

Table S1: Full proteomic dataset of human proteins obtained from MIND model experiment as processed by XenoSWATH species-specific deconvolution pipeline. Confidence of the protein identification is reported as FDR-adjusted p-value.

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Table S2: Full proteomic dataset of mouse proteins obtained from MIND model experiment as processed by XenoSWATH species-specific deconvolution pipeline. Confidence of the protein identification is reported as FDR-adjusted p-value.

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Table S3: List of human proteins with significantly altered expression in 10w samples compared to 4w & 6w samples. Log₂ fold change (Log₂FC) for each protein is reported along with the FDR-adjusted p-value from the two-tailed Student's t-test.

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Table S4: List of mouse proteins with significantly altered expression in 10w samples compared to 4w & 6w samples. Log₂ fold change (Log₂FC) for each protein is reported along with the FDR-adjusted p-value from the two-tailed Student's t-test.

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Table S5: Overlapping ontologies enriched in both human and mouse dataset (Figure 4E). GSEA normalized enrichment scores (NES) and FDR-adjusted p-values are shown based on analysis of 10w versus 4w & 6w samples.

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Table S6: Detailed Spectronaut settings used for XenoSWATH analysis

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