Network analysis of the PD map: Intermodular communication

Integrating pathways of Parkinson's disease in a molecular interaction map
Molecular Neurobiology

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Supplementary Table 2: Intermodular communication in PD map

This file contains the list of PD map elements prioritized according to their intermodular communication in the PD map. P value and Z-score are calculated on the basis of a given element participating in different moules (subnetworks) in the map. The module classes are the according to article: Guimerà, R., Sales-Pardo, M. & Amaral, L. A. N. Classes of complex networks defined by role-to-role connectivity profiles. Nature Physics 3, 63–69 (2007).

Intermodular communication class

R1: Ultra peripheral - All links within one module
R2: Peripheral - Most links within one module
R3: Satellite connector - High fraction of links to multiple modules
R4: Kinless node - Links homogenously distributed among all modules
R5: Provincial hub - Most links within own module
R6: Connector hub - Many links to most of other modules
R7: Global hub - Links homogenously distributed among all modules

name	P	z	class
H2O2	0.71	5.41	R6
PINK1:PARK2	0.69	3.2	R6
26S hybrid proteasome	0.56	2.87	R6
CoA-SH	0.52	6.18	R6
L-Lactate	0.5	3	R6
ubiquitin	0.45	5.84	R6
2-Oxoglutarate	0.43	3.75	R6
Acetyl-CoA	0.42	2.52	R6
SNCA (protfibril)	0.42	4.1	R6

H2O2	0.38	3.14	R6
O2-	0.38	3.14	R6
MAPK8	0.34	2.84	R6
extracellular exosome	0.33	4.53	R6
Dopamine	0.3	2.5	R6
activated LRRK2	0.15	4.95	R5a
GADD45G	1	-0.37	R4
GADD45B	1	-0.37	R4
BCL6	1	-0.37	R4
BTG2	1	-0.37	R4
ATF3	1	-0.37	R4
PPARGC1A	1	-0.37	R4
SLC25A5	1	-0.37	R4
SLC25A4	1	-0.37	R4
SDHB	1	-0.37	R4
SDHA	1	-0.37	R4
NDUFS5	1	-0.37	R4
NDUFS3	1	-0.37	R4
NDUFC1	1	-0.37	R4
COX7B	1	-0.37	R4
NDUFB5	1	-0.37	R4
NDUFB3	1	-0.37	R4
NDUFAB1	1	-0.37	R4
NDUFA8	1	-0.37	R4
ATP5C1	1	-0.37	R4
ATP5D	1	-0.37	R4
ATP5L	1	-0.37	R4
ATP5O	1	-0.37	R4
COX5B	1	-0.37	R4
COX6A1	1	-0.37	R4
COX7A2	1	-0.37	R4
COX7A2L	1	-0.37	R4

COX7C	1	-0.37	R4
CYCS	1	-0.37	R4
ATP5A1	1	-0.37	R4
UQCRC1	1	-0.37	R4
UQCRB	1	-0.37	R4
NDUFB6	1	-0.37	R4
COX7A1	1	-0.37	R4
SIRT3	1	-0.37	R4
SLC25A14	1	-0.37	R4
SLC25A27	1	-0.37	R4
PTGS2	1	-1.32	R4
ATP	0.83	-0.98	R4
GK	0.82	-0.11	R4
Glycerol	0.82	-0.11	R4
PKLR	0.82	-1.45	R4
PFKM	0.82	-1.45	R4
PFKL	0.82	-1.45	R4
H+	0.82	-1.11	R4
PAK2	0.82	-0.28	R4
MAPK1	0.81	-0.11	R4
ADP	0.81	-1.33	R4
paraquat	0.8	-0.71	R3
Raf/Mek	0.8	0.32	R3
Cytochrome C:Apaf-1:ATP:Procaspase-9	0.8	0.8	R3
CASP3	0.79	0.13	R3
HOO•	0.78	-0.28	R3
O2-	0.78	-3.13	R3
G3P	0.78	2.02	R3
ACC1	0.78	-0.91	R3
HCO3-	0.78	-0.91	R3
GCK	0.78	-1.05	R3
HK1	0.78	-1.05	R3

caspase-7	0.78	0.13	R3
CASP7	0.78	0.13	R3
PAK2 (p34)	0.78	0.24	R3
ATXN3	0.78	-0.05	R3
H+	0.78	-0.55	R3
Apoptosome	0.76	0.47	R3
PAK2 (p34)	0.76	0.76	R3
CACNA1D	0.75	-1.44	R3
UPS	0.75	-1.57	R3
ACC2	0.74	-0.68	R3
Oxaloacetate	0.74	-0.68	R3
Citrate lyase	0.74	-0.68	R3
Citrate	0.74	-0.68	R3
beta-D-Glucose	0.74	-0.64	R3
Phosphoenolpyruvate	0.74	-0.64	R3
ROS	0.74	-0.97	R3
UBL-acyl adenylate intermediate	0.74	0.74	R3
SNCA oligomer	0.74	0.74	R3
SNCA (A30P)	0.74	0.74	R3
SNCA (A53T)	0.74	0.74	R3
ATP-dependent unfoldase	0.74	0.74	R3
PAK2	0.74	0.76	R3
ROS	0.73	0.24	R3
Acetyl-CoA	0.73	0.92	R3
CRTC1	0.73	-0.05	R3
AMPK	0.73	0.32	R3
MAP3K5	0.73	0.24	R3
Pyruvate	0.73	0.71	R3
H+	0.73	-1.65	R3
stearoyl-CoA	0.72	-0.68	R3
Akt pathway	0.72	-0.11	R3
calcineurin	0.72	-1.1	R3

BCL2:VDAC1	0.72	-0.2	R3
SNCA	0.72	-0.27	R3
PPP2CA	0.72	-0.55	R3
MAPT (fragment 422-758)	0.72	-0.2	R3
MAPT (fragment 2-421)	0.72	-0.2	R3
VDAC1	0.72	-0.2	R3
BCL2	0.72	-0.98	R3
Ca2+	0.72	-0.82	R3
Dopa-quinone SNCA adduct	0.72	-0.55	R3
Dopamine-quinone SNCA adduct	0.72	-0.55	R3
SNCA	0.72	-0.58	R3
s5319	0.72	-0.11	R3
Ca channel:RIMBP	0.72	-0.55	R3
UNC13B	0.72	-0.55	R3
permiable pore	0.72	-0.27	R3
NADP+	0.71	-0.68	R3
alpha-D-Glucose	0.7	-0.24	R3
DUB	0.7	1.17	R3
IKK complex	0.69	0.76	R3
H2O	0.69	0.66	R3
SNCA	0.69	-0.22	R3
Ca2+	0.69	0.91	R3
SNCA	0.69	-1.32	R3
BECN1	0.69	-0.95	R3
SLC16A3:BSG	0.69	-0.64	R3
SLC16A1:BSG	0.69	-0.64	R3
lactate dehydrogenase AB3 complex	0.69	-0.24	R3
lactate dehydrogenase A2B2 complex	0.69	-0.24	R3
lactate dehydrogenase A4 complex	0.69	-0.24	R3
lactate dehydrogenase B4 complex	0.69	-0.24	R3
lactate dehydrogenase A3B complex	0.69	-0.24	R3
SLC16A8:BSG	0.69	-0.64	R3

Mitochondrial permeability transition pore (open)	0.69	-0.3	R3
Peroxides	0.69	0.76	R3
Fe(III)	0.68	-1.23	R3
EPB41L1	0.68	2.36	R3
AKAP5	0.68	2.36	R3
DOPAL	0.68	1.28	R3
SOD1	0.67	-1.47	R3
3-hydroxyoctadecanoyl-CoA	0.67	-0.22	R3
NADP+	0.67	-0.57	R3
Ca2+	0.67	-1	R3
AMPA receptor ligand complex	0.67	-0.75	R3
Free Faty Acid	0.67	-0.58	R3
Purine Nucleotide	0.67	-0.58	R3
misfolded SNCA	0.67	2.35	R3
Apoptosis	0.67	-1.07	R3
docked synaptic vesicle	0.67	0.06	R3
CYCS	0.67	-0.05	R3
RHOT2	0.67	-0.54	R3
RHOT1	0.67	-0.54	R3
arachidonoyl-CoA	0.66	-0.22	R3
ubiquinol, cytochrome-c reductase (complex III)	0.66	-0.3	R3
MYO6	0.66	0.63	R3
DLG1	0.66	0.63	R3
TARP:DLG4:MDM2	0.66	0.63	R3
AMPA receptors containing GluR2 (homomers)	0.66	0.63	R3
Orthophosphate	0.66	-1.66	R3
beta-D-Fructose 6-phosphate	0.66	0.17	R3
ALDH2	0.66	-0.1	R3
MAPK1	0.66	0.53	R3
NH3	0.66	0.67	R3
H2O2	0.66	0.67	R3
MAPT	0.66	-0.86	R3

Palmitate	0.65	0.46	R3
isocitrate dehydrogenase	0.65	0.1	R3
NNT dimer	0.65	-0.51	R3
NADPH	0.65	-0.58	R3
NAD+	0.65	-0.58	R3
F0F1-ATP synthase (complex V)	0.64	-0.71	R3
ROS	0.64	0.91	R3
H+	0.64	-0.24	R3
L-Lactate	0.64	-0.24	R3
NADH-Q oxireductase (complex I)	0.64	0.1	R3
CaMKII	0.63	0.98	R3
Pyruvate	0.63	2.19	R3
OH•	0.62	0.66	R3
GSR	0.62	-4.08	R3
PRDX4	0.62	-4.08	R3
PRDX5	0.62	-4.08	R3
PRDX3	0.62	-4.08	R3
PRDX2	0.62	-4.08	R3
PRDX1	0.62	-4.08	R3
CAT	0.62	-4.08	R3
UCP3	0.62	-0.71	R3
UCP2	0.62	-0.71	R3
beta-D-Glucose 6-phosphate	0.62	0.57	R3
beta-D-Fructose 1,6-bisphosphate	0.62	0.57	R3
VDAC1	0.62	-0.22	R3
SIRT3	0.62	0.27	R3
VDAC1	0.62	-0.95	R3
DNM1L	0.62	-0.71	R3
MAPT	0.62	-0.82	R3
Caspase-2	0.62	-0.28	R3
tBID:BCL-2	0.62	-0.28	R3
phospho-dynein(DLC2) on microtubules	0.62	-0.2	R3

phospho-dynein(DLC1) on microtubules	0.62	-0.2	R3
Bcl2:BH3-only protein complex	0.62	-0.28	R3
GPX4	0.62	-1.07	R3
GPX1	0.62	-1.07	R3
PRDX4	0.62	-1.07	R3
PRDX5	0.62	-1.07	R3
PRDX3	0.62	-1.07	R3
PRDX2	0.62	-1.07	R3
PRDX1	0.62	-1.07	R3
CAT	0.62	-1.07	R3
s5073	0.62	-0.55	R3
s4933	0.62	-0.27	R3