Stable. The enrichment analysis of Kyoto Encyclopedia of Genes and Genomes for potential targets.

|  |  |  |
| --- | --- | --- |
| ACE2 |  |  |
| NAME | ES | P-value |
| KEGG\_PRIMARY\_IMMUNODEFICIENCY | 0.770972 | <0.001 |
| KEGG\_INTESTINAL\_IMMUNE\_NETWORK\_FOR\_IGA\_PRODUCTION | 0.698396 | <0.001 |
| KEGG\_T\_CELL\_RECEPTOR\_SIGNALING\_PATHWAY | 0.60218 | <0.001 |
| KEGG\_ALLOGRAFT\_REJECTION | 0.712923 | <0.001 |
| KEGG\_ANTIGEN\_PROCESSING\_AND\_PRESENTATION | 0.608839 | <0.001 |
| KEGG\_RIBOSOME | -0.70054 | <0.001 |
| KEGG\_PARKINSONS\_DISEASE | -0.60675 | <0.001 |
| KEGG\_OXIDATIVE\_PHOSPHORYLATION | -0.57062 | <0.001 |
| KEGG\_ALZHEIMERS\_DISEASE | -0.54152 | <0.001 |
| KEGG\_HUNTINGTONS\_DISEASE | -0.53134 | <0.001 |
|  |  |  |
| TMPRSS2 |  |  |
| NAME | ES | P-value |
| KEGG\_ADHERENS\_JUNCTION | 0.488246 | <0.001 |
| KEGG\_DORSO\_VENTRAL\_AXIS\_FORMATION | 0.601149 | 0.009 |
| KEGG\_TIGHT\_JUNCTION | 0.403737 | <0.001 |
| KEGG\_ARRHYTHMOGENIC\_RIGHT\_VENTRICULAR\_CARDIOMYOPATHY\_ARVC | 0.392556 | 0.036 |
| KEGG\_ECM\_RECEPTOR\_INTERACTION | 0.411209 | 0.008 |
| KEGG\_RIBOSOME | -0.92289 | <0.001 |
| KEGG\_OXIDATIVE\_PHOSPHORYLATION | -0.78406 | <0.001 |
| KEGG\_PARKINSONS\_DISEASE | -0.75122 | <0.001 |
| KEGG\_HUNTINGTONS\_DISEASE | -0.65673 | <0.001 |
| KEGG\_ALZHEIMERS\_DISEASE | -0.63094 | <0.001 |
|  |  |  |
| SARS |  |  |
| NAME | ES | P-value |
| KEGG\_RIBOSOME | 0.968285 | <0.001 |
| KEGG\_OXIDATIVE\_PHOSPHORYLATION | 0.782626 | <0.001 |
| KEGG\_PARKINSONS\_DISEASE | 0.732734 | <0.001 |
| KEGG\_PROTEASOME | 0.850487 | <0.001 |
| KEGG\_ALZHEIMERS\_DISEASE | 0.6072 | <0.001 |
| KEGG\_TASTE\_TRANSDUCTION | -0.5854 | 0.002 |
| KEGG\_DORSO\_VENTRAL\_AXIS\_FORMATION | -0.64126 | 0.007 |
| KEGG\_PHOSPHATIDYLINOSITOL\_SIGNALING\_SYSTEM | -0.53513 | 0.002 |
| KEGG\_ABC\_TRANSPORTERS | -0.54584 | 0.012 |
| KEGG\_NOTCH\_SIGNALING\_PATHWAY | -0.54008 | 0.013 |
|  |  |  |
| SARS2 |  |  |
| NAME | ES | P-value |
| KEGG\_PHOSPHATIDYLINOSITOL\_SIGNALING\_SYSTEM | 0.603246 | <0.001 |
| KEGG\_BASE\_EXCISION\_REPAIR | 0.626733 | 0.002 |
| KEGG\_INOSITOL\_PHOSPHATE\_METABOLISM | 0.57875 | 0.001 |
| KEGG\_LYSINE\_DEGRADATION | 0.588268 | 0.003 |
| KEGG\_NOTCH\_SIGNALING\_PATHWAY | 0.577436 | 0.004 |
| KEGG\_RIBOSOME | -0.90528 | <0.001 |
| KEGG\_PROTEASOME | -0.73568 | <0.001 |
| KEGG\_OXIDATIVE\_PHOSPHORYLATION | -0.60583 | <0.001 |
| KEGG\_PROTEIN\_EXPORT | -0.56908 | <0.001 |
| KEGG\_GRAFT\_VERSUS\_HOST\_DISEASE | -0.45776 | <0.001 |
|  |  |  |
| ITGA2B |  |  |
| NAME | ES | P-value |
| KEGG\_RIBOSOME | -0.65206 | <0.001 |
| KEGG\_BASAL\_CELL\_CARCINOMA | -0.54661 | <0.001 |
| KEGG\_LYSINE\_DEGRADATION | -0.53011 | <0.001 |
| KEGG\_VALINE\_LEUCINE\_AND\_ISOLEUCINE\_DEGRADATION | -0.51277 | 0.0149 |
| KEGG\_DNA\_REPLICATION | -0.52125 | 0.005 |
| KEGG\_NATURAL\_KILLER\_CELL\_MEDIATED\_CYTOTOXICITY | 0.55427 | <0.001 |
| KEGG\_GRAFT\_VERSUS\_HOST\_DISEASE | 0.649061 | <0.001 |
| KEGG\_NOD\_LIKE\_RECEPTOR\_SIGNALING\_PATHWAY | 0.528379 | <0.001 |
| KEGG\_CHEMOKINE\_SIGNALING\_PATHWAY | 0.434106 | <0.001 |
| KEGG\_OTHER\_GLYCAN\_DEGRADATION | 0.659061 | 0.022151899 |
|  |  |  |
| ATM |  |  |
| NAME | ES | P-value |
| KEGG\_CARDIAC\_MUSCLE\_CONTRACTION | -0.46354 | <0.001 |
| KEGG\_SYSTEMIC\_LUPUS\_ERYTHEMATOSUS | -0.20982 | <0.001 |
| KEGG\_OXIDATIVE\_PHOSPHORYLATION | -0.67875 | <0.001 |
| KEGG\_RIBOSOME | -0.92306 | <0.001 |
| KEGG\_COMPLEMENT\_AND\_COAGULATION\_CASCADES | -0.33698 | <0.001 |
| KEGG\_PHOSPHATIDYLINOSITOL\_SIGNALING\_SYSTEM | 0.607915 | <0.001 |
| KEGG\_LYSINE\_DEGRADATION | 0.600482 | 0.004 |
| KEGG\_PRIMARY\_IMMUNODEFICIENCY | 0.612421 | 0.017 |
| KEGG\_ABC\_TRANSPORTERS | 0.585634 | 0.014 |
| KEGG\_HOMOLOGOUS\_RECOMBINATION | 0.609224 | 0.03 |
|  |  |  |
| AGTR1 |  |  |
| NAME | ES | P-value |
| KEGG\_OTHER\_GLYCAN\_DEGRADATION | -0.72145 | 0.005 |
| KEGG\_ONE\_CARBON\_POOL\_BY\_FOLATE | -0.64487 | 0.018 |
| KEGG\_PRIMARY\_IMMUNODEFICIENCY | -0.54944 | 0.012 |
| KEGG\_LYSOSOME | -0.44112 | 0.007 |
| KEGG\_FRUCTOSE\_AND\_MANNOSE\_METABOLISM | -0.518 | 0.032 |
| KEGG\_RIBOSOME | 0.757497 | <0.001 |
| KEGG\_VASCULAR\_SMOOTH\_MUSCLE\_CONTRACTION | 0.575647 | <0.001 |
| KEGG\_TGF\_BETA\_SIGNALING\_PATHWAY | 0.545437 | <0.001 |
| KEGG\_FOCAL\_ADHESION | 0.466559 | <0.001 |
| KEGG\_DILATED\_CARDIOMYOPATHY | 0.504329 | <0.001 |
| CD69 |  |  |
| NAME | ES | P-value |
| KEGG\_ECM\_RECEPTOR\_INTERACTION | -0.50742 | 0.001 |
| KEGG\_ADHERENS\_JUNCTION | -0.50416 | <0.001 |
| KEGG\_ARRHYTHMOGENIC\_RIGHT\_VENTRICULAR\_CARDIOMYOPATHY\_ARVC | -0.4268 | 0.037 |
| KEGG\_RIBOSOME | 0.798034 | <0.001 |
| KEGG\_OXIDATIVE\_PHOSPHORYLATION | 0.594467 | <0.001 |
| KEGG\_PARKINSONS\_DISEASE | 0.579369 | <0.001 |
| KEGG\_GRAFT\_VERSUS\_HOST\_DISEASE | 0.694562 | <0.001 |
| KEGG\_ALLOGRAFT\_REJECTION | 0.669805 | <0.001 |
| KEGG\_CYTOKINE\_CYTOKINE\_RECEPTOR\_INTERACTION | 0.49171 | <0.001 |
| KEGG\_AUTOIMMUNE\_THYROID\_DISEASE | 0.612635 | <0.001 |
|  |  |  |
| ACE |  |  |
| NAME | ES | P-value |
| KEGG\_PHOSPHATIDYLINOSITOL\_SIGNALING\_SYSTEM | 0.615199 | <0.001 |
| KEGG\_FOCAL\_ADHESION | 0.530289 | <0.001 |
| KEGG\_ADHERENS\_JUNCTION | 0.585654 | <0.001 |
| KEGG\_ECM\_RECEPTOR\_INTERACTION | 0.564557 | <0.001 |
| KEGG\_ACUTE\_MYELOID\_LEUKEMIA | 0.582122 | 0.001 |
| KEGG\_RIBOSOME | -0.95841 | <0.001 |
| KEGG\_OXIDATIVE\_PHOSPHORYLATION | -0.80802 | <0.001 |
| KEGG\_PARKINSONS\_DISEASE | -0.78605 | <0.001 |
| KEGG\_HUNTINGTONS\_DISEASE | -0.6547 | <0.001 |
| KEGG\_ALZHEIMERS\_DISEASE | -0.64663 | <0.001 |

Note. ES, Enrichment score; KEGG, Kyoto Encyclopedia of Genes and Genomes.