

## ANALYTICAL AND BIOANALYTICAL CHEMISTRY

## Electronic Supplementary Material

## Microscale depletion of high abundance proteins in human biofluids using IgY14 immunoaffinity resin: analysis of human plasma and cerebrospinal fluid

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**Table S1.** A summary table of literature results for recent CSF studies

# Proteins	Method	Reference	Affiliation
798	2.5 ml pooled CSF, 2 ml of individual CSF, 10 kDa cutoff filtration (high and low molecular weight ranges)	<b>Journal of Proteome Research</b> 2008, 7, 386–399	Max-Planck-Institute for Biochemistry
1,212	ProteoMiner, 1,290 ml pooled CSF → SDS-PAGE using 150 µg of FF or nontreated of CSF → cut 20 lanes → digestion → LC-MS/MS (Orbitrap)	<b>Molecular &amp; Cellular Proteomics</b> 9:1006–1021, 2010.	Institut de Pharmacologie et de Biologie Structurale
2,594	CSF proteome characterization in three groups based on the proteomic platforms.	<b>Proteomics</b> 2007, 7, 469–473	Department of Pathology, University of Washington
	1 <sup>st</sup> group: 1. SDS-PAGE → CSF digest → SCX-RPLC online or offline (each 100 µg) → LTQ-FT, LCQ. 2. Pooled CSF → ICAT labeling → LC-MS/MS → 1,474 protein IDs.		
	2 <sup>nd</sup> group: 400 µg of CSF tryptic digest → ACN fractionation → RP-LC, MALDI TOF/TOF → 1,583 protein IDs with single peptides		
	3 <sup>rd</sup> group: Glycoprotein analysis → 2 ml of pooled CSF → MudPIT, LCQ → 359 protein IDs		
156 and 535	750 µg of CSF → IgY14 → FF (3 replicates) → LTQ-FT → 156 unique protein IDs	<b>Clinical Proteomics</b> 2011, 8:6	Laboratoire de Neurobiochimie, Université Jean Monnet, Saint Etienne, France
	750 µg of CSF → IgYHSA RP30 → FF (3 replicates) → LTQ-FT → 535 unique protein IDs		

1,506	18 ml of CSF → IgY14 LC10 → 30 fractions of SCX with 300 µg of FF and BF → RPLC LTQ and LTQ-Orbitrap	<i>PLoS ONE</i> 2010;5:e 10980	University of Medicine and Dentistry of New Jersey-New Jersey Medical School and Pacific Northwest National Lab.
219	4 ml of pooled CSF → MARS (for 6 abundant proteins) column → iTRAQ with digests → SCX → LC-MS/MS (QSTAR Pulsar i quadrupole-TOF)	<i>Proteomics</i> 2007, 7, 3726	Department of Chemistry, North Carolina State University
289	100 µL of pooled CSF (3 control and 3 transgenic) → IgY14 depletion → 90 min RPLC → amaZon ETD ion trap	Journal of Proteome Research 2013,12, 719-728	Department of Chemistry & School of Pharmacy, University of Wisconsin-Madison
242	10 µL of CSF (41 animals) → 180 min RPLC → LTQ Orbitrap XL	Journal of Proteome Research 2012, 11, 4315-4325	Department of Analytical Biochemistry, Centre for Pharmacy, University of Groningen
368	1 mL CSF → Gelfree 8100 (12 fractions) → 70 min RPLC → LTQ Orbitrap	Journal of Proteome Research 2012, 11, 3143-3149	Department of Pharmacology and Molecular Sciences, Johns Hopkins School of Medicine

**Table S2.** All identified proteins obtained from human plasma and CSF in this study are including protein identifications consisting of ≥1 unique peptide - 216\_2014\_8058\_MOESM2\_ESM.xlsx