

Introduction

Description

Nuclear receptor subfamily 4 group A member 3, a transcription factor that acts in cell cycle, apoptosis, and embryonic development, downregulated in acute myeloid leukemia and atherosclerosis; genetic translocation correlates with chondrosarcoma

Gene symbol

NR4A3

Synonyms

(CHN); (TEC); (NOR1); CSMF; NOR-1; NR4A3; (MINOR); RP11-60I3.3; neuron derived orphan receptor; nuclear hormone receptor NOR-1; neuron-derived orphan receptor 1; nuclear receptor subfamily 4 group A member 3; nuclear receptor subfamily 4, group A, member 3

Gene Ontology [what is this?](#)

Molecular function

binding [S], RNA polymerase II transcription factor activity, ligand-activated sequence-specific DNA binding, steroid hormone receptor activity [S]... [details](#)

Biological process

cell death [E], inflammatory response [P], intracellular steroid hormone receptor signaling pathway [S], phosphatidylinositol 3-kinase signaling [E]... [details](#)

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

Hierachy of orthologous relationships for this locus

+ View orthologous relationships

Biomarker Associations [what is this?](#)

Diseases associated with NR4A3 (21 entries)

Show 5 entries

Search:

Disease details-all	Significance	Type of Association				Indication		
		Causal 3 associations	Correlative 41 associations	Preventative 1 associations	Negative	Disease Mechanism 3 associations	Prognosis 5 associations	Therapeutic Target 1 associations
Chondrosarcoma	13 associations	2 associations	11 associations			2 associations	4 associations	

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Atherosclerosis	4 associations		4 associations				
Leiomyoma	3 associations		3 associations				
Soft Tissue Neoplasms	2 associations	1 associations	1 associations			1 associations	

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GENE

Mutant Phenotype [what is this?](#)

Mutant phenotype of closely related homolog(s)



- Mouse **Nr4a3** (73.1% identity to Human NR4A3 [0.0])
- Anatomical effects : brain; dentate gyrus; ear; hippocampus; neurons; pyramidal cells [details](#)
- Physiological effects : cell death/apoptosis; motor function [details](#)
- C. elegans **nhr-6** (77.1% identity to Human NR4A3 [6e-35])

Show

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Search:

Phenotypic effect details	Mutation type
Gonad development is defective	RNAi
Gonad development is defective	Recessive

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Expression [what is this?](#)

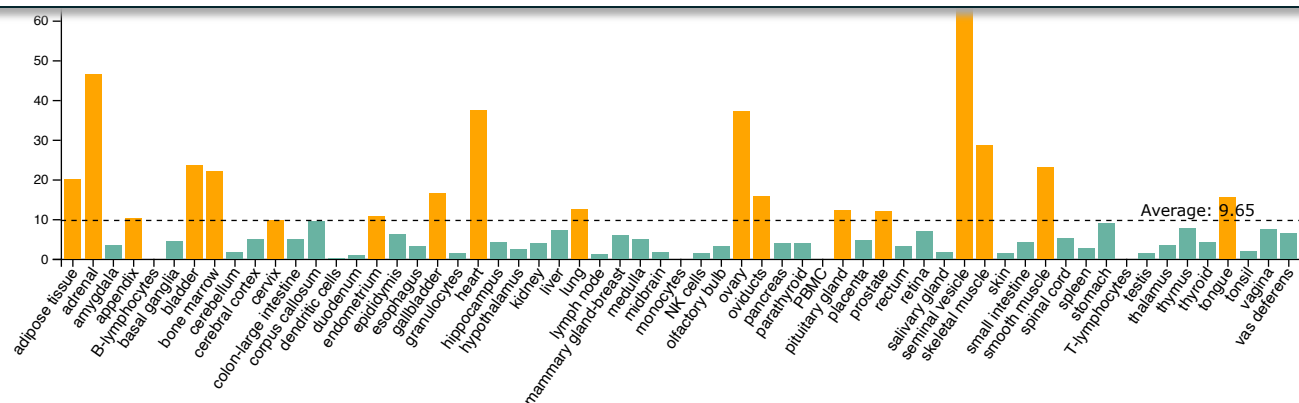
Tissue expression

Consensus normalized transcript expression levels provided by Human Protein Atlas (v20)

Relative tissue specificity: 0.15

Sorting:

Alphabetical



Proteins, complexes, or pathways that influence NR4A3 expression (1 entry)

Search:

Regulator details	Effect
VEGF-A	Upregulated by

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what is this?

Analyze NR4A3 with MATCH Suite →

Predicted promoter sequences :  Match →

All promoters for the gene : [PM000910856](#), [PM000582174](#)



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Search:

Identifier	Relative Location	Genomic Location	Binding Factor(s)	DNA Binding Reaction	Effect
HS\$NR4A3_01	-83 to -42	Chr9 99821772 99821814 +	CREB(h)	CREB(h) --> NR4A3(h)	DNA binding

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In vivo fragments within the promoter(s) of the NR4A3 gene that are bound by transcription factors (3080 entries)

Show 5 entries

Search:

Promoter	Transcription Factor	Genomic Location	Cell Source	Matrix	Relative Location	CSS	MSS	Sequence	Reference
PM000910856	CUX-1(h)	9:99811712..99811963	GM12878	V\$CDP_Q6_01	-10212	0.953	0.956	TATTGCTCAATGA	ENCODE Data 22955616
PM000582174	HD2(h)	9:99816400..99816815	K562	V\$HDAC2_02	-10176	0.980	0.896	ATAGCAAAT	ENCODE Data 22955616
PM000910856	ZNF217(h)	9:99811611..99812070	GM12878	V\$ZABC1_01	-10170	1.000	1.000	ATTCCAAC	ENCODE Data 22955616
PM000910856	NF-1C(h)	9:99811554..99812149	GM12878	V\$CTF1_01	-10155	1.000	0.771	TTAACTGACTGCCA	ENCODE Data 22955616
PM000910856	Runx3(h)	9:99811670..99812039	GM12878	V\$AML2_Q3_01	-10132	0.962	0.918	TATTGCTGAGG	ENCODE Data 22955616

Showing 1 to 5 of 3,080 entries

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Predicted enhancers / silencers for NR4A3 regulation (73 entries)

Show 5 entries

Search:

Accession	Effect	Chromosomal location	Length (bp)	Identification method	Active in tissue (cell type or line)	Reference
EN000060532	activation	chr9:99181732..99181953	222	chromatin interaction study	blood (natural killer cells), blood (monocytes), placenta (placental epithelial cell), small intestine (intestinal epithelial cells)	HACER
EN000060542	activation	chr9:99419203..99419322	120	pair-wise expression correlation with RefSeq promoter	skin (skin fibroblasts)	FANTOM5
EN000060543	activation	chr9:99430181..99430642	462	pair-wise expression correlation with RefSeq promoter	blood (monocytes)	FANTOM5
EN000060544	activation	chr9:99431261..99431354	94	pair-wise expression correlation with RefSeq promoter	blood (monocytes)	FANTOM5

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				promoter	associated smooth muscle cell), neurons (neuronal stem cell), placenta (placental epithelial cell), small intestine (intestinal epithelial cells), teeth (fibroblast of periodontium)	
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Translational Regulation [what is this?](#)

Regulation of NR4A3 mRNA expression

miRNA binding sites within NR4A3 mRNA (9 entries)

Show

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 entries

Search:

Identifier	Region	Location	Location Reference Point	Binding Factor(s)
HS\$NR4A3_02	3' UTR			hsa-miR-638(h)
HS\$NR4A3_03	3' UTR	490 to 518		hsa-miR-7-5p(h)
HS\$NR4A3_04	3' UTR	568 to 596		hsa-miR-7-5p(h)
HS\$NR4A3_05	3' UTR	2612 to 2640		hsa-miR-7-5p(h)
HS\$NR4A3_06	3' UTR	262 to 290		hsa-miR-17-5p(h)

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RNA Features [what is this?](#)

Overview of RNA sequence

Nucleotide Sequence : ATAAATG...AATGGCA (1..5635; 5635 nt) [details](#)

Sequence source : REFSEQ#NM_006981

FASTA

PROTEIN

Pathways & Interactions [what is this?](#)

Pathways

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Name	Reactome pathway report link	Reactome pathway browser link
Gene expression (Transcription)	R-HSA-74160	Open in Reactome Browser
Generic Transcription Pathway	R-HSA-212436	Open in Reactome Browser
Nuclear Receptor transcription pathway	R-HSA-383280	Open in Reactome Browser
RNA Polymerase II Transcription	R-HSA-73857	Open in Reactome Browser
RUNX1 regulates genes involved in megakaryocyte differentiation and platelet function	R-HSA-8936459	Open in Reactome Browser

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Pathways from WikiPathways (2 entries)

Provided by the [WikiPathways](#) database.

Show

5

 entries

Search:

Name	Display below	WikiPathways external link
Hypertrophy model	View	WikiPathways
Orexin receptor pathway	View	WikiPathways

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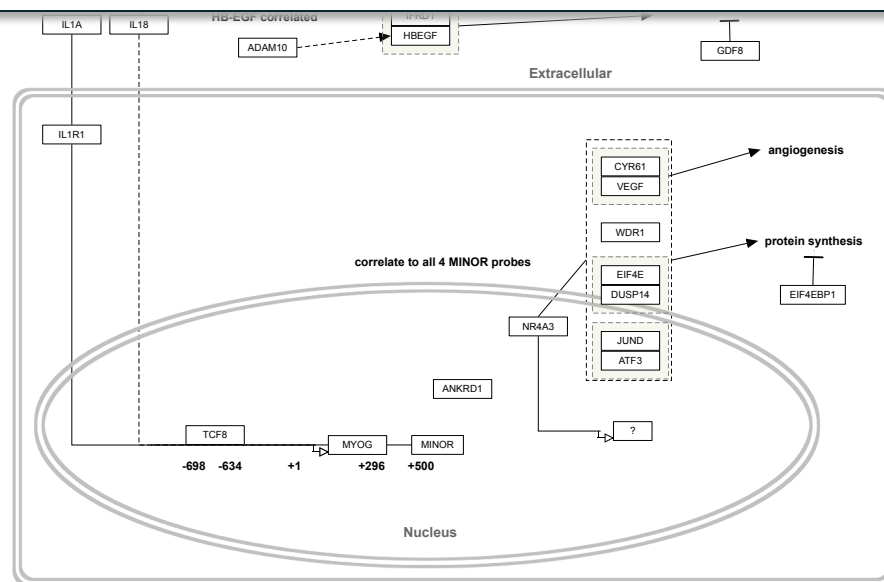
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Protein-protein interactions

+ Proteins bound by NR4A3 (41 partners)

Events acting on NR4A3

+ Proteins or complexes that affect NR4A3 in other ways (25 partners)

Events triggered by NR4A3

+ Proteins or complexes affected by NR4A3 in other ways (8 partners)

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

Regulation of gene expression by NR4A3

Transcription factor classification :

NOR1 (NR4A3); [2.1.4.0.3](#)

Nuclear receptors with C4 zinc fingers; [2.1](#) (Zinc finger motif of nuclear receptor type. Two such motifs differing in size, composition and function are present in each receptor molecule. Each finger comprises 4 cysteine residues coordinating one zinc ion. The second half including the second cysteine pair has alpha-helix conformation, the helix of the first finger binds to the DNA through the major groove. The sequence between the first two cysteines of the second finger

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Gene	Location within Gene	Binding Site Identifier	DNA Binding Reaction	Effect	Quality Score
A2M(h)	-80 to -55	HS\$A2M_04			6

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Positional weight matrices for NR4A3 (1 entry)

Show5entries

Search:

Sequence logo	PWM ID	Matrix type	Matrix category
	V\$NOR1_02	factor-specific	3D structure-based energy calculations

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Transcription factors which interact with NR4A3

Show5entries

Search:

Species	Factor
Human	PARP, SIX3

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Protein Features

what is this?

Overview of protein sequence and structure

Chromosome : 9q22

Family membership : Nuclear hormone receptor

Isoforms : NOR1 -alpha , NOR1 -beta , NOR1 -isoform3 , NOR1/MINOR

+View associated sequences and their domains

+View related proteins

View complexes containing NR4A3 protein

+View complexes (41 entry)

Annotations

what is this?

Display all annotations

Editor's Notes

- Nuclear receptor

Disease related

- Aberrant mRNA expression may act as therapeutic target for acute myeloid leukemia 17515897
- Chondrosarcoma, extraskeletal myxoid pid1779547
- Chromosomal translocation is associated with extraskeletal myxoid chondrosarcoma 18330902
- Decreased mRNA expression causes acute myeloid leukemia 17515897
- Downregulated in follicular carcinoma 20668010

more



Identifiers [what is this?](#)

Accessions mapped to this record

BIOBASE gene accession : GN000007582, G002785, MO000030595

BIOBASE protein accession : PR000457675, MO000150839, T15532

Gene

Affymetrix	11729058_s_at, 11741458_a_at, 11741705_at, 17087517, 190_at, 207978_s_at, 209959_at, 216979_at, 3181977, 3181978, 3181979, 3181980, 3181981, 3181982, 3181987, 3181989, 3181990, 3181993, 3181994, 3181995, 3181996, 3181997, 3181998, 3182004, 3182005, 3182006, 3182007, 3182008, 3182010, 3182012, 3182014, 3182015, 3182016, 40659_at, 40660_at, 40661_at, 40662_g_at, 8156848, g11276070_3p_a_at, g924281_3p_at, Hs.80561.2.S1_3p_at, S81243_s_at, TC09000508.hg, U12767_at, X89894_at,
Agilent	A_14_P121401
Ensembl	ENSG00000119508, ENST00000330847, ENST00000338488, ENST00000395097, ENST00000618101
EntrezGene	8013
Genbank	11276070, 1165104, 1311504, 15620620, 1651190, 16973850, 27894354, 27894356, 27894358, 27894360, 3168579, 3168581, 34368261, 924281, AL358937, AL359710, BX649089, D78579, D85241, D85242, NM_006981, NM_173198, NM_173199, NM_173200, S81243, U12767, X89894
HumanProteinAtlas	ENSG00000119508
ILLumina	0001500139, 0003870603, ILMN_1774586
OMIM	600542
RefSeq	NM_006981.4, NM_173199.4, NM_173200.3, NP_008912.2, NP_775291.1, NP_775292.1, XM_017015162.1, XP_016870651.1
UniGene	Hs&279522
WikiPathways	WP5094, WP516



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Genbank	CAI95320.1 , NP_008912.1 , NP_008912.2 , NP_775290.1 , NP_775291.1 , NP_775292.1
UniProt	Q92570

References (76 entries)

Show 5 entries Search:

Sl.No	PMID	Citation
1	32296183	A reference map of the human binary protein interactome. Nature 580 402-408 (2020) Show abstract
2	28818916	A pathology atlas of the human cancer transcriptome. Science 357 (2017) Show abstract
3	28383167	Urbini, M, Astolfi, A, Pantaleo, MA, Serravalle, S, Dei Tos, AP, Picci, P, Indio, V, Sbaraglia, M, Benini, S, Righi, A, Gambarotti, M, Gronchi, A, Colombo, C, Dagrada, GP, Pilotti, S, Maestro, R, Polano, M, Saponara, M, Tarantino, G, Pession, A, Biasco, G, Casali, PG, Stacchiotti, S, HSPA8 as a novel fusion partner of NR4A3 in extraskeletal myxoid chondrosarcoma. Genes Chromosomes Cancer 56 (7) 582-586 (2017) Show abstract
4	27992436	Corley, SM, Tsai, SY, Wilkins, MR, Shannon Weickert, C, Transcriptomic Analysis Shows Decreased Cortical Expression of NR4A1, NR4A2 and RXRB in Schizophrenia and Provides Evidence for Nuclear Receptor Dysregulation. PLoS ONE 11 (12) e0166944-e016694 (2016) Show abstract
5	27159982	Montarolo, F, Perga, S, Martire, S, Navone, DN, Marchet, A, Leotta, D, Bertolotto, A, Altered NR4A Subfamily Gene Expression Level in Peripheral Blood of Parkinson's and Alzheimer's Disease Patients. Neurotox Res 30 (3) 338-344 (2016) Show abstract

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