

Sublist	Category	Term	RT	Genes	Count	%	P-Value	B
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cell chemotaxis</a>	RT		6	0,0	4,3E-3	1,
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of defense response to virus by virus</a>	RT		4	0,0	1,1E-2	1,
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Adherens junction</a>	RT		6	0,0	1,1E-2	1,
<input type="checkbox"/>	UP_SEQ_FEATURE	<a href="#">mutagenesis site</a>	RT		50	0,1	1,2E-2	1,
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to gamma radiation</a>	RT		4	0,0	1,4E-2	1,
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">hemoglobin complex</a>	RT		3	0,0	1,6E-2	1,
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cell-matrix adhesion</a>	RT		6	0,0	1,7E-2	1,
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein kinase B signaling</a>	RT		4	0,0	1,7E-2	1,
<input type="checkbox"/>	UP_SEQ_FEATURE	<a href="#">metal ion-binding site:Iron (heme distal ligand)</a>	RT		3	0,0	1,8E-2	1,
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Oxygen transport</a>	RT		3	0,0	1,9E-2	1,
<input type="checkbox"/>	INTERPRO	<a href="#">Globin-like</a>	RT		3	0,0	2,0E-2	1,
<input type="checkbox"/>	INTERPRO	<a href="#">Globin</a>	RT		3	0,0	2,0E-2	1,
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to organonitrogen compound</a>	RT		3	0,0	2,2E-2	1,
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">viral genome replication</a>	RT		3	0,0	2,2E-2	1,
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">somatic stem cell population maintenance</a>	RT		5	0,0	2,2E-2	1,
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Nucleus</a>	RT		104	0,2	2,3E-2	1,
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">dendrite morphogenesis</a>	RT		4	0,0	2,3E-2	1,
<input type="checkbox"/>	INTERPRO	<a href="#">Globin, structural domain</a>	RT		3	0,0	2,3E-2	1,
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">MAPK signaling pathway</a>	RT		11	0,0	2,3E-2	1,
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">oxygen transporter activity</a>	RT		3	0,0	2,4E-2	1,
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein kinase activity</a>	RT		13	0,0	2,4E-2	1,
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">oxygen transport</a>	RT		3	0,0	2,5E-2	1,
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">intracellular membrane-bounded organelle</a>	RT		17	0,0	2,6E-2	1,
<input type="checkbox"/>	UP_SEQ_FEATURE	<a href="#">metal ion-binding site:Iron (heme proximal ligand)</a>	RT		3	0,0	2,7E-2	1,
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator</a>	RT		3	0,0	2,8E-2	1,
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of calcium ion import</a>	RT		3	0,0	2,8E-2	1,
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of ossification</a>	RT		3	0,0	2,8E-2	1,
<input type="checkbox"/>	UP_SEQ_FEATURE	<a href="#">active site:Glycyl thioester intermediate</a>	RT		5	0,0	2,8E-2	1,
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">nucleoplasm</a>	RT		60	0,1	3,1E-2	1,
<input type="checkbox"/>	UP_SEQ_FEATURE	<a href="#">site:Involved in GAG binding</a>	RT		2	0,0	3,2E-2	1,
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">focal adhesion</a>	RT		13	0,0	3,2E-2	1,
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">protein heterodimerization activity</a>	RT		15	0,0	3,4E-2	1,
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cell-cell junction assembly</a>	RT		3	0,0	3,5E-2	1,

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Ben
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">MyD88-independent toll-like receptor signaling pathway</a>	RT		4	0,0	1,1E-3	8,1E
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ER to Golgi vesicle-mediated transport</a>	RT		10	0,0	1,2E-3	8,1E
<input type="checkbox"/>	KEGG_PATHWAY	<a href="#">Lysosome</a>	RT		9	0,0	2,0E-3	4,0E
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">toll-like receptor 4 signaling pathway</a>	RT		4	0,0	2,8E-3	1,0E
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">G-protein alpha-subunit binding</a>	RT		4	0,0	3,2E-3	1,0E
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">dendritic spine</a>	RT		7	0,0	5,2E-3	1,0E
<input type="checkbox"/>	UP_SEQ_FEATURE	topological domain: Cytoplasmic	RT		72	0,2	6,0E-3	1,0E
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of MyD88-independent toll-like receptor signaling pathway</a>	RT		3	0,0	6,8E-3	1,0E
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Membrane</a>	RT		136	0,3	8,0E-3	1,0E
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Polymorphism</a>	RT		205	0,5	8,9E-3	1,0E
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">SH3 domain binding</a>	RT		7	0,0	1,2E-2	1,0E
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">phospholipid binding</a>	RT		6	0,0	1,2E-2	1,0E
<input type="checkbox"/>	UP_SEQ_FEATURE	compositionally biased region: Ser/Thr-rich	RT		4	0,0	1,4E-2	1,0E
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Lysosome</a>	RT		10	0,0	2,0E-2	1,0E
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Signal-anchor</a>	RT		14	0,0	2,3E-2	1,0E
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Alternative splicing</a>	RT		180	0,4	2,3E-2	1,0E
<input type="checkbox"/>	INTERPRO	<a href="#">Immunoglobulin E-set</a>	RT		6	0,0	2,7E-2	1,0E
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">lysosome</a>	RT		9	0,0	2,8E-2	1,0E
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">heat shock protein binding</a>	RT		4	0,0	2,9E-2	1,0E
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">oxidative single-stranded DNA demethylation</a>	RT		2	0,0	3,2E-2	1,0E
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Signal</a>	RT		78	0,2	3,2E-2	1,0E
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Disulfide bond</a>	RT		66	0,1	3,3E-2	1,0E
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Transmembrane</a>	RT		102	0,2	3,3E-2	1,0E
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">phosphatidylglycerol acyl-chain remodeling</a>	RT		3	0,0	3,3E-2	1,0E
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">necroptotic process</a>	RT		3	0,0	3,3E-2	1,0E
<input type="checkbox"/>	INTERPRO	<a href="#">Nucleic acid-binding, OB-fold</a>	RT		5	0,0	3,4E-2	1,0E
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Hydrolase</a>	RT		36	0,1	3,4E-2	1,0E
<input type="checkbox"/>	SMART	<a href="#">PX</a>	RT		4	0,0	3,6E-2	1,0E
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">myoblast fusion</a>	RT		3	0,0	3,7E-2	1,0E
<input type="checkbox"/>	UP_SEQ_FEATURE	domain: PX	RT		4	0,0	3,8E-2	1,0E
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway</a>	RT		4	0,0	4,0E-2	1,0E
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Phosphoprotein</a>	RT		142	0,3	4,0E-2	1,0E
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of transcription, DNA-templated</a>	RT		15	0,0	4,0E-2	1,0E
<input type="checkbox"/>	UP_SEQ_FEATURE	DNA-binding region: Basic motif	RT		7	0,0	4,1E-2	1,0E
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">integral component of plasma membrane</a>	RT		32	0,1	4,2E-2	1,0E
<input type="checkbox"/>	INTERPRO	<a href="#">EGF, extracellular</a>	RT		3	0,0	4,3E-2	1,0E
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Acetylation</a>	RT		65	0,1	4,3E-2	1,0E



Category	Term	RT	Genes	Count	%	P-Value	Benjamini
GOTERM_BP_DIRECT	<a href="#">sodium ion transport</a>	RT		7	0,0	3,2E-3	1,0E0
UP_KEYWORDS	<a href="#">Sodium transport</a>	RT		8	0,0	4,2E-3	9,1E-1
GOTERM_CC_DIRECT	<a href="#">apical plasma membrane</a>	RT		13	0,0	5,3E-3	1,0E0
UP_KEYWORDS	<a href="#">Sodium</a>	RT		8	0,0	5,8E-3	9,1E-1
GOTERM_BP_DIRECT	<a href="#">axoogenesis</a>	RT		7	0,0	8,0E-3	1,0E0
GOTERM_BP_DIRECT	<a href="#">associative learning</a>	RT		4	0,0	8,5E-3	1,0E0
GOTERM_CC_DIRECT	<a href="#">adherens junction</a>	RT		5	0,0	1,1E-2	1,0E0
GOTERM_CC_DIRECT	<a href="#">fascia adherens</a>	RT		3	0,0	1,2E-2	1,0E0
GOTERM_BP_DIRECT	<a href="#">long-term memory</a>	RT		4	0,0	1,3E-2	1,0E0
UP_KEYWORDS	<a href="#">Cardiomyopathy</a>	RT		6	0,0	1,3E-2	1,0E0
KEGG_PATHWAY	<a href="#">Insulin secretion</a>	RT		6	0,0	1,4E-2	1,0E0
GOTERM_CC_DIRECT	<a href="#">lateral plasma membrane</a>	RT		5	0,0	1,4E-2	1,0E0
UP_KEYWORDS	<a href="#">Transmembrane helix</a>	RT		117	0,2	1,5E-2	1,0E0
UP_SEQ_FEATURE	<a href="#">topological domain:Extracellular</a>	RT		62	0,1	1,6E-2	1,0E0
UP_KEYWORDS	<a href="#">Transmembrane</a>	RT		117	0,2	1,6E-2	1,0E0
GOTERM_BP_DIRECT	<a href="#">cell growth</a>	RT		5	0,0	1,7E-2	1,0E0
UP_SEQ_FEATURE	<a href="#">transmembrane region</a>	RT		103	0,2	1,8E-2	1,0E0
GOTERM_BP_DIRECT	<a href="#">trophoblastic cell differentiation</a>	RT		3	0,0	2,2E-2	1,0E0
GOTERM_MF_DIRECT	<a href="#">transcription factor activity, RNA polymerase II transcription factor binding</a>	RT		3	0,0	2,4E-2	1,0E0
UP_KEYWORDS	<a href="#">Antibiotic</a>	RT		6	0,0	2,4E-2	1,0E0
UP_KEYWORDS	<a href="#">Developmental protein</a>	RT		26	0,1	2,5E-2	1,0E0
GOTERM_CC_DIRECT	<a href="#">nuclear matrix</a>	RT		6	0,0	2,7E-2	1,0E0
GOTERM_BP_DIRECT	<a href="#">neuromuscular process</a>	RT		3	0,0	2,8E-2	1,0E0
UP_KEYWORDS	<a href="#">Membrane</a>	RT		148	0,3	2,8E-2	1,0E0
GOTERM_MF_DIRECT	<a href="#">cofactor binding</a>	RT		3	0,0	3,0E-2	1,0E0
INTERPRO	<a href="#">Major facilitator superfamily domain</a>	RT		7	0,0	3,3E-2	1,0E0
UP_SEQ_FEATURE	<a href="#">domain:Calx-beta</a>	RT		2	0,0	3,3E-2	1,0E0
GOTERM_MF_DIRECT	<a href="#">neurotrophin TRKB receptor binding</a>	RT		2	0,0	3,4E-2	1,0E0
GOTERM_MF_DIRECT	<a href="#">pyrimidine nucleotide transmembrane transporter activity</a>	RT		2	0,0	3,4E-2	1,0E0
GOTERM_BP_DIRECT	<a href="#">pyrimidine nucleotide transport</a>	RT		2	0,0	3,5E-2	1,0E0
UP_SEQ_FEATURE	<a href="#">topological domain:Cytoplasmic</a>	RT		72	0,2	3,5E-2	1,0E0
GOTERM_BP_DIRECT	<a href="#">blood vessel morphogenesis</a>	RT		3	0,0	3,6E-2	1,0E0
INTERPRO	<a href="#">NAD(P)-binding domain</a>	RT		8	0,0	3,6E-2	1,0E0
GOTERM_CC_DIRECT	<a href="#">integral component of membrane</a>	RT		106	0,2	3,7E-2	1,0E0
UP_KEYWORDS	<a href="#">Antimicrobial</a>	RT		6	0,0	3,9E-2	1,0E0
UP_KEYWORDS	<a href="#">Cell adhesion</a>	RT		15	0,0	4,0E-2	1,0E0

Category	Term	RT	Genes	Count	%	P-Value	Benjam
Biocarta	<a href="#">Growth Hormone Signaling Pathway</a>	RT		4	0,0	8,2E-3	6,2E-1
GoTerm_MF_DIRECT	<a href="#">endopeptidase activity</a>	RT		5	0,0	9,0E-3	1,0E0
InterPro	<a href="#">Epidermal growth factor-like domain</a>	RT		10	0,0	1,0E-2	1,0E0
UP_KEYWORDS	<a href="#">EGF-like domain</a>	RT		10	0,0	1,1E-2	1,0E0
GoTerm_BP_DIRECT	<a href="#">cholesterol homeostasis</a>	RT		5	0,0	1,7E-2	1,0E0
GoTerm_BP_DIRECT	<a href="#">somatic stem cell population maintenance</a>	RT		5	0,0	1,8E-2	1,0E0
GoTerm_BP_DIRECT	<a href="#">detection of calcium ion</a>	RT		3	0,0	1,9E-2	1,0E0
SMART	<a href="#">EGF</a>	RT		8	0,0	1,9E-2	1,0E0
GoTerm_MF_DIRECT	<a href="#">serum response element binding</a>	RT		2	0,0	3,0E-2	1,0E0
GoTerm_BP_DIRECT	<a href="#">platelet formation</a>	RT		3	0,0	3,4E-2	1,0E0
InterPro	<a href="#">EGF-like, conserved site</a>	RT		8	0,0	3,6E-2	1,0E0
UP_SEQ_FEATURE	<a href="#">domain:EGF-like 1</a>	RT		6	0,0	3,6E-2	1,0E0
GoTerm_BP_DIRECT	<a href="#">regulation of vasoconstriction</a>	RT		3	0,0	3,7E-2	1,0E0
GoTerm_MF_DIRECT	<a href="#">sucrose:proton symporter activity</a>	RT		2	0,0	4,5E-2	1,0E0
GoTerm_BP_DIRECT	<a href="#">sucrose transport</a>	RT		2	0,0	4,5E-2	1,0E0
UP_SEQ_FEATURE	<a href="#">domain:EGF-like 2</a>	RT		5	0,0	4,6E-2	1,0E0
GoTerm_MF_DIRECT	<a href="#">hyaluronic acid binding</a>	RT		3	0,0	4,7E-2	1,0E0
GoTerm_BP_DIRECT	<a href="#">embryonic digit morphogenesis</a>	RT		4	0,0	5,5E-2	1,0E0
GoTerm_BP_DIRECT	<a href="#">thyroid gland development</a>	RT		3	0,0	5,6E-2	1,0E0
GoTerm_MF_DIRECT	<a href="#">transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding</a>	RT		5	0,0	5,6E-2	1,0E0
UP_SEQ_FEATURE	<a href="#">compositionally biased region:Poly-Pro</a>	RT		12	0,0	5,7E-2	1,0E0
GoTerm_MF_DIRECT	<a href="#">chromatin DNA binding</a>	RT		4	0,0	5,8E-2	1,0E0
UP_KEYWORDS	<a href="#">Endoplasmic reticulum</a>	RT		24	0,1	5,8E-2	1,0E0
GoTerm_MF_DIRECT	<a href="#">BAT3 complex binding</a>	RT		2	0,0	5,9E-2	1,0E0
GoTerm_BP_DIRECT	<a href="#">positive regulation of transcription via serum response element binding</a>	RT		2	0,0	6,0E-2	1,0E0
UP_SEQ_FEATURE	<a href="#">domain:EGF-like 4</a>	RT		4	0,0	6,0E-2	1,0E0
InterPro	<a href="#">Bile acid transporter</a>	RT		2	0,0	6,1E-2	1,0E0
InterPro	<a href="#">NAD(P)-binding domain</a>	RT		7	0,0	6,1E-2	1,0E0
InterPro	<a href="#">Prefoldin</a>	RT		3	0,0	6,1E-2	1,0E0
Biocarta	<a href="#">Hop Pathway in Cardiac Development</a>	RT		2	0,0	6,3E-2	1,0E0
GoTerm_CC_DIRECT	<a href="#">presynaptic membrane</a>	RT		4	0,0	6,7E-2	1,0E0
Biocarta	<a href="#">EGF Signaling Pathway</a>	RT		3	0,0	6,8E-2	1,0E0
UP_SEQ_FEATURE	<a href="#">domain:EGF-like 3</a>	RT		4	0,0	6,8E-2	1,0E0



Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjam
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Protein biosynthesis</a>	RT		9	0,0	3,3E-3	1,0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Lipid biosynthesis</a>	RT		8	0,0	1,3E-2	1,0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of transcription from RNA polymerase III promoter</a>	RT		3	0,0	1,9E-2	1,0E0
<input type="checkbox"/>	SMART	<a href="#">LINK</a>	RT		3	0,0	2,3E-2	1,0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Link</a>	RT		3	0,0	2,4E-2	1,0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">phosphatidylethanolamine biosynthetic process</a>	RT		3	0,0	2,5E-2	1,0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	<a href="#">short sequence motif:Nuclear export signal</a>	RT		4	0,0	3,2E-2	1,0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Phospholipid biosynthesis</a>	RT		4	0,0	3,6E-2	1,0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">calcium ion transport</a>	RT		5	0,0	3,9E-2	1,0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">drug binding</a>	RT		5	0,0	3,9E-2	1,0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">neural tube closure</a>	RT		5	0,0	4,0E-2	1,0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">cytoplasmic vesicle</a>	RT		9	0,0	4,1E-2	1,0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">RNA-binding</a>	RT		18	0,0	4,3E-2	1,0E0
<input type="checkbox"/>	SMART	<a href="#">FA58C</a>	RT		3	0,0	4,4E-2	1,0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Phospholipid metabolism</a>	RT		4	0,0	4,4E-2	1,0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Zinc-finger</a>	RT		39	0,1	4,6E-2	1,0E0
<input type="checkbox"/>	INTERPRO	<a href="#">SUZ-C domain</a>	RT		2	0,0	4,8E-2	1,0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">cyclic-nucleotide phosphodiesterase activity</a>	RT		2	0,0	4,9E-2	1,0E0
<input type="checkbox"/>	GOTERM_CC_DIRECT	<a href="#">excitatory synapse</a>	RT		3	0,0	5,0E-2	1,0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Hypotrichosis</a>	RT		3	0,0	5,3E-2	1,0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Ligase</a>	RT		11	0,0	5,6E-2	1,0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">hyaluronic acid binding</a>	RT		3	0,0	5,6E-2	1,0E0
<input type="checkbox"/>	UP_KEYWORDS	<a href="#">Transport</a>	RT		42	0,1	5,7E-2	1,0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of cell cycle</a>	RT		6	0,0	5,7E-2	1,0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	<a href="#">zinc finger region:C2H2-type 19</a>	RT		4	0,0	6,0E-2	1,0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Coagulation factor 5/8 C-terminal type domain</a>	RT		3	0,0	6,3E-2	1,0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	<a href="#">compositionally biased region:Poly-His</a>	RT		4	0,0	6,3E-2	1,0E0
<input type="checkbox"/>	INTERPRO	<a href="#">Aspartic peptidase, DDI1-type</a>	RT		2	0,0	6,4E-2	1,0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	<a href="#">binding site:Nucleotide</a>	RT		2	0,0	6,5E-2	1,0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	<a href="#">chain:TP53-target gene 3 protein</a>	RT		2	0,0	6,5E-2	1,0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">ethanolamine kinase activity</a>	RT		2	0,0	6,5E-2	1,0E0
<input type="checkbox"/>	PIR_SUPERFAMILY	<a href="#">importin subunit alpha</a>	RT		2	0,0	6,8E-2	1,0E0
<input type="checkbox"/>	UP_SEQ_FEATURE	<a href="#">zinc finger region:C2H2-type 21</a>	RT		3	0,0	6,9E-2	1,0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">glycosaminoglycan catabolic process</a>	RT		3	0,0	7,0E-2	1,0E0
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">phosphatidylinositol biosynthetic process</a>	RT		4	0,0	7,3E-2	1,0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">RNA binding</a>	RT		15	0,0	7,9E-2	1,0E0
<input type="checkbox"/>	GOTERM_MF_DIRECT	<a href="#">histone acetyltransferase binding</a>	RT		3	0,0	8,0E-2	1,0E0