INSTITUTE FOR
Protein Design
UNIVERSITY of WASHINGTON

I would like to thank Cancer Computer for supporting Rosetta@Home, which provides my team at the University of Washington with round-the-clock access to the computing resources we need to conduct research on protein structure prediction and protein design.

Proteins are the molecular machines and building blocks of life. Their functions, which are critical for all living things, are largely determined by their intricate three-dimensional structures. Understanding protein structure is therefore one of the central problems of biology.

Currently, tens of millions of dollars are spent per year to determine the structures of proteins using laboratory techniques such as X-ray crystallography and nuclear magnetic resonance. If this work could instead be done on a computer, it would significantly shrink costs and discovery timelines, with near-term benefits in medicine, including for cancer therapy.

Scientists in my laboratory created Rosetta, a powerful scientific software package for modeling protein structures, to do this. These simulations are accurate but incredibly demanding to compute, so in 2005 we launched Rosetta@Home to gain access to the power of crowd computing. The volunteers at the heart of Rosetta@Home have greatly accelerated our research.

Compute cycles donated through Rosetta@Home are used by scientists in my laboratory to both model natural proteins and design new ones. Designing proteins offers significant scientific and practical benefits: By creating new protein structures, one can design novel molecular machines that carry out new therapeutic functions.

We rely on Rosetta@Home for virtually all of our protein design projects, including efforts to create safer cancer immunotherapies, tumor-targeting proteins and novel antibiotics. Finally, there's the evolutionary question of whether the protein structures sampled by evolution are the limit of what's possible, or whether there are quite different proteins can also be made. Understanding the rules that govern folding and design may help answer this important question.

We are grateful to Cancer Computer for their generous support as we explore this frontier of science and pursue tomorrow's cures.

Sincerely,

David Baker

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Director, Institute for Protein Design
Professor in Biochemistry, University of Washington