

Supplementary material

Title: The RNA A-helix architects the evolution of the ribosome

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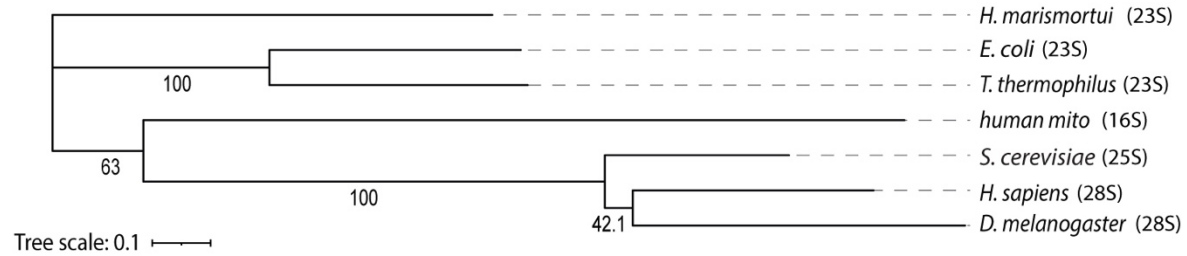


Figure S1. The LSU rRNA phylogenetic tree.

The phylogenetic tree was built using intact LSU rRNA sequences from seven species under the multiple sequence alignment (MSA) approach. The MSA was performed using the Clustal Omega algorithm ¹, implemented as a sequence analysis tool within the EMBL-EBI Job Dispatcher ² framework. The numbers at the nodes represent bootstrap values, which provide a measure of confidence for each grouping. Higher bootstrap values indicate stronger support for that branch ³.

Table S1. The LSU ribosome data were employed in the present study.

Species	PDB ID	Data methodology	Data resolution (Å)
<i>Escherichia coli</i>	4V9D ⁴	X-ray Diffraction	3.00
<i>Thermus thermophilus</i>	4V51 ⁵	X-ray Diffraction	2.80
<i>Haloarcula marismortui</i>	1JJ2 ⁶	X-ray Diffraction	2.40
<i>Saccharomyces cerevisiae</i>	4V88 ⁷	X-ray Diffraction	3.00
<i>Drosophila melanogaster</i>	4V6W ⁸	Cryogenic electron microscopy	6.00
Homo sapiens	4V6X ⁸	Cryogenic electron microscopy	5.00
Human mitochondria	7L20 ⁹	Cryogenic electron microscopy	3.15

Table S2. The LSU A-helices in bin.

<i>E. coli</i> (23S)						
Helix	Sequence	State	Composite Sequence	Bin no.	D _{COM}	D _{COM: H-LSU} ¹
74	CCCGUGAUCCGGG	A-core	CCCGUGAUCCGGG CCCGGUACCGGA CCUUAAGGUGGUG AAAGGCCCCGUGA GGUGUUUAUUAAA AACAGAACGUCGU GAGACAGUUCCCG ACUAAUGUUGAAA AAUUAGCGGACCU UUUGUAUAAUGGG UCAGCGCUGACGA CUGGGGCGGUCAU AAGUAACGUGAAA UUCCGGGGGAACU GAAACAUCUAAGU ACCCCGAG	1	13.38	0.00
32	CCCGGUACCGGG			2	21.63	8.25
70	ACCUUAAGGU			2	22.01	8.63
35a	GGUGAAAGGCC			2	22.48	9.10
23	CCGUGAGG			2	25.92	12.54
65	UGUUUAUUAAAAACA			2	26.99	13.60
93	GAACGUCGUGAGACAG UUC			3	27.91	14.53
35	CCGACUAAUGUUGAAA AAUUAGCGG			3	28.58	15.20
25a	ACCUUUUGUAUAAUGG			3	29.23	15.85
26	GUCAGCGCUGAC			3	30.14	16.76
80	GACUGGGGCGGUC			3	31.86	18.48
26a	AUAAGUAACGUGAAA U			3	33.35	19.96
11	CCGGGGGAACUGAAACA UCUAAGUACCCCGAG			3	34.01	20.63
33	CUAGCCAUGGGCGACUU GUGGCUGGG			4	34.72	21.34
37	GCUAUUUAGGUAGC			4	35.99	22.61
90	CGGCUCAUCACGUGGUA CGCGAGCUGG			4	36.29	22.91
73	CCCGCGGCAAGACGGCC UAUCUGCCGUGGG			4	38.51	25.13
75	ACUAUAGCUUGACAUG UCUGGUGGGUAGU			4	41.20	27.82
72	GCUGUGAAGAUGCAGU G			5	42.19	28.81
64	CUGGCUGCAUGAUGGCC AG			5	43.80	30.42
66	GCACUGUGCAAACACGA AAGUGGACGUUAACGG UGU			5	45.01	31.63
39	CACGGCGGGUGCUAACG UCCGUCGUG			5	46.05	32.67
92	AUGGCUGUUCGCCAU			5	46.31	32.93
52	CCUAAGGCGAGGCCGAA AGGCGUAGUCGAUGG			5	47.18	33.80
61	CUCGGGUGAAGGAAUG UCUCCACCCGAG			5	47.28	33.90
3	CCGG			5	48.31	34.93
36	CUCCCCGGGGAG	A- mofa	CUCCCCGGGGAGG ACCAGGUCAAGGA	6	48.39	35.01
49	GACCAGGUCA			6	48.56	35.18

5	AGGACCGA		CCGACGCCGGCGCC	6	49.11	35.73
67	CGCCGGCG		UGUCCAACGUUAA	6	49.70	36.32
50	CCUGUCCAACGUUAAUC		UCGGGGCAGGGGG	6	50.27	36.89
	GGGGCAGGG		GAAACAACCCGGC			
40	GGGAAACAACCC		AGUCAGAGCUCCU	6	50.65	37.27
4	GGCAGUCAGAGCUCCUG		GACUGACCUAUAU	6	50.75	37.37
	ACUGACC		UCUGUAGCGUUGC			
27	UAUAUUCUGUAGCGUU		AGGGUAUAGGGGA	6	51.25	37.86
	GCAGGGUAUA		AACCCGUCGGGUA			
8	GGGGAAACCC		AGUUCCGACUCCCC	6	51.39	38.01
71	GUCGGGUAAGUUCCGAC		CAGUAGCGGCGAG	6	51.55	38.17
13	UCCCCCAGUAGCGGCGA		CGAACGGGGAUCC	6	51.56	38.18
	GCGAACGGGGA		UCCUAAAAGAGUAA			
81	UCCUCCUAAAGAGUAAC		CGGAGGACGCCGG	6	52.20	38.81
	GGAGGA		CGCGGGCGGGACA			
48	CGCCGGCGC		CGUGGUAUCCUGU	6	52.34	38.96
21	GGGCGGGACACGUGGU		CUGCGUACACGGG	6	53.22	39.84
	AUCCUGUCU		UGUACGUACAGGC			
2	GCGUACACGGGUGUACG		UGAUACCGCCCAA	6	53.96	40.58
	UAC		GAGUUCAUAUCGA			
89	AGGCUGAUACCGCCCAA		CGGCGGUGUUUGG	6	55.10	41.71
	GAGUUCAUAUCGACGGC		CACCCGUGCUAUU			
	GGUGUUUGGCACC		CUGCGCGAUCGGG	6	56.30	42.92
6	CGUGC UAAUCUGCG		UGUGCUGUGAGGC	7	56.40	43.02
51	CGAUCG		AUGCUGGUAGAGA	7	56.94	43.56
46	GGUGUGCUGUGAGGCA		AUACCGGUAGAGA	7	56.99	43.60
	UGC U		AUACCGCCCGGUG	7	56.99	43.60
49a	GGUAGAGAAUACC		CCGGAAGGUUAAU	7	58.26	44.88
60	GGUAGAGAAUACC		UGAUGGGGUUAGC			
68	GCCCGGUGCCGGAAGGU		GCAAGCGAAGCUC	7	59.89	46.51
	UAAUUGAUGGGGUUAG		UUGAUCGAAGCCC	7	60.36	46.98
	CGCAAGCGAAGCUCUUG		CGGUAACGGCGG	7	60.96	47.58
	AUCGAAGCCCCGGUAAA		AGCUUCAGCGGGU			
	CGGC		GAAAAGCCCGCUA			
55a	GGAGCUUC		CGCAUCACUGGUG			
47	AGCGGGUGAAAAGCCCG		UUCGGGUUGUCAU			
	CU		GCCAAUGGCACUG			
96	ACGCAUCACUGGUGUUC		CCCGGUAGCUAAA	7	59.89	46.51
	GGGUUGUCAUGCCAAU		UGC GGCGUUGAAG	7	60.36	46.98
	GGCACUGCCCGGUAGCU		ACGACGACGCACCC	7	60.96	47.58
	AAAUGCGG		CGGCGAGGGGGUG			
100	CGUUGAAGACGACGACG		GGAGCACGCUUAG			
82	CA		GCGUGUGACUGCC			
24	CCCCGGCGAGGGG		GGUGGUUCUGAAU			
25	GUGGGAGCACGCUUAG		GGAAGGGCCAUCG	8	62.65	49.27
	GCGUGUGACUGC		GUGCCGGCACGGU	8	62.94	49.56
88	CGGUGGUUCUGAAUGG		UAACCGAAUAGGG	8	63.31	49.93
	AAGGGCCAUCG		GAGCCUAAACGUUG	8	64.52	51.14
			ACCCGUAAUCCGG	8	64.61	51.23
			GUUGCGGAGGCCG			
			UAACUUAACGGU			
			CCUCGUGAAUUCA			

62	GUGCCGGCAC		UCUCCGGGGGUAG	8	65.13	51.75
28	GGUUAACCGAAUAGGG GAGCC		AGCACUGUUUCGG CAAGGGGGUCACU	8	65.26	51.88
79	UAACGUUGACCCGUAAU CCGGGUUGCGGA		UACCAACCCGAUG CAAACUGCGAAUA	8	65.50	52.12
69	GGCCGUAAACUUAACGG UC		CCGGAGAAUGUUA UCACGGGCUGCGA	8	66.00	52.62
38	CUCGUGAAUUCAUCUCC GGGGGUAGAGCACUGU UUCGGCAAGGGGGUCAC UUACCAACCCGAUGCAA ACUGCGAAUACCGGAGA AUGUUAUCACGGG		GCGUGACGGCGCG AGCAGGGCGCCGG UUGAAGGUUGGGU AACACUAACUGGA GGACCACAGGUUA AUAUUCUGUCCG CCAGCUAAGGUCC CAAAGUCAUGGUU AACCAUGCACCGA AGCUGCGGCCUGG GGCUGAAGUAGGU CCCAAGGGGGGAA ACCGGGUGACAGC CCC	8	66.66	53.28
86	CUGCGAGCGUGACGGCG CGAGCAG			8	66.74	53.36
56	GGCGCC			8	67.03	53.64
34	GGUUGAAGGUUGGGUA ACACUAAUGGAGGACC			8	67.52	54.14
53	ACAGGUUAAUAUCCU GU			8	67.79	54.41
41	CCGCCAGCUAAGGUCCC AAAGUCAUGGUUAACC AUGCACCGAAGCUGCGG			8	68.38	55.00
91	CCUGGGGCUGAAGUAG GUCCCAAGGG			8	68.40	55.02
29	GGGAAACC			8	68.79	55.41
20	GGGUGACAGCCCC			8	68.88	55.50
14	AGCCGGCU	A-rest	AGCCGGCUUCAUU	9	69.39	56.01
10	UCAUUAACUGAAUCCAU AGGUUAAUGA		AACUGAAUCCAUA GGUUA AUGAAAGG GGGGCCUCUCGUC GGUAAGGUGAUUA GAACCGUUAUAAC CGGCGCGAAGGGG GGGACCAUCCUCC AGCGACGCUUAUG CGUUGUUGUCAAC CGAAGGAAAACCG AGUCUUAACUGGG CGCAGUGUGUGUG UUAGUGCACAAAA AUGCACAUGCUGA GUGUGUUAGUUCU CCGCGUCUGGAAA GGCGCUAGGCCGG GUGUGUAAGCGCA GCGAUGCGUUGAG CUAACCGGUACUA AUUAAGCGUGUAG	9	70.40	57.02
55	AAGGGGGGCCUCU			9	71.43	58.05
7	CGUCGGUAAGGUGAUA UGAACCGUUAUAACCGG CG			9	71.50	58.12
63a	CGAAG			9	71.52	58.14
22	GGGGGGACCAUCCUCC			9	71.87	58.49
45	AGCGACGCUUAUGCGUU GUUG			9	72.22	58.83
12	UCAACCGA			9	72.30	58.92
99	AGGAAAACCG			9	72.51	59.13
31	AGUCUUAACUGGGCG			9	74.01	60.63
18	CAGUGUGUGUGUUAGU GCACAAAAAUGCACAUG CUG			9	74.50	61.11
9	AGUGUGUU			9	75.16	61.77
94	AGUUCUCC			10	77.77	64.39
19	GCGUCUGGAAAGGCGC			10	78.24	64.86

101	UAGGCCGGGUGUGUAA GCGCAGCGAUGCGUUGA GCUAACCGGUACUAA		GCUGGUUUUCCAG GCAAAUCCGGAAA AUCAAGGCUGAGG	10	78.38	65.00
58	UUAAGCGUGUAGGCUG GUUUUCCAGGCAAUCC GGAAAAUCAAGGCUGA GGCGUGAUGA		CGUGAUGAGAGGC ACUACGGUGCUGA CUGCUCCUAGUAC GAGAGGACCGGAG	10	78.43	65.05
59	GAGGCACUACGGUGCUG A		UGGGAGAUAAAGUG CUGAAAGCAUCUA	10	79.71	66.32
95	CUGCUCCUAGUACGAGA GGACCGGAGUGG		AGCACGAAACUUG ACCCUUUAAGGGU	10	79.83	66.45
97	GAGAUAAAGUGCUGAAA GCAUCUAAGCACGAAAC UU		CUUGGUGUUACUA GGUAACAUAACC	10	80.25	66.87
98	GACCCUUUAAGGGUC		GGGCGACGGUUGU CCCGGUCGAUGUG	10	82.40	69.01
54	UUGGUGUUACUAGGUA ACAUCA		GGAAGGCGUCGGC CUGCGCGGCUGAU	10	82.90	69.52
57	CCGGGCGACGGUUGUCC CGGU		AUGUAGGUGAGGU CCCUCGCGGAUGG	10	83.00	69.62
42	CGAUGUGGGAAGGCGU CGGCCUGCGCG		AGCUGAAAUCAGU GAACAUUGAGCCU	11	83.73	70.35
63	GCUGAUUAGUAGGUGA GGUCCCUCGCGGAUGGA GCUGAAAUCAGU		UGAUGCUUUAAUG UUUGAUGUUCAGG	11	84.26	70.88
76	GAACAUUGAGCCUUGA UGC UUUAUGUUUGAU GUUC		UUGGCGCCAGCUU GGUUAAGCGCUUA	11	84.69	71.31
83	AGGUUGGCGCCAGCUU		ACCGAGCGCUCUG CGAAAGCUAAUCC	11	84.80	71.42
1	GGUUAAGCGCUUAACC		UGGUCGGACAUCA GGAGGUUAGAAAG	11	86.47	73.09
16	GAGCGCUC		CGUAAUAGCUCAA UGUUGGCUUAGAA	11	89.15	75.77
87	UGC GAAAGC		GCAGCCAUCAUGG UGGCACCCGGCUU	11	90.07	76.69
84	UAAUCCUGGUCGGACAU CAGGAGGUUA		UGAAGUGUGGACG CCAGUCUGCAUGG	12	91.10	77.72
44	GAAAGCGUAAUAGCUC A		AGCC	13	97.65	84.26
43	AUGUUGGCUUAGAAGC AGCCAUCAU			13	101.82	88.44
77	GGUGGCACCC			14	106.09	92.70
78	GGCUUUGAAGUGUGGA CGCCAGUCUGCAUGGAG CC			15	114.26	100.88

Table S2 (cont'd)

<i>H. marismortui</i> (23S)						
Helix	Sequence	State	Composite Sequence	Bin no.	D _{COM}	D _{COM: H-LSU} ¹
74	CCCUAUGGAGCUUAA GCUACCCUAGGG	A-core	CCCUAUGGAGCUUAA AGCUACCCUAGGGC	1	16.62	0.00
25a	CGUUUUGAAAAACGA		GUUUUUGAAAAACGA	2	24.22	7.60
32	CCGGACGUCCGG		CCGGACGUCCGGGC	2	24.48	7.86
26	GCCAGGUCCUGG		CAGGUCCUGGGGUG	2	25.35	8.74
35a	GGUGAAAGGCC		AAAGGCCGUGUGAA	2	27.49	10.87
23	GUGUGAAC		CGACUGGGGCGAGU	2	27.82	11.20
80	GACUGGGGC		UGGUGUCCUACAAU	2	29.34	12.72
35	GAGUUGGUGUCCUAC AAUACCCUCUC		ACCCUCUCUGUCUA	2	29.42	12.80
65	UGUCUAGUAACAACA		GUAACAACAGACCG	2	30.48	13.86
93	GACCGUCGUGAGACA GGUC		UCGUGAGACAGGUC	2	31.07	14.46
49a	CCGACACAGG		CCGACACAGGCGGU	2	31.42	14.80
90	CGGUUCCCUCCGGAG GUCGUGAGCUGG		UCCCUCCGGAGGUC	3	34.26	17.64
73	CACCCAGGGGGAAGC GCUAUCUACUGGGUG		GUGAGCUGGCACCC	3	34.87	18.25
11	CCCGAGAACUGAAAC AUCUCAGUAUCGGG		AGGGGGAAGCGCUA	3	35.07	18.45
37	CAUGUCGAAGCAUG		UCUACUGGGUGCCC	3	35.15	18.54
72	UCCAGUGCGGAGUCU GGA		GAGAACUGAAACAU	3	37.26	20.64
33	CUACGCAUGGACGAU CUAUGUGUAG		CUCAGUAUCGGGCA	4	39.91	23.29
39	GGUGCGCGGGGUAAG CCUGUGUACC		UGUCGAAGCAUGUC	4	43.17	26.55
92	AGGUUGUUCGCCU		CAGUGCGGAGUCUG GA	5	44.68	28.07
36	CCAAUCGAUUGG			5	45.31	28.69
75	ACUGCAGGCUGUCGC GAUAGCCGGGCAG			5	46.21	29.59
64	GAAGCUCGGCCAGAG CUUC			5	46.25	29.63
3	GCGC			5	46.45	29.83
2	UGCCAGCUGGUGUCA GUUGGC			5	46.57	29.96
40	GGGGAACAACCC			5	46.64	30.03
61	CCAACGUUAGGCCCA ACGUUG			5	47.31	30.69
4	UCGGCUCAGGCGCAA CCUGAGACCGA			5	48.44	31.82
49	GGAUUAUGUCC			5	48.77	32.15

81	GUACGCGCUCGAAAA GAUAUCGAGCGC			5	49.51	32.89
27	GUGUCUGCAUGGCGC CAUGUGGACAC			5	49.55	32.94
50	CCUCAGCACUGCUGA UCAGCUGAGG			5	49.71	33.10
52	CCUAAGUCAUACCGC AACUCGACUAUGACG AAAUGG			5	50.12	33.51
66	GGUGACCGCAAUCC GCAAGGACUCGUACG GUCACU			5	50.17	33.55
13	UCGUUAGUAACCGCG AGUGAACGCGA	A- mofa	UCGUUAGUAACCGC GAGUGAACGCGAAA UCCUAUGGAUUGGA UCCGCCGCAUCAGU AGCGGCCUCUAAUU GGAUGGAAGUAGGG GUGAAAACUCCUUAU GGACCGAUUAGUGG GCCGGCCGCCAGU GCAGGUUAUACCCUG UCAACGGCGAGAAU CUCGCGGGGGUUGG AUAUCCCUCCCGU GCCAAGCUGCGAGU CGUCACUCGCAAGA GCACAUUUCGACCG AGUGGCUUGCUGGC GGCGAAAGCCCCGC CGAGUCGGGUGAGA ACCCCGACGUGGCC ACUGGUGUACCGGU UGUUCGAGAGAGCA CGUGCCGGGUAGCC ACGCCACCUUCGGG GUCGACCGGGGGUC CCUCAGAAGGGCAG UGUUCUUCCCAACG AGGAACGCUGCUC GCCGAGGUAGUCUG UGAGGUAGAGCGAC CGAUUGGUCCUGUC AAACUCCAAACUUA CAGACGCCGUUUGA CGCGGGGGAUAGGU UAAGGUCCCCAAGU GUGGAUUAUCCAC CACCGAGACCUGUC GUCUAACCGGAGUA UCCGGGGAGGCCGU ACCACUCAUACUGG	6	52.06	35.44
67	AAUCCUAUGGAUU			6	52.19	35.58
5	GGAUCC			6	52.24	35.62
71	GCCGCAUCAGUAGCG GC			6	53.31	36.69
46	CUCUAAUUGGAUGGA AGUAGGGGUGAAAAC UCCUAUGGACCGAUU AGUG			6	53.71	37.09
48	GGCCGGCC			6	54.88	38.27
69	GCCCAGUGCAGGUUAU CACCUGUCAACGGC			6	55.29	38.68
8	GAGAAUCUC			6	55.45	38.83
21	GCGGGGGUUGGAUUAU CCCUCGC			6	55.67	39.05
6	CGUGCCAAGCUGCG			6	55.69	39.07
89	AGUCGUCACUCGCAA GAGCACAUAUCGACC GAGUGGCUUGCU			6	56.27	39.66
60	GGCGGCGAAAGCC			7	59.35	42.74
51	CGGCCG			7	59.41	42.79
47	AGUCGGGUGAGAACC CCGAC			7	59.46	42.85
96	GUGGCCACUGGUGUA CCGGUUGUUCGAGAG AGCACGUGCCGGGUA GCCACGCCAC			7	60.55	43.94
62	CUUCGG			7	61.32	44.70
100	GGUCGACC			7	61.35	44.74
70	GGGGGUC			7	61.61	45.00
24	CCUCAGAAGGG			7	61.94	45.33
86	CAGUGUUCUUCCCAA CGAGGAACGCUG			7	62.36	45.74
38	CUCCGCCGAGGUAGU CUGUGAGGUAGAGCG ACCGAUUGGUCCUGU			7	62.86	46.25

	CAAACUCCAAACUUA CAGACGCCGUUUGAC GCGGGG		UAAUCGCAAUAGC CUGCUUGAUGCGGG CAAUUGCCUGCCCC UGCAGAAGCGGGCA AGGGGGGUGACAAC CCCCCCCUGGGGUA ACCUGGGGCUAACC GGGUGCAAGAGCGG GAAACCGGUCGACC GGUCGACCACGGGU UAAUAUUCCCGUGA CAGGGCAUACAAGG UCCCUCGACGAAUG ACCGACGCGCGAGC GUCCAGUAAGACUC ACGGGAAGCCGAUG UUCUGUCCCAUGGG GAGCCGCACGGAGG CGAAGAACCAUGGG UCUCGAUCGAGACA UUGCUUCGCGCAAU AGAUGAAGCGUGCC GAAAGGCACGUGGA AGUCUCCUCGUACA AGAGGAGCCGGCUA CUCCGGGAGGAGCG CAG			
41	GAUAGGUUAAGGUCC CCAAGUGUGGAUUA UCCACCACCGAGACC UGUC			7	64.44	47.82
28	GUCUAACCGGAGUAU CCGGGGGAGGC			7	64.78	48.17
45	CGUACCACUCAUACU GGUAAUCG			8	66.01	49.40
88	CAAUUAGCCUGCUUG AUGCGGGCAAUUG			8	66.60	49.99
91	CCUGCCCGUGCAGAA GCGGGCAAGGG			8	66.98	50.36
20	GGGUGACAACCCC			8	67.27	50.66
56	GCCCUGGGGUAACCU GGGGC			8	67.75	51.13
9	UAA			8	68.42	51.81
82	CCGG			8	68.53	51.91
85	GUGCAAGAGC			8	68.86	52.24
29	GGGAAACC			8	68.97	52.36
98	GGUCGACC			8	69.37	52.75
99	GGUCGACC			8	69.37	52.75
53	ACGGGUUAAUAUCC CGU			8	69.92	53.31
25	GACAGGGCAUACAAG GUCCCUCGACGAAUG ACCGACGCGCGAGCG UCCAGUAAGACUCAC GGGAAGCCGAUGUUC UGUC			8	69.99	53.38
7	CCAUGGGGAGCCGCA CGGAGGCGAAGAACC AUGG			8	70.76	54.15
18	GUCUCGAUCGAGAC			8	70.86	54.24
10	AUUGCUUCGCGCAAU			8	70.93	54.31
34	AGAUGAAGCGUGCCG AAAGGCACGUGGAAG UCU			8	71.70	55.09
68	CCUCGUACAAGAGG			8	71.78	55.16
14	AGCCGGCU			8	72.12	55.50
79	ACUCCGGGAGGAG			8	72.36	55.74
63a	CGCAG			8	72.44	55.82
19	UCUCGACGAAGUCUC UUGGAACAGAGC	A-rest	UCUCGACGAAGUCU CUUGGAACAGAGCC CGUCUUCAAGGGCG GACGCAAUGUGGUG UCUAGACACCGCGC	9	72.69	56.07
31	CCGUCUUAAGGGCG G			9	72.87	56.26
12	ACGCAAUGU			9	73.99	57.37

94	GGUGUCUAGACACCG	AGGCAUCGACUGCG GUACGGGGUAAGAG CUGAACGCAUCUAA GCUCGAAACCCGAC CGUAUAGUACGAGA GGAACUACGGUUUA GACUCGGGGUGUGC GCGUCGAGGUAACG AGACGUUAAGCCCA CGAGCACUAGAGGA CUUGGGCAUCGCCC ACCUGCUCCGGAAC GGAGCAGGUGGUGG UCUCGAGCCGGUUU GAGGCGCCGGCCGC AGGGCUUGCCCGAG GGCCGGAACACCU AUGCGCAUAGUGCG AACCGUCCAACUCC GUGGAAGCCGUAAU GGCAGGAAGCGGAC GAACGGCGGCAUAG CAUCAGCCGAUACG ACGUGGGCUAUGAU AGCCGCGAGCGUCC AGUCGCGAAAGCGC UCAGCCGGGGACCC GGCGAAGAGGGCUA CCGGUAGUGCCAAA AAGCGUAACAGCUU AAGGUGAGCUUAGA AGCAGCUACCCUCU AAG	9	74.47	57.86
22	CGCAGGCAUCGACUG CG		9	74.98	58.37
55	GUAC		9	75.54	58.93
97	GGGGUAAGAGCUGAA CGCAUCUAAGCUCGA AACCC		9	77.10	60.49
95	GACCGUAUAGUACGA GAGGAACUACGGUU		9	78.65	62.03
101	UAGACUCGGGGUGUG CGCGUCGAGGUAACG AGACGUUAAGCCAC GAGCACUA		10	79.70	63.09
76	GAGGACU		10	79.87	63.26
57	UGGGCAUCGCCCA		10	81.15	64.53
63	CCUGCUCCGGAACGG AGCAGGU		10	81.27	64.65
42	GGUGGUCUCGAGCCG GUUUGAGGCGCC		10	81.29	64.67
30	GGCCGCAGGGCUUGC CCGAGGGCC		10	81.79	65.17
59	GGAAAC		10	82.52	65.90
54	CACUAUGCGCAUAGU G		10	84.29	67.67
58	CGAACCGUCCAACUC CGUGGAAGCCGUAAU GGCAGGAAGCGGACG AACGGCGGCAUAG		10	84.34	67.73
17	CAUCAGCCGAUACGA CGUG		10	84.65	68.04
83	GGCUAUGAUAGC		10	85.77	69.16
15	CGCGAGCGUCCAGU		10	86.17	69.56
87	CGCGAAAGCG		11	87.85	71.24
84	CUCAGCCGGGGACCC GGCGAAGA		11	91.52	74.91
16	GGGCUACCGGUAGUG CCA		12	94.91	78.29
44	AAAAGCGUACAGCU UA		13	103.48	86.86
43	AGGUGAGCUUAGAAG CAGCUACCCU		14	111.60	94.98
43a	CUAAG		15	118.17	101.56

Table S2 (cont'd)

<i>T. thermophilus</i> (23S)						
Helix	Sequence	State	Composite Sequence	Bin no.	D _{COM}	D _{COM: H-LSU} ¹
74	CCCCGUGGAGCUUAAGU	A-core	CCCCGUGGAGCU	1	15.51	0.00
	UACCCCGGG		UAAGUUACCCCG			
32	CCGGGCGCCCGG		GGCCGGGCGCCCG	1	20.38	4.87
35a	AGUGAAAAGCU		GAGUGAAAAGCU	2	22.60	7.09
70	AGCUUAAGUU		AGCUUAAGUUC			
			GUGAGGUGUUUA	2	22.88	7.37
23	CCGUGAGG		CCAAAAACACCG	2	24.56	9.05
65	UGUUUACCAAAAACA		GUGGGGGAUGCA	2	27.75	12.24
35	CCGGUGGGGGAUGCAAA		AACCCUCGGA			
	CCCCUCGG		ACGUCGUGAGAC	2	29.07	13.56
93	GAACGUCGUGAGACAGU		AGUUCGCCGCG			
	UC		CCGGCGCCUAUU	2	29.17	13.66
26	GCCGGCGCCGCGC		GAAGCAUGACUG			
			GGAACUGAAAC	2	29.30	13.79
25a	GCCUAUUGAAGCAUGA		AUCUCAGUACCC	3	29.82	14.31
11	CUGGGGAACUGAAACAU		AGGACUGGGGCG	3	31.77	16.26
	CUCAGUACCCAG		GUCAUGAGUAAC			
80	GACUGGGGCGGUC		GUGAAAUUCUAG	3	33.08	17.57
26a	AUGAGUAACGUGAAAUU		CCCUGGCCGAGCU	3	33.10	17.59
33	CUAGCCCUGGCCGAGCU		GGGGCUAGGUGA	3	34.87	19.36
	GGGGCUAGG		CUUUAGGGUCA			
37	UGACUUUAGGGUCA			3	36.40	20.90
90	CGGCUCGUCGCGGCGCAC			4	37.89	22.38
	GCGAGCUGG					
73	CCCGUGGCAGGACGAUC			4	39.01	23.50
	UAUCCGCCACGGG					
75	ACUGCAGCCUGGUGCGC			4	41.37	25.86
	UUGGCGGGCAGU					
72	GGCCGUGAAGAUGC			4	43.40	27.89
	GC					
64	GCUCUGGCGCGACCGGA			5	45.12	29.61
	GC					
66	GCUCUCUGCGAACUCGU			5	45.25	29.74
	AAGAGGAGGUUAUAGGGA					
	GC					
52	CCUAAGGUGAAGCCGAA			5	46.86	31.35
	AGGCGUAGCCGAAGG					
39	GGGCGCGAGCGAUAACG			5	47.21	31.70
	UCCGCGUCC					
61	CGGGAGAACCCUCGCCA			5	47.22	31.71
	AGGUCUCGGCGAGGG					
3	CCGG			5	47.23	31.72
36	CUCCCCGGGGAG			5	48.34	32.83
92	UGGGCUGUUCGCCCA			5	48.34	32.83
4	GGCACCCGAGCCUCCGGG			5	48.43	32.92
	UGACC					

49	GCCCAGGGCG			5	48.68	33.17
5	GGAUCCG			5	49.41	33.91
50	CCUACGCAAUGGUCGUC AGCGUAGGG			5	49.75	34.24
8	GGGGGAACCC			5	50.31	34.80
67	ACGCUAGCGU			5	50.42	34.91
27	CACGGUCGUGGGCGUCC GCGGCCGUG			6	50.76	35.25
13	UCCCUGAGUAGCGGCGA GCGAAAGGGGA			6	50.86	35.35
2	GGGCCACGGCCGUGGG CUU			6	52.46	36.95
48	CGCCGGCGC			6	52.55	37.04
21	CCCCGUGGUUCGUGGAG CCAUGGGG			6	53.32	37.81
81	GCCUCCUAAAAGGUAAC GGAGGC			6	53.42	37.91
71	GUCGGGUAAGUUCGAC			6	53.48	37.97
6	CGUGGCUACCUGCG			6	55.42	39.91
51	CGGCCG			6	55.92	40.42
68	GCCCGGUGCCGGAAGGU CAAGGGGAGGGGUGCAA GCCCCGAACCGAAGCCCC GGUGAACGGC			6	56.62	41.11
46	GGCCGACCCGCGAGGGC GGCU			6	56.77	41.26
49a	GGUGCAAGAGCACU	A- mofa	GGUGCAAGAGCA CUGGUGCAAGAG CACUAGAGGGUG AGAAUCCCUCUG CUGAUCUCCCCCG AGCGUCCACAGC GGCGGGGAGGUU UGGCACGCACCUC UGGUUUCCCAGC UGUCCCUCCAGG GGCAUAAGCUGG GUAGCCAUGUGC GGAAGGGAUAAC CGCUGAAAGCAU CUAAGCGGGAAG CCCGCUCGAGCGC CCCGUAACUUCG GGAGAAGGGGUG UCACGGCCCCAAG GGGUUGUGGCC GGGAAGACCACC CGGCCCCGGGAG GGGCUUAAGCC	7	57.77	42.26
60	GGUGCAAGAGCACU			7	57.77	42.26
47	AGAGGGUGAGAAUCCCU CU			7	60.21	44.70
89	GCUGAUCUCCCCGAGCG UCCACAGCGGCGGGGAG GUUUGGC			7	60.33	44.82
96	ACGCACCUCUGGUUCCC AGCUGUCCCUCCAGGGG CAUAAGCUGGGUAGCCA UGUGCGGAAGGGAUAAC CGCUGAAAGCAUCUAAG CGGGAAGCCC			7	60.52	45.01
55a	GCUCGAGC			7	60.53	45.02
62	GCCCCGUAACUUCGGGA GAAGGGGU			7	61.31	45.80
25	GUCACGGCCCCAAGGGG UUGUGGC			7	62.24	46.73
92a	CCGGGAAGACCACCCGG			7	62.98	47.47
24	CCCCGGGAGGGG			7	63.11	47.60
28	GCUUAAGCCGUUGAGGC GGAGGC			7	63.65	48.15

88	CGGUGGUCCCGUGUGGA AGGGCCAUCG	GUUGAGGCGGAG GCCGGUGGUCCC GUGUGGAAGGGC CAUCGCCGCGCUG CGCGGCCGCCAGC UAAGGCGCCGAA GCUGCGGCCUCG GAUGGGGGGCCG GUUAAUAUUCG GCCUGCGAGGCC UGCAAGCCGAGC AGAGCCGGCUCU CAGGCGCUGACU GGGGCCUGUAGA GCACUGAUAGGG CUAGGGGGCGCC UACCAAACCCUG UCAACUCCGAA GGGUCCCAGGUG GAGCCUGGGGGG UGAAAGCCCCGG GUGAAGCUGGGG UGAGACCCAGUG GAGGCCCGGGAA ACCCCGGCCGUA CUAUAACGGUCC CGCCAGCUAAGG CCCCAAGUCUGG GCUAGCCCAGCGC CGAAGCUGCGGG AGAAAUCGCGCA AGGGUCCAGGGG GAGCCGGUAGCG GGCGUGGAUCC UGGCCUGGGGCU GAAGAAGGUCC AAGGGGGGCGGA CCACCGCCUGGCU AGGGGGACCCCC GAAGCCAUGGGG GGCCUCUUCUGG GGGAUGACCCA GGCGGCCGGCGG GAUAACCGCUGA AAGCAUCUAAGC GGGAAGCCCGCCC CAAGAUGAGGCC UCCACGGCGUCA AGCCGCGCAGUCC CCAGCCUAGCCGG CGAAAGGUGGGG GGGGAGUCCAGU CCGAACAGGGCG	7	64.27	48.76
10	CCGCGCUGCGCGG		8	66.00	50.50
40	CCGCCAGCUAAGGCGCCG AAGCUGCGG		8	66.35	50.84
79	CCCUCGGAUGGGGG		8	66.99	51.48
53	GCCGGUUAUAUUCGG C		8	67.24	51.73
86	CUGCGAGGCCUGCAAGC CGAGCAG		8	67.31	51.80
14	AGCCGVCU		8	67.69	52.18
38	CUCAGGCGCUGACUGGG GCCUGUAGAGCACUGAU AGGGCUAGGGGGCGCCU ACCAAACCCUGUCAAAC UCCGAAGGGUCCAGGU GGAGCCUGGG		8	68.01	52.50
20	GGGUGAAAGCCCC		8	68.21	52.70
34	GGGUGAAGCUGGGGUGA GACCCAGUGGAGGCC		8	68.25	52.74
29	GGGAAACC		8	68.28	52.77
82	CC		8	68.79	53.28
69	GGCCGUAACUAUAACGG UC		8	69.03	53.52
41	CCGCCAGCUAAGGCCCCC AAGUCUGGGCUAGCCCA GCGCCGAAGCUGCGG		8	69.37	53.86
12	GAGAAAUC		8	70.05	54.54
85	GCGCAAGGGU		8	70.17	54.66
7	CCAGGGGGAGCCGUAG CGGGCGUGGAUCCUGG		8	70.42	54.91
91	CCUGGGGCUAGAAGG UCCCAAGGG		8	70.76	55.25
22	GGGCGGACCACGCCU		8	71.04	55.53
56	GGCUAGGGGGACCCCC GAAGCC		9	71.53	56.02
55	AUGGGGGGCCUCU		9	71.69	56.18
45	UCUGGGGGAUGACCCCA GGC		9	71.74	56.23
9	GGCCGGC		9	71.94	56.43
97	GGGAUAACCGCUGAAAG CAUCUAAGCGGGAAGCC CGCCCCAAGAUGAGGCC UCCACGGCGUCAAGCCG		9	72.13	56.62
63a	CGCAG		9	72.21	56.70
18	UCCCCAGCCUAGCCGGCG AAAGGUGGGGGG		9	72.95	57.44
99	GGAGUCC		9	73.00	57.49
31	AGUCCGAACAGGGCG		9	74.41	58.90

100	UGGGCCGGGGGCCGACC GGUCCCA		UGGGCCGGGGGC CGACCGGUCCCAG	9	76.07	60.56
94	GGAGGCUUAGGCCUCC		GAGGCUUAGGCC	9	76.67	61.16
19	GCUGUUGGGAAGCAGC		UCCGCUGUUGGG	9	78.27	62.76
59	GAAGCCCCG		AAGCAGCGAAGC CCG	9	78.27	62.77
58	CCAGAAGCGCAGGGUGG GAGGUAGGCAAAUCCGC CUCCCAACAAGCUCUGCG UGGUGG	A-rest	CCAGAAGCGCAG GGUGGGAGGUAG GCAAAUCCGCCUC CCAACAAGCUCU GCGUGGUGGGUC UGGGCUGCCCAG CCGGCGUCAAGCC GGGCUCUUGGUC GCGCCGGCGCGGC UGGGGGCCGCUC CCUGGGGUGAUG AGCCCCGGGGAG CAGAUCUCUCUU CCUAGUACGAGA GGACCGGAAGGG UUCCCGCAGGUA ACCUGCGGGAAC GGAGCCAUGGAC GAGCCCGGAACC GUCCGGCUUGUC CGGGCGGGGUCG GGGGCCCUCGGG GUGAGGGUACCC AGGUCCCCGGGG GCCUGCGCCGCGA GGCGUGGCGAAA GCCUCAGGCGGG ACGGAUAUCCGC CGGAGAGGUGGC CACCCUGGC	10	78.53	63.02
42	GUCUGGGCUGCCCAGC			10	79.19	63.68
98	CGGCGUCAAGCCG			10	80.13	64.62
76	GGCUCUUGGUCGCGCCG GCGCGGCUGGGGGCC			10	81.06	65.55
63	GCUCCUGGGGUGAUGA GCCCCGGGGAGC			10	81.64	66.13
1	AGAUCU			10	82.14	66.63
95	CUCUUCCUAGUACGAGA GGACCGGAAGGG			10	82.49	66.98
54	UUCCCGCAGGUAACCUG CGGGAA			10	83.24	67.73
57	CGGAGCCAUGGACGAGC CCGG			10	83.73	68.22
16	AACCGUCCGGCUUGUCC GGGCGGGGUCGGGGGCC CUCGGGGUGAGGGUACC C			11	86.18	70.67
83	AGGUCCCCGGGGGCCU			11	86.31	70.80
101	GCGCCGCGAGGCGU			11	89.10	73.59
87	GGCGAAAGCC			11	90.13	74.62
84	UCAGGCGGGACGGAAAU CCGCCGAGA			11	92.14	76.63
77	GGUGGCCACC			13	102.9 6	87.45
78	CUGGC			16	121.1 4	105.63

Table S2 (cont'd)

<i>S. cerevisiae</i> (25S)						
Helix	Sequence	State	Composite Sequence	Bin no.	D _{COM}	D _{COM: H-LSU} ¹
h74	CCCUGUUGAGCUUAAG UUACCACAGGG	A-core	CCCUGUUGAGCUU AAGUUACCACAGG	1	17.25	0.00
h32	CCCGAAAGAUGGUACC AUCUAGUAGCUGG		GCCCGAAAGAUGG UACCAUCUAGUAG	1	20.33	3.07
h25a	CCGUCUUGAAACACGG		CUGGCCGUCUUGA AACACGGACCAAG	1	21.53	4.27
h26	ACCAAGUCUUGGU		UCUUGGUCGGCUC	2	25.59	8.34
h90	CGGCUCUCCUAGGGA ACGUGAGCUGG		UUCCUAGGGAACG UGAGCUGGCGGUU	2	26.28	9.03
h35	CGGUUCUGACGUGCAA AUCGAUCG		CUGACGUGCAAAU CGAUCGGGUAGUA	2	30.08	12.83
h26a	GGUAGUAGCGCGAAAC C		GCGCGAAACCAUC AGCGGGGAAAUU	2	30.28	13.03
h73	AUCAGCGGGGAAAUA CCCUACUGAU		ACCCUACUGAUGG CUGGGGCGGCACG	2	30.61	13.36
h80	GGCUGGGGCGGCAC		GCGAAAGACACCG	2	30.75	13.50
h35a	GGCGAAAGAC		UCGUGAGACAGGU	2	30.93	13.68
h93	ACCGUCGUGAGACAGG U		UGUCUAAUUA ACACAGUGAUGCC	3	32.11	14.86
h65	UGUCUAAUUAACA		AAGGGAACGGGCU	3	32.63	15.38
h23	CAGUGAUG		UGGCCGCAGCAGG	3	32.75	15.50
h72	CCAAGGGAACGGGCUU GG		UUUCCUCAGGAU A	3	33.90	16.65
h49a	CCGCAGCAGG			3	34.20	16.94
h37	UUUCCUCAGGAUA			3	34.38	17.13
h11	CCCGCUGAACUUAAGC AUAUCAUAAGCGGA			4	38.84	21.59
h39	GCCAUUUUUGGUAAGC AGAACUGGC			4	40.75	23.50
h70	AAAUGCCU			4	42.99	25.74
h33	CUAUGCCUGAAUAAUU UGGGUAUAG			4	43.34	26.09
h40	CGGGAUGAACCG			4	43.65	26.39
h36	CCUGCCGGCAGG			4	43.98	26.73
h92	UGGAUUGUUCACCCA			4	44.05	26.79
h61	UAGAAUAAUGUAGAUA AGGCCCUAUCUACUAU CUA			4	44.09	26.83
h89	GCAGUCAAGCGUUCAU AGCGACAUUGCUIUUU GAUUCUUCGAUGUCGG CUCUCCUA			4	44.31	27.06
h64	GGGAAUCUGCGAGAUU CCC			5	46.72	29.47

h75	ACUCUAGUUUGACAUG UCAGGUGGGGAGU			5	48.15	30.90
h27	CUAACGUCUAUGCGCA UAGCUGUUGG			5	50.06	32.81
h50	GGGAAAGGUUCCACGU CAACAGCAGUUGGACG UGG			5	50.27	33.02
h71	GUCAUCUAAUUAGUGA C	A- mofa	GUCAUCUAAUUAG UGACUGGAGGUCA GUGACGAAGCCUA GACCGUAAGGUCG GGUCGAACGGCCU CUACAUUGCGAUG GUCAGAAAGUGA UGUUGACGCAAUG GGGGAUCUCCGGC AUUUGAUC AUGG UUAUAUGCCUUCG GAAUGGGGAAGC UCCGUUUGCCUUA GUAACGGCGAGUG AAGCGGCAAAGAA GCUCGAGCUUUUU UUGUAUACGACUU AACUAGUGAGUU GUUUGGGAAUGC AGCUCGCCCAGUG CUCUGAAUGUCAA AGUGAAGAAAU CAACCAAGCGCGG GUAAACGGCCGGA UAAUUGGUUUUU GCGGCUGUCUGAU CAGGCAUUGCCGC GAAGCUACCAUCC GGUAGAGUUAAG GUGCCGGAUACA CGCGCGUGUUACC UAUACUCUACAGG UGAACAGCCUUUC AAAUGAGAACUU UGAAUGUAUGAU UUUUACCGCAAUA GCUAGAACGCGGU GACGAUCGUUUUG AUUUUCAGUGUG AAUACAAAGGUAC CUUUGAAAAGAG GUGUUUGGGUGU AAAACCCAUACGC UACCGAAGCAGAA UUCGGUACUUUAG	6	52.51	35.26
h46	UGGAGGUCAGUGACGA AGCCUAGACCGUAAGG UCGGGUCGAACGGCCU CUA			6	53.58	36.33
h66	CAUUGCGAUGGUCAGA AAGUGAUGUUGACGCA AUG			6	53.65	36.39
h49	GGGGAUCUCC			6	54.15	36.89
h25	GGCAUUUGAUC AUGGU UAUAUGCC			6	54.33	37.08
h67	UUCGGA			6	55.11	37.85
h52	AUGGGGAAGCUCCGU			6	55.18	37.93
h13	UUGCCUAGUAACGGC GAGUGAAGCGGCAA			6	55.43	38.17
h38	AGAAGCUCGAGCUUUU			6	56.03	38.78
h100	UUUGUAUACGACUUA			6	56.25	39.00
h48	ACUAGU			6	57.47	40.22
h21	GAGUUGUUUGGGAUG CAGCUC			6	58.14	40.89
h68	GCCAGUGCUCUGAAU GUCAAAGUGAAGAAU UCAACCAAGCGCGGU AAACGGC			7	59.83	42.57
h96	CGGAUAAUUGGUUUUU GCGGCUGUCUGAUCAG GCAUUGCCGCGAAGCU ACCAUCCG			7	60.40	43.14
h41	GUAGAGUUAAGGUGCC GGAAUACACGCGCGUG UUACCUAUACUCUAC			7	61.04	43.79
h60	AGGUGAACAGCCU			7	61.61	44.36
h47	UUCAAAUGAGAACUUU GAA			7	61.64	44.39
h94	UGUAUGAUUU			7	61.68	44.42
h51	UUACCGCAAUAGCUAG AACGCGGUGA			7	61.96	44.70
h86	CGAUCG			7	62.95	45.70
63a	UUUUGAUUUUCAGUGU GAAUACAAA			7	63.08	45.83
h24	GGUAC			7	63.65	46.39
h99	CUUUGAAAAGAG			7	63.82	46.57

h28	GUGUUUGGGUGUAAAA CCCAUACGC		UCCCUCGGAUUU GAGGCUAGAGCCU	8	67.19	49.94
h91	UACCGAAGCAGAAUUC GGUA		GACAAAAGGGUA GGGAGUAAACUAU	8	67.65	50.40
h88	CUUUAGUCCCUCGGAA UUUGAGGCUAGAG		GACUCUCCGUCAG GGUUGAUUAUGAU	8	67.98	50.73
h82	CCUG		GCCCUGACGGGGU GAGAAUCCCAUCC	8	68.34	51.08
h85	ACAAAAGGGUA		GGAUAUGAAAGU GUCGGCGCGAGCC	8	68.50	51.24
h69	GGGAGUAACUAUGACU CUC		CUGCGGUGCGCUU GUGACGGCUCCGG	8	68.54	51.28
h45	CGUCAGGGUUGAUUAUG AUGCCCUGACG		UUAAGAUAUCCGGA UUCAAUUGAAGG	8	68.63	51.37
h20	GGGUGAGAAUCCC		GUGAAGCCAGAGG AAACUCUGGUGGA	8	69.01	51.76
h62	AUCCGGAU		GGCUCGAUUAUGG CUGAACGCCUCUA	8	69.40	52.15
h29	AUGAAAGU		AGUCAGAAUCCAA AGCUAGCUAUUGA	8	69.56	52.30
h56	GUCGGCGCGAGCCCUG CGGUGCGCUUGUGACG GC		ACUUAGUACGAGA GGAACAGUUCAUU	8	72.49	55.24
h53	UCCGGUUAAGAUUCCG GA		GGGUGGUAAAUAU CCAUCCCAACCGG	9	73.27	56.02
h79	UUCAAUUGAA		GUUCCUUGGAACA GGACAGGUGUUA	9	74.00	56.75
h34	GGGUGAAGCCAGAGGA AACUCUGGUGGAGGCU C		GUUCAUAUGAACU AGCCCUCUCCACA	9	74.68	57.43
h97	GAUUAUGGCUGAACGC CUCUAAGUCAGAAUCC A		CAAUAUAUUUUGC GUGGGGUCCUUGU	9	74.70	57.44
h14	AAGCUAGCU		CGGCGAGGA	9	74.88	57.63
h95	AUUGAACUUAGUACGA GAGGAACAGUUCAUU			9	74.94	57.69
h22	GGGUGGUAAAUCCAU C			9	75.86	58.60
h12	CCAACCGG			9	75.95	58.69
h19	GUUCCUUGGAACAGGA C			9	76.96	59.70
h42	AGGUGUUAGUUCAUAU GAACUAGCCCU			9	77.00	59.75
h98	CUCCACACAAUAUAUU UUGCGUGGGG			9	78.10	60.85
h18	UCCUUGUCGGCGAGGA			9	78.90	61.65
h25hs 1	GCCAGCAUGCUGGC	A-rest	GCCAGCAUGCUGG CACCGAUCCUGAU	10	81.16	63.91
h31	ACCGAUCCUGAUGUCU UCGGAUGGAUUUGAGU		GUCUUCGGAUGGA UUUGAGUUGUGG	10	81.17	63.91
h55	UGUGGAUCCACA		AUCCACAGGUUGG GGCCUCGCAAGAG	10	81.85	64.59
h30	GGUUGGGGCCUCGCAA GAGGUGCACAAC		GUGCACAAUCCA GAAAGUGAGGGG	10	82.52	65.27
h87	CAUGAAAGUG		GGCGCCCCCUAC	10	83.66	66.40
h83	AGGGGGGCGCCCCCUU			10	83.81	66.56

h101	ACAACGGGGUAUUGUA AGCAGUAGAGUAGCCU UGUUGUUACGAUCUGC UGAGAUUAAGCCUUUG UUGU		AACGGGGUAUUG UAAGCAGUAGAG UAGCCUUGUUGUU ACGAUCUGCUGAG AUUAAGCCUUUGU	10	84.08	66.83
h57	GAGGAGUUAUCUUUUC UUC		UGUGAGGAGUUA UCUUUUCUUCGCU	10	84.70	67.45
h63	GCUCUAAGGGUCGCGA UCAACUUAGAAC		CUAAGGGUCGCGA UCAACUUAGAACG	10	85.49	68.24
h59	GCCAGCACC UUUGCUG GC		CCAGCACC UUUGC UGGCUCAUGGAGA	11	89.34	72.09
h84	UCAUGGAGAACAGAAA UCUCCAGUAGA		ACAGAAAUCUCCA GUAGACAGCUUAU	11	90.19	72.94
h58	CAGCUUAUCACCCCGG AAUUGGUUUAUCCGGA GAUGGGGUCUUAUGGC UG		CACCCCGGAAUUG GUUUAUCCGGAGA UGGGGUCUUAUG GCUGCUCAAAUUU	11	90.49	73.24
h15	CUCAAAUUUGAAAUCU GGUACCUUCGGUGCCC GAGUUGUAAU		GAAAUCUGGUACC UUCGGUGCCCGAG UUGUAAUGGACU	11	91.01	73.76
h25es 7c	GGACUGCGACGUAAGU CAAGG		GCGACGUAAGUCA AGGCUGGAUAUG	11	91.32	74.06
h54	CUGGAUAUGGAUUCAU GCCAG		GAUUCAUGCCAGU GGCGGGCCGCGGU	11	91.72	74.46
h25s	UGGC		UCGCCUGAUUUUA	11	92.70	75.45
h17	GGGCCGCGGUUC		UGCAGGCGGACCG	11	93.05	75.80
h52E S19	GCCUGAUUUUAUGCAG GC		GCUAGCAACGGUG CACUUGGCGGAAA	11	93.67	76.42
h79E S31	GGACCG		GGCCUUGGGUGCU UGCUGGCGACGUA	12	97.36	80.11
h98b	GCUAGCAACGGUGCAC UUGGCGGAAAGGCCUU GGGUGCUUGCUGGC		AGUCGGCGUCCUU GUGGCGUCGAGGG	12	98.98	81.72
h25hs 2	GACGUAAGUC		CAACUUUAAAGUG CCUUCGAGUGUGU	12	100.32	83.07
h98a	GGCGUCCUUGUGGCGU C		AACAACUCGGUCC CAUUCGGGGCUGG	13	101.58	84.33
h16	GAGGGCAACUUUAAAG UGCCUUC		AAUUCAUUUCCA CCAUAGGAAUGUA	13	102.77	85.51
h44	GAGUGUGUAACAACUC		GCUUGCCUCGGUA AGUAUUAUAGCCU	14	109.83	92.57
h79E S31b	GGUCCAUUCGGGGC		GUGGCGGUGGCCA UGGAAGUCGGAA	14	111.96	94.71
h79E S31a	UGGAAUUCAUUUCCA		UCCG	14	112.94	95.69
h25es 7	CCAUAGGAAUGUAGCU UGCCUCGGUAAGUAUU AUAGCCUGUGG			14	114.17	96.92
h43	CGGUGGCCAUGGAAGU CGGAAUCCG			14	114.78	97.52

Table S2 (cont'd)

<i>D. melanogaster</i> (28S)						
Helix	Sequence	State	Composite Sequence	Bin no.	D _{COM}	D _{COM: H-LSU} ¹
74	CUUUUGAGCUAGUU ACCAUAG	A-core	CUUUUGAGCUAGUUAC CAUAGCCAAGCUUGGU GGAUGGUACCAUCCCG UGAGGGGGCGAAAGAC CGACUGGGGGCGGUACU UUCCCUCAGGAUAAUU AGCGGGGAAAUUACCC UACUAAUGUCUAAUUA AAACGACCGUCGUGAG ACAGGUUGGGAACGUG AGCUGGACAGUUCUGA CGUGCAAUUCGAUUGU CCCCCUGAAUUUAAGC AUAUAAUUAAGGGGAG CCAAGGGAACGGGCUU GG	1	16.39	0.00
26	CCAAGCUUGGUG			2	24.91	8.53
32	GAUGGUACCAUC			2	24.99	8.61
23	CCGUGAGG			2	29.48	13.09
35a	GGGCGAAAGACC			2	29.84	13.46
80	GACUGGGGGCGGUAC			3	30.67	14.29
37	UUUCCCUCAGGAUA			3	31.05	14.66
73	AUUAGCGGGGAAAU UACCCUACUAAU			3	32.75	16.36
65	GUCUAAUUAAC			3	32.78	16.40
93	GACCGUCGUGAGAC AGGUU			3	32.91	16.53
90	GGAACGUGAGCUG G			3	33.20	16.81
35	ACAGUUCUGACGUG CAAUUCGAUUGU			3	33.27	16.89
11	CCCCCUGAAUUUAA GCAUAAUAAUAGG GGAG			3	34.92	18.54
72	CCAAGGGAACGGGC UUGG			3	35.46	19.07
36	CCUUCGGGAAGG			4	40.11	23.73
39	GCCACUUUUGGUAA GCAGAACUGGC			4	40.25	23.87
27	CUAACAU AUGUGCA GCAUAUAUGCUGUG AC			4	43.31	26.92
40	UGGGAUGAACCA			4	43.42	27.04
33	AUACUUGAU AUUGA GUAUA			4	44.38	27.99
49b	GG			5	44.46	28.07
75	ACUCUAAUCUGGCA UGCCAGGUAGGGAG U			5	45.12	28.73
38	GCUGGUGCAUAAAU GUCCCAGU			5	46.69	30.30
92	UGGAUUGUUCACCC A			5	47.90	31.52
81	AUCUCUCAAUAAU AACGGAGGU			5	48.16	31.78
46	UACAAUGGUAUGCG CUGCCAUUGGUA			5	48.76	32.38
13	UUUCUUAGUAGCGG CGAGCGAAAAGAAA			5	49.36	32.98

61	GUAGGUAAGGCCCU AUCUACU			5	49.55	33.17
70	GCGCAU			5	50.43	34.05
25	CCCGAUGCUUCGGG			5	50.44	34.05
50	UCGUGUGAACAGUG GUUGAUCACGAGU	A- mofa	UCGUGUGAACAGUGGU UGAUCACGAGUGGAAU CCGGCAUUGUGAUGGC CCUAGCGGGUGUUGAC ACAAUGUGUGUUGCUU GAUAGUGCAGCACGGA GCUCCGGCUUGUGGCG GCCAAGCGUUCAUAGC GACGUCGCUUUUUGAU CCGUUAACUUUCUGGA UGUCAUCUAAUAGUG ACGGGUGAACCACGUG CCCAGUGCUCUGAAUG UCAAGUGAAGAAAU CAAGUAAGCGCGGGUC AACGGCCUCGGUGUUC AGUACACACAGGGUUG UAAACGACUUCGGCCG UCGAAUGAGAGCCUUG GAGUUAUUGGGAUAUA AACCUAUAGCGCUAA AGUAACUUUAGUGCUC UGAAUAGAGAGGUGAA GAGUCUAGGUGAAGAG UCUCGGACCAAUGGCA CAAUACUUGUUCGAGC GAACAGUGGUAUGACG CUACGUCCGCAAAAGG GCUUUUGGUUUAAGA GUUUUUAACAAGAGAU UAACUUCGGGGGUGC CAGGCCCCCUGAUCAG GAAUCGAUUCUUGUG AAGCAAAAUUCACCAA GCGGUUCAAUUGUUG UUGCACAAUGAUGGGA UAUCCCUUAACAACGU UGUAUAGGGAGUAACU AUGACUCUCCUAACAA GCCGUCGAGAGAUUUC GUCGAUUAUUUCUCCU CGGGAUCCGGGAUUAG GCGUUGGUUGCUAGCA ACUAGCCC	6	51.57	35.19
64	GGAAUCCG			6	51.86	35.47
66	GCAUUGUGAUGGCC CUAGCGGGUGUUGA CACAAUGU			6	52.32	35.94
21	GUGUUGCUUGAUAG UGCAGCAC			6	53.79	37.41
49	GGAGCUCC			6	53.85	37.47
89	GGCUUGUGGCGGCC AAGCGUUCUAGCG ACGUCGCUUUUUGA UCC			6	54.19	37.81
52	GUUAAC			6	54.27	37.88
67	UUUCUGGAU			6	54.91	38.53
71	GUCAUCUAAUAGU GAC			6	55.36	38.97
22	GGGUGAACC			6	56.22	39.83
48	ACGU			6	56.85	40.47
68	GCCCAGUGCUCUGA AUGUCAAGUGAAG AAAUUCAAGUAAGC GCGGGUCAACGGC			6	57.58	41.20
86	CUCGGUGUUCAGUA CACACAGGG			6	57.89	41.50
100	UUGUAAACGACUU			7	58.65	42.26
51	CGGCCG			7	61.19	44.81
47	UCGAAUGAGAGCCU UGGA			7	61.30	44.92
28	GUUAUUGGGAUAUA AACCUAUAGC			7	61.40	45.02
45	GCUAAAGUAACUUU AGUG			7	61.44	45.05
24	CUCUGAAUAGAG			7	61.75	45.36
49a	AGGUGAAGAGUCU			7	62.47	46.08
60	AGGUGAAGAGUCU			7	62.47	46.08
96	CGGACCAAUGGCAC AAUACUUGUUCGAG CGAACAGUGGUAUG ACGCUACGUCCG			7	62.92	46.53
85	CAAAAGGG			7	63.02	46.64
88	CUUUUGGUUAAAG AGUUUUUAACAAGA G			7	63.54	47.15

29	AUUAACUU			7	64.11	47.72
82	CCGG			7	64.14	47.76
20	GGGUGCCAGGCCC			7	64.87	48.49
25ES 7	CCUGAUCAGG			7	65.28	48.89
99	AAUCGAUU			8	66.52	50.14
91	CAUUGUGAAGCAAA AUUCACCAAGCG			8	66.67	50.29
14	GUUCAAAAU			8	68.50	52.12
94	GUUGUUGCGCAAUG AU			8	69.95	53.57
30	GGGAUAUCCC			8	70.27	53.89
41	UUAACAACGUUGUA UA			8	70.38	54.00
69	GGGAGUAACUAUGA CUCUC			8	70.54	54.16
12	CUAACAAG			8	70.71	54.33
62	CCGUCGAGAGAUAU CGUCGAUAUUUUCU CCUCGG			8	70.78	54.40
79	GAUCCGGGAUU			8	71.84	55.46
53	AGGCGUUGGUUGCU AGCAACUAGCCC			8	72.06	55.68
19	GUCCUUCUAAAUG AGGC	A-rest	GUCCUUCUAAAUGAG GCUACGGUCCAAUUC CGUAGGUUGAAGUCAG GGGAAACCCUGAUGGA AGACCAAUAACGAUA ACGUAAAUUGGAUUUAU GCCUGAACGCCUCUAA GGUCGUAUCCGUUAUC UGGUAAAGCGAAUGAU UAGAGGCCUUAGGGUC GAAACGAUCUUAACCU AUUCUCAACUUUAAA UGGCAAGGUGUGCUUA UCCUUUGCUGGGUAAC AUUGUACAAUGGGCCA GCGCUGACUGGGCGUU CUAUUAAGUUUUUAU GCCUCUACUGGAACG UACCAGCAAAAGCUAC CAUAAGAAGAGUUUUC UUUUCUGUGGCAUUU AAGCCGGCUCUGAAGA UAUCAAUUCAGAACUC CUUAACUUUCUUGAUA UGAAGAUC AAGCUGUU GAGCUCAACAGGUAAG GAGACAU AAGAGAAUA	9	72.81	56.42
56	UACGGUCCAAUUC CGUA			9	74.15	57.77
34	GGUUGAAGUCAGGG GAAACCCUGAUGGA AGACC			9	75.41	59.02
18ES 43	AAUUAACGAUAACG UUAAU			9	75.97	59.59
97	UGGAUUAUGCCUGA ACGCCUCUAAGGUC GUAUCCG			9	76.40	60.02
38a	UUAUCUGGUA AAGC GAAUGAUUAGAGGC CUUAGGGUCGAAAC GAUCUUAACCUAUU CUCAAACUUUAAA			9	76.56	60.17
101	GGCAAGGUGUGCUU AUCCUUUGCU			9	77.78	61.39
42	GGGUAA			9	78.61	62.22
98ES 39	CAUUGUACAAUG			9	78.74	62.36
83	GGCCAGCGCUGACU			10	81.30	64.91
31	GGGCGUUCUAUAUA GUUAUUUAUGCCUC UAACUGGAACGUAC C			10	81.80	65.41

87	AGCAAAAGCU		CCACUACUCUUAUUGU	10	82.96	66.57
55	ACCAUAA		UUCCUUACCAUGACAU	10	83.01	66.63
57	GAAGAGUUUUCUUU UCUGU		AUACUGUUGUGGUUUU	10	84.84	68.45
98	GGCAAUUUAAGCC		UUAGCUAUUUUAUAGCU	10	85.41	69.02
63	GGCUCUGAAGAUAU CAAUUCAGAACU		AAUUAACUAGCCGUAC			
38ES 12	CCUUAACUUUCUUG AUAUGAAGAUCAAG		UACCAUGGAAGUCUUU	10	85.41	69.02
54	CUGUUGAGCUCAAC AG		CGCAGAGAGAU AUGGU	11	86.48	70.10
76	GUAAGGAGACAUAA GAGAAUACCACUAC UCUUAUUGUUUCCU UAC		AGAUGGGCUACUAGUA	11	86.75	70.36
59	CAUGACAUAUACUG UUGUG		AUUACUAGGUGCGGAC			
30ES 9	GUUUUUUAGCUAUU UAUAGCUAAUUAAC		AGAAACCACACUGGAU	11	86.95	70.57
58	UAGCCGUACUACCA UGGAAGUCUUUCGC AGAGAGAU AUGGUA GAUGGGCUA		CCACACUAAUUUCCAC			
17	CUAGUAAUUA CUAG		AGUGCGCACUUGUAGA	11	87.83	71.44
84	GUGCGGACAGAAAC CACAC		GUGUGUAACAACUCGU			
79ES 31	UGGAUCCA		GGUUGAGCAGCUGCCA	11	88.00	71.61
16	CACUAAUUUCC		UACUGCGAUCCACCUG			
25ES 7c	ACAGUGCGCACUUG UA		GCAACAGUCUAUUAGC	11	89.01	72.62
44	GAGUGUGUAACAAC UC		AUAUACCAAAUUUAUC			
101E S41	GUGGUUGAGCAGCU GCCAUACUGCGAUC CAC		AUAAAAUUAACUUAU	11	89.89	73.50
54ES 20b	CUGGCAACAG		AGUUUAUUCCAAUUAA			
25ES 7b	UCUAUUAGCAUAUA CCAAAUUUAUCAUA AAAUUAACUUAUA GUUUAUUCCAAUUA AAUUGCUUGCAUUU UAACACAGAAUAAA UGUUAUUAAUUUGA UAAAGUGCUGAUAG A		AUUGCUUGCAUUUUA	11	90.75	74.36
98ES 39b	UGUAACAUAGUAAA UUGGGAGGAUCUUC GAUCACCUGAUGCC GCGCUAGUUACA		CUUCGAUCACCUGAUG			
			CCGCGCUAGUUACACG	11	91.86	75.48
			GUGAUCAUGGAAGUCG	12	93.71	77.33
			AAAUCCGUUAUAAUUU			
			ACUUUAUAAGUAUAAU	12	94.49	78.10
			GUAUAUUUAUAUUUAU			
			UAUGCUAUA AUGGCAU	12	97.28	80.89
			AAUUAUCAUUGAUUUU			
			UGUGUUUAUUUAUGUA	12	97.70	81.32
			UUCCAAAUUUUUCGGA			
			AUUAGGGAGAU AUUAG	12	99.15	82.76
			ACCUCGGUUUGGUAUC			
			GUCAAUGAAAUACCGA	12	99.64	83.25
			UAGUCGCGAUUAUCCU			
			UGAUUGGGAAACAAUA	12	100.2 3	83.84
			UUGUGGAACUUUCUUG			
			CUUUGUUUAUUAAUGGG	13	102.1 3	85.74
			CCUCGUGCUCAUAUUA			
			GACCUCGGUUUGGUUAU			
			UGUAUCAUUUCCUAGC			
			CAUUAUACGGAUAUAU			
			UUAUUAUAUCUUAUGG			
			UAUUGGGUUUUGAUGC			
			AAAAAUUUUAAUUUAU			
			UAAUUAUA			

43	CGGUGAUCAUGGAA GUCGAAAUCCG			13	102.3 1	85.92
98ES 39a	UUAUAAUUUACUUU AUA			13	103.6 2	87.23
31ES 9	GUAUAAUGUAUAUU UAUAUUUUUAUGC			13	104.7 3	88.35
25ES 7e	UAUAAUGGCAUAAU UAUCAUUGAUUUUU GUGUUUAUUUA			13	104.8 1	88.42
79ES 31b	GUAUCCA			14	113.5 1	97.13
25ES 7d	AAUUUUUCGGAUU A			15	115.0 0	98.61
77	GGGAGAUUUAGAC CUCGGUUUGGUAUC GUCAAUGAAAUACC			15	119.6 5	103.26
63ES 27	GAUAGUCGCGAUUA UC			15	121.2 3	104.84
63ES 27a	CUUGAUUGGGAAAC AAUAUUGUGGAACU UUCUUGC			16	128.3 4	111.95
54ES 20c	UUUGUUAUUA			17	128.8 0	112.41
54ES 20a	UGGGCCUCGUGCUC			17	129.3 2	112.93
78	AUAUUAGACCUCGG UUUGGUUAU			17	129.5 6	113.17
79ES 31a	UGUAUCAUUUCCUA GCCAUUAUACGGAU AUAUUUAUUAUAUC UUAUGGUUUUGGU UUUGAUGCA			17	130.0 5	113.67
63ES 27b	AAAAUUUUUAAUUA UUAUUUAU			18	135.7 6	119.37

Table S2 (cont'd)

<i>H. sapiens</i> (28S)						
Helix	Sequence	State	Composite Sequence	Bin no.	D _{COM}	D _{COM: H-LSU} ¹
25a	CCGUCUUGAAACAC GG	A-core	CCGUCUUGAAACAC GGCCUGUUGAGCUA GUUACCACAGGACC AAGCUUGGUUUUCC CUCAGGAUAGGAUG GUACCAUCGACUGG GGCGGUACCCUUCG AUGUCGGCUCUUC UAGGGAACGUGAGC UGGCCAAGGGAACG GGCUUGGCCCUCCG GAGGGCCGUAAGGG CCACUUUUGGUAAG CAGAACUGGCAAUC AGCGGGGAAAUAUAC CCUACUGAUGCCCGC UGAAUUUAAGCAUA UUAGUCAGCGGAG	1	16.17	0.00
74	CCUGUUGAGCUAGU UACCACAGG			1	18.59	2.42
26	ACCAAGCUUGGU			2	23.84	7.67
37	UUUCCCUCAGGAUA G			2	26.79	10.62
32	GAUGGUACCAUC			2	29.28	13.11
80	GACUGGGGCGGUAC			2	29.69	13.52
90	CCUUCGAUGUCGGC UCUUCCUAGGGAAC GUGAGCUGG			3	31.71	15.54
72	CCAAGGGAACGGGC UUGG			3	32.62	16.45
36	CCCUCGAGGG			3	34.52	18.35
23	CCGUAAGG			3	34.75	18.58
39	GCCACUUUUGGUAA GCAGAACUGGC			3	35.59	19.42
73	AAUCAGCGGGGAAA UUACCCUACUGAUG			3	36.10	19.93
11	CCCGCUGAAUUUAA GCAUAUUAGUCAGC GGAG			3	36.34	20.17
35a	GGCGAAAGAC			4	37.94	21.77
93	ACCGUCGUGAGACA GGU			4	38.15	21.98
40	CGGGAUGAACCG			4	38.17	22.00
35	CGGUCCUGACGUGC AAAUCGGUCG			4	39.95	23.78
65	GUUUAUUAAAAC			4	40.33	24.16
27	CUAACACGUGCGCG CGCACGUGUUAG			4	40.36	24.19
49a	CCGCAGCAGG			4	41.34	25.16
38	CUGGCGCUCGAGUG CCUAG			4	43.06	26.89
81	ACCUGUCAAACGGU AACGCAGGU			5	44.92	28.75
46	CGCUGCGGUGAGCC UUGAAGCCUAGGGC GCGGGCCCGGGUGG AGCCGCCGCAGGUG			5	45.61	29.44
25	CGGGUGGGCCCACC CG			5	46.41	30.24
13	UCCCUACAGUAACGG CGAGUGAACAGGGA			5	48.05	31.88

92	UGGAUUGUUCACCC A	A-mofa	UGGAUUGUUCACCC AUAUGCCUGGGGAC	6	51.29	35.12
33	UAUGCCUGGGGACC UGGGUAAU		CUGGGUAUGGCUUG UGGCGGCCAAGCGU	6	52.68	36.51
89	GGCUUGUGGCGGCC AAGCGUUCAUAGCG ACGUCGCUUUUUGA UCC		UCAUAGCGACGUCG CUUUUUGAUCCACU CUAGUCUGGCACGU GCCAGGUGCCCGCG GCGGGGCGGAGCGC CCGUCGCCGGCGCCG	6	53.51	37.34
75	ACUCUAGUCUGGCA CGUGCCAGGU		CGACGUCUUGAUUU UCAGUACGAAUACA GAGGGUUGCUUGGG AAUGCAGCCCGUAG GUAAGGCCCUACCU ACGCCGGGUUAAGG CGCCCGAUGCCGACG CUAGCGUCGGGCC AUACCCGGCGGGAA UCCGCGAGAUUCCCC CAUGUGAACAGCAG UUGAACAUGGGGAU GCCCAUCGCGCGAU GGUCGGGGGCUCGC ACGAAAGCCGCCGU GGCGUAGACGACGU CAUCUAAUUAGUGA CCCUACGAGCUCG CCCAGUGCUCUGAA UGUCAAGUGAAGA AAUUCAAUGAAGCG CGGGUAAACGGCAU GAAGGUGCCCGGAG CGCAGAAGGGCCCG G CUUCUGACCUUUUG GGUUUUAAGCAGGA G CGGUGUGAGGCCGC CGCGCGUCGGCUUU GAAGAGAGGCCGGC UUGUUGCCAUGGCC AGGCGGAACGAGGU GGCCACCUUCAAC GAGAACUUUGAACG GCCGCCACCAGACAU UUGGUGUAUGUGCU UGGCUGAGGAGCCA AUGGGGCGAAGCUA CCAUCUGAAACCGG UUUCUAACCAGAGG UGAACAGCCUGGGU	6	54.29	38.12
66	GCCCGCGGCGGG			6	54.30	38.13
52	GGCGAGCGCC			6	55.15	38.98
45	CGUCGCCGGCGCCG CGACG			6	55.26	39.09
86	UCUUGAUUUUCAGU ACGAAUACAGA			6	55.68	39.51
21	GGGUUGCUUGGGAA UGCAGCCC			6	55.71	39.54
61	GUAGGUAAGGCCC ACCUAC			6	55.87	39.70
41	GCCGGGUUAAGGCG CCCGAUGCCGACGC UAGCGUCGGGCCCA UACCCGGC			6	56.13	39.96
64	GGGAAUCCGCGAGA UUCCC			6	56.15	39.98
50	CCAUGUGAACAGCA GUUGAACAUGG			6	56.53	40.36
70	GAUAGUACG			6	57.82	41.65
49b	UGCC			7	58.35	42.18
67	CAUCGCGCGAUG			7	59.22	43.05
28	GUCGGGGGCUCGCA CGAAAGCCGCCGUG GC			7	59.24	43.07
100	GUAGACGAC			7	59.68	43.51
71	GUCAUCUAAUUAGU GAC			7	60.29	44.12
49	GGAGCUC			7	60.70	44.53
68	GCCCAGUGCUCUGA AUGUCAAGUGAAG AAAUUCAUGAAGC GCGGGUAAACGGC			7	61.52	45.35
29	AUGAAGGU			7	61.80	45.63
31	GCCCGGAGC			7	62.37	46.20
85	GCAGAAGGGC			7	62.81	46.64
82	CCGG			7	63.05	46.88
88	CUUCUGACCUUUUG GGUUUUAAGCAGGA G			7	63.39	47.22

20	CGGUGUGAGGCCG		GGUAAACUCCAUCG UCCUUCUGAUCGAG GC	7	64.20	48.03
25ES7	CCGCGCGUCGG			7	64.56	48.39
24	CUUUGAAGAGAG			7	64.56	48.39
48	GCCGGC			7	64.72	48.55
94	UUGUUGCCAUGGCC AGGCGGAACGA			7	64.95	48.78
30	GGUGGCCACC			8	66.04	49.87
47	UUCAAACGAGAACU UUGAA			8	67.61	51.44
51	CGGCCG			8	68.27	52.10
98ES3 9	CCAC			8	68.59	52.42
96	CAGACAUUUGGUGU AUGUGCUUGGCUGA GGAGCCAAUGGGGC GAAGCUACCAUCUG			8	69.01	52.84
99	AAACCGGUUU			8	70.10	53.93
12	CUAACCAG			8	70.16	53.99
60	AGGUGAACAGCCU			8	70.48	54.31
22	GGGUGGUAAACUCC AUC			8	71.64	55.47
19	GUCCUUCUGAUCGA GGC			8	72.09	55.92
14	GCCGGC	A-rest	GCCGGCGGGAGUAA CUAUGACUCUCGUG AAGCAGAAUUCACU AUCCGGUAAAGCGA AUGAUUAGAGGUCU UGGGGCCGAAACGA UCUCAACCUAUUCU CAAACUUUAAAUGG GUAAAUCCGUAACU UCGGGAUAAGGAUA GGUGUUGGUUGAUA UCAACUAGCCCUGG GAUUAUGACUGAAC GCCUCUAAGUCAGA AUCCCGGGGGCCGG CCCCCCCCGGCCGGG UCGGGUUCAGAUCC CCGAGGCGAGCGCU CGCUUAUCCUGCUC AGUACGAGAGGAAC CGCAGGUUCCGCCCG GAGGAUUAACCCG GCGGCGGGUCCGGC CGUGUCGGCGGCC GGCGGAUCUUUCCC	9	72.39	56.22
69	GGGAGUAACUAUGA CUCUC			9	73.30	57.13
91	GUGAAGCAGAAUUC AC			9	73.45	57.28
38a	UAUCCGGUAAAGCG AAUGAUUAGAGGUC UUGGGGCCGAAACG AUCUCAACCUAUUC UCAAAACUUUAAAUG GGUAA			9	73.84	57.67
62	AUCCGUAACUUCGG GAUAAGGAU			9	74.16	57.99
42	AGGUGUUGGUUGAU AUCAACUAGCCCU			9	75.47	59.30
97	GGGAUUAUGACUGA ACGCCUCUAAGUCA GAAUCCC			9	75.74	59.57
18ES4 3	GGGGGCCGGCCCCC			9	75.87	59.70
79	CCCGGCCGGG			9	77.40	61.23
53	UCGGGUUCAGAUCC CCGA			10	79.28	63.11
83	GGCGAGCGCUCGCU U			10	79.36	63.19

95	AUCCUGCUCAGUAC GAGAGGAACCGCAG GUU		GCCCCCGUCCUCC CGACCCUCCACCCG CCUCCCUUCCCCCG CCGCCCCGGGCUCCG GCGGGUGCGGGGGU GGGCGGGCGGGGCC GGGGGUGGGGUCGG CGGGGGACCGUCCCC CGACCGGCGACCGGC CGCCGCCGGGCGCAU UCCACCGCGGCGGC GUGAAAGCGCUCGC CCGCCGCGCCGGGA GGCCGGCGGGAGCC CCGGCCGGUGAGCU CUCGCUGGCCCCGGC UCGCUGGCGUGGAG CCGGGCUGGGUCGG GGUUUAGUCAGCCC UCGACACAGGGCGA AGCCAGAGGAAACU CUGGUGGAGGUCCG CGCCGCGGCCUUGCG CCCCGAGGCCUCUCC AGUCCGCCGAGGGG UGAAGAGACAUGAG AGCUCUGAUCGUUU UUUCACGGCCGGCG CGCUCGCCGGCCCC GGCGCCGCGCGCGCC GGGGCGCCGAAUCC CCGCCCCGCGGCGGG GCGCGGGACAUGUG GCGGGAGGACAGAA ACCUCCAGAGUUC UCUUUUCUGACCCC CGCCGAUCCCGGAUC CGGGGGAGAGCGUC GCGGUUCCGGCGGC GGCCGCGCUCGAGC GCACCCGAGUGGC GCGCGCCGGGAGUG UGUAACAACUCGCU CUAAGGGCUGCAGC CGACUUAGAACUGG GAAACGGGGCGCGG CCGAGAGGCGGCC GCCCCUCGCCAGG GCAGGGCGCCUGG AAUGGGUUCGCCCC GAGAGAGGGGCCCG	10	80.70	64.53
25ES7 a	CCGCCCCGAGGAUU CAACCCGGCGGCGG GUCCGGCCGUGUCG GCGGCCCCGCGGAU CUUCCCCGCCCCC GUUCCUCCCGACCC CUCCACCCGCCUCC CUUCCCCCGCCGCC CGGGCUCGCGGGG UGCGGGGGUGGG CGGGCGGGGCCGGG GGUGGGGUCGGCGG GGGACCGUCCCCCG ACCGGCGACCGGCC GCCGCCGGGCGCAU UCCACCGCGGCGG		10	80.87	64.70	
87	CGUGAAAGCG		10	80.88	64.71	
31ES9	CUCGCCCCCGCGCC GGGGAG		10	81.54	65.36	
56	GCCGGCGGGAGCCC CGGCCGGUGAGCUC UCGCUGGC		10	81.87	65.70	
38ES1 2	CCCGGCUCGCUGGC GUGGAGCCGGGC		10	83.45	67.28	
101	UGGGUCGGGGUUUA GUCAGCCUCGACA CA		10	83.66	67.49	
34	GGGCGAAGCCAGAG GAAACUCUGGUGGA GGUCC		10	84.07	67.90	
98	GCGCCGCGGCCUGG CGC		10	84.66	68.49	
30ES9	CCCGAGGCCUCUCC AGUCCGCCGAGGG		11	88.76	72.59	
76	GUGAAGAGACAUGA GAGCUCUGAUCGUU UUUUCAC		11	89.27	73.10	
30ES9 a	GGCCGGCGCGCUCG CCGGCC		11	89.52	73.35	
17	CCCGGCGCCGCGCG CGCCGGG		11	90.20	74.03	
15	GCGCCGAAUCCCCG CCCCGCGGCGGGGC GCGGGACAUGUGGC		11	90.33	74.16	
84	GGGAGGACAGAAAC CUCCC		11	91.63	75.46	
57	AGAGUUCUCUUUUC U		11	92.57	76.40	

38ES1 0	GCACCCCCGC		UGCCUUGAAGACCC	11	92.58	76.41
55	CGAUCCCGGAUCCG GGGGAGA		GCGGGUCUUCGGC	12	93.57	77.40
59	GCGUCGCGGUUCCG GCGGCG		GGGGGCGGCGCGC	12	94.33	78.16
25ES7 c	GCCGCGCUCGAGCG CAC		CGGACGGGCGAUGG	12	95.39	79.22
54	CCGGAGUGGCGCGC GCCGG		CCUCCGUUGCCCUCG	12	96.31	80.14
44	GAGUGUGUAACAAC UC		CGGGCCCCGCGGCUC	12	97.61	81.44
63	GCUCUAAGGGCUGC AGCCGACUUAGAAC U		GGGACGGCUGGGAA	12	97.96	81.79
98ES3 9b	GGGAAACGGGGCGC GGCCGGAGAGGCGG CCGCCCCCUCGCCC		GGCCCCGCGGGGAA	12	98.32	82.15
58	AGGGCAGGGCGCCC UGGAAUGGGUUCGC CCCGAGAGAGGGGC CCGUGCCUU		GGUGGCUCGGGGGG	12	98.47	82.30
16	GAAGACCCGCGGGU CUUC		CCCCGUCCGUCCGUC	12	99.23	83.06
45ES1 5a	CGGCGGGGGCGGCG CGCGCG		CGGCGGCGGCGGCG	12	99.75	83.58
52ES1 9	GACGGGCGAUGGCC UCCGUUGCCCUCG		ACCCCCCGAGUGU	12	99.84	83.67
79ES3 1	CGGGCCCCG		UACAGCCCCCCCCGC	13	100.17	84.00
25ES7 b	CGGCUCCGGGACGG CUGGGAAGGCCCGG CGGGGAAGGUGGCU CGGGGGGCCCCGUC CGUCCGUCCGGCGG CGGCGGCGGCGGCG GGACCGAAACCCCC CCCGAGUGUUACAG CCCCCCCCGCGAGCA GCACUCGCCGAAUC CCGGGGCCG		AGCAGCACUCGCCG	13	100.98	84.81
43	CGGUGGCCAUGGAA GUCGGAUCCG		AAUCCCGGGGCCGC	13	101.77	85.60
77	AGUGGCCACU		GGUGGCCAUGGAAG	13	104.26	88.09
101ES 41	UAGCAGAGCAGCUC CCUCGCUGCGAUCU A		UCGAAUCCGAGUG	13	107.14	90.97
54ES2 0b	UGCGGUAACGCG		GCCACUCCGCCC	14	107.89	91.72
25ES7 e	GGGGCGGACUGUCC CCAGUGCGCCCC		CGCGGGGGCGGACU	15	115.91	99.73

25ES7 h	CGUCCCCCGAAGAG GGGGACG		GCCCCAGUCCGCCGG CGCGCGCGUGUGGU	15	119.18	103.01
25ES7 d	CCCCCUCCCGGCGC CCACCCCCGCGGGG ACUCCCCCGCGGGG GCGCGCCGGCGUCU CCUCGUGGGGGGG		GUGCGUCGAGGGC GGCCUCCUCCCGCCC ACGCCCCGCUCCCCG CGGCGGGCGUCGCG GCCGCGCGGUUCCGC GCGGCGCCUCGCCCC CCCCCGGUGUCCCCG CGAGGGGGCCCGGG CGG	15	119.87	103.70
79ES3 1a	GGCGAGCCCCGAGG GGCUCUC			15	120.10	103.93
98ES3 9a	CCGUCCCCCGCCU GUCCCCGCGGCGG GCCGCCCCCCCCCUC CACGGGAGGGCGCG UGCCCCGCGCGC GCCGGGACCGGGGU CCGG			15	120.56	104.39
25ES7 g	GAGGUUCUCUCGGG			15	121.15	104.98
79ES3 1b	GCGCCCGGCCGCGC GCCGCGCGGGCGC			16	122.54	106.36
78	GGCCCCCGCGGGCC			17	128.54	112.37
25ES7 f	CACCCUCCUCCCCG CGCCCCCGGGGUGC CGCGCGCGGGUCGG GGG			17	132.89	116.72
63ES2 7	CGGUCGCGGCCG			17	133.15	116.98
54ES2 0a	UGGCGCGCGGAGG CGUCCA			18	135.40	119.22
63ES2 7a	UGGGGCGCGAAGCG GGGCUGGGCGCGCG CCGCGGCUGGAUCU GGACGCGAGCCGGG CCCUUCCCGUGGAU CGCCCCA			18	135.54	119.37
78ES3 0a	GUCCGCCGGC			18	139.76	123.58
45ES1 5	GCGCGCGUGUGGUG UGCGUCGAGGGCG GCCUCCUCCCGCCA CGCCCCGCUCCCCG			19	142.32	126.15
63ES2 7b	GGCGGGCGUCGCGG CCGCGCGGUUCCGC GCGGCGCCUCGCC			19	143.01	126.84
78ES3 0	CCCCCGGUGUCCC CGCGAGGGGCCCGG GGCGG			19	149.13	132.96

Table S2 (cont'd)

human mitochondria (16S)						
Helix	Sequence	State	Composite Sequence	Bin no.	D _{COM}	D _{COM: H-LSU} ¹
59	GUAAUCCAGGUCGG UUUCUAUCUACUUU C	A-core	GUAAUCCAGGUCGGUU UCUAUCUACUUUCAGC AAGACGACUGAGUUA GGGGUUUACGACCUCG AUGUUGGAUCAUGACC AACGGAACAAGUUACC CUAGGGAUAAACAGCGC AAUCCUAUUCACCUUC UGCAUAAUGACCCGGC UGGAACUUUGCAAGGA GAGCCAUAUAAAAUUU CGGUUGGGGCGAGCCC GUGAAGAGGCGGGCAG GCGACAAACCUACCCC GUCUAUGUAGCAAAAU AGUGGGUGUUUACCAA AAACAGUUAGUGAAUC UUAGUUCAUAAGUAAC GUGAAAUU	1	12.61	0.00
47	AGCAAGACGACUGA GUUCAG			1	15.59	2.98
56	GGGUUUACGACCUC GAUGUUGGAUCA			1	17.18	4.57
54	UGACCAACGGAACA AGUUACCCUAGGGA UACAGCGCAAUCC UAUUC			2	20.07	7.46
8	ACCUUCUGCAUAAU GA			2	22.16	9.55
12	CCCGGCUGG			2	24.69	12.08
11	AACUUUGCAAGGAG AGCCAAAGCUAAGA CCCCGAAACCAGA CGAGCUACCUAAGA ACAGCUAAAAGAGC ACACCCGUCUAUGU AGCAAAAUAGUGGG AAGAUUUUAUAGGUA GAGGCG			3	27.05	14.44
51	AUUAAAAAUUUCGG UUGGGGCGA			3	30.05	17.44
46	GCCCGUGAAGAGGC GGGC			3	31.40	18.79
17	AGGCGACAAACCUA C			3	31.66	19.05
16	CCCGUCUAUGUAGC AAAAUAGUGGG			3	31.97	19.36
40	UGUUUACCAAAAAC A			3	32.16	19.55
10	GUUAGU			3	32.97	20.36
19	GAAUCUUAGUUC			3	33.06	20.45
28	AUAAGUAACGUGAA AUU			3	33.51	20.90
13	CCAGACAG			4	34.51	21.90
9	AUUAAC			4	34.93	22.32
21	GUCCAAAGAGGAAC AGCUCUUUGGAC			4	36.00	23.39
58	CAACGAUUAAGUC CUACG			4	36.53	23.92
48	CCUAUGGAGCUUCU CAAUUGAUCCA			4	36.83	24.22

3	UAGCCAAACCAUUU AC			4	38.29	25.68
5	CCGCAAGG			4	38.82	26.21
36	CCAACACAGG			4	39.01	26.40
22	AGGAAAAAACCU	A- mofa	AGGAAAAAACCUAAAA AGUAAAAGGAACUCGG CCUGUCUCUUACUUUU ACCCCGCGAGGGUGCA UAAUCACUUGUCCUU AAAUAGGGACCUGUAU CUACCUAAGAACGAUU UAUAGGUAGAGUCCAA UUGGACGCGCAGGUAC CAGCAAGGACUAACCC CUCAUAUCAACAAGCU AUUAAAGGUUCGUCCG CCGGCUCACAUCCCGA UGGUGUCGGAGCAGAA CCCAACCUCGAGCAG UACAUGCUAAGACUUC ACGCCUGCAACGCCCA GUGACACAUGUUUAA GGCAUAAGGCCUACUU CACAAAGCGGCCCGGC GCCCUAGGAACUUUAA AUUUGCCACAGAACC CUCUAAAUCCCUUGU AAAUUUAAACUGUGCAU AUGCGUCAGAUUAAAA CACUGAACUGACUAAA GUAUAGGCGAUAGAAA UUCCUCUAGCAUACCC AGUAUUAGAGGGCUAA AAGAGCGAGAGAGUAC UCCUC	5	40.66	28.05
38	AAAAAGUAAAAGGA ACUCGGCCUGUCUC UUACUUUU			5	40.83	28.22
39	ACCCCGCGAGGGU			5	41.00	28.39
45	GCAUAAUCACUUGU UCCUUAUUAGGGA CCUGUAU			5	42.65	30.04
14	CUACCUAAGAACGA UUUAUAGGUAGA			5	46.23	33.62
18	GUCCAAUUGGAC			5	46.87	34.26
1	GCGC			6	47.81	35.20
37	AGGUACCA			6	47.95	35.34
7	GCAAGGACUAACCC CU			6	48.52	35.91
55	CAUAUCAACAAGCU AUUAAAGGUUCGU			6	48.67	36.06
42	CCGCCGGCUC			6	52.23	39.62
57	ACAUCCCGAUGGUG			6	53.13	40.52
52	UCGGAGCAGAACCC AACCUCGAGCAGU ACAUGCUAAGACUU CAC			6	53.79	41.18
32	GCCUGCAAC			6	54.58	41.97
43	GCCCAGUGACACAU GUUUAACGGC			6	54.59	41.98
61	AUAAGGCCUACUUC ACAAAGCG			7	55.03	42.42
2	GCCCGGCGC			7	56.10	43.49
30	CCUAGGA			7	56.73	44.12
20	ACUUUAAAUUUGCC CACAGAACCCUCUA AAUCCCCUUGUAAA UUUAACUGU			7	56.96	44.35
31	GCAUAUGC			7	57.15	44.54
33	GUCAGAUUAAAACA CUGAACUGAC			7	57.29	44.68
4	UAAAGUAUAGGCGA UAGAAAUU			7	57.43	44.82
41	CCUCUAGCAUACCC AGUAUUAGAGG			7	58.32	45.71
15	GCUAAAAGAGC			7	58.83	46.22
23	GAGAGAGUACUCCU C			7	60.22	47.61

6	AUGAAAAAUUAUAA CCAAG	A-rest	AUGAAAAAUUAUAAACC AAGCGCGGUACCCUAA CCGUGAUCUAUCACCC UAUAGAAUUUAUUAAU GCAAACAGUAGAAAAC AUUCAAAUCCUCCCU GUACGAAAGGACACAG UCAAGCGCAGCACUG AAUAUCUACAAUCAAC CAACAAGUCAUUUUU AUCAUCUCAACUAAA AGCGUUCAAGCUCCAC CCAACACCCGUAGGCC UAAAAGCAGCCACC	8	61.68	49.07
44	CGCGGUACCCUAA CGUG			8	61.71	49.10
27	AUCUAUCACCCU AGA			8	62.56	49.95
49	AUUUAUUAAUGCA ACAGUA			8	64.41	51.80
29	GAAAACAUUC			8	66.84	54.23
60	AAAUUCCUCCCUG ACGAAAGGACA			8	67.78	55.17
53	CAGUCAAGCG			9	68.84	56.23
34	CAGCACUG			9	69.64	57.03
35	AAUAUCUACAAUC ACCAACAAGUCAU AUU			9	75.03	62.42
62	UAUCAUCUACU A			9	75.45	62.84
26	AAAGCGUUCAAGC C			11	85.53	72.92
24	CACCCAACACCC			12	90.71	78.10
25	GUAGGCCUAAAAG AGCCACC			12	92.12	79.51

1. $D_{\text{COM: H-LSU}}$ is the regenerated set of geometric distances for binning. It utilizes the D_{COM} (the distance between the center of mass (COM) of an A-helix and the LSU] subtracted from the smallest distance.

Reference.

- 1 Sievers, F. *et al.* Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. *Mol Syst Biol* **7**, 539 (2011).
<https://doi.org/10.1038/msb.2011.75>
- 2 Madeira, F. *et al.* The EMBL-EBI Job Dispatcher sequence analysis tools framework in 2024. *Nucleic acids research* **52**, W521–W525 (2024).
<https://doi.org/10.1093/nar/gkae241>
- 3 Hillis, D. M. & Bull, J. J. An empirical test of bootstrapping as a method for assessing confidence in phylogenetic analysis. *Systematic biology* **42**, 182–192 (1993).
- 4 Dunkle, J. A. *et al.* Structures of the bacterial ribosome in classical and hybrid states of tRNA binding. *Science* **332**, 981–984 (2011).
- 5 Selmer, M. *et al.* Structure of the 70S ribosome complexed with mRNA and tRNA. *Science* **313**, 1935–1942 (2006).
- 6 Klein, D. J., Schmeing, T. M., Moore, P. B. & Steitz, T. A. The kink-turn: a new RNA secondary structure motif. *The EMBO journal* **20**, 4214–4221 (2001).
- 7 Ben-Shem, A. *et al.* The structure of the eukaryotic ribosome at 3.0 Å resolution. *Science* **334**, 1524–1529 (2011).
- 8 Anger, A. M. *et al.* Structures of the human and Drosophila 80S ribosome. *Nature* **497**, 80–85 (2013).
- 9 Koripella, R. K. *et al.* Distinct mechanisms of the human mitoribosome recycling and antibiotic resistance. *Nature Communications* **12**, 1–13 (2021).