

***Logical Analysis of Data (LAD) applied to mass spectrometry data  
to Predict Rate of Decline of kidney function***

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**Abstract:**

Even proteinuria, the best predictor of progression rate of chronic kidney disease (CKD), is inadequate in many situations. We therefore used SELDI-TOF mass spectrometry (MS) to assay the serum proteome in the African American Study of Kidney Disease and Hypertension (AASK) Cohort study which examines traditional and non-traditional risk factors for progression of renal disease and analyzed the data with Logical Analysis of Data (LAD) to develop combinatorial biomarkers that predict GFR slope. Sera from 57 rapid and 59 slow progressors (GFR slope -6.64 1.38 vs +2.18 1.13ml/min/yr) were bound to Cu-loaded IMAC30 Protein Chips, SELDI-TOF MS performed. Serum MS and LAD allow the generation of a model consisting of 7 combinatorial biomarkers using just 7 of the 5721 SELDI protein peaks that predicts GFR slope more accurately than proteinuria. Eventual identification of these peaks may lead to a better understanding of progression of CKD and/or new therapeutic modalities.