

**Table 2. Gene ontology (GO) categories enriched in the set of genes bound by NF- $\kappa$ B**

GO system	GO category	Number of bound genes	Total number of genes in category	P value
Biological process	Response to biotic stimulus	44	516	6.3E-07
Biological process	Immune response	38	425	1.3E-06
Biological process	Defense response	39	475	7.8E-06
Biological process	Response to pest/pathogen/parasite	26	276	3E-05
Molecular function	Cytokine activity	15	133	0.00011
Molecular function	Transcription factor activity	32	468	0.00046
Biological process	Response to stress	33	465	0.00068
Biological process	Response to wounding	16	163	0.0007
Molecular function	Tumor necrosis factor receptor binding	4	12	0.00072
Biological process	Response to external stimulus	49	793	0.00083
Molecular function	Transcription regulator activity	38	635	0.00172
Biological process	Antigen processing, endogenous antigen via MHC class I	3	7	0.00193
Biological process	Inflammatory response	12	116	0.00207
Molecular function	Receptor binding	23	332	0.00255
Biological process	Antigen processing	3	8	0.003
Biological process	Response to stimulus	53	934	0.00345
Biological process	Transcription	50	869	0.00347
Biological process	Innate immune response	12	125	0.00387
Biological process	Regulation of transcription from Pol II promoter	13	143	0.0043
Biological process	Response to virus	5	28	0.00442
Molecular function	GTP binding	12	139	0.00517
Molecular function	Chemokine receptor binding	5	32	0.00592
Molecular function	Chemokine activity	5	32	0.00592
Molecular function	Guanyl nucleotide binding	12	143	0.00648
Molecular function	G-protein-coupled receptor binding	5	33	0.00677
Biological process	Transcription, DNA-dependent	47	833	0.00681
Biological process	Cell motility	14	169	0.00707
Biological process	Viral life cycle	4	20	0.00714
Molecular function	DNA binding	48	930	0.00858
Biological process	Transcription from Pol II promoter	20	285	0.00902
Molecular function	Binding	149	3,561	0.0091

Fisher exact scores were generated using the EASEonline tool ([aaps1.niaid.nih.gov/david](http://aaps1.niaid.nih.gov/david)). A total of 5,707 genes present of the arrays were annotated by GO biological process information; 227 of these were bound by NF- $\kappa$ B.