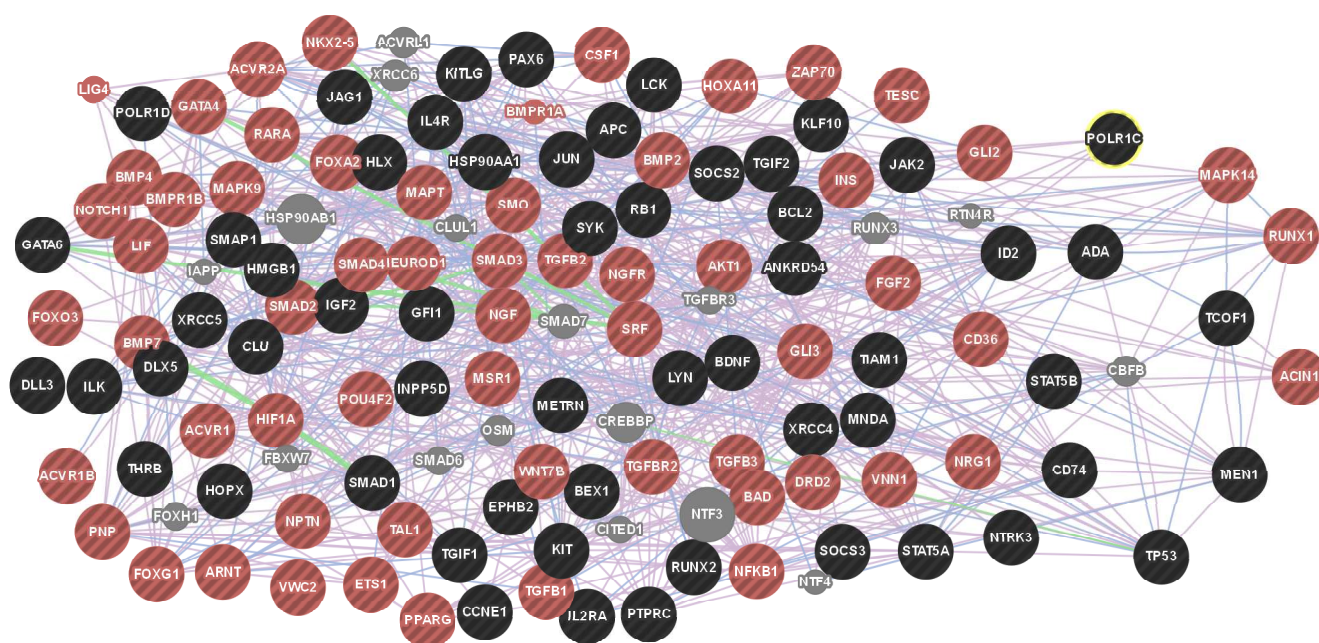


GENEMANIA

Created on: 5 December 2012 08:06:55
Last database update: 19 July 2012 20:00:00
Application version: 3.1.1

Report of GeneMANIA search

Network image



Functions legend

- positive regulation of cell differentiation
- query genes

Networks legend

- Co-expression
- Co-localization
- Genetic interactions
- Pathway
- Physical interactions
- Predicted
- Shared protein domains

3.01

Search parameters

Organism: *H. sapiens* (human)

Genes: BAD; HOXA11; PAX6; CD74; MSR1; KITLG; MAPK9; NGFR; TCOF1; GLI2; IL4RA; XRCC5; HSP90AA1; PTPRC; TESC; DLL3; TGFB2; JAK2; ANKRD54; HIF1A; ACIN1; BMP7; JAG1; METRN; CCNE1; TGFB1; DLX5; GLI3; NFKB1; MAPK14; VNN1; SMAP1; SRF; ZAP70; ACVR1; ID2; FOXO3; TGIF2; TGFB3; SOCS2; CLU; ACVR2A; RUNX2; BMP4; FOXA2; BMP2; STAT5A; LIF; SMO; RARA; PPARG; BEX1; EPHB2; MEN1; NGF; IL2RA; ETS1; APC; CD36; ACVR1B; GATA4; HLX; FGF2; BMPR1B; RB1; NTRK3; GATA6; TP53; SMAD4; AKT1; ARNT; NOTCH1; DRD2; THRB; POU4F2; XRCC4; KLF10; TIAM1; NPTN; NRG1; KIT; RUNX1; TAL1; GFI1; NEUROD1; TGFB2; MND4; SYK; ILK; SMAD3; IGF2; INPP5D; SMAD1; POLR1C; HOPX; BCL2; STAT5B; SMAD2; FOXG1; BDNF; TGIF1; JUN; LCK; NKX2-5; CSF1; SOCS3; POLR1D; MAPT; WNT7B; VWC2; HMGB1; ADA; PNP; LYN; INS

Networks:

Attributes:

Network weighting: Automatically selected weighting method (Assigned based on query genes)

Number of gene results: 20

Networks

Predicted	43.79 %
I2D-Li-Vidal-2004-CORE-1-Worm2Human A map of the interactome network of the metazoan C. elegans. Li et al. (2004). <i>Science</i> . Note: I2D predictions of protein protein interactions using Li-Vidal-2004 Caenorhabditis elegans data Source: Direct interaction with 103 interactions from I2D	8.17 %
I2D-Li-Vidal-2004-CE-DATA-Worm2Human A map of the interactome network of the metazoan C. elegans. Li et al. (2004). <i>Science</i> . Note: I2D predictions of protein protein interactions using Li-Vidal-2004 Caenorhabditis elegans data Source: Direct interaction with 97 interactions from I2D	7.51 %
I2D-Yu-Vidal-2008-GoldStd-Yeast2Human High-quality binary protein interaction map of the yeast interactome network. Yu et al. (2008). <i>Science</i> . Note: I2D predictions of protein protein interactions using Yu Gold Standard Saccharomyces cerevisiae data Source: Direct interaction with 386 interactions from I2D Tags: transcription factors; signal transduction	6.59 %
I2D-Tarassov-PCA-Yeast2Human An in vivo map of the yeast protein interactome. Tarassov et al. (2008). <i>Science</i> . Note: I2D predictions of protein protein interactions using Tarassov-Michnick-2008 Saccharomyces cerevisiae data Source: Direct interaction with 441 interactions from I2D Tags: cell proliferation	4.23 %
I2D-Tewari-Vidal-2004-TGFb-Worm2Human Systematic interactome mapping and genetic perturbation analysis of a C. elegans TGF-beta signaling network. Tewari et al. (2004). <i>Mol Cell</i> . Note: I2D predictions of protein protein interactions using Tewari-Vidal-2004 Caenorhabditis elegans data Source: Direct interaction with 18 interactions from I2D Tags: development; cultured cells; cell line; signal transduction; cell signalling; transcription factors; kidney	3.86 %
I2D-MINT-Rat2Human MINT: a Molecular INTERaction database. Zanzoni et al. (2002). <i>FEBS Lett</i> . Note: I2D predictions of protein protein interactions using MINT Rattus norvegicus data Source: Direct interaction with 574 interactions from I2D	3.83 %
I2D-BIND-Yeast2Human BIND--a data specification for storing and describing biomolecular interactions, molecular complexes and pathways. Bader et al. (2000). <i>Bioinformatics</i> . Note: I2D predictions of protein protein interactions using BIND Saccharomyces cerevisiae data Source: Direct interaction with 1,543 interactions from I2D	2.11 %
I2D-IntAct-Fly2Human The IntAct molecular interaction database in 2010. Aranda et al. (2010). <i>Nucleic Acids Res</i> . Note: I2D predictions of protein protein interactions using IntAct Drosophila melanogaster data Source: Direct interaction with 3,920 interactions from I2D	1.83 %
I2D-BIND-Rat2Human BIND--a data specification for storing and describing biomolecular interactions, molecular complexes and pathways. Bader et al. (2000). <i>Bioinformatics</i> . Note: I2D predictions of protein protein interactions using BIND Rattus norvegicus data Source: Direct interaction with 556 interactions from I2D	1.46 %
I2D-INNATEDB-Mouse2Human	1.15 %

InnateDB: facilitating systems-level analyses of the mammalian innate immune response. Lynn et al. (2008). <i>Mol Syst Biol</i> .	
Note: I2D predictions of protein protein interactions using INNATEDB Mus musculus data	
Source: Direct interaction with 1,455 interactions from I2D	
Tags: signal transduction; immune system	
I2D-Formstecher-Daviet-2005-Embryo-Fly2Human	1.01 %
Protein interaction mapping: a Drosophila case study. Formstecher et al. (2005). <i>Genome Res</i> .	
Note: I2D predictions of protein protein interactions using Formstecher-Daviet-2005 Drosophila melanogaster data	
Source: Direct interaction with 488 interactions from I2D	
Tags: cancer	
I2D-IntAct-Mouse2Human	0.91 %
The IntAct molecular interaction database in 2010. Aranda et al. (2010). <i>Nucleic Acids Res</i> .	
Note: I2D predictions of protein protein interactions using IntAct Mus musculus data	
Source: Direct interaction with 3,422 interactions from I2D	
I2D-BIND-Mouse2Human	0.73 %
BIND--a data specification for storing and describing biomolecular interactions, molecular complexes and pathways. Bader et al. (2000). <i>Bioinformatics</i> .	
Note: I2D predictions of protein protein interactions using BIND Mus musculus data	
Source: Direct interaction with 1,198 interactions from I2D	
Stuart-Kim-2003	0.40 %
A gene-coexpression network for global discovery of conserved genetic modules. Stuart et al. (2003). <i>Science</i> .	
Source: 24,952 interactions from supplementary material	
Tags: cell proliferation; cultured cells; signal transduction; cancer	
Co-expression	19.22 %
Kang-Willman-2010	< 0.01 %
Gene expression classifiers for relapse-free survival and minimal residual disease improve risk classification and outcome prediction in pediatric B-precursor acute lymphoblastic leukemia. Kang et al. (2010). <i>Blood</i> .	
Source: Pearson correlation with 549,783 interactions from GEO	
Tags: transcription factors; lymphoma; cancer	
Perou-Botstein-1999	3.90 %
Distinctive gene expression patterns in human mammary epithelial cells and breast cancers. Perou et al. (1999). <i>Proc Natl Acad Sci U S A</i> .	
Source: Pearson correlation with 50,804 interactions from supplementary material	
Tags: cultured cells; cancer; epithelial cells; signal transduction; breast; stromal cells; transcription factors; breast cancer	
Ramaswamy-Golub-2001	3.29 %
Multiclass cancer diagnosis using tumor gene expression signatures. Ramaswamy et al. (2001). <i>Proc Natl Acad Sci U S A</i> .	
Source: Pearson correlation with 226,615 interactions from supplementary material	
Tags: cancer	
Bild-Nevins-2006 B	2.86 %
Oncogenic pathway signatures in human cancers as a guide to targeted therapies. Bild et al. (2006). <i>Nature</i> .	
Note: One of 3 datasets produced from this publication.	
Source: Pearson correlation with 254,105 interactions from GEO	
Tags: cultured cells; signal transduction; cancer; epithelial cells; cell line; disease; breast; transcription factors; breast cancer	
Rieger-Chu-2004	2.40 %
Toxicity from radiation therapy associated with abnormal transcriptional responses to DNA damage. Rieger et al. (2004).	

Proc Natl Acad Sci U S A.

Source: [Pearson correlation](#) with 220,846 interactions from [GEO](#)

Tags: cultured cells; cell line

Nakayama-Hasegawa-2007 **1.68 %**

[Gene expression analysis of soft tissue sarcomas: characterization and reclassification of malignant fibrous histiocytoma.](#) Nakayama et al. (2007). *Mod Pathol.*

Source: [Pearson correlation](#) with 361,398 interactions from [GEO](#)

Tags: transcription factors; cancer

Wang-Maris-2006 **1.64 %**

[Integrative genomics identifies distinct molecular classes of neuroblastoma and shows that multiple genes are targeted by regional alterations in DNA copy number.](#) Wang et al. (2006). *Cancer Res.*

Source: [Pearson correlation](#) with 231,830 interactions from [GEO](#)

Tags: transcription factors; cancer

Berchtold-Cotman-2008 **1.53 %**

[Gene expression changes in the course of normal brain aging are sexually dimorphic.](#) Berchtold et al. (2008). *Proc Natl Acad Sci U S A.*

Source: [Pearson correlation](#) with 507,933 interactions from [GEO](#)

Tags: aging; brain

Wu-Garvey-2007 **1.01 %**

[The effect of insulin on expression of genes and biochemical pathways in human skeletal muscle.](#) Wu et al. (2007). *Endocrine.*

Source: [Pearson correlation](#) with 223,988 interactions from [GEO](#)

Tags: transcription factors; muscle; cultured cells

Hummel-Siebert-2006 **0.47 %**

[A biologic definition of Burkitt's lymphoma from transcriptional and genomic profiling.](#) Hummel et al. (2006). *N Engl J Med.*

Source: [Pearson correlation](#) with 466,765 interactions from [GEO](#)

Tags: cancer

Burington-Shaughnessy-2008 **0.42 %**

[Tumor cell gene expression changes following short-term in vivo exposure to single agent chemotherapeutics are related to survival in multiple myeloma.](#) Burington et al. (2008). *Clin Cancer Res.*

Source: [Pearson correlation](#) with 266,464 interactions from [GEO](#)

Tags: transcription factors; time series; cancer; chemotherapy

Pathway **11.20 %**

Wu-Stein-2010 **5.50 %**

[A human functional protein interaction network and its application to cancer data analysis.](#) Wu et al. (2010). *Genome Biol.*

Source: 78,448 interactions from supplementary material

Tags: transcription factors; cancer

PATHWAYCOMMONS-IMID **2.21 %**

Source: [Direct interaction](#) with 937 interactions from [Pathway Commons](#)

PATHWAYCOMMONS-NCI_NATURE **1.66 %**

Source: [Direct interaction](#) with 10,118 interactions from [Pathway Commons](#)

PATHWAYCOMMONS-REACTOME **0.91 %**

Source: [Direct interaction](#) with 24,924 interactions from [Pathway Commons](#)

PATHWAYCOMMONS-CELL_MAP **0.91 %**

Source: [Direct interaction](#) with 598 interactions from [Pathway Commons](#)

Physical interactions **10.83 %**

IREF-BIND-TRANSLATION	3.70 %
Source: Direct interaction with 680 interactions from iRefIndex	
IREF-MPPI	2.36 %
Source: Direct interaction with 385 interactions from iRefIndex	
IREF-DIP	2.04 %
Source: Direct interaction with 12,700 interactions from iRefIndex	
IREF-BIND	1.21 %
Source: Direct interaction with 5,310 interactions from iRefIndex	
IREF-CORUM	0.52 %
Source: Direct interaction with 637 interactions from iRefIndex	
IREF-INTACT	0.41 %
Source: Direct interaction with 21,448 interactions from iRefIndex	
Bandyopadhyay-Ideker-2010	0.37 %
A human MAP kinase interactome. Bandyopadhyay et al. (2010). <i>Nat Methods</i> .	
Source: Direct interaction with 556 interactions from iRefIndex	
Tags: transcription factors; signal transduction; cell line; cultured cells	
Miyamoto-Sato-Yanagawa-2010	0.16 %
A comprehensive resource of interacting protein regions for refining human transcription factor networks. Miyamoto-Sato et al. (2010). <i>PLoS One</i> .	
Source: Direct interaction with 921 interactions from iRefIndex	
Tags: transcription factors	
IREF-GRID	0.07 %
Source: Direct interaction with 33,623 interactions from iRefIndex	
Co-localization	8.24 %
Schadt-Shoemaker-2004	4.92 %
A comprehensive transcript index of the human genome generated using microarrays and computational approaches. Schadt et al. (2004). <i>Genome Biol</i> .	
Note: Predicted transcript array	
Source: Pearson correlation with 60,454 interactions from GEO	
Johnson-Shoemaker-2003	3.32 %
Genome-wide survey of human alternative pre-mRNA splicing with exon junction microarrays. Johnson et al. (2003). <i>Science</i> .	
Source: Pearson correlation with 426,934 interactions from GEO	
Tags: cultured cells; cell line	
Shared protein domains	4.56 %
INTERPRO	3.46 %
Source: Pearson correlation with 488,822 interactions from InterPro	
PFAM	1.11 %
Source: Pearson correlation with 530,357 interactions from Pfam	
Genetic interactions	2.17 %
BIOGRID-SMALL-SCALE-STUDIES	2.17 %
Source: Direct interaction with 345 interactions from BioGRID	

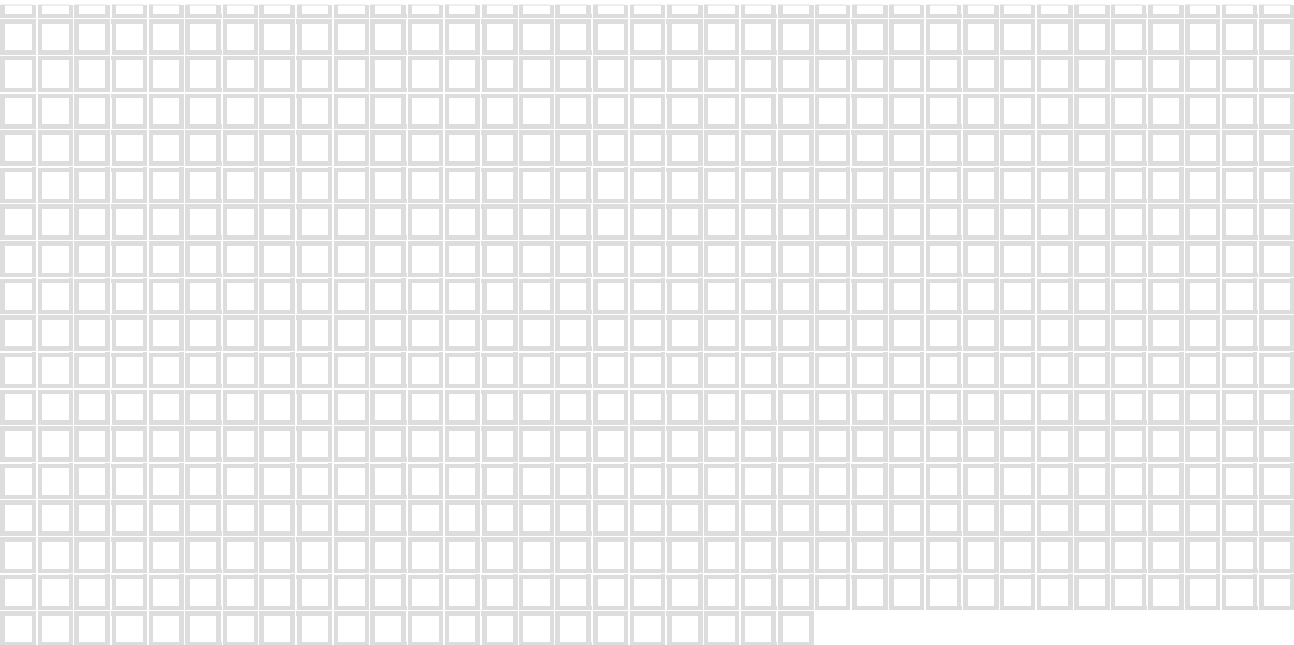
Attributes

Attribute	Gene
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VWC2 von Willebrand factor C domain containing 2 [Source:HGNC Symbol;Acc:30200]

More at [Entrez](#)

METR meteorin, glial cell differentiation regulator [Source:HGNC Symbol;Acc:14151]

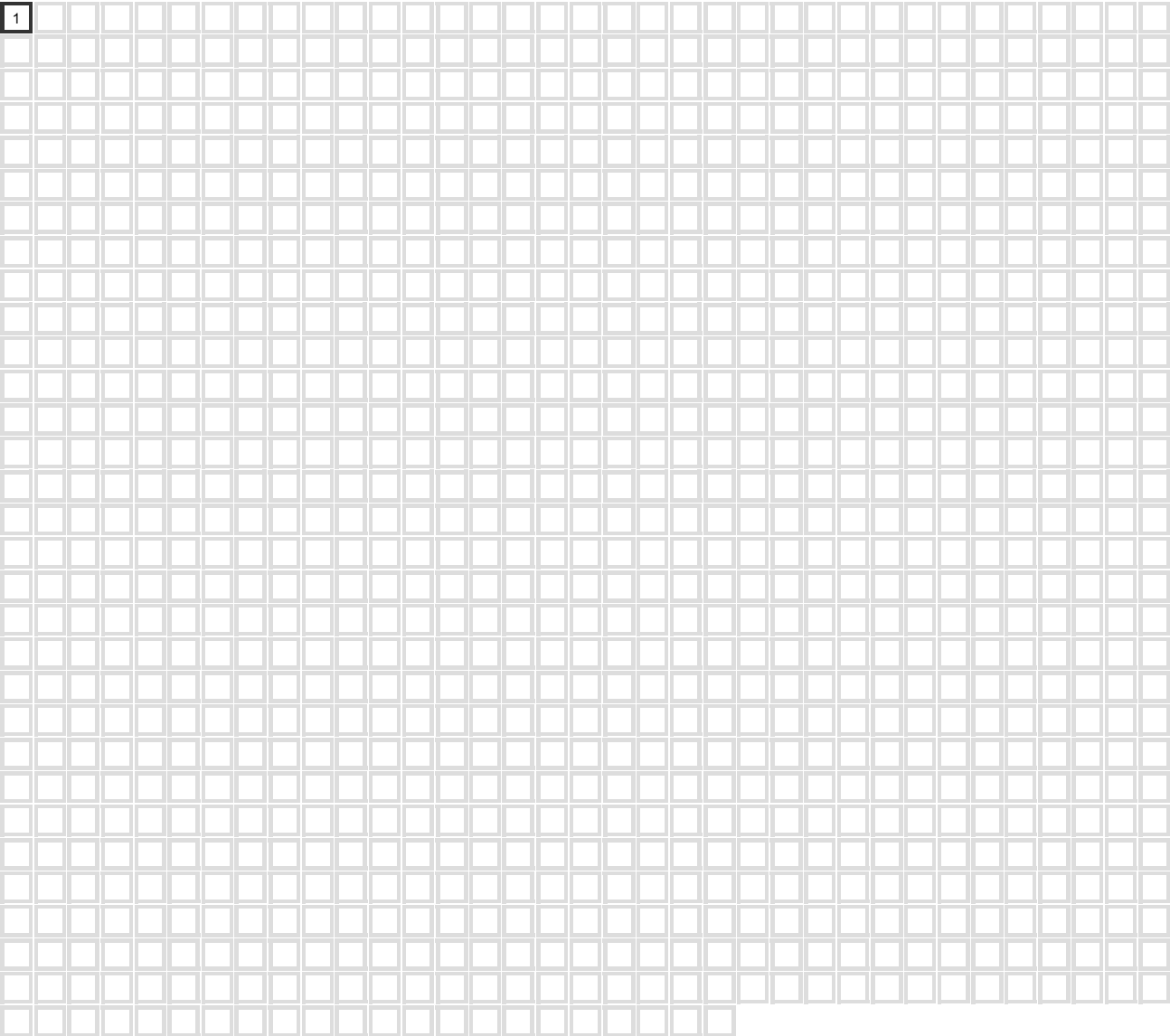


Synonyms: ENSG00000103260; ENSP00000219542; 79006; METRN; NP_076947; NM_024042; C16orf23; c380A1.2; MGC2601; METRN_HUMAN; Q9UJH8;

More at [Entrez](#)

ANKRD54 ankyrin repeat domain 54 [Source:HGNC Symbol;Acc:25185]

Functions:



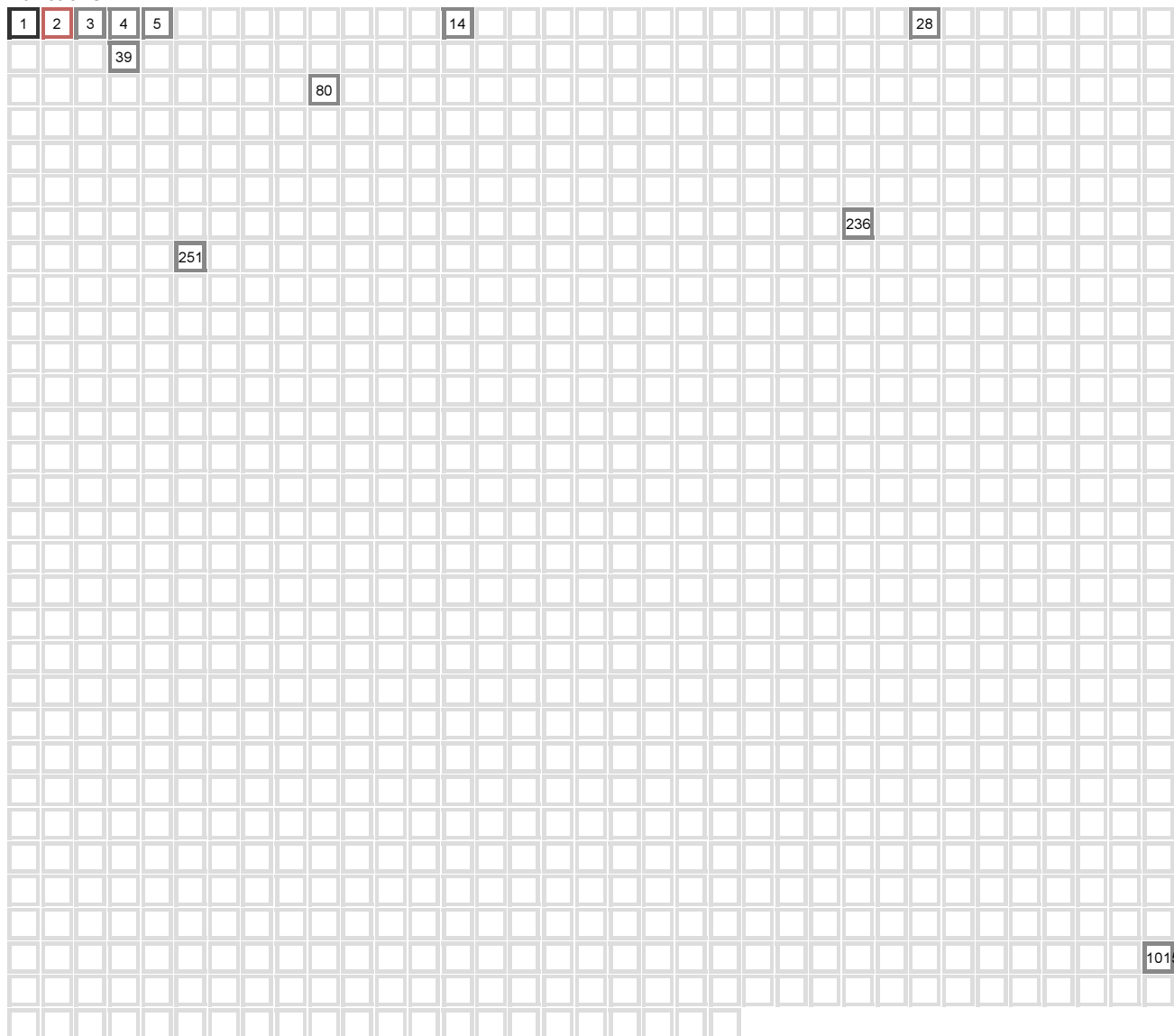
Synonyms: ENSG00000100124; ENSP00000215941; ENSP00000384392; ENSP00000385180; ENSP00000387507;

ENSP00000391744; ENSP00000393035; ENSP00000405782; ENSP00000412534; 129138; ANKRD54; NP_620152; NM_138797; NR_036556; LIAR; ANR54_HUMAN; Q6NXT1;

More at [Entrez](#)

TESC tescalcin [Source:HGNC Symbol;Acc:26065]

Functions:

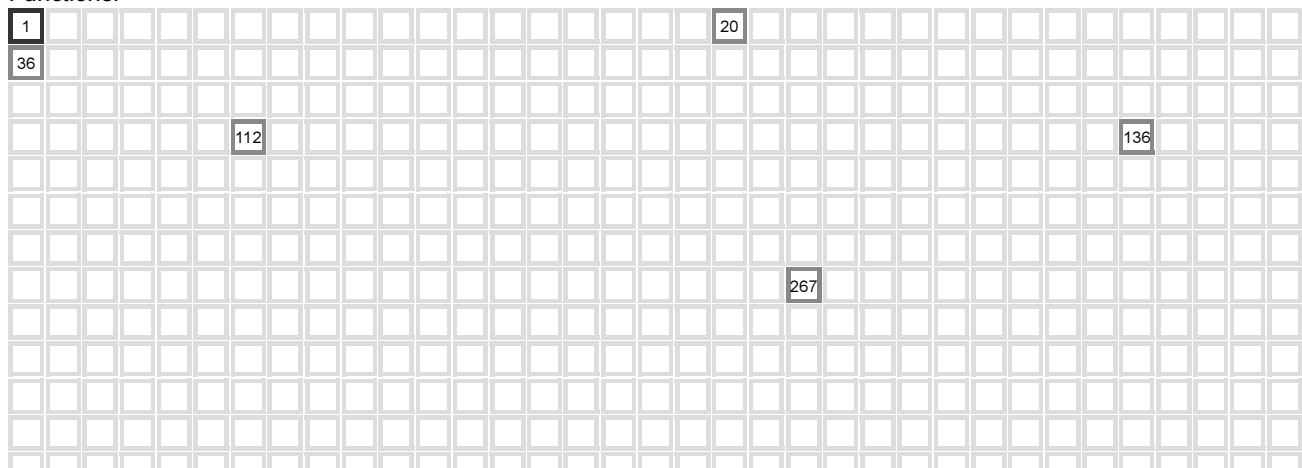


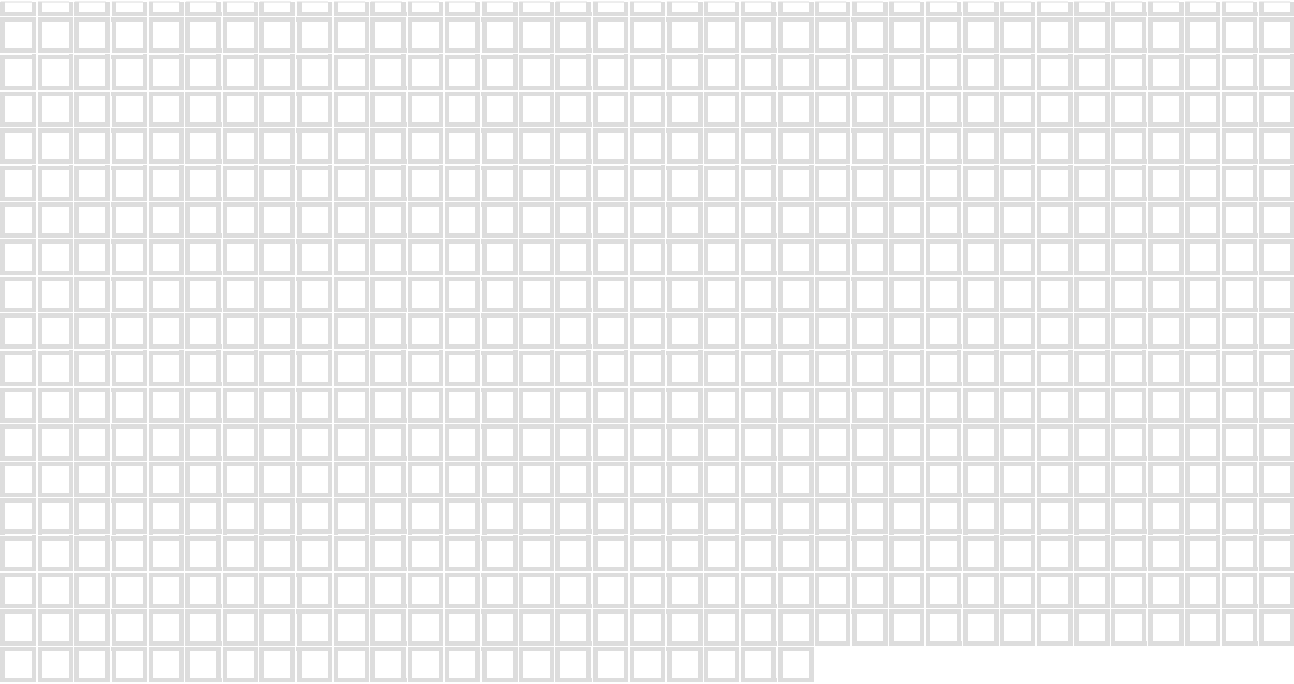
Synonyms: ENSG00000088992; ENSP00000334785; ENSP00000376328; ENSP00000432608; ENSP00000432716; ENSP00000445689; ENSP00000450386; 54997; TESC; NP_001161797; NP_060369; NM_001168325; NM_017899; NR_031766; CHP3; FLJ20607; Q96BS2; TESC_HUMAN;

More at [Entrez](#)

HOPX HOP homeobox [Source:HGNC Symbol;Acc:24961]

Functions:



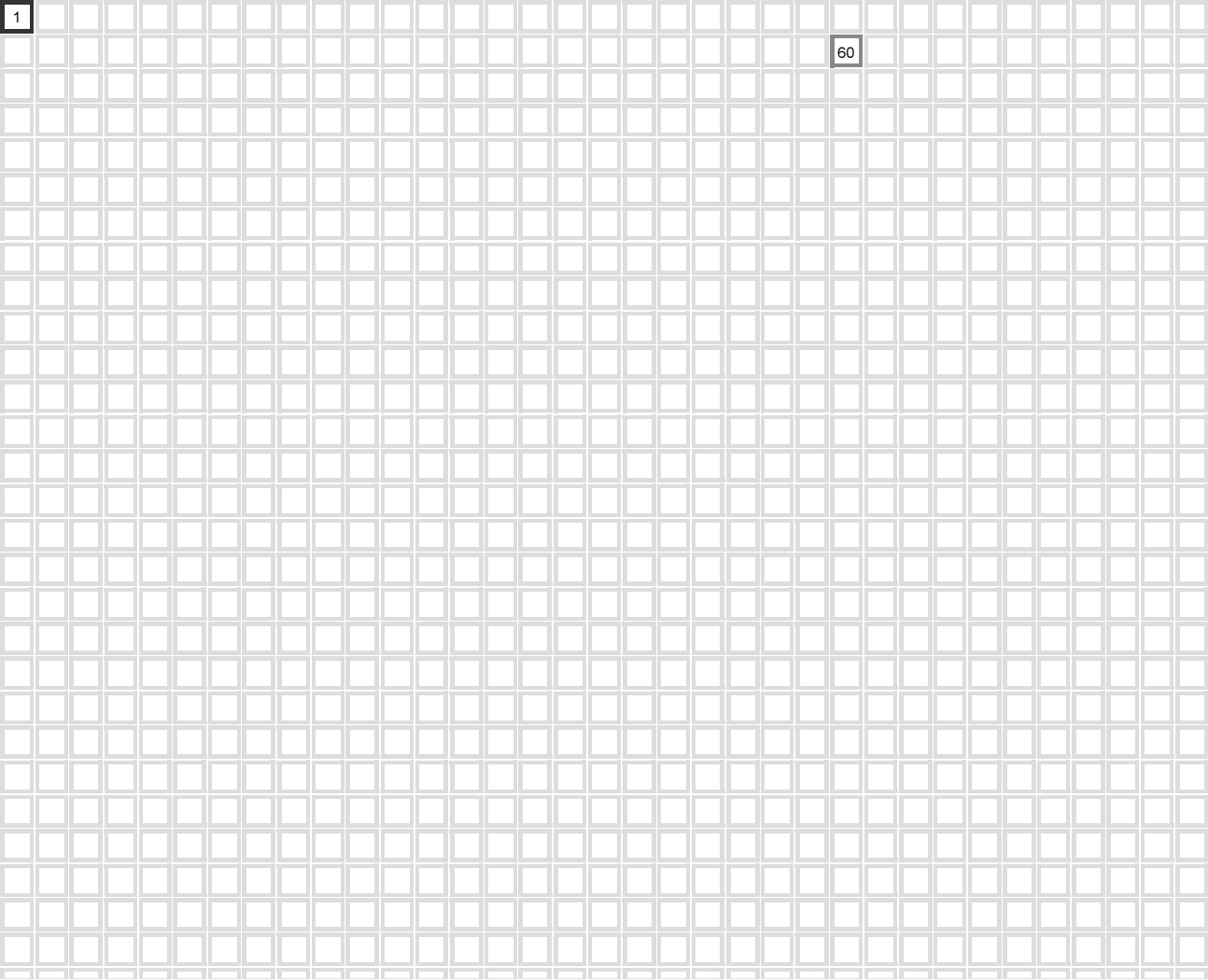


Synonyms: ENSG00000171476; ENSP00000315198; ENSP00000337330; ENSP00000370654; ENSP00000370659; ENSP00000396275; ENSP00000421272; ENSP00000421831; ENSP00000422083; ENSP00000422175; ENSP00000423239; ENSP00000424101; ENSP00000450527; ENSP00000451631; ENSP00000451794; ENSP00000452003; ENSP00000452098; ENSP00000452340; 84525; HOPX; NP_001138931; NP_001138932; NP_115884; NP_631957; NP_631958; NM_001145459; NM_001145460; NM_032495; NM_139211; NM_139212; CAMEO; HOD; LAGY; OB1; SMAP31; TOTO; HOP_HUMAN; Q9BPY8;

More at [Entrez](#)

DLL3 delta-like 3 (Drosophila) [Source:HGNC Symbol;Acc:2909]

Functions:



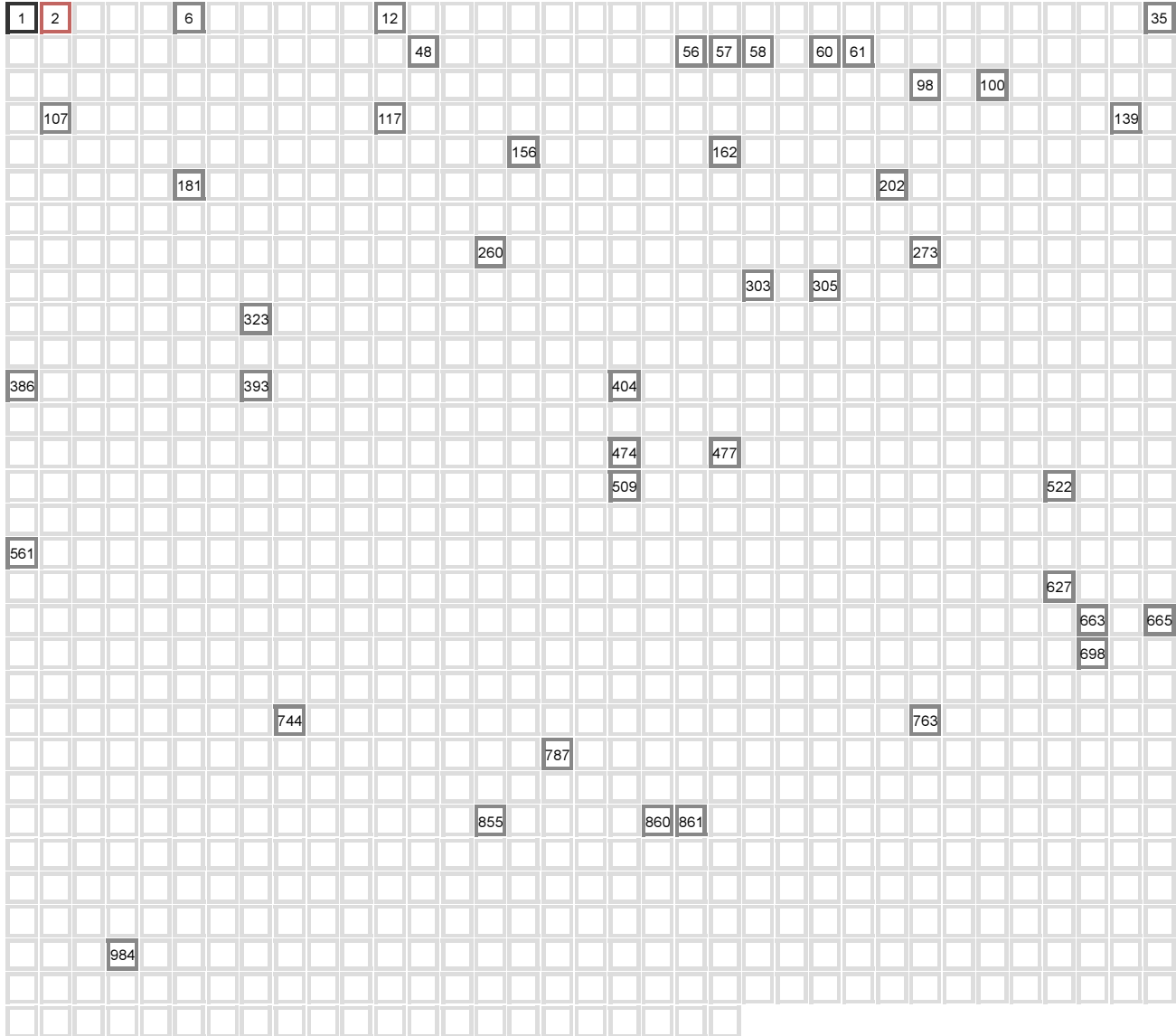


Synonyms: ENSG00000090932; ENSP00000205143; ENSP00000348810; 10683; DLL3; NP_058637; NP_982353; NM_016941; NM_203486; SCDO1; DLL3_HUMAN; Q9NYJ7;

More at [Entrez](#)

HOXA11 homeobox A11 [Source:HGNC Symbol;Acc:5101]

Functions:

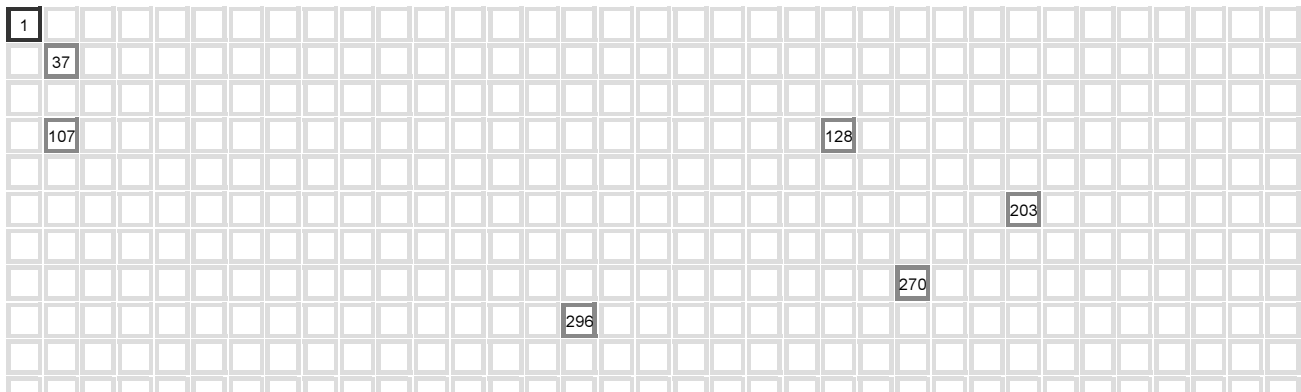


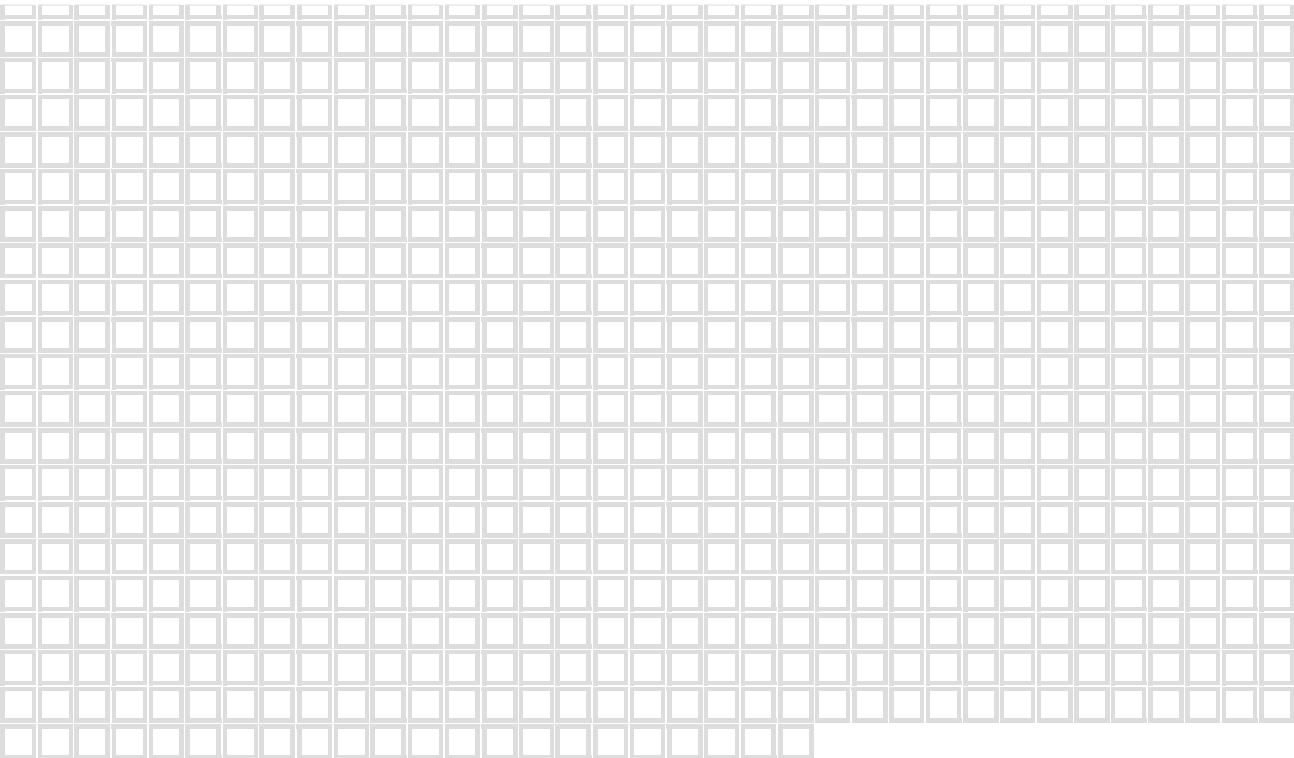
Synonyms: ENSG00000005073; ENSP00000006015; ENSP00000448962; 3207; HOXA11; NP_005514; NM_005523; HOX11; HXA11_HUMAN; P31270;

More at [Entrez](#)

BEX1 brain expressed, X-linked 1 [Source:HGNC Symbol;Acc:1036]

Functions:



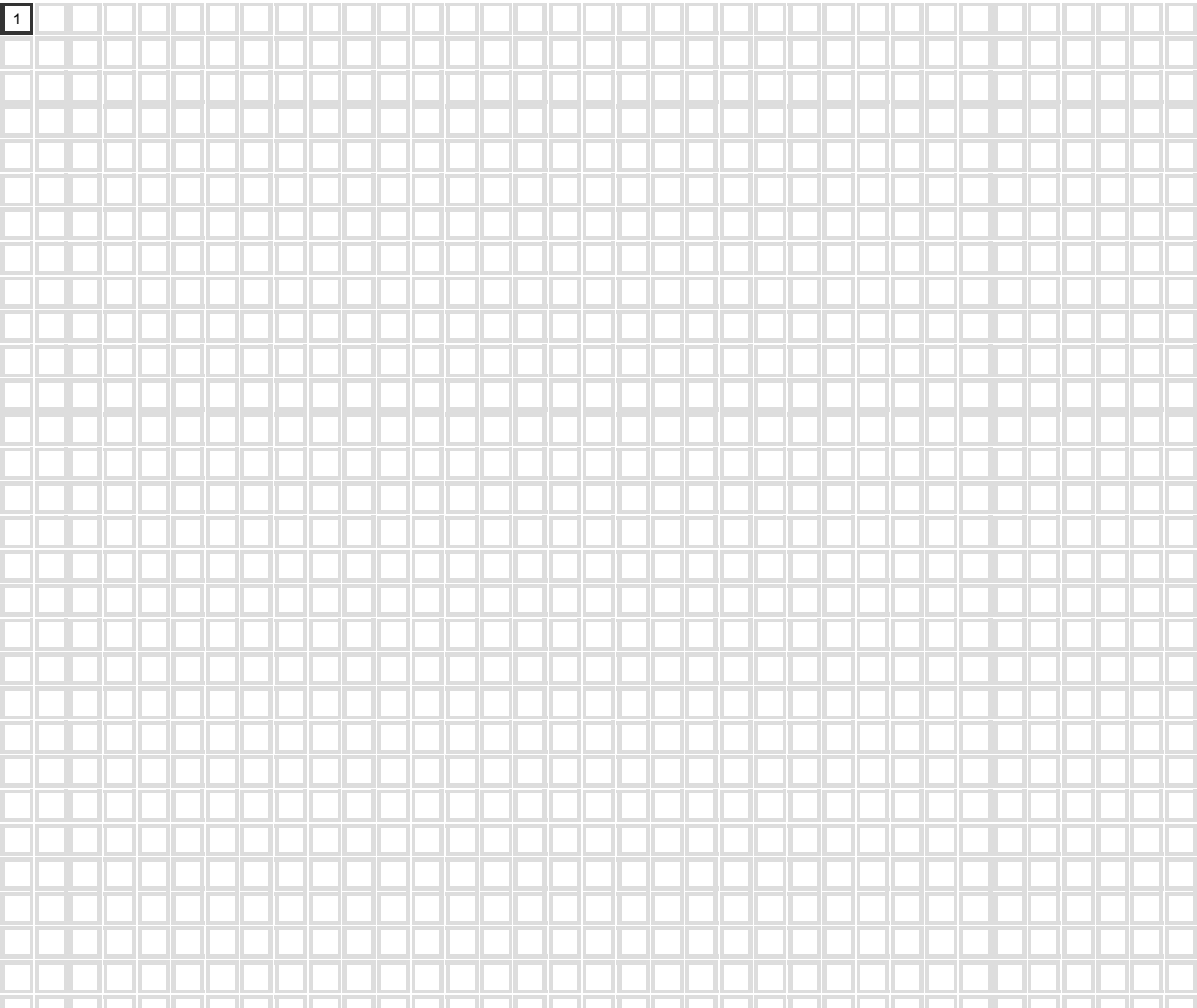


Synonyms: ENSG00000133169; ENSP00000361813; 55859; BEX1; NP_060946; NM_018476; HBEX2; HGR74-h; BEX1_HUMAN; Q9HBH7;

More at [Entrez](#)

TGIF2 TGFB-induced factor homeobox 2 [Source:HGNC Symbol;Acc:15764]

Functions:



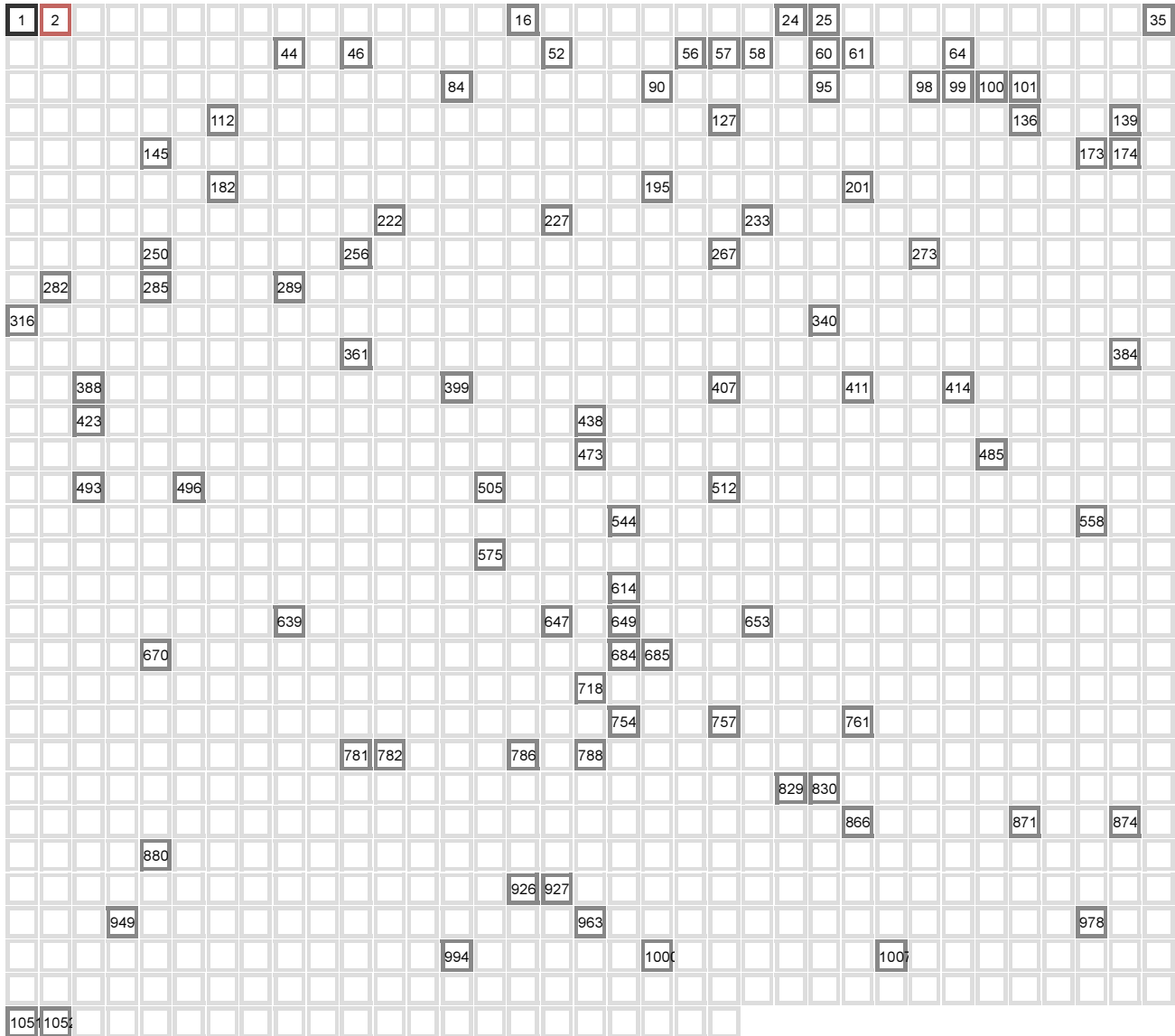


Synonyms: ENSG00000118707; ENSP00000362979; ENSP00000362981; ENSP00000452878; ENSP00000453773; 60436; TGIF2; NP_001186442; NP_001186443; NP_001186444; NP_068581; NM_001199513; NM_001199514; NM_001199515; NM_021809; Q9GZN2; TGIF2_HUMAN;

More at [Entrez](#)

WNT7B wingless-type MMTV integration site family, member 7B [Source:HGNC Symbol;Acc:12787]

Functions:

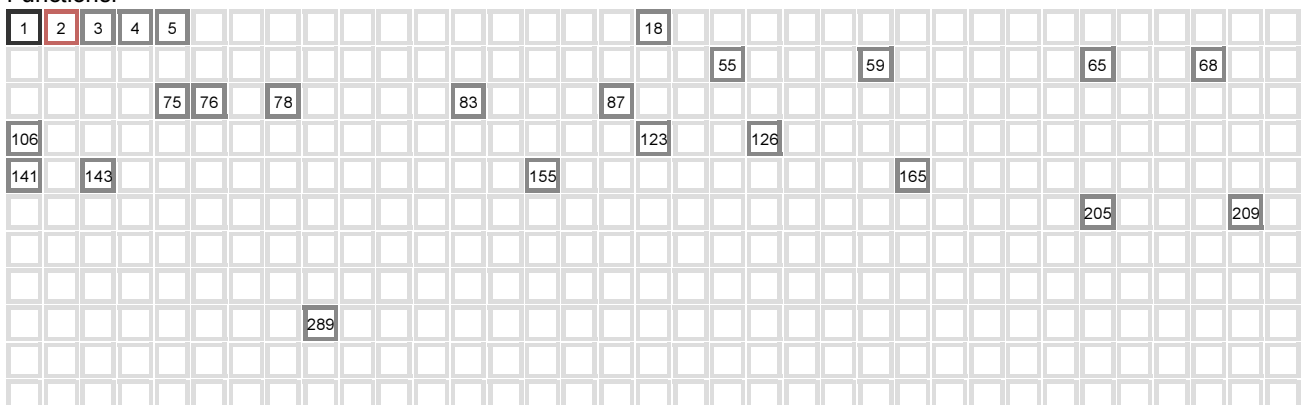


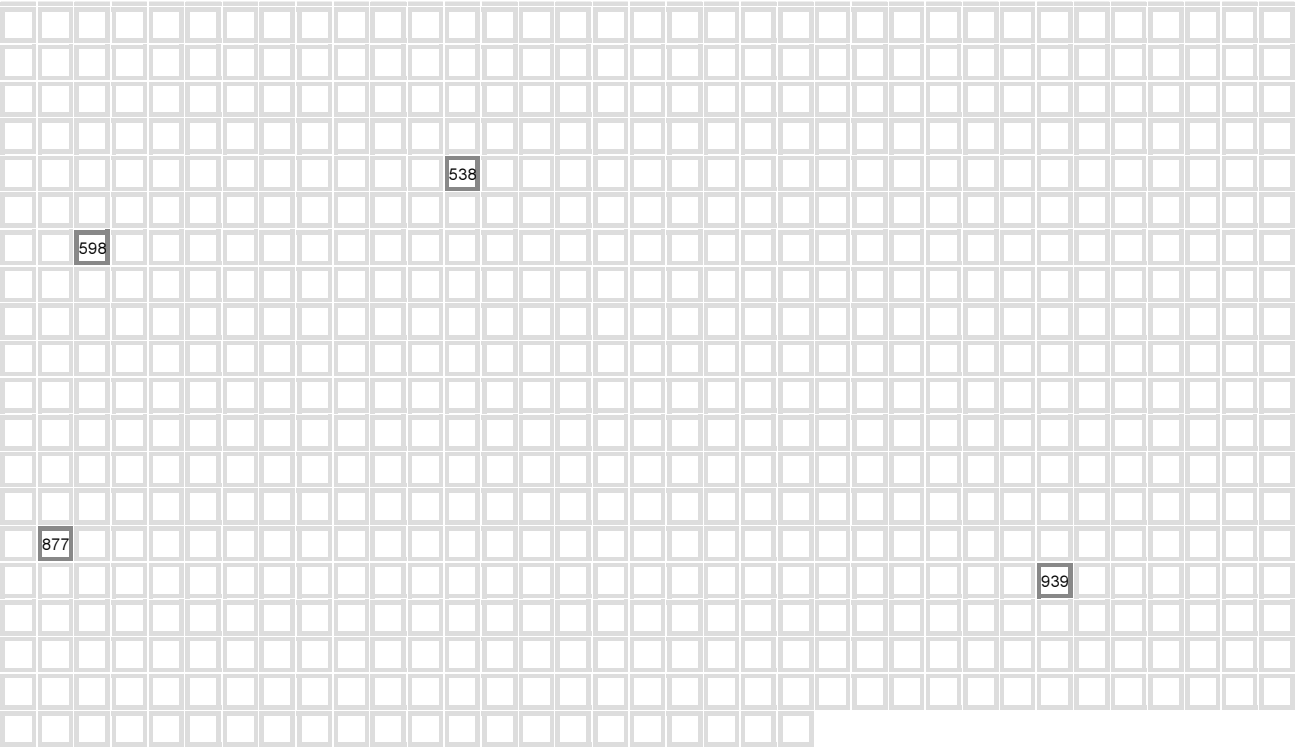
Synonyms: ENSG00000188064; ENSP00000341032; ENSP00000386546; ENSP00000386781; ENSP00000387217; ENSP00000392750; 7477; WNT7B; NP_478679; NM_058238; P56706; WNT7B_HUMAN;

More at [Entrez](#)

VNN1 vanin 1 [Source:HGNC Symbol;Acc:12705]

Functions:



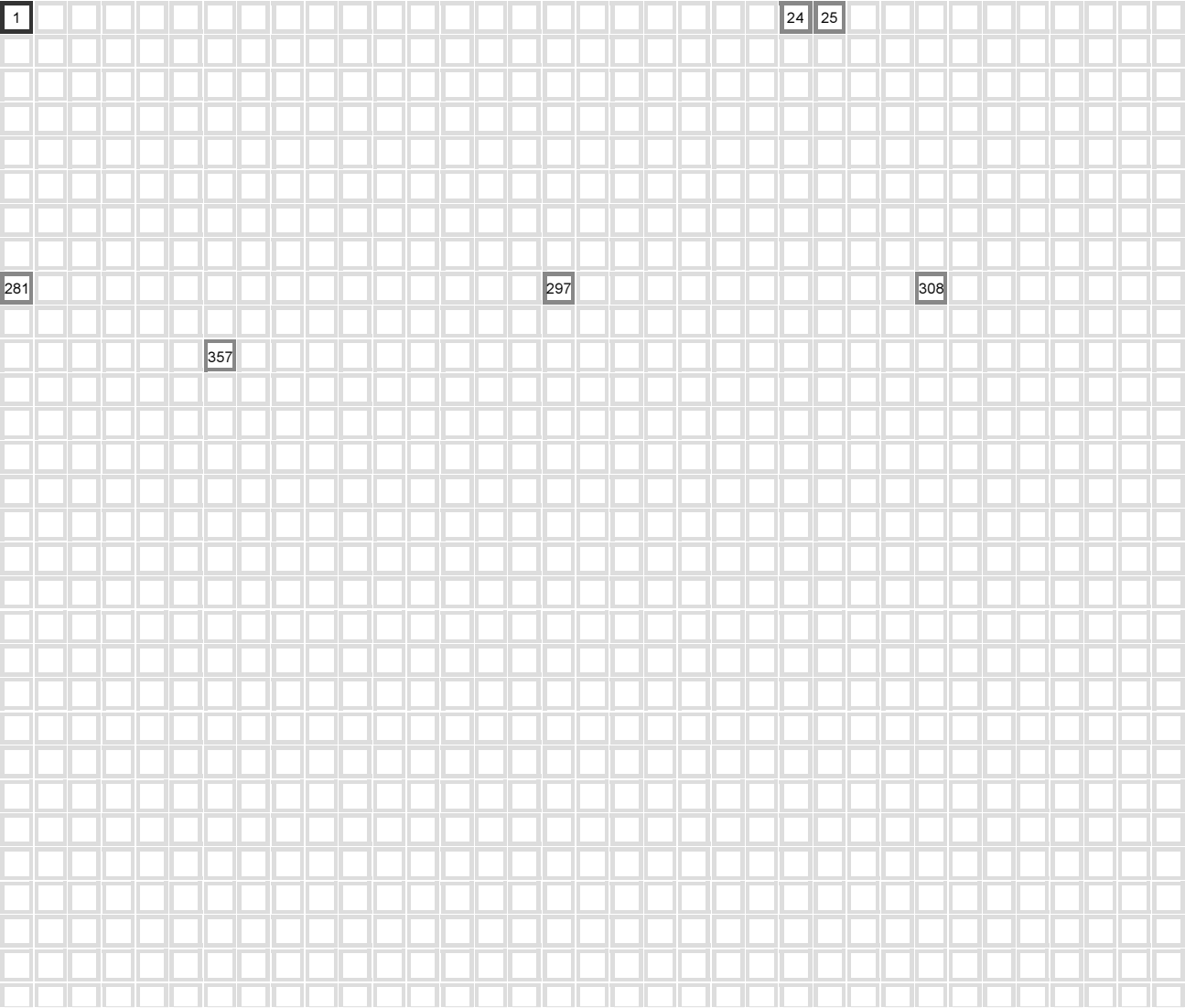


Synonyms: ENSG00000112299; ENSP00000356905; 8876; VNN1; NP_004657; NM_004666; HDLCQ8; Tiff66; O95497; VNN1_HUMAN;

More at [Entrez](#)

RUNX2 runt-related transcription factor 2 [Source:HGNC Symbol;Acc:10472]

Functions:



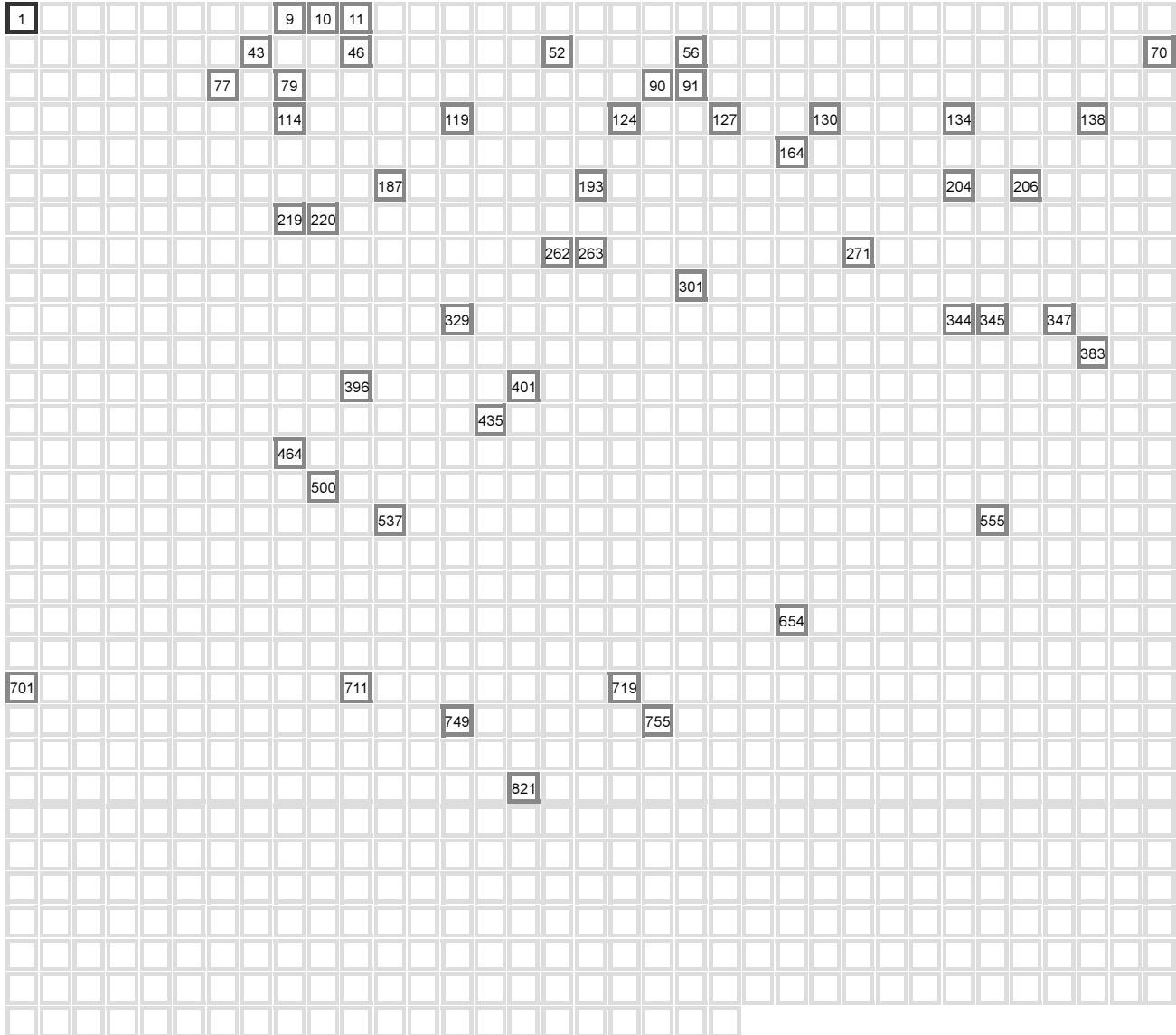


Synonyms: ENSG00000124813; ENSP00000319087; ENSP00000352514; ENSP00000360486; ENSP00000360491; ENSP00000360493; ENSP00000420707; ENSP00000446290; 860; RUNX2; NP_001015051; NP_001019801; NP_004339; NM_001015051; NM_001024630; NM_004348; AML3; CBFA1; CCD; PEA2aA; PEBP2A1; PEBP2aA; PEBP2aA1; Q13950; RUNX2_HUMAN;

More at [Entrez](#)

GATA6 GATA binding protein 6 [Source:HGNC Symbol;Acc:4174]

Functions:

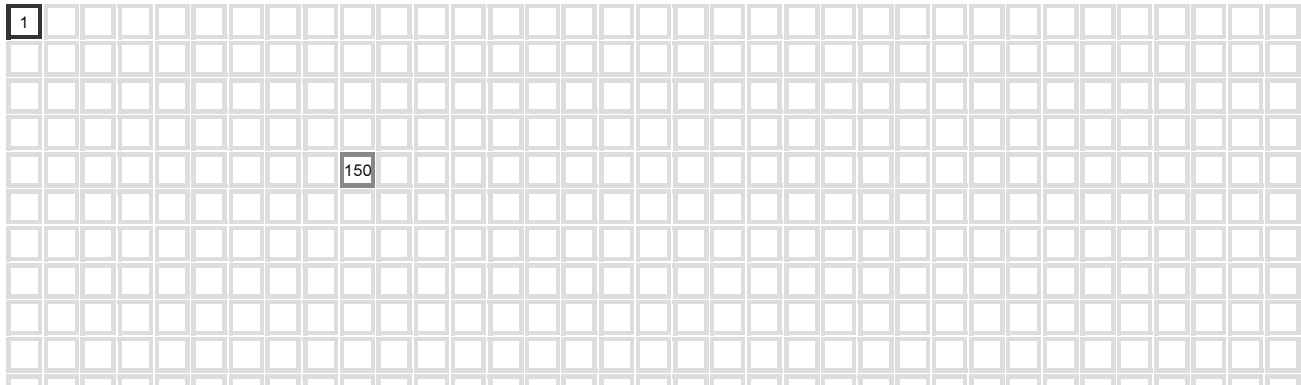


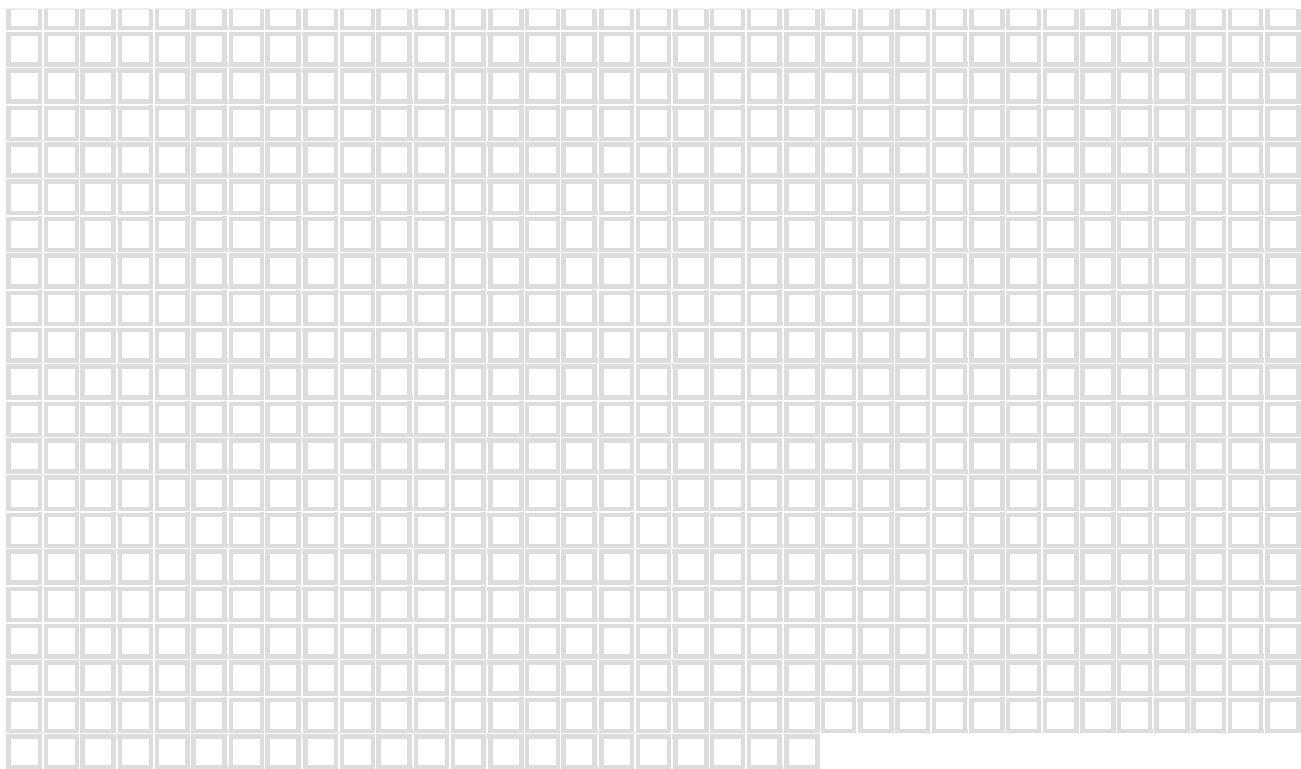
Synonyms: ENSG00000141448; ENSP00000269216; 2627; GATA6; NP_005248; NM_005257; GATA6_HUMAN; Q92908;

More at [Entrez](#)

NTRK3 neurotrophic tyrosine kinase, receptor, type 3 [Source:HGNC Symbol;Acc:8033]

Functions:



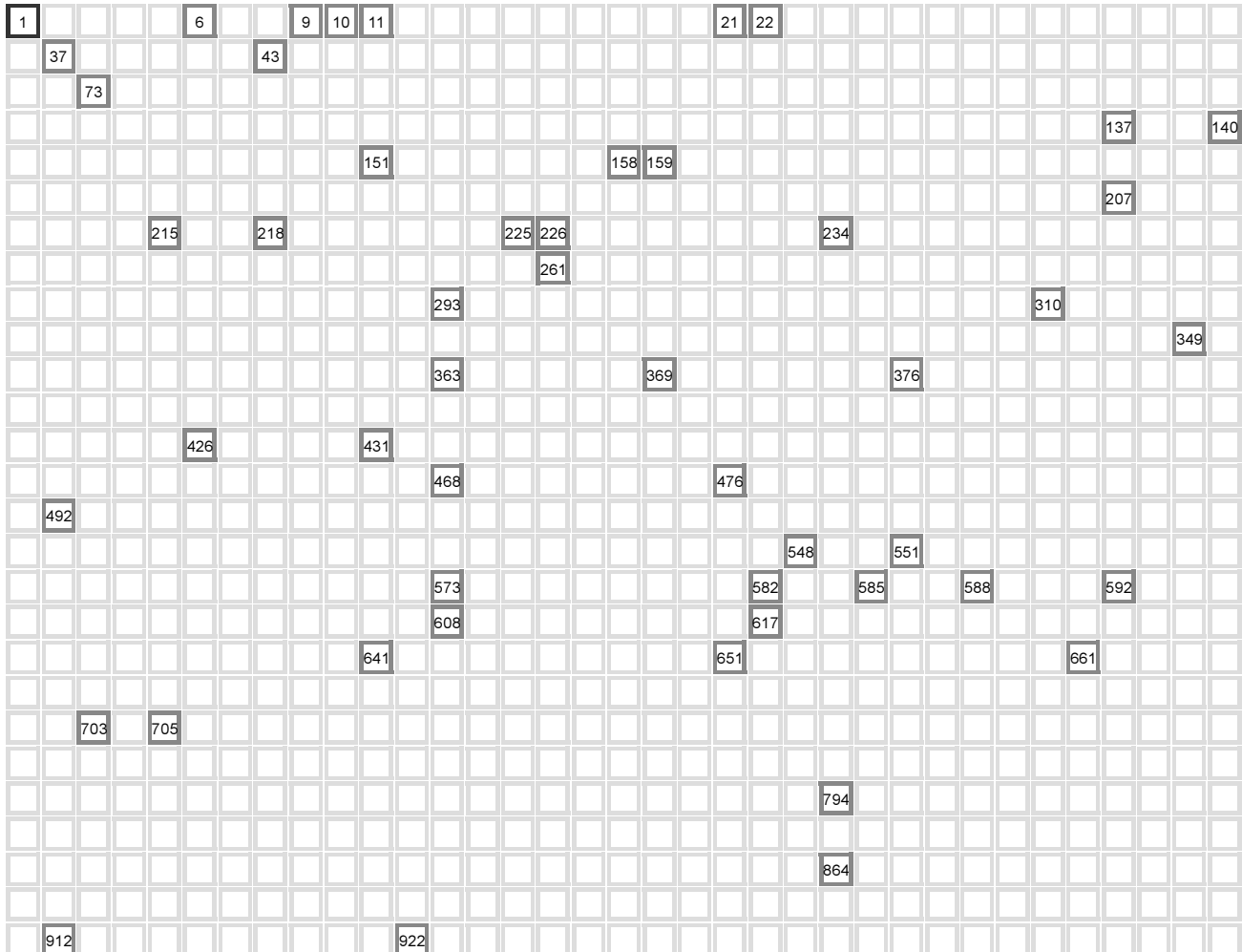


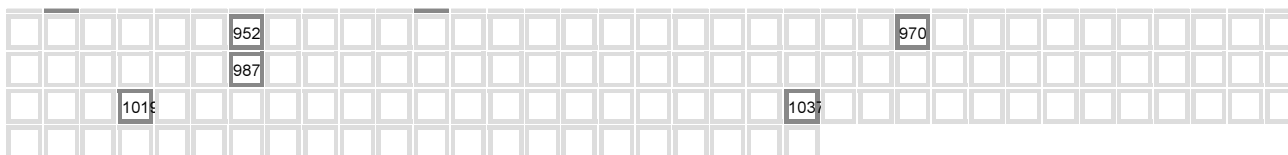
Synonyms: ENSG00000140538; ENSP00000318328; ENSP00000342792; ENSP00000347397; ENSP00000350356; ENSP00000354207; ENSP00000377990; ENSP00000437773; ENSP00000444673; ENSP00000453511; ENSP00000453624; ENSP00000453959; 4916; NTRK3; NP_001007157; NP_001012338; NP_001230030; NP_002521; NM_001007156; NM_001012338; NM_001243101; NM_002530; gp145(trkC); TRKC; NTRK3_HUMAN; Q16288;

More at [Entrez](#)

GF11 growth factor independent 1 transcription repressor [Source:HGNC Symbol;Acc:4237]

Functions:



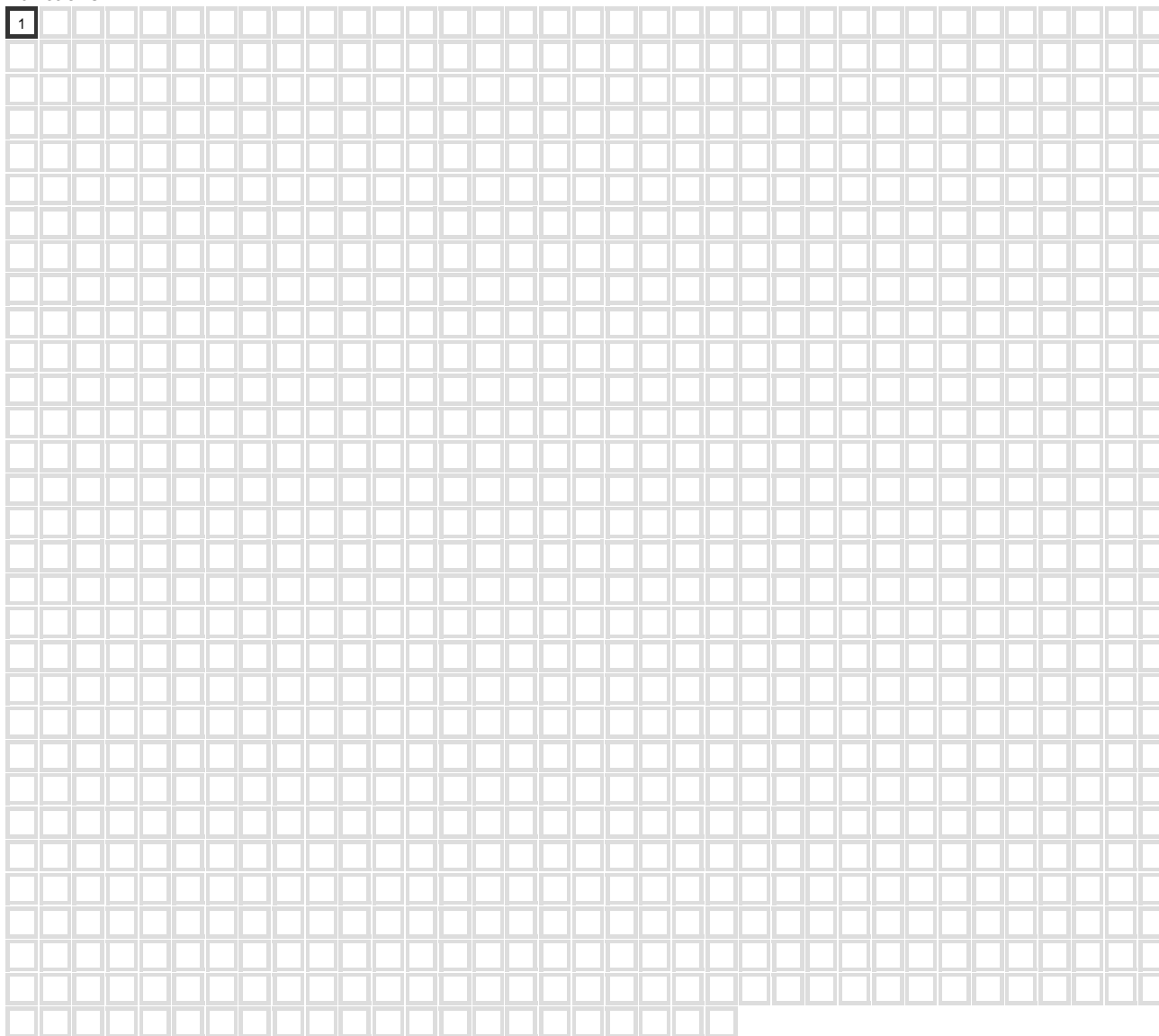


Synonyms: ENSG00000162676; ENSP00000294702; ENSP00000359357; ENSP00000399719; 2672; GFI1; NP_001120687; NP_001120688; NP_005254; NM_001127215; NM_001127216; NM_005263; GFI-1; SCN2; ZNF163; GFI1_HUMAN; Q99684;

More at [Entrez](#)

SMAP1 small ArfGAP 1 [Source:HGNC Symbol;Acc:19651]

Functions:

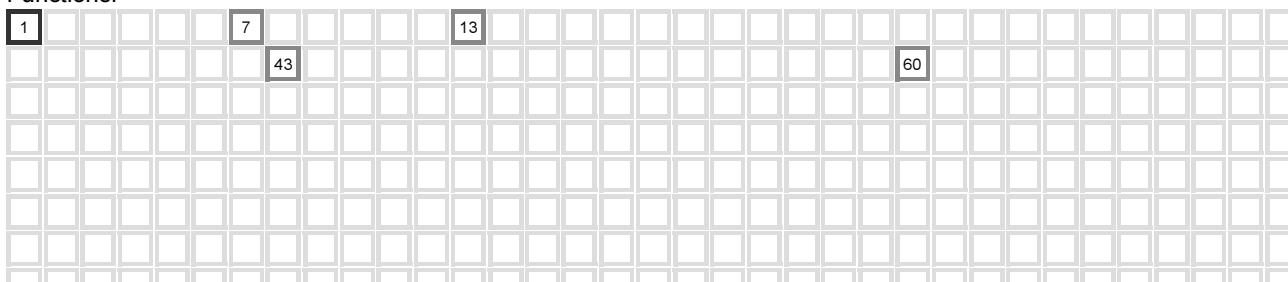


Synonyms: ENSG00000112305; ENSP00000313382; ENSP00000359471; ENSP00000359481; ENSP00000359484; ENSP00000398306; ENSP00000398541; ENSP00000415426; 60682; SMAP1; NP_001037770; NP_068759; NM_001044305; NM_021940; FLJ13159; Q8IYB5; SMAP1_HUMAN;

More at [Entrez](#)

KLF10 Kruppel-like factor 10 [Source:HGNC Symbol;Acc:11810]

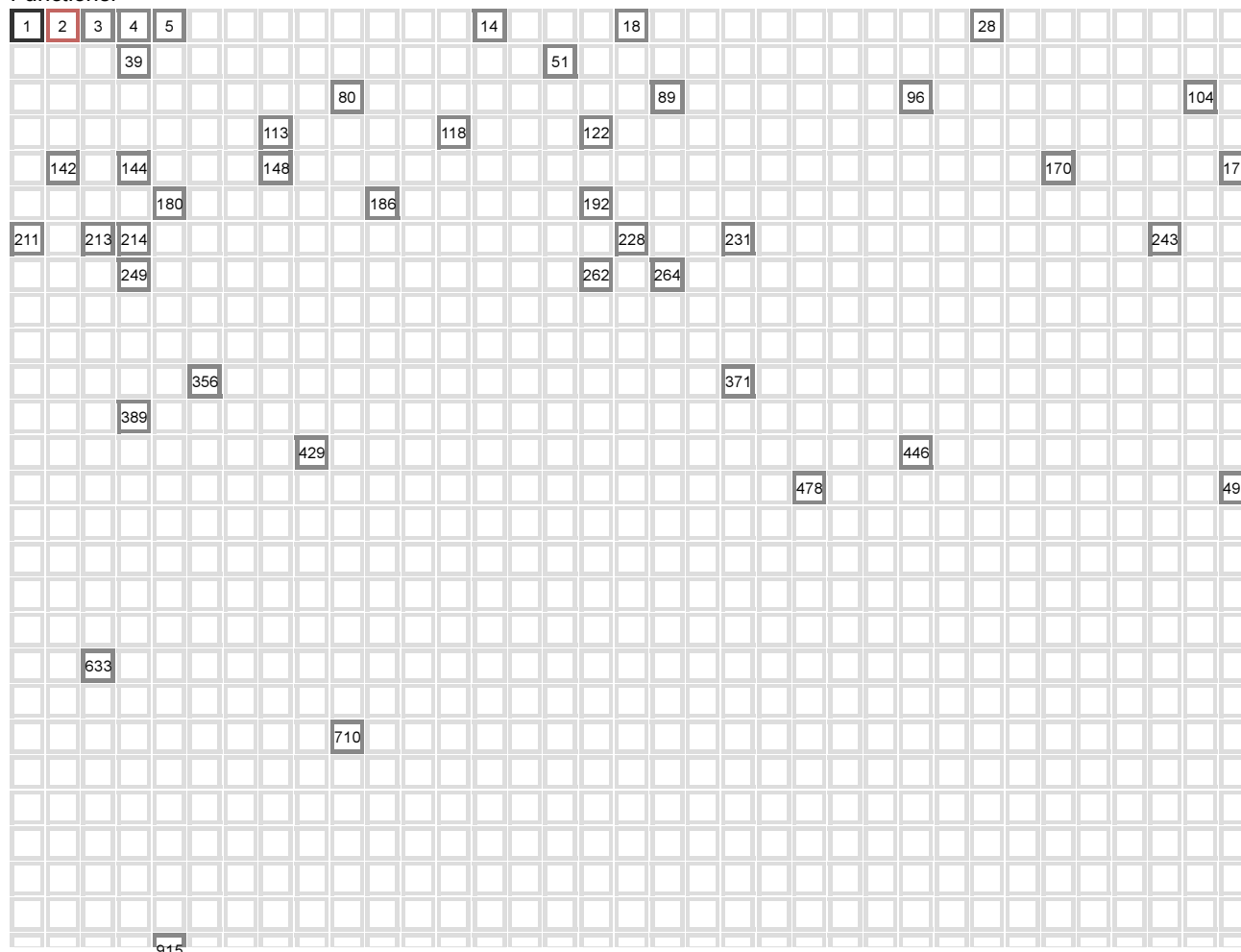
Functions:

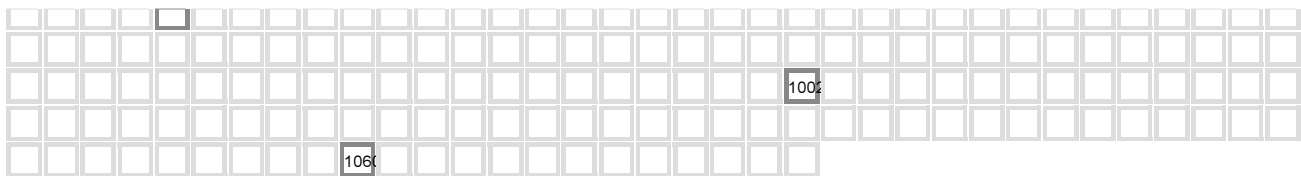


More at [Entrez](#)

CSF1 colony stimulating factor 1 (macrophage) [Source:HGNC Symbol;Acc:2432]

Functions:



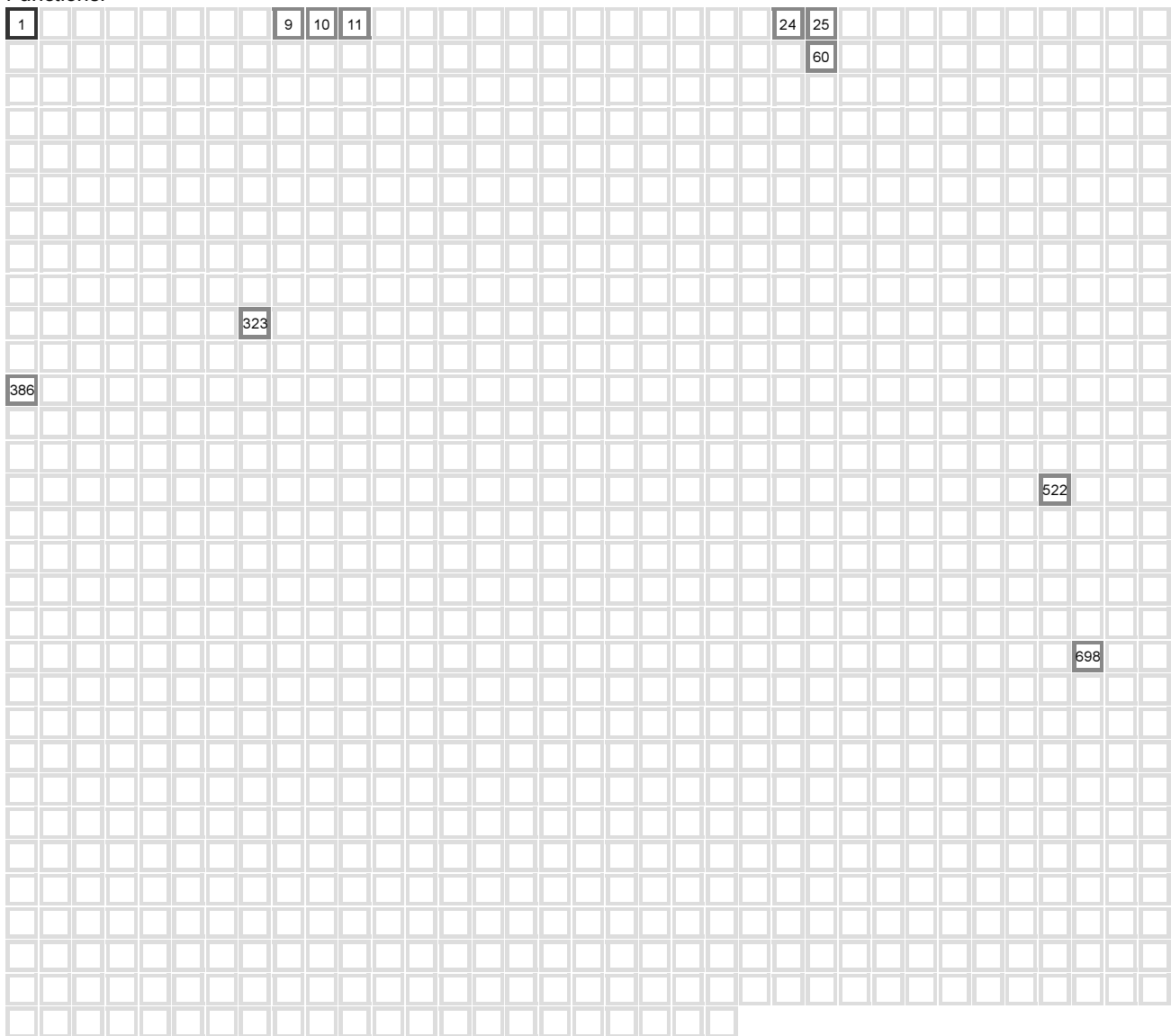


Synonyms: ENSG00000184371; ENSP00000327513; ENSP00000342718; ENSP00000349854; ENSP00000358816; ENSP00000358817; ENSP00000407317; ENSP00000431547; ENSP00000433837; ENSP00000434527; 1435; CSF1; NP_000748; NP_757349; NP_757350; NP_757351; NM_000757; NM_172210; NM_172211; NM_172212; CSF-1; M-CSF; MCSF; MGC31930; CSF1_HUMAN; P09603;

More at [Entrez](#)

DLX5 distal-less homeobox 5 [Source:HGNC Symbol;Acc:2918]

Functions:

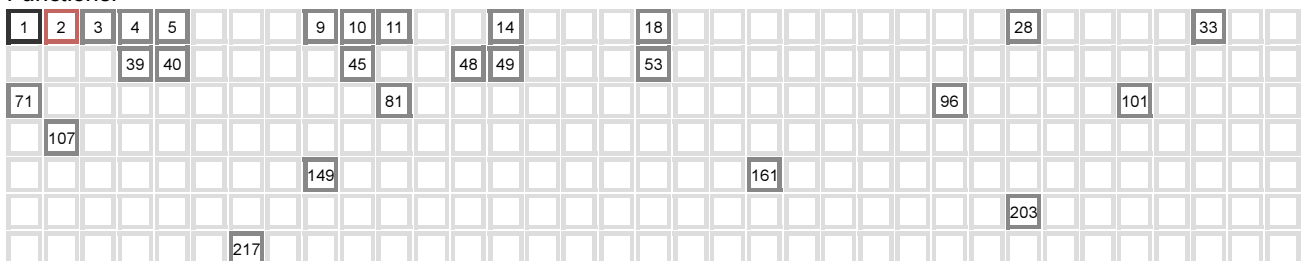


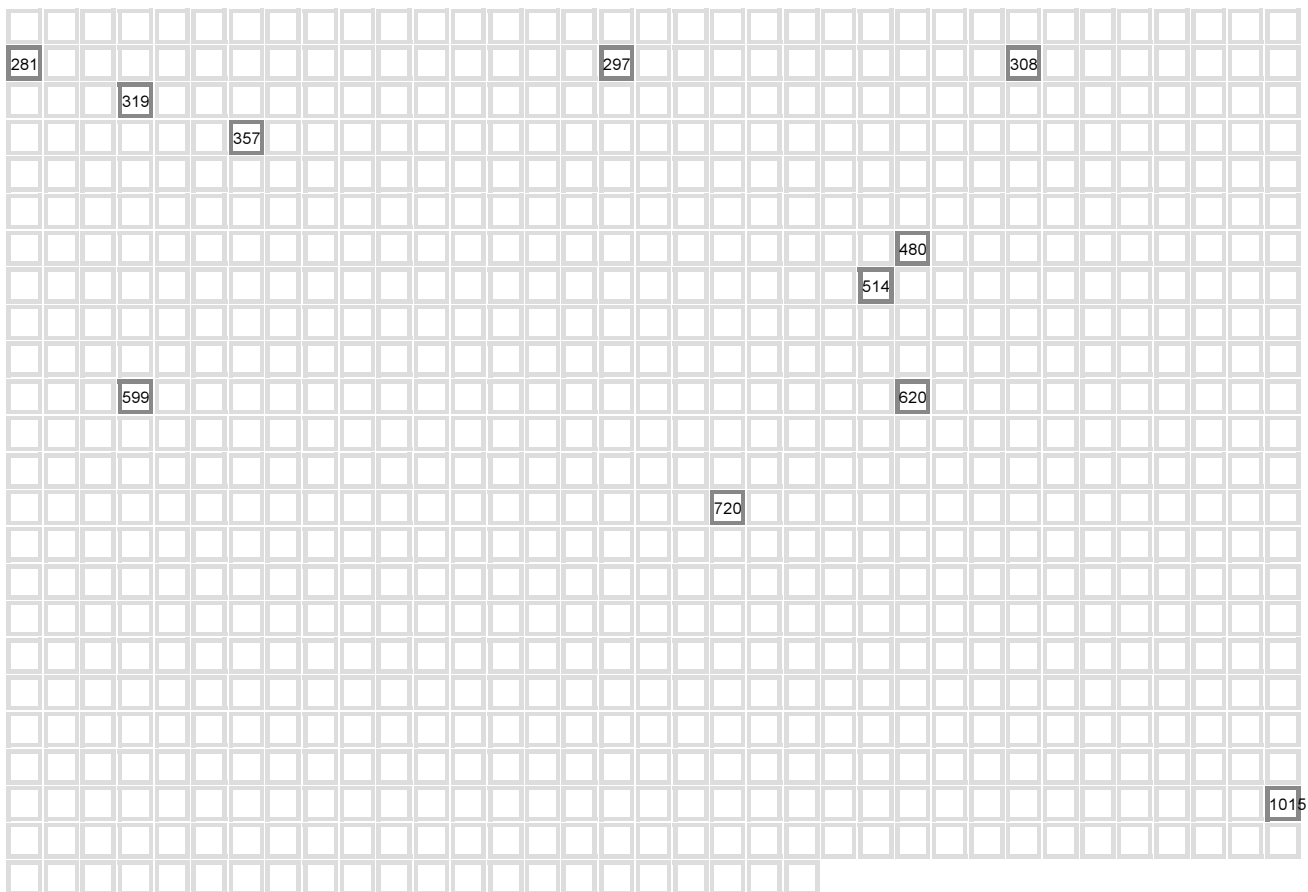
Synonyms: ENSG00000105880; ENSP00000222598; 1749; DLX5; NP_005212; NM_005221; DLX5_HUMAN; P56178;

More at [Entrez](#)

TAL1 T-cell acute lymphocytic leukemia 1 [Source:HGNC Symbol;Acc:11556]

Functions:



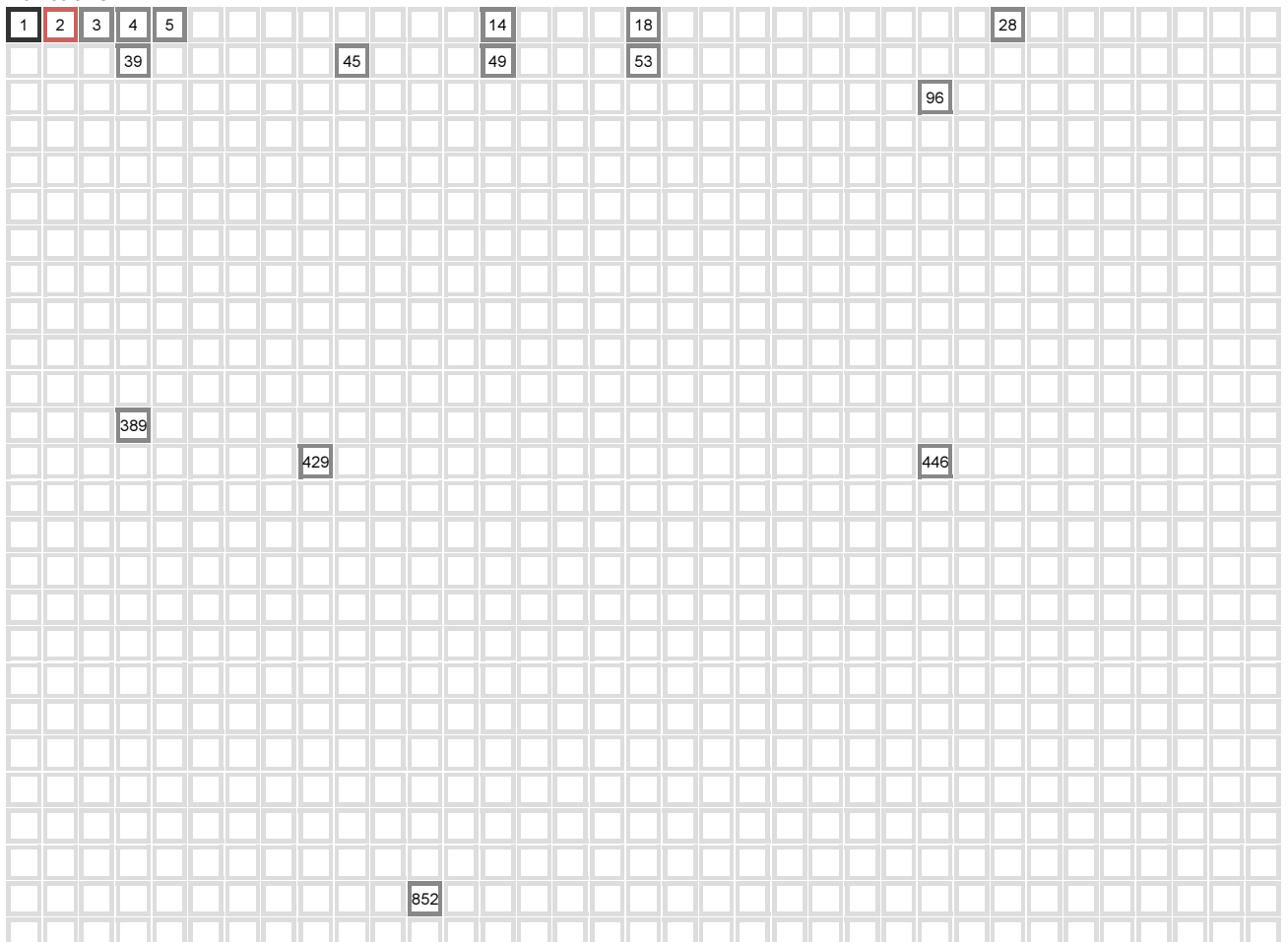


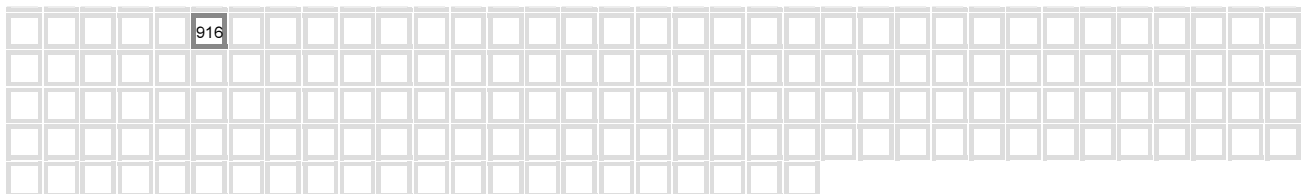
Synonyms: ENSG00000162367; ENSP00000294339; ENSP00000360950; ENSP00000360951; 6886; TAL1; NP_003180; NM_003189; bHLHa17; tal-1; TCL5; P17542; TAL1_HUMAN;

More at [Entrez](#)

ACIN1 apoptotic chromatin condensation inducer 1 [Source:HGNC Symbol;Acc:17066]

Functions:



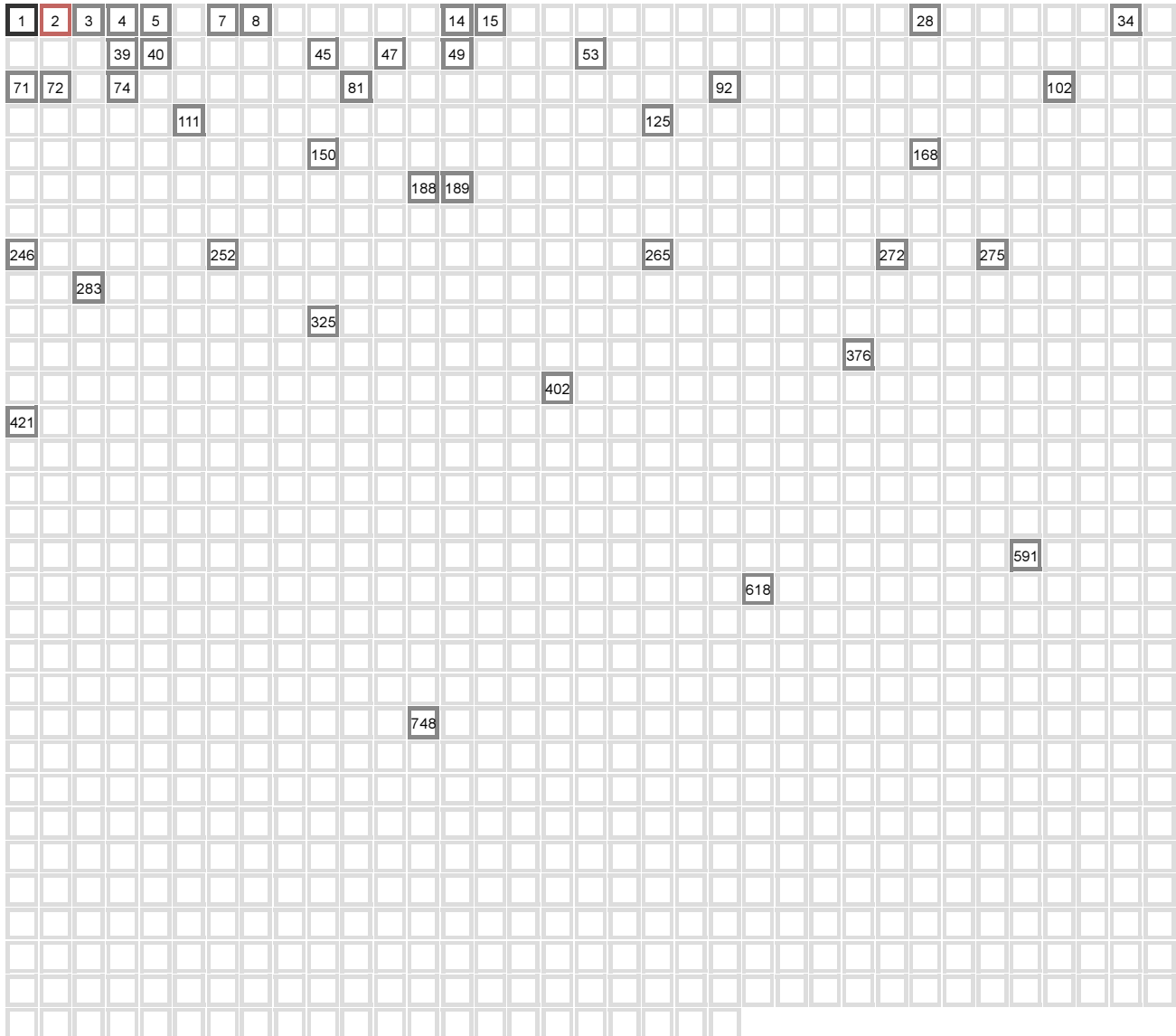


Synonyms: ENSG00000100813; ENSP00000262710; ENSP00000345541; ENSP00000350073; ENSP00000380502; ENSP00000405677; ENSP00000451138; ENSP00000451328; ENSP00000451410; 22985; ACIN1; NP_001158286; NP_001158287; NP_001158288; NP_001158289; NP_055792; NM_001164814; NM_001164815; NM_001164816; NM_001164817; NM_014977; ACINUS; fSAP152; KIAA0670; ACINU_HUMAN; Q9UKV3;

More at [Entrez](#)

ACVR1B activin A receptor, type IB [Source:HGNC Symbol;Acc:172]

Functions:

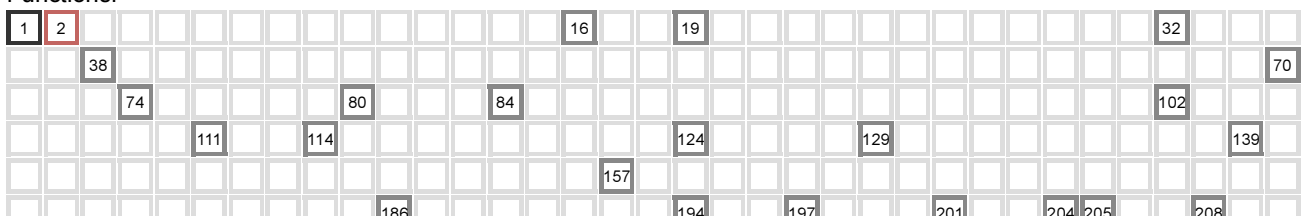


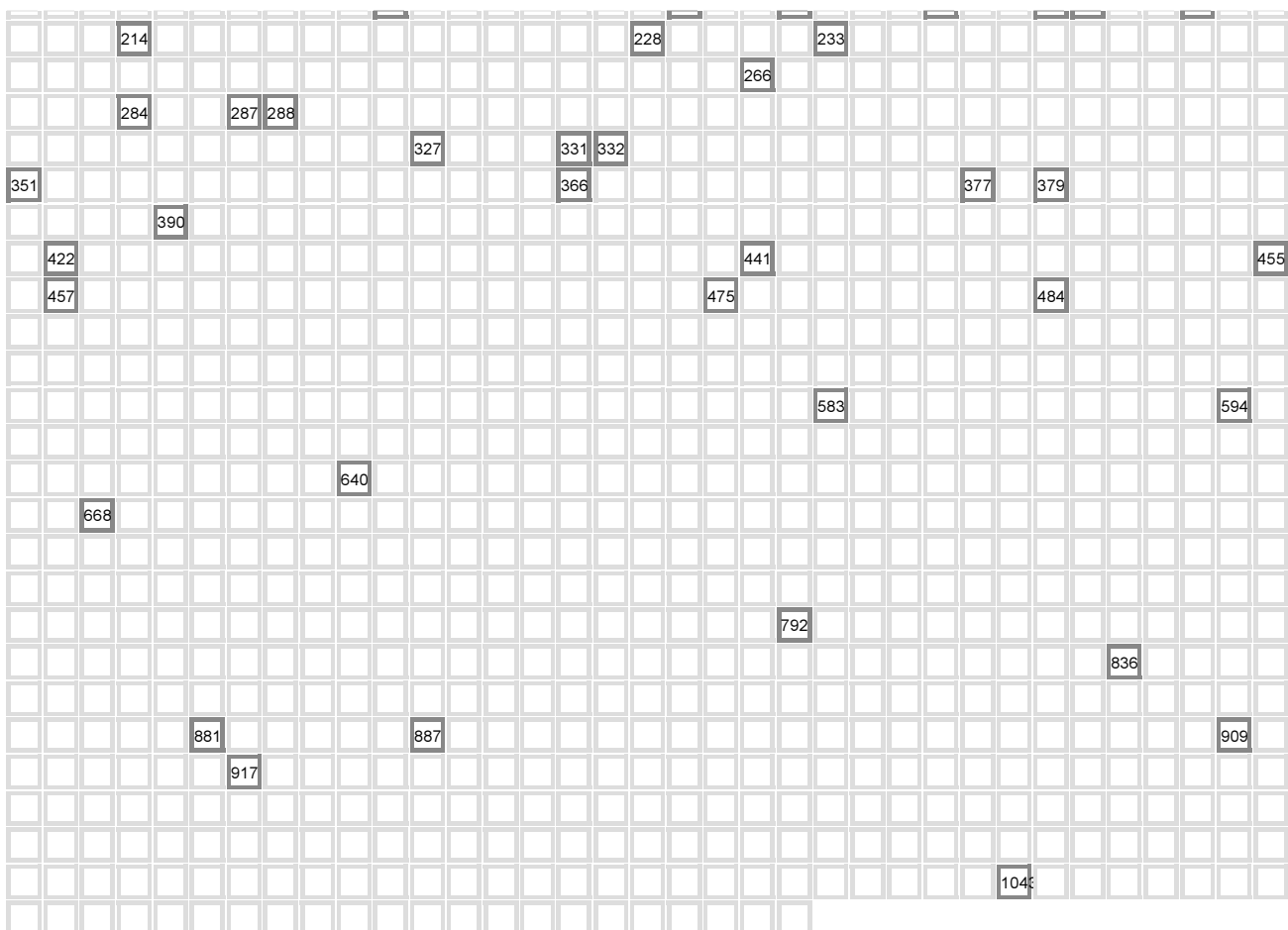
Synonyms: ENSG00000135503; ENSP00000257963; ENSP00000390477; ENSP00000397550; ENSP00000442656; ENSP00000442885; ENSP00000443218; 91; ACVR1B; NP_004293; NP_064732; NP_064733; NM_004302; NM_020327; NM_020328; ACTRIB; ALK4; SKR2; ACV1B_HUMAN; P36896;

More at [Entrez](#)

NRG1 neuregulin 1 [Source:HGNC Symbol;Acc:7997]

Functions:



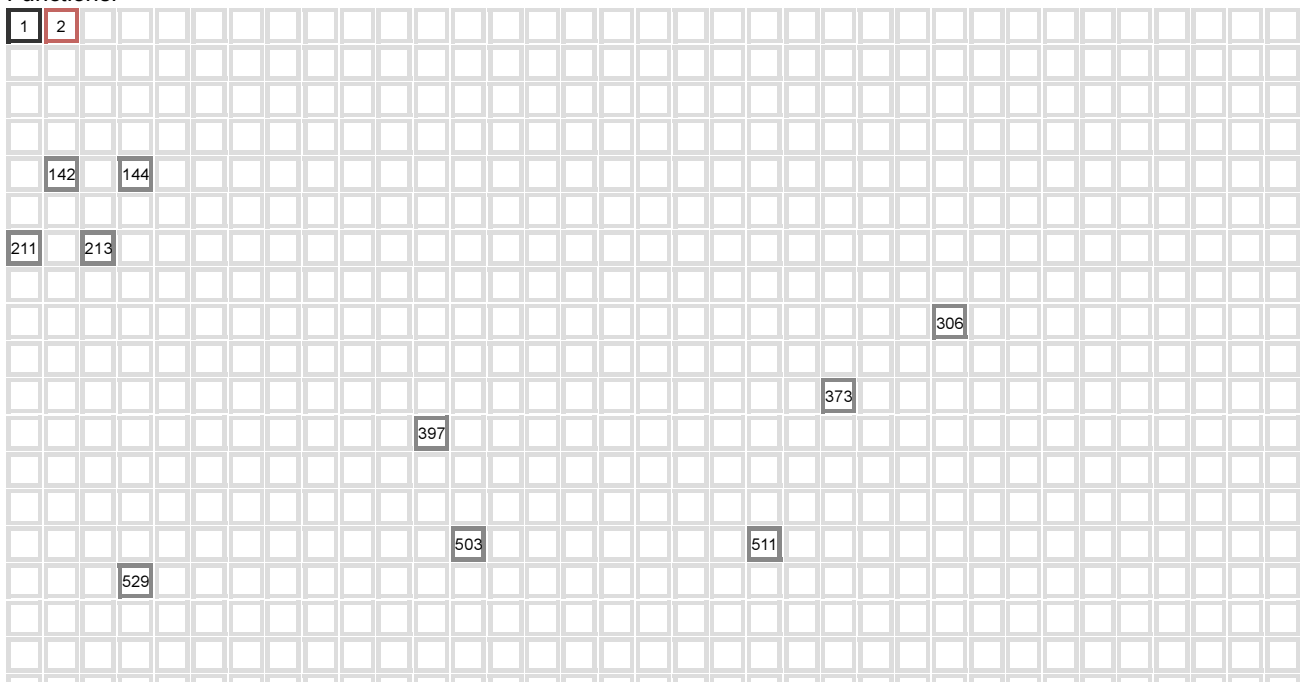


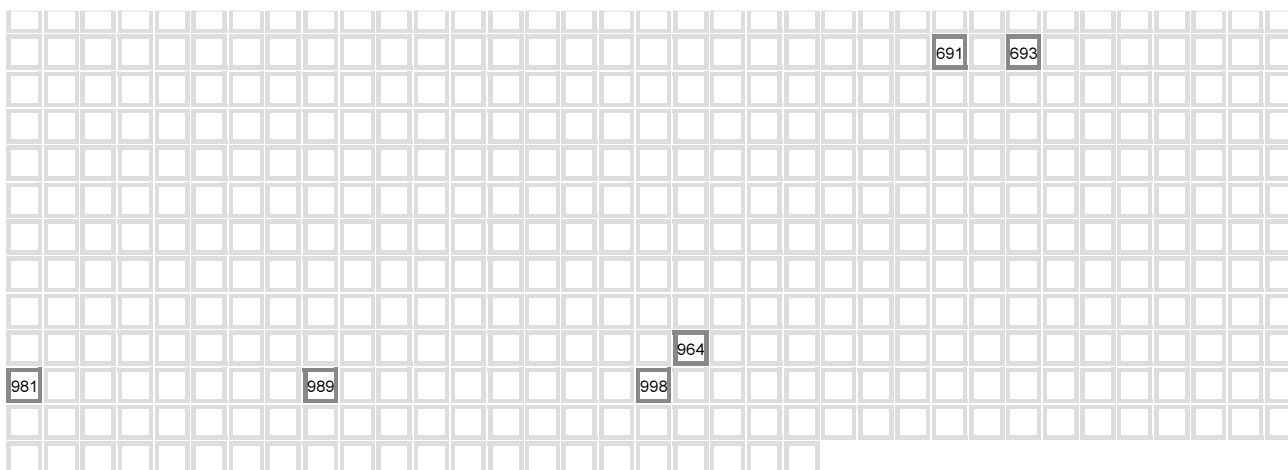
Synonyms: ENSG00000157168; ENSP00000287840; ENSP00000287842; ENSP00000287845; ENSP00000340497; ENSP00000343395; ENSP00000349275; ENSP00000384620; ENSP00000428411; ENSP00000428546; ENSP00000428828; ENSP00000429067; ENSP00000429582; ENSP00000430053; ENSP00000430120; ENSP00000430862; ENSP00000432052; ENSP00000433289; ENSP00000433350; ENSP00000434640; ENSP00000439276; 3084; NRG1; NP_001153467; NP_001153468; NP_001153471; NP_001153473; NP_001153474; NP_001153476; NP_001153477; NP_001153479; NP_001153480; NP_004486; NP_039250; NP_039251; NP_039252; NP_039253; NP_039254; NP_039256; NP_039258; NM_001159995; NM_001159996; NM_001159999; NM_001160001; NM_001160002; NM_001160004; NM_001160005; NM_001160007; NM_001160008; NM_004495; NM_013956; NM_013957; NM_013958; NM_013959; NM_013960; NM_013962; NM_013964; GGF; GGF2; HRGA; MST131; NDF; SMDF; NRG1_HUMAN; Q02297;

More at [Entrez](#)

MSR1 macrophage scavenger receptor 1 [Source:HGNC Symbol;Acc:7376]

Functions:



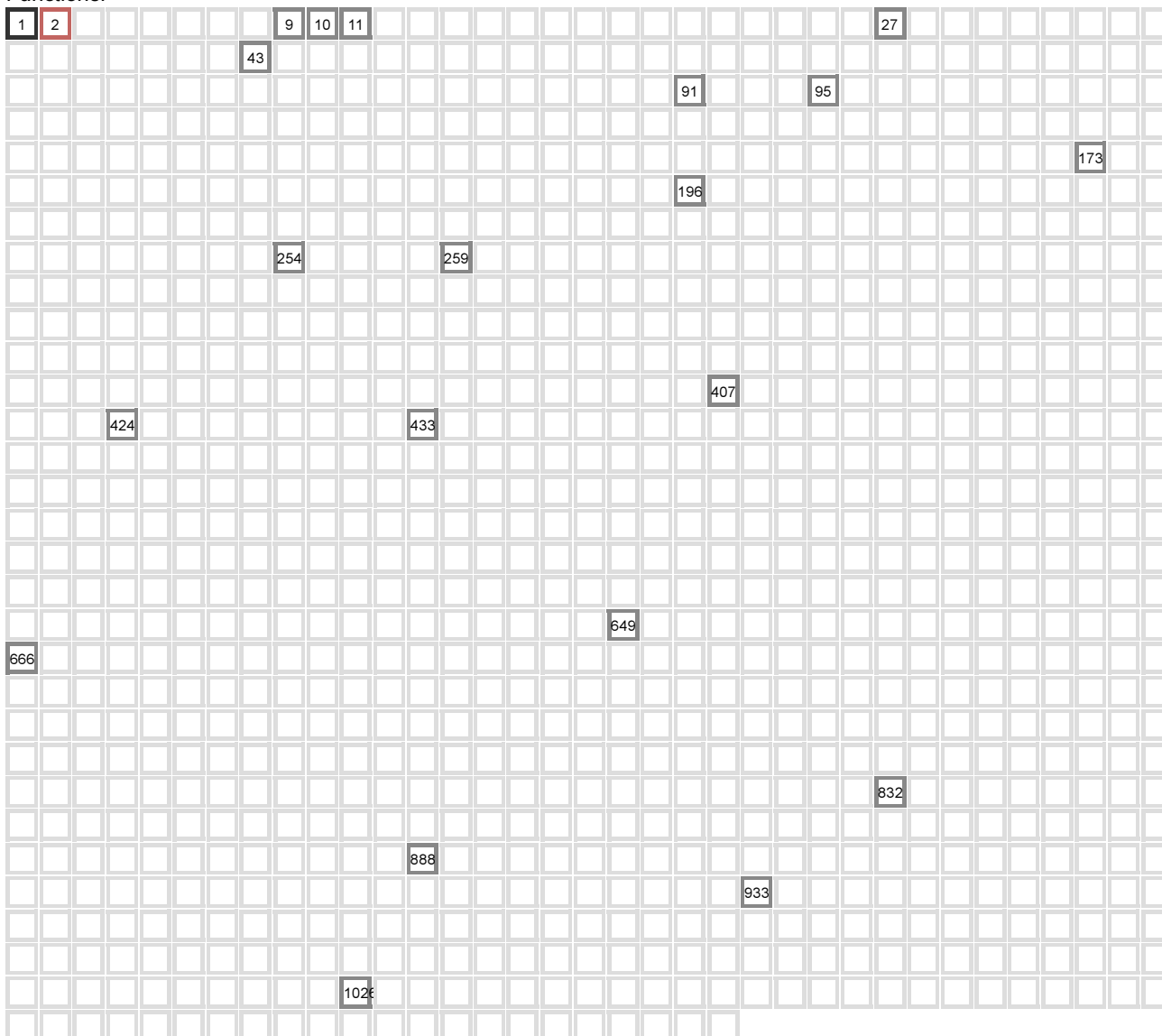


Synonyms: ENSG00000038945; ENSP00000262100; ENSP00000262101; ENSP00000347430; ENSP00000371428; ENSP00000405453; ENSP00000427905; ENSP00000428865; ENSP00000429498; ENSP00000430536; ENSP00000444414; 4481; MSR1; NP_002436; NP_619729; NP_619730; NM_002445; NM_138715; NM_138716; CD204; phSR1; phSR2; SCARA1; SR-A; MSRE_HUMAN; P21757;

More at [Entrez](#)

POU4F2 POU class 4 homeobox 2 [Source:HGNC Symbol;Acc:9219]

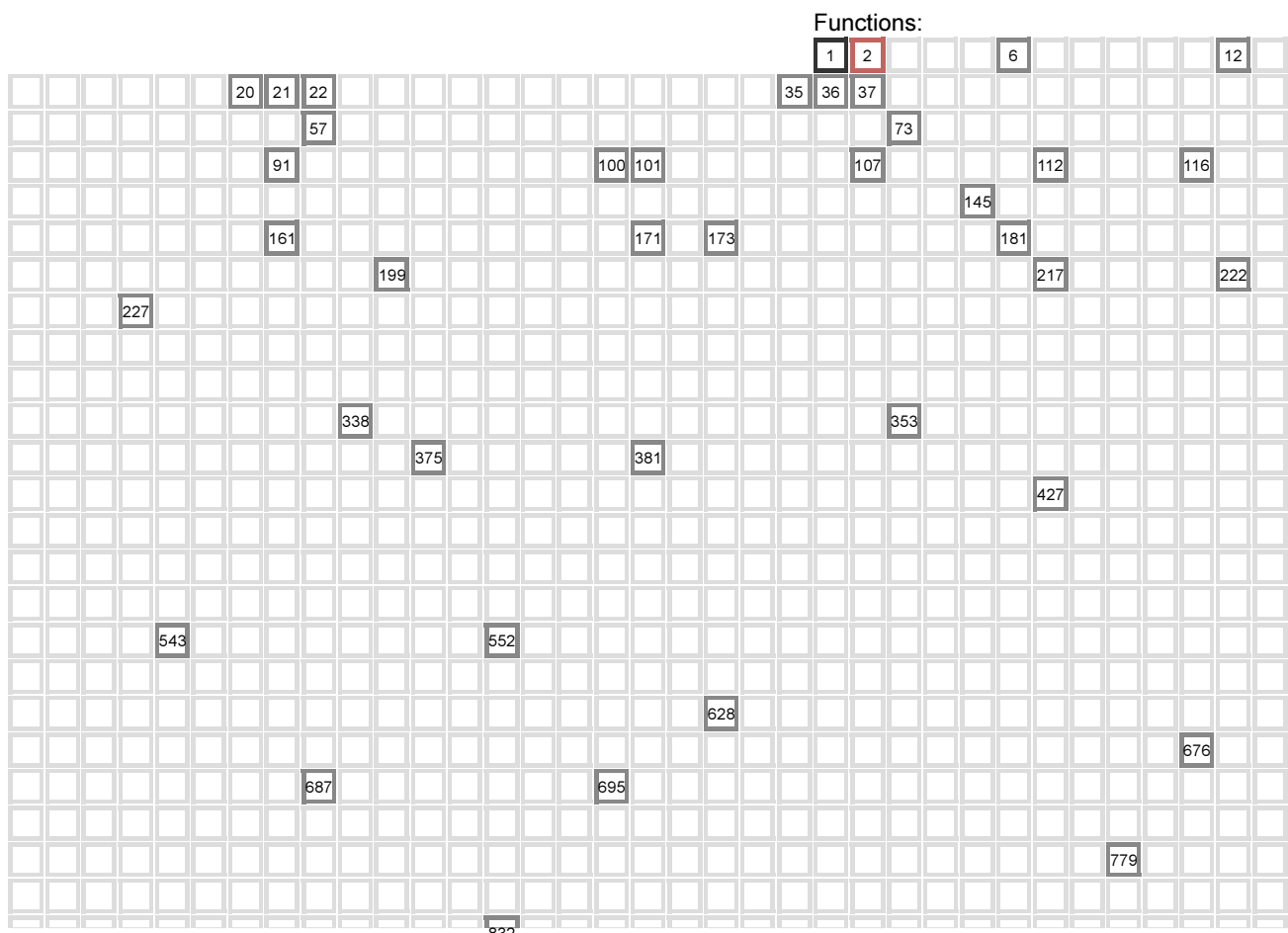
Functions:

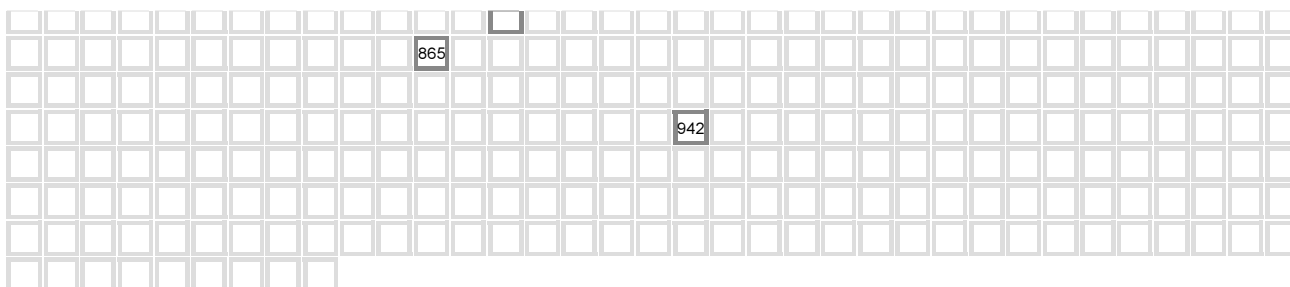


Synonyms: ENSG00000151615; ENSP00000281321; 5458; POU4F2; NP_004566; NM_004575; Brn-3b; BRN3.2; BRN3B; PO4F2_HUMAN; Q12837;

More at [Entrez](#)

FOXG1 forkhead box G1 [Source:HGNC Symbol;Acc:3811]



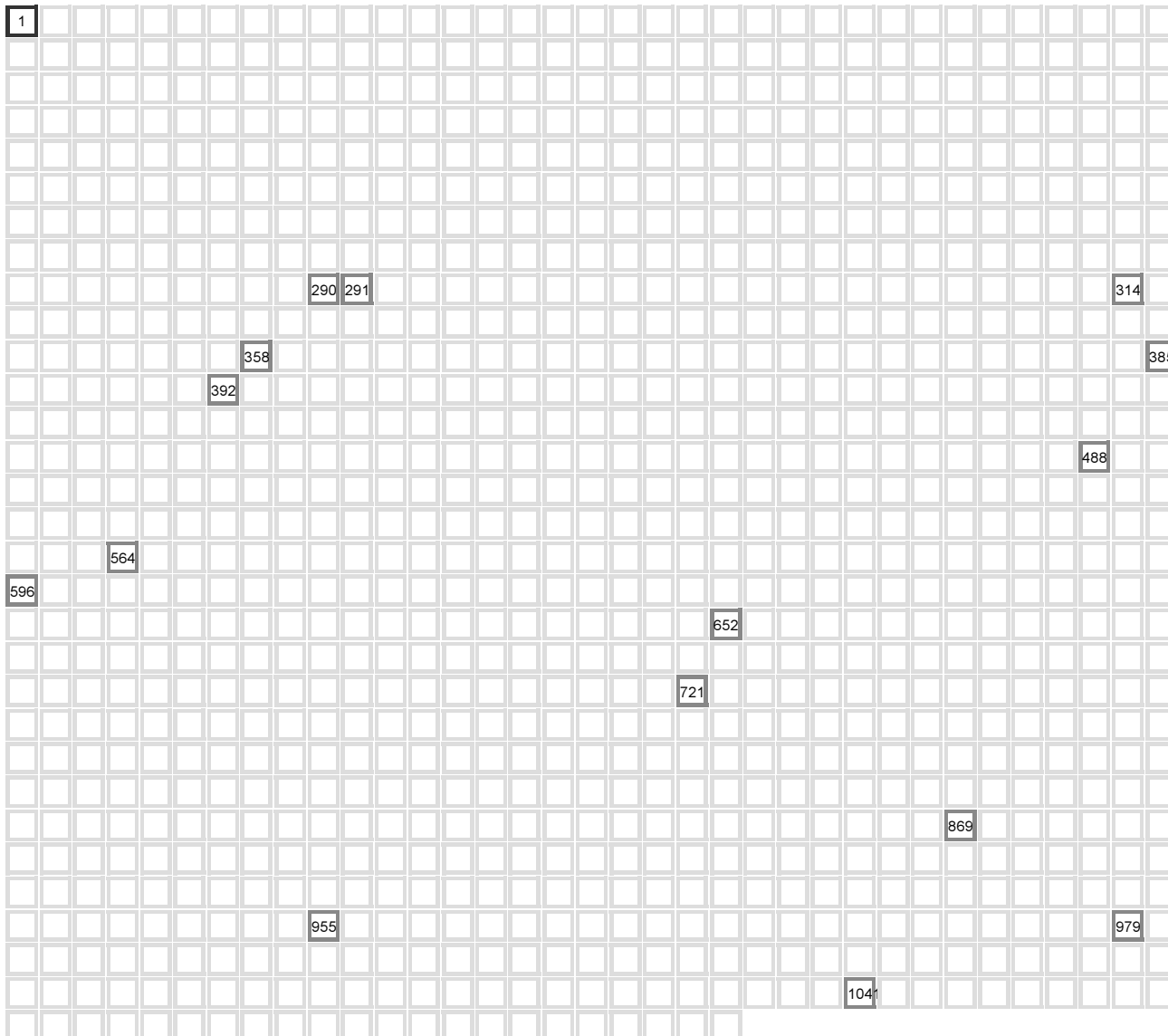


Synonyms: ENSG00000176165; ENSP00000339004; ENSP00000371975; 2290; FOXG1; NP_005240; NM_005249; BF1; BF2; FHKL3; FKHL2; FKHL1; FKHL2; FKHL3; FKHL4; FOXG1A; FOXG1B; FOXG1C; HBF-1; HBF-2; HBF-3; HBF-G2; HBF2; HFK1; HFK2; HFK3; KHL2; QIN; FOXG1_HUMAN; P55316;

More at [Entrez](#)

XRCC4 X-ray repair complementing defective repair in Chinese hamster cells 4 [Source:HGNC Symbol;Acc:12831]

Functions:

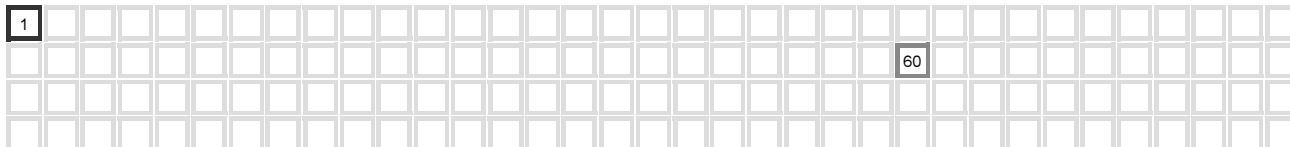


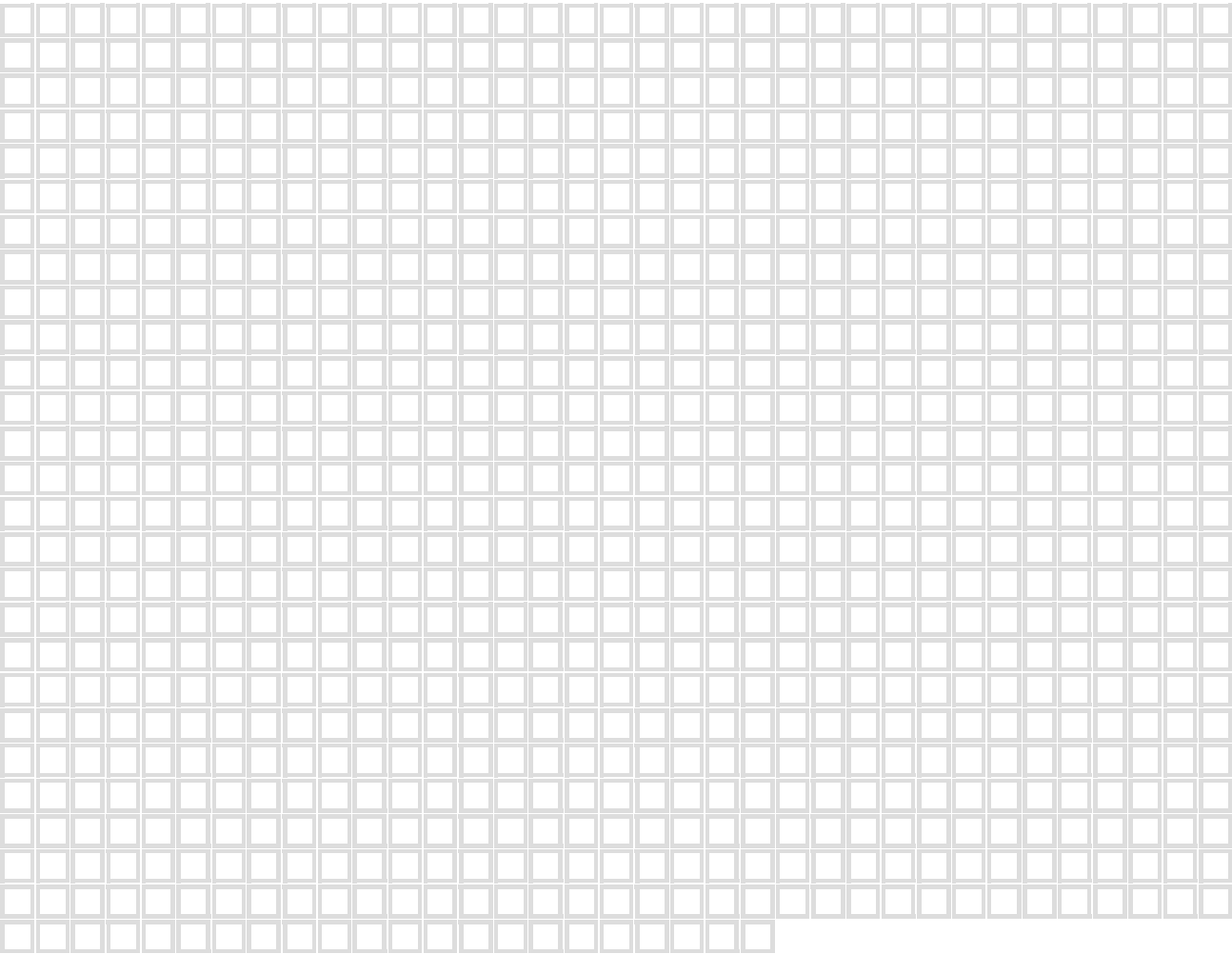
Synonyms: ENSG00000152422; ENSP00000282268; ENSP00000342011; ENSP00000379344; ENSP00000421491; ENSP00000439891; 7518; XRCC4; NP_003392; NP_071801; NP_072044; NM_003401; NM_022406; NM_022550; Q13426; XRCC4_HUMAN;

More at [Entrez](#)

TCOF1 Treacher Collins-Franceschetti syndrome 1 [Source:HGNC Symbol;Acc:11654]

Functions:



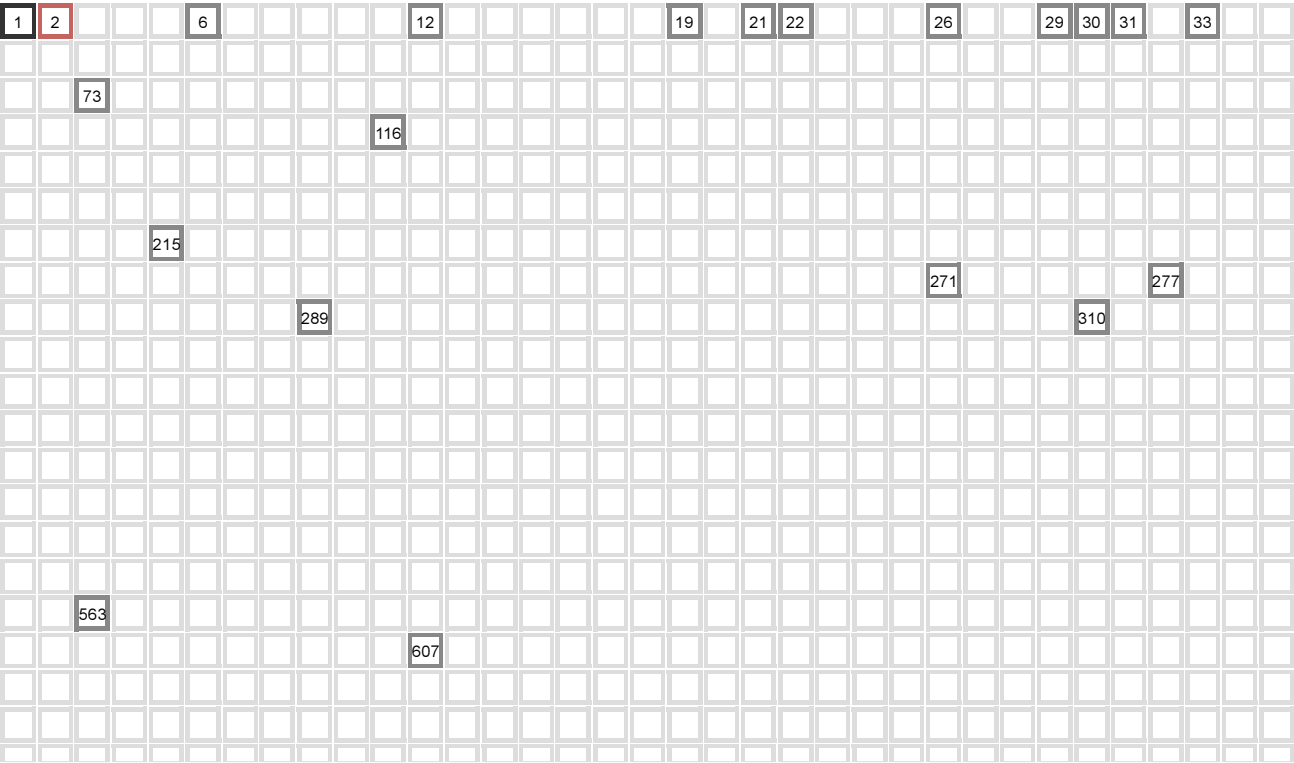


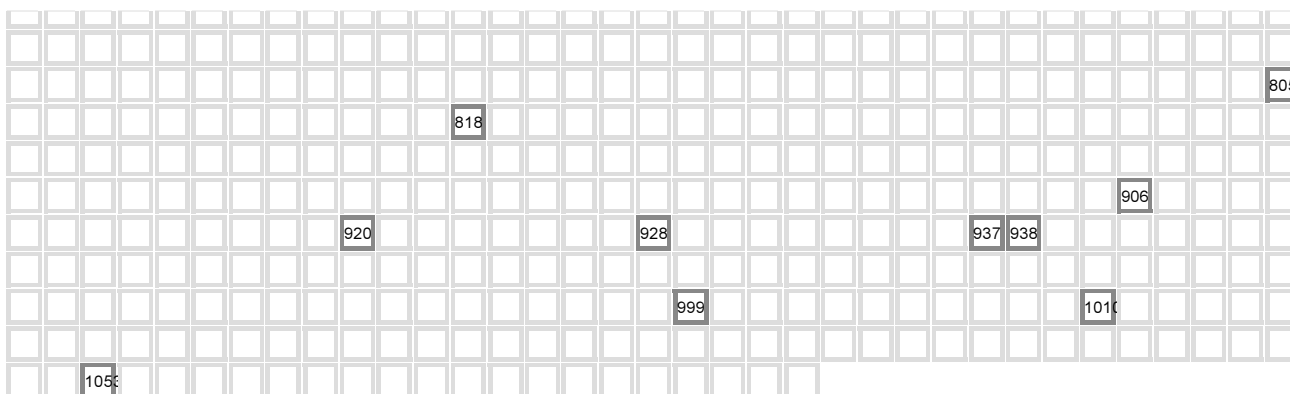
Synonyms: ENSG00000070814; ENSP000000325223; ENSP000000367028; ENSP000000377811; ENSP000000390717; ENSP000000400939; ENSP000000406888; ENSP000000409944; ENSP000000421655; ENSP000000422567; ENSP000000426471; ENSP000000426587; ENSP000000427484; 6949; TCOF1; NP_000347; NP_001008657; NP_001128715; NP_001128716; NP_001128717; NP_001182070; NM_000356; NM_001008656; NM_001008657; NM_001135243; NM_001135244; NM_001135245; NM_001195141; MFD1; treacle; Q13428; TCOF_HUMAN;

More at [Entrez](#)

NPTN neuroplastin [Source:HGNC Symbol;Acc:17867]

Functions:



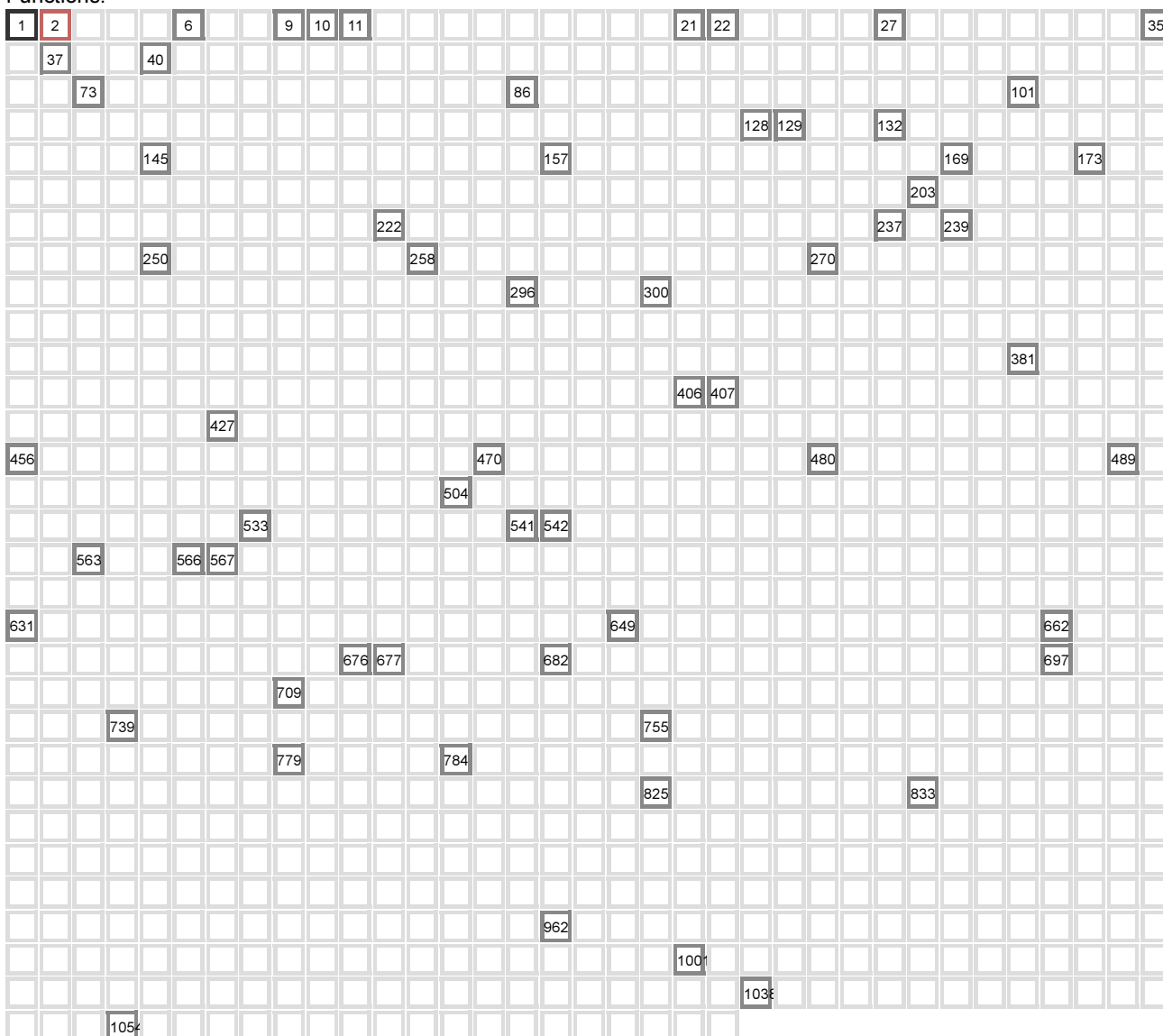


Synonyms: ENSG00000156642; ENSP00000287226; ENSP00000290401; ENSP00000342958; ENSP00000440593; ENSP00000444548; 27020; NPTN; NP_001154835; NP_001154836; NP_036560; NP_059429; NM_001161363; NM_001161364; NM_012428; NM_017455; GP55; GP65; np55; np65; SDFR1; NPTN_HUMAN; Q9Y639;

More at [Entrez](#)

NEUROD1 neurogenic differentiation 1 [Source:HGNC Symbol;Acc:7762]

Functions:



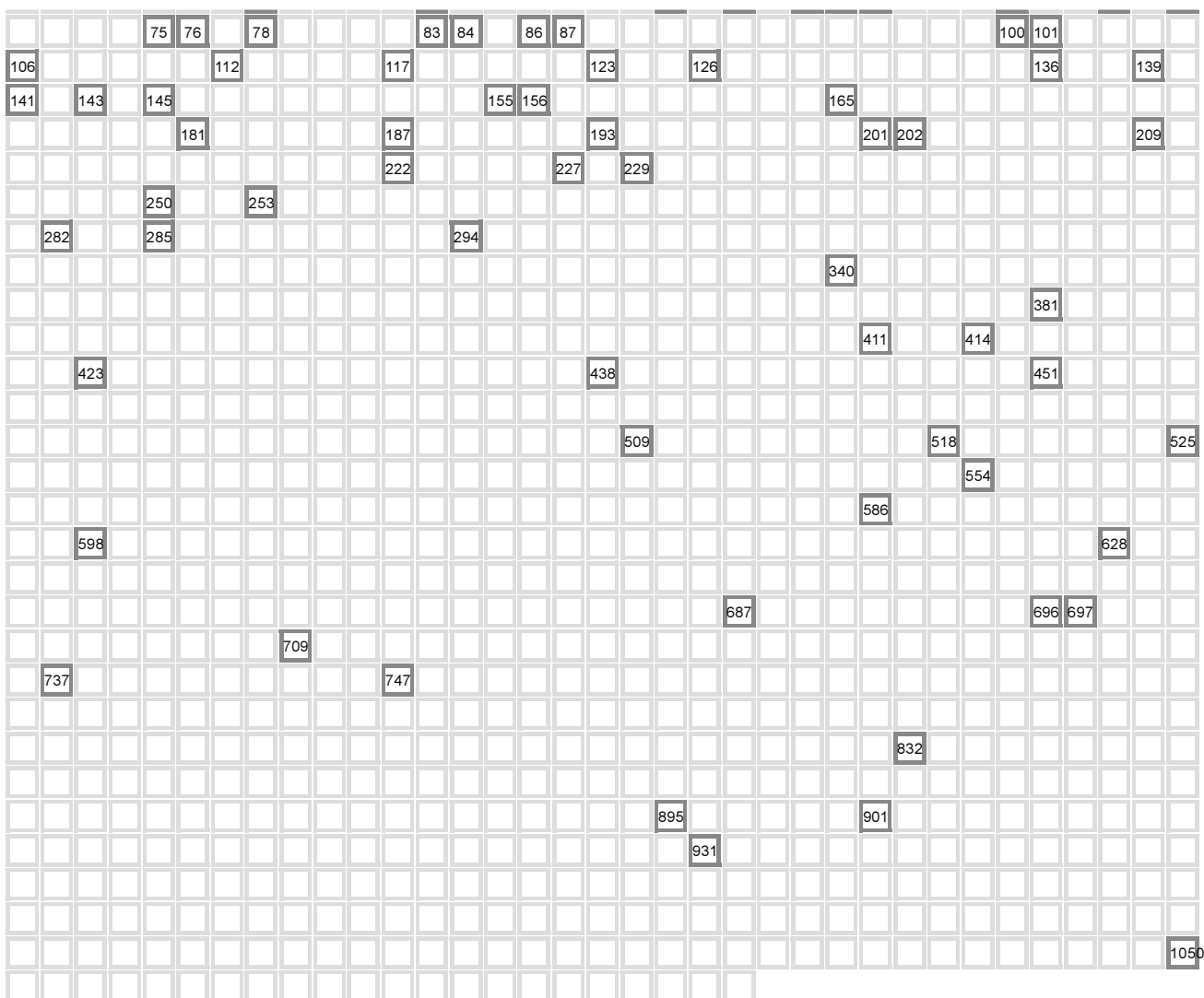
Synonyms: ENSG00000162992; ENSP00000295108; 4760; NEUROD1; NP_002491; NM_002500; BHF-1; bHLHa3; MODY6; NEUROD; NDF1_HUMAN; Q13562;

More at [Entrez](#)

GLI2 GLI family zinc finger 2 [Source:HGNC Symbol;Acc:4318]

Functions:



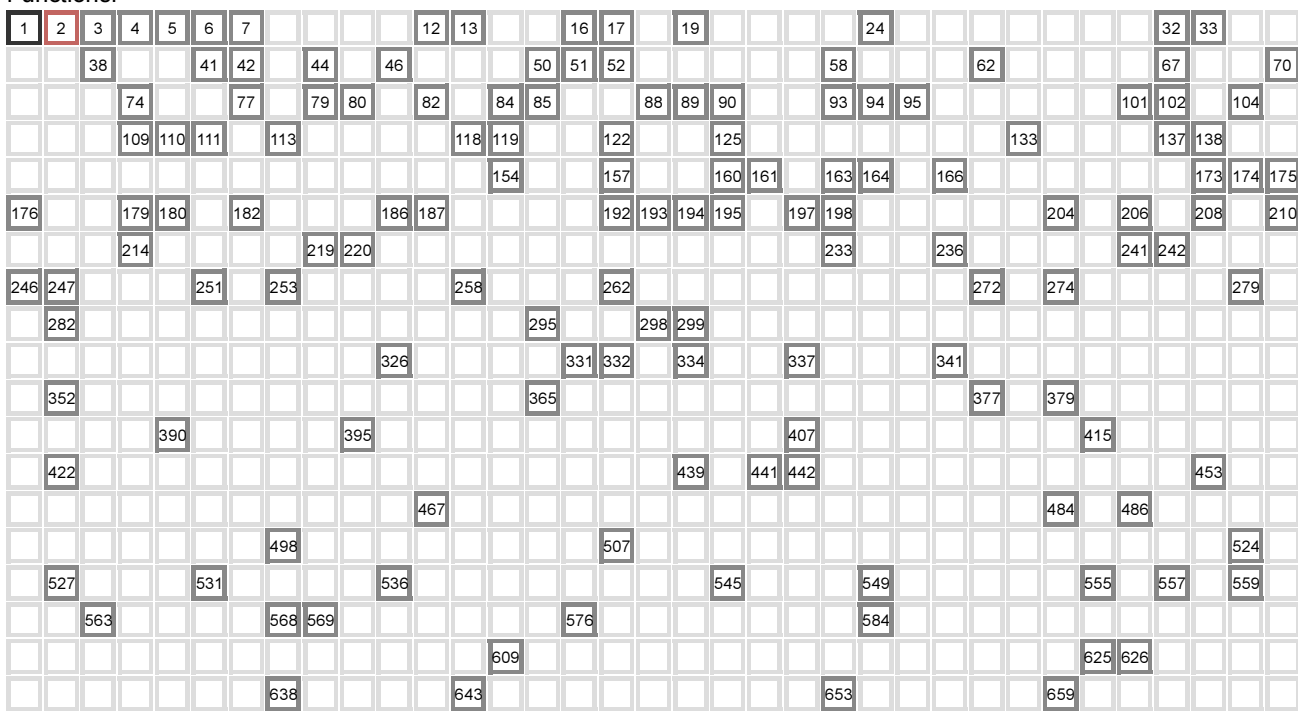


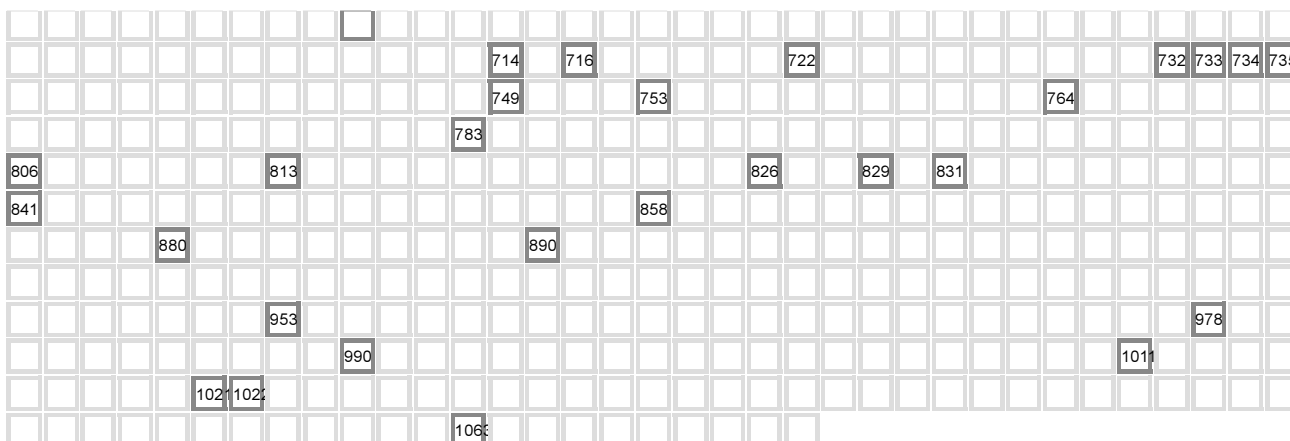
Synonyms: ENSG00000074047; ENSP00000312694; ENSP00000344473; ENSP00000354586; ENSP00000390436; ENSP00000395688; ENSP00000397488; ENSP00000398992; ENSP00000400593; ENSP00000402383; ENSP00000403715; ENSP00000415773; ENSP00000441454; 2736; GLI2; NP_005261; NM_005270; NM_030379; NM_030380; NM_030381; HPE9; THP1; THP2; GLI2_HUMAN; P10070;

More at [Entrez](#)

TGFB2 transforming growth factor, beta 2 [Source:HGNC Symbol;Acc:11768]

Functions:



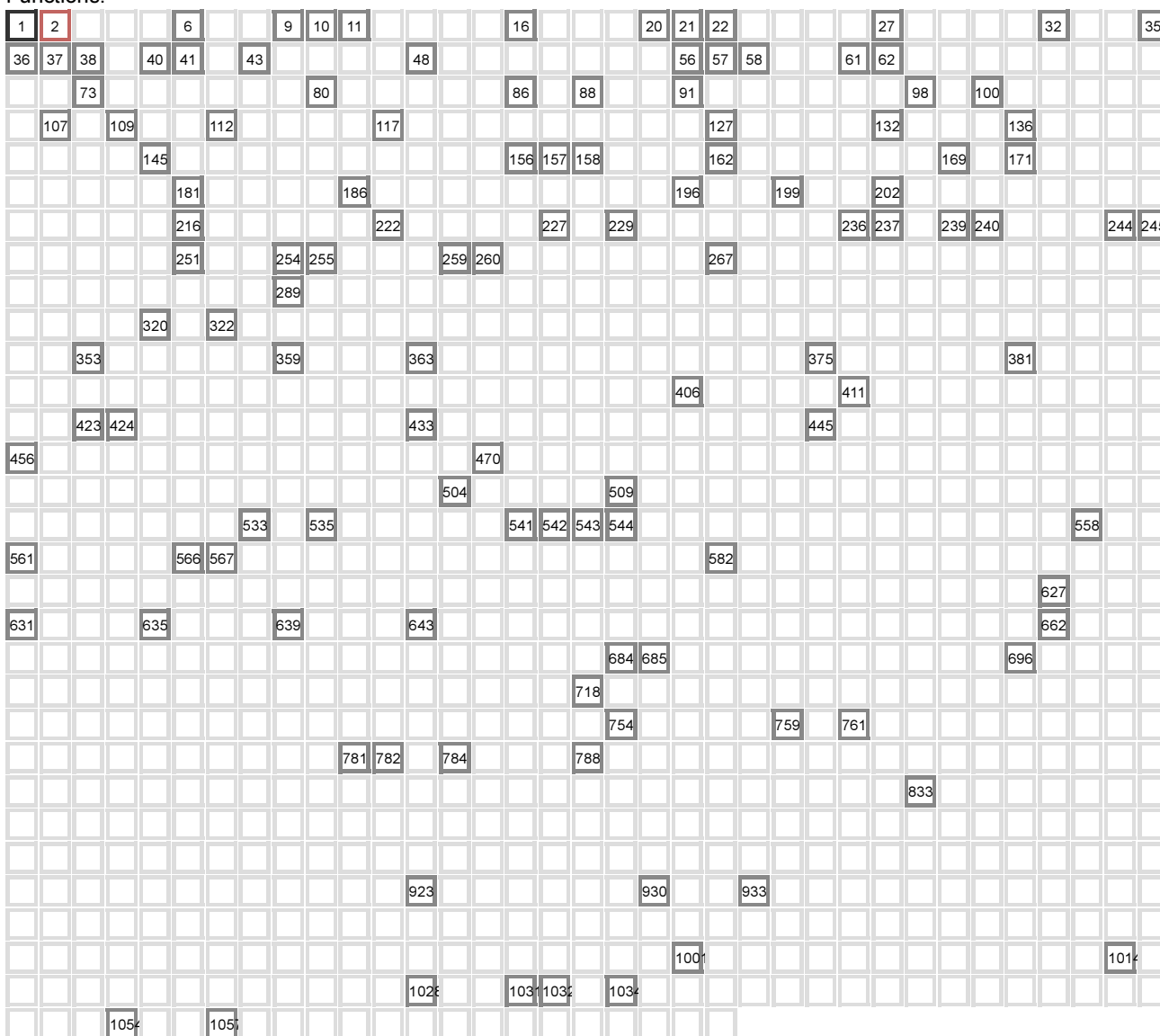


Synonyms: ENSG00000092969; ENSP00000355896; ENSP00000355897; 7042; TGFB2; NP_001129071; NP_003229; NM_001135599; NM_003238; TGF-beta2; P61812; TGFB2_HUMAN;

More at [Entrez](#)

FOXA2 forkhead box A2 [Source:HGNC Symbol;Acc:5022]

Functions:



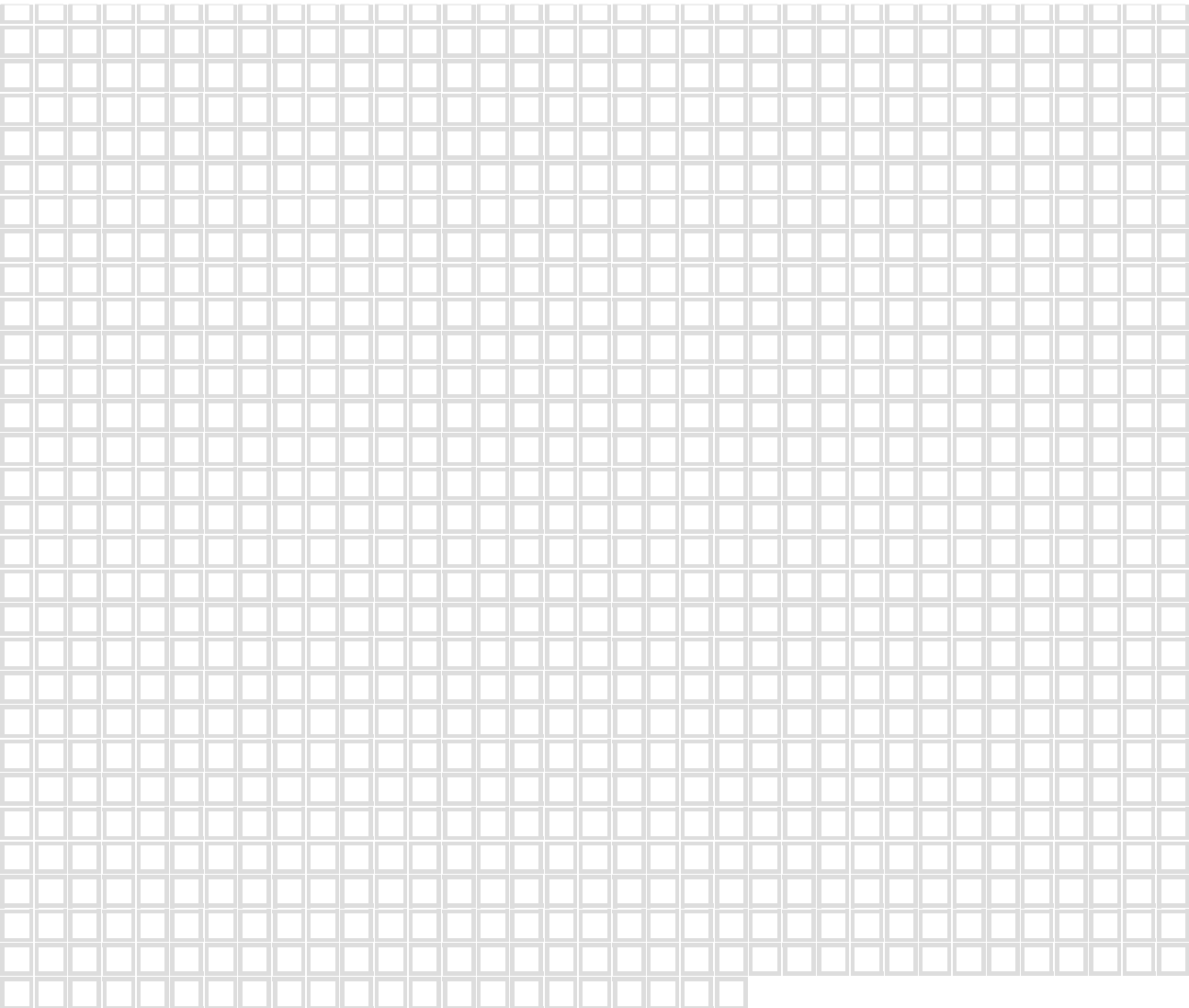
Synonyms: ENSG00000125798; ENSP00000315955; ENSP00000366319; ENSP00000400341; ENSP00000414472; 3170; FOXA2; NP_068556; NP_710141; NM_021784; NM_153675; HNF3B; TCF3B; FOXA2_HUMAN; Q9Y261;

More at [Entrez](#)

THRB thyroid hormone receptor, beta [Source:HGNC Symbol;Acc:11799]

Functions:



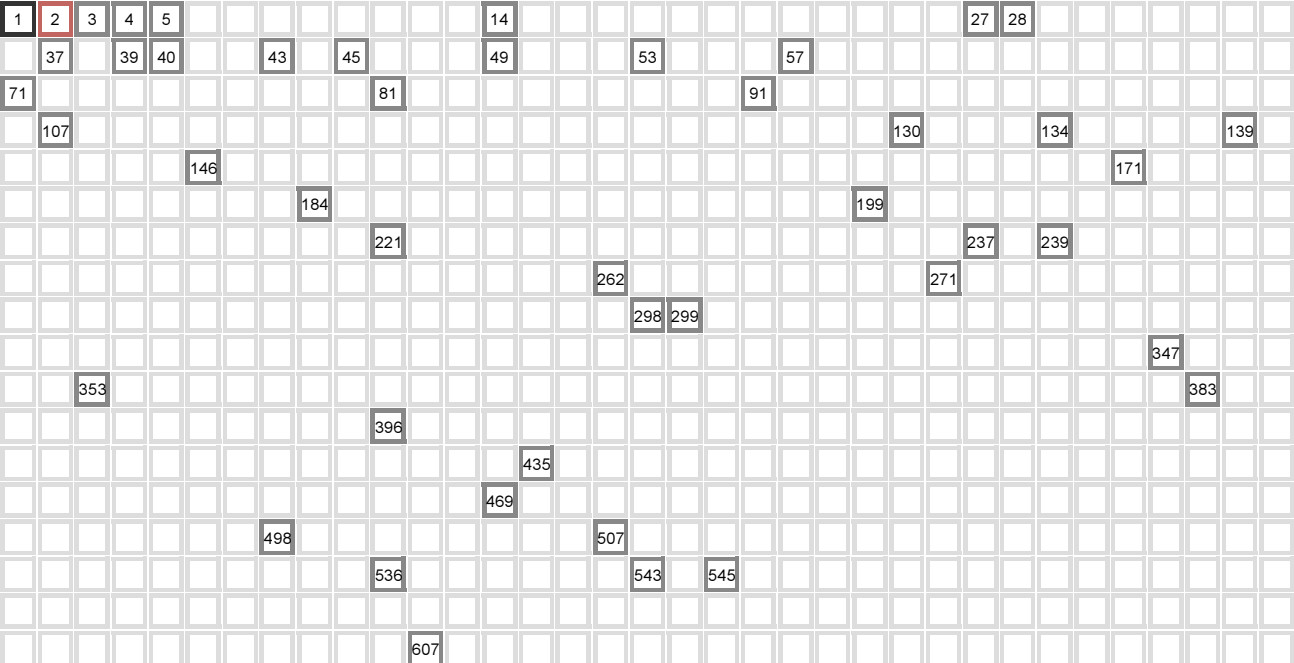


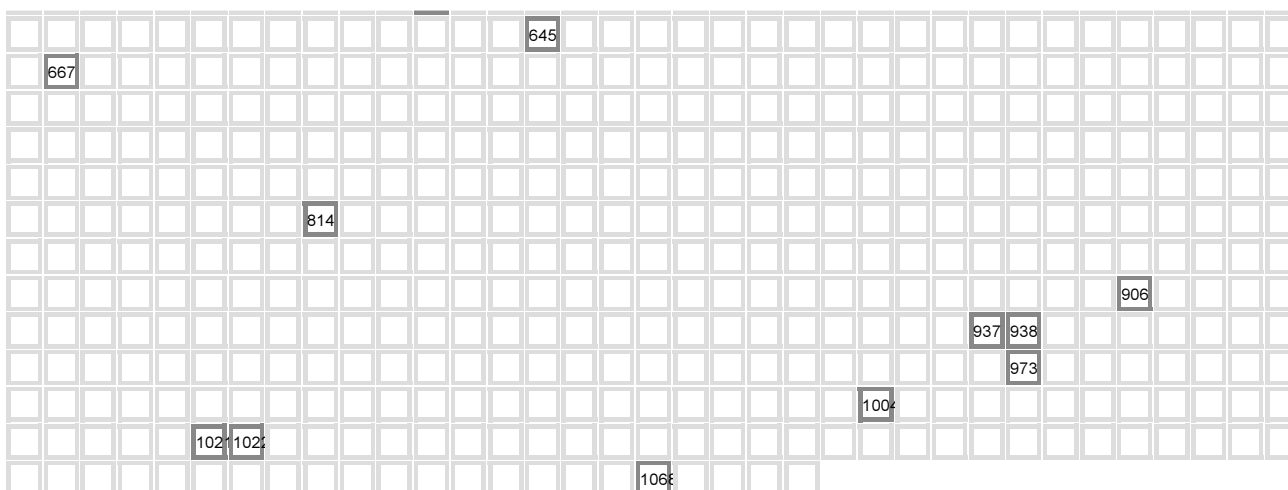
Synonyms: ENSG00000151090; ENSP00000280696; ENSP00000348827; ENSP00000379904; ENSP00000388467; ENSP00000393932; ENSP00000395362; ENSP00000399573; ENSP00000404233; ENSP00000404898; ENSP00000414100; ENSP00000414401; ENSP00000414444; ENSP00000414910; 7068; THRB; NP_000452; NP_001121648; NP_001121649; NP_001239563; NM_000461; NM_001128176; NM_001128177; NM_001252634; C-ERBA-2; C-ERBA-BETA; ERBA-BETA; ERBA2; NR1A2; PRTH; THR1; THRB1; THRB2; P10828; THB_HUMAN;

More at [Entrez](#)

FOXO3 forkhead box O3 [Source:HGNC Symbol;Acc:3821]

Functions:



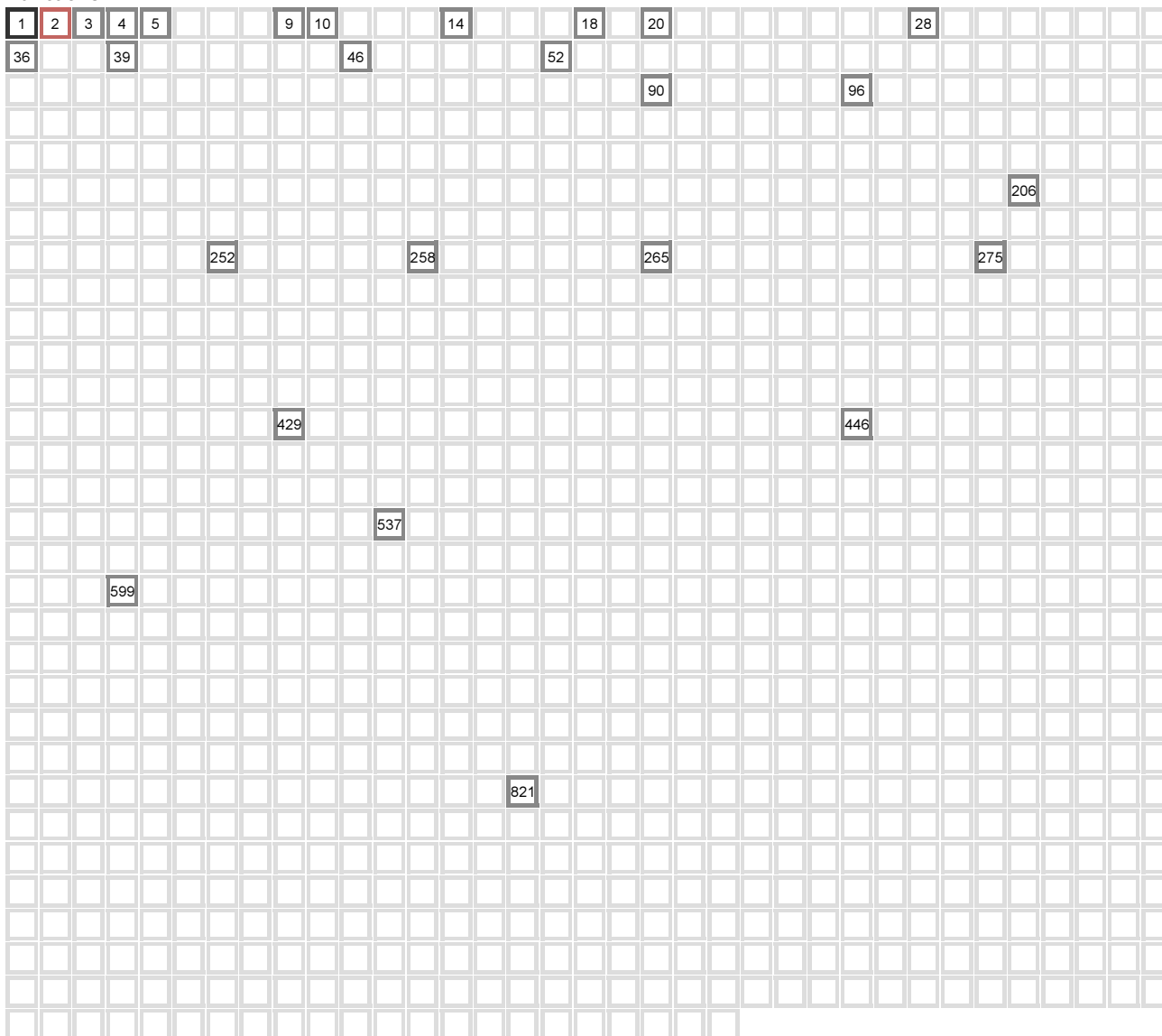


Synonyms: ENSG00000118689; ENSP00000339527; ENSP00000385824; ENSP00000442607; ENSP00000446316; 2309; FOXO3; NP_001446; NP_963853; NM_001455; NM_201559; AF6q21; FKHL1; FKHL1P2; FOXO2; FOXO3A; FOXO3_HUMAN; O43524;

More at [Entrez](#)

RUNX1 runt-related transcription factor 1 [Source:HGNC Symbol;Acc:10471]

Functions:



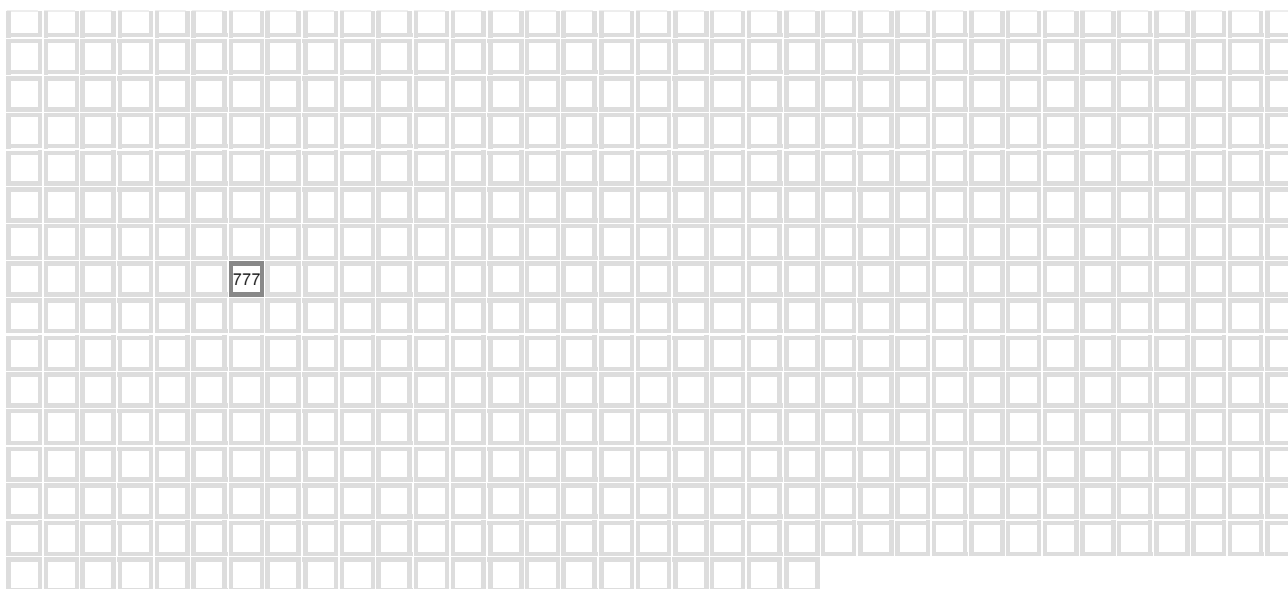
Synonyms: ENSG00000159216; ENSP00000300305; ENSP00000319459; ENSP00000340690; ENSP00000351123; ENSP00000382182; ENSP00000382184; ENSP00000382189; ENSP00000388189; ENSP00000395947; ENSP00000405158; ENSP00000409227; ENSP00000438019; 861; RUNX1; NP_001001890; NP_001116079; NP_001745; NM_001001890; NM_001122607; NM_001754; AML1; AMLCR1; CBFA2; EVI-1; PEBP2aB; Q01196; RUNX1_HUMAN;

MNDA myeloid cell nuclear differentiation antigen [Source:HGNC Symbol;Acc:7183]

A 100x100 grid with 25 numbered points scattered across it. The numbers are: 1, 55, 59, 65, 68, 137, 140, 148, 151, 159, 170, 176, 231, 235, 248, 257, 264, 315, 324, 364, 382, 434, 495, 574, 765, 913, 993, and 1066.

More at [Entrez](#)

POLR1D polymerase (RNA) I polypeptide D, 16kDa [Source:HGNC Symbol;Acc:20422]

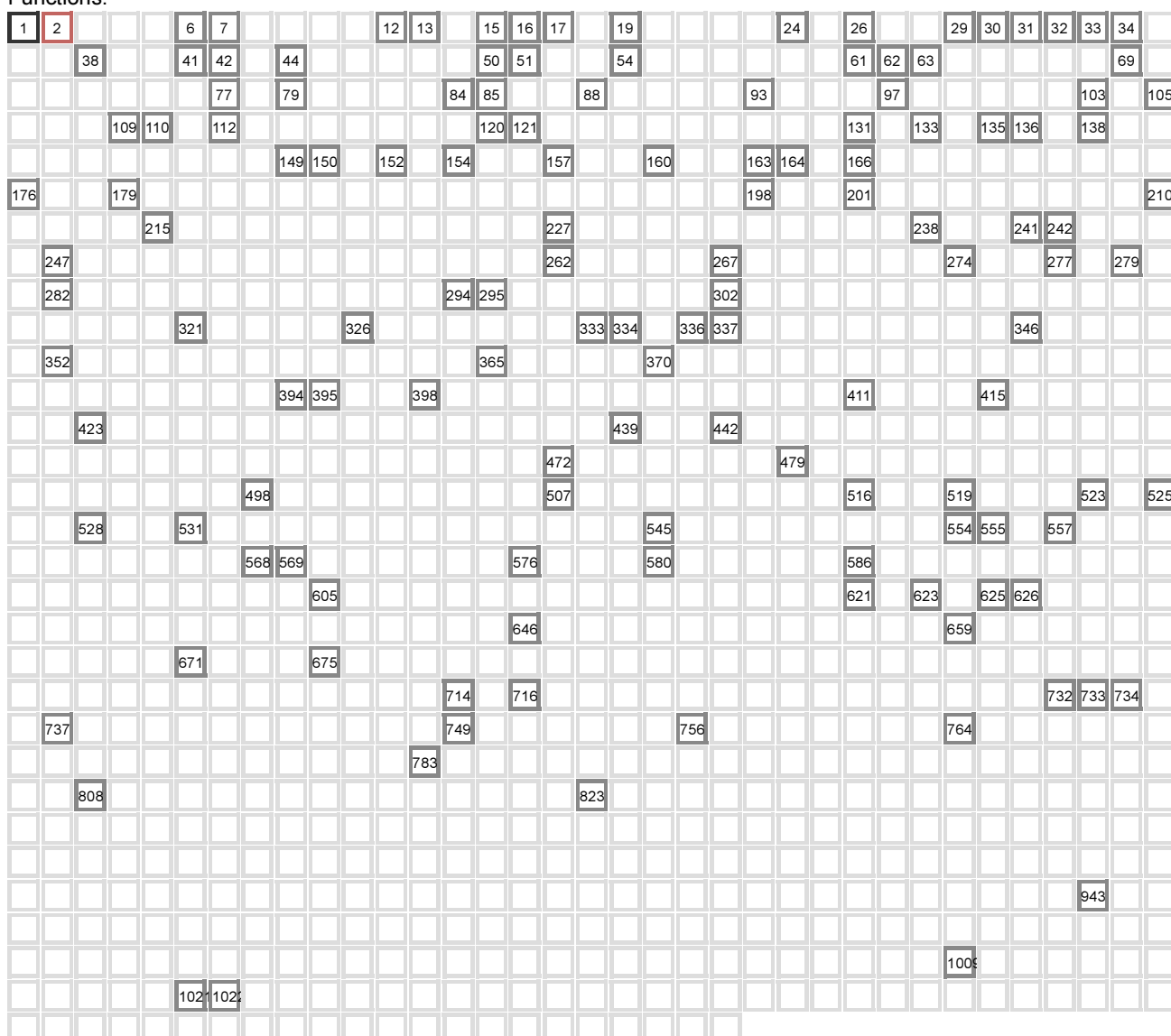


Synonyms: ENSG00000186184; ENSP00000302478; ENSP00000382603; ENSP00000382604; 51082; POLR1D; NP_001193488; NP_057056; NP_689918; NM_001206559; NM_015972; NM_152705; AC19; MGC9850; RPA16; RPA9; RPAC2; RPC16; RPO1-3; TCS2; Q9Y2S0; RPAC2_HUMAN;

More at [Entrez](#)

TGFB3 transforming growth factor, beta 3 [Source:HGNC Symbol;Acc:11769]

Functions:

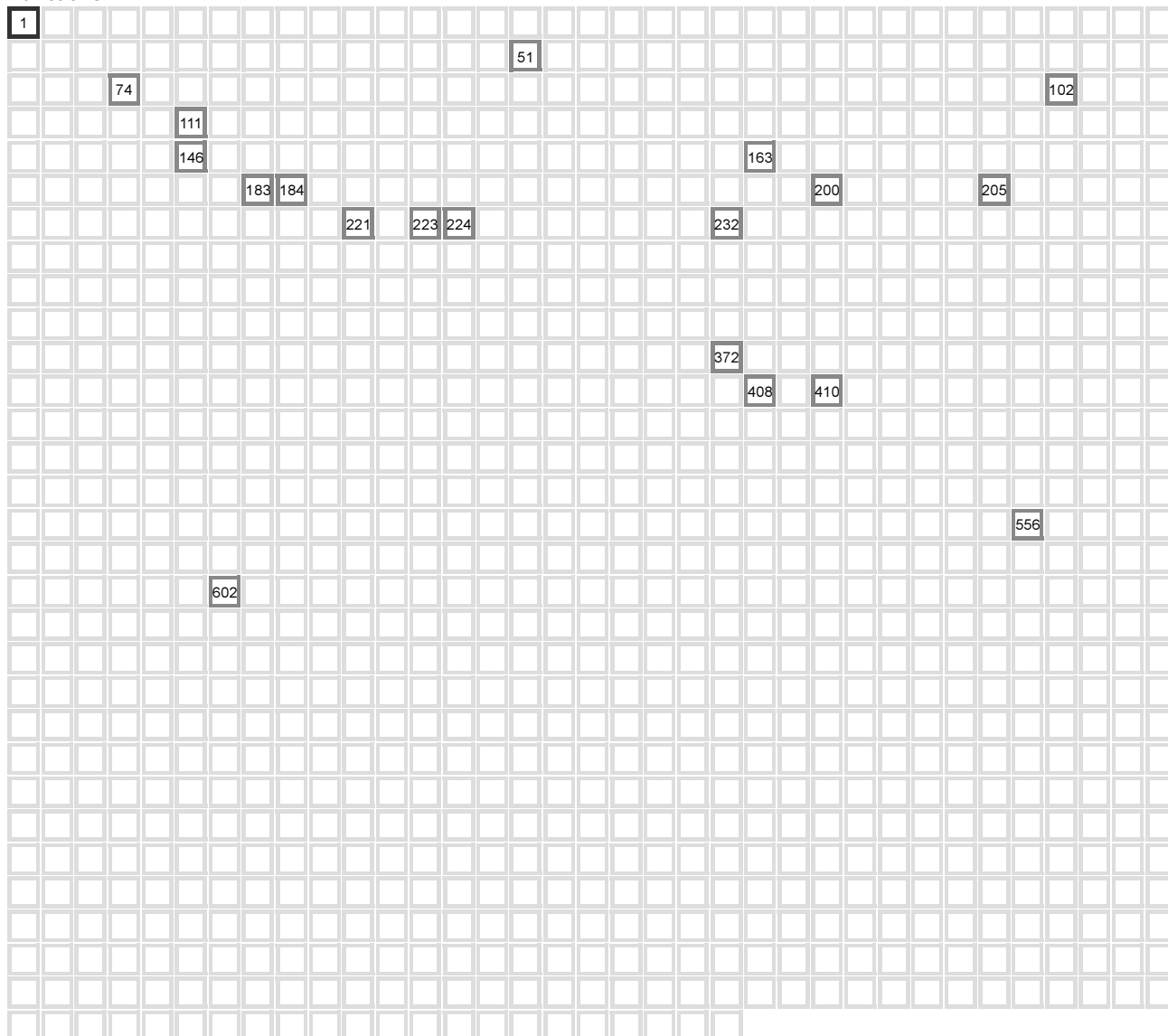


Synonyms: ENSG00000119699; ENSP00000238682; ENSP00000451110; 7043; TGFB3; NP_003230; NM_003239; ARVD; TGF-beta3; P10600; TGFB3_HUMAN;

More at [Entrez](#)

SOCS2 suppressor of cytokine signaling 2 [Source:HGNC Symbol;Acc:19382]

Functions:

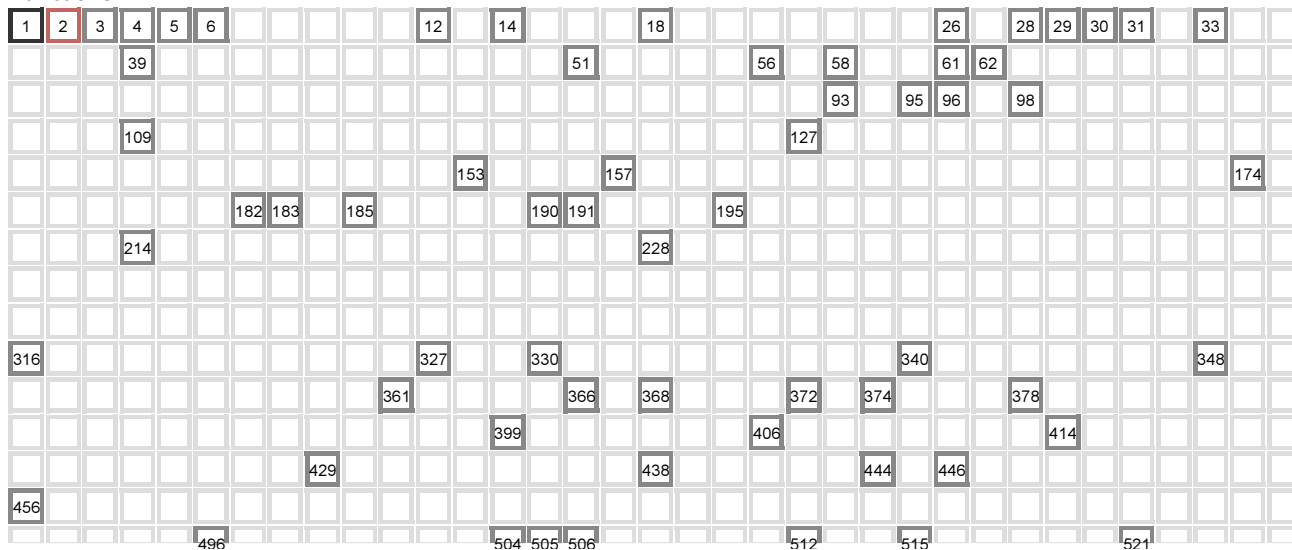


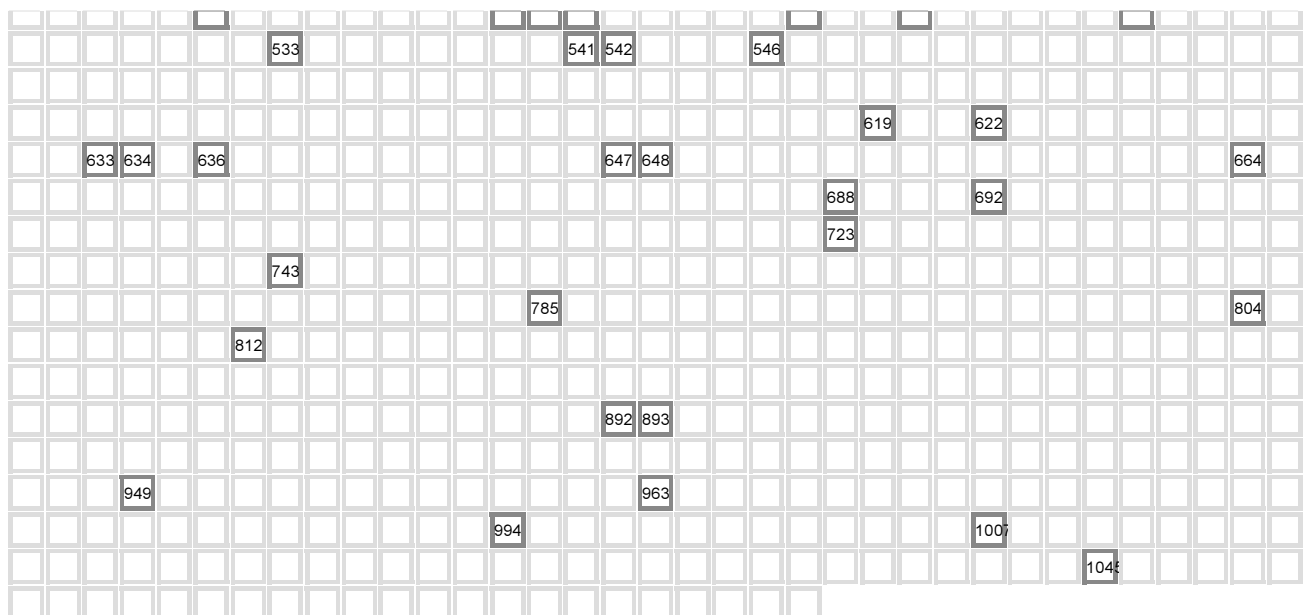
Synonyms: ENSG00000120833; ENSP00000339428; ENSP00000442898; ENSP00000445369; ENSP00000447161; ENSP00000447902; ENSP00000448611; ENSP00000448709; ENSP00000448815; ENSP00000449227; 8835; SOCS2; NP_003868; NM_003877; CIS2; Cish2; SOCS-2; SSI-2; SSI2; STATI2; O14508; SOCS2_HUMAN;

More at [Entrez](#)

LIF leukemia inhibitory factor (cholinergic differentiation factor) [Source:HGNC Symbol;Acc:6596]

Functions:



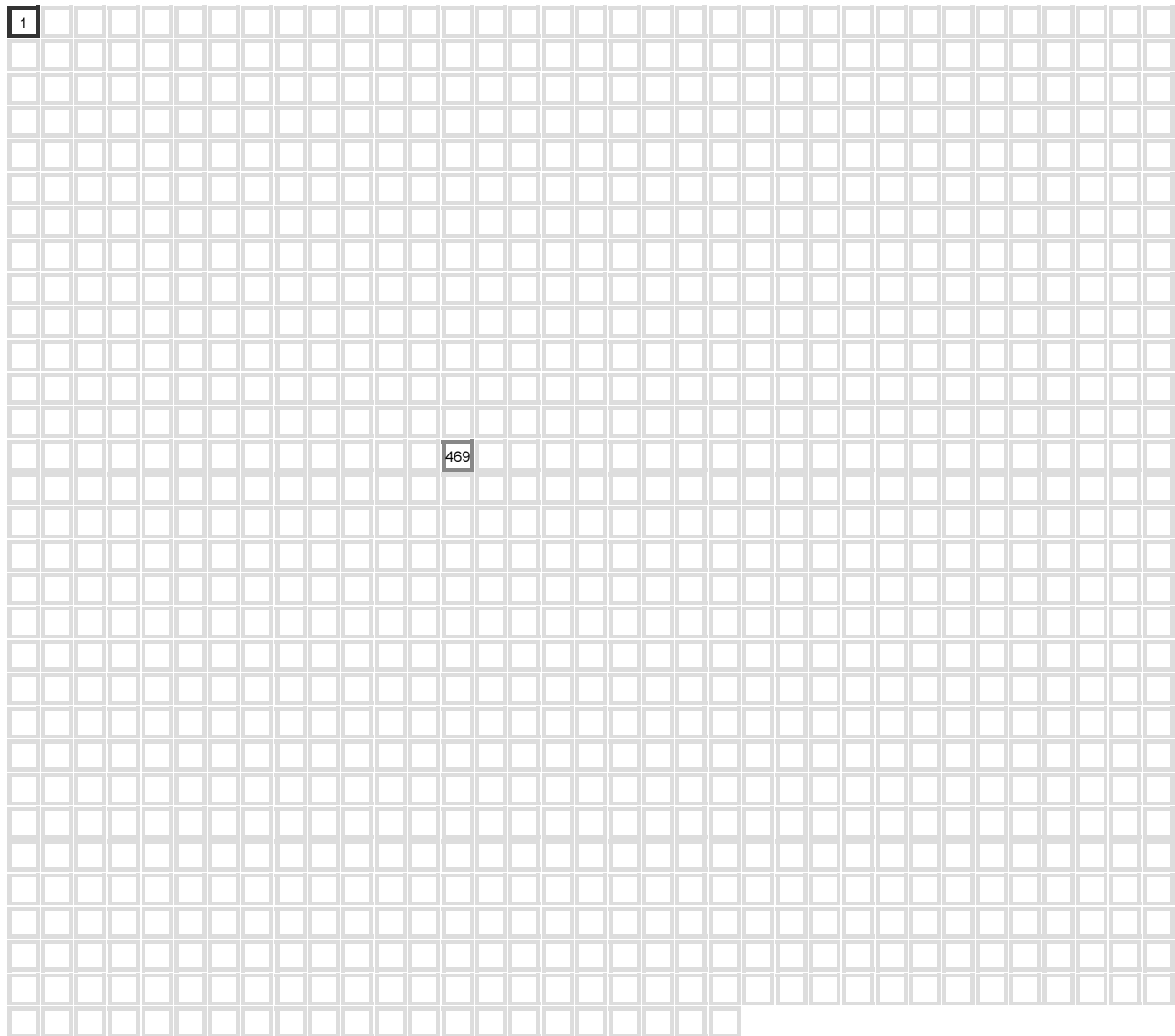


Synonyms: ENSG00000128342; ENSP00000249075; ENSP00000384450; 3976; LIF; NP_002300; NM_002309; CDF; HILDA; LIF_HUMAN; P15018;

More at [Entrez](#)

TIAM1 T-cell lymphoma invasion and metastasis 1 [Source:HGNC Symbol;Acc:11805]

Functions:

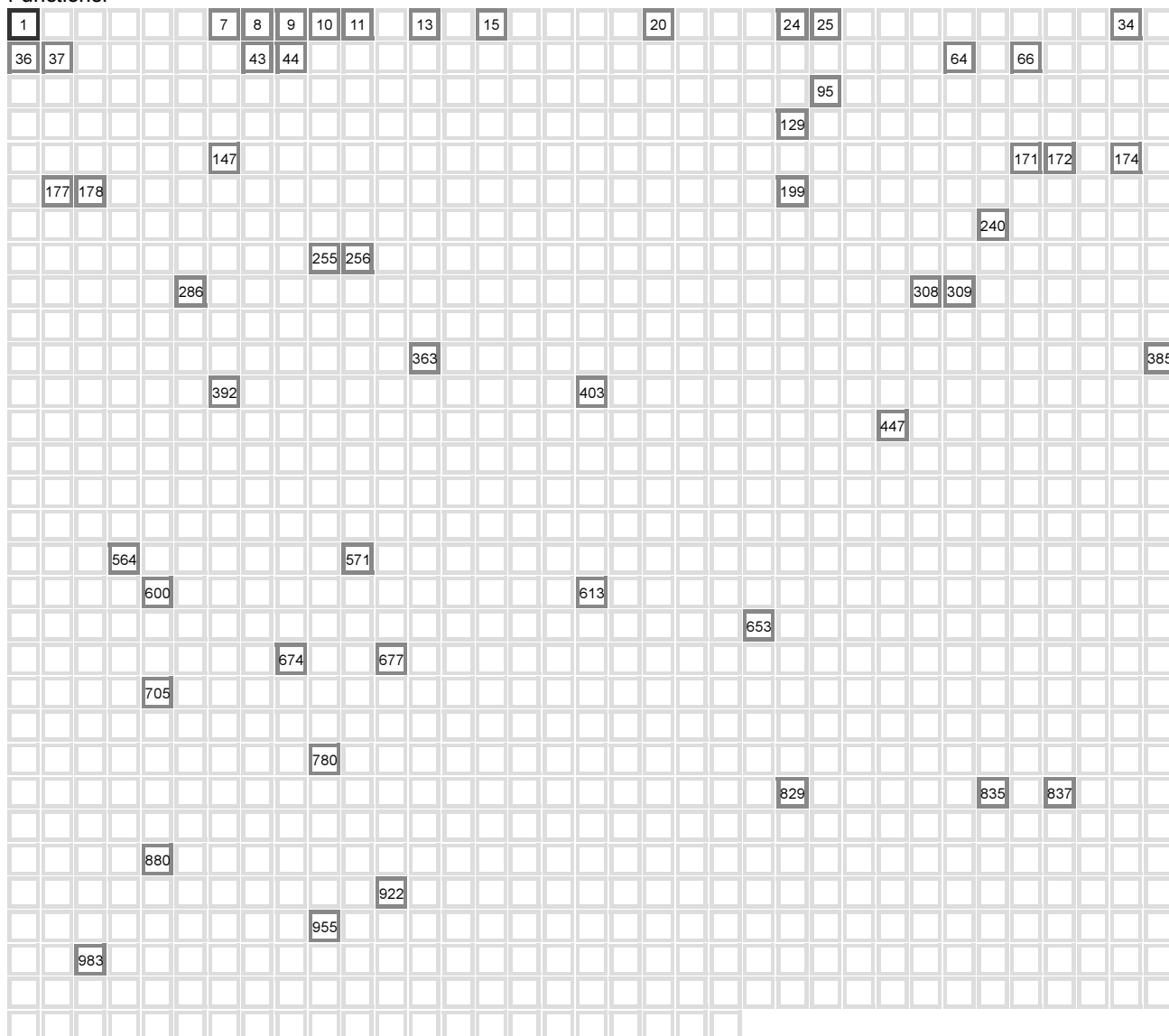


Synonyms: ENSG00000156299; ENSP00000286827; ENSP00000382735; ENSP00000388217; ENSP00000393384; ENSP00000417828; ENSP00000441570; 7074; TIAM1; NP_003244; NM_003253; Q13009; TIAM1_HUMAN;

More at [Entrez](#)

MEN1 multiple endocrine neoplasia I [Source:HGNC Symbol;Acc:7010]

Functions:

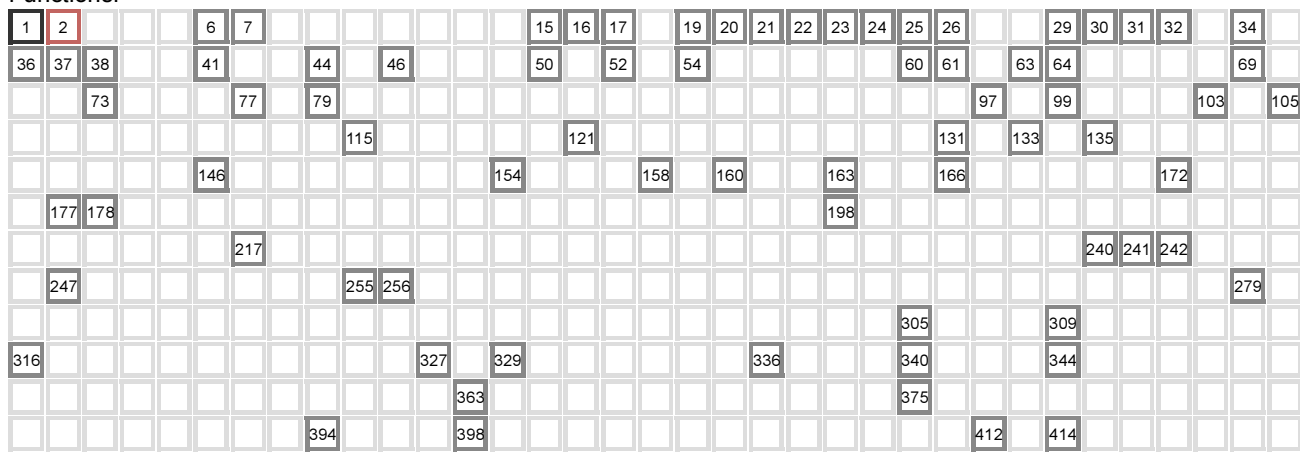


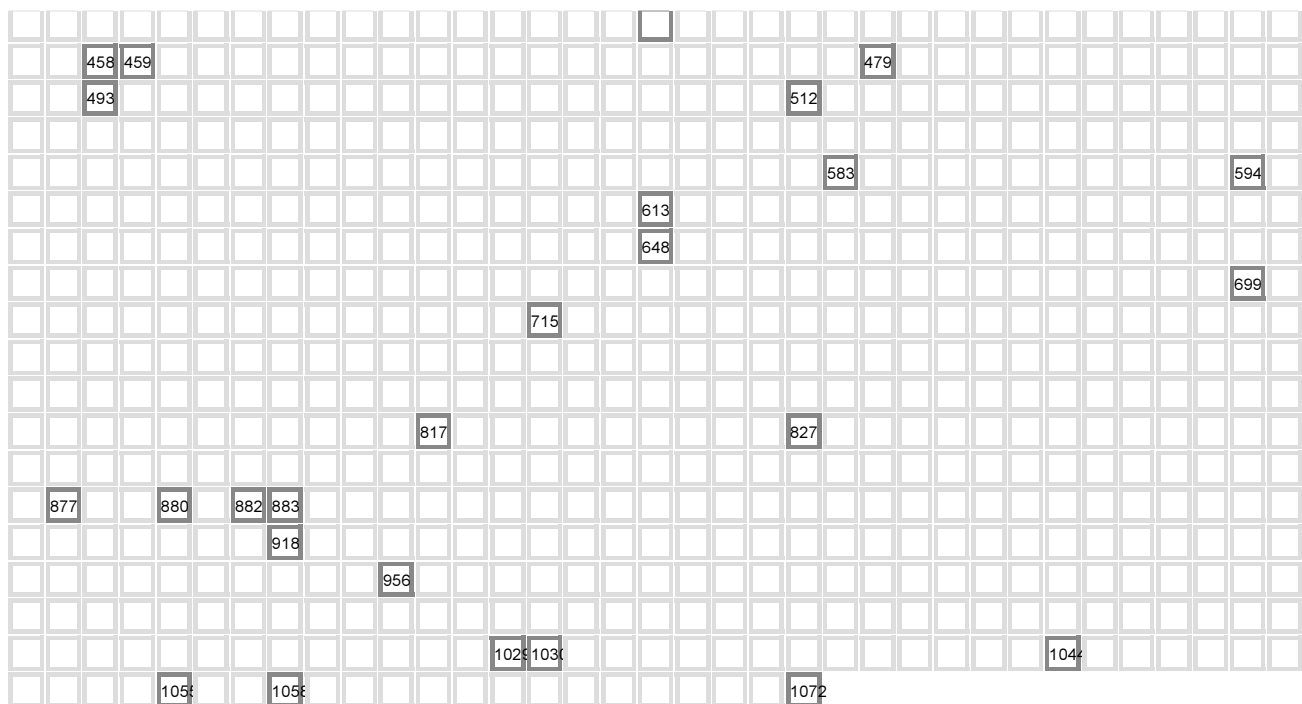
Synonyms: ENSG00000133895; ENSP00000308975; ENSP00000323747; ENSP00000337088; ENSP00000366530; ENSP00000366533; ENSP00000366538; ENSP00000366543; ENSP00000377899; ENSP00000377901; ENSP00000388016; ENSP00000394933; ENSP00000396940; ENSP00000402752; ENSP00000411218; ENSP00000413944; 4221; MEN1; NP_000235; NP_570711; NP_570712; NP_570713; NP_570714; NP_570715; NP_570716; NM_000244; NM_130799; NM_130800; NM_130801; NM_130802; NM_130803; NM_130804; MEAI; MENIN; MEN1_HUMAN; O00255;

More at [Entrez](#)

BMP7 bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1074]

Functions:



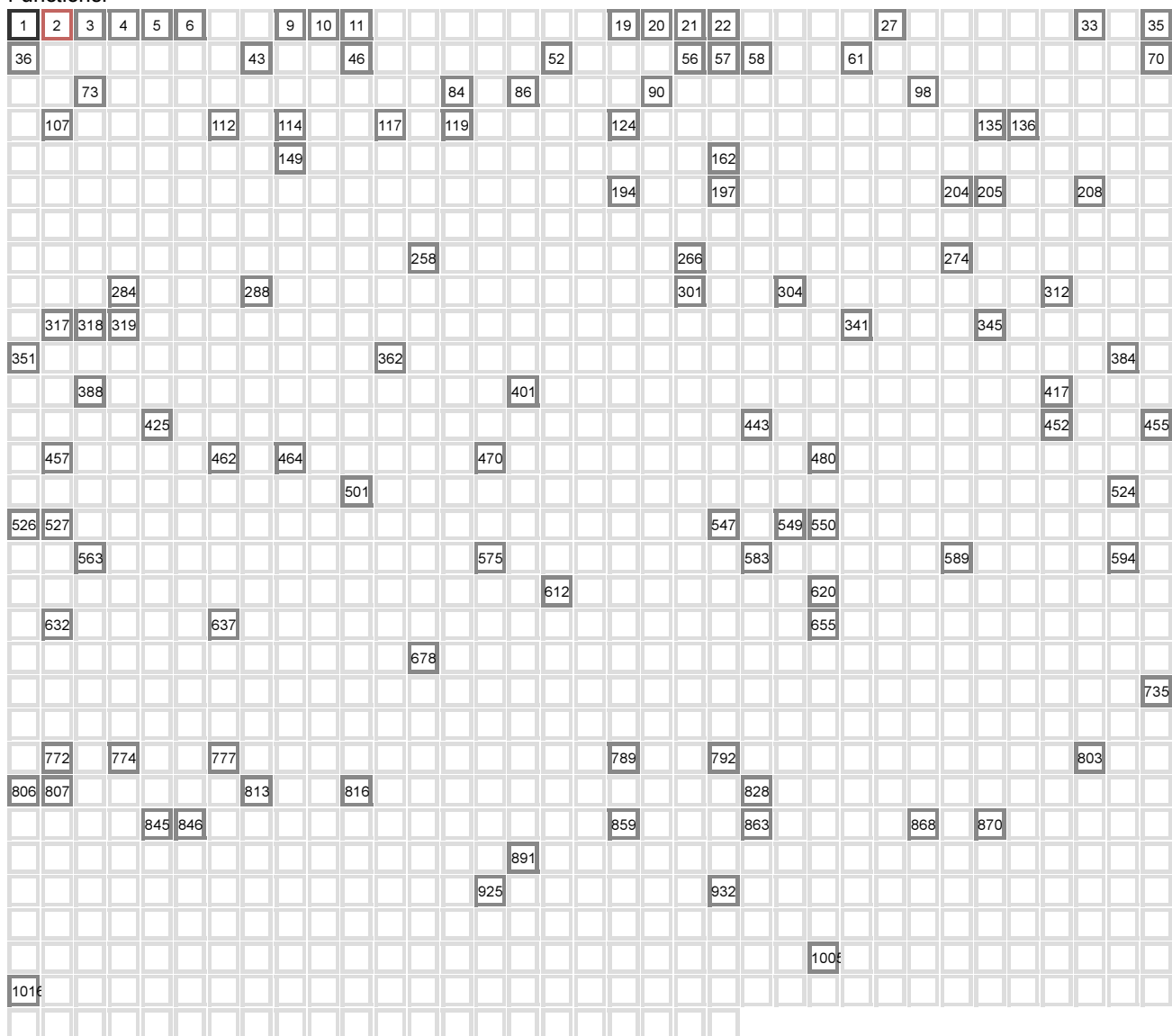


Synonyms: ENSG00000101144; ENSP00000379204; ENSP00000379205; ENSP00000390814; ENSP00000398687; 655; BMP7; NP_001710; NM_001719; OP-1; BMP7_HUMAN; P18075;

More at [Entrez](#)

NKX2-5 NK2 homeobox 5 [Source:HGNC Symbol;Acc:2488]

Functions:

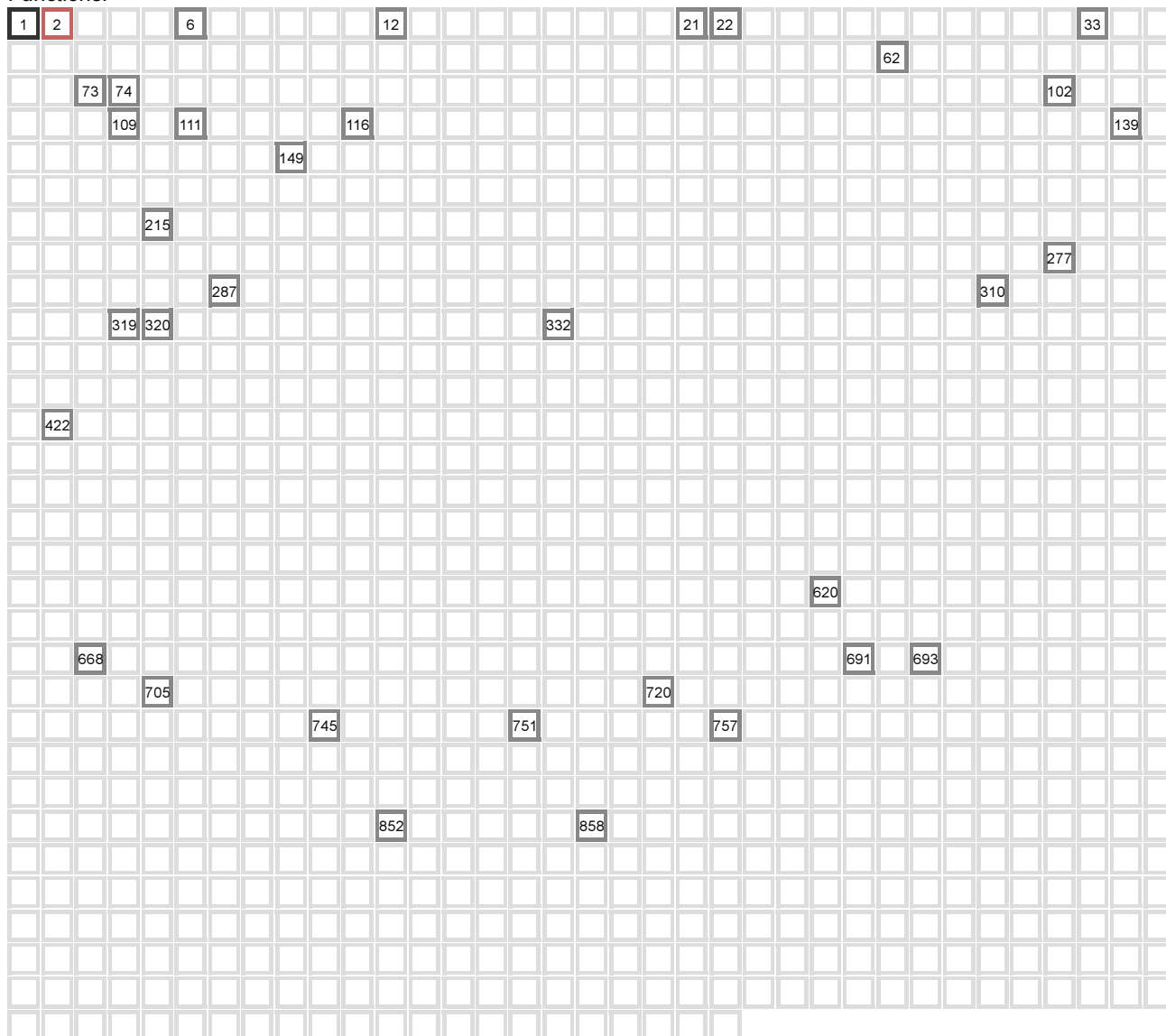


Synonyms: ENSG00000183072; ENSP00000327758; ENSP00000395378; ENSP00000427906; ENSP00000429905; 1482; NKX2-5; NP_001159647; NP_001159648; NP_004378; NM_001166175; NM_001166176; NM_004387; CHNG5; CSX; CSX1; HLHS2; NKX2.5; NKX2E; NKX4-1; VSD3; NKX25_HUMAN; P52952;

More at [Entrez](#)

MAPT microtubule-associated protein tau [Source:HGNC Symbol;Acc:6893]

Functions:

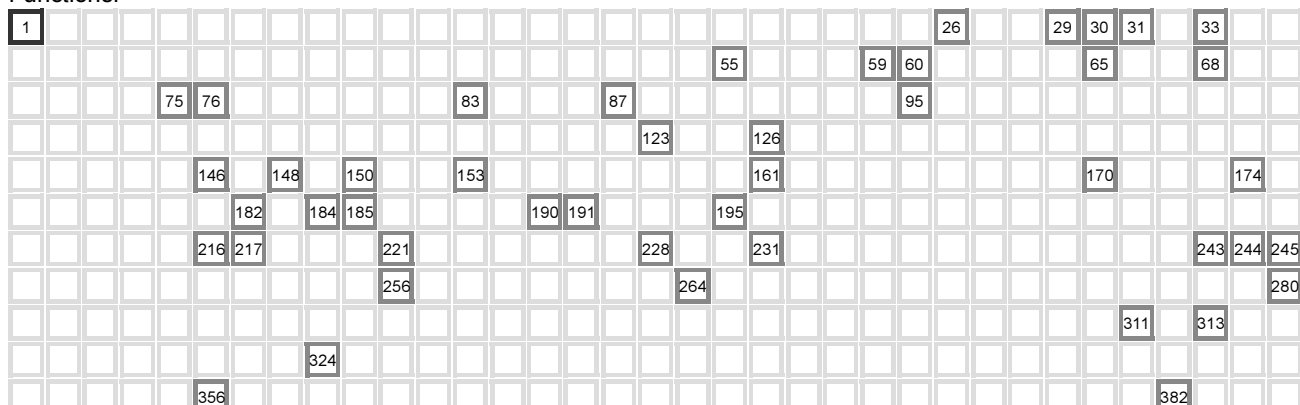


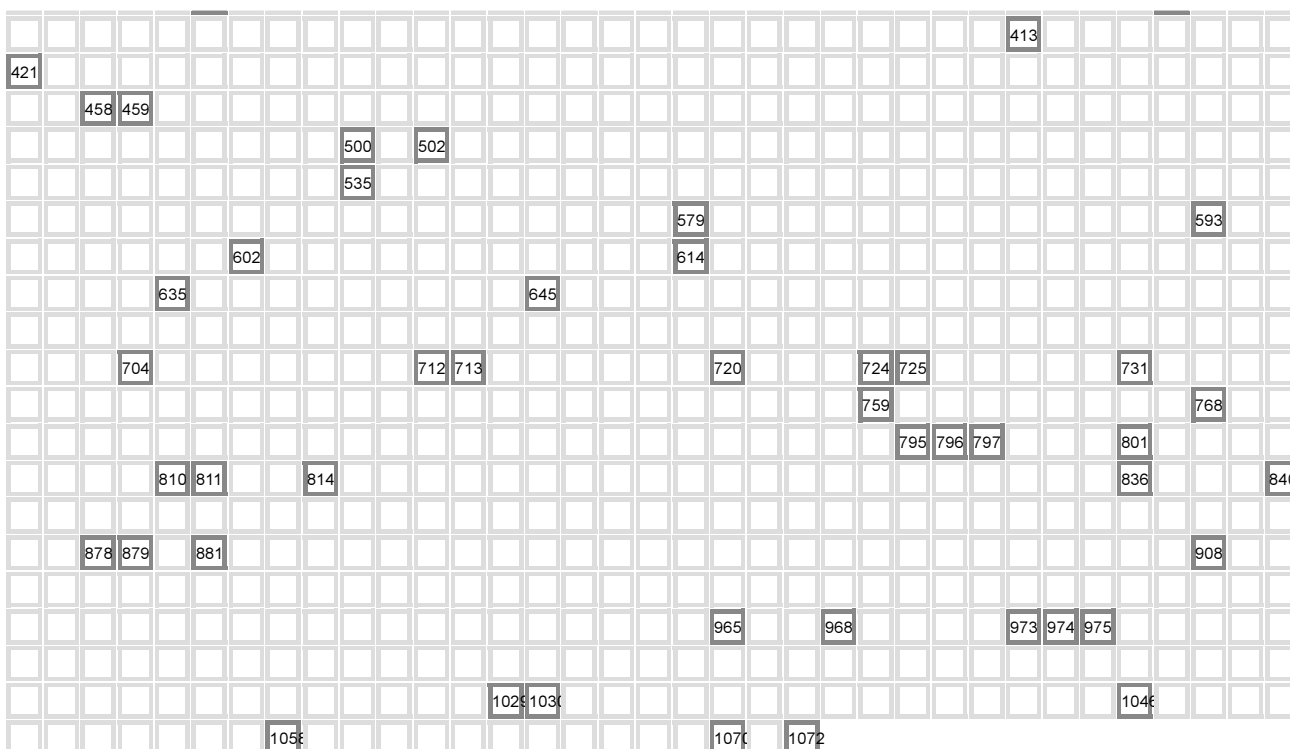
Synonyms: ENSG00000186868; ENSP00000262410; ENSP00000302706; ENSP00000303214; ENSP00000334886; ENSP00000340438; ENSP00000340820; ENSP00000346287; ENSP00000389250; ENSP00000408975; ENSP00000410838; ENSP00000413056; ENSP00000443028; 4137; MAPT; FLJ31424; MGC138549; P10636; TAU_HUMAN;

More at [Entrez](#)

IGF2 insulin-like growth factor 2 (somatomedin A) [Source:HGNC Symbol;Acc:5466]

Functions:



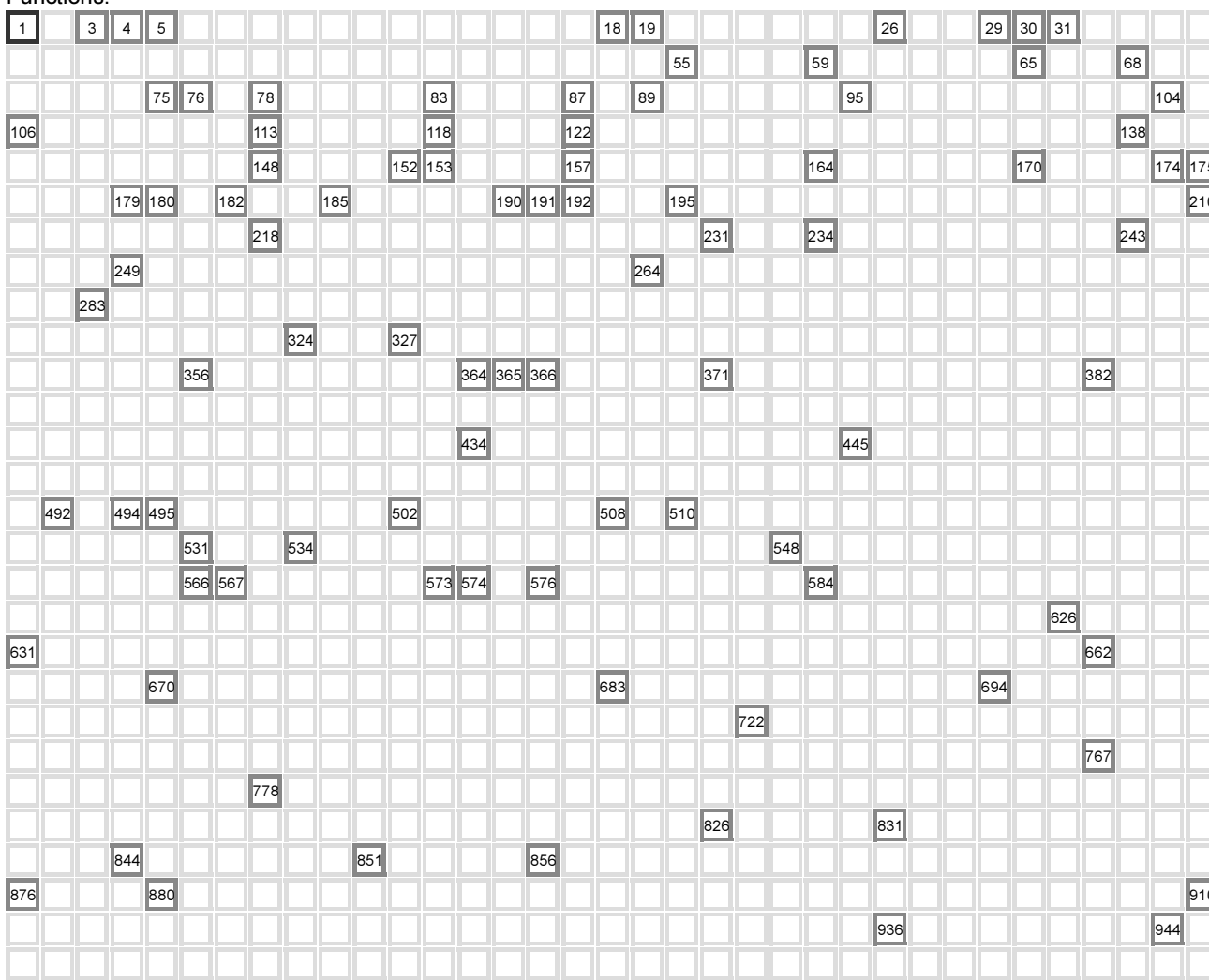


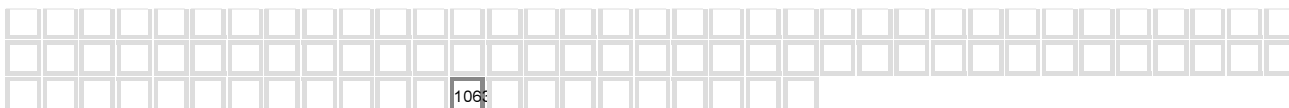
Synonyms: ENSG00000167244; ENSP00000300632; ENSP00000338297; ENSP00000370720; ENSP00000370786; ENSP00000370796; ENSP00000370799; ENSP00000370802; ENSP00000370813; ENSP00000391826; ENSP00000402047; ENSP00000414497; 3481; IGF2; NP_000603; NP_001007140; NP_001121070; NM_000612; NM_001007139; NM_001127598; C11orf43; FLJ44734; IGF-II; PP9974; IGF2_HUMAN; P01344;

More at [Entrez](#)

CD74 CD74 molecule, major histocompatibility complex, class II invariant chain [Source:HGNC Symbol;Acc:1697]

Functions:



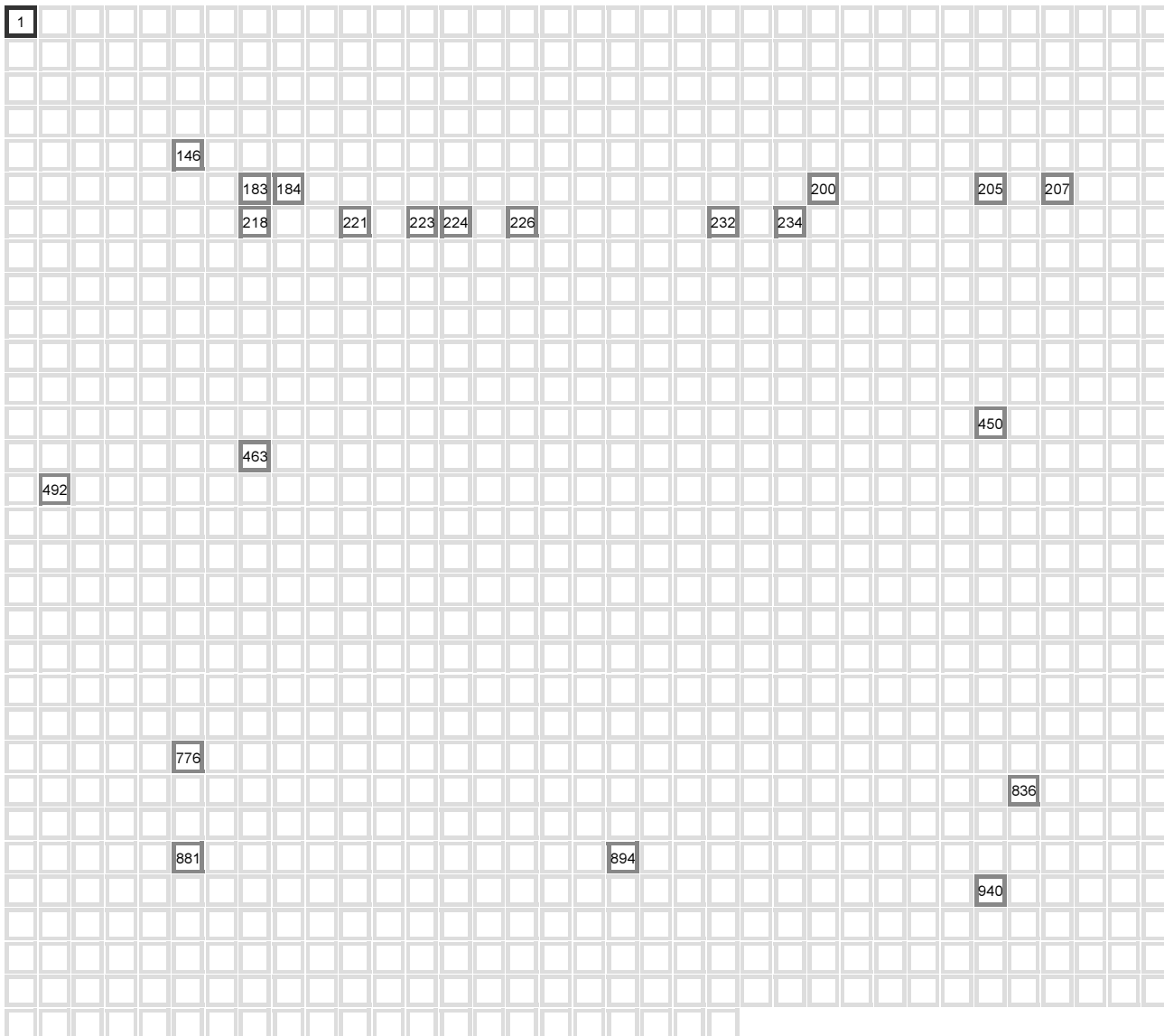


Synonyms: ENSG00000019582; ENSP00000009530; ENSP000000230685; ENSP000000367026; ENSP000000429024; ENSP000000429478; ENSP000000429641; ENSP000000430614; ENSP000000430654; 972; CD74; NP_001020329; NP_001020330; NP_004346; NM_001025158; NM_001025159; NM_004355; DHLAG; HLADG; Ia-GAMMA; HG2A_HUMAN; P04233;

More at [Entrez](#)

SOCS3 suppressor of cytokine signaling 3 [Source:HGNC Symbol;Acc:19391]

Functions:

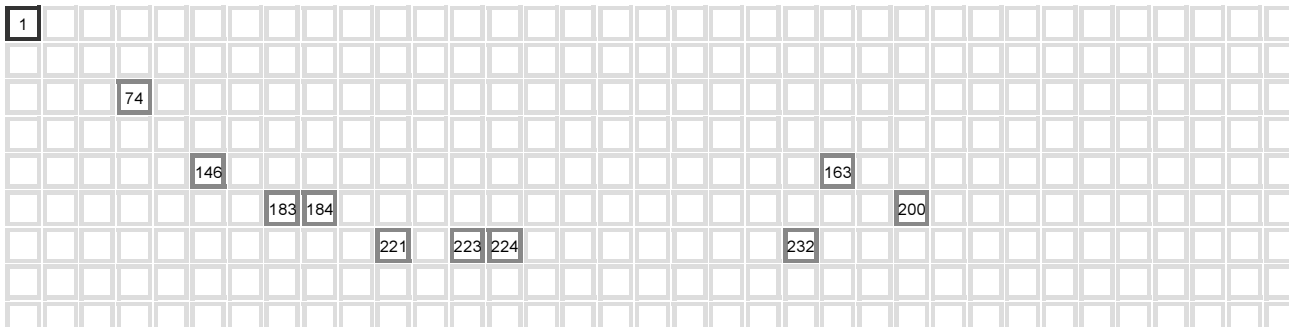


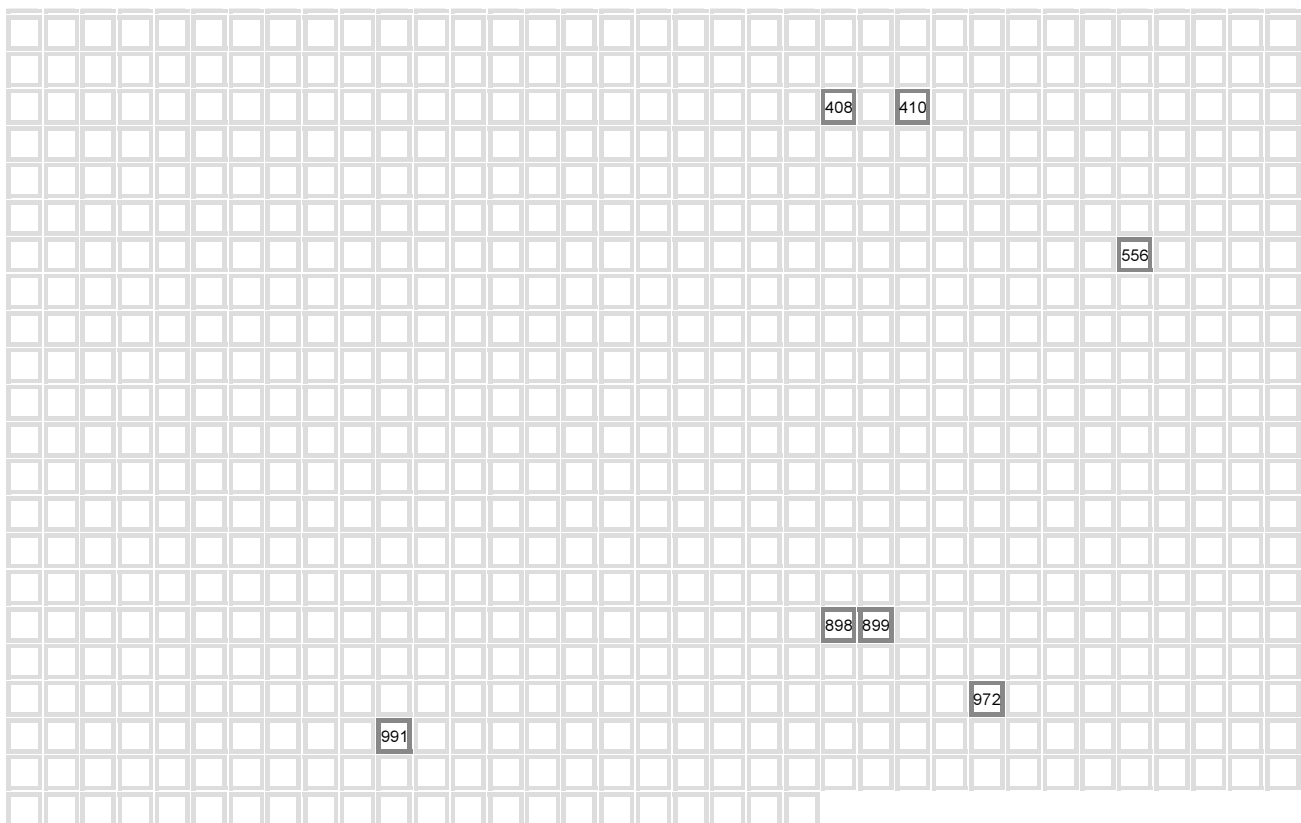
Synonyms: ENSG00000184557; ENSP000000330341; 9021; SOCS3; NP_003946; NM_003955; ATOD4; CIS3; Cish3; SOCS-3; SSI-3; SSI3; O14543; SOCS3_HUMAN;

More at [Entrez](#)

STAT5B signal transducer and activator of transcription 5B [Source:HGNC Symbol;Acc:11367]

Functions:



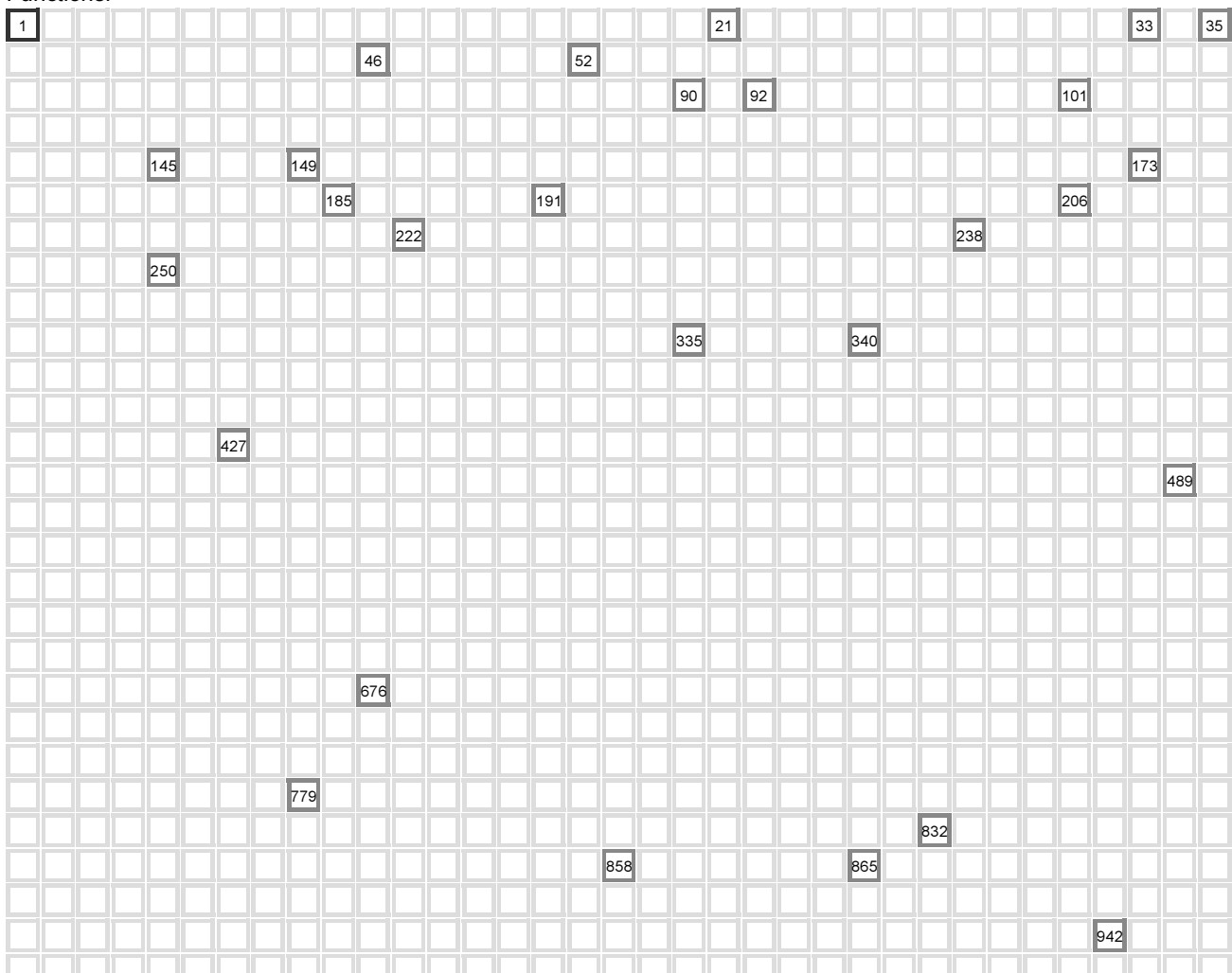


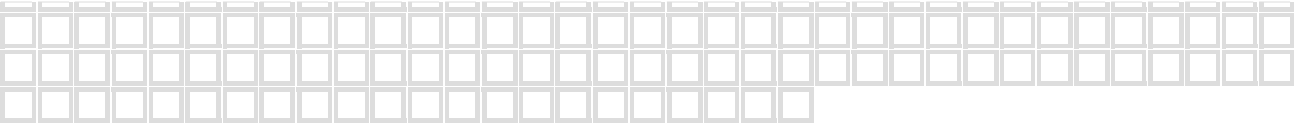
Synonyms: ENSG00000173757; ENSP00000293328; ENSP00000398379; 6777; STAT5B; NP_036580; NM_012448; P51692; STA5B_HUMAN;

More at [Entrez](#)

EPHB2 EPH receptor B2 [Source:HGNC Symbol;Acc:3393]

Functions:



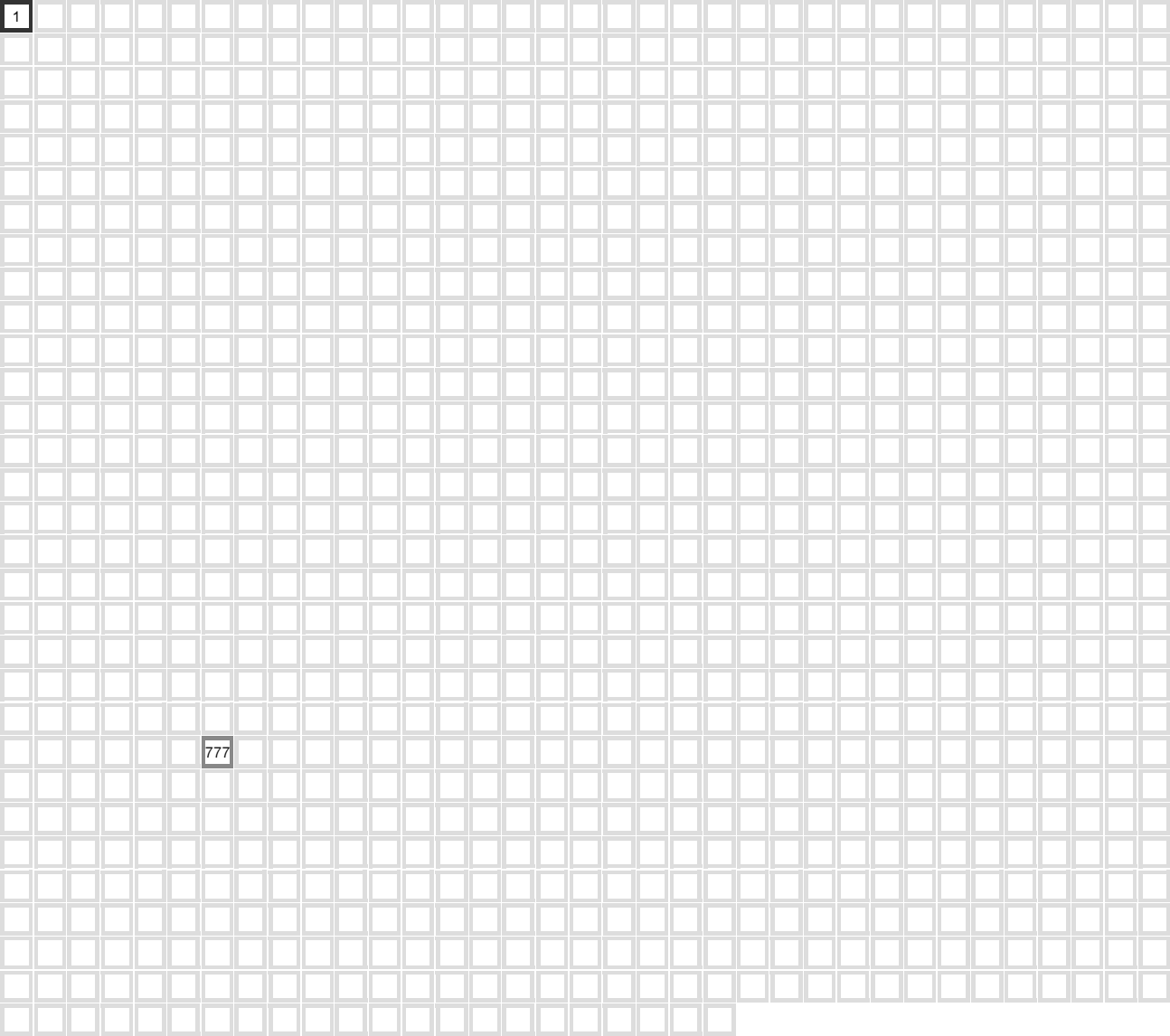


Synonyms: ENSG00000133216; ENSP00000363755; ENSP00000363758; ENSP00000363761; ENSP00000363763; ENSP00000383053; ENSP00000444174; 2048; EPHB2; NP_004433; NP_059145; NM_004442; NM_017449; DRT; EK5; EPHT3; Hek5; PCBC; Tyro5; EPHB2_HUMAN; P29323;

More at [Entrez](#)

POLR1C polymerase (RNA) I polypeptide C, 30kDa [Source:HGNC Symbol;Acc:20194]

Functions:

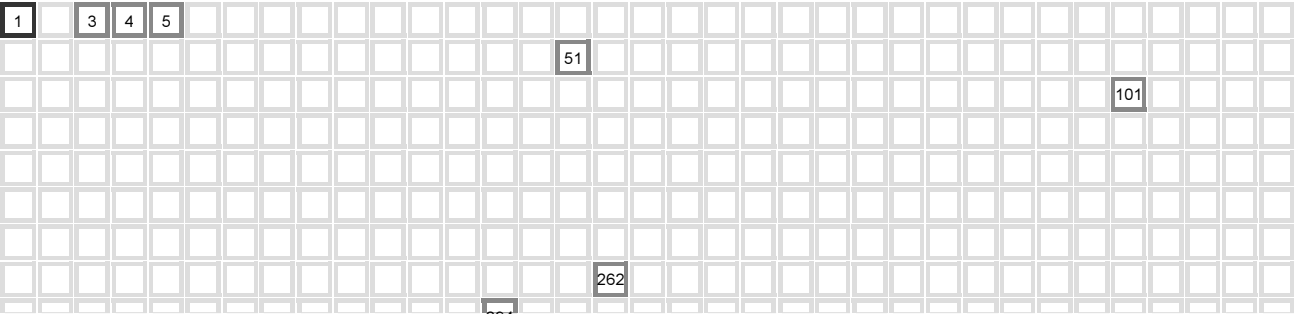


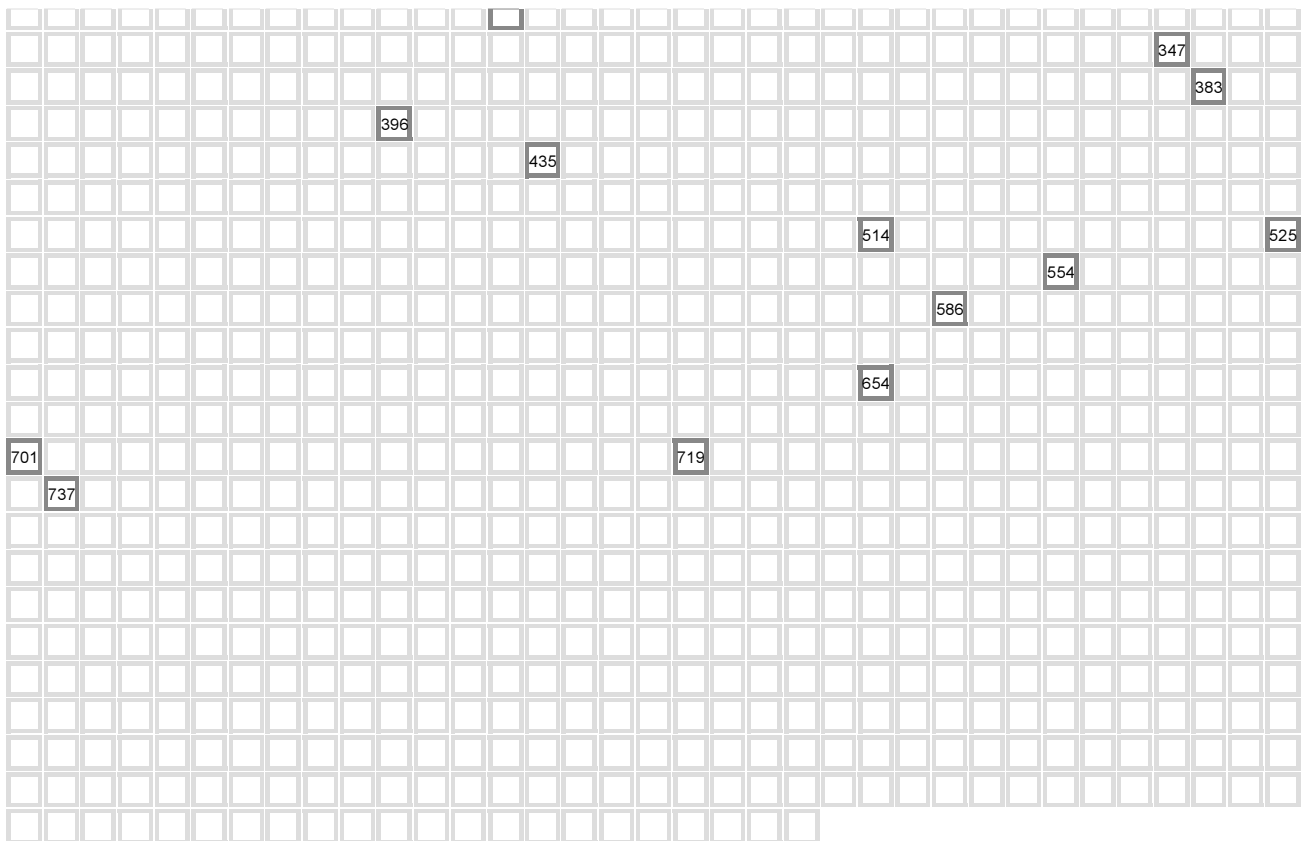
Synonyms: ENSG00000171453; ENSP00000307212; ENSP00000361419; ENSP00000361448; ENSP00000361465; ENSP00000395401; ENSP00000409536; ENSP00000423773; 9533; POLR1C; NP_976035; NM_004875; NM_203290; RPA39; RPA40; RPA5; RPAC1; TCS3; O15160; RPAC1_HUMAN;

More at [Entrez](#)

KITLG KIT ligand [Source:HGNC Symbol;Acc:6343]

Functions:



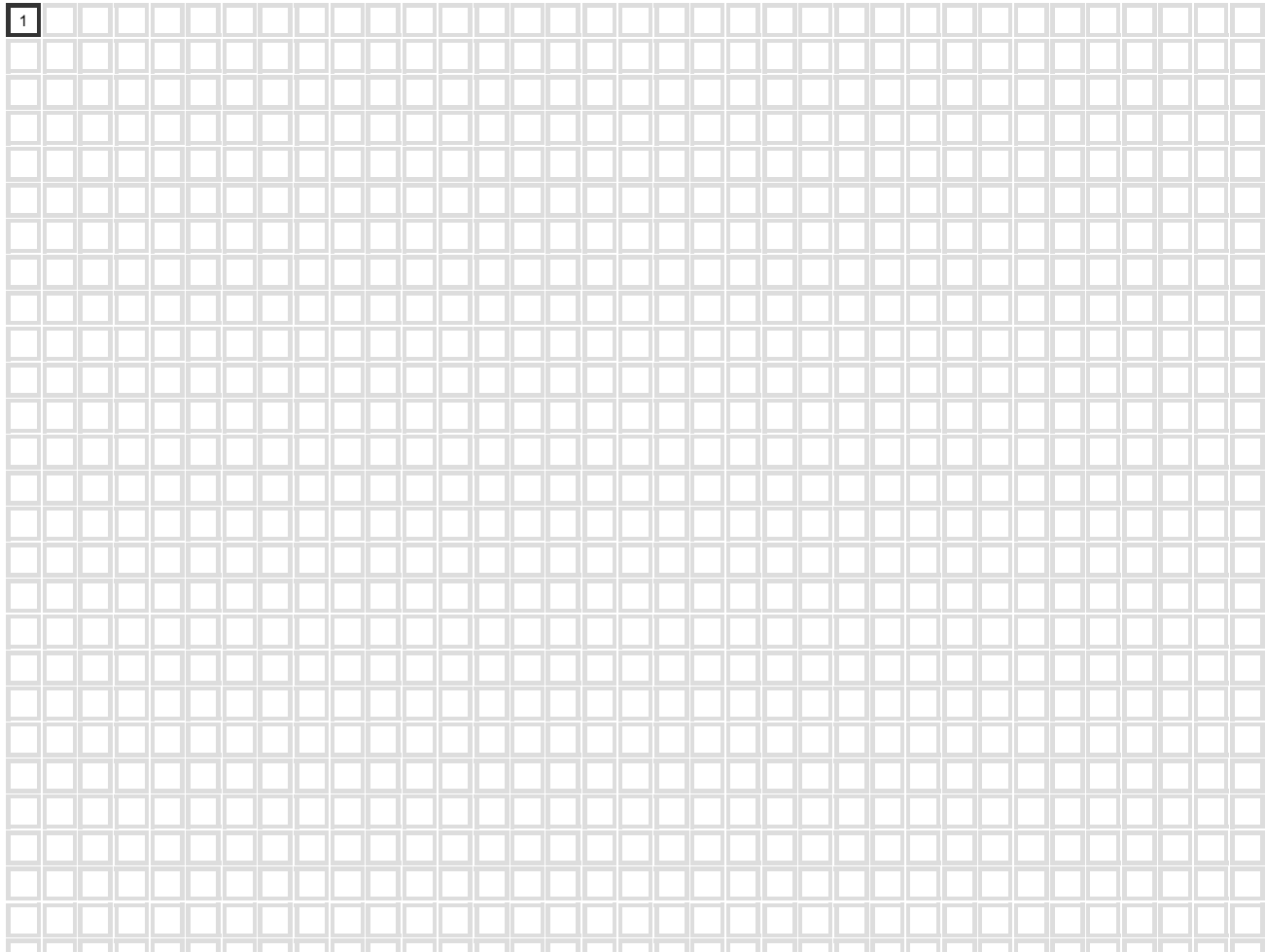


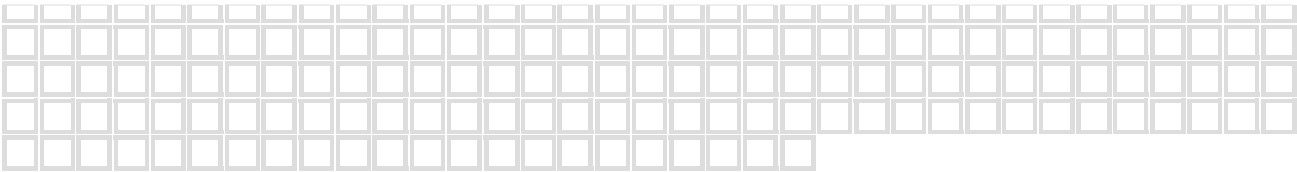
Synonyms: ENSG00000049130; ENSP00000054216; ENSP00000228280; ENSP00000367796; ENSP00000438889; 4254; KITLG; NP_000890; NP_003985; NM_000899; NM_003994; FPH2; kit-ligand; Kitl; KL-1; SCF; SHEP7; P21583; SCF_HUMAN;

More at [Entrez](#)

IL2RA interleukin 2 receptor, alpha [Source:HGNC Symbol;Acc:6008]

Functions:



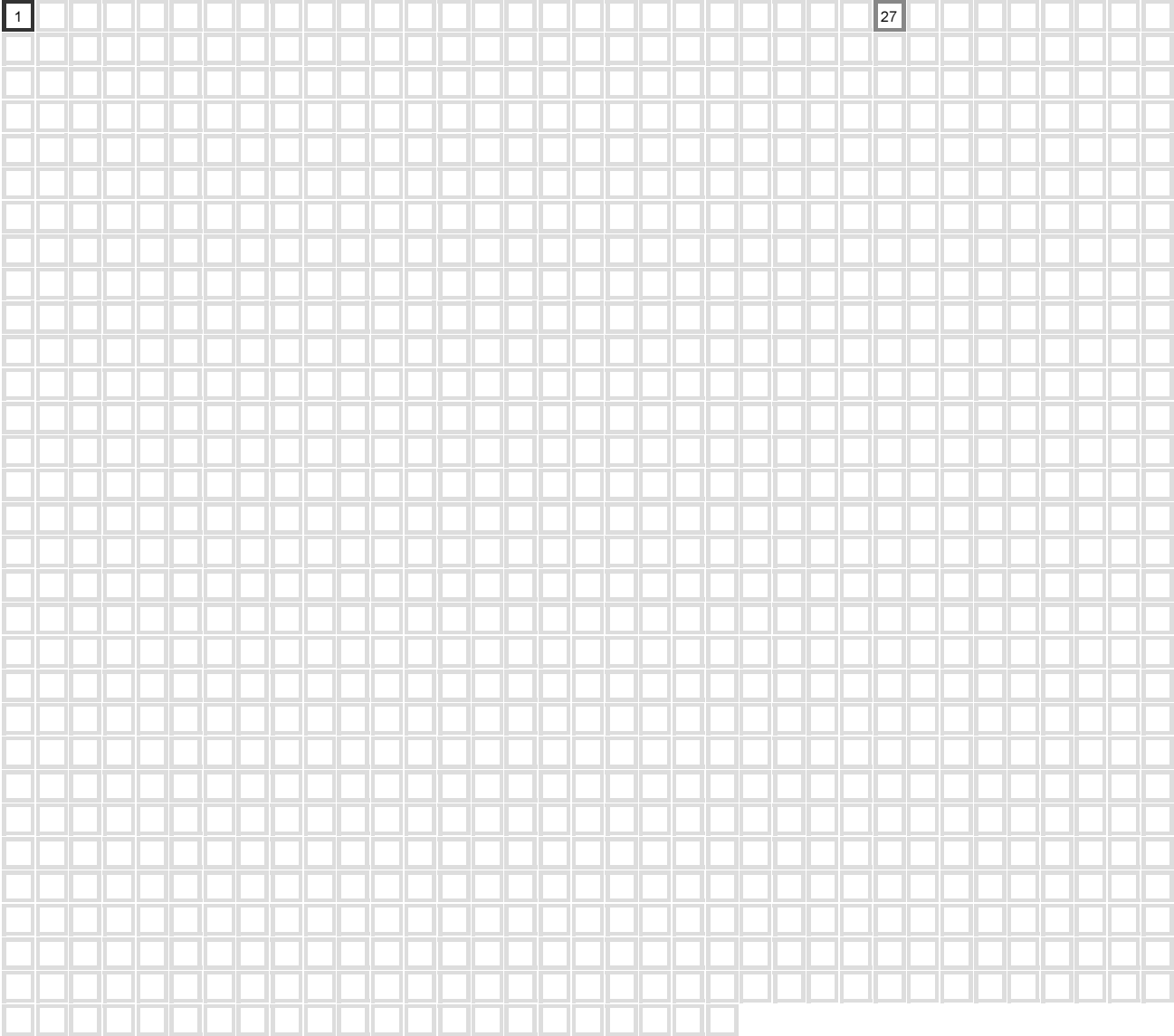


Synonyms: ENSG00000134460; ENSP00000256876; ENSP00000369287; ENSP00000369293; ENSP00000380415; ENSP00000402024; 3559; IL2RA; NP_000408; NM_000417; IDDM10; IL2R; TCGFR; IL2RA_HUMAN; P01589;

More at [Entrez](#)

HLX H2.0-like homeobox [Source:HGNC Symbol;Acc:4978]

Functions:

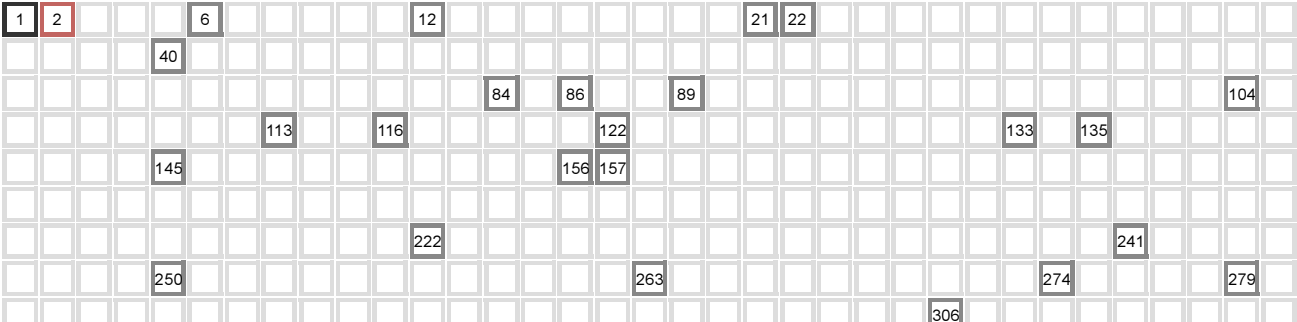


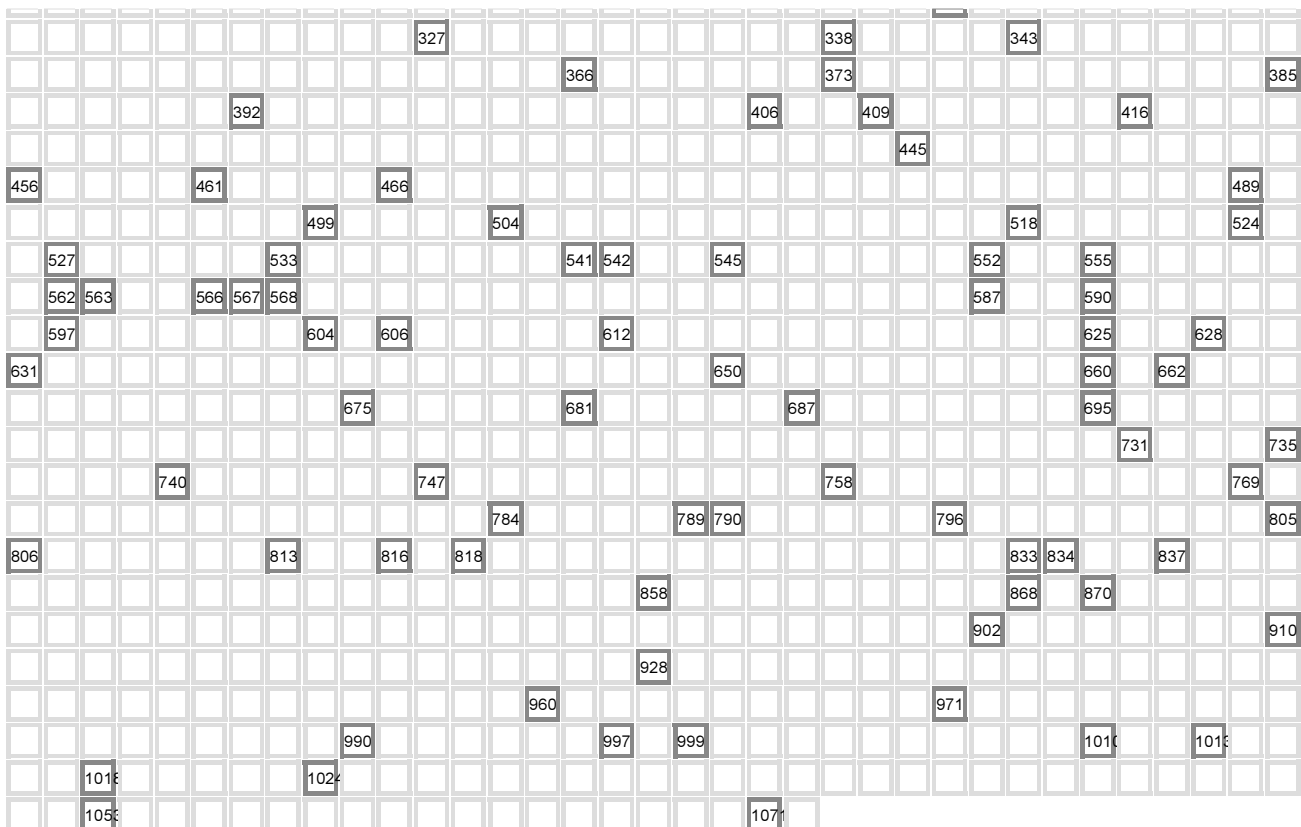
Synonyms: ENSG00000136630; ENSP00000355870; ENSP00000408248; ENSP00000449882; 3142; HLX; NP_068777; NM_021958; HB24; HLX1; HLX_HUMAN; Q14774;

More at [Entrez](#)

DRD2 dopamine receptor D2 [Source:HGNC Symbol;Acc:3023]

Functions:



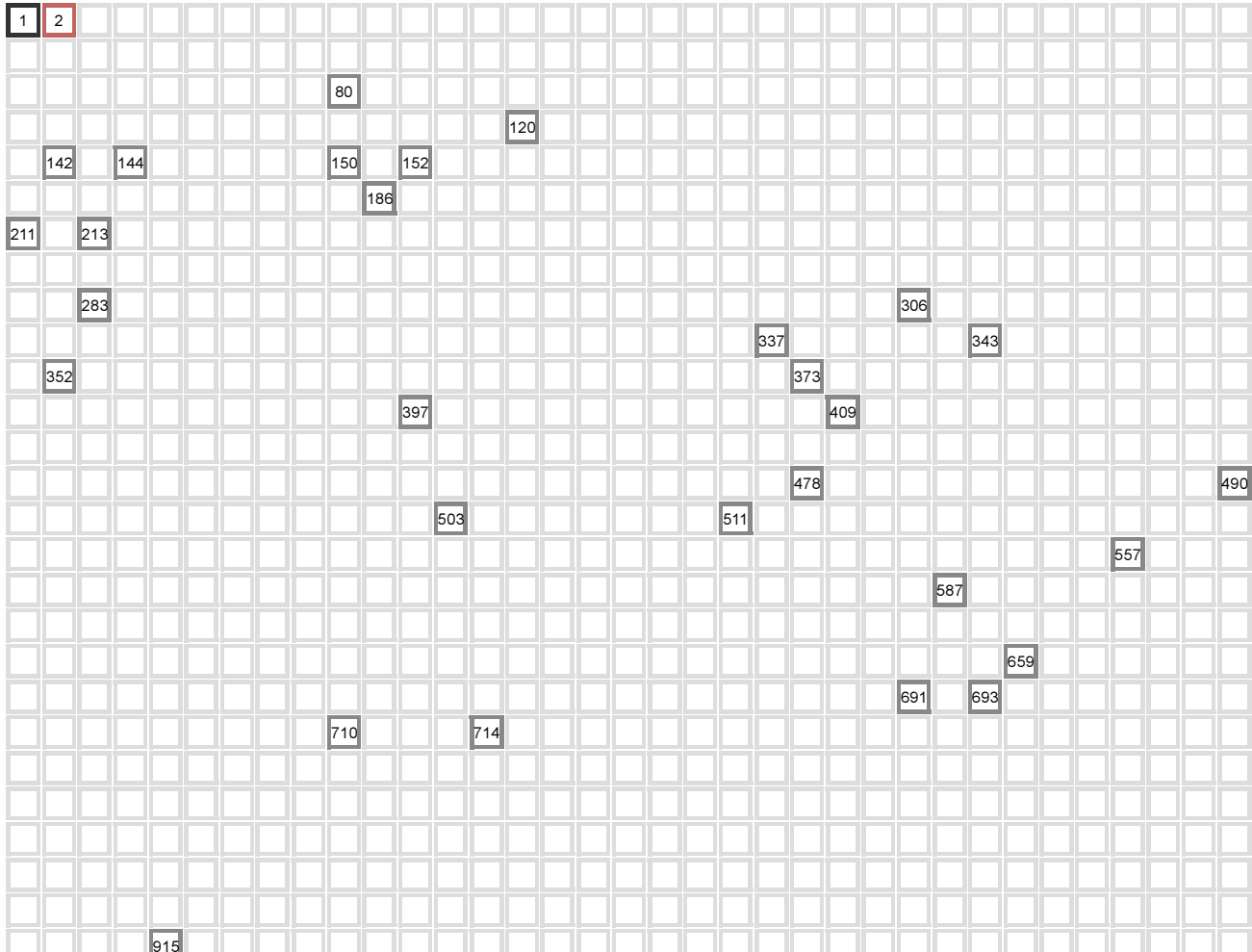


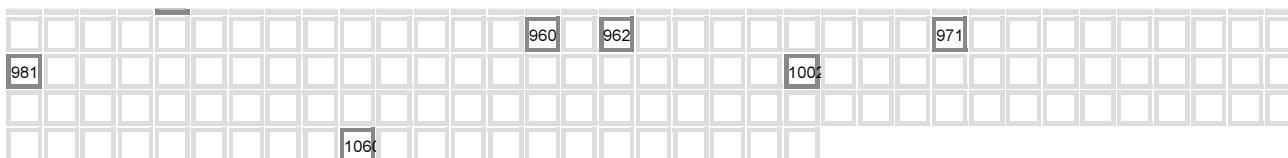
Synonyms: ENSG00000149295; ENSP00000278597; ENSP00000347474; ENSP00000354859; ENSP00000438215; ENSP00000438419; ENSP00000441068; ENSP00000441474; ENSP00000442172; 1813; DRD2; NP_000786; NP_057658; NM_000795; NM_016574; D2DR; D2R; DRD2_HUMAN; P14416;

More at [Entrez](#)

CD36 CD36 molecule (thrombospondin receptor) [Source:HGNC Symbol;Acc:1663]

Functions:



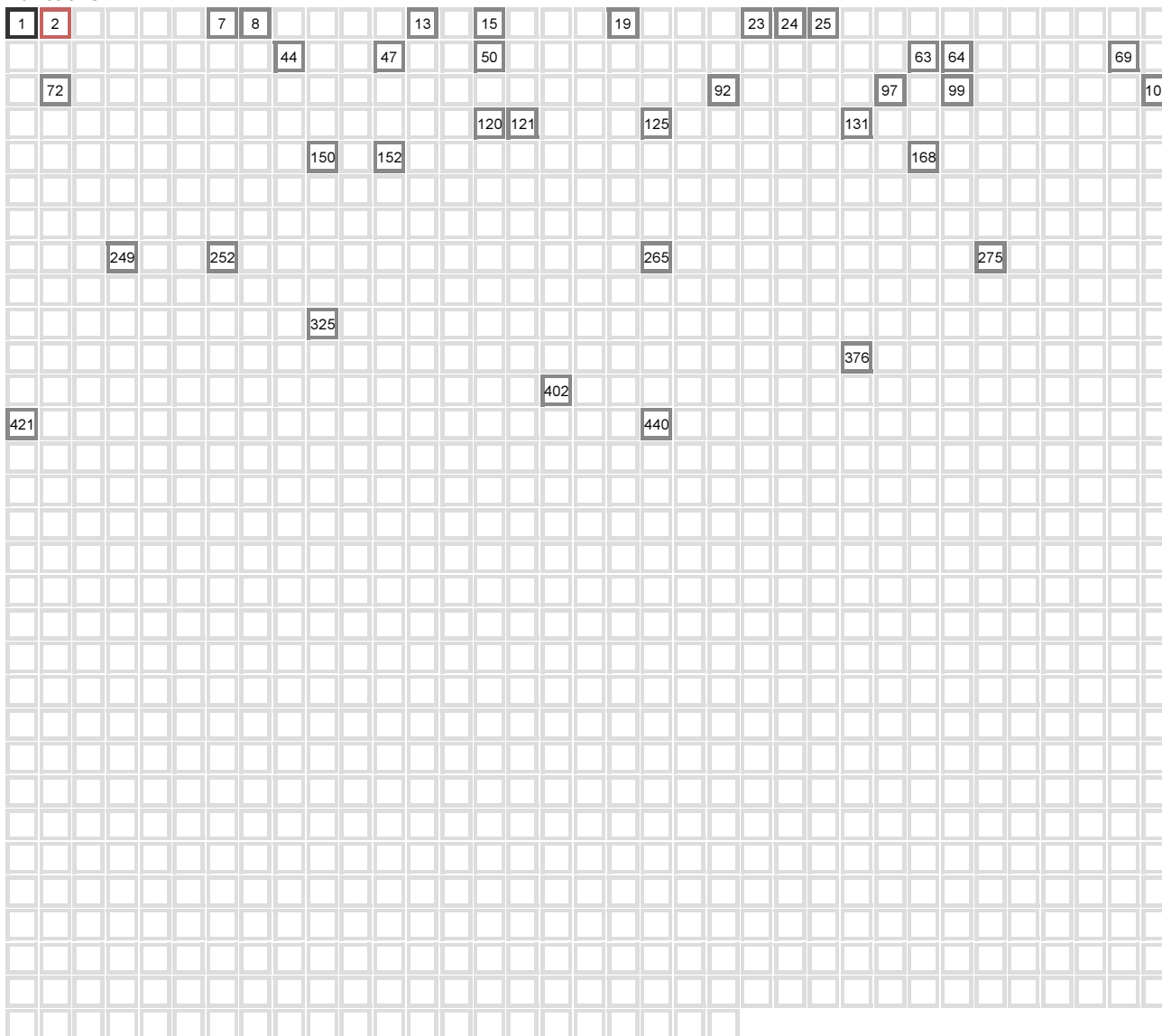


Synonyms: ENSG00000135218; ENSP00000308165; ENSP00000378268; ENSP00000392298; ENSP00000396258; ENSP00000398760; ENSP00000399421; ENSP00000401863; ENSP00000407690; ENSP00000409762; ENSP00000410371; ENSP00000411411; ENSP00000415743; ENSP00000416388; ENSP00000431296; ENSP00000433659; ENSP00000435698; ENSP00000439543; ENSP00000441956; 948; CD36; NP_000063; NP_001001547; NP_001001548; NP_001120915; NP_001120916; NM_000072; NM_001001547; NM_001001548; NM_001127443; NM_001127444; BDPLT10; CHDS7; GP3B; GP4; PASIV; SCARB3; CD36_HUMAN; P16671;

More at [Entrez](#)

ACVR1 activin A receptor, type I [Source:HGNC Symbol;Acc:171]

Functions:

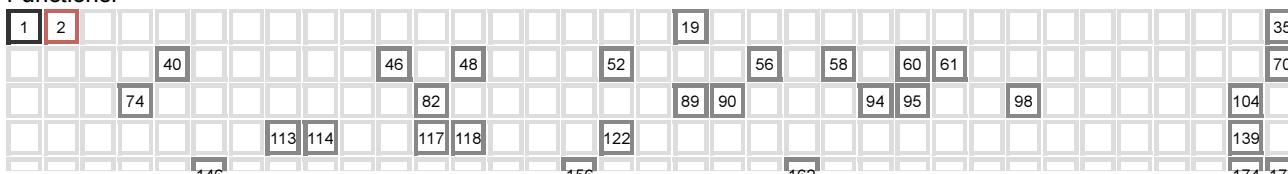


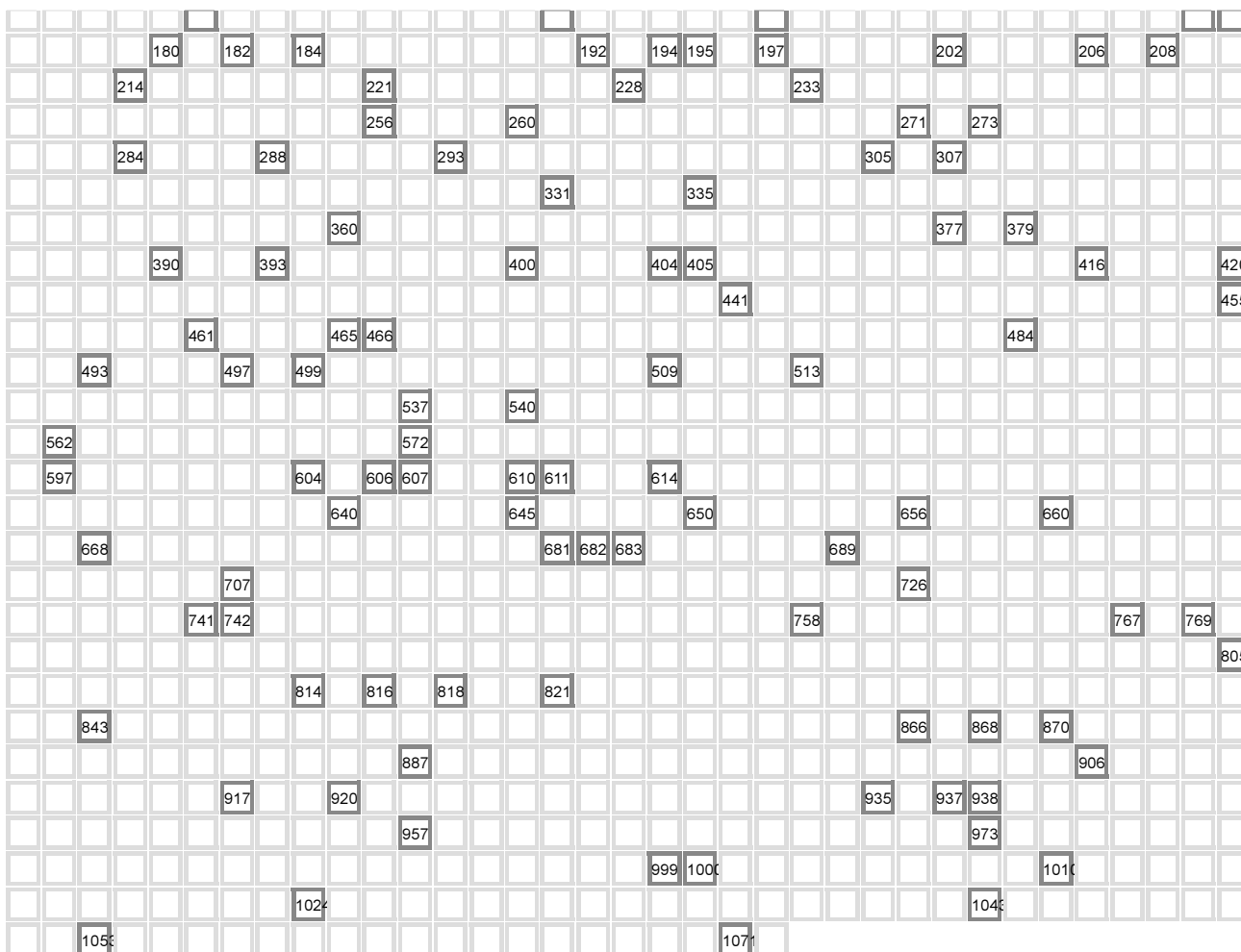
Synonyms: ENSG00000115170; ENSP00000263640; ENSP00000387127; ENSP00000387273; ENSP00000399322; ENSP00000400767; ENSP00000401189; ENSP00000403006; ENSP00000405004; ENSP00000440091; 90; ACVR1; NP_001096; NP_001104537; NM_001105; NM_001111067; ACTRI; ACVR1A; ACVRLK2; ALK2; SKR1; TSRI; ACVR1_HUMAN; Q04771;

More at [Entrez](#)

FGF2 fibroblast growth factor 2 (basic) [Source:HGNC Symbol;Acc:3676]

Functions:



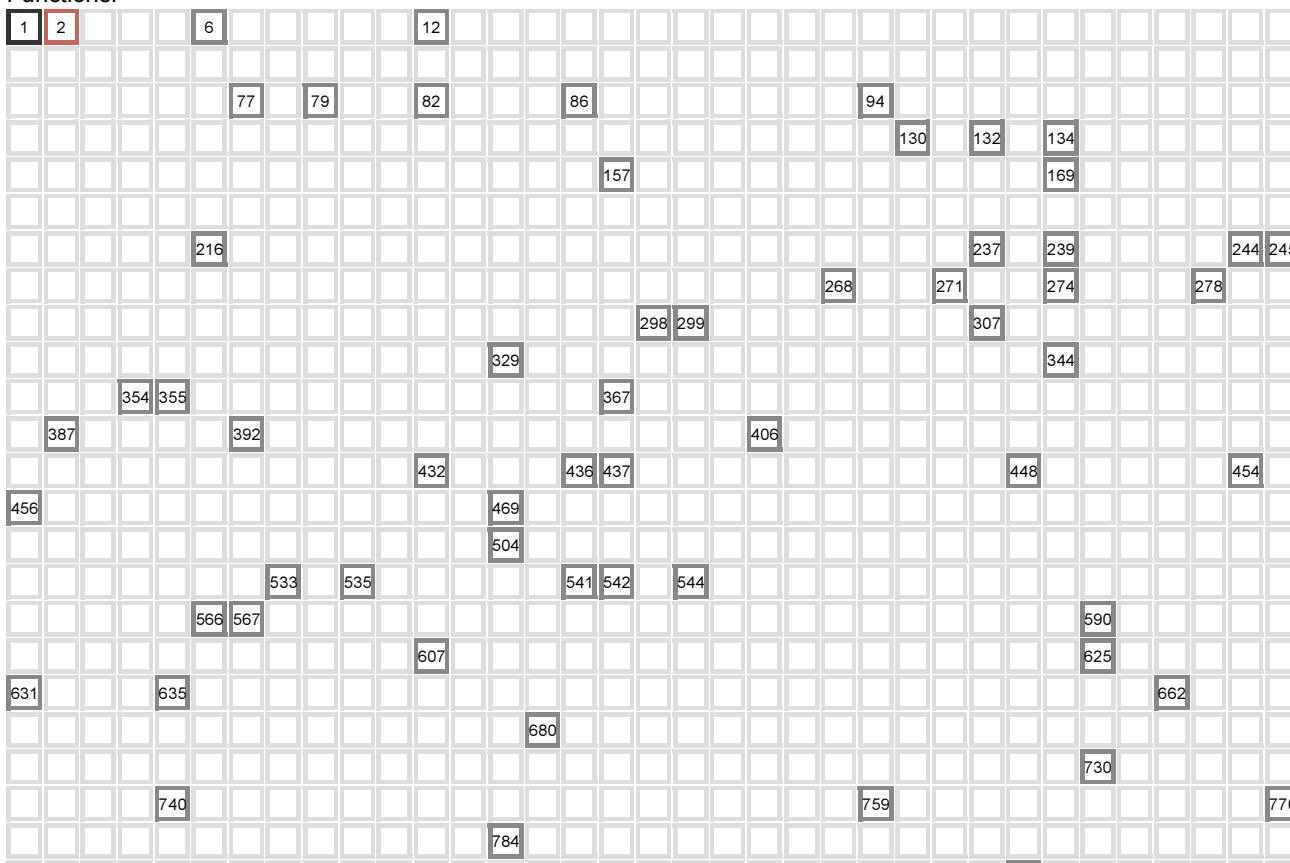


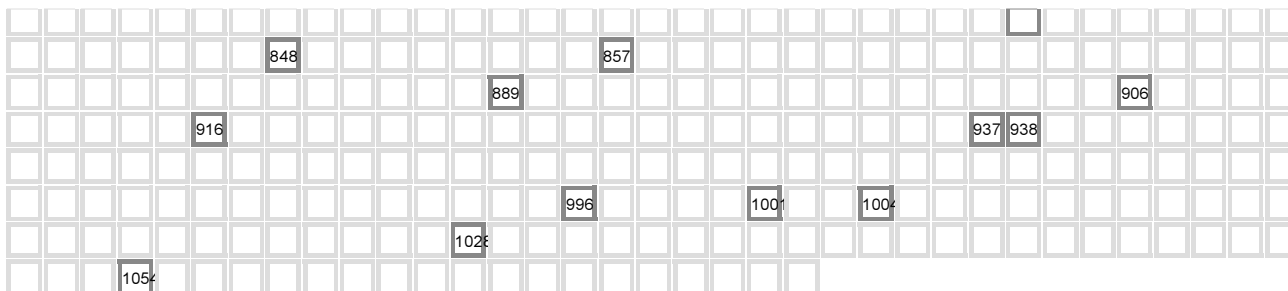
Synonyms: ENSG00000138685; ENSP00000264498; 2247; FGF2; NP_001997; NM_002006; BFGF; FGFB; HBGF-2; FGF2_HUMAN; P09038;

More at [Entrez](#)

BAD BCL2-associated agonist of cell death [Source:HGNC Symbol;Acc:936]

Functions:



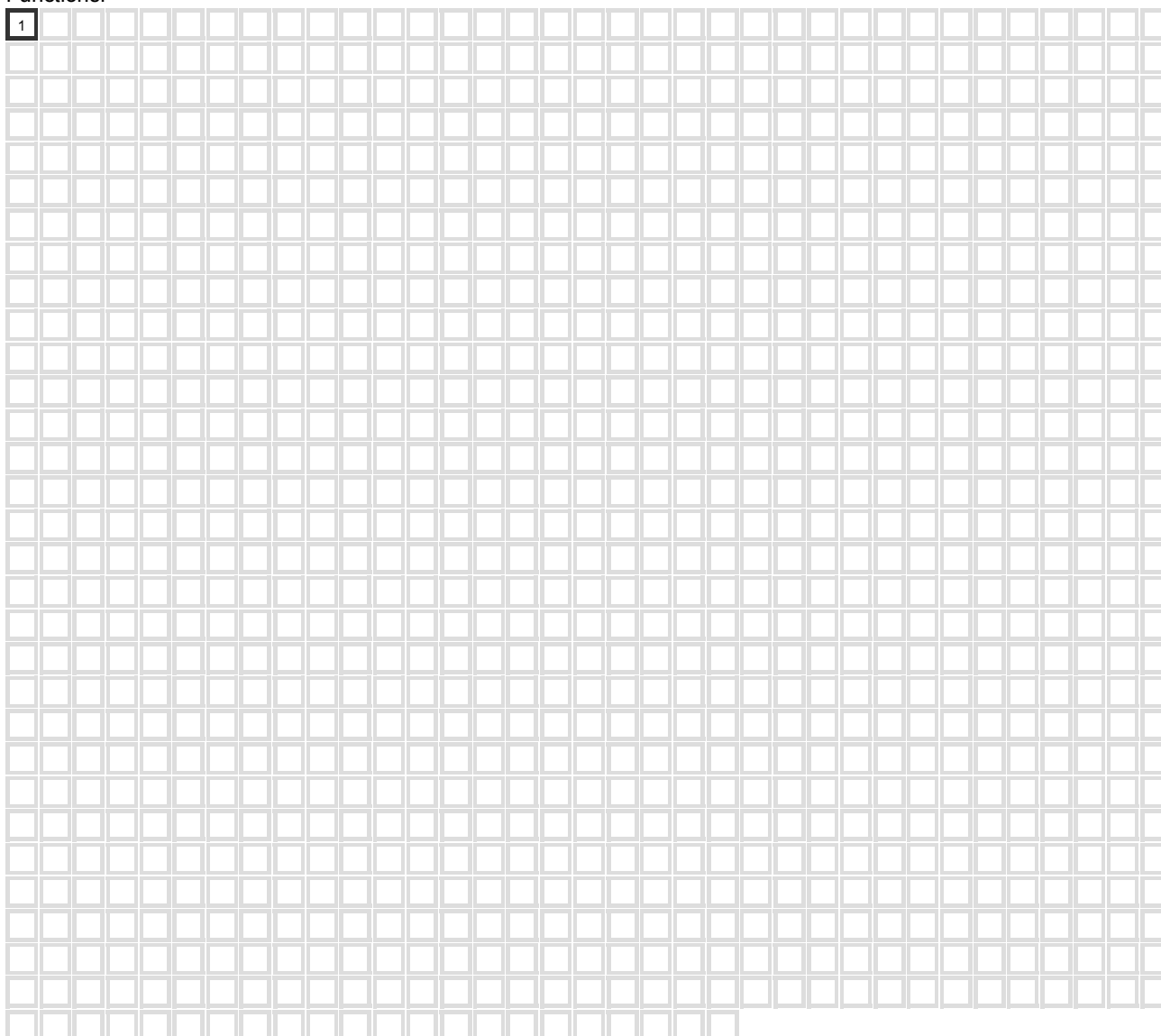


Synonyms: ENSG00000002330; ENSP00000309103; ENSP00000378039; ENSP00000378040; ENSP00000438975; ENSP00000439202; ENSP00000440575; ENSP00000440807; 572; BAD; NP_004313; NP_116784; NM_004322; NM_032989; BBC2; BCL2L8; BAD_HUMAN; Q92934;

More at [Entrez](#)

TGIF1 TGFB-induced factor homeobox 1 [Source:HGNC Symbol;Acc:11776]

Functions:



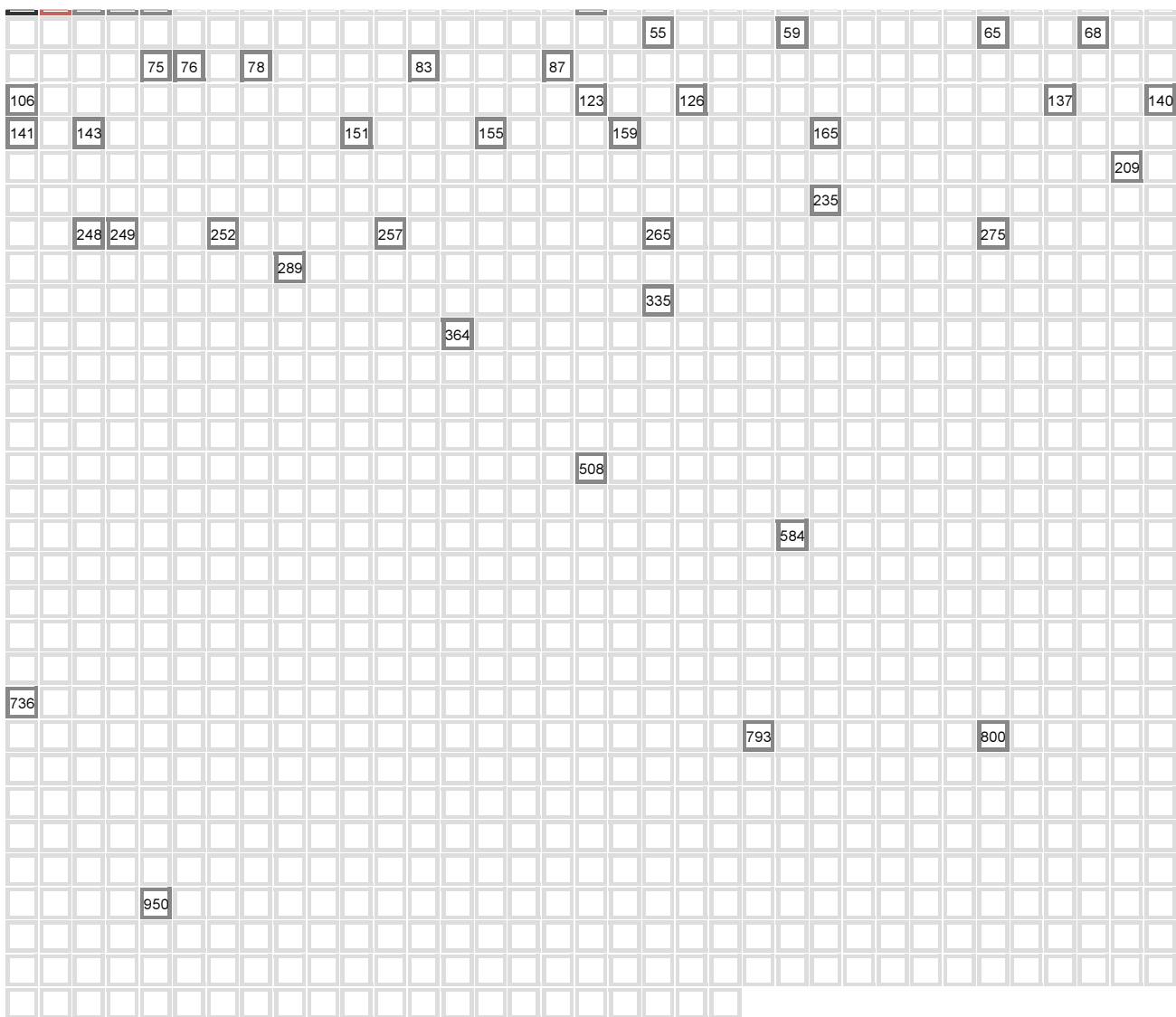
Synonyms: ENSG00000177426; ENSP00000327959; ENSP00000339631; ENSP00000343969; ENSP00000383031; ENSP00000384133; ENSP00000384970; ENSP00000385206; ENSP00000446838; ENSP00000446944; ENSP00000447747; ENSP00000448121; ENSP00000448934; ENSP00000449287; ENSP00000449501; ENSP00000449531; ENSP00000449580; ENSP00000449722; ENSP00000449973; ENSP00000450025; 7050; TGIF1; NP_003235; NP_733796; NP_775299; NP_775300; NP_775301; NP_775302; NP_775303; NP_777480; NM_003244; NM_170695; NM_173207; NM_173208; NM_173209; NM_173210; NM_173211; NM_174886; HPE4; Q15583; TGIF1_HUMAN;

More at [Entrez](#)

ZAP70 zeta-chain (TCR) associated protein kinase 70kDa [Source:HGNC Symbol;Acc:12858]

Functions:



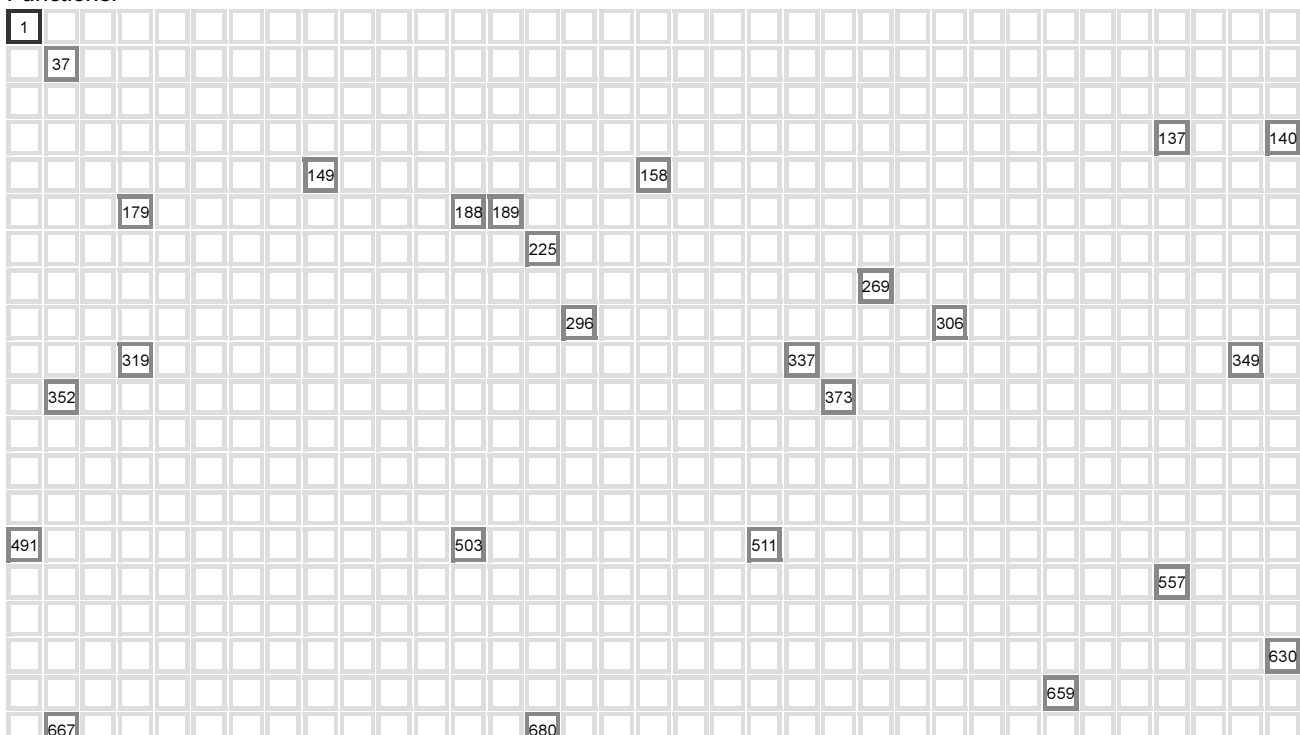


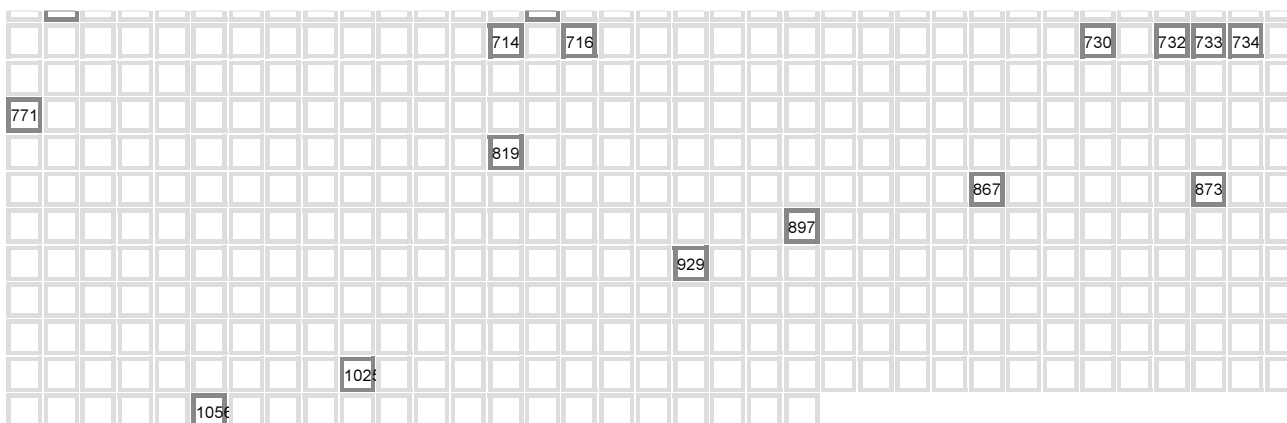
Synonyms: ENSG00000115085; ENSP00000264972; ENSP00000400475; ENSP00000411141; 7535; ZAP70; NP_001070; NP_997402; NM_001079; NM_207519; TZK; ZAP-70; P43403; ZAP70_HUMAN;

More at [Entrez](#)

CLU clusterin [Source:HGNC Symbol;Acc:2095]

Functions:



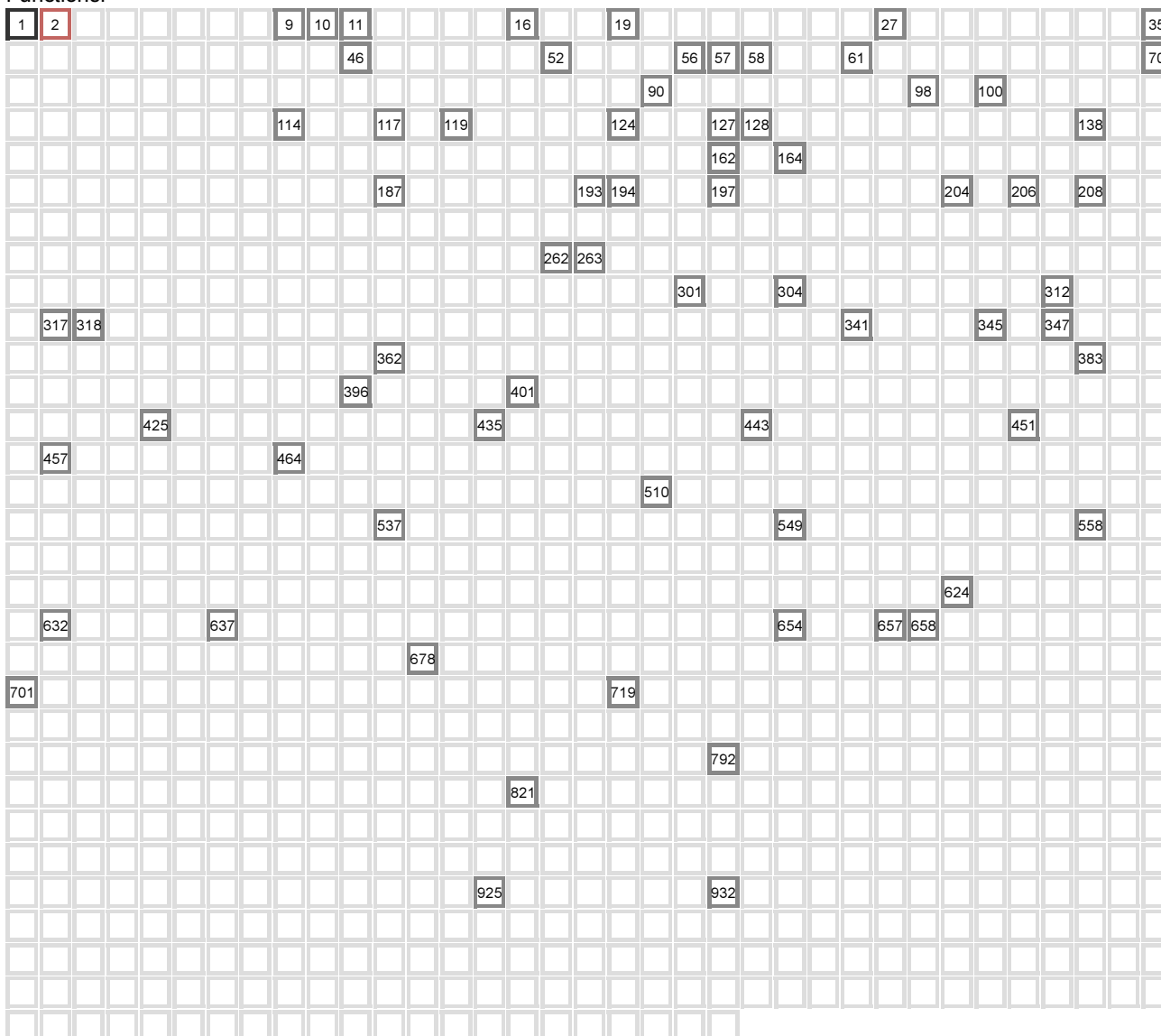


Synonyms: ENSG00000120885; ENSP00000315130; ENSP00000369812; ENSP00000385419; ENSP00000427868; ENSP00000428033; ENSP00000428526; ENSP00000428779; ENSP00000429087; ENSP00000429336; ENSP00000429620; ENSP00000429881; ENSP00000430821; ENSP00000431026; ENSP00000431070; ENSP00000431096; ENSP00000446413; ENSP00000453247; ENSP00000453939; 1191; CLU; NP_001822; NP_976084; NM_001831; NM_203339; NR_038335; NR_045494; APO-J; APOJ; CLI; KUB1; NA1/NA2; SGP-2; SGP2; SP-40; TRPM-2; CLUS_HUMAN; P10909;

More at [Entrez](#)

GATA4 GATA binding protein 4 [Source:HGNC Symbol;Acc:4173]

Functions:

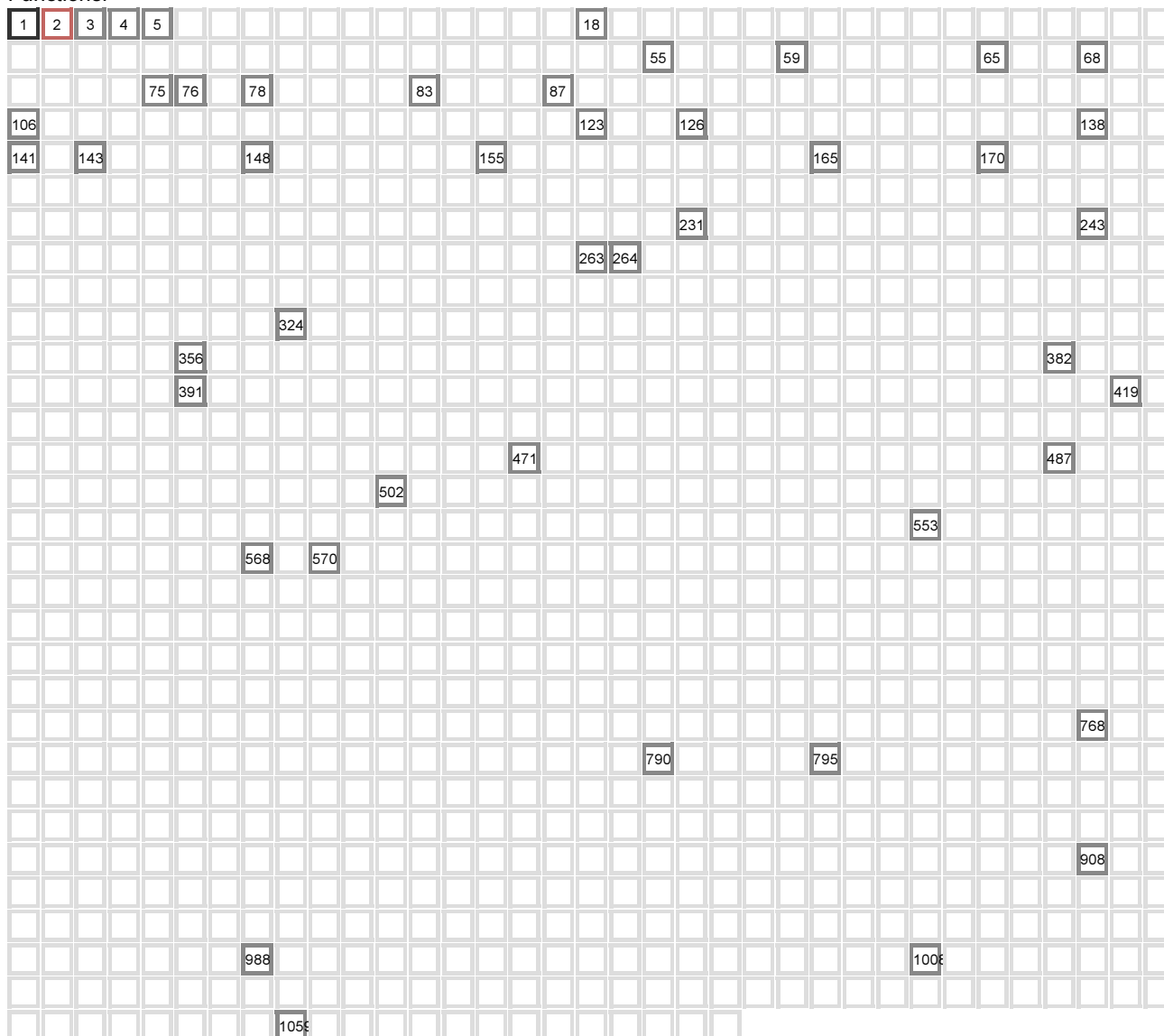


Synonyms: ENSG00000136574; ENSP00000259090; ENSP00000334458; ENSP00000432278; ENSP00000435043; ENSP00000435347; ENSP00000435712; 2626; GATA4; NP_002043; NM_002052; ASD2; VSD1; GATA4_HUMAN; P43694;

More at [Entrez](#)

PNP purine nucleoside phosphorylase [Source:HGNC Symbol;Acc:7892]

Functions:

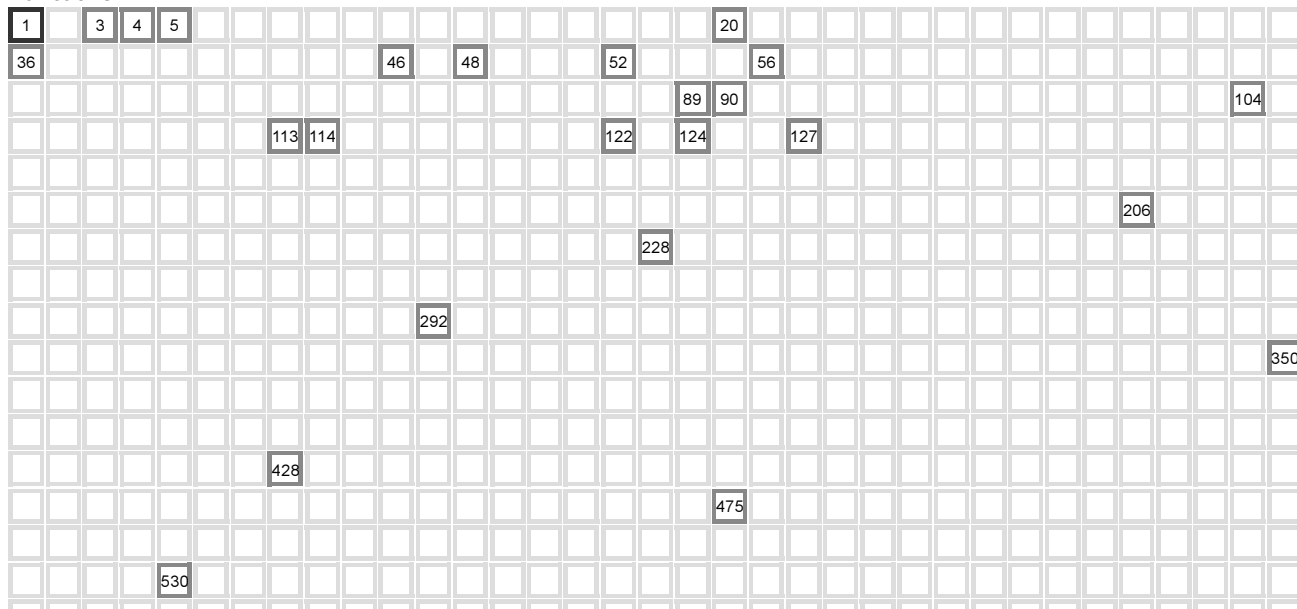


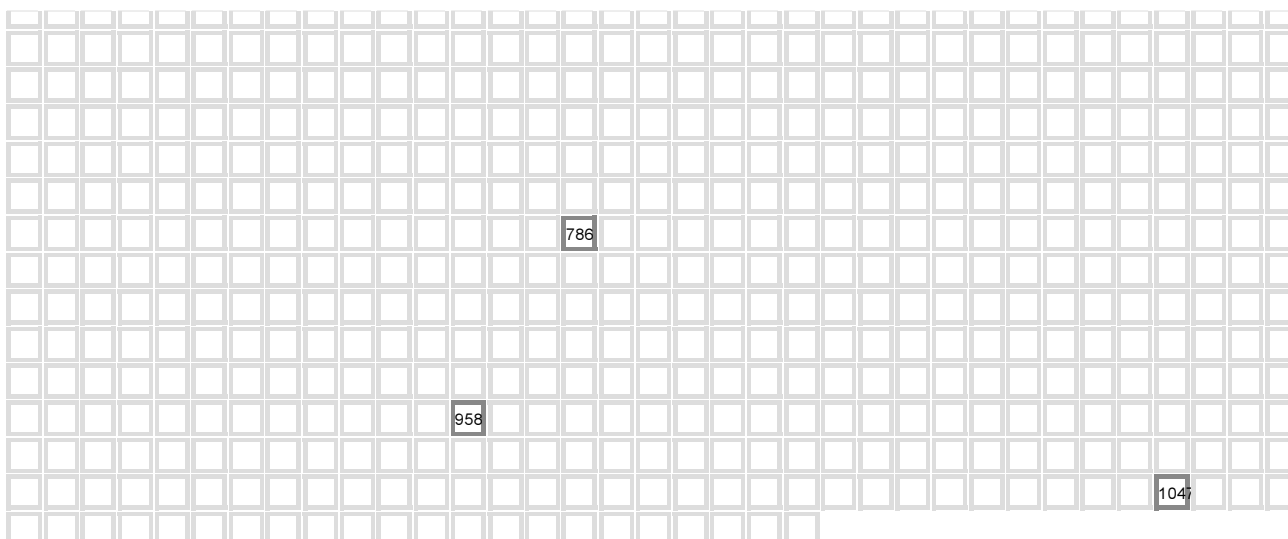
Synonyms: ENSG00000198805; ENSP00000354532; ENSP00000450663; ENSP00000450966; ENSP00000451108; ENSP00000452421; 4860; PNP; NP_000261; NM_000270; PRO1837; PUNP; P00491; PNPH_HUMAN;

More at [Entrez](#)

JAG1 jagged 1 [Source:HGNC Symbol;Acc:6188]

Functions:



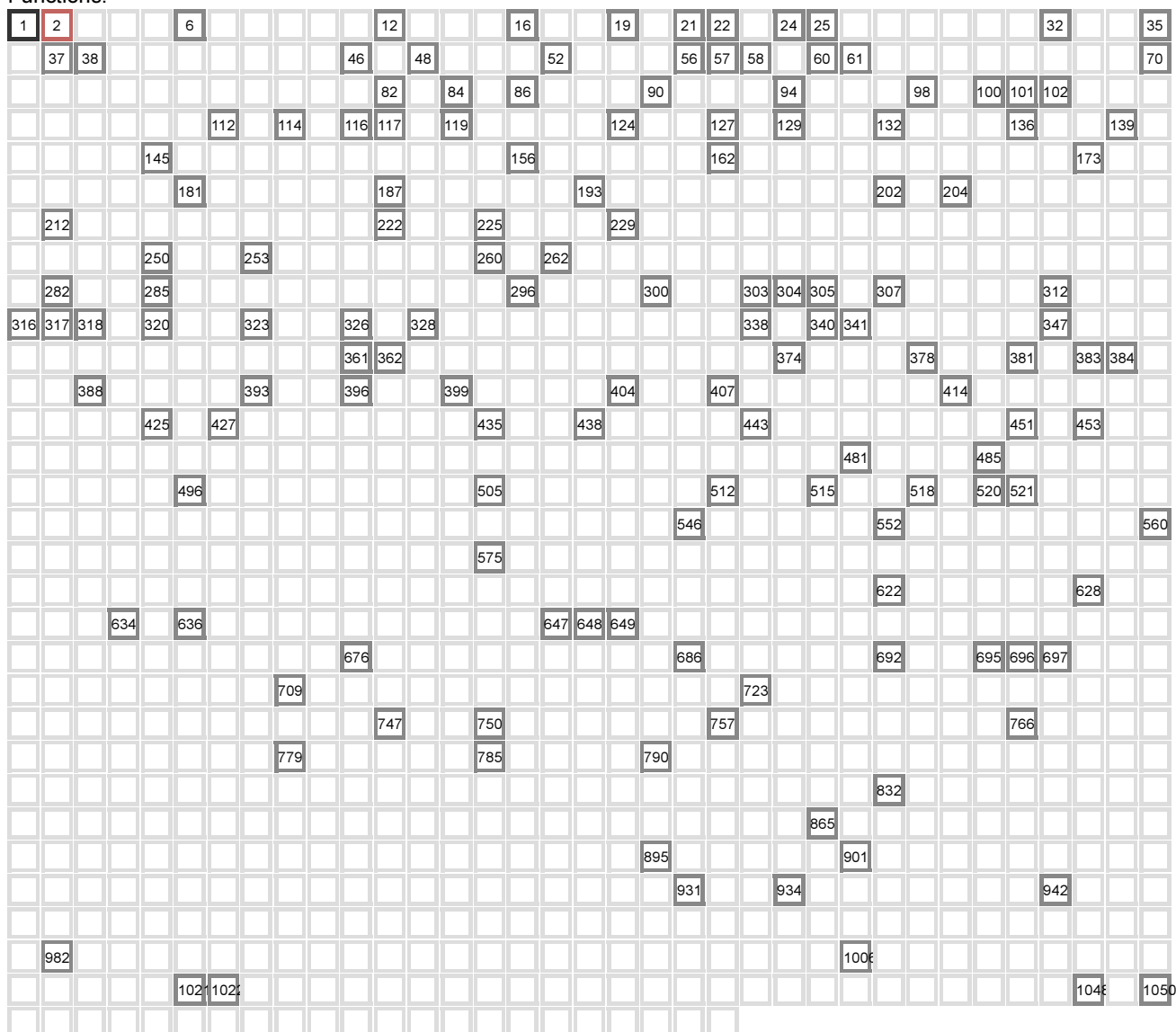


Synonyms: ENSG00000101384; ENSP00000254958; ENSP00000389519; 182; JAG1; NP_000205; NM_000214; AGS; AHD; AWS; CD339; HJ1; JAGL1; JAG1_HUMAN; P78504;

More at [Entrez](#)

SMO smoothened, frizzled family receptor [Source:HGNC Symbol;Acc:11119]

Functions:

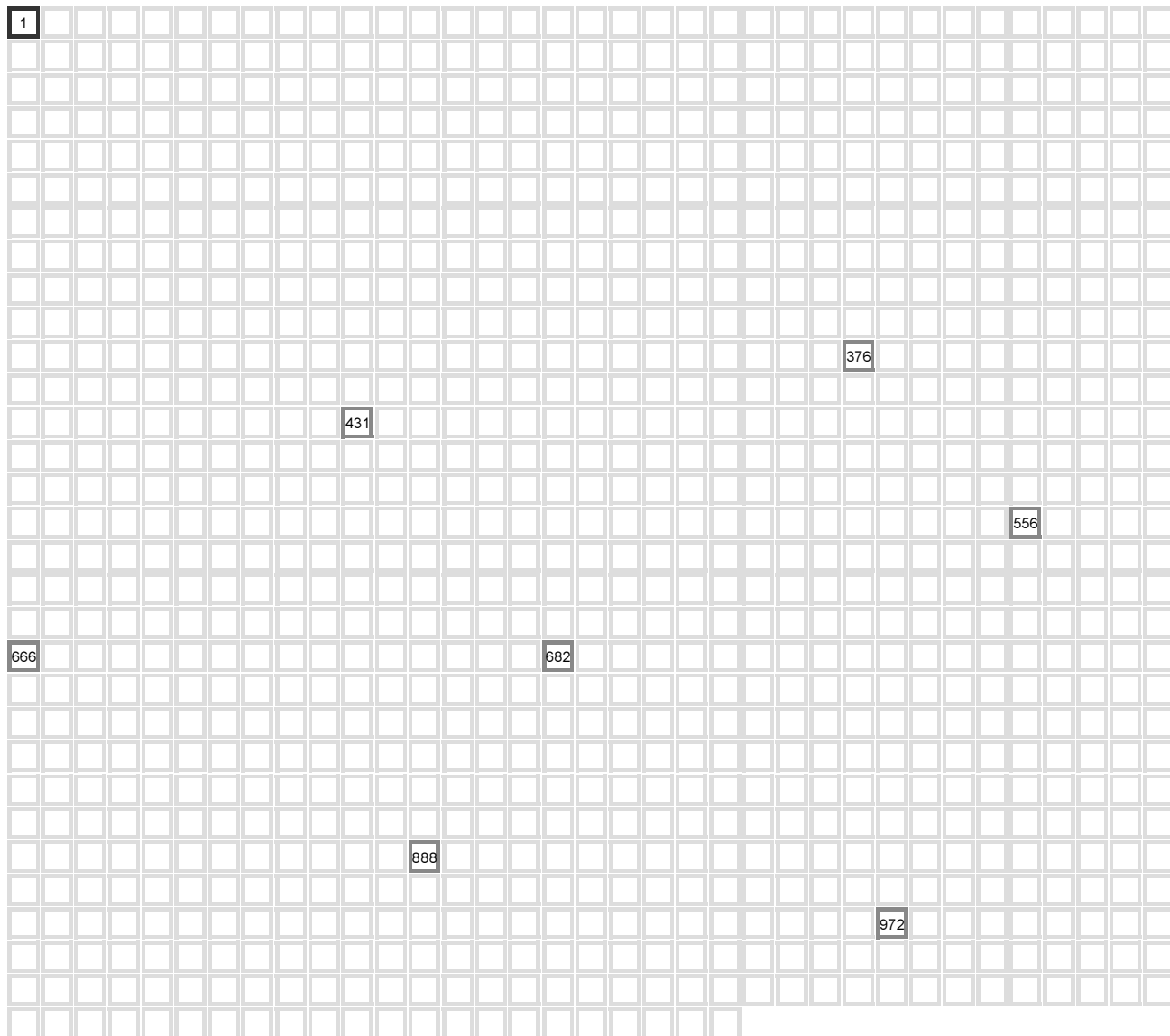


Synonyms: ENSG00000128602; ENSP00000249373; ENSP00000418720; ENSP00000420749; 6608; SMO; NP_005622; NM_005631; FZD11; SMOH; Q99835; SMO_HUMAN;

More at [Entrez](#)

CCNE1 cyclin E1 [Source:HGNC Symbol;Acc:1589]

Functions:

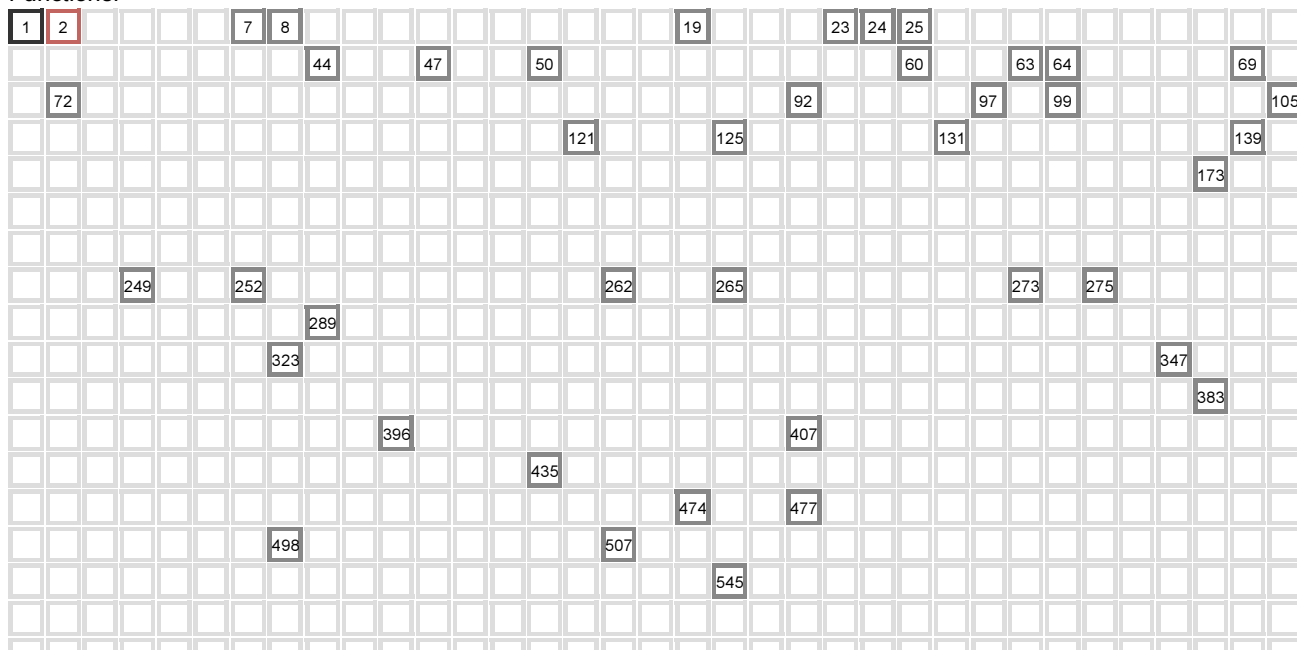


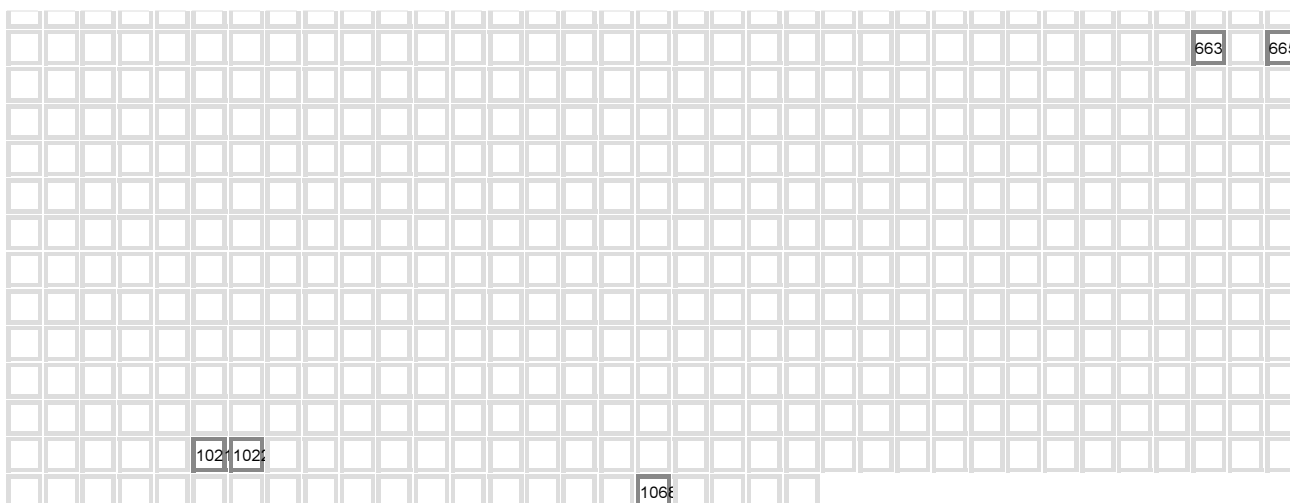
Synonyms: ENSG00000105173; ENSP00000262643; ENSP00000350625; ENSP00000410179; 898; CCNE1; NP_001229; NM_001238; NM_057182; CCNE; CCNE1_HUMAN; P24864;

More at [Entrez](#)

BMPR1B bone morphogenetic protein receptor, type IB [Source:HGNC Symbol;Acc:1077]

Functions:



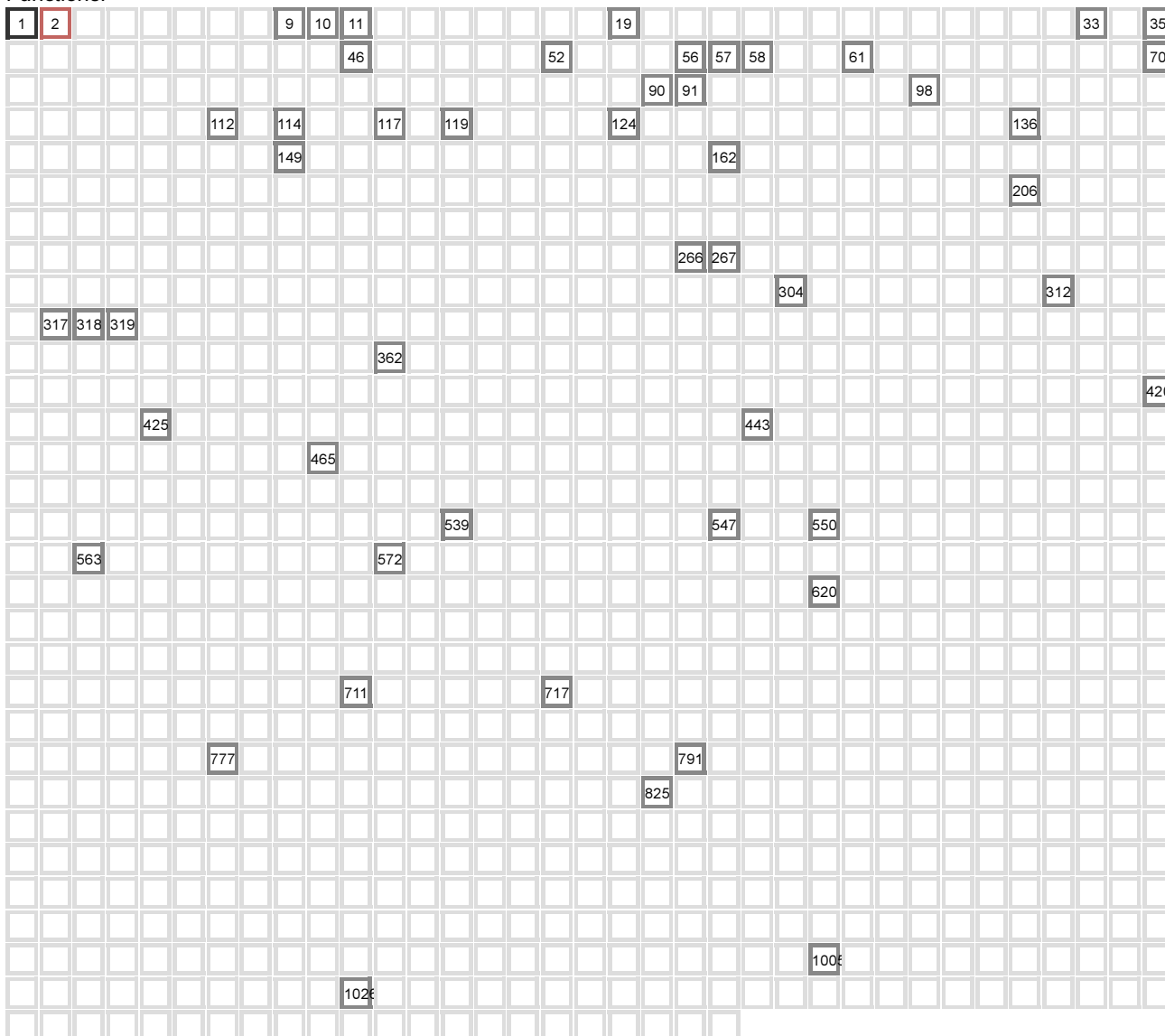


Synonyms: ENSG00000138696; ENSP00000264568; ENSP00000378389; ENSP00000401907; ENSP00000421144; ENSP00000421671; ENSP00000424693; ENSP00000425444; ENSP00000426617; 658; BMPR1B; NP_001194; NM_001203; ALK-6; ALK6; CDw293; BMR1B_HUMAN; O00238;

More at [Entrez](#)

SRF serum response factor (c-fos serum response element-binding transcription factor) [Source:HGNC Symbol;Acc:11291]

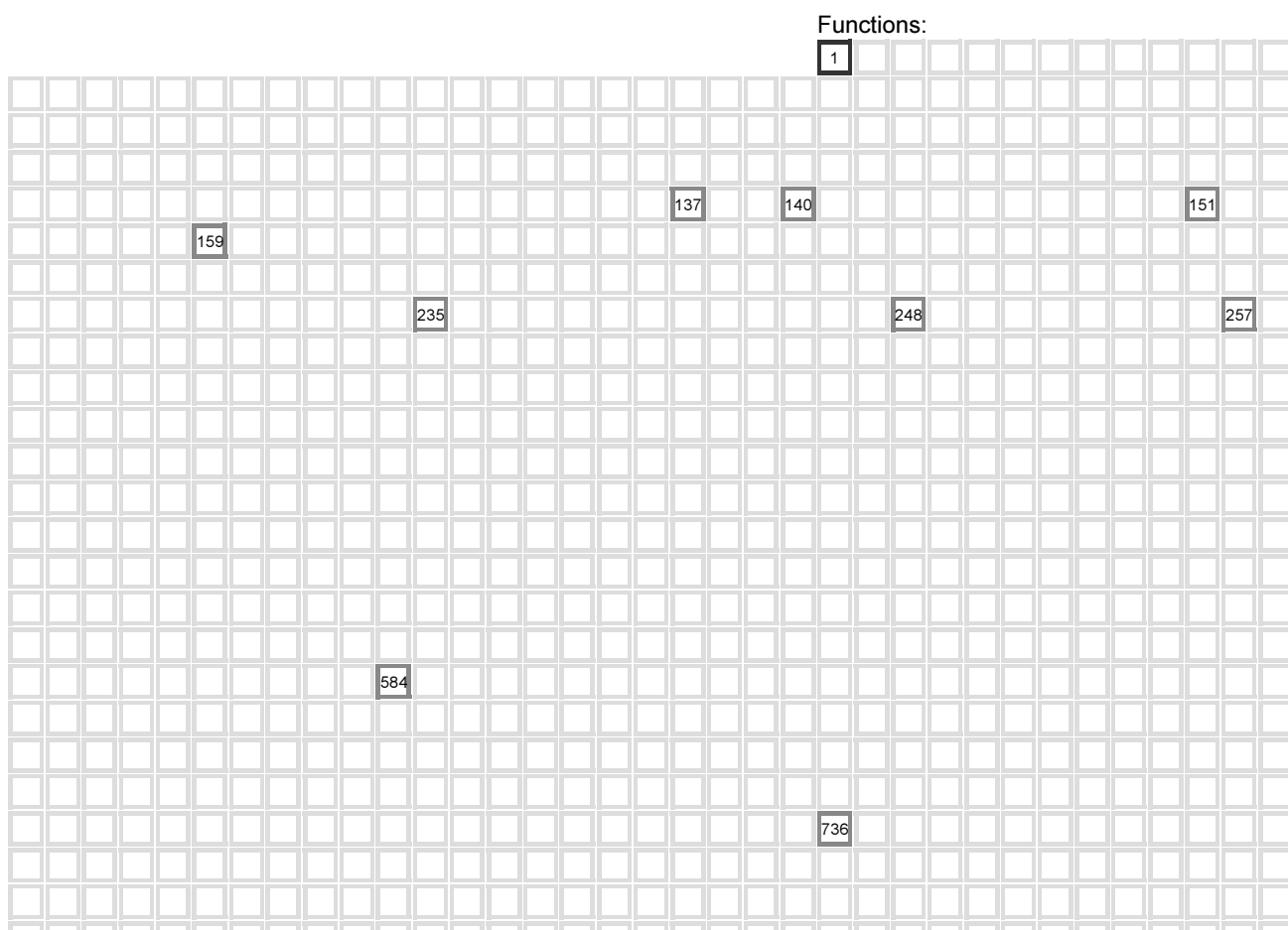
Functions:

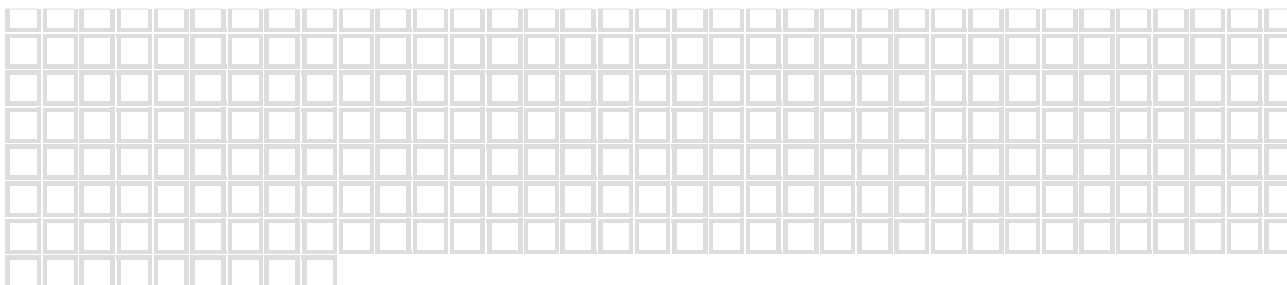


Synonyms: ENSG00000112658; ENSP00000265354; ENSP00000401320; 6722; SRF; NP_003122; NM_003131; MCM1; P11831; SRF_HUMAN;

More at [Entrez](#)

INPP5D inositol polyphosphate-5-phosphatase, 145kDa [Source:HGNC Symbol;Acc:6079]



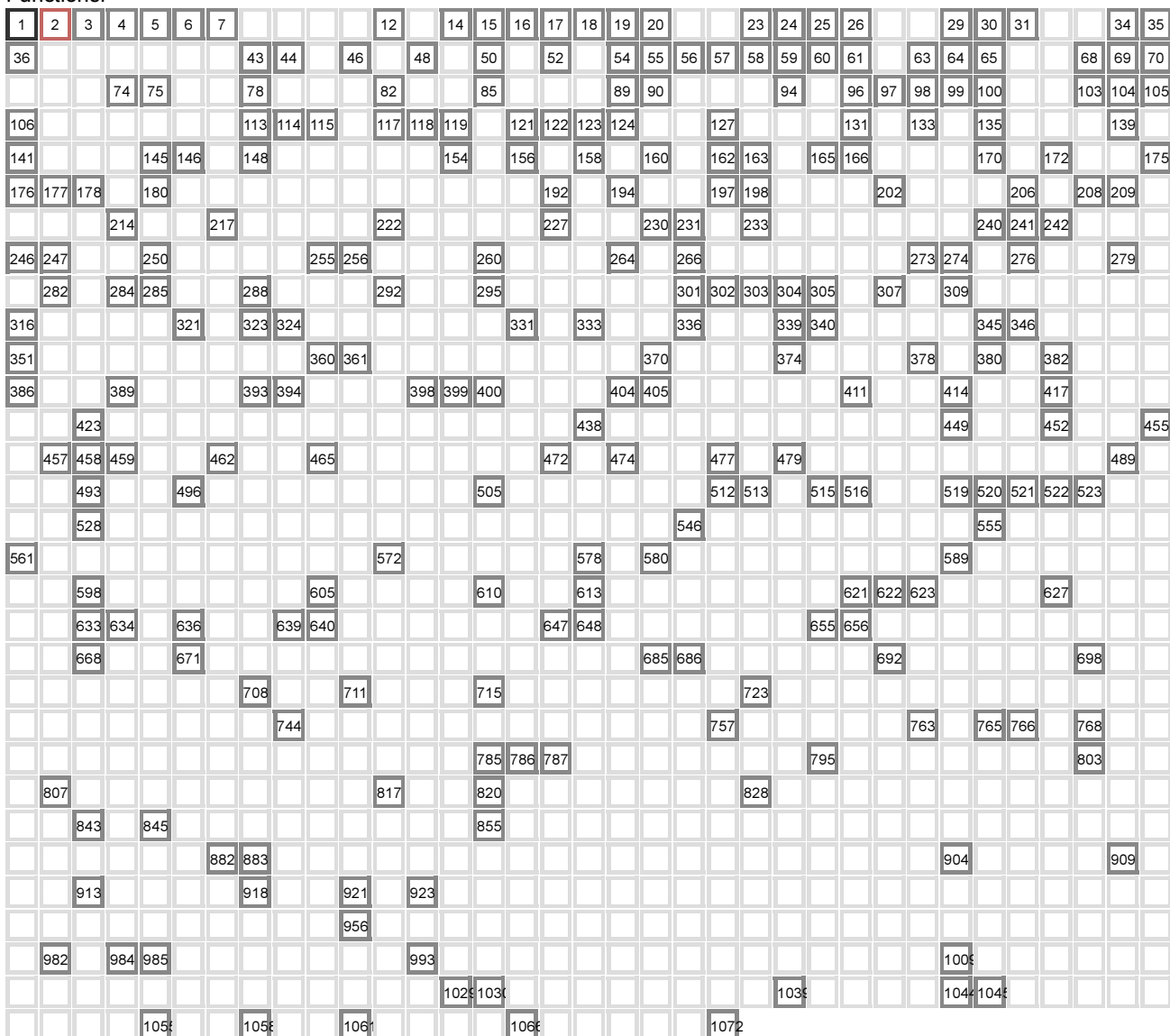


Synonyms: ENSG00000168918; ENSP00000352575; ENSP00000397421; ENSP00000400151; ENSP00000404610; ENSP00000405338; ENSP00000407916; ENSP00000409018; ENSP00000414835; ENSP00000415253; ENSP00000441010; 3635; INPP5D; NP_001017915; NP_005532; NM_001017915; NM_005541; hp51CN; SHIP; SHIP1; SIP-145; Q92835; SHIP1_HUMAN;

More at [Entrez](#)

BMP4 bone morphogenetic protein 4 [Source:HGNC Symbol;Acc:1071]

Functions:



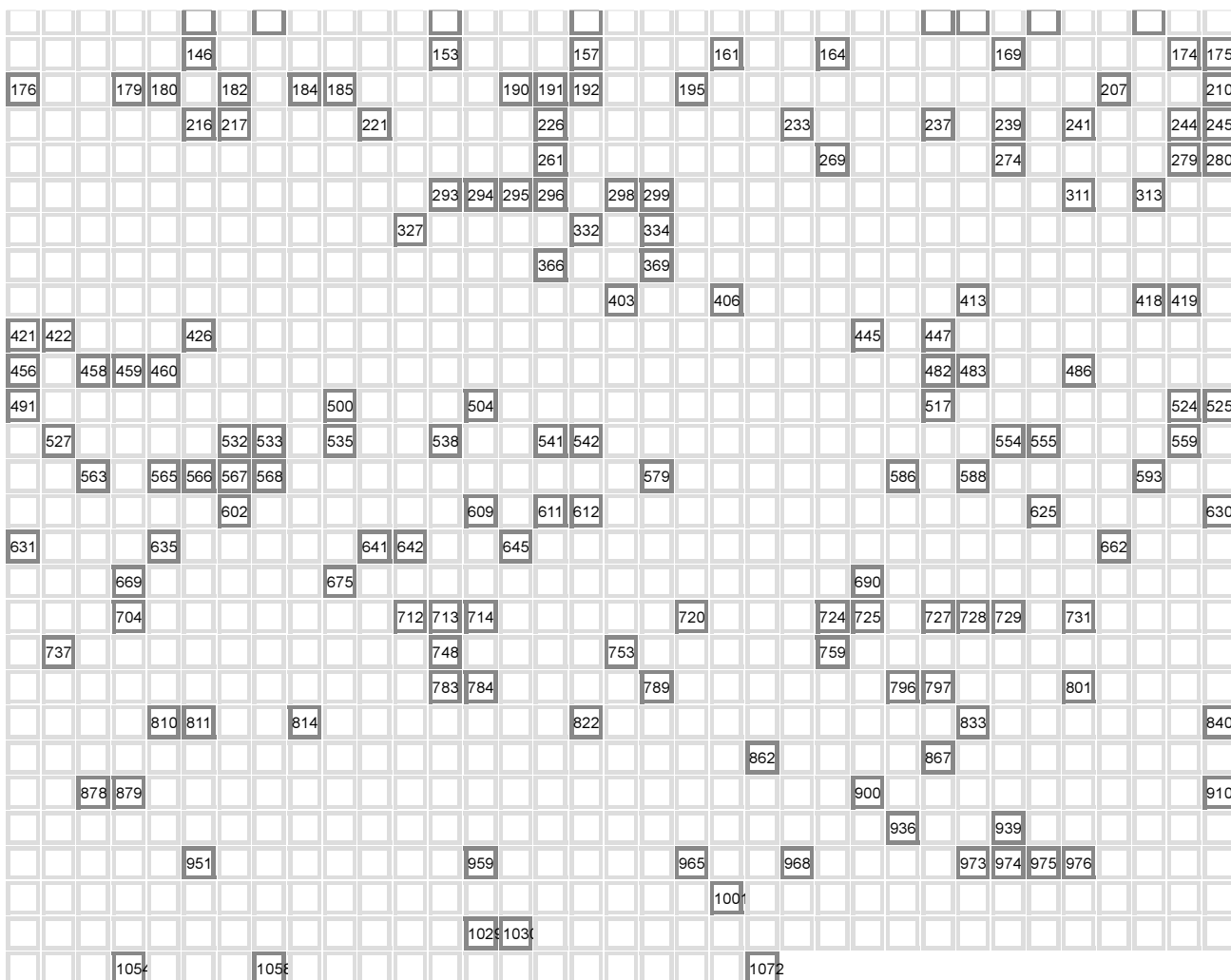
Synonyms: ENSG00000125378; ENSP00000245451; ENSP00000394165; ENSP00000453365; ENSP00000453467; ENSP00000453485; ENSP00000453691; ENSP00000454134; 652; BMP4; NP_001193; NP_570911; NP_570912; NM_001202; NM_130850; NM_130851; BMP2B; BMP2B1; MCOPS6; OFC11; ZYME; BMP4_HUMAN; P12644;

More at [Entrez](#)

INS insulin [Source:HGNC Symbol;Acc:6081]

Functions:



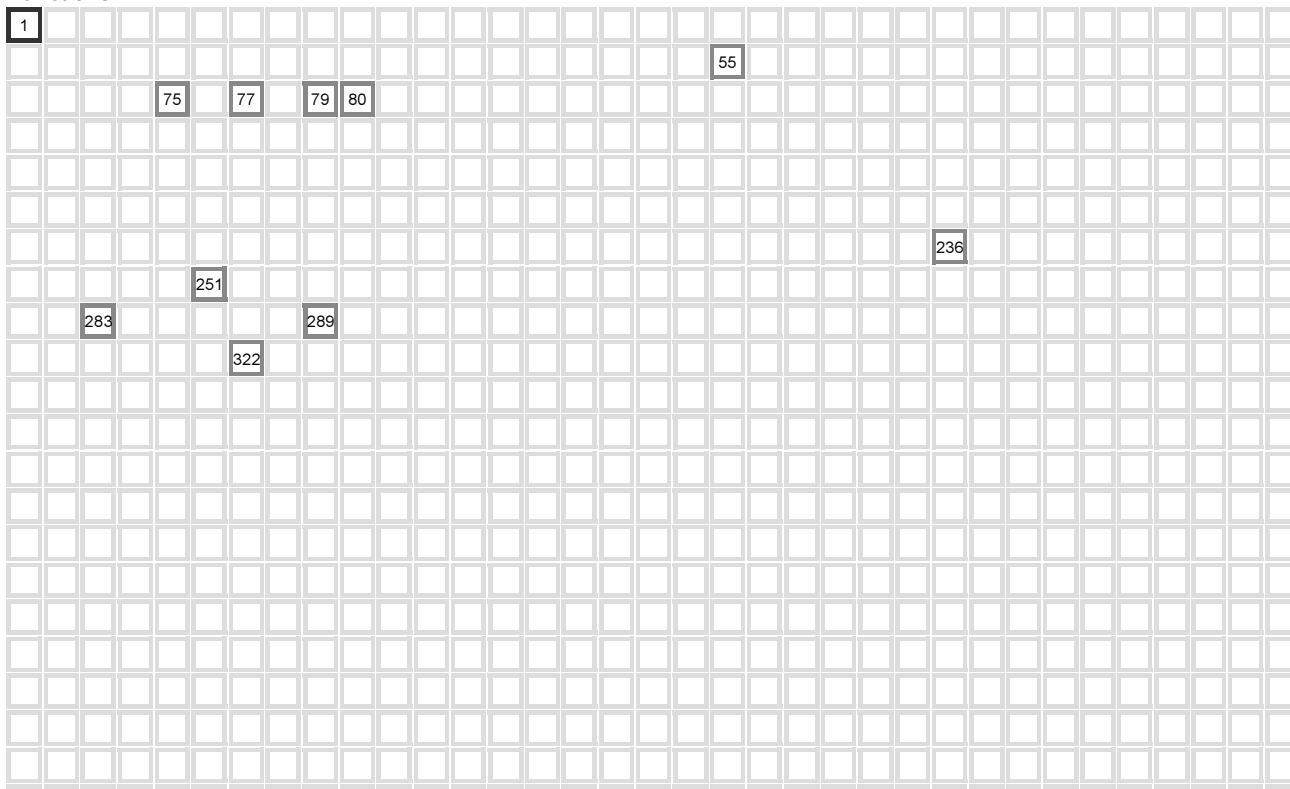


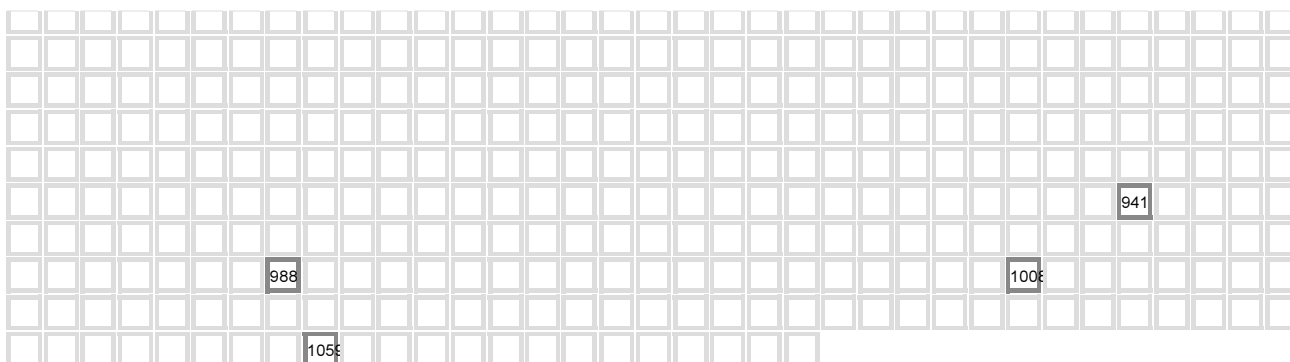
Synonyms: ENSG00000254647; ENSP00000250971; ENSP00000370731; ENSP00000380432; ENSP00000408400; ENSP00000424008; 3630; INS; NP_000198; NP_001172026; NP_001172027; NM_000207; NM_001185097; NM_001185098; IDDM2; ILPR; IRDN; MODY10; INS_HUMAN; P01308;

More at [Entrez](#)

ADA adenosine deaminase [Source:HGNC Symbol;Acc:186]

Functions:



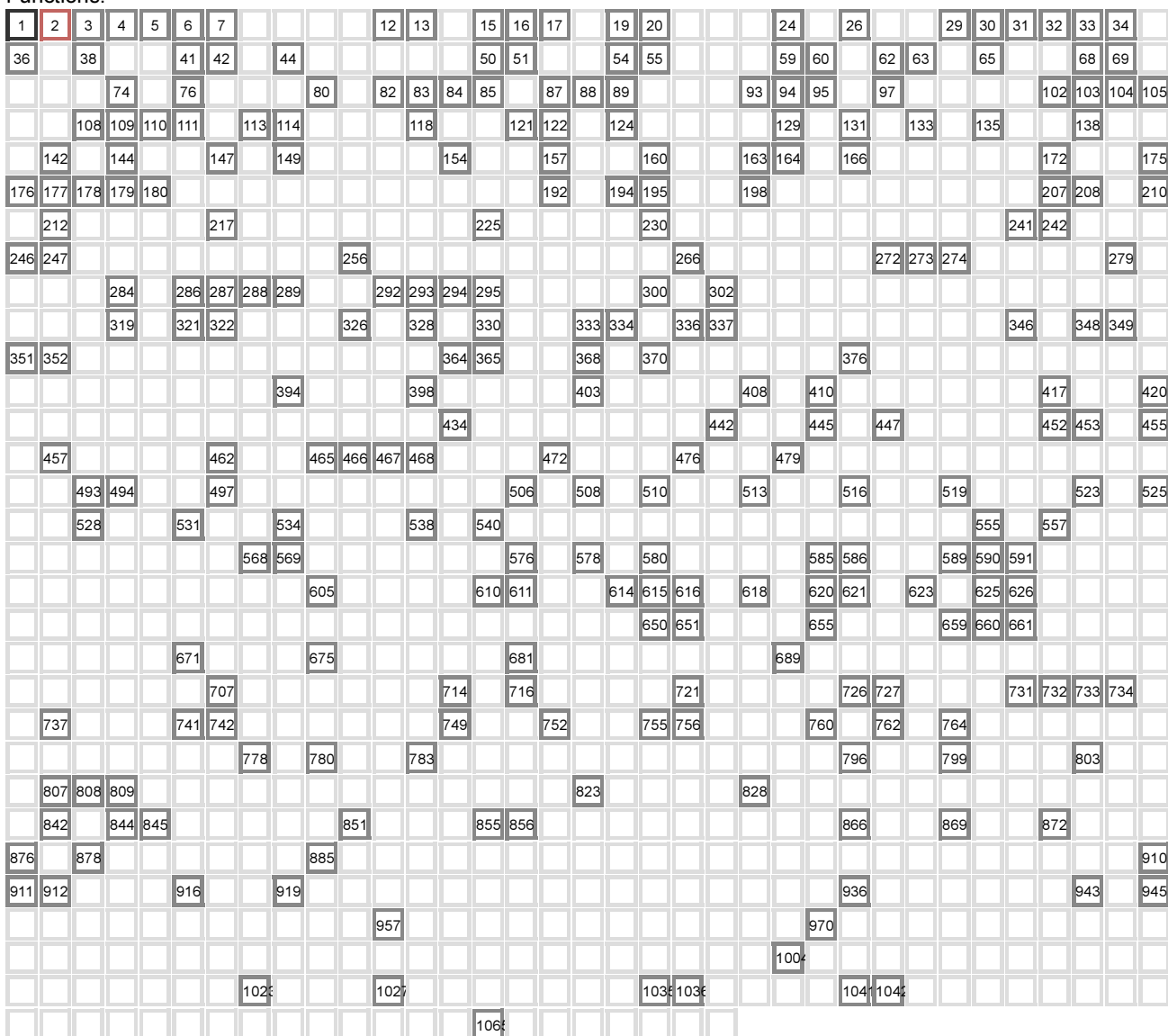


Synonyms: ENSG00000196839; ENSP00000361965; ENSP00000440946; ENSP00000441818; ENSP00000446464; 100; ADA; NP_000013; NM_000022; ADA_HUMAN; P00813;

More at [Entrez](#)

TGFBI transforming growth factor, beta 1 [Source:HGNC Symbol;Acc:11766]

Functions:

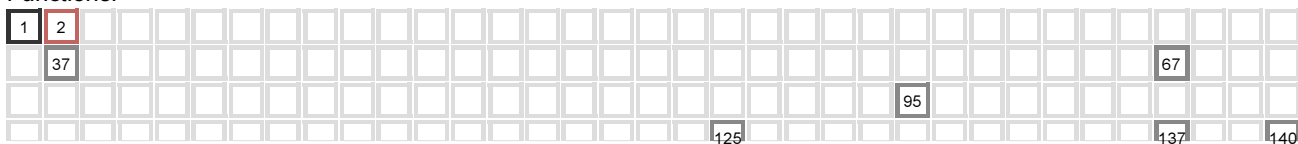


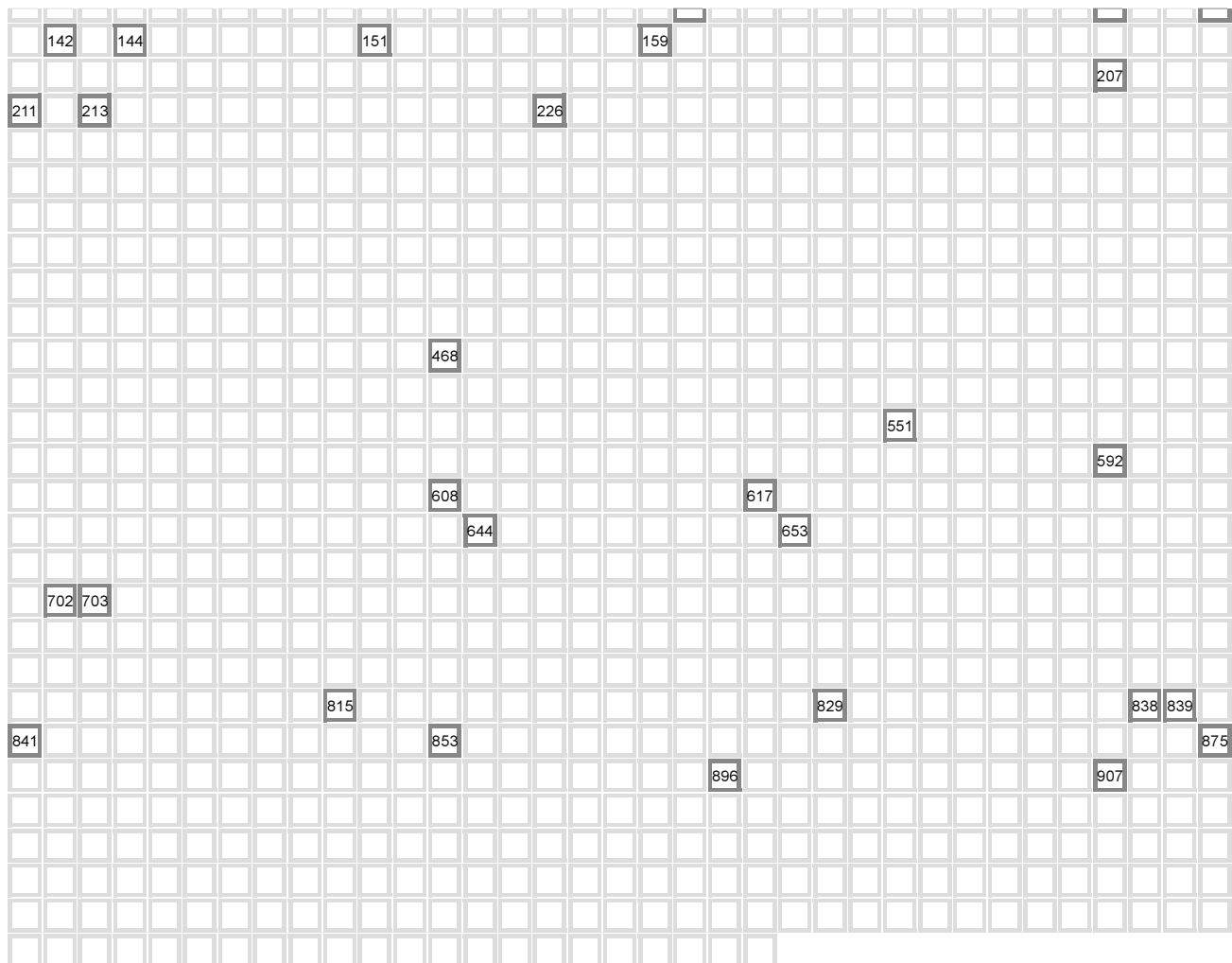
Synonyms: ENSG00000105329; ENSP00000221930; 7040; TGFBI; NP_000651; NM_000660; DPD1; TGFBI; TGFbeta; P01137; TGFBI_HUMAN;

More at [Entrez](#)

MAPK9 mitogen-activated protein kinase 9 [Source:HGNC Symbol;Acc:6886]

Functions:



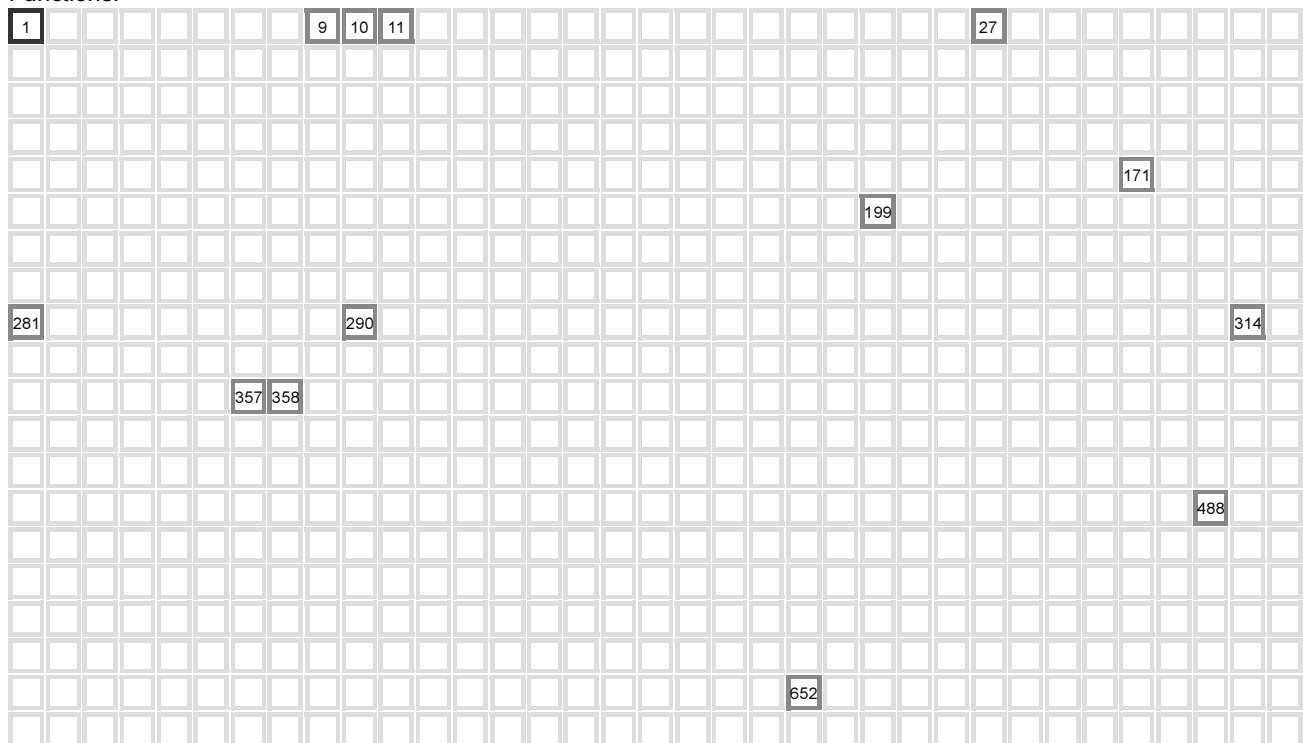


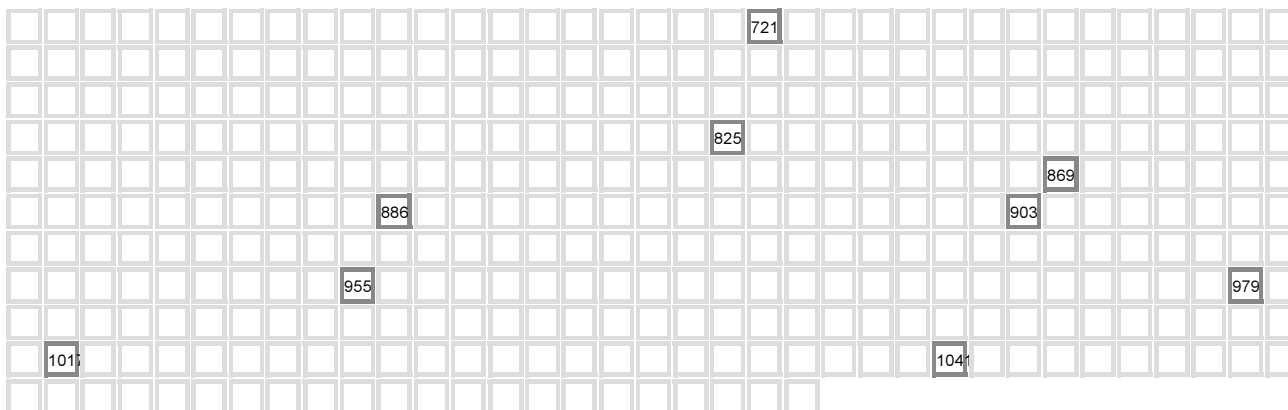
Synonyms: ENSG00000050748; ENSP00000321410; ENSP00000345524; ENSP00000377028; ENSP00000377029; ENSP00000380262; ENSP00000389338; ENSP00000394560; ENSP00000397422; ENSP00000430608; ENSP00000443149; 5601; MAPK9; NP_001128516; NP_002743; NP_620707; NP_620708; NP_620709; NM_001135044; NM_002752; NM_139068; NM_139069; NM_139070; JNK-55; JNK2; JNK2A; JNK2ALPHA; JNK2B; JNK2BETA; p54a; p54aSAPK; PRKM9; SAPK; SAPK1a; MK09_HUMAN; P45984;

More at [Entrez](#)

XRCC5 X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining) [Source:HGNC Symbol;Acc:12833]

Functions:



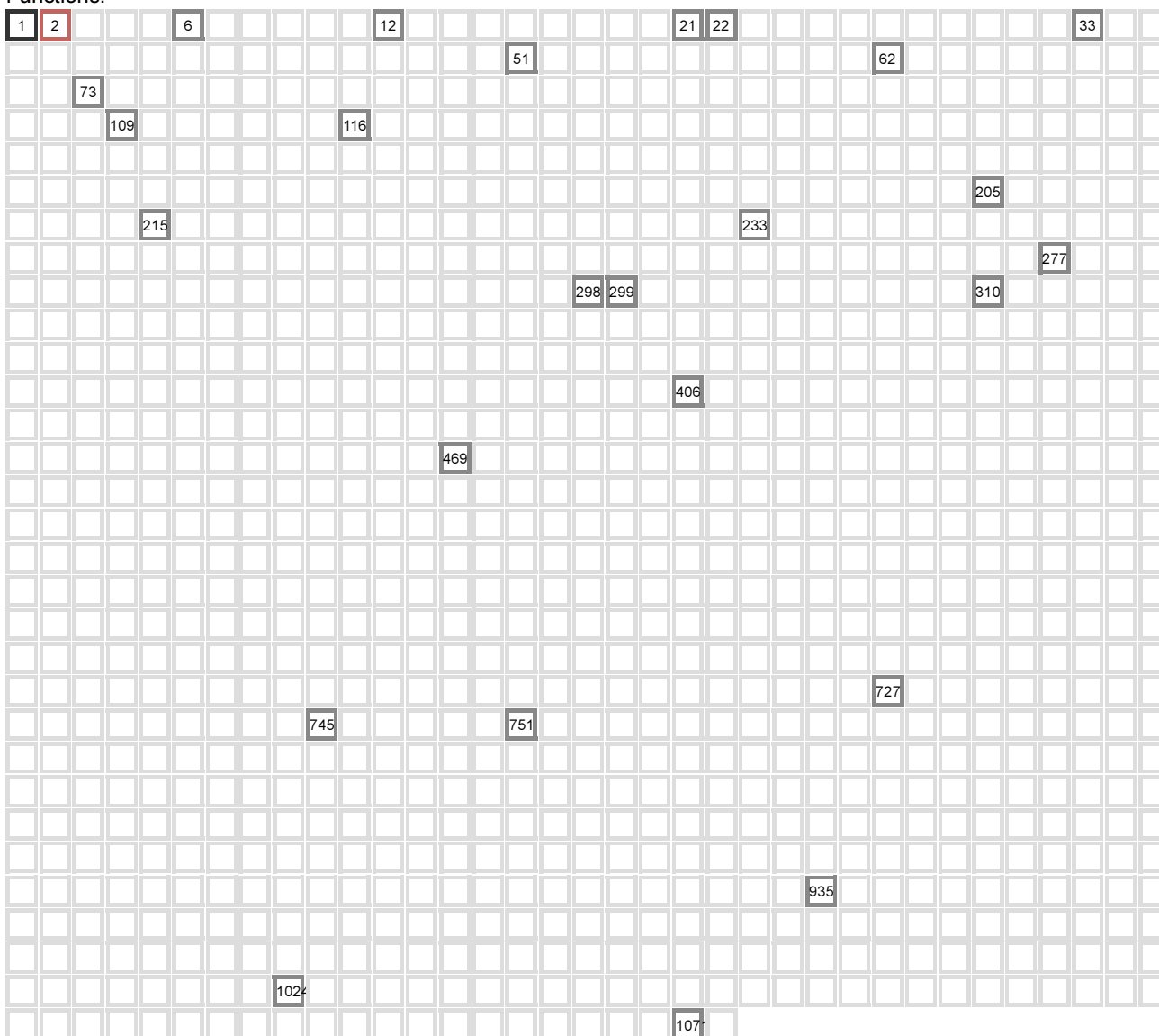


Synonyms: ENSG00000079246; ENSP00000375977; ENSP00000375978; ENSP00000395108; ENSP00000401318; 7520; XRCC5; NP_066964; NM_021141; KARP-1; KARP1; KU80; Ku86; KUB2; NFIV; P13010; XRCC5_HUMAN;

More at [Entrez](#)

NGF nerve growth factor (beta polypeptide) [Source:HGNC Symbol;Acc:7808]

Functions:

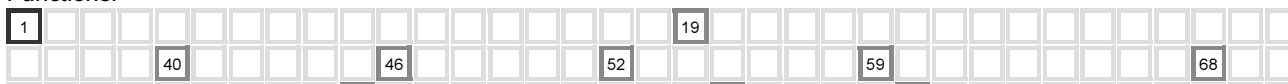


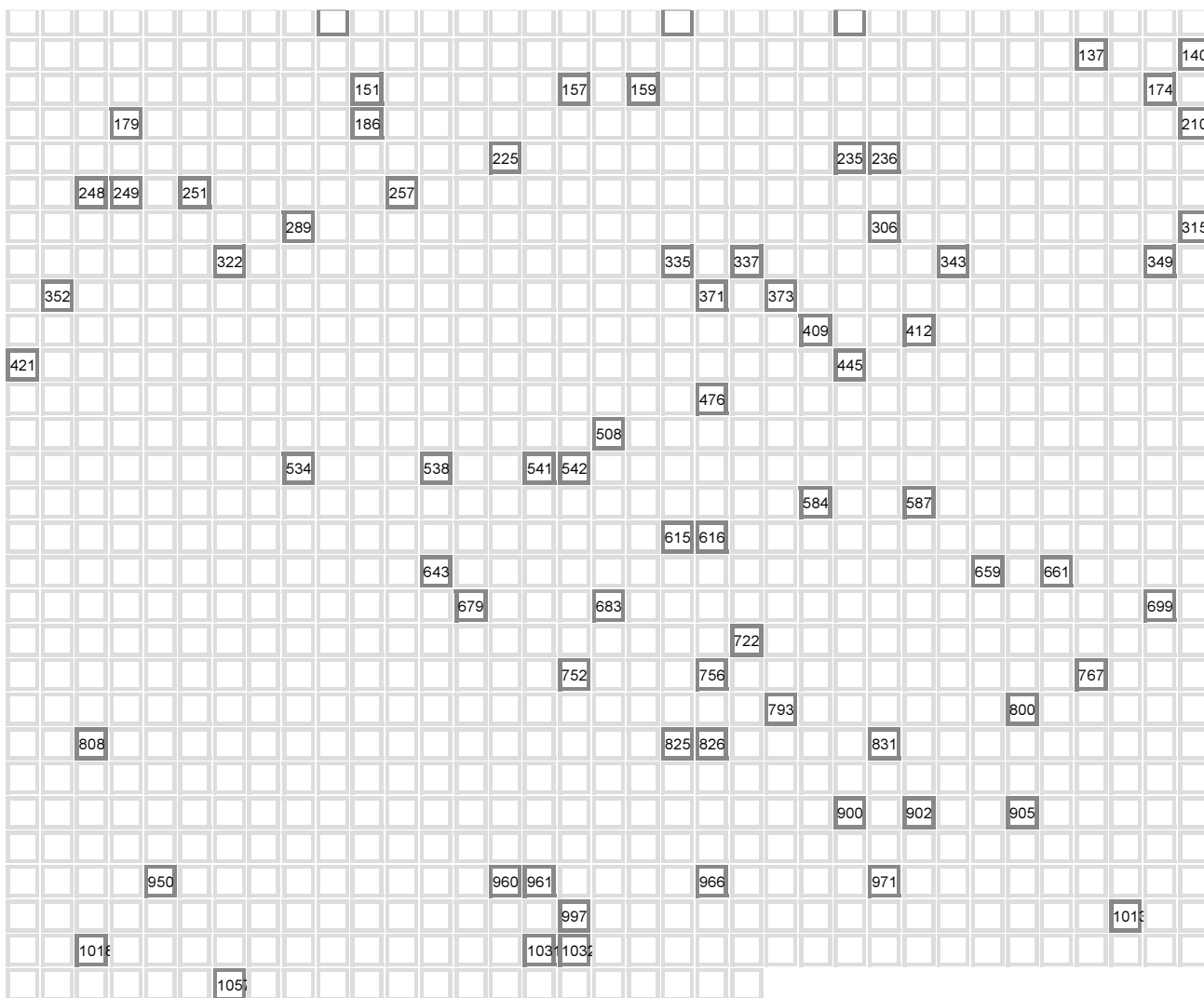
Synonyms: ENSG00000134259; ENSP00000358525; 4803; NGF; NP_002497; NM_002506; Beta-NGF; HSAN5; NGFB; NGF_HUMAN; P01138;

More at [Entrez](#)

SYK spleen tyrosine kinase [Source:HGNC Symbol;Acc:11491]

Functions:



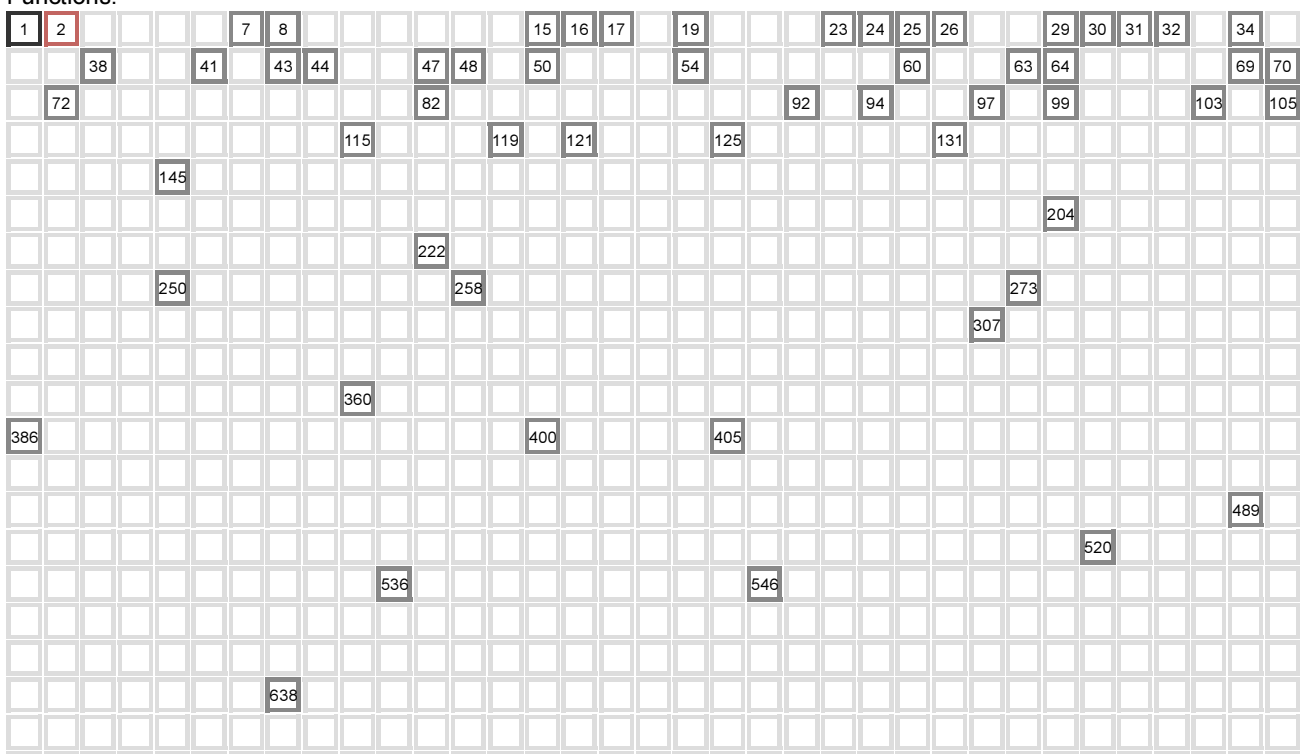


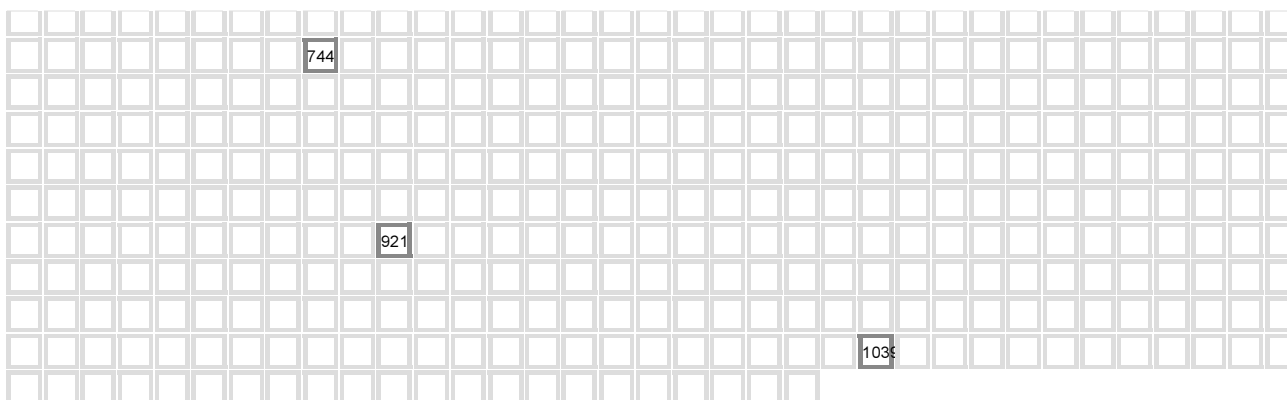
Synonyms: ENSG00000165025; ENSP00000364898; ENSP00000364899; ENSP00000364904; ENSP00000364907; 6850; SYK; NP_001128524; NP_001167638; NP_001167639; NP_003168; NM_001135052; NM_001174167; NM_001174168; NM_003177; KSYK_HUMAN; P43405;

More at [Entrez](#)

BMP2 bone morphogenetic protein 2 [Source:HGNC Symbol;Acc:1069]

Functions:



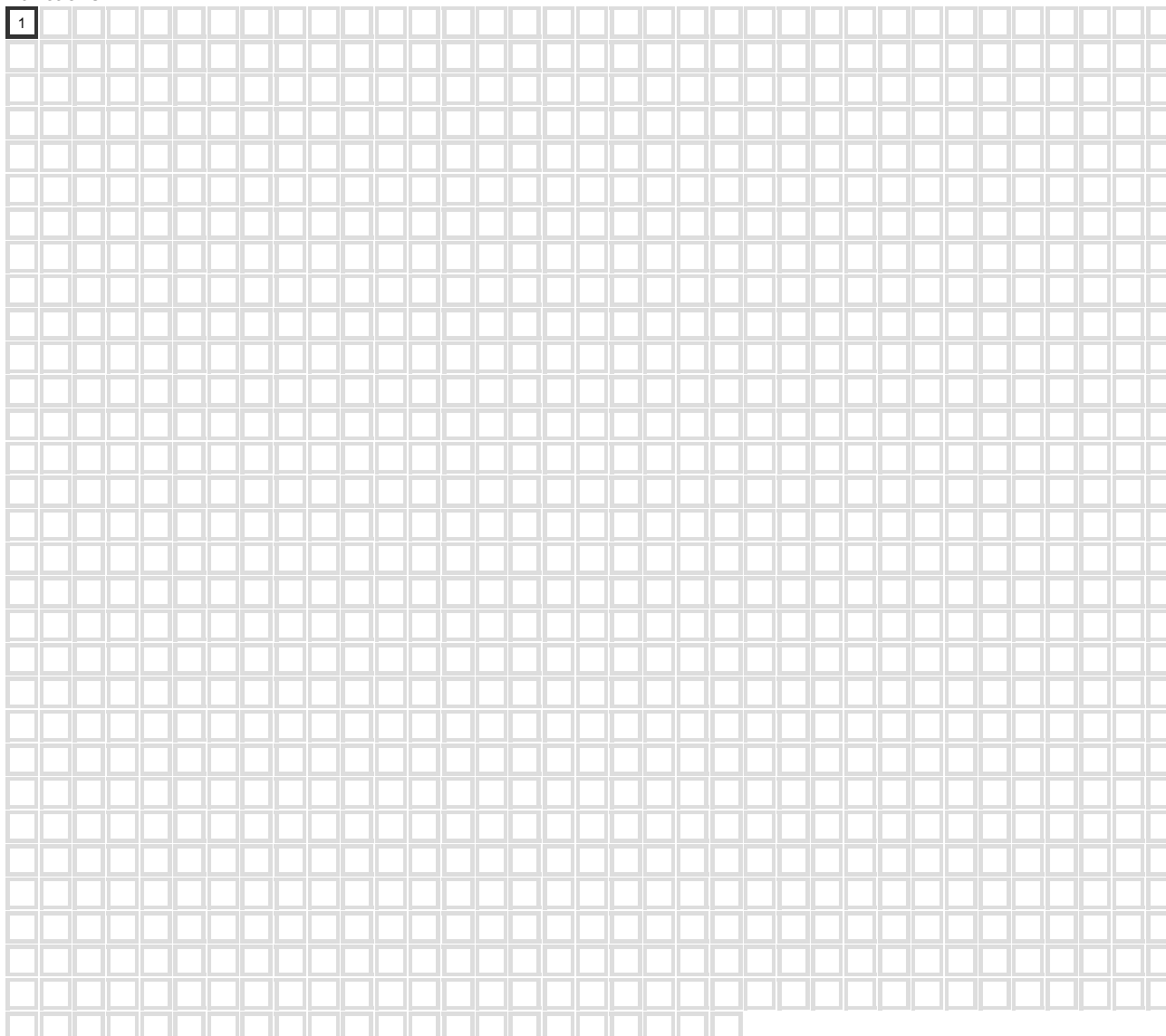


Synonyms: ENSG00000125845; ENSP00000368104; 650; BMP2; NP_001191; NM_001200; BDA2; BMP2A; BMP2_HUMAN; P12643;

More at [Entrez](#)

BDNF brain-derived neurotrophic factor [Source:HGNC Symbol;Acc:1033]

Functions:

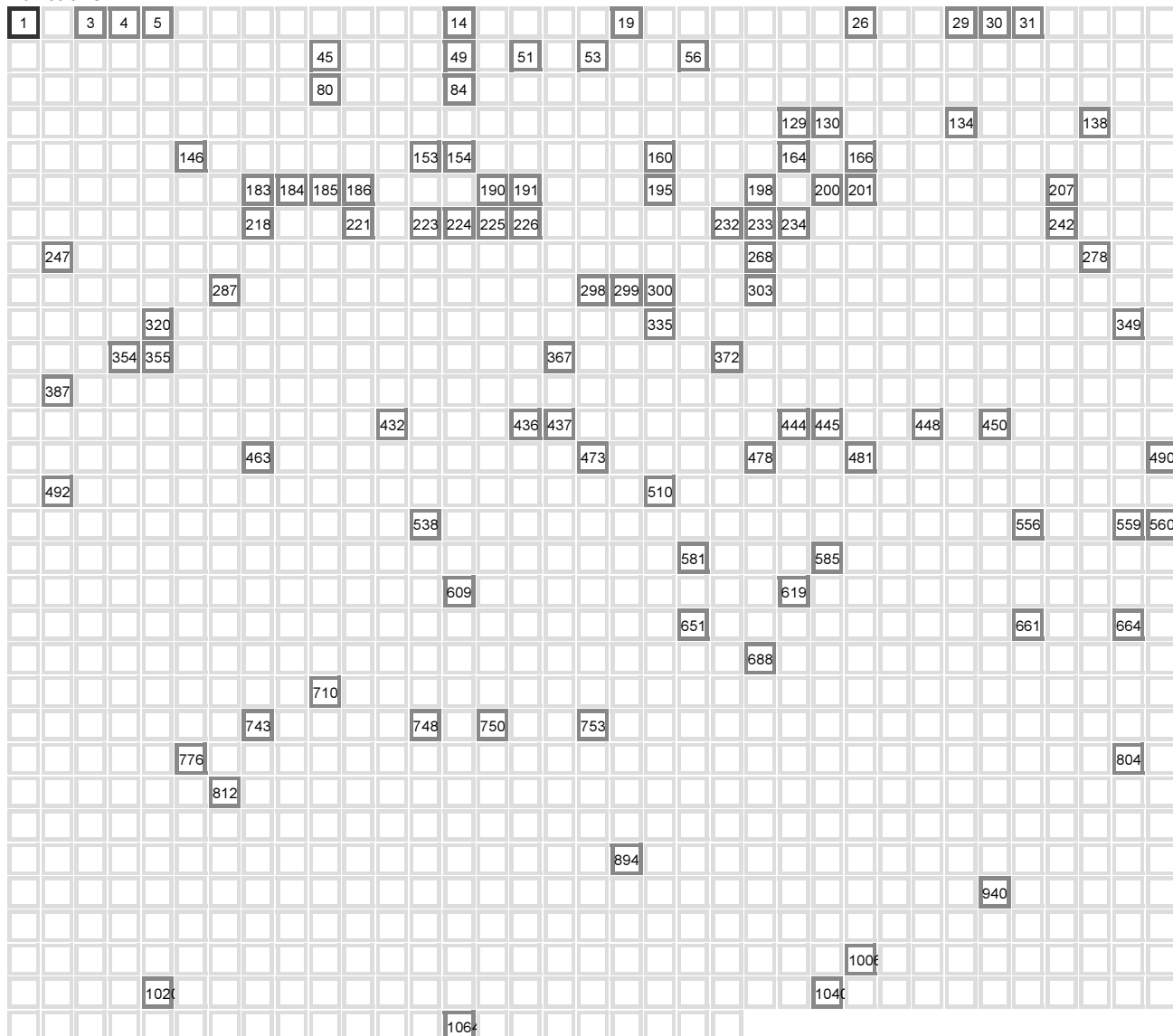


Synonyms: ENSG00000176697; ENSP00000320002; ENSP00000349084; ENSP00000379302; ENSP00000379304; ENSP00000379305; ENSP00000379307; ENSP00000379309; ENSP00000389345; ENSP00000389564; ENSP00000400502; ENSP00000414303; ENSP00000431998; ENSP00000432035; ENSP00000432376; ENSP00000432727; ENSP00000433003; ENSP00000435564; ENSP00000435805; ENSP00000437138; 627; BDNF; NP_001137277; NP_001137278; NP_001137279; NP_001137280; NP_001137281; NP_001137282; NP_001137283; NP_001137284; NP_001137285; NP_001137286; NP_001137288; NP_001700; NP_733927; NP_733928; NP_733929; NP_733930; NP_733931; NM_001143805; NM_001143806; NM_001143807; NM_001143808; NM_001143809; NM_001143810; NM_001143811; NM_001143812; NM_001143813; NM_001143814; NM_001143815; NM_001143816; NM_001709; NM_170731; NM_170732; NM_170733; NM_170734; NM_170735; BDNF_HUMAN; P23560;

More at [Entrez](#)

JAK2 Janus kinase 2 [Source:HGNC Symbol;Acc:6192]

Functions:

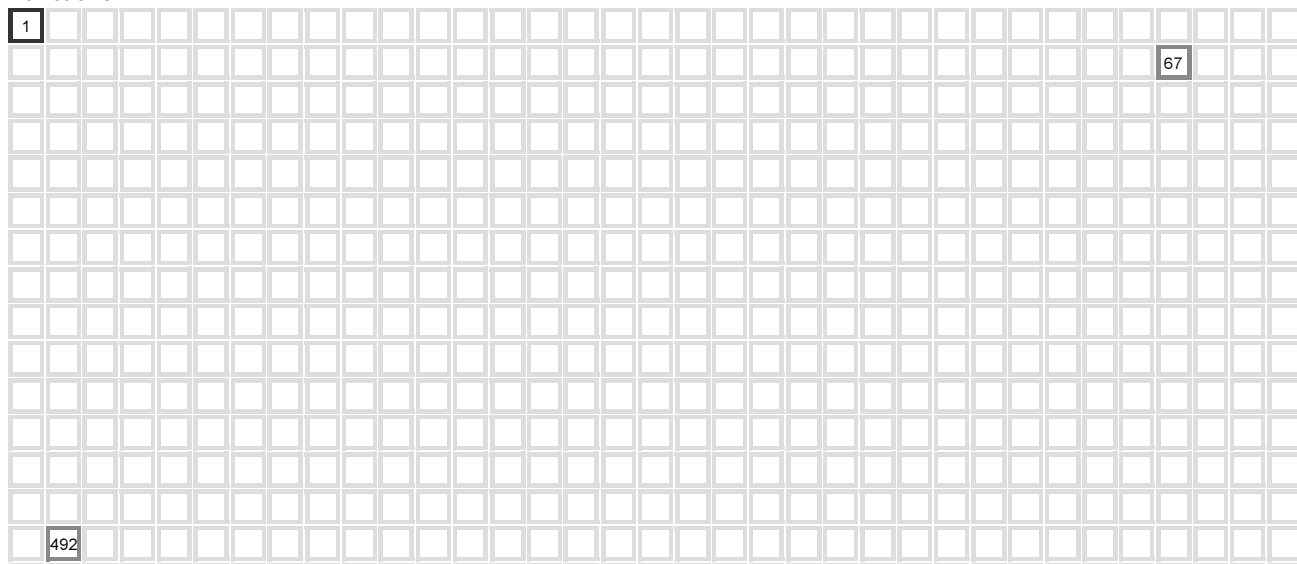


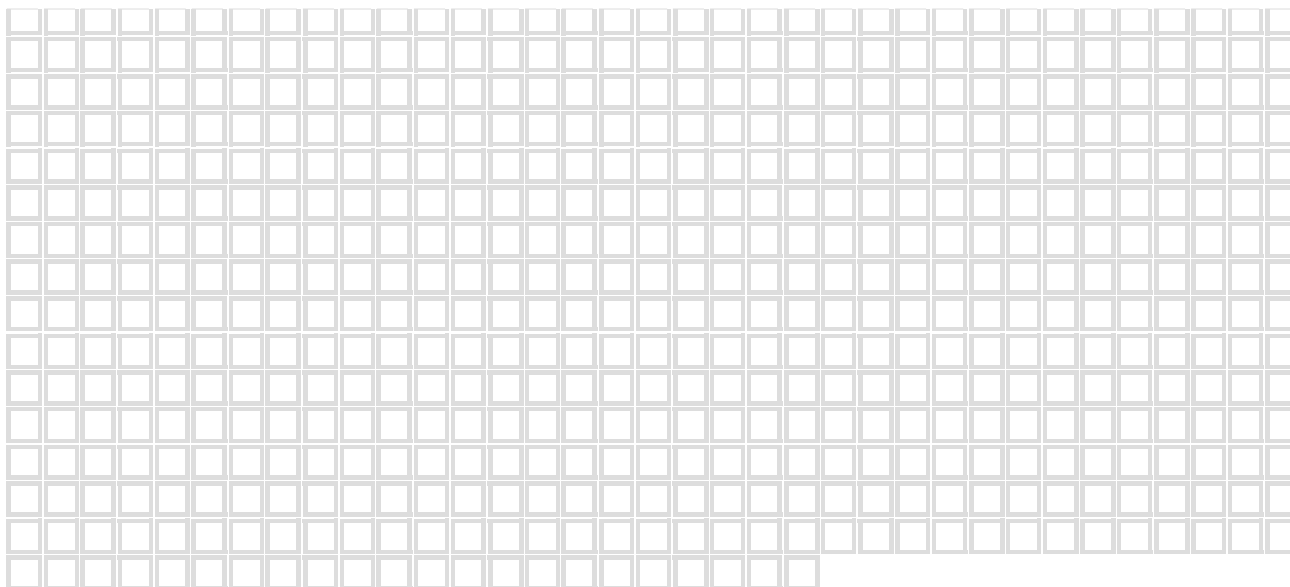
Synonyms: ENSG00000096968; ENSP00000371067; ENSP00000440387; ENSP00000443103; 3717; JAK2; NP_004963; NM_004972; JTK10; JAK2_HUMAN; O60674;

More at [Entrez](#)

IL4R (IL4RA) interleukin 4 receptor [Source:HGNC Symbol;Acc:6015]

Functions:



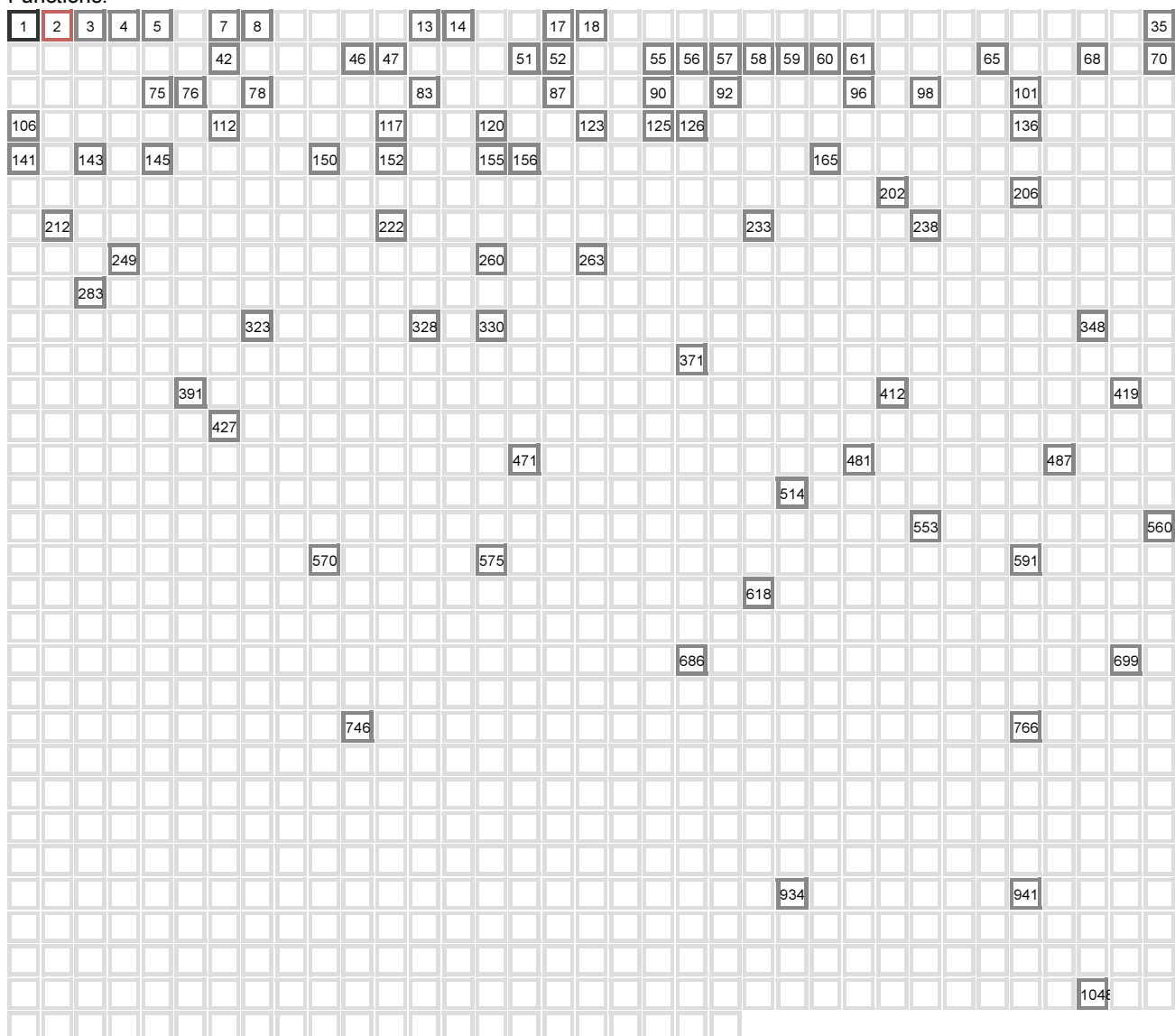


Synonyms: ENSG00000077238; ENSP00000170630; ENSP00000370309; ENSP00000370312; ENSP00000379111; ENSP00000410322; ENSP00000441667; 3566; IL4R; NP_000409; NP_001008699; NM_000418; NM_001008699; CD124; IL4RA; IL4RA_HUMAN; P24394;

More at [Entrez](#)

TGFBR2 transforming growth factor, beta receptor II (70/80kDa) [Source:HGNC Symbol;Acc:11773]

Functions:

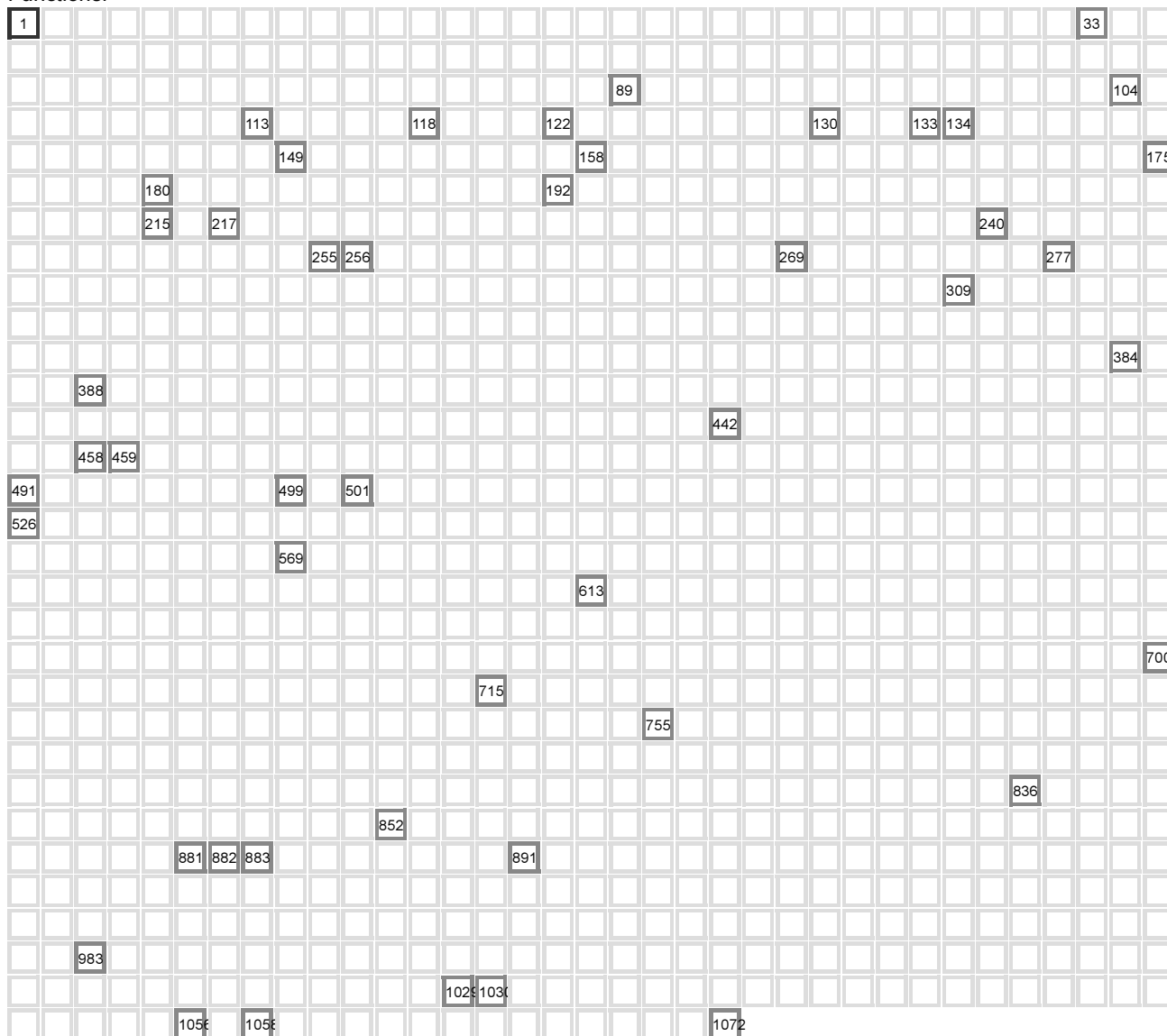


Synonyms: ENSG00000163513; ENSP00000295754; ENSP00000351905; ENSP00000373275; ENSP00000392572; 7048; TGFBR2; NP_001020018; NP_003233; NM_001024847; NM_003242; AAT3; FAA3; LDS1B; LDS2B; MFS2;

RIIC; TAAD2; TGFbeta-RII; TGFR-2; P37173; TGFR2_HUMAN;

More at [Entrez](#)**APC** adenomatous polyposis coli [Source:HGNC Symbol;Acc:583]

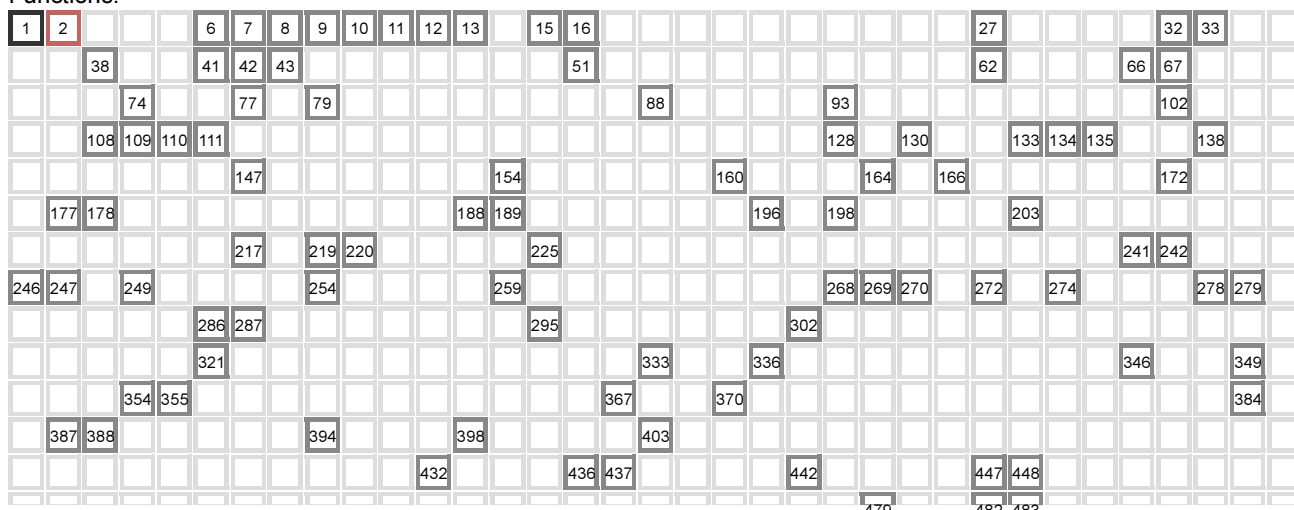
Functions:

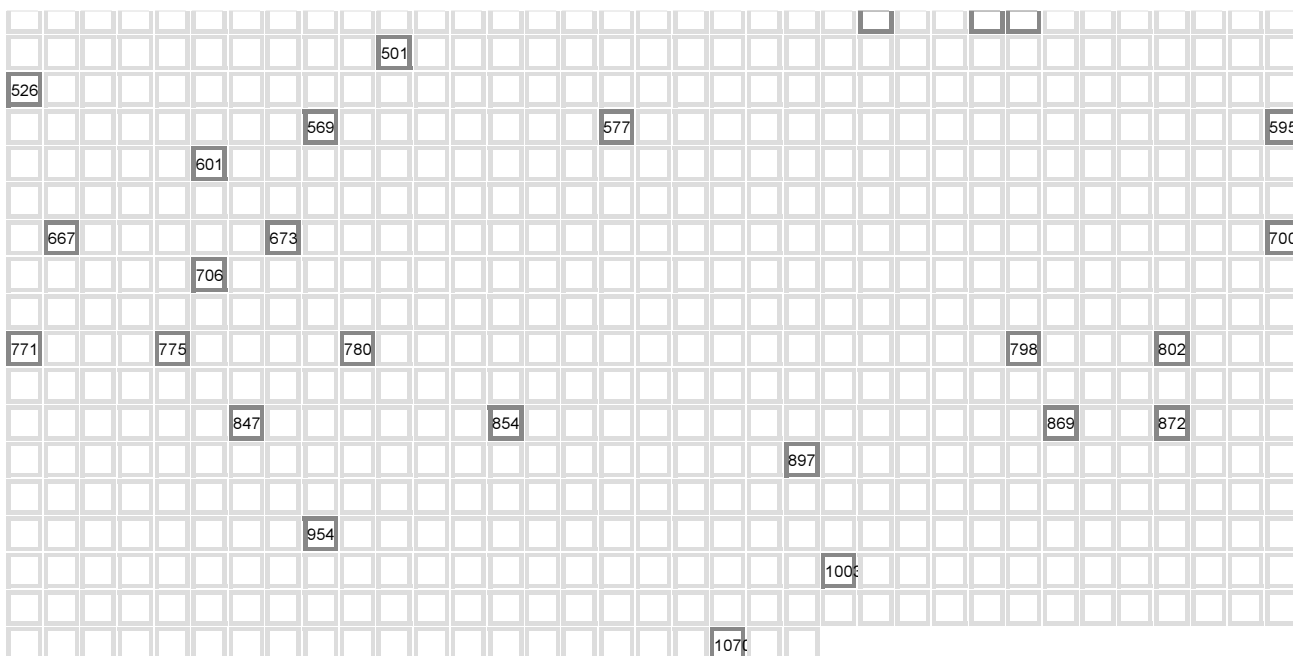


Synonyms: ENSG00000134982; ENSP00000257430; ENSP00000413133; ENSP00000423224; ENSP00000423828; ENSP00000424265; ENSP00000426541; ENSP00000427089; 324; APC; NP_000029; NP_001120982; NP_001120983; NM_000038; NM_001127510; NM_001127511; BTPS2; DP2.5; PPP1R46; APC_HUMAN; P25054;

More at [Entrez](#)**SMAD3** SMAD family member 3 [Source:HGNC Symbol;Acc:6769]

Functions:



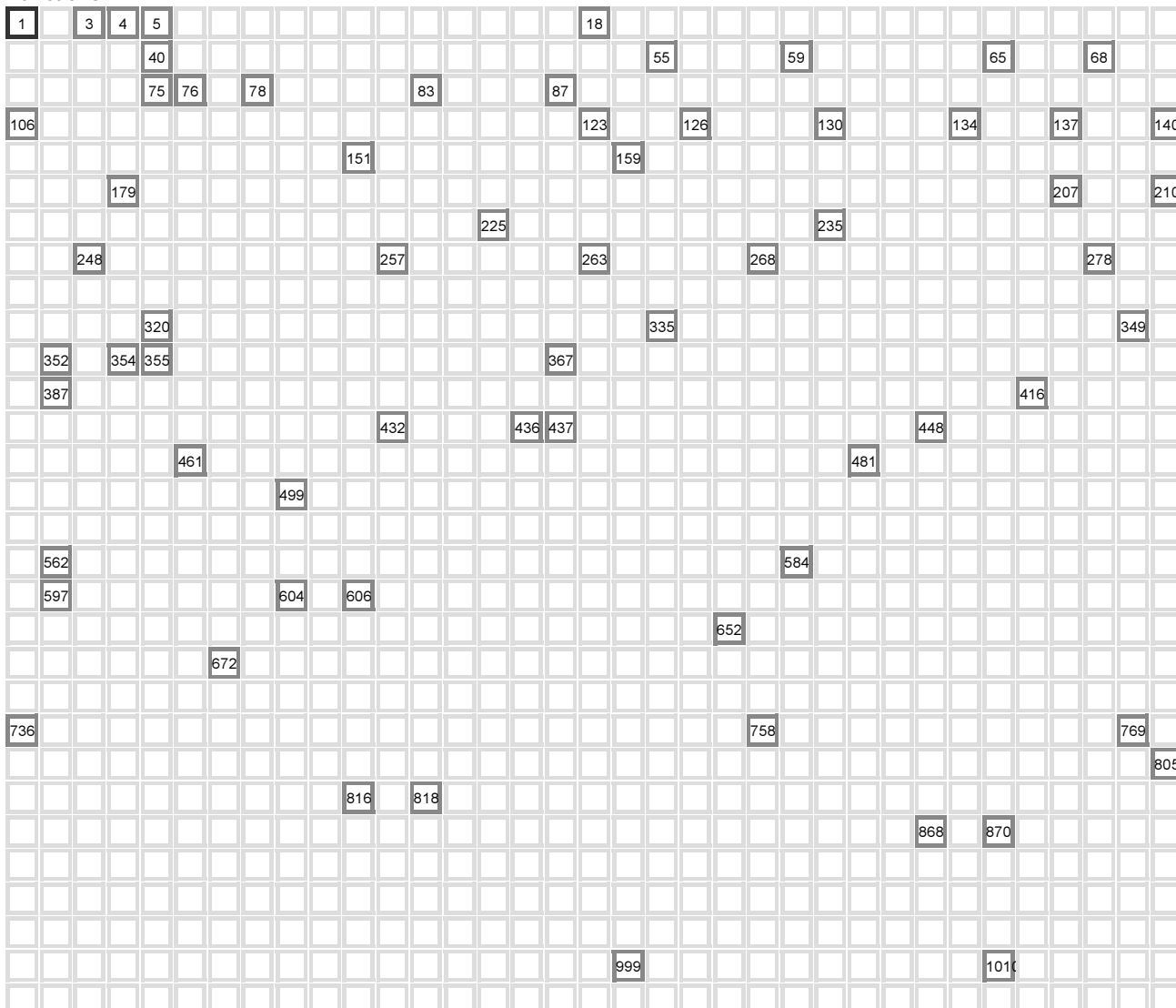


Synonyms: ENSG00000166949; ENSP00000332973; ENSP00000401133; ENSP00000437757; ENSP00000441856; ENSP00000445348; ENSP00000452767; ENSP00000453049; ENSP00000453082; ENSP00000453684; ENSP00000453788; ENSP00000454165; 4088; SMAD3; NP_001138574; NP_001138575; NP_001138576; NP_005893; NM_001145102; NM_001145103; NM_001145104; NM_005902; HSPC193; HsT17436; JV15-2; LDS1C; MADH3; P84022; SMAD3_HUMAN;

More at [Entrez](#)

LCK lymphocyte-specific protein tyrosine kinase [Source:HGNC Symbol;Acc:6524]

Functions:



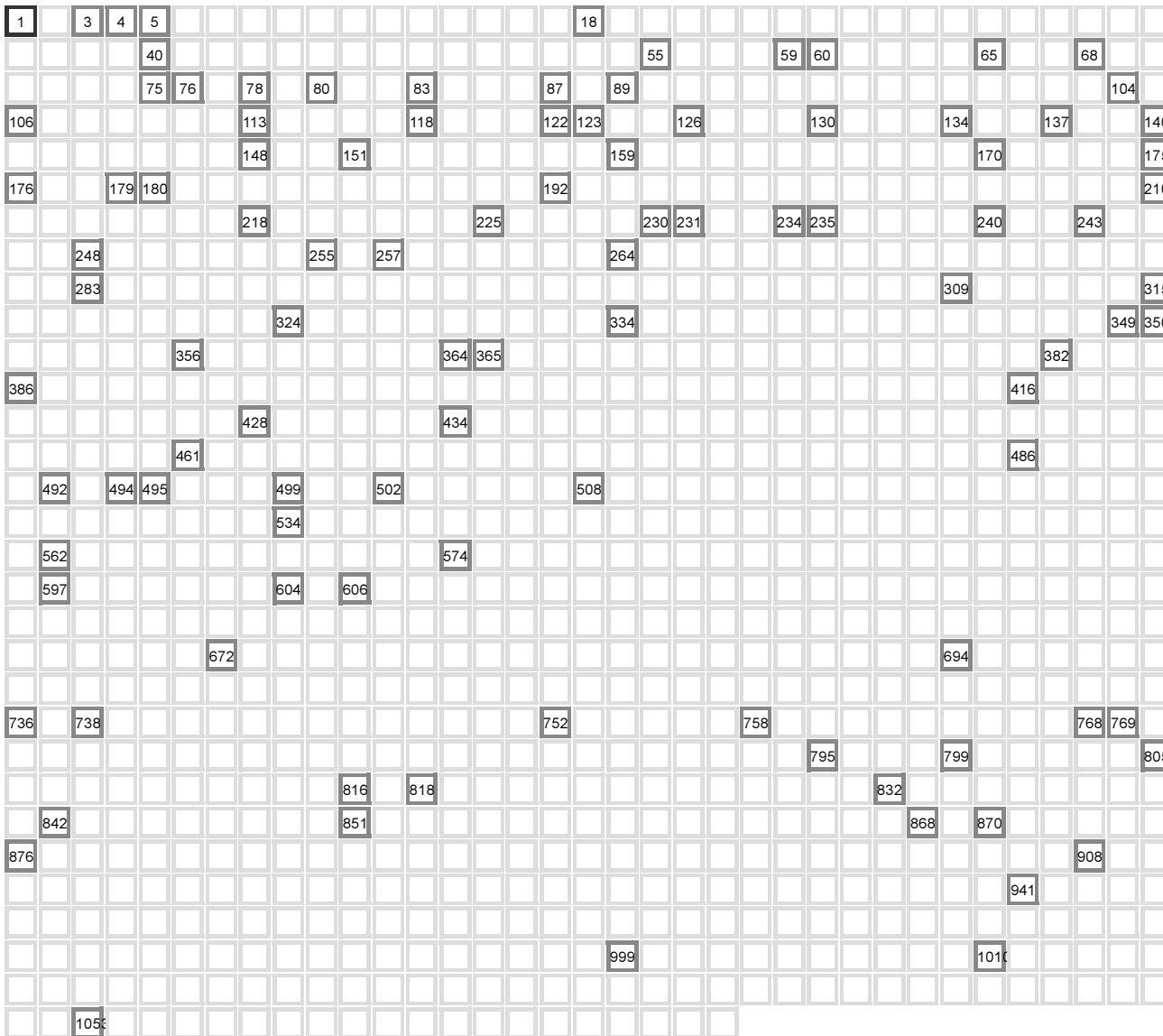


Synonyms: ENSG00000182866; ENSP00000328213; ENSP00000337825; ENSP00000362658; ENSP00000362663; ENSP00000362665; ENSP00000381387; ENSP00000400092; ENSP00000431517; ENSP00000434525; ENSP00000435605; ENSP00000436554; 3932; LCK; NP_001036236; NP_005347; NM_001042771; NM_005356; p56lck; pp58lck; YT16; LCK_HUMAN; P06239;

More at [Entrez](#)

PTPRC protein tyrosine phosphatase, receptor type, C [Source:HGNC Symbol;Acc:9666]

Functions:

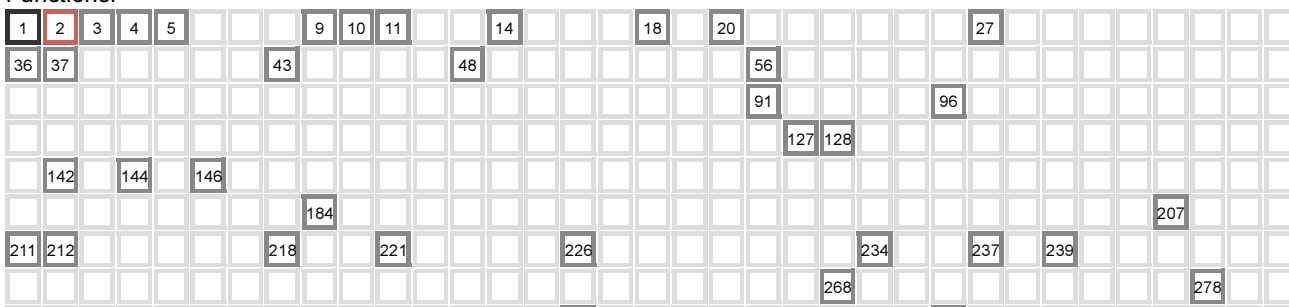


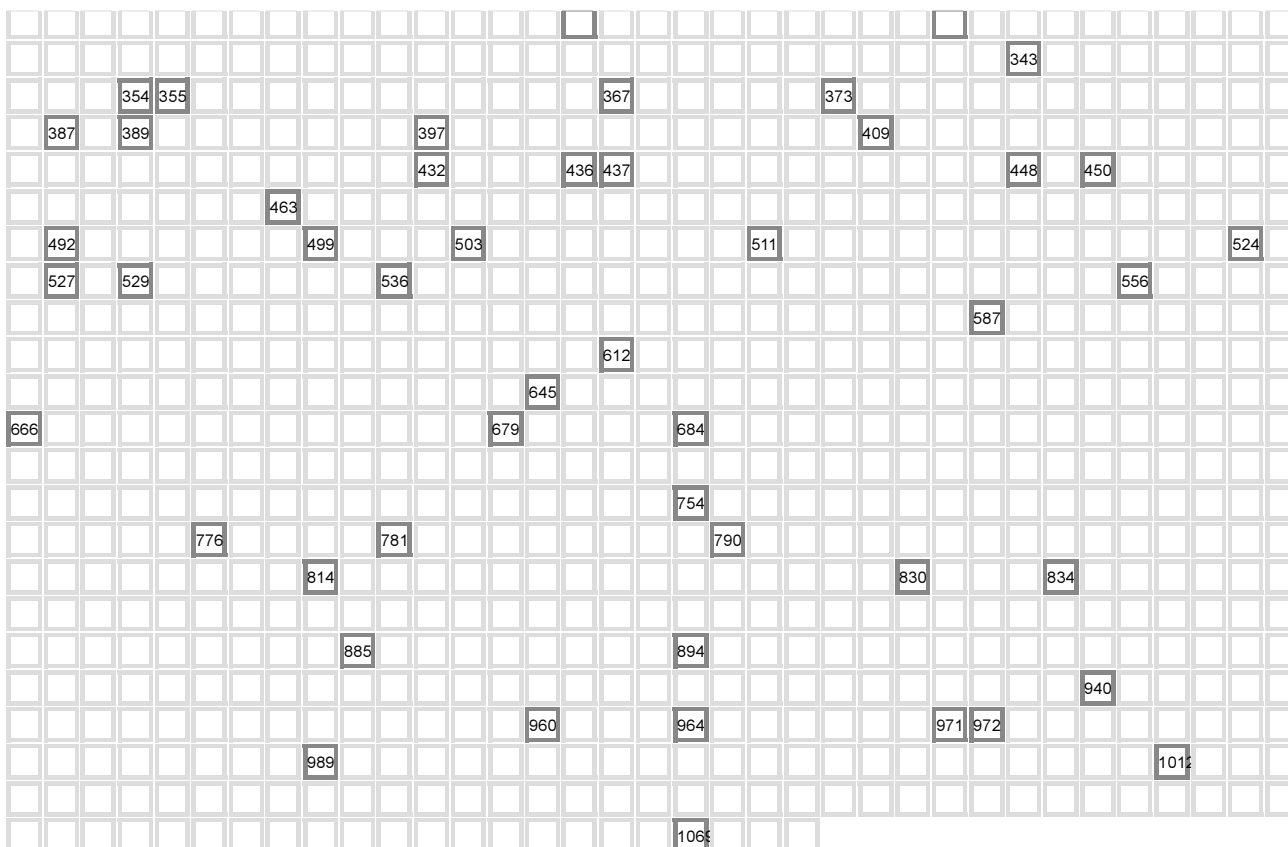
Synonyms: ENSG00000081237; ENSP00000193532; ENSP00000271610; ENSP00000306782; ENSP00000356334; ENSP00000356336; ENSP00000356337; ENSP00000356346; ENSP00000356349; ENSP00000393360; ENSP00000405494; ENSP00000411355; ENSP00000433536; ENSP00000444735; 5788; PTPRC; NP_002829; NP_563578; NP_563580; NM_002838; NM_080921; NM_080922; NM_080923; B220; CD45; CD45R; L-CA; LY5; T200; P08575; PTPRC_HUMAN;

More at [Entrez](#)

PPARG peroxisome proliferator-activated receptor gamma [Source:HGNC Symbol;Acc:9236]

Functions:



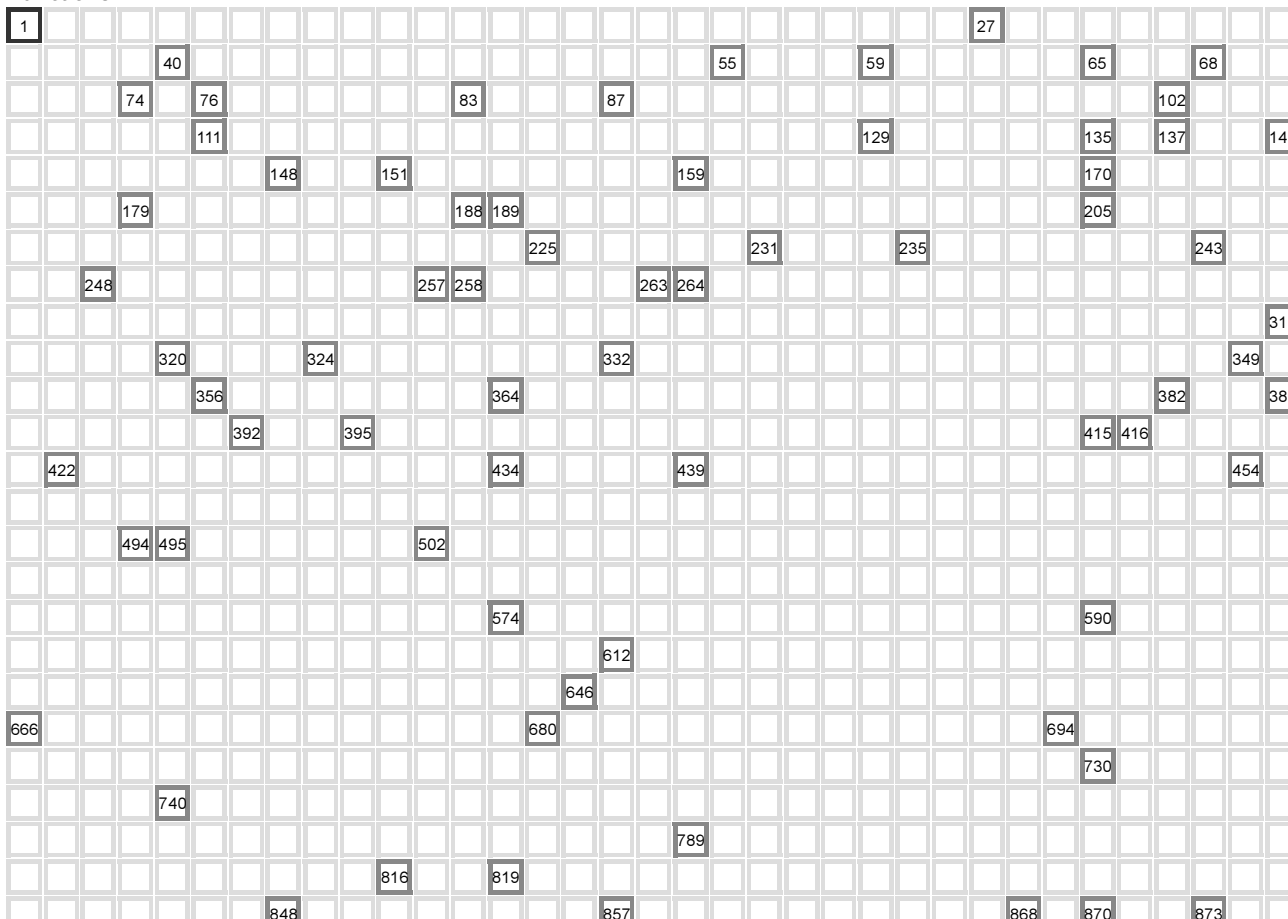


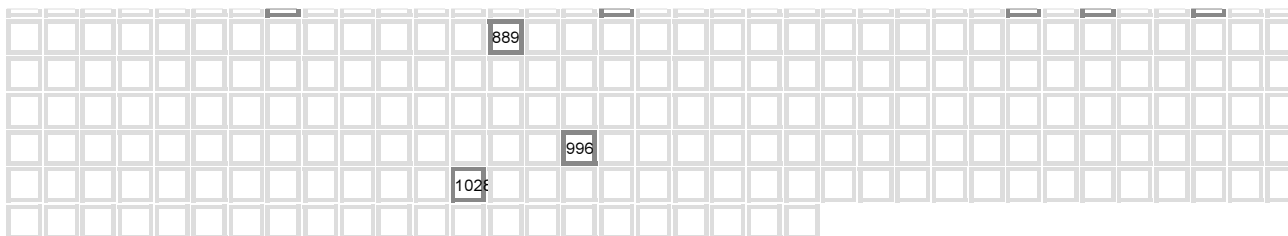
Synonyms: ENSG00000132170; ENSP00000287820; ENSP00000312472; ENSP00000380195; ENSP00000380196; ENSP00000380205; ENSP00000380207; ENSP00000380210; ENSP00000380218; ENSP00000380221; ENSP00000380224; ENSP00000392285; ENSP00000411931; ENSP00000438940; 5468; PPARG; NP_005028; NP_056953; NP_619725; NP_619726; NM_005037; NM_015869; NM_138711; NM_138712; CIMT1; GLM1; NR1C3; PPARG1; PPARG2; PPARGgamma; P37231; PPARG_HUMAN;

More at [Entrez](#)

BCL2 B-cell CLL/lymphoma 2 [Source:HGNC Symbol;Acc:990]

Functions:



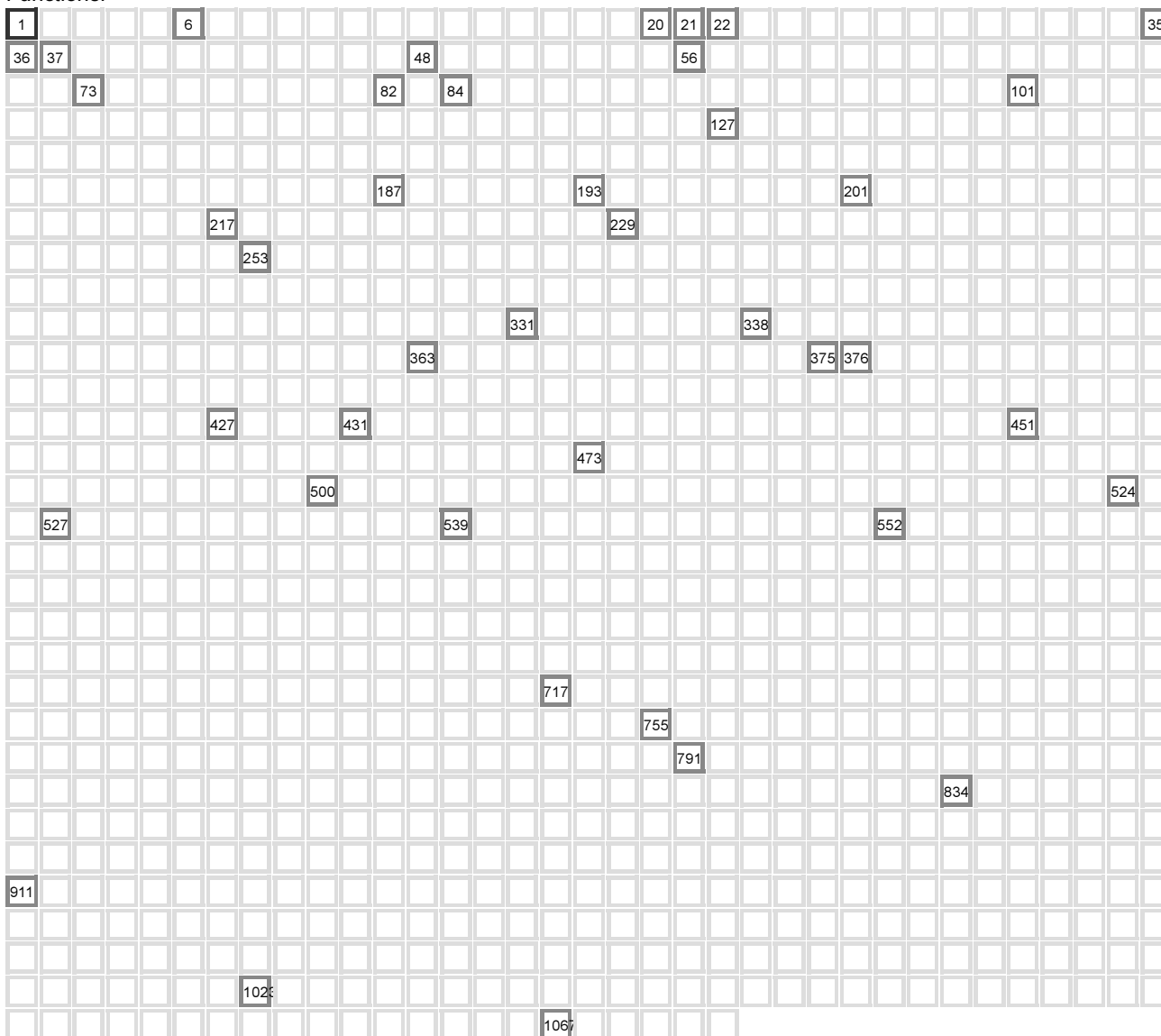


Synonyms: ENSG00000171791; ENSP00000329623; ENSP00000381185; ENSP00000404214; 596; BCL2; NP_000624; NP_000648; NM_000633; NM_000657; Bcl-2; PPP1R50; BCL2_HUMAN; P10415;

More at [Entrez](#)

ID2 inhibitor of DNA binding 2, dominant negative helix-loop-helix protein [Source:HGNC Symbol;Acc:5361]

Functions:

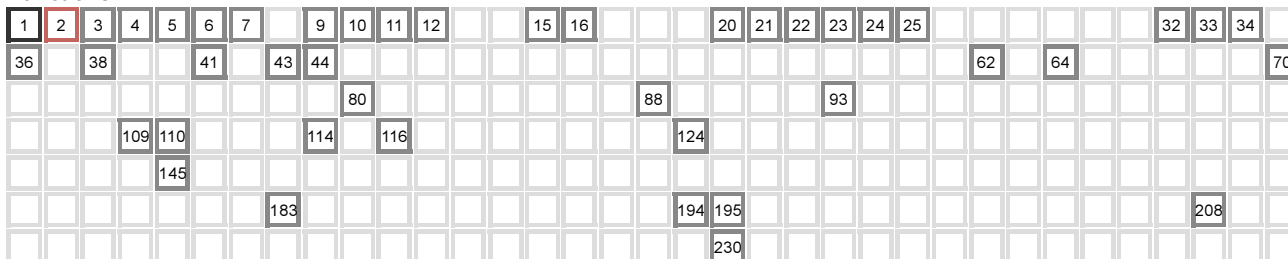


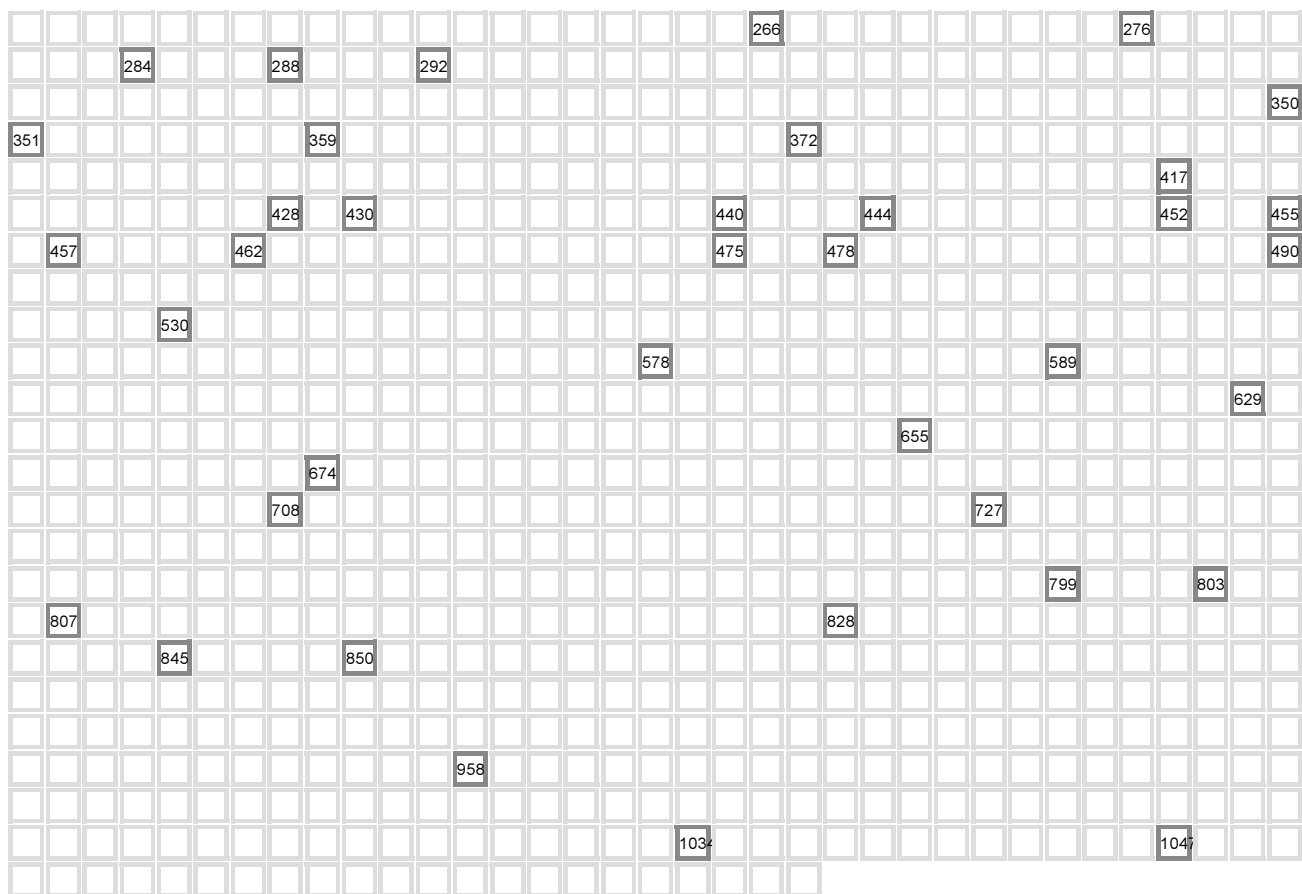
Synonyms: ENSG00000115738; ENSP00000234091; ENSP00000379585; ENSP00000385465; 3398; ID2; NP_002157; NM_002166; bHLHb26; GIG8; ID2A; ID2H; ID2_HUMAN; Q02363;

More at [Entrez](#)

NOTCH1 notch 1 [Source:HGNC Symbol;Acc:7881]

Functions:



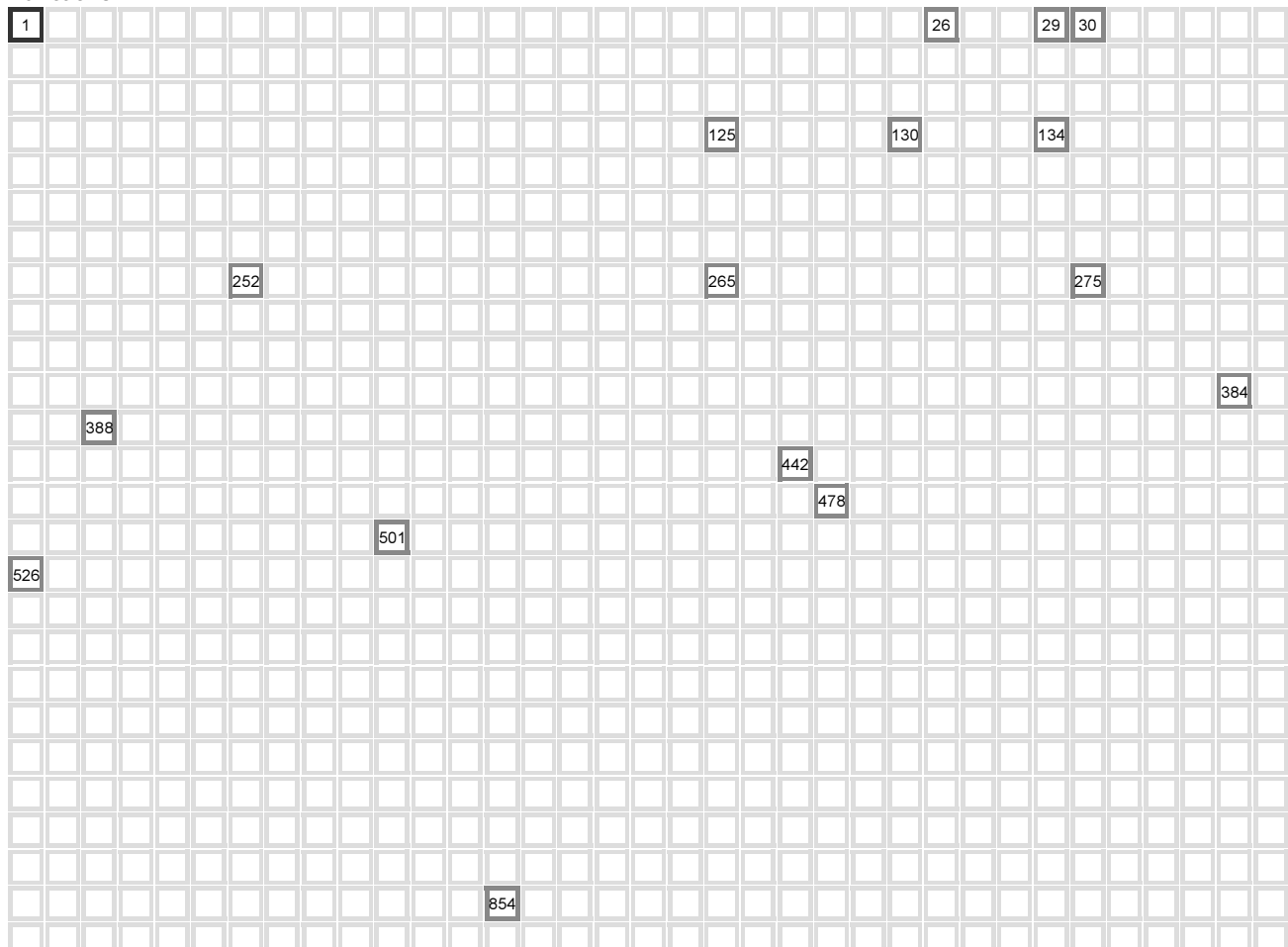


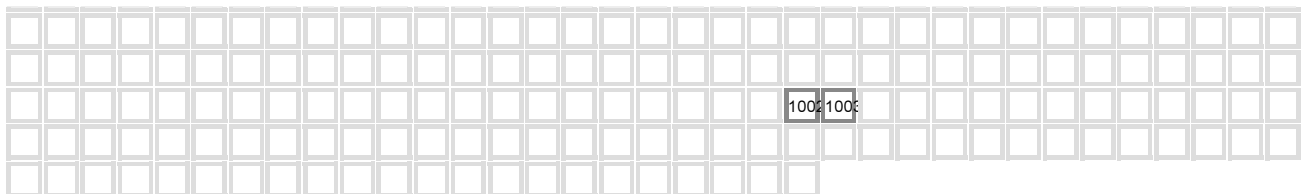
Synonyms: ENSG00000148400; ENSP00000277541; 4851; NOTCH1; NP_060087; NM_017617; TAN1; NOTC1_HUMAN; P46531;

More at [Entrez](#)

ILK integrin-linked kinase [Source:HGNC Symbol;Acc:6040]

Functions:



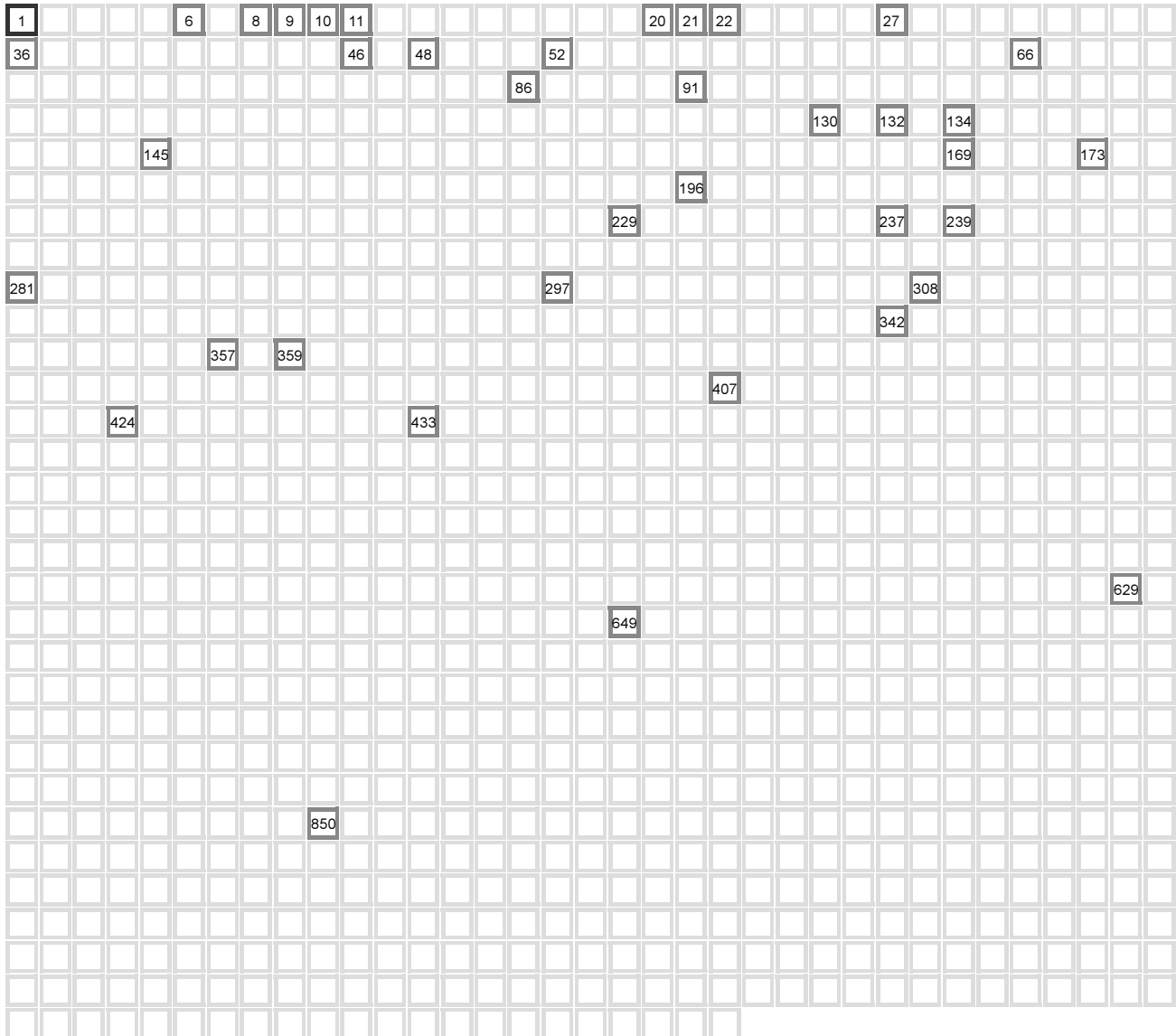


Synonyms: ENSG00000166333; ENSP00000299421; ENSP00000379975; ENSP00000403487; ENSP00000432617; ENSP00000432796; ENSP00000433129; ENSP00000434492; ENSP00000435323; ENSP00000436062; ENSP00000439606; 3611; ILK; NP_001014794; NP_001014795; NP_004508; NM_001014794; NM_001014795; NM_004517; ILK-2; ILK_HUMAN; Q13418;

More at [Entrez](#)

PAX6 paired box 6 [Source:HGNC Symbol;Acc:8620]

Functions:

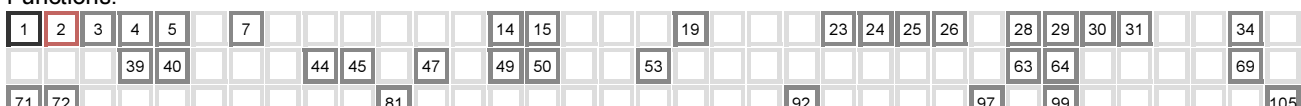


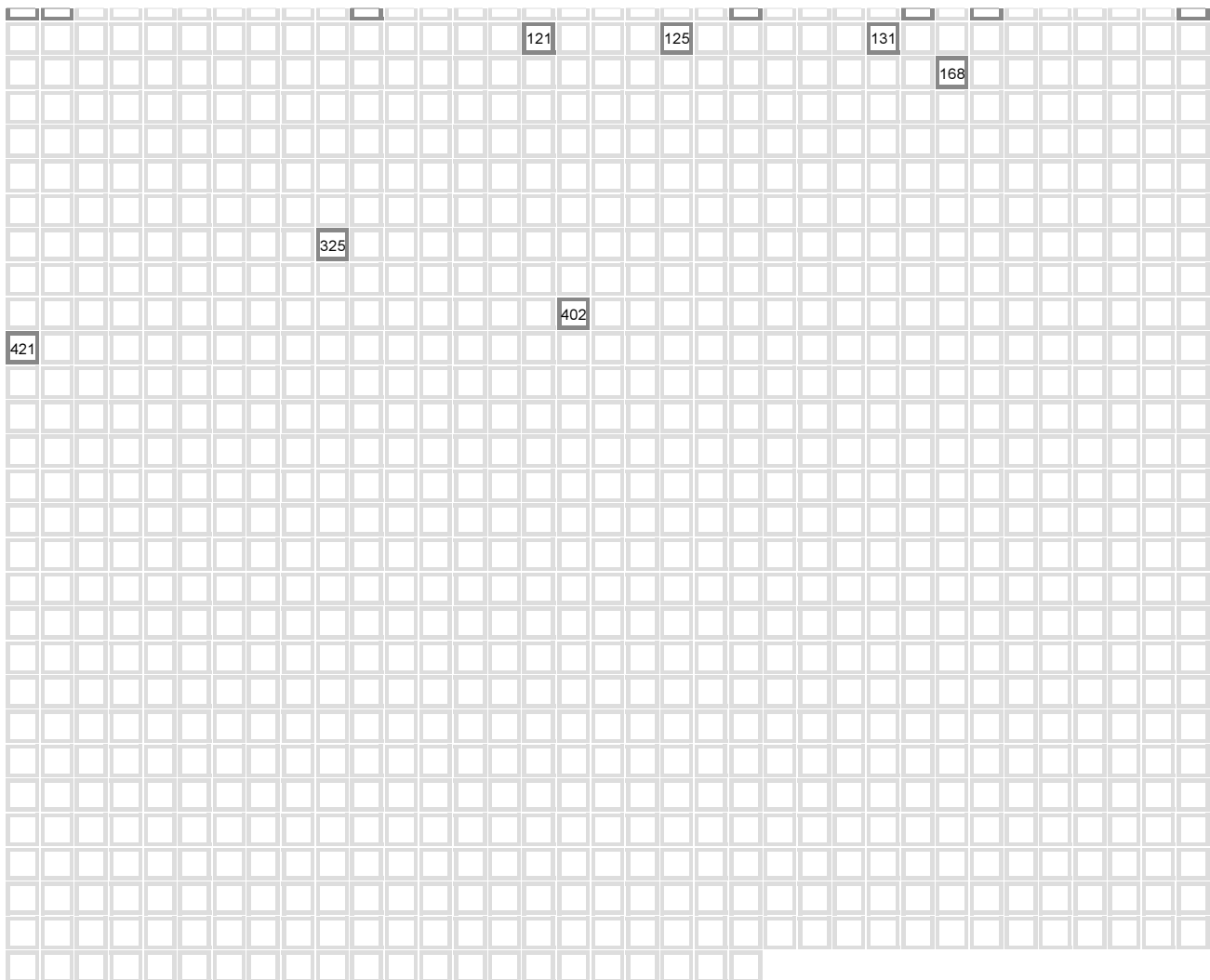
Synonyms: ENSG00000007372; ENSP00000241001; ENSP00000368401; ENSP00000368403; ENSP00000368406; ENSP00000368410; ENSP00000368418; ENSP00000368424; ENSP00000368427; ENSP00000388132; ENSP00000397384; ENSP00000404100; ENSP00000404356; ENSP00000431585; ENSP00000431961; ENSP00000435884; ENSP00000435975; ENSP00000436365; ENSP00000450552; ENSP00000450579; ENSP00000450775; ENSP00000451372; ENSP00000451885; ENSP00000451901; ENSP00000452202; ENSP00000452558; 5080; PAX6; NP_000271; NP_001121084; NP_001595; NM_000280; NM_001127612; NM_001604; AN2; D11S812E; MGDA; P26367; PAX6_HUMAN;

More at [Entrez](#)

ACVR2A activin A receptor, type IIA [Source:HGNC Symbol;Acc:173]

Functions:



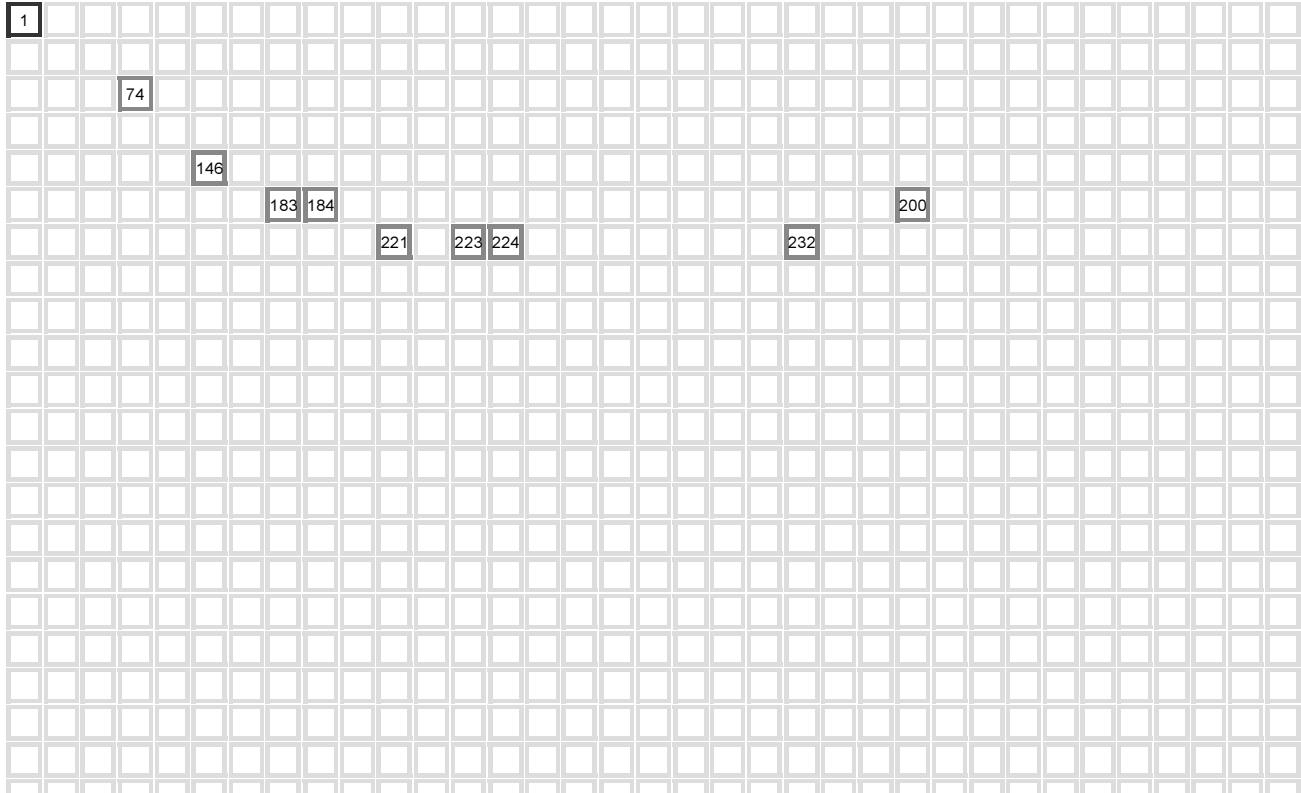


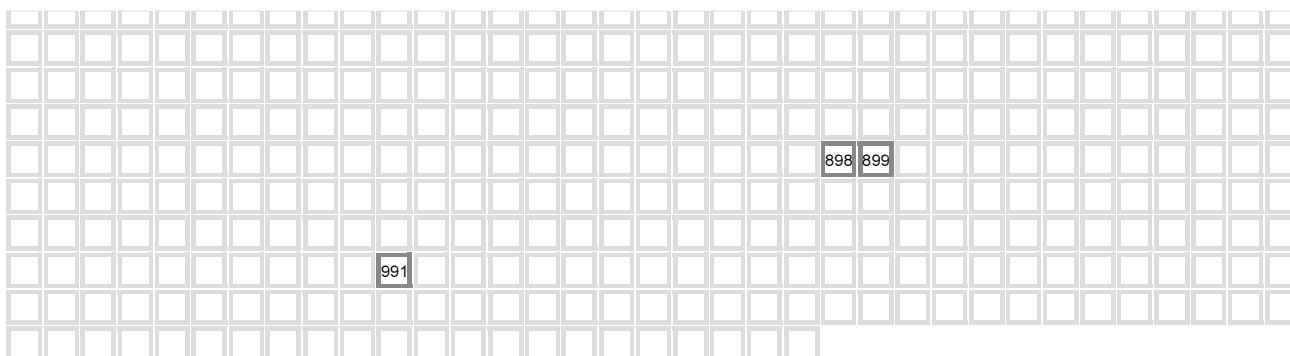
Synonyms: ENSG00000121989; ENSP00000241416; ENSP00000384338; ENSP00000439988; 92; ACVR2A; NP_001607; NM_001616; ACTRII; ACVR2; AVR2A_HUMAN; P27037;

More at [Entrez](#)

STAT5A signal transducer and activator of transcription 5A [Source:HGNC Symbol;Acc:11366]

Functions:



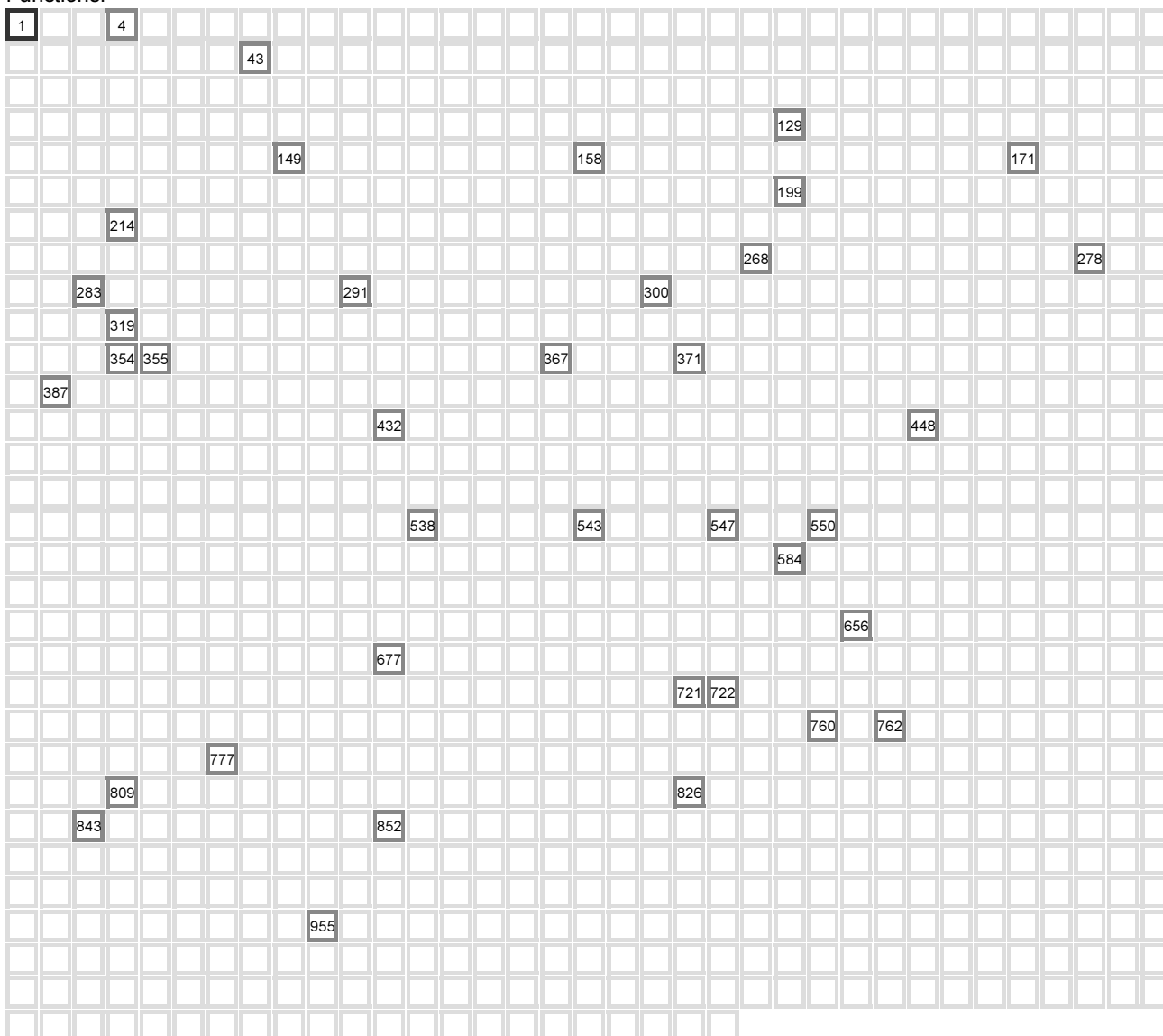


Synonyms: ENSG00000126561; ENSP00000341208; ENSP00000400320; ENSP00000407327; ENSP00000441234; ENSP00000443107; 6776; STAT5A; NP_003143; NM_003152; P42229; STA5A_HUMAN;

More at [Entrez](#)

HMGB1 high mobility group box 1 [Source:HGNC Symbol;Acc:4983]

Functions:

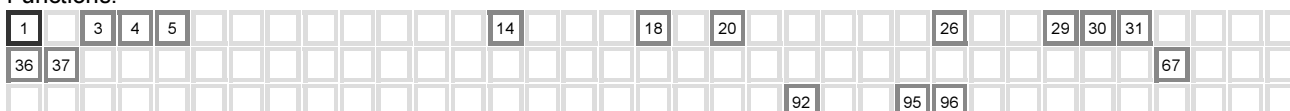


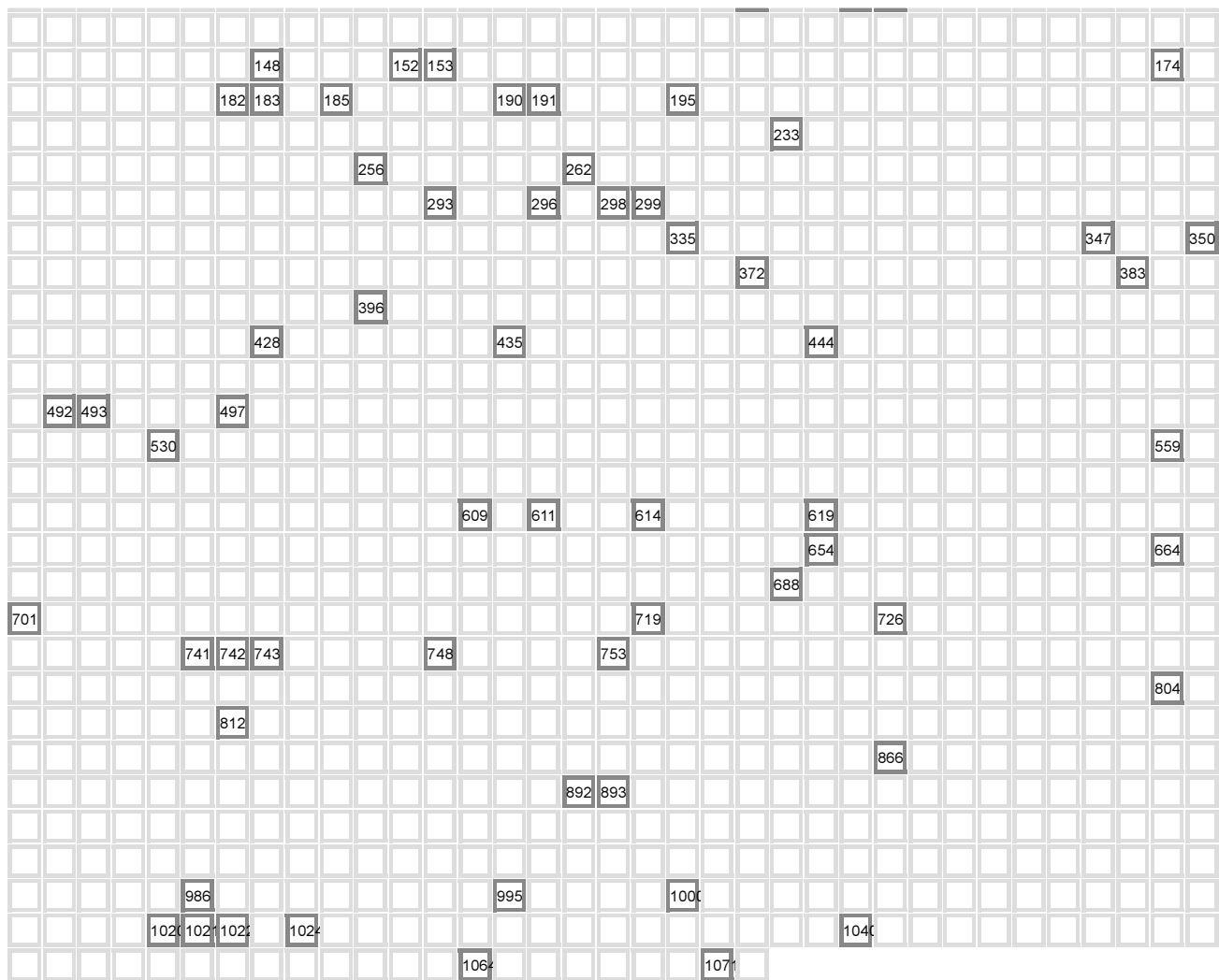
Synonyms: ENSG00000189403; ENSP00000343040; ENSP00000345347; ENSP00000369904; ENSP00000382412; ENSP00000382417; ENSP00000384678; ENSP00000410465; ENSP00000411269; 3146; HMGB1; NP_002119; NM_002128; DKFZp686A04236; HMG1; HMG3; SBP-1; HMGB1_HUMAN; P09429;

More at [Entrez](#)

KIT v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog [Source:HGNC Symbol;Acc:6342]

Functions:



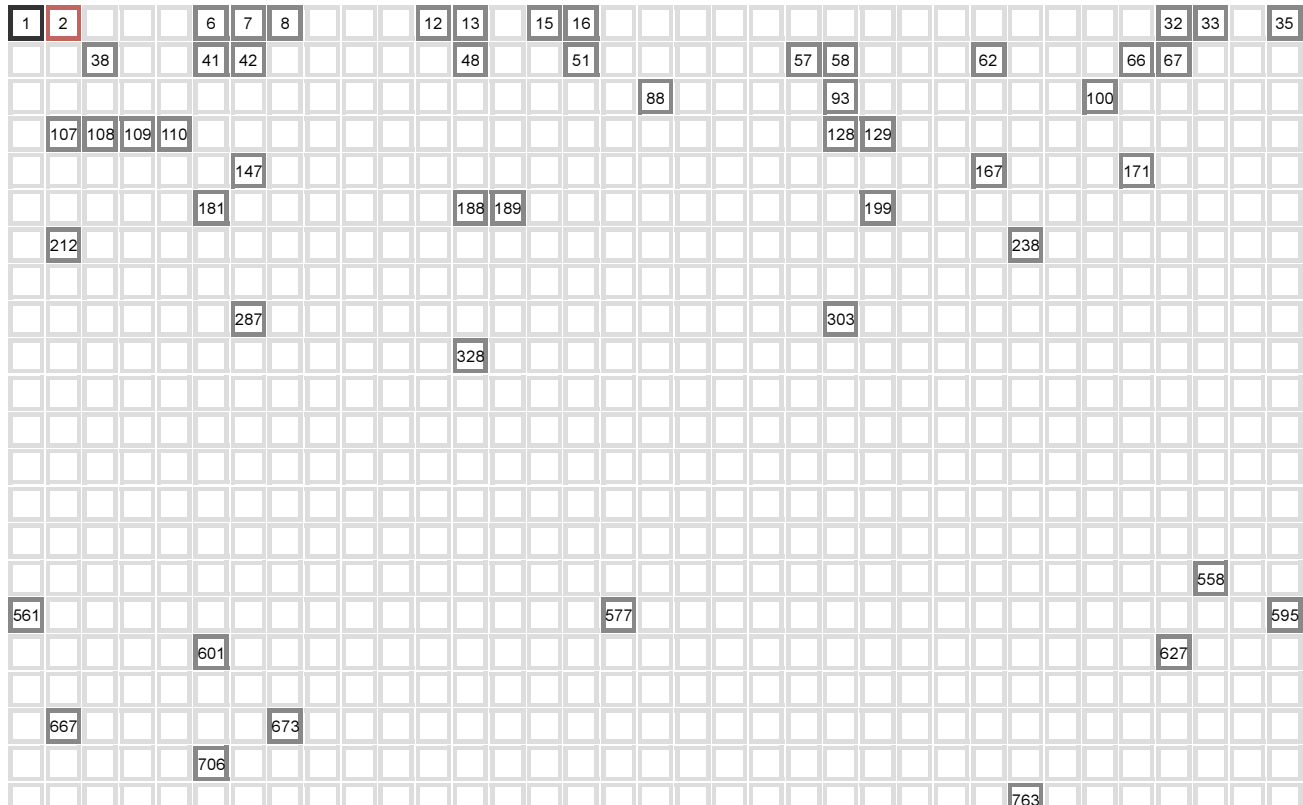


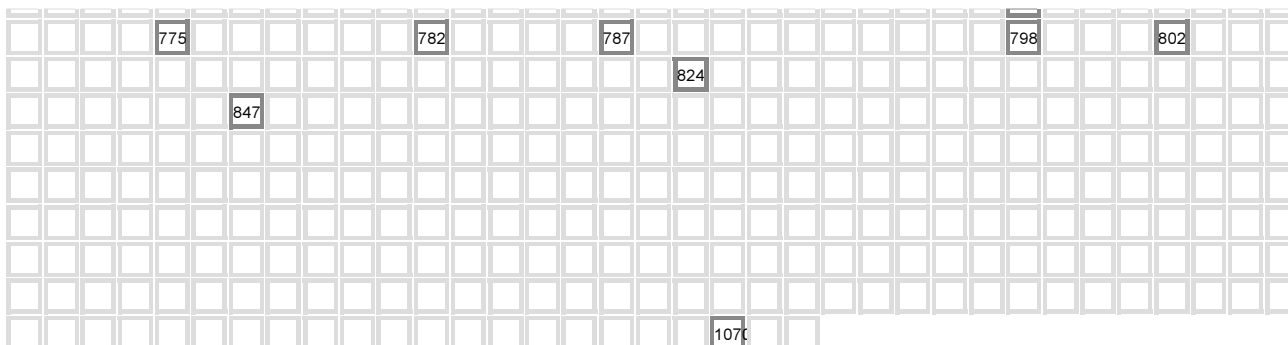
Synonyms: ENSG00000157404; ENSP00000288135; ENSP00000390987; ENSP00000443604; 3815; KIT; NP_000213; NP_001087241; NM_000222; NM_001093772; C-Kit; CD117; PBT; SCFR; KIT_HUMAN; P10721;

More at [Entrez](#)

SMAD2 SMAD family member 2 [Source:HGNC Symbol;Acc:6768]

Functions:



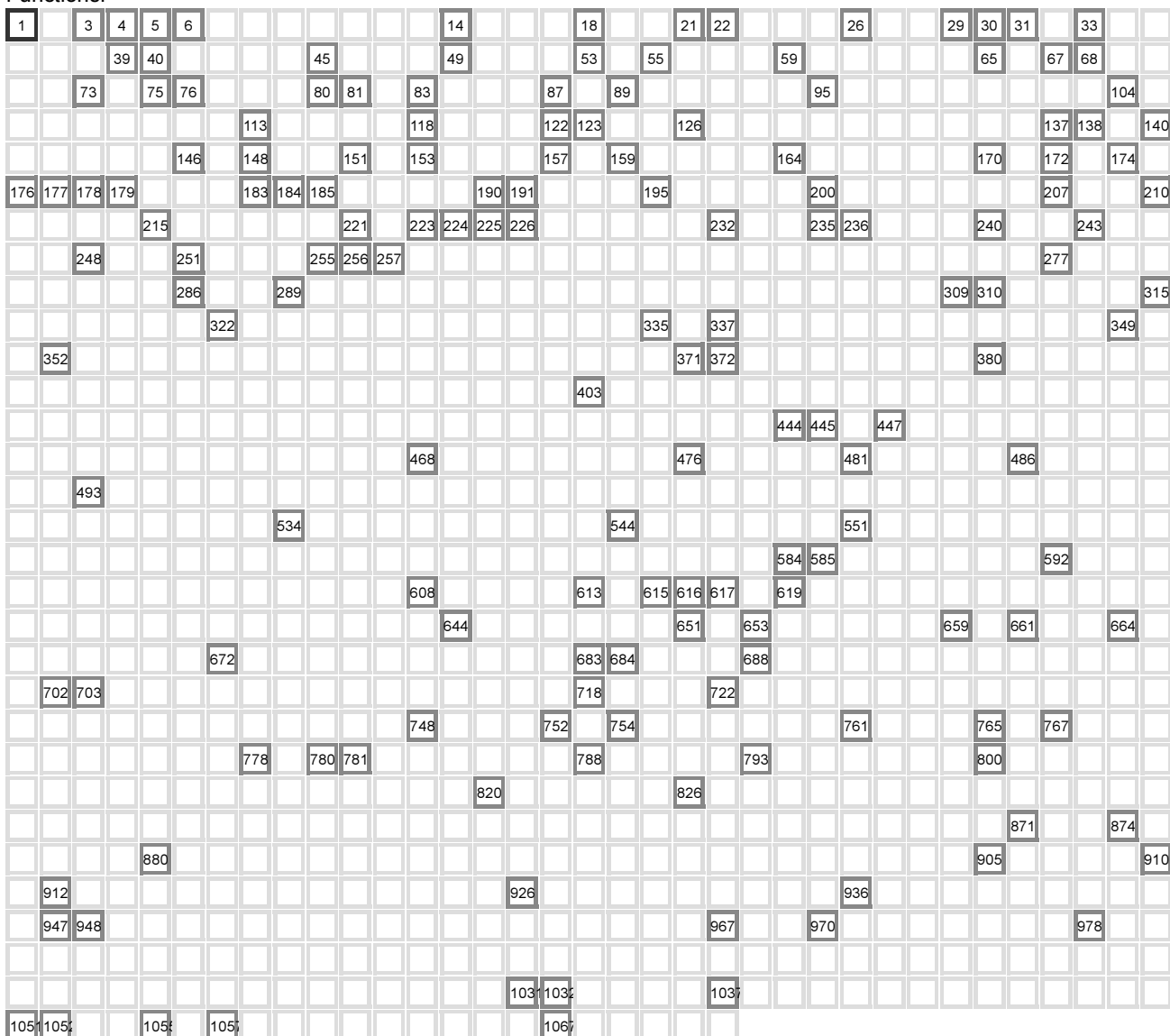


Synonyms: ENSG00000175387; ENSP00000262160; ENSP00000349282; ENSP00000384449; 4087; SMAD2; NP_001003652; NP_001129409; NP_005892; NM_001003652; NM_001135937; NM_005901; hMAD-2; JV18; JV18-1; MADH2; MADR2; Q15796; SMAD2_HUMAN;

More at [Entrez](#)

LYN v-yes-1 Yamaguchi sarcoma viral related oncogene homolog [Source:HGNC Symbol;Acc:6735]

Functions:

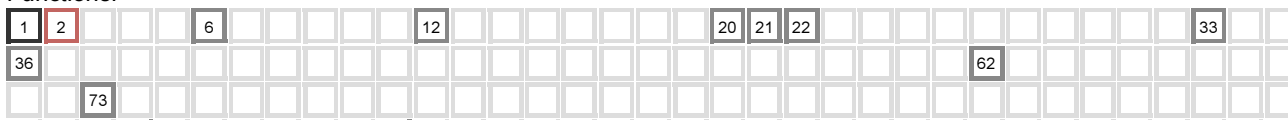


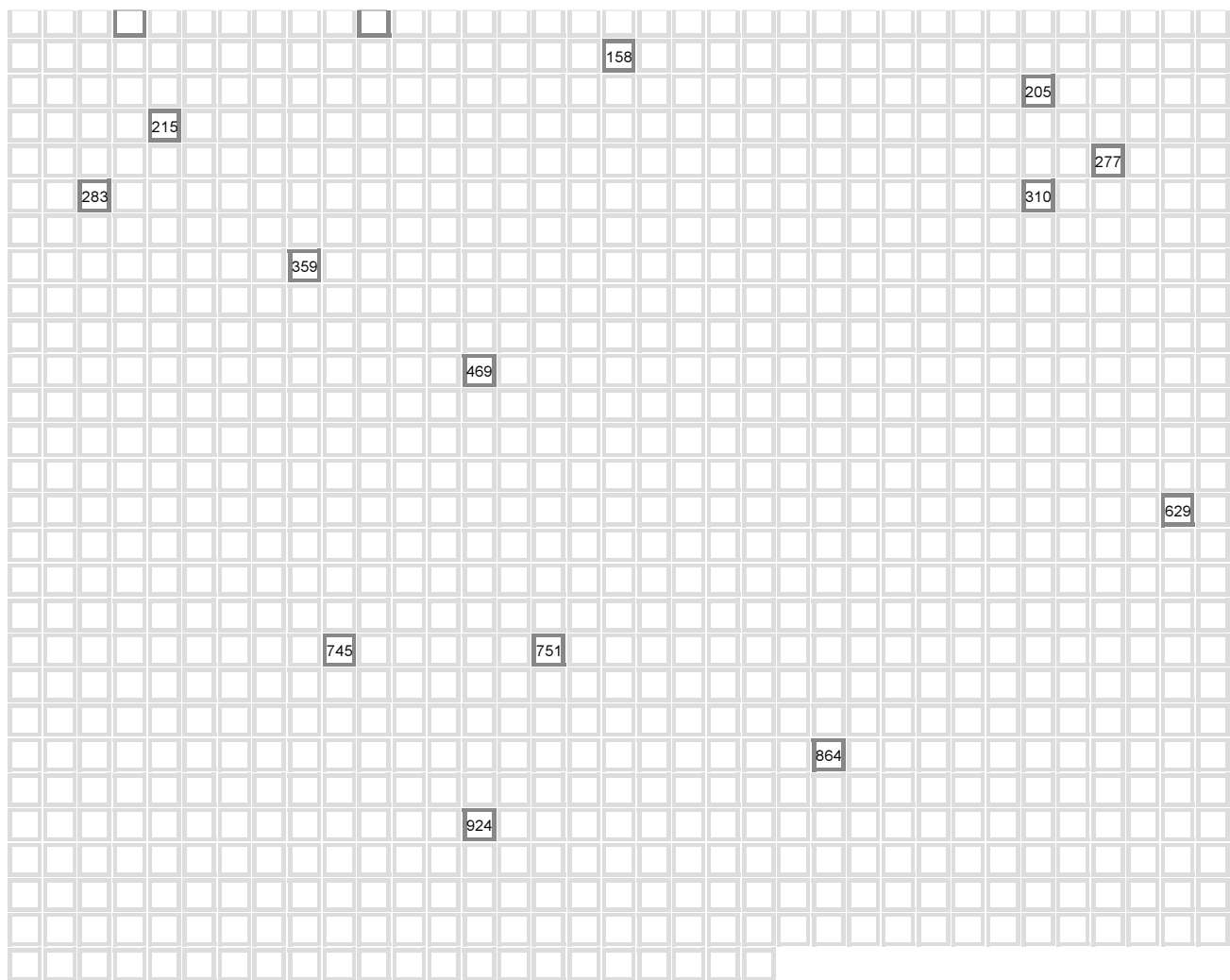
Synonyms: ENSG00000254087; ENSP00000428313; ENSP00000428424; ENSP00000428924; 4067; LYN; NP_001104567; NP_002341; NM_001111097; NM_002350; JTK8; p53Lyn; p56Lyn; LYN_HUMAN; P07948;

More at [Entrez](#)

NGFR nerve growth factor receptor [Source:HGNC Symbol;Acc:7809]

Functions:



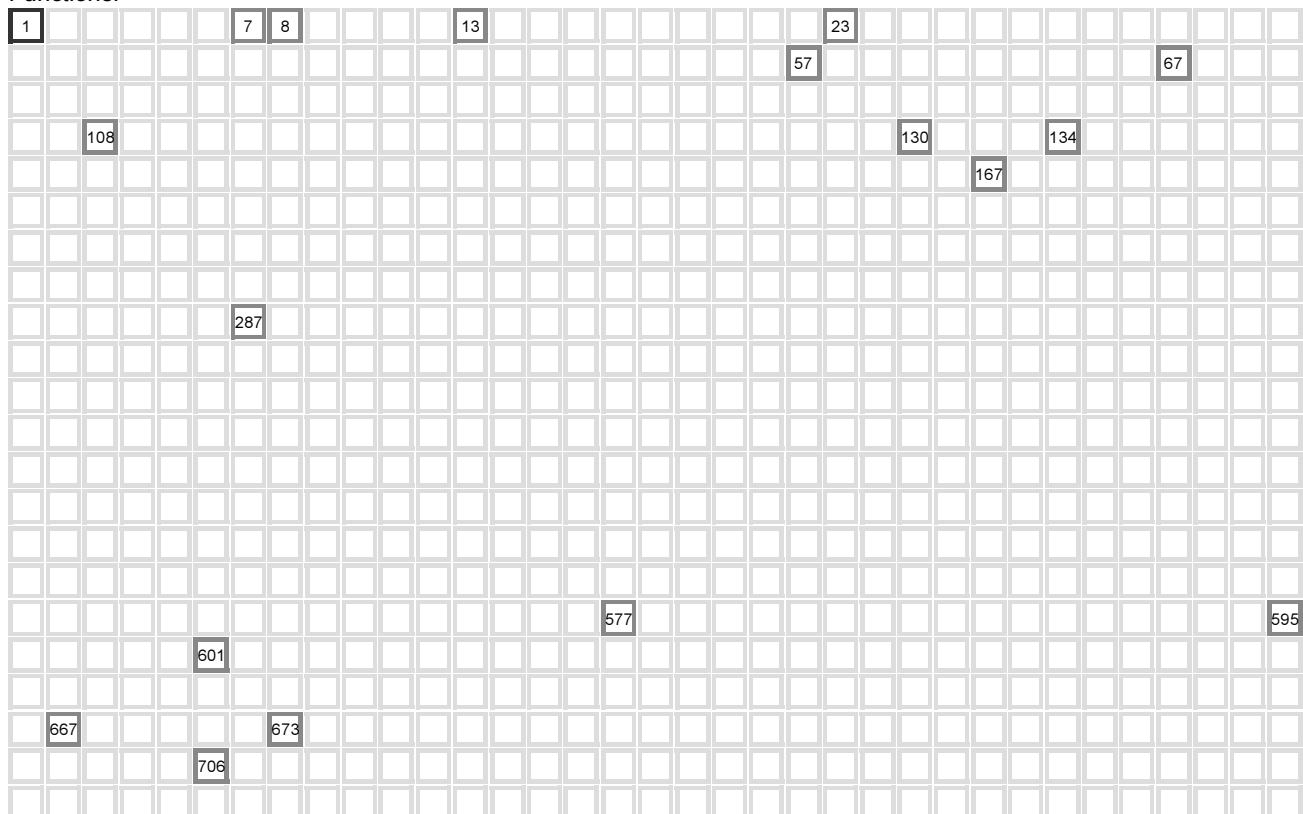


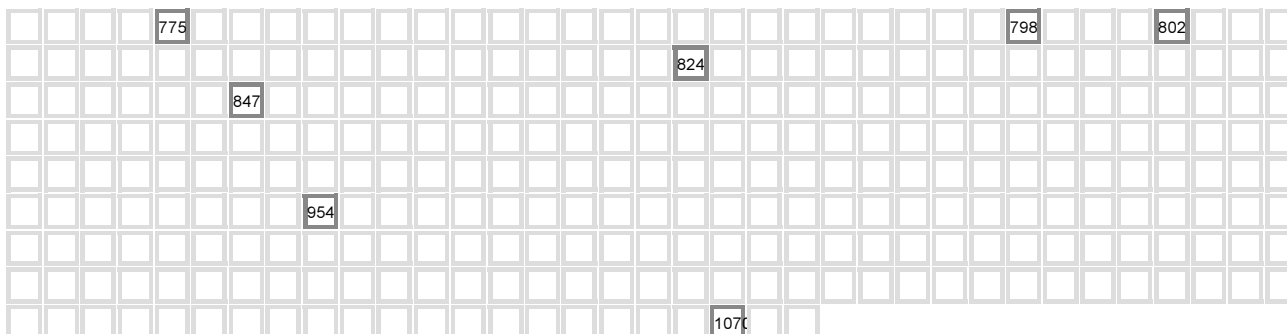
Synonyms: ENSG00000064300; ENSP00000172229; ENSP00000421514; ENSP00000421731; 4804; NGFR; NP_002498; NM_002507; CD271; Gp80-LNGFR; p75(NTR); p75NTR; TNFRSF16; P08138; TNR16_HUMAN;

More at [Entrez](#)

SMAD1 SMAD family member 1 [Source:HGNC Symbol;Acc:6767]

Functions:



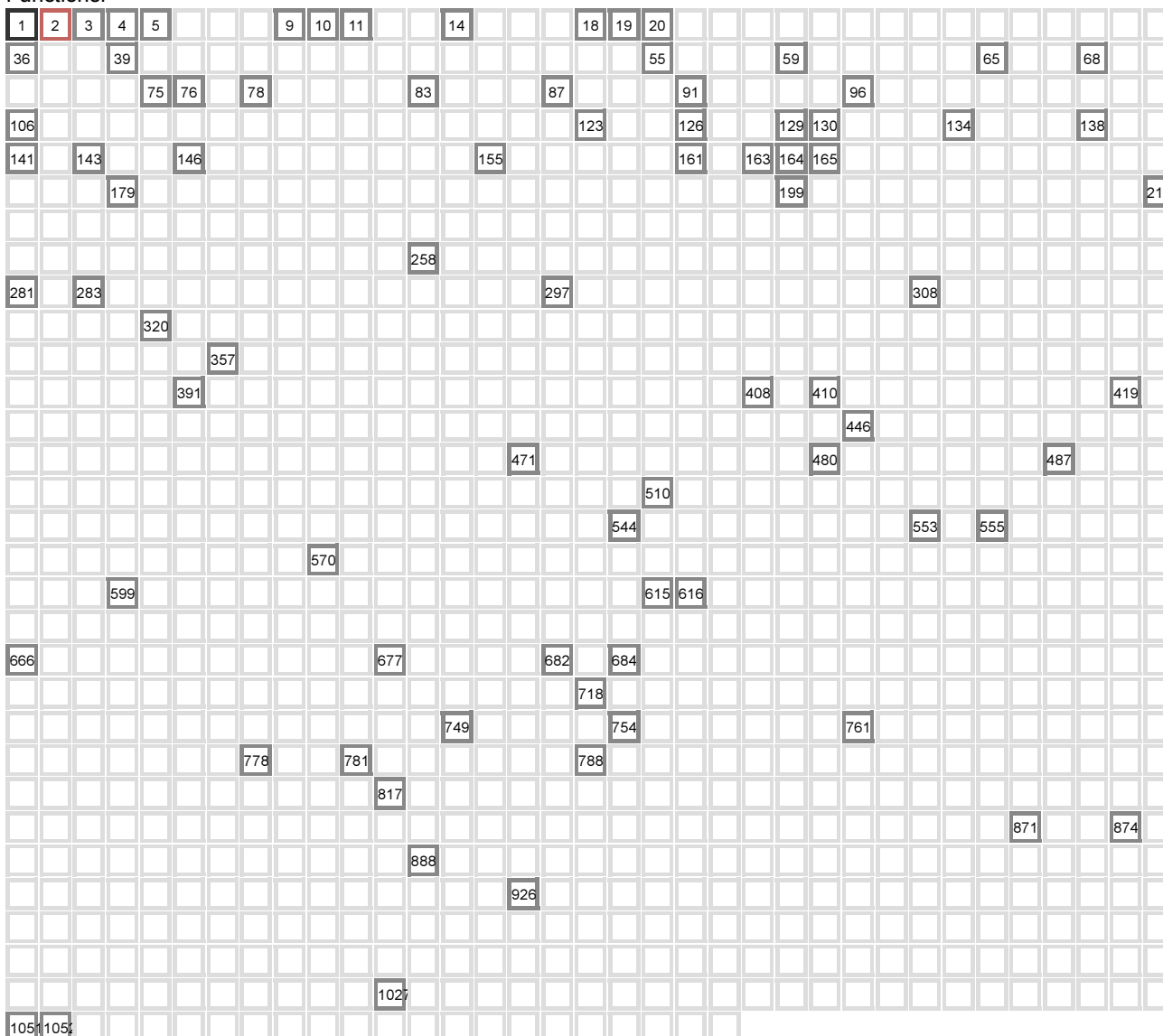


Synonyms: ENSG00000170365; ENSP00000305769; ENSP00000377652; ENSP00000421601; ENSP00000422706; ENSP00000424649; ENSP00000424959; ENSP00000425270; ENSP00000426568; ENSP00000427002; 4086; SMAD1; NP_001003688; NP_005891; NM_001003688; NM_005900; BSP-1; JV4-1; JV41; MADH1; MADR1; Q15797; SMAD1_HUMAN;

More at [Entrez](#)

RARA retinoic acid receptor, alpha [Source:HGNC Symbol;Acc:9864]

Functions:



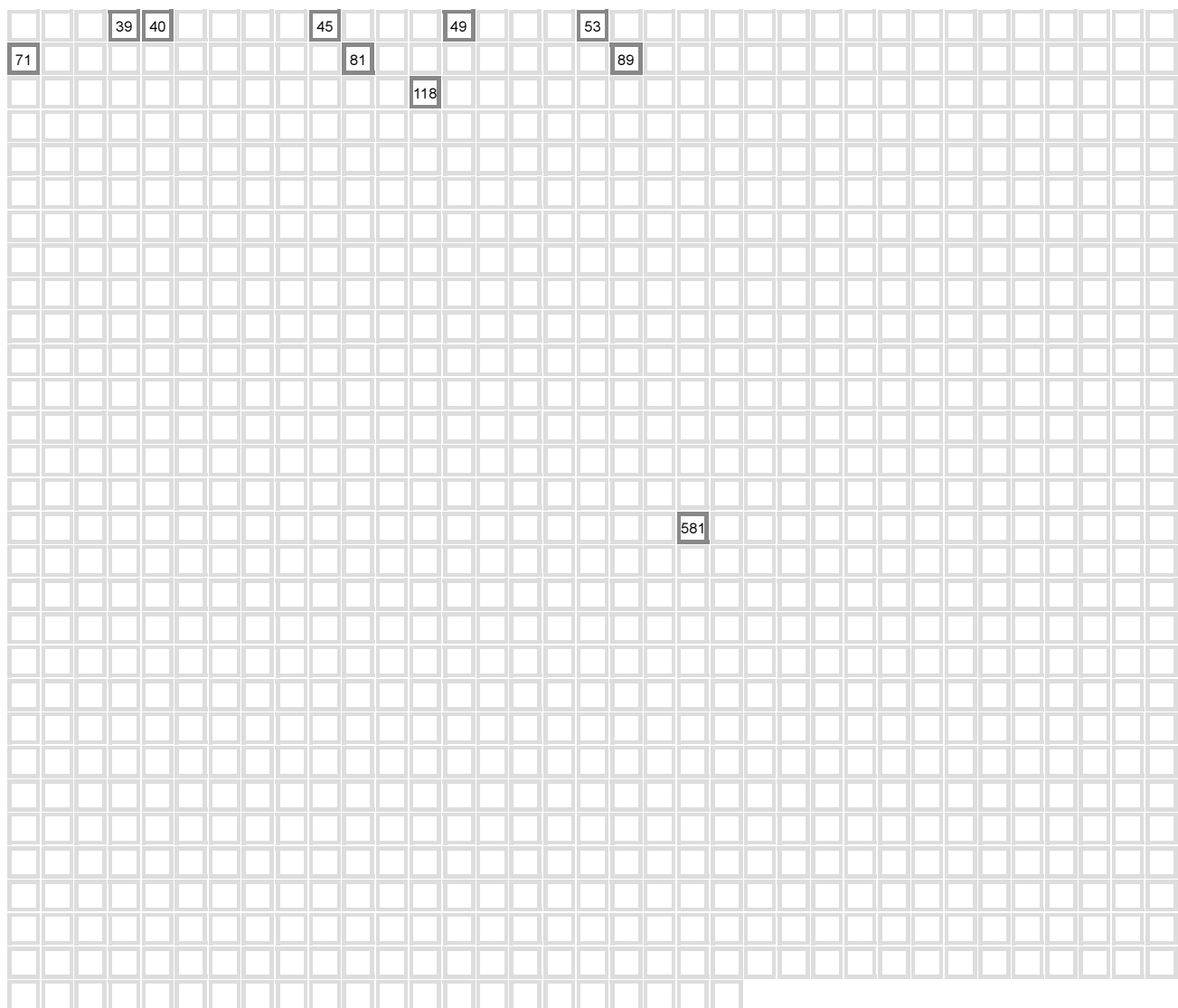
Synonyms: ENSG00000131759; ENSP00000254066; ENSP00000316769; ENSP00000377643; ENSP00000377648; ENSP00000377649; ENSP00000388570; ENSP00000389993; 5914; RARA; NP_000955; NP_001019980; NP_001138773; NP_001138774; NM_000964; NM_001024809; NM_001033603; NM_001145301; NM_001145302; NR1B1; P10276; RARA_HUMAN;

More at [Entrez](#)

ETS1 v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) [Source:HGNC Symbol;Acc:3488]

Functions:



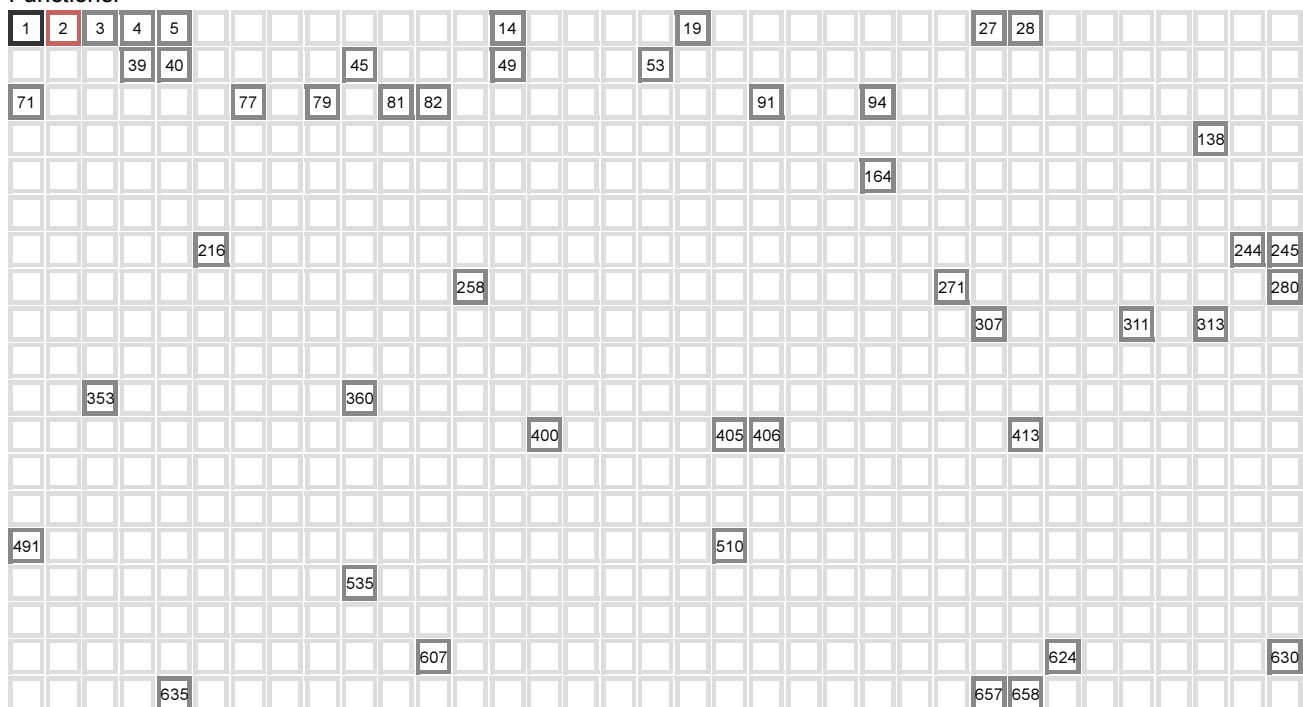


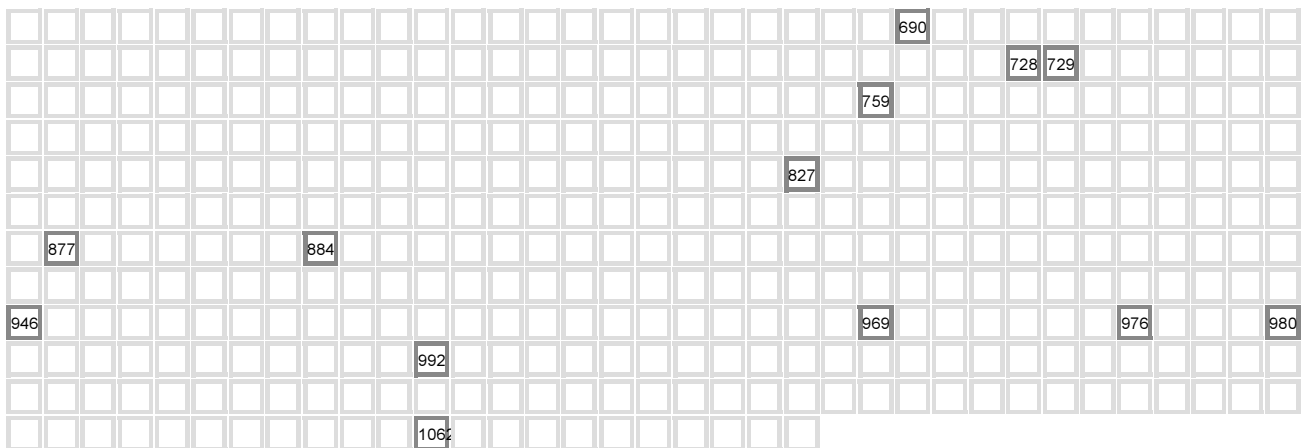
Synonyms: ENSG00000134954; ENSP00000324578; ENSP00000340485; ENSP00000376436; ENSP00000433500; ENSP00000435666; ENSP00000441430; 2113; ETS1; NP_001137292; NP_001155894; NP_005229; NM_001143820; NM_001162422; NM_005238; ETS-1; FLJ10768; ETS1_HUMAN; P14921;

More at [Entrez](#)

ARNT aryl hydrocarbon receptor nuclear translocator [Source:HGNC Symbol;Acc:700]

Functions:



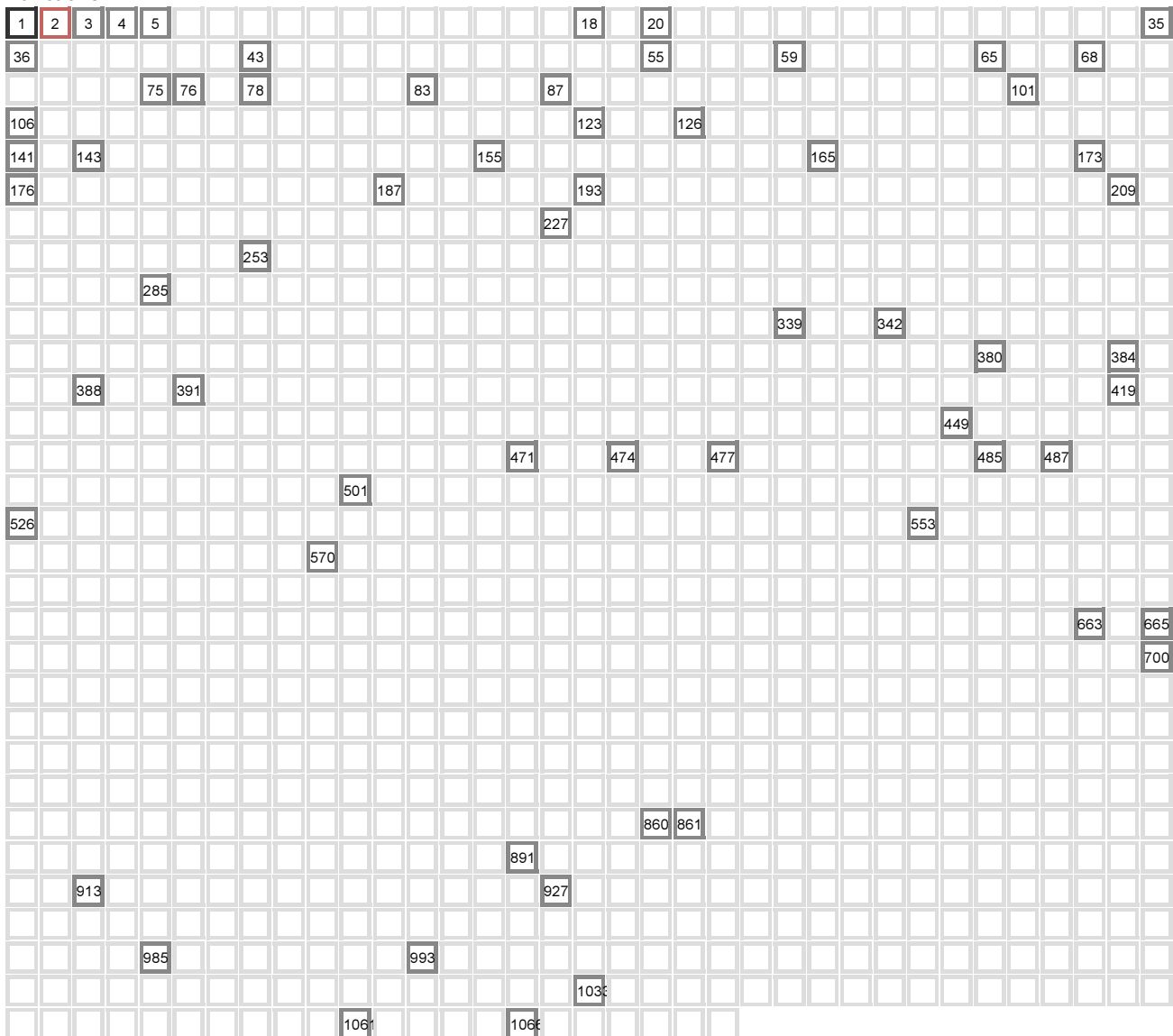


Synonyms: ENSG00000143437; ENSP00000346372; ENSP00000351407; ENSP00000357971; ENSP00000378190; ENSP00000423851; ENSP00000425363; ENSP00000425899; ENSP00000427571; 405; ARNT; NP_001184254; NP_001659; NP_848514; NM_001197325; NM_001668; NM_178426; NM_178427; bHLHe2; HIF-1-beta; HIF-1beta; HIF1-beta; HIF1B; HIF1BETA; ARNT_HUMAN; P27540;

More at [Entrez](#)

GLI3 GLI family zinc finger 3 [Source:HGNC Symbol;Acc:4319]

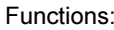
Functions:

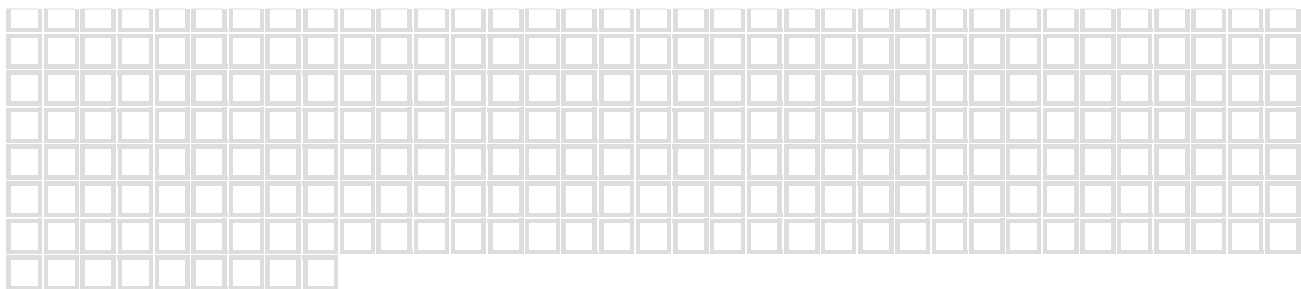


Synonyms: ENSG00000106571; ENSP00000379258; ENSP00000406135; ENSP00000407963; 2737; GLI3; NP_000159; NM_000168; GCPS; GLI3-190; GLI3FL; PAP-A; PAPA1; PAPB; PPDIV; GLI3_HUMAN; P10071;

More at [Entrez](#)

SMAD4 SMAD family member 4 [Source:HGNC Symbol;Acc:6770]



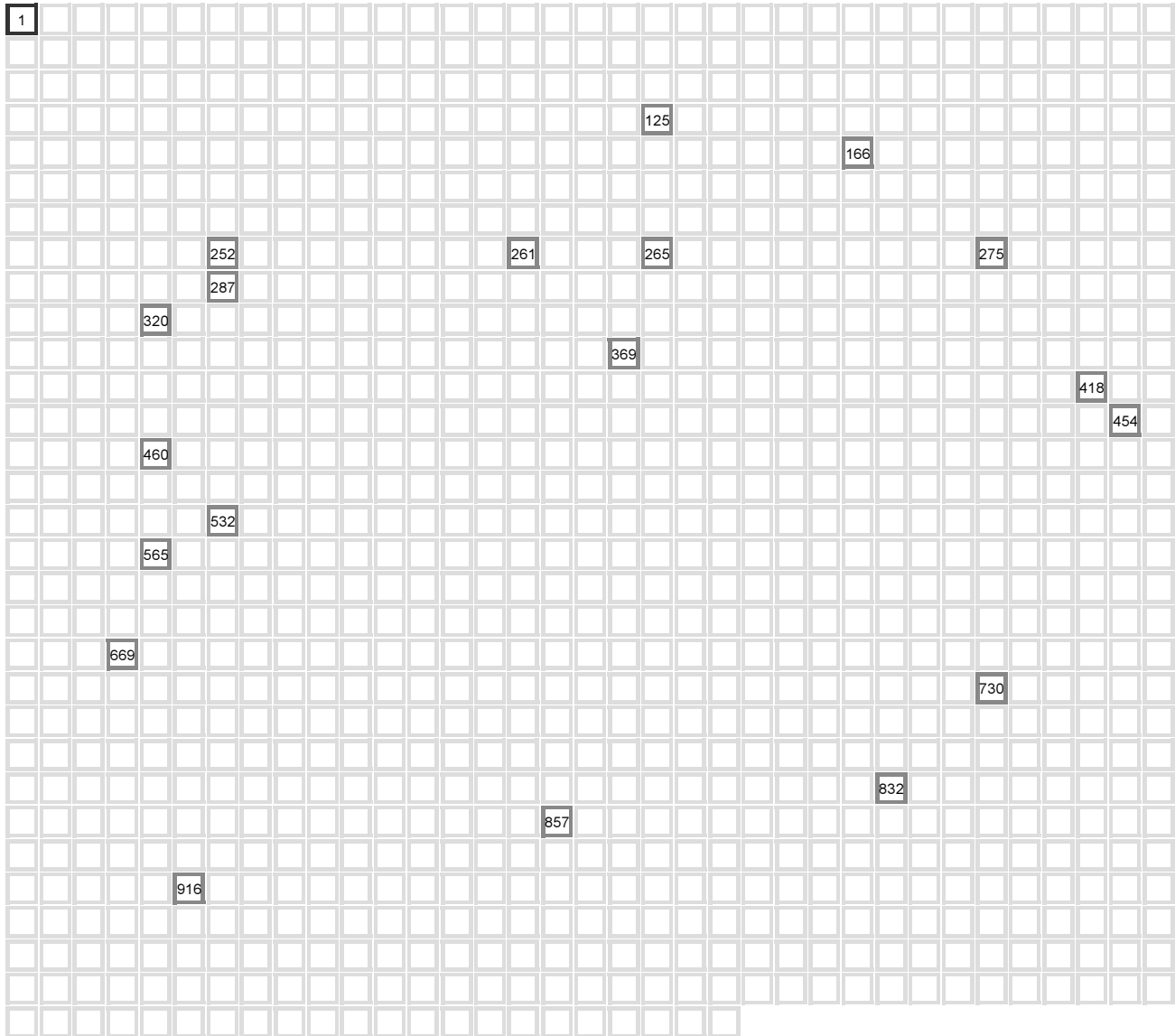


Synonyms: ENSG00000141646; ENSP00000341551; ENSP00000381452; ENSP00000409551; ENSP00000443830; 4089; SMAD4; NP_005350; NM_005359; DPC4; JIP; MADH4; Q13485; SMAD4_HUMAN;

More at [Entrez](#)

HSP90AA1 heat shock protein 90kDa alpha (cytosolic), class A member 1 [Source:HGNC Symbol;Acc:5253]

Functions:

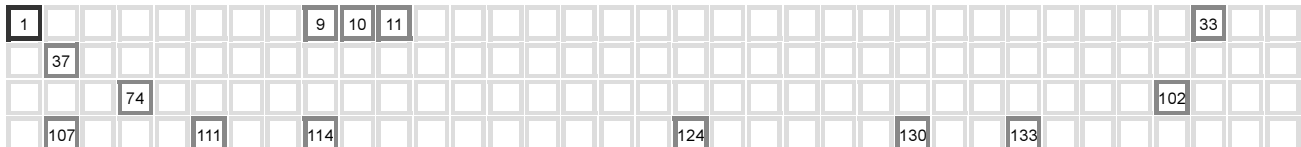


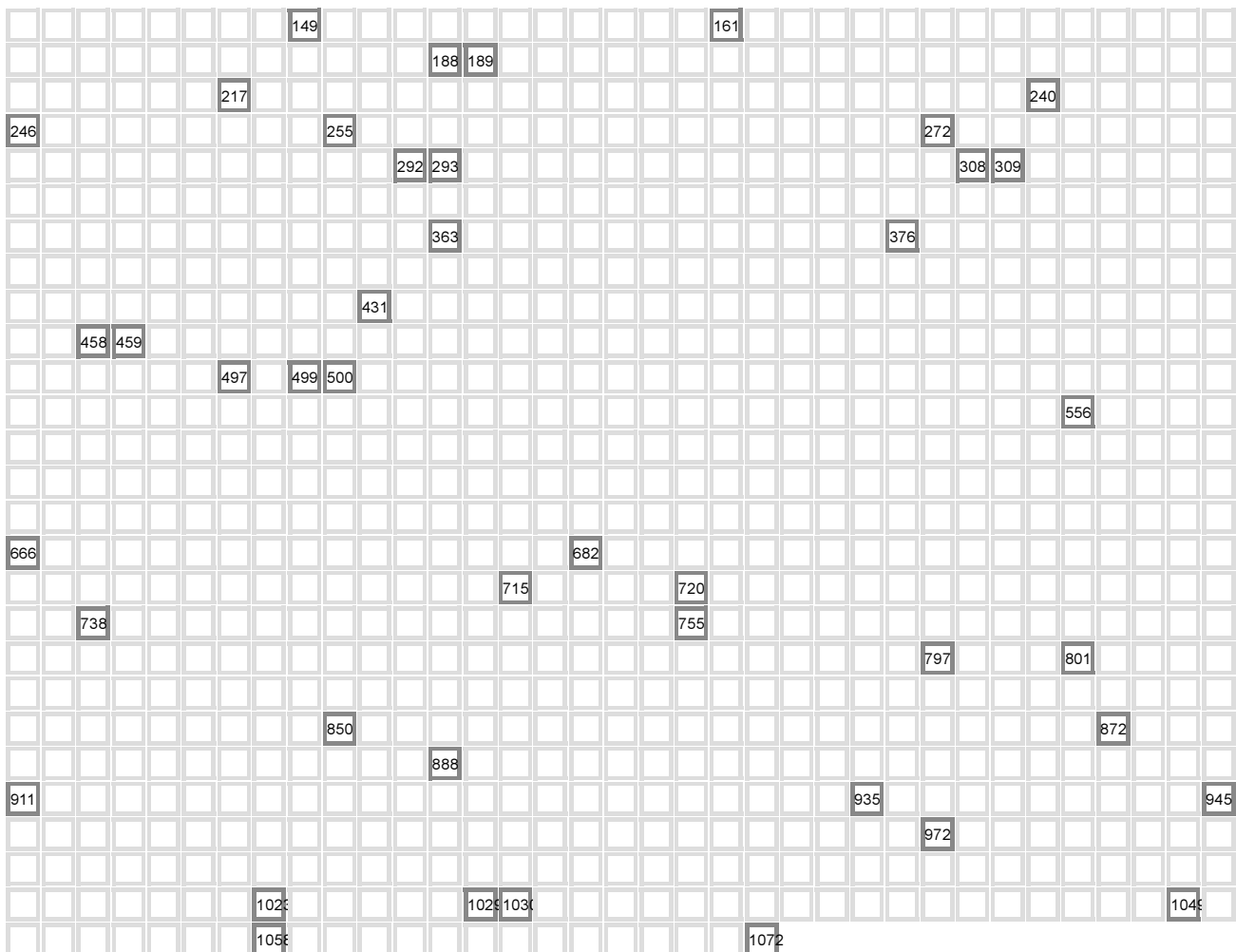
Synonyms: ENSG00000080824; ENSP00000216281; ENSP00000335153; ENSP00000396189; ENSP00000450712; ENSP00000451400; ENSP00000452241; 3320; HSP90AA1; NP_001017963; NP_005339; NM_001017963; NM_005348; FLJ31884; HSP86; Hsp89; HSP89A; Hsp90; HSP90A; HSP90N; HSPC1; HSPCA; HSPCAL1; HSPCAL4; HSPN; HS902_HUMAN; HS90A_HUMAN; P07900; Q14568;

More at [Entrez](#)

RB1 retinoblastoma 1 [Source:HGNC Symbol;Acc:9884]

Functions:



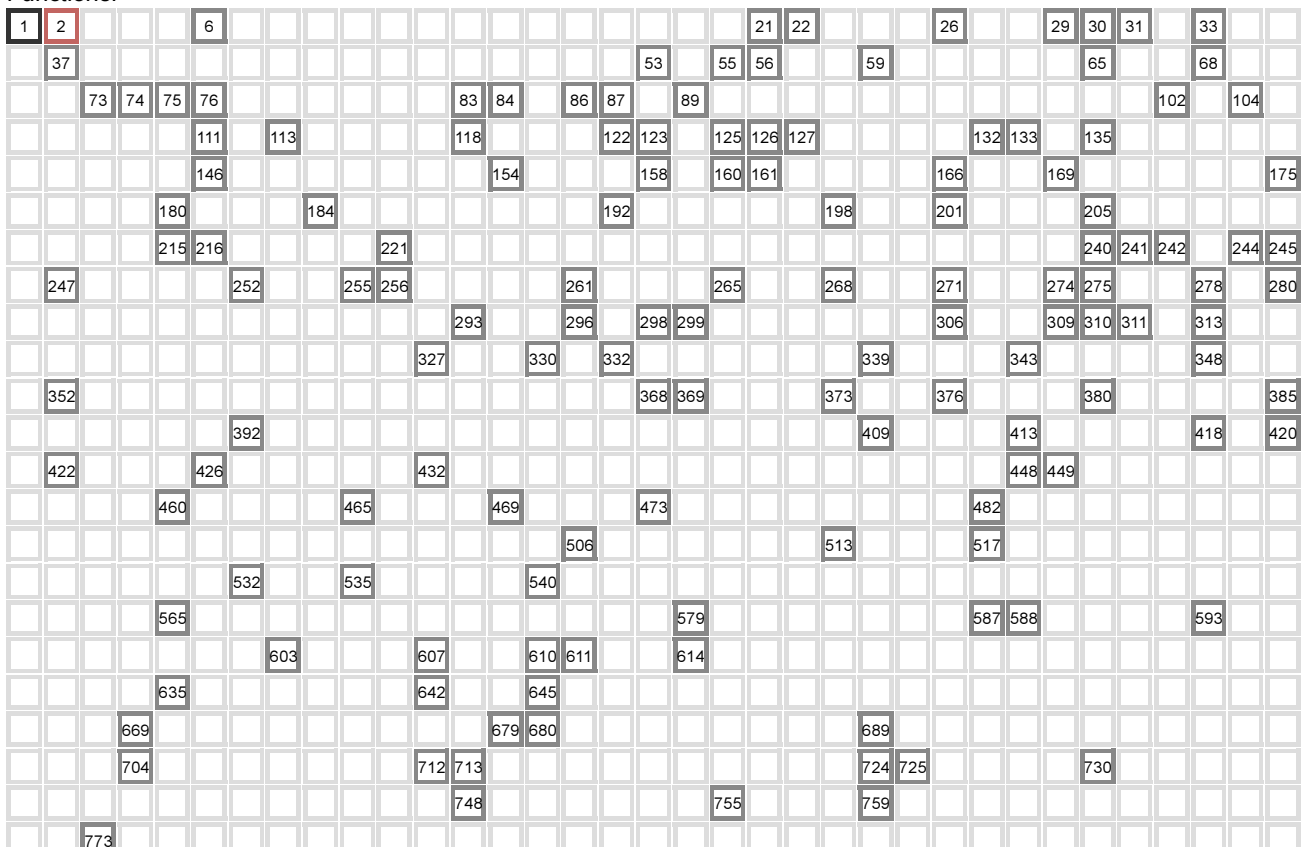


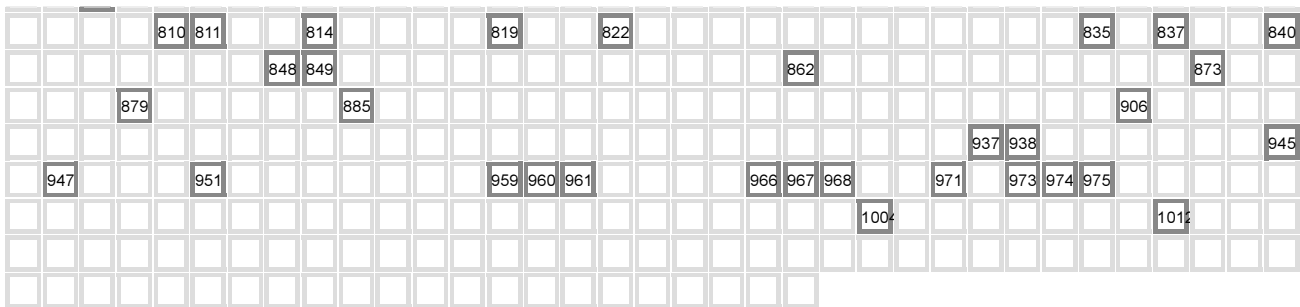
Synonyms: ENSG00000139687; ENSP00000267163; ENSP00000434702; ENSP00000437642; 5925; RB1; NP_000312; NM_000321; OSRC; p105-Rb; pp110; pRb; RB; P06400; RB_HUMAN;

More at [Entrez](#)

AKT1 v-akt murine thymoma viral oncogene homolog 1 [Source:HGNC Symbol;Acc:391]

Functions:



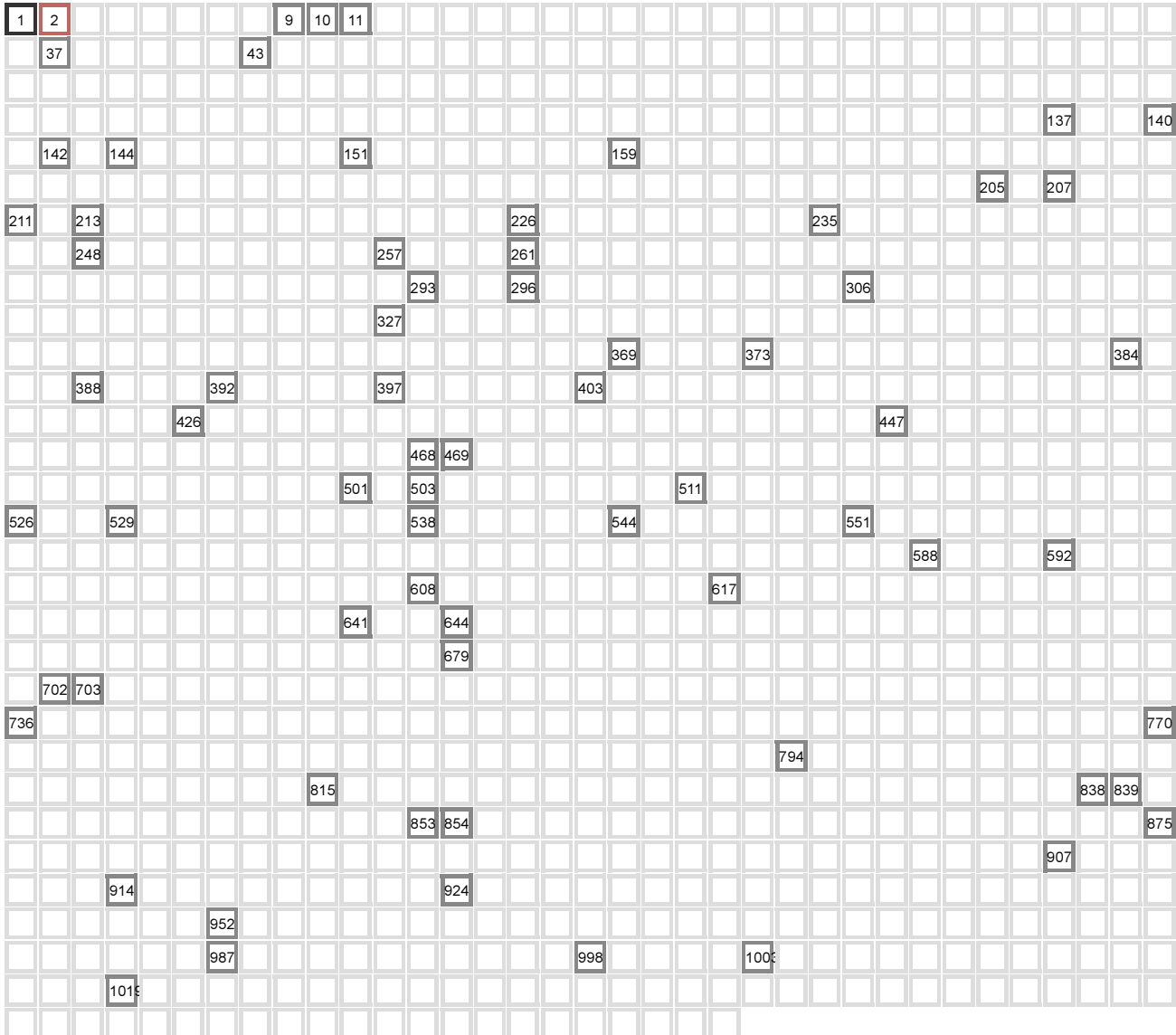


Synonyms: ENSG00000142208; ENSP00000270202; ENSP00000384293; ENSP00000385326; ENSP00000443897; ENSP00000450681; ENSP00000450688; ENSP00000451166; ENSP00000451290; ENSP00000451470; ENSP00000451824; ENSP00000451828; 207; AKT1; NP_001014431; NP_001014432; NP_005154; NM_001014431; NM_001014432; NM_005163; AKT; PKB-ALPHA; PRKBA; RAC; RAC-ALPHA; AKT1_HUMAN; P31749;

More at [Entrez](#)

NFKB1 nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 [Source:HGNC Symbol;Acc:7794]

Functions:



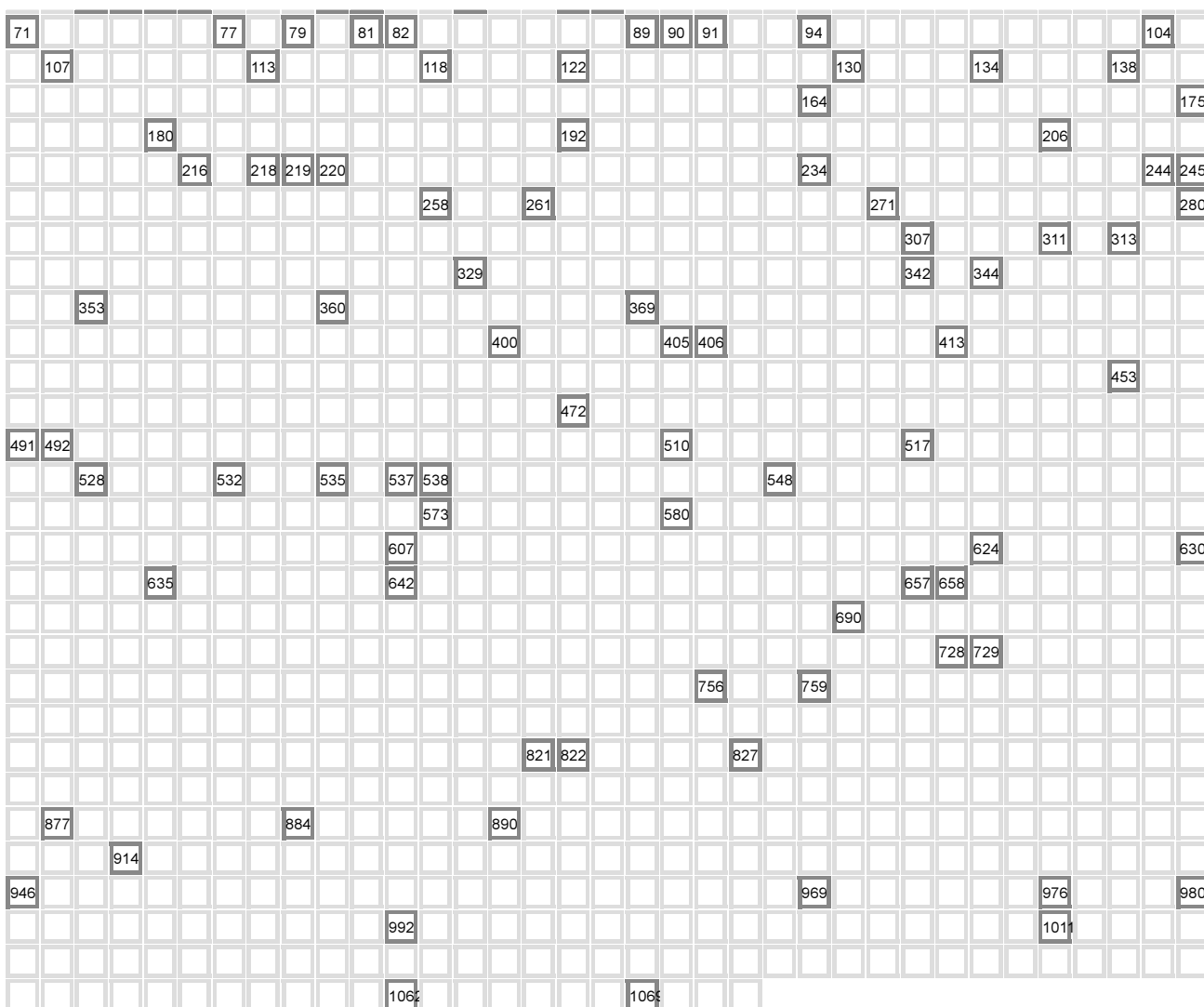
Synonyms: ENSG00000109320; ENSP00000226574; ENSP00000378297; ENSP00000420904; ENSP00000423877; ENSP00000424790; ENSP00000424815; ENSP00000426147; 4790; NFKB1; NP_001158884; NP_003989; NM_001165412; NM_003998; EBP-1; KBF1; NF-kappa-B; NF-kappaB; NFkappaB; NFKB-p105; NFKB-p50; NFKB1_HUMAN; P19838;

More at [Entrez](#)

HIF1A hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) [Source:HGNC Symbol;Acc:4910]

Functions:



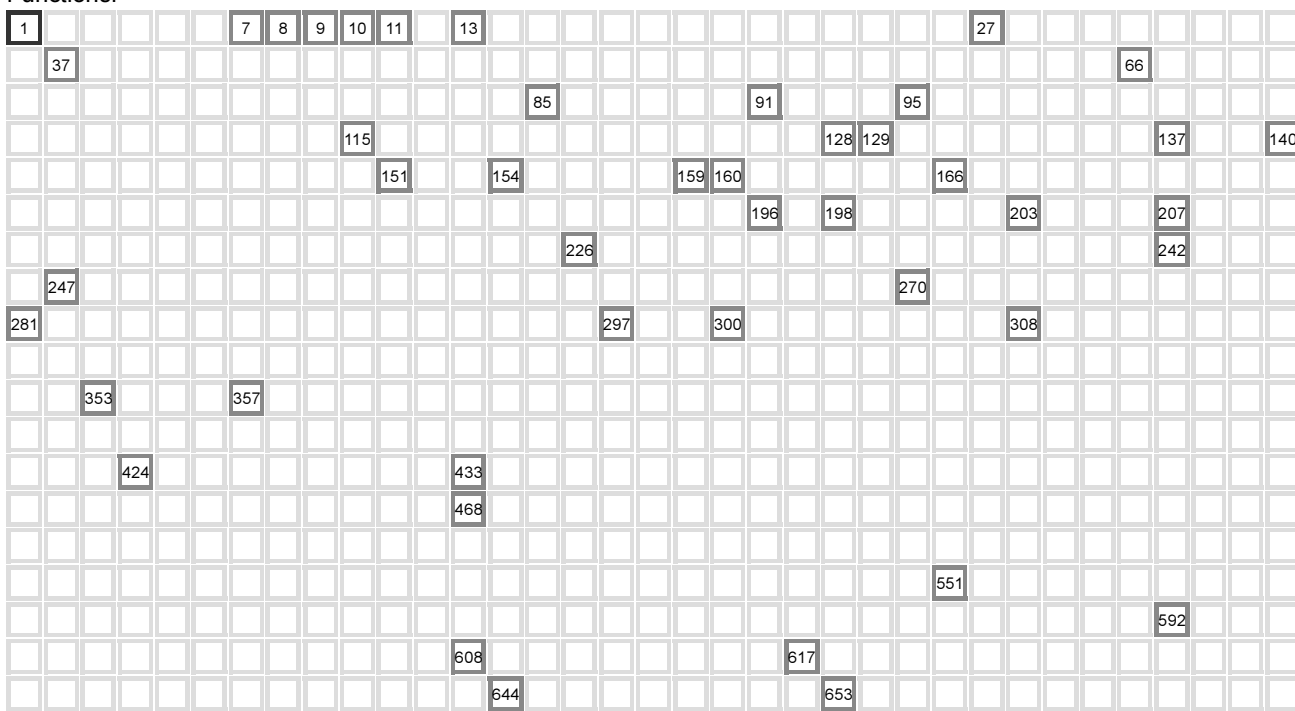


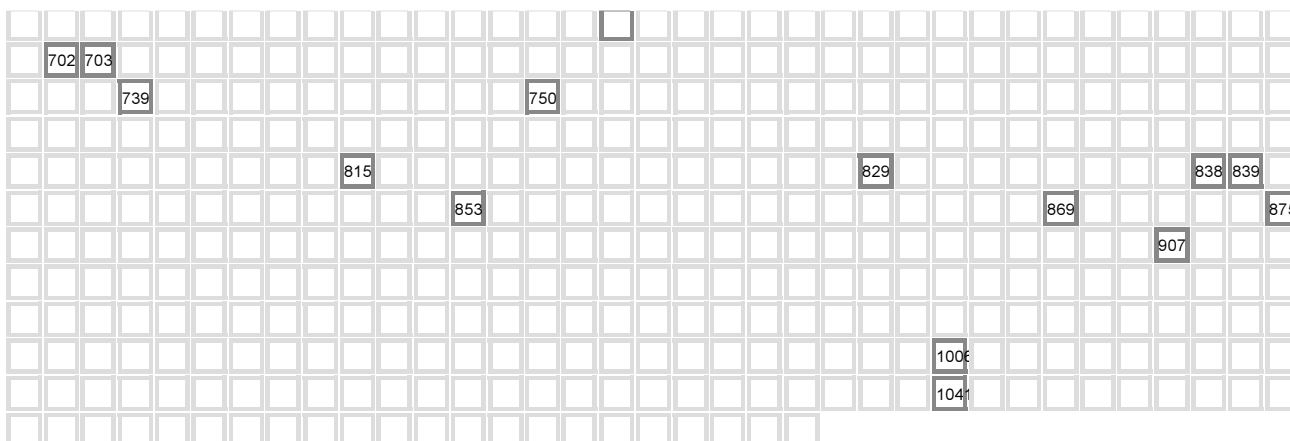
Synonyms: ENSG00000100644; ENSP00000323326; ENSP00000338018; ENSP00000378439; ENSP00000378446; ENSP00000437955; ENSP00000446436; ENSP00000451696; 3091; HIF1A; NP_001230013; NP_001521; NP_851397; NM_001243084; NM_001530; NM_181054; bHLHe78; HIF-1alpha; HIF1; HIF1-ALPHA; MOP1; PASD8; HIF1A_HUMAN; Q16665;

More at [Entrez](#)

JUN jun proto-oncogene [Source:HGNC Symbol;Acc:6204]

Functions:



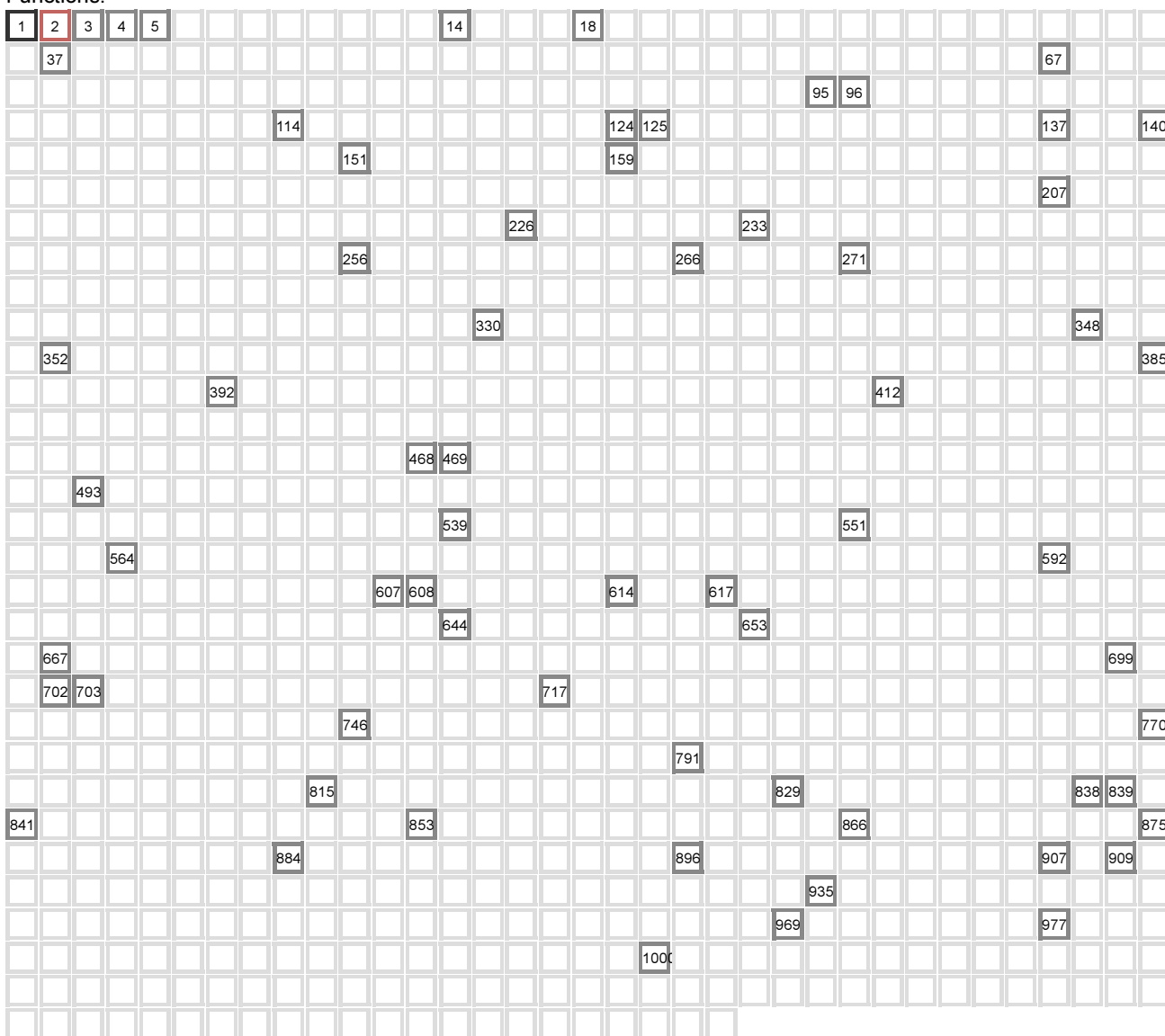


Synonyms: ENSG00000177606; ENSP00000360266; 3725; JUN; NP_002219; NM_002228; AP1; c-Jun; JUN_HUMAN; P05412;

More at [Entrez](#)

MAPK14 mitogen-activated protein kinase 14 [Source:HGNC Symbol;Acc:6876]

Functions:

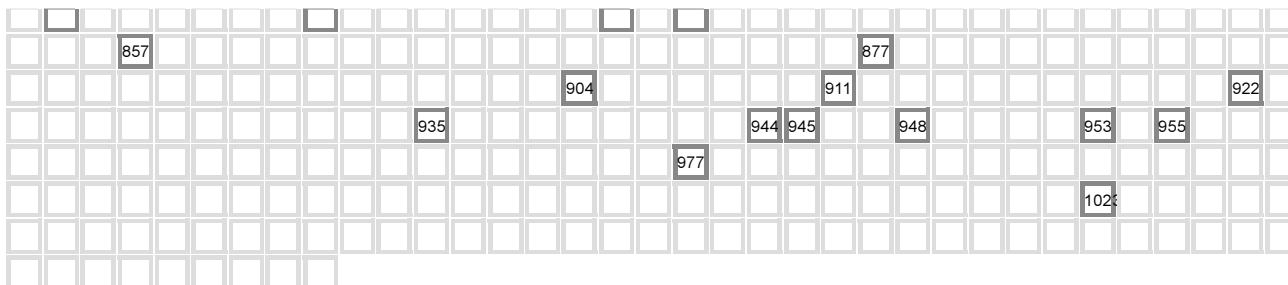


Synonyms: ENSG00000112062; ENSP00000229794; ENSP00000229795; ENSP00000308669; ENSP00000417065; ENSP00000417531; ENSP00000419141; ENSP00000419837; 1432; MAPK14; NP_001306; NP_620581; NP_620582; NP_620583; NM_001315; NM_139012; NM_139013; NM_139014; CSBP1; CSBP2; CSPB1; EXIP; Mxi2; p38ALPHA; PRKM14; PRKM15; SAPK2A; MK14_HUMAN; Q16539;

More at [Entrez](#)

TP53 tumor protein p53 [Source:HGNC Symbol;Acc:11998]



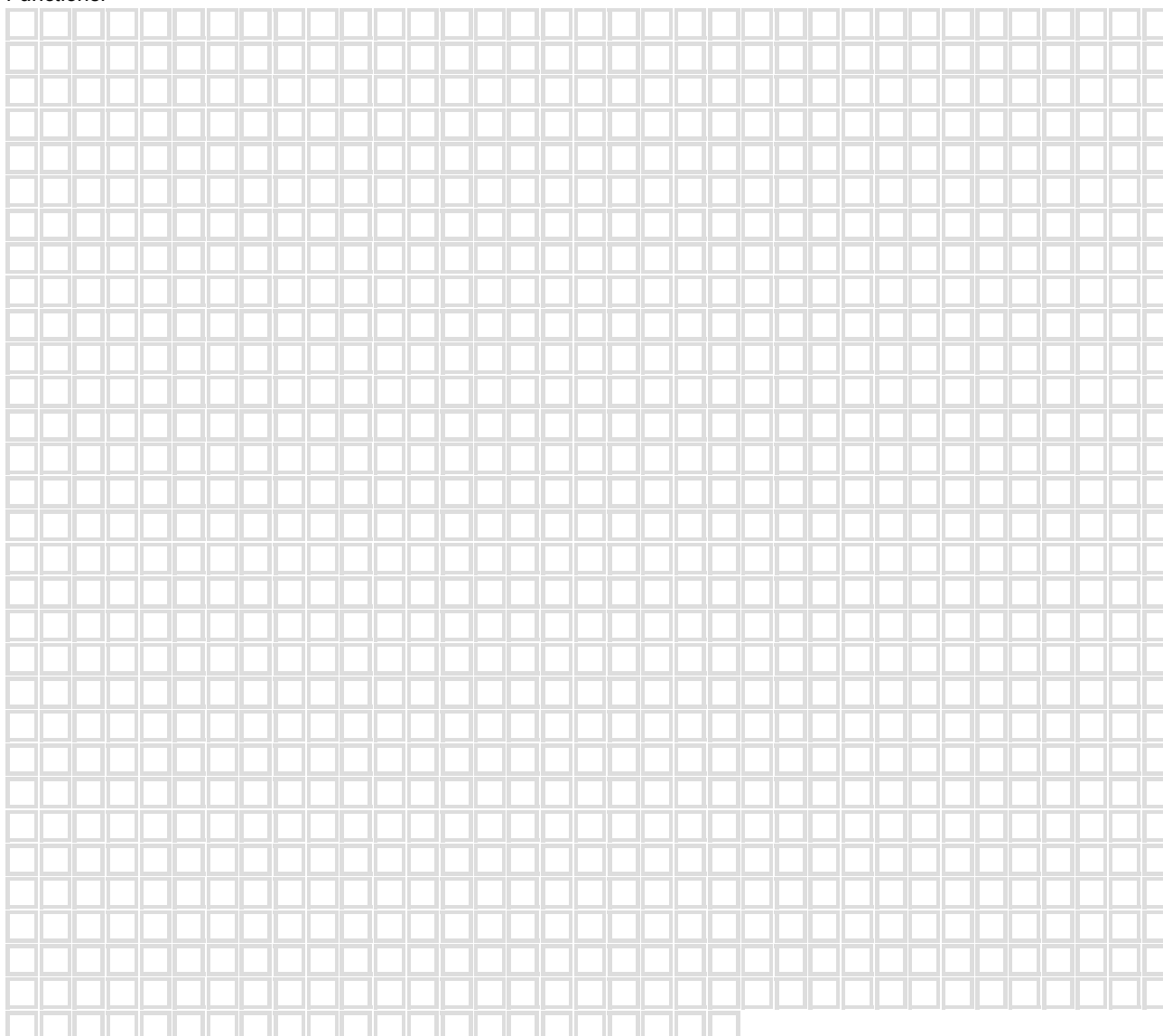


Synonyms: ENSG00000141510; ENSP00000269305; ENSP00000352610; ENSP00000379735; ENSP00000391127; ENSP00000391478; ENSP00000394195; ENSP00000398846; ENSP00000402130; ENSP00000410739; ENSP00000423862; ENSP00000424104; ENSP00000425104; ENSP00000426252; ENSP00000437792; 7157; TP53; NP_000537; NP_001119584; NP_001119585; NP_001119586; NP_001119587; NP_001119588; NP_001119589; NP_001119590; NM_000546; NM_001126112; NM_001126113; NM_001126114; NM_001126115; NM_001126116; NM_001126117; NM_001126118; LFS1; P53; TRP53; P04637; P53_HUMAN;

More at [Entrez](#)

NTF3 neurotrophin 3 [Source:HGNC Symbol;Acc:8023]

Functions:



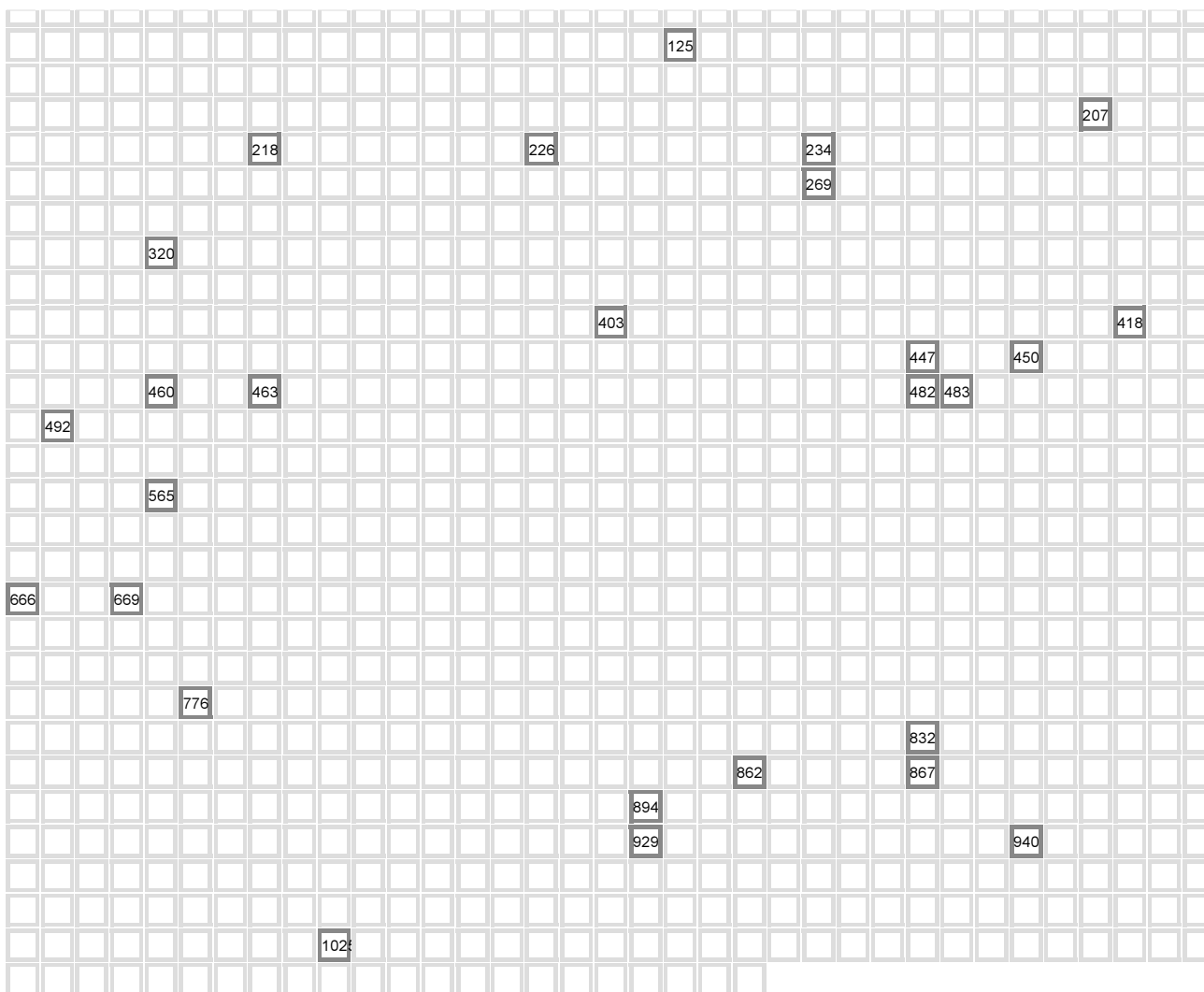
Synonyms: ENSG00000185652; ENSP00000328738; ENSP00000397297; 4908; NTF3; NP_001096124; NP_002518; NM_001102654; NM_002527; HDNF; NGF-2; NGF2; NTF3_HUMAN; P20783;

More at [Entrez](#)

HSP90AB1 heat shock protein 90kDa alpha (cytosolic), class B member 1 [Source:HGNC Symbol;Acc:5258]

Functions:



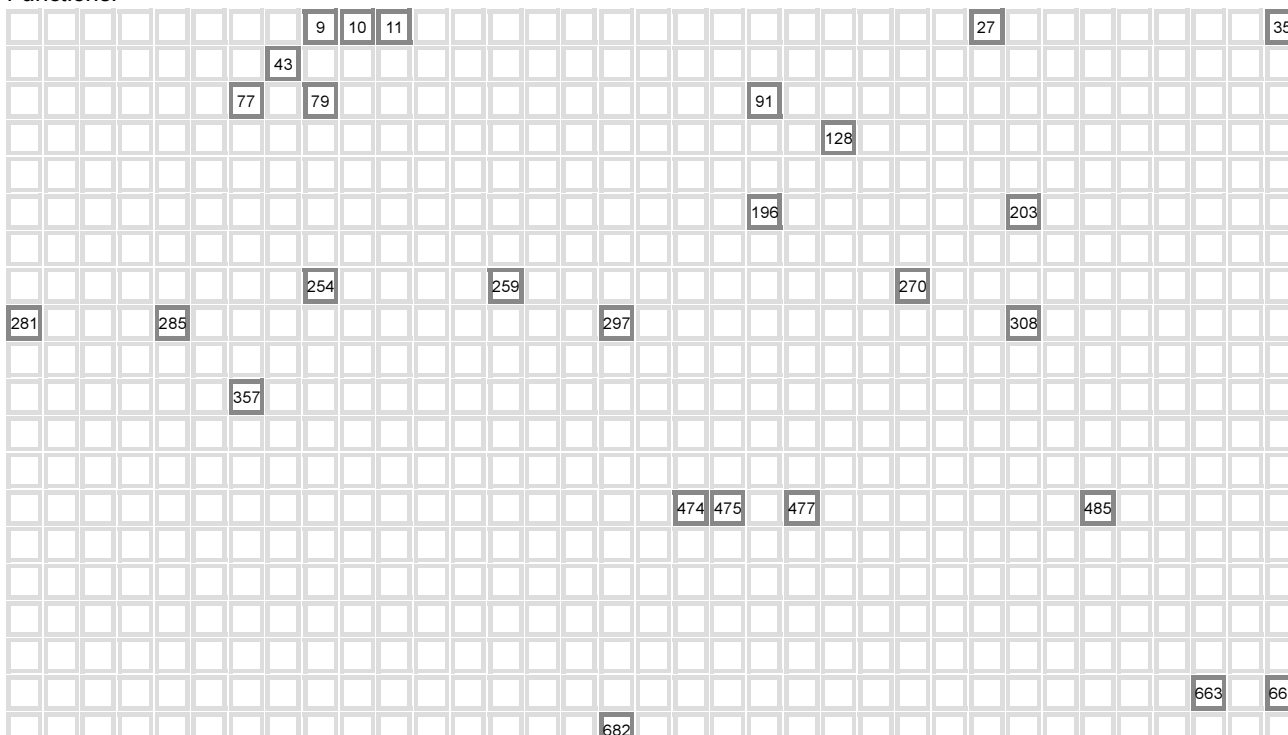


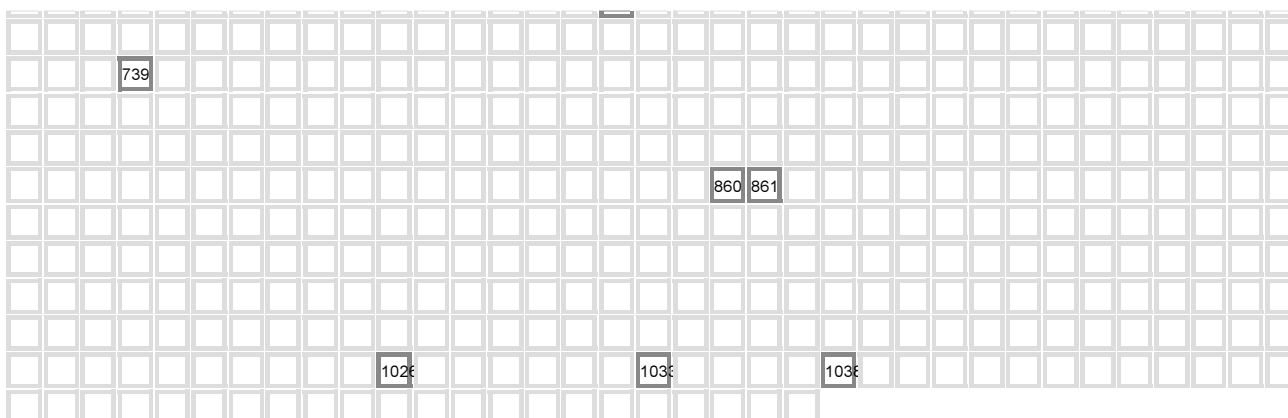
Synonyms: ENSG00000096384; ENSP00000325875; ENSP00000360609; ENSP00000360611; ENSP00000360617; ENSP00000360620; ENSP00000360709; ENSP00000397409; ENSP00000399096; ENSP00000400457; ENSP00000405093; 3326; HSP90AB1; NP_031381; NM_007355; D6S182; HSP90-BETA; HSP90B; HSPC2; HSPCB; HS90B_HUMAN; P08238;

More at [Entrez](#)

CREBBP CREB binding protein [Source:HGNC Symbol;Acc:2348]

Functions:



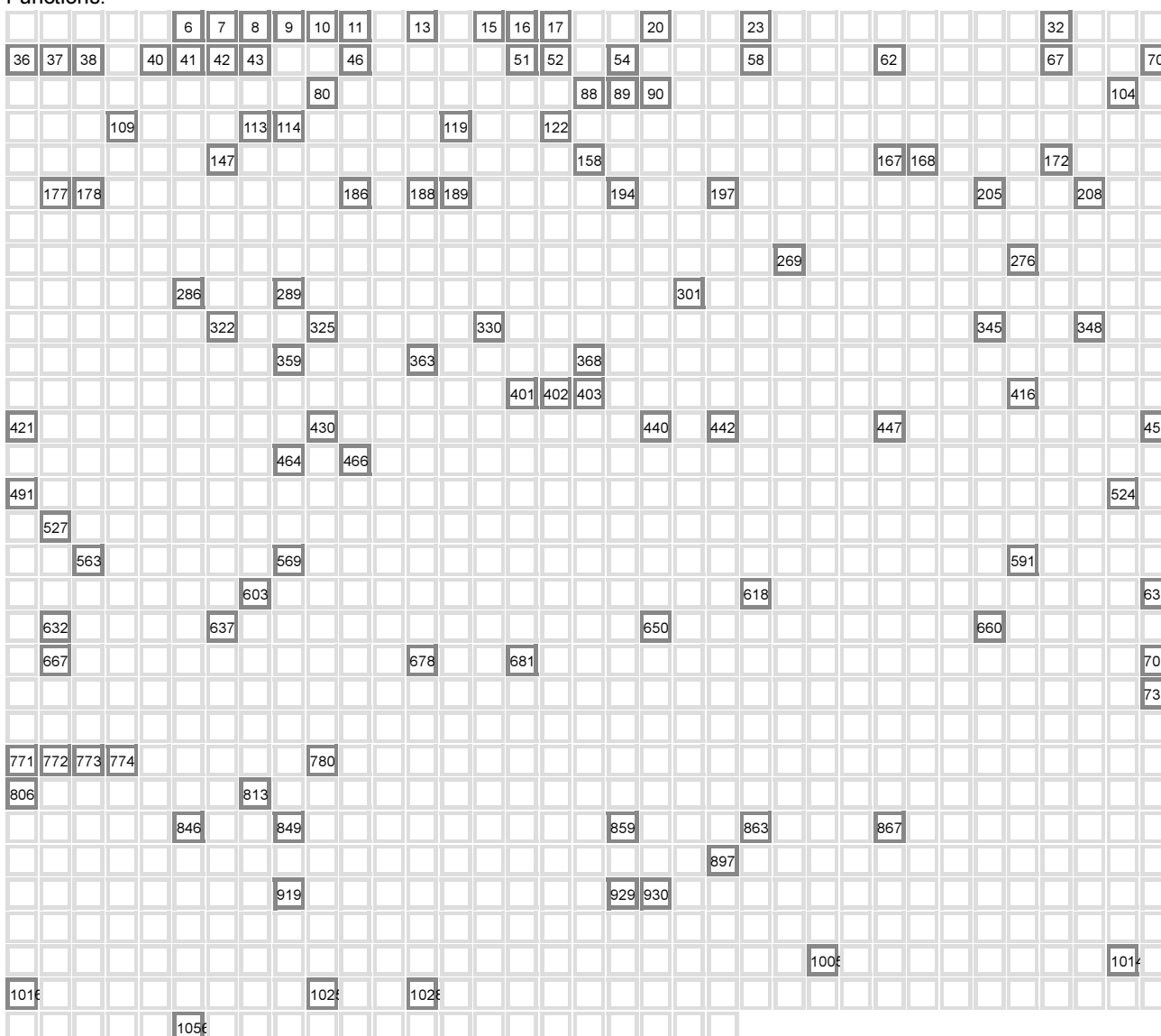


Synonyms: ENSG0000005339; ENSP00000262367; ENSP00000323550; ENSP00000371502; ENSP00000441978; 1387; CREBBP; NP_001073315; NP_004371; NM_001079846; NM_004380; KAT3A; RSTS; CBP_HUMAN; Q92793;

More at [Entrez](#)

SMAD7 SMAD family member 7 [Source:HGNC Symbol;Acc:6773]

Functions:



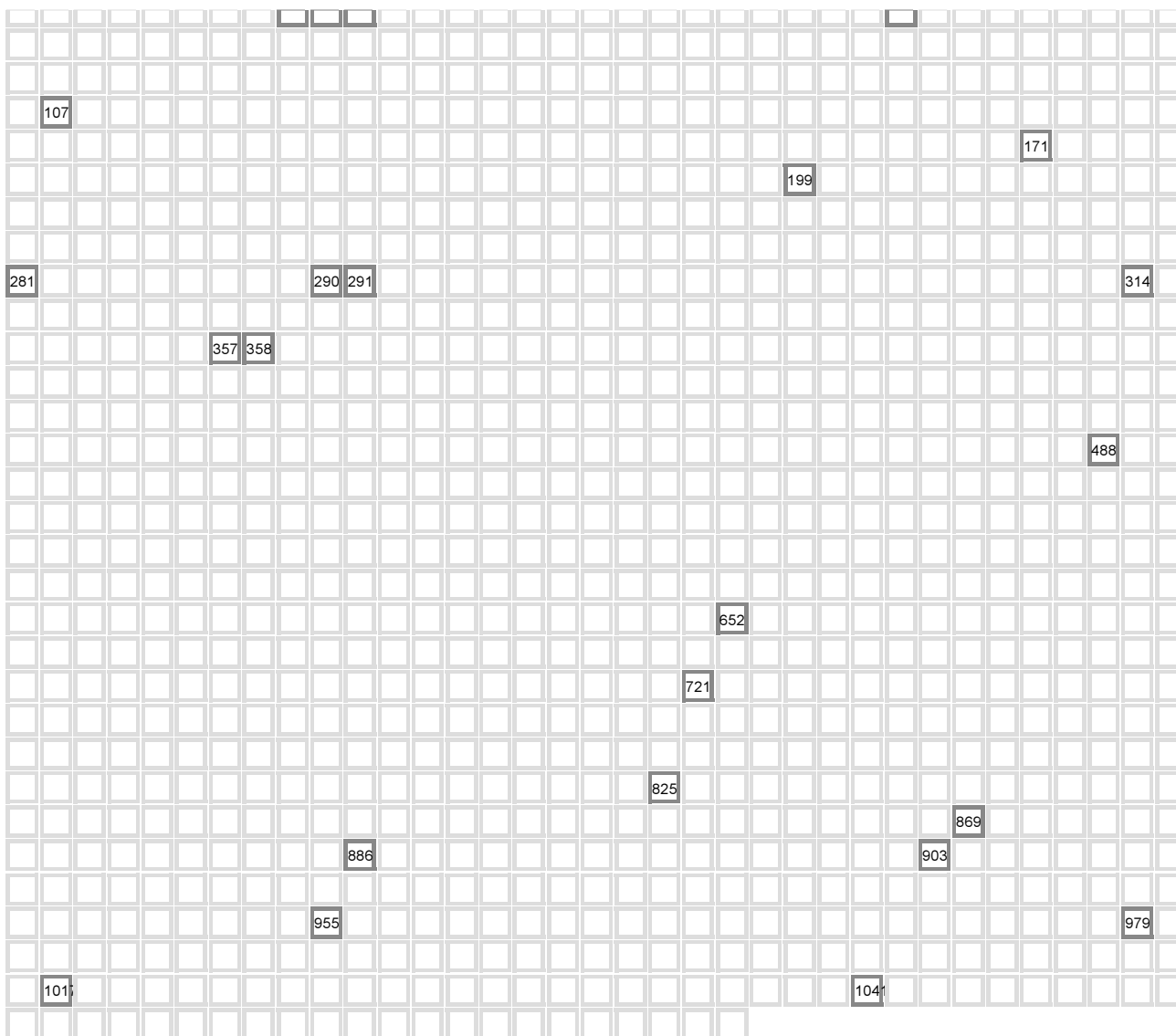
Synonyms: ENSG00000101665; ENSP00000262158; ENSP00000438103; 4092; SMAD7; NP_001177750; NP_001177751; NP_001177752; NP_005895; NM_001190821; NM_001190822; NM_001190823; NM_005904; CRCS3; MADH8; O15105; SMAD7_HUMAN;

More at [Entrez](#)

XRCC6 X-ray repair complementing defective repair in Chinese hamster cells 6 [Source:HGNC Symbol;Acc:4055]

Functions:



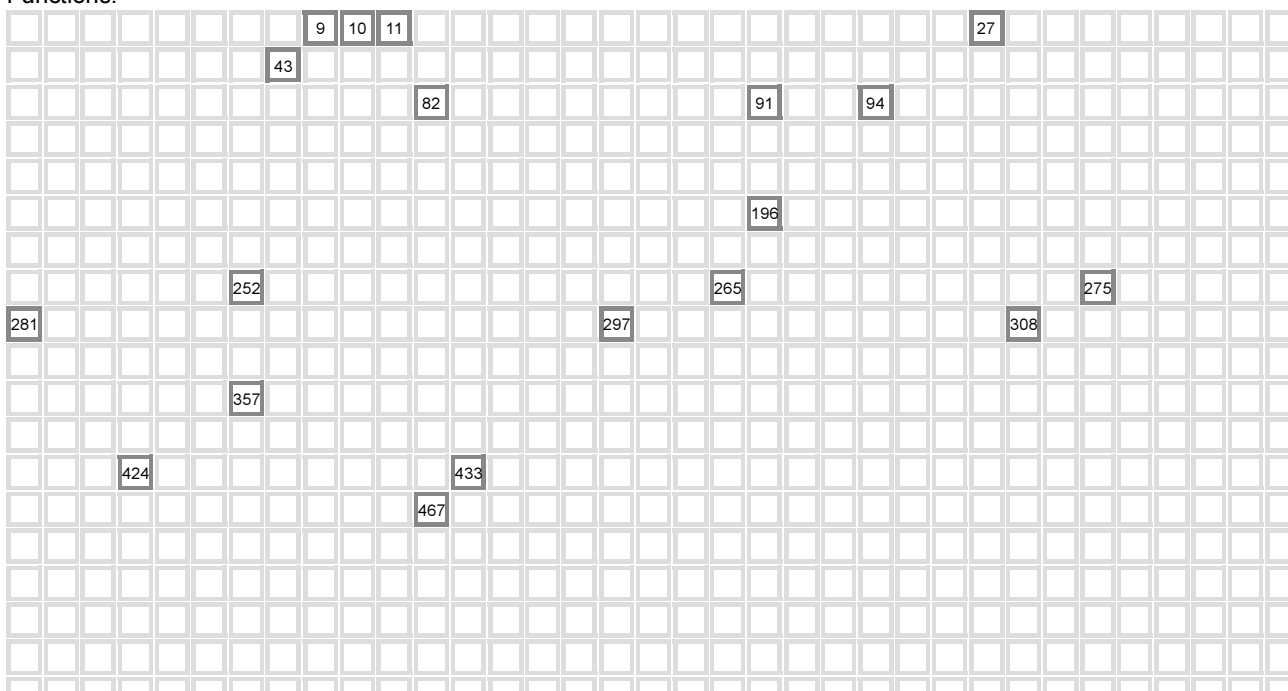


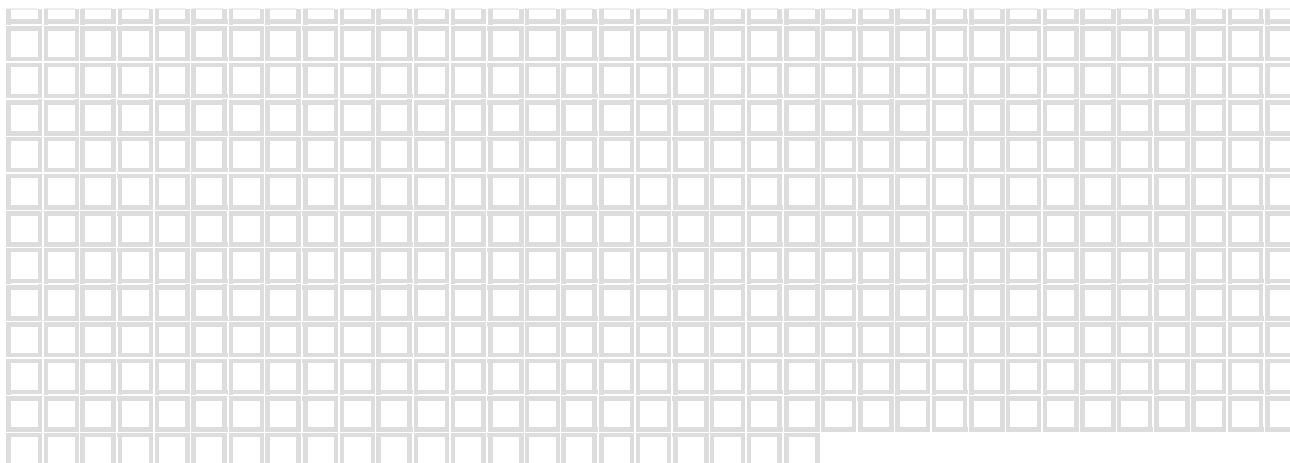
Synonyms: ENSG00000196419; ENSP00000352257; ENSP00000353192; ENSP00000384082; ENSP00000384104; ENSP00000384257; ENSP00000384941; ENSP00000403679; 2547; XRCC6; NP_001460; NM_001469; CTC75; CTCBF; D22S671; D22S731; G22P1; KU70; ML8; TLAA; P12956; XRCC6_HUMAN;

More at [Entrez](#)

RUNX3 runt-related transcription factor 3 [Source:HGNC Symbol;Acc:10473]

Functions:



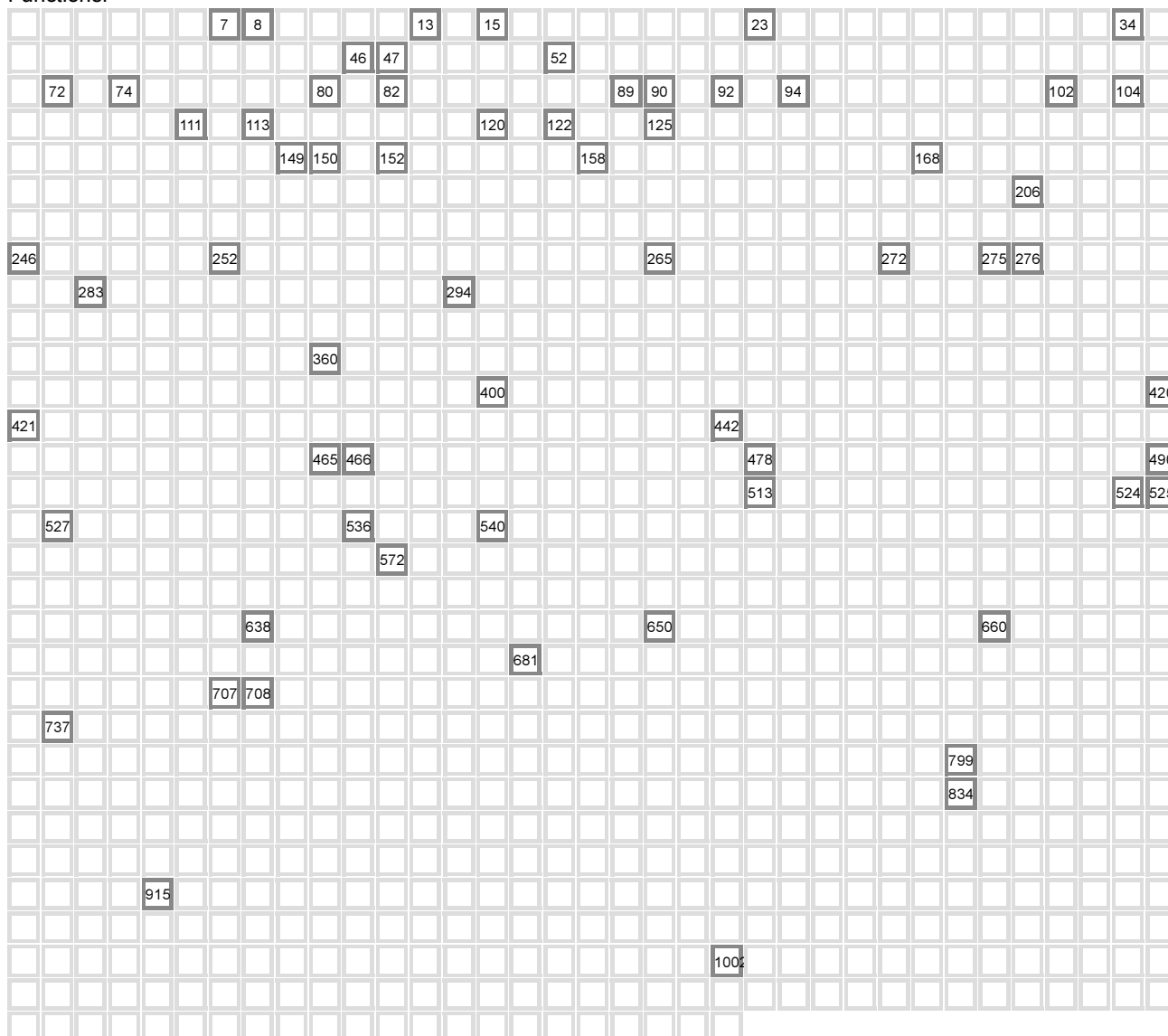


Synonyms: ENSG00000020633; ENSP000000308051; ENSP000000343477; ENSP000000382800; ENSP000000387686; ENSP000000444872; 864; RUNX3; NP_001026850; NP_004341; NM_001031680; NM_004350; AML2; CBFA3; PEBP2A3; PEBP2aC; Q13761; RUNX3_HUMAN;

More at [Entrez](#)

ACVRL1 activin A receptor type II-like 1 [Source:HGNC Symbol;Acc:175]

Functions:

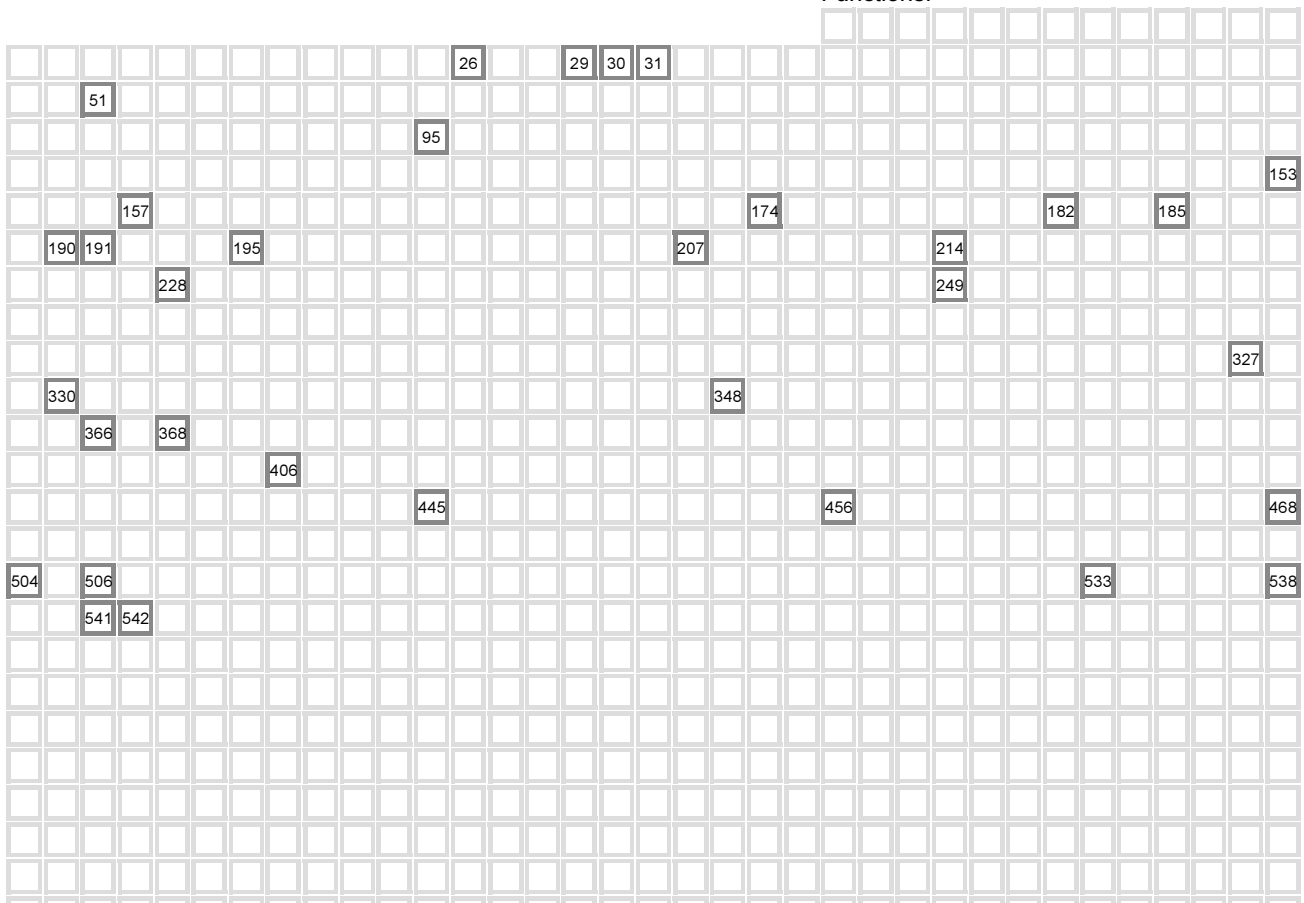


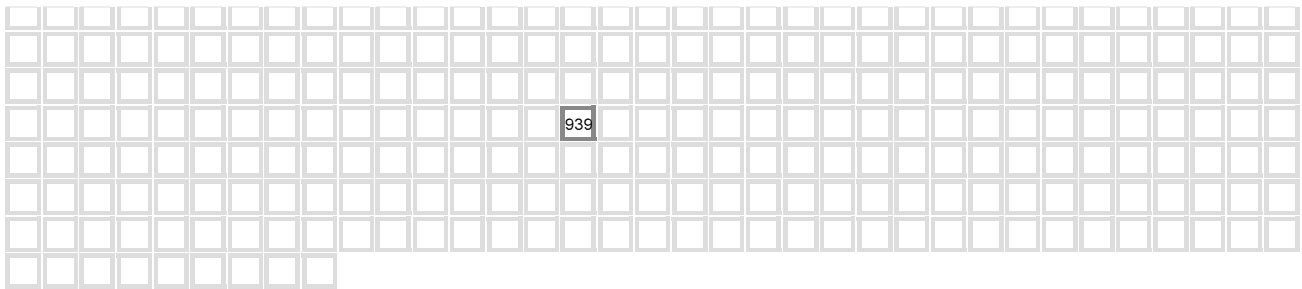
Synonyms: ENSG000000139567; ENSP000000267008; ENSP000000373574; ENSP000000392492; ENSP000000446724; ENSP000000447884; ENSP000000449992; 94; ACVRL1; NP_000011; NP_001070869; NM_000020; NM_001077401; ACVRLK1; ALK-1; HHT; HHT2; ORW2; SKR3; TSR-I; ACVL1_HUMAN; P37023;

More at [Entrez](#)

OSM oncostatin M [Source:HGNC Symbol;Acc:8506]

Functions:



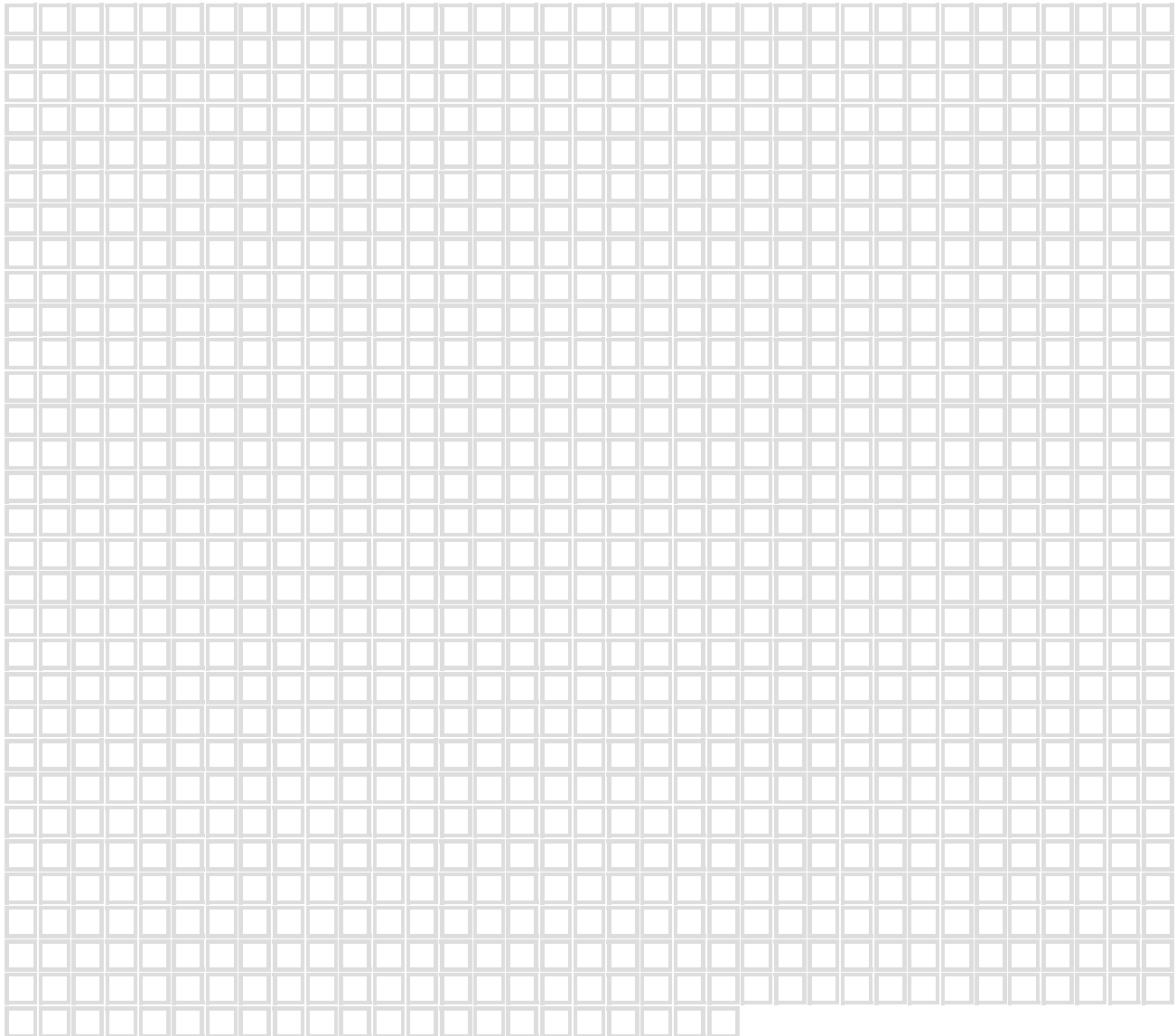


Synonyms: ENSG00000099985; ENSP00000215781; ENSP00000383893; ENSP00000384543; 5008; OSM; NP_065391; NM_020530; MGC20461; ONCM_HUMAN; P13725;

More at [Entrez](#)

CBFβ core-binding factor, beta subunit [Source:HGNC Symbol;Acc:1539]

Functions:

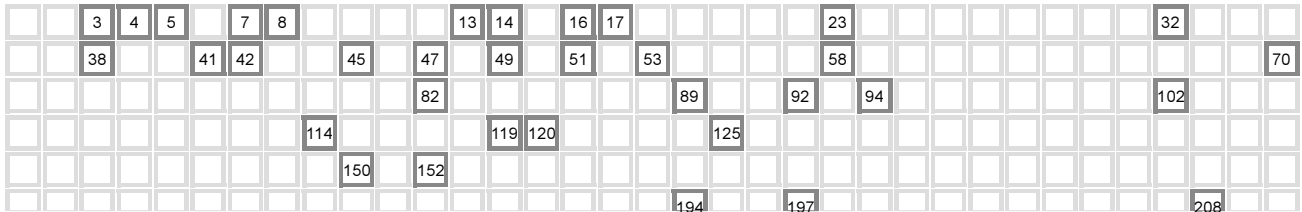


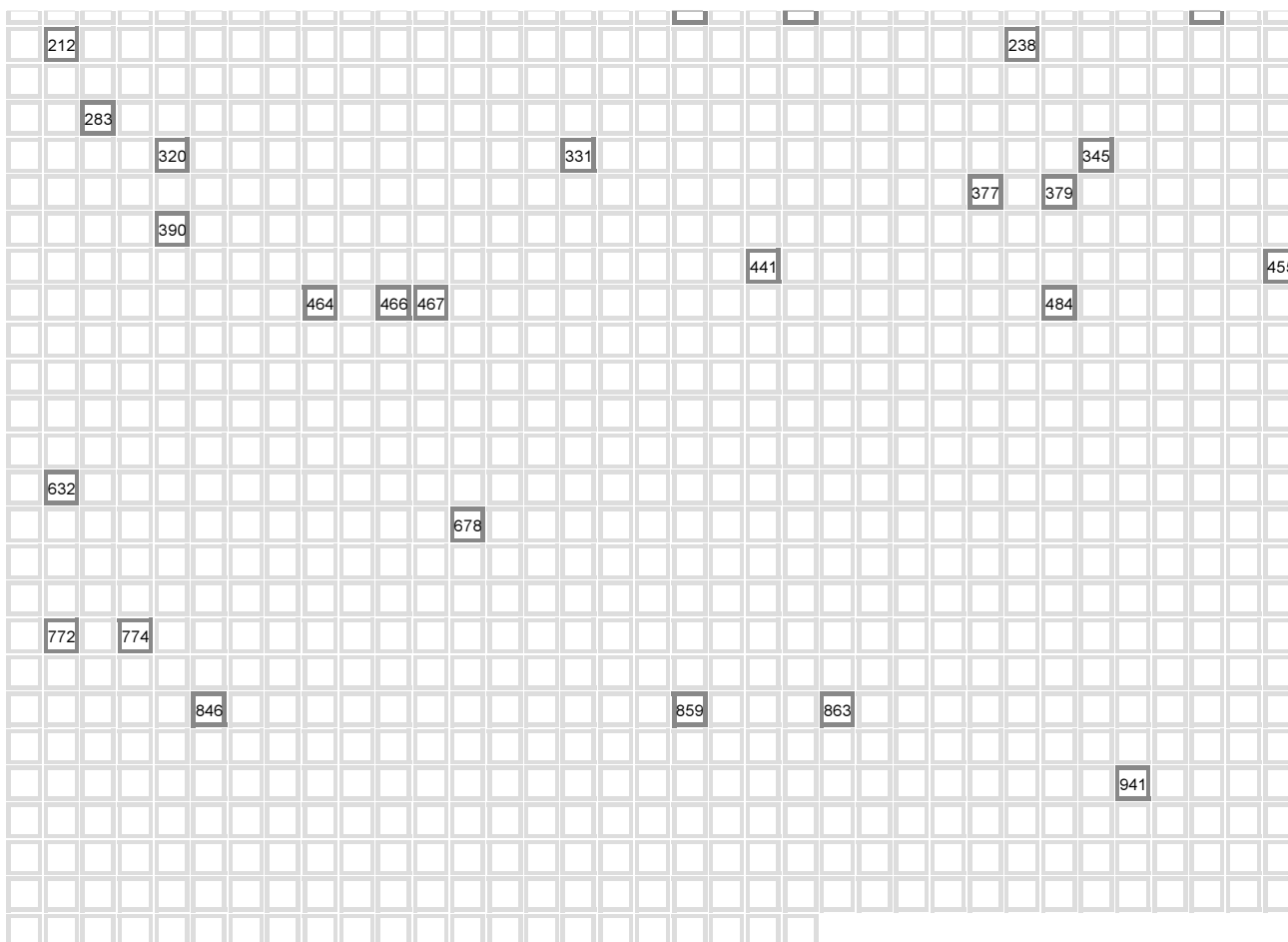
Synonyms: ENSG00000067955; ENSP00000290858; ENSP00000415151; 865; CBFβ; NP_001746; NP_074036; NM_001755; NM_022845; PEBP2B; PEBB_HUMAN; Q13951;

More at [Entrez](#)

TGFβR3 transforming growth factor, beta receptor III [Source:HGNC Symbol;Acc:11774]

Functions:



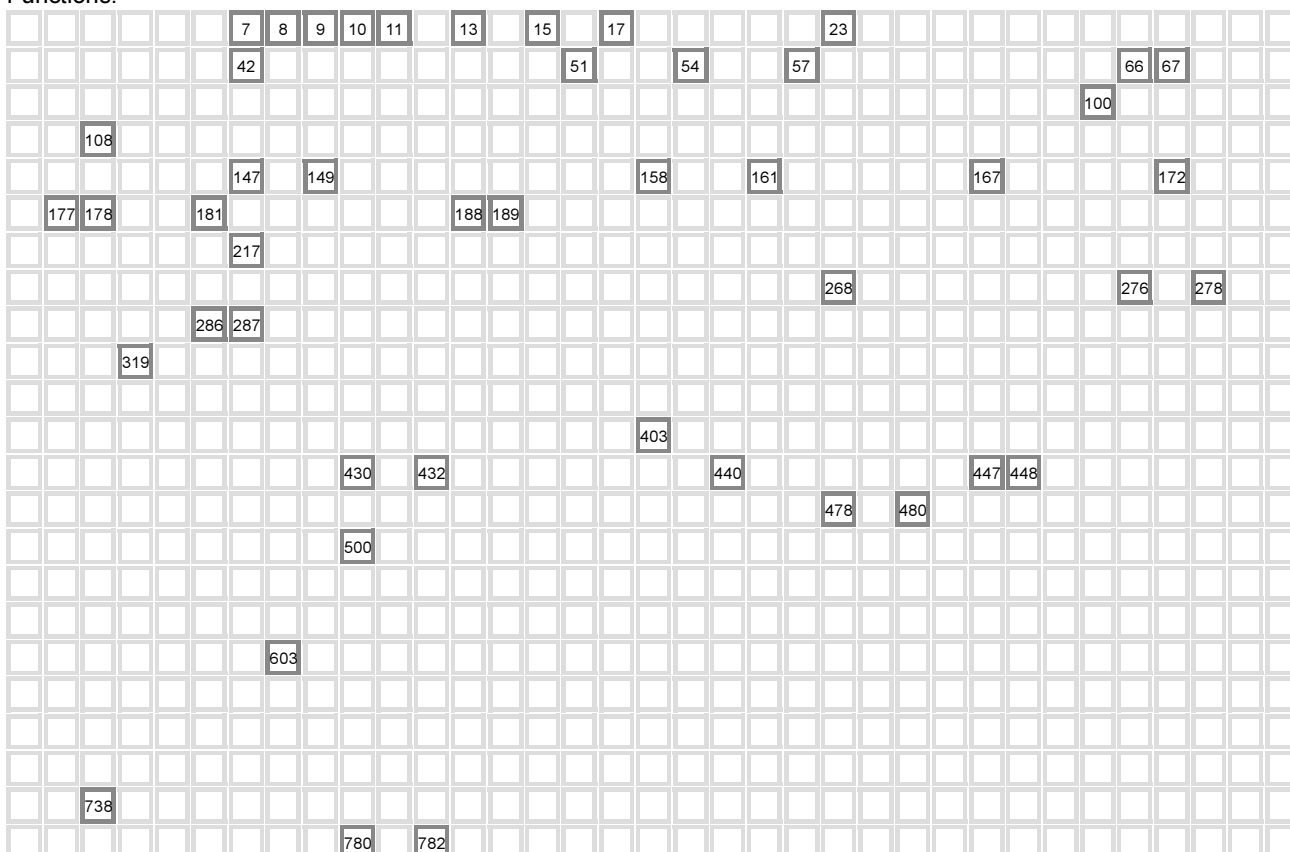


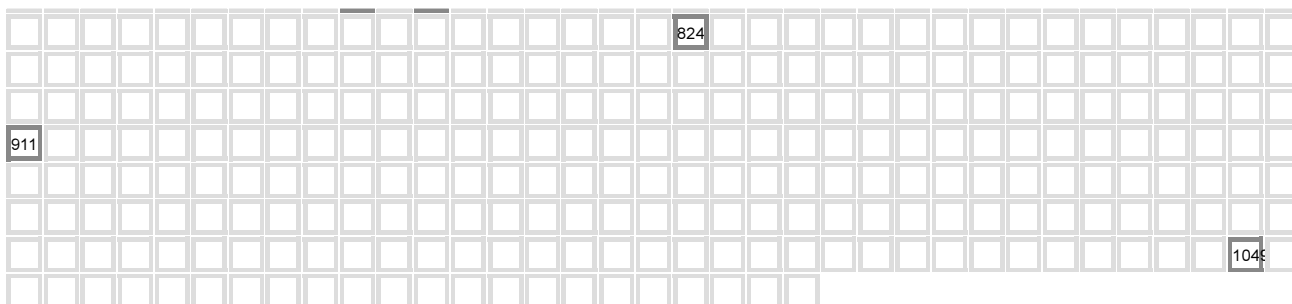
Synonyms: ENSG00000069702; ENSP00000212355; ENSP00000359426; ENSP00000395975; ENSP00000432638; ENSP00000433477; ENSP00000434994; ENSP00000436127; 7049; TGFB3; NP_001182612; NP_001182613; NP_003234; NM_001195683; NM_001195684; NM_003243; NR_036634; betaglycan; BGCAN; Q03167; TGBR3_HUMAN;

More at [Entrez](#)

SMAD6 SMAD family member 6 [Source:HGNC Symbol;Acc:6772]

Functions:



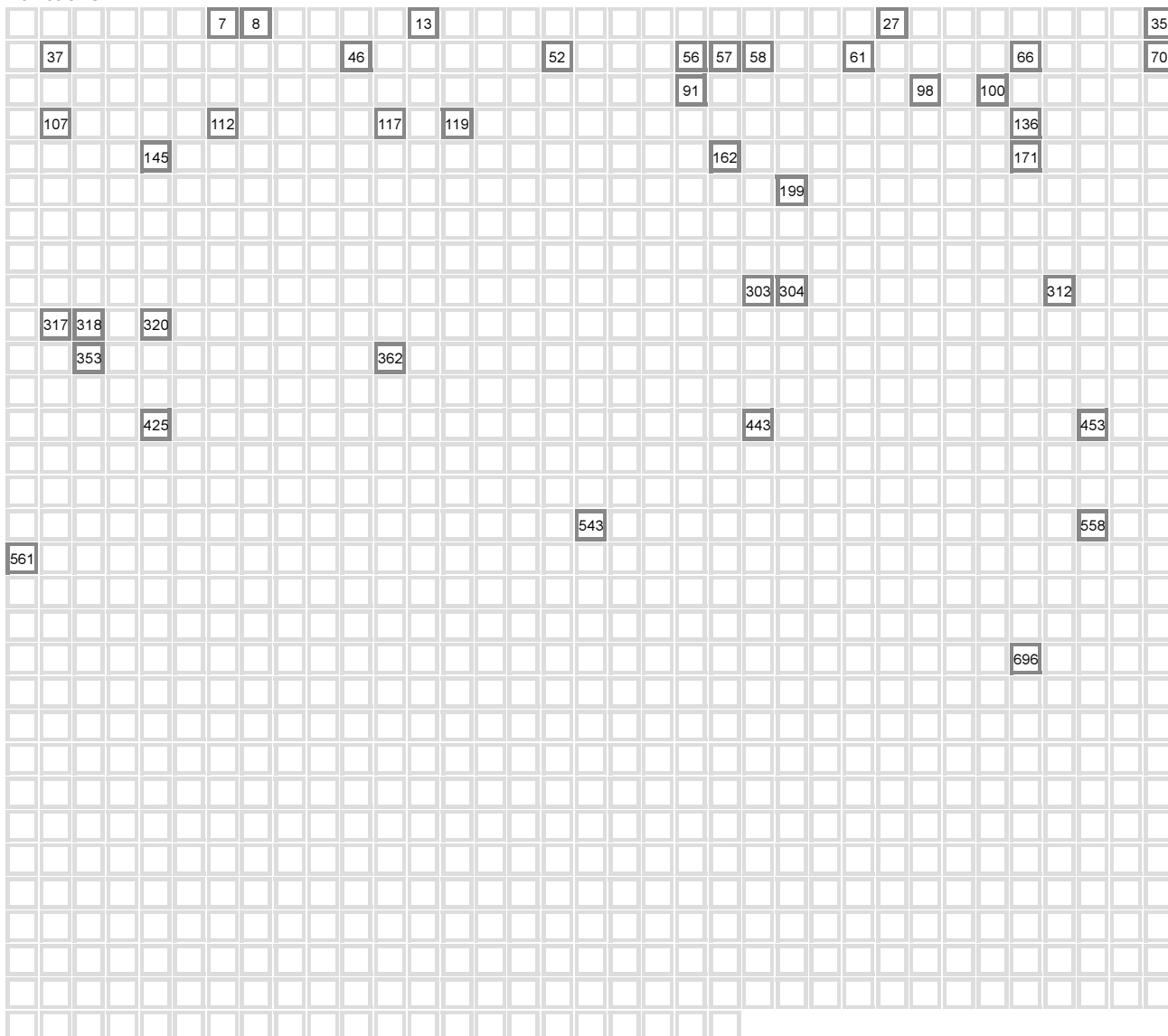


Synonyms: ENSG00000137834; ENSP00000288840; ENSP00000345054; ENSP00000396961; ENSP00000452694; ENSP00000452955; ENSP00000453446; 4091; SMAD6; NP_001136333; NP_005576; NM_001142861; NM_005585; NR_027654; HsT17432; O43541; SMAD6_HUMAN;

More at [Entrez](#)

FOXH1 forkhead box H1 [Source:HGNC Symbol;Acc:3814]

Functions:

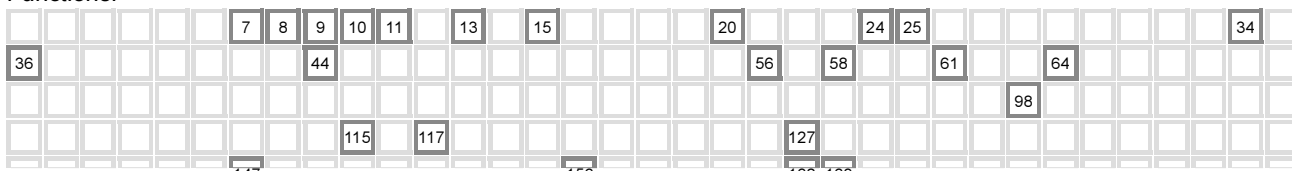


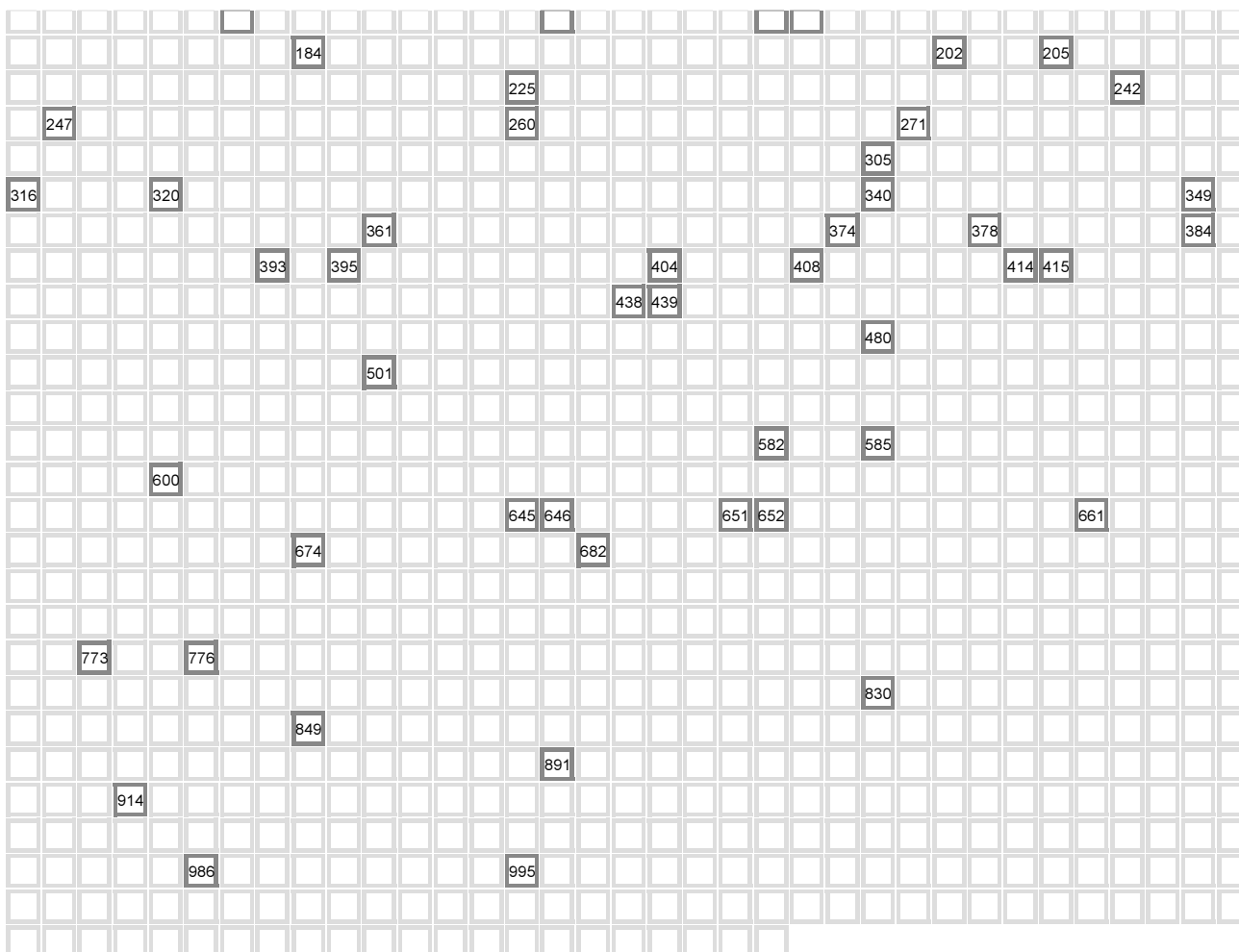
Synonyms: ENSG00000160973; ENSP00000292541; ENSP00000366534; 8928; FOXH1; NP_003914; NM_003923; FAST-1; FAST1; FOXH1_HUMAN; O75593;

More at [Entrez](#)

CITED1 Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1 [Source:HGNC Symbol;Acc:1986]

Functions:



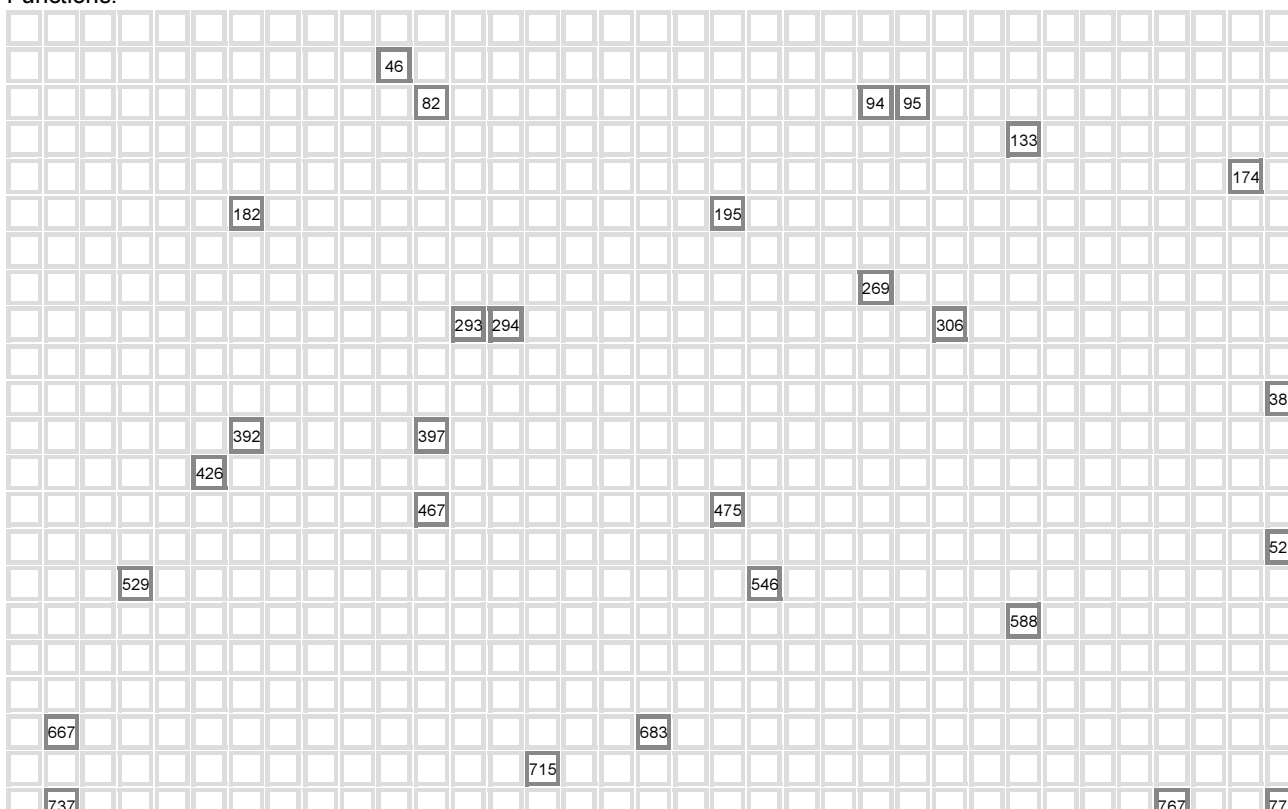


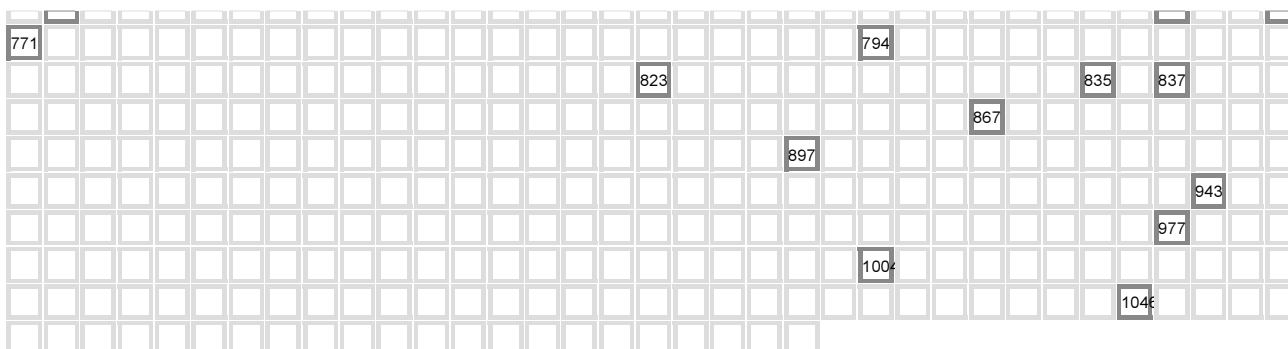
Synonyms: ENSG00000125931; ENSP00000246139; ENSP00000362721; ENSP00000388548; ENSP00000391407; ENSP00000401764; ENSP00000403274; ENSP00000405765; ENSP00000407496; ENSP00000412769; ENSP00000414781; 4435; CITED1; NP_001138357; NP_001138358; NP_001138359; NP_004134; NM_001144885; NM_001144886; NM_001144887; NM_004143; MSG1; CITE1_HUMAN; Q99966;

More at [Entrez](#)

FBXW7 F-box and WD repeat domain containing 7 [Source:HGNC Symbol;Acc:16712]

Functions:



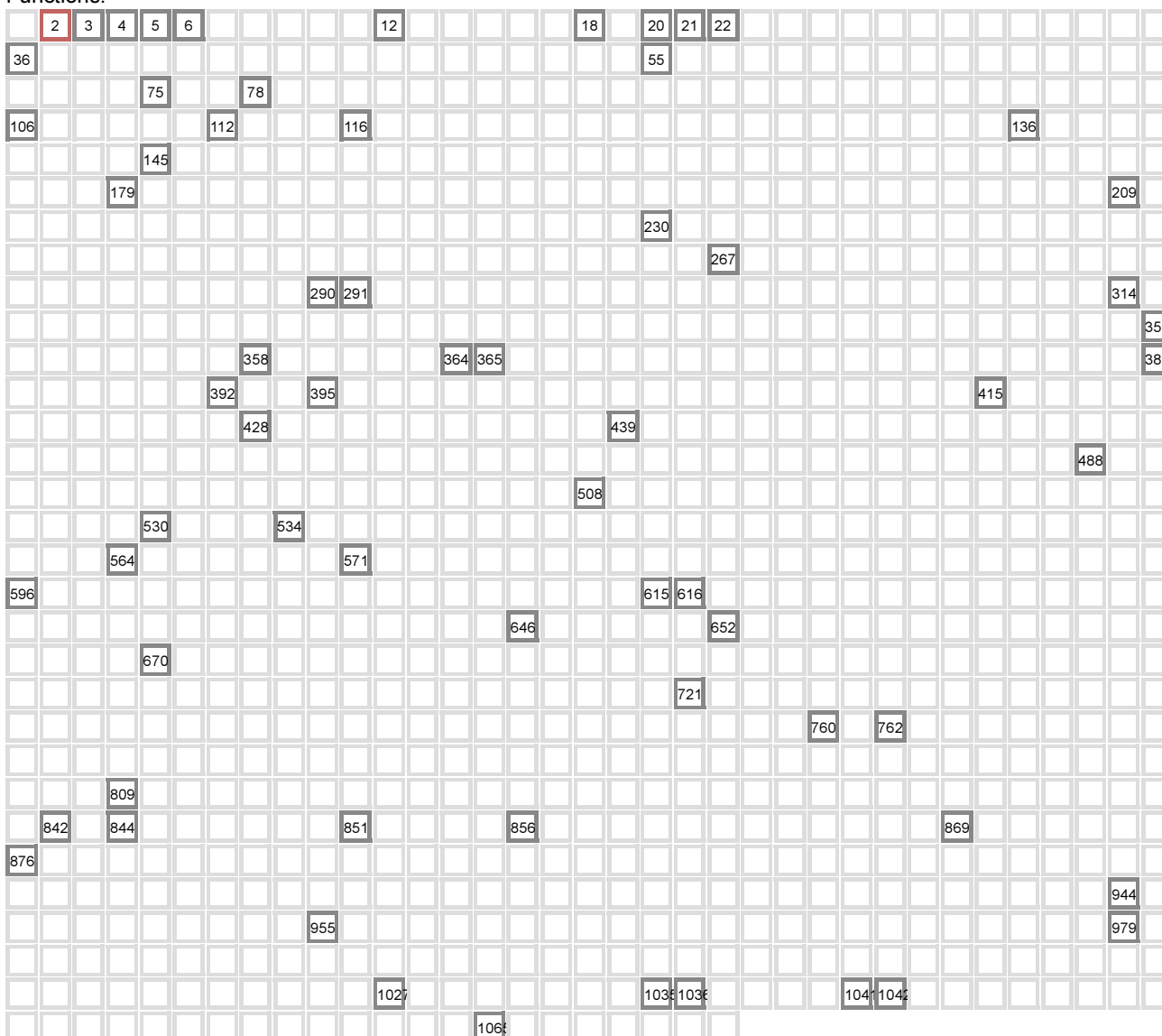


Synonyms: ENSG00000109670; ENSP00000263981; ENSP00000281708; ENSP00000296555; ENSP00000377528; 55294; FBXW7; NP_001013433; NP_060785; NP_361014; NM_001013415; NM_018315; NM_033632; AGO; CDC4; FBW7; FLJ11071; SEL-10; SEL10; FBXW7_HUMAN; Q969H0;

More at [Entrez](#)

LIG4 ligase IV, DNA, ATP-dependent [Source:HGNC Symbol;Acc:6601]

Functions:

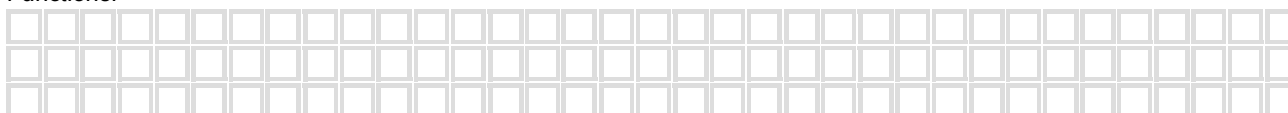


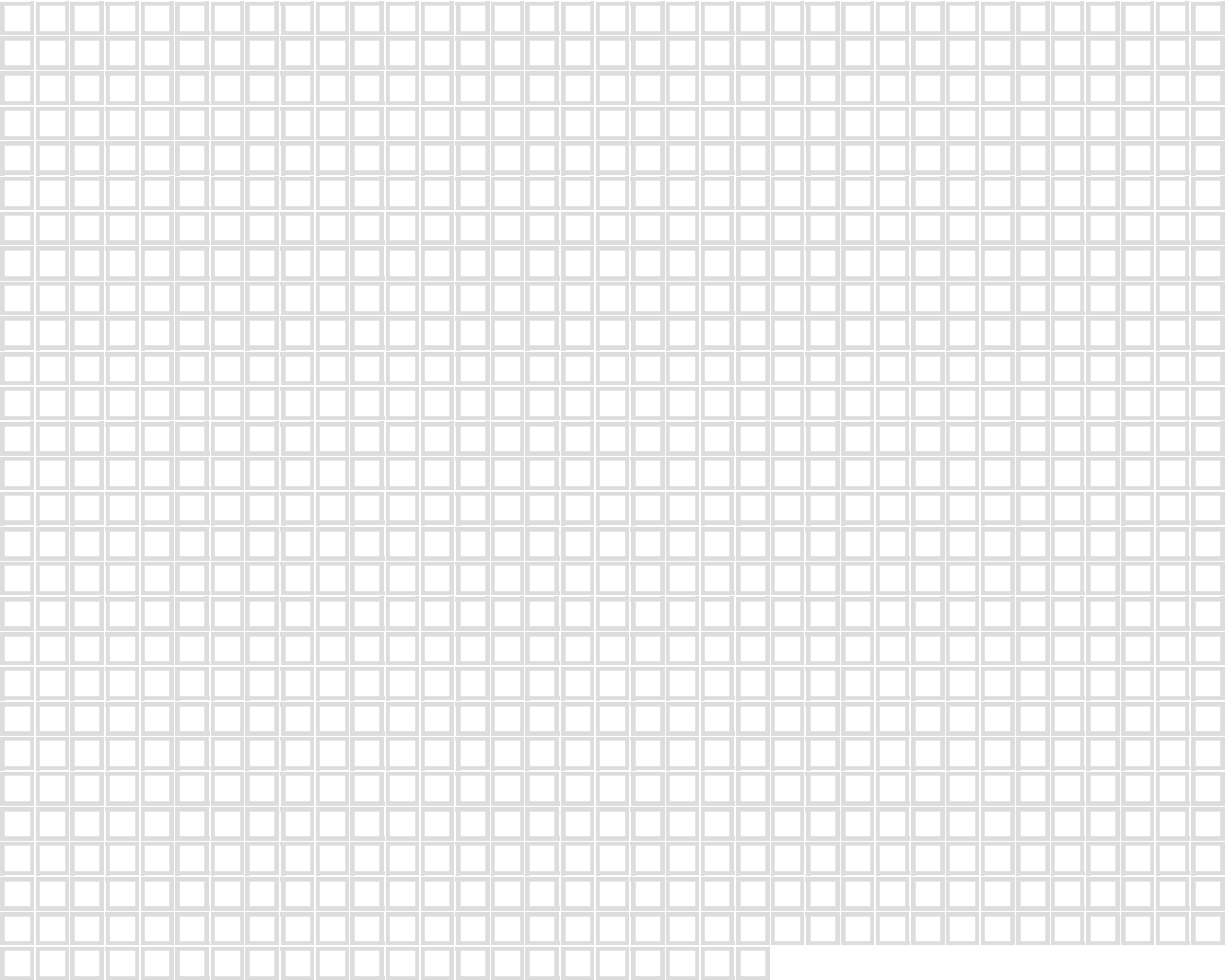
Synonyms: ENSG00000174405; ENSP00000349393; ENSP00000385955; ENSP00000402030; 3981; LIG4; NP_001091738; NP_002303; NP_996820; NM_001098268; NM_002312; NM_206937; DNLI4_HUMAN; P49917;

More at [Entrez](#)

CLUL1 clusterin-like 1 (retinal) [Source:HGNC Symbol;Acc:2096]

Functions:



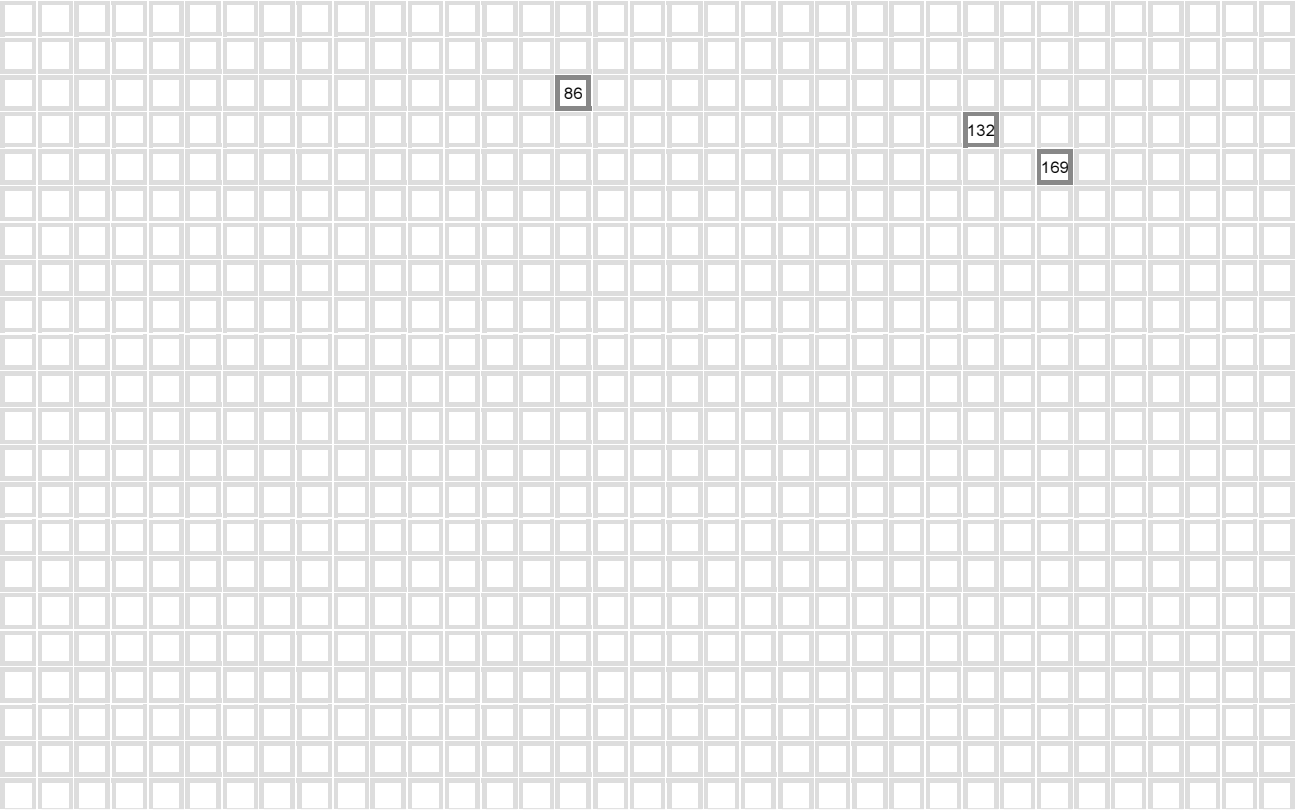


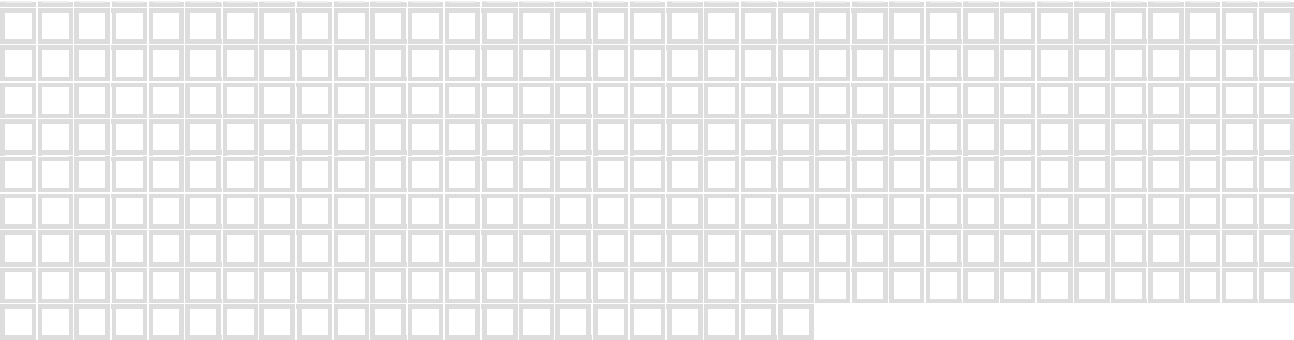
Synonyms: ENSG00000079101; ENSP00000341128; ENSP00000383449; ENSP00000441726; 27098; CLUL1; NP_055225; NP_954636; NM_014410; NM_199167; RA337M; CLUL1_HUMAN; Q15846;

More at [Entrez](#)

IAPP islet amyloid polypeptide [Source:HGNC Symbol;Acc:5329]

Functions:



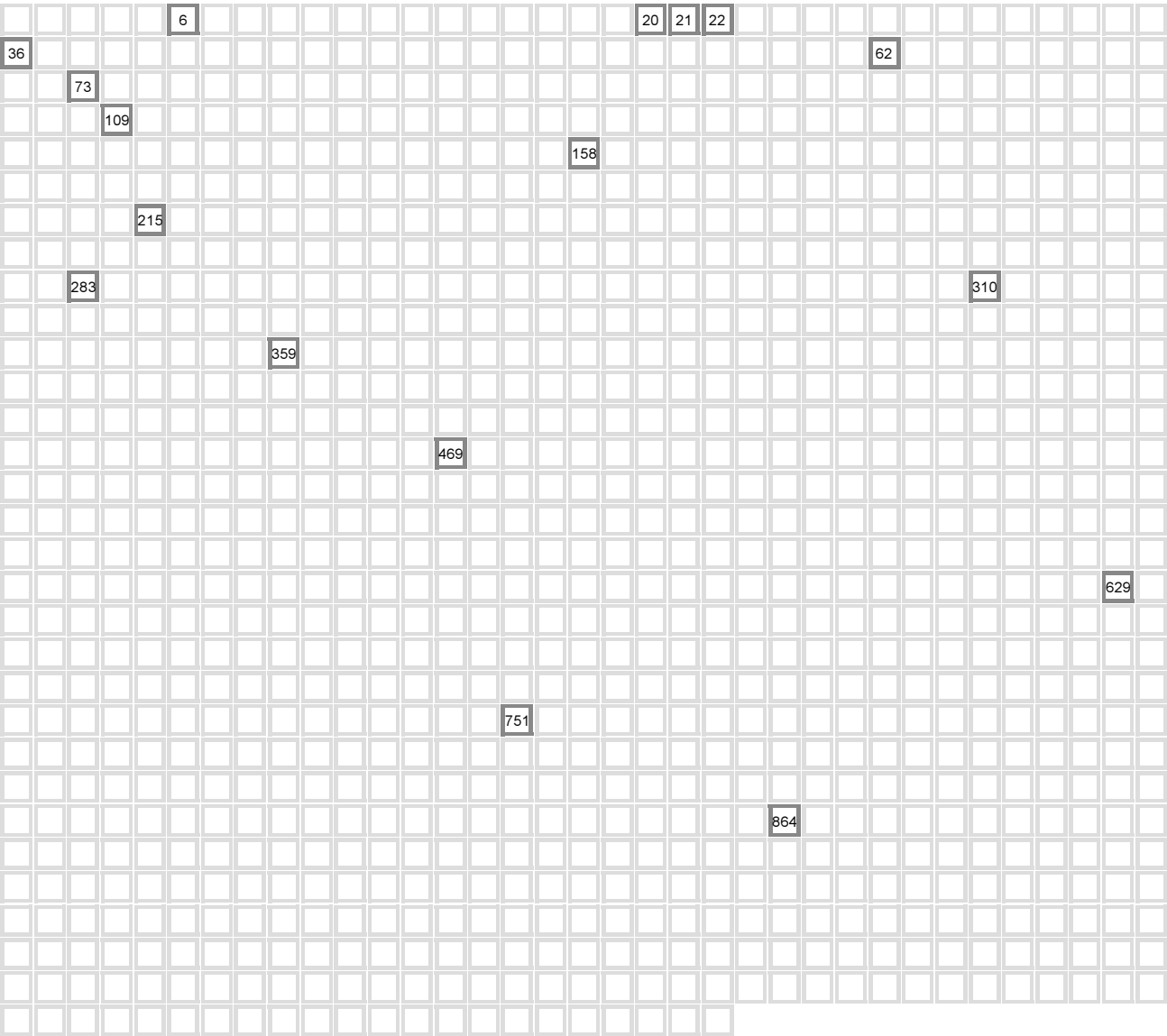


Synonyms: ENSG00000121351; ENSP00000240652; ENSP00000437357; ENSP00000437559; ENSP00000445711; ENSP00000445980; 3375; IAPP; NP_000406; NM_000415; AMYLIN; IAPP_HUMAN; P10997;

More at [Entrez](#)

RTN4R reticulon 4 receptor [Source:HGNC Symbol;Acc:18601]

Functions:

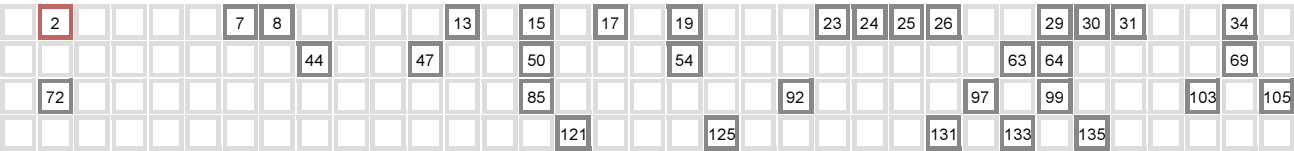


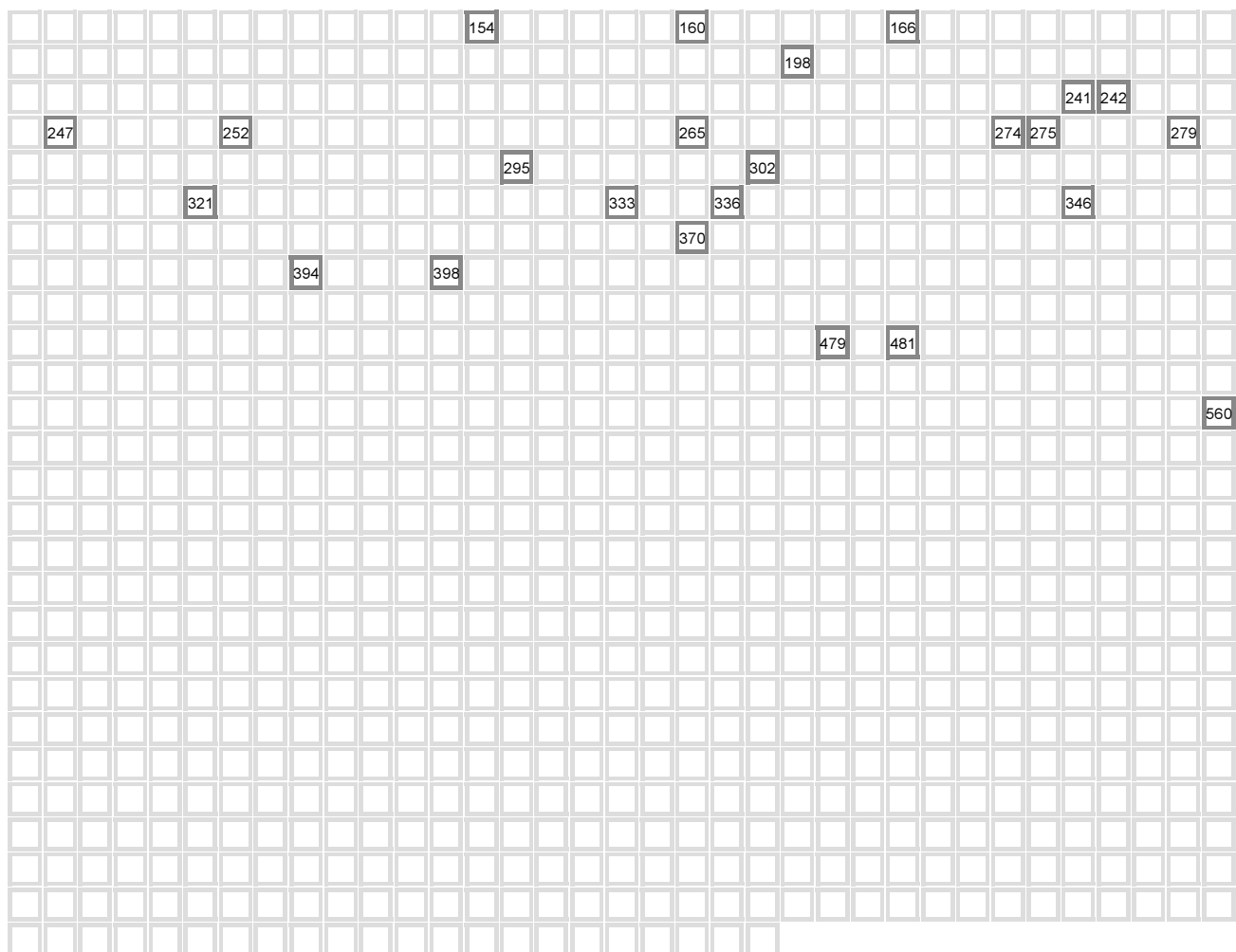
Synonyms: ENSG00000040608; ENSP00000043402; ENSP00000396872; ENSP00000403535; 65078; RTN4R; NP_075380; NM_023004; NGR; NOGOR; Q9BZR6; RTN4R_HUMAN;

More at [Entrez](#)

BMPR1A bone morphogenetic protein receptor, type IA [Source:HGNC Symbol;Acc:1076]

Functions:



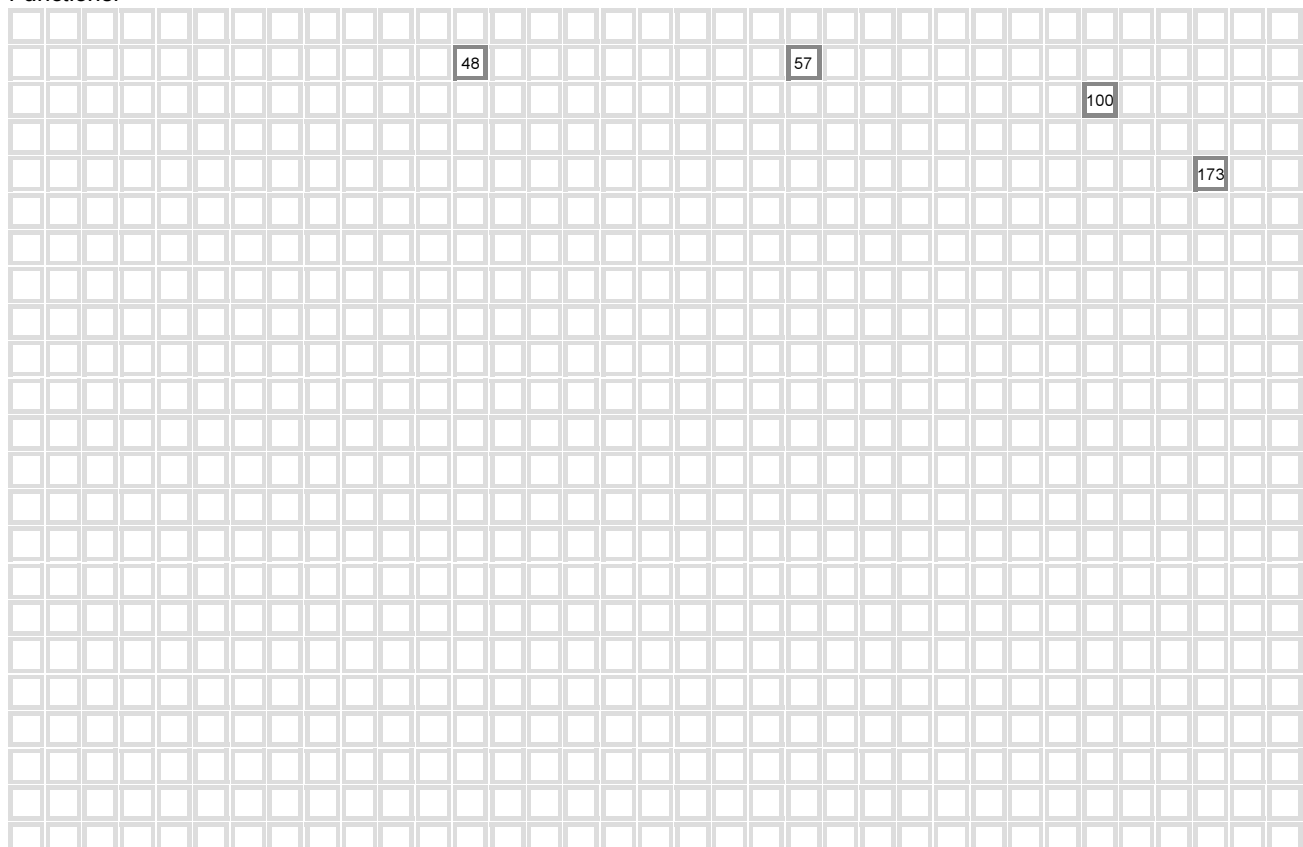


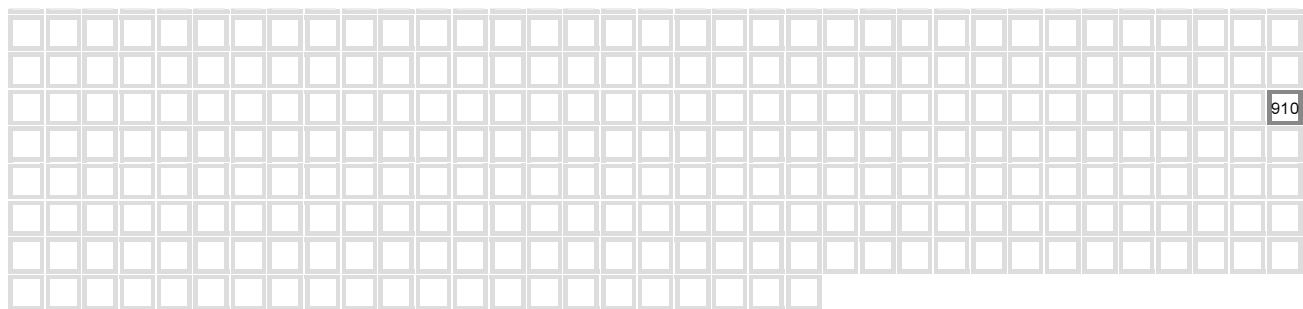
Synonyms: ENSG00000107779; ENSP00000224764; ENSP00000361107; 657; BMPR1A; NP_004320; NM_004329; ACVRLK3; ALK3; CD292; SKR5; BMR1A_HUMAN; P36894;

More at [Entrez](#)

NTF4 neurotrophin 4 [Source:HGNC Symbol;Acc:8024]

Functions:





Synonyms: ENSG00000167744; ENSP00000301411; 4909; NTF4; NP_006170; NM_006179; GLC10; GLC10; NT-4; NT-4/5; NT-5; NT4; NTF5; NTF4_HUMAN; P34130;

More at [Entrez](#)

Functions

Function	FDR	Coverage
1 query genes	n/a	115 / 115
2 positive regulation of cell differentiation	5.71E-73	60 / 262
3 hemopoiesis	3.33E-32	36 / 271
4 immune system development	3.33E-32	37 / 299
5 hemopoietic or lymphoid organ development	1.01E-31	36 / 284
6 regulation of cell development	1.92E-28	32 / 242
7 transmembrane receptor protein serine/threonine kinase signaling pathway	1.42E-27	27 / 147
8 SMAD binding	1.59E-26	19 / 45
9 regulatory region nucleic acid binding	3.66E-26	30 / 236
10 regulatory region DNA binding	3.66E-26	30 / 236
11 transcription regulatory region DNA binding	7.57E-25	29 / 235
12 positive regulation of cell development	1.33E-21	19 / 76
13 transforming growth factor beta receptor signaling pathway	2.66E-20	19 / 88
14 myeloid cell differentiation	3.44E-20	21 / 126
15 regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	2.57E-19	19 / 99
16 mesenchyme development	9.25E-18	18 / 99
17 pathway-restricted SMAD protein phosphorylation	2.4E-17	12 / 24
18 leukocyte differentiation	3.74E-17	21 / 176
19 positive regulation of multicellular organismal process	4.73E-17	24 / 266
20 negative regulation of cell differentiation	8.74E-17	22 / 212
21 regulation of nervous system development	3.45E-16	21 / 197
22 regulation of neurogenesis	7.6E-16	20 / 177
23 BMP signaling pathway	8.89E-16	15 / 70
24 ossification	8.89E-16	18 / 129
25 osteoblast differentiation	1.31E-15	15 / 72
26 positive regulation of phosphorylation	1.55E-15	20 / 185
27 sequence-specific DNA binding	2.01E-15	21 / 217
28 positive regulation of myeloid cell differentiation	2.72E-15	12 / 34
29 positive regulation of phosphorus metabolic process	2.81E-15	20 / 192
30 positive regulation of phosphate metabolic process	2.81E-15	20 / 192
31 positive regulation of protein phosphorylation	5.16E-15	19 / 170
32 mesenchymal cell development	5.39E-15	15 / 80
33 positive regulation of cellular component organization	5.39E-15	23 / 297
34 positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	6.22E-15	13 / 49
35 embryonic morphogenesis	8.82E-15	19 / 176
36 negative regulation of developmental process	1.23E-14	22 / 274
37 regulation of sequence-specific DNA binding transcription factor activity	1.39E-14	22 / 276
38 mesenchymal cell differentiation	1.77E-14	15 / 87
39 regulation of myeloid cell differentiation	2.76E-14	14 / 71
40 regulation of homeostatic process	3.9E-14	17 / 137
41 epithelial to mesenchymal transition	5.85E-14	13 / 58
42 transforming growth factor beta receptor binding	6.69E-14	9 / 15
43 negative regulation of transcription from RNA polymerase II promoter	8.82E-14	21 / 267
44 regulation of ossification	9.95E-14	14 / 78
45 erythrocyte differentiation	1.96E-13	11 / 35
46 vasculature development	2.32E-13	21 / 281
47 transmembrane receptor protein serine/threonine kinase activity	2.86E-13	9 / 17

Function	FDR	Coverage
48 cell fate commitment	4.56E-13	14 / 87
49 erythrocyte homeostasis	5.09E-13	11 / 38
50 positive regulation of ossification	5.75E-13	10 / 27
51 cytokine receptor binding	6.12E-13	16 / 136
52 blood vessel development	7.67E-13	20 / 263
53 homeostasis of number of cells	7.84E-13	12 / 54
54 regulation of pathway-restricted SMAD protein phosphorylation	2.93E-12	9 / 21
55 lymphocyte activation	2.95E-12	20 / 283
56 epithelium development	3.05E-12	19 / 247
57 pattern specification process	3.1E-12	17 / 181
58 tissue morphogenesis	3.23E-12	17 / 182
59 regulation of leukocyte activation	3.23E-12	18 / 214
60 skeletal system development	3.23E-12	17 / 182
61 tube development	4.16E-12	16 / 155
62 regulation of cell morphogenesis involved in differentiation	4.68E-12	14 / 104
63 positive regulation of bone mineralization	6.86E-12	9 / 23
64 regulation of osteoblast differentiation	6.86E-12	11 / 48
65 regulation of lymphocyte activation	7.93E-12	17 / 193
66 R-SMAD binding	8.23E-12	8 / 15
67 receptor signaling protein activity	1E-11	12 / 67
68 regulation of cell activation	1.07E-11	18 / 231
69 positive regulation of biomineral tissue development	1.55E-11	9 / 25
70 heart development	2.06E-11	16 / 173
71 positive regulation of erythrocyte differentiation	2.18E-11	7 / 10
72 activin-activated receptor activity	2.18E-11	7 / 10
73 regulation of neuron differentiation	2.6E-11	15 / 146
74 regulation of growth	2.71E-11	18 / 245
75 T cell activation	3.24E-11	17 / 212
76 positive regulation of lymphocyte activation	4.13E-11	15 / 151
77 response to hypoxia	4.26E-11	12 / 76
78 T cell differentiation	5.75E-11	12 / 78
79 response to oxygen levels	5.75E-11	12 / 78
80 regulation of cell adhesion	7.67E-11	15 / 158
81 regulation of erythrocyte differentiation	7.68E-11	8 / 19
82 epithelial cell proliferation	9.26E-11	14 / 131
83 positive regulation of leukocyte activation	1.07E-10	15 / 162
84 gland development	1.17E-10	12 / 83
85 SMAD protein import into nucleus	1.2E-10	7 / 12
86 endocrine system development	1.27E-10	11 / 63
87 positive regulation of cell activation	1.59E-10	15 / 167
88 regulation of epithelial to mesenchymal transition	1.6E-10	9 / 32
89 regulation of cellular component movement	1.63E-10	18 / 275
90 blood vessel morphogenesis	1.91E-10	17 / 239
91 sequence-specific DNA binding RNA polymerase II transcription factor activity	1.98E-10	15 / 170
92 transmembrane receptor protein kinase activity	2.42E-10	11 / 67
93 positive regulation of cell morphogenesis involved in differentiation	2.77E-10	8 / 22
94 regulation of epithelial cell proliferation	3.9E-10	13 / 118
95 MAPK cascade	4.45E-10	18 / 293
96 myeloid leukocyte differentiation	7.22E-10	11 / 74
97 regulation of bone mineralization	1.05E-9	9 / 39

Function	FDR	Coverage
98 morphogenesis of an epithelium	1.07E-9	13 / 128
99 positive regulation of osteoblast differentiation	1.23E-9	8 / 26
100 regionalization	1.23E-9	12 / 102
101 embryonic organ development	1.36E-9	12 / 103
102 cell growth	1.94E-9	16 / 238
103 positive regulation of pathway-restricted SMAD protein phosphorylation	2.36E-9	7 / 17
104 regulation of cell migration	2.94E-9	16 / 245
105 regulation of biomineral tissue development	3.15E-9	9 / 44
106 lymphocyte differentiation	3.19E-9	12 / 111
107 transcription factor complex	3.25E-9	14 / 173
108 SMAD protein complex assembly	3.78E-9	6 / 10
109 regulation of cell morphogenesis	4.34E-9	14 / 177
110 positive regulation of epithelial to mesenchymal transition	5.66E-9	7 / 19
111 regulation of cell growth	6.68E-9	14 / 183
112 embryo development ending in birth or egg hatching	6.93E-9	12 / 119
113 regulation of cell motility	7.41E-9	16 / 262
114 muscle structure development	7.41E-9	15 / 222
115 SMAD protein signal transduction	7.77E-9	6 / 11
116 positive regulation of neurogenesis	8.02E-9	9 / 49
117 tube morphogenesis	8.09E-9	12 / 121
118 positive regulation of cellular component movement	9.43E-9	13 / 154
119 heart morphogenesis	1.08E-8	11 / 96
120 transforming growth factor beta binding	1.48E-8	6 / 12
121 bone mineralization	1.62E-8	9 / 53
122 regulation of locomotion	1.66E-8	16 / 278
123 regulation of T cell activation	1.71E-8	13 / 162
124 muscle cell differentiation	1.78E-8	12 / 130
125 protein serine/threonine kinase activity	2.1E-8	16 / 283
126 positive regulation of T cell activation	2.1E-8	12 / 132
127 epithelial cell differentiation	2.71E-8	12 / 135
128 activating transcription factor binding	2.8E-8	8 / 38
129 regulation of binding	2.95E-8	11 / 106
130 kinase binding	3.66E-8	15 / 251
131 biomineral tissue development	4.09E-8	9 / 59
132 pancreas development	5.21E-8	8 / 41
133 regulation of protein localization	5.72E-8	14 / 218
134 protein kinase binding	7.2E-8	14 / 222
135 regulation of transmembrane transport	7.44E-8	12 / 148
136 chordate embryonic development	8.19E-8	11 / 117
137 positive regulation of immune response	1.06E-7	15 / 272
138 cytokine production	1.16E-7	15 / 274
139 developmental growth	1.19E-7	10 / 92
140 activation of immune response	1.23E-7	14 / 232
141 regulation of T cell differentiation	1.55E-7	8 / 47
142 foam cell differentiation	1.64E-7	7 / 30
143 positive regulation of T cell differentiation	1.64E-7	7 / 30
144 macrophage derived foam cell differentiation	1.64E-7	7 / 30
145 central nervous system development	1.72E-7	15 / 283
146 cellular response to hormone stimulus	1.72E-7	15 / 283
147 regulation of transforming growth factor beta receptor signaling pathway	1.77E-7	8 / 48

Function	FDR	Coverage
148 leukocyte proliferation	1.89E-7	10 / 97
149 regulation of cellular component biogenesis	1.92E-7	13 / 200
150 growth factor binding	1.97E-7	9 / 71
151 immune response-activating signal transduction	2.02E-7	13 / 201
152 cytokine binding	2.04E-7	8 / 49
153 positive regulation of peptidyl-tyrosine phosphorylation	2.2E-7	9 / 72
154 protein import into nucleus	2.43E-7	11 / 131
155 positive regulation of lymphocyte differentiation	2.48E-7	7 / 32
156 morphogenesis of a branching structure	2.75E-7	9 / 74
157 regulation of secretion	2.75E-7	14 / 249
158 negative regulation of cellular component organization	2.91E-7	13 / 208
159 immune response-regulating signaling pathway	2.91E-7	13 / 208
160 nuclear import	2.98E-7	11 / 134
161 positive regulation of cell cycle	3.03E-7	9 / 75
162 epithelial tube morphogenesis	3.13E-7	10 / 103
163 response to steroid hormone stimulus	3.37E-7	9 / 76
164 regulation of cytokine production	3.56E-7	14 / 255
165 regulation of lymphocyte differentiation	3.6E-7	8 / 53
166 protein import	3.63E-7	12 / 173
167 I-SMAD binding	4.32E-7	5 / 10
168 activin binding	4.32E-7	5 / 10
169 endocrine pancreas development	4.47E-7	7 / 35
170 regulation of leukocyte proliferation	5.14E-7	9 / 80
171 double-stranded DNA binding	5.17E-7	10 / 109
172 negative regulation of phosphorylation	5.44E-7	8 / 56
173 sensory organ development	5.91E-7	11 / 144
174 regulation of MAPK cascade	6.17E-7	13 / 223
175 positive regulation of cell migration	6.29E-7	11 / 145
176 negative regulation of immune system process	6.91E-7	9 / 83
177 negative regulation of phosphorus metabolic process	7.01E-7	8 / 58
178 negative regulation of phosphate metabolic process	7.01E-7	8 / 58
179 immune effector process	7.42E-7	13 / 227
180 positive regulation of cell motility	7.58E-7	11 / 148
181 dorsal/ventral pattern formation	7.69E-7	7 / 38
182 positive regulation of MAPK cascade	8.19E-7	10 / 115
183 JAK-STAT cascade	8.22E-7	9 / 85
184 response to peptide hormone stimulus	8.45E-7	13 / 230
185 peptidyl-tyrosine phosphorylation	8.77E-7	10 / 116
186 positive regulation of cell adhesion	8.85E-7	8 / 60
187 digestive tract development	9.02E-7	7 / 39
188 ubiquitin protein ligase binding	9.75E-7	9 / 87
189 small conjugating protein ligase binding	9.75E-7	9 / 87
190 regulation of peptidyl-tyrosine phosphorylation	9.75E-7	9 / 87
191 peptidyl-tyrosine modification	1E-6	10 / 118
192 positive regulation of locomotion	1.01E-6	11 / 153
193 digestive system development	1.05E-6	7 / 40
194 striated muscle tissue development	1.07E-6	10 / 119
195 positive regulation of intracellular protein kinase cascade	1.08E-6	14 / 282
196 transcription regulatory region sequence-specific DNA binding	1.09E-6	8 / 62
197 cardiac muscle tissue development	1.09E-6	8 / 62

Function	FDR	Coverage
198 protein localization to nucleus	1.11E-6	11 / 155
199 structure-specific DNA binding	1.11E-6	11 / 155
200 JAK-STAT cascade involved in growth hormone signaling pathway	1.2E-6	6 / 24
201 mammary gland development	1.45E-6	7 / 42
202 branching morphogenesis of a tube	1.56E-6	8 / 65
203 RNA polymerase II transcription factor binding	1.68E-6	7 / 43
204 cardiac cell differentiation	1.68E-6	7 / 43
205 anti-apoptosis	1.68E-6	12 / 202
206 angiogenesis	1.77E-6	12 / 203
207 regulation of defense response	1.8E-6	14 / 295
208 muscle tissue development	1.87E-6	10 / 127
209 T cell differentiation in thymus	1.95E-6	6 / 26
210 regulation of immune effector process	2.32E-6	10 / 130
211 regulation of macrophage derived foam cell differentiation	2.45E-6	6 / 27
212 response to lipid	2.45E-6	6 / 27
213 positive regulation of macrophage derived foam cell differentiation	2.64E-6	5 / 14
214 cytokine activity	2.67E-6	8 / 70
215 regulation of cell projection organization	3.03E-6	10 / 134
216 regulation of glucose metabolic process	3.05E-6	7 / 47
217 regulation of mitotic cell cycle	3.08E-6	13 / 260
218 regulation of cytokine-mediated signaling pathway	3.29E-6	8 / 72
219 transforming growth factor beta production	3.81E-6	5 / 15
220 regulation of transforming growth factor beta production	3.81E-6	5 / 15
221 cellular response to peptide hormone stimulus	4.02E-6	12 / 220
222 brain development	4.19E-6	11 / 178
223 cellular response to growth hormone stimulus	4.58E-6	6 / 30
224 growth hormone receptor signaling pathway	4.58E-6	6 / 30
225 response to biotic stimulus	5.04E-6	13 / 272
226 regulation of innate immune response	5.16E-6	11 / 182
227 respiratory system development	5.19E-6	7 / 51
228 growth factor activity	5.19E-6	7 / 51
229 neuron fate commitment	5.28E-6	5 / 16
230 hemopoietic progenitor cell differentiation	5.28E-6	5 / 16
231 regulation of mononuclear cell proliferation	5.3E-6	8 / 77
232 response to growth hormone stimulus	5.45E-6	6 / 31
233 activation of protein kinase activity	5.6E-6	11 / 184
234 regulation of response to cytokine stimulus	5.79E-6	8 / 78
235 antigen receptor-mediated signaling pathway	6.23E-6	9 / 110
236 regulation of cell adhesion mediated by integrin	6.51E-6	6 / 32
237 carbohydrate homeostasis	6.51E-6	7 / 53
238 palate development	6.51E-6	6 / 32
239 glucose homeostasis	6.51E-6	7 / 53
240 negative regulation of kinase activity	7.7E-6	9 / 113
241 regulation of establishment of protein localization	7.92E-6	11 / 191
242 nucleocytoplasmic transport	7.93E-6	12 / 236
243 positive regulation of leukocyte proliferation	8.27E-6	7 / 55
244 regulation of carbohydrate metabolic process	8.27E-6	7 / 55
245 regulation of cellular carbohydrate metabolic process	8.27E-6	7 / 55
246 negative regulation of growth	8.75E-6	9 / 115
247 nuclear transport	8.91E-6	12 / 239

Function	FDR	Coverage
248 immune response-activating cell surface receptor signaling pathway	9.35E-6	9 / 116
249 receptor complex	1E-5	9 / 117
250 forebrain development	1.07E-5	8 / 85
251 cell adhesion mediated by integrin	1.09E-5	6 / 35
252 ATP binding	1.14E-5	12 / 245
253 embryonic digestive tract development	1.25E-5	5 / 19
254 core promoter proximal region sequence-specific DNA binding	1.25E-5	5 / 19
255 negative regulation of transferase activity	1.31E-5	9 / 121
256 regulation of protein serine/threonine kinase activity	1.34E-5	12 / 249
257 immune response-regulating cell surface receptor signaling pathway	1.39E-5	9 / 122
258 protein heterodimerization activity	1.61E-5	10 / 163
259 core promoter proximal region DNA binding	1.62E-5	5 / 20
260 morphogenesis of a branching epithelium	1.62E-5	7 / 61
261 regulation of monooxygenase activity	1.74E-5	6 / 38
262 developmental process involved in reproduction	1.77E-5	10 / 165
263 response to drug	1.88E-5	8 / 92
264 mononuclear cell proliferation	1.88E-5	8 / 92
265 adenylyl ribonucleotide binding	1.9E-5	12 / 258
266 regulation of muscle cell differentiation	1.98E-5	7 / 63
267 in utero embryonic development	2E-5	6 / 39
268 regulation of cysteine-type endopeptidase activity involved in apoptotic process	2.01E-5	9 / 128
269 regulation of protein catabolic process	2.01E-5	8 / 93
270 RNA polymerase II activating transcription factor binding	2.03E-5	5 / 21
271 response to growth factor stimulus	2.03E-5	11 / 212
272 negative regulation of cell growth	2.15E-5	8 / 94
273 cartilage development	2.16E-5	7 / 64
274 positive regulation of transport	2.25E-5	12 / 263
275 adenylyl nucleotide binding	2.25E-5	12 / 263
276 regulation of BMP signaling pathway	2.27E-5	6 / 40
277 positive regulation of cell projection organization	2.37E-5	7 / 65
278 regulation of cysteine-type endopeptidase activity	2.37E-5	9 / 131
279 regulation of protein transport	2.45E-5	10 / 172
280 positive regulation of glucose metabolic process	2.52E-5	5 / 22
281 nuclear chromosome part	2.55E-5	10 / 173
282 odontogenesis	2.55E-5	6 / 41
283 cell surface	2.55E-5	12 / 267
284 regulation of striated muscle tissue development	2.55E-5	6 / 41
285 smoothened signaling pathway	2.55E-5	6 / 41
286 negative regulation of protein phosphorylation	2.55E-5	6 / 41
287 cellular protein complex assembly	2.65E-5	10 / 174
288 regulation of muscle organ development	2.93E-5	6 / 42
289 cell-cell adhesion	3E-5	11 / 222
290 DNA integration	3.05E-5	4 / 10
291 DNA ligation	3.05E-5	4 / 10
292 myoblast differentiation	3.08E-5	5 / 23
293 regulation of lipid metabolic process	3.29E-5	9 / 137
294 regulation of DNA replication	3.38E-5	7 / 69
295 positive regulation of protein transport	3.46E-5	8 / 101
296 positive regulation of sequence-specific DNA binding transcription factor activity	3.68E-5	9 / 139
297 nuclear chromatin	3.68E-5	8 / 102

Function	FDR	Coverage
298 inositol lipid-mediated signaling	3.68E-5	8 / 102
299 phosphatidylinositol-mediated signaling	3.68E-5	8 / 102
300 regulation of DNA binding	3.73E-5	6 / 44
301 cardiac septum development	3.73E-5	5 / 24
302 positive regulation of protein import into nucleus	3.73E-5	6 / 44
303 mesoderm development	4.23E-5	6 / 45
304 specification of symmetry	4.23E-5	6 / 45
305 ureteric bud development	4.23E-5	6 / 45
306 lipid localization	4.26E-5	9 / 142
307 positive regulation of epithelial cell proliferation	4.34E-5	7 / 72
308 chromatin	4.34E-5	10 / 185
309 negative regulation of protein kinase activity	4.44E-5	8 / 105
310 regulation of neuron projection development	4.44E-5	8 / 105
311 positive regulation of carbohydrate metabolic process	4.45E-5	5 / 25
312 heart looping	4.45E-5	5 / 25
313 positive regulation of cellular carbohydrate metabolic process	4.45E-5	5 / 25
314 double-strand break repair via nonhomologous end joining	4.45E-5	4 / 11
315 B cell receptor signaling pathway	4.45E-5	5 / 25
316 metanephros development	4.67E-5	6 / 46
317 embryonic heart tube morphogenesis	5.43E-5	5 / 26
318 determination of heart left/right asymmetry	5.43E-5	5 / 26
319 regulation of protein complex assembly	5.74E-5	8 / 109
320 protein domain specific binding	5.86E-5	12 / 292
321 positive regulation of transmembrane transport	5.91E-5	6 / 48
322 regulation of cell-cell adhesion	5.91E-5	6 / 48
323 skeletal system morphogenesis	5.91E-5	6 / 48
324 regulation of lymphocyte proliferation	5.96E-5	7 / 76
325 regulation of activin receptor signaling pathway	6.31E-5	4 / 12
326 exocrine system development	6.31E-5	4 / 12
327 negative regulation of transport	6.31E-5	9 / 150
328 response to cholesterol	6.31E-5	4 / 12
329 cellular response to hypoxia	6.4E-5	5 / 27
330 peptidyl-serine phosphorylation	6.4E-5	7 / 77
331 muscle cell proliferation	6.54E-5	6 / 49
332 positive regulation of cell growth	7.34E-5	6 / 50
333 positive regulation of nucleocytoplasmic transport	7.34E-5	6 / 50
334 negative regulation of immune effector process	7.63E-5	5 / 28
335 protein tyrosine kinase activity	7.69E-5	8 / 114
336 regulation of protein import into nucleus	8.13E-5	7 / 80
337 platelet degranulation	8.13E-5	7 / 80
338 regulation of neural precursor cell proliferation	8.7E-5	4 / 13
339 T cell apoptosis	8.7E-5	4 / 13
340 urogenital system development	8.7E-5	8 / 116
341 cardioblast differentiation	8.7E-5	4 / 13
342 histone acetyltransferase binding	8.7E-5	4 / 13
343 long-chain fatty acid transport	8.91E-5	5 / 29
344 cellular response to oxygen levels	8.91E-5	5 / 29
345 cardiac chamber development	8.95E-5	6 / 52
346 positive regulation of intracellular protein transport	8.95E-5	6 / 52
347 gonad development	9.34E-5	7 / 82

Function	FDR	Coverage
348 peptidyl-serine modification	1.01E-4	7 / 83
349 response to other organism	1.04E-4	11 / 257
350 stem cell development	1.04E-4	5 / 30
351 regulation of striated muscle cell differentiation	1.04E-4	5 / 30
352 platelet activation	1.05E-4	10 / 207
353 sequence-specific distal enhancer binding RNA polymerase II transcription factor activity	1.08E-4	7 / 84
354 positive regulation of cysteine-type endopeptidase activity	1.08E-4	7 / 84
355 positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	1.08E-4	7 / 84
356 positive regulation of mononuclear cell proliferation	1.09E-4	6 / 54
357 nuclear chromosome	1.09E-4	10 / 208
358 non-recombinational repair	1.16E-4	4 / 14
359 negative regulation of cell development	1.2E-4	6 / 55
360 regulation of endothelial cell proliferation	1.2E-4	6 / 55
361 epithelial cell development	1.2E-4	5 / 31
362 embryonic heart tube development	1.2E-4	5 / 31
363 negative regulation of sequence-specific DNA binding transcription factor activity	1.23E-4	7 / 86
364 B cell activation	1.23E-4	7 / 86
365 production of molecular mediator of immune response	1.32E-4	6 / 56
366 negative regulation of secretion	1.32E-4	6 / 56
367 positive regulation of endopeptidase activity	1.32E-4	7 / 87
368 regulation of peptidyl-serine phosphorylation	1.39E-4	5 / 32
369 regulation of oxidoreductase activity	1.44E-4	6 / 57
370 positive regulation of intracellular transport	1.44E-4	6 / 57
371 myeloid leukocyte activation	1.44E-4	6 / 57
372 regulation of JAK-STAT cascade	1.44E-4	6 / 57
373 lipid transport	1.47E-4	8 / 126
374 mesenchymal to epithelial transition	1.48E-4	4 / 15
375 negative regulation of neuron differentiation	1.48E-4	4 / 15
376 G1/S transition of mitotic cell cycle	1.48E-4	9 / 169
377 striated muscle cell proliferation	1.48E-4	4 / 15
378 epithelial cell morphogenesis	1.48E-4	4 / 15
379 cardiac muscle cell proliferation	1.48E-4	4 / 15
380 leukocyte apoptosis	1.57E-4	5 / 33
381 hindbrain development	1.57E-4	5 / 33
382 lymphocyte proliferation	1.59E-4	7 / 90
383 development of primary sexual characteristics	1.59E-4	7 / 90
384 Wnt receptor signaling pathway	1.59E-4	9 / 171
385 response to radiation	1.59E-4	9 / 171
386 bone development	1.81E-4	5 / 34
387 positive regulation of peptidase activity	1.82E-4	7 / 92
388 canonical Wnt receptor signaling pathway	1.89E-4	8 / 131
389 monocyte differentiation	1.9E-4	4 / 16
390 cardiac muscle tissue growth	1.9E-4	4 / 16
391 positive regulation of alpha-beta T cell differentiation	1.9E-4	4 / 16
392 response to abiotic stimulus	1.99E-4	11 / 278
393 branching involved in ureteric bud morphogenesis	2.06E-4	5 / 35
394 regulation of nucleocytoplasmic transport	2.07E-4	7 / 94
395 regulation of neuron apoptosis	2.24E-4	6 / 62
396 reproductive structure development	2.36E-4	7 / 96
397 lipid storage	2.36E-4	5 / 36

Function	FDR	Coverage
398 regulation of intracellular protein transport	2.36E-4	7 / 96
399 metanephros morphogenesis	2.41E-4	4 / 17
400 endothelial cell proliferation	2.41E-4	6 / 63
401 cardiac septum morphogenesis	2.41E-4	4 / 17
402 activin receptor signaling pathway	2.41E-4	4 / 17
403 negative regulation of protein metabolic process	2.55E-4	10 / 232
404 ureteric bud morphogenesis	2.65E-4	5 / 37
405 positive regulation of endothelial cell proliferation	2.65E-4	5 / 37
406 regulation of hormone levels	2.73E-4	10 / 234
407 eye development	2.83E-4	7 / 99
408 response to estrogen stimulus	3.01E-4	5 / 38
409 fatty acid transport	3.01E-4	5 / 38
410 response to estradiol stimulus	3.02E-4	4 / 18
411 lung development	3.4E-4	5 / 39
412 regulation of reactive oxygen species metabolic process	3.4E-4	5 / 39
413 regulation of generation of precursor metabolites and energy	3.4E-4	5 / 39
414 kidney development	3.61E-4	7 / 103
415 neuron apoptosis	3.65E-4	6 / 68
416 regulation of ion homeostasis	3.65E-4	6 / 68
417 negative regulation of muscle cell differentiation	3.73E-4	4 / 19
418 positive regulation of nitric oxide biosynthetic process	3.73E-4	4 / 19
419 alpha-beta T cell activation	3.8E-4	5 / 40
420 blood vessel endothelial cell migration	3.8E-4	5 / 40
421 protein complex binding	3.89E-4	8 / 146
422 positive regulation of growth	3.92E-4	6 / 69
423 respiratory tube development	4.22E-4	5 / 41
424 RNA polymerase II regulatory region sequence-specific DNA binding	4.22E-4	5 / 41
425 determination of left/right symmetry	4.22E-4	5 / 41
426 negative regulation of lipid metabolic process	4.22E-4	5 / 41
427 embryonic organ morphogenesis	4.22E-4	6 / 70
428 stem cell differentiation	4.22E-4	5 / 41
429 positive regulation of myeloid leukocyte differentiation	4.5E-4	4 / 20
430 negative regulation of BMP signaling pathway	4.5E-4	4 / 20
431 regulation of transcription involved in G1/S phase of mitotic cell cycle	4.5E-4	4 / 20
432 regulation of endopeptidase activity	4.66E-4	9 / 198
433 RNA polymerase II regulatory region DNA binding	4.7E-4	5 / 42
434 regulation of B cell activation	4.7E-4	5 / 42
435 sex differentiation	4.7E-4	7 / 108
436 activation of cysteine-type endopeptidase activity	4.85E-4	6 / 72
437 activation of cysteine-type endopeptidase activity involved in apoptotic process	4.85E-4	6 / 72
438 renal system development	4.96E-4	7 / 109
439 neuron death	5.22E-4	6 / 73
440 negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	5.22E-4	5 / 43
441 heart growth	5.4E-4	4 / 21
442 cell junction organization	5.47E-4	8 / 154
443 determination of bilateral symmetry	5.77E-4	5 / 44
444 positive regulation of JAK-STAT cascade	5.77E-4	5 / 44
445 regulation of response to external stimulus	5.77E-4	9 / 204
446 regulation of myeloid leukocyte differentiation	5.77E-4	5 / 44
447 negative regulation of cellular protein metabolic process	5.94E-4	9 / 205

Function	FDR	Coverage
448 regulation of peptidase activity	5.94E-4	9 / 205
449 lymphocyte apoptosis	6.38E-4	4 / 22
450 regulation of interferon-gamma-mediated signaling pathway	6.38E-4	4 / 22
451 digestive tract morphogenesis	6.38E-4	4 / 22
452 regulation of skeletal muscle fiber development	6.38E-4	4 / 22
453 ameboidal cell migration	6.38E-4	5 / 45
454 mitochondrial membrane organization	6.38E-4	4 / 22
455 muscle organ development	6.41E-4	8 / 158
456 regulation of hormone secretion	6.77E-4	7 / 115
457 striated muscle cell differentiation	6.81E-4	6 / 77
458 regulation of nuclear division	6.81E-4	6 / 77
459 regulation of mitosis	6.81E-4	6 / 77
460 regulation of nitric oxide biosynthetic process	7.53E-4	4 / 23
461 sequestering of calcium ion	7.53E-4	4 / 23
462 regulation of skeletal muscle tissue development	7.53E-4	4 / 23
463 regulation of response to interferon-gamma	7.53E-4	4 / 23
464 cardiac chamber morphogenesis	7.71E-4	5 / 47
465 endothelial cell migration	7.79E-4	6 / 79
466 negative regulation of cellular component movement	8.36E-4	6 / 80
467 negative regulation of epithelial cell proliferation	8.5E-4	5 / 48
468 positive regulation of defense response	8.52E-4	8 / 165
469 nerve growth factor receptor signaling pathway	8.59E-4	9 / 216
470 positive regulation of neuron differentiation	8.8E-4	4 / 24
471 regulation of alpha-beta T cell differentiation	8.8E-4	4 / 24
472 collagen metabolic process	8.8E-4	4 / 24
473 mammary gland epithelium development	8.8E-4	4 / 24
474 limb development	9.22E-4	5 / 49
475 Notch signaling pathway	9.22E-4	5 / 49
476 cellular response to biotic stimulus	9.22E-4	5 / 49
477 appendage development	9.22E-4	5 / 49
478 cell-substrate adhesion	9.48E-4	7 / 122
479 regulation of intracellular transport	9.96E-4	7 / 123
480 chromatin binding	9.96E-4	7 / 123
481 membrane raft	1E-3	6 / 83
482 negative regulation of catabolic process	1.01E-3	5 / 50
483 negative regulation of protein catabolic process	1.01E-3	4 / 25
484 organ growth	1.01E-3	4 / 25
485 regulation of smoothened signaling pathway	1.01E-3	4 / 25
486 negative regulation of immune response	1.01E-3	4 / 25
487 positive regulation of alpha-beta T cell activation	1.01E-3	4 / 25
488 initiation of viral infection	1.01E-3	4 / 25
489 telencephalon development	1.09E-3	5 / 51
490 regulation of cell-substrate adhesion	1.09E-3	5 / 51
491 positive regulation of catabolic process	1.12E-3	6 / 85
492 cytokine-mediated signaling pathway	1.13E-3	10 / 282
493 regulation of MAP kinase activity	1.14E-3	8 / 173
494 positive regulation of B cell activation	1.16E-3	4 / 26
495 regulation of B cell proliferation	1.16E-3	4 / 26
496 kidney morphogenesis	1.16E-3	4 / 26
497 regulation of lipid kinase activity	1.16E-3	4 / 26

Function	FDR	Coverage
498 ovulation cycle process	1.16E-3	4 / 26
499 maintenance of location	1.18E-3	7 / 127
500 positive regulation of cell cycle process	1.29E-3	7 / 129
501 regulation of Wnt receptor signaling pathway	1.29E-3	7 / 129
502 positive regulation of lymphocyte proliferation	1.29E-3	5 / 53
503 cholesterol transport	1.29E-3	5 / 53
504 hormone secretion	1.29E-3	7 / 129
505 nephron epithelium development	1.33E-3	4 / 27
506 positive regulation of peptidyl-serine phosphorylation	1.33E-3	4 / 27
507 ovulation cycle	1.33E-3	4 / 27
508 adaptive immune response	1.33E-3	6 / 88
509 cell fate specification	1.33E-3	4 / 27
510 positive regulation of cytokine production	1.34E-3	7 / 130
511 sterol transport	1.38E-3	5 / 54
512 nephron development	1.38E-3	5 / 54
513 regulation of endothelial cell migration	1.38E-3	5 / 54
514 embryonic hemopoiesis	1.42E-3	3 / 10
515 metanephric renal vesicle morphogenesis	1.42E-3	3 / 10
516 positive regulation of multicellular organismal metabolic process	1.42E-3	3 / 10
517 positive regulation of nitric-oxide synthase activity	1.42E-3	3 / 10
518 pituitary gland development	1.42E-3	3 / 10
519 positive regulation of collagen metabolic process	1.42E-3	3 / 10
520 regulation of heart morphogenesis	1.42E-3	3 / 10
521 mesenchymal to epithelial transition involved in metanephros morphogenesis	1.42E-3	3 / 10
522 endochondral bone morphogenesis	1.42E-3	3 / 10
523 positive regulation of collagen biosynthetic process	1.42E-3	3 / 10
524 blood circulation	1.42E-3	8 / 180
525 regulation of DNA metabolic process	1.43E-3	7 / 132
526 regulation of canonical Wnt receptor signaling pathway	1.45E-3	6 / 90
527 circulatory system process	1.47E-3	8 / 181
528 multicellular organismal macromolecule metabolic process	1.47E-3	4 / 28
529 regulation of lipid storage	1.47E-3	4 / 28
530 stem cell maintenance	1.47E-3	4 / 28
531 regulation of cytokine production involved in immune response	1.47E-3	4 / 28
532 regulation of nitric-oxide synthase activity	1.47E-3	4 / 28
533 hormone transport	1.48E-3	7 / 133
534 leukocyte mediated immunity	1.52E-3	6 / 91
535 glucose metabolic process	1.55E-3	7 / 134
536 developmental maturation	1.58E-3	5 / 56
537 positive regulation of angiogenesis	1.58E-3	5 / 56
538 inflammatory response	1.65E-3	9 / 239
539 cellular senescence	1.68E-3	4 / 29
540 regulation of blood vessel endothelial cell migration	1.68E-3	4 / 29
541 signal release	1.73E-3	8 / 186
542 generation of a signal involved in cell-cell signaling	1.73E-3	8 / 186
543 DNA binding, bending	1.84E-3	5 / 58
544 cellular response to external stimulus	1.84E-3	7 / 138
545 rhythmic process	1.84E-3	5 / 58
546 regulation of organ morphogenesis	1.84E-3	5 / 58
547 regulation of transcription initiation from RNA polymerase II promoter	1.85E-3	3 / 11

Function	FDR	Coverage
548 positive regulation of cytokine-mediated signaling pathway	1.85E-3	3 / 11
549 regulation of cardioblast differentiation	1.85E-3	3 / 11
550 regulation of transcription initiation, DNA-dependent	1.85E-3	3 / 11
551 toll-like receptor signaling pathway	1.87E-3	6 / 95
552 neural precursor cell proliferation	1.87E-3	4 / 30
553 alpha-beta T cell differentiation	1.87E-3	4 / 30
554 positive regulation of DNA replication	1.87E-3	4 / 30
555 negative regulation of multicellular organismal process	1.97E-3	8 / 190
556 hormone receptor binding	1.97E-3	6 / 96
557 platelet alpha granule	2.1E-3	5 / 60
558 anterior/posterior pattern specification	2.1E-3	5 / 60
559 positive regulation of phosphatidylinositol 3-kinase cascade	2.1E-3	4 / 31
560 caveola	2.1E-3	4 / 31
561 gastrulation	2.1E-3	5 / 60
562 sequestering of metal ion	2.1E-3	4 / 31
563 regulation of system process	2.1E-3	8 / 192
564 response to ionizing radiation	2.1E-3	5 / 60
565 nitric oxide biosynthetic process	2.1E-3	4 / 31
566 regulation of peptide transport	2.17E-3	6 / 98
567 regulation of peptide secretion	2.17E-3	6 / 98
568 protein secretion	2.29E-3	6 / 99
569 cell-cell junction organization	2.29E-3	6 / 99
570 regulation of alpha-beta T cell activation	2.31E-3	4 / 32
571 response to gamma radiation	2.31E-3	3 / 12
572 sprouting angiogenesis	2.31E-3	4 / 32
573 positive regulation of response to cytokine stimulus	2.31E-3	3 / 12
574 B cell proliferation	2.31E-3	4 / 32
575 vasculogenesis	2.31E-3	4 / 32
576 cytokine production involved in immune response	2.31E-3	4 / 32
577 production of miRNAs involved in gene silencing by miRNA	2.31E-3	3 / 12
578 regulation of myoblast differentiation	2.31E-3	3 / 12
579 positive regulation of glycogen biosynthetic process	2.31E-3	3 / 12
580 multicellular organismal metabolic process	2.31E-3	4 / 32
581 response to antibiotic	2.31E-3	3 / 12
582 response to interleukin-6	2.31E-3	3 / 12
583 regulation of muscle cell apoptosis	2.31E-3	3 / 12
584 leukocyte migration	2.41E-3	8 / 197
585 response to lipopolysaccharide	2.55E-3	5 / 63
586 positive regulation of DNA metabolic process	2.55E-3	5 / 63
587 monocarboxylic acid transport	2.55E-3	5 / 63
588 regulation of lipid biosynthetic process	2.55E-3	5 / 63
589 skeletal muscle fiber development	2.58E-3	4 / 33
590 response to organic cyclic compound	2.58E-3	4 / 33
591 peptidyl-threonine phosphorylation	2.58E-3	4 / 33
592 pattern recognition receptor signaling pathway	2.75E-3	6 / 103
593 positive regulation of glycogen metabolic process	2.87E-3	3 / 13
594 muscle cell apoptosis	2.87E-3	3 / 13
595 dsRNA fragmentation	2.87E-3	3 / 13
596 response to X-ray	2.87E-3	3 / 13
597 negative regulation of sequestering of calcium ion	2.87E-3	4 / 34

Function	FDR	Coverage
598 regulation of T cell differentiation in thymus	2.87E-3	3 / 13
599 granulocyte differentiation	2.87E-3	3 / 13
600 positive regulation of transforming growth factor beta receptor signaling pathway	2.87E-3	3 / 13
601 production of small RNA involved in gene silencing by RNA	2.87E-3	3 / 13
602 insulin-like growth factor receptor binding	2.87E-3	3 / 13
603 response to fluid shear stress	2.87E-3	3 / 13
604 regulation of sequestering of calcium ion	2.87E-3	4 / 34
605 regulation of collagen biosynthetic process	2.87E-3	3 / 13
606 release of sequestered calcium ion into cytosol	2.87E-3	4 / 34
607 cellular response to growth factor stimulus	2.96E-3	8 / 204
608 innate immune response-activating signal transduction	3.14E-3	6 / 106
609 regulation of phosphatidylinositol 3-kinase cascade	3.17E-3	4 / 35
610 positive regulation of endothelial cell migration	3.17E-3	4 / 35
611 positive regulation of lipid metabolic process	3.27E-3	5 / 67
612 regulation of transporter activity	3.27E-3	5 / 67
613 negative regulation of protein serine/threonine kinase activity	3.27E-3	5 / 67
614 positive regulation of protein serine/threonine kinase activity	3.27E-3	7 / 154
615 leukocyte activation involved in immune response	3.27E-3	5 / 67
616 cell activation involved in immune response	3.27E-3	5 / 67
617 activation of innate immune response	3.43E-3	6 / 108
618 peptidyl-threonine modification	3.49E-3	4 / 36
619 positive regulation of tyrosine phosphorylation of STAT protein	3.49E-3	4 / 36
620 positive regulation of protein complex assembly	3.49E-3	5 / 68
621 regulation of multicellular organismal metabolic process	3.53E-3	3 / 14
622 renal vesicle morphogenesis	3.53E-3	3 / 14
623 regulation of collagen metabolic process	3.53E-3	3 / 14
624 positive regulation vascular endothelial growth factor production	3.53E-3	3 / 14
625 positive regulation of secretion	3.74E-3	6 / 110
626 regulation of production of molecular mediator of immune response	3.83E-3	4 / 37
627 formation of primary germ layer	3.83E-3	4 / 37
628 central nervous system neuron differentiation	3.83E-3	4 / 37
629 negative regulation of neurogenesis	3.83E-3	4 / 37
630 positive regulation of cellular catabolic process	3.94E-3	5 / 70
631 peptide secretion	4.1E-3	6 / 112
632 cardiac ventricle morphogenesis	4.24E-3	4 / 38
633 macrophage differentiation	4.26E-3	3 / 15
634 renal vesicle development	4.26E-3	3 / 15
635 hexose metabolic process	4.26E-3	7 / 162
636 metanephric nephron morphogenesis	4.26E-3	3 / 15
637 ventricular septum development	4.26E-3	3 / 15
638 anatomical structure maturation	4.26E-3	3 / 15
639 lung epithelium development	4.26E-3	3 / 15
640 regulation of cardiac muscle tissue development	4.26E-3	3 / 15
641 negative regulation of oxidoreductase activity	4.26E-3	3 / 15
642 positive regulation of monooxygenase activity	4.26E-3	3 / 15
643 positive regulation of cell adhesion mediated by integrin	4.26E-3	3 / 15
644 toll-like receptor 2 signaling pathway	4.4E-3	5 / 72
645 response to insulin stimulus	4.58E-3	7 / 164
646 negative regulation of neuron apoptosis	4.58E-3	4 / 39
647 kidney epithelium development	4.58E-3	4 / 39

Function	FDR	Coverage
648 regulation of kidney development	4.58E-3	4 / 39
649 camera-type eye development	4.65E-3	5 / 73
650 negative regulation of cell migration	4.65E-3	5 / 73
651 response to molecule of bacterial origin	4.65E-3	5 / 73
652 protein C-terminus binding	4.81E-3	6 / 116
653 stress-activated protein kinase signaling cascade	4.88E-3	7 / 166
654 male gonad development	5.01E-3	4 / 40
655 muscle fiber development	5.01E-3	4 / 40
656 chemoattractant activity	5.1E-3	3 / 16
657 regulation of vascular endothelial growth factor production	5.1E-3	3 / 16
658 vascular endothelial growth factor production	5.1E-3	3 / 16
659 exocytosis	5.2E-3	7 / 168
660 negative regulation of cell motility	5.21E-3	5 / 75
661 response to bacterium	5.21E-3	6 / 118
662 peptide transport	5.44E-3	6 / 119
663 appendage morphogenesis	5.44E-3	4 / 41
664 regulation of tyrosine phosphorylation of STAT protein	5.44E-3	4 / 41
665 limb morphogenesis	5.44E-3	4 / 41
666 intracellular receptor mediated signaling pathway	5.54E-3	7 / 170
667 posttranscriptional regulation of gene expression	5.78E-3	8 / 228
668 regulation of developmental growth	5.93E-3	4 / 42
669 nitric oxide metabolic process	5.93E-3	4 / 42
670 fibroblast proliferation	5.93E-3	4 / 42
671 collagen biosynthetic process	6.02E-3	3 / 17
672 regulation of antigen receptor-mediated signaling pathway	6.02E-3	3 / 17
673 cellular response to dsRNA	6.02E-3	3 / 17
674 negative regulation of osteoblast differentiation	6.02E-3	3 / 17
675 regulation of protein secretion	6.13E-3	5 / 78
676 inner ear development	6.42E-3	4 / 43
677 positive regulation of binding	6.42E-3	4 / 43
678 cardiac ventricle development	6.42E-3	4 / 43
679 regulation of lipid transport	6.42E-3	4 / 43
680 induction of apoptosis by intracellular signals	6.45E-3	5 / 79
681 negative regulation of locomotion	6.45E-3	5 / 79
682 transcription coactivator activity	6.75E-3	8 / 234
683 regulation of ERK1 and ERK2 cascade	6.81E-3	5 / 80
684 response to nutrient	6.81E-3	5 / 80
685 lung morphogenesis	6.94E-3	3 / 18
686 regulation of mesenchymal cell proliferation	6.94E-3	3 / 18
687 central nervous system neuron development	6.94E-3	3 / 18
688 tyrosine phosphorylation of STAT protein	6.94E-3	4 / 44
689 positive regulation of blood vessel endothelial cell migration	6.94E-3	3 / 18
690 regulation of glycolysis	6.94E-3	3 / 18
691 lipoprotein particle binding	6.94E-3	3 / 18
692 nephron epithelium morphogenesis	6.94E-3	3 / 18
693 protein-lipid complex binding	6.94E-3	3 / 18
694 positive regulation of B cell proliferation	6.94E-3	3 / 18
695 neuroblast proliferation	6.94E-3	3 / 18
696 neural tube development	6.94E-3	4 / 44
697 cerebellum development	6.94E-3	3 / 18

Function	FDR	Coverage
698 bone morphogenesis	6.94E-3	3 / 18
699 reactive oxygen species metabolic process	7.07E-3	5 / 81
700 beta-catenin binding	7.43E-3	4 / 45
701 development of primary male sexual characteristics	7.43E-3	4 / 45
702 toll-like receptor 4 signaling pathway	7.89E-3	5 / 83
703 positive regulation of innate immune response	7.94E-3	6 / 129
704 regulation of glycogen biosynthetic process	8.02E-3	3 / 19
705 nuclear periphery	8.02E-3	4 / 46
706 response to dsRNA	8.02E-3	3 / 19
707 negative regulation of endothelial cell migration	8.02E-3	3 / 19
708 positive regulation of BMP signaling pathway	8.02E-3	3 / 19
709 metencephalon development	8.02E-3	3 / 19
710 positive regulation of cell-substrate adhesion	8.02E-3	3 / 19
711 smooth muscle cell differentiation	8.02E-3	3 / 19
712 regulation of glucan biosynthetic process	8.02E-3	3 / 19
713 regulation of polysaccharide biosynthetic process	8.02E-3	3 / 19
714 secretory granule	8.15E-3	6 / 130
715 negative regulation of cell cycle process	8.19E-3	5 / 84
716 platelet alpha granule lumen	8.58E-3	4 / 47
717 cell aging	8.58E-3	4 / 47
718 cellular response to nutrient	8.58E-3	4 / 47
719 male sex differentiation	8.58E-3	4 / 47
720 positive regulation of organelle organization	8.76E-3	6 / 132
721 DNA recombination	8.76E-3	6 / 132
722 leukocyte chemotaxis	9.05E-3	5 / 86
723 nephron morphogenesis	9.18E-3	3 / 20
724 regulation of glycogen metabolic process	9.18E-3	3 / 20
725 regulation of polysaccharide metabolic process	9.18E-3	3 / 20
726 positive regulation of phosphatidylinositol 3-kinase activity	9.18E-3	3 / 20
727 Golgi lumen	9.18E-3	4 / 48
728 regulation of cellular carbohydrate catabolic process	9.18E-3	3 / 20
729 regulation of carbohydrate catabolic process	9.18E-3	3 / 20
730 mitochondrion organization	9.76E-3	6 / 135
731 regulation of protein kinase B signaling cascade	9.86E-3	4 / 49
732 secretory granule lumen	9.86E-3	4 / 49
733 cytoplasmic membrane-bounded vesicle lumen	9.86E-3	4 / 49
734 vesicle lumen	9.86E-3	4 / 49
735 regulation of heart contraction	9.86E-3	4 / 49
736 T cell receptor signaling pathway	9.87E-3	5 / 88
737 DNA replication	1.02E-2	7 / 191
738 regulation of S phase	1.04E-2	3 / 21
739 RNA polymerase II transcription factor binding transcription factor activity involved in positive regulation of transcription	1.04E-2	3 / 21
740 response to alkaloid	1.04E-2	3 / 21
741 regulation of phosphatidylinositol 3-kinase activity	1.04E-2	3 / 21
742 positive regulation of lipid kinase activity	1.04E-2	3 / 21
743 positive regulation of tyrosine phosphorylation of Stat3 protein	1.04E-2	3 / 21
744 regulation of cartilage development	1.04E-2	3 / 21
745 positive regulation of axonogenesis	1.04E-2	3 / 21
746 positive regulation of reactive oxygen species metabolic process	1.04E-2	3 / 21
747 diencephalon development	1.04E-2	3 / 21

Function	FDR	Coverage
748 protein autophosphorylation	1.04E-2	6 / 137
749 negative regulation of cytokine production	1.04E-2	5 / 89
750 negative regulation of DNA binding	1.04E-2	3 / 21
751 regulation of axonogenesis	1.04E-2	4 / 50
752 regulation of leukocyte mediated immunity	1.04E-2	4 / 50
753 phosphatidylinositol 3-kinase cascade	1.04E-2	4 / 50
754 response to nutrient levels	1.06E-2	6 / 138
755 regulation of cell cycle arrest	1.08E-2	8 / 255
756 tissue remodeling	1.12E-2	4 / 51
757 developmental growth involved in morphogenesis	1.12E-2	4 / 51
758 calcium ion transport into cytosol	1.12E-2	4 / 51
759 monosaccharide metabolic process	1.15E-2	7 / 196
760 somatic cell DNA recombination	1.17E-2	3 / 22
761 cellular response to nutrient levels	1.17E-2	5 / 92
762 somatic diversification of immune receptors via germline recombination within a single locus	1.17E-2	3 / 22
763 mesoderm formation	1.17E-2	3 / 22
764 gland morphogenesis	1.17E-2	3 / 22
765 negative regulation of leukocyte proliferation	1.17E-2	3 / 22
766 mesenchymal cell proliferation	1.17E-2	3 / 22
767 ERK1 and ERK2 cascade	1.17E-2	5 / 92
768 regulation of T cell proliferation	1.18E-2	4 / 52
769 cytosolic calcium ion transport	1.18E-2	4 / 52
770 cellular response to abiotic stimulus	1.22E-2	5 / 93
771 protein stabilization	1.27E-2	4 / 53
772 ventricular cardiac muscle tissue morphogenesis	1.32E-2	3 / 23
773 positive regulation of anti-apoptosis	1.32E-2	3 / 23
774 ventricular cardiac muscle tissue development	1.32E-2	3 / 23
775 gene silencing by miRNA	1.32E-2	3 / 23
776 response to interferon-gamma	1.33E-2	5 / 95
777 transcription initiation, DNA-dependent	1.33E-2	5 / 95
778 positive regulation of immune effector process	1.35E-2	4 / 54
779 ear development	1.35E-2	4 / 54
780 negative regulation of protein modification process	1.38E-2	6 / 146
781 response to extracellular stimulus	1.38E-2	6 / 146
782 axis specification	1.44E-2	4 / 55
783 positive regulation of protein secretion	1.44E-2	4 / 55
784 regulation of peptide hormone secretion	1.45E-2	5 / 97
785 metanephric nephron development	1.48E-2	3 / 24
786 endothelium development	1.48E-2	3 / 24
787 mesoderm morphogenesis	1.48E-2	3 / 24
788 cellular response to extracellular stimulus	1.51E-2	5 / 98
789 regulation of transmembrane transporter activity	1.53E-2	4 / 56
790 drug binding	1.64E-2	4 / 57
791 aging	1.64E-2	4 / 57
792 cardiac muscle cell differentiation	1.66E-2	3 / 25
793 homotypic cell-cell adhesion	1.66E-2	3 / 25
794 negative regulation of lipid biosynthetic process	1.66E-2	3 / 25
795 T cell proliferation	1.74E-2	4 / 58
796 protein kinase B signaling cascade	1.74E-2	4 / 58
797 positive regulation of mitosis	1.84E-2	3 / 26

Function	FDR	Coverage
798 posttranscriptional gene silencing by RNA	1.84E-2	3 / 26
799 negative regulation of cell adhesion	1.84E-2	4 / 59
800 non-membrane spanning protein tyrosine kinase activity	1.84E-2	3 / 26
801 positive regulation of nuclear division	1.84E-2	3 / 26
802 posttranscriptional gene silencing	1.84E-2	3 / 26
803 striated muscle cell development	1.84E-2	4 / 59
804 regulation of tyrosine phosphorylation of Stat3 protein	1.84E-2	3 / 26
805 elevation of cytosolic calcium ion concentration	1.86E-2	5 / 103
806 heart contraction	1.95E-2	4 / 60
807 skeletal muscle tissue development	1.95E-2	4 / 60
808 bone remodeling	2.04E-2	3 / 27
809 somatic diversification of immune receptors	2.04E-2	3 / 27
810 glycogen biosynthetic process	2.04E-2	3 / 27
811 glucan biosynthetic process	2.04E-2	3 / 27
812 tyrosine phosphorylation of Stat3 protein	2.04E-2	3 / 27
813 heart process	2.06E-2	4 / 61
814 cellular response to insulin stimulus	2.14E-2	6 / 160
815 TRIF-dependent toll-like receptor signaling pathway	2.18E-2	4 / 62
816 calcium ion transport	2.21E-2	6 / 161
817 cellular response to steroid hormone stimulus	2.24E-2	3 / 28
818 cytosolic calcium ion homeostasis	2.24E-2	5 / 108
819 release of cytochrome c from mitochondria	2.24E-2	3 / 28
820 regulation of leukocyte apoptosis	2.24E-2	3 / 28
821 regulation of angiogenesis	2.24E-2	5 / 108
822 positive regulation of oxidoreductase activity	2.24E-2	3 / 28
823 negative regulation of DNA replication	2.24E-2	3 / 28
824 embryonic pattern specification	2.24E-2	3 / 28
825 anatomical structure homeostasis	2.24E-2	5 / 108
826 cell chemotaxis	2.33E-2	5 / 109
827 cellular response to oxidative stress	2.42E-2	4 / 64
828 skeletal muscle organ development	2.42E-2	4 / 64
829 stress-activated MAPK cascade	2.47E-2	6 / 165
830 placenta development	2.47E-2	3 / 29
831 neutrophil chemotaxis	2.47E-2	3 / 29
832 axon guidance	2.49E-2	8 / 294
833 peptide hormone secretion	2.51E-2	5 / 111
834 regulation of blood pressure	2.54E-2	4 / 65
835 response to UV	2.54E-2	4 / 65
836 protein kinase regulator activity	2.54E-2	4 / 65
837 response to light stimulus	2.6E-2	5 / 112
838 MyD88-independent toll-like receptor signaling pathway	2.68E-2	4 / 66
839 toll-like receptor 3 signaling pathway	2.68E-2	4 / 66
840 regulation of carbohydrate biosynthetic process	2.68E-2	3 / 30
841 receptor signaling protein serine/threonine kinase activity	2.68E-2	3 / 30
842 immunoglobulin production	2.68E-2	3 / 30
843 positive chemotaxis	2.68E-2	3 / 30
844 immunoglobulin mediated immune response	2.68E-2	3 / 30
845 muscle cell development	2.82E-2	4 / 67
846 cardiac muscle tissue morphogenesis	2.94E-2	3 / 31
847 gene silencing by RNA	2.94E-2	3 / 31

Function	FDR	Coverage
848 activation of pro-apoptotic gene products	2.94E-2	3 / 31
849 regulation of anti-apoptosis	2.94E-2	3 / 31
850 core promoter binding	2.94E-2	3 / 31
851 lymphocyte mediated immunity	2.95E-2	4 / 68
852 cellular component disassembly involved in apoptosis	2.95E-2	4 / 68
853 toll-like receptor 1 signaling pathway	3.11E-2	4 / 69
854 positive regulation of canonical Wnt receptor signaling pathway	3.2E-2	3 / 32
855 chondrocyte differentiation	3.2E-2	3 / 32
856 B cell mediated immunity	3.2E-2	3 / 32
857 mitochondrial transport	3.27E-2	4 / 70
858 axon	3.44E-2	4 / 71
859 muscle organ morphogenesis	3.47E-2	3 / 33
860 embryonic appendage morphogenesis	3.47E-2	3 / 33
861 embryonic limb morphogenesis	3.47E-2	3 / 33
862 negative regulation of cellular catabolic process	3.47E-2	3 / 33
863 muscle tissue morphogenesis	3.47E-2	3 / 33
864 negative regulation of cell projection organization	3.47E-2	3 / 33
865 inner ear morphogenesis	3.47E-2	3 / 33
866 positive regulation of MAP kinase activity	3.54E-2	5 / 121
867 regulation of proteolysis	3.54E-2	5 / 121
868 divalent metal ion transport	3.58E-2	6 / 179
869 viral reproductive process	3.62E-2	7 / 244
870 divalent inorganic cation transport	3.67E-2	6 / 180
871 cellular response to vitamin A	3.74E-2	3 / 34
872 negative regulation of mitotic cell cycle	3.74E-2	3 / 34
873 apoptotic mitochondrial changes	3.74E-2	3 / 34
874 cellular response to retinoic acid	3.74E-2	3 / 34
875 MyD88-dependent toll-like receptor signaling pathway	3.93E-2	4 / 74
876 adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	3.93E-2	4 / 74
877 response to oxidative stress	4.04E-2	5 / 125
878 positive regulation of protein kinase B signaling cascade	4.05E-2	3 / 35
879 cellular polysaccharide biosynthetic process	4.05E-2	3 / 35
880 regulation of cellular response to stress	4.17E-2	6 / 185
881 kinase regulator activity	4.31E-2	4 / 76
882 negative regulation of nuclear division	4.37E-2	3 / 36
883 negative regulation of mitosis	4.37E-2	3 / 36
884 vascular endothelial growth factor receptor signaling pathway	4.37E-2	3 / 36
885 regulation of fat cell differentiation	4.37E-2	3 / 36
886 telomere cap complex	4.48E-2	2 / 10
887 regulation of cardiac muscle cell proliferation	4.48E-2	2 / 10
888 intracellular steroid hormone receptor signaling pathway	4.48E-2	4 / 77
889 response to nicotine	4.48E-2	2 / 10
890 positive regulation of epithelial cell migration	4.48E-2	2 / 10
891 negative regulation of Wnt receptor signaling pathway	4.48E-2	4 / 77
892 regulation of tyrosine phosphorylation of Stat1 protein	4.48E-2	2 / 10
893 tyrosine phosphorylation of Stat1 protein	4.48E-2	2 / 10
894 interferon-gamma-mediated signaling pathway	4.48E-2	4 / 77
895 cerebellum morphogenesis	4.48E-2	2 / 10
896 MAP kinase activity	4.48E-2	2 / 10
897 regulation of protein stability	4.48E-2	4 / 77

Function	FDR	Coverage
898 creatine metabolic process	4.48E-2	2 / 10
899 phosphagen metabolic process	4.48E-2	2 / 10
900 production of molecular mediator involved in inflammatory response	4.48E-2	2 / 10
901 cerebellar cortex development	4.48E-2	2 / 10
902 arachidonic acid secretion	4.48E-2	2 / 10
903 nuclear telomere cap complex	4.48E-2	2 / 10
904 regulation of T cell apoptosis	4.48E-2	2 / 10
905 regulation of homotypic cell-cell adhesion	4.48E-2	2 / 10
906 fibroblast growth factor receptor signaling pathway	4.49E-2	5 / 129
907 Toll signaling pathway	4.6E-2	4 / 78
908 positive regulation of T cell proliferation	4.6E-2	3 / 37
909 positive regulation of muscle cell differentiation	4.6E-2	3 / 37
910 behavior	4.61E-2	6 / 190
911 regulation of interphase of mitotic cell cycle	4.62E-2	5 / 130
912 cellular response to lipopolysaccharide	4.94E-2	3 / 38
913 negative regulation of lymphocyte activation	4.94E-2	3 / 38
914 response to interleukin-1	4.94E-2	3 / 38
915 regulation of cell-matrix adhesion	4.94E-2	3 / 38
916 ATP metabolic process	5E-2	4 / 80
917 regulation of cardiac muscle tissue growth	5.28E-2	2 / 11
918 cell proliferation involved in kidney development	5.28E-2	2 / 11
919 regulation of peptidyl-threonine phosphorylation	5.28E-2	2 / 11
920 fibroblast growth factor receptor binding	5.28E-2	2 / 11
921 organ induction	5.28E-2	2 / 11
922 nuclear matrix	5.28E-2	3 / 39
923 epithelial tube branching involved in lung morphogenesis	5.28E-2	2 / 11
924 membrane protein intracellular domain proteolysis	5.28E-2	2 / 11
925 cardiac atrium morphogenesis	5.28E-2	2 / 11
926 cellular response to vitamin	5.28E-2	3 / 39
927 negative regulation of smoothened signaling pathway	5.28E-2	2 / 11
928 regulation of neuronal synaptic plasticity	5.28E-2	2 / 11
929 regulation of proteasomal ubiquitin-dependent protein catabolic process	5.28E-2	3 / 39
930 negative regulation of epithelial to mesenchymal transition	5.28E-2	2 / 11
931 hindbrain morphogenesis	5.28E-2	2 / 11
932 cardiac atrium development	5.28E-2	2 / 11
933 RNA polymerase II core promoter proximal region sequence-specific DNA binding	5.28E-2	2 / 11
934 embryonic cranial skeleton morphogenesis	5.28E-2	2 / 11
935 Ras protein signal transduction	5.3E-2	5 / 135
936 regulation of behavior	5.35E-2	4 / 82
937 response to fibroblast growth factor stimulus	5.46E-2	5 / 136
938 cellular response to fibroblast growth factor stimulus	5.46E-2	5 / 136
939 acute inflammatory response	5.56E-2	3 / 40
940 cellular response to interferon-gamma	5.56E-2	4 / 83
941 external side of plasma membrane	5.56E-2	4 / 83
942 ear morphogenesis	5.56E-2	3 / 40
943 negative regulation of DNA metabolic process	5.96E-2	3 / 41
944 regulation of fibroblast proliferation	5.96E-2	3 / 41
945 G1/S transition checkpoint	6.04E-2	4 / 85
946 regulation of DNA-dependent transcription in response to stress	6.09E-2	2 / 12
947 leukocyte homeostasis	6.09E-2	2 / 12

Function	FDR	Coverage
948 positive regulation of leukocyte apoptosis	6.09E-2	2 / 12
949 metanephric nephron epithelium development	6.09E-2	2 / 12
950 T cell receptor complex	6.09E-2	2 / 12
951 negative regulation of fatty acid metabolic process	6.09E-2	2 / 12
952 negative regulation of steroid biosynthetic process	6.09E-2	2 / 12
953 positive regulation of neuron apoptosis	6.09E-2	2 / 12
954 nuclear inner membrane	6.09E-2	2 / 12
955 DNA repair	6.09E-2	7 / 272
956 glomerulus vasculature development	6.09E-2	2 / 12
957 negative regulation of blood vessel endothelial cell migration	6.09E-2	2 / 12
958 regulation of stem cell differentiation	6.09E-2	2 / 12
959 negative regulation of lipid catabolic process	6.09E-2	2 / 12
960 carboxylic acid transport	6.09E-2	5 / 140
961 regulation of organic acid transport	6.09E-2	2 / 12
962 nitric oxide mediated signal transduction	6.09E-2	2 / 12
963 metanephric nephron tubule development	6.09E-2	2 / 12
964 regulation of cholesterol storage	6.09E-2	2 / 12
965 insulin receptor binding	6.09E-2	2 / 12
966 regulation of fatty acid transport	6.09E-2	2 / 12
967 lymphocyte homeostasis	6.09E-2	2 / 12
968 glycogen metabolic process	6.21E-2	3 / 42
969 cellular response to vascular endothelial growth factor stimulus	6.21E-2	3 / 42
970 cellular response to molecule of bacterial origin	6.21E-2	3 / 42
971 organic acid transport	6.35E-2	5 / 142
972 nuclear hormone receptor binding	6.39E-2	4 / 87
973 insulin receptor signaling pathway	6.53E-2	5 / 143
974 glucan metabolic process	6.59E-2	3 / 43
975 cellular glucan metabolic process	6.59E-2	3 / 43
976 glycolysis	6.59E-2	3 / 43
977 cellular response to radiation	6.59E-2	3 / 43
978 positive regulation of stress-activated protein kinase signaling cascade	6.59E-2	3 / 43
979 double-strand break repair	6.61E-2	4 / 88
980 positive regulation of vascular endothelial growth factor receptor signaling pathway	6.94E-2	2 / 13
981 low-density lipoprotein particle binding	6.94E-2	2 / 13
982 regulation of branching involved in ureteric bud morphogenesis	6.94E-2	2 / 13
983 negative regulation of cyclin-dependent protein kinase activity	6.94E-2	2 / 13
984 mesodermal cell differentiation	6.94E-2	2 / 13
985 negative regulation of T cell differentiation	6.94E-2	2 / 13
986 melanocyte differentiation	6.94E-2	2 / 13
987 vitamin biosynthetic process	6.94E-2	2 / 13
988 ribonucleoside catabolic process	6.94E-2	2 / 13
989 cholesterol storage	6.94E-2	2 / 13
990 dopamine metabolic process	6.94E-2	2 / 13
991 2-oxoglutarate metabolic process	6.94E-2	2 / 13
992 regulation of hormone metabolic process	6.94E-2	2 / 13
993 negative regulation of leukocyte activation	6.94E-2	3 / 44
994 metanephric tubule development	6.94E-2	2 / 13
995 pigment cell differentiation	6.94E-2	2 / 13
996 regulation of mitochondrial membrane potential	6.94E-2	2 / 13
997 acid secretion	6.94E-2	2 / 13

Function	FDR	Coverage
998 positive regulation of lipid storage	6.94E-2	2 / 13
999 cellular calcium ion homeostasis	6.95E-2	5 / 146
1000 activation of MAPK activity	7.02E-2	4 / 90
1001 regulation of insulin secretion	7.28E-2	4 / 91
1002 cell-matrix adhesion	7.28E-2	4 / 91
1003 positive regulation of Wnt receptor signaling pathway	7.32E-2	3 / 45
1004 epidermal growth factor receptor signaling pathway	7.33E-2	5 / 148
1005 regulation of muscle contraction	7.76E-2	3 / 46
1006 negative regulation of binding	7.76E-2	3 / 46
1007 metanephric epithelium development	7.89E-2	2 / 14
1008 purine-containing compound salvage	7.89E-2	2 / 14
1009 lung alveolus development	7.89E-2	2 / 14
1010 calcium ion homeostasis	7.89E-2	5 / 151
1011 regulation of epithelial cell migration	7.89E-2	2 / 14
1012 positive regulation of fat cell differentiation	7.89E-2	2 / 14
1013 icosanoid secretion	7.89E-2	2 / 14
1014 negative regulation of cell morphogenesis involved in differentiation	7.89E-2	2 / 14
1015 megakaryocyte differentiation	7.89E-2	2 / 14
1016 regulation of cardiac muscle contraction	7.89E-2	2 / 14
1017 telomeric DNA binding	7.89E-2	2 / 14
1018 icosanoid transport	7.89E-2	2 / 14
1019 negative regulation of steroid metabolic process	7.89E-2	2 / 14
1020 positive regulation of tyrosine phosphorylation of Stat5 protein	7.89E-2	2 / 14
1021 multicellular organism reproduction	7.9E-2	6 / 217
1022 multicellular organismal reproductive process	7.9E-2	6 / 217
1023 regulation of G1/S transition of mitotic cell cycle	8E-2	4 / 94
1024 positive regulation of phospholipase C activity	8E-2	4 / 94
1025 regulation of proteasomal protein catabolic process	8.08E-2	3 / 47
1026 RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity	8.08E-2	3 / 47
1027 lymphocyte activation involved in immune response	8.08E-2	3 / 47
1028 regulation of membrane potential	8.28E-2	4 / 95
1029 mitosis	8.38E-2	6 / 220
1030 nuclear division	8.38E-2	6 / 220
1031 regulation of hemostasis	8.54E-2	3 / 48
1032 regulation of blood coagulation	8.54E-2	3 / 48
1033 embryonic digit morphogenesis	8.8E-2	2 / 15
1034 oligodendrocyte differentiation	8.8E-2	2 / 15
1035 isotype switching	8.8E-2	2 / 15
1036 somatic recombination of immunoglobulin genes involved in immune response	8.8E-2	2 / 15
1037 regulation of toll-like receptor signaling pathway	8.8E-2	2 / 15
1038 RNA polymerase II transcription coactivator activity	8.8E-2	2 / 15
1039 regulation of organ formation	8.8E-2	2 / 15
1040 regulation of tyrosine phosphorylation of Stat5 protein	8.8E-2	2 / 15
1041 viral infectious cycle	8.8E-2	6 / 223
1042 somatic diversification of immunoglobulins involved in immune response	8.8E-2	2 / 15
1043 regulation of heart growth	8.8E-2	2 / 15
1044 steroid hormone mediated signaling pathway	8.8E-2	2 / 15
1045 regulation of metanephros development	8.8E-2	2 / 15
1046 positive regulation of receptor activity	8.8E-2	2 / 15
1047 Notch receptor processing	8.8E-2	2 / 15

Function	FDR	Coverage
1048 positive regulation of mesenchymal cell proliferation	8.8E-2	2 / 15
1049 regulation of S phase of mitotic cell cycle	8.8E-2	2 / 15
1050 odontogenesis of dentin-containing tooth	8.8E-2	2 / 15
1051 response to vitamin A	8.88E-2	3 / 49
1052 response to retinoic acid	8.88E-2	3 / 49
1053 cellular divalent inorganic cation homeostasis	8.97E-2	5 / 157
1054 insulin secretion	9.35E-2	4 / 99
1055 negative regulation of MAP kinase activity	9.35E-2	3 / 50
1056 positive regulation of protein catabolic process	9.35E-2	3 / 50
1057 regulation of coagulation	9.35E-2	3 / 50
1058 organelle fission	9.83E-2	6 / 229
1059 purine ribonucleoside metabolic process	9.83E-2	2 / 16
1060 positive regulation of cell-matrix adhesion	9.83E-2	2 / 16
1061 negative regulation of lymphocyte differentiation	9.83E-2	2 / 16
1062 regulation of vascular endothelial growth factor receptor signaling pathway	9.83E-2	2 / 16
1063 beta-amyloid binding	9.83E-2	2 / 16
1064 tyrosine phosphorylation of Stat5 protein	9.83E-2	2 / 16
1065 immunoglobulin production involved in immunoglobulin mediated immune response	9.83E-2	2 / 16
1066 negative regulation of cell activation	9.83E-2	3 / 51
1067 ion channel binding	9.83E-2	2 / 16
1068 ovarian follicle development	9.83E-2	2 / 16
1069 regulation of receptor biosynthetic process	9.83E-2	2 / 16
1070 regulation of gene expression, epigenetic	9.87E-2	4 / 101
1071 positive regulation of phospholipase activity	9.87E-2	4 / 101
1072 M phase of mitotic cell cycle	9.97E-2	6 / 230

Interactions

Gene 1	Gene 2	Weight	Network group	Networks
SMAD4	SMAD2	0.09168746881186962	Co-expression	Bild-Nevins-2006 B Burlington-Shaughnessy-2008 Hummel-Siebert-2006 Rieger-Chu-2004
HSP90AB1	HSP90AA1	0.07092966372147202	Co-expression	Berchtold-Cotman-2008 Bild-Nevins-2006 B Kang-Willman-2010 Nakayama-Hasegawa-2007 Ramaswamy-Golub-2001
LIG4	SMAD1	0.05450665485113859	Co-expression	Hummel-Siebert-2006 Kang-Willman-2010 Ramaswamy-Golub-2001
SMAD7	TGIF1	0.05414937250316143	Co-expression	Kang-Willman-2010 Nakayama-Hasegawa-2007 Rieger-Chu-2004 Wang-Maris-2006
LIG4	RB1	0.05335725285112858	Co-expression	Bild-Nevins-2006 B Burlington-Shaughnessy-2008 Wang-Maris-2006
JAG1	ACVR1	0.05155155621469021	Co-expression	Berchtold-Cotman-2008 Bild-Nevins-2006 B Nakayama-Hasegawa-2007
STAT5A	STAT5B	0.05045503377914429	Co-expression	Bild-Nevins-2006 B Hummel-Siebert-2006
SMAD7	ID2	0.04825983941555023	Co-expression	Kang-Willman-2010 Rieger-Chu-2004 Wang-Maris-2006
LYN	SYK	0.04402371495962143	Co-expression	Hummel-Siebert-2006 Nakayama-Hasegawa-2007 Wang-Maris-2006
CBFB	SMAD4	0.03993440233170986	Co-expression	Berchtold-Cotman-2008 Ramaswamy-Golub-2001 Wu-Garvey-2007
MAPK14	ARNT	0.039857231080532074	Co-expression	Burlington-Shaughnessy-2008 Hummel-Siebert-2006
SMAD2	SMAP1	0.03799214493483305	Co-expression	Bild-Nevins-2006 B Nakayama-Hasegawa-2007
LYN	PTPRC	0.035695469938218594	Co-expression	Bild-Nevins-2006 B Burlington-Shaughnessy-2008 Nakayama-Hasegawa-2007
RARA	SMAD3	0.03547972720116377	Co-expression	Bild-Nevins-2006 B Ramaswamy-Golub-2001
LCK	ZAP70	0.0350326644256711	Co-expression	Bild-Nevins-2006 B Kang-Willman-2010 Ramaswamy-Golub-2001
HSP90AA1	SMAP1	0.0348156588152051	Co-expression	Burlington-Shaughnessy-2008 Rieger-Chu-2004
EPHB2	FOXG1	0.0344112403690815	Co-expression	Bild-Nevins-2006 B
SYK	INPP5D	0.034010024741292	Co-expression	Bild-Nevins-2006 B Hummel-Siebert-2006 Wang-Maris-2006
BMP2	CD36	0.033818915486335754	Co-expression	Burlington-Shaughnessy-2008
NFKB1	LYN	0.033628868870437145	Co-expression	Hummel-Siebert-2006 Ramaswamy-Golub-2001 Wang-Maris-2006
ID2	TGIF1	0.03331202082335949	Co-expression	Kang-Willman-2010 Rieger-Chu-2004 Wu-Garvey-2007
LYN	INPP5D	0.033197433687746525	Co-expression	Bild-Nevins-2006 B Nakayama-Hasegawa-2007 Wu-Garvey-2007

Gene 1	Gene 2	Weight	Network group	Networks
AKT1	MAPK9	0.03287607338279486	Co-expression	Kang-Willman-2010 Rieger-Chu-2004
OSM	SOCS3	0.032460618764162064	Co-expression	Kang-Willman-2010
BMPR1A	SMAD2	0.03234745375812054	Co-expression	Kang-Willman-2010 Wang-Maris-2006
LCK	TGFBR2	0.031974432058632374	Co-expression	Kang-Willman-2010 Perou-Botstein-1999
IL4R	CD74	0.03156293788924813	Co-expression	Hummel-Siebert-2006 Nakayama-Hasegawa-2007 Ramaswamy-Golub-2001
SMAD7	KLF10	0.031519277952611446	Co-expression	Bild-Nevins-2006 B Kang-Willman-2010
ILK	BAD	0.031116542406380177	Co-expression	Hummel-Siebert-2006 Wang-Maris-2006
STAT5A	INPP5D	0.030677043367177248	Co-expression	Bild-Nevins-2006 B Burington-Shaughnessy-2008 Wang-Maris-2006
HSP90AA1	HMGB1	0.03057844005525112	Co-expression	Hummel-Siebert-2006 Wang-Maris-2006
GLI3	SMO	0.030051090754568577	Co-expression	Berchtold-Cotman-2008 Kang-Willman-2010
JAG1	GATA6	0.029969326220452785	Co-expression	Hummel-Siebert-2006 Nakayama-Hasegawa-2007
ACVR2A	CD36	0.02985968254506588	Co-expression	Kang-Willman-2010
NEUROD1	TAL1	0.029504990205168724	Co-expression	Nakayama-Hasegawa-2007
IGF2	CSF1	0.029051654040813446	Co-expression	Wang-Maris-2006
BCL2	SMAD3	0.028530972078442574	Co-expression	Burington-Shaughnessy-2008
SRF	POLR1C	0.028238126076757908	Co-expression	Bild-Nevins-2006 B Kang-Willman-2010
JAK2	TIAM1	0.02814759872853756	Co-expression	Bild-Nevins-2006 B
AKT1	RARA	0.0280342074111104	Co-expression	Burington-Shaughnessy-2008 Rieger-Chu-2004
SRF	KLF10	0.027619299478828907	Co-expression	Berchtold-Cotman-2008 Nakayama-Hasegawa-2007
GATA4	BMP7	0.027609989047050476	Co-expression	Bild-Nevins-2006 B
LYN	PNP	0.02747542830184102	Co-expression	Berchtold-Cotman-2008 Ramaswamy-Golub-2001 Wu-Garvey-2007
SMAD7	SMAD1	0.0272242221981287	Co-expression	Wu-Garvey-2007
NGF	SMO	0.026653219014406204	Co-expression	Rieger-Chu-2004
ACVR2A	JAG1	0.02636973187327385	Co-expression	Perou-Botstein-1999
CLU	HOPX	0.026110898703336716	Co-expression	Bild-Nevins-2006 B
TGIF1	LIF	0.02586931735277176	Co-expression	Berchtold-Cotman-2008 Nakayama-Hasegawa-2007
ETS1	ZAP70	0.02562770899385214	Co-expression	Ramaswamy-Golub-2001 Rieger-Chu-2004
SMAD1	FOXO3	0.025555658154189587	Co-expression	Kang-Willman-2010 Wang-Maris-2006
JAK2	ACVR1	0.025434140115976334	Co-expression	Kang-Willman-2010
CLUL1	ACVR1	0.025256844237446785	Co-expression	Bild-Nevins-2006 B
GATA4	FOXG1	0.025174632668495178	Co-expression	Nakayama-Hasegawa-2007 Rieger-Chu-2004
MNDA	MSR1	0.02516944333910942	Co-expression	Nakayama-Hasegawa-2007 Wang-Maris-2006
AKT1	CD74	0.025165939703583717	Co-expression	Wu-Garvey-2007
BDNF	NRG1	0.02515152469277382	Co-expression	Nakayama-Hasegawa-2007
BMPR1B	TGFB2	0.024942884221673012	Co-expression	Berchtold-Cotman-2008
SYK	CD74	0.024919923394918442	Co-expression	Nakayama-Hasegawa-2007 Ramaswamy-Golub-2001
CLU	MAPT	0.024890608619898558	Co-expression	Perou-Botstein-1999 Rieger-Chu-2004

Gene 1	Gene 2	Weight	Network group	Networks
ARNT	ETS1	0.024809246882796288	Co-expression	Hummel-Siebert-2006 Rieger-Chu-2004
FGF2	SOCS2	0.024693841114640236	Co-expression	Hummel-Siebert-2006
BMP2	DLX5	0.02461368776857853	Co-expression	Bild-Nevins-2006 B
JUN	KLF10	0.024568046908825636	Co-expression	Berchtold-Cotman-2008 Ramaswamy-Golub-2001
RB1	ETS1	0.02453891560435295	Co-expression	Bild-Nevins-2006 B
BMP7	METRN	0.024498112499713898	Co-expression	Berchtold-Cotman-2008
LYN	MNDA	0.024248364381492138	Co-expression	Nakayama-Hasegawa-2007 Wu-Garvey-2007
TGFB1	NEUROD1	0.0242238100618124	Co-expression	Ramaswamy-Golub-2001
CCNE1	POLR1C	0.024129534140229225	Co-expression	Burington-Shaughnessy-2008 Perou-Botstein-1999
HIF1A	PTPRC	0.024044647812843323	Co-expression	Burington-Shaughnessy-2008
TGFBR3	TGFBR2	0.023960103280842304	Co-expression	Wang-Maris-2006 Wu-Garvey-2007
TGFBR3	GFI1	0.02386941760778427	Co-expression	Hummel-Siebert-2006
IL4R	INPP5D	0.023826470132917166	Co-expression	Bild-Nevins-2006 B Hummel-Siebert-2006 Wang-Maris-2006
CITED1	FOXG1	0.023776240646839142	Co-expression	Kang-Willman-2010
LIG4	ARNT	0.02375366911292076	Co-expression	Ramaswamy-Golub-2001
BAD	STAT5B	0.023646008223295212	Co-expression	Hummel-Siebert-2006
SRF	TGIF1	0.02362861018627882	Co-expression	Ramaswamy-Golub-2001 Wang-Maris-2006
NPTN	KLF10	0.023605138063430786	Co-expression	Bild-Nevins-2006 B Nakayama-Hasegawa-2007
PTPRC	STAT5B	0.023489883169531822	Co-expression	Perou-Botstein-1999
SMO	GATA4	0.02342734206467867	Co-expression	Rieger-Chu-2004 Wang-Maris-2006
HIF1A	RB1	0.023328172974288464	Co-expression	Rieger-Chu-2004 Wu-Garvey-2007
SMAD6	NOTCH1	0.023156311362981796	Co-expression	Nakayama-Hasegawa-2007 Perou-Botstein-1999
KIT	SYK	0.02298440970480442	Co-expression	Burington-Shaughnessy-2008
GLI3	NEUROD1	0.02297944761812687	Co-expression	Rieger-Chu-2004
TGFB2	GATA6	0.02267659828066826	Co-expression	Nakayama-Hasegawa-2007
CLUL1	BDNF	0.02254449389874935	Co-expression	Hummel-Siebert-2006
NOTCH1	FOXG1	0.02248748578131199	Co-expression	Kang-Willman-2010
TGIF1	HLX	0.022385938093066216	Co-expression	Kang-Willman-2010
BMPR1A	ACVR1	0.022346634417772293	Co-expression	Ramaswamy-Golub-2001
SMO	THRB	0.02232656255364418	Co-expression	Ramaswamy-Golub-2001
TGFB1	TGIF2	0.022289371117949486	Co-expression	Wu-Garvey-2007
SMAD3	IL4R	0.022153387777507305	Co-expression	Rieger-Chu-2004 Wang-Maris-2006
MAPK14	ACVR2A	0.02213389240205288	Co-expression	Wu-Garvey-2007
KITLG	TGFB3	0.021985990926623344	Co-expression	Bild-Nevins-2006 B
CITED1	TGFBR3	0.021890314295887947	Co-expression	Bild-Nevins-2006 B
ACVRL1	CD36	0.021654412150382996	Co-expression	Rieger-Chu-2004
FGF2	NRG1	0.021597133949398994	Co-expression	Bild-Nevins-2006 B
NFKB1	TGIF2	0.021580936387181282	Co-expression	Rieger-Chu-2004
KITLG	MSR1	0.02147693559527397	Co-expression	Ramaswamy-Golub-2001
JAK2	VNN1	0.02142908424139023	Co-expression	Rieger-Chu-2004
NGFR	CLU	0.021387636195868254	Co-expression	Rieger-Chu-2004 Wang-Maris-2006
NKX2-5	RUNX1	0.02135641500353813	Co-expression	Hummel-Siebert-2006
RUNX3	NFKB1	0.021110589616000652	Co-expression	Hummel-Siebert-2006 Kang-Willman-2010
MAPK14	SMAD3	0.021059874445199966	Co-expression	Hummel-Siebert-2006
ID2	HOPX	0.021046658977866173	Co-expression	Wang-Maris-2006
RB1	KLF10	0.021021492779254913	Co-expression	Nakayama-Hasegawa-2007

Gene 1	Gene 2	Weight	Network group	Networks
CBFB	POU4F2	0.021005690097808838	Co-expression	Wang-Maris-2006
TP53	TGIF2	0.020965378265827894	Co-expression	Nakayama-Hasegawa-2007 Wang-Maris-2006
PPARG	THRB	0.020918432623147964	Co-expression	Kang-Willman-2010
ADA	EPHB2	0.020712118595838547	Co-expression	Bild-Nevins-2006 B
NFKB1	CSF1	0.020692041143774986	Co-expression	Berchtold-Cotman-2008
TP53	XRCC5	0.020633612759411335	Co-expression	Nakayama-Hasegawa-2007 Ramaswamy-Golub-2001
INPP5D	MNDA	0.02043072134256363	Co-expression	Berchtold-Cotman-2008
EPHB2	IGF2	0.020240159705281258	Co-expression	Rieger-Chu-2004 Wu-Garvey-2007
KIT	TGFB2	0.020177306607365608	Co-expression	Bild-Nevins-2006 B
BMPR1B	GATA4	0.020164284855127335	Co-expression	Burington-Shaughnessy-2008
SMAD3	BMPR1B	0.020008837804198265	Co-expression	Bild-Nevins-2006 B
ACVR2A	BMPR1B	0.020004384219646454	Co-expression	Kang-Willman-2010
LIG4	TP53	0.019680801779031754	Co-expression	Burington-Shaughnessy-2008
GFI1	TESC	0.01958276890218258	Co-expression	Hummel-Siebert-2006
LIF	FOXG1	0.01946423202753067	Co-expression	Bild-Nevins-2006 B
PAX6	BMP7	0.01945630833506584	Co-expression	Rieger-Chu-2004
SMAD3	NRG1	0.01944870874285698	Co-expression	Ramaswamy-Golub-2001
ACVR2A	ID2	0.01937408186495304	Co-expression	Ramaswamy-Golub-2001
SMAD1	IL2RA	0.019372297450900078	Co-expression	Ramaswamy-Golub-2001
NGFR	MSR1	0.01919521577656269	Co-expression	Rieger-Chu-2004
MAPK14	AKT1	0.01917402632534504	Co-expression	Nakayama-Hasegawa-2007
NFKB1	TGFB2	0.019164062570780516	Co-expression	Bild-Nevins-2006 B Kang-Willman-2010
LCK	INPP5D	0.019148088991642	Co-expression	Bild-Nevins-2006 B Wang-Maris-2006
SMAD6	KITLG	0.019082525745034218	Co-expression	Rieger-Chu-2004
PAX6	CLU	0.019053014926612377	Co-expression	Berchtold-Cotman-2008 Rieger-Chu-2004
SMAD6	DLX5	0.018918294459581375	Co-expression	Bild-Nevins-2006 B
GLI3	LCK	0.018907349556684494	Co-expression	Perou-Botstein-1999
CLU	TAL1	0.018824132159352303	Co-expression	Burington-Shaughnessy-2008
BMP4	KITLG	0.018815267831087112	Co-expression	Bild-Nevins-2006 B
NKX2-5	THRB	0.01877574808895588	Co-expression	Nakayama-Hasegawa-2007
PTPRC	CD74	0.018687117844820023	Co-expression	Bild-Nevins-2006 B Nakayama-Hasegawa-2007 Wang-Maris-2006
OSM	PNP	0.018625492230057716	Co-expression	Wang-Maris-2006
KLF10	SMAP1	0.01858752779662609	Co-expression	Hummel-Siebert-2006
HIF1A	ID2	0.018528727814555168	Co-expression	Hummel-Siebert-2006
HMGB1	NGF	0.01851152186281979	Co-expression	Bild-Nevins-2006 B Perou-Botstein-1999
FBXW7	ACVR2A	0.018511086702346802	Co-expression	Kang-Willman-2010
BDNF	FOXO3	0.01842688024044037	Co-expression	Rieger-Chu-2004
SMAD6	PAX6	0.018324004486203194	Co-expression	Burington-Shaughnessy-2008
BCL2	MEN1	0.018292113207280636	Co-expression	Ramaswamy-Golub-2001 Wu-Garvey-2007
SMAD7	ACVR1	0.018275246489793062	Co-expression	Hummel-Siebert-2006 Nakayama-Hasegawa-2007
ADA	ZAP70	0.018204934895038605	Co-expression	Bild-Nevins-2006 B Ramaswamy-Golub-2001
SMAD6	CD36	0.018179746344685555	Co-expression	Perou-Botstein-1999
NFKB1	HLX	0.018092120066285133	Co-expression	Perou-Botstein-1999 Ramaswamy-Golub-2001
SYK	ZAP70	0.018074996769428253	Co-expression	Bild-Nevins-2006 B Kang-Willman-2010
BMP2	TGIF1	0.017873652279376984	Co-expression	Wang-Maris-2006
GLI3	SOCS3	0.01785321719944477	Co-expression	Wang-Maris-2006
BMP2	HLX	0.017667800188064575	Co-expression	Hummel-Siebert-2006

Gene 1	Gene 2	Weight	Network group	Networks
MAPK14	IL2RA	0.017617756500840187	Co-expression	Wang-Maris-2006
TGFBR3	TAL1	0.01754610985517502	Co-expression	Wang-Maris-2006
NFKB1	STAT5A	0.01739482581615448	Co-expression	Wang-Maris-2006
HIF1A	JAG1	0.017389990389347076	Co-expression	Ramaswamy-Golub-2001
PTPRC	MNDA	0.017262699082493782	Co-expression	Berchtold-Cotman-2008
CITED1	DRD2	0.01722211018204689	Co-expression	Hummel-Siebert-2006
GLI3	EPHB2	0.017106618732213974	Co-expression	Hummel-Siebert-2006
NTF3	PPARG	0.017075609415769577	Co-expression	Kang-Willman-2010
RUNX3	ZAP70	0.016974654980003834	Co-expression	Bild-Nevins-2006 B Wang-Maris-2006
RUNX3	SYK	0.016917718574404716	Co-expression	Bild-Nevins-2006 B
LIG4	ACVR2A	0.016900867223739624	Co-expression	Wu-Garvey-2007
BMPR1A	GATA6	0.016849009320139885	Co-expression	Ramaswamy-Golub-2001
IAPP	POU4F2	0.016774801071733236	Co-expression	Bild-Nevins-2006 B Hummel-Siebert-2006
RUNX3	RUNX1	0.016698097810149193	Co-expression	Wu-Garvey-2007
CBFB	JUN	0.01665894314646721	Co-expression	Wu-Garvey-2007
RB1	XRCC5	0.016475297510623932	Co-expression	Ramaswamy-Golub-2001
IAPP	ACVR1B	0.016468532383441925	Co-expression	Wang-Maris-2006
CREBBP	ACVR1	0.016334036365151405	Co-expression	Wu-Garvey-2007
TGFBR3	STAT5A	0.01630791649222374	Co-expression	Wang-Maris-2006
INPP5D	CD74	0.016251899302005768	Co-expression	Hummel-Siebert-2006 Nakayama-Hasegawa-2007
ETS1	LCK	0.016244810074567795	Co-expression	Ramaswamy-Golub-2001
IL4R	FGF2	0.016214663162827492	Co-expression	Burington-Shaughnessy-2008
GLI3	SMAD3	0.016207044944167137	Co-expression	Nakayama-Hasegawa-2007
SMAD1	BMP7	0.01620492897927761	Co-expression	Hummel-Siebert-2006
KIT	DRD2	0.015910981222987175	Co-expression	Ramaswamy-Golub-2001
HIF1A	LYN	0.015888167079538107	Co-expression	Nakayama-Hasegawa-2007 Perou-Botstein-1999
TP53	HMGB1	0.015824420377612114	Co-expression	Wang-Maris-2006
DRD2	NKX2-5	0.01577940210700035	Co-expression	Bild-Nevins-2006 B
RUNX3	TGFB1	0.015726614743471146	Co-expression	Ramaswamy-Golub-2001
SMAD7	SMAD2	0.015646034851670265	Co-expression	Burington-Shaughnessy-2008
PTPRC	LCK	0.01563969301059842	Co-expression	Nakayama-Hasegawa-2007 Wang-Maris-2006
FGF2	CD74	0.015587645582854748	Co-expression	Burington-Shaughnessy-2008
SMAD7	HOPX	0.015516763553023338	Co-expression	Hummel-Siebert-2006
PAX6	DLX5	0.015486026182770729	Co-expression	Wu-Garvey-2007
KIT	CD36	0.01542868372052908	Co-expression	Perou-Botstein-1999
APC	FOXO3	0.015425564721226692	Co-expression	Rieger-Chu-2004
ACVR2A	BMP2	0.015368836000561714	Co-expression	Perou-Botstein-1999
IAPP	ETS1	0.015333067625761032	Co-expression	Perou-Botstein-1999
STAT5A	IL4R	0.015291995368897915	Co-expression	Rieger-Chu-2004 Wang-Maris-2006
SMAD1	FGF2	0.015279892832040787	Co-expression	Berchtold-Cotman-2008
STAT5A	RUNX1	0.01526802871376276	Co-expression	Ramaswamy-Golub-2001
IL2RA	CD74	0.015264827758073807	Co-expression	Ramaswamy-Golub-2001
LIG4	HSP90AB1	0.01524015050381422	Co-expression	Bild-Nevins-2006 B
TGFB2	XRCC4	0.015185129828751087	Co-expression	Ramaswamy-Golub-2001
INPP5D	HLX	0.015144518576562405	Co-expression	Burington-Shaughnessy-2008
SMAD7	SMAD4	0.01513982005417347	Co-expression	Burington-Shaughnessy-2008
HIF1A	PNP	0.015066707506775856	Co-expression	Nakayama-Hasegawa-2007
CREBBP	NFKB1	0.015044637024402618	Co-expression	Wu-Garvey-2007
HIF1A	SMAD1	0.01500045508146286	Co-expression	Berchtold-Cotman-2008
STAT5A	SYK	0.014835170470178127	Co-expression	Wang-Maris-2006
TGFBR2	SOCS2	0.014830635860562325	Co-expression	Burington-Shaughnessy-2008
CLU	FGF2	0.014826457016170025	Co-expression	Berchtold-Cotman-2008
NTF3	BMP7	0.014789164997637272	Co-expression	Hummel-Siebert-2006

Gene 1	Gene 2	Weight	Network group	Networks
STAT5A	SOCS2	0.014763821847736835	Co-expression	Rieger-Chu-2004
PTPRC	SYK	0.014738695695996284	Co-expression	Bild-Nevins-2006 B
CITED1	BDNF	0.014655741630122066	Co-expression	Berchtold-Cotman-2008 Wang-Maris-2006
IL2RA	MNDA	0.014645054936408997	Co-expression	Hummel-Siebert-2006
FOXH1	GLI3	0.014635000377893448	Co-expression	Hummel-Siebert-2006
LCK	SMAD3	0.014544375240802765	Co-expression	Hummel-Siebert-2006
NFKB1	SYK	0.01441972702741623	Co-expression	Wang-Maris-2006
TP53	RB1	0.014419361017644405	Co-expression	Ramaswamy-Golub-2001
PPARG	CLU	0.014411445707082748	Co-expression	Burington-Shaughnessy-2008
RARA	INS	0.014261210337281227	Co-expression	Nakayama-Hasegawa-2007
NGF	GATA4	0.014204475097358227	Co-expression	Rieger-Chu-2004
HSP90AB1	POLR1C	0.01417803205549717	Co-expression	Burington-Shaughnessy-2008 Nakayama-Hasegawa-2007
SMAD1	POU4F2	0.014102627523243427	Co-expression	Wang-Maris-2006
FGF2	TGFB2	0.014024253934621811	Co-expression	Berchtold-Cotman-2008
PTPRC	INPP5D	0.0139940045773983	Co-expression	Nakayama-Hasegawa-2007 Wang-Maris-2006
PAX6	BMPR1B	0.013975005596876144	Co-expression	Berchtold-Cotman-2008
TGFBR3	TGFB2	0.013925460167229176	Co-expression	Berchtold-Cotman-2008
OSM	ACVRL1	0.013861631043255329	Co-expression	Ramaswamy-Golub-2001
KITLG	CSF1	0.01385705266147852	Co-expression	Burington-Shaughnessy-2008
FOXH1	NGF	0.01384820882230997	Co-expression	Hummel-Siebert-2006
BMPR1B	IL2RA	0.013843282125890255	Co-expression	Kang-Willman-2010
GLI3	PAX6	0.013709837570786476	Co-expression	Berchtold-Cotman-2008
APC	CCNE1	0.013690393418073654	Co-expression	Wu-Garvey-2007
HIF1A	KLF10	0.013665822334587574	Co-expression	Nakayama-Hasegawa-2007
NTF3	ACVR1	0.013639001175761223	Co-expression	Berchtold-Cotman-2008
RARA	KLF10	0.013613268733024597	Co-expression	Ramaswamy-Golub-2001
NTRK3	BEX1	0.013605279847979546	Co-expression	Nakayama-Hasegawa-2007
TGFBR3	CLU	0.013598838821053505	Co-expression	Berchtold-Cotman-2008
BMPR1A	TGFBR3	0.01355715375393629	Co-expression	Berchtold-Cotman-2008
KIT	STAT5A	0.013510044664144516	Co-expression	Nakayama-Hasegawa-2007
SMAD4	SOCS2	0.01341210212558508	Co-expression	Ramaswamy-Golub-2001
KIT	ACVR1	0.013350557535886765	Co-expression	Berchtold-Cotman-2008
CREBBP	CD74	0.013329505920410156	Co-expression	Perou-Botstein-1999
LCK	IL4R	0.013325413689017296	Co-expression	Hummel-Siebert-2006
PNP	TGIF1	0.013297813944518566	Co-expression	Berchtold-Cotman-2008
ID2	KLF10	0.013175396248698235	Co-expression	Kang-Willman-2010
PNP	TGFB2	0.013109778054058552	Co-expression	Bild-Nevins-2006 B
CREBBP	CD36	0.013095029629766941	Co-expression	Perou-Botstein-1999
RUNX3	INPP5D	0.013088750187307596	Co-expression	Bild-Nevins-2006 B Wang-Maris-2006
CREBBP	POLR1C	0.013068100437521935	Co-expression	Perou-Botstein-1999
MAPT	LIF	0.013058546930551529	Co-expression	Wu-Garvey-2007
HLX	VNN1	0.013058308511972427	Co-expression	Burington-Shaughnessy-2008
ACVR1	KLF10	0.013028580695390701	Co-expression	Rieger-Chu-2004
AKT1	ANKRD54	0.01302102766931057	Co-expression	Kang-Willman-2010
SMAD7	TGFBR2	0.013011857867240906	Co-expression	Burington-Shaughnessy-2008
SMO	BMP7	0.01297042891383171	Co-expression	Berchtold-Cotman-2008
ETS1	PNP	0.012963257730007172	Co-expression	Wu-Garvey-2007
INPP5D	ZAP70	0.012962981592863798	Co-expression	Bild-Nevins-2006 B Wang-Maris-2006
APC	NPTN	0.012856153771281242	Co-expression	Kang-Willman-2010
GLI3	TGFBR2	0.01278216578066349	Co-expression	Perou-Botstein-1999
FOXH1	BEX1	0.012711492367088795	Co-expression	Nakayama-Hasegawa-2007
PAX6	EPHB2	0.012677688151597977	Co-expression	Wang-Maris-2006
JUN	MNDA	0.012675328180193901	Co-expression	Hummel-Siebert-2006
GATA4	IGF2	0.012566971592605114	Co-expression	Perou-Botstein-1999

Gene 1	Gene 2	Weight	Network group	Networks
NTF3	NTRK3	0.012553674168884754	Co-expression	Nakayama-Hasegawa-2007
LYN	TAL1	0.012505786493420601	Co-expression	Wang-Maris-2006
LYN	CLU	0.01248995866626501	Co-expression	Perou-Botstein-1999
HIF1A	LIF	0.012488553300499916	Co-expression	Nakayama-Hasegawa-2007
NGFR	PAX6	0.01247795857489109	Co-expression	Rieger-Chu-2004
JAK2	GFI1	0.012457642704248428	Co-expression	Hummel-Siebert-2006
ACVRL1	STAT5A	0.012434176169335842	Co-expression	Nakayama-Hasegawa-2007
FGF2	TGFB3	0.012433418072760105	Co-expression	Perou-Botstein-1999
HSP90AA1	PNP	0.012413534335792065	Co-expression	Burington-Shaughnessy-2008
BCL2	IL4R	0.012406312860548496	Co-expression	Rieger-Chu-2004
NGF	SOCS3	0.012394048273563385	Co-expression	Wu-Garvey-2007
TP53	TIAM1	0.012347506359219551	Co-expression	Ramaswamy-Golub-2001
ADA	RUNX1	0.012308372184634209	Co-expression	Ramaswamy-Golub-2001
BMP4	PNP	0.012211834080517292	Co-expression	Wu-Garvey-2007
PTPRC	HLX	0.012105201371014118	Co-expression	Wu-Garvey-2007
CREBBP	KIT	0.012007132172584534	Co-expression	Perou-Botstein-1999
JUN	LIF	0.011965018697082996	Co-expression	Berchtold-Cotman-2008
XRCC6	ACIN1	0.011941852048039436	Co-expression	Burington-Shaughnessy-2008
NOTCH1	POLR1C	0.01192822027951479	Co-expression	Perou-Botstein-1999
BMP2	LIF	0.011889087967574596	Co-expression	Berchtold-Cotman-2008
NKX2-5	VNN1	0.011878862977027893	Co-expression	Wang-Maris-2006
ARNT	SMO	0.011815392412245274	Co-expression	Wang-Maris-2006
NFKB1	AKT1	0.011783776804804802	Co-expression	Hummel-Siebert-2006
ID2	JAG1	0.01172269694507122	Co-expression	Rieger-Chu-2004
TGFB1	ADA	0.011708241887390614	Co-expression	Perou-Botstein-1999
HMGB1	POLR1D	0.011686976999044418	Co-expression	Nakayama-Hasegawa-2007
HIF1A	RARA	0.0116854477673769	Co-expression	Ramaswamy-Golub-2001
RUNX3	IL4R	0.011664293706417084	Co-expression	Bild-Nevins-2006 B
TGFB3	JAK2	0.011639190837740898	Co-expression	Hummel-Siebert-2006
BDNF	MSR1	0.011571087874472141	Co-expression	Wu-Garvey-2007
TP53	PNP	0.011563011445105076	Co-expression	Berchtold-Cotman-2008
MEN1	TCOF1	0.011548996903002262	Co-expression	Wu-Garvey-2007
HLX	SOCS2	0.011422382667660713	Co-expression	Kang-Willman-2010
HIF1A	HLX	0.011382526718080044	Co-expression	Kang-Willman-2010
RUNX3	TGFB2	0.011371619068086147	Co-expression	Rieger-Chu-2004
LCK	EPHB2	0.011332783848047256	Co-expression	Perou-Botstein-1999
CREBBP	RB1	0.011327026411890984	Co-expression	Rieger-Chu-2004
LCK	ADA	0.011326047591865063	Co-expression	Ramaswamy-Golub-2001
TGFB3	JAG1	0.011319425888359547	Co-expression	Berchtold-Cotman-2008
SMAD6	PNP	0.01131749339401722	Co-expression	Wu-Garvey-2007
AKT1	ID2	0.011275344528257847	Co-expression	Ramaswamy-Golub-2001
SOCS2	MNDA	0.011255279183387756	Co-expression	Hummel-Siebert-2006
PNP	RUNX1	0.01125526987016201	Co-expression	Wu-Garvey-2007
ID2	BMP2	0.011216840706765652	Co-expression	Nakayama-Hasegawa-2007
IAPP	CCNE1	0.01108609326183796	Co-expression	Wu-Garvey-2007
INS	RUNX2	0.011015940457582474	Co-expression	Berchtold-Cotman-2008
NGFR	CD74	0.010960891842842102	Co-expression	Wang-Maris-2006
RARA	ILK	0.010876295156776905	Co-expression	Rieger-Chu-2004
ACVR1	NPTN	0.010802917182445526	Co-expression	Nakayama-Hasegawa-2007
CLUL1	RUNX2	0.01080134604126215	Co-expression	Nakayama-Hasegawa-2007
LCK	SMAP1	0.010655581019818783	Co-expression	Kang-Willman-2010
PNP	SOCS3	0.01064732950180769	Co-expression	Berchtold-Cotman-2008
LYN	ACVR1	0.010561073198914528	Co-expression	Perou-Botstein-1999
MEN1	TGIF2	0.01054809894412756	Co-expression	Hummel-Siebert-2006
XRCC4	GATA6	0.010343123227357864	Co-expression	Wu-Garvey-2007
ADA	JAG1	0.010316720232367516	Co-expression	Perou-Botstein-1999
STAT5A	TGIF2	0.010308625176548958	Co-expression	Berchtold-Cotman-2008
ID2	TGFB2	0.01027731690555811	Co-expression	Rieger-Chu-2004
CD74	MEN1	0.01027196366339922	Co-expression	Rieger-Chu-2004

Gene 1	Gene 2	Weight	Network group	Networks
LYN	TGIF1	0.010242313146591187	Co-expression	Hummel-Siebert-2006
BAD	HLX	0.010207302868366241	Co-expression	Wu-Garvey-2007
OSM	SMO	0.010158143704757094	Co-expression	Bild-Nevins-2006 B Burlington-Shaughnessy-2008
NGFR	INPP5D	0.010093571618199348	Co-expression	Wu-Garvey-2007
ARNT	INPP5D	0.009995552711188793	Co-expression	Ramaswamy-Golub-2001
TGIF1	ACVR1	0.009848738089203835	Co-expression	Nakayama-Hasegawa-2007
NFKB1	MNDA	0.009795596823096275	Co-expression	Bild-Nevins-2006 B
RUNX3	LYN	0.009759042412042618	Co-expression	Bild-Nevins-2006 B
HIF1A	FGF2	0.009708140976727009	Co-expression	Berchtold-Cotman-2008
RARA	LYN	0.009671247564256191	Co-expression	Ramaswamy-Golub-2001
PTPRC	ZAP70	0.009669489227235317	Co-expression	Wang-Maris-2006
IL4R	RUNX1	0.009661329910159111	Co-expression	Rieger-Chu-2004
PAX6	HLX	0.009635702706873417	Co-expression	Perou-Botstein-1999
ID2	PPARG	0.009615076705813408	Co-expression	Rieger-Chu-2004
INS	TGFB3	0.009591788984835148	Co-expression	Wang-Maris-2006
LYN	HLX	0.009506721049547195	Co-expression	Ramaswamy-Golub-2001
RB1	MNDA	0.009443209506571293	Co-expression	Nakayama-Hasegawa-2007
NFKB1	INPP5D	0.009375657886266708	Co-expression	Hummel-Siebert-2006
BDNF	IL2RA	0.009286521933972836	Co-expression	Wu-Garvey-2007
PTPRC	JAK2	0.009279023855924606	Co-expression	Nakayama-Hasegawa-2007
BMP7	MEN1	0.009173995815217495	Co-expression	Hummel-Siebert-2006
TGFB1	CD74	0.009118885733187199	Co-expression	Rieger-Chu-2004
INPP5D	SOCS2	0.009107468649744987	Co-expression	Kang-Willman-2010
SRF	LIF	0.009066116996109486	Co-expression	Berchtold-Cotman-2008
CITED1	LCK	0.009061806835234165	Co-expression	Burlington-Shaughnessy-2008
FOXG1	BEX1	0.009016506373882294	Co-expression	Berchtold-Cotman-2008
STAT5A	PTPRC	0.008968863636255264	Co-expression	Wang-Maris-2006
HSP90AB1	NPTN	0.008878517895936966	Co-expression	Wu-Garvey-2007
PNP	EPHB2	0.008858299814164639	Co-expression	Perou-Botstein-1999
ACVR1	TGFB2	0.008824551478028297	Co-expression	Perou-Botstein-1999
CBFB	MAPK9	0.008771130815148354	Co-expression	Rieger-Chu-2004
LIF	TAL1	0.008755821734666824	Co-expression	Wu-Garvey-2007
NGFR	POU4F2	0.008733177557587624	Co-expression	Ramaswamy-Golub-2001
RARA	NGF	0.008717562071979046	Co-expression	Berchtold-Cotman-2008
NFKB1	LCK	0.008690367452800274	Co-expression	Nakayama-Hasegawa-2007
LCK	GFI1	0.008651496842503548	Co-expression	Nakayama-Hasegawa-2007
CREBBP	ACIN1	0.008650075644254684	Co-expression	Hummel-Siebert-2006
AKT1	ACIN1	0.008603736758232117	Co-expression	Rieger-Chu-2004
HSP90AB1	JUN	0.008523243479430676	Co-expression	Ramaswamy-Golub-2001
SMO	MAPT	0.008422274142503738	Co-expression	Burlington-Shaughnessy-2008
INS	KITLG	0.008419353514909744	Co-expression	Wang-Maris-2006
IAPP	THRB	0.008406275883316994	Co-expression	Nakayama-Hasegawa-2007
BMP4	TGFB2	0.008273957297205925	Co-expression	Nakayama-Hasegawa-2007
NFKB1	RARA	0.008234232664108276	Co-expression	Kang-Willman-2010
CLU	TIAM1	0.008215146139264107	Co-expression	Rieger-Chu-2004
IL4R	PNP	0.008168277330696583	Co-expression	Nakayama-Hasegawa-2007
TGIF1	NPTN	0.008129199035465717	Co-expression	Nakayama-Hasegawa-2007
NFKB1	SMAD3	0.008127238601446152	Co-expression	Ramaswamy-Golub-2001
INPP5D	ACIN1	0.008081371895968914	Co-expression	Rieger-Chu-2004
OSM	INS	0.008070423267781734	Co-expression	Wang-Maris-2006
PTPRC	IL4R	0.008063577115535736	Co-expression	Wu-Garvey-2007
CBFB	HMGB1	0.008017931133508682	Co-expression	Ramaswamy-Golub-2001
SMAD7	NPTN	0.007981358096003532	Co-expression	Bild-Nevins-2006 B
MAPK9	NPTN	0.007908514700829983	Co-expression	Bild-Nevins-2006 B
ID2	ACVR1	0.007878110744059086	Co-expression	Hummel-Siebert-2006
PNP	LIF	0.007803258951753378	Co-expression	Berchtold-Cotman-2008
IL4R	ADA	0.007787610869854689	Co-expression	Wang-Maris-2006
LYN	MSR1	0.007687859237194061	Co-expression	Nakayama-Hasegawa-2007

Gene 1	Gene 2	Weight	Network group	Networks
RUNX3	PTPRC	0.007681102957576513	Co-expression	Wang-Maris-2006
TP53	BDNF	0.007654133252799511	Co-expression	Berchtold-Cotman-2008
ID2	NPTN	0.0075850640423595905	Co-expression	Berchtold-Cotman-2008
FOXH1	FOXG1	0.007536794990301132	Co-expression	Burington-Shaughnessy-2008
SMAD7	JUN	0.007331468164920807	Co-expression	Rieger-Chu-2004
ARNT	MEN1	0.007290789391845465	Co-expression	Ramaswamy-Golub-2001
FOXH1	RUNX2	0.007272780407220125	Co-expression	Bild-Nevins-2006 B
HIF1A	TGFB2	0.007269333582371473	Co-expression	Wu-Garvey-2007
SYK	MEN1	0.007225850131362677	Co-expression	Kang-Willman-2010
NGFR	NTRK3	0.007173951715230942	Co-expression	Burington-Shaughnessy-2008
CBFB	RB1	0.007121953647583723	Co-expression	Ramaswamy-Golub-2001
INPP5D	NPTN	0.00711909681558609	Co-expression	Rieger-Chu-2004
IAPP	WNT7B	0.007112038787454367	Co-expression	Nakayama-Hasegawa-2007
BDNF	NGF	0.0071106040850281715	Co-expression	Perou-Botstein-1999
HIF1A	NFKB1	0.007109369616955519	Co-expression	Perou-Botstein-1999
RUNX3	NKX2-5	0.007069000508636236	Co-expression	Berchtold-Cotman-2008
NGFR	NRG1	0.0070580109022557735	Co-expression	Burington-Shaughnessy-2008
SYK	NPTN	0.007001503370702267	Co-expression	Burington-Shaughnessy-2008
HSP90AA1	NPTN	0.006983407773077488	Co-expression	Bild-Nevins-2006 B
RUNX3	HLX	0.006979699246585369	Co-expression	Berchtold-Cotman-2008
HMGB1	TGIF2	0.006916561163961887	Co-expression	Nakayama-Hasegawa-2007
IL4R	ZAP70	0.006868333090096712	Co-expression	Bild-Nevins-2006 B
BMP4	GATA6	0.006735648028552532	Co-expression	Nakayama-Hasegawa-2007
NFKB1	IL4R	0.00672589847818017	Co-expression	Wang-Maris-2006
MEN1	RUNX1	0.006705774925649166	Co-expression	Ramaswamy-Golub-2001
HSP90AB1	KLF10	0.00658777542412281	Co-expression	Ramaswamy-Golub-2001
ZAP70	GFI1	0.006554048974066973	Co-expression	Bild-Nevins-2006 B
SMO	ACIN1	0.0065277754329144955	Co-expression	Nakayama-Hasegawa-2007
NFKB1	PNP	0.006500383373349905	Co-expression	Ramaswamy-Golub-2001
NGFR	GLI2	0.006490181665867567	Co-expression	Burington-Shaughnessy-2008
NPTN	SMAP1	0.00645954255014658	Co-expression	Hummel-Siebert-2006
TCOF1	ACIN1	0.006416196469217539	Co-expression	Hummel-Siebert-2006
NGFR	BDNF	0.006335606798529625	Co-expression	Berchtold-Cotman-2008
STAT5A	MEN1	0.006304657086730003	Co-expression	Ramaswamy-Golub-2001
NGFR	LIF	0.006236812565475702	Co-expression	Wu-Garvey-2007
CITED1	BMP2	0.0061853318475186825	Co-expression	Berchtold-Cotman-2008
STAT5A	ZAP70	0.006153095979243517	Co-expression	Bild-Nevins-2006 B
CITED1	NGFR	0.005998457781970501	Co-expression	Berchtold-Cotman-2008
PPARG	HLX	0.005985211580991745	Co-expression	Berchtold-Cotman-2008
HIF1A	GATA6	0.005980293732136488	Co-expression	Wu-Garvey-2007
SMAD7	ETS1	0.0059766885824501514	Co-expression	Rieger-Chu-2004
BMP4	NKX2-5	0.00594694446772337	Co-expression	Ramaswamy-Golub-2001
RUNX3	ILK	0.005935875698924065	Co-expression	Rieger-Chu-2004
NGF	BMP4	0.005925455130636692	Co-expression	Nakayama-Hasegawa-2007
BDNF	BMP2	0.005923738703131676	Co-expression	Berchtold-Cotman-2008
IL4R	SYK	0.005910660605877638	Co-expression	Wang-Maris-2006
BMP2	KLF10	0.005772590171545744	Co-expression	Berchtold-Cotman-2008
ACVR1	SOCS2	0.0056998408399522305	Co-expression	Hummel-Siebert-2006
IL4R	LIF	0.005639415699988604	Co-expression	Wu-Garvey-2007
MAPK14	MAPK9	0.00562028493732214	Co-expression	Berchtold-Cotman-2008
TGFB3	KIT	0.005604473873972893	Co-expression	Kang-Willman-2010
LIF	KLF10	0.00555048044770956	Co-expression	Berchtold-Cotman-2008
RUNX3	ID2	0.0055362749844789505	Co-expression	Rieger-Chu-2004
BDNF	LIF	0.005511140450835228	Co-expression	Berchtold-Cotman-2008
NGFR	INS	0.005489529576152563	Co-expression	Burington-Shaughnessy-2008
GATA4	NKX2-5	0.005467310547828674	Co-expression	Ramaswamy-Golub-2001
CD74	CSF1	0.005453747697174549	Co-expression	Nakayama-Hasegawa-2007
NGFR	RUNX2	0.005406286101788282	Co-expression	Burington-Shaughnessy-2008
NGFR	CD36	0.005401852540671825	Co-expression	Burington-Shaughnessy-2008

Gene 1	Gene 2	Weight	Network group	Networks
IGF2	NKX2-5	0.0053892070427536964	Co-expression	Wu-Garvey-2007
CBFB	XRCC5	0.005377198103815317	Co-expression	Ramaswamy-Golub-2001
NGFR	HOXA11	0.005357855465263128	Co-expression	Burington-Shaughnessy-2008
NFKB1	CD74	0.0053559523075819016	Co-expression	Nakayama-Hasegawa-2007
PNP	NKX2-5	0.005340928677469492	Co-expression	Ramaswamy-Golub-2001
PPARG	TIAM1	0.005334846675395966	Co-expression	Nakayama-Hasegawa-2007
NGFR	GATA4	0.005319212097674608	Co-expression	Ramaswamy-Golub-2001
CITED1	VNN1	0.005275672301650047	Co-expression	Burington-Shaughnessy-2008
SMO	NTRK3	0.005263183731585741	Co-expression	Bild-Nevins-2006 B
TP53	MEN1	0.005261209327727556	Co-expression	Ramaswamy-Golub-2001
PPARG	CD36	0.0051940008997917175	Co-expression	Nakayama-Hasegawa-2007
ACVRL1	SMO	0.005144515540450811	Co-expression	Bild-Nevins-2006 B
LYN	IL4R	0.0050579397939145565	Co-expression	Wang-Maris-2006
BMPR1B	SMO	0.005046057049185038	Co-expression	Burington-Shaughnessy-2008
TGFB1	SMO	0.005045323166996241	Co-expression	Bild-Nevins-2006 B
ZAP70	CD74	0.004852088168263435	Co-expression	Bild-Nevins-2006 B
BDNF	SRF	0.004835817031562328	Co-expression	Berchtold-Cotman-2008
CBFB	TP53	0.004824026487767696	Co-expression	Ramaswamy-Golub-2001
CITED1	LIF	0.004772816319018602	Co-expression	Berchtold-Cotman-2008
JAK2	CD74	0.004747674334794283	Co-expression	Nakayama-Hasegawa-2007
MAPK9	KITLG	0.0047028628177940845	Co-expression	Berchtold-Cotman-2008
BDNF	KITLG	0.004673744551837444	Co-expression	Wu-Garvey-2007
ID2	BMP4	0.004639922175556421	Co-expression	Nakayama-Hasegawa-2007
NGFR	KIT	0.004600147716701031	Co-expression	Kang-Willman-2010
SMO	FOXG1	0.004466351121664047	Co-expression	Bild-Nevins-2006 B
RUNX3	SMAD7	0.0044213528744876385	Co-expression	Rieger-Chu-2004
BMP4	FOXG1	0.004419235046952963	Co-expression	Nakayama-Hasegawa-2007
CITED1	HMGB1	0.004357414785772562	Co-expression	Burington-Shaughnessy-2008
CBFB	MAPK14	0.0043133883737027645	Co-expression	Ramaswamy-Golub-2001
CBFB	ADA	0.004309426993131638	Co-expression	Ramaswamy-Golub-2001
IL4R	SOC3	0.004160996526479721	Co-expression	Wu-Garvey-2007
STAT5A	PPARG	0.004077814519405365	Co-expression	Nakayama-Hasegawa-2007
NGFR	CSF1	0.0038967749569565058	Co-expression	Burington-Shaughnessy-2008
SMO	TGIF2	0.0038166611921042204	Co-expression	Nakayama-Hasegawa-2007
SMO	VNN1	0.0037918835878372192	Co-expression	Bild-Nevins-2006 B
MAPT	POU4F2	0.0036381627433001995	Co-expression	Kang-Willman-2010
BDNF	KLF10	0.003586831269785762	Co-expression	Berchtold-Cotman-2008
TP53	SMO	0.003565228544175625	Co-expression	Bild-Nevins-2006 B
SMO	DLX5	0.0035613386426120996	Co-expression	Burington-Shaughnessy-2008
INS	SMO	0.003529809881001711	Co-expression	Bild-Nevins-2006 B
HMGB1	THRB	0.0035149212926626205	Co-expression	Bild-Nevins-2006 B
SMO	GATA6	0.00337424804456532	Co-expression	Bild-Nevins-2006 B
HMGB1	GLI2	0.003203413914889097	Co-expression	Bild-Nevins-2006 B
FOXH1	SMO	0.0031966035021468997	Co-expression	Bild-Nevins-2006 B Burington-Shaughnessy-2008
SMO	LIF	0.003109097946435213	Co-expression	Bild-Nevins-2006 B
HMGB1	FOXG1	0.0030558600556105375	Co-expression	Bild-Nevins-2006 B
HMGB1	ID2	0.0029801209457218647	Co-expression	Bild-Nevins-2006 B
CD74	MNDA	0.002898246282711625	Co-expression	Nakayama-Hasegawa-2007
LYN	CD74	0.0028734880033880472	Co-expression	Nakayama-Hasegawa-2007
SMAD6	POU4F2	0.002827234100550413	Co-expression	Kang-Willman-2010
HLX	NKX2-5	0.002792586572468281	Co-expression	Berchtold-Cotman-2008
HMGB1	NRG1	0.002770462539047003	Co-expression	Bild-Nevins-2006 B
JAG1	POU4F2	0.0027621383778750896	Co-expression	Kang-Willman-2010
CBFB	MEN1	0.0027558777946978807	Co-expression	Ramaswamy-Golub-2001
NTF4	INS	0.002586949383839965	Co-expression	Berchtold-Cotman-2008
NKX2-5	POU4F2	0.002541680820286274	Co-expression	Kang-Willman-2010
NGFR	IGF2	0.002523518167436123	Co-expression	Burington-Shaughnessy-2008
POU4F2	DLX5	0.002343768486753106	Co-expression	Kang-Willman-2010

Gene 1	Gene 2	Weight	Network group	Networks
BDNF	POU4F2	0.001856622751802206	Co-expression	Kang-Willman-2010
HMGB1	PAX6	0.0017307167872786522	Co-expression	Bild-Nevins-2006 B
MAPK14	HMGB1	0.03822549432516098	Co-localization	Johnson-Shoemaker-2003 Schadt-Shoemaker-2004
STAT5A	STAT5B	0.03707068786025047	Co-localization	Johnson-Shoemaker-2003
AKT1	GATA6	0.02982565015554428	Co-localization	Johnson-Shoemaker-2003
NTF4	MEN1	0.027753623202443123	Co-localization	Johnson-Shoemaker-2003
ADA	RUNX1	0.0269040884450078	Co-localization	Johnson-Shoemaker-2003 Schadt-Shoemaker-2004
MAPK14	ADA	0.025643298402428627	Co-localization	Schadt-Shoemaker-2004
GLI2	GATA6	0.025482870638370514	Co-localization	Johnson-Shoemaker-2003
NGFR	RUNX2	0.024600375443696976	Co-localization	Johnson-Shoemaker-2003
INS	GATA4	0.024173887446522713	Co-localization	Johnson-Shoemaker-2003
ARNT	KIT	0.023951295763254166	Co-localization	Schadt-Shoemaker-2004
CREBBP	ACVR2A	0.02336900122463703	Co-localization	Johnson-Shoemaker-2003
ARNT	JAG1	0.023059481754899025	Co-localization	Schadt-Shoemaker-2004
IL4R	IL2RA	0.022349888458848	Co-localization	Schadt-Shoemaker-2004
SYK	BMP7	0.021328428760170937	Co-localization	Johnson-Shoemaker-2003
BMPR1A	KIT	0.020683210343122482	Co-localization	Johnson-Shoemaker-2003
TGFB3	ARNT	0.02006889134645462	Co-localization	Johnson-Shoemaker-2003
SMAD3	NRG1	0.019660091027617455	Co-localization	Johnson-Shoemaker-2003
NTF4	BDNF	0.019410019740462303	Co-localization	Johnson-Shoemaker-2003
JAK2	CD36	0.018102794885635376	Co-localization	Johnson-Shoemaker-2003
FBXW7	MAPT	0.01779078133404255	Co-localization	Johnson-Shoemaker-2003
KIT	KITLG	0.01775994524359703	Co-localization	Johnson-Shoemaker-2003
RB1	RUNX1	0.017706818878650665	Co-localization	Johnson-Shoemaker-2003
OSM	TESC	0.017566118389368057	Co-localization	Johnson-Shoemaker-2003
ACVR2A	JAG1	0.017108360305428505	Co-localization	Johnson-Shoemaker-2003
SMAD7	TAL1	0.016962477937340736	Co-localization	Johnson-Shoemaker-2003
SYK	RUNX2	0.01694803312420845	Co-localization	Johnson-Shoemaker-2003
SMAD1	HOXA11	0.016934378072619438	Co-localization	Johnson-Shoemaker-2003
ID2	IL4R	0.01691608317196369	Co-localization	Schadt-Shoemaker-2004
SRF	HOXA11	0.016831837594509125	Co-localization	Johnson-Shoemaker-2003
SMO	JAG1	0.01666690595448017	Co-localization	Johnson-Shoemaker-2003
PAX6	NEUROD1	0.016196591779589653	Co-localization	Johnson-Shoemaker-2003
GLI2	HOXA11	0.016117682680487633	Co-localization	Johnson-Shoemaker-2003
TGFB1	IL2RA	0.01562516950070858	Co-localization	Schadt-Shoemaker-2004
TP53	TCOF1	0.015287617221474648	Co-localization	Johnson-Shoemaker-2003
SMAD2	NRG1	0.01520499400794506	Co-localization	Johnson-Shoemaker-2003
SMAD2	SMAD3	0.014917352236807346	Co-localization	Johnson-Shoemaker-2003
PAX6	BDNF	0.014569546096026897	Co-localization	Schadt-Shoemaker-2004
SMAD6	ARNT	0.014465227723121643	Co-localization	Johnson-Shoemaker-2003
IAPP	IL4R	0.01446493063122034	Co-localization	Schadt-Shoemaker-2004
TGFB2	HLX	0.014441605657339096	Co-localization	Johnson-Shoemaker-2003
RB1	BMP7	0.014125408604741096	Co-localization	Schadt-Shoemaker-2004
TGFB3	JAG1	0.013856839388608932	Co-localization	Johnson-Shoemaker-2003
GLI3	NGFR	0.013837054371833801	Co-localization	Johnson-Shoemaker-2003
NGF	HOXA11	0.01377896498888731	Co-localization	Johnson-Shoemaker-2003
RARA	TGFB2	0.01374336238950491	Co-localization	Johnson-Shoemaker-2003
TGFB2	GATA6	0.01369240041822195	Co-localization	Johnson-Shoemaker-2003
IL4R	TGFB1	0.013556449674069881	Co-localization	Schadt-Shoemaker-2004
JUN	RB1	0.013302212581038475	Co-localization	Schadt-Shoemaker-2004
GLI3	RUNX2	0.013247865252196789	Co-localization	Johnson-Shoemaker-2003
SMAD6	ACVRL1	0.01320160087198019	Co-localization	Johnson-Shoemaker-2003
RUNX3	LYN	0.01285848394036293	Co-localization	Johnson-Shoemaker-2003
FBXW7	SMAP1	0.012842466123402119	Co-localization	Johnson-Shoemaker-2003
IAPP	INS	0.012820589356124401	Co-localization	Johnson-Shoemaker-2003
RARA	RUNX1	0.012560809031128883	Co-localization	Schadt-Shoemaker-2004
APC	MAPT	0.012425502762198448	Co-localization	Johnson-Shoemaker-2003

Gene 1	Gene 2	Weight	Network group	Networks
STAT5A	ADA	0.012231742031872272	Co-localization	Johnson-Shoemaker-2003
ETS1	IL4R	0.012187417596578598	Co-localization	Johnson-Shoemaker-2003
GLI3	BMP4	0.012010257691144943	Co-localization	Johnson-Shoemaker-2003
SMAD3	LIF	0.011872544884681702	Co-localization	Johnson-Shoemaker-2003
LYN	BCL2	0.011795340105891228	Co-localization	Johnson-Shoemaker-2003
SMO	TGIF1	0.011782333254814148	Co-localization	Johnson-Shoemaker-2003
TP53	SYK	0.011717121116816998	Co-localization	Johnson-Shoemaker-2003
ADA	TCOF1	0.011618578806519508	Co-localization	Schadt-Shoemaker-2004
NFKB1	CD74	0.01147613488137722	Co-localization	Johnson-Shoemaker-2003
TP53	BMP7	0.011288645677268505	Co-localization	Johnson-Shoemaker-2003
RB1	ADA	0.011230025440454483	Co-localization	Johnson-Shoemaker-2003
ARNT	BMP2	0.011196746490895748	Co-localization	Schadt-Shoemaker-2004
TGFB3	TGFB2	0.011129519902169704	Co-localization	Johnson-Shoemaker-2003
BMP2	CSF1	0.011116285808384418	Co-localization	Schadt-Shoemaker-2004
TGIF1	LIF	0.011071203276515007	Co-localization	Johnson-Shoemaker-2003
ACVRL1	CSF1	0.011030885390937328	Co-localization	Schadt-Shoemaker-2004
XRCC6	ADA	0.010974017903208733	Co-localization	Schadt-Shoemaker-2004
TGFB2	KITLG	0.010965542867779732	Co-localization	Johnson-Shoemaker-2003
RARA	PNP	0.010957911610603333	Co-localization	Schadt-Shoemaker-2004
CLUL1	PAX6	0.010863829404115677	Co-localization	Johnson-Shoemaker-2003
IL2RA	CD74	0.010818318463861942	Co-localization	Johnson-Shoemaker-2003
MAPK14	RUNX1	0.010443801991641521	Co-localization	Schadt-Shoemaker-2004
CLUL1	TGFB2	0.010312872007489204	Co-localization	Johnson-Shoemaker-2003
JUN	BMP4	0.010288403369486332	Co-localization	Schadt-Shoemaker-2004
IAPP	GATA4	0.010133441537618637	Co-localization	Johnson-Shoemaker-2003
IAPP	ACVR1B	0.010025115683674812	Co-localization	Johnson-Shoemaker-2003
KITLG	MSR1	0.009893832728266716	Co-localization	Johnson-Shoemaker-2003
TIAM1	NEUROD1	0.009862212464213371	Co-localization	Johnson-Shoemaker-2003
XRCC6	RARA	0.00976585503667593	Co-localization	Schadt-Shoemaker-2004
IL4R	CD74	0.00956089049577713	Co-localization	Johnson-Shoemaker-2003
TP53	HMGB1	0.009547731839120388	Co-localization	Johnson-Shoemaker-2003
GLI2	FOXG1	0.009461931884288788	Co-localization	Johnson-Shoemaker-2003
APC	SMAP1	0.009446419775485992	Co-localization	Johnson-Shoemaker-2003
ILK	SRF	0.009413983672857285	Co-localization	Johnson-Shoemaker-2003
TGFB1	PNP	0.009277034550905228	Co-localization	Schadt-Shoemaker-2004
SRF	POLR1D	0.009262689389288425	Co-localization	Johnson-Shoemaker-2003
CLUL1	NEUROD1	0.009115700609982014	Co-localization	Johnson-Shoemaker-2003
ACVRL1	ACVR2A	0.009101614356040955	Co-localization	Schadt-Shoemaker-2004
RB1	CLU	0.009027276188135147	Co-localization	Schadt-Shoemaker-2004
JUN	CLU	0.009014843963086605	Co-localization	Schadt-Shoemaker-2004
SOCS2	VNN1	0.00892684981226921	Co-localization	Johnson-Shoemaker-2003
ID2	IL2RA	0.00888284295797348	Co-localization	Johnson-Shoemaker-2003
SMAD1	FOXG1	0.008727057836949825	Co-localization	Johnson-Shoemaker-2003
MAPK14	TCOF1	0.008682138286530972	Co-localization	Schadt-Shoemaker-2004
SOCS2	TGFB3	0.00866633839905262	Co-localization	Johnson-Shoemaker-2003
MEN1	TCOF1	0.00849950686097145	Co-localization	Schadt-Shoemaker-2004
KITLG	CSF1	0.008215275593101978	Co-localization	Schadt-Shoemaker-2004
ACVR2A	CSF1	0.008055729791522026	Co-localization	Schadt-Shoemaker-2004
XRCC5	XRCC4	0.007895725779235363	Co-localization	Johnson-Shoemaker-2003
SMAD6	BDNF	0.007876154966652393	Co-localization	Johnson-Shoemaker-2003
XRCC6	HIF1A	0.007796869613230228	Co-localization	Schadt-Shoemaker-2004
SMO	FOXG1	0.007775422651320696	Co-localization	Johnson-Shoemaker-2003
BMP2	KITLG	0.007623921148478985	Co-localization	Schadt-Shoemaker-2004
XRCC6	MEN1	0.0075502716936171055	Co-localization	Schadt-Shoemaker-2004
ILK	NGF	0.007221202831715345	Co-localization	Johnson-Shoemaker-2003
FOXH1	POLR1D	0.007177673280239105	Co-localization	Johnson-Shoemaker-2003
ACVR2A	CLU	0.007164594251662493	Co-localization	Schadt-Shoemaker-2004
CBFB	TCOF1	0.007140946574509144	Co-localization	Johnson-Shoemaker-2003
FOXG1	HOXA11	0.0070470767095685005	Co-localization	Johnson-Shoemaker-2003

Gene 1	Gene 2	Weight	Network group	Networks
LYN	TGFB1	0.0069535281509160995	Co-localization	Johnson-Shoemaker-2003
SMAD4	POLR1D	0.006913880351930857	Co-localization	Johnson-Shoemaker-2003
ACVR2A	KITLG	0.0068956161849200726	Co-localization	Schadt-Shoemaker-2004
CLU	KITLG	0.006887275725603104	Co-localization	Schadt-Shoemaker-2004
BMPR1A	ILK	0.00686898035928607	Co-localization	Johnson-Shoemaker-2003
SMAD1	ILK	0.006804003845900297	Co-localization	Johnson-Shoemaker-2003
ID2	SOCS2	0.0067411381751298904	Co-localization	Johnson-Shoemaker-2003
SMAD3	POLR1D	0.006670613307505846	Co-localization	Johnson-Shoemaker-2003
IAPP	XRCC6	0.006585367955267429	Co-localization	Schadt-Shoemaker-2004
PNP	RUNX1	0.006575313862413168	Co-localization	Schadt-Shoemaker-2004
ACVR2A	BMP2	0.0065209586173295975	Co-localization	Schadt-Shoemaker-2004
SMAD7	ID2	0.006501839961856604	Co-localization	Johnson-Shoemaker-2003
ACVR2A	CD36	0.006437818519771099	Co-localization	Schadt-Shoemaker-2004
ILK	JAG1	0.006114363204687834	Co-localization	Johnson-Shoemaker-2003
JUN	ACVR2A	0.006113705690950155	Co-localization	Schadt-Shoemaker-2004
ID2	VNN1	0.006088517606258392	Co-localization	Johnson-Shoemaker-2003
XRCC6	PNP	0.005700803827494383	Co-localization	Schadt-Shoemaker-2004
RUNX1	TCOF1	0.00568779744207859	Co-localization	Schadt-Shoemaker-2004
FBXW7	APC	0.005631111096590757	Co-localization	Johnson-Shoemaker-2003
ILK	HOXA11	0.005470371339470148	Co-localization	Johnson-Shoemaker-2003
ID2	TGFB3	0.005430538207292557	Co-localization	Johnson-Shoemaker-2003
TGFB1	MNDA	0.005004832986742258	Co-localization	Johnson-Shoemaker-2003
ID2	TGIF1	0.004706614650785923	Co-localization	Johnson-Shoemaker-2003
ILK	TGFB2	0.004621392581611872	Co-localization	Johnson-Shoemaker-2003
CBFB	PTPRC	0.0038271844387054443	Co-localization	Johnson-Shoemaker-2003
CBFB	ETS1	0.0033476650714874268	Co-localization	Johnson-Shoemaker-2003
CBFB	TP53	0.003309819847345352	Co-localization	Johnson-Shoemaker-2003
CBFB	XRCC4	0.002128621796146035	Co-localization	Johnson-Shoemaker-2003
SMAD1	BMP7	0.7962251901626587	Genetic interactions	BIOGRID-SMALL-SCALE-STUDIES
SRF	GATA6	0.40824830532073975	Genetic interactions	BIOGRID-SMALL-SCALE-STUDIES
SRF	NKX2-5	0.40824830532073975	Genetic interactions	BIOGRID-SMALL-SCALE-STUDIES
SRF	GATA4	0.40824830532073975	Genetic interactions	BIOGRID-SMALL-SCALE-STUDIES
SMAD7	SMAD4	0.35090553760528564	Genetic interactions	BIOGRID-SMALL-SCALE-STUDIES
SMAD2	SMAD3	0.27765947580337524	Genetic interactions	BIOGRID-SMALL-SCALE-STUDIES
SMAD7	SMAD3	0.19676916301250458	Genetic interactions	BIOGRID-SMALL-SCALE-STUDIES
SMAD7	SMAD2	0.19676916301250458	Genetic interactions	BIOGRID-SMALL-SCALE-STUDIES
CREBBP	TP53	0.03027477115392685	Genetic interactions	BIOGRID-SMALL-SCALE-STUDIES
CREBBP	GLI3	0.8774421159178019	Pathway	PATHWAYCOMMONS-CELL_MAP Wu-Stein-2010
SMAD4	FOXO3	0.7759389663115144	Pathway	PATHWAYCOMMONS-REACTOME Wu-Stein-2010
LYN	SYK	0.7531962990760803	Pathway	PATHWAYCOMMONS-IMID Wu-Stein-2010
ACVRL1	TGFB1	0.6766772083938122	Pathway	PATHWAYCOMMONS-CELL_MAP PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
IAPP	NEUROD1	0.6578707695007324	Pathway	Wu-Stein-2010
TGFB3	TGFB3	0.614339217543602	Pathway	PATHWAYCOMMONS-CELL_MAP Wu-Stein-2010
CBFB	RUNX3	0.5804541707038879	Pathway	Wu-Stein-2010
JAG1	DLL3	0.47579325735569	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
SRF	HOPX	0.4569915533065796	Pathway	Wu-Stein-2010
RB1	ID2	0.43419080693274736	Pathway	PATHWAYCOMMONS-CELL_MAP Wu-Stein-2010
FOXH1	NKX2-5	0.416493222117424	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
LIG4	XRCC4	0.4135868176817894	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010

Gene 1	Gene 2	Weight	Network group	Networks
FBXW7	NOTCH1	0.39235105738043785	Pathway	PATHWAYCOMMONS-CELL_MAP Wu-Stein-2010
ACVR2A	ACVR1	0.3490579817444086	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
TGFBR3	TGFB1	0.3446703776717186	Pathway	PATHWAYCOMMONS-CELL_MAP Wu-Stein-2010
CREBBP	STAT5A	0.340660959482193	Pathway	PATHWAYCOMMONS-IMID
CREBBP	NFKB1	0.340660959482193	Pathway	PATHWAYCOMMONS-IMID
FOXH1	FOXG1	0.31668516993522644	Pathway	Wu-Stein-2010
SMAD2	FOXO3	0.31644043046981096	Pathway	PATHWAYCOMMONS-CELL_MAP Wu-Stein-2010
STAT5A	STAT5B	0.31131829461082816	Pathway	PATHWAYCOMMONS-CELL_MAP Wu-Stein-2010
ACVRL1	TGFBR2	0.31069324631243944	Pathway	PATHWAYCOMMONS-CELL_MAP PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
TP53	SMAD2	0.30289020005147904	Pathway	PATHWAYCOMMONS-CELL_MAP Wu-Stein-2010
SMAD4	TGIF2	0.283001609146595	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
ACVRL1	TGFB3	0.2371333073824644	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
XRCC5	XRCC4	0.2357436865568161	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
CBFB	RUNX1	0.22999447584152222	Pathway	Wu-Stein-2010
LIG4	XRCC5	0.22732391953468323	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
NTF3	NTRK3	0.2143251746892929	Pathway	Wu-Stein-2010
NTF4	NGFR	0.20879659056663513	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
XRCC6	XRCC4	0.20338109880685806	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
LIG4	XRCC6	0.1970188170671463	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
IAPP	PAX6	0.19631515443325043	Pathway	Wu-Stein-2010
NGFR	BEX1	0.19481293112039566	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
NTF3	TIAM1	0.18848907947540283	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
SOCS3	SOCS2	0.18190004117786884	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
CITED1	TGIF1	0.18058979511260986	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
CREBBP	SRF	0.17330874502658844	Pathway	PATHWAYCOMMONS-IMID
TGFBR3	TGFBR2	0.15837412513792515	Pathway	PATHWAYCOMMONS-CELL_MAP Wu-Stein-2010
SMAD6	BMP7	0.158004492521286	Pathway	PATHWAYCOMMONS-NCI_NATURE
ACVR1	BMP7	0.15565195865929127	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
LYN	JAK2	0.1538992254063487	Pathway	PATHWAYCOMMONS-REACTOME Wu-Stein-2010
NGF	BEX1	0.14713158458471298	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
MAPK14	JUN	0.14666029333602637	Pathway	PATHWAYCOMMONS-IMID Wu-Stein-2010
FOXO3	FOXG1	0.14204971492290497	Pathway	Wu-Stein-2010
SMAD6	SMAD1	0.127581050619483	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
RTN4R	NGFR	0.12601908296346664	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
NOTCH1	DLL3	0.12458140775561333	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010

Gene 1	Gene 2	Weight	Network group	Networks
SMAD2	NKX2-5	0.12415706925094128	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
SMAD4	FOXG1	0.12394754402339458	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
XRCC6	XRCC5	0.12154677137732506	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
TIAM1	NTRK3	0.1180737316608429	Pathway	Wu-Stein-2010
RB1	RUNX2	0.11432065069675446	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
SMAD3	TGIF2	0.10476242005825043	Pathway	Wu-Stein-2010
LCK	SOCS2	0.10380022879689932	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
FOXH1	SMAD2	0.0975470170378685	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
POLR1C	POLR1D	0.0969071201980114	Pathway	PATHWAYCOMMONS-REACTOME Wu-Stein-2010
BCL2	BAD	0.09622331708669662	Pathway	PATHWAYCOMMONS-IMID Wu-Stein-2010
JUN	LIF	0.09483317285776138	Pathway	PATHWAYCOMMONS-NCI_NATURE
TGFB2	TGFB3	0.09395973943173885	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
ID2	TAL1	0.08909934759140015	Pathway	Wu-Stein-2010
SMAD1	BMP7	0.08778093475848436	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
NTF3	NGFR	0.08500148355960846	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
CREBBP	JUN	0.07979671005159616	Pathway	PATHWAYCOMMONS-IMID Wu-Stein-2010
CBFB	SMAD4	0.07975723780691624	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
NFKB1	NGFR	0.07366471295244992	Pathway	PATHWAYCOMMONS-REACTOME Wu-Stein-2010
SMO	GLI2	0.07045906968414783	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
ZAP70	CD74	0.07010714709758759	Pathway	Wu-Stein-2010
TP53	LIF	0.06906388700008392	Pathway	PATHWAYCOMMONS-NCI_NATURE
KIT	STAT5B	0.06826247414574027	Pathway	PATHWAYCOMMONS-CELL_MAP Wu-Stein-2010
KIT	STAT5A	0.06649362621828914	Pathway	PATHWAYCOMMONS-CELL_MAP Wu-Stein-2010
GATA4	BMP7	0.06622301042079926	Pathway	Wu-Stein-2010
PAX6	FOXA2	0.06603877246379852	Pathway	Wu-Stein-2010
SRF	GATA4	0.06595595180988312	Pathway	Wu-Stein-2010
SMAD6	GATA4	0.06498925387859344	Pathway	Wu-Stein-2010
NOTCH1	JAG1	0.06457595713436604	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
GATA4	NKX2-5	0.06426174938678741	Pathway	Wu-Stein-2010
SMAD4	RUNX2	0.06384122930467129	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
INS	NEUROD1	0.06361944228410721	Pathway	Wu-Stein-2010
KIT	JAK2	0.06304522836580873	Pathway	PATHWAYCOMMONS-REACTOME Wu-Stein-2010
GLI3	SMO	0.059320561587810516	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
CREBBP	KIT	0.057984162122011185	Pathway	PATHWAYCOMMONS-NCI_NATURE
CREBBP	BCL2	0.057836998254060745	Pathway	PATHWAYCOMMONS-NCI_NATURE
ETS1	IL4R	0.05592810269445181	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
SMAD4	NKX2-5	0.05592318717390299	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
IL4R	INPP5D	0.054381631314754486	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010

Gene 1	Gene 2	Weight	Network group	Networks
KIT	KITLG	0.05417484138160944	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
CITED1	SMAD2	0.053883678279817104	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
SMAD7	TGFB1	0.05196873005479574	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
RARA	THRB	0.050492655485868454	Pathway	Wu-Stein-2010
RB1	CCNE1	0.05025110300630331	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
FOXH1	SMAD4	0.05022619850933552	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
OSM	STAT5B	0.04898572713136673	Pathway	Wu-Stein-2010
ACVRL1	SMAD7	0.04834604635834694	Pathway	PATHWAYCOMMONS-NCI_NATURE
NKX2-5	BMP7	0.048154138028621674	Pathway	Wu-Stein-2010
SRF	NKX2-5	0.04795994609594345	Pathway	Wu-Stein-2010
SMAD6	NKX2-5	0.04725700989365578	Pathway	Wu-Stein-2010
RB1	TGFB2	0.04711659625172615	Pathway	PATHWAYCOMMONS-NCI_NATURE
SMAD7	SMAD1	0.04697143007069826	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
ETS1	MSR1	0.04628290981054306	Pathway	Wu-Stein-2010
NFKB1	NGF	0.045741269597783685	Pathway	PATHWAYCOMMONS-REACTOME Wu-Stein-2010
RB1	PPARG	0.04549416666850448	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
NGFR	BDNF	0.045314500108361244	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
RB1	TAL1	0.044894345104694366	Pathway	Wu-Stein-2010
OSM	STAT5A	0.043954987078905106	Pathway	Wu-Stein-2010
SMAD6	TGFB2	0.04344901815056801	Pathway	Wu-Stein-2010
BMP4	GATA4	0.04274741932749748	Pathway	Wu-Stein-2010
RUNX3	SMAD3	0.04204902797937393	Pathway	Wu-Stein-2010
LCK	CD74	0.039772942662239075	Pathway	Wu-Stein-2010
SMAD4	TGIF1	0.03964038472622633	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
RUNX3	SMAD4	0.03707566112279892	Pathway	Wu-Stein-2010
BMP2	GATA4	0.036689452826976776	Pathway	Wu-Stein-2010
SMAD2	RUNX2	0.036454904824495316	Pathway	Wu-Stein-2010
SMAD2	FOXG1	0.03621974587440491	Pathway	Wu-Stein-2010
FOXA2	GLI2	0.03557542338967323	Pathway	Wu-Stein-2010
HIF1A	ID2	0.035543620586395264	Pathway	PATHWAYCOMMONS-NCI_NATURE
ETS1	LIF	0.03534933924674988	Pathway	Wu-Stein-2010
SMAD6	TGFB3	0.035276442766189575	Pathway	Wu-Stein-2010
FOXH1	SMAD1	0.0344601534307003	Pathway	Wu-Stein-2010
MAPK14	IL4R	0.03408800112083554	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
SYK	INPP5D	0.03345303609967232	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
CBFB	SMAD3	0.0328950360417366	Pathway	Wu-Stein-2010
EPHB2	TIAM1	0.03242342919111252	Pathway	Wu-Stein-2010
LYN	KITLG	0.03164057806134224	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
TGFBR2	TGFB1	0.03163613099604845	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
ARNT	ID2	0.031551722437143326	Pathway	PATHWAYCOMMONS-NCI_NATURE
IL2RA	SOCS3	0.03129758592694998	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
BMP4	NKX2-5	0.031083837151527405	Pathway	Wu-Stein-2010
LYN	INPP5D	0.030575189739465714	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
JUN	CLU	0.03035767562687397	Pathway	Wu-Stein-2010

Gene 1	Gene 2	Weight	Network group	Networks
LCK	ZAP70	0.030351359397172928	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
INS	INPP5D	0.030129927210509777	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
ACVRL1	BMP7	0.029424432665109634	Pathway	Wu-Stein-2010
NOTCH1	APC	0.028552830684930086	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
SMAD3	RUNX2	0.028414525091648102	Pathway	Wu-Stein-2010
SMAD3	FOXG1	0.02823123149573803	Pathway	Wu-Stein-2010
SMAD6	TGFB1	0.02747735194861889	Pathway	Wu-Stein-2010
INS	FOXA2	0.02742699161171913	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
JAK2	HLX	0.0273786298930645	Pathway	Wu-Stein-2010
BMP7	ACVR1B	0.02736244723200798	Pathway	Wu-Stein-2010
CREBBP	IL2RA	0.02726430632174015	Pathway	PATHWAYCOMMONS-NCI_NATURE
SMAD6	BMP2	0.0269808080047369	Pathway	Wu-Stein-2010
FOXH1	SMAD3	0.026731066405773163	Pathway	Wu-Stein-2010
BMP2	NKX2-5	0.0266787800937891	Pathway	Wu-Stein-2010
ACVR1	TGFB2	0.026554344221949577	Pathway	Wu-Stein-2010
ACVR2A	BMP7	0.026390139013528824	Pathway	Wu-Stein-2010
ACVRL1	TGFB2	0.02625218592584133	Pathway	Wu-Stein-2010
SYK	IL2RA	0.02611454948782921	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
SMAD7	TGFB2	0.026012607384473085	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
PPARG	CD36	0.025971395894885063	Pathway	Wu-Stein-2010
AKT1	RARA	0.025918217143043876	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
SMAD6	ACVR2A	0.025898480787873268	Pathway	Wu-Stein-2010
JUN	MAPK9	0.02551863668486476	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
LCK	SOCS3	0.025172322057187557	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
TP53	POU4F2	0.025116849690675735	Pathway	PATHWAYCOMMONS-NCI_NATURE
MAPK14	SOCS3	0.02468014694750309	Pathway	PATHWAYCOMMONS-NCI_NATURE
TGFB2	ACVR1B	0.024412501603364944	Pathway	Wu-Stein-2010
IL4R	JAK2	0.02422172948718071	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
AKT1	SMO	0.023663719184696674	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
ACVR2A	TGFB2	0.02354501746594906	Pathway	Wu-Stein-2010
SMAD7	TGFB2	0.022794637829065323	Pathway	Wu-Stein-2010
AKT1	GLI2	0.02254018234089017	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
GLI3	BMP7	0.022070856764912605	Pathway	Wu-Stein-2010
ACVR1	TGFB3	0.021559584885835648	Pathway	Wu-Stein-2010
SMAD2	TGIF1	0.021532226353883743	Pathway	Wu-Stein-2010
GLI3	FOXA2	0.021372279152274132	Pathway	Wu-Stein-2010
BMPR1B	BMP7	0.02118348516523838	Pathway	Wu-Stein-2010
BMPR1A	BMP7	0.02118348516523838	Pathway	Wu-Stein-2010
NFKB1	TAL1	0.02079213224351406	Pathway	Wu-Stein-2010
SMAD6	BMPR1B	0.020788827911019325	Pathway	Wu-Stein-2010
BMPR1A	SMAD6	0.020788827911019325	Pathway	Wu-Stein-2010
SMAD2	TGFB2	0.020626578014343977	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
IL4R	SOCS2	0.02022894285619259	Pathway	Wu-Stein-2010
LCK	SYK	0.020227160304784775	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
CREBBP	TGIF1	0.020152557641267776	Pathway	Wu-Stein-2010
MAPK14	LYN	0.0199787225574255	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010

Gene 1	Gene 2	Weight	Network group	Networks
TGFB3	ACVR1B	0.019820615649223328	Pathway	Wu-Stein-2010
CREBBP	CD36	0.01960306614637375	Pathway	PATHWAYCOMMONS-REACTOME
NGFR	NGF	0.01957476744428277	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
LYN	PTPRC	0.01935463398694992	Pathway	Wu-Stein-2010
BDNF	MAPK9	0.019233811646699905	Pathway	Wu-Stein-2010
BMP4	ACVR1	0.01921229436993599	Pathway	Wu-Stein-2010
ACVR2A	TGFB3	0.019116301089525223	Pathway	Wu-Stein-2010
LCK	IL2RA	0.019070837646722794	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
ACVRL1	BMP4	0.0189936812967062	Pathway	Wu-Stein-2010
PAX6	INS	0.01898467168211937	Pathway	Wu-Stein-2010
BMPR1B	TGFB2	0.018899692222476006	Pathway	Wu-Stein-2010
BMPR1A	TGFB2	0.018899692222476006	Pathway	Wu-Stein-2010
TGFBR2	GATA4	0.018790055066347122	Pathway	Wu-Stein-2010
SMAD1	GATA4	0.01870785653591156	Pathway	Wu-Stein-2010
BCL2	GLI2	0.018551625311374664	Pathway	Wu-Stein-2010
SMAD7	TGFB3	0.018507063388824463	Pathway	Wu-Stein-2010
JAK2	KITLG	0.01827019825577736	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
HMGB1	POLR1D	0.018099740147590637	Pathway	Wu-Stein-2010
JUN	PPARG	0.017966487212106586	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
BMP4	ACVR1B	0.01766265369951725	Pathway	Wu-Stein-2010
JAK2	SOCS3	0.017657019663602114	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
SMAD4	SMAD1	0.01759151229634881	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
NFKB1	CSF1	0.017458610236644745	Pathway	Wu-Stein-2010
ACVR2A	BMP4	0.017035022377967834	Pathway	Wu-Stein-2010
ETS1	RUNX1	0.016993755474686623	Pathway	Wu-Stein-2010
TGFB1	ACVR1	0.016793085262179375	Pathway	Wu-Stein-2010
AKT1	FOXA2	0.01676840055733919	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
SMAD3	RUNX1	0.01666116528213024	Pathway	Wu-Stein-2010
MAPK9	BAD	0.01661389134824276	Pathway	Wu-Stein-2010
TP53	XRCC5	0.016596457920968533	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
SMAD7	BMP4	0.016492115333676338	Pathway	Wu-Stein-2010
BMP2	ACVR1	0.01648961566388607	Pathway	Wu-Stein-2010
LIG4	TP53	0.016405193135142326	Pathway	Wu-Stein-2010
ACVRL1	BMP2	0.01630198210477829	Pathway	Wu-Stein-2010
LYN	EPHB2	0.015735814347863197	Pathway	Wu-Stein-2010
ACVRL1	ACVR2A	0.01564803533256054	Pathway	Wu-Stein-2010
TGFB1	ACVR1B	0.015438576228916645	Pathway	Wu-Stein-2010
BMPR1B	TGFB3	0.015344741754233837	Pathway	Wu-Stein-2010
BMPR1A	TGFB3	0.015344741754233837	Pathway	Wu-Stein-2010
CITED1	SMAD1	0.015269950963556767	Pathway	Wu-Stein-2010
BMP2	ACVR1B	0.015159583650529385	Pathway	Wu-Stein-2010
GLI3	WNT7B	0.015146179124712944	Pathway	Wu-Stein-2010
PTPRC	LCK	0.015145143494009972	Pathway	Wu-Stein-2010
ACVR2A	TGFB1	0.01488997507840395	Pathway	Wu-Stein-2010
IL4R	SOCS3	0.01482166163623333	Pathway	Wu-Stein-2010
SMAD4	RUNX1	0.014690560288727283	Pathway	Wu-Stein-2010
XRCC6	TP53	0.014665261376649141	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
ACVR2A	BMP2	0.014620895497500896	Pathway	Wu-Stein-2010
HIF1A	ETS1	0.014582080766558647	Pathway	PATHWAYCOMMONS-NCI_NATURE
ACVR2A	ACVR1B	0.014551461674273014	Pathway	Wu-Stein-2010

Gene 1	Gene 2	Weight	Network group	Networks
NFKB1	SYK	0.014397267950698733	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
GLI3	BMP4	0.014246894977986813	Pathway	Wu-Stein-2010
AKT1	INS	0.01423815661109984	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
CITED1	CREBBP	0.014223076403141022	Pathway	Wu-Stein-2010
SMAD7	BMP2	0.014154927805066109	Pathway	Wu-Stein-2010
NFKB1	LYN	0.014088688418269157	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
TGFB2	BMP7	0.014080210588872433	Pathway	Wu-Stein-2010
AKT1	ILK	0.013943969272077084	Pathway	Wu-Stein-2010
JUN	TGFB1	0.013828381197527051	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
SMAD6	TGFB2	0.013817890547215939	Pathway	Wu-Stein-2010
HSP90AB1	TP53	0.013730872422456741	Pathway	Wu-Stein-2010
SMAD6	SMAD2	0.013691543601453304	Pathway	Wu-Stein-2010
BMP4	BMPR1B	0.013674089685082436	Pathway	Wu-Stein-2010
BMPR1A	BMP4	0.013674089685082436	Pathway	Wu-Stein-2010
TGFB2	NKX2-5	0.013663209974765778	Pathway	Wu-Stein-2010
RARA	TGFB2	0.013633889146149158	Pathway	Wu-Stein-2010
SMAD1	NKX2-5	0.013603439554572105	Pathway	Wu-Stein-2010
SMAD7	ACVR2A	0.013587108813226223	Pathway	Wu-Stein-2010
ARNT	ETS1	0.012944369576871395	Pathway	PATHWAYCOMMONS-NCI_NATURE
TP53	BDNF	0.012866624630987644	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
SMAD4	GATA4	0.012795464135706425	Pathway	Wu-Stein-2010
SMAD4	SMAD2	0.012586714699864388	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
TGFB2	TGFB2	0.012562221847474575	Pathway	Wu-Stein-2010
SMAD1	TGFB2	0.01250726729631424	Pathway	Wu-Stein-2010
SMAD2	TGFB2	0.0124473562464118	Pathway	Wu-Stein-2010
MAPK14	NFKB1	0.012446110020391643	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
IL2RA	SOCS2	0.012425578199326992	Pathway	Wu-Stein-2010
LCK	EPHB2	0.012313393875956535	Pathway	Wu-Stein-2010
GLI3	BMP2	0.012227890081703663	Pathway	Wu-Stein-2010
AKT1	HSP90AA1	0.012012711958959699	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
SMAD3	FOXO3	0.011990267783403397	Pathway	Wu-Stein-2010
BCL2	MAPK9	0.01196334045380354	Pathway	Wu-Stein-2010
TGFB1	BMPR1B	0.011952250264585018	Pathway	Wu-Stein-2010
BMPR1A	TGFB1	0.011952250264585018	Pathway	Wu-Stein-2010
CITED1	SMAD3	0.01184504572302103	Pathway	Wu-Stein-2010
MAPK14	MAPT	0.011785873211920261	Pathway	Wu-Stein-2010
JUN	ETS1	0.011750963400118053	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
BMP2	BMPR1B	0.011736259795725346	Pathway	Wu-Stein-2010
BMPR1A	BMP2	0.011736259795725346	Pathway	Wu-Stein-2010
HIF1A	ARNT	0.011630590539425611	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
IL4R	STAT5B	0.011485518887639046	Pathway	Wu-Stein-2010
ACVR2A	BMPR1B	0.011265465058386326	Pathway	Wu-Stein-2010
BMPR1A	ACVR2A	0.011265465058386326	Pathway	Wu-Stein-2010
HIF1A	HSP90AA1	0.011210531229153275	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
MAPK14	CD36	0.011171109043061733	Pathway	Wu-Stein-2010
NFKB1	LCK	0.011124899378046393	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
AKT1	FOXO3	0.010926761664450169	Pathway	Wu-Stein-2010
SMAD7	BMPR1B	0.010906433686614037	Pathway	Wu-Stein-2010

Gene 1	Gene 2	Weight	Network group	Networks
BMPR1A	SMAD7	0.010906433686614037	Pathway	Wu-Stein-2010
LCK	JAK2	0.010783068835735321	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
MAPK9	IL2RA	0.010709461756050587	Pathway	Wu-Stein-2010
SMAD6	SMAD3	0.010671778582036495	Pathway	Wu-Stein-2010
SMAD4	ARNT	0.010519922943785787	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
CITED1	SMAD4	0.010444067418575287	Pathway	Wu-Stein-2010
NGFR	MAPK9	0.010372201912105083	Pathway	Wu-Stein-2010
STAT5A	IL4R	0.0103059783577919	Pathway	Wu-Stein-2010
SMAD1	TGFB3	0.010154703631997108	Pathway	Wu-Stein-2010
SMAD2	TGFB3	0.010106061585247517	Pathway	Wu-Stein-2010
LYN	ZAP70	0.009781714528799057	Pathway	Wu-Stein-2010
SMAD4	TGFB2	0.009745075134560466	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
SMAD3	TGFB2	0.009702005423605442	Pathway	Wu-Stein-2010
JAK2	INPP5D	0.009529362432658672	Pathway	PATHWAYCOMMONS-NCI_NATURE
JUN	TGIF1	0.009449665434658527	Pathway	Wu-Stein-2010
SMAD6	SMAD4	0.009409569203853607	Pathway	Wu-Stein-2010
LYN	KIT	0.009322765283286572	Pathway	Wu-Stein-2010
AKT1	IL2RA	0.00917424913495779	Pathway	PATHWAYCOMMONS-NCI_NATURE
CREBBP	ARNT	0.009104084223508835	Pathway	Wu-Stein-2010
TGFB2	BMP4	0.00908887479454279	Pathway	Wu-Stein-2010
SMAD1	ID2	0.009056629613041878	Pathway	Wu-Stein-2010
SMAD1	BMP4	0.00904911570250988	Pathway	Wu-Stein-2010
BMPR1A	BMPR1B	0.009042839519679546	Pathway	Wu-Stein-2010
RB1	POLR1D	0.00887453742325306	Pathway	Wu-Stein-2010
STAT5B	SOCS2	0.00864496361464262	Pathway	Wu-Stein-2010
RARA	TGFB1	0.008622132241725922	Pathway	Wu-Stein-2010
JUN	ILK	0.008615231141448021	Pathway	Wu-Stein-2010
SMAD4	TGFB2	0.008554496802389622	Pathway	Wu-Stein-2010
SMAD2	ACVR1	0.00836773682385683	Pathway	Wu-Stein-2010
ACVRL1	SMAD2	0.008272521197795868	Pathway	Wu-Stein-2010
SMAD7	JUN	0.008215798065066338	Pathway	PATHWAYCOMMONS-NCI_NATURE
NFKB1	AKT1	0.008068881812505424	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
HIF1A	TGFB3	0.007954577915370464	Pathway	Wu-Stein-2010
AKT1	LCK	0.007942869327962399	Pathway	PATHWAYCOMMONS-NCI_NATURE
SMAD1	TGFB1	0.007909651845693588	Pathway	Wu-Stein-2010
SMAD3	TGFB3	0.007877100259065628	Pathway	Wu-Stein-2010
SMAD2	TGFB1	0.007871763780713081	Pathway	Wu-Stein-2010
TGFB2	BMP2	0.0078008417040109634	Pathway	Wu-Stein-2010
BCL2	PPARG	0.0077818771824240685	Pathway	Wu-Stein-2010
SMAD1	BMP2	0.007766715716570616	Pathway	Wu-Stein-2010
TGFB2	ACVR1B	0.007763795554637909	Pathway	Wu-Stein-2010
STAT5A	SOCS2	0.007757142186164856	Pathway	Wu-Stein-2010
RB1	MAPK9	0.0077120098285377026	Pathway	Wu-Stein-2010
JUN	RB1	0.007711443351581693	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
NFKB1	JAK2	0.007701994385570288	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
SMAD2	ACVR1B	0.007692805025726557	Pathway	Wu-Stein-2010
ARNT	SMAD3	0.0075819240882992744	Pathway	Wu-Stein-2010
SMAD1	ACVR2A	0.007455156650394201	Pathway	Wu-Stein-2010
NGF	MAPK9	0.007401291746646166	Pathway	Wu-Stein-2010
TP53	NGFR	0.007252832176163793	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
ETS1	FGF2	0.007242236752063036	Pathway	Wu-Stein-2010
JAK2	SOCS2	0.007204084657132626	Pathway	Wu-Stein-2010
SMAD7	SMAD2	0.0071829878725111485	Pathway	Wu-Stein-2010

Gene 1	Gene 2	Weight	Network group	Networks
TP53	APC	0.0071795047260820866	Pathway	PATHWAYCOMMONS-NCI_NATURE
CREBBP	POLR1D	0.00717361643910408	Pathway	Wu-Stein-2010
ETS1	BMP4	0.007159606087952852	Pathway	Wu-Stein-2010
JUN	ARNT	0.007098523899912834	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
IL2RA	STAT5B	0.007054950576275587	Pathway	Wu-Stein-2010
LCK	MAPK9	0.007008230313658714	Pathway	Wu-Stein-2010
AKT1	BAD	0.0069494303315877914	Pathway	Wu-Stein-2010
SMAD4	TGFB3	0.006945433095097542	Pathway	Wu-Stein-2010
AKT1	ARNT	0.0069094267673790455	Pathway	Wu-Stein-2010
MAPK14	SRF	0.006601868662983179	Pathway	Wu-Stein-2010
SMAD3	ACVR1	0.006522174458950758	Pathway	Wu-Stein-2010
ACVRL1	SMAD3	0.006447959691286087	Pathway	Wu-Stein-2010
HIF1A	SMAD4	0.00644171261228621	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
STAT5B	SOCS3	0.006334128323942423	Pathway	Wu-Stein-2010
STAT5A	IL2RA	0.006330420728772879	Pathway	Wu-Stein-2010
HIF1A	TGFB1	0.006195941008627415	Pathway	Wu-Stein-2010
SMAD4	ID2	0.006194392219185829	Pathway	Wu-Stein-2010
SMAD3	TGFB1	0.006135592237114906	Pathway	Wu-Stein-2010
SMAD3	ACVR1B	0.00599610386416316	Pathway	Wu-Stein-2010
SMAD1	BMPR1B	0.005984288640320301	Pathway	Wu-Stein-2010
BMPR1A	SMAD1	0.005984288640320301	Pathway	Wu-Stein-2010
MAPK14	TGFB2	0.005913970991969109	Pathway	Wu-Stein-2010
LYN	STAT5B	0.005899921525269747	Pathway	Wu-Stein-2010
JAK2	IL2RA	0.0058790841139853	Pathway	Wu-Stein-2010
JUN	IL2RA	0.005709401331841946	Pathway	PATHWAYCOMMONS-NCI_NATURE
STAT5A	SOCS3	0.0056836255826056	Pathway	Wu-Stein-2010
ETS1	BCL2	0.005600819829851389	Pathway	Wu-Stein-2010
SMAD7	SMAD3	0.005598730407655239	Pathway	Wu-Stein-2010
TP53	MAPK14	0.005494703189469874	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
SMAD4	TGFB1	0.005409902427345514	Pathway	Wu-Stein-2010
LYN	STAT5A	0.005294010974466801	Pathway	Wu-Stein-2010
SMAD4	ACVR1B	0.0052869124338030815	Pathway	Wu-Stein-2010
NOTCH1	LCK	0.005143371410667896	Pathway	Wu-Stein-2010
NFKB1	HMGB1	0.004966852255165577	Pathway	Wu-Stein-2010
SMAD7	SMAD4	0.00493653817102313	Pathway	Wu-Stein-2010
SMAD1	NOTCH1	0.004911832045763731	Pathway	Wu-Stein-2010
RARA	STAT5B	0.004806043114513159	Pathway	Wu-Stein-2010
MAPK14	TGFB3	0.004801578354090452	Pathway	Wu-Stein-2010
MAPK14	BAD	0.00464840792119503	Pathway	Wu-Stein-2010
LCK	STAT5B	0.004616732243448496	Pathway	Wu-Stein-2010
CREBBP	NOTCH1	0.004575088154524565	Pathway	Wu-Stein-2010
JUN	HIF1A	0.004542468348518014	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
JUN	SMAD4	0.004258818458765745	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
CREBBP	RB1	0.004250496160238981	Pathway	Wu-Stein-2010
STAT5A	LCK	0.004142602905631065	Pathway	Wu-Stein-2010
MAPK14	CCNE1	0.004139158874750137	Pathway	Wu-Stein-2010
JAK2	STAT5B	0.004090310074388981	Pathway	Wu-Stein-2010
JUN	HMGB1	0.004064925014972687	Pathway	Wu-Stein-2010
CREBBP	RARA	0.004020994063466787	Pathway	Wu-Stein-2010
SMAD1	TGFBR2	0.003977628890424967	Pathway	Wu-Stein-2010
NFKB1	BCL2	0.0037778052501380444	Pathway	Wu-Stein-2010
TP53	HIF1A	0.003764076391234994	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
MAPK14	TGFB1	0.0037400214932858944	Pathway	Wu-Stein-2010

Gene 1	Gene 2	Weight	Network group	Networks
CREBBP	SMAD1	0.0036887237802147865	Pathway	Wu-Stein-2010
CREBBP	SMAD2	0.0036710540298372507	Pathway	Wu-Stein-2010
STAT5A	JAK2	0.0036702428478747606	Pathway	Wu-Stein-2010
TP53	POLR1D	0.0035816568415611982	Pathway	Wu-Stein-2010
ETS1	RARA	0.003415549173951149	Pathway	Wu-Stein-2010
SMAD7	MAPK14	0.0034127712715417147	Pathway	Wu-Stein-2010
NFKB1	IL2RA	0.00338185322470963	Pathway	Wu-Stein-2010
PPARG	SMAD3	0.003377030836418271	Pathway	Wu-Stein-2010
JUN	POLR1D	0.0033637555316090584	Pathway	Wu-Stein-2010
MAPK14	BCL2	0.0033472285140305758	Pathway	Wu-Stein-2010
MAPK14	SYK	0.0033302230294793844	Pathway	Wu-Stein-2010
TP53	BCL2	0.0032920800149440765	Pathway	Wu-Stein-2010
ETS1	LCK	0.0032810100819915533	Pathway	Wu-Stein-2010
ETS1	TGFBR2	0.0031470763497054577	Pathway	Wu-Stein-2010
AKT1	STAT5B	0.0031166786793619394	Pathway	Wu-Stein-2010
SMAD3	TGFBR2	0.0030854842625558376	Pathway	Wu-Stein-2010
JUN	SYK	0.003076088149100542	Pathway	Wu-Stein-2010
SMAD2	SMAD3	0.0030572712421417236	Pathway	Wu-Stein-2010
NFKB1	SOCS3	0.0030363204423338175	Pathway	Wu-Stein-2010
MAPK14	IL2RA	0.00299640535376966	Pathway	Wu-Stein-2010
CREBBP	HIF1A	0.0028895221184939146	Pathway	Wu-Stein-2010
CREBBP	SMAD3	0.0028613777831196785	Pathway	Wu-Stein-2010
AKT1	STAT5A	0.0027966019697487354	Pathway	Wu-Stein-2010
NFKB1	NOTCH1	0.002621286315843463	Pathway	Wu-Stein-2010
CREBBP	AKT1	0.0026075809728354216	Pathway	Wu-Stein-2010
CREBBP	SMAD4	0.0025229472666978836	Pathway	Wu-Stein-2010
TP53	JUN	0.0024572184775024652	Pathway	PATHWAYCOMMONS-NCI_NATURE Wu-Stein-2010
HIF1A	SMAD3	0.002406407380476594	Pathway	Wu-Stein-2010
JUN	LYN	0.0023146122694015503	Pathway	Wu-Stein-2010
HIF1A	AKT1	0.002192965243011713	Pathway	Wu-Stein-2010
AKT1	SMAD3	0.0021716055925935507	Pathway	Wu-Stein-2010
MAPK14	RB1	0.0021577468141913414	Pathway	Wu-Stein-2010
JUN	NOTCH1	0.002145288744941354	Pathway	Wu-Stein-2010
TP53	RB1	0.002122195903211832	Pathway	Wu-Stein-2010
SMAD4	SMAD3	0.0021011224016547203	Pathway	Wu-Stein-2010
MAPK14	RARA	0.0020412409212440252	Pathway	Wu-Stein-2010
TP53	HSP90AA1	0.0019976277835667133	Pathway	Wu-Stein-2010
MAPK14	LCK	0.0019608361180871725	Pathway	Wu-Stein-2010
JUN	NGF	0.0019127839477732778	Pathway	Wu-Stein-2010
CREBBP	MAPK14	0.0017441862728446722	Pathway	Wu-Stein-2010
MAPK14	JAK2	0.001737251877784729	Pathway	Wu-Stein-2010
JUN	SMAD1	0.0017296667210757732	Pathway	Wu-Stein-2010
JUN	SMAD2	0.0017213814426213503	Pathway	Wu-Stein-2010
NFKB1	ETS1	0.0016721459105610847	Pathway	Wu-Stein-2010
TP53	ETS1	0.001457152422517538	Pathway	Wu-Stein-2010
JUN	SMAD3	0.001341718714684248	Pathway	Wu-Stein-2010
TP53	AKT1	0.0013019179459661245	Pathway	Wu-Stein-2010
JUN	AKT1	0.001222711754962802	Pathway	Wu-Stein-2010
TP53	NFKB1	9.828627808019519E-4	Pathway	Wu-Stein-2010
TGFBR2	TGFB3	2.1570912450551987	Physical interactions	IREF-BIND IREF-CORUM IREF-DIP IREF-GRID IREF-INTACT
NTF3	BDNF	2.1223801374435425	Physical interactions	IREF-BIND IREF-DIP IREF-INTACT

Gene 1	Gene 2	Weight	Network group	Networks
LIG4	XRCC4	2.077696815133095	Physical interactions	IREF-BIND IREF-CORUM IREF-GRID IREF-INTACT
CBFB	RUNX1	1.8360343873500824	Physical interactions	IREF-BIND IREF-CORUM IREF-GRID IREF-INTACT
CITED1	STAT5A	1.6979542672634125	Physical interactions	IREF-BIND IREF-BIND-TRANSLATION IREF-MPPI
SMAD4	SMAD3	1.5549770705401897	Physical interactions	IREF-BIND IREF-DIP IREF-GRID IREF-INTACT IREF-MPPI
FBXW7	CCNE1	1.452228419482708	Physical interactions	IREF-BIND IREF-BIND-TRANSLATION IREF-GRID
TGFB3	TGFB2	1.3931087851524353	Physical interactions	IREF-BIND IREF-DIP
BMPR1A	BMP2	1.3698308616876602	Physical interactions	IREF-DIP IREF-GRID IREF-INTACT
ACVR2A	ACVR1B	1.3287160694599152	Physical interactions	IREF-BIND IREF-DIP IREF-GRID IREF-MPPI
NTF3	NTRK3	1.243940144777298	Physical interactions	IREF-DIP IREF-GRID
HIF1A	ARNT	1.231044651940465	Physical interactions	IREF-BIND IREF-CORUM IREF-DIP IREF-GRID IREF-INTACT IREF-MPPI
XRCC6	XRCC5	1.206141959875822	Physical interactions	IREF-BIND IREF-CORUM IREF-GRID IREF-INTACT IREF-MPPI
SRF	GATA4	1.1804500296711922	Physical interactions	IREF-BIND IREF-BIND-TRANSLATION IREF-GRID
BMPR1A	BMP4	1.1747714951634407	Physical interactions	IREF-BIND IREF-DIP IREF-GRID
TGFB2	TGFB1	1.1190376169979572	Physical interactions	IREF-BIND IREF-CORUM IREF-DIP IREF-GRID
KIT	KITLG	1.1047692894935608	Physical interactions	IREF-GRID IREF-INTACT
ACVRL1	ACVR2A	1.009182333946228	Physical interactions	IREF-BIND IREF-DIP IREF-MPPI
NGFR	NGF	0.9552624970674515	Physical interactions	IREF-BIND IREF-CORUM IREF-DIP IREF-GRID
ACVR2A	BMP7	0.9202205911278725	Physical interactions	IREF-BIND IREF-GRID IREF-INTACT
SMAD6	RUNX2	0.7962251901626587	Physical interactions	IREF-INTACT
ACVR2A	ACVR1	0.7919175922870636	Physical interactions	IREF-DIP IREF-MPPI

Gene 1	Gene 2	Weight	Network group	Networks
BMP4	BMPR1B	0.7399471029639244	Physical interactions	IREF-BIND IREF-DIP IREF-GRID
NOTCH1	JAG1	0.6843582391738892	Physical interactions	IREF-DIP IREF-GRID
POLR1C	POLR1D	0.6232312023639679	Physical interactions	IREF-GRID IREF-INTACT
NTF3	NGFR	0.6077812314033508	Physical interactions	IREF-CORUM
ACVR2A	BMPR1B	0.601166345179081	Physical interactions	IREF-BIND IREF-DIP IREF-MPPI
CBFB	RUNX3	0.5877852439880371	Physical interactions	IREF-BIND
BMPR1A	BMPR1B	0.5586157590150833	Physical interactions	IREF-DIP IREF-GRID IREF-MPPI
GATA4	NKX2-5	0.5269390642642975	Physical interactions	IREF-BIND IREF-GRID
TGFBR3	TGFBR2	0.506669357419014	Physical interactions	IREF-DIP IREF-GRID
FOXH1	SMAD2	0.48329441249370575	Physical interactions	IREF-BIND IREF-CORUM IREF-GRID
HIF1A	HSP90AA1	0.43957401905208826	Physical interactions	IREF-BIND IREF-DIP IREF-GRID IREF-MPPI
SRF	HOPX	0.428779661655426	Physical interactions	IREF-BIND
TGFBR3	TGFB1	0.4159679412841797	Physical interactions	IREF-DIP IREF-GRID
NTF4	BDNF	0.3523203134536743	Physical interactions	IREF-BIND
HIF1A	FOXO3	0.34357577562332153	Physical interactions	IREF-DIP
CREBBP	SMAD1	0.34204160142689943	Physical interactions	IREF-CORUM IREF-GRID
JUN	MAPK9	0.34192137978971004	Physical interactions	IREF-BIND IREF-DIP IREF-GRID IREF-INTACT
ACVRL1	TGFB1	0.32375162839889526	Physical interactions	IREF-DIP IREF-GRID
JUN	HSP90AA1	0.32162908697500825	Physical interactions	Bandyopadhyay-Ideker-2010 IREF-GRID IREF-INTACT Miyamoto-Sato-Yanagawa-2010
BMPR1B	BMP7	0.30772707238793373	Physical interactions	IREF-DIP IREF-GRID
FBXW7	NOTCH1	0.2792393546551466	Physical interactions	IREF-DIP IREF-GRID
CREBBP	TP53	0.27869068284053355	Physical interactions	IREF-BIND IREF-GRID IREF-INTACT IREF-MPPI
ACVRL1	TGFB3	0.26684802770614624	Physical interactions	IREF-DIP
SMAD4	SMAD2	0.25901729753240943	Physical interactions	IREF-BIND IREF-DIP IREF-GRID IREF-INTACT
LYN	SYK	0.2582435915246606	Physical interactions	IREF-DIP IREF-GRID
FOXO3	FOXG1	0.256315678358078	Physical interactions	IREF-BIND
FOXH1	FOXG1	0.2536062002182007	Physical interactions	IREF-GRID
TGFBR2	CLU	0.24327119067311287	Physical interactions	IREF-BIND IREF-GRID
TP53	FOXO3	0.23088566772639751	Physical interactions	IREF-BIND IREF-CORUM

Gene 1	Gene 2	Weight	Network group	Networks
LCK	ZAP70	0.21141947619616985	Physical interactions	IREF-GRID IREF-INTACT
BCL2	BAD	0.20863651484251022	Physical interactions	IREF-BIND IREF-GRID IREF-INTACT
TP53	BCL2	0.19963097758591175	Physical interactions	IREF-CORUM IREF-DIP
RUNX1	TAL1	0.19960516691207886	Physical interactions	IREF-DIP
ACVR2A	BMP2	0.19756053388118744	Physical interactions	IREF-DIP
RB1	RUNX2	0.18773458898067474	Physical interactions	IREF-BIND
PPARG	CLU	0.17990311235189438	Physical interactions	IREF-INTACT Miyamoto-Sato-Yanagawa-2010
ACVRL1	TGFBR2	0.17004704475402832	Physical interactions	IREF-DIP
RTN4R	NGFR	0.16914978623390198	Physical interactions	IREF-BIND
CREBBP	SMAD2	0.16367157362401485	Physical interactions	IREF-BIND IREF-CORUM
HSP90AB1	PPARG	0.16271859034895897	Physical interactions	IREF-INTACT Miyamoto-Sato-Yanagawa-2010
FOXH1	TGIF1	0.16099822521209717	Physical interactions	IREF-GRID
NTF4	NGFR	0.15682004392147064	Physical interactions	IREF-BIND
LYN	KIT	0.1492357524111867	Physical interactions	IREF-BIND IREF-GRID
CREBBP	SMAD3	0.14693060610443354	Physical interactions	IREF-BIND IREF-CORUM
FOXH1	SMAD3	0.13712387531995773	Physical interactions	IREF-BIND IREF-GRID
XRCC6	CLU	0.11867846921086311	Physical interactions	IREF-BIND IREF-GRID
AKT1	MAPT	0.11159626394510269	Physical interactions	IREF-DIP
ETS1	HMGB1	0.11016082763671875	Physical interactions	IREF-INTACT Miyamoto-Sato-Yanagawa-2010
IL4R	INPP5D	0.1059093028306961	Physical interactions	IREF-GRID
SRF	GATA6	0.09882982820272446	Physical interactions	IREF-GRID
TP53	HMGB1	0.09848623746074736	Physical interactions	IREF-BIND IREF-DIP IREF-GRID IREF-INTACT
ID2	NKX2-5	0.09805718809366226	Physical interactions	IREF-GRID
TP53	THRB	0.09103599307127297	Physical interactions	IREF-DIP IREF-GRID
PTPRC	LCK	0.0810762494802475	Physical interactions	IREF-DIP IREF-GRID IREF-INTACT
ETS1	RUNX2	0.08032746613025665	Physical interactions	IREF-GRID
XRCC6	NOTCH1	0.07492367830127478	Physical interactions	IREF-GRID IREF-INTACT
BMPR1A	BMP7	0.0743701308965683	Physical interactions	IREF-GRID
RB1	MNDA	0.07384765893220901	Physical interactions	IREF-DIP
NFKB1	MEN1	0.07141177915036678	Physical interactions	IREF-DIP IREF-GRID
HIF1A	NOTCH1	0.07012082636356354	Physical interactions	IREF-DIP
TGFBR2	TGFB2	0.0688038095831871	Physical interactions	IREF-GRID
HSP90AB1	HIF1A	0.06789062172174454	Physical interactions	IREF-DIP
RUNX3	SMAD1	0.06653089821338654	Physical interactions	IREF-GRID
SMAD3	TGIF2	0.06322960555553436	Physical interactions	IREF-GRID
ID2	GATA4	0.06317011266946793	Physical interactions	IREF-GRID
SMAD1	FOXG1	0.057344675064086914	Physical interactions	IREF-GRID
TP53	MNDA	0.05525964871048927	Physical interactions	IREF-DIP
RB1	MAPK9	0.055164072662591934	Physical interactions	IREF-BIND
ETS1	RUNX1	0.05377354472875595	Physical interactions	IREF-GRID
SMAD4	FOXO3	0.05157012678682804	Physical interactions	IREF-BIND IREF-GRID

Gene 1	Gene 2	Weight	Network group	Networks
TGFB1	TGFB2	0.04922926425933838	Physical interactions	IREF-GRID
SRF	NKX2-5	0.04785706102848053	Physical interactions	IREF-GRID
SMAD3	FOXO3	0.04443326219916344	Physical interactions	IREF-BIND IREF-GRID
TP53	PNP	0.04411103390157223	Physical interactions	IREF-GRID IREF-INTACT
CITED1	SMAD4	0.04194407910108566	Physical interactions	IREF-GRID
HSP90AA1	LCK	0.04053952172398567	Physical interactions	IREF-DIP
RB1	HMGB1	0.04012775467708707	Physical interactions	IREF-BIND IREF-GRID
SMAD6	SMAD7	0.03938949480652809	Physical interactions	IREF-GRID
SMAD7	ACVR1B	0.03891828656196594	Physical interactions	IREF-GRID
CITED1	CREBBP	0.038791753351688385	Physical interactions	IREF-GRID
SMAD1	BMP7	0.03851953521370888	Physical interactions	IREF-GRID
KIT	INPP5D	0.03847891092300415	Physical interactions	IREF-GRID
XRCC6	SMAD7	0.036977268755435944	Physical interactions	IREF-BIND
BMPR1A	SMAD7	0.03685181960463524	Physical interactions	IREF-GRID
CBFB	JUN	0.03646202106028795	Physical interactions	IREF-INTACT Miyamoto-Sato-Yanagawa-2010
SMAD1	TGIF1	0.036404434591531754	Physical interactions	IREF-GRID
RUNX3	SMAD2	0.03622758015990257	Physical interactions	IREF-GRID
SMAD6	SMAD1	0.035186681896448135	Physical interactions	IREF-GRID
JUN	ETS1	0.03479645075276494	Physical interactions	IREF-GRID IREF-INTACT Miyamoto-Sato-Yanagawa-2010
SMAD1	RUNX2	0.033553965389728546	Physical interactions	IREF-GRID
TP53	HIF1A	0.033283940982073545	Physical interactions	IREF-BIND IREF-GRID
FOXH1	SMAD4	0.03258991986513138	Physical interactions	IREF-GRID
SMAD4	TGFBR2	0.03166759014129639	Physical interactions	IREF-BIND
RUNX3	SMAD3	0.0316334031522274	Physical interactions	IREF-GRID
BMP2	BMPR1B	0.028357544913887978	Physical interactions	IREF-GRID
SMAD7	TGFBR2	0.02812250144779682	Physical interactions	IREF-GRID
ACVR1	BMP7	0.027597801759839058	Physical interactions	IREF-GRID
JAK2	STAT5B	0.02560833841562271	Physical interactions	IREF-GRID
ACVR1	ACVR1B	0.024908360093832016	Physical interactions	IREF-GRID
HSP90AB1	AKT1	0.024694208055734634	Physical interactions	IREF-GRID
CREBBP	APC	0.024148749420419335	Physical interactions	Bandyopadhyay-Ideker-2010 IREF-GRID
JAK2	SOCS3	0.02307949587702751	Physical interactions	IREF-GRID
SMAD6	BMPR1B	0.02299601212143898	Physical interactions	IREF-GRID
SMAD3	TGFBR2	0.02297462709248066	Physical interactions	IREF-BIND
SMAD1	RUNX1	0.02246199920773506	Physical interactions	IREF-GRID
LYN	CD36	0.022186780348420143	Physical interactions	IREF-GRID
LYN	INPP5D	0.02185654453933239	Physical interactions	IREF-GRID
BCL2	EPHB2	0.020992206409573555	Physical interactions	IREF-GRID
XRCC6	TP53	0.020143350353464484	Physical interactions	IREF-BIND IREF-GRID IREF-INTACT
STAT5A	JAK2	0.019936036318540573	Physical interactions	IREF-GRID
SMAD2	TGIF1	0.019823037087917328	Physical interactions	IREF-GRID
SMAD6	SMAD2	0.019159944728016853	Physical interactions	IREF-GRID
SMAD2	ACVR1B	0.018930738791823387	Physical interactions	IREF-GRID
AKT1	BAD	0.018800057470798492	Physical interactions	IREF-GRID
SMAD3	BMP7	0.01831485889852047	Physical interactions	IREF-GRID
SMAD2	RUNX2	0.018270891159772873	Physical interactions	IREF-GRID
TGFBR2	ACVR1	0.017998874187469482	Physical interactions	IREF-GRID
RB1	TAL1	0.01736266165971756	Physical interactions	IREF-DIP
SMAD3	TGIF1	0.017309194430708885	Physical interactions	IREF-GRID
NOTCH1	LCK	0.017308207228779793	Physical interactions	IREF-GRID

Gene 1	Gene 2	Weight	Network group	Networks
JUN	TGIF1	0.01684398204088211	Physical interactions	IREF-GRID
SMAD3	ACVR1B	0.016530049964785576	Physical interactions	IREF-GRID
SMAD3	RUNX2	0.01595388352870941	Physical interactions	IREF-GRID
KIT	LCK	0.015941103920340538	Physical interactions	IREF-GRID
JUN	RUNX2	0.015525097027420998	Physical interactions	IREF-GRID
SMAD6	SMAD4	0.01520741917192936	Physical interactions	IREF-GRID
JUN	SMAD2	0.014826163649559021	Physical interactions	IREF-GRID IREF-INTACT Miyamoto-Sato-Yanagawa-2010
LYN	PTPRC	0.014815556816756725	Physical interactions	IREF-GRID
NFKB1	NOTCH1	0.014216439798474312	Physical interactions	IREF-GRID
HSP90AA1	ARNT	0.01409261766821146	Physical interactions	IREF-GRID
HSP90AA1	TGFB2	0.013986745849251747	Physical interactions	IREF-GRID
CREBBP	GLI3	0.013961213640868664	Physical interactions	IREF-GRID
SMAD4	SMAD1	0.013798704836517572	Physical interactions	IREF-BIND IREF-GRID
KIT	JAK2	0.013732079416513443	Physical interactions	IREF-GRID
JUN	RB1	0.013037987519055605	Physical interactions	IREF-BIND IREF-GRID
SMAD7	BMPR1B	0.012474283576011658	Physical interactions	IREF-GRID
SMAD2	RUNX1	0.012231066823005676	Physical interactions	IREF-GRID
SMAD1	ACVR1	0.012216105125844479	Physical interactions	IREF-GRID
LCK	SYK	0.012057275511324406	Physical interactions	IREF-GRID
SMAD7	AKT1	0.01193909989831448	Physical interactions	IREF-GRID
SMAD3	MEN1	0.011892559006810188	Physical interactions	IREF-GRID
XRCC6	SMAD3	0.011743846349418163	Physical interactions	IREF-BIND
RB1	ARNT	0.011196661740541458	Physical interactions	IREF-GRID
XRCC6	TAL1	0.011051087640225887	Physical interactions	IREF-GRID
NFKB1	HMGB1	0.010837143287062645	Physical interactions	IREF-GRID
SMAD3	RUNX1	0.010679992847144604	Physical interactions	IREF-GRID
RB1	PAX6	0.010504008270800114	Physical interactions	IREF-GRID
SMAD7	SMAD2	0.010393393225967884	Physical interactions	IREF-GRID
JUN	RUNX1	0.010392951779067516	Physical interactions	IREF-GRID
NOTCH1	SMAD3	0.009856047108769417	Physical interactions	IREF-GRID
SMAD7	MAPK14	0.009635044261813164	Physical interactions	IREF-GRID
AKT1	ILK	0.009603360667824745	Physical interactions	IREF-GRID
SMAD7	SMAD3	0.009075362235307693	Physical interactions	IREF-GRID
SMAD7	SMAD4	0.008249328471720219	Physical interactions	IREF-GRID
RB1	PPARG	0.008171905763447285	Physical interactions	IREF-GRID
SMAD2	SMAD3	0.007960853865370154	Physical interactions	IREF-BIND IREF-GRID
LYN	JAK2	0.00780000863596797	Physical interactions	IREF-GRID
JUN	HIF1A	0.007568481378257275	Physical interactions	IREF-GRID
CREBBP	PPARG	0.0073842694982886314	Physical interactions	IREF-GRID
CREBBP	HIF1A	0.006538290064781904	Physical interactions	IREF-GRID
CREBBP	SRF	0.0061632189899683	Physical interactions	IREF-GRID
AKT1	HSP90AA1	0.005937919951975346	Physical interactions	IREF-GRID
AKT1	SMAD2	0.005807449575513601	Physical interactions	IREF-GRID
MAPK14	AKT1	0.005383711773902178	Physical interactions	IREF-GRID
AKT1	SMAD3	0.005070981569588184	Physical interactions	IREF-GRID
AKT1	SMAD4	0.0046094246208667755	Physical interactions	IREF-GRID
TP53	MAPK9	0.00410738680511713	Physical interactions	IREF-GRID
XRCC6	CREBBP	0.004018891602754593	Physical interactions	IREF-GRID
JUN	SMAD3	0.003751045325770974	Physical interactions	IREF-GRID
CREBBP	JUN	0.003153375815600157	Physical interactions	IREF-GRID
TP53	HSP90AA1	0.0019446308724582195	Physical interactions	IREF-GRID
POLR1C	POLR1D	3.083118749782443	Predicted	I2D-BIND-Yeast2Human I2D-IntAct-Fly2Human I2D-Tarassov-PCA-Yeast2Human I2D-Yu-Vidal-2008-GoldStd-

Gene 1	Gene 2	Weight	Network group	Networks
				Yeast2Human Stuart-Kim-2003
CBFB	RUNX1	1.8765486478805542	Predicted	I2D-BIND-Mouse2Human I2D-IntAct-Fly2Human
RTN4R	NGFR	1.6077812314033508	Predicted	I2D-BIND-Rat2Human I2D-MINT-Rat2Human
JUN	MAPK9	1.419400155544281	Predicted	I2D-BIND-Rat2Human I2D-MINT-Rat2Human
STAT5A	STAT5B	1.0	Predicted	I2D-Li-Vidal-2004-CORE-1-Worm2Human
CREBBP	HIF1A	1.0	Predicted	I2D-MINT-Rat2Human
CREBBP	SMAD3	1.0	Predicted	I2D-BIND-Rat2Human
SMAD7	SMAD3	1.0	Predicted	I2D-IntAct-Mouse2Human
XRCC6	CLU	1.0	Predicted	I2D-BIND-Mouse2Human
JAK2	STAT5B	0.9321110248565674	Predicted	I2D-INNATEDB-Mouse2Human I2D-IntAct-Fly2Human
XRCC6	XRCC5	0.9314934611320496	Predicted	I2D-IntAct-Mouse2Human
GATA4	NKX2-5	0.9052254557609558	Predicted	I2D-BIND-Mouse2Human I2D-IntAct-Mouse2Human
FOXH1	NKX2-5	0.7962251901626587	Predicted	I2D-BIND-Mouse2Human
TGFB3	TGFB1	0.7345095276832581	Predicted	I2D-BIND-Mouse2Human
ACVR2A	SMAD3	0.7113714218139648	Predicted	I2D-MINT-Rat2Human
HSP90AA1	SMAD4	0.7071067690849304	Predicted	I2D-Li-Vidal-2004-CORE-1-Worm2Human
HSP90AB1	SMAD4	0.7071067690849304	Predicted	I2D-Li-Vidal-2004-CORE-1-Worm2Human
TP53	HMGB1	0.7071067690849304	Predicted	I2D-BIND-Rat2Human
HIF1A	ARNT	0.6762251555919647	Predicted	I2D-INNATEDB-Mouse2Human I2D-IntAct-Mouse2Human
PTPRC	LCK	0.6051100492477417	Predicted	I2D-BIND-Mouse2Human I2D-IntAct-Mouse2Human
ACVR2A	BMPR1B	0.553432047367096	Predicted	I2D-BIND-Mouse2Human
HSP90AA1	XRCC5	0.52464759349823	Predicted	I2D-Li-Vidal-2004-CE-DATA-Worm2Human
HSP90AB1	XRCC5	0.52464759349823	Predicted	I2D-Li-Vidal-2004-CE-DATA-Worm2Human
SMAD6	SMAD7	0.5	Predicted	I2D-INNATEDB-Mouse2Human
ACVR2A	ACVR1	0.5	Predicted	I2D-BIND-Mouse2Human
BCL2	BAD	0.43513987958431244	Predicted	I2D-BIND-Mouse2Human I2D-IntAct-Mouse2Human
NOTCH1	JAG1	0.38260239362716675	Predicted	I2D-IntAct-Fly2Human
HIF1A	FOXA2	0.3807545006275177	Predicted	I2D-IntAct-Mouse2Human
NOTCH1	XRCC5	0.3716626763343811	Predicted	I2D-Formstecher-Daviet-2005-Embryo-Fly2Human
AKT1	SMAD2	0.36535391211509705	Predicted	I2D-MINT-Rat2Human
AKT1	SMAD4	0.36535391211509705	Predicted	I2D-MINT-Rat2Human
SMAD7	AKT1	0.36535391211509705	Predicted	I2D-MINT-Rat2Human
FBXW7	JUN	0.3606799244880676	Predicted	I2D-BIND-Mouse2Human
AKT1	SMAD3	0.3541731983423233	Predicted	I2D-INNATEDB-Mouse2Human I2D-MINT-Rat2Human
HSP90AB1	HSP90AA1	0.3235439360141754	Predicted	I2D-Tewari-Vidal-2004-TGFB-Worm2Human
BMP4	BMPR1B	0.29470255970954895	Predicted	I2D-BIND-Mouse2Human
ARNT	FOXA2	0.2943146526813507	Predicted	I2D-IntAct-Mouse2Human
FOXG1	DLX5	0.26905712485313416	Predicted	Stuart-Kim-2003
LYN	ANKRD54	0.2660134434700012	Predicted	I2D-IntAct-Mouse2Human
CREBBP	IL2RA	0.26470470428466797	Predicted	I2D-INNATEDB-Mouse2Human
HSP90AA1	ACVR2A	0.264690101146698	Predicted	I2D-Tewari-Vidal-2004-TGFB-Worm2Human
HSP90AB1	ACVR2A	0.264690101146698	Predicted	I2D-Tewari-Vidal-2004-TGFB-Worm2Human
SMAD4	SMAD2	0.26332011818885803	Predicted	I2D-INNATEDB-Mouse2Human

Gene 1	Gene 2	Weight	Network group	Networks
HLX	BMP7	0.22581854462623596	Predicted	I2D-IntAct-Fly2Human
SMAD4	SMAD1	0.2193576842546463	Predicted	I2D-INNATEDB-Mouse2Human
LYN	JAK2	0.20454076677560806	Predicted	I2D-BIND-Mouse2Human I2D-INNATEDB-Mouse2Human
RB1	NEUROD1	0.1982966512441635	Predicted	I2D-BIND-Mouse2Human
LCK	ZAP70	0.19746579229831696	Predicted	I2D-INNATEDB-Mouse2Human
AKT1	BAD	0.17264260351657867	Predicted	I2D-BIND-Mouse2Human
RB1	ID2	0.156843900680542	Predicted	I2D-BIND-Mouse2Human
MAPK14	MAPK9	0.13639622926712036	Predicted	I2D-IntAct-Mouse2Human
CREBBP	LYN	0.12914153933525085	Predicted	I2D-INNATEDB-Mouse2Human
NFKB1	AKT1	0.12252085655927658	Predicted	I2D-MINT-Rat2Human
SMAD3	SOCS3	0.11608617007732391	Predicted	I2D-INNATEDB-Mouse2Human
RB1	RUNX2	0.08309318125247955	Predicted	I2D-BIND-Mouse2Human
LYN	SYK	0.07589130848646164	Predicted	I2D-INNATEDB-Mouse2Human
STAT5A	JAK2	0.052403487265110016	Predicted	I2D-INNATEDB-Mouse2Human
SYK	CSF1	0.04722074419260025	Predicted	I2D-IntAct-Mouse2Human
JAK2	CSF1	0.03984596207737923	Predicted	I2D-IntAct-Mouse2Human
HSP90AB1	MAPK14	0.038143593817949295	Predicted	I2D-BIND-Yeast2Human
NFKB1	BCL2	0.031253453344106674	Predicted	I2D-INNATEDB-Mouse2Human
JAK2	SOCS3	0.028265556320548058	Predicted	I2D-INNATEDB-Mouse2Human
OSM	LIF	2.0	Shared protein domains	INTERPRO PFAM
CLUL1	CLU	2.0	Shared protein domains	INTERPRO PFAM
RUNX1	RUNX2	1.0	Shared protein domains	INTERPRO PFAM
RUNX3	RUNX2	1.0	Shared protein domains	INTERPRO PFAM
RUNX3	RUNX1	1.0	Shared protein domains	INTERPRO PFAM
XRCC6	XRCC5	0.8412725478410721	Shared protein domains	INTERPRO PFAM
NTF3	BDNF	0.6666669547557831	Shared protein domains	INTERPRO PFAM
NTF4	BDNF	0.6666669547557831	Shared protein domains	INTERPRO PFAM
NTF4	NTF3	0.6666669547557831	Shared protein domains	INTERPRO PFAM
BDNF	NGF	0.6666663885116577	Shared protein domains	INTERPRO PFAM
NTF3	NGF	0.6666663885116577	Shared protein domains	INTERPRO PFAM
NTF4	NGF	0.6666663885116577	Shared protein domains	INTERPRO PFAM
POLR1C	POLR1D	0.3599122613668442	Shared protein domains	INTERPRO PFAM
GATA4	GATA6	0.3098515421152115	Shared protein domains	INTERPRO PFAM
SMAD7	SMAD4	0.29401640594005585	Shared protein domains	INTERPRO PFAM
SMAD6	SMAD4	0.29401640594005585	Shared protein domains	INTERPRO PFAM
SMAD6	SMAD7	0.29401640594005585	Shared protein domains	INTERPRO PFAM
HSP90AB1	HSP90AA1	0.27668698877096176	Shared protein domains	INTERPRO PFAM
INS	IGF2	0.2329198494553566	Shared protein domains	INTERPRO PFAM
SMAD4	SMAD3	0.21181202679872513	Shared protein domains	INTERPRO PFAM
SMAD4	SMAD2	0.21181202679872513	Shared protein domains	INTERPRO PFAM

Gene 1	Gene 2	Weight	Network group	Networks
SMAD4	SMAD1	0.21181202679872513	Shared protein domains	INTERPRO PFAM
SMAD7	SMAD3	0.21181202679872513	Shared protein domains	INTERPRO PFAM
SMAD7	SMAD2	0.21181202679872513	Shared protein domains	INTERPRO PFAM
SMAD7	SMAD1	0.21181202679872513	Shared protein domains	INTERPRO PFAM
SMAD6	SMAD3	0.21181202679872513	Shared protein domains	INTERPRO PFAM
SMAD6	SMAD2	0.21181202679872513	Shared protein domains	INTERPRO PFAM
SMAD6	SMAD1	0.21181202679872513	Shared protein domains	INTERPRO PFAM
SMAD2	SMAD3	0.21137941628694534	Shared protein domains	INTERPRO PFAM
SMAD1	SMAD3	0.21137941628694534	Shared protein domains	INTERPRO PFAM
SMAD1	SMAD2	0.21137941628694534	Shared protein domains	INTERPRO PFAM
STAT5A	STAT5B	0.15050295740365982	Shared protein domains	INTERPRO PFAM
TGFB3	TGFB2	0.1391255185008049	Shared protein domains	INTERPRO PFAM
XRCC6	ACIN1	0.10193119198083878	Shared protein domains	INTERPRO PFAM
TGFB1	TGFB2	0.08552314341068268	Shared protein domains	INTERPRO PFAM
TGFB1	TGFB3	0.08552314341068268	Shared protein domains	INTERPRO PFAM
TGIF1	TGIF2	0.0833843257278204	Shared protein domains	INTERPRO PFAM
BMP2	BMP7	0.06807868182659149	Shared protein domains	INTERPRO PFAM
TGFB1	BMP4	0.06138192117214203	Shared protein domains	INTERPRO PFAM
SOCS3	SOCS2	0.0612266156822443	Shared protein domains	INTERPRO PFAM
BMP4	TGFB2	0.06002816930413246	Shared protein domains	INTERPRO PFAM
BMP4	TGFB3	0.06002816930413246	Shared protein domains	INTERPRO PFAM
BMP4	BMP7	0.057676929980516434	Shared protein domains	INTERPRO PFAM
BMP2	BMP4	0.057676929980516434	Shared protein domains	INTERPRO PFAM
TGFB1	BMP7	0.056532058864831924	Shared protein domains	INTERPRO PFAM
BMP2	TGFB1	0.056532058864831924	Shared protein domains	INTERPRO PFAM
BMP7	TGFB2	0.05539081618189812	Shared protein domains	INTERPRO PFAM
BMP7	TGFB3	0.05539081618189812	Shared protein domains	INTERPRO PFAM
BMP2	TGFB2	0.05539081618189812	Shared protein domains	INTERPRO PFAM
BMP2	TGFB3	0.05539081618189812	Shared protein domains	INTERPRO PFAM
JAG1	DLL3	0.05461818724870682	Shared protein domains	INTERPRO PFAM
LYN	LCK	0.053967636078596115	Shared protein domains	INTERPRO PFAM
KIT	NTRK3	0.04856158047914505	Shared protein domains	INTERPRO PFAM

Gene 1	Gene 2	Weight	Network group	Networks
SYK	ZAP70	0.047666437923908234	Shared protein domains	INTERPRO PFAM
BMPR1B	ACVR1	0.047233978286385536	Shared protein domains	INTERPRO PFAM
ACVRL1	BMPR1B	0.047233978286385536	Shared protein domains	INTERPRO PFAM
ACVRL1	ACVR1	0.047232743352651596	Shared protein domains	INTERPRO PFAM
RARA	THRB	0.045653752982616425	Shared protein domains	INTERPRO PFAM
HIF1A	ARNT	0.04344249330461025	Shared protein domains	INTERPRO PFAM
FOXO3	FOXG1	0.04327800124883652	Shared protein domains	INTERPRO PFAM
FOXH1	FOXG1	0.04323924705386162	Shared protein domains	INTERPRO PFAM
FOXH1	FOXO3	0.04323924705386162	Shared protein domains	INTERPRO PFAM
JAK2	SYK	0.04305198509246111	Shared protein domains	INTERPRO PFAM
JAK2	ZAP70	0.0430510425940156	Shared protein domains	INTERPRO PFAM
BMPR1A	ACVR1B	0.04246009141206741	Shared protein domains	INTERPRO PFAM
BMPR1A	BMPR1B	0.041699085384607315	Shared protein domains	INTERPRO PFAM
BMPR1A	ACVR1	0.04169791378080845	Shared protein domains	INTERPRO PFAM
BMPR1A	ACVRL1	0.04169791378080845	Shared protein domains	INTERPRO PFAM
PPARG	THRB	0.04169074073433876	Shared protein domains	INTERPRO PFAM
BMPR1B	ACVR1B	0.041567808017134666	Shared protein domains	INTERPRO PFAM
ACVR1	ACVR1B	0.0415666364133358	Shared protein domains	INTERPRO PFAM
ACVRL1	ACVR1B	0.0415666364133358	Shared protein domains	INTERPRO PFAM
RARA	PPARG	0.03881804086267948	Shared protein domains	INTERPRO PFAM
LCK	JAK2	0.0383489653468132	Shared protein domains	INTERPRO PFAM
LYN	JAK2	0.0383489653468132	Shared protein domains	INTERPRO PFAM
FOXA2	FOXG1	0.038302335888147354	Shared protein domains	INTERPRO PFAM
FOXO3	FOXA2	0.038302335888147354	Shared protein domains	INTERPRO PFAM
FOXH1	FOXA2	0.038268039003014565	Shared protein domains	INTERPRO PFAM
LCK	SYK	0.03374485671520233	Shared protein domains	INTERPRO PFAM
LYN	SYK	0.03374485671520233	Shared protein domains	INTERPRO PFAM
LCK	ZAP70	0.03374376520514488	Shared protein domains	INTERPRO PFAM
LYN	ZAP70	0.03374376520514488	Shared protein domains	INTERPRO PFAM
ACVR2A	BMPR1B	0.03305115643888712	Shared protein domains	INTERPRO PFAM
ACVR2A	ACVR1	0.03305035550147295	Shared protein domains	INTERPRO PFAM
ACVRL1	ACVR2A	0.03305035550147295	Shared protein domains	INTERPRO PFAM

Gene 1	Gene 2	Weight	Network group	Networks
NOTCH1	DLL3	0.03251044638454914	Shared protein domains	INTERPRO PFAM
NOTCH1	JAG1	0.03190816380083561	Shared protein domains	INTERPRO PFAM
NPTN	NRG1	0.02769915573298931	Shared protein domains	INTERPRO PFAM
BMPR1A	ACVR2A	0.02696016989648342	Shared protein domains	INTERPRO PFAM
ACVR2A	ACVR1B	0.026869794353842735	Shared protein domains	INTERPRO PFAM
NFKB1	NGFR	0.023593857884407043	Shared protein domains	INTERPRO PFAM
NEUROD1	TAL1	0.022450877353549004	Shared protein domains	INTERPRO PFAM
STAT5B	SOCS3	0.021747739054262638	Shared protein domains	INTERPRO PFAM
STAT5A	SOCS3	0.02174764685332775	Shared protein domains	INTERPRO PFAM
STAT5B	SOCS2	0.021746926940977573	Shared protein domains	INTERPRO PFAM
STAT5A	SOCS2	0.021746834740042686	Shared protein domains	INTERPRO PFAM
ID2	NEUROD1	0.021506750024855137	Shared protein domains	INTERPRO PFAM
ARNT	ID2	0.020095229614526033	Shared protein domains	INTERPRO PFAM
INPP5D	STAT5B	0.02000562846660614	Shared protein domains	INTERPRO PFAM
STAT5A	INPP5D	0.020005540922284126	Shared protein domains	INTERPRO PFAM
HLX	DLX5	0.019978195428848267	Shared protein domains	INTERPRO PFAM
NKX2-5	HOXA11	0.01991607854142785	Shared protein domains	INTERPRO PFAM
ID2	TAL1	0.018555731512606144	Shared protein domains	INTERPRO PFAM
ACVR2A	TGFBR2	0.015906967222690582	Shared protein domains	INTERPRO
NKX2-5	DLX5	0.015572668053209782	Shared protein domains	INTERPRO PFAM
TGIF1	HOPX	0.015394419897347689	Shared protein domains	INTERPRO PFAM
TGIF2	HOPX	0.015329858288168907	Shared protein domains	INTERPRO PFAM
TGFBR2	BMPR1B	0.01522082556039095	Shared protein domains	INTERPRO
TGFBR2	ACVR1	0.015220657922327518	Shared protein domains	INTERPRO
ACVRL1	TGFBR2	0.015220657922327518	Shared protein domains	INTERPRO
PAX6	HOPX	0.01484523992985487	Shared protein domains	INTERPRO PFAM
RB1	CCNE1	0.014798241667449474	Shared protein domains	INTERPRO
HLX	POU4F2	0.014086015522480011	Shared protein domains	PFAM
HLX	NKX2-5	0.013914674753323197	Shared protein domains	INTERPRO PFAM
INPP5D	ZAP70	0.013626051135361195	Shared protein domains	PFAM
SYK	INPP5D	0.013626051135361195	Shared protein domains	PFAM
JAK2	INPP5D	0.013626051135361195	Shared protein domains	PFAM
MAPK14	MAPK9	0.013552912510931492	Shared protein domains	INTERPRO PFAM
JAG1	VWC2	0.013239278458058834	Shared protein domains	INTERPRO
POU4F2	HOPX	0.012741212267428637	Shared protein domains	INTERPRO PFAM
PAX6	NKX2-5	0.012291313149034977	Shared protein domains	PFAM
ZAP70	STAT5B	0.012047665193676949	Shared protein domains	PFAM

Gene 1	Gene 2	Weight	Network group	Networks
SYK	STAT5B	0.012047665193676949	Shared protein domains	PFAM
JAK2	STAT5B	0.012047665193676949	Shared protein domains	PFAM
STAT5A	ZAP70	0.01204756461083889	Shared protein domains	PFAM
STAT5A	SYK	0.01204756461083889	Shared protein domains	PFAM
STAT5A	JAK2	0.01204756461083889	Shared protein domains	PFAM
ARNT	TAL1	0.011233795434236526	Shared protein domains	INTERPRO PFAM
KLF10	GFI1	0.008782967692241073	Shared protein domains	INTERPRO PFAM
DLX5	HOPX	0.0059745474718511105	Shared protein domains	PFAM
HOXA11	HOPX	0.005757870152592659	Shared protein domains	PFAM
HIF1A	TAL1	0.005058014765381813	Shared protein domains	INTERPRO
HIF1A	ID2	0.00490269111469388	Shared protein domains	INTERPRO
HLX	HOXA11	0.004865808878093958	Shared protein domains	PFAM
TGIF1	HLX	0.004341624211519957	Shared protein domains	PFAM
NFKB1	ANKRD54	0.004339497536420822	Shared protein domains	PFAM
HLX	TGIF2	0.004287065006792545	Shared protein domains	PFAM
TGIF1	NKX2-5	0.0041547855362296104	Shared protein domains	PFAM
NKX2-5	TGIF2	0.004102574195712805	Shared protein domains	PFAM
PAX6	HLX	0.00404316745698452	Shared protein domains	PFAM
NKX2-5	POU4F2	0.0038421167992055416	Shared protein domains	PFAM
HLX	HOPX	0.003645345102995634	Shared protein domains	PFAM
GLI2	GFI1	0.0035777029115706682	Shared protein domains	INTERPRO
GLI2	KLF10	0.0035777029115706682	Shared protein domains	INTERPRO
GLI3	GFI1	0.0035777029115706682	Shared protein domains	INTERPRO
GLI3	KLF10	0.0035777029115706682	Shared protein domains	INTERPRO
GLI3	GLI2	0.0035777029115706682	Shared protein domains	INTERPRO
NKX2-5	HOPX	0.003488470334559679	Shared protein domains	PFAM

Search results generated by the GeneMANIA algorithm (genemania.org)