



PROTEOMEBINDERS

A European Infrastructure of Ligand Binding Molecules against the Human Proteome

EC FP6 Research Infrastructures
Coordination Action 026008



ProteomeBinders

is a European consortium planning the establishment of a comprehensive infrastructure resource of binding molecules for detection of the human proteome, together with tools for their use and applications in studying proteome function and organisation. This 4-year FP6 Research Infrastructures Coordination Action, started in March 2006, is funded with 1.8 M€ and links EU and USA partners (see overleaf), leaders in the area of binders and their applications. We advocate the organisation of an infrastructure of binders, available at cost and with no restrictions for research use.

Currently there is no pan-European platform for the systematic development and quality control for these essential reagents. We aim to provide a set of consistently characterised binders, required to detect all the relevant human proteins in tissues and fluids in health and disease. As the size of the human proteome is at least an order of magnitude greater than the ~ 21.000 protein coding genes known to date, and as for many applications several binders against each target are needed, the scale of our project is potentially immense. To date, antibodies are the most widely used protein-binders, but novel binder types based on alternative protein scaffolds or nucleic acids each have significant advantages and will be vital elements of a research resource for the 21st century.

Picking up the momentum created by ProteomeBinders, practical pilot projects initiating the creation of a binder resource are emerging.

Literature:

ProteomeBinders: planning a European resource of affinity reagents for analysis of the human proteome. MJ Taussig et al., *Nature Methods*. 4:13 (2007)

Proteomics' framework for success? Editorial, *Nature Methods*. 4:1 (2007)

Affinity reagent resources for human proteome detection: initiatives and perspectives. O Stoevesandt & MJ Taussig, *Proteomics*. 7:2738 (2007)

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www.proteomebinders.org

Community Resources for Affinity Proteomics developed within ProteomeBinders

Antibodypedia

Community-based portal showing application-specific validation of publicly available antibodies to human protein targets. Each protein binder has been scored according to a standardised format. www.antibodypedia.org

EpiC - The ProteomeBinders Epitope Choice Resource (alpha release)

EpiC collates and presents a structure-function summary of your proteins of interest to help you design antibodies against epitopes that are appropriate to your planned experiments. <http://epic.emble.de>

HUPO PSI-PAR: a standard format for protein affinity reagents

The Proteomics Standards Initiative (PSI) aims to define community standards for data representation to facilitate data comparison, exchange and verification. The PSI-PAR format is a standardised means of representing binder data and is designed to facilitate the exchange between different databases or LIMS systems. <http://www.psicodev.info/index.php?q=node/281>

Protein Array Resource Page

Protein and binder arrays are rapidly becoming established as a powerful means to detect proteins, monitor expression levels, investigate interactions and characterise binders. The Resource Page collates state of the art information. http://www.functionalgenomics.org.uk/sections/resources/protein_arrays.htm

MolMeth - Free Protocols Online (beta release)

The MolMeth database is built with the vision to provide free, up-to-date and community-validated protocols for molecular methods. MolMeth needs your help through submitting your own methods or lab protocols. <http://www.molmeth.org/>



The ProteomeBinders Consortium at Alpbach, March 2007

Participants in ProteomeBinders

Carl Borrebaeck	Recombinant antibody libraries, phage display, antibody microarrays, biomarkers	Department of Immunotechnology, Lund University, Sweden
Andrew Bradbury	Recombinant antibody libraries and novel formats, phage display	Biosciences Division, Los Alamos National Laboratory, USA
Dolores Cahill	Protein expression and arrays, binder specificity profiling	University College, Dublin, Ireland
Christian Cambillau	Protein expression systems	CNRS-Universités Aix-Marseille I & II, France
Stefan Dübel	Recombinant antibody libraries, phage display, antibody engineering	Technical University Braunschweig, Germany
Ronald Frank	Small molecule binding entities (peptides, chemicals)	Helmholtz Centre for Infection Research, Braunschweig, Germany
Toby Gibson	Epitope selection software	EMBL, Heidelberg, Germany
Larry Gold	Aptamers and SELEX selection	SomaLogic Inc., Boulder CO, USA
Friedrich Herberg	Binder characterisation, SPR	Department of Biochemistry, University of Kassel, Germany
Henning Hermjakob Sandra Orchard	Bioinformatics, standards for binder data representation	European Bioinformatics Institute, Hinxton, UK
Jörg Hoheisel Bernhard Korn	Protein and antibody microarrays, cancer biomarkers, Proteomics facilities	German Cancer Research Center, Heidelberg, Germany
Thomas Joos Markus Templin	Quality control, protein microarray formats, epitope mapping	NMI, Tübingen, Germany
Olli Kallioniemi Petri Saviranta	Reverse (lysate) arrays, cell arrays	VTT Technical Research Centre of Finland, Turku, Finland
Johannes Maurer	cDNA clone collections, protein microarrays, protein expression	imaGenes, Berlin, Germany
Zoltán Konthur Sylvia Krobitsch	Recombinant antibodies, phage display, automation	Max Planck Institute of Molecular Genetics, Berlin, Germany
Ulf Landegren	Sensitive protein detection, proximity ligation	The Rudbeck Laboratory, Uppsala University, Sweden
Silvère van der Maarel	Heavy chain (camelid) antibodies, intrabodies, phage display	Leiden University Medical Center, Leiden, The Netherlands
Serge Muyldermans	Heavy chain (camelid) antibodies, single domains	Vrije Universiteit Brussels, Belgium
Per-Åke Nygren	Alternative binder protein scaffolds, affibodies, phage display	School of Biotechnology, KTH, Stockholm, Sweden
Andreas Plückthun	Recombinant antibody libraries, phage and ribosome display, ankyrins	Department of Biochemistry, University of Zurich, Switzerland
Bojan Polic	High throughput mouse monoclonal antibody production facility	Medical Faculty University of Rijeka, Croatia
Michael Przybylski	Epitope and paratope analysis by high performance FT-MS	University of Konstanz, Germany
Alan Sawyer	High throughput mouse monoclonal antibody production facility	EMBL Monoclonal Antibody Core Facility, Monterotondo, Italy
David Sherman	Bioinformatics, binder ontology, database schema	Laboratoire Bordelais de Recherche en Informatique, France
Arne Skerra	Alternative binder protein scaffolds, anticalins, phage display	Biological Chemistry, Technische Universität München, Germany
Mike Taussig Oda Stoevesandt	Ribosome display, protein arrays, project coordination and management	The Babraham Institute, Cambridge, UK
Marius Ueffing Elisabeth Kremmer	European Protein Initiative, functional proteomics, monoclonal antibodies	National Research Center for Environment and Health, Munich, Germany
Mathias Uhlén	Human proteome expression atlas, systematic polyclonal antibody programme	School of Biotechnology, KTH, Stockholm, Sweden