



# Neuroinflammation and neuroaxonal damage in multiple sclerosis: a cross-sectional cerebrospinal fluid-based proteomic study



Gaetani Lorenzo [1], Höglund Kina [2], Eusebi Paolo [1], Mancini Andrea [1], Di Gregorio Maria [1], Sarchielli Paola [1], Calabresi Paolo [1], Blennow Kaj [2], Parnetti Lucilla [1], Zetterberg Henrik [2], Di Filippo Massimiliano [1]

[1] Clinica Neurologica, Università degli Studi di Perugia, Perugia, Italy

[2] Institute of Neuroscience and Physiology, Department of Psychiatry and Neurochemistry, The Sahlgrenska Academy at University of Gothenburg, Gothenburg, Sweden

## INTRODUCTION AND AIM

Neuroaxonal damage is strongly related to disease progression in multiple sclerosis (MS) [1]. In MS, axonal loss is considered the detrimental consequence of central nervous system (CNS) inflammation [2]. While several treatments are effective in reducing the inflammatory activity of the disease, no therapy is available to directly counteract axonal damage [3]. The study of cerebrospinal fluid (CSF) inflammatory markers closely related to axonal damage can help to identify novel immunological pathways responsible for a more severe neuronal injury.

The aim of this study was to explore the correlations between a panel of CSF inflammation-related proteins (IRPs) and a well-established marker of neuro-axonal damage, namely CSF neurofilament light (NfL).

## PATIENTS AND METHODS

The levels of NfL and of 92 IRPs were determined in the CSF of patients with radiologically isolated syndrome (RIS, n=6), clinically isolated syndrome (CIS, n=32), relapsing remitting MS (RRMS, n=51), progressive MS (PMS, n=8) and in the CSF of patients with other neurological diseases as control group (OND, n=36). NfL was assessed through a newly developed in-house ELISA while the 92 IRPs were determined with a proximity extension assay (PEA) using the Proseek Multiplex Inflammation I kit (Olink Bioscience, Uppsala, Sweden) (Figure 1) (Figure 2).

FIGURE 1. Study design. Collection of CSF samples and subsequent analyses.

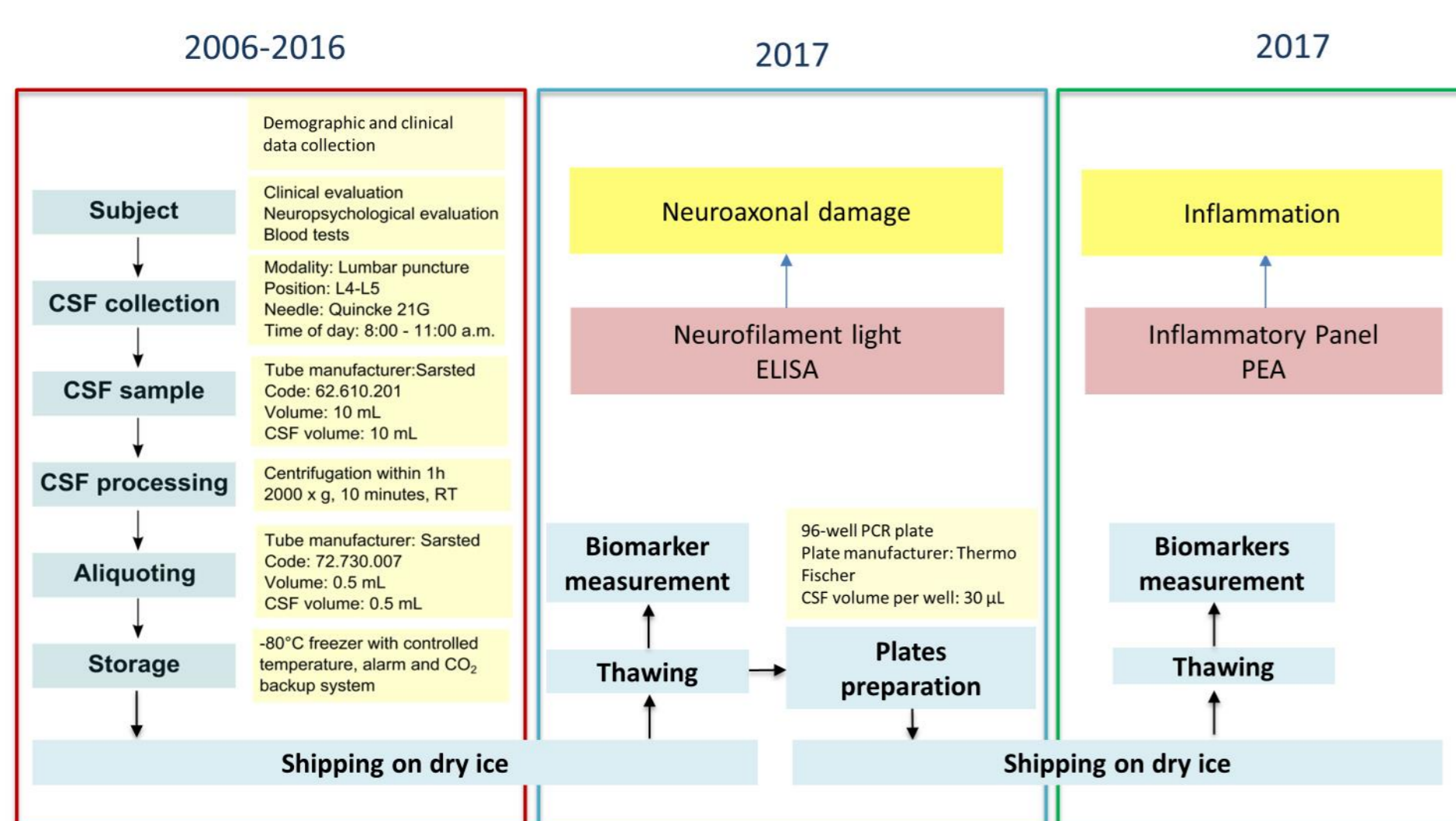
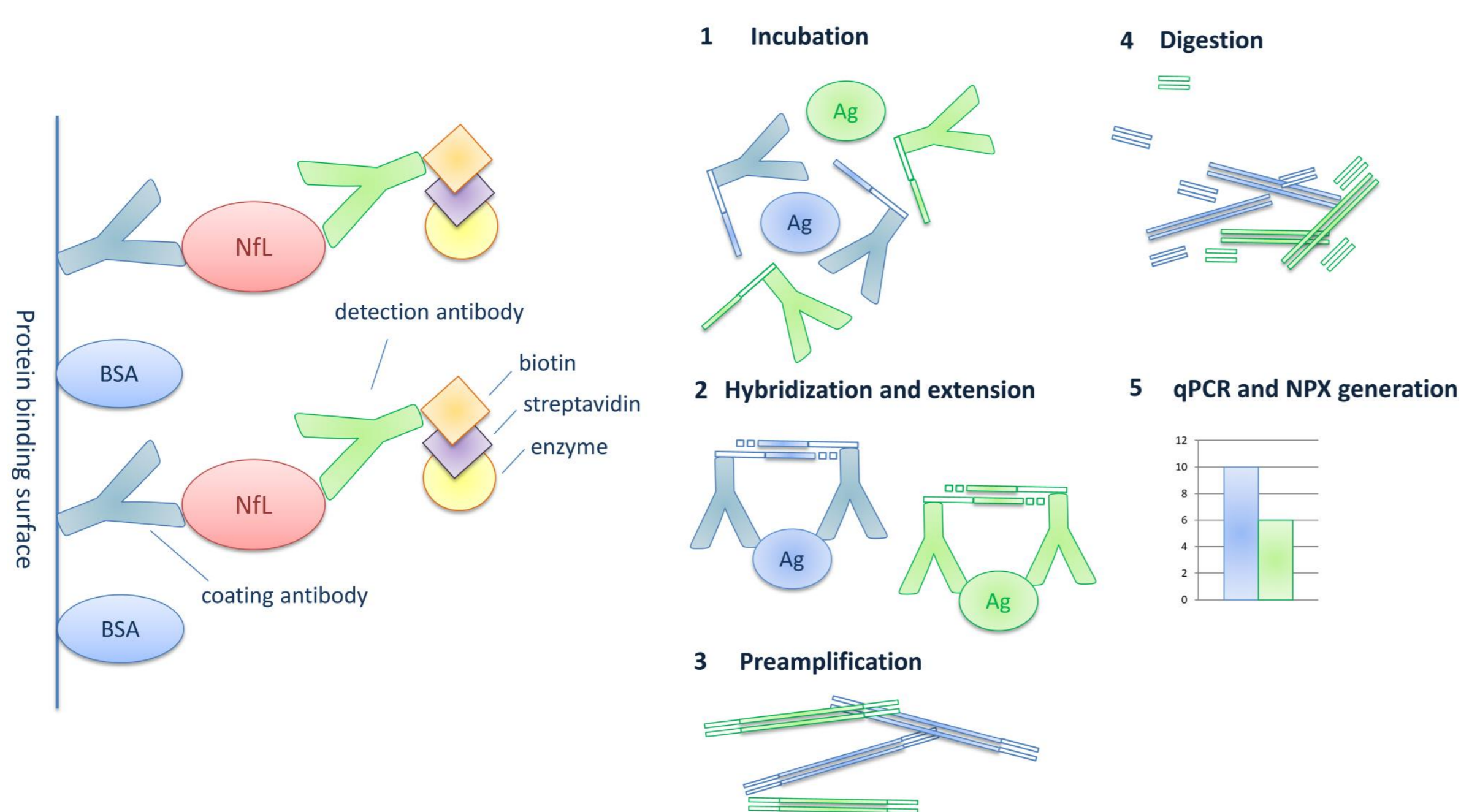


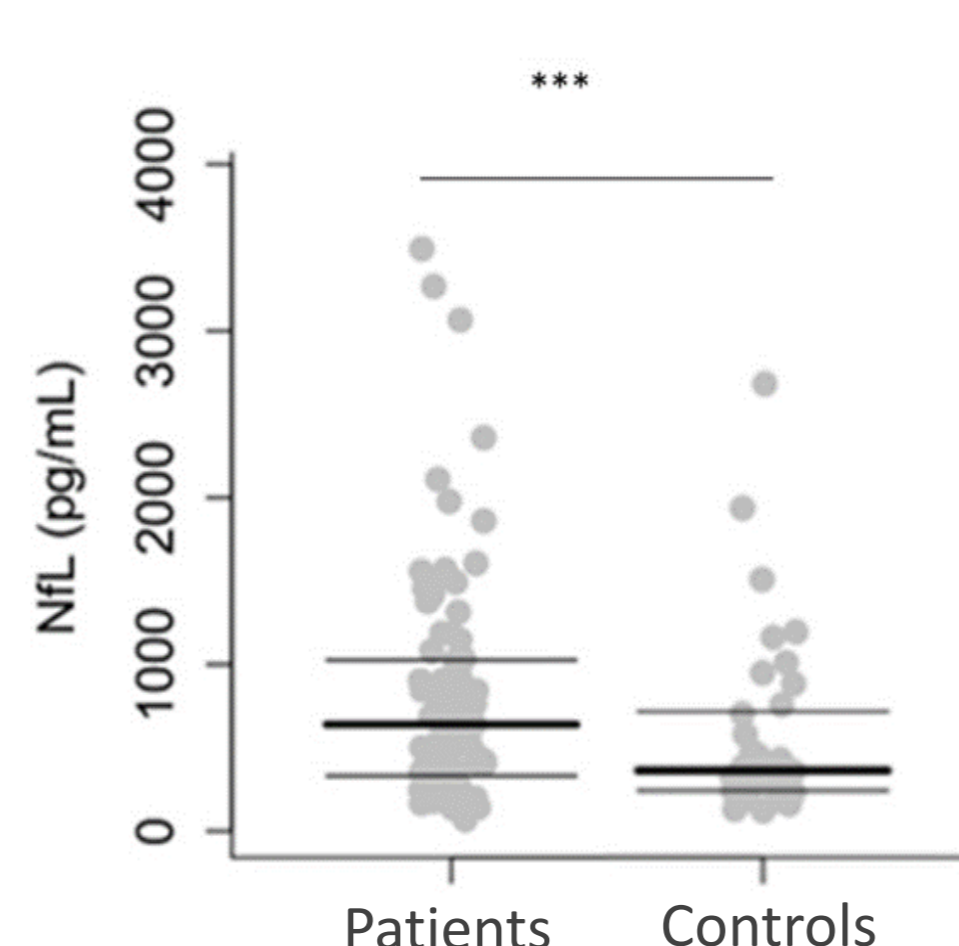
FIGURE 2. ELISA for NfL (left) and proximity extension assay analysis (PEA) (right).



## RESULTS - NfL

- CSF NfL levels were significantly higher in RIS, CIS, RRMS and PMS patients as compared to controls ( $p < 0.001$ ) (Figure 3).
- No significant differences in CSF NfL values were found between RIS, CIS, RRMS and PMS patients.

FIGURE 3. CSF NfL values in patients vs ONDs.



## RESULTS - IRPs

- Out of the 92 IRPs, 41 were excluded from the analysis because of a call rate  $< 75\%$  ( $>75\%$  of all the patients had values below the lower limit of detection).
- 44 IRPs were not significantly different between patients and controls.
- 8 proteins (listed according to p-values from  $p < 0.0001$  to  $p = 0.049$ : CD5, IL12B, TNF $\beta$ , MIP1 $\alpha$ , TNFSF14, TNFSF9, CXCL11) were significantly increased in the CSF of MS patients (Figure 4) (Figure 5).

FIGURE 4. IRPs fold change in MS patients as compared to OND controls. The arrows indicate the significant differences (Adjusted ANOVA + Tukey contrasts)

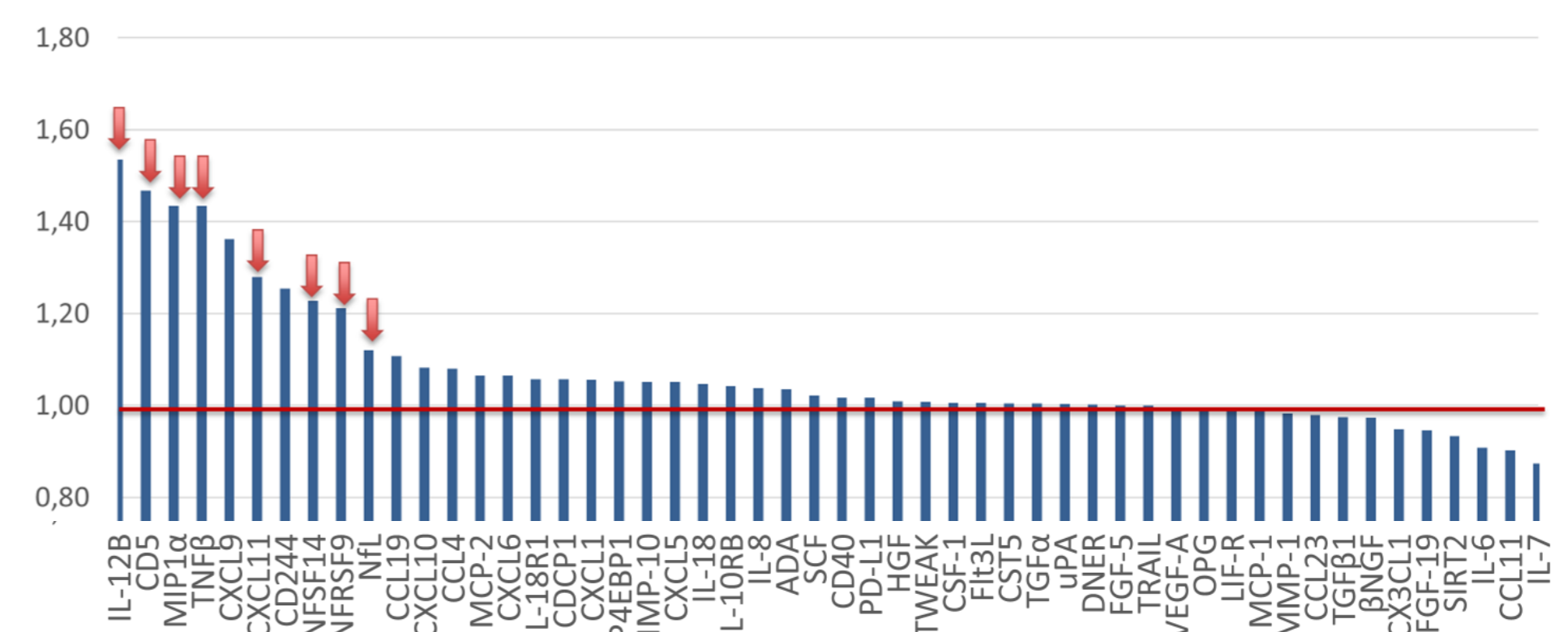
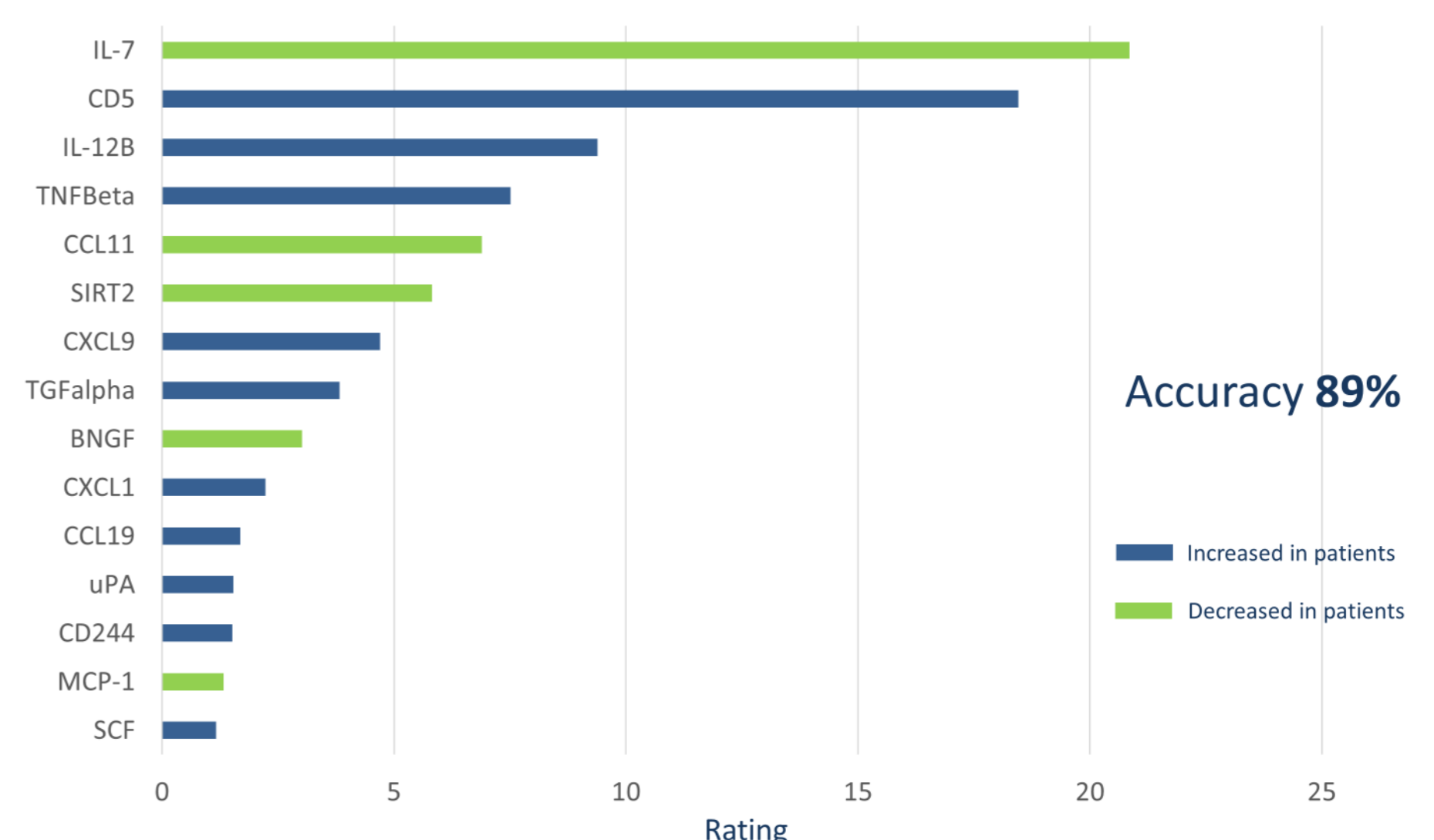


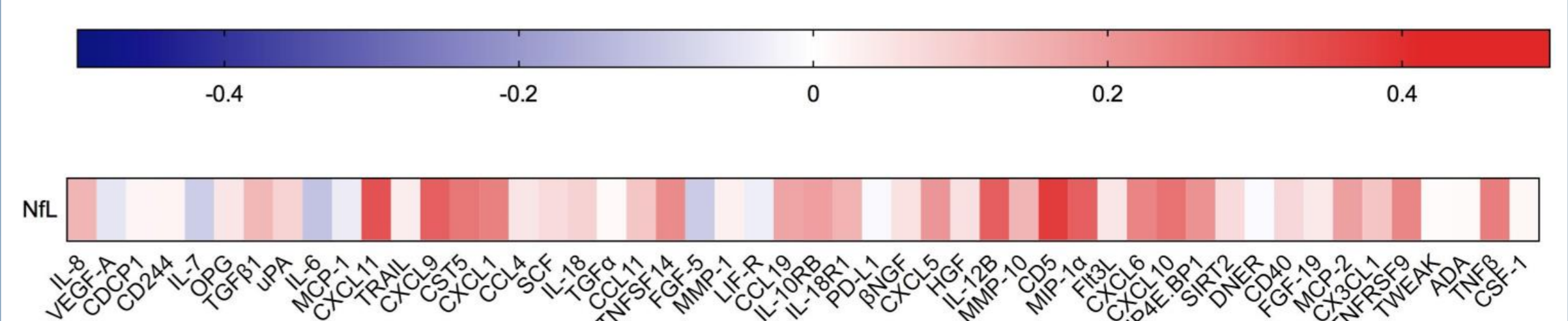
FIGURE 5. Stochastic gradient boosting rating values of each of the IRPs in the discrimination between MS patients and OND controls. The model reaches a high diagnostic accuracy (89%).



## RESULTS - IRPs and NfL

- 15 proteins (including the 7 proteins with higher concentrations in the CSF of MS patients plus CXCL1, CXCL6, CXCL9, CXCL10, CCL23, CCL28, CST5, EIF4BP1) positively correlated with the levels of CSF NfL in MS patients (Figure 6).

FIGURE 6. Spearman's rank correlation coefficients for the correlation between IRPs and NfL.



## CONCLUSIONS

- In MS patients several IRPs are increased as compared to controls.
- Several IRPs positively correlate with the degree of neuroaxonal damage.
- The IRPs we have found to be increased in MS and to correlate with neuroaxonal damage reflect different immunological pathways including B cell activity and lymphoid neogenesis.