Pfam ID (# of sequences × # of sites)	Elapsed time (sec.)				
# of threads	(i) All-to-all	(ii) Progressive	(iii) Refinement	Total	Efficiency
Cas_Cas1 (1000 × 640)					
1	489	16.7	3270	3770	-
2	248	17.0	1760	2020	0.93
8	67.8	15.4	654	737	0.64
Cob_adeno_trans (997 × 388)					
1	226	9.94	2160	2390	-
2	115	9.05	1190	1310	0.91
8	31.8	9.59	466	507	0.59
CstA (1001 × 712)					
1	639	17.4	4010	4660	-
2	323	15.3	2170	2510	0.93
8	85.0	14.9	687	787	0.74
ArgJ (1001 × 747)					
1	1050	20.9	6180	7250	-
2	540	17.3	3360	3920	0.92
8	139	18.9	1480	1640	0.55
MHYT (1001 × 157)					
1	44.7	4.36	628	677	-
2	23.5	4.39	368	396	0.85
8	7.80	4.53	133	145	0.58
Average percentages of elapsed times for the three stages					
1	13%	0.37%	87%		
2	12%	0.62%	87%		
8	8.7%	1.7%	90%		

Supplemental table: To examine the efficiency of the simple hill-climbing strategy for larger datasets than for those in the main part, elapsed time was measured for five datasets, each with ∼1000 sequences, taken from Pfam (Finn *et al.* 2010). Elapsed times for stages i - iii are also separately shown to compare the parallelization efficiency in more detail. For the iterative refinement stage (iii), average elapsed time in ten runs with different random numbers is shown. The G-INS-i option of MAFFT was used in this test, because these Pfam alignments can be assumed to have global homology.

Finn, R. D., Mistry, J., Tate, J., Coggill, P., Heger, A., Pollington, J. E., Gavin, O. L., Gunasekaran, P., Ceric, G., Forslund, K., Holm, L., Sonnhammer, E. L., Eddy, S. R. & Bateman, A. (2010) The pfam protein families database. *Nucleic Acids Res.,* **38**, D211–D222.