

Table S1. Similarity index of PfFSmat60 and Blosum50 (comparison of odd ratios)

	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
A	1.661	0.218	0.158	0.181	0.788	0.241	0.175	0.469	0.114	0.181	0.230	0.148	0.315	0.208	0.463	0.459	0.403	0.223	0.140	0.460
R	0.320	1.495	0.207	0.183	0.255	0.338	0.237	0.189	0.292	0.155	0.212	0.288	0.274	0.137	0.245	0.292	0.310	0.123	0.122	0.168
N	0.607	0.666	0.659	0.609	0.318	0.723	0.557	0.683	0.473	0.160	0.404	0.460	0.356	0.366	0.518	0.529	0.484	0.435	0.286	0.419
D	0.430	0.370	0.292	0.850	0.253	0.525	0.624	0.327	0.345	0.128	0.224	0.282	0.308	0.255	0.421	0.429	0.326	0.242	0.190	0.231
C	1.917	0.572	0.517	0.502	0.725	0.303	0.412	0.559	0.558	0.678	0.670	0.196	0.717	0.417	0.407	0.970	0.748	0.567	0.495	0.961
Q	0.598	0.535	0.390	0.464	0.252	1.472	0.516	0.353	0.424	0.243	0.291	0.376	0.416	0.267	0.423	0.367	0.491	0.179	0.154	0.336
E	0.604	0.394	0.304	0.551	0.268	0.549	0.916	0.307	0.339	0.203	0.271	0.313	0.380	0.203	0.392	0.393	0.345	0.144	0.137	0.346
G	0.507	0.220	0.169	0.197	0.302	0.149	0.214	0.962	0.168	0.089	0.114	0.133	0.188	0.118	0.263	0.265	0.165	0.094	0.077	0.156
H	0.576	0.485	0.241	0.444	0.275	0.562	0.371	0.342	1.068	0.149	0.269	0.250	0.286	0.279	0.360	0.365	0.378	0.490	0.302	0.380
I	0.559	0.500	0.207	0.241	0.522	0.502	0.328	0.185	0.255	0.668	0.516	0.316	0.745	0.335	0.366	0.258	0.403	0.440	0.191	0.782
L	0.501	0.413	0.230	0.236	0.484	0.471	0.308	0.151	0.226	0.345	0.915	0.308	0.738	0.387	0.409	0.261	0.297	0.265	0.185	0.484
K	0.638	0.820	0.370	0.426	0.350	0.633	0.473	0.399	0.419	0.270	0.357	0.700	0.378	0.236	0.547	0.465	0.470	0.361	0.187	0.455
M	0.388	0.295	0.202	0.232	0.341	0.311	0.371	0.115	0.162	0.417	0.530	0.261	1.908	0.415	0.182	0.252	0.367	0.225	0.181	0.514
F	0.478	0.280	0.189	0.218	0.425	0.318	0.207	0.247	0.384	0.286	0.496	0.173	0.669	0.907	0.386	0.268	0.277	0.715	0.444	0.399
P	0.574	0.362	0.192	0.257	0.243	0.281	0.186	0.165	0.211	0.143	0.203	0.180	0.200	0.141	1.048	0.387	0.229	0.195	0.102	0.325
S	1.038	0.381	0.316	0.440	0.547	0.403	0.384	0.455	0.400	0.180	0.250	0.270	0.487	0.212	0.604	1.072	0.617	0.474	0.153	0.312
T	0.655	0.450	0.264	0.340	0.426	0.525	0.313	0.290	0.301	0.206	0.243	0.252	0.394	0.224	0.450	0.584	1.297	0.148	0.168	0.384
W	0.223	0.429	0.307	0.172	0.141	0.179	0.079	0.140	0.445	0.162	0.169	0.054	0.490	0.546	0.072	0.194	0.178	1.330	0.343	0.232
Y	0.504	0.369	0.260	0.288	0.289	0.279	0.296	0.207	0.416	0.210	0.341	0.250	0.478	0.580	0.520	0.341	0.317	0.696	0.754	0.320
V	0.637	0.352	0.197	0.212	0.579	0.372	0.313	0.220	0.380	0.400	0.375	0.247	0.511	0.254	0.377	0.290	0.430	0.239	0.146	1.219

Each element of the table is a ratio of the odd ratios of PfFSmat60 and Blosum50 substitution matrices, a measure of similarity of the two matrices. The text highlighted in bold are the diagonal elements.

Table S2. Alignment scores of the PFB0090C protein of *Plasmodium falciparum* and human DnaJ homolog, Q9UDY4, with PfSSM series of matrices

Clustering %	Smat	SSmat	PfFmat	PfFSmat
50	235.8 (338)	142.7 (339)	199.6 (346)	53.5 (343)
60	235.9 (348)	148.0 (339)	203.5* (346)	53.0 (343)
70	236.8 (348)	148.0 (339)	201.4 (346)	54.8 (343)
80	238.9* † (348)	151.9 (339)	196.2 (337)	57.7 (343)
90	230.2 (348)	179.4* (339)	183.0 (346)	62.5* (340)

Smat = Symmetric matrix; SSmat = Symmetric Scaled matrix; PfFmat = *Plasmodium falciparum* Fixed matrix; PfFSmat = *Plasmodium falciparum* Fixed Scaled matrix. The first column of the table represents the clustering % at which the matrices (represented in the subsequent columns along the first row) were calculated. Columns 2-5 represent the alignment scores obtained for each matrix series at different clustering percentages. The values in the closed brackets are the amino acid overlap for the alignment.

* The highest obtained scores for the respective columns

† The score for the best performing matrix series

Table S3. Alignment scores for the FASTA local pairwise alignment of *Plasmodium falciparum* hypothetical protein, PFB0090C and human DnaJ protein, Q9UDY4, with the PfSSM series of matrices

Clustering %	Smat	SSmat	PfFmat	PfFSmat
50	428.6* (339)	479.5 (339)	239.1 (346)	806.0 (343)
60	288.2 (348)	477.2 (339)	243.7* (346)	810.0* [†] (343)
70	287.6 (348)	476.6 (339)	239.6 (346)	806.0 (343)
80	295.2 (348)	484.2* (339)	226.8 (346)	792.6 (343)
90	274.2 (348)	463.2 (339)	212.7 (346)	775.6 (340)

Smat = Symmetric matrix; SSmat = Symmetric Scaled matrix; PfFmat = *Plasmodium falciparum* Fixed matrix; PfFSmat = *Plasmodium falciparum* Fixed Scaled matrix. The first column of the table represents the clustering % at which the matrices (represented in the subsequent columns along the first row) were calculated. Columns 2-7 represent the alignment scores obtained for each matrix series at different clustering percentages. The values in the closed brackets are the amino acid overlap for the alignment.

* The highest obtained scores for the respective columns

[†] The score for the best performing matrix series