

Introduction

Description

Interferon regulatory factor 1, a transcription factor that acts in toll-like receptor signaling, JAK-STAT cascade, antiapoptosis, and inflammatory response, aberrantly expressed in psoriasis and sclerosis; mRNA is downregulated in leukemia

Gene symbol

IRF1



Synonyms

MAR; IRF1; ISGF2; IRF-1; Interferon regulatory factor 1

Gene Ontology [what is this?](#)

Molecular function

glucocorticoid receptor binding [E], transcription factor activity, sequence-specific DNA binding [E] [details](#)

Biological process

cell growth [E, P], cellular process [E], immune response [P], inflammatory response [P], JAK-STAT cascade [E], nitric oxide biosynthetic process [P]... [details](#)

Cellular component

cytosol [Y], nucleoplasm [Y], nucleus [E] [details](#)

Orthologs & Molecular Hierarchy [what is this?](#)

Hierarchy of orthologous relationships for this locus

[+](#) View orthologous relationships

Biomarker Associations [what is this?](#)

Diseases associated with IRF1 (22 entries)

Show entries

Search:

	Type of Association	Indication

[Table of Contents](#) ↓

Stomach Neoplasms	9 associations	5 associations	4 associations			5 associations	
Asthma	7 associations	2 associations	5 associations			2 associations	
COVID-19	5 associations		5 associations				5 associations
Psoriasis	4 associations		3 associations		1 associations		
Ovarian Neoplasms	3 associations		3 associations				

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GENE

Mutations

Inherited IRF1 mutations

The [Human Gene Mutation Database \(HGMD®\) report](#) provides information on the following inherited IRF1 mutations (subscription required):

Mutation Type	Count	Mutation Type	Count
Missense/nonsense	0	Small indels	0
Splicing	0	Gross deletions	0
Regulatory	2	Gross insertions	0
Small deletions	0	Complex rearrangements	0
Small insertions	0	Repeat variations	0

Mutant Phenotype [what is this?](#)

Mutant phenotype of closely related homolog(s)

Mouse **Irf1** (76.0% identity to Human IRF1 [1e-147])

Viability effects : decreased viability; increased viability; inviable [details](#)

Anatomical effects : B-lymphocytes; blood; bone marrow; brain; central nervous system; chondrocytes; colon/large intestine; fibroblasts; glial cells; heart; hepatocytes ... [details](#)

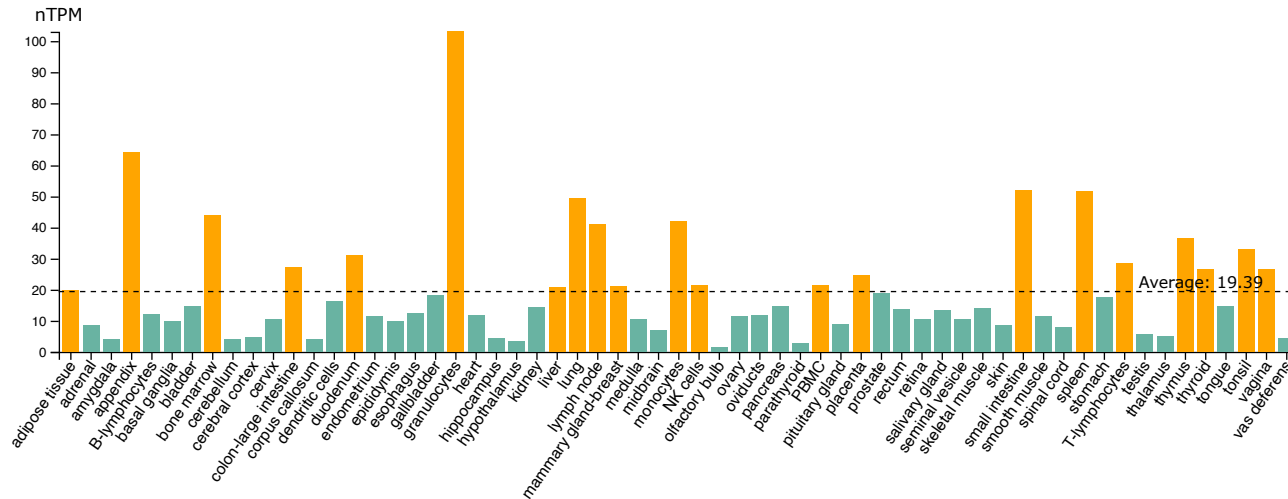
Physiological effects : anti-bacterial response; anti-pathogen response; anti-viral response; cell adhesion; cell cycle control; cell death/apoptosis; cell migration; DNA repair; drug response; immunity and inflammation; infertile ... [details](#)

Expression [what is this?](#)

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Relative tissue specificity: 0.08

Sorting: Alphabetical ▾



+ View organ or tissue, cell type, and tumor type entries in detail

Regulation of IRF1 expression

Proteins, complexes, or pathways that influence IRF1 expression (14 entries)

Show 5 ▾ entries Search:

Regulator details	Effect
C/EBPdelta	Upregulated by
cd40	Upregulated by
IFNgamma	Upregulated by
IFNGR	Upregulated by
IL-10	Upregulated by

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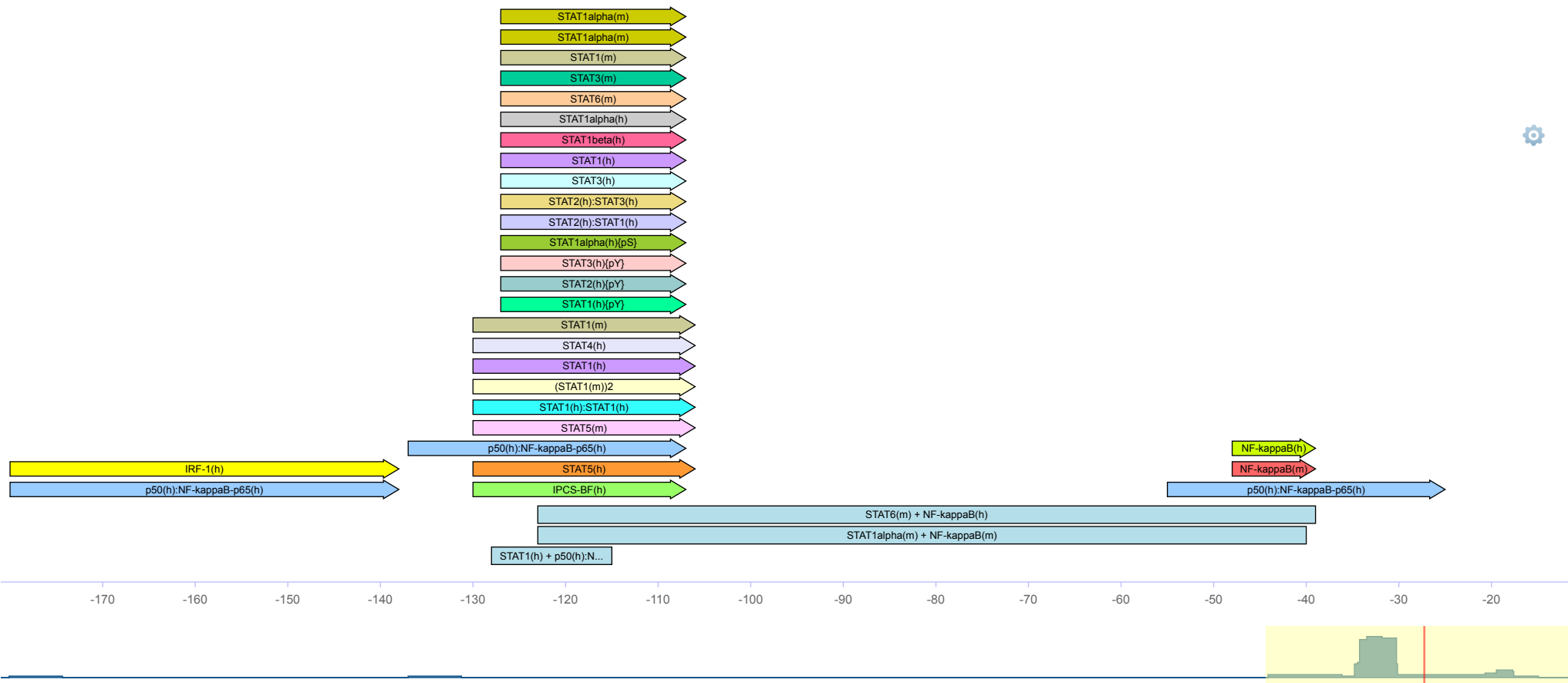
Transcriptional Regulation [what is this?](#)

Regulation of IRF1 gene expression

Analyze IRF1 with MATCH Suite →

Best supported : [PM001006905](#)

All promoters for the gene : [PM001006907](#), [PM001006906](#), [PM001006905](#)



Viewing nucleotides -181 to 1

* Note: Only binding sites whose location is relative to the TSS are graphically displayed. Binding sites with an asterisk (*) are not included in the graphical display.

Transcription factor binding sites within the IRF1 gene (59 entries)

Show **5** entries

Search:

Identifier	Relative Location	Genomic Location	Binding Factor(s)	DNA Binding Reaction	Effect
HS\$IRF1_15	-180 to -138	Chr5 132490913 132490955 -	IRF-1(h)	IRF-1(h) --> IRF1(h)	DNA binding

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HS\$IRF1_07	-130 to -106	Chr5 132490881 132490905 -	STAT5(h)	STAT5(h) --> IRF1(h)	DNA binding
HS\$IRF1_07	-130 to -106	Chr5 132490881 132490905 -	STAT5(m)	STAT5(m) --> IRF1(h)	DNA binding

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Composite element binding sites within the IRF1 gene (3 entries)

Show 5 entries

Search:

Identifier	Relative Location	Genomic Location	Factors	Type
C00544	-128 to -115	Chr5:132490889..132490902	STAT1(h), p50(h):NF-kappaB-p65(h)	synergism
C00307	-123 to -39	Chr5:132490814..132490898	NF-kappaB(h), STAT6(m)	antagonism
C00192	-123 to -40	Chr5:132490814..132490898	NF-kappaB(m), STAT1alpha(m)	synergism

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In vivo fragments within the promoter(s) of the IRF1 gene that are bound by transcription factors (0 entries)

Show 5 entries

Search:

Promoter	Transcription Factor	Genomic Location	Cell Source	Matrix	Relative Location	CSS	MSS	Sequence	Reference
Loading...									

Showing 0 to 0 of 0 entries

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Predicted enhancers / silencers for IRF1 regulation (22 entries)

Show 5 entries

Search:

Accession	Effect	Chromosomal location	Length (bp)	Identification method	Active in tissue (cell type or line)	Reference
EN000047302	activation	chr5:132019986..132020067	82	pair-wise expression correlation with RefSeq promoter, pair-wise expression correlation with robust FANTOM5 promoter	blood (natural killer cells), blood (T cells), cartilage (chondrocytes), neurons (neuronal stem cell)	FANTOM5 ↗
EN000047303	activation	chr5:132020286..132020469	184	pair-wise expression correlation with RefSeq promoter, pair-wise expression correlation with robust FANTOM5 promoter	blood (natural killer cells), blood (T cells), cartilage (chondrocytes), neurons (neuronal stem cell)	FANTOM5 ↗

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EN000047305	activation	chr5:132069604..132069783	180	promoter pair-wise expression correlation with RefSeq promoter	blood (monocytes)	FANTOM5 ↗
EN000047308	activation	chr5:132094304..132095137	834	pair-wise expression correlation with RefSeq promoter, pair-wise expression correlation with robust FANTOM5 promoter	blood (monocytes), fat (preadipocyte)	FANTOM5 ↗

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Translational Regulation [what is this?](#)

Regulation of IRF1 mRNA expression

miRNA binding sites within IRF1 mRNA (15 entries)

Show entriesSearch:

Identifier	Region	Location	Location Reference Point	Binding Factor(s)
HS\$IRF1_05	3' UTR	609 to 615	stop codon	hsa-miR-203a-3p(h)
HS\$IRF1_06	3' UTR	638 to 644	stop codon	hsa-miR-203a-3p(h)
HS\$IRF1_17	3' UTR	602 to 624	stop codon (end of coding sequence (CDS))	hsa-miR-383-5p(h)
HS\$IRF1_18	3' UTR	473 to 494	stop codon (end of coding sequence (CDS))	hsa-miR-23a-3p(h)
HS\$IRF1_19	3' UTR	383 to 402	stop codon (end of coding sequence (CDS))	hsa-miR-130b-3p(h)

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RNA Features [what is this?](#)

Overview of RNA sequence

Nucleotide Sequence : CGAGCCC...AATTGTT (1..2035; 2035 nt) [details](#)

Sequence source : RefSeq:NM_002198

[FASTA](#) ↓

Drug Interactions [what is this?](#)**Drug(s) targeting IRF1 (1 entry)**



Show 5 entries Search:

Drug(s)	Status	Interaction Data Source	Reference(s)
Cyc065	small molecule, investigational	DrugBank ↗	29137393 ↗

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Pathways & Interactions [what is this?](#)**Pathways****Canonical pathways assembled from experiments involving orthologous proteins (2 entries)**



Show 5 entries Search:

Name	View Supporting Reactions	View Graphic Representation	Load in PathFinder
IFNgamma signaling	View Supporting Reactions	View Graphic Representation	 Load in PathFinder →
TLR9 pathway	View Supporting Reactions	View Graphic Representation	 Load in PathFinder →

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Subcomponents assembled from experiments involving orthologous proteins (2 entries)

Show 5 entries Search:

Name	View Supporting Reactions	View Graphic Representation	Load in PathFinder
STAT1 ---IRF-1---> IRF2	View Supporting Reactions		 Load in PathFinder →
TLR9 ---IRF-1---> NOS2, IFNB1, IL12A	View Supporting Reactions		 Load in PathFinder →

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Pathways from Reactome (10 entries)

Provided by the [Reactome](#) database, release 81 ([ReactomePathways.gmt ↗](#)).

Show 5 entries Search:

Name	Reactome pathway report link	Reactome pathway browser link
Cytokine Signaling in Immune system	R-HSA-1280215 ↗	Open in Reactome Browser ↗
Factors involved in megakaryocyte development and platelet production	R-HSA-983231 ↗	Open in Reactome Browser ↗
Hemostasis	R-HSA-109582 ↗	Open in Reactome Browser ↗

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Pathways from WikiPathways (7 entries)

Provided by the WikiPathways database.

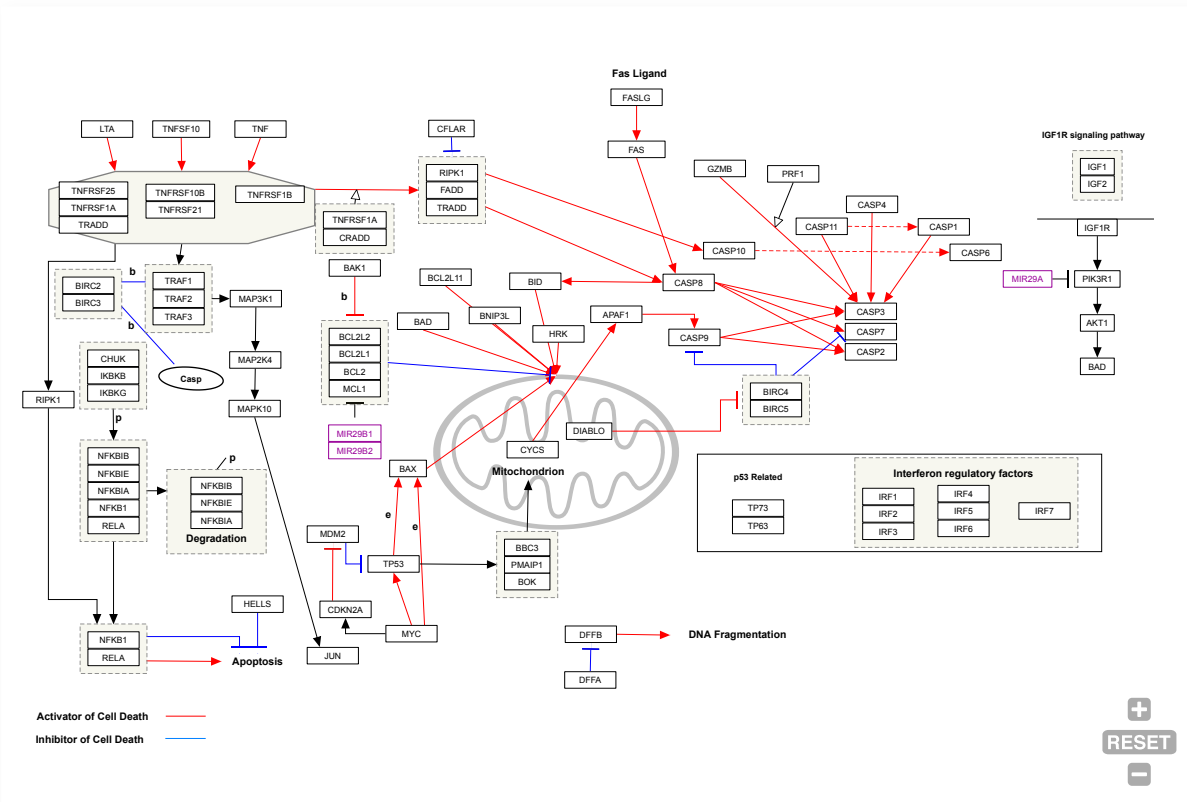
Show 5 entries

Search:

Name	Display below	WikiPathways external link
Apoptosis	View ↗	WikiPathways ↗
IL-18 signaling pathway	View ↗	WikiPathways ↗
IL6 signaling pathway	View ↗	WikiPathways ↗
Immune response to tuberculosis	View ↗	WikiPathways ↗
miRNAs involvement in the immune response in sepsis	View ↗	WikiPathways ↗

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[+](#) Protein-protein associations (8 partners)

Events acting on IRF1

- [+](#) Proteins or complexes that phosphorylate IRF1 (4 partners)
- [+](#) Proteins or complexes that affect IRF1 in other ways (76 partners)

Events triggered by IRF1

- [+](#) Proteins or complexes affected by IRF1 in other ways (227 partners)

Genes regulated (directly or indirectly) by IRF1

Show entries Search:

Gene details	Effect
ANXA2	Downregulated by
BAX	Downregulated by
BIRC5	Downregulated by
BRIP1	Upregulated by
CD38	Upregulated by

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Transcription Factor Activity [what is this?](#)

Regulation of gene expression by IRF1

Transcription factor classification :

IRF-1; [3.5.3.0.1](#)

Tryptophan cluster factors; [3.5](#) (The tryptophan clusters comprise several tryptophan residues with a spacing of 12-21 amino acid residues; the subclass of myb-type DNA-binding domains typically exhibit a spacing of 19-21 amino acid residues. All IRF family members, except IRF-1 and IRF-2, contain conserved IAD, IRF association domain that is responsible for protein-protein interactions with other IRF family members or with Ets factor PU.1 and/or bHLH factor E47. IRF-1 and IRF-2 contain IAD2 that is conserved between them and, like IAD, involved in protein-protein interactions.)

IRF1 binding sites in gene promoters and enhancers, experimentally proven (104 entries)

Show entries Search:

Gene	Location within Gene	Binding Site Identifier	DNA Binding Reaction	Effect	Quality Score
APOL1(h)	-45 to -28	HS\$APOL1_01	IRF-1(h) --> APOL1(h)	transactivation	3
B2M(h)		HS\$B2M_03	IRF-1(h) --> B2M(h)	DNA binding	3
B2M(h)		HS\$B2M_04	IRF-1(h) --> B2M(h)	DNA binding	3
BLMH(h)	-130 to -119	HS\$BLMH_03	IRF-1(h) --> BLMH(h)	DNA binding	5
CASP8(h)	-38 to -13	HS\$CASP8_03	IRF-1(h) --> CASP8(h)	transactivation	3

Composite regulatory elements with IRF1 (4 entries)

Show 5 entries

Search:

Gene	Identifier	Relative Location	Genomic Location	Factors	Type
CYBB	C00249	-63 to -50	ChrX:37780003..37780016	IRF-1(h) , IRF-8(h) , PU.1(m) , PU.1-isoform1(h)	synergism
CYBB	C00386	-104 to -82	ChrX:37779962..37779984	IRF-1(h) , STAT1alpha(h)	synergism
H2-L	C00340	-172 to -144	Chr17:35481899..35481927	IRF-1(h) , NF-kappaB(h) , NF-kappaB-p65-isoform1(h)	synergism
IDO1	C00300	-449 to -402	Chr8:39912765..39912812	IRF-1(h) , STAT1alpha(h)	synergism

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Artificial sites bound by IRF1 (7 entries)

Show 5 entries

Search:

Description	Binding Site Identifier	Quality Score
artificial sequence	AS\$IRF_01	3
artificial sequence	AS\$IRF_02	4
Artificial sequence	AS\$IRF_03	3
Artificial sequence	AS\$IRF1_23	3
Artificial sequence	AS\$IRF1_24	4

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ChIP-seq or similar experiments for IRF1 (9 entries)

Show 5 entries

Search:

ChIP Experiment Report	Chromosome	Binding Fragments	Cell	Reference
View Report	Human Genome	1299	K562 + IFN-alpha (30min)	ENCODE Data 22955616
View Report	Human Genome	8349	K562 + IFN-alpha (6h)	ENCODE Data 22955616
View Report	Human Genome	10318	K562 + IFN-gamma (30min)	ENCODE Data 22955616
View Report	Human Genome	12570	K562 + IFN-gamma (6h)	ENCODE Data 22955616
View Report	Human Genome	13280	K562	ENCODE Data 22955616

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Positional weight matrices for IRF1 (10 entries)

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	V\$IRF1_Q6	factor-specific	matrix compiled from individual genomic sites
	V\$IRF_Q6	family	matrix compiled from individual genomic sites
	V\$IRF_Q6_01	family	matrix compiled from individual genomic sites
	V\$IRF1_03	factor-specific, recommended by evaluation	ChIP-Seq

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IRF1 consensus site (2 entries)

Show 5 entries

Search:

Description	Binding Site Identifier	Quality Score
consensus	ISGF2\$CONS	6
consensus	IRF1\$CONS_01	6

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Transcription factors which interact with IRF1

Show 5 entries

Search:

Species	Factor
Human	ARID1A, ARID1B, ARID2, DPF1, DPF2, E2F-6, IRF-9, KLF11-isoform1, L3MBTL2, Mad5, PB-1, SATB-2, SMARCA2, SMARCD1, SS18, STAT1

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Protein Features [what is this?](#)

Overview of protein sequence and structure

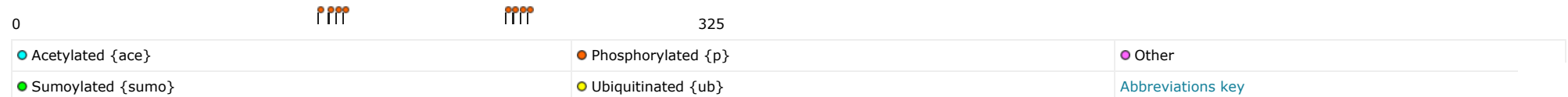
Chromosome : 5q31.1

Isoforms : [IRF-1](#)

+ View associated sequences and their domains

+ View related proteins

Post-translational modifications of IRF1 protein



View complexes containing IRF1 protein

+ View complexes (37 entry)

Annotations [what is this?](#)

Display all annotations

Description

- Interferon regulatory factor 1, a transcription factor that acts in toll-like receptor signaling, JAK-STAT cascade, antiapoptosis, and inflammatory response, aberrantly expressed in psoriasis and sclerosis; mRNA is downregulated in leukemia [11278357](#) [8438156](#) [18216101](#) [9389691](#) [10954537](#) [2475256](#) [9202213](#)

Editor's Notes

- IFN γ induced IRF-1 protein expression was suppressed in TGF β 1 treated HEp-2 cells but not in THP-1 cells [17371985](#)
- Inducible by alpha and gamma interferons and virus infection, ubiquitously expressed factor.

Function

- Activated by ISGF3 and thus being a target gene of STAT1 [8306959](#) [7507207](#)
- Cooperates with STAT-1 α for IFN- γ -dependent gene induction in myeloid cells [11781315](#)
- Deleted in some leukemias and myelodysplasias showing cytogenetic abnormalities of chromosome 5 [8438156](#)
- Inducible by IFN- γ (and weakly by IFN- α) through an inverted GAAANN repeat, no autoregulation observed [7678055](#)
- Inducible by IL-6 [8168491](#)

more

Domains

- HTH, Tryptophan clusters, IRF family
- IAD2 domain is conserved between IRF-1 and IRF-2, but is different in other family members [10586038](#)
- IAD2 is responsible for protein-protein interactions [10586038](#)
- M-form appears as 56-kDa protein

Disease related

- De novo synthesis and nuclear translocation is induced by infection with respiratory syncytial virus (RSV) and this translocation is inhibited by the antioxidant butylated hydroxyanisole [11259439](#)
- Decreased mRNA expression correlates with risk of recurrence of breast cancer [19697121](#)
- Gene deletion is associated with leukemia and myelodysplasia [8438156](#)
- Increased expression correlates with acute coronary syndrome [20177960](#)
- Increased mRNA expression correlates with chronic hepatitis C [19858727](#)

Accessions mapped to this record

BIOBASE gene accession : GN000007328, G000324, MO000022842

BIOBASE protein accession : PR000014130, f00254, MO000007686, MO000480730, MO000481834, T00423

Gene

Affymetrix	11716733_at, 11716734_at, 11754035_a_at, 11761782_at, 16999773, 16999776, 202531_at, 238725_at, 2875331, 2875332, 2875337, 2875338, 2875339, 2875340, 2875342, 2875347, 2875349, 2875350, 2875351, 2875352, 2875353, 2875354, 2875355, 2875356, 2875357, 2875358, 2875359, 2875360, 2875361, 2875362, 2875363, 2875364, 2875365, 2875366, 2875367, 2875368, 2875369, 2875370, 2875371, 2875372, 2875373, 2875374, 2875375, 46648_g_at, 59777_at, 669_s_at, 8114010, g4504720_3p_at, Hs.180559.0.A1_3p_at, L05072_s_at, TC05001767.hg, TC05001768.hg,
Agilent	A_19_P00318006
Ensembl	ENSG00000125347 , ENST00000245414 , ENST00000405885 , ENST00000437654 , ENST00000439555 , ENST00000443093 , ENST00000458069 , ENST00000459982 , ENST00000463784 , ENST00000472045 , ENST00000476613 , ENST00000493208 , ENST00000613424 , ENST00000679440 , ENST00000679499 , ENST00000679500 , ENST00000679522 , ENST00000679620 , ENST00000679633 , ENST00000679700 , ENST00000679743 , ENST00000679762 , ENST00000679786 , ENST00000679820 , ENST00000679860 , ENST00000679921 , ENST00000679945 , ENST00000679964 , ENST00000680139 , ENST00000680237 , ENST00000680352 , ENST00000680380 , ENST00000680562 , ENST00000680594 , ENST00000680796 , ENST00000680848 , ENST00000680903 , ENST00000681049 , ENST00000681197 , ENST00000681240 , ENST00000681336 , ENST00000681458 , ENST00000681462 , ENST00000681573 , ENST00000681584 , ENST00000681595 , ENST00000681603 , ENST00000681634 , ENST00000681694 , ENST00000681715 , ENST00000681749
EntrezGene	3659
Genbank	111117523 , 14550468 , 184648 , 2731598 , 4504720 , 49456386 , 54696375 , 54696377 , 580208 , 58737030 , 62088827 , AB103081 , AB209624 , AC003959 , BC009483 , BT019755 , BT019756 , CR541713 , DQ789232 , L05072 , NM_002198 , X14454
HGMD	IRF1
HumanProteinAtlas	ENSG00000125347
Illumina	0007100435, ILMN_1708375
OMIM	147575
Pfam	PF08368
RefSeq	NM_001354924.1 , NM_001354925.1 , NM_002198.3 , NP_001341853.1 , NP_001341854.1 , NP_002189.1 , NR_149068.1 , NR_149069.2 , XM_011543379.2 , XP_011541681.1
UniGene	Hs&436061
WikiPathways	WP2037 , WP254 , WP364 , WP4197 , WP4329 , WP4754 , WP619

mRNA

Pfam	PF11390
-------------	-------------------------

Protein

PROSITE	PS00601
Pfam	PF11510
UniProt	P10914

References (321 entries)

Show 5 entries

Search:

Sl.No	PMID	Citation
1	35140242	Human transcription factor protein interaction networks. 13 766 (2022) Show abstract
2	33531712	Flament, H, Rouland, M, Beaudoin, L, Toubal, A, Bertrand, L, Lebourgeois, S, Rousseau, C, Soulard, P, Gouda, Z, Cagninacci, L, Monteiro, AC, Hurtado-Nedelec, M, Luce, S, Bailly, K, Andrieu, M, Saintpierre, B, Letourneur, F, Jouan, Y, Si-Tahar, M, Baranek, T, Paget, C, Boitard, C, Vallet-Pichard, A, Gautier, JF, Ajzenberg, N, Terrier, B, Pene, F, Ghosn, J, Lescure, X, Yazdanpanah, Y, Visseaux, B, Descamps, D, Timsit, JF, Monteiro, RC, Lehuen, A, Outcome of SARS-CoV-2 infection is linked to MAIT cell activation and cytotoxicity. Nat Immunol 22 (3) 322-335 (2021) Show abstract
3	33278357	Karki, R, Sharma, BR, Tuladhar, S, Williams, EP, Zalduondo, L, Samir, P, Zheng, M, Sundaram, B, Banoth, B, Malireddi, RKS, Schreiner, P, Neale, G, Vogel, P, Webby, R, Jonsson, CB, Kanneganti, TD, Synergism of TNF- α and IFN- γ Triggers Inflammatory Cell Death, Tissue Damage, and Mortality in SARS-CoV-2 Infection and Cytokine Shock Syndromes. Cell 184 (1) 149-168 (2021) Show abstract
4	33248817	Vadillo, E, Taniguchi-Ponciano, K, Lopez-Macias, C, Carvente-Garcia, R, Mayani, H, Ferat-Osorio, E, Flores-Padilla, G, Torres, J, Gonzalez-Bonilla, CR, Majluf, A, Albarran-Sanchez, A, Galan, JC, Pe?a-Martinez, E, Silva-Roman, G, Vela-Pati?o, S, Ferreira-Hermosillo, A, Ramirez-Renteria, C, Espinoza-Sanchez, NA, Pelayo-Camacho, R, Bonifaz, L, Arriaga-Pizano, L, Mata-Lozano, C, Andonegui-Elguera, S, Wachter, N, Blanco-Favela, F, De-Lira-Barraza, R, Villanueva-Compean, H, Esquivel-Pineda, A, Ramirez-Montes-de-Oca, R, Anda-Garay, C, Noyola-Garcia, M, Guizar-Garcia, L, Cerbulo-Vazquez, A, Zamudio-Meza, H, Marrero-Rodriguez, D, Mercado, M, A Shift Towards an Immature Myeloid Profile in Peripheral Blood of Critically Ill COVID-19 Patients. Arch Med Res - (2020) Show abstract
5	29126285	ReMap 2018: an updated atlas of regulatory regions from an integrative analysis of DNA-binding ChIP-seq experiments. Nucleic Acids Res 46 D267-D275 (2018) Show abstract

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