a more focused approach, the JCSG is leveraging its HTSB platform to address more challenging targets and capitalize on our extensive experience to develop the best strategies to enhance chances of success. In parallel, we process our internal biomedical-theme targets in a HT mode. This project is centered the microbial communities that inhabit specific niches and environments of the human body to investigate the structural basis for host/commensal-microbe interactions. We are initially focusing on secreted proteins from commensal bacteria in the human gut to explore their symbiotic relationship with their human host. The gut microbiota is dominated by poorly characterized bacterial phyla, which contain an unusually high number of uncharacterized proteins and remain largely unstudied. Their influence upon human development, physiology, immunity, and nutrition are only starting to surface and, thus, represents an exciting new frontier for HTSB where we can investigate the contributions of these microorganisms to human health, as well as to disease. Supported by NIGMS: U54-GM094586

Keywords: structural genomics, high-throughput structural biology, human microbiome

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ARCIMBOLDO goes super: *ab Initio* phasing on the supercomputer Calendula FCSCL

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A supercomputer (FCSCL: www.fcsc.es) provides the ideal environment for ARCIMBOLDO, as it opens new dimensions to the incorporation of prior knowledge, allowing to tackle increasingly difficult structures. Extensions in the method and its successes will be reported. It also makes the method accessible to users who do not have a grid.

Ab Initio phasing of macromolecular structures with no heavy atoms has been limited to cases with up to around 1000 atoms in the asymmetric unit, diffracting to atomic resolution [1].

Both the size and resolution barriers have been overcome in the case of several test and previously unknown structures. Thus, cases with a few thousand atoms, diffracting to 2Å have been solved through a combination of location of model fragments such as polyalanine alpha-helices with the program PHASER [2] and density modification with the program SHELXE [3]. Given the difficulties in discriminating correctly positioned fragments, the method has to test many putative groups of fragments in parallel, thus calculations are performed in a grid. The method has been called after the Italian painter Arcimboldo [4], who used to compose portraits out of fruits and vegetables. In the case of our program, most collections of fragments remain a "still-life", but some are correct enough for density modification to reveal the protein's portrait.

[1] G.M. Sheldrick, H.A. Hauptman, C.M. Weeks, R. Miller, I. Usón, *International Tables for Macromolecular Crystallography vol. F,* (eds., M.G. Rossmann and E. Arnold), Boston, **2001,** 333–345. [2] A.J. McCoy et al. *J. Appl. Crystallogr* **2007,** *40*, 658–674. [3] G.M. Sheldrick *Z. Kristallogr* **2002,** *217*, 644–650. [4] T. Tannenbaum, D. Wright, K. Miller, M. Livny, *in Beowulf Cluster Computing with Linux* (ed., T. Sterling) (MIT Press, Cambridge, Massachusetts, USA). **2002** 307–350 [4] D. Rodríguez, C. Grosse, S. Himmel, C. González, I. M de Ilarduya, S. Becker, G.M. Sheldrick, I. Usón, *Nature Meth.* **2009,** *6*, 651–654.

Keywords: ab initio phasing, macromolecule, supercomputing

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Accelerating ab initio phasing with de novo models

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The *ab initio* phasing is one of remaining challenges in protein crystallography. Recent progress in computational structure prediction has enabled the generation of *de novo* models with high enough accuracy to solve the phase problem *ab initio*. This "*ab initio* phasing with *de novo* models" method first generates a huge number of *de novo* models and then selects some lowest energy models to solve the phase problem using molecular replacement. The amount of CPU time required is huge even for small proteins and this has limited the utility of this method. Here, we describe an approach that significantly reduces the computing time required to perform the "*ab initio* phasing with *de novo* models". Instead of performing molecular replacement after the completion of all models, we initiate molecular replacement during the course of each simulation. Our approach principally focuses on avoiding the refinement of the best and the worst models and terminating the entire simulation early once suitable models for phasing have been obtained. In a benchmark dataset of 20 proteins, our method is over two orders of magnitude faster than the conventional approach. We have observed that in most cases molecular replacement solutions were determined soon after the coarse-grained models were turned into full atom representations. We have also found that all-atom refinement could hardly change the models sufficiently to enable successful molecular replacement if the coarse-grained models were not very close to the native structure. Therefore, it remains critical to generate good quality coarse-grained models to enable subsequent all-atom refinement for successful *ab initio* phasing by molecular replacement.

Keywords: phasing, prediction, computation

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Structure analysis of 2D membrane proteins using X-ray powder diffraction data

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The majority of known integral membrane proteins (IMPs) have a natural propensity to form two-dimensional (2D) crystals during the crystallization processes [1]. This limits the possibility that their molecular structures may be obtained using the standard methods of protein crystallography. Powder diffraction methods are, in contrast, not critically sensitive to the quality and dimensions of crystals, which suggests their use in the structure analysis of protein crystals [2]. The application of powder diffraction methods for the structure analysis of proteins, however, is still regarded as intractable because of the large number of unresolved (overlapping) reflections. The development of new methodologies for powder diffraction structure analysis is, therefore, timely and desirable and could significantly expand the list