

**Table 8. Composition-specific BLOSUM-62 scores**

A	207	-135	-203	-175	-68	-105	-122	-14	-190	-129	-128	-119	-92	-217	-80	11	-34	-222	-202	-45
R	-76	301	-108	-134	-212	30	-47	-128	-80	-196	-138	79	-86	-219	-124	-68	-66	-201	-167	-150
N	-39	-3	294	78	-126	16	-12	26	13	-167	-166	-12	-89	-188	-75	55	41	-217	-146	-129
D	-80	-99	10	315	-201	-30	65	-54	-114	-188	-207	-70	-169	-244	-72	-23	-46	-275	-231	-172
C	-2	-206	-224	-230	504	-184	-239	-126	-226	-79	-73	-209	-75	-181	-152	-61	-37	-165	-195	-37
Q	-22	54	-65	-42	-167	300	86	-80	-21	-166	-120	48	-13	-224	-59	-12	-23	-140	-134	-116
E	-27	-12	-81	65	-210	98	263	-100	-55	-193	-162	17	-107	-227	-51	-16	-35	-194	-170	-131
G	-16	-189	-139	-151	-193	-165	-196	301	-217	-272	-256	-166	-196	-270	-159	-74	-126	-223	-278	-220
H	-38	13	2	-57	-139	48	2	-63	427	-162	-125	-37	-48	-79	-78	-25	-49	-131	82	-137
I	-49	-175	-249	-202	-64	-168	-207	-190	-233	235	99	-179	81	-44	-142	-140	-21	-174	-125	167
L	-60	-129	-261	-233	-70	-134	-188	-187	-209	87	233	-169	130	-12	-150	-148	-52	-121	-111	61
K	1	139	-55	-45	-155	85	42	-45	-70	-140	-118	257	-49	-199	-24	2	-2	-180	-137	-99
M	-23	-76	-184	-196	-72	-28	-133	-126	-132	69	131	-100	336	-30	-122	-86	-15	-103	-102	61
F	-63	-124	-198	-185	-93	-153	-168	-115	-77	30	74	-165	56	359	-152	-102	-63	71	165	7
P	-77	-181	-236	-164	-214	-139	-143	-155	-228	-220	-216	-141	-188	-303	394	-107	-100	-295	-275	-177
S	82	-57	-38	-47	-56	-24	-40	-2	-107	-150	-146	-47	-84	-185	-39	213	90	-197	-157	-91
T	8	-84	-81	-100	-61	-64	-88	-83	-160	-60	-79	-80	-41	-176	-61	61	269	-183	-158	-4
W	-83	-121	-241	-231	-91	-84	-150	-82	-144	-115	-50	-161	-32	56	-159	-128	-85	631	117	-113
Y	-48	-73	-156	-173	-107	-63	-112	-124	83	-52	-26	-104	-17	165	-125	-75	-47	131	368	-27
V	2	-163	-246	-220	-56	-152	-179	-172	-243	133	39	-172	39	-100	-134	-115	1	-206	-133	222
	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V

A composition-adjusted BLOSUM-62 amino acid substitution matrix, based on the amino acid frequencies of the two proteins under consideration, each adjusted with 20 pseudocounts proportional to the implicit BLOSUM-62 background frequencies. In the context of these two sequences, this matrix has the same scale ( $\lambda = 0.00635$ ) and relative entropy (0.74 bits) as that in Table 7. This matrix is used in conjunction with  $-550$ - $50k$  gap costs to produce the optimal local alignment shown in Fig. 1*b*.