Supporting Text S4: Model-quality statistics. A common method for assessing the quality of a protein structure relative to a reference is GDT[13]. Briefly, this algorithm measures the average number of residues superimposable under a variety of distance thresholds. We use an approach that differs slightly from the canonical GDT implementation, in that superposition is done using Mammoth [14] rather than the Maxsub [15]. Mammoth begins superimposition between the two sets of coordinates using 7-mer seeds. The seeds are extended so long as the average RMSD across the aligned coordinates does not exceed a user-specified threshold. Once the alignment extension is finished, one set of coordinates is superimposed onto the other and the function reports the percentage of aligned atoms that superimpose beneath a user-defined threshold. It is important to note that GDTMM is a sequence-dependent algorithm, which means that the *i*th coordinate in the first list is always superimposed onto the *i*th coordinate of the second.

The GDTMM function is thus given the two sets of coordinates, a distance threshold used for extending alignments, and a second distance threshold under which two aligned coordinates are considered equivalent. The final value of GDTMM is the average computed across the following sets of distance thresholds:

Function Call Name	**Alignment Threshold**	**Equivalence Threshold**
gdtmm1_1	1Å	1Å
gdtmm2_2	2Å	2Å
gdtmm3_3	3Å	3Å
gdtmm4_3	4Å	3Å
gdtmm7_4	7Å	4Å

A routine for calculating GDTMM is provided as part of the standard Rosetta software suite of programs, and can be activated using following command-line flags:
-bGDT
-evaluation:gdtmm
-in:file:native native.pdb