SysPTM

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SysPTM entry: [illegible]

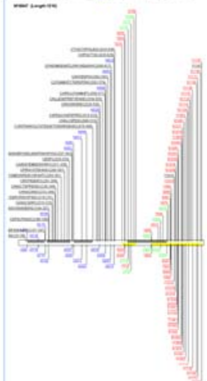
Summary

PTM Site	[illegible]
Protein Description	epidermal growth factor receptor isoform a precursor [Homo sapiens] ; ISOFORM 1 OF EPIDERMAL GROWTH FACTOR RECEPTOR; ISOFORM 1 OF EPIDERMAL GROWTH FACTOR RECEPTOR ; Receptor tyrosine-protein kinase ErbB-1 [Flags: Precursor] Receptor tyrosine-protein kinase ErbB-1 [Flags: Precursor]
Gene Name	EGFR ; EGFR ; ERBB-EGFR ; ERBB1
Species	Homo sapiens
Related ID	[illegible]
Protein Length	[illegible]
Protein Structure	[illegible]

PTMsite - Statistics

PTM_Type	Source	Site_Number
Diphosphorylation	SysPTM-A	[illegible]
Disulfide Bridge	SysPTM-A	[illegible]
Glycosylation	SysPTM-A/SysPTM-B	[illegible]
Phosphorylation	SysPTM-A/SysPTM-B	[illegible]
Phosphorylation	SysPTM-B	[illegible]
Phosphorylation	SysPTM-A	[illegible]
Ubiquitination	SysPTM-A/SysPTM-B	[illegible]
Ubiquitination	SysPTM-A	[illegible]

PTMsite - Map



PTMsite - Table

Start	End	Sites_aa	PTM_Type	Source	Paper_Number
[illegible]	[illegible]	[illegible]	Disulfide Bridge	SysPTM-A	[illegible]
[illegible]	[illegible]	N	Glycosylation	SysPTM-A/SysPTM-B	[illegible]
[illegible]	[illegible]	N	Glycosylation	SysPTM-A/SysPTM-B	[illegible]
[illegible]	[illegible]	[illegible]	Disulfide Bridge	SysPTM-A	[illegible]
[illegible]	[illegible]	N	Glycosylation	SysPTM-A/SysPTM-B	[illegible]
[illegible]	[illegible]	[illegible]	Disulfide Bridge	SysPTM-A	[illegible]
[illegible]	[illegible]	[illegible]	Disulfide Bridge	SysPTM-A	[illegible]
[illegible]	[illegible]	N	Glycosylation	SysPTM-A/SysPTM-B	[illegible]
[illegible]	[illegible]	[illegible]	Disulfide Bridge	SysPTM-A	[illegible]
[illegible]	[illegible]	[illegible]	Disulfide Bridge	SysPTM-A	[illegible]

PTMsite - Source

SysPTM-A

Original_ID	Start	End	Keyword	PTM_Type	Source
[illegible]	[illegible]	[illegible]	Disulfide Bridge	Disulfide Bridge	[illegible]
[illegible]	[illegible]	[illegible]		Disulfide Bridge	[illegible]
[illegible]	[illegible]	[illegible]	Glycosylation	Glycosylation	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	Glycosylation	[illegible]
[illegible]	[illegible]	[illegible]	Glycosylation	Glycosylation	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	Glycosylation	[illegible]
[illegible]	[illegible]	[illegible]	Disulfide Bridge	Disulfide Bridge	[illegible]
[illegible]	[illegible]	[illegible]		Disulfide Bridge	[illegible]
[illegible]	[illegible]	[illegible]	Glycosylation	Glycosylation	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	Glycosylation	[illegible]
[illegible]	[illegible]	[illegible]	Disulfide Bridge	Disulfide Bridge	[illegible]

SysPTM-B

Original_ID	Site_aa	Peptide
[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]

PTMsite - Cluster

Cluster	P-value
[illegible]	[illegible]
[illegible]	[illegible]

PTMprotein - Sequence

[illegible]

PTMprotein - Annotation

Domain from Pfam

Start	End	Pfam_id	Pfam_ID	Pfam_Description	E-value
[illegible]	[illegible]	[illegible]	Recep_L_domain	Receptor L domain	[illegible]
[illegible]	[illegible]	[illegible]	Furin-like	Furin-like cysteine rich region	[illegible]
[illegible]	[illegible]	[illegible]	Recep_L_domain	Receptor L domain	[illegible]
[illegible]	[illegible]	[illegible]	Pkinase	Protein kinase domain	[illegible]
[illegible]	[illegible]	[illegible]	Pkinase_Tyr	Protein tyrosine kinase	[illegible]

Pathway from KEGG

KEGG_ID	KEGG_Name
[illegible]	Melanoma
[illegible]	MAPK signaling pathway
[illegible]	ErbB signaling pathway
[illegible]	Calcium signaling pathway
[illegible]	Cytokine-cytokine receptor interaction
[illegible]	Focal adhesion
[illegible]	Adherens junction
[illegible]	Gap junction
[illegible]	Regulation of actin cytoskeleton
[illegible]	GnRH signaling pathway
[illegible]	Epithelial cell signaling in Helicobacter pylori infection
[illegible]	Colorectal cancer
[illegible]	Pancreatic cancer
[illegible]	Endometrial cancer
[illegible]	Glioma
[illegible]	Prostate cancer
[illegible]	Bladder cancer
[illegible]	Non-small cell lung cancer

Association with Disease from OMIM

OMIM_ID	OMIM_Name	OMIM_Type
[illegible]	EPIDERMAL GROWTH FACTOR RECEPTOR; EGFR	Gene with known sequence
[illegible]	LUNG CANCER	Phenotype description, molecular basis known

Molecular Function from GO

GO_ID	GO_Evidence	GO_Name
[illegible]	IEA	nucleotide binding
[illegible]	NAS	double-stranded DNA binding
[illegible]	NAS	MAP/ERK kinase kinase activity
[illegible]	IEA	transmembrane receptor activity
[illegible]	IEA	epidermal growth factor receptor activity
[illegible]	NAS	epidermal growth factor receptor activity
[illegible]	IEA	ATP binding
[illegible]	IEA	transferase activity
[illegible]	IEA	nitric-oxide synthase regulator activity
[illegible]	IPI	identical protein binding
[illegible]	IEA	protein heterodimerization activity
[illegible]	IEA	actin filament binding

Biological Process from GO

GO_ID	GO_Evidence	GO_Name
[illegible]	NAS	ossification
[illegible]	NAS	response to stress
[illegible]	IEA	cell surface receptor linked signal transduction
[illegible]	IEA	epidermal growth factor receptor signaling pathway
[illegible]	TAS	activation of phospholipase C activity
[illegible]	IMP	cell-cell adhesion
[illegible]	IMP	positive regulation of cell migration
[illegible]	IEA	positive regulation of phosphorylation
[illegible]	TAS	calcium-dependent phospholipase A2 activation
[illegible]	IEA	positive regulation of MAP kinase activity
[illegible]	IEA	positive regulation of nitric oxide biosynthetic process
[illegible]	IEA	negative regulation of cell cycle
[illegible]	IEA	protein amino acid autophosphorylation
[illegible]	IEA	positive regulation of epithelial cell proliferation
[illegible]	IMP	regulation of peptidyl-tyrosine phosphorylation
[illegible]	IEA	regulation of nitric-oxide synthase activity
[illegible]	TAS	protein insertion into membrane
[illegible]	IEA	epidermal growth factor receptor signaling ...
[illegible]	IEA	positive regulation of epithelial cell prol...
[illegible]	IEA	positive regulation of nitric oxide biosynt...
[illegible]	IMP	regulation of peptidyl-tyrosine phosphoryla...

Cell Component from GO

GO_ID	GO_Evidence	GO_Name
[illegible]	IEA	extracellular region
[illegible]	NAS	extracellular space
[illegible]	IEA	intracellular
[illegible]	IEA	nucleus
[illegible]	IEA	cytoplasm
[illegible]	IEA	endosome
[illegible]	IEA	endoplasmic reticulum
[illegible]	EXP	plasma membrane
[illegible]	IEA	plasma membrane
[illegible]	IEA	integral to membrane
[illegible]	IEA	basolateral plasma membrane
[illegible]	TAS	AP-2 adaptor complex
[illegible]	IEA	endocytic vesicle
[illegible]	IEA	basolateral plasma membrane

Ortholog Group from HomoloGene

Group: [illegible]

Species	Gene_Symbol	NCBI_accession	SysPTM_ID
Bos taurus	EGFR	[illegible]	
Canis lupus familiaris	EGFR	[illegible]	
Danio rerio	egfr	[illegible]	
Homo sapiens	EGFR	[illegible]	[illegible]
Mus musculus	Egfr	[illegible]	[illegible]
Pan troglodytes	EGFR	[illegible]	
Rattus norvegicus	Egfr	[illegible]	