functional annotation (up + down)

Legend:
- expected (blue)
- observed (red)

Categories (top to bottom):
- gap junction
- GO:0005539~glycosaminoglycan binding
- GO:0048732~gland development
- region of interest:Triple−helical region
- GO:0044421~extracellular region part
- IPR002048:Calcium−binding EF−hand
- GO:0044420~extracellular matrix part
- calcium−binding region:4
- GO:0001655~urogenital system development
- domain:EF−hand 5
- Albinism
- transmembrane
- GO:0006707~cholesterol catabolic process
- GO:0016127~sterol catabolic process
- GO:0048753~pigment granule organization
- hsa04916:Melanogenesis
- Isomerase
- GO:0048770~pigment granule
- GO:0042470~melanosome
- GO:0032438~melanosome organization
- GO:0005788~endoplasmic reticulum lumen
- domain:EF−hand 6
- GO:0019748~secondary metabolic process
- calcium−binding region:5
- GO:0031012~extracellular matrix
- endoplasmic reticulum
- GO:0005783~endoplasmic reticulum
- topological domain:Cytoplasmic
- metal ion−binding site:Copper B
- metal ion−binding site:Copper A
- Melanin biosynthesis
- PIRSF036326:reticulocalbin
- GO:0005578~proteinaceous extracellular matrix
- Two newly identified genetic determinants of pigmentation in Europeans
- GO:0043473~pigmentation
- lipoprotein
- polymorphism
- incorporation or reduction of molecular oxygen, another compound as one donor, and incorporation of one atom of oxygen
- sequence variant
- GO:0005509~calcium ion binding
- IPR008922:Di−copper centre−containing
- IPR002227:Tyrosinase
- topological domain:Lumenal, melanosome
- GO:0042440~pigment metabolic process
- Secreted
- calcium
- GO:0046148~pigment biosynthetic process
- disease mutation
- disulfide bond
- disulfide bond
- extracellular matrix
- short sequence motif:Prevents secretion from ER
- GO:0006582~melanin metabolic process
- GO:0042438~melanin biosynthetic process
- IPR000886:Endoplasmic reticulum, targeting sequence
- signal peptide
- signal
- glycosylation site:N−linked (GlcNAc...)
- glycoprotein

X-axis: 0, 5, 10, 15, 20, 25, 30