

Table S3. GO terms that are overrepresented among top regulated**Duodenum: overrepresented terms among top 500 genes regul.**

GO Term	P-val	Frequency	Genome frequency
GO:0016020	2.42E-12	240/500 (48.0%)	5797/17360 (33.4%)
GO:0005783	8.11E-11	56/500 (11.2%)	760/17360 (4.4%)
GO:0019752	1.16E-08	39/500 (7.8%)	492/17360 (2.8%)
GO:0006082	1.23E-08	39/500 (7.8%)	493/17360 (2.8%)
GO:0005792	1.34E-08	21/500 (4.2%)	166/17360 (1.0%)
GO:0042598	2.52E-08	21/500 (4.2%)	172/17360 (1.0%)
GO:0016491	1.65E-07	49/500 (9.8%)	769/17360 (4.4%)
GO:0009055	1.99E-07	24/500 (4.8%)	246/17360 (1.4%)
GO:0055114	3.27E-07	42/500 (8.4%)	625/17360 (3.6%)
GO:0044420	1.18E-06	13/500 (2.6%)	87/17360 (0.5%)
GO:0032787	1.73E-06	23/500 (4.6%)	258/17360 (1.5%)
GO:0018958	2.21E-06	12/500 (2.4%)	78/17360 (0.4%)
GO:0006066	2.28E-06	28/500 (5.6%)	362/17360 (2.1%)
GO:0044444	2.58E-06	149/500 (29.8%)	3675/17360 (21.2%)
GO:0044432	2.91E-06	34/500 (6.8%)	496/17360 (2.9%)
GO:0006519	8.09E-06	24/500 (4.8%)	303/17360 (1.7%)
GO:0003824	8.53E-06	202/500 (40.4%)	5439/17360 (31.3%)
GO:0003823	1.09E-05	6/500 (1.2%)	19/17360 (0.1%)
GO:0006807	1.29E-05	27/500 (5.4%)	375/17360 (2.2%)
GO:0005789	1.36E-05	30/500 (6.0%)	442/17360 (2.5%)
GO:0051186	1.89E-05	19/500 (3.8%)	218/17360 (1.3%)
GO:0009308	2.09E-05	25/500 (5.0%)	342/17360 (2.0%)
GO:0007050	2.13E-05	9/500 (1.8%)	54/17360 (0.3%)
GO:0005583	2.22E-05	4/500 (0.8%)	7/17360 (0.0%)
GO:0043259	2.38E-05	3/500 (0.6%)	3/17360 (0.0%)
GO:0044255	2.72E-05	36/500 (7.2%)	599/17360 (3.5%)
GO:0007155	3.41E-05	38/500 (7.6%)	654/17360 (3.8%)
GO:0022610	3.41E-05	38/500 (7.6%)	654/17360 (3.8%)
GO:0034641	3.53E-05	25/500 (5.0%)	353/17360 (2.0%)
GO:0005201	3.78E-05	8/500 (1.6%)	45/17360 (0.3%)
GO:0048407	4.34E-05	4/500 (0.8%)	8/17360 (0.0%)
GO:0005509	4.81E-05	48/500 (9.6%)	918/17360 (5.3%)
GO:0008667	5.24E-05	8/500 (1.6%)	47/17360 (0.3%)
GO:0009237	5.24E-05	8/500 (1.6%)	47/17360 (0.3%)
GO:0009238	5.24E-05	8/500 (1.6%)	47/17360 (0.3%)
GO:0009239	5.24E-05	8/500 (1.6%)	47/17360 (0.3%)
GO:0009712	5.24E-05	8/500 (1.6%)	47/17360 (0.3%)
GO:0019184	5.24E-05	8/500 (1.6%)	47/17360 (0.3%)
GO:0019290	5.24E-05	8/500 (1.6%)	47/17360 (0.3%)
GO:0019540	5.24E-05	8/500 (1.6%)	47/17360 (0.3%)
GO:0030155	5.41E-05	11/500 (2.2%)	90/17360 (0.5%)
GO:0006631	5.46E-05	17/500 (3.4%)	196/17360 (1.1%)
GO:0006518	5.81E-05	9/500 (1.8%)	61/17360 (0.4%)
GO:0006725	6.60E-05	15/500 (3.0%)	161/17360 (0.9%)
GO:0043043	7.14E-05	8/500 (1.6%)	49/17360 (0.3%)
GO:0016627	7.34E-05	11/500 (2.2%)	93/17360 (0.5%)
GO:0016712	7.54E-05	9/500 (1.8%)	63/17360 (0.4%)
GO:0031012	8.27E-05	22/500 (4.4%)	306/17360 (1.8%)
GO:0042420	9.30E-05	3/500 (0.6%)	4/17360 (0.0%)

Duodenum: overrepresented terms among top 500 genes regul.

GO Term	P-val	Frequency	Genome frequency
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GO:0055114	4.52E-25	73/500 (14.6%)	625/17360 (3.6%)
GO:0016491	7.49E-23	78/500 (15.6%)	769/17360 (4.4%)
GO:0003824	2.41E-19	251/500 (50.2%)	5439/17360 (31.3%)
GO:0008152	4.00E-12	279/500 (55.8%)	7112/17360 (41.0%)
GO:0004091	8.78E-12	20/500 (4.0%)	102/17360 (0.6%)
GO:0006629	1.19E-11	55/500 (11.0%)	705/17360 (4.1%)
GO:0016616	4.14E-11	21/500 (4.2%)	123/17360 (0.7%)
GO:0016614	7.58E-11	22/500 (4.4%)	140/17360 (0.8%)
GO:0044255	1.10E-10	48/500 (9.6%)	599/17360 (3.5%)
GO:0004364	2.84E-10	10/500 (2.0%)	23/17360 (0.1%)
GO:0051186	8.81E-10	26/500 (5.2%)	218/17360 (1.3%)
GO:0032787	1.80E-09	28/500 (5.6%)	258/17360 (1.5%)
GO:0009055	2.73E-09	27/500 (5.4%)	246/17360 (1.4%)
GO:0019752	3.63E-09	40/500 (8.0%)	492/17360 (2.8%)
GO:0020037	3.79E-09	21/500 (4.2%)	155/17360 (0.9%)
GO:0046906	3.79E-09	21/500 (4.2%)	155/17360 (0.9%)
GO:0006082	3.83E-09	40/500 (8.0%)	493/17360 (2.8%)
GO:0006066	5.53E-09	33/500 (6.6%)	362/17360 (2.1%)
GO:0006631	1.17E-08	23/500 (4.6%)	196/17360 (1.1%)
GO:0005792	1.34E-08	21/500 (4.2%)	166/17360 (1.0%)
GO:0004104	1.51E-08	8/500 (1.6%)	18/17360 (0.1%)
GO:0016712	2.25E-08	13/500 (2.6%)	63/17360 (0.4%)
GO:0042598	2.52E-08	21/500 (4.2%)	172/17360 (1.0%)
GO:0044444	3.78E-08	157/500 (31.4%)	3675/17360 (21.2%)
GO:0006725	4.05E-08	20/500 (4.0%)	161/17360 (0.9%)
GO:0004497	6.45E-08	19/500 (3.8%)	150/17360 (0.9%)
GO:0042287	8.30E-08	7/500 (1.4%)	15/17360 (0.1%)
GO:0018958	3.21E-07	13/500 (2.6%)	78/17360 (0.4%)
GO:0016705	3.26E-07	19/500 (3.8%)	166/17360 (1.0%)
GO:0005506	7.01E-07	28/500 (5.6%)	341/17360 (2.0%)
GO:0042288	8.00E-07	6/500 (1.2%)	13/17360 (0.1%)
GO:0016765	1.31E-06	10/500 (2.0%)	50/17360 (0.3%)
GO:0051188	1.57E-06	16/500 (3.2%)	134/17360 (0.8%)
GO:0005783	1.68E-06	46/500 (9.2%)	760/17360 (4.4%)
GO:0002478	1.85E-06	7/500 (1.4%)	22/17360 (0.1%)
GO:0002495	2.22E-06	6/500 (1.2%)	15/17360 (0.1%)
GO:0019886	2.22E-06	6/500 (1.2%)	15/17360 (0.1%)
GO:0042613	2.22E-06	5/500 (1.0%)	9/17360 (0.1%)
GO:0006766	2.53E-06	12/500 (2.4%)	79/17360 (0.5%)
GO:0016627	2.55E-06	13/500 (2.6%)	93/17360 (0.5%)
GO:0006749	2.59E-06	7/500 (1.4%)	23/17360 (0.1%)
GO:0044432	2.91E-06	34/500 (6.8%)	496/17360 (2.9%)
GO:0006732	3.10E-06	16/500 (3.2%)	141/17360 (0.8%)
GO:0005777	4.63E-06	13/500 (2.6%)	98/17360 (0.6%)
GO:0042579	5.19E-06	13/500 (2.6%)	99/17360 (0.6%)
GO:0002504	5.23E-06	6/500 (1.2%)	17/17360 (0.1%)
GO:0008667	6.53E-06	9/500 (1.8%)	47/17360 (0.3%)
GO:0009237	6.53E-06	9/500 (1.8%)	47/17360 (0.3%)
GO:0009238	6.53E-06	9/500 (1.8%)	47/17360 (0.3%)
GO:0009239	6.53E-06	9/500 (1.8%)	47/17360 (0.3%)
GO:0009712	6.53E-06	9/500 (1.8%)	47/17360 (0.3%)
GO:0019184	6.53E-06	9/500 (1.8%)	47/17360 (0.3%)
GO:0019290	6.53E-06	9/500 (1.8%)	47/17360 (0.3%)
GO:0019540	6.53E-06	9/500 (1.8%)	47/17360 (0.3%)
GO:0042825	7.78E-06	5/500 (1.0%)	11/17360 (0.1%)
GO:0019884	8.49E-06	7/500 (1.4%)	27/17360 (0.2%)

GO:0043043	9.35E-06	9/500 (1.8%)	49/17360 (0.3%)
GO:0008202	1.46E-05	16/500 (3.2%)	159/17360 (0.9%)
GO:0006790	1.55E-05	10/500 (2.0%)	65/17360 (0.4%)
GO:0006955	2.15E-05	28/500 (5.6%)	408/17360 (2.4%)
GO:0070330	2.27E-05	7/500 (1.4%)	31/17360 (0.2%)
GO:0034045	2.38E-05	3/500 (0.6%)	3/17360 (0.0%)
GO:0048002	2.84E-05	7/500 (1.4%)	32/17360 (0.2%)
GO:0005771	4.34E-05	4/500 (0.8%)	8/17360 (0.0%)
GO:0016628	4.43E-05	9/500 (1.8%)	59/17360 (0.3%)
GO:0006776	4.79E-05	6/500 (1.2%)	24/17360 (0.1%)
GO:0006518	5.81E-05	9/500 (1.8%)	61/17360 (0.4%)
GO:0016125	6.23E-05	10/500 (2.0%)	76/17360 (0.4%)

Duodenum: overrepresented terms among top 500 genes where

GO Term	P-val	Frequency	Genome frequency
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Jejunum: overrepresented terms among top 500 genes regulated

GO Term	P-val	Frequency	Genome frequency
GO:0003824	9.99E-09	216/500 (43.2%)	5439/17360 (31.3%)
GO:0005783	1.16E-07	49/500 (9.8%)	760/17360 (4.4%)
GO:0055114	1.23E-07	43/500 (8.6%)	625/17360 (3.6%)
GO:0002682	6.84E-07	25/500 (5.0%)	282/17360 (1.6%)
GO:0002684	1.35E-06	19/500 (3.8%)	182/17360 (1.0%)
GO:0045582	1.50E-06	8/500 (1.6%)	30/17360 (0.2%)
GO:0016491	2.31E-06	46/500 (9.2%)	769/17360 (4.4%)
GO:0045621	2.56E-06	8/500 (1.6%)	32/17360 (0.2%)
GO:0003823	1.09E-05	6/500 (1.2%)	19/17360 (0.1%)
GO:0045321	1.19E-05	19/500 (3.8%)	211/17360 (1.2%)
GO:0050870	1.35E-05	10/500 (2.0%)	64/17360 (0.4%)
GO:0006082	1.72E-05	32/500 (6.4%)	493/17360 (2.8%)
GO:0001775	1.84E-05	20/500 (4.0%)	237/17360 (1.4%)
GO:0045597	2.32E-05	16/500 (3.2%)	165/17360 (1.0%)
GO:0045580	2.67E-05	8/500 (1.6%)	43/17360 (0.2%)
GO:0051251	2.82E-05	11/500 (2.2%)	84/17360 (0.5%)
GO:0002376	3.45E-05	37/500 (7.4%)	630/17360 (3.6%)
GO:0005789	3.51E-05	29/500 (5.8%)	442/17360 (2.5%)
GO:0050778	3.55E-05	13/500 (2.6%)	118/17360 (0.7%)
GO:0008238	3.94E-05	11/500 (2.2%)	87/17360 (0.5%)
GO:0019752	4.11E-05	31/500 (6.2%)	492/17360 (2.8%)
GO:0002696	4.38E-05	11/500 (2.2%)	88/17360 (0.5%)
GO:0044432	4.78E-05	31/500 (6.2%)	496/17360 (2.9%)
GO:0016614	5.32E-05	14/500 (2.8%)	140/17360 (0.8%)
GO:0006066	5.33E-05	25/500 (5.0%)	362/17360 (2.1%)
GO:0016616	5.50E-05	13/500 (2.6%)	123/17360 (0.7%)
GO:0050867	6.00E-05	11/500 (2.2%)	91/17360 (0.5%)
GO:0002253	6.23E-05	10/500 (2.0%)	76/17360 (0.4%)
GO:0051249	9.02E-05	13/500 (2.6%)	129/17360 (0.7%)
GO:0045619	9.59E-05	8/500 (1.6%)	51/17360 (0.3%)
GO:0016829	9.75E-05	14/500 (2.8%)	148/17360 (0.9%)
GO:0046942	9.75E-05	14/500 (2.8%)	148/17360 (0.9%)

Jejunum: overrepresented terms among top 500 genes regulated

GO Term	P-val	Frequency	Genome frequency
GO:0006955	2.83E-18	50/500 (10.0%)	408/17360 (2.4%)
GO:0002376	2.00E-16	60/500 (12.0%)	630/17360 (3.6%)
GO:0042287	5.36E-11	9/500 (1.8%)	15/17360 (0.1%)

GO:0042825	6.79E-11	8/500 (1.6%)	11/17360 (0.1%)
GO:0042288	5.00E-10	8/500 (1.6%)	13/17360 (0.1%)
GO:0048002	7.19E-10	11/500 (2.2%)	32/17360 (0.2%)
GO:0009615	1.82E-09	13/500 (2.6%)	52/17360 (0.3%)
GO:0019882	1.45E-08	14/500 (2.8%)	72/17360 (0.4%)
GO:0002478	1.00E-07	8/500 (1.6%)	22/17360 (0.1%)
GO:0032553	1.34E-07	94/500 (18.8%)	1915/17360 (11.0%)
GO:0032555	1.34E-07	94/500 (18.8%)	1915/17360 (11.0%)
GO:0007049	1.64E-07	36/500 (7.2%)	479/17360 (2.8%)
GO:0000280	1.82E-07	19/500 (3.8%)	160/17360 (0.9%)
GO:0007067	1.82E-07	19/500 (3.8%)	160/17360 (0.9%)
GO:0050896	2.05E-07	111/500 (22.2%)	2409/17360 (13.9%)
GO:0017076	2.66E-07	96/500 (19.2%)	1999/17360 (11.5%)
GO:0002449	2.93E-07	10/500 (2.0%)	43/17360 (0.2%)
GO:0042611	2.93E-07	10/500 (2.0%)	43/17360 (0.2%)
GO:0048285	3.26E-07	19/500 (3.8%)	166/17360 (1.0%)
GO:0019884	6.14E-07	8/500 (1.6%)	27/17360 (0.2%)
GO:0002443	7.14E-07	10/500 (2.0%)	47/17360 (0.3%)
GO:0002250	1.08E-06	10/500 (2.0%)	49/17360 (0.3%)
GO:0002460	1.08E-06	10/500 (2.0%)	49/17360 (0.3%)
GO:0051301	1.52E-06	23/500 (4.6%)	256/17360 (1.5%)
GO:0002252	1.67E-06	14/500 (2.8%)	104/17360 (0.6%)
GO:0000166	1.78E-06	102/500 (20.4%)	2256/17360 (13.0%)
GO:0002495	2.22E-06	6/500 (1.2%)	15/17360 (0.1%)
GO:0019886	2.22E-06	6/500 (1.2%)	15/17360 (0.1%)
GO:0042613	2.22E-06	5/500 (1.0%)	9/17360 (0.1%)
GO:0003824	3.59E-06	204/500 (40.8%)	5439/17360 (31.3%)
GO:0002504	5.23E-06	6/500 (1.2%)	17/17360 (0.1%)
GO:0005524	5.48E-06	76/500 (15.2%)	1579/17360 (9.1%)
GO:0009607	5.63E-06	22/500 (4.4%)	257/17360 (1.5%)
GO:0051707	7.57E-06	16/500 (3.2%)	151/17360 (0.9%)
GO:0032559	8.80E-06	76/500 (15.2%)	1600/17360 (9.2%)
GO:0022403	1.08E-05	21/500 (4.2%)	248/17360 (1.4%)
GO:0006952	1.39E-05	31/500 (6.2%)	465/17360 (2.7%)
GO:0030554	1.62E-05	78/500 (15.6%)	1684/17360 (9.7%)
GO:0005771	4.34E-05	4/500 (0.8%)	8/17360 (0.0%)
GO:0043368	4.34E-05	4/500 (0.8%)	8/17360 (0.0%)
GO:0045059	4.34E-05	4/500 (0.8%)	8/17360 (0.0%)
GO:0045061	4.59E-05	5/500 (1.0%)	15/17360 (0.1%)
GO:0044432	4.78E-05	31/500 (6.2%)	496/17360 (2.9%)
GO:0016064	4.79E-05	6/500 (1.2%)	24/17360 (0.1%)
GO:0043383	7.64E-05	4/500 (0.8%)	9/17360 (0.1%)
GO:0045060	7.64E-05	4/500 (0.8%)	9/17360 (0.1%)
GO:0016817	7.74E-05	44/500 (8.8%)	832/17360 (4.8%)
GO:0022402	8.00E-05	24/500 (4.8%)	349/17360 (2.0%)
GO:0019724	9.79E-05	6/500 (1.2%)	27/17360 (0.2%)

Jejunum: overrepresented terms among top 500 genes where λ

GO Term	P-val	Frequency	Genome frequency
GO:0042287	5.36E-11	9/500 (1.8%)	15/17360 (0.1%)
GO:0044432	4.55E-09	40/500 (8.0%)	496/17360 (2.9%)
GO:0042288	2.32E-08	7/500 (1.4%)	13/17360 (0.1%)
GO:0006695	4.16E-08	8/500 (1.6%)	20/17360 (0.1%)
GO:0048002	1.97E-07	9/500 (1.8%)	32/17360 (0.2%)
GO:0042825	2.26E-07	6/500 (1.2%)	11/17360 (0.1%)
GO:0002376	4.05E-07	42/500 (8.4%)	630/17360 (3.6%)

GO:0008203	5.66E-07	12/500 (2.4%)	69/17360 (0.4%)
GO:0016126	6.14E-07	8/500 (1.6%)	27/17360 (0.2%)
GO:0050863	1.32E-06	14/500 (2.8%)	102/17360 (0.6%)
GO:0016125	1.66E-06	12/500 (2.4%)	76/17360 (0.4%)
GO:0005783	1.68E-06	46/500 (9.2%)	760/17360 (4.4%)
GO:0002478	1.85E-06	7/500 (1.4%)	22/17360 (0.1%)
GO:0002495	2.22E-06	6/500 (1.2%)	15/17360 (0.1%)
GO:0019886	2.22E-06	6/500 (1.2%)	15/17360 (0.1%)
GO:0042613	2.22E-06	5/500 (1.0%)	9/17360 (0.1%)
GO:0006955	2.80E-06	30/500 (6.0%)	408/17360 (2.4%)
GO:0008610	4.80E-06	23/500 (4.6%)	274/17360 (1.6%)
GO:0005789	5.05E-06	31/500 (6.2%)	442/17360 (2.5%)
GO:0002504	5.23E-06	6/500 (1.2%)	17/17360 (0.1%)
GO:0019882	6.26E-06	11/500 (2.2%)	72/17360 (0.4%)
GO:0019884	8.49E-06	7/500 (1.4%)	27/17360 (0.2%)
GO:0002252	9.00E-06	13/500 (2.6%)	104/17360 (0.6%)
GO:0044255	1.15E-05	37/500 (7.4%)	599/17360 (3.5%)
GO:0016491	1.19E-05	44/500 (8.8%)	769/17360 (4.4%)
GO:0008202	1.46E-05	16/500 (3.2%)	159/17360 (0.9%)
GO:0051249	2.13E-05	14/500 (2.8%)	129/17360 (0.7%)
GO:0055114	2.91E-05	37/500 (7.4%)	625/17360 (3.6%)
GO:0044444	4.11E-05	143/500 (28.6%)	3675/17360 (21.2%)
GO:0002694	4.18E-05	14/500 (2.8%)	137/17360 (0.8%)
GO:0016020	4.18E-05	209/500 (41.8%)	5797/17360 (33.4%)
GO:0005771	4.34E-05	4/500 (0.8%)	8/17360 (0.0%)
GO:0043368	4.34E-05	4/500 (0.8%)	8/17360 (0.0%)
GO:0045059	4.34E-05	4/500 (0.8%)	8/17360 (0.0%)
GO:0045061	4.59E-05	5/500 (1.0%)	15/17360 (0.1%)
GO:0031090	4.67E-05	66/500 (13.2%)	1400/17360 (8.1%)
GO:0050865	5.32E-05	14/500 (2.8%)	140/17360 (0.8%)
GO:0006694	6.23E-05	10/500 (2.0%)	76/17360 (0.4%)
GO:0043383	7.64E-05	4/500 (0.8%)	9/17360 (0.1%)
GO:0045060	7.64E-05	4/500 (0.8%)	9/17360 (0.1%)
GO:0050868	9.17E-05	7/500 (1.4%)	38/17360 (0.2%)
GO:0016705	9.36E-05	15/500 (3.0%)	166/17360 (1.0%)

Ileum: overrepresented terms among top 500 genes regulated t

GO Term	P-val	Frequency	Genome frequency
GO:0002376	7.36E-25	73/500 (14.6%)	630/17360 (3.6%)
GO:0016020	3.52E-17	256/500 (51.2%)	5797/17360 (33.4%)
GO:0009897	4.42E-17	30/500 (6.0%)	152/17360 (0.9%)
GO:0006955	7.17E-17	48/500 (9.6%)	408/17360 (2.4%)
GO:0002682	2.59E-13	35/500 (7.0%)	282/17360 (1.6%)
GO:0002684	3.39E-13	28/500 (5.6%)	182/17360 (1.0%)
GO:0019882	1.24E-12	18/500 (3.6%)	72/17360 (0.4%)
GO:0050865	1.11E-11	23/500 (4.6%)	140/17360 (0.8%)
GO:0051249	1.46E-11	22/500 (4.4%)	129/17360 (0.7%)
GO:0048002	3.65E-11	12/500 (2.4%)	32/17360 (0.2%)
GO:0055114	4.43E-11	50/500 (10.0%)	625/17360 (3.6%)
GO:0002694	4.92E-11	22/500 (4.4%)	137/17360 (0.8%)
GO:0045321	6.98E-11	27/500 (5.4%)	211/17360 (1.2%)
GO:0050863	7.38E-11	19/500 (3.8%)	102/17360 (0.6%)
GO:0050867	8.27E-11	18/500 (3.6%)	91/17360 (0.5%)
GO:0019884	8.38E-11	11/500 (2.2%)	27/17360 (0.2%)
GO:0051251	1.90E-10	17/500 (3.4%)	84/17360 (0.5%)
GO:0007159	1.98E-10	8/500 (1.6%)	12/17360 (0.1%)

GO:0050870	2.51E-10	15/500 (3.0%)	64/17360 (0.4%)
GO:0002696	4.06E-10	17/500 (3.4%)	88/17360 (0.5%)
GO:0050776	4.07E-10	23/500 (4.6%)	166/17360 (1.0%)
GO:0016491	4.22E-10	55/500 (11.0%)	769/17360 (4.4%)
GO:0001775	1.17E-09	27/500 (5.4%)	237/17360 (1.4%)
GO:0003824	1.88E-09	219/500 (43.8%)	5439/17360 (31.3%)
GO:0042287	2.39E-09	8/500 (1.6%)	15/17360 (0.1%)
GO:0002478	4.49E-09	9/500 (1.8%)	22/17360 (0.1%)
GO:0042825	4.68E-09	7/500 (1.4%)	11/17360 (0.1%)
GO:0050778	7.51E-09	18/500 (3.6%)	118/17360 (0.7%)
GO:0044459	1.23E-08	75/500 (15.0%)	1328/17360 (7.6%)
GO:0045621	1.31E-08	10/500 (2.0%)	32/17360 (0.2%)
GO:0050896	1.63E-08	115/500 (23.0%)	2409/17360 (13.9%)
GO:0042288	2.32E-08	7/500 (1.4%)	13/17360 (0.1%)
GO:0006952	2.53E-08	37/500 (7.4%)	465/17360 (2.7%)
GO:0046649	2.56E-08	22/500 (4.4%)	188/17360 (1.1%)
GO:0005886	3.45E-08	95/500 (19.0%)	1888/17360 (10.9%)
GO:0009055	4.98E-08	25/500 (5.0%)	246/17360 (1.4%)
GO:0042221	5.73E-08	52/500 (10.4%)	812/17360 (4.7%)
GO:0002495	8.30E-08	7/500 (1.4%)	15/17360 (0.1%)
GO:0019886	8.30E-08	7/500 (1.4%)	15/17360 (0.1%)
GO:0044255	1.03E-07	42/500 (8.4%)	599/17360 (3.5%)
GO:0045582	1.06E-07	9/500 (1.8%)	30/17360 (0.2%)
GO:0006629	2.06E-07	46/500 (9.2%)	705/17360 (4.1%)
GO:0002504	2.39E-07	7/500 (1.4%)	17/17360 (0.1%)
GO:0005783	2.89E-07	48/500 (9.6%)	760/17360 (4.4%)
GO:0042110	3.10E-07	16/500 (3.2%)	119/17360 (0.7%)
GO:0045058	3.81E-07	7/500 (1.4%)	18/17360 (0.1%)
GO:0070666	5.66E-07	12/500 (2.4%)	69/17360 (0.4%)
GO:0044444	5.68E-07	152/500 (30.4%)	3675/17360 (21.2%)
GO:0032944	1.06E-06	12/500 (2.4%)	73/17360 (0.4%)
GO:0050670	1.06E-06	12/500 (2.4%)	73/17360 (0.4%)
GO:0070663	1.06E-06	12/500 (2.4%)	73/17360 (0.4%)
GO:0044432	1.07E-06	35/500 (7.0%)	496/17360 (2.9%)
GO:0048584	1.35E-06	18/500 (3.6%)	165/17360 (1.0%)
GO:0045619	1.59E-06	10/500 (2.0%)	51/17360 (0.3%)
GO:0006954	1.64E-06	20/500 (4.0%)	202/17360 (1.2%)
GO:0045061	2.22E-06	6/500 (1.2%)	15/17360 (0.1%)
GO:0042613	2.22E-06	5/500 (1.0%)	9/17360 (0.1%)
GO:0043383	2.22E-06	5/500 (1.0%)	9/17360 (0.1%)
GO:0045060	2.22E-06	5/500 (1.0%)	9/17360 (0.1%)
GO:0048518	2.78E-06	68/500 (13.6%)	1335/17360 (7.7%)
GO:0016614	2.82E-06	16/500 (3.2%)	140/17360 (0.8%)
GO:0042611	2.99E-06	9/500 (1.8%)	43/17360 (0.2%)
GO:0045580	2.99E-06	9/500 (1.8%)	43/17360 (0.2%)
GO:0009605	4.25E-06	37/500 (7.4%)	573/17360 (3.3%)
GO:0001772	4.34E-06	5/500 (1.0%)	10/17360 (0.1%)
GO:0048583	4.84E-06	24/500 (4.8%)	294/17360 (1.7%)
GO:0032787	5.99E-06	22/500 (4.4%)	258/17360 (1.5%)
GO:0046635	6.44E-06	7/500 (1.4%)	26/17360 (0.1%)
GO:0019752	6.45E-06	33/500 (6.6%)	492/17360 (2.8%)
GO:0006082	6.73E-06	33/500 (6.6%)	493/17360 (2.8%)
GO:0002252	9.00E-06	13/500 (2.6%)	104/17360 (0.6%)
GO:0020037	1.06E-05	16/500 (3.2%)	155/17360 (0.9%)
GO:0046906	1.06E-05	16/500 (3.2%)	155/17360 (0.9%)
GO:0009611	1.08E-05	21/500 (4.2%)	248/17360 (1.4%)

GO:0016616	1.23E-05	14/500 (2.8%)	123/17360 (0.7%)
GO:0006725	1.71E-05	16/500 (3.2%)	161/17360 (0.9%)
GO:0006066	1.94E-05	26/500 (5.2%)	362/17360 (2.1%)
GO:0019955	1.95E-05	14/500 (2.8%)	128/17360 (0.7%)
GO:0050853	2.06E-05	5/500 (1.0%)	13/17360 (0.1%)
GO:0043235	2.24E-05	11/500 (2.2%)	82/17360 (0.5%)
GO:0046983	2.33E-05	24/500 (4.8%)	323/17360 (1.9%)
GO:0030852	2.38E-05	3/500 (0.6%)	3/17360 (0.0%)
GO:0000267	2.68E-05	34/500 (6.8%)	551/17360 (3.2%)
GO:0042129	2.88E-05	9/500 (1.8%)	56/17360 (0.3%)
GO:0002757	3.18E-05	8/500 (1.6%)	44/17360 (0.3%)
GO:0008305	3.51E-05	7/500 (1.4%)	33/17360 (0.2%)
GO:0050851	3.51E-05	7/500 (1.4%)	33/17360 (0.2%)
GO:0050871	3.51E-05	7/500 (1.4%)	33/17360 (0.2%)
GO:0032946	3.78E-05	8/500 (1.6%)	45/17360 (0.3%)
GO:0050671	3.78E-05	8/500 (1.6%)	45/17360 (0.3%)
GO:0070665	3.78E-05	8/500 (1.6%)	45/17360 (0.3%)
GO:0070668	3.78E-05	8/500 (1.6%)	45/17360 (0.3%)
GO:0005626	3.80E-05	31/500 (6.2%)	490/17360 (2.8%)
GO:0042102	4.32E-05	7/500 (1.4%)	34/17360 (0.2%)
GO:0005771	4.34E-05	4/500 (0.8%)	8/17360 (0.0%)
GO:0043368	4.34E-05	4/500 (0.8%)	8/17360 (0.0%)
GO:0045059	4.34E-05	4/500 (0.8%)	8/17360 (0.0%)
GO:0050798	4.34E-05	4/500 (0.8%)	8/17360 (0.0%)
GO:0055069	4.34E-05	4/500 (0.8%)	8/17360 (0.0%)
GO:0005624	5.03E-05	30/500 (6.0%)	474/17360 (2.7%)
GO:0017076	5.06E-05	87/500 (17.4%)	1999/17360 (11.5%)
GO:0002443	5.24E-05	8/500 (1.6%)	47/17360 (0.3%)
GO:0046634	5.26E-05	7/500 (1.4%)	35/17360 (0.2%)
GO:0005506	5.57E-05	24/500 (4.8%)	341/17360 (2.0%)
GO:0002526	6.13E-05	8/500 (1.6%)	48/17360 (0.3%)
GO:0002764	6.13E-05	8/500 (1.6%)	48/17360 (0.3%)
GO:0002819	6.13E-05	8/500 (1.6%)	48/17360 (0.3%)
GO:0002822	6.13E-05	8/500 (1.6%)	48/17360 (0.3%)
GO:0050864	6.13E-05	8/500 (1.6%)	48/17360 (0.3%)
GO:0002253	6.23E-05	10/500 (2.0%)	76/17360 (0.4%)
GO:0002250	7.14E-05	8/500 (1.6%)	49/17360 (0.3%)
GO:0002460	7.14E-05	8/500 (1.6%)	49/17360 (0.3%)
GO:0005887	7.62E-05	20/500 (4.0%)	262/17360 (1.5%)
GO:0002429	9.17E-05	7/500 (1.4%)	38/17360 (0.2%)
GO:0005415	9.30E-05	3/500 (0.6%)	4/17360 (0.0%)
GO:0002821	9.79E-05	6/500 (1.2%)	27/17360 (0.2%)
GO:0002824	9.79E-05	6/500 (1.2%)	27/17360 (0.2%)

Ileum: overrepresented terms among top 500 genes regulated t

GO Term	P-val	Frequency	Genome frequency
GO:0006955	7.17E-17	48/500 (9.6%)	408/17360 (2.4%)
GO:0002376	2.95E-15	58/500 (11.6%)	630/17360 (3.6%)
GO:0002252	6.68E-09	17/500 (3.4%)	104/17360 (0.6%)
GO:0006952	7.84E-08	36/500 (7.2%)	465/17360 (2.7%)
GO:0045087	1.28E-07	15/500 (3.0%)	98/17360 (0.6%)
GO:0003824	1.34E-07	211/500 (42.2%)	5439/17360 (31.3%)
GO:0032020	6.80E-07	4/500 (0.8%)	4/17360 (0.0%)
GO:0050776	1.47E-06	18/500 (3.6%)	166/17360 (1.0%)
GO:0050778	1.50E-06	15/500 (3.0%)	118/17360 (0.7%)
GO:0004364	2.59E-06	7/500 (1.4%)	23/17360 (0.1%)

GO:0009611	3.15E-06	22/500 (4.4%)	248/17360 (1.4%)
GO:0003924	4.96E-06	20/500 (4.0%)	217/17360 (1.3%)
GO:0009607	5.63E-06	22/500 (4.4%)	257/17360 (1.5%)
GO:0019882	6.26E-06	11/500 (2.2%)	72/17360 (0.4%)
GO:0006954	6.35E-06	19/500 (3.8%)	202/17360 (1.2%)
GO:0016787	8.14E-06	105/500 (21.0%)	2422/17360 (14.0%)
GO:0016020	8.30E-06	213/500 (42.6%)	5797/17360 (33.4%)
GO:0005525	9.16E-06	27/500 (5.4%)	368/17360 (2.1%)
GO:0002253	1.07E-05	11/500 (2.2%)	76/17360 (0.4%)
GO:0032561	1.42E-05	27/500 (5.4%)	377/17360 (2.2%)
GO:0019001	1.49E-05	27/500 (5.4%)	378/17360 (2.2%)
GO:0050896	1.84E-05	103/500 (20.6%)	2409/17360 (13.9%)
GO:0048584	2.32E-05	16/500 (3.2%)	165/17360 (1.0%)
GO:0002682	2.43E-05	22/500 (4.4%)	282/17360 (1.6%)
GO:0016817	3.76E-05	45/500 (9.0%)	832/17360 (4.8%)
GO:0042221	4.40E-05	44/500 (8.8%)	812/17360 (4.7%)
GO:0006959	4.46E-05	8/500 (1.6%)	46/17360 (0.3%)
GO:0002443	5.24E-05	8/500 (1.6%)	47/17360 (0.3%)
GO:0002684	7.66E-05	16/500 (3.2%)	182/17360 (1.0%)

Ileum: overrepresented terms among top 500 genes where Myd

GO Term	P-val	Frequency	Genome frequency
GO:0006695	4.16E-08	8/500 (1.6%)	20/17360 (0.1%)
GO:0016126	6.14E-07	8/500 (1.6%)	27/17360 (0.2%)
GO:0006066	2.28E-06	28/500 (5.6%)	362/17360 (2.1%)
GO:0008202	3.49E-06	17/500 (3.4%)	159/17360 (0.9%)
GO:0008203	4.09E-06	11/500 (2.2%)	69/17360 (0.4%)
GO:0006694	1.07E-05	11/500 (2.2%)	76/17360 (0.4%)
GO:0016125	1.07E-05	11/500 (2.2%)	76/17360 (0.4%)
GO:0044255	1.15E-05	37/500 (7.4%)	599/17360 (3.5%)
GO:0006629	1.63E-05	41/500 (8.2%)	705/17360 (4.1%)
GO:0008299	2.06E-05	5/500 (1.0%)	13/17360 (0.1%)
GO:0008152	3.18E-05	249/500 (49.8%)	7112/17360 (41.0%)
GO:0006720	3.51E-05	7/500 (1.4%)	33/17360 (0.2%)
GO:0008610	4.79E-05	21/500 (4.2%)	274/17360 (1.6%)
GO:0055114	6.56E-05	36/500 (7.2%)	625/17360 (3.6%)

Proximal colon: overrepresented terms among top 500 genes r

GO Term	P-val	Frequency	Genome frequency
GO:0003824	2.90E-08	214/500 (42.8%)	5439/17360 (31.3%)
GO:0016324	5.34E-08	17/500 (3.4%)	119/17360 (0.7%)
GO:0005903	3.81E-07	7/500 (1.4%)	18/17360 (0.1%)
GO:0042598	5.67E-07	19/500 (3.8%)	172/17360 (1.0%)
GO:0016491	9.82E-07	47/500 (9.4%)	769/17360 (4.4%)
GO:0005792	1.47E-06	18/500 (3.6%)	166/17360 (1.0%)
GO:0016712	1.61E-06	11/500 (2.2%)	63/17360 (0.4%)
GO:0004497	6.95E-06	16/500 (3.2%)	150/17360 (0.9%)
GO:0000267	1.11E-05	35/500 (7.0%)	551/17360 (3.2%)
GO:0055114	1.25E-05	38/500 (7.6%)	625/17360 (3.6%)
GO:0016020	1.26E-05	212/500 (42.4%)	5797/17360 (33.4%)
GO:0005626	1.53E-05	32/500 (6.4%)	490/17360 (2.8%)
GO:0044432	1.94E-05	32/500 (6.4%)	496/17360 (2.9%)
GO:0032787	1.97E-05	21/500 (4.2%)	258/17360 (1.5%)
GO:0001730	2.38E-05	3/500 (0.6%)	3/17360 (0.0%)
GO:0020037	4.26E-05	15/500 (3.0%)	155/17360 (0.9%)
GO:0046906	4.26E-05	15/500 (3.0%)	155/17360 (0.9%)

GO:0005624	5.03E-05	30/500 (6.0%)	474/17360 (2.7%)
GO:0007623	5.26E-05	7/500 (1.4%)	35/17360 (0.2%)
GO:0005783	8.87E-05	41/500 (8.2%)	760/17360 (4.4%)
GO:0001523	9.02E-05	5/500 (1.0%)	17/17360 (0.1%)
GO:0006721	9.02E-05	5/500 (1.0%)	17/17360 (0.1%)
GO:0016101	9.02E-05	5/500 (1.0%)	17/17360 (0.1%)

Proximal colon: overrepresented terms among top 500 genes r

GO Term	P-val	Frequency	Genome frequency
GO:0046777	1.78E-05	10/500 (2.0%)	66/17360 (0.4%)
GO:0003824	2.94E-05	199/500 (39.8%)	5439/17360 (31.3%)
GO:0044237	4.12E-05	214/500 (42.8%)	5961/17360 (34.3%)
GO:0005488	9.34E-05	376/500 (75.2%)	11727/17360 (67.6%)
GO:0008152	9.72E-05	246/500 (49.2%)	7112/17360 (41.0%)

Proximal colon: overrepresented terms among top 500 genes w

GO Term	P-val	Frequency	Genome frequency
GO:0000280	9.17E-14	27/500 (5.4%)	160/17360 (0.9%)
GO:0007067	9.17E-14	27/500 (5.4%)	160/17360 (0.9%)
GO:0048285	2.29E-13	27/500 (5.4%)	166/17360 (1.0%)
GO:0022403	9.62E-13	32/500 (6.4%)	248/17360 (1.4%)
GO:0051301	1.15E-11	31/500 (6.2%)	256/17360 (1.5%)
GO:0003824	6.77E-11	224/500 (44.8%)	5439/17360 (31.3%)
GO:0007049	1.04E-10	42/500 (8.4%)	479/17360 (2.8%)
GO:0022402	1.10E-10	35/500 (7.0%)	349/17360 (2.0%)
GO:0002376	2.41E-09	47/500 (9.4%)	630/17360 (3.6%)
GO:0006955	2.62E-09	36/500 (7.2%)	408/17360 (2.4%)
GO:0000776	2.53E-08	11/500 (2.2%)	43/17360 (0.2%)
GO:0016126	3.75E-08	9/500 (1.8%)	27/17360 (0.2%)
GO:0000775	6.91E-08	11/500 (2.2%)	47/17360 (0.3%)
GO:0009615	2.10E-07	11/500 (2.2%)	52/17360 (0.3%)
GO:0006695	8.83E-07	7/500 (1.4%)	20/17360 (0.1%)
GO:0044427	1.06E-06	27/500 (5.4%)	328/17360 (1.9%)
GO:0016125	1.66E-06	12/500 (2.4%)	76/17360 (0.4%)
GO:0017076	1.72E-06	93/500 (18.6%)	1999/17360 (11.5%)
GO:0005694	3.16E-06	18/500 (3.6%)	175/17360 (1.0%)
GO:0050896	3.72E-06	106/500 (21.2%)	2409/17360 (13.9%)
GO:0000166	5.53E-06	100/500 (20.0%)	2256/17360 (13.0%)
GO:0032553	1.02E-05	87/500 (17.4%)	1915/17360 (11.0%)
GO:0032555	1.02E-05	87/500 (17.4%)	1915/17360 (11.0%)
GO:0006694	1.07E-05	11/500 (2.2%)	76/17360 (0.4%)
GO:0006996	1.51E-05	53/500 (10.6%)	1005/17360 (5.8%)
GO:0030554	1.62E-05	78/500 (15.6%)	1684/17360 (9.7%)
GO:0000777	1.80E-05	7/500 (1.4%)	30/17360 (0.2%)
GO:0016787	2.30E-05	103/500 (20.6%)	2422/17360 (14.0%)
GO:0006950	2.32E-05	63/500 (12.6%)	1287/17360 (7.4%)
GO:0001730	2.38E-05	3/500 (0.6%)	3/17360 (0.0%)
GO:0033554	2.46E-05	26/500 (5.2%)	367/17360 (2.1%)
GO:0008203	2.66E-05	10/500 (2.0%)	69/17360 (0.4%)
GO:0005524	5.96E-05	72/500 (14.4%)	1579/17360 (9.1%)
GO:0006323	6.15E-05	6/500 (1.2%)	25/17360 (0.1%)
GO:0016779	6.49E-05	12/500 (2.4%)	108/17360 (0.6%)
GO:0016817	7.74E-05	44/500 (8.8%)	832/17360 (4.8%)
GO:0032559	9.02E-05	72/500 (14.4%)	1600/17360 (9.2%)
GO:0032020	9.30E-05	3/500 (0.6%)	4/17360 (0.0%)

genes from 2-way ANOVA tests.

ated by microbiota

Description

membrane
endoplasmic reticulum
carboxylic acid metabolic process
organic acid metabolic process
microsome
vesicular fraction
oxidoreductase activity
electron carrier activity
oxidation reduction
extracellular matrix part
monocarboxylic acid metabolic process
phenol metabolic process
cellular alcohol metabolic process
cytoplasmic part
endoplasmic reticulum part
cellular amino acid and derivative metabolic process
catalytic activity
antigen binding
nitrogen compound metabolic process
endoplasmic reticulum membrane
cofactor metabolic process
cellular amine metabolic process
cell cycle arrest
fibrillar collagen
laminin-10 complex
cellular lipid metabolic process
cell adhesion
biological adhesion
cellular nitrogen compound metabolic process
extracellular matrix structural constituent
platelet-derived growth factor binding
calcium ion binding
2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase activity
siderophore metabolic process
enterobactin metabolic process
enterobactin biosynthetic process
catechol metabolic process
nonribosomal peptide biosynthetic process
siderophore biosynthetic process
siderophore biosynthetic process from catechol
regulation of cell adhesion
fatty acid metabolic process
peptide metabolic process
cellular aromatic compound metabolic process
peptide biosynthetic process
oxidoreductase activity, acting on the CH-CH group of donors
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen...
extracellular matrix
dopamine catabolic process

ated by Myd88 genotype

Description

oxidation reduction
oxidoreductase activity
catalytic activity
metabolic process
carboxylesterase activity
lipid metabolic process
oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
oxidoreductase activity, acting on CH-OH group of donors
cellular lipid metabolic process
glutathione transferase activity
cofactor metabolic process
monocarboxylic acid metabolic process
electron carrier activity
carboxylic acid metabolic process
heme binding
tetrapyrrole binding
organic acid metabolic process
cellular alcohol metabolic process
fatty acid metabolic process
microsome
cholinesterase activity
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen...
vesicular fraction
cytoplasmic part
cellular aromatic compound metabolic process
monooxygenase activity
MHC protein binding
phenol metabolic process
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
iron ion binding
MHC class I protein binding
transferase activity, transferring alkyl or aryl (other than methyl) groups
cofactor biosynthetic process
endoplasmic reticulum
antigen processing and presentation of exogenous peptide antigen
antigen processing and presentation of peptide antigen via MHC class II
antigen processing and presentation of exogenous peptide antigen via MHC class II
MHC class II protein complex
vitamin metabolic process
oxidoreductase activity, acting on the CH-CH group of donors
glutathione metabolic process
endoplasmic reticulum part
coenzyme metabolic process
peroxisome
microbody
antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase activity
siderophore metabolic process
enterobactin metabolic process
enterobactin biosynthetic process
catechol metabolic process
nonribosomal peptide biosynthetic process
siderophore biosynthetic process
siderophore biosynthetic process from catechol
TAP complex
antigen processing and presentation of exogenous antigen

peptide biosynthetic process
steroid metabolic process
sulfur metabolic process
immune response
aromatase activity
pre-autophagosomal structure membrane
antigen processing and presentation of peptide antigen
multivesicular body
oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor
vitamin A metabolic process
peptide metabolic process
sterol metabolic process

e Myd88 genotype modulates response to microbiota

Description

enriched by microbiota

Description

catalytic activity
endoplasmic reticulum
oxidation reduction
regulation of immune system process
positive regulation of immune system process
positive regulation of T cell differentiation
oxidoreductase activity
positive regulation of lymphocyte differentiation
antigen binding
leukocyte activation
positive regulation of T cell activation
organic acid metabolic process
cell activation
positive regulation of cell differentiation
regulation of T cell differentiation
positive regulation of lymphocyte activation
immune system process
endoplasmic reticulum membrane
positive regulation of immune response
exopeptidase activity
carboxylic acid metabolic process
positive regulation of leukocyte activation
endoplasmic reticulum part
oxidoreductase activity, acting on CH-OH group of donors
cellular alcohol metabolic process
oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
positive regulation of cell activation
activation of immune response
regulation of lymphocyte activation
regulation of lymphocyte differentiation
lyase activity
carboxylic acid transport

enriched by Myd88 genotype

Description

immune response
immune system process
MHC protein binding

TAP complex
MHC class I protein binding
antigen processing and presentation of peptide antigen
response to virus
antigen processing and presentation
antigen processing and presentation of exogenous peptide antigen
ribonucleotide binding
purine ribonucleotide binding
cell cycle
nuclear division
mitosis
response to stimulus
purine nucleotide binding
lymphocyte mediated immunity
MHC protein complex
organelle fission
antigen processing and presentation of exogenous antigen
leukocyte mediated immunity
adaptive immune response
adaptive immune response based on somatic recombination of immune receptors built from...
cell division
immune effector process
nucleotide binding
antigen processing and presentation of peptide antigen via MHC class II
antigen processing and presentation of exogenous peptide antigen via MHC class II
MHC class II protein complex
catalytic activity
antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
ATP binding
response to biotic stimulus
response to other organism
adenyl ribonucleotide binding
cell cycle phase
defense response
adenyl nucleotide binding
multivesicular body
positive T cell selection
positive thymic T cell selection
thymic T cell selection
endoplasmic reticulum part
immunoglobulin mediated immune response
negative T cell selection
negative thymic T cell selection
hydrolase activity, acting on acid anhydrides
cell cycle process
B cell mediated immunity

lyd88 genotype modulates response to microbiota

Description

MHC protein binding
endoplasmic reticulum part
MHC class I protein binding
cholesterol biosynthetic process
antigen processing and presentation of peptide antigen
TAP complex
immune system process

cholesterol metabolic process
sterol biosynthetic process
regulation of T cell activation
sterol metabolic process
endoplasmic reticulum
antigen processing and presentation of exogenous peptide antigen
antigen processing and presentation of peptide antigen via MHC class II
antigen processing and presentation of exogenous peptide antigen via MHC class II
MHC class II protein complex
immune response
lipid biosynthetic process
endoplasmic reticulum membrane
antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
antigen processing and presentation
antigen processing and presentation of exogenous antigen
immune effector process
cellular lipid metabolic process
oxidoreductase activity
steroid metabolic process
regulation of lymphocyte activation
oxidation reduction
cytoplasmic part
regulation of leukocyte activation
membrane
multivesicular body
positive T cell selection
positive thymic T cell selection
thymic T cell selection
organelle membrane
regulation of cell activation
steroid biosynthetic process
negative T cell selection
negative thymic T cell selection
negative regulation of T cell activation
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen

by microbiota

Description

immune system process
membrane
external side of plasma membrane
immune response
regulation of immune system process
positive regulation of immune system process
antigen processing and presentation
regulation of cell activation
regulation of lymphocyte activation
antigen processing and presentation of peptide antigen
oxidation reduction
regulation of leukocyte activation
leukocyte activation
regulation of T cell activation
positive regulation of cell activation
antigen processing and presentation of exogenous antigen
positive regulation of lymphocyte activation
leukocyte adhesion

positive regulation of T cell activation
positive regulation of leukocyte activation
regulation of immune response
oxidoreductase activity
cell activation
catalytic activity
MHC protein binding
antigen processing and presentation of exogenous peptide antigen
TAP complex
positive regulation of immune response
plasma membrane part
positive regulation of lymphocyte differentiation
response to stimulus
MHC class I protein binding
defense response
lymphocyte activation
plasma membrane
electron carrier activity
response to chemical stimulus
antigen processing and presentation of peptide antigen via MHC class II
antigen processing and presentation of exogenous peptide antigen via MHC class II
cellular lipid metabolic process
positive regulation of T cell differentiation
lipid metabolic process
antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
endoplasmic reticulum
T cell activation
T cell selection
regulation of mast cell proliferation
cytoplasmic part
regulation of mononuclear cell proliferation
regulation of lymphocyte proliferation
regulation of leukocyte proliferation
endoplasmic reticulum part
positive regulation of response to stimulus
regulation of lymphocyte differentiation
inflammatory response
thymic T cell selection
MHC class II protein complex
negative T cell selection
negative thymic T cell selection
positive regulation of biological process
oxidoreductase activity, acting on CH-OH group of donors
MHC protein complex
regulation of T cell differentiation
response to external stimulus
immunological synapse
regulation of response to stimulus
monocarboxylic acid metabolic process
positive regulation of alpha-beta T cell activation
carboxylic acid metabolic process
organic acid metabolic process
immune effector process
heme binding
tetrapyrrole binding
response to wounding

oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
cellular aromatic compound metabolic process
cellular alcohol metabolic process
cytokine binding
B cell receptor signaling pathway
receptor complex
protein dimerization activity
regulation of granulocyte differentiation
cell fraction
regulation of T cell proliferation
immune response-activating signal transduction
integrin complex
antigen receptor-mediated signaling pathway
positive regulation of B cell activation
positive regulation of mononuclear cell proliferation
positive regulation of lymphocyte proliferation
positive regulation of leukocyte proliferation
positive regulation of mast cell proliferation
insoluble fraction
positive regulation of T cell proliferation
multivesicular body
positive T cell selection
positive thymic T cell selection
activated T cell proliferation
zinc ion homeostasis
membrane fraction
purine nucleotide binding
leukocyte mediated immunity
regulation of alpha-beta T cell activation
iron ion binding
acute inflammatory response
immune response-regulating signal transduction
regulation of adaptive immune response
regulation of adaptive immune response based on somatic recombination of immune receptors...
regulation of B cell activation
activation of immune response
adaptive immune response
adaptive immune response based on somatic recombination of immune receptors built from...
integral to plasma membrane
immune response-activating cell surface receptor signaling pathway
nucleoside:sodium symporter activity
positive regulation of adaptive immune response
positive regulation of adaptive immune response based on somatic recombination of immune...

Myd88 genotype

Description

immune response
immune system process
immune effector process
defense response
innate immune response
catalytic activity
ISG15-protein conjugation
regulation of immune response
positive regulation of immune response
glutathione transferase activity

response to wounding
GTPase activity
response to biotic stimulus
antigen processing and presentation
inflammatory response
hydrolase activity
membrane
GTP binding
activation of immune response
guanyl ribonucleotide binding
guanyl nucleotide binding
response to stimulus
positive regulation of response to stimulus
regulation of immune system process
hydrolase activity, acting on acid anhydrides
response to chemical stimulus
humoral immune response
leukocyte mediated immunity
positive regulation of immune system process

188 genotype modulates response to microbiota

Description

cholesterol biosynthetic process
sterol biosynthetic process
cellular alcohol metabolic process
steroid metabolic process
cholesterol metabolic process
steroid biosynthetic process
sterol metabolic process
cellular lipid metabolic process
lipid metabolic process
isoprenoid biosynthetic process
metabolic process
isoprenoid metabolic process
lipid biosynthetic process
oxidation reduction

regulated by microbiota

Description

catalytic activity
apical plasma membrane
brush border
vesicular fraction
oxidoreductase activity
microsome
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen...
monooxygenase activity
cell fraction
oxidation reduction
membrane
insoluble fraction
endoplasmic reticulum part
monocarboxylic acid metabolic process
2'-5'-oligoadenylate synthetase activity
heme binding
tetrapyrrole binding

membrane fraction
circadian rhythm
endoplasmic reticulum
retinoid metabolic process
terpenoid metabolic process
diterpenoid metabolic process

regulated by Myd88 genotype

Description

protein amino acid autophosphorylation
catalytic activity
cellular metabolic process
binding
metabolic process

where Myd88 genotype modulates response to microbiota

Description

nuclear division
mitosis
organelle fission
cell cycle phase
cell division
catalytic activity
cell cycle
cell cycle process
immune system process
immune response
kinetochore
sterol biosynthetic process
chromosome, centromeric region
response to virus
cholesterol biosynthetic process
chromosomal part
sterol metabolic process
purine nucleotide binding
chromosome
response to stimulus
nucleotide binding
ribonucleotide binding
purine ribonucleotide binding
steroid biosynthetic process
organelle organization
adenyl nucleotide binding
condensed chromosome kinetochore
hydrolase activity
response to stress
2'-5'-oligoadenylate synthetase activity
cellular response to stress
cholesterol metabolic process
ATP binding
DNA packaging
nucleotidyltransferase activity
hydrolase activity, acting on acid anhydrides
adenyl ribonucleotide binding
ISG15-protein conjugation