<https://www.ncbi.nlm.nih.gov/pubmed/26063326>

Top 10 genetic markers associated with CFS based on weighted genetic variation (WGV) estimated by the Bayesian model

| **SNP ID** | **Proxy SNP** | **Gene symbola** | **SNP annotationa** | **WGV** | **SE of WGVb** |
| --- | --- | --- | --- | --- | --- |
| rs2288831 | rs3212227 | IL12B | Intron (UTR-3) | 3.95 | 0.0299 |

<https://www.ncbi.nlm.nih.gov/pubmed/26063326>

| Sr. no. | Gene symbol | NCBI rsID | Chr. | Position | Homo-zygous-1 | Homo-zygous-2 | Hetero-zygous | Weighted genetic variation |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| 51 | *IL12B* | rs2288831 | 5 | 158682591 | 0.10 | 0.65 | 0.25 | 3.95 |
| 49 | *IL12B* | rs1368439 | 5 | 158674592 | 0.03 | 0.65 | 0.32 | 1.39 |

t is interesting to note that SNPs from 7 out of 9 immune function genes were represented in this group that showed greater prediction, and SNPs in three of them (IL12B rs2288831, IL1A rs2071376, and IFNG rs2069718) showed the highest association with CFS in terms of WGV values. All three SNPs showed replicated or moderate association with other diseases as well. SNP rs2288831 is in complete LD with rs3212227 located in the 3′-untranslated region (3′UTR) of IL12B (Table [2](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4479222/table/Tab2/)), and this proxy SNP was reported to be associated with psoriasis in a large-scale association study, confirming the results of a previous study [[55](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4479222/#CR55)].

<https://www.ncbi.nlm.nih.gov/pubmed/28596683>

Chronic inﬂammation plays a crucial role in GC development, thus multiple genes in inﬂammatory pathways may be associated with GC risk[[29](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5442083/#B29)]. To date, different gene polymorphism related to inflammatory pathways have been evaluated, with IL-1B and IL-1RN being the most widely studied ones[[18](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5442083/#B18),[30](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5442083/#B30)-[34](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5442083/#B34)]. Computational analysis tools that we used in our study suggested two genes polymorphisms - IL12B (rs1368439) and IL10 (rs3024498) - situated in inflammatory pathways, that might be the involved in miRNA-target gene interaction[[16](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5442083/#B16)]. The other studies evaluated some gene polymorphisms located in IL12 and IL10; however, they were different from the ones selected for our study. IL12B encodes a subunit p40 of interleukin (IL) 12. Proinflammatory cytokine IL12 is expressed by activated macrophages and favors the differentiation of T helper 1 (Th1) cells[[35](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5442083/#B35)]. Th1 lymphocytes prevail over Th2 in H. pylori associated chronic gastritis[[36](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5442083/#B36)]. IL10 down-regulates the expression of Th1 cytokines and enhances B cell survival, proliferation, and antibody production[[37](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5442083/#B37)]. Our study did not find significant association between polymorphisms in IL12Bor IL10 genes with GC risk. Our results support the previous data to other populations, which analyzed associations between SNPs in genes regulating the inflammatory response and GC[[30](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5442083/#B30)-[32](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5442083/#B32),[34](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5442083/#B34)].

<https://www.ncbi.nlm.nih.gov/pubmed/21339808>

We examined whether polymorphisms in interleukin-12B (IL12B) associate with susceptibility to pulmonary tuberculosis (PTB) in two West African populations (from The Gambia and Guinea-Bissau) and in two independent populations from North and South America. Nine polymorphisms (seven SNPs, one insertion/deletion, one microsatellite) were analyzed in 321 PTB cases and 346 controls from Guinea-Bissau and 280 PTB cases and 286 controls from The Gambia. For replication we studied 281 case and 179 control African-American samples and 221 cases and 144 controls of European ancestry from the US and Argentina. First-stage single locus analyses revealed signals of association at IL12B 3′ UTR SNP rs3212227 (unadjusted allelic p = 0.04; additive genotypic p = 0.05, OR = 0.78, 95% CI [0.61–0.99]) in Guinea-Bissau and rs11574790 (unadjusted allelic p = 0.05; additive genotypic p = 0.05, OR = 0.76, 95% CI [0.58–1.00]) in The Gambia. Association of rs3212227 was then replicated in African-Americans (rs3212227 allelic p = 0.002; additive genotypic p = 0.05, OR = 0.78, 95% CI [0.61–1.00]); most importantly, in the African-American cohort, multiple significant signals of association (seven of the nine polymorphisms tested) were detected throughout the gene. These data suggest that genetic variation in IL12B, a highly relevant candidate gene, is a risk factor for PTB in populations of African ancestry, although further studies will be required to confirm this association and identify the precise mechanism underlying it.

. Single locus tests of association in the African-Americans identified seven significant allelic associations at IL12B polymorphisms rs3212227 (p = 0.002), rs2421047 (p = 0.008), rs2288831

<https://www.ncbi.nlm.nih.gov/pubmed/20525402>

Even though none of the other IL12B polymorphisms investigated were associated with TB in the single-point analysis (similar to the results published by Kusuhara et al. [[77](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2891757/#B77)] for rs11135058, rs2288831 and rs6870828), we found a nominally significant association between a haplotype in IL12B and resistance to TB in the SAC population (Figure [​(Figure1,1](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2891757/figure/F1/), Table [​Table3).3](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2891757/table/T3/)).

<https://www.ncbi.nlm.nih.gov/pubmed/28415696>

e observed a significant association between IL-12B rs3212227 and overall cancer risk, especially in hepatocellular carcinoma, nasopharyngeal cancer, and among Asians.

<https://www.ncbi.nlm.nih.gov/pubmed/27896842>

Frequencies of the rs3212227CC genotype were statistically higher in patients with RA compared with the healthy control group in both codominant and recessive models (P = 0.037; P = 0.04, respectively). The frequency of rs3212227C allele also showed similar tendency (P = 0.07). IL-12 level in serum was significantly higher in RA group compared with control (P < 0.0001). We observed that increased IL-12 serum level was correlated with higher number of tender and swollen joints, ExRA presence and higher levels of haemoglobin, CRP and PLT. Also higher IL-12 level in serum was observed within RA patients with hypertension. Present findings indicated that IL-12p40 + 1188A/C polymorphism as well as IL-12p70 protein levels may be associated with RA in the Polish population.

<https://www.ncbi.nlm.nih.gov/pubmed/27876593>

IFN-γ production by C. burnetii-stimulated PBMCs from chronic Q fever patients was significantly higher than in healthy controls. Many IFN-γ response genes were strongly upregulated in PBMCs of patients. Neopterin levels were significantly higher in PBMC supernatants and sera of patients. The IL12B polymorphisms rs3212227 and rs2853694 were associated with chronic Q fever.

<https://www.ncbi.nlm.nih.gov/pubmed/27312970>

The aim of this study was to investigate the association of two common interleukin 12B (IL-12B) polymorphisms (rs3212227 and rs6887695) with rheumatoid arthritis (RA) susceptibility through meta-analyses. A systematic literature search of PubMed, Web of Science, Cochrane Library, and Embase databases was conducted on articles published before 28 February 2016. Then odds ratio (OR) with 95 % confidence interval (CI) was used to quantify the strength of association for homozygote, heterozygote, dominant, and recessive genetic models. Nine articles with a total of 17 case-control studies (12 for IL-12B rs3212227 polymorphism and 5 for IL-12B rs6887695 polymorphism) met our inclusion criteria. The pooled results demonstrated that IL-12B rs3212227 (homozygote model: OR = 0.96, 95 % CI = 0.81-1.15; heterozygote model: OR = 1.07, 95 % CI = 0.93-1.23; dominant model: OR = 1.05, 95 % CI = 0.91-1.20; recessive model: OR = 0.93, 95 % CI = 0.79-1.10) and rs6887695 (homozygote model: OR = 1.01, 95 % CI = 0.84-1.21; heterozygote model: OR = 1.14, 95 % CI = 0.86-1.51; dominant model: OR = 1.14, 95 % CI = 0.87-1.48; recessive model: OR = 1.01, 95 % CI = 0.85-1.21) polymorphisms may not be associated with RA risk. Our meta-analyses demonstrated that IL-12B rs3212227 and rs6887695 polymorphisms do not confer susceptibility to RA.

<https://www.ncbi.nlm.nih.gov/pubmed/27059274>

To investigate the potential association between IL-12B and IL-27 gene polymorphisms and systemic lupus erythematosus (SLE), we performed a case-control study based on the Polish population. Patients with SLE and healthy individuals were examined for -6415 CTCTAA/GC (rs17860508) and +1188A/C (rs3212227) in IL-12B and -924A/G (rs153109) and 4730T/C (rs181206) in IL-27 gene polymorphisms using the high-resolution melting method, PCR-RFLP method and TaqMan SNP genotyping assay, respectively. An increased frequency of GC/GC genotype as well as GC allele of the IL-12B rs17860508 was found in patients with SLE, as compared with healthy subjects (P < 0.001). We did not find differences in genotype and allele frequencies of the IL-12B rs3212227 and IL-27 rs153109 and rs181206 variants between patients with SLE and controls. IL-27 haplotype rs181206C/rs153109G indicated higher risk for SLE (P = 0.002), whereas haplotype rs181206T/rs153109G indicated reduced risk for SLE (P = 0.005). The IL-12B rs3212227 A/C polymorphism was associated with the mean value of the platelets (PLT), urea and complement C3 level. Furthermore, IL-12B rs17860508 genetic variant showed correlation with PLT, prothrombin time, international normalized ratio and alkaline phosphatase. Our results revealed that IL-12B rs17860508 and IL-27 haplotype CG are genetic risk factors for SLE and that both IL-12B rs17860508 and rs3212227 predict disease phenotype.

[**https://www.ncbi.nlm.nih.gov/pubmed/26915668**](https://www.ncbi.nlm.nih.gov/pubmed/26915668)

**OBJECTIVES:**

The purpose of this study was to evaluate whether a single-nucleotide polymorphism (SNP) IL12B 3(')UTR +1188A/C (rs3212227) confers susceptibility to several autoimmune diseases.

**METHODS:**

A systematic literature search was conducted to identify relevant studies. Pooled odds ratio (OR) with 95% confidence interval (CI) was used to estimate the strength of association.

**RESULTS:**

Twenty-five studies were included in the meta-analysis, which contained 9794 cases and 11,330 controls. Our result indicated that IL12B +1188A/C (rs3212227) polymorphism was associated with type-1 diabetes (T1D) in the dominant model (p = 0.008), and an increased risk was found in East Asians in the dominant model (p < 0.001). East Asians rheumatoid arthritis (RA) patients seemed to be at risk of allelic model (p = 0.011). As to Behcet's disease (BD), there was a risk in dominant model (p = 0.020) and positive associations of dominant model, allelic model in East Asians (p = 0.009; p < 0.001, respectively). But we failed to find any association between IL12B +1188A/C (rs3212227) polymorphism with Graves' disease (GD) and ankylosing spondylitis (AS).

**CONCLUSIONS:**

The present study suggests that the IL12B +1188A/C (rs3212227) polymorphism might be associated with genetic susceptibility to autoimmune diseases, such as T1D, RA, BD, but not GD and AS.

<https://www.ncbi.nlm.nih.gov/pubmed/26850223>

In early onset autoimmune thyroid disease (AITD) showing a strong genetic tendency, cytokines have been suggested to play a critical role in the development of AITD. To directly compare the influences of several cytokine gene polymorphisms, 25 single nucleotide polymorphisms (SNPs) in 17 cytokine genes were analyzed on 104 Korean children with AITD [Hashimoto's disease (HD) = 44, Graves' disease (GD) = 60 (thyroid-associated ophthalmopathy (TAO) = 29, non-TAO = 31)] and 192 controls. Compared with healthy controls, any significant association with polymorphisms of cytokine genes was not found in HD and GD. Among GD patients, non-TAO group only showed significant associations with IL-12 C allele (rs3212227: A > C) (76.6% vs. 51.6%, OR = 0.3 [0.15-0.71], Pc = 0.007). Particularly, the frequency of IL-12C allele was significantly lower in the non-TAO group than in the TAO group (82.8% vs. 51.6%, Pc = 0.018). Our comprehensive analysis of cytokine gene polymorphisms suggests that IL-12 gene may play impact on specific pathogenesis of ophthalmopathy in Korean children with AITD.

#### <https://www.ncbi.nlm.nih.gov/pubmed/26800664>

#### RESULTS:

Meta-analysis indicated associations between IL‑6 rs1800795, IL‑12B rs3212227, and IL‑18 rs1946518 in all study subjects: IL‑18 rs1946518 in the dominant model (IL‑18 rs1946518: OR = 0.48, 95 % CI: 0.34-0.70, P = 0.000) and the homozygote model (IL‑18 rs1946518: OR = 0.40, 95 % CI: 0.25-0.65, P = 0.000); and IL‑6 rs1800795 and IL‑12B rs3212227 in the dominant model (IL‑6 rs1800795: OR = 0.53, 95 % CI: 0.39-0.72, P = 0.000; IL‑12B rs3212227: OR = 1.26, 95 % CI: 1.06-1.48, P = 0.007; IL‑18 rs1946518: OR = 0.46, 95 % CI: 0.33-0.65, P = 0.000). No significant evidence for associations of IL‑18 rs187238 polymorphisms with BD susceptibility was detected.

#### CONCLUSION:

In summary, this meta-analysis finds that IL‑6 rs1800795 and IL‑18 rs1946518 polymorphisms decrease the risk of BD. However, IL‑12B rs3212227 increases BD susceptibility. Further large-scale investigation of this association is necessary.

<https://www.ncbi.nlm.nih.gov/pubmed/26375522>

A significantly increased risk for RA associated with the IL-12A rs2243115 GG (GG versus TT: OR=4.81, 95% CI 1.33-17.36, P=0.017; and GG versus TG+TT: OR=4.55, 95% CI 1.27-16.36, P=0.020) genotype was evident among rheumatoid factor (RF) negative patients, and with the IL-12B rs3212227 AC (AC versus AA) and AC+CC (AC+CC versus AA) genotypes were evident among older patients (OR=1.48, 95% CI 1.06-2.06, P=0.020), RF positive patients (OR=1.35, 95% CI 1.04-1.75, P=0.026) and anti-cyclic citrullinated peptide antibodies (ACPA) negative patients (OR=1.53, 95% CI 1.11-2.10, P=0.009). The plasma level of IL-12 was significantly higher in RA patients (P<0.001). IL-12 plasma level of IL-12A rs2243115 TT (P<0.001) and IL-12B rs3212227 C allele (P<0.001) were significantly higher in RA patients than controls respectively. The plasma level of IL-12 of RF positive RA patients was significantly higher than RF negative patients (P=0.008), especially in rs3212227 AC patients (P=0.01).

#### CONCLUSIONS:

These findings suggested that the functional single nucleotide polymorphism (SNP) IL-12A rs2243115 GG genotype may increase the risk of RA in RF negative patients, and the IL-12B rs3212227 AC and AC+CC genotypes are associated with RA risk in older patients, RF positive patients and ACPA negative patients. The IL-12A rs2243115 T/G and IL-12B rs3212227 A/C allele might also impact the inflammatory reaction of IL-12 in patients with RA.

<http://www.uniprot.org/uniprot/P29460>

**Interleukin-12 subunit beta**

Cytokine that can act as a growth factor for activated T and NK cells, enhance the lytic activity of NK/lymphokine-activated killer cells, and stimulate the production of IFN-gamma by resting PBMC.1 Publication

Associates with IL23A to form the IL-23 interleukin, a heterodimeric cytokine which functions in innate and adaptive immunity. IL-23 may constitute with IL-17 an acute response to infection in peripheral tissues. IL-23 binds to a heterodimeric receptor complex composed of IL12RB1 and IL23R, activates the Jak-Stat signaling cascade, stimulates memory rather than naive T-cells and promotes production of proinflammatory cytokines. IL-23 induces autoimmune inflammation and thus may be responsible for autoimmune inflammatory diseases and may be important for tumorigenesis.

* [cytokine activity](https://www.ebi.ac.uk/QuickGO/term/GO:0005125) Source: UniProtKB-KW
* [cytokine receptor activity](https://www.ebi.ac.uk/QuickGO/term/GO:0004896) Source: InterPro
* [identical protein binding](https://www.ebi.ac.uk/QuickGO/term/GO:0042802) Source: IntAct
* [interleukin-12 alpha subunit binding](https://www.ebi.ac.uk/QuickGO/term/GO:0042164) Source: AgBase
* [interleukin-12 receptor binding](https://www.ebi.ac.uk/QuickGO/term/GO:0005143) Source: UniProtKB
* [protein heterodimerization activity](https://www.ebi.ac.uk/QuickGO/term/GO:0046982) Source: UniProtKB
* [protein homodimerization activity](https://www.ebi.ac.uk/QuickGO/term/GO:0042803) Source: Ensembl

[View the complete GO annotation on QuickGO ...](http://www.ebi.ac.uk/QuickGO/annotations?geneProductId=P29460)

#### GO - Biological processi

* [cell cycle arrest](https://www.ebi.ac.uk/QuickGO/term/GO:0007050) Source: BHF-UCL
* [cell migration](https://www.ebi.ac.uk/QuickGO/term/GO:0016477) Source: UniProtKB
* [cell proliferation](https://www.ebi.ac.uk/QuickGO/term/GO:0008283) Source: Ensembl
* [cellular response to interferon-gamma](https://www.ebi.ac.uk/QuickGO/term/GO:0071346) Source: Ensembl
* [cellular response to lipopolysaccharide](https://www.ebi.ac.uk/QuickGO/term/GO:0071222) Source: Ensembl
* [cytokine-mediated signaling pathway](https://www.ebi.ac.uk/QuickGO/term/GO:0019221) Source: Reactome
* [defense response to Gram-negative bacterium](https://www.ebi.ac.uk/QuickGO/term/GO:0050829) Source: BHF-UCL
* [defense response to protozoan](https://www.ebi.ac.uk/QuickGO/term/GO:0042832) Source: Ensembl
* [defense response to virus](https://www.ebi.ac.uk/QuickGO/term/GO:0051607) Source: Ensembl
* [interferon-gamma biosynthetic process](https://www.ebi.ac.uk/QuickGO/term/GO:0042095) Source: UniProtKB
* [interleukin-12-mediated signaling pathway](https://www.ebi.ac.uk/QuickGO/term/GO:0035722) Source: Reactome
* [interleukin-23-mediated signaling pathway](https://www.ebi.ac.uk/QuickGO/term/GO:0038155) Source: Reactome
* [natural killer cell activation](https://www.ebi.ac.uk/QuickGO/term/GO:0030101) Source: UniProtKB
* [natural killer cell activation involved in immune response](https://www.ebi.ac.uk/QuickGO/term/GO:0002323) Source: Ensembl
* [negative regulation of growth of symbiont in host](https://www.ebi.ac.uk/QuickGO/term/GO:0044130) Source: Ensembl
* [negative regulation of inflammatory response to antigenic stimulus](https://www.ebi.ac.uk/QuickGO/term/GO:0002862) Source: Ensembl
* [negative regulation of interleukin-10 production](https://www.ebi.ac.uk/QuickGO/term/GO:0032693) Source: BHF-UCL
* [negative regulation of interleukin-17 production](https://www.ebi.ac.uk/QuickGO/term/GO:0032700) Source: BHF-UCL
* [negative regulation of smooth muscle cell proliferation](https://www.ebi.ac.uk/QuickGO/term/GO:0048662) Source: BHF-UCL
* [positive regulation of activated T cell proliferation](https://www.ebi.ac.uk/QuickGO/term/GO:0042104) Source: UniProtKB
* [positive regulation of activation of Janus kinase activity](https://www.ebi.ac.uk/QuickGO/term/GO:0010536) Source: BHF-UCL
* [positive regulation of cell adhesion](https://www.ebi.ac.uk/QuickGO/term/GO:0045785) Source: UniProtKB
* [positive regulation of defense response to virus by host](https://www.ebi.ac.uk/QuickGO/term/GO:0002230) Source: BHF-UCL
* [positive regulation of granulocyte macrophage colony-stimulating factor production](https://www.ebi.ac.uk/QuickGO/term/GO:0032725) Source: BHF-UCL
* [positive regulation of inflammatory response](https://www.ebi.ac.uk/QuickGO/term/GO:0050729) Source: BHF-UCL
* [positive regulation of interferon-gamma biosynthetic process](https://www.ebi.ac.uk/QuickGO/term/GO:0045078) Source: UniProtKB
* [positive regulation of interferon-gamma production](https://www.ebi.ac.uk/QuickGO/term/GO:0032729) Source: UniProtKB
* [positive regulation of interleukin-10 production](https://www.ebi.ac.uk/QuickGO/term/GO:0032733) Source: BHF-UCL
* [positive regulation of interleukin-12 production](https://www.ebi.ac.uk/QuickGO/term/GO:0032735) Source: BHF-UCL
* [positive regulation of interleukin-17 production](https://www.ebi.ac.uk/QuickGO/term/GO:0032740) Source: BHF-UCL
* [positive regulation of lymphocyte proliferation](https://www.ebi.ac.uk/QuickGO/term/GO:0050671) Source: UniProtKB
* [positive regulation of memory T cell differentiation](https://www.ebi.ac.uk/QuickGO/term/GO:0043382) Source: BHF-UCL
* [positive regulation of mononuclear cell proliferation](https://www.ebi.ac.uk/QuickGO/term/GO:0032946) Source: AgBase
* [positive regulation of natural killer cell activation](https://www.ebi.ac.uk/QuickGO/term/GO:0032816) Source: UniProtKB
* [positive regulation of natural killer cell mediated cytotoxicity directed against tumor cell target](https://www.ebi.ac.uk/QuickGO/term/GO:0002860) Source: UniProtKB
* [positive regulation of natural killer cell proliferation](https://www.ebi.ac.uk/QuickGO/term/GO:0032819) Source: BHF-UCL
* [positive regulation of NF-kappaB import into nucleus](https://www.ebi.ac.uk/QuickGO/term/GO:0042346) Source: BHF-UCL
* [positive regulation of NK T cell activation](https://www.ebi.ac.uk/QuickGO/term/GO:0051135) Source: BHF-UCL
* [positive regulation of NK T cell proliferation](https://www.ebi.ac.uk/QuickGO/term/GO:0051142) Source: BHF-UCL
* [positive regulation of osteoclast differentiation](https://www.ebi.ac.uk/QuickGO/term/GO:0045672) Source: BHF-UCL
* [positive regulation of smooth muscle cell apoptotic process](https://www.ebi.ac.uk/QuickGO/term/GO:0034393) Source: BHF-UCL
* [positive regulation of T cell mediated cytotoxicity](https://www.ebi.ac.uk/QuickGO/term/GO:0001916) Source: BHF-UCL
* [positive regulation of T cell proliferation](https://www.ebi.ac.uk/QuickGO/term/GO:0042102) Source: BHF-UCL
* [positive regulation of T-helper 17 cell lineage commitment](https://www.ebi.ac.uk/QuickGO/term/GO:2000330) Source: BHF-UCL
* [positive regulation of T-helper 17 type immune response](https://www.ebi.ac.uk/QuickGO/term/GO:2000318) Source: BHF-UCL
* [positive regulation of T-helper 1 type immune response](https://www.ebi.ac.uk/QuickGO/term/GO:0002827) Source: BHF-UCL
* [positive regulation of tissue remodeling](https://www.ebi.ac.uk/QuickGO/term/GO:0034105) Source: BHF-UCL
* [positive regulation of tumor necrosis factor production](https://www.ebi.ac.uk/QuickGO/term/GO:0032760) Source: BHF-UCL
* [positive regulation of tyrosine phosphorylation of STAT protein](https://www.ebi.ac.uk/QuickGO/term/GO:0042531) Source: BHF-UCL
* [regulation of cytokine biosynthetic process](https://www.ebi.ac.uk/QuickGO/term/GO:0042035) Source: UniProtKB
* [regulation of tyrosine phosphorylation of STAT protein](https://www.ebi.ac.uk/QuickGO/term/GO:0042509) Source: BHF-UCL
* [response to UV-B](https://www.ebi.ac.uk/QuickGO/term/GO:0010224) Source: UniProtKB
* [sensory perception of pain](https://www.ebi.ac.uk/QuickGO/term/GO:0019233) Source: Ensembl
* [sexual reproduction](https://www.ebi.ac.uk/QuickGO/term/GO:0019953) Source: BHF-UCL
* [T-helper 1 cell cytokine production](https://www.ebi.ac.uk/QuickGO/term/GO:0035744) Source: Ensembl
* [T-helper 1 type immune response](https://www.ebi.ac.uk/QuickGO/term/GO:0042088) Source: UniProtKB
* [T-helper cell differentiation](https://www.ebi.ac.uk/QuickGO/term/GO:0042093) Source: UniProtKB

###### [**Immunodeficiency 29 (IMD29)**](http://www.uniprot.org/diseases/DI-04222)**2 Publications**

The disease is caused by mutations affecting the gene represented in this entry.

Disease descriptionA form of Mendelian susceptibility to mycobacterial disease, a rare condition caused by impairment of interferon-gamma mediated immunity. It is characterized by predisposition to illness caused by moderately virulent mycobacterial species, such as Bacillus Calmette-Guerin (BCG) vaccine, environmental non-tuberculous mycobacteria, and by the more virulent Mycobacterium tuberculosis. Other microorganisms rarely cause severe clinical disease in individuals with susceptibility to mycobacterial infections, with the exception of Salmonella which infects less than 50% of these individuals. Clinical outcome severity depends on the degree of impairment of interferon-gamma mediated immunity. Some patients die of overwhelming mycobacterial disease with lepromatous-like lesions in early childhood, whereas others develop, later in life, disseminated but curable infections with tuberculoid granulomas. IMD29 is characterized by undetectable IL12B secretion from leukocytes. Affected individuals generally present with BCG disease after vaccination in childhood, and at least half also have Salmonella infection. Disease phenotype is relatively mild, and patients have a good prognosis.

[See also OMIM:614890](http://www.omim.org/entry/614890)

###### [**Psoriasis 11 (PSORS11)**](http://www.uniprot.org/diseases/DI-02669)

Disease susceptibility is associated with variations affecting the gene represented in this entry.

Disease descriptionA common, chronic inflammatory disease of the skin with multifactorial etiology. It is characterized by red, scaly plaques usually found on the scalp, elbows and knees. These lesions are caused by abnormal keratinocyte proliferation and infiltration of inflammatory cells into the dermis and epidermis.

[See also OMIM:612599](http://www.omim.org/entry/612599)

|  |  |
| --- | --- |
| DrugBanki | [DB02763](https://www.drugbank.ca/drugs/DB02763) 5-Mercapto-2-Nitro-Benzoic Acid [DB05459](https://www.drugbank.ca/drugs/DB05459) Briakinumab [DB05848](https://www.drugbank.ca/drugs/DB05848) humanized SMART Anti-IL-12 Antibody [DB05679](https://www.drugbank.ca/drugs/DB05679) Ustekinumab |

<https://www.ncbi.nlm.nih.gov/gene/3593>

This gene encodes a subunit of interleukin 12, a cytokine that acts on T and natural killer cells, and has a broad array of biological activities. Interleukin 12 is a disulfide-linked heterodimer composed of the 40 kD cytokine receptor like subunit encoded by this gene, and a 35 kD subunit encoded by IL12A. This cytokine is expressed by activated macrophages that serve as an essential inducer of Th1 cells development. This cytokine has been found to be important for sustaining a sufficient number of memory/effector Th1 cells to mediate long-term protection to an intracellular pathogen. Overexpression of this gene was observed in the central nervous system of patients with multiple sclerosis (MS), suggesting a role of this cytokine in the pathogenesis of the disease. The promoter polymorphism of this gene has been reported to be associated with the severity of atopic and non-atopic asthma in children.