

instrument. The instrument had an active anti-coincidence shield that effectively removed the contaminating spacecraft background. In the end, the NEAR gamma ray spectrometer did return a spectacular data set, but from the surface of Eros after the spacecraft landed—something neither the instrument nor the spacecraft was originally designed to do.

ANDREW F. CHENG

NEAR Project Scientist, Johns Hopkins University Applied Physics Laboratory, 11100 Johns Hopkins Road, Laurel, MD 20723, USA.

Structural Genomics: Current Progress

IN HIS NEWS FOCUS "TAPPING DNA FOR structures produces a trickle" (1 Nov., p. 948), Robert Service presents an informative viewpoint about the progress of the structural genomics consortia. He describes how a number of consortia have targeted a vast number of proteins but only solved a small fraction of them. Although this is true, it is important to realize that structural genomics projects have been organized to evaluate large numbers of candidate targets, often of the same protein in different organisms, and simultaneously work on them in parallel. The aim is to determine the structure of representatives of particular protein families; thus, the representatives that do not come to fruition are not necessarily failures but are often simply the consequence of success elsewhere. For example, according to the International Structural Genomics Target Tracking Database (1), over 360 new three-dimensional protein structures have been completed by the various consortia and many more are nearly done. These proteins, which were selected because of their unique position in sequence space, have actually

shed light on further thousands of homologous proteins whose structures can now be modeled for the first time. Thus, the output of structural genomics is highly leveraged, being much greater than the absolute number of new experimental structures.

Moreover, the number of targets selected does not represent a final end-point for the current structural genomics consortia in the way that the entire human genome represented an end-point for genome sequencing. The current consortia, in fact, represent pilot projects with a primary mandate of testing multiple technologies in order to identify the best procedures for scaling up. Accordingly, the "success rates" reported by Service represent snapshots of an ongoing iterative process. For many of the protein targets reported as being "selected," no effort has even been made yet to clone or express them. Consequently, comparing outcome versus number of "selected" targets can result in a somewhat misleading picture of the current progress of the nascent structural genomics efforts.

M. GERSTEIN,^{1*} A. EDWARDS,^{2*} C. H. ARROWSMITH,^{3*} G. T. MONTELIONE^{4*}

¹Department of Molecular Biophysics and Biochemistry, Yale University, New Haven, CT 06520, USA. ²Banting and Best Department of Medical Research, C. H. Best Institute, University of Toronto, Toronto M5G 2M9, Canada. ³Department of Medical Biophysics, Ontario Cancer Institute, University of Toronto, Toronto M5G 2M9, Canada. ⁴Department of Molecular Biology and Biochemistry, Center for Advanced Biotechnology and Medicine, Rutgers University and Robert Wood Johnson Medical School, UMDNJ, Piscataway, NJ 08854, USA.

*Members of the Northeast Structural Genomics Consortium (nsg.org) of the NIH-sponsored Protein Structure Initiative

Reference

1. See <http://targetdb.rutgers.edu>.

CORRECTIONS AND CLARIFICATIONS

Research Articles:

"Corepressor-dependent silencing of chromosomal regions encoding neuronal genes" by V. V. Lunyak *et al.* (29 Nov., p. 1747). In Fig. 3B, the bands shown for the NaCh III gene up-regulated by CoREST RID and the HoxD9 genes up-regulated by REST DBD were incorrectly inserted during the preparation of the figures. The correct bands are included in the figure shown here. This error in figure preparation does not alter the conclusions in the manuscript.

