

**Table 7. Scaled BLOSUM-62 scores**

A	222	-80	-87	-99	-23	-45	-49	9	-92	-75	-83	-42	-53	-125	-46	63	-3	-143	-100	-11
R	-80	310	-25	-91	-192	56	-7	-130	-14	-169	-122	119	-77	-158	-119	-43	-63	-152	-96	-142
N	-87	-25	320	72	-150	0	-15	-24	33	-182	-191	-10	-122	-169	-113	34	-3	-209	-118	-163
D	-99	-91	72	327	-196	-18	85	-74	-63	-177	-204	-40	-173	-197	-84	-15	-59	-238	-173	-178
C	-23	-192	-150	-196	485	-164	-204	-141	-169	-69	-72	-172	-80	-134	-158	-50	-49	-130	-136	-46
Q	-45	56	0	-18	-164	299	105	-101	25	-157	-121	72	-24	-179	-73	-6	-38	-110	-80	-124
E	-49	-7	-15	85	-204	105	277	-119	-7	-181	-161	44	-113	-181	-63	-8	-49	-160	-114	-138
G	9	-130	-24	-74	-141	-101	-119	315	-115	-211	-205	-86	-151	-176	-121	-17	-89	-141	-172	-178
H	-92	-14	33	-63	-169	25	-7	-115	425	-183	-158	-41	-88	-70	-122	-50	-95	-132	96	-176
I	-75	-169	-182	-177	-69	-157	-181	-211	-183	226	86	-151	64	-9	-156	-133	-41	-146	-75	144
L	-83	-122	-191	-204	-72	-121	-161	-205	-158	86	218	-138	113	23	-162	-138	-68	-92	-60	45
K	-42	119	-10	-40	-172	72	44	-86	-41	-151	-138	255	-77	-174	-57	-12	-38	-167	-103	-128
M	-53	-77	-122	-173	-80	-24	-113	-151	-88	64	113	-77	305	1	-140	-84	-38	-81	-56	39
F	-125	-158	-169	-197	-134	-179	-181	-176	-70	-9	23	-174	1	342	-204	-134	-119	52	166	-48
P	-46	-119	-113	-84	-158	-73	-63	-121	-122	-156	-162	-57	-140	-204	417	-46	-61	-207	-165	-133
S	63	-43	34	-15	-50	-6	-8	-17	-50	-133	-138	-12	-84	-134	-46	220	78	-156	-95	-93
T	-3	-63	-3	-59	-49	-38	-49	-89	-95	-41	-68	-38	-38	-119	-61	78	257	-137	-91	-3
W	-143	-152	-209	-238	-130	-110	-160	-141	-132	-146	-92	-167	-81	52	-207	-156	-137	594	122	-160
Y	-100	-96	-118	-173	-136	-80	-114	-172	96	-75	-60	-103	-56	166	-165	-95	-91	122	373	-68
V	-11	-142	-163	-178	-46	-124	-138	-178	-176	144	45	-128	39	-48	-133	-93	-3	-160	-68	213
	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V

The standard BLOSUM-62 amino acid substitution matrix, scaled so that in the context of the compositions of two proteins under consideration, it has  $\lambda$  equal to 0.00635. Rows correspond to amino acids from the *Plasmodium falciparum* protein, and columns to amino acids from the *Mycobacterium tuberculosis* protein. To produce the alignment shown in Fig. 1a, this matrix is used in conjunction with gap costs of  $-550-50k$  for a gap of length  $k$ . This is equivalent to  $-11-k$  gap costs in the context of a standard BLAST search.