

All Enrichment of Significant Genes						All Enrichment of Genes Thresholded at 95 percentile							
	term	N-term	N-query	overlap	p-value	domain		term	N-term	N-query	overlap	p-value	domain
	anatomical structure morphogenesis	2598	1237	379	1.38e-60	BP		collagen-containing extracellular matrix	249	849	76	3.45e-40	CC
	collagen-containing extracellular matrix	249	621	81	3.48e-56	CC		extracellular matrix organization	332	849	80	4.16e-34	BP
	extracellular matrix structural constituent	126	679	54	6.32e-42	MF		extracellular matrix structural constituent	126	849	49	1.11e-30	MF
	growth factor binding	130	276	30	1.35e-24	MF		cell-substrate junction	404	824	58	5.09e-13	CC
	adherens junction	513	897	83	8.21e-21	CC		response to wounding	667	844	68	8.74e-08	BP
	plasma membrane	5424	996	397	5.66e-15	CC		dna-dependent dna replication	145	504	18	9.7e-05	BP
	cell surface	770	1278	115	1.73e-14	CC		collagen metabolic process	100	814	18	0.000389	BP
	cell leading edge	375	960	59	3.56e-12	CC		regulation of hydrolase activity	1256	843	91	0.00151	BP
	collagen metabolic process	100	1176	26	2.56e-07	BP		ribosome biogenesis	281	323	18	0.00296	BP
	glycosaminoglycan metabolic process	158	1158	33	3.23e-07	BP		regulation of phosphorylation	1515	844	103	0.00525	BP
	actin cytoskeleton	468	1021	58	1.67e-06	CC		calcium ion binding	707	849	58	0.00614	MF
	transmembrane receptor protein kinase activity	80	1219	22	4.23e-06	MF		platelet alpha granule	92	772	15	0.0081	CC
	molecular function regulator	1830	1007	149	1.23e-05	MF		glycosaminoglycan biosynthetic process	107	844	17	0.00865	BP
	erase ii proximal promoter sequence-specific dna binding	402	1276	57	3.24e-05	MF		caveola	78	812	14	0.00964	CC
	pdz domain binding	90	1054	19	0.000615	MF		regulation of cardiac epithelial to mesenchymal transition	8	772	5	0.0137	BP
	bleb assembly	11	275	5	0.00067	BP		base-excision repair	43	212	6	0.0182	BP
	receptor complex	326	1053	41	0.000828	CC		positive regulation of rho protein signal transduction	27	815	8	0.0272	BP
	cellular response to vitamin	29	1167	11	0.00101	BP		platelet degranulation	127	772	17	0.0286	BP
	platelet alpha granule	92	657	15	0.00108	CC		cellular response to amino acid stimulus	63	834	12	0.033	BP
	neuromuscular junction	54	900	13	0.00201	CC		membrane microdomain	306	812	30	0.033	CC
	plasma membrane organization	78	79	6	0.00203	BP		dna replication, okazaki fragment processing	5	210	3	0.0341	BP
	growth factor activity	161	1278	28	0.00337	MF		response to steroid hormone	386	812	35	0.0353	BP
	erase ii proximal promoter sequence-specific dna binding	472	1276	58	0.00348	MF		ribonucleoprotein complex	825	428	38	0.0363	CC
	egative regulation of nitrogen compound metabolic process	2384	1123	187	0.00398	BP		catalytic activity, acting on dna	185	278	12	0.0384	MF
	oncostatin-m receptor activity	3	243	3	0.00555	MF		cellular protein complex disassembly	202	599	19	0.04	BP
	dystrophin-associated glycoprotein complex	21	619	7	0.00691	CC		pdz domain binding	90	793	14	0.0412	MF
	membrane assembly	27	1253	10	0.00849	BP							
	laminin-1 binding	6	115	3	0.0113	MF							
	regulation of cell size	160	456	15	0.0154	BP							
		behavior	588	1284	66	0.0191		BP					
endocytosis		749	759	54	0.023	BP							
protease binding		134	154	8	0.0318	MF							
polymerase ii distal enhancer sequence-specific binding		100	901	16	0.035	MF							
	positive regulation of programmed cell death	628	745	46	0.0461	BP							

Autoimmune Enrichment of Significant Genes						Autoimmune Enrichment of Genes Thresholded at 95 percentile					
term	N-term	N-query	overlap	p.value	domain	term	N-term	N-query	overlap	p.value	domain
enzyme linked receptor protein signaling pathway	1031	1081	123	4.47e-14	BP	intracellular part	14266	847	723	3.1e-19	CC
intracellular part	14266	500	426	1.05e-10	CC	protein binding	11522	839	579	2.33e-08	MF
metal ion binding	4139	1054	306	1.25e-08	MF	cellular metabolic process	10713	787	504	6.85e-06	BP
collagen-containing extracellular matrix	249	909	37	5.41e-07	CC	rna processing	896	784	67	0.00121	BP
cell adhesion	1343	1030	117	1.83e-05	BP	enzyme linked receptor protein signaling pathway	1031	764	72	0.00213	BP
transcription regulator activity	2059	1015	158	9.46e-05	MF	embryonic skeletal system development	124	4	3	0.00312	BP
extracellular matrix structural constituent	126	968	23	0.000104	MF	canonical wnt signaling pathway	276	3	3	0.00877	BP
actin binding	415	1134	50	0.000767	MF	cellular response to growth factor stimulus	685	751	51	0.0103	BP
ventricular compact myocardium morphogenesis	8	616	5	0.00515	BP	proteolysis involved in cellular protein catabolic process	678	715	48	0.0219	BP
membrane receptor protein serine/threonine kinase activity	17	757	7	0.00539	MF	transferase activity	2479	786	139	0.0338	MF
cell adhesion via plasma membrane adhesion molecules	159	1103	25	0.0054	BP	histone h2a ubiquitination	25	656	7	0.0375	BP
glycosaminoglycan biosynthetic process	107	926	18	0.00595	BP						
growth factor binding	130	757	18	0.00712	MF						
regulation of binding	362	1138	43	0.0086	BP						
actin-based cell projection	195	560	19	0.00968	CC						
phosphotransferase activity, alcohol group as acceptor	796	893	64	0.0103	MF						
vasoconstriction	79	171	7	0.0163	BP						
regulation of cell projection organization	625	899	53	0.0196	BP						
actin cytoskeleton	468	1134	50	0.0259	CC						
anterior/posterior pattern specification	203	1088	27	0.042	BP						
axon extension	109	839	16	0.0421	BP						
neural tube formation	104	690	14	0.048	BP						
positive regulation of gtpase activity	410	26	6	0.048	BP						

EMT Enrichment of Significant Genes						EMT Enrichment of Genes Thresholded at 95 percentile							
	term	N-term	N-query	overlap	p.value	domain		term	N-term	N-query	overlap	p.value	domain
	anatomical structure morphogenesis	2598	1114	283	2.33e-27	BP		extracellular matrix	376	829	50	4.24e-10	CC
	extracellular matrix	376	754	68	5.92e-24	CC		anatomical structure morphogenesis	2598	829	170	2.17e-07	BP
	endoplasmic reticulum lumen	298	865	48	1.04e-11	CC		extracellular matrix organization	332	829	41	7.27e-07	BP
	extracellular matrix structural constituent	126	951	32	1.11e-11	MF		regulation of cell proliferation	1708	817	119	3.38e-06	BP
	ion binding	6165	1301	512	1.84e-09	MF		extracellular matrix structural constituent	126	829	23	4.09e-06	MF
	cell junction	1253	1260	135	6.31e-07	CC		response to growth factor	713	825	59	0.000458	BP
	cell projection	2002	1287	195	1.48e-06	CC		growth factor binding	130	806	20	0.000583	MF
	cell surface	770	689	61	4.64e-06	CC		regulation of biological quality	3656	829	205	0.000754	BP
	membrane region	317	831	36	0.00017	CC		enzyme linked receptor protein signaling pathway	1031	825	76	0.000829	BP
	platelet alpha granule	92	54	6	0.000592	CC		wound healing	558	829	47	0.00623	BP
	vesicle	3788	563	155	0.00104	CC		cell periphery	5522	830	283	0.00659	CC
	platelet degranulation	127	54	6	0.00399	BP		cell adhesion	1343	829	89	0.00918	BP
	growth factor activity	161	544	17	0.006	MF		negative regulation of transmission of nerve impulse	5	584	4	0.0104	BP
	protein-lysine 6-oxidase activity	3	27	2	0.0163	MF		endoplasmic reticulum	1824	829	112	0.0163	CC
	cell periphery	5522	397	150	0.0172	CC		positive regulation of phospholipase activity	56	772	11	0.0208	BP
	cytoskeleton	2115	1232	178	0.018	CC		vesicle	3788	820	201	0.0219	CC
	ovulation cycle	66	410	9	0.0228	BP		positive regulation of hair follicle maturation	5	18	2	0.0238	BP
	chordate embryonic development	574	1136	59	0.0238	BP		activation of protein kinase b activity	34	453	7	0.0259	BP
	serine-type endopeptidase inhibitor activity	94	221	8	0.0298	MF		regulation of signaling	3482	777	178	0.0261	BP
	membrane assembly	27	589	7	0.0299	BP		hormone secretion	307	804	29	0.0408	BP
adhesion via plasma membrane cell adhesion molecules	31	1289	10	0.0405	BP								
homeostasis of number of cells	246	688	23	0.048	BP								

Fibrosis Enrichment of Significant Genes					
term	N-term	N-query	overlap	p.value	domain
anatomical structure morphogenesis	2598	1013	251	7.02e-22	BP
collagen-containing extracellular matrix	249	785	53	1.84e-20	CC
extracellular matrix structural constituent	126	452	28	2.23e-16	MF
anchoring junction	530	836	70	7.5e-14	CC
platelet-derived growth factor binding	11	104	6	3.03e-08	MF
regulation of gtpase activity	482	718	48	1.2e-06	BP
response to wounding	667	672	54	1.62e-05	BP
glycosaminoglycan biosynthetic process	107	1099	22	0.000248	BP
gtpase activator activity	284	479	23	0.00199	MF
ventricular trabecula myocardium morphogenesis	16	565	6	0.0124	BP
growth	964	678	61	0.0137	BP
smooth muscle cell migration	91	565	12	0.0407	BP
pdz domain binding	90	311	9	0.0472	MF

Fibrosis Enrichment of Genes Thresholded at 95 percentile					
term	N-term	N-query	overlap	p.value	domain
extracellular matrix structural constituent	126	823	31	9.95e-13	MF
extracellular matrix organization	332	823	49	1.34e-11	BP
extracellular matrix	376	823	50	4.54e-10	CC
cell adhesion	1343	823	110	2.75e-09	BP
endoplasmic reticulum lumen	298	824	37	5.31e-06	CC
anatomical structure morphogenesis	2598	834	165	1.33e-05	BP
enzyme linked receptor protein signaling pathway	1031	834	79	0.000223	BP
endomembrane system	4393	826	241	0.000369	CC
cytoskeleton organization	1235	817	85	0.00273	BP
cell periphery	5522	820	284	0.00298	CC
actin cytoskeleton	468	817	42	0.00389	CC
growth factor binding	130	822	19	0.00434	MF
response to growth factor	713	834	57	0.0045	BP
notochord morphogenesis	10	4	2	0.00507	BP
heparin metabolic process	8	59	3	0.00521	BP
n of g-protein coupled receptor protein signaling pathway	31	774	9	0.00541	BP
regulation of cell proliferation in midbrain	2	26	2	0.00611	BP
cell proliferation	2121	532	89	0.011	BP
bounding membrane of organelle	2019	480	79	0.0111	CC
proteoglycan biosynthetic process	59	709	11	0.0179	BP
response to wounding	667	788	50	0.0246	BP
regulation of secretion	738	323	29	0.0268	BP
generation of neurons	1450	527	65	0.0274	BP
anchoring involved in mammary gland duct morphogenesis	23	4	2	0.0285	BP
amino sugar metabolic process	38	766	9	0.0315	BP
phosphorus metabolic process	3255	792	172	0.0329	BP
of plasma membrane bounded cell projection organization	616	503	34	0.0356	BP
mammary gland epithelial cell proliferation	28	4	2	0.0425	BP

ILD_PAH Enrichment of Significant Genes					
term	N-term	N-query	overlap	p.value	domain
anatomical structure morphogenesis	2598	1362	317	1.14e-26	BP
extracellular matrix	376	1293	90	1.31e-25	CC
extracellular matrix structural constituent	126	593	29	1.09e-14	MF
cell periphery	5522	1320	486	1.22e-13	CC
cell projection	2002	1299	214	7.9e-12	CC
calcium ion binding	707	1364	102	1.29e-10	MF
integrin binding	121	1006	28	1.43e-08	MF
heparin binding	158	1427	38	2.1e-08	MF
cell junction	1253	1317	141	5.43e-08	CC
wnt-activated receptor activity	21	1152	11	1.11e-05	MF
wnt-protein binding	31	1152	13	1.32e-05	MF
actin cytoskeleton	468	570	38	1.81e-05	CC
transmembrane receptor protein kinase activity	80	160	9	4.5e-05	MF
synapse	859	1452	104	7.21e-05	CC
actin binding	415	569	34	8.95e-05	MF
endoplasmic reticulum lumen	298	1103	41	0.000104	CC
collagen binding	63	60	6	0.00011	MF
cell adhesion mediator activity	41	1283	13	0.00218	MF
axoneme assembly	59	1166	15	0.00225	BP
cell surface	770	693	53	0.00348	CC
behavior	588	1432	72	0.0045	BP
positive regulation of phosphorus metabolic process	1078	1329	109	0.0046	BP
regulation of lipase activity	92	1362	20	0.00552	BP
axoneme	113	1195	21	0.00607	CC
pdz domain binding	90	515	12	0.00891	MF
olfactory bulb interneuron development	7	9	2	0.0124	BP
arterial endothelial cell differentiation	6	1311	5	0.0185	BP
receptor complex	326	1242	41	0.0218	CC
phosphatidylinositol biphosphate kinase activity	71	1307	16	0.0228	MF
growth factor binding	130	1324	23	0.0258	MF
positive regulation of phosphatidylinositol 3-kinase signaling	69	1046	14	0.0264	BP
sensory perception of sound	148	1432	26	0.0287	BP
peptidyl-tyrosine phosphorylation	387	1287	47	0.0322	BP
on by regulation of the release of sequestered calcium ion	22	126	4	0.0336	BP
rho protein signal transduction	186	915	23	0.0343	BP
pulmonary valve development	19	911	7	0.0345	BP
regulation of secretion	738	1174	71	0.0377	BP
receptor-mediated endocytosis	325	1050	36	0.0385	BP
regulation of melanin biosynthetic process	7	152	3	0.0449	BP
acting on the ch-nh2 group of donors, oxygen as acceptor	16	746	6	0.0449	MF

ILD_PAH Enrichment of Genes Thresholded at 95 percentile					
term	N-term	N-query	overlap	p.value	domain
collagen-containing extracellular matrix	249	866	44	1.43e-12	CC
cellular component organization or biogenesis	6297	806	335	1.68e-08	BP
extracellular matrix structural constituent	126	866	26	4.06e-08	MF
cell adhesion	1343	860	103	3.54e-06	BP
collagen trimer	98	866	19	6.82e-05	CC
tube development	1079	865	83	0.000197	BP
renal system development	281	860	33	0.000275	BP
ion binding	6165	855	325	0.000346	MF
protein binding	11522	807	519	0.000537	MF
organelle lumen	5205	696	233	0.00126	CC
aorta development	55	860	12	0.00677	BP
negative regulation of canonical wnt signaling pathway	127	5	3	0.00835	BP
positive regulation of cellular process	5100	844	265	0.0143	BP
cell development	2040	813	120	0.015	BP
locomotion	1842	827	112	0.0159	BP
blood vessel development	743	865	57	0.0272	BP
ossification	380	169	13	0.0376	BP
embryo development ending in birth or egg hatching	593	295	23	0.0418	BP
midgut development	12	88	3	0.0445	BP

Lung
Enrichment of Significant Genes

term	N-term	N-query	overlap	p-value	domain
anatomical structure morphogenesis	2598	1206	320	9.22e-35	BP
extracellular matrix	376	1251	99	4.73e-32	CC
extracellular matrix structural constituent	126	782	43	3.19e-25	MF
growth factor binding	130	732	33	3.01e-15	MF
endoplasmic reticulum lumen	298	953	52	2.05e-12	CC
cell surface	770	1066	92	1.69e-09	CC
actin cytoskeleton	468	844	55	3.97e-08	CC
collagen trimer	98	1251	26	6.9e-07	CC
transmembrane receptor protein kinase activity	80	370	14	8.47e-07	MF
cell projection	2002	1278	198	8.69e-07	CC
glycosaminoglycan biosynthetic process	107	1221	25	1.64e-05	BP
molecular function regulator	1830	989	144	8.81e-05	MF
platelet alpha granule membrane	17	1043	9	0.000156	CC
plasma membrane organization	78	514	12	0.00255	BP
response to oxygen levels	339	985	39	0.00353	BP
filopodium	97	1027	18	0.00705	CC
receptor complex	326	1026	38	0.00906	CC
ovulation cycle	66	1285	16	0.0102	BP
epithelial cell apoptotic process	111	483	13	0.0107	BP
corticospinal tract morphogenesis	6	468	4	0.0138	BP
platelet-derived growth factor receptor binding	15	356	5	0.0148	MF
gtpase activator activity	284	1069	35	0.0153	MF
intracellular	14606	603	496	0.0156	CC
platelet degranulation	127	1097	21	0.0202	BP
cytokine production involved in immune response	87	62	5	0.0245	BP
muscle system process	465	602	33	0.025	BP
macrophage cytokine production	14	62	3	0.032	BP
regulation of protein binding	216	701	22	0.0326	BP
peptidyl-tyrosine modification	390	510	26	0.0393	BP
pdz domain binding	90	1026	16	0.0441	MF
wnt signaling pathway, planar cell polarity pathway	62	1200	14	0.0462	BP
neuromuscular junction	54	1024	12	0.0492	CC
response to calcium ion	139	378	12	0.0496	BP

Lung
Enrichment of Genes Thresholded at 95 percentile

term	N-term	N-query	overlap	p-value	domain
collagen-containing extracellular matrix	249	821	47	6.85e-15	CC
cellular component organization or biogenesis	6297	801	369	3.79e-14	BP
cytoplasm	11390	771	549	8.8e-12	CC
extracellular matrix structural constituent	126	821	28	8.26e-10	MF
protein binding	11522	801	560	1.43e-08	MF
focal adhesion	396	804	45	1.9e-06	CC
regulation of catalytic activity	2262	798	146	1.77e-05	BP
response to wounding	667	819	61	2.26e-05	BP
cell proliferation	2121	819	139	9.33e-05	BP
catalytic activity, acting on rna	378	554	31	0.00037	MF
response to oxygen-containing compound	1571	807	106	0.000662	BP
ossification	380	816	38	0.00175	BP
caveola	78	807	15	0.00177	CC
growth	964	807	72	0.00199	BP
embryo development	969	821	73	0.0023	BP
response to endogenous stimulus	1588	819	106	0.00231	BP
response to growth factor	713	818	58	0.00277	BP
skeletal system development	495	821	45	0.00284	BP
regulation of protein modification process	1801	797	113	0.005	BP
biological adhesion	1351	816	92	0.00509	BP
enzyme linked receptor protein signaling pathway	1031	821	75	0.00601	BP
adenyl ribonucleotide binding	1542	686	88	0.00898	MF
response to antimetabolite	12	200	4	0.016	BP
muscle structure development	659	807	52	0.0167	BP
transmembrane receptor protein kinase activity	80	821	14	0.0167	MF
rna binding	1848	704	102	0.0191	MF
regulation of small gtpase mediated signal transduction	320	791	31	0.0197	BP
collagen binding	63	797	12	0.0236	MF
response to inorganic substance	542	613	37	0.0246	BP
fibrinogen complex	9	729	5	0.0255	CC
response to antineoplastic agent	90	222	8	0.027	BP
cellular response to stress	1870	620	92	0.0337	BP
regulation of phosphate metabolic process	1714	797	105	0.0352	BP
response to calcium ion	139	793	18	0.0407	BP
purine ntp-dependent helicase activity	97	726	14	0.0416	MF
amide biosynthetic process	833	509	43	0.0435	BP
cellular localization	2673	208	51	0.0483	BP

	Skin							Skin						
	Enrichment of Significant Genes							Enrichment of Genes Thresholded at 95 percentile						
	term	N-term	N-query	overlap	p.value	domain		term	N-term	N-query	overlap	p.value	domain	
donors, with incorporation or reduction of molecular oxygen	skeletal system development	495	1124	86	7.53e−18	BP		protein binding	11522	828	598	6.92e−14	MF	
	extracellular matrix	376	806	61	5.07e−17	CC		intracellular part	14266	866	724	2.79e−12	CC	
	extracellular matrix structural constituent	126	747	33	1.65e−15	MF		cellular component organization	6120	586	257	4.48e−08	BP	
	metal ion binding	4139	888	270	1.34e−08	MF		extracellular matrix	376	865	44	1e−05	CC	
	collagen binding	63	747	17	3.8e−07	MF		n of g-protein coupled receptor protein signaling pathway	31	14	4	1.52e−05	BP	
	focal adhesion	396	825	47	3.86e−07	CC		extracellular matrix structural constituent	126	853	22	6.56e−05	MF	
	transcription regulator activity	2059	1102	175	5.03e−06	MF		anchoring junction	530	482	36	9.82e−05	CC	
	sequence-specific dna binding	1076	1100	96	0.00458	MF		protein-containing complex	5095	589	207	0.000543	CC	
	cellular response to nutrient levels	212	867	26	0.00737	BP		error-prone translesion synthesis	20	65	4	0.00154	BP	
	golgi vesicle transport	341	695	30	0.0156	BP		regulation of catalytic activity	2262	586	106	0.00293	BP	
	negative regulation of cellular protein localization	112	509	13	0.0242	BP		intracellular signal transduction	2713	446	98	0.00311	BP	
	regulation of protein import into nucleus	66	1059	14	0.0245	BP		regulation of canonical wnt signaling pathway	226	3	3	0.00452	BP	
	l-ascorbic acid binding	20	276	5	0.0255	MF		membrane microdomain	306	234	15	0.0118	CC	
	regulation of hydrolase activity	1256	546	62	0.0274	BP		cell junction assembly	206	560	19	0.0198	BP	
	cell surface	770	926	63	0.0322	CC		regulation of multicellular organismal process	2957	850	174	0.0223	BP	
	response to vitamin	94	985	16	0.0476	BP		negative regulation of peptidyl-tyrosine phosphorylation	48	120	5	0.0331	BP	
	cellular carbohydrate biosynthetic process	76	134	6	0.0496	BP		catalytic activity, acting on dna	185	236	11	0.0428	MF	

SSc Enrichment of Significant Genes							SSc Enrichment of Genes Thresholded at 95 percentile						
	term	N-term	N-query	overlap	p.value	domain		term	N-term	N-query	overlap	p.value	domain
cell adhesion via plasma membrane	multicellular organismal process	7414	1073	514	5.01e-16	BP	extracellular matrix	extracellular matrix	376	806	32	0.0466	CC
	plasma membrane	5424	863	332	1.26e-13	CC			NA	NA	NA	NA	
	adhesion molecules	159	1177	34	3.19e-08	BP							
	cell-cell signaling	1559	1073	135	1.85e-06	BP							
	transmembrane signaling receptor activity	1239	465	63	3.52e-06	MF							
	ion gated channel activity	332	485	26	0.000327	MF							
	regulation of hemostasis	78	891	16	0.000525	BP							
	axon guidance	227	728	25	0.0016	BP							
	extracellular matrix	376	534	28	0.00205	CC							
	golgi lumen	101	273	10	0.00343	CC							
g-protein coupled receptor signaling pathway	extracellular region	4453	989	270	0.00353	CC							
	ion transport	1609	839	102	0.00811	BP							
	calcium ion binding	707	1184	70	0.00927	MF							
	g-protein coupled receptor signaling pathway	1342	480	58	0.0126	BP							
	transcription activator activity, rna polymerase ii-specific	414	1162	46	0.0169	MF							
	postsynaptic membrane	238	409	17	0.0228	CC							
	ion channel complex	290	409	19	0.0229	CC							
	cardiac muscle cell development	77	933	14	0.0243	BP							
	voltage-gated potassium channel activity	96	746	14	0.0299	MF							
	peptide cross-linking	59	373	8	0.039	BP							
erase ii regulatory region sequence-specific dna binding	synapse	859	1069	73	0.0399	CC							
	response to stimulus	9017	480	254	0.0434	BP							
	erase ii regulatory region sequence-specific dna binding	674	1207	66	0.0466	MF							