**Supplementary Table 2: Analysis of the enrichment of biological annotations using the DAVID knowledgebase.** The 217 confidently identified protein IDs were matched to 161 genes, which then were submitted to the DAVID enrichment analysis tool containing a total of 12983 annotated genes. For example, 27 of the submitted gene codes (15.2%) were annotated with peptidase inhibitor activity, which represents a ~14 fold increase over the number of matches observed in the entire gene population.

| Term | Count | % | PValue | Genes | Pop Hits | Fold Enrich. | Bonferroni | Benjamini | FDR |
|---|---|---|---|---|---|---|---|---|---|
| GO:0005198~structural molecule activity | 48 | 27.1 | 1.86E-24 | K1C10_HUMAN,UBIQ_HUMAN,K1C28_HUMAN,CH3L1_HUMAN,K2C7_HUMAN,ACTS_HUMAN,ACTN3_HUMAN,K2C6C_HUMAN,K1C9_HUMAN,K1C15_HUMAN,K22E_HUMAN,K2C4_HUMAN,KRT38_HUMAN,ACTB_HUMAN,CYTA_HUMAN,K2C6A_HUMAN,K1C16_HUMAN,K2C72_HUMAN,LMNA_HUMAN,K2C1_HUMAN,K2C5_HUMAN,K1C25_HUMAN,K2C6B_HUMAN,K2C71_HUMAN,K2C73_HUMAN,TSP1_HUMAN,MOES_HUMAN,K22O_HUMAN,K1C17_HUMAN,K2C8_HUMAN,K2C3_HUMAN,K2C79_HUMAN,K2C80_HUMAN,K1C19_HUMAN,K1C13_HUMAN,K1C24_HUMAN,K1C27_HUMAN,K1C14_HUMAN,EMIL2_HUMAN,CO1A1_HUMAN,ACTN2_HUMAN,TITIN_HUMAN,K2C75_HUMAN,FINC_HUMAN,ACTG_HUMAN | 634 | 6.11 | 5.06E-22 | 5.06E-22 | 2.45E-21 |
| GO:0004866~endopeptidase inhibitor activity | 27 | 15.2 | 2.83E-23 | AMBP_HUMAN,A2MG_HUMAN,ITIH2_HUMAN,CYTB_HUMAN,CO3_HUMAN,ANGT_HUMAN,ITIH4_HUMAN,GRP78_HUMAN,CO4B_HUMAN,KNG1_HUMAN,A1AT_HUMAN,ILEU_HUMAN,ITIH1_HUMAN,CYTA_HUMAN,CYTT_HUMAN,ANT3_HUMAN,PEBP1_HUMAN,AACT_HUMAN,PZP_HUMAN,HRG_HUMAN,FETUA_HUMAN,CO5_HUMAN,IC1_HUMAN,PEDF_HUMAN,CYTN_HUMAN,CYTS_HUMAN,CO4A_HUMAN | 145 | 15.02 | 7.69E-21 | 3.84E-21 | 3.72E-20 |
| GO:0030414~peptidase inhibitor activity | 27 | 15.2 | 1.20E-22 | AMBP_HUMAN,A2MG_HUMAN,ITIH2_HUMAN,CYTB_HUMAN,CO3_HUMAN,ANGT_HUMAN,ITIH4_HUMAN,GRP78_HUMAN,CO4B_HUMAN,KNG1_HUMAN,A1AT_HUMAN,ILEU_HUMAN,ITIH1_HUMAN,CYTA_HUMAN,CYTT_HUMAN,ANT3_HUMAN,PEBP1_HUMAN,AACT_HUMAN,PZP_HUMAN,HRG_HUMAN,FETUA_HUMAN,CO5_HUMAN,IC1_HUMAN,PEDF_HUMAN,CYTN_HUMAN,CYTS_HUMAN,CO4A_HUMAN | 153 | 14.23 | 3.26E-20 | 1.09E-20 | 1.58E-19 |
| GO:0004857~enzyme inhibitor activity | 28 | 15.8 | 2.39E-17 | AMBP_HUMAN,A2MG_HUMAN,ITIH2_HUMAN,CYTB_HUMAN,CO3_HUMAN,ANGT_HUMAN,ITIH4_HUMAN,GRP78_HUMAN,CO4B_HUMAN,KNG1_HUMAN,A1AT_HUMAN,ILEU_HUMAN,ITIH1_HUMAN,CYTA_HUMAN,CYTT_HUMAN,ANT3_HUMAN,PEBP1_HUMAN,AACT_HUMAN,PZP_HUMAN,HRG_HUMAN,FETUA_HUMAN,CO5_HUMAN,IC1_HUMAN,CYTN_HUMAN,PEDF_HUMAN,CYTS_HUMAN,APOA2_HUMAN,CO4A_HUMAN | 270 | 8.36 | 6.50E-15 | 1.62E-15 | 3.14E-14 |
| GO:0005200~structural constituent of cytoskeleton | 15 | 8.47 | 2.53E-13 | K2C6B_HUMAN,MOES_HUMAN,K1C17_HUMAN,K1C19_HUMAN,ACTS_HUMAN,K1C9_HUMAN,K1C15_HUMAN,K22E_HUMAN,K1C14_HUMAN,K2C6A_HUMAN,ACTB_HUMAN,K1C16_HUMAN,K2C1_HUMAN,ACTG_HUMAN,K2C5_HUMAN | 74 | 16.35 | 6.88E-11 | 1.38E-11 | 3.33E-10 |
| GO:0003823~antigen binding | 13 | 7.34 | 2.83E-12 | KV304_HUMAN,KV401_HUMAN,IGHA1_HUMAN,IGHG3_HUMAN,IGHA2_HUMAN,IGHM_HUMAN,IGKC_HUMAN,LAC_HUMAN,HV303_HUMAN,KV102_HUMAN,IGHG1_HUMAN,IGHG2_HUMAN,KV101_HUMAN,IGHG4_HUMAN,KV312_HUMAN | 56 | 18.72 | 7.70E-10 | 1.28E-10 | 3.73E-09 |

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|---|---|---|---|---|---|---|---|---|---|
| GO:0004867~serine-type endopeptidase inhibitor activity | 15 | 8.47 | 5.77E-12 | HRG_HUMAN,AMBP_HUMAN,A2MG_HUMAN,ITIH2_HUMAN,IC1_HUMAN,ITIH4_HUMAN,ANGT_HUMAN,PEDF_HUMAN,A1AT_HUMAN,ILEU_HUMAN,ITIH1_HUMAN,ANT3_HUMAN,PZP_HUMAN,AACT_HUMAN,PEBP1_HUMAN | 92 | 13.15 | 1.57E-09 | 2.24E-10 | 7.60E-09 |
| GO:0004869~cysteine-type endopeptidase inhibitor activity | 9 | 5.08 | 1.27E-08 | HRG_HUMAN,FETUA_HUMAN,CYTB_HUMAN,CYTA_HUMAN,CYTT_HUMAN,GRP78_HUMAN,CYTN_HUMAN,CYTS_HUMAN,KNG1_HUMAN | 37 | 19.62 | 3.46E-06 | 4.33E-07 | 1.67E-05 |
| GO:0005344~oxygen transporter activity | 6 | 3.39 | 3.17E-07 | HBD_HUMAN,HBG1_HUMAN,HBB_HUMAN,HBG2_HUMAN,HBA_HUMAN,MYG_HUMAN | 13 | 37.22 | 8.63E-05 | 9.59E-06 | 4.18E-04 |
| GO:0019825~oxygen binding | 7 | 3.95 | 1.33E-05 | HBD_HUMAN,HBG1_HUMAN,HBB_HUMAN,ALBU_HUMAN,HBG2_HUMAN,HBA_HUMAN,MYG_HUMAN | 43 | 13.13 | 0.003620 | 3.63E-04 | 0.017552 |
| GO:0043499~eukaryotic cell surface binding | 5 | 2.82 | 4.67E-05 | TSP1_HUMAN,FIBA_HUMAN,FIBG_HUMAN,FIBB_HUMAN,APOH_HUMAN | 17 | 23.72 | 0.012610 | 0.001153 | 0.061397 |
| GO:0043498~cell surface binding | 5 | 2.82 | 4.15E-04 | TSP1_HUMAN,FIBA_HUMAN,FIBG_HUMAN,FIBB_HUMAN,APOH_HUMAN | 29 | 13.90 | 0.106750 | 0.009363 | 0.544826 |
| GO:0016160~amylase activity | 3 | 1.69 | 4.49E-04 | AMY1_HUMAN,AMYP_HUMAN,AMY2B_HUMAN | 3 | 80.64 | 0.115023 | 0.009355 | 0.589602 |
| GO:0004556~alpha-amylase activity | 3 | 1.69 | 4.49E-04 | AMY1_HUMAN,AMYP_HUMAN,AMY2B_HUMAN | 3 | 80.64 | 0.115023 | 0.009355 | 0.589602 |
| GO:0020037~heme binding | 8 | 4.52 | 7.38E-04 | AMBP_HUMAN,HBD_HUMAN,HBG1_HUMAN,HBB_HUMAN,HBG2_HUMAN,HBA_HUMAN,HERC2_HUMAN,MYG_HUMAN | 121 | 5.33 | 0.181993 | 0.014246 | 0.967454 |
| GO:0046906~tetrapyrrole binding | 8 | 4.52 | 0.001076 | AMBP_HUMAN,HBD_HUMAN,HBG1_HUMAN,HBB_HUMAN,HBG2_HUMAN,HBA_HUMAN,HERC2_HUMAN,MYG_HUMAN | 129 | 5.00 | 0.254029 | 0.019348 | 1.408271 |
| GO:0002020~protease binding | 4 | 2.26 | 0.001539 | A1AT_HUMAN,CYTB_HUMAN,CYTA_HUMAN,ANT3_HUMAN | 19 | 16.98 | 0.342361 | 0.025853 | 2.007769 |
| GO:0003779~actin binding | 12 | 6.78 | 0.002364 | VTDB_HUMAN,ACTN4_HUMAN,MOES_HUMAN,COF1_HUMAN,COTL1_HUMAN,GELS_HUMAN,PROF1_HUMAN,MYO5B_HUMAN,ACTN2_HUMAN,ACTN3_HUMAN,TITIN_HUMAN,ACTN1_HUMAN | 326 | 2.97 | 0.474746 | 0.037166 | 3.067925 |
| GO:0004252~serine-type endopeptidase activity | 8 | 4.52 | 0.002972 | CFAD_HUMAN,TRY1_HUMAN,HPTR_HUMAN,PLMN_HUMAN,HPT_HUMAN,TRFL_HUMAN,MMP8_HUMAN,CFAB_HUMAN,ENOA_HUMAN | 154 | 4.19 | 0.555045 | 0.043990 | 3.843078 |
| GO:0051082~unfolded protein binding | 7 | 3.95 | 0.002974 | HSP7C_HUMAN,PPIA_HUMAN,HSP72_HUMAN,HSP71_HUMAN,GRP78_HUMAN,TCPG_HUMAN,PPIB_HUMAN | 115 | 4.91 | 0.555257 | 0.041748 | 3.845303 |
| GO:0008092~cytoskeletal protein binding | 15 | 8.47 | 0.003799 | VTDB_HUMAN,ACTN4_HUMAN,MOES_HUMAN,COF1_HUMAN,GELS_HUMAN,MYO5B_HUMAN,ACTS_HUMAN,ACTN3_HUMAN,COTL1_HUMAN,PROF1_HUMAN,ACTC_HUMAN,CALM_HUMAN,ACTN2_HUMAN,TITIN_HUMAN,ACTN1_HUMAN | 504 | 2.40 | 0.644909 | 0.050451 | 4.887188 |
| GO:0005506~iron ion binding | 11 | 6.21 | 0.004849 | AMBP_HUMAN,HBD_HUMAN,HBG1_HUMAN,HBB_HUMAN,HBG2_HUMAN,TRFL_HUMAN,HBA_HUMAN,HERC2_HUMAN,HEMO_HUMAN,MYG_HUMAN,TRFE_HUMAN | 308 | 2.88 | 0.733487 | 0.061026 | 6.198869 |
| GO:0016861~intramolecular oxidoreductase activity, interconverting aldoses and ketoses | 3 | 1.69 | 0.005133 | HYI_HUMAN,TPIS_HUMAN,G6PI_HUMAN | 9 | 26.88 | 0.753374 | 0.061648 | 6.550240 |
| GO:0005178~integrin binding | 5 | 2.82 | 0.005975 | ACTN4_HUMAN,TSP1_HUMAN,ACTN2_HUMAN,ACTN3_HUMAN,ACTN1_HUMAN | 59 | 6.83 | 0.804098 | 0.068422 | 7.585798 |
| GO:0008236~serine-type peptidase activity | 8 | 4.52 | 0.006532 | CFAD_HUMAN,TRY1_HUMAN,HPTR_HUMAN,PLMN_HUMAN,HPT_HUMAN,TRFL_HUMAN,MMP8_HUMAN,CFAB_HUMAN,ENOA_HUMAN | 178 | 3.62 | 0.831791 | 0.071581 | 8.264892 |
| GO:0017171~serine hydrolase activity | 8 | 4.52 | 0.006920 | CFAD_HUMAN,TRY1_HUMAN,HPTR_HUMAN,PLMN_HUMAN,HPT_HUMAN,TRFL_HUMAN,MMP8_HUMAN,CFAB_HUMAN,ENOA_HUMAN | 180 | 3.58 | 0.848755 | 0.072770 | 8.735632 |

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|---|---|---|---|---|---|---|---|---|---|
| GO:0008201~heparin binding | 6 | 3.39 | 0.008875 | HRG_HUMAN,TSP1_HUMAN,ANT3_HUMAN,KNG1_HUMAN,APOH_HUMAN,FINC_HUMAN | 103 | 4.70 | 0.911521 | 0.089051 | 11.07310 |
| GO:0005509~calcium ion binding | 21 | 11.7 | 0.009187 | ACTN4_HUMAN,TSP1_HUMAN,S10AB_HUMAN,AMY1_HUMAN,GELS_HUMAN,AMY2B_HUMAN,S10A8_HUMAN,GRP78_HUMAN,ACTN3_HUMAN,TRY1_HUMAN,ITIH1_HUMAN,PLMN_HUMAN,AMYP_HUMAN,CALM_HUMAN,MMP8_HUMAN,S10A9_HUMAN,ACTN2_HUMAN,MMP9_HUMAN,FIBG_HUMAN,TITIN_HUMAN,ACTN1_HUMAN | 919 | 1.84 | 0.918783 | 0.088794 | 11.44091 |
| GO:0001871~pattern binding | 7 | 3.95 | 0.012064 | HRG_HUMAN,TSP1_HUMAN,ANT3_HUMAN,CHIT1_HUMAN,KNG1_HUMAN,APOH_HUMAN,FINC_HUMAN | 154 | 3.67 | 0.963173 | 0.111225 | 14.76640 |
| GO:0030247~polysaccharide binding | 7 | 3.95 | 0.012064 | HRG_HUMAN,TSP1_HUMAN,ANT3_HUMAN,CHIT1_HUMAN,KNG1_HUMAN,APOH_HUMAN,FINC_HUMAN | 154 | 3.67 | 0.963173 | 0.111225 | 14.76640 |
| GO:0008307~structural constituent of muscle | 4 | 2.26 | 0.014839 | ACTN2_HUMAN,K1C19_HUMAN,ACTN3_HUMAN,TITIN_HUMAN | 42 | 7.68 | 0.982862 | 0.130836 | 17.86402 |
| GO:0051015~actin filament binding | 4 | 2.26 | 0.027462 | ACTN4_HUMAN,MYO5B_HUMAN,TITIN_HUMAN,ACTN1_HUMAN | 53 | 6.09 | 0.999486 | 0.223127 | 30.68817 |
| GO:0030674~protein binding, bridging | 5 | 2.82 | 0.028813 | CYTA_HUMAN,GRP78_HUMAN,FIBA_HUMAN,FIBG_HUMAN,FIBB_HUMAN | 94 | 4.29 | 0.999648 | 0.226264 | 31.94431 |
| GO:0005539~glycosaminoglycan binding | 6 | 3.39 | 0.029531 | HRG_HUMAN,TSP1_HUMAN,ANT3_HUMAN,KNG1_HUMAN,APOH_HUMAN,FINC_HUMAN | 140 | 3.46 | 0.999712 | 0.224930 | 32.60437 |
| GO:0032403~protein complex binding | 7 | 3.95 | 0.034468 | AMBP_HUMAN,ACTN4_HUMAN,TSP1_HUMAN,1433Z_HUMAN,ACTN2_HUMAN,ACTN3_HUMAN,ACTN1_HUMAN | 196 | 2.88 | 0.999928 | 0.251076 | 36.98033 |
| GO:0034190~apolipoprotein receptor binding | 2 | 1.13 | 0.036520 | APOA2_HUMAN,APOA1_HUMAN | 3 | 53.76 | 0.999959 | 0.257425 | 38.72046 |
| GO:0030492~hemoglobin binding | 2 | 1.13 | 0.036520 | HPTR_HUMAN,HBB_HUMAN,HPT_HUMAN | 3 | 53.76 | 0.999959 | 0.257425 | 38.72046 |
| GO:0070653~high-density lipoprotein receptor binding | 2 | 1.13 | 0.036520 | APOA2_HUMAN,APOA1_HUMAN | 3 | 53.76 | 0.999959 | 0.257425 | 38.72046 |
| GO:0004083~2,3-bisphospho-D-glycerate 2-phosphohydrolase activity | 2 | 1.13 | 0.048396 | PGAM2_HUMAN,PGAM1_HUMAN | 4 | 40.32 | 0.999998 | 0.319902 | 47.95132 |
| GO:0004082~bisphosphoglycerate mutase activity | 2 | 1.13 | 0.048396 | PGAM2_HUMAN,PGAM1_HUMAN | 4 | 40.32 | 0.999998 | 0.319902 | 47.95132 |
| GO:0004619~phosphoglycerate mutase activity | 2 | 1.13 | 0.048396 | PGAM2_HUMAN,PGAM1_HUMAN | 4 | 40.32 | 0.999998 | 0.319902 | 47.95132 |
| GO:0034416~bisphosphoglycerate phosphatase activity | 2 | 1.13 | 0.060127 | PGAM2_HUMAN,PGAM1_HUMAN | 5 | 32.26 | 0.999999 | 0.374079 | 55.79225 |
| GO:0060228~phosphatidylcholine-sterol O-acyltransferase activator activity | 2 | 1.13 | 0.060127 | APOA2_HUMAN,APOA1_HUMAN | 5 | 32.26 | 0.999999 | 0.374079 | 55.79225 |
| GO:0008034~lipoprotein binding | 3 | 1.69 | 0.068928 | TSP1_HUMAN,APOA2_HUMAN,APOA1_HUMAN | 35 | 6.91 | 0.999999 | 0.408459 | 60.94113 |
| GO:0030246~carbohydrate binding | 9 | 5.08 | 0.071697 | HRG_HUMAN,TSP1_HUMAN,CH3L1_HUMAN,ANT3_HUMAN,CHIT1_HUMAN,KNG1_HUMAN,K2C1_HUMAN,APOH_HUMAN,FINC_HUMAN | 354 | 2.05 | 0.999999 | 0.412883 | 62.44313 |
| GO:0005518~collagen binding | 3 | 1.69 | 0.072409 | TSP1_HUMAN,MMP9_HUMAN,FINC_HUMAN | 36 | 6.72 | 0.999999 | 0.407989 | 62.82068 |

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|---|---|---|---|---|---|---|---|---|---|
| GO:0003755~peptidyl-prolyl cis-trans isomerase activity | 3 | 1.69 | 0.075947 | PPIA_HUMAN,PAL4B_HUMAN,PPIB_HUMAN | 37 | 6.54 | 1 | 0.415563 | 64.64445 |
| GO:0016860~intramolecular oxidoreductase activity | 3 | 1.69 | 0.079539 | HYI_HUMAN,TPIS_HUMAN,G6PI_HUMAN | 38 | 6.37 | 1 | 0.422959 | 66.41114 |
| GO:0008035~high-density lipoprotein binding | 2 | 1.13 | 0.083160 | APOA2_HUMAN,APOA1_HUMAN | 7 | 23.04 | 1 | 0.43009 | 68.10965 |
| GO:0031432~titin binding | 2 | 1.13 | 0.083160 | CALM_HUMAN,ACTN2_HUMAN | 7 | 23.04 | 1 | 0.430092 | 68.10965 |
| GO:0016859~cis-trans isomerase activity | 3 | 1.69 | 0.083182 | PPIA_HUMAN,PAL4B_HUMAN,PPIB_HUMAN | 39 | 6.20 | 1 | 0.422679 | 68.11978 |
| GO:0005201~extracellular matrix structural constituent | 4 | 2.26 | 0.089876 | CH3L1_HUMAN,CO1A1_HUMAN,EMIL2_HUMAN,FINC_HUMAN | 86 | 3.75 | 1 | 0.441318 | 71.05145 |
| GO:0004175~endopeptidase activity | 9 | 5.08 | 0.092554 | CFAD_HUMAN,TRY1_HUMAN,HPTR_HUMAN,PLMN_HUMAN,HPT_HUMAN,TRFL_HUMAN,MMP8_HUMAN,CFAB_HUMAN,MMP9_HUMAN,ENOA_HUMAN | 375 | 1.94 | 1 | 0.444032 | 72.15257 |
| GO:0001848~complement binding | 2 | 1.13 | 0.094465 | IC1_HUMAN,CFAB_HUMAN | 8 | 20.16 | 1 | 0.443868 | 72.91484 |
| GO:0004568~chitinase activity | 2 | 1.13 | 0.094465 | CH3L1_HUMAN,CHIT1_HUMAN | 8 | 20.16 | 1 | 0.443868 | 72.91484 |