

Table S1: Percentage of cases in which the SPS and CS scores become better (the first number for each algorithm) and worse (the second number for each algorithm) on full length protein sequences in BALiBASE 3.0 when comparing the results of the modified algorithm NRAlign to the original algorithm.

SPS	TCoffee		MUSCLE		ProbCons		MUMMALS	
1V1 {38}	44.74	36.84	60.53	39.47	47.37	47.37	10.53	34.21
1V2 {44}	65.91	29.55	75.00	20.45	54.55	18.18	36.36	25.00
1 (V1-V2) {82}	56.10	32.93	68.29	29.27	51.22	31.71	24.39	29.27
2 {41}	39.02	46.34	51.22	41.46	26.83	19.51	58.54	19.51
3 {30}	50.00	36.67	50.00	46.67	20.00	26.67	26.67	50.00
4 {49}	53.06	34.69	55.10	40.82	32.65	28.57	36.73	28.57
5 {16}	56.25	43.75	50.00	50.00	75.00	6.25	68.75	25.00
All (1-5) {218}	51.38	37.16	58.26	38.07	39.91	26.15	37.16	29.82
CS	TCoffee		MUSCLE		ProbCons		MUMMALS	
1V1 {38}	36.84	10.53	36.84	31.58	23.68	15.79	0.00	10.53
1V2 {44}	59.09	15.91	65.91	27.27	29.55	6.82	27.27	11.36
1 (V1-V2) {82}	48.78	13.41	52.44	29.27	26.83	10.98	14.63	10.98
2 {41}	48.78	4.88	41.46	21.95	9.76	7.32	26.83	12.20
3 {30}	36.67	20.00	40.00	33.33	13.33	6.67	26.67	16.67
4 {49}	38.78	14.29	36.73	20.41	16.33	10.20	18.37	12.24
5 {16}	50.00	25.00	50.00	31.25	25.00	12.50	37.50	12.50
All (1-5) {218}	44.95	13.76	44.95	26.61	19.27	9.63	21.10	12.39

Table S2: Percentage of cases in which the SPS and CS scores become better and worse on HOM-STRAD.

SPS	TCoffee		MUSCLE		ProbCons		MUMMALS	
0-20% {156}	41.03	30.13	59.62	31.41	62.82	22.44	28.85	16.67
20-40% {459}	56.43	24.18	57.30	34.64	70.15	23.53	33.77	20.48
40-70% {348}	41.67	14.94	42.24	28.74	53.74	20.98	28.45	17.24
70-100% {69}	13.04	8.70	13.04	18.84	14.49	15.94	24.64	10.14
All {1032}	46.22	20.93	49.61	31.10	59.79	22.00	30.62	18.12
CS	TCoffee		MUSCLE		ProbCons		MUMMALS	
0-20% {156}	44.23	25.00	55.77	33.97	60.26	21.79	23.72	15.38
20-40% {459}	56.43	21.35	56.64	33.33	66.45	21.79	28.98	19.39
40-70% {348}	39.94	12.64	41.67	27.59	50.86	19.83	27.59	13.22
70-100% {69}	13.04	8.70	13.04	18.84	14.49	15.94	24.64	8.70
All {1032}	46.12	18.12	48.55	30.52	56.78	20.74	27.42	15.99

Table S3: Percentage of cases in which the Q score becomes better and worse on PREFAB 4.0.

$Q(2)$	TCoffee		MUSCLE		ProbCons		MUMMALS	
0-20% {887}	28.30	18.60	43.86	28.07	48.70	18.15	13.53	8.79
20-40% {588}	44.90	24.66	64.12	22.45	67.35	19.22	23.98	13.95
40-70% {112}	26.79	10.71	33.93	27.68	48.21	12.50	23.21	8.93
70-100% {95}	8.42	5.26	13.68	12.63	22.11	3.16	15.79	5.26
All {1682}	32.88	19.44	48.57	25.21	53.69	17.30	17.95	10.40
$Q(50)$	TCoffee		MUSCLE		ProbCons		MUMMALS	
0-20% {887}	42.05	31.23	43.63	40.14	26.72	18.26	30.55	26.27
20-40% {588}	48.81	33.84	47.28	41.67	33.84	14.63	37.41	29.93
40-70% {112}	24.11	37.50	39.29	32.14	25.89	6.25	22.32	19.64
70-100% {95}	18.95	13.68	23.16	13.68	16.84	1.05	17.89	5.26
All {1682}	41.91	31.57	43.46	38.64	28.60	15.22	31.69	25.92

Table S4: Percentage of cases in which the f_D and f_M scores and the normalized Dali Z-score, GDT_TS score, and ContactA and ContactB scores become better and worse on the Twilight and Superfamily subsets of SABmark 1.65.

Twilight {205}	TCoffee		MUSCLE		ProbCons		MUMMALS	
f_D	49.27	41.95	57.07	37.56	53.66	38.05	39.02	28.78
f_M	43.90	50.24	54.15	40.49	43.41	50.73	44.39	31.22
Dali Z-score	57.07	42.93	56.59	43.41	63.41	36.59	53.17	39.02
GDT_TS	57.07	42.93	55.12	44.88	59.02	40.98	48.78	41.46
ContactA	53.66	46.34	56.59	43.41	53.66	46.34	47.80	44.39
ContactB	54.15	45.85	57.07	42.93	53.66	46.34	47.80	44.39
Superfamily {422}	TCoffee		MUSCLE		ProbCons		MUMMALS	
f_D	54.50	35.78	52.61	40.76	59.00	31.04	36.97	29.86
f_M	53.32	39.10	52.37	41.71	50.24	41.71	40.52	31.52
Dali Z-score	54.03	45.02	56.87	41.47	69.43	29.62	50.95	37.20
GDT_TS	55.45	43.36	56.16	42.18	67.06	31.99	48.34	38.39
ContactA	52.61	46.45	55.92	42.42	62.56	36.49	46.68	41.47
ContactB	47.16	51.90	55.69	42.65	56.87	42.18	46.45	41.71

Table S5: Percentage of cases in which the SPS, CS and SCI scores become better and worse on Data-set 1 of BRAliBase II.

SPS	TCoffee		MUSCLE		ProbConsRNA	
0-55% {96}	82.29	17.71	61.46	38.54	69.79	30.21
55-75% {218}	80.28	19.72	51.38	45.41	58.72	30.28
75-100% {167}	39.52	35.33	28.74	33.53	43.11	23.35
All {481}	66.53	24.74	45.53	39.92	55.51	27.86
CS	TCoffee		MUSCLE		ProbConsRNA	
0-55% {96}	65.62	28.12	56.25	35.42	54.17	35.42
55-75% {218}	80.28	16.51	49.08	40.37	50.92	29.36
75-100% {167}	29.94	29.94	24.55	26.95	34.13	22.75
All {481}	59.88	23.49	42.00	34.72	45.74	28.27
SCI	TCoffee		MUSCLE		ProbConsRNA	
0-55% {96}	77.08	8.33	56.25	28.12	77.08	8.33
55-75% {218}	80.28	12.39	50.00	32.11	80.28	12.39
75-100% {167}	33.53	26.35	28.74	21.56	33.53	26.35
All {481}	63.41	16.42	43.87	27.65	50.52	14.97

Table S6: Percentage of cases in which the Q score becomes better and worse on the mdsa_all set of DNA PREFAB.

Q	TCoffee		MUSCLE		ProbConsRNA	
0-20% {123}	16.26	7.32	27.64	10.57	19.51	5.69
20-40% {1030}	56.31	10.78	57.48	18.74	58.83	9.81
40-70% {436}	92.43	2.75	91.75	4.82	93.58	2.06
70-100% {87}	26.44	4.60	17.24	21.84	48.28	8.05
All {1676}	61.22	8.11	62.11	14.68	64.44	7.40

Table S7: Percentage of cases in which the number of gaps in an alignment (num_gap, a string of consecutive indels within a sequence is counted as one gap), the average length of gaps (len_gap) and the length of the alignment (len_aln) become smaller, larger and smaller respectively (the first number for each algorithm), and larger, smaller and larger respectively (the second number for each algorithm), on full length protein sequences in BALiBASE 3.0. For each algorithm, the third number is the p -value of the number of gaps in an alignment, the average length of gaps and the length of the alignment becoming smaller, larger and smaller respectively.

num_gap	TCoffee			MUSCLE			ProbCons			MUMMALS		
1V1 {38}	92.11	0.00		92.11	7.89		94.74	0.00		76.32	10.53	
1V2 {44}	95.45	0.00		93.18	4.55		86.36	6.82		68.18	11.36	
1 (V1-V2) {82}	93.90	0.00	8×10^{-15}	92.68	6.10	8×10^{-15}	90.24	3.66	3×10^{-13}	71.95	10.98	8×10^{-9}
2 {41}	100.00	0.00		92.68	7.32		73.17	26.83		60.98	36.59	
3 {30}	100.00	0.00		96.67	3.33		80.00	20.00		46.67	50.00	
4 {49}	97.96	2.04		95.92	4.08		77.55	18.37		75.51	20.41	
5 {16}	100.00	0.00		100.00	0.00		100.00	0.00		93.75	6.25	
All (1-5) {218}	97.25	0.46	5×10^{-37}	94.50	5.05	8×10^{-36}	83.49	13.30	2×10^{-21}	68.81	22.94	2×10^{-8}
len_gap	TCoffee			MUSCLE			ProbCons			MUMMALS		
1V1 {38}	86.84	7.89		92.11	7.89		97.37	0.00		68.42	15.79	
1V2 {44}	90.91	6.82		88.64	9.09		77.27	18.18		65.91	13.64	
1 (V1-V2) {82}	89.02	7.32	2×10^{-13}	90.24	8.54	1×10^{-11}	86.59	9.76	6×10^{-12}	67.07	14.63	3×10^{-6}
2 {41}	100.00	0.00		95.12	4.88		70.73	29.27		58.54	39.02	
3 {30}	96.67	3.33		96.67	3.33		70.00	30.00		50.00	46.67	
4 {49}	97.96	2.04		89.80	10.20		75.51	22.45		73.47	24.49	
5 {16}	87.50	12.50		100.00	0.00		87.50	12.50		87.50	12.50	
All (1-5) {218}	94.04	4.59	6×10^{-35}	92.66	6.88	3×10^{-31}	78.90	19.27	9×10^{-18}	66.06	25.69	5×10^{-11}
len_aln	TCoffee			MUSCLE			ProbCons			MUMMALS		
1V1 {38}	76.32	7.89		68.42	23.68		76.32	10.53		52.63	7.89	
1V2 {44}	75.00	2.27		68.18	6.82		68.18	18.18		29.55	15.91	
1 (V1-V2) {82}	75.61	4.88	1×10^{-10}	68.29	14.63	3×10^{-8}	71.95	14.63	9×10^{-9}	40.24	12.20	5×10^{-4}
2 {41}	87.80	12.20		73.17	21.95		63.41	36.59		51.22	31.71	
3 {30}	90.00	10.00		80.00	20.00		63.33	30.00		50.00	43.33	
4 {49}	77.55	22.45		65.31	32.65		59.18	38.78		63.27	28.57	
5 {16}	93.75	6.25		75.00	12.50		75.00	25.00		62.50	25.00	
All (1-5) {218}	81.65	11.01	6×10^{-22}	70.64	20.64	5×10^{-12}	66.51	27.06	2×10^{-6}	50.46	24.77	0.008

Table S8: Percentage of cases in which the number of gaps in an alignment (num_gap), the average length of gaps (len_gap) and the length of the alignment (len_aln) become smaller, larger and smaller respectively, and larger, smaller and larger respectively, on HOMSTRAD.

num_gap	TCoffee			MUSCLE			ProbCons			MUMMALS		
0-20% {156}	42.31	0.00	6×10^{-13}	80.13	0.00	8×10^{-23}	75.00	1.92	2×10^{-19}	19.23	4.49	2×10^{-4}
20-40% {459}	42.70	2.40	2×10^{-33}	60.78	3.49	8×10^{-41}	58.82	2.40	3×10^{-41}	16.99	4.36	2×10^{-7}
40-70% {348}	21.26	2.01	5×10^{-13}	30.75	0.57	4×10^{-19}	27.59	1.44	3×10^{-15}	11.21	3.16	3×10^{-4}
70-100% {69}	5.80	0.00	—	2.90	0.00	—	2.90	0.00	—	1.45	0.00	—
All {1032}	32.95	1.74	3×10^{-56}	49.71	1.74	2×10^{-78}	47.00	1.84	5×10^{-72}	14.34	3.68	6×10^{-13}
len_gap	TCoffee			MUSCLE			ProbCons			MUMMALS		
0-20% {156}	37.82	5.13	5×10^{-8}	72.44	9.62	8×10^{-19}	67.95	11.54	1×10^{-15}	17.95	7.05	9×10^{-4}
20-40% {459}	40.09	4.79	1×10^{-26}	55.99	9.80	8×10^{-34}	55.56	5.88	3×10^{-39}	14.81	6.75	2×10^{-5}
40-70% {348}	20.69	2.87	3×10^{-9}	26.72	5.46	3×10^{-14}	26.72	1.72	7×10^{-15}	10.06	5.17	0.004
70-100% {69}	5.80	0.00	—	1.45	2.90	—	2.90	0.00	—	1.45	0.00	—
All {1032}	30.91	3.88	6×10^{-41}	44.96	7.85	3×10^{-62}	44.19	4.94	2×10^{-64}	12.79	5.81	3×10^{-9}
len_aln	TCoffee			MUSCLE			ProbCons			MUMMALS		
0-20% {156}	26.92	5.13	3×10^{-5}	56.41	8.97	8×10^{-12}	55.13	3.21	4×10^{-14}	8.33	3.21	—
20-40% {459}	20.26	2.18	6×10^{-14}	37.91	6.75	8×10^{-18}	34.42	2.83	3×10^{-23}	7.19	1.09	5×10^{-6}
40-70% {348}	7.47	0.00	2×10^{-6}	14.94	2.01	3×10^{-9}	9.20	1.15	3×10^{-5}	4.31	1.72	0.006
70-100% {69}	1.45	0.00	—	2.90	0.00	—	0.00	0.00	—	0.00	0.00	—
All {1032}	15.70	1.74	9×10^{-21}	30.62	5.04	1×10^{-34}	26.74	2.13	3×10^{-39}	5.91	1.55	1×10^{-7}

Table S9: Percentage of cases in which the number of gaps in an alignment (num_gap), the average length of gaps (len_gap) and the length of the alignment (len_aln) become smaller, larger and smaller respectively, and larger, smaller and larger respectively, on PREFAB 4.0. (a) Only the original input protein sequence pair are aligned. (b) The full set of protein sequences (at most 50) that also include random hits from database search are aligned.

num_gap(2)	TCoffee			MUSCLE			ProbCons			MUMMALS		
0-20% {887}	20.41	0.56	9×10^{-33}	81.06	0.34	1×10^{-120}	73.73	0.11	5×10^{-111}	10.03	0.56	2×10^{-17}
20-40% {588}	27.89	0.51	9×10^{-31}	57.99	0.17	2×10^{-59}	51.53	0.00	1×10^{-53}	6.80	0.17	2×10^{-9}
40-70% {112}	2.68	0.00	—	13.39	0.00	6×10^{-5}	13.39	0.00	9×10^{-5}	8.04	0.89	0.007
70-100% {95}	3.16	0.00	—	3.16	0.00	—	5.26	0.00	0.03	3.16	0.00	—
All {1682}	20.87	0.48	2×10^{-62}	64.09	0.24	2×10^{-180}	58.09	0.06	1×10^{-165}	8.38	0.42	8×10^{-27}
len_gap(2)	TCoffee			MUSCLE			ProbCons			MUMMALS		
0-20% {887}	18.94	2.82	8×10^{-23}	76.89	6.88	9×10^{-106}	69.90	4.85	2×10^{-95}	9.70	1.47	2×10^{-14}
20-40% {588}	27.89	1.36	2×10^{-25}	50.34	8.16	2×10^{-42}	45.58	5.27	5×10^{-38}	6.46	0.51	1×10^{-6}
40-70% {112}	2.68	0.00	—	10.71	2.68	0.002	9.82	2.68	0.009	6.25	4.46	—
70-100% {95}	3.16	0.00	—	3.16	0.00	—	4.21	2.11	—	3.16	0.00	—
All {1682}	20.10	1.96	2×10^{-46}	59.04	6.66	7×10^{-150}	53.69	4.70	3×10^{-133}	7.97	1.25	3×10^{-19}
len_aln(2)	TCoffee			MUSCLE			ProbCons			MUMMALS		
0-20% {887}	10.37	1.24	7×10^{-12}	47.01	10.15	2×10^{-39}	41.83	1.69	3×10^{-53}	2.37	0.11	3×10^{-5}
20-40% {588}	6.12	1.36	1×10^{-5}	31.97	2.21	9×10^{-29}	30.27	0.17	7×10^{-31}	1.53	0.00	0.004
40-70% {112}	0.00	0.00	—	5.36	0.89	—	6.25	0.00	0.01	7.14	0.89	0.01
70-100% {95}	0.00	0.00	—	0.00	0.00	—	5.26	0.00	0.03	1.05	0.00	—
All {1682}	7.61	1.13	5×10^{-16}	36.33	6.18	2×10^{-63}	33.35	0.95	2×10^{-83}	2.32	0.12	3×10^{-8}

(a)

num_gap(50)	TCoffee			MUSCLE			ProbCons			MUMMALS		
0-20% {887}	96.17	1.35	1×10^{-142}	91.43	6.65	1×10^{-131}	73.84	20.63	5×10^{-70}	60.20	33.60	6×10^{-19}
20-40% {588}	95.75	1.53	4×10^{-95}	88.27	7.48	2×10^{-84}	71.09	21.09	5×10^{-40}	59.52	34.01	2×10^{-10}
40-70% {112}	88.39	2.68	1×10^{-18}	72.32	10.71	4×10^{-15}	58.04	18.75	8×10^{-7}	60.71	30.36	1×10^{-4}
70-100% {95}	76.84	4.21	3×10^{-14}	63.16	9.47	4×10^{-11}	58.95	13.68	5×10^{-6}	51.58	25.26	0.004
All {1682}	94.41	1.66	7×10^{-264}	87.46	7.37	4×10^{-236}	70.99	20.27	1×10^{-116}	59.51	33.06	2×10^{-31}
len_gap(50)	TCoffee			MUSCLE			ProbCons			MUMMALS		
0-20% {887}	89.29	8.34	3×10^{-121}	85.34	13.08	1×10^{-97}	63.36	29.88	2×10^{-28}	57.05	36.41	3×10^{-12}
20-40% {588}	91.50	5.10	1×10^{-85}	82.65	12.76	4×10^{-67}	59.86	30.61	5×10^{-14}	55.27	37.59	6×10^{-5}
40-70% {112}	81.25	9.82	9×10^{-17}	69.64	13.39	1×10^{-11}	45.54	31.25	0.01	51.79	38.39	0.02
70-100% {95}	72.63	8.42	1×10^{-12}	53.68	17.89	4×10^{-7}	45.26	27.37	0.008	49.47	25.26	0.005
All {1682}	88.59	7.31	6×10^{-229}	81.57	13.26	5×10^{-177}	59.93	30.08	3×10^{-42}	55.65	36.33	1×10^{-17}
len_aln(50)	TCoffee			MUSCLE			ProbCons			MUMMALS		
0-20% {887}	88.39	4.51	9×10^{-119}	72.94	15.11	2×10^{-65}	55.13	26.83	7×10^{-19}	47.24	25.70	9×10^{-11}
20-40% {588}	88.10	1.36	1×10^{-83}	70.58	9.86	2×10^{-52}	52.04	26.36	3×10^{-12}	45.41	20.58	2×10^{-12}
40-70% {112}	83.93	0.89	3×10^{-17}	54.46	14.29	4×10^{-6}	50.89	16.07	8×10^{-6}	46.43	17.86	0.001
70-100% {95}	64.21	3.16	4×10^{-10}	51.58	7.37	5×10^{-9}	45.26	12.63	6×10^{-4}	33.68	12.63	0.003
All {1682}	86.62	3.09	1×10^{-221}	69.68	12.78	1×10^{-123}	53.21	25.15	9×10^{-35}	45.78	22.65	1×10^{-23}

(b)

Table S10: Percentage of cases in which the number of gaps in an alignment (num_gap), the average length of gaps (len_gap) and the length of the alignment (len_aln) become smaller, larger and smaller respectively, and larger, smaller and larger respectively, on the Twilight and Superfamily subsets of SABmark 1.65.

Twilight {205}	TCoffee			MUSCLE			ProbCons			MUMMALS		
num_gap	84.69	7.66	8×10^{-28}	85.17	7.18	1×10^{-27}	85.65	7.18	8×10^{-27}	50.72	20.57	2×10^{-6}
len_gap	68.42	23.92	1×10^{-11}	75.12	19.62	5×10^{-23}	76.08	17.70	3×10^{-21}	50.24	24.88	3×10^{-6}
len_aln	66.51	13.88	5×10^{-14}	56.94	30.62	5×10^{-5}	61.24	20.57	3×10^{-7}	33.01	21.05	0.02
Superfamily {422}	TCoffee			MUSCLE			ProbCons			MUMMALS		
num_gap	79.06	4.71	7×10^{-52}	82.12	4.47	2×10^{-56}	76.00	6.35	5×10^{-47}	44.71	16.94	7×10^{-11}
len_gap	72.00	12.71	2×10^{-34}	76.71	12.00	2×10^{-44}	72.24	10.59	1×10^{-42}	41.41	20.71	4×10^{-8}
len_aln	53.65	7.76	6×10^{-26}	57.41	19.53	1×10^{-17}	53.18	12.47	7×10^{-18}	26.59	12.00	6×10^{-5}

Table S11: Percentage of cases in which the number of gaps in an alignment (num_gap), the average length of gaps (len_gap) and the length of the alignment (len_aln) become smaller, larger and smaller respectively, and larger, smaller and larger respectively, on Data-set 1 of BRAlIbase II.

num_gap	TCoffee			MUSCLE			ProbConsRNA		
0-55% {96}	98.96	0.00	9×10^{-18}	77.08	7.29	2×10^{-13}	89.58	3.12	4×10^{-16}
55-75% {218}	96.79	0.00	7×10^{-37}	66.06	4.59	8×10^{-26}	73.39	0.92	3×10^{-28}
75-100% {167}	46.11	1.20	1×10^{-14}	20.36	0.60	2×10^{-7}	29.94	1.20	4×10^{-10}
All {481}	79.63	0.42	5×10^{-65}	52.39	3.74	2×10^{-42}	61.54	1.46	1×10^{-50}
len_gap	TCoffee			MUSCLE			ProbConsRNA		
0-55% {96}	90.62	8.33	5×10^{-15}	48.96	38.54	—	83.33	8.33	1×10^{-14}
55-75% {218}	65.14	26.15	1×10^{-9}	41.28	29.82	—	68.35	6.42	1×10^{-23}
75-100% {167}	30.54	13.77	4×10^{-4}	16.77	3.59	2×10^{-4}	25.75	4.19	9×10^{-8}
All {481}	58.21	18.30	1×10^{-25}	34.30	22.45	0.005	56.55	6.03	2×10^{-42}
len_aln	TCoffee			MUSCLE			ProbConsRNA		
0-55% {96}	89.58	4.17	3×10^{-15}	68.75	9.38	2×10^{-9}	63.54	5.21	6×10^{-11}
55-75% {218}	92.66	0.46	2×10^{-35}	55.50	3.21	6×10^{-19}	53.21	2.29	5×10^{-21}
75-100% {167}	35.33	0.00	4×10^{-12}	8.98	0.00	3×10^{-4}	17.37	0.00	4×10^{-7}
All {481}	72.14	1.04	8×10^{-58}	42.00	3.33	2×10^{-28}	42.83	2.08	6×10^{-35}

Table S12: Percentage of cases in which the number of gaps in an alignment (num_gap), the average length of gaps (len_gap) and the length of the alignment (len_aln) become smaller, larger and smaller respectively, and larger, smaller and larger respectively, on the mdsa_all set of DNA PREFAB.

num_gap	TCoffee			MUSCLE			ProbConsRNA		
0-20% {123}	100.00	0.00	2×10^{-22}	100.00	0.00	2×10^{-22}	100.00	0.00	2×10^{-22}
20-40% {1030}	100.00	0.00	1×10^{-170}	100.00	0.00	1×10^{-170}	100.00	0.00	1×10^{-170}
40-70% {436}	97.94	0.00	3×10^{-72}	95.18	0.00	4×10^{-70}	96.79	0.00	2×10^{-71}
70-100% {87}	21.84	0.00	6×10^{-5}	13.79	0.00	6×10^{-4}	25.29	0.00	2×10^{-5}
All {1676}	95.41	0.00	3×10^{-263}	94.27	0.00	4×10^{-260}	95.29	0.00	7×10^{-263}
len_gap	TCoffee			MUSCLE			ProbConsRNA		
0-20% {123}	100.00	0.00	2×10^{-22}	100.00	0.00	2×10^{-22}	100.00	0.00	2×10^{-22}
20-40% {1030}	100.00	0.00	1×10^{-170}	95.73	4.27	2×10^{-166}	99.90	0.10	2×10^{-170}
40-70% {436}	96.33	1.15	1×10^{-71}	85.55	9.17	7×10^{-61}	94.95	1.61	7×10^{-71}
70-100% {87}	19.54	2.30	2×10^{-4}	13.79	0.00	0.001	25.29	0.00	2×10^{-5}
All {1676}	94.87	0.42	3×10^{-262}	89.14	5.01	3×10^{-249}	94.75	0.48	2×10^{-262}
len_aln	TCoffee			MUSCLE			ProbConsRNA		
0-20% {123}	85.37	9.76	3×10^{-17}	87.80	10.57	7×10^{-18}	91.06	4.07	7×10^{-18}
20-40% {1030}	86.12	6.89	9×10^{-132}	82.72	13.79	1×10^{-114}	83.20	4.85	1×10^{-128}
40-70% {436}	88.99	2.75	1×10^{-61}	86.47	4.82	4×10^{-60}	81.88	2.29	4×10^{-57}
70-100% {87}	10.34	1.15	0.006	2.30	1.15	—	2.30	0.00	—
All {1676}	82.88	5.73	2×10^{-207}	79.89	10.56	3×10^{-188}	79.24	3.88	4×10^{-199}