

Supplementary Table 3: results of the pathway analysis by the David tool on the proteins modulated in response to PET nanoparticles					
Annotation Cluster 1 Category	Enrichment Score: 7.062983323505796 Term	Count	PValue	Genes	FDR
GOTERM_MF_DIRECT	GO:0000166~nucleotide binding	45	2.27E-09	O70551, P46471, Q81ZRO, Q2NL51, P50516, P70388, P70303, P70248, Q91YH5, P68181, P36371, Q8VEH6, P70704, P61222, Q91V92, Q04899, P61087, P48722, P04184, Q9J111, P49615, Q8CGK3, Q9D0F6, Q8C111, Q9DBC7, P80314, Q61687, P28650, Q9CZ30, Q6ZQB6, Q9WUK4, Q61881, Q04692, Q61102, Q35379, Q8BP47, P21958, Q9WTT7, P08113, Q9EPE9, Q9Z110, Q9D1G2, E9Q634, P60843, P43346	5.69E-07
GOTERM_MF_DIRECT	GO:0005524~ATP binding	42	2.46E-09	O70551, P46471, Q81ZRO, Q2NL51, P50516, P70388, P70303, P70248, P68181, P36371, P70704, P61222, Q6A028, Q91V92, Q04899, P61087, P48722, P04184, Q9J111, P49615, Q8CGK3, Q9D0F6, P80314, Q61687, Q8BH61, Q9CZ30, Q6ZQB6, Q9WUK4, Q61881, Q04692, Q61102, Q35379, Q8BP47, P21958, Q9WTT7, P08113, Q9EPE9, Q9Z110, Q9D1G2, E9Q634, P60843, P43346	5.69E-07
GOTERM_MF_DIRECT	GO:0016887~ATPase activity	21	4.70E-09	P80314, Q61687, P46471, Q9CZ30, P50516, P70388, Q9WUK4, Q61881, Q04692, Q61102, P36371, Q35379, P70704, P61222, P21958, P08113, Q9EPE9, E9Q634, P60843, Q8CGK3, Q9D0F6, P46471, P50516, P70388, P70303, P70248, Q91YH5, P36371, Q8VEH6, P61222, P04184, Q8CGK3, Q9D0F6, Q8C111, Q61687, P28650, Q9CZ30, Q9WUK4, Q61881, Q04692, Q61102, Q35379, P21958, Q9WTT7, Q9D1G2, E9Q634, P60843, P43346	7.26E-07
INTERPRO	IPR027417:P-loop_NTPase	27	2.84E-07	O70551, P46471, Q81ZRO, Q2NL51, P50516, P70388, P70303, P70248, P68181, P36371, P70704, P61222, Q91V92, Q04899, P61087, P48722, P04184, Q9J111, P49615, Q8CGK3, Q9D0F6, P80314, Q61687, Q8BH61, Q9CZ30, Q6ZQB6, Q9WUK4, Q61881, Q04692, Q61102, Q35379, Q8BP47, P21958, Q9WTT7, P08113, Q9EPE9, Q9Z110, Q9D1G2, E9Q634, P60843, P43346	2.21E-04
UP_KW_LIGAND	KW-0067~ATP-binding	41	2.55E-06	O70551, P46471, Q81ZRO, Q2NL51, P50516, P70388, P70303, P70248, Q91YH5, P68181, P36371, Q8VEH6, P70704, P61222, Q91V92, Q04899, P61087, P48722, P04184, Q9J111, P49615, Q8CGK3, Q9D0F6, P28650, Q9CZ30, Q6ZQB6, Q9WUK4, Q61881, Q04692, Q61102, Q35379, Q8BP47, P21958, Q9WTT7, P08113, Q9EPE9, Q9Z110, Q9D1G2, E9Q634, P60843, P43346	7.15E-05
UP_KW_LIGAND	KW-0547~Nucleotide-binding	46	2.20E-05	O70551, P46471, Q81ZRO, Q2NL51, P50516, P70388, P70303, P70248, Q91YH5, P68181, P36371, Q8VEH6, P70704, P61222, Q91V92, Q04899, P61087, P48722, P04184, Q9J111, P49615, Q8CGK3, Q9D0F6, Q8C111, Q9DBC7, P80314, Q61687, Q8BH61, P28650, Q9CZ30, Q6ZQB6, Q9WUK4, Q61881, Q04692, Q61102, Q35379, Q8BP47, P21958, Q9WTT7, P08113, Q9EPE9, Q9Z110, Q9D1G2, E9Q634, P60843, P43346	3.08E-04
Annotation Cluster 2 Category	Enrichment Score: 6.637692151981012 Term	Count	PValue	Genes	
UP_KW_CELLULAR_COMPONENT	KW-0256~Endoplasmic reticulum	38	4.78E-09	O70551, Q81ZRO, Q8R2E9, Q9J1J5, O08547, Q91YH5, P36371, P70704, Q6ZW07, Q9JHP7, P35441, Q8BLN5, O08992, Q9DC16, Q8CHK3, P08003, O88455, Q8C3X8, Q9EQH2, Q8BSY0, Q9D1R9, Q3TYS2, O08715, Q64310, P35564, Q61263, Q8CGZ0, Q8R180, P35821, Q54692, Q9JK23, P21958, Q8R0X7, P08113, B9E186, Q9EPE9, Q70503, Q9DBS1	1.53E-07
GOTERM_CC_DIRECT	GO:0005783~endoplasmic reticulum	39	1.73E-07	O70551, Q81ZRO, Q8R2E9, Q9J1J5, O08547, Q91YH5, Q9CPU4, P36371, P70704, Q6ZW07, Q9JHP7, P35441, Q8BLN5, O08992, Q9DC16, Q8CHK3, P08003, O88455, Q8C3X8, Q9EQH2, Q8BSY0, Q9D1R9, Q3TYS2, O08715, Q64310, P35564, Q61263, Q8CGZ0, Q8R180, P35821, Q54692, Q9JK23, P21958, Q8R0X7, P08113, B9E186, Q9EPE9, Q70503, Q9DBS1	2.95E-05

GOTERM_CC_DIRECT	GO:0005789~endoplasmic reticulum membrane	26	1.48E-05	Q81ZR0, Q8R2E9, Q9JL15, O08547, P36371, Q6ZWO7, Q8BLN5, O08992, Q9DC16, Q8CHK3, O08455, Q8C3X8, Q9EQH2, Q8BSY0, Q3TVS2, Q64310, P35564, Q61263, Q8R180, O54692, P21958, Q8R0X7, P08113, B9EI86, Q9EPE9, Q9DBS1	1.69E-03
Annotation Cluster 3 Category	Enrichment Score: 3.253692744687441 Term	Count	PV value	Genes	
UP_SEQ_FEATURE	CROSSLNK:Glycyl lysine isopeptide (Lys-Gly) (interchain wi	26	4.22E-06	P62717, Q5SU73, P11103, Q8BX09, P10852, P97822, P12970, O35226, Q1HFEZ0, Q9IKX6, Q6NS46, Q99JF8, Q8C111, P80314, Q61687, Q60973, Q9CX56, Q9DIR9, Q8C4I7, Q8CGZ0, Q61881, Q3UEB3, Q04692, P17225, Q9DDE1, P60843	3.17E-03
UP_KW_PTM	KW-1017~Isopeptide bond	37	1.45E-03	P62717, Q5SU73, P11103, Q8BX09, P10852, P97822, P12970, O35226, Q9QUN7, P09055, Q91V92, P61087, Q1HFEZ0, Q9IKX6, Q6NS46, Q99JF8, Q8C111, P80314, Q61687, Q60972, Q60973, Q9CX56, Q9DIR9, Q8C4I7, Q9CO71, Q9WTK5, Q8CGZ0, Q61881, Q3UEB3, P14685, Q9DBG5, Q04692, P17225, Q61093, Q9QXK7, Q9DDE1, P60843	8.70E-03
UP_KW_PTM	KW-0832~Ubl conjugation	44	2.84E-02	Q9D8Y7, P62717, P46471, Q5SU73, P11103, Q8BX09, P10852, P97822, P12970, O35226, P61222, Q9QUN7, P09055, Q91V92, P61087, Q1HFEZ0, Q9IKX6, P04184, A1L314, Q6NS46, Q99JF8, Q8C111, P80314, Q61687, Q60973, Q9CX56, Q9DIR9, Q8C4I7, P35564, Q9CO71, Q9WTK5, Q8CGZ0, Q61881, Q3UEB3, P11157, P14685, Q9DBG5, Q04692, P17225, Q61093, Q9QXK7, Q9DDE1, P60843	1.28E-01
Annotation Cluster 4 Category	Enrichment Score: 2.5204718720181813 Term	Count	PV value	Genes	
GOTERM_MF_DIRECT	GO:0016491~oxidoreductase activity	17	2.94E-04	Q9D6R2, Q8BSY0, P47199, Q8R2E9, Q9ESY9, Q8BV14, Q9JH15, Q8R180, P11157, Q9CPL4, P20108, Q61093, Q99L27, Q9Z110, O08455, Q70503, Q9D616	1.94E-02
UP_KW_MOLECULAR_FUNCTION	KW-0560~Oxidoreductase	17	2.08E-03	Q9D6R2, Q8BSY0, P47199, Q8R2E9, Q9ESY9, Q8BV14, Q9JH15, Q8R180, P11157, Q9CPL4, P20108, Q61093, Q99L27, Q9Z110, O08455, Q70503, Q9D616	3.07E-02
Annotation Cluster 5 Category	Enrichment Score: 2.5073306149579513 Term	Count	PV value	Genes	
UP_KW_BIOLOGICAL_PROCESS	KW-0653~Protein transport	16	2.93E-03	O08920, P61924, Q8BFEY9, Q9CRL6, Q99P88, Q64310, P35585, O08547, Q64324, P36371, O54692, O35344, P21958, Q8BU7, Q9EPE9, P61967	1.39E-01
UP_KW_BIOLOGICAL_PROCESS	KW-0813~Transport	35	6.40E-03	P61924, Q8R2E9, Q99P88, P10852, P50516, O08547, Q64324, P36371, P70704, O35344, Q9DC16, Q8BIJ7, P84104, P61967, Q9DD66, Q8R111, O70318, O08920, Q8BFEY9, Q9CRL6, Q64310, P35585, Q9CQX2, Q8R180, Q9DBG5, Q61102, O35379, O54692, Q61093, P21958, B9EI86, P24668, Q9EPE9, Q9Z111, Q9DB43	1.43E-01
Annotation Cluster 6 Category	Enrichment Score: 2.0912919704661483 Term	Count	PV value	Genes	
GOTERM_MF_DIRECT	GO:0001968~fibronectin binding	6	2.49E-05	P35441, Q64281, P09055, Q08879, O70503	2.31E-03
GOTERM_MF_DIRECT	GO:0005178~integrin binding	8	9.38E-04	Q8K1B8, P35441, Q64281, P09055, Q08879, P08003, P26039	4.82E-02
Annotation Cluster 7 Category	Enrichment Score: 2.0767119854304092 Term	Count	PV value	Genes	

UP_SEQ_FEATURE	REGION:2 X 8 AA tandem repeats of A-X-A-K-A-P-A-[KQ]	3	2.21E-04	P47915	8.30E-02
GOTERM_CC_DIRECT	GO:0042788~polyosomal ribosome	5	2.99E-04	P47915, P62717, P12970	1.05E-02
GOTERM_CC_DIRECT	GO:0022626~cytosolic ribosome	8	3.20E-04	P47915, P61222, P62717, Q9D1R9, Q8CCP0, P12970	1.05E-02
GOTERM_CC_DIRECT	GO:0022625~cytosolic large ribosomal subunit	7	3.39E-04	P47915, P62717, Q9D1R9, Q9D8M4, P12970	1.05E-02
INTERPRO	IPR002673:Ribosomal_e129	3	4.74E-04	P47915	1.23E-01
UP_KW_MOLECULAR_FUNCTION	KW-0687~Ribonucleoprotein	12	9.82E-04	P47915, Q9D7S7, P62717, Q9D1R9, Q9D8M4, Q9QXK7, Q9D0E1, P12970, Q9D883, Q3UEB3	2.14E-02
GOTERM_CC_DIRECT	GO:1990904~ribonucleoprotein complex	11	7.76E-03	P47915, Q9D7S7, P62717, Q9D1R9, Q9D8M4, Q9QXK7, Q9D0E1, P12970, Q3UEB3	1.37E-01
GOTERM_CC_DIRECT	GO:0098793~presynapse	9	8.03E-03	P47915, Q9D7S7, P62717, Q9D1R9, Q9D8M4, Q9QXK7, Q9D0E1, P12970, Q3UEB3	1.37E-01
UP_KW_MOLECULAR_FUNCTION	KW-0689~Ribosomal protein	8	9.55E-03	P47915, Q9D7S7, P62717, Q9D1R9, Q9D8M4, P12970	1.13E-01
Annotation Cluster 8	Enrichment Score: 2.0635147646282004				
Category	Term	Count	PV alue	Genes	
INTERPRO	IPR011012:Longin-like_dom_sf	4	1.97E-03	P61924, P35585, P61967, O08547	1.68E-01
Annotation Cluster 9	Enrichment Score: 2.033959040426288				
Category	Term	Count	PV alue	Genes	
GOTERM_CC_DIRECT	GO:0042470~melanosome	7	3.21E-04	P09055, O08992, P08003, P08113, P10852, P35564, O08547	1.05E-02
Annotation Cluster 10	Enrichment Score: 1.9872865481398783				
Category	Term	Count	PV alue	Genes	
UP_KW_BIOLOGICAL_PROCESS	KW-0235~DNA replication	6	3.40E-03	Q60972, Q60973, Q9CQ71, Q9WUK4, Q61881, Q9D0F6	1.39E-01
Annotation Cluster 11	Enrichment Score: 1.9778910425748917				
Category	Term	Count	PV alue	Genes	
BIOCARTA	m_mCalpainPathway:mCalpain and friends in Cell motility	5	7.24E-04	Q9DBCT, P09055, O88456, P68181, P26039	7.89E-02
Annotation Cluster 12	Enrichment Score: 1.9327840195181778				
Category	Term	Count	PV alue	Genes	
UP_KW_DOMAIN	KW-0676~Redox-active center	5	1.22E-03	P20108, Q8R2E9, P08003, Q9ESY9, Q8R180	2.13E-02
Annotation Cluster 13	Enrichment Score: 1.857541978200378				
Annotation Cluster 14	Enrichment Score: 1.797125927425803				
Category	Term	Count	PV alue	Genes	
INTERPRO	IPR003593:AAA+_ATPase	10	6.97E-06	P36371, O35379, P61222, P46471, P21958, Q9WUK4, Q61881, Q8CGK3, Q9D0F6, Q61102	2.71E-03
SMART	SM00382:AAA	10	9.04E-06	Q8CGK3, Q9D0F6, Q61102	9.95E-04
UP_SEQ_FEATURE	DOMAIN:ABC transporter	5	7.18E-04	P36371, O35379, P61222, P21958, Q61102	1.80E-01
INTERPRO	IPR017871:ABC_transporter-like_CS	5	8.94E-04	P36371, O35379, P61222, P21958, Q61102	1.68E-01
UP_KW_MOLECULAR_FUNCTION	KW-1278~Translocase	7	1.09E-03	P36371, O35379, P70704, P21958, P50516, Q9EPE9, Q9D6I6	2.14E-02
UP_SEQ_FEATURE	DOMAIN:ABC transmembrane type-1	4	1.27E-03	P36371, O35379, P21958, Q61102	2.07E-01
INTERPRO	IPR003439:ABC_transporter-like_ATP_bd	5	1.30E-03	P36371, O35379, P61222, P21958, Q61102	1.68E-01
INTERPRO	IPR036640:ABCI_TM_sf	4	1.58E-03	P36371, O35379, P21958, Q61102	1.68E-01
INTERPRO	IPR011527:ABCI_TM_dom	4	1.77E-03	P36371, O35379, P21958, Q61102	1.68E-01

[illegible]

Category	Term	Count	PV alue	Genes	
UP_KW_BIOLOGICAL_PROCESS	KW:0249~Electron transport	6	6.98E-03	Q61093, Q8R2E9, Q9CQX2, Q9D6I6, Q8RII1, Q8RI80	1.43E-01
Annotation Cluster 24	Enrichment Score: 1.0512318624944594				
Category	Term	Count	PV alue	Genes	
UP_KW_BIOLOGICAL_PROCESS	KW:0931~ER-Golgi transport	5	1.72E-02	O54692, P61924, Q9DCI6, O08547, Q9DB43	2.02E-01
Annotation Cluster 25	Enrichment Score: 0.6890457016707101				
Category	Term	Count	PV alue	Genes	
GOTERM_MF_DIRECT	GO:0005178~integrin binding	8	9.38E-04	Q8K1B8, P35441, Q64281, P09055, Q08879, P08003, P26039	4.82E-02