



- 144/227 cofactor binding
 - 36/50 pyridoxal phosphate binding
- 28/46 NAD binding
 - 7/9 oxidoreductase, acting on the CH–NH2 group of donors, oxygen as acceptor
 - 11/15 oxidoreductase, acting on the CH–NH2 group of donors
 - 18/25 carboxy-lyase
- 98/148 lyase
 - 30/44 carbon–oxygen lyase
- 20/26 oxidoreductase, acting on the aldehyde or oxo group of donors
 - 8/9 glutathione peroxidase
 - 20/25 peroxidase
- 30/41 antioxidant
 - 4/5 glutathione binding
 - 6/7 oxidoreductase, acting on superoxide radicals as acceptor
- 28/35 oxidoreductase, acting on a sulfur group of donors
 - 15/18 disulfide oxidoreductase
- 394/580 oxidoreductase
 - 9/14 NADH dehydrogenase (quinone)
 - 26/42 oxidoreductase, acting on NAD(P)H
 - 12/19 oxidoreductase, acting on NAD(P)H, quinone or similar compound as acceptor
 - 48/83 dioxygenase
 - 6/10 steroid dehydrogenase, acting on the CH–OH group of donors, NAD or NADP as acceptor
 - 5/7 estradiol 17–beta–dehydrogenase
- 71/109 oxidoreductase, acting on CH–OH group of donors
 - 9/11 retinol dehydrogenase
- 7/8 aldo–keto reductase (NADP)
 - 29/40 transferase, transferring alkyl or aryl (other than methyl) groups
- 17/19 glutathione transferase
 - 190/270 structural molecule
- 89/114 structural constituent of ribosome
 - 27/40 extracellular matrix structural constituent
 - 6/6 structural constituent of eye lens
- 17/20 oxidoreductase, acting on the CH–NH group of donors, NAD or NADP as acceptor
 - 22/31 intramolecular oxidoreductase
 - 13/16 protein disulfide isomerase
 - 68/92 isomerase
 - 22/26 cis–trans isomerase
 - 7/7 intramolecular transferase, phosphotransferases
 - 11/13 intramolecular transferase
 - 5/8 hydrolase, acting on carbon–nitrogen (but not peptide) bonds, in linear amidines
- 46/75 hydrolase, acting on carbon–nitrogen (but not peptide) bonds
 - 97/166 transferase, transferring one–carbon groups
- 196/346 receptor binding
 - 35/55 G–protein coupled receptor binding
 - 17/23 frizzled binding
 - 13/21 Wnt–protein binding
 - 4/6 fibroblast growth factor receptor binding
- 373/658 signal transducer
 - 33/54 peptide receptor
 - 259/432 signaling receptor
 - 9/10 neuropeptide Y receptor
 - 43/67 neurotransmitter receptor
 - 8/13 opioid receptor binding
 - 7/18 adrenergic receptor
- 135/244 G–protein coupled receptor
 - 18/36 G–protein coupled amine receptor
- 246/451 kinase
 - 5/6 protein histidine kinase
 - 125/243 protein serine/threonine kinase
 - 14/23 fibroblast growth factor–activated receptor
- 66/118 protein tyrosine kinase
 - 48/75 transmembrane receptor protein kinase
- 374/686 transferase, transferring phosphorus–containing groups
 - 98/166 DNA polymerase
 - 126/223 nucleotidyltransferase
- 9/23 antiporter
 - 72/109 divalent inorganic cation transmembrane transporter
 - 14/18 voltage–gated calcium channel
- 65/91 voltage–gated ion channel
 - 5/6 cyclic nucleotide–gated ion channel
 - 8/11 intracellular ligand–gated ion channel
- 231/357 cation transmembrane transporter
 - 193/291 inorganic cation transmembrane transporter
 - 14/22 delayed rectifier potassium channel
 - 36/50 voltage–gated potassium channel
 - 46/70 potassium ion transmembrane transporter
 - 6/9 outward rectifier potassium channel
 - 15/26 sodium channel
 - 4/6 voltage–gated sodium channel
- 119/183 monovalent inorganic cation transmembrane transporter
 - 39/69 sodium ion transmembrane transporter
- 10/11 toxic substance binding
 - 13/18 beta–amyloid binding
 - 17/24 neurotransmitter binding
- 405/666 transporter
 - 14/19 acetylcholine–activated cation–selective channel
 - 165/253 channel
 - 35/53 extracellular ligand–gated ion channel
 - 27/39 excitatory extracellular ligand–gated ion channel
 - 360/591 transmembrane transporter
 - 62/95 ligand–gated ion channel
 - 121/182 gated channel
 - 14/18 acetylcholine receptor
 - 22/37 inorganic anion transmembrane transporter
 - 6/7 extracellular–glycine–gated ion channel
 - 16/30 chloride transmembrane transporter
 - 5/10 GABA–A receptor
 - 53/107 anion transmembrane transporter
- 6/8 transmitter–gated channel
 - 7/14 ion gated channel
 - 24/39 channel regulator
- 5/8 cAMP binding
 - 11/18 cyclic nucleotide binding
 - 6/11 cGMP binding
- 9/10 ATPase, coupled to transmembrane movement of ions, rotational mechanism
 - 38/49 hydrogen ion transmembrane transporter
 - 6/7 proton–transporting ATP synthase, rotational mechanism
 - 17/24 cation–transporting ATPase
- 8/12 actinin binding
 - 325/524 calcium ion binding
 - 42/75 cell adhesion molecule binding
- 29/51 protein tyrosine phosphatase
 - 47/90 phosphoprotein phosphatase
 - 91/170 phosphoric ester hydrolase
 - 8/11 cyclic–nucleotide phosphodiesterase
- 70/128 motor
 - 9/12 microfilament motor
 - 5/8 actin–dependent ATPase
 - 51/91 calmodulin binding
- 51/94 microtubule motor
 - 32/71 phosphatase binding
 - 292/517 enzyme binding
 - 4/6 ubiquitin conjugating enzyme binding
 - 36/63 small conjugating protein binding
 - 16/28 polyubiquitin binding
- 22/34 thioesterase binding
 - 452/815 zinc ion binding
- 184/322 ligase, forming carbon–nitrogen bonds
 - 249/432 ligase
 - 14/22 WW domain binding
 - 54/90 small conjugating protein ligase binding
 - 5/8 ligase, forming carbon–carbon bonds
 - 19/35 PDZ domain binding
 - 135/219 protein domain specific binding
 - 4/5 BH domain binding
 - 19/32 Rho guanyl–nucleotide exchange factor
 - 27/44 Ras guanyl–nucleotide exchange factor
- 60/91 exopeptidase
 - 21/33 aminopeptidase
 - 12/17 dipeptidase
 - 23/33 carboxypeptidase
- 124/195 metallopeptidase
 - 76/125 metalloendopeptidase
 - 43/65 aspartic–type peptidase
 - 242/379 endopeptidase
 - 347/549 peptidase
 - 15/15 threonine–type peptidase
- 89/136 serine hydrolase
 - 43/77 peptidase regulator
 - 36/59 endopeptidase regulator
 - 5/6 hydrolase, acting on ether bonds
 - 21/37 thiolester hydrolase
 - 6/8 CoA hydrolase
- 7/13 RNA polymerase II transcription factor binding transcription factor involved in positive regulation of tr
 - 67/140 protein binding transcription factor
 - 39/79 transcription coactivator
 - 19/38 histone acetyltransferase
 - 38/62 transcription regulatory region sequence–specific DNA binding
 - 65/126 regulatory region DNA binding
 - 27/41 RNA polymerase II regulatory region DNA binding
- 140/241 sequence–specific DNA binding
 - 16/23 RNA polymerase II transcription regulatory region sequence–specific DNA binding transcription fac
 - 30/50 sequence–specific DNA binding RNA polymerase II transcription factor
- 153/283 sequence–specific DNA binding transcription factor
 - 33/43 unfolded protein binding
 - 8/12 chitinase
- 67/100 hydrolase, acting on glycosyl bonds
 - 22/32 chitin binding
 - 9/10 glucosidase
 - 42/61 translation factor, nucleic acid binding
- 30/45 translation initiation factor
 - 10/11 translation elongation factor
 - 9/12 sulfuric ester hydrolase

p < 0.01
p < 0.05
p < 0.1