Identifiers found:

Below is a list of the input identifiers that have been found or mapped to an equivalent element in Reactome, classified by resource.

Entities (181)

Input	UniProt Id	Input	UniProt Id	Input	UniProt Id
ABR	Q12979	ACAT2	O75908	AHRR	A9YTQ3
ANO7	Q6IWH7	ARFGAP3	Q9NP61	ARFRP1	Q13795
ARHGAP12	Q8IWW6	ARL3	P36405	ARL6IP5	O75915
ARNT	P27540	AS3MT	Q9HBK9	ASAH1	Q13510
ASNS	P08243	ATM	Q13315	ATP2B1	P20020
ATP9B	O43861	AURKB	Q96GD4	B3GAT1	Q9P2W7
BMPR1B	O00238	BRI3	O95415	CABLES2	Q9BTV7 CAPZB
				P47756 CASP8	Q14790 CATSPERG Q6ZRH7
CDKN1B	P46527	CFLAR	O15519-1, O15519-2	CHMP2B	Q9UQN3
CHMP7	Q8WUX9	COL23A1	Q86Y22	COL2A1	P02458
COMMD10	Q9Y6G5	CPD	O75976	CREB3L4	Q8TEY5
CTBP1	Q13363	CTBP2	P56545	CTSK	P43235
CTSS	P25774	DDX52	Q9Y2R4	DTX4	Q9Y2E6
EEFSEC	P57772	EIF4B	P23588	FAM96B	Q9Y3D0
FGFR2	P21802, P21802-1, P21802-18, P21802-3, P21802-5	GCHFR	P30047	GEMIN4	P57678
GGCX	P38435	GJB1	P08034	GOT2	P00505
GPR143	P51810	GPRC6A	Q5T6X5	GRHL1	Q9NZI5
GUCA1B	Q9UMX6	GUCY2D	Q02846	HAAO	P46952
HAPLN1	P10915	HAUS6	Q7Z4H7	HLA-A	P01891, P01892, P04439, P05534, P10314, P10316, P13746, P16188, P16189, P16190, P18462, P30443, P30447, P30450, P30453, P30455, P30456, P30457, P30459, P30512, Q09160
HLA-C	P04222, P10321, P30499, P30501, P30504, P30505, P30508, P30510, Q07000, Q29865, Q29960, Q29963, Q95604, Q9TNN7	HLA-DQA1	P01906, P01909	HLA-DQA2	P01906
HLA-DQB1	P01920, P05538	HLA-DQB2	P05538	HLA-DRB1	P01911, P01912, P04229, P04440, P05538, P13760, P13761, P20039, Q29974, Q30134, Q30154, Q30167, Q5Y7A7, Q95IE3, Q9GIY3, Q9TQE0
HLA-DRB5	Q30154	HLA-E	P13747	HLA-F	P30511
HLA-G	P17693	HLA-H	P01893	HNF1B	P35680
ITGA6	P23229	KCNK6	Q9Y257	KCNN3	Q9UGI6
KDM6B	O15054	KDSR	Q06136	KLK2	P20151
KLK3	P03952	KRT18	P05783	KRT8	P04264, P05787
KRT86	O43790, P78385, Q14533	LASS2	Q96G23	LGMN	Q99538
LILRB2	Q8N423	LOXL2	Q9Y4K0	LYVE1	Q9Y5Y7
MAP2K1	Q02750	MAPRE1	Q15691	MCAT	Q8IVS2
MCM3	P25205	MDM4	O15151	MICA	Q29983

Input	UniProt Id	Input	UniProt Id	Input	UniProt Id
MMP16	P51512	MMP7	P08254, P09237	MPHOSPH6	Q99547
MRPL18	Q9H0U6	MYB	P10242	MYC	P01106
MYO6	Q9UM54	MYO9B	Q13459	NDUFA9	Q16795
NOTCH4	Q99466	NT5C2	P49902	NUDT10	Q8NFP7, Q96G61
NUDT11	Q96G61	NUDT13	Q86X67	OR13A1	Q8NGR1
P2RX2	Q9UBL9	PCYOX1L	Q8NBM8	PDCD4	Q53EL6
PDLIM5	Q96HC4	PGD	P52209	PHC3	Q8NDX5
PIK3C2B	O00750	PLCD1	P51178	PLOD2	O00469
PMVK	Q15126	POLI	Q9UNA4	PPA2	Q15181, Q9H2U2
PPP1R14A	Q96A00	PRR3	Q9NQS3	PSMB7	Q99436
PSMD5	Q16401	PYGB	P11216	RAB17	Q9H0T7
RAB7L1	O14966	RAD51C	O43502	RAD9A	Q99638
RALB	P11234	RFX6	Q8HWS3	RGS17	Q9UGC6
RPL22L1	Q6P5R6	RPL3	P39023	RPS9	P46781
RUVBL1	Q9Y265	SEPT2	Q15019	SESN1	Q9Y6P5-1, Q9Y6P5-3
SKIL	P12757	SLC22A2	O15244	SLC22A3	O75751
SLC25A37	Q9NYZ2	SLC39A1	Q9NP94, Q9NY26	SLC41A1	Q8IVJ1
SLC7A3	Q8WY07	SLC9A8	Q9Y2E8	SNRPC	P09234
SOX9	P48436	SPINT2	O43291	STARD8	Q92502
STC2	O76061	STXBP1	P61764	SUPT4H1	P63272
SUV420H1	Q4FZB7	SV2A	Q7L0J3	TAX1BP1	Q86VP1
TBX5	Q99593	TDRKH	Q9Y2W6	TERT	O14746
TLE4	Q04727	TNS3	Q68CZ2	TOR1A	O14656
TOR1B	O14656, O14657	TPM3	P06753, P09493	TRDMT1	O14717
TRIM26	Q12899	TRIM31	Q9BZY9	TRIM8	Q9BZR9
TTLL12	Q14166	TUBA1B	P68363	TUBA1C	Q9BQE3
UBE2R2	Q712K3	UGP2	Q16851	USP20	Q9Y2K6
USP39	Q53GS9	VAMP8	Q9BV40	VARS2	P26640
VPS53	Q5VIR6	WIF1	Q9Y5W5	WTAP	Q15007
ZFP36L1	Q07352	ZNF266	Q14584	ZNRD1	Q9P1U0
ZRANB1	Q9UGI0				

Input	Ensembl Id	Input	Ensembl Id	Input	Ensembl Id
ASNS	ENSG00000070669	ATM	ENSG00000149311, ENST00000278616	CDKN1B	ENSG00000111276
GRHL1	ENSG00000134317	HLA-A	ENSG00000206503	HLA-C	ENSG00000204525
HLA-DQA1	ENSG00000196735	HLA-DQA2	ENSG00000237541	HLA-DQB1	ENSG00000179344
HLA-DQB2	ENSG00000232629	HLA-DRB1	ENSG00000196126	HLA-DRB5	ENSG00000198502
HLA-E	ENSG00000204592	HLA-F	ENSG00000204642	HLA-G	ENSG00000204632
HLA-H	ENSG00000206341	HNF1B	ENSG00000275410	KDM6B	ENSG00000132510
KLK2	ENSG00000167751	KLK3	ENSG00000142515	MRPL18	ENSG00000112110
MYB	ENSG00000118513	MYC	ENSG00000136997	NOTCH4	ENSG00000206312, ENST00000383264
PDCD4	ENSG00000150593	PMVK	ENSG00000163344	SESN1	ENSG00000080546
TRIM26	ENSG00000234127	TRIM31	ENSG00000204616	TRIM8	ENSG00000171206

Most significant pathways including HLA genes:

The following table shows the 25 most relevant pathways sorted by p-value.

Pathway name	Entities				Reactions	
	found	ratio	p-value	FDR*	found	ratio
Endosomal/Vacuolar pathway	40 / 82	0.004	1.11e-16	2.10e-14	4 / 4	3.34e-04
Antigen Presentation: Folding, assembly and peptide loading of class I MHC	40 / 217	0.011	1.11e-16	2.10e-14	13 / 16	0.001
ER-Phagosome pathway	43 / 298	0.015	1.11e-16	2.10e-14	7 / 10	8.34e-04
Antigen processing-Cross	44 / 320	0.016	1.11e-16	2.10e-14	12 / 23	0.002
Interferon gamma signaling	81 / 427	0.021	1.11e-16	2.10e-14	4 / 15	0.001
Interferon Signaling	87 / 957	0.048	1.11e-16	2.10e-14	16 / 66	0.006
Interferon alpha/beta signaling	49 / 388	0.019	1.11e-16	2.10e-14	4 / 20	0.002
PD-1 signaling	19 / 74	0.004	9.80e-14	1.63e-11	1 / 4	3.34e-04
Translocation of ZAP-70 to Immunological synapse	19 / 79	0.004	3.03e-13	4.46e-11	4 / 4	3.34e-04
Phosphorylation of CD3 and TCR zeta	19 / 95	0.005	7.04e-12	9.30e-10	5 / 7	5.84e-04
Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	50 / 621	0.031	6.64e-09	7.39e-07	17 / 43	0.004
Class I MHC mediated antigen	46 / 670	0.034	6.72e-09	7.39e-07	30 / 48	0.004
MHC class II antigen presentation	25 / 281	0.014	6.25e-08	6.38e-06	25 / 26	0.002
Generation of second messenger	22 / 289	0.014	1.39e-04	0.013	10 / 17	0.001
Downstream TCR signaling	27 / 351	0.018	2.25e-04	0.02	6 / 24	0.002
Signaling by FGFR2 IIIa TM	5 / 30	0.002	9.82e-04	0.082	2 / 2	1.67e-04
Adaptive Immune System	92 / 2,019	0.101	0.002	0.119	113 / 261	0.022
TCF7L2 mutants don't bind CTBP	2 / 3	1.50e-04	0.003	0.189	1 / 1	8.34e-05
Costimulation by the CD28 family	22 / 379	0.019	0.003	0.224	5 / 34	0.003
Activation of Matrix	6 / 65	0.003	0.006	0.393	17 / 27	0.002
CASP8 activity is inhibited	4 / 15	7.52e-04	0.006	0.4	3 / 3	2.50e-04
Assembly of collagen fibrils and	6 / 74	0.004	0.011	0.649	11 / 26	0.002
FGFR2 mutant receptor activation	6 / 81	0.004	0.016	0.902	17 / 18	0.002
Pyrophosphate hydrolysis	2 / 8	4.01e-04	0.017	0.902	2 / 2	1.67e-04

Pathway name	Entities				Reactions	
	found	ratio	p-value	FDR*	found	ratio
Aryl hydrocarbon receptor signalling	2 / 8	4.01e-04	0.017	0.902	2 / 5	4.17e-04

* False Discovery Rate

Most significant pathways excluding HLA genes:

The following table shows the 25 most relevant pathways sorted by p-value.

Pathway name	Entities				Reactions	
	found	ratio	p-value	FDR*	found	ratio
Signaling by FGFR2 IIIa TM	5 / 30	0.002	4.84e-04	0.64	2 / 2	1.67e-04
TCF7L2 mutants don't bind CTBP	2 / 3	1.50e-04	0.002	0.934	1 / 1	8.34e-05
Activation of Matrix Metalloproteinases	6 / 65	0.003	0.003	0.934	17 / 27	0.002
CASP8 activity is inhibited	4 / 15	7.52e-04	0.004	0.934	3 / 3	2.50e-04
Assembly of collagen fibrils and other multimeric structures	6 / 74	0.004	0.005	0.934	11 / 26	0.002
FGFR2 mutant receptor activation	6 / 81	0.004	0.008	0.934	17 / 18	0.002
Collagen formation	8 / 142	0.007	0.011	0.934	36 / 77	0.006
Pyrophosphate hydrolysis	2 / 8	4.01e-04	0.013	0.934	2 / 2	1.67e-04
Aryl hydrocarbon receptor signalling	2 / 8	4.01e-04	0.013	0.934	2 / 5	4.17e-04
Collagen degradation	5 / 75	0.004	0.022	0.934	13 / 34	0.003
Carboxyterminal post-translational modifications of tubulin	4 / 52	0.003	0.025	0.934	6 / 6	5.01e-04
Regulation by c-FLIP	3 / 12	6.02e-04	0.027	0.934	4 / 4	3.34e-04
Degradation of the extracellular matrix	9 / 202	0.01	0.029	0.934	45 / 105	0.009
FGFR2 ligand binding and activation	4 / 55	0.003	0.03	0.934	4 / 5	4.17e-04
Caspase activation via Death Receptors in the presence of ligand	5 / 35	0.002	0.038	0.934	9 / 9	7.51e-04
Regulation of necroptotic cell death	4 / 37	0.002	0.044	0.934	4 / 5	4.17e-04
Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane	2 / 22	0.001	0.079	0.934	1 / 2	1.67e-04
Tandem of pore domain in a weak inwardly rectifying K+ channels (TWIK)	1 / 4	2.01e-04	0.081	0.934	1 / 1	8.34e-05
Transport of connexons to the plasma membrane	2 / 23	0.001	0.085	0.934	1 / 3	2.50e-04
Dimerization of procaspase-8	4 / 26	0.001	0.104	0.934	3 / 3	2.50e-04
SHC-mediated cascade:FGFR2	4 / 85	0.004	0.106	0.934	4 / 4	3.34e-04
Defective LFNG causes SCDO3	1 / 6	3.01e-04	0.118	0.934	1 / 1	8.34e-05
Defective AVP does not bind AVPR2 and causes neurohypophyseal diabetes insipidus (NDI)	1 / 6	3.01e-04	0.118	0.934	1 / 1	8.34e-05
Activated point mutants of FGFR2	3 / 58	0.003	0.124	0.934	9 / 10	8.34e-04

Pathway name	Entities				Reactions	
	found	ratio	p-value	FDR*	found	ratio
Defective Mismatch Repair Associated With MSH2	1 / 7	3.51e-04	0.137	0.934	1 / 2	1.67e-04

* False Discovery Rate