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Metallomics approach for the identification of the iron transport protein transferrin in the blood of harbour seals (*Phoca vitulina*)

Mechthild Grebe, Daniel Pröfrock, Antje Kakuschke, Jose A.C. Broekaert and Andreas Prange

Table S-1: Compilation of the average retention times and peak area RSDs (n=3) obtained during the repetitive, highly resolved separation of seal Tf isoforms using anion exchange HPLC-ICP-MS.

Peak No.	Average Retention time (min)	Retention time RSD [%]	Peak area RSD [%]
1	4.97	0.9	8.8
2	7.11	1.4	9.3
3	10.6	0.9	6.1
4	12.9	0.3	2.4
5	14.6	0.2	8.6
6	16.5	0.3	2.8
7	18.6	0.3	4.6
8	20.0	0.2	3.5

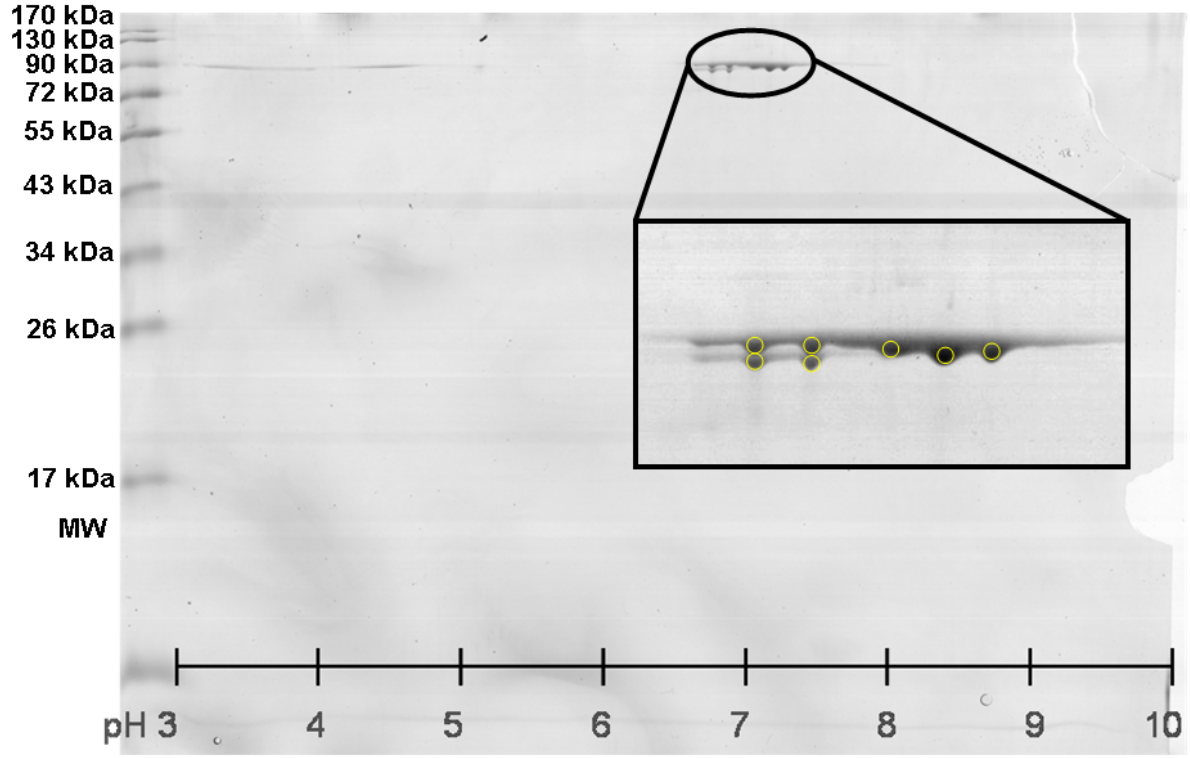

Figure S-1

Figure S-1

2D gel electrophoretic separation of the combined collected iron containing protein species derived after the anion exchange HPLC-ICP-MS analysis and fractionation of a depleted seal plasma sample.

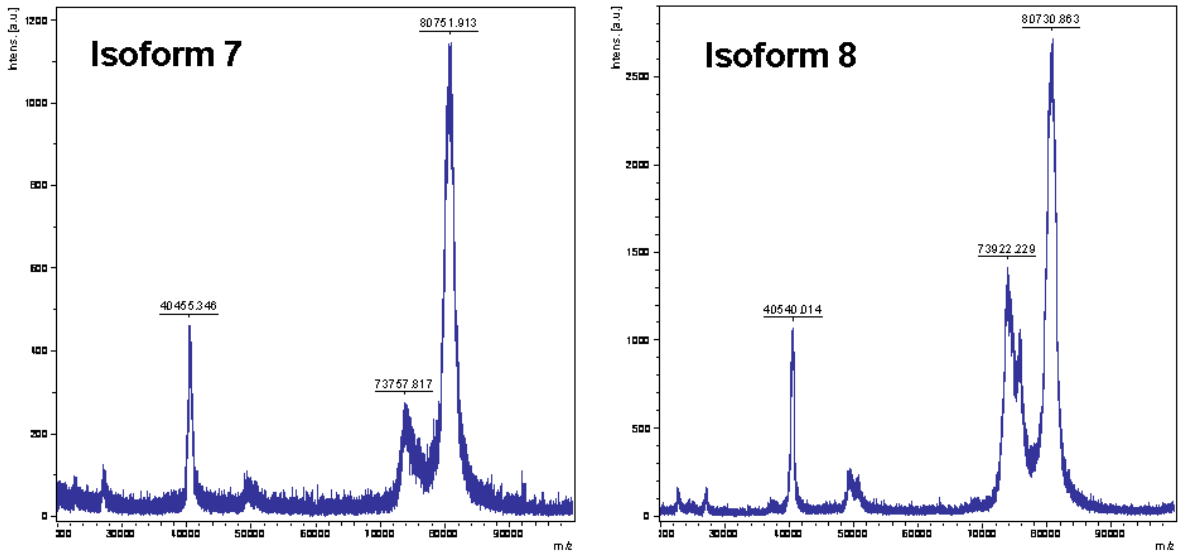

Figure S-2

Figure S-2

Annotated MALDI-TOF spectra of the further iron containing protein species (peak 7 and 8) obtained by element guided fractionation using anion exchange HPLC-ICP-MS.

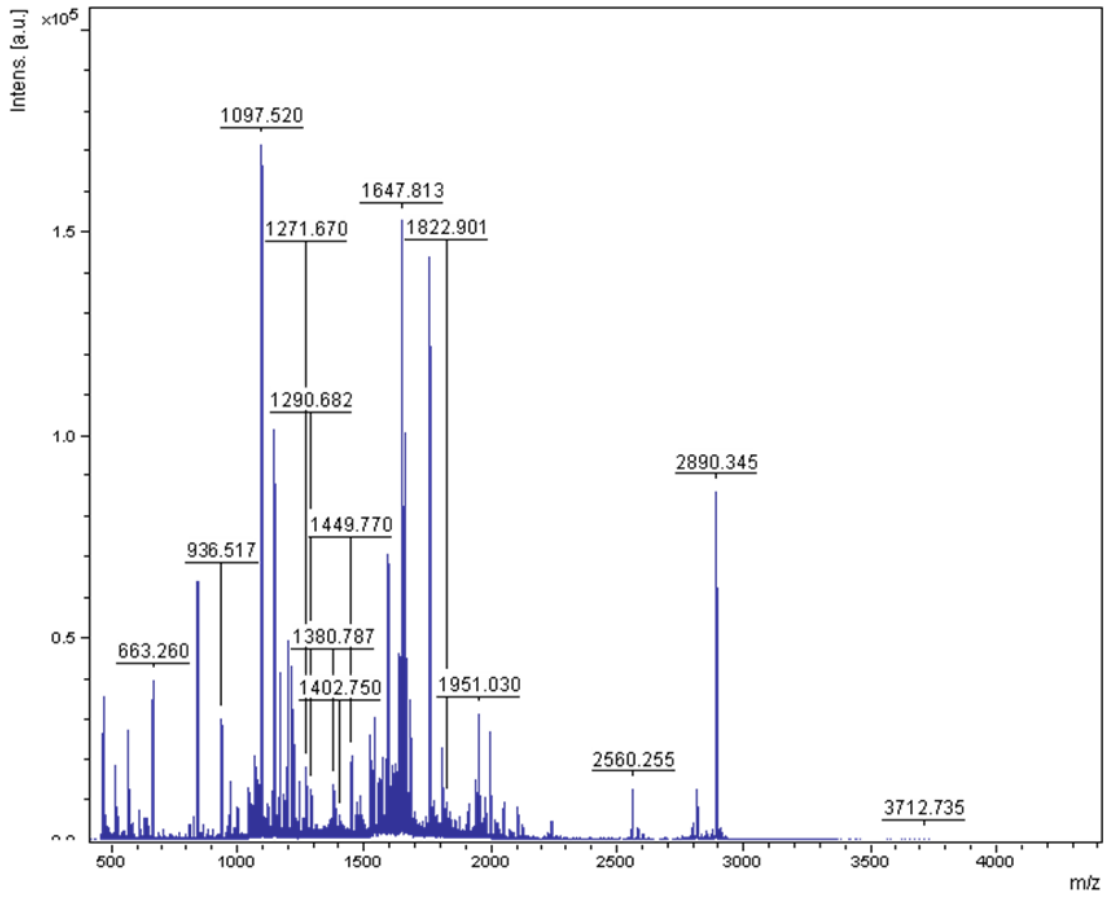

Figure S-3

Figure S-3

MALDI-TOF peptide mass fingerprint spectra of spot 5 (see Figure S-1) after digestion with PNGaseF and Trypsin, respectively, used for cross species protein identification.

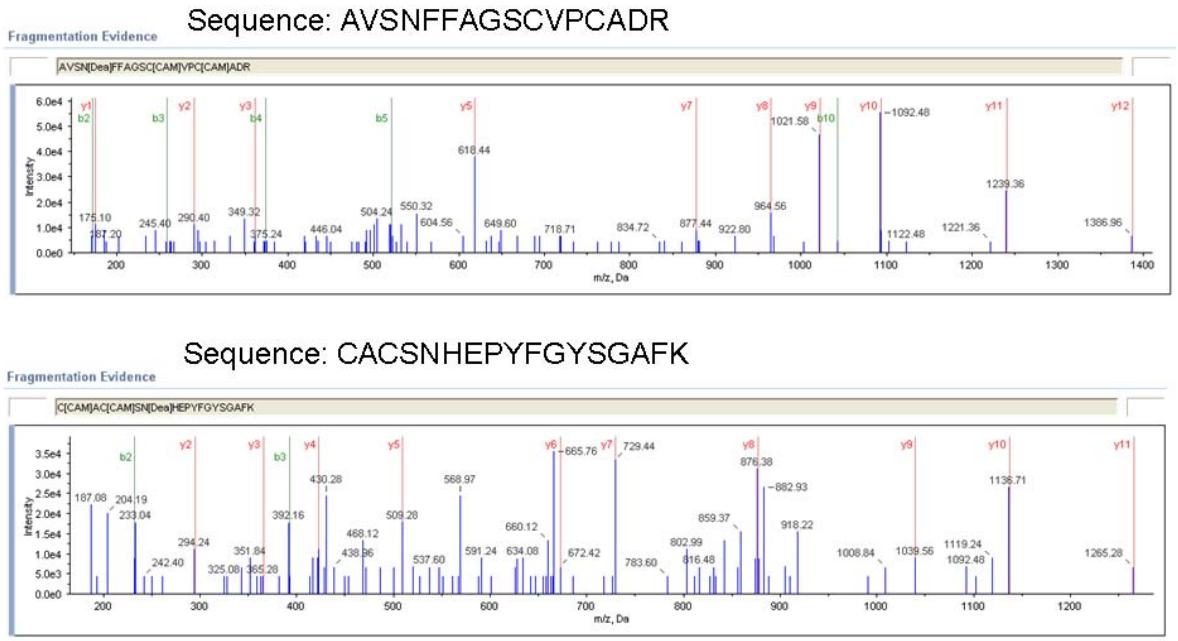

Figure S-4

Figure S-4

NanoLC-ESI-MS-MS analysis allowed the sequence identification and verification of the two peptides with the sequences AVSNFFAGSCVPCADR and CACSNHEPYFGYSGAFK, respectively, which were also observed during PMF experiments.