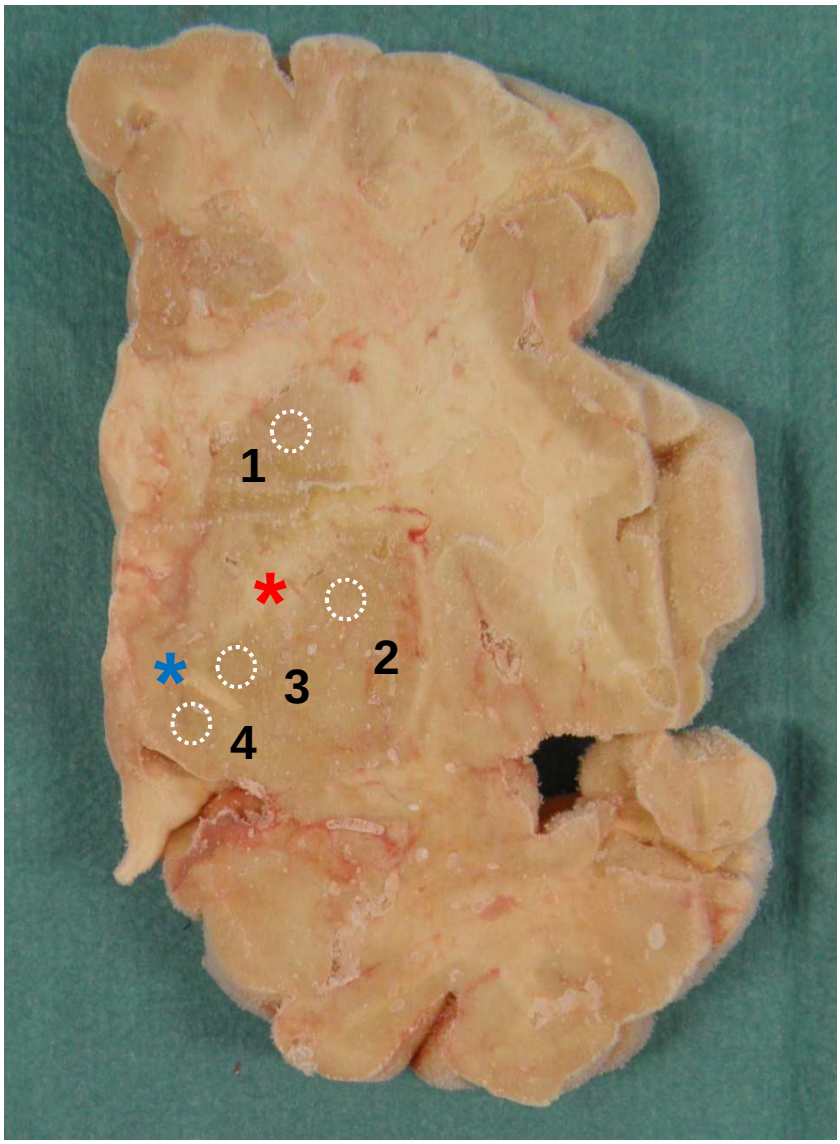
Anatomo-Proteomic Characterization of Human Basal Ganglia:
Focus on striatum and Globus Pallidus

Joaquín Fernández-Irigoyen[1], María Victoria Zelaya[2], Teresa Tuñon[3], Enrique Santamaría[1*]

[1]Proteomics Unit, Clinical Neuroproteomics Group, Navarrabiomed, Fundación Miguel Servet, Pamplona, Spain
[2]Neurological Tissue Bank, Navarrabiomed, Fundación Miguel Servet, 31008 Pamplona, Spain
[3]Pathological Anatomy Department, Navarra Hospital Complex, Pamplona, Spain

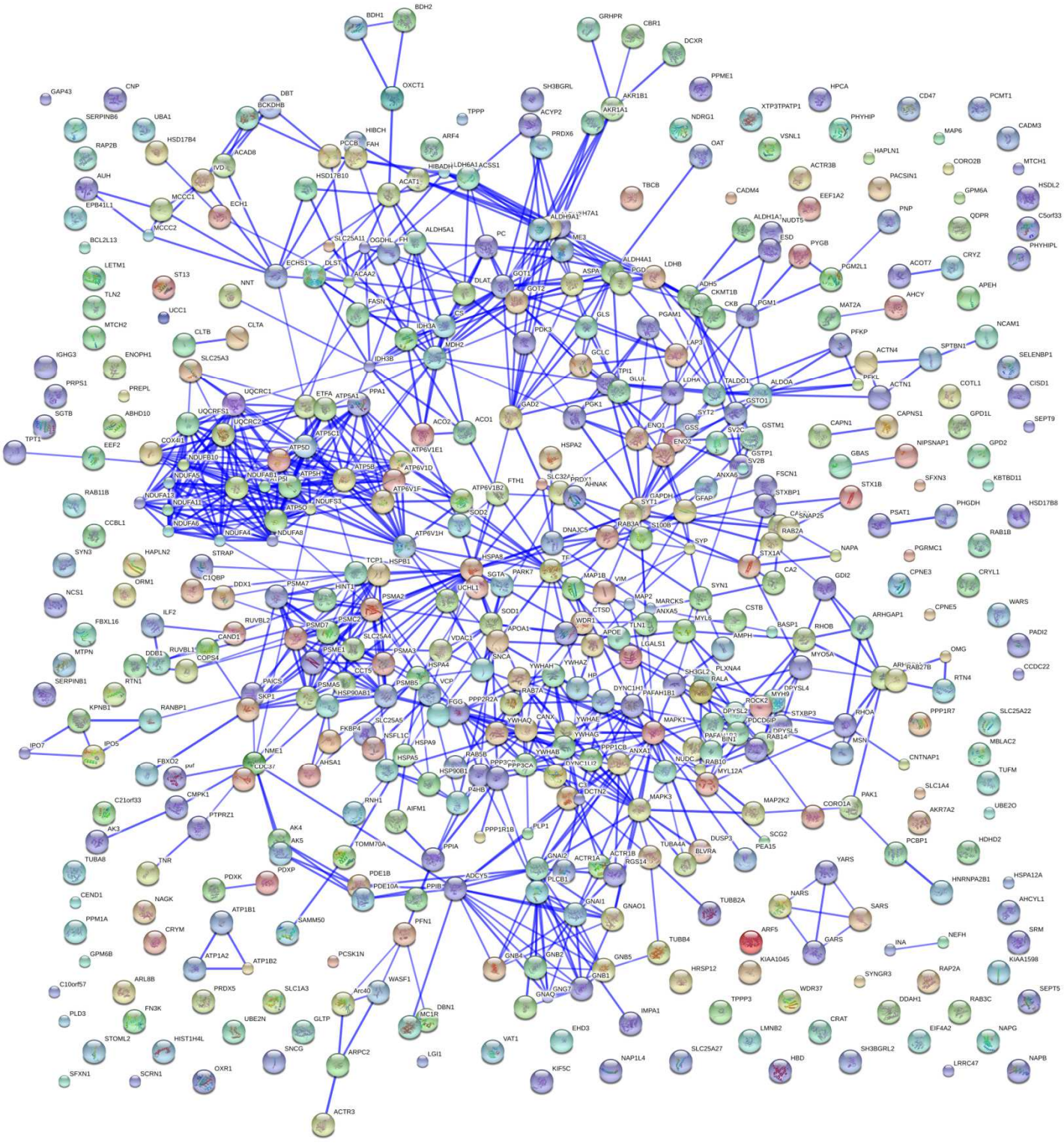
Case	Sex	Age	Macroscopy analysis	PMI (hours)	Immunohistochemistry analysis (Tau, β-amyloide, TDP43, PrP, α-syn, Ub, αβ cryst)	Diagnostic
BCN 34	M	54	normal	3.25	negative	control
BCN 115	M	54	normal	> 8	negative	control
BCN 169	M	41	normal	3.5	negative	control
BCN 174	M	29	normal	7	negative	control
BCN 251	M	53	normal	7	negative	control
BCN 294	M	61	normal	8	negative	control

Supporting figure 1: General characteristics of the subjects included in the proteomic study

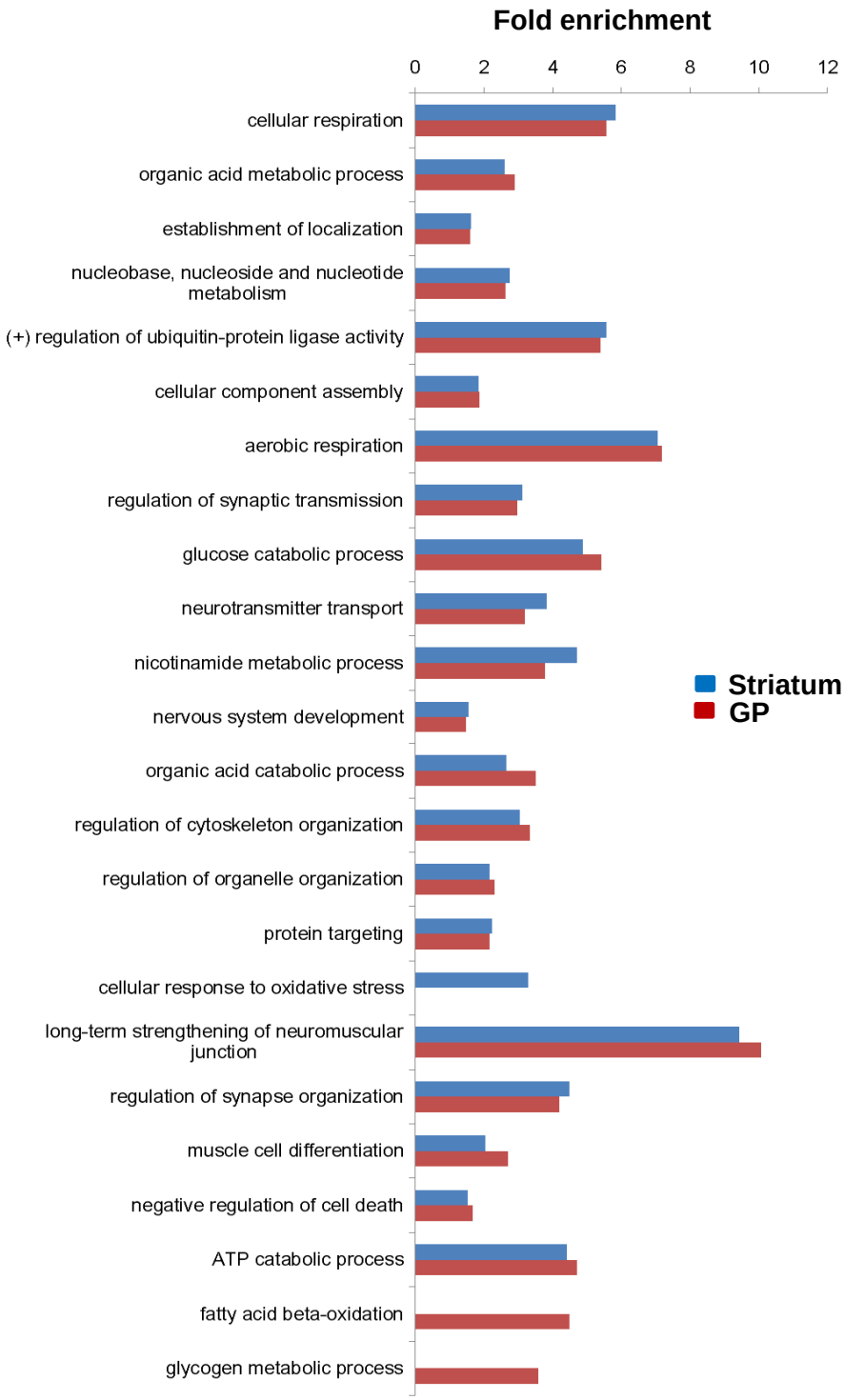


Supporting figure 2: A representative image of BG structures analyzed in this study. The internal capsule and the medial medullary lamina are indicated as a reference. 1) Caudate nucleus, 2) Putamen, 3) Lateral globus pallidus (external), 4) Medial globus pallidus (internal)

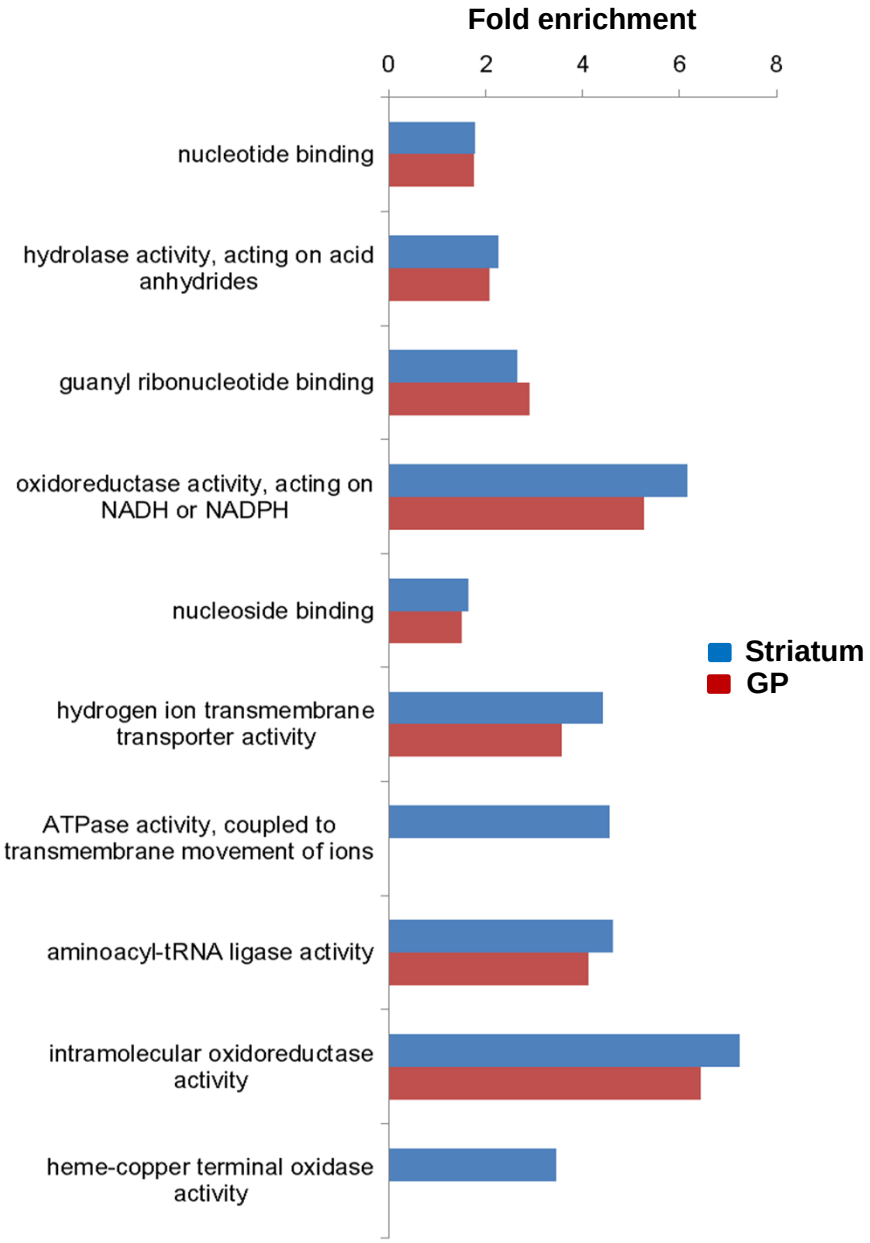
*) internal capsule
*) Medial medullary lamina



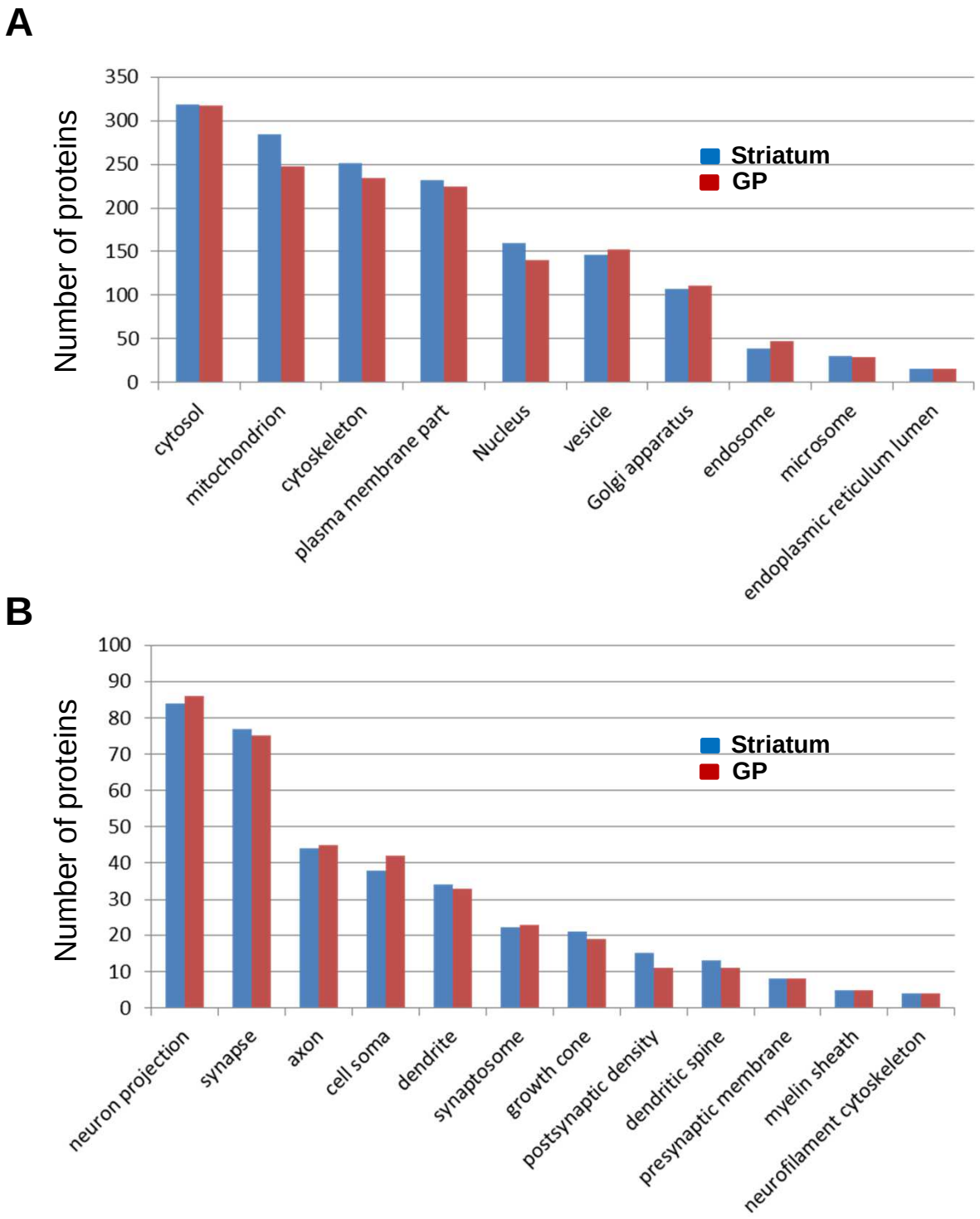
Supporting figure 3: BG interactome network.



Supporting figure 4: Biological Process Ontology for the striatal and pallidal proteomic expression profiles. Representative enriched GO biological process terms from 24 significantly annotation clusters are shown (fold enrichment > 1.5, EASE p-value <0.01). Fold enrichment refers to the number of relevant basal ganglia protein species represented in each category relative to random expression of all genes in the human genome. A complete characterization of each cluster is shown in supplementary table 9.



Supporting figure 5: Molecular Function Ontology for the striatal and pallidal proteomic expression profiles. Representative enriched GO molecular function terms from 10 significantly annotation clusters are shown (fold enrichment > 1.5, EASE p-value <0.01). Fold enrichment refers to the number of relevant basal ganglia protein species represented in each category relative to random expression of all genes in the human genome. A complete characterization of each cluster is shown in supplementary table 10.



Supporting figure 6: Cellular Component Ontology for the striatal and pallidal proteomic expression profiles. A) Classification of BG proteomes based on cellular localization. B) Neuron-specific localization detected by DAVID software (see supplementary table 10).