%)	94 (96%)	4 (4%)	26	50
49	ld	98/98 (100%)	96 (98%)	2 (2%)	50	68
50	Le	114/114 (100%)	110 (96%)	4 (4%)	31	54
50	le	114/114 (100%)	108 (95%)	6 (5%)	19	44
51	Lf	88/88 (100%)	88 (100%)	0	100	100
51	lf	88/88 (100%)	86 (98%)	2 (2%)	45	63
52	Lg	98/98 (100%)	97 (99%)	1 (1%)	73	80
52	lg	98/98 (100%)	93 (95%)	5 (5%)	20	45
53	Lh	109/109 (100%)	104 (95%)	5 (5%)	23	47
53	lh	109/109 (100%)	105 (96%)	4 (4%)	29	53
54	Li	86/86 (100%)	81 (94%)	5 (6%)	17	42
54	li	86/86 (100%)	86 (100%)	0	100	100
55	Lj	73/73 (100%)	70 (96%)	3 (4%)	26	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	lj	73/73 (100%)	66 (90%)	7 (10%)	7	26
56	Lk	64/64 (100%)	63 (98%)	1 (2%)	58	73
56	lk	64/64 (100%)	62 (97%)	2 (3%)	35	56
57	Ll	47/47 (100%)	46 (98%)	1 (2%)	48	66
57	ll	47/47 (100%)	44 (94%)	3 (6%)	14	39
58	Lm	48/48 (100%)	48 (100%)	0	100	100
58	lm	48/48 (100%)	45 (94%)	3 (6%)	15	40
59	Ln	23/23 (100%)	20 (87%)	3 (13%)	3	18
59	ln	23/23 (100%)	22 (96%)	1 (4%)	25	49
60	Lo	93/93 (100%)	89 (96%)	4 (4%)	25	49
60	lo	93/93 (100%)	86 (92%)	7 (8%)	11	35
61	Lp	74/74 (100%)	71 (96%)	3 (4%)	26	50
61	lp	74/74 (100%)	70 (95%)	4 (5%)	18	43
62	Lr	109/109 (100%)	104 (95%)	5 (5%)	23	47
62	lr	109/109 (100%)	107 (98%)	2 (2%)	54	71
63	Lz	195/196 (100%)	185 (95%)	10 (5%)	20	45
63	lz	195/196 (100%)	181 (93%)	14 (7%)	12	36
64	SR	122/122 (100%)	116 (95%)	6 (5%)	21	45
64	sR	122/122 (100%)	116 (95%)	6 (5%)	21	45
65	SD	190/190 (100%)	181 (95%)	9 (5%)	22	46
65	sD	190/190 (100%)	179 (94%)	11 (6%)	17	42
66	SF	159/159 (100%)	151 (95%)	8 (5%)	20	45
66	sF	159/159 (100%)	152 (96%)	7 (4%)	24	48
67	SK	89/89 (100%)	82 (92%)	7 (8%)	10	34
67	sK	89/89 (100%)	85 (96%)	4 (4%)	23	47
68	SP	107/107 (100%)	99 (92%)	8 (8%)	11	35
68	sP	107/107 (100%)	102 (95%)	5 (5%)	22	46
69	SQ	119/119 (100%)	116 (98%)	3 (2%)	42	62
69	sQ	119/119 (100%)	108 (91%)	11 (9%)	7	28
70	SS	126/126 (100%)	121 (96%)	5 (4%)	27	50
70	sS	126/126 (100%)	117 (93%)	9 (7%)	12	36

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

All (1026) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	cH	31	ARG
1	cH	113	ARG
2	sE	47	PHE
2	sE	73	ASP
2	sE	94	LYS
2	sE	142	HIS

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Mol	Chain	Res	Type
2	sE	181	CYS
2	sE	224	ASN
2	sE	226	PHE
3	sI	13	LYS
3	sI	52	ASN
3	sI	61	ASP
3	sI	66	SER
3	sI	105	ASP
3	sI	123	ARG
3	sI	150	ASP
3	sI	153	LYS
3	sI	178	ARG
4	sL	48	LYS
4	sL	57	ASP
4	sL	69	ARG
4	sL	73	LEU
4	sL	74	SER
4	sL	82	MET
4	sL	90	ARG
4	sL	91	ASP
4	sL	116	CYS
4	sL	118	ARG
5	sX	14	ARG
5	sX	64	SER
5	sX	90	CYS
5	sX	105	PHE
5	sX	110	HIS
5	sX	140	ARG
5	sX	142	ARG
6	sG	6	SER
6	sG	7	PHE
6	sG	22	ARG
6	sG	25	ARG
6	sG	27	PHE
6	sG	48	TYR
6	sG	57	ASP
6	sG	83	CYS
6	sG	85	ARG
6	sG	98	ARG
6	sG	107	SER
6	sG	119	LYS
6	sG	126	ASP

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Mol	Chain	Res	Type
6	sG	156	TYR
6	sG	167	LYS
6	sG	178	ARG
6	sG	204	GLU
6	sG	224	ARG
7	sJ	23	SER
7	sJ	169	ARG
8	sY	12	PHE
8	sY	23	MET
8	sY	49	LYS
8	sY	72	PHE
8	sY	81	TYR
8	sY	97	TYR
8	sY	101	LYS
8	sY	113	ARG
8	sY	122	LYS
9	se	37	GLN
10	sA	18	PHE
10	sA	52	LYS
10	sA	69	GLU
10	sA	70	ASN
10	sA	85	ARG
10	sA	130	ASP
10	sA	148	CYS
10	sA	184	ARG
10	sA	193	HIS
10	sA	200	ASP
11	sB	53	GLN
11	sB	65	ARG
11	sB	78	GLU
11	sB	84	PHE
11	sB	96	CYS
11	sB	113	MET
11	sB	146	ARG
11	sB	202	GLN
11	sB	209	ASP
11	sB	223	PHE
12	sH	32	MET
12	sH	41	ARG
12	sH	72	PHE
12	sH	78	ARG
12	sH	87	PHE

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Mol	Chain	Res	Type
12	sH	135	PHE
12	sH	138	GLU
12	sH	168	HIS
12	sH	173	PHE
12	sH	177	TYR
12	sH	180	LEU
13	sV	1	MET
13	sV	10	ASP
13	sV	12	TYR
13	sV	14	PRO
13	sV	17	CYS
13	sV	21	ASN
13	sV	66	ASP
14	sa	15	ARG
14	sa	59	PHE
14	sa	68	TYR
15	sC	115	GLN
15	sC	159	LYS
15	sC	167	ARG
15	sC	194	ARG
15	sC	221	ASP
15	sC	229	CYS
15	sC	269	PHE
15	sC	275	LYS
16	sN	34	LYS
16	sN	39	LYS
16	sN	77	SER
16	sN	108	ASP
17	sO	25	GLU
17	sO	31	CYS
17	sO	67	ASP
17	sO	83	GLN
17	sO	94	HIS
17	sO	98	ARG
17	sO	128	ARG
17	sO	141	ARG
18	sW	15	ASN
18	sW	37	PHE
18	sW	72	CYS
18	sW	111	MET
19	sb	13	GLU
19	sb	31	TYR

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Mol	Chain	Res	Type
19	sb	34	ASP
22	1A	30	ARG
22	1A	34	PHE
22	1A	54	ARG
22	1A	92	LYS
22	1A	102	LEU
22	1A	154	SER
22	1A	160	SER
22	1A	217	GLN
22	1A	245	ARG
23	1B	84	MET
23	1B	123	HIS
23	1B	248	LEU
23	1B	258	HIS
23	1B	271	GLN
23	1B	298	LEU
23	1B	315	ASN
23	1B	332	MET
23	1B	382	MET
24	1C	5	ARG
24	1C	122	TYR
24	1C	178	ASN
24	1C	188	ARG
24	1C	208	CYS
24	1C	245	HIS
24	1C	257	PHE
24	1C	291	ARG
24	1C	310	HIS
24	1C	366	ASP
25	1D	23	ARG
25	1D	62	CYS
25	1D	76	CYS
25	1D	111	ASN
25	1D	113	PHE
25	1D	187	SER
25	1D	196	ARG
25	1D	221	LYS
25	1D	222	GLN
25	1D	224	SER
25	1D	228	LYS
25	1D	236	MET
25	1D	259	LYS

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Mol	Chain	Res	Type
25	1D	272	SER
26	1E	52	ARG
26	1E	62	MET
26	1E	100	LYS
26	1E	204	SER
26	1E	205	ASN
26	1E	211	HIS
26	1E	216	TYR
26	1E	226	ARG
26	1E	254	ASP
27	1F	25	PHE
27	1F	186	CYS
27	1F	232	ASP
28	1G	35	ARG
28	1G	75	LYS
28	1G	87	LEU
28	1G	100	HIS
28	1G	131	LYS
28	1G	225	ASN
28	1G	229	ARG
28	1G	259	LYS
29	1H	40	HIS
29	1H	50	LYS
29	1H	51	LYS
29	1H	56	ARG
29	1H	130	PRO
30	1I	83	ASP
30	1I	141	LYS
30	1I	142	LEU
31	1J	43	LEU
31	1J	60	PHE
31	1J	95	ARG
31	1J	100	SER
31	1J	111	GLU
31	1J	119	TYR
31	1J	128	LEU
31	1J	131	TYR
32	1L	8	MET
32	1L	67	HIS
32	1L	103	ARG
32	1L	104	ASN
32	1L	136	LYS

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Mol	Chain	Res	Type
32	1L	208	GLU
33	1M	4	ARG
33	1M	35	ARG
33	1M	69	HIS
33	1M	81	ASP
34	1N	17	ASP
34	1N	68	ARG
34	1N	125	SER
34	1N	166	SER
34	1N	171	SER
34	1N	195	ARG
35	1O	42	ASN
35	1O	59	ARG
35	1O	117	ARG
35	1O	183	LYS
35	1O	190	ASP
35	1O	202	LEU
36	1P	3	ARG
36	1P	18	ARG
36	1P	30	ARG
36	1P	50	ASP
36	1P	69	ARG
36	1P	87	SER
36	1P	97	ASN
36	1P	103	GLU
36	1P	108	ASP
37	1Q	54	SER
37	1Q	66	MET
37	1Q	107	SER
37	1Q	160	HIS
37	1Q	183	SER
37	1Q	188	ASN
38	1R	17	CYS
38	1R	59	SER
38	1R	157	ASP
38	1R	176	ARG
38	1R	186	LYS
39	1S	21	LYS
39	1S	23	HIS
39	1S	173	ASN
40	1T	35	LYS
40	1T	38	ASP

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Mol	Chain	Res	Type
40	IT	103	ASP
40	IT	115	LYS
40	IT	158	PHE
41	IU	19	LEU
41	IU	21	PHE
41	IU	52	LYS
41	IU	90	TYR
41	IU	99	TRP
41	IU	115	PHE
41	IU	116	GLN
42	IV	100	ASP
42	IV	101	ASN
42	IV	112	MET
42	IV	134	SER
43	IX	72	ASP
43	IX	118	ASP
43	IX	139	ARG
43	IX	148	ASP
44	IY	74	TYR
44	IY	78	TYR
44	IY	84	ARG
44	IY	91	ASN
44	IY	112	ASP
44	IY	125	SER
44	IY	130	LYS
45	IZ	5	MET
45	IZ	12	LEU
45	IZ	39	SER
45	IZ	57	MET
45	IZ	61	LYS
45	IZ	77	TYR
45	IZ	85	TYR
45	IZ	135	ARG
46	la	32	ARG
46	la	92	LYS
46	la	106	SER
46	la	116	LYS
46	la	125	LYS
47	lb	32	LEU
47	lb	33	LYS
47	lb	39	PHE
47	lb	43	MET

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Mol	Chain	Res	Type
47	lb	58	GLN
47	lb	63	LYS
47	lb	65	MET
48	lc	23	LYS
48	lc	31	TYR
48	lc	57	LYS
48	lc	94	LEU
48	lc	106	ARG
49	ld	31	LYS
49	ld	59	THR
50	le	11	LYS
50	le	37	LYS
50	le	47	ARG
50	le	102	ASN
50	le	108	ARG
50	le	129	LEU
51	lf	36	ARG
51	lf	47	CYS
52	lg	7	TYR
52	lg	32	TYR
52	lg	44	SER
52	lg	53	LEU
52	lg	105	LYS
53	lh	7	ARG
53	lh	13	LYS
53	lh	27	GLU
53	lh	45	SER
55	lj	3	LYS
55	lj	11	ARG
55	lj	22	CYS
55	lj	32	SER
55	lj	50	SER
55	lj	57	ASN
55	lj	67	LEU
56	lk	11	PHE
56	lk	60	LEU
57	ll	16	LYS
57	ll	37	TYR
57	ll	45	ARG
58	lm	89	TYR
58	lm	109	ASN
58	lm	128	LYS

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Mol	Chain	Res	Type
59	ln	6	ARG
60	lo	15	CYS
60	lo	26	TYR
60	lo	31	ASP
60	lo	46	SER
60	lo	77	CYS
60	lo	96	ASP
60	lo	99	ARG
61	lp	40	SER
61	lp	41	PHE
61	lp	42	CYS
61	lp	59	SER
62	lr	19	LYS
62	lr	118	LEU
63	lz	7	ARG
63	lz	10	LEU
63	lz	12	GLU
63	lz	15	ARG
63	lz	22	GLN
63	lz	39	LYS
63	lz	56	LYS
63	lz	68	LEU
63	lz	156	LYS
63	lz	161	LYS
63	lz	173	LYS
63	lz	174	MET
63	lz	178	GLU
63	lz	193	LEU
64	sR	14	ARG
64	sR	29	HIS
64	sR	53	TYR
64	sR	82	ASP
64	sR	114	LEU
64	sR	118	GLN
65	sD	35	SER
65	sD	57	ASN
65	sD	76	ARG
65	sD	90	LYS
65	sD	134	CYS
65	sD	142	LEU
65	sD	143	ARG
65	sD	151	LYS

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Mol	Chain	Res	Type
65	sD	169	ASP
65	sD	189	MET
65	sD	192	TRP
66	sF	48	TYR
66	sF	61	PHE
66	sF	65	GLN
66	sF	79	HIS
66	sF	106	GLU
66	sF	127	ARG
66	sF	204	ARG
67	sK	5	LYS
67	sK	34	GLU
67	sK	55	ARG
67	sK	60	GLU
68	sP	46	ASN
68	sP	51	ARG
68	sP	82	ASP
68	sP	97	TYR
68	sP	106	GLU
69	sQ	7	LEU
69	sQ	13	PHE
69	sQ	41	MET
69	sQ	49	TYR
69	sQ	57	LEU
69	sQ	110	ASP
69	sQ	115	TYR
69	sQ	127	CYS
69	sQ	131	LYS
69	sQ	138	ARG
69	sQ	144	SER
70	sS	40	TYR
70	sS	73	ASN
70	sS	81	ASP
70	sS	83	PHE
70	sS	97	GLN
70	sS	99	LEU
70	sS	108	ARG
70	sS	121	ARG
70	sS	126	PHE
71	sT	33	TRP
71	sT	48	TYR
71	sT	53	PHE

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Mol	Chain	Res	Type
71	sT	116	ASP
71	sT	133	ARG
72	sU	41	ARG
72	sU	70	CYS
73	sc	34	PHE
73	sc	35	MET
73	sc	37	ASP
73	sc	51	ARG
74	sd	9	SER
74	sd	40	ARG
75	sg	27	PHE
75	sg	56	GLN
75	sg	65	PHE
75	sg	68	ASP
75	sg	101	PHE
75	sg	125	ARG
75	sg	138	CYS
75	sg	156	PHE
75	sg	259	TRP
75	sg	271	LYS
75	sg	305	ASN
76	sM	33	ARG
76	sM	42	LEU
76	sM	45	ARG
76	sM	59	PRO
76	sM	60	MET
76	sM	61	TYR
76	sM	63	LYS
76	sM	119	GLN
76	sM	122	ASP
77	sZ	57	LYS
77	sZ	58	LEU
77	sZ	76	ARG
77	sZ	78	LYS
77	sZ	96	LEU
78	sf	90	LYS
78	sf	95	ARG
78	sf	106	TYR
78	sf	119	ARG
78	sf	146	LEU
80	cB	20	ARG
80	cB	42	LYS

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Mol	Chain	Res	Type
80	cB	48	SER
80	cB	55	ARG
80	cB	65	GLU
80	cB	79	TYR
80	cB	93	LYS
80	cB	123	ASP
80	cB	130	ASP
80	cB	200	MET
80	cB	214	PHE
80	cB	231	MET
80	cB	235	LYS
80	cB	266	PHE
80	cB	275	LYS
80	cB	290	CYS
80	cB	302	ASP
80	cB	330	LYS
80	cB	333	LYS
80	cB	348	ASP
80	cB	359	PRO
80	cB	366	LYS
80	cB	367	TYR
80	cB	383	MET
80	cB	405	SER
80	cB	439	LYS
80	cB	453	MET
80	cB	454	MET
80	cB	457	TYR
80	cB	481	LYS
80	cB	488	PHE
80	cB	553	HIS
80	cB	578	SER
80	cB	594	LYS
80	cB	609	PHE
80	cB	625	ARG
80	cB	671	TYR
80	cB	688	LYS
80	cB	705	HIS
80	cB	739	ARG
80	cB	745	TYR
80	cB	751	CYS
80	cB	858	LEU
83	ls	28	PHE

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Mol	Chain	Res	Type
83	ls	38	LYS
83	ls	47	LEU
83	ls	55	MET
83	ls	58	ASN
83	ls	101	MET
83	ls	112	ARG
83	ls	183	PHE
84	lt	106	PHE
84	lt	138	SER
86	LW	2	LYS
86	LW	40	PHE
86	LW	55	TYR
86	LW	56	ARG
86	LW	73	ARG
86	LW	74	ARG
86	LW	102	LYS
86	LW	116	LYS
2	SE	32	SER
2	SE	41	CYS
2	SE	113	ARG
2	SE	182	MET
2	SE	188	ASN
2	SE	198	ARG
2	SE	226	PHE
3	SI	5	ARG
3	SI	19	LYS
3	SI	42	ARG
3	SI	52	ASN
3	SI	124	LYS
3	SI	139	LYS
3	SI	140	LYS
3	SI	141	ARG
3	SI	157	LYS
3	SI	184	ARG
3	SI	188	TYR
3	SI	206	LYS
4	SL	17	PHE
4	SL	49	GLU
4	SL	58	LYS
4	SL	69	ARG
4	SL	81	LYS
4	SL	104	LYS

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Mol	Chain	Res	Type
4	SL	124	ASP
4	SL	132	ARG
5	SX	69	CYS
5	SX	130	LEU
6	SG	1	MET
6	SG	20	ASP
6	SG	59	GLN
6	SG	83	CYS
6	SG	105	ASN
6	SG	131	ARG
6	SG	140	ARG
6	SG	154	ARG
6	SG	172	LYS
6	SG	175	LYS
6	SG	198	ARG
6	SG	217	MET
6	SG	237	LEU
7	SJ	7	TRP
7	SJ	17	ARG
7	SJ	72	PHE
7	SJ	75	ASN
7	SJ	79	ARG
7	SJ	115	PHE
7	SJ	152	ASP
7	SJ	155	LYS
7	SJ	169	ARG
8	SY	23	MET
8	SY	44	LEU
8	SY	46	LYS
8	SY	63	HIS
8	SY	79	LEU
8	SY	101	LYS
8	SY	103	SER
8	SY	113	ARG
8	SY	118	ARG
9	Se	25	LYS
9	Se	26	LYS
9	Se	37	GLN
10	SA	52	LYS
10	SA	117	ARG
10	SA	131	HIS
10	SA	142	LEU

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Mol	Chain	Res	Type
10	SA	175	TRP
10	SA	195	TRP
10	SA	198	MET
10	SA	206	ASP
10	SA	212	LYS
11	SB	38	MET
11	SB	76	ASN
11	SB	85	LYS
11	SB	90	ASP
11	SB	96	CYS
11	SB	144	LYS
11	SB	172	MET
11	SB	182	LYS
11	SB	201	CYS
11	SB	211	PHE
11	SB	214	LYS
11	SB	229	MET
12	SH	57	ARG
12	SH	58	LYS
12	SH	72	PHE
12	SH	87	PHE
12	SH	143	ARG
12	SH	157	HIS
12	SH	163	GLN
12	SH	164	ASN
12	SH	193	GLN
13	SV	4	ASP
13	SV	8	PHE
13	SV	11	LEU
13	SV	12	TYR
13	SV	17	CYS
13	SV	22	ARG
13	SV	33	GLN
13	SV	56	CYS
13	SV	76	ASP
13	SV	83	PHE
14	Sa	3	LYS
14	Sa	29	CYS
14	Sa	39	PHE
14	Sa	52	ASP
14	Sa	64	LEU
14	Sa	102	ARG

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Mol	Chain	Res	Type
15	SC	121	ARG
15	SC	132	ASP
15	SC	167	ARG
15	SC	176	LYS
15	SC	220	ASP
16	SN	25	TRP
16	SN	34	LYS
16	SN	109	LYS
17	SO	25	GLU
17	SO	46	ASP
17	SO	54	CYS
17	SO	80	ASP
17	SO	104	ARG
17	SO	150	ARG
17	SO	151	LEU
18	SW	7	LEU
18	SW	38	LEU
18	SW	50	PHE
19	Sb	3	LEU
19	Sb	34	ASP
19	Sb	51	GLN
19	Sb	56	CYS
19	Sb	70	LYS
19	Sb	72	ARG
22	LA	54	ARG
22	LA	90	CYS
22	LA	107	MET
22	LA	155	LYS
22	LA	176	ASP
22	LA	194	ASN
22	LA	245	ARG
23	LB	53	MET
23	LB	112	ASP
23	LB	120	LYS
23	LB	135	LYS
23	LB	174	ARG
23	LB	200	ARG
23	LB	214	ASP
23	LB	258	HIS
23	LB	271	GLN
23	LB	300	LYS
23	LB	310	SER

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Mol	Chain	Res	Type
23	LB	329	ASP
24	LC	5	ARG
24	LC	95	MET
24	LC	122	TYR
24	LC	156	ASP
24	LC	188	ARG
24	LC	261	ASP
24	LC	269	LYS
24	LC	290	SER
24	LC	325	MET
24	LC	343	GLN
24	LC	352	ASP
25	LD	3	PHE
25	LD	34	LYS
25	LD	72	ASP
25	LD	76	CYS
25	LD	113	PHE
25	LD	115	MET
25	LD	128	ASP
25	LD	190	PHE
25	LD	206	ASP
25	LD	210	TYR
25	LD	228	LYS
25	LD	235	MET
25	LD	239	MET
25	LD	256	LYS
25	LD	259	LYS
25	LD	268	ARG
25	LD	271	MET
26	LE	99	ASP
26	LE	110	ARG
26	LE	114	ARG
26	LE	130	LYS
26	LE	135	GLN
26	LE	210	LYS
26	LE	240	TYR
26	LE	251	LYS
26	LE	260	LYS
27	LF	25	PHE
27	LF	74	MET
27	LF	99	ASN
27	LF	119	ASN

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Mol	Chain	Res	Type
27	LF	186	CYS
27	LF	232	ASP
28	LG	26	LYS
28	LG	71	TYR
28	LG	73	ARG
28	LG	97	LYS
28	LG	113	ARG
28	LG	115	LEU
28	LG	117	ARG
28	LG	162	ASP
28	LG	181	TYR
28	LG	192	ARG
28	LG	228	ASP
28	LG	230	TYR
28	LG	240	ASN
28	LG	259	LYS
29	LH	37	ASP
29	LH	50	LYS
29	LH	51	LYS
29	LH	108	ASN
29	LH	128	MET
29	LH	170	LYS
29	LH	177	ASP
29	LH	180	TYR
30	LI	21	ARG
30	LI	71	CYS
30	LI	79	SER
30	LI	82	ARG
30	LI	136	MET
30	LI	175	LYS
30	LI	187	LYS
30	LI	213	HIS
31	LJ	28	GLU
31	LJ	60	PHE
31	LJ	64	ARG
31	LJ	95	ARG
31	LJ	107	PHE
31	LJ	112	HIS
31	LJ	137	PRO
32	LL	8	MET
32	LL	21	ARG
32	LL	67	HIS

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Mol	Chain	Res	Type
32	LL	69	LYS
32	LL	104	ASN
32	LL	111	GLN
32	LL	155	MET
33	LM	4	ARG
33	LM	35	ARG
33	LM	50	MET
33	LM	70	GLN
33	LM	118	MET
33	LM	128	LYS
34	LN	26	ARG
34	LN	90	ASN
34	LN	153	LYS
34	LN	193	ARG
34	LN	195	ARG
35	LO	118	MET
35	LO	179	LYS
35	LO	187	LYS
35	LO	191	LYS
36	LP	30	ARG
36	LP	69	ARG
36	LP	94	MET
36	LP	115	GLU
36	LP	118	GLN
36	LP	139	TYR
36	LP	148	MET
37	LQ	16	LYS
37	LQ	49	LYS
37	LQ	66	MET
37	LQ	101	CYS
37	LQ	150	ARG
37	LQ	188	ASN
38	LR	109	TYR
38	LR	111	GLU
38	LR	136	ARG
38	LR	153	LYS
38	LR	183	GLU
38	LR	186	LYS
39	LS	17	LEU
39	LS	29	ARG
39	LS	76	LYS
39	LS	82	LEU

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Mol	Chain	Res	Type
39	LS	111	ARG
39	LS	127	MET
39	LS	160	ARG
40	LT	3	ASN
40	LT	52	MET
40	LT	83	LYS
40	LT	106	LEU
41	LU	67	LYS
41	LU	82	TYR
41	LU	99	TRP
41	LU	116	GLN
42	LV	48	ARG
42	LV	90	ARG
43	LX	63	LYS
43	LX	68	ARG
43	LX	116	LEU
43	LX	118	ASP
44	LY	1	MET
44	LY	10	ASP
44	LY	41	LYS
44	LY	47	MET
44	LY	50	ARG
44	LY	74	TYR
44	LY	109	LEU
45	LZ	30	ASP
45	LZ	81	MET
45	LZ	84	ARG
45	LZ	103	ASP
45	LZ	109	LYS
45	LZ	112	ARG
45	LZ	123	LYS
46	La	89	ASN
46	La	92	LYS
47	Lb	16	TRP
47	Lb	43	MET
47	Lb	92	LYS
48	Lc	9	LYS
48	Lc	10	SER
48	Lc	23	LYS
48	Lc	51	ASN
49	Ld	67	ARG
49	Ld	87	ARG

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Mol	Chain	Res	Type
49	Ld	121	ASN
49	Ld	123	ASP
50	Le	7	LEU
50	Le	11	LYS
50	Le	33	ARG
50	Le	83	LYS
52	Lg	32	TYR
53	Lh	19	LYS
53	Lh	68	ASN
53	Lh	87	LYS
53	Lh	91	MET
53	Lh	112	ARG
54	Li	7	MET
54	Li	13	LYS
54	Li	38	LYS
54	Li	55	ARG
54	Li	86	LYS
55	Lj	22	CYS
55	Lj	34	CYS
55	Lj	63	ARG
56	Lk	9	LYS
57	Ll	45	ARG
59	Ln	4	LYS
59	Ln	10	MET
59	Ln	24	SER
60	Lo	32	SER
60	Lo	77	CYS
60	Lo	90	HIS
60	Lo	99	ARG
61	Lp	32	SER
61	Lp	48	LYS
61	Lp	85	ARG
62	Lr	46	ARG
62	Lr	72	LYS
62	Lr	83	ASN
62	Lr	90	LEU
62	Lr	122	LYS
64	SR	1	MET
64	SR	5	ARG
64	SR	7	LYS
64	SR	33	ARG
64	SR	73	LEU

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Mol	Chain	Res	Type
64	SR	105	MET
65	SD	24	PHE
65	SD	94	ARG
65	SD	107	TYR
65	SD	134	CYS
65	SD	143	ARG
65	SD	146	ARG
65	SD	148	LYS
65	SD	150	MET
65	SD	227	LYS
66	SF	26	ASP
66	SF	37	ASP
66	SF	77	MET
66	SF	94	LYS
66	SF	97	PHE
66	SF	145	ARG
66	SF	175	ASP
66	SF	194	ASP
67	SK	7	ASN
67	SK	13	GLU
67	SK	25	LYS
67	SK	50	GLN
67	SK	53	LYS
67	SK	81	ASP
67	SK	95	ARG
68	SP	37	TYR
68	SP	40	ARG
68	SP	58	LYS
68	SP	59	ARG
68	SP	65	LYS
68	SP	77	LYS
68	SP	81	ARG
68	SP	100	LYS
69	SQ	126	ARG
69	SQ	138	ARG
69	SQ	145	TYR
70	SS	19	ASN
70	SS	77	TYR
70	SS	81	ASP
70	SS	83	PHE
70	SS	104	ASP
71	ST	21	PHE

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Mol	Chain	Res	Type
71	ST	24	LYS
71	ST	25	SER
71	ST	27	LYS
71	ST	51	ASN
71	ST	91	HIS
71	ST	93	SER
71	ST	118	ASP
72	SU	36	CYS
72	SU	78	ASP
72	SU	79	ARG
72	SU	83	ARG
72	SU	88	LEU
73	Sc	5	ARG
73	Sc	40	ARG
74	Sd	8	TRP
74	Sd	39	CYS
74	Sd	40	ARG
74	Sd	48	LYS
75	Sg	25	PRO
75	Sg	44	LYS
75	Sg	52	TYR
75	Sg	64	HIS
75	Sg	65	PHE
75	Sg	101	PHE
75	Sg	113	PHE
75	Sg	125	ARG
75	Sg	138	CYS
75	Sg	144	ASP
75	Sg	155	ARG
75	Sg	194	TYR
75	Sg	215	GLN
75	Sg	228	TYR
75	Sg	249	CYS
75	Sg	271	LYS
75	Sg	310	TRP
76	SM	26	LEU
76	SM	33	ARG
76	SM	45	ARG
76	SM	50	CYS
76	SM	63	LYS
76	SM	69	CYS
76	SM	99	LYS

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Mol	Chain	Res	Type
76	SM	112	LYS
76	SM	119	GLN
76	SM	127	TYR
77	SZ	51	ASP
77	SZ	55	TYR
77	SZ	104	ARG
78	Sf	89	LYS
78	Sf	104	LYS
78	Sf	117	LEU
78	Sf	131	PHE
78	Sf	132	MET
88	CF	20	LYS
88	CF	37	ARG
88	CF	51	LYS
88	CF	55	LYS
88	CF	58	TRP
88	CF	69	ARG
88	CF	84	LYS
88	CF	86	TYR
88	CF	141	TYR
88	CF	159	GLU
88	CF	205	SER
88	CF	208	MET
88	CF	219	LYS
88	CF	220	ASP
88	CF	232	LEU
88	CF	252	ASP
88	CF	290	LYS
88	CF	294	MET
88	CF	321	ARG
88	CF	415	PHE
88	CF	417	ASP
88	CF	444	LYS
84	Lt	57	ARG
63	Lz	15	ARG
63	Lz	42	ASP
63	Lz	56	LYS
63	Lz	105	LYS
63	Lz	113	SER
63	Lz	122	ARG
63	Lz	124	LEU
63	Lz	156	LYS

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Mol	Chain	Res	Type
63	Lz	161	LYS
63	Lz	178	GLU
83	Ls	10	LYS
83	Ls	15	LEU
83	Ls	38	LYS
83	Ls	66	ARG
83	Ls	77	LYS
83	Ls	101	MET
83	Ls	106	LYS
83	Ls	146	LYS
83	Ls	162	LYS
83	Ls	197	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (93) such sidechains are listed below:

Mol	Chain	Res	Type
1	cH	48	GLN
2	sE	98	ASN
4	sL	5	GLN
4	sL	11	GLN
4	sL	13	GLN
4	sL	19	ASN
6	sG	59	GLN
6	sG	197	GLN
7	sJ	177	ASN
8	sY	15	ASN
8	sY	22	GLN
12	sH	25	GLN
12	sH	76	GLN
13	sV	29	HIS
16	sN	90	HIS
18	sW	90	GLN
18	sW	98	GLN
22	lA	8	GLN
23	lB	213	GLN
23	lB	271	GLN
24	lC	310	HIS
26	lE	250	GLN
28	lG	43	GLN
30	lI	51	HIS
38	lR	34	ASN
38	lR	118	HIS

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Mol	Chain	Res	Type
45	lZ	127	ASN
47	lb	6	ASN
48	lc	51	ASN
50	le	43	ASN
52	lg	114	GLN
58	lm	90	ASN
64	sR	31	ASN
67	sK	28	HIS
67	sK	61	GLN
69	sQ	11	GLN
69	sQ	77	HIS
69	sQ	86	GLN
70	sS	101	ASN
71	sT	126	GLN
71	sT	128	GLN
75	sg	285	GLN
77	sZ	106	GLN
78	sf	91	ASN
80	cB	27	HIS
80	cB	468	ASN
80	cB	492	HIS
80	cB	588	ASN
80	cB	600	ASN
80	cB	705	HIS
83	ls	105	ASN
2	SE	161	GLN
4	SL	5	GLN
6	SG	56	ASN
6	SG	65	GLN
7	SJ	39	ASN
7	SJ	113	GLN
10	SA	111	GLN
10	SA	149	ASN
10	SA	165	ASN
12	SH	157	HIS
13	SV	35	ASN
15	SC	267	GLN
16	SN	49	GLN
23	LB	302	ASN
23	LB	315	ASN
25	LD	39	GLN
25	LD	111	ASN

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Mol	Chain	Res	Type
30	LI	143	GLN
30	LI	147	HIS
31	LJ	104	ASN
31	LJ	155	HIS
34	LN	87	HIS
36	LP	137	ASN
37	LQ	77	ASN
40	LT	131	GLN
42	LV	84	GLN
43	LX	151	ASN
44	LY	72	GLN
46	La	66	ASN
47	Lb	58	GLN
50	Le	92	ASN
57	Ll	43	HIS
65	SD	101	GLN
70	SS	17	ASN
70	SS	87	GLN
75	Sg	119	GLN
76	SM	19	GLN
77	SZ	45	ASN
88	CF	343	GLN
88	CF	349	HIS
84	Lt	115	GLN
83	Ls	58	ASN

5.3.3 RNA ⓘ

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

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
89	Pt	72/74 (97%)	16 (22%)	0
All	All	11747/11884 (98%)	2902 (24%)	36 (0%)

All (2902) 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
20	17	38	U
20	17	53	U
20	17	54	A
20	17	63	C
20	17	64	G
20	17	76	U
20	17	97	G
20	17	100	A
20	17	111	C
21	18	34	U
21	18	35	C
21	18	39	G
21	18	46	G
21	18	48	A
21	18	59	A
21	18	62	A
21	18	63	U
21	18	68	G
21	18	80	A
21	18	82	A
21	18	83	C
21	18	84	A
21	18	85	U
21	18	86	U
21	18	87	G
21	18	94	G
21	18	103	A
21	18	105	C
21	18	110	U
21	18	111	U
21	18	112	G

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Mol	Chain	Res	Type
21	l8	114	G
21	l8	123	U
21	l8	124	U
21	l8	125	C
21	l8	126	C
21	l8	127	U
21	l8	147	G
21	l8	151	G
79	s2	4	C
79	s2	11	A
79	s2	13	C
79	s2	14	C
79	s2	17	C
79	s2	25	A
79	s2	33	G
79	s2	37	C
79	s2	41	G
79	s2	42	A
79	s2	45	A
79	s2	46	A
79	s2	56	G
79	s2	58	C
79	s2	62	G
79	s2	64	A
79	s2	66	G
79	s2	67	C
79	s2	68	A
79	s2	72	C
79	s2	73	C
79	s2	74	G
79	s2	76	U
79	s2	77	A
79	s2	92	A
79	s2	103	A
79	s2	113	G
79	s2	114	G
79	s2	115	U
79	s2	116	U
79	s2	126	G
79	s2	130	G
79	s2	139	C
79	s2	143	U

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Mol	Chain	Res	Type
79	s2	147	A
79	s2	149	A
79	s2	158	A
79	s2	160	U
79	s2	161	U
79	s2	162	C
79	s2	163	U
79	s2	168	C
79	s2	170	A
79	s2	175	A
79	s2	179	C
79	s2	182	C
79	s2	190	G
79	s2	191	A
79	s2	196	C
79	s2	197	U
79	s2	198	U
79	s2	200	G
79	s2	202	G
79	s2	203	G
79	s2	204	G
79	s2	206	G
79	s2	207	G
79	s2	208	G
79	s2	209	A
79	s2	212	C
79	s2	214	U
79	s2	220	U
79	s2	291	G
79	s2	292	A
79	s2	294	U
79	s2	295	C
79	s2	303	C
79	s2	305	U
79	s2	306	C
79	s2	307	G
79	s2	308	G
79	s2	309	G
79	s2	310	C
79	s2	311	C
79	s2	312	G
79	s2	317	C

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Mol	Chain	Res	Type
79	s2	318	A
79	s2	319	C
79	s2	323	C
79	s2	324	C
79	s2	325	C
79	s2	326	C
79	s2	327	G
79	s2	328	U
79	s2	329	G
79	s2	332	G
79	s2	335	G
79	s2	338	G
79	s2	339	A
79	s2	340	C
79	s2	347	G
79	s2	351	G
79	s2	360	A
79	s2	361	U
79	s2	362	C
79	s2	363	A
79	s2	364	A
79	s2	368	U
79	s2	370	G
79	s2	374	G
79	s2	384	U
79	s2	385	G
79	s2	386	C
79	s2	407	G
79	s2	408	A
79	s2	409	C
79	s2	421	G
79	s2	437	G
79	s2	442	C
79	s2	448	A
79	s2	449	A
79	s2	450	C
79	s2	452	G
79	s2	464	A
79	s2	465	A
79	s2	471	G
79	s2	472	C
79	s2	473	A

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Mol	Chain	Res	Type
79	s2	474	G
79	s2	476	A
79	s2	487	U
79	s2	488	U
79	s2	492	C
79	s2	493	A
79	s2	496	C
79	s2	502	C
79	s2	503	C
79	s2	516	A
79	s2	517	C
79	s2	532	C
79	s2	533	A
79	s2	534	G
79	s2	536	A
79	s2	537	C
79	s2	540	U
79	s2	541	U
79	s2	542	U
79	s2	544	G
79	s2	546	G
79	s2	547	G
79	s2	551	U
79	s2	553	U
79	s2	555	A
79	s2	557	U
79	s2	558	G
79	s2	559	G
79	s2	563	G
79	s2	564	A
79	s2	576	A
79	s2	583	A
79	s2	585	C
79	s2	587	A
79	s2	589	G
79	s2	590	A
79	s2	591	U
79	s2	593	C
79	s2	594	A
79	s2	603	C
79	s2	608	C
79	s2	610	G

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Mol	Chain	Res	Type
79	s2	614	C
79	s2	615	C
79	s2	616	A
79	s2	617	G
79	s2	623	G
79	s2	627	U
79	s2	628	A
79	s2	629	A
79	s2	631	U
79	s2	638	C
79	s2	643	A
79	s2	644	G
79	s2	660	C
79	s2	664	A
79	s2	668	A
79	s2	669	A
79	s2	671	A
79	s2	672	A
79	s2	673	G
79	s2	684	G
79	s2	688	U
79	s2	689	U
79	s2	692	G
79	s2	693	A
79	s2	694	G
79	s2	695	C
79	s2	696	G
79	s2	697	G
79	s2	698	G
79	s2	731	G
79	s2	732	U
79	s2	734	C
79	s2	736	C
79	s2	738	C
79	s2	749	U
79	s2	750	C
79	s2	751	G
79	s2	752	G
79	s2	753	C
79	s2	788	G
79	s2	791	C
79	s2	792	C

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Mol	Chain	Res	Type
79	s2	794	A
79	s2	797	C
79	s2	798	G
79	s2	799	U
79	s2	801	U
79	s2	812	A
79	s2	821	G
79	s2	822	U
79	s2	823	U
79	s2	824	C
79	s2	827	A
79	s2	830	A
79	s2	833	C
79	s2	834	C
79	s2	835	C
79	s2	836	G
79	s2	837	A
79	s2	838	G
79	s2	839	C
79	s2	842	C
79	s2	844	U
79	s2	847	A
79	s2	869	A
79	s2	870	A
79	s2	871	U
79	s2	872	A
79	s2	873	G
79	s2	874	G
79	s2	877	C
79	s2	878	G
79	s2	882	U
79	s2	888	U
79	s2	889	U
79	s2	890	U
79	s2	891	G
79	s2	892	U
79	s2	893	U
79	s2	896	U
79	s2	898	U
79	s2	899	U
79	s2	900	C
79	s2	901	G

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Mol	Chain	Res	Type
79	s2	903	A
79	s2	905	C
79	s2	913	A
79	s2	917	U
79	s2	919	A
79	s2	920	A
79	s2	925	G
79	s2	933	G
79	s2	934	G
79	s2	943	U
79	s2	949	G
79	s2	954	U
79	s2	955	A
79	s2	963	A
79	s2	971	G
79	s2	972	A
79	s2	979	C
79	s2	988	C
79	s2	990	A
79	s2	992	A
79	s2	997	A
79	s2	999	G
79	s2	1001	A
79	s2	1002	U
79	s2	1008	A
79	s2	1017	U
79	s2	1023	A
79	s2	1027	A
79	s2	1042	A
79	s2	1045	U
79	s2	1047	C
79	s2	1058	A
79	s2	1061	U
79	s2	1062	A
79	s2	1067	C
79	s2	1083	A
79	s2	1085	C
79	s2	1088	U
79	s2	1100	A
79	s2	1109	C
79	s2	1110	G
79	s2	1113	A

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Mol	Chain	Res	Type
79	s2	1114	U
79	s2	1115	U
79	s2	1116	C
79	s2	1117	C
79	s2	1118	C
79	s2	1119	A
79	s2	1121	G
79	s2	1124	C
79	s2	1133	A
79	s2	1138	C
79	s2	1148	A
79	s2	1149	A
79	s2	1153	C
79	s2	1154	U
79	s2	1155	U
79	s2	1170	A
79	s2	1195	A
79	s2	1200	A
79	s2	1207	G
79	s2	1208	A
79	s2	1213	C
79	s2	1215	C
79	s2	1216	C
79	s2	1217	A
79	s2	1220	A
79	s2	1224	G
79	s2	1227	G
79	s2	1237	C
79	s2	1240	A
79	s2	1242	U
79	s2	1243	U
79	s2	1251	A
79	s2	1253	A
79	s2	1256	G
79	s2	1257	G
79	s2	1259	A
79	s2	1263	U
79	s2	1264	C
79	s2	1274	G
79	s2	1275	G
79	s2	1281	G
79	s2	1283	C

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Mol	Chain	Res	Type
79	s2	1284	A
79	s2	1286	G
79	s2	1287	A
79	s2	1290	G
79	s2	1294	G
79	s2	1295	A
79	s2	1301	A
79	s2	1302	G
79	s2	1303	C
79	s2	1306	U
79	s2	1308	U
79	s2	1342	U
79	s2	1354	G
79	s2	1355	C
79	s2	1356	G
79	s2	1357	A
79	s2	1358	U
79	s2	1369	A
79	s2	1370	A
79	s2	1371	U
79	s2	1372	U
79	s2	1373	C
79	s2	1375	G
79	s2	1376	A
79	s2	1378	A
79	s2	1388	A
79	s2	1389	C
79	s2	1393	G
79	s2	1401	A
79	s2	1402	A
79	s2	1406	G
79	s2	1407	U
79	s2	1408	U
79	s2	1411	G
79	s2	1413	G
79	s2	1415	C
79	s2	1419	C
79	s2	1420	G
79	s2	1421	A
79	s2	1422	G
79	s2	1423	C
79	s2	1424	G

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Mol	Chain	Res	Type
79	s2	1425	G
79	s2	1428	G
79	s2	1433	C
79	s2	1434	C
79	s2	1435	C
79	s2	1436	C
79	s2	1438	A
79	s2	1442	U
79	s2	1449	G
79	s2	1450	G
79	s2	1452	A
79	s2	1453	C
79	s2	1454	A
79	s2	1456	G
79	s2	1459	G
79	s2	1463	U
79	s2	1464	C
79	s2	1476	A
79	s2	1478	U
79	s2	1479	G
79	s2	1486	A
79	s2	1489	A
79	s2	1490	G
79	s2	1494	U
79	s2	1495	G
79	s2	1497	G
79	s2	1498	A
79	s2	1507	G
79	s2	1508	A
79	s2	1521	C
79	s2	1522	A
79	s2	1533	A
79	s2	1535	U
79	s2	1536	G
79	s2	1537	A
79	s2	1544	C
79	s2	1546	G
79	s2	1551	U
79	s2	1552	G
79	s2	1555	U
79	s2	1556	A
79	s2	1567	G

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Mol	Chain	Res	Type
79	s2	1570	G
79	s2	1574	C
79	s2	1578	U
79	s2	1579	A
79	s2	1580	A
79	s2	1581	C
79	s2	1585	U
79	s2	1586	U
79	s2	1587	G
79	s2	1588	A
79	s2	1594	A
79	s2	1599	U
79	s2	1600	G
79	s2	1601	A
79	s2	1603	G
79	s2	1604	G
79	s2	1606	G
79	s2	1621	U
79	s2	1623	A
79	s2	1629	C
79	s2	1630	A
79	s2	1633	A
79	s2	1637	A
79	s2	1638	G
79	s2	1639	G
79	s2	1640	A
79	s2	1646	C
79	s2	1648	G
79	s2	1649	U
79	s2	1654	G
79	s2	1663	A
79	s2	1664	A
79	s2	1665	G
79	s2	1671	G
79	s2	1680	G
79	s2	1694	U
79	s2	1695	A
79	s2	1696	C
79	s2	1699	A
79	s2	1712	A
79	s2	1715	A
79	s2	1722	G

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Mol	Chain	Res	Type
79	s2	1729	U
79	s2	1743	G
79	s2	1744	G
79	s2	1745	A
79	s2	1752	C
79	s2	1753	C
79	s2	1754	G
79	s2	1755	C
79	s2	1757	G
79	s2	1758	G
79	s2	1759	G
79	s2	1761	U
79	s2	1772	C
79	s2	1773	C
79	s2	1774	C
79	s2	1777	G
79	s2	1780	G
79	s2	1781	A
79	s2	1782	G
79	s2	1783	C
79	s2	1784	G
79	s2	1785	C
79	s2	1787	G
79	s2	1789	G
79	s2	1798	C
79	s2	1809	A
79	s2	1810	U
79	s2	1812	U
79	s2	1813	A
79	s2	1820	G
79	s2	1822	A
79	s2	1823	A
79	s2	1825	A
79	s2	1826	G
79	s2	1835	A
79	s2	1838	U
79	s2	1849	G
79	s2	1852	C
79	s2	1861	G
79	s2	1862	G
79	s2	1863	A
79	s2	1865	C

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Mol	Chain	Res	Type
81	aP	8	U
81	aP	9	A
81	aP	10	G
81	aP	11	U
81	aP	13	U
81	aP	14	A
81	aP	19	G
81	aP	20(A)	U
81	aP	21	A
81	aP	25	C
81	aP	26	G
81	aP	31	C
81	aP	47	U
81	aP	48	C
81	aP	49	C
81	aP	54	U
81	aP	55	U
81	aP	56	C
81	aP	58	A
81	aP	66	C
81	aP	67	G
81	aP	70	A
82	pE	4	C
82	pE	8	U
82	pE	9	A
82	pE	10	G
82	pE	11	C
82	pE	16	C
82	pE	19	G
82	pE	20	U
82	pE	21	A
82	pE	25	C
82	pE	26	A
82	pE	27	U
82	pE	31	A
82	pE	34	U
82	pE	35	U
82	pE	38	A
82	pE	39	U
82	pE	40	C
82	pE	46	G
82	pE	47	U

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Mol	Chain	Res	Type
82	pE	48	C
82	pE	50	A
82	pE	52	G
82	pE	54	U
82	pE	55	U
82	pE	56	C
82	pE	58	A
82	pE	61	C
82	pE	65	G
82	pE	67	U
82	pE	68	C
82	pE	69	G
82	pE	70	G
82	pE	71	G
82	pE	76	A
85	l5	2	G
85	l5	6	C
85	l5	17	A
85	l5	25	A
85	l5	26	C
85	l5	30	C
85	l5	39	A
85	l5	42	A
85	l5	48	G
85	l5	56	A
85	l5	59	A
85	l5	64	A
85	l5	65	A
85	l5	73	A
85	l5	74	G
85	l5	91	G
85	l5	104	G
85	l5	108	A
85	l5	109	G
85	l5	110	C
85	l5	119	G
85	l5	120	A
85	l5	132	G
85	l5	133	C
85	l5	134	G
85	l5	135	G
85	l5	136	C

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Mol	Chain	Res	Type
85	l5	144	G
85	l5	152	U
85	l5	159	C
85	l5	165	A
85	l5	170	C
85	l5	171	U
85	l5	172	C
85	l5	181	C
85	l5	183	C
85	l5	184	U
85	l5	185	C
85	l5	187	U
85	l5	188	G
85	l5	189	G
85	l5	200	U
85	l5	209	U
85	l5	216	C
85	l5	218	A
85	l5	220	C
85	l5	234	G
85	l5	235	A
85	l5	237	G
85	l5	255	C
85	l5	256	G
85	l5	261	G
85	l5	263	G
85	l5	264	C
85	l5	265	C
85	l5	266	C
85	l5	267	G
85	l5	269	G
85	l5	275	C
85	l5	276	C
85	l5	280	G
85	l5	297	U
85	l5	306	A
85	l5	315	G
85	l5	316	U
85	l5	340	C
85	l5	350	C
85	l5	373	G
85	l5	385	A

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Mol	Chain	Res	Type
85	15	387	G
85	15	388	A
85	15	396	A
85	15	401	G
85	15	407	A
85	15	409	G
85	15	410	A
85	15	411	G
85	15	412	G
85	15	413	G
85	15	431	G
85	15	432	U
85	15	433	A
85	15	438	G
85	15	449	C
85	15	450	G
85	15	452	A
85	15	453	G
85	15	454	U
85	15	456	C
85	15	457	G
85	15	465	G
85	15	467	U
85	15	468	U
85	15	469	C
85	15	472	C
85	15	483	G
85	15	485	C
85	15	486	C
85	15	489	C
85	15	493	G
85	15	494	U
85	15	497	G
85	15	498	C
85	15	499	G
85	15	500	G
85	15	501	C
85	15	502	C
85	15	503	C
85	15	504	G
85	15	505	G
85	15	506	C

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Mol	Chain	Res	Type
85	15	509	A
85	15	510	U
85	15	512	U
85	15	513	U
85	15	514	U
85	15	518	G
85	15	519	C
85	15	643	C
85	15	644	G
85	15	645	G
85	15	646	G
85	15	655	C
85	15	656	C
85	15	657	C
85	15	658	C
85	15	659	G
85	15	666	G
85	15	667	A
85	15	668	C
85	15	669	C
85	15	672	C
85	15	673	C
85	15	682	G
85	15	685	C
85	15	686	A
85	15	687	U
85	15	696	C
85	15	703	G
85	15	704	C
85	15	706	C
85	15	708	G
85	15	731	G
85	15	738	C
85	15	739	G
85	15	742	G
85	15	753	C
85	15	754	U
85	15	758	G
85	15	759	G
85	15	904	C
85	15	905	C
85	15	906	C

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Mol	Chain	Res	Type
85	15	907	C
85	15	910	G
85	15	911	U
85	15	912	G
85	15	913	U
85	15	914	U
85	15	915	A
85	15	917	A
85	15	918	G
85	15	923	C
85	15	924	C
85	15	926	G
85	15	932	A
85	15	933	G
85	15	935	A
85	15	936	C
85	15	937	U
85	15	943	A
85	15	944	A
85	15	945	U
85	15	959	G
85	15	960	A
85	15	961	G
85	15	962	C
85	15	965	G
85	15	966	A
85	15	967	C
85	15	968	C
85	15	969	C
85	15	970	G
85	15	982	U
85	15	985	C
85	15	989	U
85	15	990	C
85	15	992	C
85	15	993	G
85	15	995	C
85	15	1048	G
85	15	1049	C
85	15	1050	C
85	15	1051	G
85	15	1066	G

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Mol	Chain	Res	Type
85	l5	1070	G
85	l5	1071	C
85	l5	1072	C
85	l5	1075	G
85	l5	1082	C
85	l5	1083	U
85	l5	1095	A
85	l5	1168	G
85	l5	1171	G
85	l5	1172	C
85	l5	1173	G
85	l5	1179	U
85	l5	1180	C
85	l5	1182	C
85	l5	1183	C
85	l5	1193	C
85	l5	1202	C
85	l5	1203	G
85	l5	1210	C
85	l5	1211	G
85	l5	1215	C
85	l5	1216	C
85	l5	1217	G
85	l5	1218	G
85	l5	1219	G
85	l5	1221	G
85	l5	1222	A
85	l5	1235	G
85	l5	1241	C
85	l5	1245	C
85	l5	1246	G
85	l5	1253	G
85	l5	1254	A
85	l5	1257	A
85	l5	1258	G
85	l5	1266	G
85	l5	1267	C
85	l5	1269	G
85	l5	1270	A
85	l5	1271	G
85	l5	1272	C
85	l5	1273	G

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Mol	Chain	Res	Type
85	l5	1274	A
85	l5	1275	G
85	l5	1280	C
85	l5	1284	G
85	l5	1287	G
85	l5	1293	G
85	l5	1294	A
85	l5	1295	C
85	l5	1296	G
85	l5	1301	C
85	l5	1313	C
85	l5	1314	C
85	l5	1326	A
85	l5	1339	U
85	l5	1354	A
85	l5	1358	G
85	l5	1359	G
85	l5	1365	C
85	l5	1367	C
85	l5	1370	G
85	l5	1378	C
85	l5	1381	U
85	l5	1387	A
85	l5	1394	G
85	l5	1397	A
85	l5	1404	G
85	l5	1405	C
85	l5	1407	C
85	l5	1409	C
85	l5	1410	U
85	l5	1411	C
85	l5	1414	C
85	l5	1415	G
85	l5	1417	C
85	l5	1418	C
85	l5	1420	A
85	l5	1425	G
85	l5	1437	C
85	l5	1439	C
85	l5	1441	C
85	l5	1443	A
85	l5	1446	C

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Mol	Chain	Res	Type
85	l5	1447	C
85	l5	1452	A
85	l5	1457	G
85	l5	1465	G
85	l5	1482	G
85	l5	1483	C
85	l5	1497	A
85	l5	1498	G
85	l5	1516	G
85	l5	1517	G
85	l5	1518	A
85	l5	1534	A
85	l5	1547	A
85	l5	1562	G
85	l5	1564	A
85	l5	1566	C
85	l5	1578	U
85	l5	1582	U
85	l5	1591	U
85	l5	1596	U
85	l5	1612	G
85	l5	1624	G
85	l5	1625	G
85	l5	1631	A
85	l5	1633	G
85	l5	1634	A
85	l5	1641	G
85	l5	1654	G
85	l5	1661	C
85	l5	1676	C
85	l5	1677	U
85	l5	1678	C
85	l5	1691	G
85	l5	1698	C
85	l5	1699	A
85	l5	1700	G
85	l5	1701	A
85	l5	1703	C
85	l5	1704	C
85	l5	1705	G
85	l5	1707	C
85	l5	1718	C

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Mol	Chain	Res	Type
85	l5	1741	G
85	l5	1742	A
85	l5	1750	G
85	l5	1753	G
85	l5	1754	U
85	l5	1757	U
85	l5	1758	G
85	l5	1760	G
85	l5	1761	G
85	l5	1762	C
85	l5	1763	C
85	l5	1764	G
85	l5	1765	A
85	l5	1766	A
85	l5	1767	A
85	l5	1768	C
85	l5	1770	A
85	l5	1785	C
85	l5	1787	A
85	l5	1804	A
85	l5	1806	G
85	l5	1810	G
85	l5	1820	C
85	l5	1821	G
85	l5	1822	U
85	l5	1836	G
85	l5	1837	A
85	l5	1842	G
85	l5	1843	A
85	l5	1855	G
85	l5	1869	G
85	l5	1881	C
85	l5	1897	A
85	l5	1917	A
85	l5	1918	U
85	l5	1919	G
85	l5	1920	C
85	l5	1921	C
85	l5	1922	G
85	l5	1925	G
85	l5	1931	C
85	l5	1932	A

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Mol	Chain	Res	Type
85	15	1935	C
85	15	1936	C
85	15	1940	G
85	15	1948	G
85	15	1949	U
85	15	1959	U
85	15	1961	G
85	15	1962	A
85	15	1965	G
85	15	1974	U
85	15	1975	G
85	15	1978	C
85	15	1980	U
85	15	1981	G
85	15	1982	G
85	15	1984	A
85	15	1985	G
85	15	1986	U
85	15	1989	G
85	15	1991	A
85	15	1992	U
85	15	1993	C
85	15	1997	U
85	15	1998	A
85	15	2001	G
85	15	2002	A
85	15	2004	U
85	15	2005	G
85	15	2011	C
85	15	2014	C
85	15	2017	A
85	15	2018	C
85	15	2024	G
85	15	2026	A
85	15	2033	A
85	15	2034	G
85	15	2046	G
85	15	2048	U
85	15	2055	G
85	15	2056	G
85	15	2069	A
85	15	2084	C

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Mol	Chain	Res	Type
85	15	2085	G
85	15	2092	G
85	15	2093	A
85	15	2094	G
85	15	2095	A
85	15	2096	G
85	15	2097	U
85	15	2098	G
85	15	2101	C
85	15	2102	G
85	15	2103	G
85	15	2106	G
85	15	2107	C
85	15	2108	G
85	15	2112	G
85	15	2250	C
85	15	2252	G
85	15	2253	A
85	15	2256	C
85	15	2257	C
85	15	2258	C
85	15	2259	G
85	15	2260	C
85	15	2262	G
85	15	2263	A
85	15	2289	C
85	15	2300	A
85	15	2301	G
85	15	2306	G
85	15	2313	A
85	15	2331	G
85	15	2332	A
85	15	2333	G
85	15	2348	G
85	15	2351	C
85	15	2360	A
85	15	2364	G
85	15	2395	A
85	15	2397	G
85	15	2398	U
85	15	2402	G
85	15	2404	A

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Mol	Chain	Res	Type
85	l5	2410	C
85	l5	2417	A
85	l5	2421	G
85	l5	2425	U
85	l5	2441	C
85	l5	2442	G
85	l5	2447	U
85	l5	2450	G
85	l5	2453	A
85	l5	2465	C
85	l5	2470	C
85	l5	2471	G
85	l5	2474	G
85	l5	2475	G
85	l5	2478	C
85	l5	2483	G
85	l5	2484	A
85	l5	2485	U
85	l5	2487	G
85	l5	2488	C
85	l5	2489	C
85	l5	2490	U
85	l5	2491	C
85	l5	2494	U
85	l5	2503	G
85	l5	2504	C
85	l5	2505	C
85	l5	2506	G
85	l5	2513	A
85	l5	2518	G
85	l5	2519	U
85	l5	2520	C
85	l5	2529	A
85	l5	2537	A
85	l5	2544	G
85	l5	2546	G
85	l5	2547	G
85	l5	2554	U
85	l5	2557	G
85	l5	2560	C
85	l5	2565	A
85	l5	2567	G

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Mol	Chain	Res	Type
85	15	2568	C
85	15	2583	C
85	15	2587	A
85	15	2588	C
85	15	2589	C
85	15	2600	A
85	15	2601	A
85	15	2627	C
85	15	2652	G
85	15	2653	C
85	15	2659	A
85	15	2662	G
85	15	2664	G
85	15	2669	C
85	15	2673	G
85	15	2676	A
85	15	2687	U
85	15	2694	G
85	15	2695	A
85	15	2696	A
85	15	2703	G
85	15	2707	U
85	15	2708	U
85	15	2710	C
85	15	2711	G
85	15	2719	C
85	15	2721	G
85	15	2724	G
85	15	2726	G
85	15	2739	C
85	15	2742	G
85	15	2743	A
85	15	2761	U
85	15	2763	U
85	15	2764	A
85	15	2769	U
85	15	2770	C
85	15	2787	A
85	15	2788	U
85	15	2790	U
85	15	2826	U
85	15	2827	G

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Mol	Chain	Res	Type
85	15	2829	U
85	15	2830	G
85	15	2846	G
85	15	2855	G
85	15	2867	C
85	15	2877	G
85	15	2900	U
85	15	2902	G
85	15	2903	G
85	15	2904	U
85	15	2905	C
85	15	2906	G
85	15	2908	U
85	15	3586	G
85	15	3590	G
85	15	3591	C
85	15	3594	C
85	15	3595	U
85	15	3596	A
85	15	3597	G
85	15	3598	C
85	15	3599	A
85	15	3605	C
85	15	3615	G
85	15	3618	C
85	15	3626	G
85	15	3630	A
85	15	3635	A
85	15	3644	U
85	15	3646	A
85	15	3648	A
85	15	3662	A
85	15	3664	G
85	15	3670	C
85	15	3673	C
85	15	3674	G
85	15	3685	C
85	15	3691	G
85	15	3692	A
85	15	3694	U
85	15	3710	G
85	15	3711	A

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Mol	Chain	Res	Type
85	15	3713	U
85	15	3727	A
85	15	3748	A
85	15	3750	G
85	15	3756	A
85	15	3759	A
85	15	3761	C
85	15	3772	U
85	15	3773	U
85	15	3774	A
85	15	3776	G
85	15	3777	G
85	15	3778	U
85	15	3784	A
85	15	3786	U
85	15	3802	U
85	15	3811	G
85	15	3812	C
85	15	3814	U
85	15	3817	A
85	15	3818	U
85	15	3819	G
85	15	3823	G
85	15	3838	U
85	15	3840	U
85	15	3841	C
85	15	3867	A
85	15	3877	A
85	15	3878	C
85	15	3879	G
85	15	3885	G
85	15	3887	C
85	15	3890	A
85	15	3892	U
85	15	3897	G
85	15	3898	G
85	15	3901	A
85	15	3906	A
85	15	3907	G
85	15	3908	A
85	15	3915	U
85	15	3923	A

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Mol	Chain	Res	Type
85	15	3938	G
85	15	3939	G
85	15	3943	A
85	15	3944	G
85	15	3947	A
85	15	3948	C
85	15	3949	A
85	15	3950	U
85	15	3953	G
85	15	3955	G
85	15	3956	G
85	15	3957	U
85	15	3959	U
85	15	3960	A
85	15	3961	G
85	15	3962	A
85	15	3963	A
85	15	3964	U
85	15	3965	A
85	15	3966	A
85	15	3967	G
85	15	3968	U
85	15	3969	G
85	15	3970	G
85	15	3972	A
85	15	3973	G
85	15	3974	G
85	15	3977	C
85	15	4034	G
85	15	4038	C
85	15	4039	G
85	15	4041	C
85	15	4042	G
85	15	4043	G
85	15	4044	U
85	15	4046	A
85	15	4047	A
85	15	4048	A
85	15	4049	U
85	15	4050	A
85	15	4051	C
85	15	4052	C

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Mol	Chain	Res	Type
85	l5	4053	A
85	l5	4054	C
85	l5	4055	U
85	l5	4056	A
85	l5	4057	C
85	l5	4058	U
85	l5	4059	C
85	l5	4060	U
85	l5	4061	G
85	l5	4062	A
85	l5	4063	U
85	l5	4064	C
85	l5	4065	G
85	l5	4067	U
85	l5	4068	U
85	l5	4069	U
85	l5	4076	G
85	l5	4084	G
85	l5	4093	G
85	l5	4096	C
85	l5	4097	G
85	l5	4099	G
85	l5	4101	C
85	l5	4102	C
85	l5	4103	C
85	l5	4104	G
85	l5	4108	G
85	l5	4111	U
85	l5	4114	C
85	l5	4115	G
85	l5	4116	C
85	l5	4117	U
85	l5	4119	C
85	l5	4121	G
85	l5	4127	A
85	l5	4133	C
85	l5	4134	C
85	l5	4140	C
85	l5	4141	G
85	l5	4142	C
85	l5	4143	G
85	l5	4144	C

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Mol	Chain	Res	Type
85	l5	4146	G
85	l5	4149	C
85	l5	4150	G
85	l5	4156	G
85	l5	4160	C
85	l5	4162	C
85	l5	4163	U
85	l5	4168	G
85	l5	4170	A
85	l5	4183	G
85	l5	4184	G
85	l5	4191	G
85	l5	4196	G
85	l5	4197	G
85	l5	4201	G
85	l5	4203	A
85	l5	4212	A
85	l5	4225	G
85	l5	4229	U
85	l5	4233	A
85	l5	4237	C
85	l5	4241	C
85	l5	4242	U
85	l5	4251	A
85	l5	4254	G
85	l5	4255	A
85	l5	4256	A
85	l5	4257	A
85	l5	4265	U
85	l5	4268	A
85	l5	4273	A
85	l5	4281	A
85	l5	4291	G
85	l5	4304	A
85	l5	4305	G
85	l5	4306	U
85	l5	4312	U
85	l5	4313	A
85	l5	4314	C
85	l5	4319	C
85	l5	4330	G
85	l5	4332	C

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Mol	Chain	Res	Type
85	l5	4339	A
85	l5	4349	C
85	l5	4354	U
85	l5	4373	G
85	l5	4377	G
85	l5	4378	A
85	l5	4380	A
85	l5	4387	C
85	l5	4394	A
85	l5	4421	C
85	l5	4422	A
85	l5	4438	U
85	l5	4448	G
85	l5	4449	A
85	l5	4453	C
85	l5	4464	A
85	l5	4466	C
85	l5	4488	A
85	l5	4500	U
85	l5	4512	U
85	l5	4513	A
85	l5	4518	A
85	l5	4524	G
85	l5	4545	G
85	l5	4548	A
85	l5	4549	G
85	l5	4557	U
85	l5	4560	C
85	l5	4567	G
85	l5	4572	U
85	l5	4573	G
85	l5	4575	G
85	l5	4584	A
85	l5	4589	A
85	l5	4590	A
85	l5	4599	A
85	l5	4600	G
85	l5	4601	U
85	l5	4617	G
85	l5	4636	U
85	l5	4637	G
85	l5	4648	A

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Mol	Chain	Res	Type
85	15	4652	G
85	15	4656	A
85	15	4659	G
85	15	4670	C
85	15	4672	A
85	15	4687	A
85	15	4694	G
85	15	4695	C
85	15	4700	A
85	15	4707	A
85	15	4708	A
85	15	4709	U
85	15	4719	G
85	15	4732	G
85	15	4733	C
85	15	4734	A
85	15	4740	G
85	15	4741	C
85	15	4742	G
85	15	4745	G
85	15	4747	C
85	15	4750	G
85	15	4754	G
85	15	4757	C
85	15	4759	C
85	15	4761	G
85	15	4764	A
85	15	4765	G
85	15	4771	C
85	15	4772	C
85	15	4773	C
85	15	4775	C
85	15	4776	G
85	15	4859	C
85	15	4864	U
85	15	4870	G
85	15	4871	C
85	15	4874	A
85	15	4875	G
85	15	4880	C
85	15	4882	U
85	15	4883	C

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Mol	Chain	Res	Type
85	15	4889	G
85	15	4893	A
85	15	4895	C
85	15	4896	G
85	15	4898	G
85	15	4900	C
85	15	4901	G
85	15	4902	C
85	15	4910	G
85	15	4912	G
85	15	4914	C
85	15	4918	C
85	15	4922	C
85	15	4923	C
85	15	4924	C
85	15	4925	U
85	15	4926	C
85	15	4927	G
85	15	4928	C
85	15	4934	A
85	15	4941	G
85	15	4943	A
85	15	4944	C
85	15	4951	G
85	15	4960	G
85	15	4963	G
85	15	4976	U
85	15	4979	A
85	15	4985	U
85	15	4988	U
85	15	4989	U
85	15	4990	C
85	15	4991	U
85	15	5006	U
85	15	5007	A
85	15	5014	A
85	15	5017	G
85	15	5020	G
85	15	5024	C
85	15	5026	U
85	15	5027	C
85	15	5028	G

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Mol	Chain	Res	Type
85	l5	5029	C
85	l5	5030	U
85	l5	5034	A
85	l5	5041	G
85	l5	5050	C
85	l5	5054	C
85	l5	5055	G
85	l5	5060	A
85	l5	5061	A
85	l5	5069	U
85	L5	2	G
85	L5	5	A
85	L5	13	U
85	L5	17	A
85	L5	25	A
85	L5	26	C
85	L5	30	C
85	L5	39	A
85	L5	42	A
85	L5	48	G
85	L5	59	A
85	L5	64	A
85	L5	65	A
85	L5	73	A
85	L5	74	G
85	L5	84	A
85	L5	91	G
85	L5	104	G
85	L5	109	G
85	L5	110	C
85	L5	119	G
85	L5	120	A
85	L5	132	G
85	L5	133	C
85	L5	134	G
85	L5	135	G
85	L5	144	G
85	L5	152	U
85	L5	159	C
85	L5	164	G
85	L5	165	A
85	L5	170	C

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Mol	Chain	Res	Type
85	L5	182	G
85	L5	183	C
85	L5	184	U
85	L5	185	C
85	L5	188	G
85	L5	189	G
85	L5	197	A
85	L5	200	U
85	L5	209	U
85	L5	216	C
85	L5	217	C
85	L5	218	A
85	L5	220	C
85	L5	233	U
85	L5	234	G
85	L5	235	A
85	L5	237	G
85	L5	250	C
85	L5	255	C
85	L5	256	G
85	L5	261	G
85	L5	264	C
85	L5	265	C
85	L5	266	C
85	L5	267	G
85	L5	275	C
85	L5	276	C
85	L5	280	G
85	L5	297	U
85	L5	306	A
85	L5	315	G
85	L5	316	U
85	L5	340	C
85	L5	350	C
85	L5	357	U
85	L5	363	A
85	L5	373	G
85	L5	385	A
85	L5	387	G
85	L5	388	A
85	L5	396	A
85	L5	399	G

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Mol	Chain	Res	Type
85	L5	407	A
85	L5	409	G
85	L5	410	A
85	L5	412	G
85	L5	413	G
85	L5	431	G
85	L5	432	U
85	L5	440	U
85	L5	449	C
85	L5	450	G
85	L5	452	A
85	L5	453	G
85	L5	454	U
85	L5	456	C
85	L5	457	G
85	L5	465	G
85	L5	467	U
85	L5	468	U
85	L5	480	C
85	L5	485	C
85	L5	486	C
85	L5	489	C
85	L5	493	G
85	L5	494	U
85	L5	497	G
85	L5	498	C
85	L5	499	G
85	L5	500	G
85	L5	501	C
85	L5	502	C
85	L5	503	C
85	L5	504	G
85	L5	505	G
85	L5	509	A
85	L5	510	U
85	L5	511	C
85	L5	512	U
85	L5	513	U
85	L5	514	U
85	L5	517	C
85	L5	518	G
85	L5	643	C

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Mol	Chain	Res	Type
85	L5	644	G
85	L5	646	G
85	L5	654	C
85	L5	655	C
85	L5	656	C
85	L5	657	C
85	L5	659	G
85	L5	663	G
85	L5	666	G
85	L5	667	A
85	L5	668	C
85	L5	669	C
85	L5	672	C
85	L5	673	C
85	L5	685	C
85	L5	686	A
85	L5	687	U
85	L5	696	C
85	L5	697	G
85	L5	703	G
85	L5	704	C
85	L5	706	C
85	L5	708	G
85	L5	730	G
85	L5	731	G
85	L5	733	A
85	L5	738	C
85	L5	739	G
85	L5	742	G
85	L5	744	G
85	L5	750	U
85	L5	753	C
85	L5	754	U
85	L5	759	G
85	L5	904	C
85	L5	905	C
85	L5	906	C
85	L5	911	U
85	L5	912	G
85	L5	913	U
85	L5	914	U
85	L5	915	A

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Mol	Chain	Res	Type
85	L5	917	A
85	L5	918	G
85	L5	923	C
85	L5	924	C
85	L5	926	G
85	L5	932	A
85	L5	933	G
85	L5	935	A
85	L5	936	C
85	L5	941	C
85	L5	944	A
85	L5	945	U
85	L5	959	G
85	L5	960	A
85	L5	961	G
85	L5	962	C
85	L5	965	G
85	L5	966	A
85	L5	967	C
85	L5	969	C
85	L5	970	G
85	L5	982	U
85	L5	985	C
85	L5	989	U
85	L5	990	C
85	L5	992	C
85	L5	993	G
85	L5	995	C
85	L5	1048	G
85	L5	1049	C
85	L5	1050	C
85	L5	1051	G
85	L5	1066	G
85	L5	1070	G
85	L5	1071	C
85	L5	1072	C
85	L5	1075	G
85	L5	1076	C
85	L5	1082	C
85	L5	1083	U
85	L5	1095	A
85	L5	1168	G

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Mol	Chain	Res	Type
85	L5	1169	G
85	L5	1170	G
85	L5	1171	G
85	L5	1172	C
85	L5	1173	G
85	L5	1174	G
85	L5	1179	U
85	L5	1180	C
85	L5	1182	C
85	L5	1183	C
85	L5	1184	A
85	L5	1202	C
85	L5	1203	G
85	L5	1205	G
85	L5	1210	C
85	L5	1211	G
85	L5	1214	C
85	L5	1215	C
85	L5	1216	C
85	L5	1217	G
85	L5	1218	G
85	L5	1219	G
85	L5	1221	G
85	L5	1222	A
85	L5	1235	G
85	L5	1241	C
85	L5	1242	G
85	L5	1246	G
85	L5	1253	G
85	L5	1254	A
85	L5	1257	A
85	L5	1258	G
85	L5	1261	G
85	L5	1266	G
85	L5	1267	C
85	L5	1269	G
85	L5	1270	A
85	L5	1271	G
85	L5	1272	C
85	L5	1273	G
85	L5	1275	G
85	L5	1277	G

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Mol	Chain	Res	Type
85	L5	1280	C
85	L5	1284	G
85	L5	1285	U
85	L5	1293	G
85	L5	1294	A
85	L5	1295	C
85	L5	1296	G
85	L5	1301	C
85	L5	1302	U
85	L5	1314	C
85	L5	1326	A
85	L5	1337	A
85	L5	1344	C
85	L5	1354	A
85	L5	1358	G
85	L5	1359	G
85	L5	1365	C
85	L5	1367	C
85	L5	1381	U
85	L5	1387	A
85	L5	1394	G
85	L5	1397	A
85	L5	1405	C
85	L5	1407	C
85	L5	1408	G
85	L5	1409	C
85	L5	1410	U
85	L5	1411	C
85	L5	1414	C
85	L5	1415	G
85	L5	1417	C
85	L5	1420	A
85	L5	1435	G
85	L5	1437	C
85	L5	1439	C
85	L5	1443	A
85	L5	1444	G
85	L5	1446	C
85	L5	1447	C
85	L5	1453	G
85	L5	1457	G
85	L5	1465	G

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Mol	Chain	Res	Type
85	L5	1482	G
85	L5	1483	C
85	L5	1497	A
85	L5	1498	G
85	L5	1502	G
85	L5	1517	G
85	L5	1518	A
85	L5	1523	A
85	L5	1525	A
85	L5	1534	A
85	L5	1547	A
85	L5	1562	G
85	L5	1564	A
85	L5	1566	C
85	L5	1574	G
85	L5	1578	U
85	L5	1591	U
85	L5	1596	U
85	L5	1624	G
85	L5	1625	G
85	L5	1631	A
85	L5	1633	G
85	L5	1634	A
85	L5	1641	G
85	L5	1649	U
85	L5	1654	G
85	L5	1661	C
85	L5	1676	C
85	L5	1677	U
85	L5	1678	C
85	L5	1681	G
85	L5	1691	G
85	L5	1698	C
85	L5	1699	A
85	L5	1700	G
85	L5	1703	C
85	L5	1704	C
85	L5	1705	G
85	L5	1707	C
85	L5	1718	C
85	L5	1719	A
85	L5	1731	C

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Mol	Chain	Res	Type
85	L5	1741	G
85	L5	1742	A
85	L5	1750	G
85	L5	1753	G
85	L5	1754	U
85	L5	1757	U
85	L5	1758	G
85	L5	1760	G
85	L5	1761	G
85	L5	1762	C
85	L5	1763	C
85	L5	1764	G
85	L5	1765	A
85	L5	1766	A
85	L5	1767	A
85	L5	1768	C
85	L5	1769	G
85	L5	1770	A
85	L5	1775	A
85	L5	1776	A
85	L5	1787	A
85	L5	1804	A
85	L5	1806	G
85	L5	1810	G
85	L5	1820	C
85	L5	1821	G
85	L5	1822	U
85	L5	1831	G
85	L5	1834	U
85	L5	1836	G
85	L5	1837	A
85	L5	1842	G
85	L5	1843	A
85	L5	1855	G
85	L5	1869	G
85	L5	1897	A
85	L5	1917	A
85	L5	1918	U
85	L5	1919	G
85	L5	1920	C
85	L5	1921	C
85	L5	1922	G

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Mol	Chain	Res	Type
85	L5	1925	G
85	L5	1931	C
85	L5	1932	A
85	L5	1938	C
85	L5	1940	G
85	L5	1941	A
85	L5	1948	G
85	L5	1949	U
85	L5	1961	G
85	L5	1962	A
85	L5	1965	G
85	L5	1972	G
85	L5	1974	U
85	L5	1975	G
85	L5	1978	C
85	L5	1980	U
85	L5	1981	G
85	L5	1982	G
85	L5	1983	A
85	L5	1984	A
85	L5	1985	G
85	L5	1986	U
85	L5	1991	A
85	L5	1992	U
85	L5	1993	C
85	L5	1997	U
85	L5	1998	A
85	L5	1999	A
85	L5	2001	G
85	L5	2002	A
85	L5	2003	G
85	L5	2004	U
85	L5	2011	C
85	L5	2017	A
85	L5	2018	C
85	L5	2024	G
85	L5	2026	A
85	L5	2033	A
85	L5	2034	G
85	L5	2046	G
85	L5	2048	U
85	L5	2052	G

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Mol	Chain	Res	Type
85	L5	2055	G
85	L5	2069	A
85	L5	2084	C
85	L5	2085	G
85	L5	2092	G
85	L5	2093	A
85	L5	2095	A
85	L5	2097	U
85	L5	2098	G
85	L5	2099	G
85	L5	2101	C
85	L5	2102	G
85	L5	2103	G
85	L5	2105	A
85	L5	2107	C
85	L5	2108	G
85	L5	2110	C
85	L5	2112	G
85	L5	2250	C
85	L5	2252	G
85	L5	2253	A
85	L5	2255	C
85	L5	2256	C
85	L5	2257	C
85	L5	2258	C
85	L5	2260	C
85	L5	2261	G
85	L5	2289	C
85	L5	2300	A
85	L5	2301	G
85	L5	2313	A
85	L5	2316	G
85	L5	2322	G
85	L5	2331	G
85	L5	2333	G
85	L5	2348	G
85	L5	2351	C
85	L5	2360	A
85	L5	2382	A
85	L5	2395	A
85	L5	2397	G
85	L5	2402	G

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Mol	Chain	Res	Type
85	L5	2411	C
85	L5	2417	A
85	L5	2421	G
85	L5	2425	U
85	L5	2441	C
85	L5	2442	G
85	L5	2450	G
85	L5	2453	A
85	L5	2463	G
85	L5	2464	C
85	L5	2465	C
85	L5	2469	C
85	L5	2474	G
85	L5	2475	G
85	L5	2478	C
85	L5	2479	G
85	L5	2483	G
85	L5	2484	A
85	L5	2485	U
85	L5	2486	G
85	L5	2487	G
85	L5	2488	C
85	L5	2489	C
85	L5	2490	U
85	L5	2491	C
85	L5	2494	U
85	L5	2503	G
85	L5	2504	C
85	L5	2505	C
85	L5	2506	G
85	L5	2511	A
85	L5	2513	A
85	L5	2519	U
85	L5	2520	C
85	L5	2529	A
85	L5	2537	A
85	L5	2544	G
85	L5	2546	G
85	L5	2547	G
85	L5	2554	U
85	L5	2555	G
85	L5	2559	G

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Mol	Chain	Res	Type
85	L5	2560	C
85	L5	2565	A
85	L5	2573	A
85	L5	2583	C
85	L5	2587	A
85	L5	2589	C
85	L5	2601	A
85	L5	2627	C
85	L5	2638	G
85	L5	2652	G
85	L5	2653	C
85	L5	2662	G
85	L5	2669	C
85	L5	2673	G
85	L5	2676	A
85	L5	2686	G
85	L5	2687	U
85	L5	2694	G
85	L5	2695	A
85	L5	2696	A
85	L5	2703	G
85	L5	2707	U
85	L5	2708	U
85	L5	2709	C
85	L5	2710	C
85	L5	2711	G
85	L5	2719	C
85	L5	2721	G
85	L5	2724	G
85	L5	2726	G
85	L5	2729	C
85	L5	2739	C
85	L5	2742	G
85	L5	2743	A
85	L5	2746	A
85	L5	2761	U
85	L5	2763	U
85	L5	2764	A
85	L5	2769	U
85	L5	2770	C
85	L5	2787	A
85	L5	2788	U

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Mol	Chain	Res	Type
85	L5	2789	A
85	L5	2790	U
85	L5	2826	U
85	L5	2827	G
85	L5	2829	U
85	L5	2835	A
85	L5	2846	G
85	L5	2855	G
85	L5	2867	C
85	L5	2877	G
85	L5	2895	A
85	L5	2899	C
85	L5	2900	U
85	L5	2902	G
85	L5	2903	G
85	L5	2904	U
85	L5	2905	C
85	L5	2906	G
85	L5	2907	G
85	L5	2908	U
85	L5	3588	C
85	L5	3590	G
85	L5	3591	C
85	L5	3594	C
85	L5	3595	U
85	L5	3596	A
85	L5	3597	G
85	L5	3605	C
85	L5	3615	G
85	L5	3616	U
85	L5	3626	G
85	L5	3630	A
85	L5	3635	A
85	L5	3644	U
85	L5	3646	A
85	L5	3648	A
85	L5	3652	A
85	L5	3662	A
85	L5	3664	G
85	L5	3673	C
85	L5	3674	G
85	L5	3692	A

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Mol	Chain	Res	Type
85	L5	3698	G
85	L5	3711	A
85	L5	3713	U
85	L5	3714	G
85	L5	3727	A
85	L5	3748	A
85	L5	3750	G
85	L5	3753	G
85	L5	3756	A
85	L5	3757	G
85	L5	3759	A
85	L5	3760	A
85	L5	3761	C
85	L5	3766	A
85	L5	3767	C
85	L5	3772	U
85	L5	3773	U
85	L5	3774	A
85	L5	3776	G
85	L5	3777	G
85	L5	3778	U
85	L5	3784	A
85	L5	3786	U
85	L5	3802	U
85	L5	3811	G
85	L5	3812	C
85	L5	3813	A
85	L5	3814	U
85	L5	3817	A
85	L5	3818	U
85	L5	3819	G
85	L5	3823	G
85	L5	3839	G
85	L5	3840	U
85	L5	3841	C
85	L5	3867	A
85	L5	3869	C
85	L5	3876	A
85	L5	3877	A
85	L5	3878	C
85	L5	3879	G
85	L5	3885	G

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Mol	Chain	Res	Type
85	L5	3887	C
85	L5	3890	A
85	L5	3892	U
85	L5	3897	G
85	L5	3901	A
85	L5	3906	A
85	L5	3907	G
85	L5	3908	A
85	L5	3915	U
85	L5	3938	G
85	L5	3939	G
85	L5	3943	A
85	L5	3944	G
85	L5	3947	A
85	L5	3949	A
85	L5	3953	G
85	L5	3955	G
85	L5	3956	G
85	L5	3957	U
85	L5	3958	G
85	L5	3959	U
85	L5	3960	A
85	L5	3961	G
85	L5	3962	A
85	L5	3963	A
85	L5	3964	U
85	L5	3965	A
85	L5	3966	A
85	L5	3968	U
85	L5	3969	G
85	L5	3973	G
85	L5	3974	G
85	L5	3975	C
85	L5	3977	C
85	L5	4034	G
85	L5	4037	C
85	L5	4038	C
85	L5	4039	G
85	L5	4041	C
85	L5	4042	G
85	L5	4043	G
85	L5	4044	U

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Mol	Chain	Res	Type
85	L5	4046	A
85	L5	4047	A
85	L5	4048	A
85	L5	4049	U
85	L5	4051	C
85	L5	4052	C
85	L5	4053	A
85	L5	4054	C
85	L5	4055	U
85	L5	4057	C
85	L5	4058	U
85	L5	4059	C
85	L5	4060	U
85	L5	4061	G
85	L5	4062	A
85	L5	4063	U
85	L5	4065	G
85	L5	4067	U
85	L5	4068	U
85	L5	4069	U
85	L5	4076	G
85	L5	4092	G
85	L5	4093	G
85	L5	4095	G
85	L5	4097	G
85	L5	4098	A
85	L5	4099	G
85	L5	4100	C
85	L5	4102	C
85	L5	4103	C
85	L5	4104	G
85	L5	4108	G
85	L5	4111	U
85	L5	4114	C
85	L5	4115	G
85	L5	4116	C
85	L5	4119	C
85	L5	4127	A
85	L5	4133	C
85	L5	4134	C
85	L5	4138	C
85	L5	4140	C

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Mol	Chain	Res	Type
85	L5	4141	G
85	L5	4142	C
85	L5	4143	G
85	L5	4144	C
85	L5	4146	G
85	L5	4149	C
85	L5	4160	C
85	L5	4162	C
85	L5	4163	U
85	L5	4164	C
85	L5	4170	A
85	L5	4183	G
85	L5	4184	G
85	L5	4191	G
85	L5	4196	G
85	L5	4203	A
85	L5	4213	A
85	L5	4222	G
85	L5	4225	G
85	L5	4229	U
85	L5	4233	A
85	L5	4234	A
85	L5	4241	C
85	L5	4251	A
85	L5	4254	G
85	L5	4255	A
85	L5	4257	A
85	L5	4258	C
85	L5	4265	U
85	L5	4268	A
85	L5	4273	A
85	L5	4279	A
85	L5	4281	A
85	L5	4286	C
85	L5	4291	G
85	L5	4304	A
85	L5	4305	G
85	L5	4306	U
85	L5	4313	A
85	L5	4314	C
85	L5	4330	G
85	L5	4332	C

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Mol	Chain	Res	Type
85	L5	4339	A
85	L5	4349	C
85	L5	4354	U
85	L5	4373	G
85	L5	4377	G
85	L5	4378	A
85	L5	4380	A
85	L5	4387	C
85	L5	4391	G
85	L5	4393	G
85	L5	4394	A
85	L5	4421	C
85	L5	4422	A
85	L5	4426	C
85	L5	4438	U
85	L5	4444	C
85	L5	4448	G
85	L5	4449	A
85	L5	4453	C
85	L5	4464	A
85	L5	4466	C
85	L5	4488	A
85	L5	4500	U
85	L5	4512	U
85	L5	4513	A
85	L5	4518	A
85	L5	4519	C
85	L5	4522	G
85	L5	4524	G
85	L5	4545	G
85	L5	4548	A
85	L5	4549	G
85	L5	4557	U
85	L5	4560	C
85	L5	4567	G
85	L5	4570	G
85	L5	4573	G
85	L5	4575	G
85	L5	4581	G
85	L5	4584	A
85	L5	4589	A
85	L5	4590	A

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Mol	Chain	Res	Type
85	L5	4594	U
85	L5	4600	G
85	L5	4601	U
85	L5	4608	G
85	L5	4617	G
85	L5	4635	A
85	L5	4636	U
85	L5	4637	G
85	L5	4648	A
85	L5	4652	G
85	L5	4656	A
85	L5	4670	C
85	L5	4672	A
85	L5	4687	A
85	L5	4694	G
85	L5	4695	C
85	L5	4700	A
85	L5	4708	A
85	L5	4709	U
85	L5	4719	G
85	L5	4734	A
85	L5	4740	G
85	L5	4741	C
85	L5	4742	G
85	L5	4745	G
85	L5	4747	C
85	L5	4750	G
85	L5	4754	G
85	L5	4757	C
85	L5	4759	C
85	L5	4761	G
85	L5	4765	G
85	L5	4771	C
85	L5	4772	C
85	L5	4775	C
85	L5	4859	C
85	L5	4862	G
85	L5	4870	G
85	L5	4871	C
85	L5	4875	G
85	L5	4880	C
85	L5	4882	U

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Mol	Chain	Res	Type
85	L5	4883	C
85	L5	4886	C
85	L5	4889	G
85	L5	4895	C
85	L5	4896	G
85	L5	4897	G
85	L5	4900	C
85	L5	4901	G
85	L5	4902	C
85	L5	4910	G
85	L5	4912	G
85	L5	4914	C
85	L5	4918	C
85	L5	4922	C
85	L5	4923	C
85	L5	4924	C
85	L5	4925	U
85	L5	4926	C
85	L5	4927	G
85	L5	4928	C
85	L5	4934	A
85	L5	4937	C
85	L5	4940	C
85	L5	4941	G
85	L5	4943	A
85	L5	4951	G
85	L5	4960	G
85	L5	4976	U
85	L5	4979	A
85	L5	4988	U
85	L5	4989	U
85	L5	4990	C
85	L5	4991	U
85	L5	4995	U
85	L5	5006	U
85	L5	5009	G
85	L5	5013	C
85	L5	5014	A
85	L5	5017	G
85	L5	5022	U
85	L5	5024	C
85	L5	5027	C

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Mol	Chain	Res	Type
85	L5	5028	G
85	L5	5030	U
85	L5	5034	A
85	L5	5041	G
85	L5	5048	A
85	L5	5050	C
85	L5	5054	C
85	L5	5055	G
85	L5	5061	A
85	L5	5069	U
20	L7	5	A
20	L7	7	G
20	L7	22	A
20	L7	24	C
20	L7	33	U
20	L7	38	U
20	L7	53	U
20	L7	54	A
20	L7	63	C
20	L7	64	G
20	L7	100	A
20	L7	110	G
21	L8	2	G
21	L8	34	U
21	L8	35	C
21	L8	39	G
21	L8	47	C
21	L8	48	A
21	L8	49	G
21	L8	59	A
21	L8	62	A
21	L8	63	U
21	L8	68	G
21	L8	70	G
21	L8	80	A
21	L8	82	A
21	L8	84	A
21	L8	85	U
21	L8	86	U
21	L8	87	G
21	L8	94	G
21	L8	103	A

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Mol	Chain	Res	Type
21	L8	105	C
21	L8	110	U
21	L8	111	U
21	L8	112	G
21	L8	114	G
21	L8	123	U
21	L8	124	U
21	L8	125	C
21	L8	126	C
21	L8	127	U
21	L8	150	C
21	L8	151	G
79	S2	13	C
79	S2	25	A
79	S2	33	G
79	S2	37	C
79	S2	41	G
79	S2	42	A
79	S2	44	U
79	S2	45	A
79	S2	46	A
79	S2	56	G
79	S2	58	C
79	S2	62	G
79	S2	64	A
79	S2	67	C
79	S2	68	A
79	S2	72	C
79	S2	73	C
79	S2	74	G
79	S2	76	U
79	S2	83	A
79	S2	92	A
79	S2	103	A
79	S2	113	G
79	S2	115	U
79	S2	116	U
79	S2	126	G
79	S2	130	G
79	S2	139	C
79	S2	142	C
79	S2	143	U

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Mol	Chain	Res	Type
79	S2	144	U
79	S2	147	A
79	S2	149	A
79	S2	158	A
79	S2	160	U
79	S2	162	C
79	S2	168	C
79	S2	170	A
79	S2	171	A
79	S2	175	A
79	S2	179	C
79	S2	182	C
79	S2	184	G
79	S2	190	G
79	S2	196	C
79	S2	197	U
79	S2	198	U
79	S2	200	G
79	S2	202	G
79	S2	203	G
79	S2	204	G
79	S2	206	G
79	S2	207	G
79	S2	208	G
79	S2	214	U
79	S2	291	G
79	S2	292	A
79	S2	295	C
79	S2	301	A
79	S2	305	U
79	S2	306	C
79	S2	307	G
79	S2	308	G
79	S2	309	G
79	S2	310	C
79	S2	311	C
79	S2	312	G
79	S2	318	A
79	S2	319	C
79	S2	322	C
79	S2	323	C
79	S2	324	C

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Mol	Chain	Res	Type
79	S2	325	C
79	S2	326	C
79	S2	328	U
79	S2	329	G
79	S2	332	G
79	S2	338	G
79	S2	339	A
79	S2	340	C
79	S2	347	G
79	S2	351	G
79	S2	360	A
79	S2	362	C
79	S2	364	A
79	S2	368	U
79	S2	369	C
79	S2	370	G
79	S2	372	U
79	S2	383	G
79	S2	385	G
79	S2	386	C
79	S2	407	G
79	S2	408	A
79	S2	409	C
79	S2	421	G
79	S2	426	A
79	S2	438	G
79	S2	448	A
79	S2	449	A
79	S2	450	C
79	S2	452	G
79	S2	464	A
79	S2	465	A
79	S2	471	G
79	S2	472	C
79	S2	473	A
79	S2	474	G
79	S2	476	A
79	S2	482	G
79	S2	485	A
79	S2	487	U
79	S2	488	U
79	S2	492	C

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Mol	Chain	Res	Type
79	S2	493	A
79	S2	502	C
79	S2	516	A
79	S2	530	U
79	S2	531	A
79	S2	532	C
79	S2	536	A
79	S2	537	C
79	S2	540	U
79	S2	542	U
79	S2	544	G
79	S2	546	G
79	S2	547	G
79	S2	557	U
79	S2	558	G
79	S2	560	A
79	S2	563	G
79	S2	564	A
79	S2	576	A
79	S2	583	A
79	S2	587	A
79	S2	589	G
79	S2	591	U
79	S2	593	C
79	S2	594	A
79	S2	603	C
79	S2	604	A
79	S2	607	U
79	S2	614	C
79	S2	617	G
79	S2	623	G
79	S2	628	A
79	S2	631	U
79	S2	643	A
79	S2	644	G
79	S2	660	C
79	S2	664	A
79	S2	668	A
79	S2	669	A
79	S2	671	A
79	S2	672	A
79	S2	673	G

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Mol	Chain	Res	Type
79	S2	688	U
79	S2	689	U
79	S2	692	G
79	S2	693	A
79	S2	695	C
79	S2	696	G
79	S2	697	G
79	S2	698	G
79	S2	732	U
79	S2	733	C
79	S2	734	C
79	S2	736	C
79	S2	738	C
79	S2	749	U
79	S2	751	G
79	S2	752	G
79	S2	753	C
79	S2	788	G
79	S2	791	C
79	S2	792	C
79	S2	798	G
79	S2	799	U
79	S2	801	U
79	S2	821	G
79	S2	822	U
79	S2	823	U
79	S2	824	C
79	S2	827	A
79	S2	830	A
79	S2	833	C
79	S2	834	C
79	S2	835	C
79	S2	836	G
79	S2	837	A
79	S2	838	G
79	S2	839	C
79	S2	844	U
79	S2	847	A
79	S2	869	A
79	S2	870	A
79	S2	873	G
79	S2	874	G

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Mol	Chain	Res	Type
79	S2	878	G
79	S2	880	G
79	S2	882	U
79	S2	888	U
79	S2	889	U
79	S2	891	G
79	S2	893	U
79	S2	896	U
79	S2	897	U
79	S2	898	U
79	S2	899	U
79	S2	900	C
79	S2	901	G
79	S2	903	A
79	S2	907	G
79	S2	908	A
79	S2	909	G
79	S2	913	A
79	S2	919	A
79	S2	920	A
79	S2	933	G
79	S2	934	G
79	S2	954	U
79	S2	963	A
79	S2	970	G
79	S2	971	G
79	S2	972	A
79	S2	978	G
79	S2	990	A
79	S2	992	A
79	S2	999	G
79	S2	1001	A
79	S2	1002	U
79	S2	1008	A
79	S2	1017	U
79	S2	1023	A
79	S2	1027	A
79	S2	1033	G
79	S2	1045	U
79	S2	1060	A
79	S2	1061	U
79	S2	1062	A

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Mol	Chain	Res	Type
79	S2	1083	A
79	S2	1085	C
79	S2	1088	U
79	S2	1099	G
79	S2	1108	G
79	S2	1109	C
79	S2	1110	G
79	S2	1113	A
79	S2	1114	U
79	S2	1115	U
79	S2	1116	C
79	S2	1121	G
79	S2	1133	A
79	S2	1138	C
79	S2	1148	A
79	S2	1150	A
79	S2	1153	C
79	S2	1154	U
79	S2	1161	U
79	S2	1195	A
79	S2	1207	G
79	S2	1208	A
79	S2	1215	C
79	S2	1216	C
79	S2	1217	A
79	S2	1220	A
79	S2	1224	G
79	S2	1227	G
79	S2	1237	C
79	S2	1240	A
79	S2	1242	U
79	S2	1243	U
79	S2	1251	A
79	S2	1253	A
79	S2	1256	G
79	S2	1257	G
79	S2	1259	A
79	S2	1264	C
79	S2	1274	G
79	S2	1275	G
79	S2	1282	A
79	S2	1283	C

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Mol	Chain	Res	Type
79	S2	1284	A
79	S2	1286	G
79	S2	1287	A
79	S2	1294	G
79	S2	1295	A
79	S2	1301	A
79	S2	1302	G
79	S2	1303	C
79	S2	1304	U
79	S2	1306	U
79	S2	1308	U
79	S2	1320	G
79	S2	1333	U
79	S2	1342	U
79	S2	1354	G
79	S2	1355	C
79	S2	1356	G
79	S2	1358	U
79	S2	1371	U
79	S2	1372	U
79	S2	1376	A
79	S2	1378	A
79	S2	1396	A
79	S2	1401	A
79	S2	1402	A
79	S2	1406	G
79	S2	1408	U
79	S2	1411	G
79	S2	1413	G
79	S2	1415	C
79	S2	1417	C
79	S2	1419	C
79	S2	1420	G
79	S2	1421	A
79	S2	1422	G
79	S2	1423	C
79	S2	1424	G
79	S2	1429	G
79	S2	1434	C
79	S2	1435	C
79	S2	1436	C
79	S2	1437	C

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Mol	Chain	Res	Type
79	S2	1438	A
79	S2	1442	U
79	S2	1449	G
79	S2	1454	A
79	S2	1463	U
79	S2	1468	C
79	S2	1480	A
79	S2	1489	A
79	S2	1490	G
79	S2	1494	U
79	S2	1495	G
79	S2	1497	G
79	S2	1498	A
79	S2	1507	G
79	S2	1508	A
79	S2	1520	G
79	S2	1521	C
79	S2	1522	A
79	S2	1531	A
79	S2	1533	A
79	S2	1535	U
79	S2	1537	A
79	S2	1544	C
79	S2	1552	G
79	S2	1553	C
79	S2	1556	A
79	S2	1570	G
79	S2	1574	C
79	S2	1575	G
79	S2	1579	A
79	S2	1580	A
79	S2	1581	C
79	S2	1582	C
79	S2	1584	G
79	S2	1585	U
79	S2	1586	U
79	S2	1587	G
79	S2	1588	A
79	S2	1599	U
79	S2	1600	G
79	S2	1601	A
79	S2	1604	G

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Mol	Chain	Res	Type
79	S2	1606	G
79	S2	1621	U
79	S2	1623	A
79	S2	1629	C
79	S2	1630	A
79	S2	1633	A
79	S2	1634	A
79	S2	1637	A
79	S2	1638	G
79	S2	1639	G
79	S2	1640	A
79	S2	1646	C
79	S2	1648	G
79	S2	1654	G
79	S2	1663	A
79	S2	1665	G
79	S2	1683	C
79	S2	1686	G
79	S2	1693	G
79	S2	1696	C
79	S2	1698	C
79	S2	1699	A
79	S2	1715	A
79	S2	1721	U
79	S2	1722	G
79	S2	1729	U
79	S2	1742	C
79	S2	1743	G
79	S2	1744	G
79	S2	1745	A
79	S2	1748	G
79	S2	1752	C
79	S2	1753	C
79	S2	1754	G
79	S2	1755	C
79	S2	1757	G
79	S2	1758	G
79	S2	1759	G
79	S2	1761	U
79	S2	1772	C
79	S2	1773	C
79	S2	1774	C

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Mol	Chain	Res	Type
79	S2	1777	G
79	S2	1782	G
79	S2	1783	C
79	S2	1784	G
79	S2	1787	G
79	S2	1809	A
79	S2	1810	U
79	S2	1812	U
79	S2	1813	A
79	S2	1822	A
79	S2	1823	A
79	S2	1824	A
79	S2	1825	A
79	S2	1826	G
79	S2	1835	A
79	S2	1838	U
79	S2	1849	G
79	S2	1851	A
79	S2	1852	C
79	S2	1861	G
79	S2	1862	G
79	S2	1863	A
79	S2	1864	U
79	S2	1865	C
87	AT	8	U
87	AT	9	A
87	AT	12	G
87	AT	14	A
87	AT	16	C
87	AT	19	G
87	AT	20	U
87	AT	21	U
87	AT	22	A
87	AT	27	G
87	AT	31	G
87	AT	33	C
87	AT	37	C
87	AT	44	A
87	AT	47	G
87	AT	49	C
87	AT	50	C
87	AT	59	A

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Mol	Chain	Res	Type
87	AT	60	A
87	AT	62	C
87	AT	72	A
87	AT	74	A
87	AT	76	C
87	AT	77	A
82	Et	4	C
82	Et	6	G
82	Et	9	A
82	Et	10	G
82	Et	11	C
82	Et	19	G
82	Et	20	U
82	Et	21	A
82	Et	26	A
82	Et	31	A
82	Et	34	U
82	Et	35	U
82	Et	38	A
82	Et	40	C
82	Et	42	G
82	Et	46	G
82	Et	47	U
82	Et	48	C
82	Et	49	C
82	Et	50	A
82	Et	55	U
82	Et	58	A
82	Et	59	G
82	Et	61	C
82	Et	66	U
82	Et	69	G
82	Et	70	G
82	Et	72	C
82	Et	73	G
82	Et	76	A
89	Pt	9	A
89	Pt	19	G
89	Pt	20(A)	U
89	Pt	21	A
89	Pt	46	G
89	Pt	47	U

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Mol	Chain	Res	Type
89	Pt	48	C
89	Pt	49	C
89	Pt	58	A
89	Pt	64	G
89	Pt	65	G
89	Pt	67	G
89	Pt	70	A
89	Pt	71	A
89	Pt	74	C
89	Pt	76	A

All (36) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
85	L5	265	C
85	L5	406	C
85	L5	493	G
85	L5	912	G
85	L5	914	U
85	L5	1082	C
85	L5	1590	C
85	L5	1633	G
85	L5	1977	C
85	L5	2003	G
85	L5	2033	A
85	L5	2055	G
85	L5	2416	G
85	L5	2485	U
85	L5	2675	G
85	L5	2760	G
85	L5	2786	C
85	L5	3614	G
85	L5	3673	C
85	L5	3948	C
85	L5	4055	U
85	L5	4061	G
85	L5	4600	G
85	L5	4699	U
85	L5	4913	G
79	S2	291	G
79	S2	420	G
79	S2	531	A

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Mol	Chain	Res	Type
79	S2	563	G
79	S2	688	U
79	S2	1355	C
79	S2	1434	C
79	S2	1455	A
79	S2	1521	C
79	S2	1693	G
79	S2	1781	A

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
88	SEP	CF	163	88	8,9,10	1.62	1 (12%)	7,12,14	1.38	1 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
88	SEP	CF	163	88	-	6/6/8/10	-

All (1) bond length outliers are listed below:

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

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
88	CF	163	SEP	OG-CB-CA	2.97	111.04	108.14

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
88	CF	163	SEP	N-CA-CB-OG
88	CF	163	SEP	C-CA-CB-OG
88	CF	163	SEP	CA-CB-OG-P
88	CF	163	SEP	CB-OG-P-O1P
88	CF	163	SEP	CB-OG-P-O2P
88	CF	163	SEP	CB-OG-P-O3P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
85	L5	12
85	l5	11
79	s2	7
79	S2	6
80	cB	1
81	aP	1
84	lt	1
89	Pt	1
84	Lt	1
82	pE	1
82	Et	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	S2	753:C	O3'	785:C	P	27.56
1	s2	753:C	O3'	785:C	P	27.07
1	L5	2910:G	O3'	3584:C	P	21.08
1	l5	2910:G	O3'	3584:C	P	20.88
1	l5	760:G	O3'	903:C	P	17.26
1	S2	698:G	O3'	730:C	P	16.92
1	l5	519:C	O3'	642:G	P	16.43
1	l5	4776:G	O3'	4858:C	P	16.16
1	cB	236:PHE	C	247:ALA	N	16.10
1	L5	760:G	O3'	903:C	P	16.08
1	L5	4776:G	O3'	4858:C	P	15.76
1	s2	698:G	O3'	730:C	P	15.53
1	L5	519:C	O3'	642:G	P	15.38
1	l5	996:G	O3'	1047:C	P	14.20
1	l5	2112:G	O3'	2249:C	P	13.86
1	L5	996:G	O3'	1047:C	P	13.44
1	s2	739:C	O3'	746:C	P	13.34
1	L5	2112:G	O3'	2249:C	P	13.25
1	S2	739:C	O3'	746:C	P	13.07
1	aP	15:G	O3'	18:G	P	12.63
1	l5	3985:C	O3'	4018:G	P	11.79
1	l5	1222:A	O3'	1234:G	P	11.12
1	L5	1222:A	O3'	1234:G	P	10.06
1	L5	1051:G	O3'	1064:G	P	9.75
1	s2	553:U	O3'	554:A	P	8.96
1	l5	1051:G	O3'	1064:G	P	8.90
1	lt	87:GLU	C	104:ILE	N	8.72
1	Pt	15:G	O3'	18:G	P	8.55
1	s2	530:U	O3'	531:A	P	8.41

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	S2	225:G	O3'	287:U	P	8.27
1	Lt	87:GLU	C	104:ILE	N	7.74
1	s2	225:G	O3'	287:U	P	7.39
1	L5	1100:U	O3'	1167:C	P	7.12
1	L5	1709:C	O3'	1714:C	P	6.48
1	l5	1100:U	O3'	1167:C	P	6.30
1	pE	16:C	O3'	18:U	P	6.16
1	l5	1709:C	O3'	1714:C	P	5.54
1	S2	1693:G	O3'	1694:U	P	5.33
1	Et	16:C	O3'	18:U	P	5.07
1	L5	3949:A	O3'	3950:U	P	4.90
1	L5	3985:C	O3'	4018:G	P	4.04
1	s2	1210:G	O3'	1211:G	P	3.45
1	S2	1210:G	O3'	1211:G	P	3.19

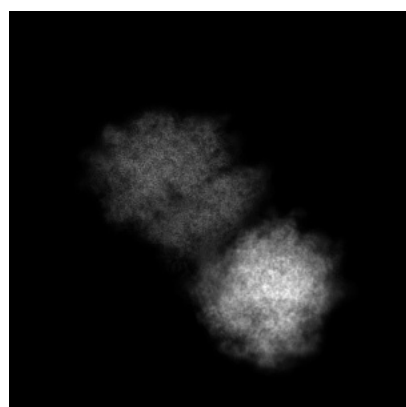
6 Map visualisation [i](#)

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

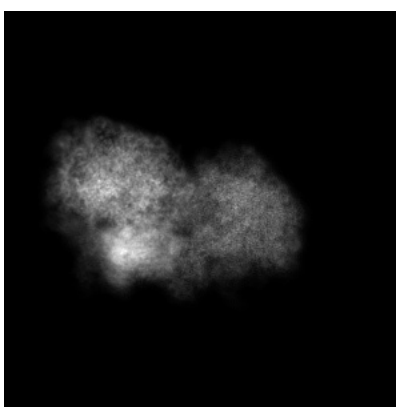
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

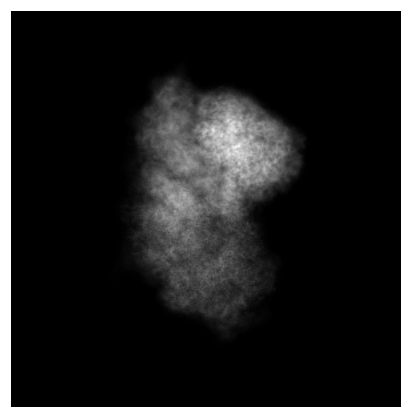
6.1.1 Primary map



X



Y

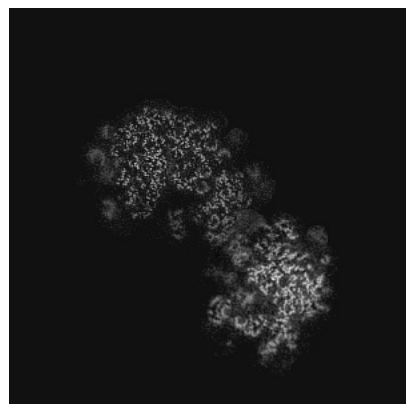


Z

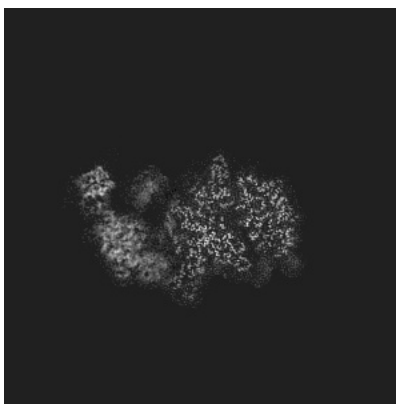
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

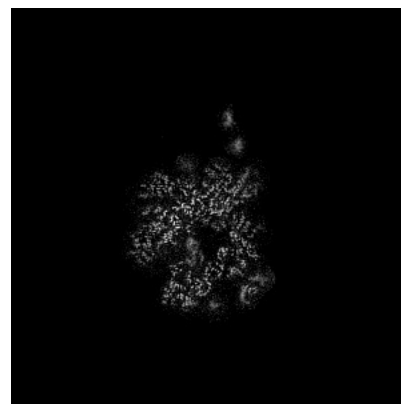
6.2.1 Primary map



X Index: 300



Y Index: 300

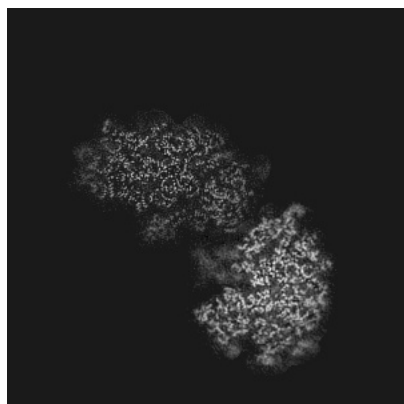


Z Index: 300

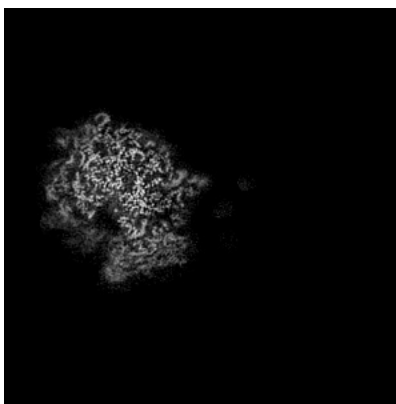
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

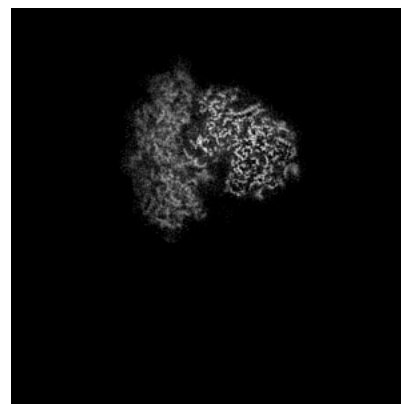
6.3.1 Primary map



X Index: 326



Y Index: 395

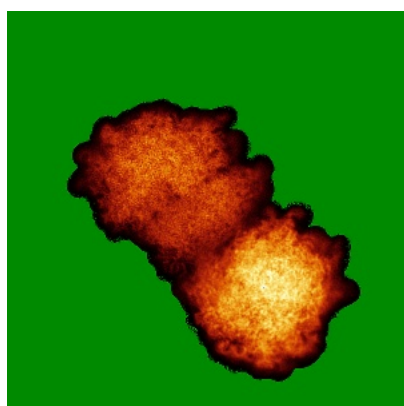


Z Index: 176

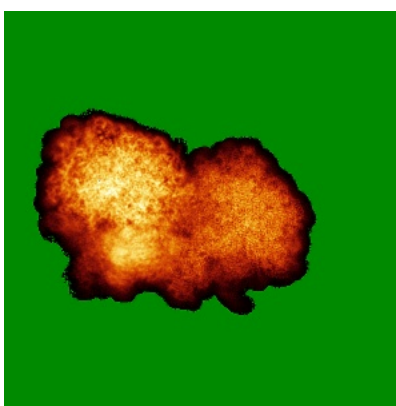
The images above show the largest variance slices of the map in three orthogonal directions.

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

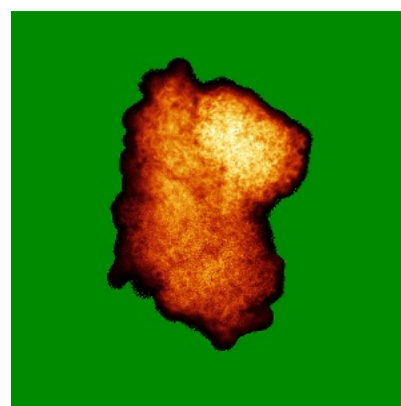
6.4.1 Primary map



X



Y

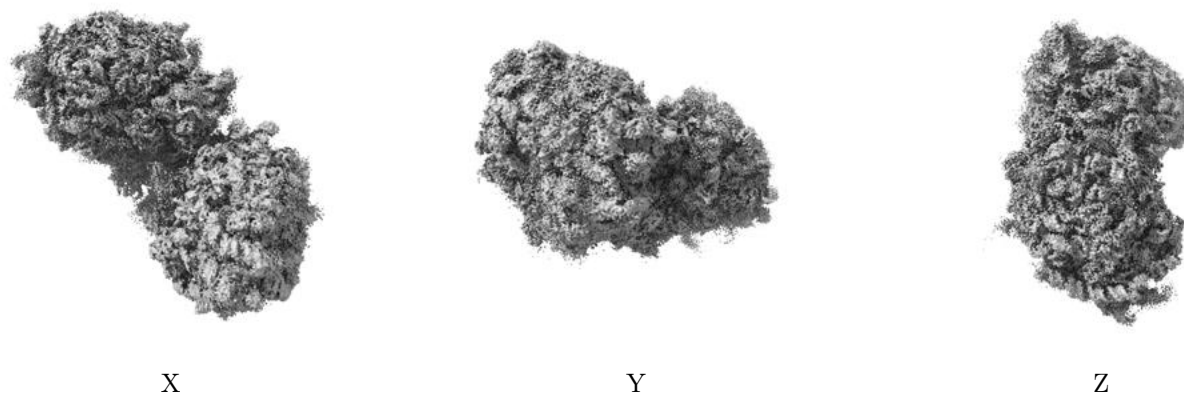


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

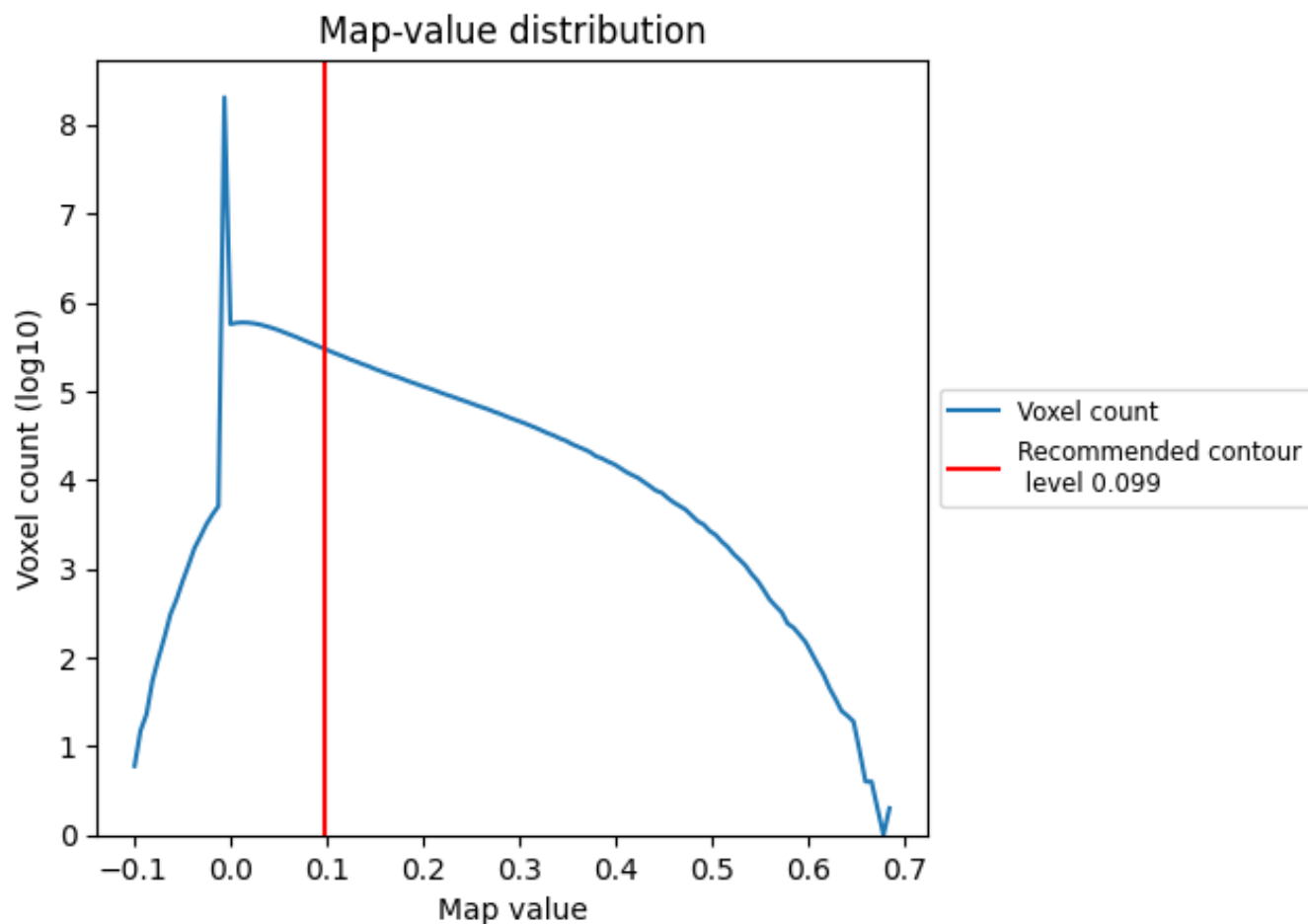
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

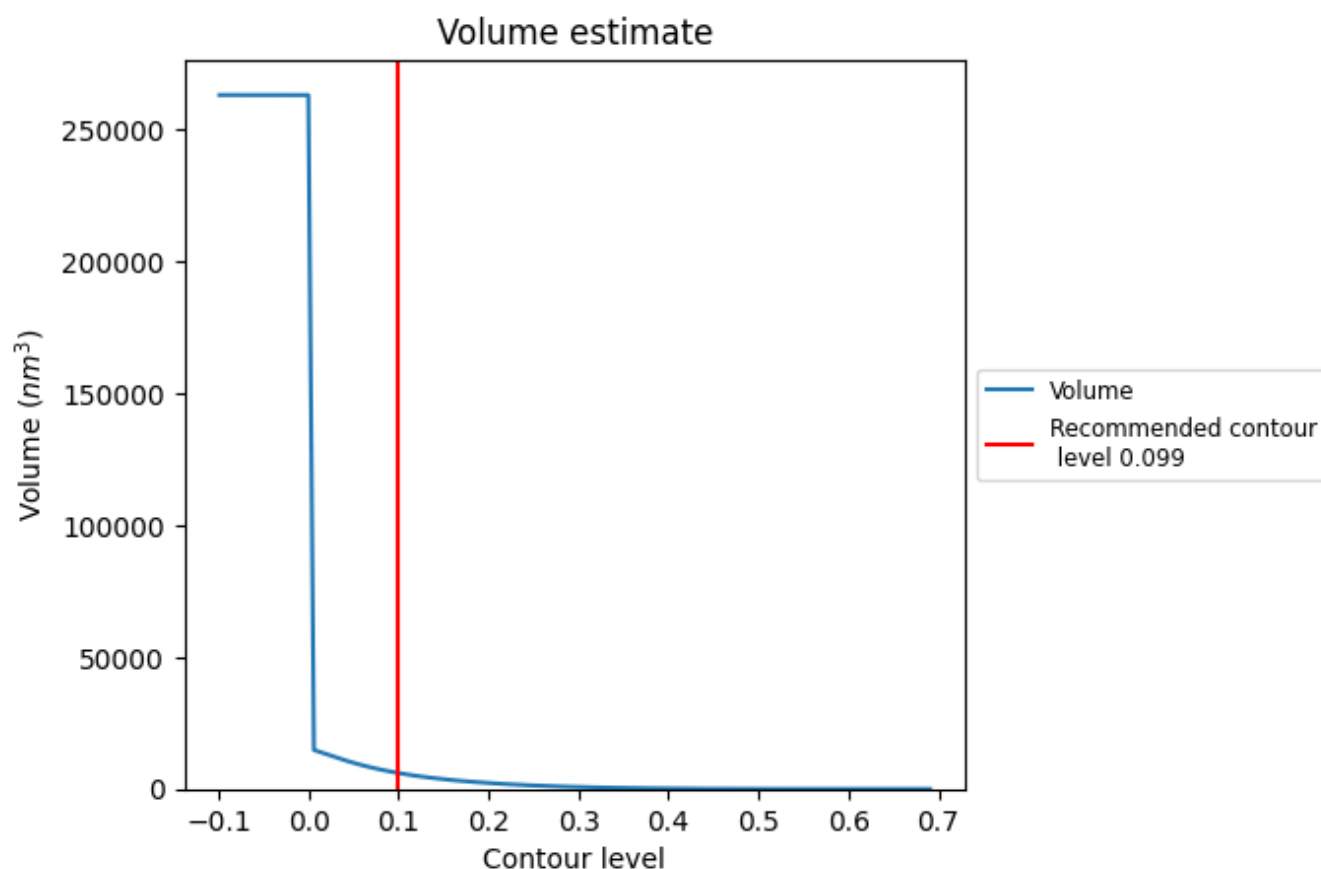
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

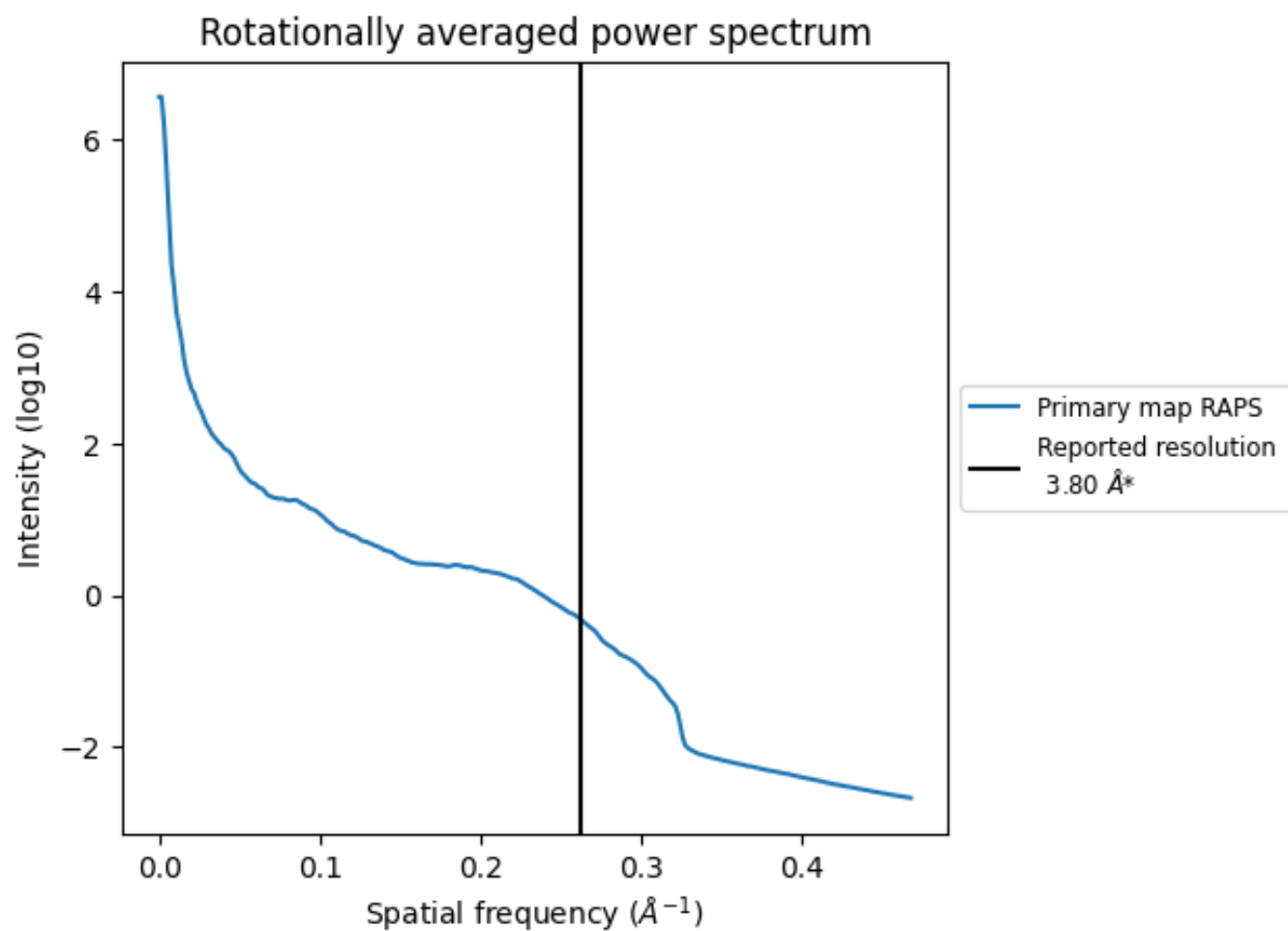
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6084 nm^3 ; this corresponds to an approximate mass of 5496 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

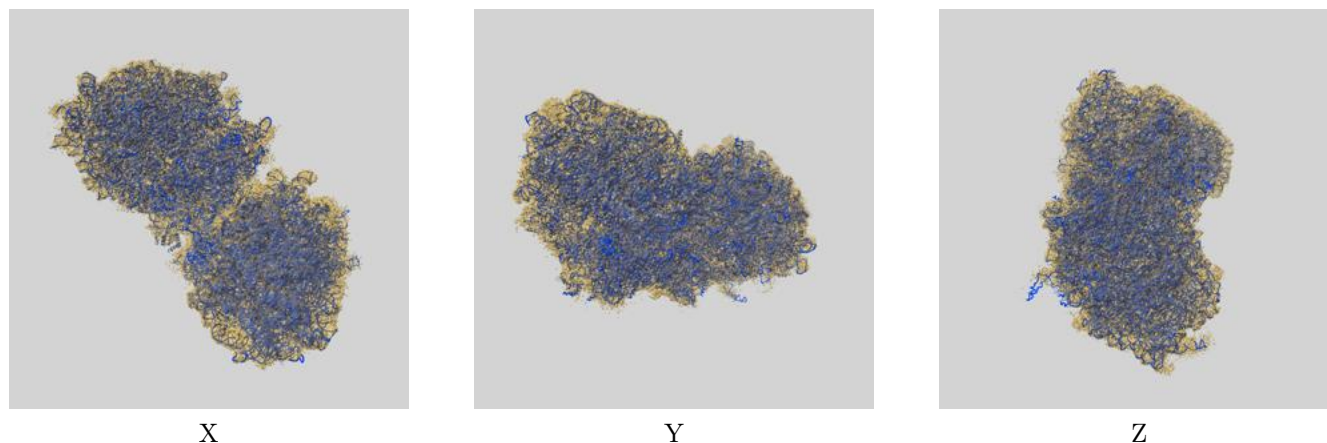
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

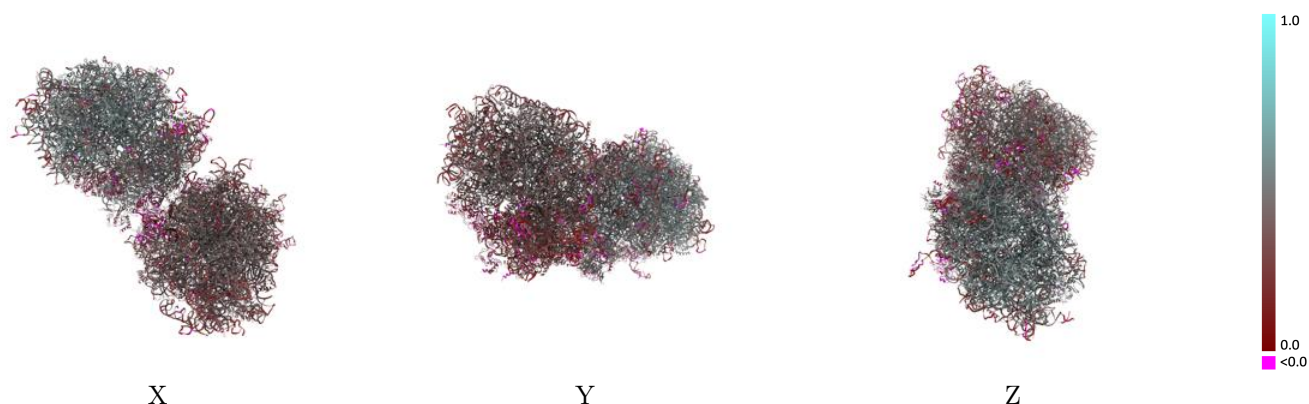
This section contains information regarding the fit between EMDB map EMD-44052 and PDB model 9B0S. Per-residue inclusion information can be found in [section 3](#) on [page 29](#).

9.1 Map-model overlay [i](#)



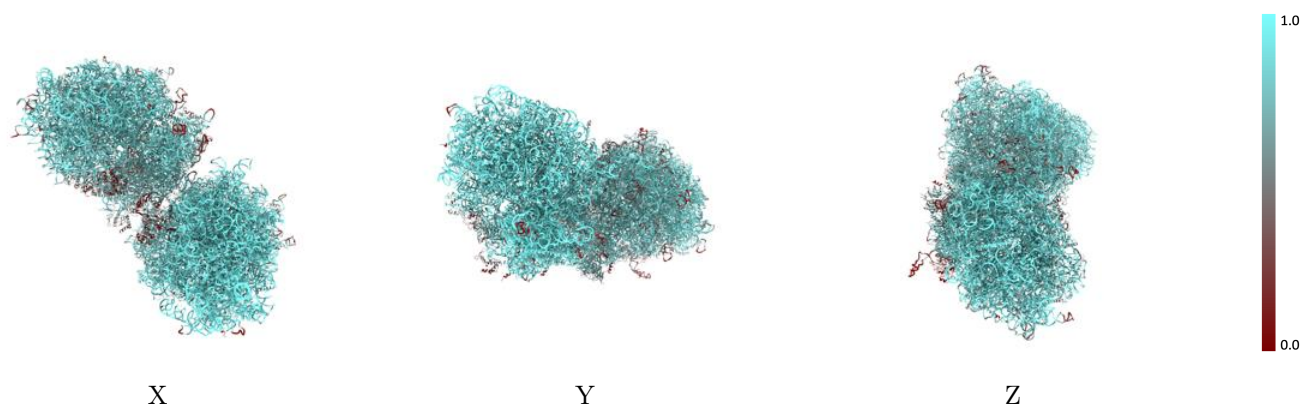
The images above show the 3D surface view of the map at the recommended contour level 0.099 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



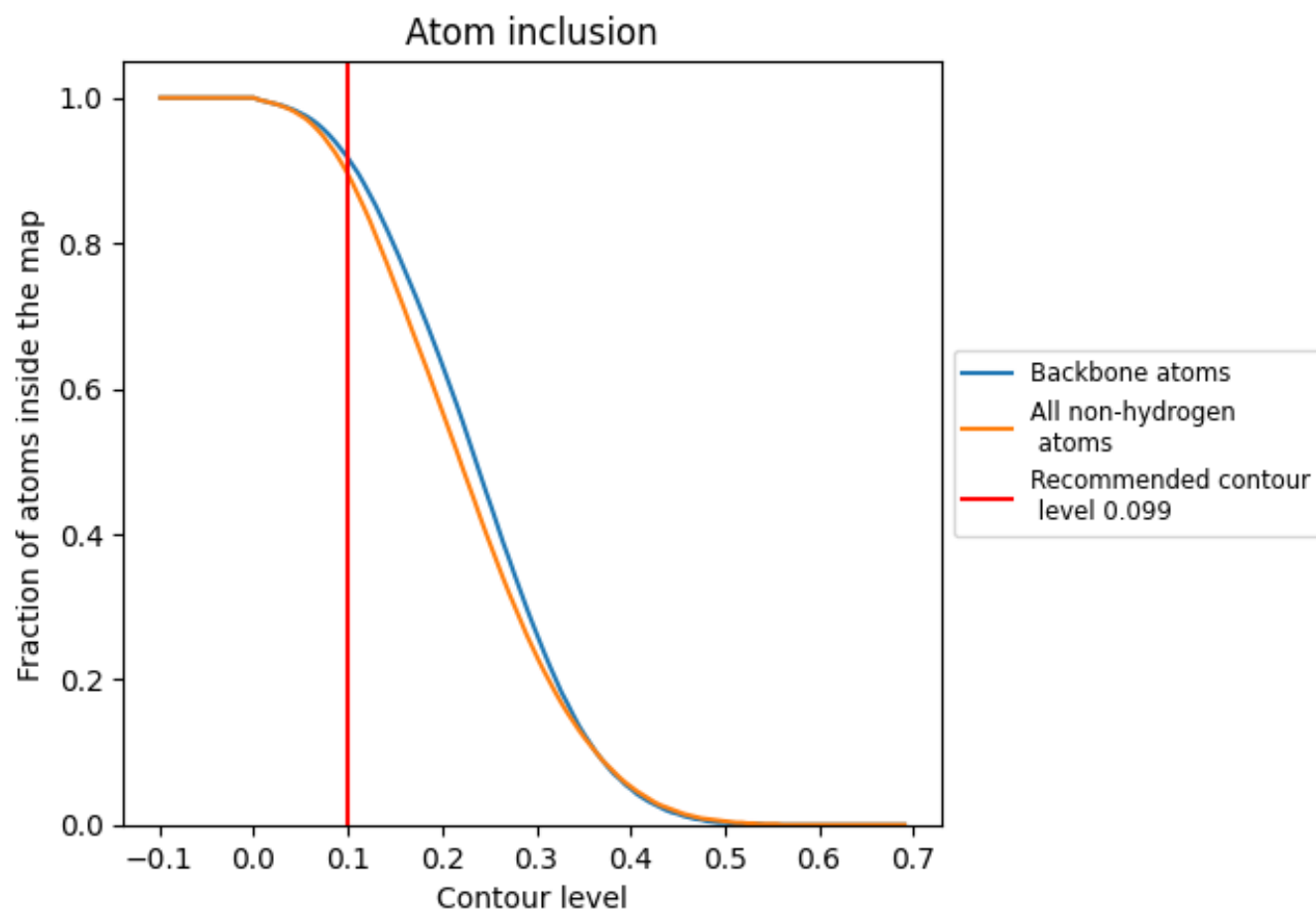
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.099).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.099) and Q-score for the entire model and for each chain.

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























































































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





















































































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























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

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