

GEPHE SUMMARY

IL4 (<a +il4+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^IL4^#gephebase-summary-title)	Gephebase Gene	GepheID	
		GP00000497	
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

		Trait Category	
Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)		Trait	
Immune response (<a +immune+response+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait=^Immune response^#gephebase-summary-title)		Trait State in Taxon A	
Homo sapiens		Trait State in Taxon B	
Homo sapiens		Ancestral State	
Data not curated		Taxonomic Status	
Intraspecific (<a +intraspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)			
Taxon A		Taxon B	
Homo sapiens		Homo sapiens	
(https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Homo sapiens^#gephebase-summary-title)		(https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Homo sapiens^#gephebase-summary-title)	
Common Name		Common Name	
human		human	
Synonyms		Synonyms	
human; man; Homo sapiens Linnaeus, 1758; Home sapiens; Homo sampiens; Homo sapeins; Homo sapian; Homo sapians; Homo sapien; Homo sapience; Homo sapiense; Homo sapients; Homo sapines; Homo spaiens; Homo spiens; Humo sapiens		human; man; Homo sapiens Linnaeus, 1758; Home sapiens; Homo sampiens; Homo sapeins; Homo sapian; Homo sapians; Homo sapien; Homo sapience; Homo sapiense; Homo sapients; Homo sapines; Homo spaiens; Homo spiens; Humo sapiens	
Rank		Rank	
species		species	
Lineage		Lineage	
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Euarchontoglires; Primates; Haplorrhini; Simiiformes; Catarrhini; Hominoidea; Hominidae; Homininae; Homo		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Euarchontoglires; Primates; Haplorrhini; Simiiformes; Catarrhini; Hominoidea; Hominidae; Homininae; Homo	
Parent		Parent	
Homo () - (Rank: genus)		Homo () - (Rank: genus)	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9605)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9605)	
NCBI Taxonomy ID		NCBI Taxonomy ID	
9606		9606	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9606)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9606)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
No		No	

GENOTYPIC CHANGE

		Generic Gene Name	
IL4		P05112 (http://www.uniprot.org/uniprot/P05112)	
		Synonyms	
BSF1; IL-4; BCGF1; BSF-1; BCGF-1		GenebankID or UniProtKB	
		M23442 (https://www.ncbi.nlm.nih.gov/nuccore/M23442)	
		String	
9606.ENSPO0000231449			
(http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPO0000231449)			
		Sequence Similarities	
Belongs to the IL-4/IL-13 family.			
		GO - Molecular Function	
GO:0005125 : cytokine activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005125)			
GO:0008083 : growth factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008083)			
GO:0005136 : interleukin-4 receptor binding			
(https://www.ebi.ac.uk/QuickGO/term/GO:0005136)			

GO - Biological Process

GO:0006955 : immune response (<https://www.ebi.ac.uk/QuickGO/term/GO:0006955>)

GO:0043066 : negative regulation of apoptotic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043066>)

GO:0045944 : positive regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)

GO:0045892 : negative regulation of transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045892>)

GO:0045893 : positive regulation of transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045893>)

GO:0008203 : cholesterol metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008203>)

GO:0010628 : positive regulation of gene expression
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010628>)

GO:0019221 : cytokine-mediated signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0019221>)

GO:0120162 : positive regulation of cold-induced thermogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0120162>)

GO:0042976 : activation of Janus kinase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042976>)

GO:0042531 : positive regulation of tyrosine phosphorylation of STAT protein
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042531>)

GO:0050776 : regulation of immune response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0050776>)

GO:0030183 : B cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030183>)

GO:0045189 : connective tissue growth factor biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045189>)

GO:0097028 : dendritic cell differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0097028>)

GO:0043011 : myeloid dendritic cell differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043011>)

GO:1903660 : negative regulation of complement-dependent cytotoxicity
(<https://www.ebi.ac.uk/QuickGO/term/GO:1903660>)

GO:2000352 : negative regulation of endothelial cell apoptotic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:2000352>)

GO:0010633 : negative regulation of epithelial cell migration
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010633>)

GO:0045671 : negative regulation of osteoclast differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045671>)

GO:0030890 : positive regulation of B cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030890>)

GO:0032736 : positive regulation of interleukin-13 production
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032736>)

GO:0048295 : positive regulation of isotype switching to IgE isotypes
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048295>)

GO:0048304 : positive regulation of isotype switching to IgG isotypes
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048304>)

GO:0016239 : positive regulation of macroautophagy
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016239>)

GO:0045348 : positive regulation of MHC class II biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045348>)

GO:0045582 : positive regulation of T cell differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045582>)

GO:0042102 : positive regulation of T cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042102>)

GO:0045191 : regulation of isotype switching
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045191>)

GO:0042325 : regulation of phosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042325>)

GO:0042110 : T cell activation (<https://www.ebi.ac.uk/QuickGO/term/GO:0042110>)

GO:0035745 : T-helper 2 cell cytokine production
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035745>)

GO:0042092 : type 2 immune response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042092>)

GO - Cellular Component

GO:0005576 : extracellular region (<https://www.ebi.ac.uk/QuickGO/term/GO:0005576>)

GO:0005615 : extracellular space (<https://www.ebi.ac.uk/QuickGO/term/GO:0005615>)

Presumptive Null

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null="No" #gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive Null=))

Molecular Type

Cis-regulatory ([https://www.gephebase.org/search-criteria?/and+Molecular Type="Cis-regulatory" #gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular Type=))

Aberration Type

SNP ([https://www.gephebase.org/search-criteria?/and+Aberration Type="SNP" #gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration Type=))

Molecular Details of the Mutation

_524T promoter single base-pair substitution affecting binding of the NFAT transcription factor

Experimental Evidence

Linkage Mapping ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence="Linkage Mapping" #gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental Evidence=))

Main Reference

Positive selection on a human-specific transcription factor binding site regulating IL4 expression. (2003) (<https://pubmed.ncbi.nlm.nih.gov/14654003>)

Authors

Rockman MV; Hahn MW; Soranzo N; Goldstein DB; Wray GA

Abstract

A single nucleotide polymorphism in the promoter of the multifunctional cytokine Interleukin 4 (IL4) affects the binding of NFAT, a key transcriptional activator of IL4 in T cells. This regulatory polymorphism influences the balance of cytokine signaling in the immune system, with important consequences-positive and negative-for human health. We determined that the NFAT binding site is unique to humans; it arose by point mutation along the lineage separating humans from other great apes. We show that its frequency distribution among human subpopulations has been shaped by the balance of selective forces on IL4's diverse roles. New statistical approaches, based on parametric and nonparametric comparisons to neutral variants typed in the same individuals, indicate that differentiation among subpopulations at the IL4 promoter polymorphism is too great to be attributed to neutral drift. The allele frequencies of this binding site represent local adaptation to diverse pathogenic challenges; disease states associated with the common derived allele are side-effects of positive selection on other IL4 functions.

Additional References

RELATED GEPHE

Related Genes

2 (TLR6-TLR1-TLR10 cluster, interleukin-4) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~9606~/and+Trait=Immune response/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS