Table 1 GO functional enrichment analysis of interacting proteins with TM4SF1 and DDR1

| Ontology | ID | Description | p. adjust | geneID | Count |
| --- | --- | --- | --- | --- | --- |
| BP | GO:0043062 | extracellular structure organization | 2.13E-09 | CDH1/COL5A2/COL1A1/COL3A1/NOTCH1/ADAM10/COL5A1/COL4A1/ITGA2/ITGB5/ITGA5/COL2A1/DDR1/APOM | 14 |
| BP | GO:0030198 | extracellular matrix organization | 3.54E-09 | CDH1/COL5A2/COL1A1/COL3A1/NOTCH1/ADAM10/COL5A1/COL4A1/ITGA2/ITGB5/ITGA5/COL2A1/DDR1 | 13 |
| BP | GO:0007229 | integrin-mediated signaling pathway | 3.71E-06 | COL3A1/PTPN11/ADAM10/ITGA2/ITGB5/ITGA5/CD63 | 7 |
| BP | GO:0038065 | collagen-activated signaling pathway | 1.04E-05 | COL1A1/COL4A1/ITGA2/DDR1 | 4 |
| BP | GO:0030199 | collagen fibril organization | 7.86E-05 | COL5A2/COL1A1/COL3A1/COL5A1/COL2A1 | 5 |
| BP | GO:0071230 | cellular response to amino acid stimulus | 0.000210175 | ZEB1/COL5A2/COL1A1/COL3A1/COL4A1 | 5 |
| BP | GO:0007492 | endoderm development | 0.000314527 | COL5A2/NOTCH1/COL5A1/ITGB5/ITGA5 | 5 |
| BP | GO:0038063 | collagen-activated tyrosine kinase receptor signaling pathway | 0.000371494 | COL1A1/COL4A1/DDR1 | 3 |
| BP | GO:0001101 | response to acid chemical | 0.000375312 | ZEB1/COL5A2/COL1A1/COL3A1/COL4A1/ITGA2/PTGS2/CD9 | 8 |
| BP | GO:0031589 | cell-substrate adhesion | 0.000427044 | COL1A1/COL3A1/NOTCH1/ITGA2/ITGB5/ITGA5/CD63/DDR1 | 8 |
| CC | GO:0098644 | complex of collagen trimers | 8.04E-10 | COL5A2/COL1A1/COL3A1/COL5A1/COL4A1/COL2A1 | 6 |
| CC | GO:0005583 | fibrillar collagen trimer | 2.07E-09 | COL5A2/COL1A1/COL3A1/COL5A1/COL2A1 | 5 |
| CC | GO:0098643 | banded collagen fibril | 2.07E-09 | COL5A2/COL1A1/COL3A1/COL5A1/COL2A1 | 5 |
| CC | GO:0044420 | extracellular matrix component | 1.26E-07 | COL5A2/COL1A1/COL3A1/COL5A1/COL4A1/COL2A1 | 6 |
| CC | GO:0005788 | endoplasmic reticulum lumen | 2.13E-06 | COL5A2/COL1A1/COL3A1/ADAM10/COL5A1/COL4A1/CDH2/COL2A1/PTGS2 | 9 |
| CC | GO:0005581 | collagen trimer | 2.20E-06 | COL5A2/COL1A1/COL3A1/COL5A1/COL4A1/COL2A1 | 6 |
| CC | GO:0005925 | focal adhesion | 0.001071564 | ADAM10/CDH2/ITGA2/ITGB5/ITGA5/TSPAN4/CD9 | 7 |
| CC | GO:0062023 | collagen-containing extracellular matrix | 0.001071564 | COL5A2/COL1A1/COL3A1/COL5A1/COL4A1/CDH2/COL2A1 | 7 |
| CC | GO:0008305 | integrin complex | 0.001071564 | ITGA2/ITGB5/ITGA5 | 3 |
| CC | GO:0005924 | cell-substrate adherens junction | 0.001071564 | ADAM10/CDH2/ITGA2/ITGB5/ITGA5/TSPAN4/CD9 | 7 |
| MF | GO:0048407 | platelet-derived growth factor binding | 4.84E-11 | COL1A1/COL3A1/COL5A1/COL4A1/COL2A1 | 5 |
| MF | GO:0005178 | integrin binding | 5.82E-11 | COL3A1/ADAM10/COL5A1/ITGA2/ITGB5/ITGA5/TSPAN4/CD9/TSPAN8 | 9 |
| MF | GO:0030020 | extracellular matrix structural constituent conferring tensile strength | 1.06E-09 | COL5A2/COL1A1/COL3A1/COL5A1/COL4A1/COL2A1 | 6 |
| MF | GO:0050839 | cell adhesion molecule binding | 4.72E-09 | CDH1/COL3A1/PTPN11/ADAM10/COL5A1/CDH2/ITGA2/ITGB5/ITGA5/TSPAN4/CD9/TSPAN8 | 12 |
| MF | GO:0019838 | growth factor binding | 1.60E-06 | COL1A1/COL3A1/COL5A1/COL4A1/SHC1/COL2A1 | 6 |
| MF | GO:0005201 | extracellular matrix structural constituent | 4.37E-06 | COL5A2/COL1A1/COL3A1/COL5A1/COL4A1/COL2A1 | 6 |
| MF | GO:0043394 | proteoglycan binding | 0.000117875 | COL5A1/ITGA2/COL2A1 | 3 |
| MF | GO:0005165 | neurotrophin receptor binding | 0.00030648 | FRS2/SHC1 | 2 |
| MF | GO:0030898 | actin-dependent ATPase activity | 0.000447983 | MYO10/MYH10 | 2 |
| MF | GO:0045295 | gamma-catenin binding | 0.000447983 | CDH1/CDH2 | 2 |

This table only displays the top 10 BP, CC, and MF results sorted by p. adjust. BP：biological process，CC：cellular constituent；MF：molecular function.

Table 2 KEGG pathway enrichment analysis of interacting proteins with TM4SF1 and DDR1

| ID | Description | p.adjust | Count |
| --- | --- | --- | --- |
| hsa04510 | Focal adhesion | 2.62E-05 | 8 |
| hsa05205 | Proteoglycans in cancer | 2.62E-05 | 8 |
| hsa04512 | ECM-receptor interaction | 2.62E-05 | 6 |
| hsa04974 | Protein digestion and absorption | 3.10E-05 | 6 |
| hsa05165 | Human papillomavirus infection | 4.47E-05 | 9 |
| hsa05412 | Arrhythmogenic right ventricular cardiomyopathy (ARVC) | 0.003324406 | 4 |
| hsa04151 | PI3K-Akt signaling pathway | 0.004130268 | 7 |
| hsa05222 | Small cell lung cancer | 0.004951827 | 4 |
| hsa04640 | Hematopoietic cell lineage | 0.005445384 | 4 |
| hsa04933 | AGE-RAGE signaling pathway in diabetic complications | 0.005445384 | 4 |
| hsa05206 | MicroRNAs in cancer | 0.008724607 | 6 |
| hsa04926 | Relaxin signaling pathway | 0.011818939 | 4 |
| hsa04145 | Phagosome | 0.019743988 | 4 |
| hsa05100 | Bacterial invasion of epithelial cells | 0.019743988 | 3 |
| hsa05220 | Chronic myeloid leukemia | 0.020672579 | 3 |
| hsa05410 | Hypertrophic cardiomyopathy (HCM) | 0.031269847 | 3 |
| hsa05414 | Dilated cardiomyopathy (DCM) | 0.03525937 | 3 |
| hsa01522 | Endocrine resistance | 0.0352713 | 3 |
| hsa05146 | Amoebiasis | 0.03590694 | 3 |
| hsa05130 | Pathogenic Escherichia coli infection | 0.03590694 | 4 |
| hsa04810 | Regulation of actin cytoskeleton | 0.041155739 | 4 |
| hsa05216 | Thyroid cancer | 0.042469257 | 2 |
| hsa04722 | Neurotrophin signaling pathway | 0.04715069 | 3 |
| hsa05219 | Bladder cancer | 0.047491525 | 2 |
| hsa04611 | Platelet activation | 0.048519869 | 3 |