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### A universal, ultra-high affinity chromatography for a one-step, high-throughput purification of complex proteins

Protein purification is an essential, primary step in numerous biological studies, including a rapidly emerging proteomics field, its structural counterpart and drug screening. Moreover, purification with high yield, purity and activity (HHH-purification) is compulsory for high-resolution structural analysis and industrial protein production. Apparently, a universal, one-step high-throughput approach for HHH-purification is a key, yet unachievable, factor of success for all these crucial studies/applications. We designed and implemented an original chromatographic technology based on the physiological, ultra-high affinity ( $K_d \sim 10^{-14}$ - $10^{-17}$  M) small ( $\sim 10/16$ kDa) protein/protein complex, which allows for a one-step HHH-purification of the traditionally challenging (eukaryotic, membrane, multi-subunit, DNA/RNA-binding, toxic) proteins. The developed system is practically indefinitely reusable, suitable for industrial-scale manufacturing, has high capacity (up to 20mg tagged protein per ml beads) and efficiently operates under nearly identical (target-independent) basic conditions. Altogether, it provides major advantages over the existing commercial analogs and may form a solid high-throughput platform for both, purification and associated “affinity” techniques (pull-down, kinetic activity/binding assays, etc.) of protein characterization.

### Biography

Dmitry G Vassilyev has completed his PhD from Institute of Molecular Biology Acad. Sci. USSR (Moscow) and Postdoctoral studies from Bioengineering Research Institute (Osaka, Japan). From 2005, he is the Full Professor at the University of Alabama at Birmingham. He is an expert in protein crystallography and has published 84 papers in the top level scientific journals.

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