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A Graphical Front End for the ARP/wARP Software in Macromolecular.
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Traditionally crystallographic protein modelling and particularly model completion involves graphical display software for manual user interference. During the last decade, a number of software packages - such as ARP/wARP [1] - emerged that do a large part of the crystallographic map interpretation and model building automatically without much manual work. This has tremendously shortened the time in which a macromolecular model could be built, from months and sometimes years to days or even a few hours. Having done a computer intensive map interpretation step there is generally no elaborate graphical communication or reporting framework, which would indicate how a model has progressed from a visually hardly interpretable density to an almost complete set of polypeptide fragments. As a result, the modelling needs to be viewed, judged and completed where needed elsewhere. At the same time, the recent past has shown that programs that allow semi-automatic modelling coupled with instantaneous graphical display - such as Coot [2] - are becoming very popular.
To bridge the gap between the automation that the ARP/wARP package offers and intuitive communication via graphical components, we have developed a graphical front end to ARP/wARP. It allows to run less time consuming tasks from the ARP/wARP suite, e.g. fitting ligands [3] or secondary structure [4]. The user can choose the input from the graphical items and get results displayed immediately. The approach behind such a graphical tool is to not only provide in total more information than logfiles do on their own, but also at the same time to instantaneously allow the user to choose from minimal intervention to very informed guidance of the software.

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Homology Modeling of VEGF-D as a Basis for Structural and Functional Analysis.
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Vascular endothelial growth factors (VEGFs) are key growth factors that induce angiogenesis and lymphangiogenesis during embryogenesis and maintain vasculature during adulthood. They are potential therapeutics for induction of blood vessel formation when normal blood flow is compromised. Most members of the VEGF family exist as covalently bound antiparallel homodimers. The mature form of human VEGF-D (VEGF-D$^{\Delta N \Delta C}$) is, however, predominantly a non-covalent dimer, although the cysteines, forming the intersubunit disulfide bonds in other VEGFs, are conserved in VEGF-D. However, VEGF-D has an extra cysteine at the subunit interface, compared to the other VEGFs. In order to investigate the importance of this cysteine, as well as other residues at the subunit interface, we constructed homology models of VEGF-D, based on the known crystal structures of VEGF-A [1] and the VEGF-F VR-1 [2]. The homology models were used as a basis for the design of site-specific mutations at the subunit interface of VEGF-D. Recombinant VEGF-D$^{\Delta N \Delta C}$ and mutant VEGF-D variants were expressed in cells and their structural and functional properties were studied and compared. Our results show that mutation of specific residues at the VEGF-D dimer interface, affects properties such as dimerization, biological activity, receptor binding affinity and protein stability [3].

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Sticky Triangles for Experimental Phasing.
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Obtaining phase information for the solution of macromolecular structures is still one of the major challenges in X-ray crystallography. 5-Amino-2,4,6-triiodoisophthalic acid (I3C) and 5-amino-2,4,6-tribromoisophthalic acid (B3C) represent a novel class of compounds that may be used for heavy-atom derivatization of biological macromolecules. I3C and B3C contain an easily recognizable arrangement of three anomalous scatterers (iodine or bromine, respectively) and three functional groups for hydrogen bonding to the protein.
I3C was synthesized and incorporated into test protein crystals using cocrystallization and soaking techniques [1,2]. Single-wavelength anomalous dispersion (SAD) phasing was successfully carried out with in-house data.
The bromine derivative B3C, suitable for multi-wavelength anomalous dispersion (MAD) experiments, was synthesized and employed for experimental phase determination using synchrotron data.
The three halogen atoms present in I3C and B3C form an equilateral triangle that can be easily identified in the heavy atom substructure. A new version of SHELXD that takes this information into account has been developed and is currently being tested.
New functional groups are currently tested to improve the