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Where are the sequences that control multicellular development in filamentous fungi?

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Abstract

We describe a wide-ranging data-mining exercise to search for homologies to gene sequences assigned to the category 'development' in the Gene Ontology Consortium AmiGo database (<http://www.geneontology.org/GO.database.shtml>) across all three of the crown group of eukaryote kingdoms. Internet web-agents were used to automate the similarity searches for 552 such developmental sequences in 1069 genomes. It emerged that only 78 of the sequences are shared between all three Kingdoms, 72 are shared only between fungi and animals, 58 sequences are shared between plants and fungi, and 4 sequences were common only to *Dictyostelium* and fungi. No sequences were strictly fungus specific, but 68 occurred only in plants (Viridiplantae) and 239 occurred only in animals (Metazoa). Although some homology was indicated for a total of 219 fungal sequences, 143 (65%) of the matches returned were assigned *E*-values of 0.05 and were not considered significant. These findings show that there are no resemblances between the crown group of eukaryotic Kingdoms in the ways they control and regulate their developmental processes. Current understanding of phylogenetic relationships is that the major kingdoms of eukaryotes separated from one another at a stage prior to the multicellular grade of organization. Consequently, in the course of their evolutionary history these very different organisms may have found different strategies to solve the same sorts of morphogenetic control problems. Finally, this means, in particular, that we are currently totally ignorant of the way fungi regulate their multicellular development.

Key words: automated, sequence analysis, homology, web-agents, eukaryotes

Introduction

Filamentous fungi inhabit every environment and habitat on planet Earth. Their success is achieved because of the apical growth of filamentous hyphae, which enables them to populate the available substratum and make efficient use of nutrient resources. Investigation of the habitat and capture of resources depends on sub-apical branching and, especially, negative autotropism which together are crucial to proliferation of the growing mycelium and, above all, to its spread through the habitat. Consequently, *the* characteristic feature of the fungal mycelium is the aggressive exploration and control of new substrate (Pringle and Taylor, 2002; Trinci *et al.*, 1994).

But this is not all that mycelia accomplish, because fungal mycelia of Ascomycota and Basidiomycota produce a range of structures that distribute spores or other propagules,

including ascomata and basidiomata – the structures that release sexual spores (meiospores) in Ascomycota and Basidiomycota respectively, as well as a range of structures that produce asexual spores (mitospores) and some somatic (vegetative) structures, such as stromata and sclerotia, that can survive adverse conditions. Obviously, the phrase ‘fruit body’, which is usually used, encompasses a very wide range of organs but their common feature is that they are multicellular, they are constructed of organised tissues that have specific functions, and their shape and form emerge as a result of a sequence of developmental adjustments. That is, they exhibit a characteristic pattern of cell and tissue morphogenesis (Moore, 1998).

As we will illustrate later, there is suggestive evidence that fungal cells within the developing tissues of a fruit body embark on their particular course of differentiation in response to the interaction of their inherent genetic programme with external physical signals (light, temperature, gravity, humidity, physical contact), and/or chemical signals from other regions of the developing structure. These chemicals may be termed organisers, inducers or morphogens, and may inhibit or stimulate entry to particular states of determination. There is also evidence for morphogenetic fields around fungal structures (cell or organ), which permits continued development of that structure but inhibits formation of another structure of the same type within the field. All of these phenomena contribute to the pattern formation that characterises the ‘body plan’ created by the particular distribution of differentiated tissues in the multicellular structure. Pattern formation depends on positional information, which prompts or allows the cell to differentiate in a way appropriate to its position in the structure and may be conveyed by concentration gradients of one or more morphogens emitted from one or more spatially distinct organisers. Pattern formation thus involves a process that provides positional information, and a second process, in which the receiving cell or tissue responds to that information.

The cells that make up a mature fungal fruit body are generally found to be totipotent (that is, able to dedifferentiate and subsequently follow any pathway of differentiation), because a mycelial culture can be produced *in vitro* from a fragment of a mature, fully differentiated structure, e.g. a mushroom stem or the inner tissues of a mushroom cap. This feature results in a morphogenetic plasticity which surpasses that of other organisms and provides an intellectual challenge in terms of developmental biology, taxonomy and genetics (Watling and Moore, 1994). The only exceptions to totipotency are the meiocytes (the cells within which meiosis occurs), which are committed to sporulation, but only when they have progressed beyond meiotic prophase (Chiu, 1996; Chiu and Moore, 1988a, b, 1990, 1993). On the other hand, even meiocytes can serve non-sporulation functions: the hymenium of *Agaricus bisporus* is packed with basidia held in an arrested meiosis and serving a purely structural function (Allen *et al.*, 1992).

It is tempting to draw parallels with morphogenesis in animals and the vocabulary established to describe morphogenetic events in animals can be used without making presumptions about the mechanisms which may be involved (Moore, 1998, 2005). For example, during the progress of the developmental process the intermediate stages represent successive reduction in developmental potential in comparison with the previous stage. Each such adjustment (or, effectively, each developmental ‘decision’) is made by cells already specified by earlier adjustments that drew them into a particular branch of the developmental pathway. Consequently, developmental decisions are made from progressively smaller numbers of alternatives until the particular structure to which the cell will contribute is finally determined. It is those decisions and that sequence of developmental adjustments that, in animals and plants, are controlled by genetic regulators of the sort that we seek in fungi.

The mating type factors are the only major morphogenetic control elements that are presently known in fungi. Mating type factors are complex genetic elements (most of which specify transcription factors) that regulate pheromone production and pheromone receptors involved in mating, ranging from recognition between sexually competent cells in yeast to regulating growth of clamp connections, internuclear recognition, and the distance between

the two nuclei in Basidiomycota (Casselton, 2002). They reach their highest expression in the basidiomycetes, where compatibility of the mating type factors permits the development of complex fruit bodies containing several different interacting tissues. However, not all fungi possess mating type factors, and, indeed, even in species that have a well-developed mating type system, haploid (that is, unmated) cultures can form apparently normal fruit bodies and fruit body formation can usually be separated from other parts of the sexual pathway by mutation (see chapter 5 in Moore, 1998). The occurrence of fruiting bodies outside the influence of mating type factors makes the real influence of the latter on events beyond the initial mating reaction difficult to judge.

Even though knowledge of major developmental gene sequences in fungi is lacking, we can at least make a comparative analysis to determine whether developmental sequences important in plants and animals can be found in fungi. There is now a sufficient number of filamentous fungal genomes, covering a representative range of fungal diversity, in the public sequence databases to make direct sequence comparisons with animal and plant genomes meaningful. A recent search of a few selected filamentous fungal genomes with a small selection of gene sequences generally considered as being essential and highly conserved components of normal animal and/or plant development failed to reveal any homologies (Moore *et al.*, 2005). This was taken to suggest that fungal and animal lineages may have diverged from their common opisthokont line (Cavalier-Smith and Chao, 1995) at the unicellular level. The unique cell biology of filamentous fungi could be presumed to cause control of multicellular development as it arose in fungi to evolve in a completely different way from that emerging concurrently in animals and plants. This line of argument was based on the current phylogenetic understanding that the major kingdoms of eukaryotes separated from one another at a very early stage in their evolution. If this is the case, these very different organisms may have needed to solve the same sorts of morphogenetic control problems in the course of their evolutionary history and may have found some common strategies, but there is no logical reason to expect that the Kingdoms will share features that contribute to multicellular developmental biology unless arrived at by convergent evolution. The fungal hypha differs from animal and plant cells in many important respects and significant differences in the way cells interact in the construction of organised tissues must be expected (Moore, 2005).

Broad conclusions like this need comprehensive comparisons and in the study described here we expanded our sequence comparisons to include all sequences assigned to the biological process ‘development’ in the Gene Ontology Consortium’s AmiGO database (<http://amigo.geneontology.org/cgi-bin/amigo/go.cgi>) (Harris *et al.*, 2004). In this database the term ‘development’ is currently defined as the biological process “whose specific outcome is the progression of the [*specific process*] over time, from its formation to the mature structure.” It is a node in the ontology and incorporates terms like morphogenesis, formation, differentiation, specification, metamorphosis, maturation, etc. Using this source of sequences allowed us to collect any and all sequences which the authors of the database entry had assigned or identified with any developmental process.

All of these ‘developmental sequences’ were then used in similarity searches against all genomes of cellular organisms included as Metazoa, Fungi or Viridiplantae in the NCBI Taxonomy database (<http://www.ncbi.nlm.nih.gov/Taxonomy/taxonomyhome.html/>). This represents an estimated total of 590,000 similarity searches. Even at 100 manual searches a day that works out to 16 years, doing 1 search every 15 minutes, 24/7, so to make such a job possible we used web agents (also known as web-robots), which are reusable programming modules that interact with the Internet seeking user-defined goals, for example ‘get the sequence data’, ‘get the taxonomy information’ or ‘get the similarity search results’, etc. We created the agents, as described below, using an application called *Sight*, which is a Java-based package that provides a user-friendly interface to generate and connect web agents for

automatic genomic data mining (visit <http://bioinformatics.org/jSight/>) (Meškauskas *et al.*, 2004).

Automated genomic data mining

To create the web agents employed in this report we used an application called *Sight*, which is a package of Java™-based programs that offers a user-friendly interface for the assembly and interconnection of agents for automatic genomic data mining (Meškauskas *et al.*, 2004).

Sight web agents are effectively scripts of active flow charts in which each element is a preprogrammed working routine. *Sight* enables the user to assemble a flow chart tailored to the task to be performed. The application was originally developed for automated analysis of the human genome but has been modified to include loops, convergences and other features that suit it to servers carrying fungal databases (version 3.2.0 beta available for free download from <http://bioinformatics.org/jSight/>).

The web agent comprises two data structures: one defines the query submitted to the selected database and the other processes the response(s) received from the database. The user provides all the necessary input information, but the program writes the code. The *Sight* application interface provides a web form appropriate to the chosen database comprising the fields, checkboxes and other controls needed by the user for entry of the initial data that generates the agent. The application itself converts these data into string values for the various named items (data fields) that represent the automated query. Single queries often generate multiple responses because, for example, several homologies may be found to the query sequence, or there may be multiple genes in a sequence, or multiple motifs in a sequence, etc.

Consequently, the *Sight* agent response data structure needs to be programmed as an array of records of multiple named fields. Because the query and response formats differ for each agent, the agents also contain explanations of the formats, defining the type, name and identifying comment for each query or response field. Default values for query fields may also be included.

The initial query in this analysis was to the Gene Ontology Consortium's AmiGO database to extract information on gene sequences involved in development (database ID GO:0032502), which belongs to the larger group 'biological process' (database ID GO:0007275). The query was sent to the AmiGo server and the responses received were stored locally as an HTML document.

Search hits from the AmiGo server contained two hyperlink references, one to the entry within the GO database itself, the other to the external server from which the original data was derived; 552 paired references were returned when the survey was first completed in January 2005 (there were 603 in July 2007). Where the GO database page contained the protein sequence, the sequence was taken from there; otherwise, the domain of the link to the original data source was checked and one of the specialized sequence retrievers was called. Sequence retrievers were written for <http://www.uniprot.org/> (Apweiler *et al.* 2004); www.tigr.org (Venter *et al.* 1992); www.arabidopsis.org (Huala *et al.* 2001); www.flybase.org (Ashburner and Drysdale, 1994); www.informatics.jax.org (MGI) (Blake *et al.*, 2003); dictybase.org (Kreppel *et al.*, 2004). DNA similarity search web agents were written for genome.jgi-psf.org/whiterot1/whiterot1.home.html (sequence data produced by the US Department of Energy Joint Genome Institute at <http://www.jgi.doe.gov/>); and protein, DNA and RNA similarity search web agents were written for tigrblast.tigr.org (Venter *et al.* 1992) and www.ncbi.nlm.nih.gov/BLAST (Wheeler *et al.*, 2005); and a taxonomy search web agent for www.ncbi.nlm.nih.gov/Taxonomy (Wheeler *et al.*, 2005). The number of links to Gramene, the database for genomes of rice, maize and other grasses (Wheeler *et al.*, 2003), the Rat Genome Database (Twigger *et al.*, 2002) and the Zebrafish Information Network, ZFIN, were too few to justify writing a tailored web agent, so these sequences were retrieved manually.

Similarity searches (Altschul *et al.*, 1990) were performed in both protein (using BLASTP) and nucleic acid (using TBLAST) sequence databases. Low complexity filters, which remove short, very widespread sequence fragments, were turned on. All other search options were left with the default values proposed by the research groups that administer the search servers. Only hits with *E*-values less than or equal to 0.05 were accepted (the significance of the *E*-value is discussed briefly below; for further information we recommend the page dealing with the statistics of sequence similarity scores at this URL: <http://www.ncbi.nlm.nih.gov/BLAST/tutorial/Altschul-1.html>).

Each and every ‘developmental’ sequence retrieved from the AmiGo server was then used in similarity searches against all genomes of cellular organisms included as Metazoa (875 genome sequences), Fungi (141 genome sequences) or Viridiplantae (53 genome sequences) in the NCBI Taxonomy database (www.ncbi.nlm.nih.gov/Taxonomy). The initial query to the Gene Ontology database retrieved a total of 552 sequences so this represents an estimated total of 590,000 similarity searches.

Some dedicated databases contain sequence data either from a single species or from several related species, so the taxonomic position was immediately evident. The taxonomic position of the organism corresponding to a sequence retrieved from a more general database was identified in several ways. Some sequences contained the Latin binomial of the organism in the sequence header; in this case the web agent submitted the organism name to the NCBI taxonomy search service referred to above, and automatically extracted the taxonomy of the organism from the web page received in response. For the NCBI nucleic acid database, the search was performed by explicitly limiting the scope of the web agent’s search to a specified Kingdom.

For processing the search data we used the *E*-value to identify the most similar sequence found in any organism from each of the Metazoa, Viridiplantae and Fungi groups for each sequence entry retrieved from the AmiGO database. These contributed to an overall comparison table for all 552 searches (in HTML format) that preserved all appropriate hyperlinks. Useful descriptive annotations for each sequence were subsequently retrieved manually from the databases using those hyperlinks. Live hyperlinks are preserved in the tables in this document (but these hyperlinks are ephemeral and subject to change).

Advantages of web agents over manual searching

We have suggested above that the number of similarity searches completed during this survey would take about 16 years to complete manually, assuming it would be possible to complete 4 searches every hour of every day of the week. Apart from speeding this process sufficiently to make the operation feasible, the web agents we used have other advantages.

The *Sight* application program permits inclusion of routines into the agent algorithm effectively to ‘anticipate’ a variety of interactions with the search server. For example, the ability to follow multiple links, conditional behaviour and loops which, for example, enable the agent to make a positive ordered response to a transient server error, or to react to server delays (for example, NCBI BLAST can tell the user to wait for a given duration a number of times before returning the results). So when constructed by an experienced bioinformatician web agents can be at least as effective as a human investigator.

As we used several independent database services (and different web servers, therefore), requests could be submitted in parallel, for which the agents ran in separate execution threads and task queues. This effectively created a kind of distributed computing, although arranging the work of ordinary web servers in parallel like this significantly differs from distributed computing as normally understood. In particular, the concept of load balancing is not applicable because each web server is specialised to its own group of tasks. Also, users have no ability to adapt software on the server(s) to suit distributed computing. Nevertheless, the possibility of reliably mimicking parallel computing gives the web agents a significant advantage over manual management of this sort of work. While it is certainly

possible for an individual worker to submit tasks in parallel from several running instances of their ordinary web browser, frequent switching of concentration between the parallel searches demands extreme skill and minor loss of attention can generate multiple errors. Web agents are greatly superior to their human equivalents in this.

As we have implied in the descriptions given above, web agents can use each other in organised workflows. For example, a sequence retrieval web agent can pass the sequence it recovers from one server to a similarity search web agent for submission to another server, and take part of the header of each similarity returned hit for submission to a third server to identify the taxonomy of the organism. Manual working of this process requires multiple copy/paste operations and switching between several browser windows. The time required for these clerical operations is comparable with the waiting time for server response, but during hours and days of such work a human operator is likely to make mistakes. Humans can use their knowledge to speed such analysis, of course. For example the Latin binomials of frequently-used organisms, such as *Homo sapiens*, *Drosophila melanogaster*, *Arabidopsis thaliana* and many other popular research organisms, were retrieved frequently in many thousands of sequence headers. A human operator recognising these repetitive features can avoid the time penalty of approximately ten seconds that it takes to execute a query to the NCBI taxonomy search server. However, this can also be mimicked in the web agents by adding retrieved names and taxonomy to a locally-stored cache. The agent can then be written to search the cache of previously-retrieved names, a matter of milliseconds only, before issuing a query for any newly-encountered name.

Researcher time is needed for creating each web agent and building the workflow system, though this is significantly reduced by using specialised development platforms like *Sight* (Meškauskas *et al.*, 2004), as used in this project. An overwhelming advantage, of course, is that while running, the agent system needs no researcher attention and web agents can run around the clock; using the night hours when servers are less loaded and respond more quickly. We believe the analysis reported here demonstrates that the web agents generated using tools like *Sight* can be extremely useful for an extensive range of highly repetitive tasks.

Comparison of the occurrence of developmental gene sequences in the genomes of eukaryotes.

The overall summary of the results of this survey (Table 1) shows that of the 552 developmental sequences retrieved by the initial query to the AmiGO database only 78 are shared between all three Kingdoms, 72 are shared only between fungi and animals, 58 sequences are shared between plants and fungi, and 4 sequences were common only to *Dictyostelium* and fungi. No sequences were strictly fungus specific, but 68 occurred only in Viridiplantae and 239 occurred only in Metazoa.

In many respects these latter two results constitute ‘control’ searches by representing positive hits within the Kingdom from which the original reference sequence was obtained. It is significant, therefore, that all of these similarities have *E*-values markedly less than our arbitrary cut-off value of 0.05. Broadly speaking, the lower the *E*-value, the better the match; an *E*-value of zero indicates identity of the compared sequences. *E*-values indicate the likelihood of the observed similarity between the sequences being found by chance. *E*-values less than 0.01 are numerically very similar to probability statements. *E*-values of 0.05 mean that there is *more* than one chance in twenty of the similarity being found by chance – ***and we do not assign any significance to these*** (because, even if not due entirely to chance, they most likely indicate possession of similar functional motifs – like shared DNA binding sites, membrane spanning regions, etc.). Consequently, ***very*** low *E*-values observed for hits within the Kingdom from which the original reference sequence was obtained validate the process by showing that the reference sequences can be shown to retrieve highly similar sequences from within their own Kingdom. Unfortunately, there are no fungal sequences that are categorised

as being involved in developmental processes. This is not a fault in the AmiGO database; rather the deficiency accurately reflects the paucity of research interest in the multicellular developmental biology of Kingdom Fungi.

Table 1. Overall summary of similarities returned

Kingdom	Hits	Remarks*
Animal only	239	all <i>E</i> -values well below 0.05
Plant only	68	all <i>E</i> -values well below 0.05
Common to fungi and <i>Dictyostelium</i>	4	of which three had <i>E</i> -values of 0.05, and the fourth an <i>E</i> -value of 0.03.
Common to animal and plant	33	13 had <i>E</i> -values of 0.05
Common to fungi and animal	72	64 had <i>E</i> -values of 0.05
Common to fungi and plant	58	55 had <i>E</i> -values of 0.05
Common to all three kingdoms	78	14 plant homologies had <i>E</i> -values of 0.05 20 fungal homologies had <i>E</i> -values of 0.05
Total	552	219 showed some homology with fungal sequences, though 143 of these had <i>E</i> -values of 0.05

*Broadly speaking, the lower the *E*-value, the better the match; an *E*-value of zero indicates identity of the compared sequences. *E*-values indicate the likelihood of the observed similarity between the sequences being found by chance. *E*-values less than 0.01 are numerically very similar to probability statements. *E*-values of 0.05 mean that there is *more* than one chance in twenty of the similarity being found by chance – ***and we do not assign any significance to these*** (because, even if not due entirely to chance, they most likely indicate possession of similar functional motifs – like shared DNA binding sites, metal ion binding domains, membrane spanning regions, etc.).

Cross-kingdom comparisons are interesting, although for Kingdom Fungi they are mostly negative. Searches with 44 ‘no apical meristem’ (NAM) family proteins failed to detect any similarities with animals or fungi (Table 2); a further 42 NAM family protein sequences showed weak (not significant) similarities (*E*-value = 0.05) with fungal genomes, but still with no similarity in Metazoa (Table 3). NAM sequences have a role in determining positions of meristems and are required for pattern formation in embryos and flowers, so there is no great surprise that the developmental functions represented by the family of NAM

proteins are restricted to plants. The one exception we discovered in this protein family is NAM locus AT4G28500 (a predicted protein of *Arabidopsis thaliana* with transcription factor activity) for which the search revealed homology (E -value = 5×10^{-5}) with clone RP11-26F2 of the *Homo sapiens* chromosome 15, and only an insignificant similarity (E -value = 0.05) with the fungal *Phanerochaete* genome (which was not annotated when the survey was carried out) (Table 4).

Table 2. Plant-only similarities found

Entries under 'genome hit' show E -value as returned by the sequence comparison software: a reference to the specific database entry and brief descriptive annotation. **NOTE** that small E -values are shown as exponential functions, i.e. $1.217E-29 = 1.217 \times 10^{-29}$

AmiGO description and hyperlinks USE Link2	Metazoan genome hit	Viridiplantae genome hit	Fungi genome hit
Link1 Link2 >49199.m00050: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	1.217E-29, 4337200 NAM (no apical meristem)-like protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >49203.m00039: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.53372E-27, 5306267 NAM (no apical meristem)-like protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >49299.m00025: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	3.53623E-29, 4544462 NAM (no apical meristem)-like protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >51050.m00108: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.07588E-29, 15217678 no apical meristem (NAM) family protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >51050.m00231: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	8.42797E-31, 15217677 <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned
Link1 Link2 >51050.m00232: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.07588E-29, 15217699 no apical meristem (NAM) family protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >51104.m00153: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	1.09927E-30, 20857250 product At2g17040/At2g17040 [<i>Arabidopsis thaliana</i>].	no hits returned

Link1 Link2 >51241.m00131: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	5.45452E-30, 34222060 product At1g54330 [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >51442.m00188: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	7.87791E-29, 5091626 Similar to gb X92204 NAM gene product from <i>Petunia hybrida</i> [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >51476.m00248: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	8.71005E-28, 6692113 product F22C12.13 [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >51641.m00076: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	1.58702E-29, 6227016 Contains similarity to gb AF123310 NAC domain protein NAM gene from <i>Arabidopsis thaliana</i> .	no hits returned
Link1 Link2 >51784.m00174: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.71119E-29, 16612277 protein product At1g01010/T25K16_1 [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >51864.m00069: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	1.3435E-28, 7715611 protein product F20B17.1 [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >60023.m00237: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.44843E-30, 4325286 NAC domain protein NAM [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >60208.m00069: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.07314E-29, 6016718 hypothetical protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >60250.m00126: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.99757E-28, 6223650 NAM-like protein (no apical meristem) [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >60460.m00049: <i>Arabidopsis</i> no apical meristem (NAM) family protein (NAC2).	no hits returned	5.45563E-30, 7021736 putative jasmonic acid regulatory protein [<i>Arabidopsis thaliana</i>].	no hits returned

Link1 Link2 >60460.m00230: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	3.53623E-29, 7021735 putative jasmonic acid regulatory protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >6548.m00385: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	7.87791E-29, 2459430 putative NAM (no apical meristem)-like protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67041.m00008: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.29166E-28, 7268195 putative NAM-like protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67041.m00010: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	6.6677E-28, 7268197 putative NAM-like protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67099.m00015: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	1.21539E-29, 22136592 putative NAM/NAP [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67170.m00140: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	9.30401E-30, 30984582 protein product At4g28530 [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67175.m00005: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.44843E-30, 7269821 putative protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67241.m00008: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	1.02889E-28, 7649380 putative protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67267.m00207: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	4.18276E-30, 24030450 putative NAC2 protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67299.m00017: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	1.43759E-30, 7594530 putative protein [<i>Arabidopsis thaliana</i>].	no hits returned

Link1 Link2 >67299.m00021: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	7.38326E-27, 7594534 putative protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67622.m00135: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.9936E-28, 30023658 protein product At5g14000 [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67644.m00021: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	6.66905E-28, 29824189 putative NAM (no apical meristem) protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67644.m00144: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	3.19839E-30, 9758912 unnamed protein product [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67651.m00128: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.9936E-28, 21592559 NAC-domain protein-like [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67651.m00132: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	9.64284E-27, 18700194 protein product AT5g22290/MWD9_7 [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67745.m00110: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	1.34377E-28, 31322199 no apical meristem-like protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67746.m00011: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.9936E-28, 10177980 NAM (no apical meristem)-like protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67757.m00015: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	6.0319E-29, 9759155 unnamed protein product [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67798.m00005: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	1.21514E-29, 8885600 NAM-like [<i>Arabidopsis thaliana</i>].	no hits returned

Link1 Link2 >67828.m00003: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	4.17723E-30, 51972128 protein product At5g50820 [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67905.m00020: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	4.17723E-30, 8809651 NAM (no apical meristem)-like protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67913.m00149: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.9936E-28, 24030239 unknown protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67919.m00003: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.61645E-32, 10178056 unnamed protein product [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >68090.m00129: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	1.217E-29, 23506087 protein product At5g13180/T19L5_140 [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >68097.m00013: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	5.11307E-28, 9955520 putative protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >68151.m00018: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	5.11307E-28, 15237698 no apical meristem (NAM) family protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >60615.m00165: <i>Arabidopsis</i> seven in absentia (SINA) protein.	no hits returned	1.09927E-30, 16323494 putative seven in absentia protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >60735.m00029: <i>Arabidopsis</i> putative seven in absentia (SINA) protein.	no hits returned	1.48571E-27, 25404638 hypothetical protein T12I7.6 of <i>Arabidopsis thaliana</i> .	no hits returned
Link1 Link2 >60735.m00031: <i>Arabidopsis</i> seven in absentia (SINA) protein.	no hits returned	1.13757E-27, 25404642 hypothetical protein T12I7.8 of <i>Arabidopsis thaliana</i> .	no hits returned
Link1 Link2 >1342.m00052: <i>Arabidopsis</i> seven in	no hits returned	1.13907E-27, 1871185 putative RING zinc finger protein; tRNA-Ser	no hits returned

absentia (SINA) protein.		[<i>Arabidopsis thaliana</i>].	
Link1 Link2 >67304.m00152: <i>Arabidopsis</i> seven in absentia (SINA) protein.	no hits returned	2.29212E-28, 21593355 putative RING zinc finger protein [<i>Arabidopsis</i> <i>thaliana</i>].	no hits returned
Link1 Link2 >67319.m00137: <i>Arabidopsis</i> seven in absentia (SINA) protein.	no hits returned	7.87632E-29, 21536945 seven in absentia-like protein [<i>Arabidopsis</i> <i>thaliana</i>].	no hits returned
Link1 Link2 >67733.m00003: <i>Arabidopsis</i> seven in absentia (SINA) protein.	no hits returned	2.9936E-28, 9758487 unnamed protein product [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67733.m00006: <i>Arabidopsis</i> seven in absentia (SINA) protein.	no hits returned	8.71005E-28, 9758490 unnamed protein product [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67908.m00010: <i>Arabidopsis</i> seven in absentia (SINA) protein.	no hits returned	1.58734E-29, 15241972 <i>Arabidopsis</i> seven in absentia (SINA) protein.	no hits returned
Link1 Link2 >67308.m00012: <i>Arabidopsis</i> putative auxin-responsive protein.	no hits returned	1.48541E-27, 7529750 putative protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >68169.m00337: <i>Arabidopsis</i> auxin- responsive family protein.	no hits returned	5.10631E-28, 27363428 product At4g17280/dl4675c [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67113.m00113: <i>Arabidopsis</i> putative auxin-responsive protein.	no hits returned	1.13757E-27, 21593814 unknown protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >60500.m00168: <i>Arabidopsis</i> auxin- responsive family protein.	no hits returned	3.30981E-27, 9294186 unnamed protein product [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67804.m00010: <i>Arabidopsis</i> putative auxin-responsive protein.	no hits returned	1.9404E-27, 9758781 unnamed protein product [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >52129.m00067: <i>Arabidopsis</i> SEUSS transcriptional co- regulator.	no hits returned	4.61846E-29, 18033922 SEUSS transcriptional co- regulator [<i>Arabidopsis</i> <i>thaliana</i>].	no hits returned
Link1 Link2 >52277.m00207: <i>Arabidopsis</i> transcription	no hits returned	4.62458E-29, 6056383 Similar to NAM protein	no hits returned

activator NAC1.		[<i>Arabidopsis thaliana</i>].	
Link 1 Link2 (Gramene) . gi 7227890 sp O24175 FL_ O: rice RYSA putative transcription factor FL (RFL).	no hits returned	0.0, 7489570 protein RFL of rice.	no hits returned
Link1 Link2 >29427.m00038: <i>Arabidopsis</i> rcd1-like cell differentiation family protein.	no hits returned	3.91494E-28, 21805678 hypothetical protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67670.m00010: <i>Arabidopsis</i> turnip crinkle virus-interacting protein / TCV-interacting protein (TIP).	no hits returned	2.07314E-29, 32441252 protein product At5g24590 [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67936.m00109: <i>Arabidopsis</i> putative AP2 domain-containing transcription factor.	no hits returned	4.93441E-31, 21593812 floral homeotic protein apetala2-like [<i>Arabidopsis</i> <i>thaliana</i>].	no hits returned
Link1 Link2 >67292.m00019: <i>Arabidopsis</i> putative AP2 domain-containing transcription factor.	no hits returned	4.77936E-26, 4678294 APETALA2-like protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >67845.m00006: <i>Arabidopsis</i> seed maturation family protein.	no hits returned	4.04597E-25, 9759173 unnamed protein product [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >68000.m00048: <i>Arabidopsis</i> root cap 1 (RCP1).	no hits returned	4.32275E-27, 20466029 putative root cap protein RCP1 [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 Antifungal protein 5 [fragment] from cheeseweed (<i>Malva</i> <i>parviflora</i>).	no hits returned	2.27601E-4, 31879432 lipid transfer protein [<i>Atriplex</i> <i>nummularia</i>].	no hits returned

Table 3. Plant – Fungal similarities found

Entries under ‘genome hit’ show *E*-value as returned by the sequence comparison software: a reference to the specific database entry and brief descriptive annotation. **NOTE** that small *E*-values are shown as exponential functions, i.e. $1.217E-29 = 1.217 \times 10^{-29}$

AmiGO description and hyperlinks USE Link2	Metazoan genome hit	Viridiplantae genome hit	Fungi genome hit
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Link1 Link2 Phosphoribosylanthranilate isomerase of <i>Arabidopsis thaliana</i> .	no hits returned	2.34934E-142, 28058927 putative phosphoribosylanthranilate isomerase of <i>Arabidopsis thaliana</i> .	1.20724E-21, 50285849 TRPF_CANGA of <i>Candida glabrata</i> .
Link1 Link2 >67844.m00001: <i>Arabidopsis</i> putative oxidoreductase.	no hits returned	9.30589E-30, 53828609 unknown protein of <i>Arabidopsis thaliana</i> .	7E-18, Aspergillus, TIGR , Putative short-chain dehydrogenase / reductase (Afu6g11650) of <i>Aspergillus fumigatus</i> .
Link1 Link2 >DDB0214816 [Protein] locus: mybC: <i>Dictyostelium myb</i> transcription factor.	no hits returned	6.27106E-10, 28829358 hypothetical protein id: At1g08840.1 of <i>Arabidopsis thaliana</i> .	4.80158E-10, 46433415 hypothetical protein CaO19.10173 of <i>Candida albicans</i> .
Link1 Link2 >60278.m00050: <i>Arabidopsis</i> NAM (no apical meristem) family protein (transcription factor?).	no hits returned	4.18276E-30, 7547102 no apical meristem hypothetical protein [<i>Arabidopsis thaliana</i>].	0.05, Cryptococcus, TIGR hypothetical protein.
Link1 Link2 >67041.m00011: <i>Arabidopsis</i> NAM (no apical meristem) family protein.	no hits returned	1.02868E-28, 7268198 putative NAM-like protein [<i>Arabidopsis thaliana</i>].	0.05, Cryptococcus, TIGR putative glutathione transferase.
Link1 Link2 >51799.m00289: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	4.17723E-30, 18396807 <i>Arabidopsis</i> no apical meristem (NAM) family protein.	0.05, Cryptococcus, TIGR putative cytoplasm protein.
Link1 Link2 >60723.m00078 <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	9.30589E-30, 25403180 unknown protein of <i>Arabidopsis thaliana</i> .	0.05, Cryptococcus, TIGR expressed protein.
Link1 Link2 >51786.m00193: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	1.217E-29, 8671840 <i>Arabidopsis</i> sequence with Strong similarity to OsNAC6 protein from <i>Oryza sativa</i> .	0.05, Cryptococcus, TIGR conserved hypothetical protein.
Link1 Link2 >51781.m00034: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	3.3142E-27, 42562475 <i>Arabidopsis</i> no apical meristem (NAM) family protein.	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 >67320.m00183 <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	4.61846E-29, 21536577 <i>Arabidopsis</i> no apical meristem (NAM) family protein.	0.05, Cryptococcus, TIGR conserved hypothetical protein.

Link1 Link2 >36000.m00043 <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	5.10528E-28, 27754598 putative <i>Arabidopsis</i> no apical meristem (NAM) family protein.	0.05, Cryptococcus , TIGR conserved hypothetical protein (as above).
Link1 Link2 >60052.m00190 <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	8.70829E-28, 32452837 cup-shaped cotyledon 3 of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein (as above).
Link1 Link2 >60085.m00279 <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.45216E-30, 30793825 putative GRAB1 protein of <i>Arabidopsis thaliana</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein (as above).
Link1 Link2 >67625.m00138 <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	8.41682E-31, 7573474 putative protein of <i>Arabidopsis thaliana</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >68152.m00941 <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.71119E-29, 19424091 unknown protein of <i>Arabidopsis thaliana</i> .	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 >67871.m00006 <i>Arabidopsis</i> no apical meristem (NAM) family protein	no hits returned	2.89282E-31, 10176766 unnamed protein product of <i>Arabidopsis thaliana</i> .	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 >50828.m00139: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	1.87469E-30, 42561659 <i>Arabidopsis</i> no apical meristem (NAM) family protein	0.05, Cryptococcus , TIGR putative vacuolar membrane protein.
Link1 Link2 >60250.m00041: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	1.03025E-28, 6223651 : NAM-like protein of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >67165.m00132: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	7.12527E-30, 24417372 unknown protein of <i>Arabidopsis thaliana</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >67119.m00016: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	9.31821E-30, 7268550 <i>Arabidopsis</i> no apical meristem (NAM) family protein	0.05, Cryptococcus , TIGR hypothetical protein.

Link1 Link2 >60242.m00298: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.07272E-29, 8567779 putative NAC (nascent polypeptide-associated complex)(chaperone) protein of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR expressed protein.
Link1 Link2 >67583.m00136: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.07588E-29, 22136362 putative protein of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR expressed protein.
Link1 Link2 >60242.m00304: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	9.62814E-27, 8567777 unknown protein of <i>Arabidopsis thaliana</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >60242.m00303: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	4.32188E-27, 18398893 <i>Arabidopsis</i> no apical meristem (NAM) family protein	0.05, Cryptococcus , TIGR conserved hypothetical protein (as above).
Link1 Link2 >67915.m00045: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	3.53623E-29, 10176954 unnamed protein product of <i>Arabidopsis thaliana</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein (as above).
Link1 Link2 >60023.m00007: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.70705E-29, 21436105 putative NAM protein of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein (as above).
Link1 Link2 >67242.m00003: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	6.67788E-28, 7529769 NAC domain-like protein [<i>Arabidopsis thaliana</i>].	0.05, Cryptococcus , TIGR putative oxidoreductase.
Link1 Link2 >60743.m00243: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	7.12383E-30, 15293163 unknown protein of <i>Arabidopsis thaliana</i> .	0.05, Cryptococcus , TIGR conserved expressed protein.
Link1 Link2 >67899.m00120: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	7.12527E-30, 9757865 NAM-like protein of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >50821.m00244: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.44843E-30, 30725366 unknown protein of <i>Arabidopsis thaliana</i> .	0.05, Cryptococcus , TIGR putative peptide-binding protein.

Link1 Link2 >60278.m00142: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	1.03025E-28, 23507759 unknown protein of <i>Arabidopsis thaliana</i> .	0.05, Cryptococcus , TIGR putative myo-inositol transporter 2.
Link1 Link2 >60507.m00052: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	4.17723E-30, 11994103 unnamed protein product of <i>Arabidopsis thaliana</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >60482.m00108: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	6.66905E-28, 30984532 unknown protein of <i>Arabidopsis thaliana</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >60025.m00139: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	7.87632E-29, 21553558 NAM-like protein of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >51903.m00352: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	6.66905E-28, 14334572 putative NAM protein of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >67601.m00151: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.44892E-30, 30102618 NAM-like protein of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >67850.m00011: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	9.94249E-32, 10177257 CUC2 (NAM-family) protein of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >60499.m00015: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	9.30589E-30, 9294586 unnamed protein product of <i>Arabidopsis thaliana</i> .	0.05, Cryptococcus , TIGR hypothetical protein.
Link1 Link2 >67637.m00010: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	1.58734E-29, 10177071 NAM-like protein of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >60247.m00053: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.45216E-30, 6714418 NAM-like protein of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein.

Link1 Link2 >43133.m00053: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	1.58734E-29, 24030186 putative NAM protein of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR hypothetical protein.
Link1 Link2 >67026.m00194: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	5.45563E-30, 34222068 similar to putative NAM protein of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >51766.m00048: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	7.87791E-29, 6714280 putative NAM-like protein of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >51442.m00191: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	3.53623E-29, 23397178 putative NAM protein of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >51079.m00082: <i>Arabidopsis</i> no apical meristem (NAM) family protein.	no hits returned	2.99757E-28, 15223376 NAM-family protein of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >67733.m00005: <i>Arabidopsis</i> putative seven in absentia (SINA) protein.	no hits returned	2.80193E-26, 9758489 unnamed protein product [<i>Arabidopsis thaliana</i>].	0.05, Cryptococcus , TIGR expressed protein.
Link1 Link2 >60737.m00068 putative seven in absentia (SINA) protein of <i>Arabidopsis thaliana</i> .	no hits returned	1.13757E-27, 12322287 hypothetical protein of <i>Arabidopsis thaliana</i> .	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 >60735.m00030: putative seven in absentia (SINA) protein of <i>Arabidopsis thaliana</i> .	no hits returned	2.29212E-28, 25404640 hypothetical protein of <i>Arabidopsis thaliana</i> .	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >67167.m00011: seven in absentia (SINA) family protein.	no hits returned	6.67788E-28, 7269641 putative zinc finger protein [<i>Arabidopsis thaliana</i>].	0.05, Cryptococcus , TIGR putative beta-fructofuranosidase.
Link1 Link2 >67733.m00009: seven in absentia (SINA) family protein.	no hits returned	1.02889E-28, 28827312 unknown protein of <i>Arabidopsis thaliana</i> .	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 >51205.m00083: <i>Arabidopsis</i> seed	no hits returned	7.87632E-29, 4587565 <i>Arabidopsis</i> protein similar to rab28 protein	0.05, Cryptococcus , TIGR putative ligand-regulated transcription factor.

maturation family protein.		gb X59138 from <i>Zea mays</i> .	
Link1 Link2 >67845.m00007 <i>Arabidopsis</i> seed maturation family protein.	no hits returned	3.09789E-25, 9759174 unnamed protein product of <i>Arabidopsis thaliana</i> .	0.05, Cryptococcus , TIGR hypothetical protein.
Link1 Link2 >67962.m00005: <i>Arabidopsis</i> seed maturation family protein.	no hits returned	3.65869E-26, 26452310 putative embryonic abundant protein of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR hypothetical protein.
Link1 Link2 >68169.m00284: putative DRE-binding transcription factor of <i>Arabidopsis</i> .	no hits returned	1.34377E-28, 7268425 apetala2 domain TINY like protein of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR putative vacuolar membrane protein.
Link1 Link2 >67824.m00008: transducin family protein.	no hits returned	2.80193E-26, 9759025 unnamed protein product of <i>Arabidopsis thaliana</i> .	0.05, Cryptococcus , TIGR hypothetical protein.
Link1 Link2 >67813.m00007: putative auxin-responsive protein.	no hits returned	1.21539E-29, 9758874 unnamed protein product of <i>Arabidopsis thaliana</i> .	0.05, Cryptococcus , TIGR putative protein-S-isoprenylcysteine O-methyltransferase.
Link1 Link2 >67617.m00015: putative rcd1-like cell differentiation protein of <i>Arabidopsis</i> (similar to protein involved in sexual development in <i>Schizosaccharomyces pombe</i>).	no hits returned	1.81856E-25, 7630054 putative protein of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR putative regulation of transcription from Pol II promoter-related protein.
Link1 Link2 >60485.m00171: putative rcd1-like cell differentiation protein of <i>Arabidopsis</i> .	no hits returned	1.64264E-26, 21689729 putative cell differentiation protein of <i>Arabidopsis</i> .	0.05, Cryptococcus , TIGR putative regulation of transcription from Pol II promoter-related protein (as above).

Table 4. Similarities found to be common to all three eukaryotic Kingdoms

Entries under 'genome hit' show *E*-value as returned by the sequence comparison software: a reference to the specific database entry and brief descriptive annotation. **NOTE** that small *E*-values are shown as exponential functions, i.e. $1.217E-29 = 1.217 \times 10^{-29}$

AmiGO description and hyperlinks USE Link2	Metazoan genome hit	Viridiplantae genome hit	Fungi genome hit
Link1 Link2 >67170.m00018: <i>Arabidopsis</i> no apical	5.06164E-5, Animal.dna <i>Homo sapiens</i> chromosome 15, clone	3.77738E-31, 7269704 predicted protein [<i>Arabidopsis thaliana</i>].	<0.05 Phanerochaete genomic homology (not annotated).

meristem (NAM) family protein.	RP11-26F2, complete sequence.		
Link1 Link2 >MGI MGI:108062 symbol:Slah2: mouse seven in absentia 2 protein.	6.41984E-23, 40254613 seven in absentia 2 [<i>Mus musculus</i>].	0.00963779, 4584086 p210 protein [<i>Spermatozopsis similis</i>] (protein is located in a membrane-microtubule- linker at the distal end of basal bodies)	0.00565021, 32422095 predicted protein [<i>Neurospora crassa</i>].
Link1 Link2 : monkey (<i>Cercopithecus aethiops</i>) cellular tumour antigen p53.	0.0, 129367 (<i>Cercopithecus aethiops</i>) cellular tumour antigen p53.	3.22101E-123, 48374980 putative tumour protein p53 [<i>Zea mays</i>].	0.0, Fungi, dna <i>Ustilago maydis</i> 521, UM04579.1 predicted mRNA.
Link1 Link2 : Chinese hamster cellular tumour antigen p53.	0.0, 1890325 Chinese hamster cellular tumour antigen p53.	2.83486E-103, 48374980 as above.	0.0, Fungi, dna as above.
Link1 Link2 : rhesus monkey cellular tumour antigen p53.	0.0, 47117801 rhesus monkey cellular tumour antigen p53.	7.17567E-123, 48374980 as above.	0.0, Fungi, dna as above.
Link1 Link2 : tree shrew cellular tumour antigen p53.	0.0, 10720194 tree shrew cellular tumour antigen p53.	8.22908E-111, 48374980 as above.	0.0, Fungi, dna as above.
Link1 Link2 : woodchuck cellular tumour antigen p53.	0.0, 2440123 tumor suppressor [<i>Marmota monax</i>].	3.91678E-113, 48374980 as above.	0.0, Fungi, dna as above.
Link1 Link2 : Mongolian gerbil P53.	0.0, 16266760 p53 [<i>Meriones unguiculatus</i>].	8.46452E-100, 48374980 as above.	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 : porcine cellular tumour antigen p53.	0.0, 47523088 tumour suppressor p53 [<i>Sus scrofa</i>].	3.72158E-108, 48374980 as above.	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 : guinea pig cellular tumour antigen p53.	0.0, 4884046 p53 protein [<i>Cavia porcellus</i>].	8.74593E-105, 48374980 as above.	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 : human putative p150 protein.	0.0, 2072958 putative p150 [<i>Homo sapiens</i>].	2.52883E-64, Plants, dna <i>Arabidopsis thaliana</i> DNA chromosome 4, ESSA I FCA contig fragment No. 4.	0.0, Fungi, dna <i>Aspergillus nidulans</i> FGSC A4, AN2724.2 predicted mRNA.
Link1 Link2 : mouse Homeobox protein A10	0.0, 30046954 Homeobox protein A10 [<i>Mus musculus</i>].	0.0, Plants, dna <i>Solanum demissum</i> chromosome 5 BAC PGEC446O19 genomic sequence, complete sequence.	0.0, Fungi, dna <i>S. cerevisiae</i> chromosome XIII cosmid 8337.
Link1 Link2 : mouse latent transforming growth factor beta binding protein 4.	0.0, 32189330 latent transforming growth factor beta binding protein 4 [<i>Mus musculus</i>].	2.46129E-14, Plants, dna <i>Oryza sativa</i> (japonica cultivar-group), mRNA.	0.0, Fungi, dna <i>Eremothecium gossypii</i> ADR210Cp (ADR210C), mRNA.

Link1 Link2 : human latent transforming growth factor-beta beta binding protein 4S.	0.0, 3327808 latent transforming growth factor-beta binding protein 4S [<i>Homo sapiens</i>].	1e-14, 42407754 , rice, putative wall-associated serine/threonine kinase [<i>Oryza sativa</i>].	0.0, Fungi, dna <i>Ashbya gossypii</i> (= <i>Eremothecium gossypii</i>) ATCC 10895 chromosome II, complete sequence.
Link1 Link2 >UNIPROT Q9JM52 symbol:M4K6: mouse mitogen-activated protein kinase kinase kinase 6.	7.08858E-22, 24850117 misshapen/NIK-related kinase isoform 2 [<i>Homo sapiens</i>].	0.05, Arabidopsis, TIGR putative cyclin-dependent kinase.	0.0, Fungi, dna <i>Saccharomyces cerevisiae</i> NRK1 gene for N-rich kinase 1.
Link2 , >gi 11131838 sp Q9SLY8 CRTC_ORYSA: rice calreticulin precursor (but no longer on godatabase.org page).	1.07201E-127, 18858381 calreticulin [<i>Danio rerio</i>].	0.0, 6682833 calcium-binding protein [<i>Oryza sativa</i>].	0.0, Fungi, dna chromosome F of strain CLIB99 of <i>Yarrowia lipolytica</i> .
Link1 Link2 >UNIPROT O15347 symbol:HMG4: human high mobility group protein 4.	7.5735E-24, 4885421 high-mobility group box 3 [<i>Homo sapiens</i>].	0.0, Plants, dna <i>Triticum aestivum</i> mRNA for high mobility group protein (HMGW).	0.0, Fungi, dna <i>Saccharomyces cerevisiae</i> clone FLH113809.01X YPR052C gene, complete cds.
Link1 Link2 : human dentin sialophosphoprotein precursor.	0.0, 11036632 dentin sialophosphoprotein preproprotein [<i>Homo sapiens</i>].	6.0953E-64, 11994784 unnamed protein product [<i>Arabidopsis thaliana</i>].	7.8507E-112, 50546453 hypothetical protein [<i>Yarrowia lipolytica</i>].
Link > MMHC188A7: Mouse casein kinase.	6.07491E-128, 46237616 casein kinase 2, beta subunit [<i>Rattus norvegicus</i>].	7.06435E-68, 37536920 putative casein kinase II beta subunit [<i>Oryza sativa japonica</i> cultivar-group].	3.506E-67, 452290 casein kinase II beta subunit [<i>Schizosaccharomyces pombe</i>].
Link2 >gi 18056667 gb AAL58107.1 AF395064_1 CSN complex subunit 6B [<i>Arabidopsis thaliana</i>] (related to COP9 signalosome).	1.5475E-58, 55741990 COP9 constitutive photomorphogenic homolog subunit 6 [<i>Xenopus tropicalis</i>].	0.0, 21593149 transcription factor-like [<i>Arabidopsis thaliana</i>].	1.11417E-40, 46095839 hypothetical protein UM00643.1 [<i>Ustilago maydis</i> 521].
Link1 Link2 : <i>Arabidopsis</i> CSN6A gene - one of two genes encoding subunit 6 of COP9 signalosome complex.	1.07168E-59, 47226158 unnamed protein product [<i>Tetraodon nigroviridis</i>].	0.0, 18056665 CSN complex subunit 6A [<i>Arabidopsis thaliana</i>].	6.11364E-39, 50257625 hypothetical protein CNBF1410 [<i>Cryptococcus neoformans</i>].
Link1 Link2 : human pProtein-tyrosine phosphatase, non-receptor type 22.	0.0, 48928054 protein tyrosine phosphatase, non-receptor type 22 (lymphoid) isoform 1 [<i>Homo sapiens</i>].	2.50413E-35, Plants, dna <i>Oryza sativa</i> (japonica cultivar-group) cDNA clone:002-166-D08, full insert sequence.	1.1738E-34, Fungi, dna <i>Yarrowia lipolytica</i> CLIB99, YALI0F24585g predicted mRNA.
Link1 >gi 18426814 ref NP_569084.1 dihydrofolate reductase [<i>Rattus</i>	1.52823E-104, 18426814 dihydrofolate reductase [<i>Rattus norvegicus</i>].	1.15727E-27, 21702230 dihydrofolate reductase-thymidylate synthase [<i>Pisum sativum</i>].	1.61483E-29, 42554965 hypothetical protein FG07210.1 [<i>Gibberella zeae</i> PH-1].

<i>norvegicus</i>].			
Link1 Link2 : human putative tyrosine phosphatase	1.37967E-164, 6650693 putative tyrosine phosphatase [<i>Homo sapiens</i>].	3.08241E-39, 30023688 At5g10480 [<i>Arabidopsis thaliana</i>].	3.77673E-29, 32421867 hypothetical protein [<i>Neurospora crassa</i>].
Link1 Link2 : mouse peroxisome proliferator-activated receptor.	0.0, 25990188 thyroid hormone receptor associated protein 220 [<i>Mus musculus</i>].	0.015399, Plants, dna <i>Oryza sativa</i> (japonica cultivar-group) cDNA clone:002-161-H03, full insert sequence.	1.3692E-28, 40645462 cell wall protein Awa1p [<i>Saccharomyces cerevisiae</i>].
Link1 Link2 Peroxisome proliferator-activated receptor binding protein.	0.0, 14193715 peroxisome proliferator-activated receptor binding protein [<i>Mus musculus</i>].	0.015399, Plants, dna <i>Oryza sativa</i> (japonica cultivar-group) cDNA clone:002-161-H03, full insert sequence.	3.99601E-28, 40645462 cell wall protein Awa1p [<i>Saccharomyces cerevisiae</i>].
Link1 Link2 : human Jagged 2 precursor.	0.0, 2605945 Jagged-2 [<i>Homo sapiens</i>].	5.29485E-51, Plants, dna <i>Oryza sativa</i> (japonica cultivar-group) cDNA clone:002-167-G01, full insert sequence.	3e-23, 3250920 , Putative wall protein. [<i>Hypocrea lixii</i>]
Link1 Link2 >tr Q80ZV1 1110033J19: mouse RIKEN cDNA 1110033J19 gene.	3.53552E-29, 55715979 LOC495812 protein [<i>Xenopus laevis</i>].	1.75873E-20, 488739 ribosomal protein, small subunit 4e (RS4e) [<i>Gossypium hirsutum</i>].	2.21965E-23, 50426545 unnamed protein product [<i>Debaryomyces hansenii</i>].
Link1 Link2 : human male-specific lethal 3-like 1.	0.0, 21411116 Male-specific lethal 3-like 1, isoform a [<i>Homo sapiens</i>].	1.83009E-18, 4006854 putative protein [<i>Arabidopsis thaliana</i>].	7.93833E-22, 40745985 hypothetical protein AN1976.2 [<i>Aspergillus nidulans</i> FGSC A4].
Link1 Link2 >MGI MGI:98158 symbol:Rps4x: mouse ribosomal protein S4, X-linked.	2.20647E-23, 46048780 ribosomal protein S4 [<i>Gallus gallus</i>].	1.8092E-17, 22138108 40S ribosomal S4 protein [<i>Glycine max</i>].	2.52453E-19, 50426545 unnamed protein product [<i>Debaryomyces hansenii</i>].
Link1 Link2 : mouse Fliih, flightless I protein homolog.	0.0, 21595485 Fliih protein [<i>Mus musculus</i>].	2.25262E-55, 22136974 putative villin 2 protein [<i>Arabidopsis thaliana</i>].	1.47563E-15, Fungi, dna <i>Aspergillus nidulans</i> FGSC A4, AN1306.2 predicted mRNA.
Link1 Link2 >UNIPROT Q9Y295 symbol:DRG1: human developmentally regulated GTP-binding protein 1.	3.88963E-20, 4758796 developmentally regulated GTP binding protein 1 [<i>Homo sapiens</i>].	2.44197E-14, 50939391 putative GTP-binding protein DRG [<i>Oryza sativa</i> (japonica cultivar-group)].	1.09615E-14, 32403724 hypothetical protein [<i>Neurospora crassa</i>].
Link1 Link2 >gi 30580409 sp O42182 FBLN1_BRARE: Zebrafish fibulin-1 precursor.	0.0, 18858663 fibulin 1 [<i>Danio rerio</i>].	0.0, Plants, dna <i>Oryza sativa</i> (japonica cultivar-group), predicted mRNA.	9e-14, 42549555 , Hypothetical protein FG02898.1 (<i>Gibberella zeae</i> , anamorph <i>Fusarium graminearum</i>).
Link1 Link2 >UNIPROT Q16576 symbol:RBB7: human	2.20647E-23, 31982059 retinoblastoma binding	1.06065E-17, 50881441 putative MSI type nucleosome/chromatin	2.70349E-13, 46100907 hypothetical protein UM04760.1 [<i>Ustilago</i>

histone acetyltransferase type B subunit 2.	protein 7 [<i>Mus musculus</i>].	assembly factor C [<i>Oryza sativa</i> (japonica cultivar-group)].	<i>maydis</i> 521].
Link1 Link2 >UNIPROT O00429 symbol:O00429: human Dynamain 1-like protein.	1.93041E-19, 19352981 Dynamain 1-like protein, isoform 2 [<i>Homo sapiens</i>].	3.64904E-10, 50902394 putative dynamain-like protein ADL2 [<i>Oryza sativa</i> (japonica cultivar-group)].	1.75003E-12, 50556172 hypothetical protein [<i>Yarrowia lipolytica</i>].
Link1 Link2 >DDB0215363 Protein locus: <i>Dictyostelium</i> alrA aldehyde reductase.	1.22079E-13, 39591260 Hypothetical protein CBG20740 [<i>Caenorhabditis briggsae</i>].	1.03346E-12, 53749361 putative aldose reductase [<i>Oryza sativa</i> (japonica cultivar-group)].	1.76282E-12, 40745643 hypothetical protein AN1679.2 [<i>Aspergillus</i> <i>nidulans</i> FGSC A4].
Link1 Link2 : human negative elongation factor A.	0.0, 11527781 Wolf- Hirshhorn syndrome candidate 2 protein [<i>Homo</i> <i>sapiens</i>].	1.49452E-10, 41400384 plus agglutinin [<i>Chlamydomonas</i> <i>reinhardtii</i>].	8.76169E-11, 46442651 hypothetical protein CaO19.11809 [<i>Candida</i> <i>albicans</i> SC5314].
Link1 Link2 >DDB0215356 Protein locus: <i>Dictyostelium</i> putative myb transcription factor.	6.27106E-10, 38787935 BMP-2 inducible kinase isoform a [<i>Homo sapiens</i>].	1.54462E-8, 4914452 putative protein [<i>Arabidopsis thaliana</i>].	2.15533E-10, 32420087 predicted protein [<i>Neurospora crassa</i>].
Link1 Link2 >UNIPROT O14807 symbol:RASM: human Ras-related protein M-Ras.	9.27024E-22, 54696976 muscle RAS oncogene homolog [<i>Homo sapiens</i>].	1.54474E-6, Plants, dna <i>Oryza sativa</i> (japonica cultivar-group) cDNA clone:002-166-D02, full insert sequence.	2.79767E-10, 19114491 hypothetical protein SPAC17H9.09c [<i>Schizosaccharomyces</i> <i>pombe</i>].
Link1 Link2 >DDB0191102 Protein locus: <i>Dictyostelium</i> apm1, clathrin-adaptor medium chain.	2.1549E-10, 48097723 similar to ENSANGP00000020532 [<i>Apis mellifera</i>].	7.6643E-8, 20466372 clathrin adaptor medium chain protein MU1B, putative [<i>Arabidopsis</i> <i>thaliana</i>].	3.11167E-9, 28949965 probable clathrin assembly protein AP47 [<i>Neurospora</i> <i>crassa</i>].
Link1 Link2 >UNIPROT Q94899 symbol:CSN2: <i>Drosophila</i> COP9 signalosome complex subunit 2.	2.87734E-23, 7297479 CG9556-PB, isoform B [<i>Drosophila</i> <i>melanogaster</i>].	2.21335E-7, 21593214 putative PCI domain protein [<i>Arabidopsis</i> <i>thaliana</i>].	9.93527E-8, 19571748 csn2 [<i>Schizosaccharomyces</i> <i>pombe</i>].
Link1 Link2 ~: human death effector domain- associated factor (RING1 and YY1 binding protein).	6.35467E-126, 15928993 RING1 and YY1 binding protein [<i>Homo sapiens</i>].	2.1166E-4, 50428710 putative FHA domain protein [<i>Oryza sativa</i> (japonica cultivar-group)].	1.01509E-6, 46435639 hypothetical protein CaO19.11553 [<i>Candida</i> <i>albicans</i> SC5314].
Link1 Link2 >UNIPROT Q92499 symbol:DDX1: human ATP-dependent helicase DDX1.	1.02359E-20, 34863163 DEAD (Asp-Glu-Ala-Asp) box polypeptide 1 [<i>Rattus</i> <i>norvegicus</i>].	2.07205E-5, 50917625 putative RNA helicase [<i>Oryza sativa</i> (japonica cultivar-group)].	2.70618E-5, 40740142 hypothetical protein AN4233.2 [<i>Aspergillus</i> <i>nidulans</i> FGSC A4].
Link1 Link2 >UNIPROT P31276 symbol:HXCD: human homeobox protein Hox- C13.	1.6872E-23, 24497536 homeo box C13 [<i>Homo</i> <i>sapiens</i>].	1.34306E-4, 50919335 putative prohibitin [<i>Oryza</i> <i>sativa</i> (japonica cultivar- group)].	3.53438E-5, 45190453 unnamed protein of <i>Eremothecium gossypii</i> (<i>Ashbya gossypii</i>).

Link1 Link2 : mouse C330013B04 product: peroxisome proliferator-activated receptor binding protein homolog [fragment].	0.0, 26339888 unnamed protein product [<i>Mus musculus</i>].	0.0131176, 55978791 hypothetical protein AT1G79480 [<i>Arabidopsis thaliana</i>].	3.68814E-5, 6322209 GPI-anchored cell surface glycoprotein required for diploid pseudohyphal formation and haploid invasive growth [<i>Saccharomyces cerevisiae</i>].
Link1 Link2 >gi 50054384 ref NP_076471.3 colony stimulating factor 1 (macrophage) [<i>Rattus norvegicus</i>].	0.0, 50054384 colony stimulating factor 1 (macrophage) [<i>Rattus norvegicus</i>].	8.26683E-4, 3063699 putative protein [<i>Arabidopsis thaliana</i>].	4.38345E-5, 50556110 hypothetical protein [<i>Yarrowia lipolytica</i>].
Link1 Link2 >UNIPROT Q8NG53 symbol:Q8NG53: human diacylglycerol kinase, delta.	4.9155E-23, 25777598 diacylglycerol kinase, delta 130kDa isoform 2 [<i>Homo sapiens</i>].	1.34484E-4, 51557999 chloroplast DnaJ-like protein 2 [<i>Chlamydomonas reinhardtii</i>].	1.02971E-4, 38100339 predicted protein [<i>Magnaporthe grisea</i> 70-15].
Link1 Link2 >UNIPROT Q9Y255 symbol:PX19: human Px19-like protein (may be important for the development of vital and immunocompetent organs).	2.87793E-23, 41190437 predicted protein similar to Px19-like protein [<i>Homo sapiens</i>].	0.05, Arabidopsis , TIGR <i>Arabidopsis</i> MSF1-like family protein similar to px19 of chicken.	1.7541E-4, 50551063 hypothetical protein [<i>Yarrowia lipolytica</i>].
Link1 Link2 >DDB0216392 [Protein] locus: <i>Dictyostelium</i> CRTF transcription factor required for expression of aggregation genes.	1.5981E-5, 23093054 CG32223-PA [<i>Drosophila melanogaster</i>].	1.03586E-4, 28829358 <i>Dictyostelium</i> protein similar to hypothetical protein; protein id: At1g08840.1 of <i>Arabidopsis thaliana</i> .	1.76691E-4, 32416082 predicted protein [<i>Neurospora crassa</i>].
Link1 Link2 >UNIPROT O14511 symbol:NRG2: human pro-neuregulin-2 precursor.	2.28032E-20, 7669536 neuregulin 2 isoform 6 [<i>Homo sapiens</i>].	0.00564273, 15230121 hypothetical protein [<i>Arabidopsis thaliana</i>].	2.29092E-4, 34809539 adhesin of <i>Candida glabrata</i> mediating adherence to human epithelial cells.
Link1 Link2 >UNIPROT Q8IN81 symbol:FRU: <i>Drosophila</i> sex determination protein fruitless.	1.05679E-25, 23171647 CG14307-PE, isoform E [<i>Drosophila melanogaster</i>].	0.0164178, 16550925 zinc transporter [<i>Eucalyptus grandis</i>].	2.99203E-4, 50260923 hypothetical protein CNBA2200 [<i>Cryptococcus neoformans</i>].
Link1 Link2 >DDB0214900: <i>Dictyostelium</i> amiB novel protein required for aggregation.	3.93627E-4, 23093054 CG32223-PA [<i>Drosophila melanogaster</i>].	5.14092E-4, 28829358 hypothetical protein; protein id: At1g08840.1 [<i>Arabidopsis thaliana</i>].	3.01389E-4, 6323816 Transcription factor involved in regulation of invasive growth and starch degradation [<i>Saccharomyces cerevisiae</i>].
Link1 Link2 >DDB0214819 [Protein] locus: <i>Dictyostelium</i> autophagy protein 7	1.22363E-5, 12652685 APG7L protein [<i>Homo sapiens</i>].	0.05, Arabidopsis , TIGR (APG7) nearly identical to autophagy 7 [<i>Arabidopsis</i>	6.71425E-4, 46100947 hypothetical protein UM04880.1 [<i>Ustilago</i>

(homologue of yeast atg7; E1-like).		<i>thaliana</i>].	<i>maydis</i> 521].
Link1 Link2 : human LIM homeobox protein cofactor	0.0, 3372807 LIM homeobox protein cofactor [<i>Homo sapiens</i>].	1.65327E-4, 7523675 Hypothetical protein [<i>Arabidopsis thaliana</i>].	8.20512E-4, 38102578 hypothetical protein MG01057.4 [<i>Magnaporthe grisea</i> 70-15].
Link1 Link2 : human nuclear LIM interactor [fragment].	0.0, 5123791 Nuclear LIM interactor [<i>Homo sapiens</i>].	1.81309E-4, 7523675 Hypothetical protein [<i>Arabidopsis thaliana</i>].	8.99825E-4, 38102578 hypothetical protein MG01057.4 [<i>Magnaporthe grisea</i> 70-15].
Link1 Link2 >UNIPROT Q9TVM2 symbol:XPO1: Drosophila Exportin-1.	2.52453E-19, 28380309 CG13387-PA [<i>Drosophila melanogaster</i>].	0.05, Arabidopsis , TIGR expressed protein.	0.00194195, 50285273 unnamed protein product [<i>Candida glabrata</i>].
Link1 Link2 >UNIPROT P31260 symbol:HXAA: human Homeobox protein Hox-A10.	2.87793E-23, 24497549 homeobox protein A10 isoform a [<i>Homo sapiens</i>].	1.02835E-4, 50909875 hypothetical protein [<i>Oryza sativa</i> (japonica cultivar-group)].	0.00330808, 32415003 hypothetical protein [<i>Neurospora crassa</i>].
Link1 Link2 : human transcription factor-like 5 protein.	0.0, 12314002 TCFL5 [<i>Homo sapiens</i>].	1.24779E-4, 7671199 flagellar autotomy protein Fa1p [<i>Chlamydomonas reinhardtii</i>].	0.00684683, 11877204 putative centromere binding factor 1 [<i>Candida albicans</i>].
Link1 Link2 >UNIPROT P25800 symbol:RHM1: human rhombotin-1.	7.5735E-24, 4505005 LIM domain only 1 [<i>Homo sapiens</i>].	0.05, Arabidopsis , TIGR LIM domain-containing protein weak similarity to LIM-homeobox protein.	0.0103, Fungi , dna S. cerevisiae (DBY874) LRG1 gene.
Link1 Link2 : human Carbohydrate sulfotransferase 2.	0.0, 27369497 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 [<i>Homo sapiens</i>].	7.63685E-4, 50934045 hypothetical protein [<i>Oryza sativa</i> (japonica cultivar-group)].	0.0110276, 38106495 hypothetical protein MG05921.4 [<i>Magnaporthe grisea</i> 70-15].
Link1 Link2 >UNIPROT P39880 symbol:CUT1: human CCAAT displacement protein.	1.74598E-20, 31652240 CCAAT displacement protein isoform a [<i>Homo sapiens</i>].	0.05, Arabidopsis , TIGR CCAAT displacement protein-related.	0.0477686, 50256507 hypothetical protein CNBH3310 [<i>Cryptococcus neoformans</i>].
Link1 Link2 >UNIPROT O60869 symbol:O60869: human endothelial differentiation-related factor 1.	3.51803E-21, 15930118 Endothelial differentiation-related factor 1, isoform alpha [<i>Homo sapiens</i>].	7.12154E-6, 50944921 putative ethylene-responsive transcriptional coactivator [<i>Oryza sativa</i> (japonica cultivar-group)].	0.0477686, 40744391 hypothetical protein AN2996.2 [<i>Aspergillus nidulans</i> FGSC A4].
Link1 Link2 >UNIPROT P52566 symbol:GDIS: human Rho GDP-dissociation inhibitor 2.	1.4283E-22, 14327952 Rho GDP dissociation inhibitor (GDI) beta [<i>Homo sapiens</i>].	0.0280046, 34906916 putative Rho GDP-dissociation inhibitor [<i>Oryza sativa</i> (japonica cultivar-group)].	0.05, Cryptococcus , TIGR putative Rho GDP-dissociation inhibitor 1.
Link1 Link2 >DDB0191390 Protein locus: <i>Dictyostelium</i> atg5	1.00099E-7, 31201617 ENSANGP00000012467	9.36897E-6, 26450228 APG5 (autophagy 5) like protein [<i>Arabidopsis</i>	0.05, Cryptococcus , TIGR putative prostatic steroid 5-alpha-reductase type I, of

autophagy protein 5.	[<i>Anopheles gambiae</i>].	<i>thaliana</i>].	<i>Cryptococcus neoformans</i> .
Link1 Link2 >UNIPROT Q15717 symbol:ELV1: human ELAV-like protein 1.	5.42754E-22, 38201714 ELAV-like 1 [<i>Homo sapiens</i>].	0.05, Arabidopsis, TIGR RNA and export factor-binding protein, putative transcriptional coactivator.	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 >67166.m00025: <i>Arabidopsis</i> oxidoreductase, forever young (FEY3).	3.93493E-11, Animal, dna Human DNA sequence from clone XXYac-65C7_A	1.217E-29, 7269630 forever young gene (FEY) (fragment) [<i>Arabidopsis thaliana</i>].	0.05, Cryptococcus, TIGR putative transposable elements-Tcn5.
Link1 Link2 >tr Q6P6K5: mouse nuclear factor, erythroid derived 2.	1.21539E-29, 40254626 nuclear factor, erythroid derived 2 [<i>Mus musculus</i>].	0.05, Arabidopsis, TIGR putative chloroplast division protein.	0.05, Cryptococcus, TIGR hypothetical protein.
Link1 Link2 >UNIPROT Q12951 symbol:FXI1: human forkhead box protein I1.	2.12937E-26, 1911185 forkhead box L1 [<i>Homo sapiens</i>].	0.05, Arabidopsis, TIGR expressed protein.	0.05, Cryptococcus, TIGR conserved hypothetical protein.
Link1 Link2 >UNIPROT Q02223 symbol:TR17: human tumour necrosis factor receptor superfamily member 17.	5.80651E-24, 23238192 tumor necrosis factor receptor superfamily, member 17 [<i>Homo sapiens</i>].	0.05, Arabidopsis, TIGR gibberellin-regulated protein 3 (GASA3).	0.05, Cryptococcus, TIGR conserved hypothetical protein.
Link1 Link2 >31052.m00046: <i>Arabidopsis</i> putative AP2 domain-containing transcription factor.	0.0, Animal, dna <i>Mus musculus</i> BAC clone RP24-121M11 from 13, complete sequence.	1.75501E-28, 20260076 putative AP2 domain transcription factor [<i>Arabidopsis thaliana</i>].	0.05, Cryptococcus, TIGR conserved hypothetical protein.
Link1 Link2 >67844.m00002: <i>Arabidopsis</i> putative oxidoreductase.	4.95871E-6, Animal, dna Homo sapiens chromosome 13q34 schizophrenia region contig 1 section 7 of 11 of the complete sequence.	7.12527E-30, 9757991 protochlorophyllide reductase; oxidoreductase required for shoot apex development [<i>Arabidopsis thaliana</i>].	0.05, Cryptococcus, TIGR putative ubiquitin-protein ligase.
Link1 Link2 >UNIPROT Q9NRW4 symbol:Q9NRW4: human mitogen-activated protein kinase phosphatase x.	5.43472E-22, 9910432 dual specificity phosphatase 22 [<i>Homo sapiens</i>].	0.05, Arabidopsis, TIGR dual specificity protein phosphatase family protein.	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 >UNIPROT P15976 symbol:GAT1: human erythroid transcription factor.	1.20913E-21, 14602571 GATA1 protein [<i>Homo sapiens</i>].	0.05, Arabidopsis, TIGR GDSL-motif lipase.	0.05, Cryptococcus, TIGR expressed protein.
Link1 Link2 >tr Q8VI44: mouse flightless I homolog (<i>Drosophila</i>) Cytoskeletal actin-modulating.	1.3435E-28, 4503743 flightless I homolog [<i>Homo sapiens</i>].	0.00114528, 37783214 resistance candidate RPP8-like protein [<i>Arabidopsis lyrata</i>].	0.05, Cryptococcus, TIGR putative adenylate cyclase.
Link1 Link2	3.75869E-23, 72239	0.05, Arabidopsis, TIGR	0.05, Cryptococcus, TIGR

>UNIPROT P14653 symbol:HXB1: human Homeobox protein Hox-B1.	homeotic protein Hox B1 - human.	zinc finger (CCCH-type) family protein.	hypothetical protein.
Link1 Link2 >UNIPROT P50221 symbol:MOX1: human Homeobox protein MOX-1.	1.38022E-25, 7710150 mesenchyme homeo box 1 isoform 2 [<i>Homo sapiens</i>].	0.05, Arabidopsis , TIGR hydroxyproline-rich glycoprotein family protein.	0.05, Cryptococcus , TIGR hypothetical protein.
Link1 Link2 : <i>Arabidopsis</i> abnormal inflorescence meristem 1 / fatty acid multifunctional protein (AIM1).	0.00568511, 50752176 predicted protein similar to enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase [<i>Gallus gallus</i>].	2.80193E-26, 20465649 putative AIM1 protein [<i>Arabidopsis thaliana</i>].	0.05, Cryptococcus , TIGR putative enoyl-CoA hydratase.
Link1 Link2 >UNIPROT Q9UGM4 symbol:Q9UGM4: human nuclear LIM interactor [fragment].	4.02113E-25, 34863521 similar to Ldb1a [<i>Rattus norvegicus</i>].	0.05, Arabidopsis , TIGR hydroxyproline-rich glycoprotein family protein similar to extension.	0.05, Cryptococcus , TIGR hypothetical protein.

The ‘seven in absentia’ (SINA) protein family has a more mixed distribution. SINA was originally discovered as a RING zinc finger-containing protein that is critically involved in development of the R7 photoreceptor cell in the *Drosophila* eye. The RING zinc finger domain (originally named for the acronym *really interesting new gene*) is a protein interaction domain consisting of two pairs of zinc ligands co-ordinately binding two zinc ions, which is implicated in a range of processes from transcriptional regulation to targeted proteolysis. Mammalian SINA homologues can act in the ubiquitin/proteasome pathway and plant (*Arabidopsis*) homologues are essential to seed (and embryo) development. The RING-finger domain is one of the most frequently detected domains in the *Arabidopsis* proteome, and is more abundant in *Arabidopsis* than in other eukaryotic genomes (Kosarev *et al.*, 2002).

No similarity in metazoan or fungal genomes can be detected for eight of the *Arabidopsis* SINA proteins (Table 2), but high levels of similarity (*E*-values less than 10^{-28}) were returned for four other *Arabidopsis* SINA proteins (Table 5), and the mouse *siah2* protein showed moderate homology with a protein from the green alga *Spermatozopsis* (*E*-value = 9.6×10^{-3}) and a predicted protein of *Neurospora crassa* (*E*-value = 5.6×10^{-3}) (Table 5). It is significant that 16 mammalian p53 protein sequences (Table 5) showed very high similarity (*E*-values less than 10^{-100}) with a protein from the *Zea mays* genome in view of the suggestion that SINA proteins may mediate p53-dependent cell-cycle arrest in man (Matsuzawa *et al.*, 1998). Eight of the mammalian p53 sequences failed to detect similarity with fungal genomes, although the sequences from African green monkey, Chinese hamster, rhesus monkey, tree shrew and woodchuck all showed complete homology (*E*-value = 0) with a predicted mRNA reported from the *Ustilago maydis* genome, whilst gerbil, porcine and guinea pig sequences were weakly similar (*E*-value reported as <0.05) to sequences in the *Phanerochaete* genome (Table 6).

Only three of the other plant development sequences from AmiGO retrieved highly similar sequences from the fungal genomes (Table 3); namely, the phosphoribosylanthranilate isomerase of *Arabidopsis thaliana* which is similar to the TRP-F sequence of *Candida glabrata* (*E*-value = 1.2×10^{-21}); a putative oxidoreductase of *Arabidopsis* that is highly similar to a putative dehydrogenase/reductase of *Aspergillus fumigatus* (*E*-value = 7×10^{-18}); and a hypothetical protein of *Arabidopsis* highly similar (with an *E*-value = 6.3×10^{-10}) to the

mybC transcription factor of *Dictyostelium* and to a hypothetical protein of *Candida albicans* (E -value = 4.8×10^{-10}). All other plant-fungus similarities were returned with E -value reported as 0.05, which corresponds to a weak similarity that is probably not significant.

Apart from the SINA and p53 homologies already noted above, very low E -values in other animal-plant similarities (Table 5) were limited to two sialyltransferases (E -value reported as zero), a cytosine methyl transferase (E -value = 4.8×10^{-9}), a transcription factor (E -value = 9.9×10^{-16}), a transcriptional co-activator (E -value = 2.5×10^{-3}), a receptor protein (E -value = 5.6×10^{-3}) and a homeobox domain protein (E -value = 2.8×10^{-2}). All other animal-plant comparisons returned E -values of 0.05 (Table 5).

Table 5. Animal-Plant similarities found

Table 5. Animal-Plant similarities found			
Entries under 'genome hit' show E -value as returned by the sequence comparison software: a reference to the specific database entry and brief descriptive annotation. NOTE that small E -values are shown as exponential functions, i.e. $1.217E-29 = 1.217 \times 10^{-29}$			
AmiGO description and hyperlinks USE Link2	Metazoan genome hit	Viridiplantae genome hit	Fungi genome hit
Link1 Link2 Bovine beta-galactoside alpha-2,6-sialyltransferase (integral membrane protein).	0.0, 29135323 Bovine beta-galactoside alpha-2,6-sialyltransferase (integral membrane protein).	0.0, Plants, dna : predicted mRNA of rice.	no hits returned
Link1 Link2 Chick CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,6-sialyltransferase.	0.0, 45382551 Chick CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,6-sialyltransferase.	0.0, Plants, dna APG5 (autophagy 5)-like protein of <i>Oryza sativa</i> .	no hits returned
Link Tair AT1G66650.1 "seven in absentia" (SINA) family protein, located in nucleus. The protein has DNA binding site.	1.06813E-17, 54641564 unnamed gene product of <i>Drosophila pseudoobscura</i> .	0.0, 12597767 hypothetical protein of <i>Arabidopsis</i> .	no hits returned
Link1 Link2 Rabbit cellular tumour antigen p53 (cell cycle regulator).	0.0, 2842741 Rabbit cellular tumour antigen p53 (tumour suppressor p53).	7.13805E-115, 48374980 putative tumour protein p53 of <i>Zea mays</i> .	no hits returned
Link1 Link2 Beluga whale P53 protein.	0.0, 18997097 Beluga whale P53 protein.	5.58669E-112, 48374980 as above.	no hits returned
Link1 Link2 : feline cellular tumour antigen p53.	0.0, 538225 feline p53 tumour-suppressor gene.	2.10835E-111, 48374980 putative tumour protein p53 of <i>Zea mays</i> .	no hits returned
Link1 Link2 Canine cellular tumour antigen p53.	0.0, 50978974 Canine cellular tumour antigen p53.	4.60588E-111, 48374980 as above.	no hits returned
Link1 Link2 Pig P53 protein.	0.0, 50979299 Pig P53 protein.	2.05624E-106, 48374980 as above.	no hits returned
Link1 Link2 Sheep cellular tumour antigen p53.	0.0, 1709531 Sheep cellular tumour antigen p53.	5.84948E-106, 48374980 as above.	no hits returned
Link1 Link2 rodent P53 [fragment]	0.0, 56829 rat unnamed protein product.	1.2865E-105, 48374980 putative tumor protein p53 [<i>Zea mays</i>].	no hits returned
Link1 Link2 mouse tumour suppressor p53.	0.0, 2961247 mouse tumour suppressor p53.	1.64813E-103, 48374980 putative tumour protein p53 of <i>Zea mays</i> .	no hits returned
Link1 Link2 >67845.m00016: manatee seven in absentia protein.	7.66585E-8, 41054792 Zebrafish seven in absentia protein.	1.09927E-30, 26449935 putative ring finger E3 ligase SINAT5	no hits returned

		[<i>Arabidopsis thaliana</i>].	
Link1 Link2 >60737.m00067: putative seven in absentia (SINA) protein of <i>Arabidopsis</i> .	0.0282149, 29293702 SINA protein of <i>Schistosoma mansoni</i> .	3.53623E-29, 33589720 product of ORF At1g66660/F4N21_20 of <i>Arabidopsis thaliana</i> .	no hits returned
Link1 Link2 >67733.m00007 : seven in absentia (SINA) family protein of <i>Arabidopsis</i> .	0.00435293, 31207365 protein of <i>Anopheles gambiae</i> .	6.66905E-28, 9758491 unnamed protein product of <i>Arabidopsis thaliana</i> .	no hits returned
Link1 Link2 >UNIPROT Q9Y6A4: human transcription factor IIB.	1.58126E-21, 55643953 predicted hypothetical protein XP_511001 of <i>Pan troglodytes</i> .	9.9274E-16, 15795151 unnamed protein product [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 : human DNA (cytosine-5)-methyltransferase 3B	0.0, 5901940 DNA cytosine-5 methyltransferase 3 beta isoform 1 [<i>Homo sapiens</i>].	4.78271E-9, 29467228 DNA methyltransferase [<i>Nicotiana tabacum</i>].	no hits returned
Link1 Link2 >UNIPROT Q8VI44 mouse flightless I protein homolog (possible coactivator in transcriptional activation).	4.9155E-23, 4503743 human flightless I protein homolog.	0.00253626, 37783214 resistance candidate RPP8-like protein [<i>Arabidopsis lyrata</i>].	no hits returned
Link1 Link2 >UNIPROT P25100 symbol:A1AD, human alpha-1D adrenergic receptor.	7.08714E-22, 4501957 human alpha-1D adrenergic receptor.	0.00564159, 15081245 glycine-rich protein GRP16 of <i>Arabidopsis</i> .	no hits returned
Link1 Link2 >UNIPROT P31310 symbol:HXAA: Homeobox protein Hox-A10 of mouse.	1.4283E-22, 6680243 Homeobox protein Hox-A10 of mouse.	0.0280046, 42391853 cold shock domain protein 2 of <i>Triticum aestivum</i> .	no hits returned
Link1 Link2 >UNIPROT P52926 symbol: human high mobility group protein HMGI-C.	1.09361E-22, 4504431 high mobility group AT-hook 2 isoform a [<i>Homo sapiens</i>].	0.0477686, 50933035 AT1 protein of rice.	no hits returned
Link1 Link2 >UNIPROT Q9NQZ9 symbol: human TCP11 protein (receptor of fertilization promoting peptide).	1.09506E-22, 54887320 human TCP11 protein.	0.05, Arabidopsis , TIGR T-complex protein 11 of <i>Arabidopsis</i> .	no hits returned
Link1 Link2 Zebrafish Wnt-4a protein precursor.	0.0, 18859563 Zebrafish Wnt-4a protein	0.05, Arabidopsis , TIGR putative ubiquitin-specific protease 1 of <i>Arabidopsis</i> .	no hits returned
Link1 Link2 >tr Q8R002 C1qtnf5 protein: mouse C1q and tumor necrosis factor related protein 5 (transmembrane receptor).	4.17638E-30, 26024327 mouse C1q and tumor necrosis factor related protein 5.	0.05, Arabidopsis , TIGR proline-rich family protein with proline rich extensin domains.	no hits returned
Link1 Link2 >UNIPROT P17483 symbol: HXB4: human homeobox protein Hox-B4.	9.8913E-24, 13273315 homeo box B4 [<i>Homo sapiens</i>].	0.05, Arabidopsis , TIGR mitochondrial transcription termination factor-related protein of <i>Arabidopsis</i> .	no hits returned
Link1 Link2 >tr Q8K5B8 HOXC12: Mouse homeo box C12.	8.41682E-31, 33859568 Mouse homeo box C12.	0.05, Arabidopsis , TIGR expressed protein identical to ORF1 [<i>Arabidopsis</i>	no hits returned

		<i>thaliana</i>].	
Link1 Link2 >UNIPROT Q96PN7 symbol:Q96PN7 human Zinc finger transcription factor TReP-132.	5.80651E-24, 15812226 transcriptional regulating factor 1 isoform 1 [<i>Homo sapiens</i>].	0.05, Arabidopsis, TIGR Rho GDP-dissociation inhibitor family protein [<i>Arabidopsis thaliana</i>].	no hits returned
Link1 Link2 >UNIPROT O00192 symbol:ARVC: human armadillo repeat protein deleted in velo-cardio- facial syndrome.	2.27986E-20, 4502247 human armadillo repeat protein.	0.05, Arabidopsis, TIGR expressed protein of <i>Arabidopsis</i> .	no hits returned
Link1 Link2 >UNIPROT P48281 symbol:VDR: mouse Vitamin D3 receptor.	1.99567E-24, 1352836 mouse Vitamin D3 receptor.	0.05, Arabidopsis, TIGR zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, of <i>Arabidopsis</i> .	no hits returned
Link1 Link2 >tr Q8C145 mouse solute carrier family 39 (metal ion transporter) protein.	1.48571E-27, 32822909 mouse Slc39a6 protein.	0.05, Arabidopsis, TIGR expressed protein of <i>Arabidopsis</i> .	no hits returned
Link1 Link2 >UNIPROT P30968 symbol:GRHR: human gonadotropin-releasing hormone receptor.	4.59468E-21, 1628390 human gonadotropin- releasing hormone receptor.	0.05, Arabidopsis, TIGR expressed protein of <i>Arabidopsis</i> .	no hits returned
Link1 Link2 Progonadoliberin I precursor of <i>Haplochromis</i> (= <i>Astatotilapia burtoni</i>).	1.2395E-50, 6226866 Progonadoliberin I precursor of <i>Astatotilapia burtoni</i> .	0.05, Arabidopsis, TIGR hypothetical protein of <i>Arabidopsis</i> .	no hits returned
Link1 Link2 >UNIPROT P13562 symbol:GON1: mouse progonadoliberin I precursor.	1.86542E-22, 51093849 gonadotropin releasing hormone [<i>Mus musculus</i>].	0.05, Arabidopsis, TIGR putative plastid developmental protein DAG (required for chloroplast differentiation).	no hits returned
Link1 Link2 Progonadoliberin I precursor of Japanese rice fish.	1.92893E-48, 34098705 Progonadoliberin I precursor of Japanese rice fish.	0.05, Arabidopsis, TIGR expressed protein with weak similarity to a bacterial urease accessory protein.	no hits returned

Table 6. Animal – fungus similarities found

<p>Entries under ‘genome hit’ show <i>E</i>-value as returned by the sequence comparison software: a reference to the specific database entry and brief descriptive annotation. NOTE that small <i>E</i>-values are shown as exponential functions, i.e. $1.217E-29 = 1.217 \times 10^{-29}$</p>			
AmiGO description and hyperlinks USE Link2	Metazoan genome hit	Viridiplantae genome hit	Fungi genome hit
Link1 Link2 >MGI MGI:101791 symbol: ISL1: mouse transcription factor, LIM/homeodomain (islet 1); may regulate insulin gene expression or islet	6.84994E-25, 8393633 ISL1 transcription factor, LIM/homeodomain 1 (<i>Rattus norvegicus</i>).	no hits returned	0.0, Fungi, dna <i>Ustilago maydis</i> 521, UM05343.1 predicted mRNA.

cell development.			
Link1 Link2 >DDB0185218 Protein locus: ifkA: <i>Dictyostelium</i> initiation factor 2 alpha (eIF2alpha) kinase.	0.00969732, 42733663 <i>Dictyostelium</i> initiation factor 2 alpha (eIF2alpha) kinase.	no hits returned	6.66905E-28, 28828088 <i>Dictyostelium</i> protein similar to Gcn2p of <i>Saccharomyces cerevisiae</i> .
Link1 Link2 >UNIPROT Q9Y3R5 symbol:CU05: human Protein C21orf5 ortholog of a <i>Caenorhabditis</i> <i>elegans</i> gene (pad-1) required for embryonic patterning.	7.83735E-21, 45827701 pad-1-like [<i>Homo sapiens</i>].	no hits returned	1.58651E-5, 46100006 hypothetical protein UM04150.1 of <i>Ustilago</i> <i>maydis</i> .
Link1 Link2 : Zebrafish nuclear respiratory factor 1.	0.0, 16200181 nuclear respiratory factor 1 [<i>Danio</i> <i>rerio</i>].	no hits returned	0.00121777, 46444519 hypothetical protein, potential cell surface flocculin of <i>Candida</i> <i>albicans</i> .
Link1 Link2 >DDB0191136 Protein locus: abpD: <i>Dictyostelium</i> actin binding protein; developmentally and cAMP-regulated; associates with intracellular membranes.	1.35288E-4, 39592126 Hypothetical protein CBG23326 [<i>Caenorhabditis briggsae</i>].	no hits returned	0.00195355, 38110842 hypothetical protein MG06475.4 [<i>Magnaporthe</i> <i>grisea</i>].
Link1 Link2 >UNIPROT O94761 symbol:RCQ4: human ATP-dependent DNA helicase Q4.	1.21073E-21, 4759030 RecQ protein-like 4 [<i>Homo</i> <i>sapiens</i>].	no hits returned	0.00565021, 45185185 hypothetical protein from <i>Eremothecium</i> (<i>Ashbya</i>) <i>gossypii</i> .
Link1 Link2 >UNIPROT O95376 symbol:ARI2: human Ariadne-2 protein homolog; might act as an ubiquitin-protein ligase.	4.908E-23, 5453557 ariadne homolog 2 [<i>Homo</i> <i>sapiens</i>].	no hits returned	0.00736814, 42546808 hypothetical protein FG00241.1 of <i>Gibberella</i> <i>zeae</i> PH-1 [anamorph = <i>Fusarium graminearum</i>].
Link 1 Link 2 >: Nrf1 protein, responsible for the mutation, named “Not really finished” which is crucial for development of the zebrafish outer retina.	0.0, 27881974 nuclear respiratory factor 1 protein of Zebra fish; transcription factor.	no hits returned	0.0180559, 46444519 hypothetical protein, potential cell surface flocculin of <i>Candida</i> <i>albicans</i> .
Link1 Link2 >UNIPROT P29762 symbol:RET3: human cellular retinoic acid- binding protein.	1.58126E-21, 4758052 Human cellular retinoic acid-binding protein.	no hits returned	0.05, Cryptococcus , TIGR putative glutathione transferase
Link1 Link2 >MGI MGI:97712 symbol:Prrx1: mouse	2.69366E-21, 5902024 paired mesoderm homeobox 1 isoform pmx-	no hits returned	0.05, Cryptococcus , TIGR conserved hypothetical protein

paired related homeobox 1.	1a [<i>Homo sapiens</i>].		
Link1 Link2 >UNIPROT Q9VB08 symbol:RNG1: <i>Drosophila melanogaster</i> polycomb complex protein Sce.	3.18614E-22, 7301619 <i>D. melanogaster</i> Polycomb group (PcG) protein.	no hits returned	0.05, Cryptococcus , TIGR conserved hypothetical protein
Link1 Link2 >UNIPROT O95285 symbol:O95285: human erythroblast macrophage protein EMP.	2.69366E-21, 5031685 human macrophage erythroblast attacher.	no hits returned	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 >UNIPROT Q02386 symbol:ZN45: human zinc finger protein 45.	3.89479E-20, 4508029 zinc finger protein 45 [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus , TIGR conserved hypothetical protein
Link1 Link2 : mouse transcription factor TFEC.	8.41682E-31, 13654264 transcription factor EC [<i>Mus musculus</i>].	no hits returned	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 >UNIPROT P80370 symbol:DLK: human Delta-like protein precursor (type I membrane protein).	8.9463E-25, 21361080 delta-like homolog (<i>Drosophila</i>), EGF-like, type I membrane protein.	no hits returned	0.05, Cryptococcus , TIGR expressed protein
Link1 Link2 >UNIPROT O14682 symbol:ENC1: human ectoderm-neural cortex-1 protein.	2.28032E-20, 4505461 ectodermal-neural cortex 1 protein; nuclear matrix- associated, actin binding protein [<i>Homo sapiens</i>].	no hits returned	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 >UNIPROT P92189 symbol:STIL: <i>Drosophila</i> stand still protein.	1.29184E-23, 7303433 stand still protein (<i>Drosophila</i>) nuclear, participates in transcriptional activation.	no hits returned	0.05, Cryptococcus , TIGR putative oxidoreductase,
Link1 Link2 >tr Q925K0: mouse peroxisome proliferator-activated receptor binding protein...	5.64569E-27, 14193715 mouse peroxisome proliferator-activated receptor binding protein.	no hits returned	0.05, Cryptococcus , TIGR putative nuclear mRNA splicing, spliceosome- related protein.
Link1 Link2 >tr Q6AXE6: mouse LIM domain binding 2. LIM- homeodomain gene expressed in the developing forebrain.	2.21496E-31, 4504971 LIM domain binding 2 [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus , TIGR putative phospholipase.
Link1 Link2 >UNIPROT P20719 symbol:HXA5: human homeobox protein Hox-A5. DNA-binding transcription	8.9463E-25, 24497517 homeobox protein A5 - HOXA5 [<i>Homo sapiens</i>].	no hits returned	<0.05 Phanerochaete genomic homology (not annotated).

factor which provides cells with specific positional identities on the anterior-posterior axis.			
Link1 Link2 >UNIPROT P09629 symbol:HXB7: human HOXB7, one of the homeobox genes that provide cells with specific positional identities on the anterior-posterior axis.	7.08858E-22, 25121963 homeo box B7 [<i>Homo sapiens</i>].	no hits returned	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 >UNIPROT P17481 symbol:HXB8: human HOXB8, one of the homeobox genes that provide cells with specific positional identities on the anterior-posterior axis.	1.6872E-23, 13273317 homeo box B8 [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus , TIGR expressed protein.
Link1 Link2 >UNIPROT Q8VDQ7 symbol:Q8VDQ7: mouse Ppar binding protein, isoform 2.	1.57917E-21, 14193715 peroxisome proliferator-activated receptor binding protein [<i>Mus musculus</i>].	no hits returned	0.05, Cryptococcus , TIGR putative nuclear mRNA splicing, via spliceosome-related protein.
Link1 Link2 >MGI MGI:108063 symbol:Siah1b: mouse seven in absentia 1B. The sina protein contains a putative zinc finger domain and localises to the cell nucleus in <i>Drosophila</i> .	3.18614E-22, 6677949 seven in absentia 1B [<i>Mus musculus</i>]	no hits returned	0.05, Cryptococcus , TIGR conserved hypothetical protein
Link1 Link2 >MGI MGI:108064 symbol:Siah1a: mouse seven in absentia homolog 1, isoform a.	1.09506E-22, 23274142 Seven in absentia homolog 1, isoform a [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus , TIGR as above.
Link1 Link2 >UNIPROT Q04900 symbol:MG24: human putative mucin core protein 24 precursor. Membrane glycoprotein with peanut agglutinin binding sites.	4.59468E-21, 219925 MGC-24 precursor [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus , TIGR expressed protein.
Link1 Link2 >UNIPROT P10244 symbol:MYBB: human MYB-related protein B, transcription factor involved in cell cycle progression.	2.20355E-23, 4505293 MYB-related protein B [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus , TIGR putative (NADP+) glutamate dehydrogenase.

Link1 Link2 >UNIPROT Q16621 symbol:NFE2: human Transcription factor NF- E2 45 kDa subunit.	5.42754E-22, 13477165 NFE2 protein [<i>Homo sapiens</i>].	no hits returned	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 >UNIPROT P91660 symbol:L259: <i>Drosophila</i> Probable multidrug resistance-associated protein lethal(2)03659.	1.4283E-22, 45445626 Integral membrane protein vital for development of <i>Drosophila melanogaster</i>	no hits returned	0.05, Cryptococcus , TIGR putative branched-chain alpha-keto acid dehydrogenase E1-alpha subunit.
Link1 Link2 >UNIPROT Q9W1A4 symbol:TAMO: <i>Drosophila</i> tamozhennic protein (modulates the nuclear import of other proteins).	1.68943E-23, 21626728 CG4057-PB, isoform B [<i>Drosophila melanogaster</i>]	no hits returned	0.05, Cryptococcus , TIGR putative adaptation to pheromone during conjugation with cellular fusion-related protein.
Link 1 Link 2 Link 3 >zfin, tr Q9DE50 Zebra fish Platelet-derived growth factor alpha polypeptide. Growth factor activity. Membrane protein.	1.08506E-111, 35903201 platelet-derived growth factor alpha polypeptide of Zebra fish.	no hits returned	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 >UNIPROT Q03014 symbol:HMPH: human Homeobox protein PRH.	3.39959E-24, 4506049 hematopoietically expressed homeobox transcription factor [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus , TIGR hypothetical protein.
Link1 Link2 >UNIPROT Q9Y5L5 symbol:L503: human lens epithelial cell protein LEP503. DNA-binding protein expressed exclusively in lens epithelial cells and may play a role in cell differentiation.	1.86542E-22, 8923830 lens epithelial protein [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus , TIGR expressed protein.
Link1 Link2 >UNIPROT Q15116 symbol:PCD1: human programmed cell death protein 1 precursor. Encodes cell surface membrane protein, induced at programmed cell death.	8.09159E-26, 4826890 programmed cell death 1 precursor [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus , TIGR hypothetical protein.
Link1 Link2 >UNIPROT Q00587 symbol:MSE5: human CDC42 effector protein 1. A member of the Rho	6.41135E-23, 23238226 CDC42 effector protein 1 isoform a [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus , TIGR putative vesicular-fusion protein.

GTPase family; a CDC42 binding protein that mediates actin cytoskeleton reorganization at the plasma membrane.			
Link1 Link2 >UNIPROT P14652 symbol:HXB2: human homeobox protein Hox-B2.	5.42754E-22, 4504465 homeo box B2 transcription factor [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus , TIGR putative Rho small monomeric GTPase.
Link1 Link2 >FB FBgn0010340 symbol:140up: <i>D. melanogaster</i> gene 'upstream of RpII140', abbreviated as 140up (may have protein transporter activity and be component of mitochondrial inner membrane).	4.15487E-22, 7299846 CG9852 [<i>Drosophila melanogaster</i>].	no hits returned	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >UNIPROT P32242 symbol:OTX1: human homeobox protein OTX1; encodes a member of the bicoid sub-family of transcription factors.	1.09361E-22, 20070107 orthodenticle 1 [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus , TIGR putative polyadenylate-binding protein.
Link1 Link2 >MGI MGI:1194883 symbol:Crx: cone-rod homeobox containing gene (transcription factor).	2.43582E-22, 6681029 cone-rod homeobox containing gene [<i>Mus musculus</i>].	no hits returned	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >UNIPROT P05549 symbol:AP2A: human transcription factor AP-2 alpha.	4.4391E-24, 31981462 transcription factor AP-2, alpha [<i>Mus musculus</i>].	no hits returned	0.05, Cryptococcus , TIGR putative chromatin modification-related protein.
Link1 Link2 >UNIPROT P11309 symbol:PIM1: human Proto-oncogene serine/threonine-protein kinase Pim-1.	5.42754E-22, 4505811 pim-1 oncogene [<i>Homo sapiens</i>].	no hits returned	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 >MGI MGI:1888519 symbol:Lmx1a: mouse LIM homeobox transcription factor 1 alpha; lmx-1 is a homeobox containing mRNA, the protein encoded also contains two amino-terminal cysteine/histidine-rich	2.28032E-20, 587461 hamster LIM homeobox transcription factor 1 alpha [<i>Mesocricetus auratus</i>].	no hits returned	<0.05 Phanerochaete genomic homology (not annotated).

"LIM" domains.			
Link1 Link2 >UNIPROT P48357 symbol:LEPR: human leptin receptor precursor (receptor for obesity factor (leptin); on ligand binding, mediates signaling).	5.24482E-25, 1589772 leptin receptor [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >MGI MGI:88005 symbol:Amelx: mouse amelogenin X chromosome (amelogenin is the major enamel protein).	6.41005E-23, 9506381 amelogenin X chromosome [<i>Rattus norvegicus</i>].	no hits returned	0.05, Cryptococcus , TIGR hypothetical protein.
Link1 Link2 >UNIPROT P07333 symbol:KFMS: human macrophage colony stimulating factor I receptor precursor (CSF-1-R)(a tyrosine-kinase transmembrane receptor).	1.86542E-22, 27262659 colony stimulating factor 1 receptor precursor [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 >UNIPROT P25116 symbol:PAR1: human proteinase activated receptor 1 precursor; belongs to the G-protein coupled receptor 1 family.	1.20913E-21, 30354672 Coagulation factor II receptor, precursor [<i>Homo sapiens</i>].	no hits returned	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 >UNIPROT P07996 symbol:TSP1: human thrombospondin-1 precursor (subunit of a disulfide-linked homotrimeric adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions).	2.43954E-22, 40317626 thrombospondin 1 precursor [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus , TIGR putative chromatin assembly complex protein.
Link1 Link2 >tr Q9R0A6: mouse T-box 21 transcription factor.	1.09927E-30, 9507179 T-box 21 transcription factor [<i>Mus musculus</i>].	no hits returned	0.05, Cryptococcus , TIGR expressed protein.
Link1 Link2 >UNIPROT P01344 symbol:IGF2: human insulin-like growth factor II precursor; potent mitogen for cultured cells.	1.4283E-22, 30582865 insulin-like growth factor 2 (IGF2) [<i>Homo sapiens</i>].	no hits returned	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 >UNIPROT Q04743 symbol:EMX2: human homeobox protein EMX2 (critical for central	5.42754E-22, 14149611 homeodomain transcription factor EMX2 [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus , TIGR conserved hypothetical protein.

nervous system and urogenital development).			
Link1 Link2 >UNIPROT P53539 symbol:FOSB: human protein fosB; interacts with Jun proteins enhancing their DNA binding activity.	5.42754E-22, 54673701 Protein fosB [<i>Homo sapiens</i>].	no hits returned	0.05, Aspergillus, TIGR putative bZIP transcription factor (AtfA) of <i>Aspergillus fumigatus</i> .
Link1 Link2 >UNIPROT Q04724 symbol:TLE1: human transducin-like enhancer protein 1 (transcriptional corepressor that binds to a number of transcription factors).	4.9155E-23, 34869030 similar to groucho protein GRG1-LDLZ2; Grg1-LDLZ2 [<i>Rattus norvegicus</i>] (record removed from further distribution at submitter's request).	no hits returned	0.05, Cryptococcus, TIGR putative kinesin family member 21A.
Link1 Link2 >UNIPROT P08151 symbol:GLI1: human Zinc finger protein GLI1; may regulate transcription.	1.52601E-24, 4885279 glioma-associated oncogene homolog 1 [<i>Homo sapiens</i>].	no hits returned	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 >UNIPROT P17097 symbol:ZN07: human Zinc finger protein 7; possible transcription factor.	3.18614E-22, 37590636 Zinc finger protein 7.	no hits returned	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 >UNIPROT P50222 symbol:MOX2: human homeobox protein MOX-2 with a role in mesoderm induction and its earliest regional specification.	8.37349E-23, 8393773 mesenchyme homeo box 2 [<i>Rattus norvegicus</i>].	no hits returned	0.05, Cryptococcus, TIGR putative tRNA binding protein.
Link1 Link2 >UNIPROT Q15699 symbol:CRT1: human cartilage homeoprotein 1; possible transcription repressor.	3.18128E-22, 55638599 predicted protein similar to cartilage paired-class homeoprotein 1 [<i>Pan troglodytes</i>].	no hits returned	0.05, Cryptococcus, TIGR hypothetical protein.
Link1 Link2 >UNIPROT P04637 symbol:P53: human cellular tumour antigen p53; involved in cell cycle regulation..	3.18192E-22, 35214 protein p53 [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus, TIGR putative sterol metabolism-related protein.
Link1 Link2 >UNIPROT P10361 symbol:P53: rat cellular tumour antigen p53.	2.43631E-22, 56829 unnamed protein product [<i>Rattus norvegicus</i>].	no hits returned	0.05, Cryptococcus, TIGR putative F-actin capping protein.
Link1 Link2 : flounder gonadotropin releasing	6.88528E-46, 18253176 salmon-type gonadotropin-	no hits returned	<0.05 Phanerochaete genomic homology (not

hormone precursor.	releasing hormone precursor [<i>Verasper moseri</i>].		annotated).
Link1 Link2 >UNIPROT P10071 symbol:GLI3: human Zinc finger protein GLI3.	1.33685E-20, 51094755 GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus , TIGR conserved hypothetical protein.
Link1 Link2 : Japanese rice fish progonadoliberin III precursor.	4.46291E-45, 34098704 gonadotropin releasing hormone precursor (Japanese rice fish).	no hits returned	0.05, Cryptococcus , TIGR hypothetical protein.
Link1 Link2 >tr O88728: mouse interferon induced transmembrane protein 5.	2.07314E-29, 33504579 haemopoiesis related membrane protein 1 [<i>Mus musculus</i>].	no hits returned	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 >tr Q8BM71: mouse integrin beta 8.	2.9936E-28, 26330087 unnamed protein product [<i>Mus musculus</i>].	no hits returned	<0.05 Phanerochaete genomic homology (not annotated).
Link1 Link2 >UNIPROT P10072 symbol:HKR1: human Krueppel-related zinc finger protein 1 (HKR1), transcription factor.	1.57917E-21, 6177785 HKR1 [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus , TIGR hypothetical protein.
Link1 Link2 >UNIPROT Q9HD85 symbol:Q9HD85: Human haematopoietic PBX-interacting protein (transcription corepressor).	2.43954E-22, 19923830 pre-B-cell leukemia transcription factor interacting protein 1 [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus , TIGR hypothetical protein.
Link1 Link2 >UNIPROT Q9Y5Y0 symbol:FVR1: human feline leukemia virus subgroup C receptor-related protein 1.	8.37349E-23, 7661708 feline leukemia virus subgroup C cellular receptor [<i>Homo sapiens</i>].	no hits returned	0.05, Cryptococcus , TIGR hypothetical protein.
Link1 Link2 >UNIPROT Q9Y458 symbol:TX22: Human T-box transcription factor TBX22.	5.08675E-20, 18375603 Human T-box transcription factor TBX22.	no hits returned	0.05, Cryptococcus , TIGR putative 30S ribosomal protein S17.
Link1 Link2 >UNIPROT O75093 symbol:SLT1: Human Slit-1; cue for cellular migration.	3.07887E-25, 55634425 chimpanzee homolog of Slit-1.	no hits returned	0.05, Cryptococcus , TIGR hypothetical protein.
Link1 Link2 >UNIPROT P00734 symbol:THRB: human	4.60077E-21, 4503635 human prothrombin precursor (coagulation	no hits returned	<0.05 Phanerochaete genomic homology (not annotated).

prothrombin precursor (coagulation factor II).	factor II).		
Link1 Link2 >UNIPROT P09919 symbol:CSF3: human granulocyte colony-stimulating factor precursor.	7.08858E-22, 27437049 human CSF1.	no hits returned	0.05, Cryptococcus , TIGR expressed protein.
Link1 Link2 >tr Q6PCS0 Itgb4 protein (Fragment): mouse integrin beta 4.	3.30981E-27, 6981108 rat integrin beta 4.	no hits returned	0.05, Cryptococcus , TIGR expressed protein.
Link1 Link2 >UNIPROT Q04741 symbol:EMX1: human homeobox protein EMX1.	4.01582E-25, 45598369 human homeobox protein EMX1.	no hits returned	<0.05 Phanerochaete genomic homology (not annotated).

Generally weak similarities were encountered in comparisons between animal developmental sequences and fungus genomes (Table 6); only six were sufficiently similar to be notable. A predicted mRNA from the *Ustilago maydis* genome proved to be homologous (E -value = 0) to the ISL1 mouse transcription factor, and a hypothetical protein of *U. maydis* was very similar (E -value = 1.6×10^{-5}) to the human ortholog of the *pad-1* gene of *Caenorhabditis elegans* which is required for embryonic patterning. E -values in the region of 10^{-3} were returned to a Zebrafish nuclear respiratory factor (compared with a potential cell surface flocculin of *Candida albicans*), a *Dictyostelium* actin binding protein (compared with a hypothetical protein of *Magnaporthe grisea*), a human ATP-dependent DNA helicase (compared with a hypothetical protein from *Eremothecium (Ashbya) gossypii*), and a human Ariadne-2 protein homolog (compared with a hypothetical protein of *Gibberella zeae* [anamorph = *Fusarium graminearum*]). E -values of 0.05 were returned for all other fungus-animal comparisons, and these are not considered significant (Table 6). The same applies to four *Dictyostelium* sequences which failed to retrieve any similarities in either Metazoa or Viridiplantae, but were just detectable in fungal genomes (Table 7). One, a putative GATA-binding transcription factor of *Dictyostelium* was marginally similar to a hypothetical protein of *Gibberella zeae* (E -value = 2.8×10^{-2}), but the other three (two transcription regulators and an adhesion modulator) returned similarities with E -values of 0.05 in *Cryptococcus* and *Phanerochaete* respectively.

Table 7. Similarities found between *Dictyostelium* sequences and fungal genomes

Entries under 'genome hit' show E -value as returned by the sequence comparison software: a reference to the specific database entry and brief descriptive annotation. NOTE that small E -values are shown as exponential functions, i.e. $1.217E-29 = 1.217 \times 10^{-29}$			
AmiGO description and hyperlinks USE Link2	Metazoan genome hit	Viridiplantae genome hit	Fungi genome hit
Link1 Link2 >DDB0214839 [Protein] locus: comH: putative GATA-binding transcription factor of	no hits returned	no hits returned	0.0282092, 42550593 Hypothetical protein FG03968.1 from <i>Gibberella zeae</i> .

<i>Dictyostelium.</i>			
Link1 Link2 >DDB0215388 [Protein] locus: dstA: signal transducer and activator of transcription (STAT) family protein of <i>Dictyostelium.</i>	no hits returned	no hits returned	0.05, Cryptococcus, TIGR putative heat shock transcription factor 2.
Link1 Link2 >DDB0191361 [Protein] locus: gbfA: G-box binding transcription factor of <i>Dictyostelium.</i>	no hits returned	no hits returned	0.05, Cryptococcus, TIGR expressed protein.
Link1 Link2 >DDB0185088 [Protein] locus: ampA: adhesion modulation protein A of <i>Dictyostelium.</i>	no hits returned	no hits returned	<0.05 Phanerochaete genomic homology (not annotated).

Overall conclusions

Our purpose was to establish whether sequences reported to be involved in development in animals or plants could be found in fungal genomes. Overall, some similarity was indicated by the comparison software for a total of 219 sequences from fungal genomes, but 143 (65%) of these returned matches were assigned *E*-values of 0.05. This level of similarity corresponds approximately to a probability of one in fewer than 20 of finding the match purely by chance, and we believe this to be too low a level of similarity for much significance to be assigned to it. The highly similar matches found in this survey between sequences labelled as being concerned in animal or plant development and fungal genomes proved to be involved in basic cell metabolism or essential eukaryotic cell processes: enzymes in common metabolic pathways, many transcription regulators, binding proteins, receptors and membrane proteins.

These findings demonstrate that there is no strong resemblance between the crown group of eukaryotic Kingdoms in the ‘higher-management’ functions that integrate and regulate their developmental processes. In particular, NAM sequences are essentially limited to plants, and *Notch*, *TGF*, *Hedgehog* and *Wnt* sequences (all widely considered as essential, highly conserved, components of normal development in animals) are limited to animals. None of the sequences most closely involved in animal or plant multicellular development can be found in the genomes of fungi. Generally, there are no *Wnt*, *Hedgehog*, *Notch*, *TGF*, *p53*, *SINA*, or *NAM* sequences in fungi.

Is there any reason to believe that there should be; if not homologous, then analogous sequences at least? We would have to say ‘yes’ to this question. Fungi, like animals and plants, have a basic ‘body plan’ which is established very early on in development. The lack of NAM (no apical meristem) sequences in fungi is easy to correlate with the fact that fungi do not have apical meristems; but fungi do have organised growth centres that need to be controlled, so where are their regulators? Tissues are demarcated in even the earliest fungal fruit body initials, so they certainly exhibit regional specification, cell differentiation, and cell co-ordination essential to establishing pattern formation (Rosin and Moore, 1985; Horner and Moore, 1987; Allen *et al.*, 1992; Chiu and Moore, 1993; Moore, 1998; Moore *et al.*, 1998). The non-random distributions of cells and tissues in the (mushroom) fruit bodies of *Coprinopsis cinerea* have been interpreted as being dependent on interplay between activating and inhibiting ‘morphogen’ factors (Horner and Moore, 1987; Moore, 1988) in a pattern-forming process similar to the model developed by Meinhardt and Gierer (1974, 1980; Meinhardt, 1984, 1998). Successful application of this morphogenetic field model to fungi as

well as to plants and animals indicates that the general rules of pattern formation apply similarly to all multicellular systems.

Many other similarities have emerged from observations of fungal, particularly mushroom, development (reviewed in Moore, 2005). These include commitment (Bastouill-Descollonges and Manachère (1984) and Chiu and Moore (1988a, b) demonstrated that basidia are specified irreversibly as meiocytes during meiotic prophase I, their maturation being an autonomous, endotrophic process that is able to proceed *in vitro*); regeneration (Chiu and Moore, 1988a, b; Brunt and Moore, 1989; Bourne *et al.*, 1996; Chiu *et al.*, 1998). Programmed cell death in fungi is used to sculpture the shape of the fruit body from the raw medium provided by the hyphal mass of the fruit body initial and primordium (Umar and Van Griensven, 1997a, b; 1998).

Thus, we reach the conclusion that fungal morphogenesis must be totally different from animals, because fungal cells have walls, and from plants (whose cells also have walls) because hyphae grow only at their tips and hyphal cross-walls form only at right angles to the long axis of the hypha, which together make fungal morphogenesis dependent on the placement of hyphal branches. On the other hand, there is no doubt that development of fungal multicellular structures involves a whole suite of cellular processes and interactions that are analogous or homologous to those that occur during animal or plant development.

Yet our findings show that there are no resemblances between the crown group of eukaryotic Kingdoms in the ways they control and regulate their developmental processes. Current understanding of phylogenetic relationships is that the major kingdoms of eukaryotes separated from one another at a stage prior to the multicellular grade of organization. Consequently, in the course of their evolutionary history these very different organisms may have found different strategies to solve the same sorts of morphogenetic control problems. Finally, this means, in particular, that we are currently totally ignorant of the way fungi regulate their multicellular development.

References

- Allen, J.J., Moore, D. and Elliott, T.J. (1992). Persistent meiotic arrest in basidia of *Agaricus bisporus*. *Mycol. Res.* **96**:125-127.
- Altschul, S.F., Gish, W., Miller, W., Myers, E.W. and Lipman, D.J. (1990). Basic local alignment search tool. *J. Mol. Biol.* **215**:403-410.
- Apweiler, R., Bairoch, A., Wu, C.H., Barker, W.C., Boeckmann, B., Ferro, S., Gasteiger, E., Huang, H., Lopez, R., Magrane, M., Martin, M.J., Natale, D.A., O'Donovan, C., Redaschi, N. and Yeh, L.S. (2004). UniProt: the Universal Protein knowledgebase. *Nucleic Acids Res.* **32**: D115-D119.
- Ashburner, M. and Drysdale, R. (1994). FlyBase-the *Drosophila* genetic database. *Development* **120**:2077-2079.
- Bastouill-Descollonges, Y. and Manachère, G. (1984). Photosporogenesis of *Coprinus congregatus*: correlations between the physiological age of lamellae and the development of their potential for renewed fruiting. *Physiol. Plant.* **61**:607-610.
- Blake, J.A., Richardson, J.E., Bult, C.J., Kadin, J.A. and Eppig, J.T. (2003). MGD: the Mouse Genome Database. *Nucleic Acids Res.* **31**:193-195.
- Brunt, I.C. and Moore, D. (1989). Intracellular glycogen stimulates fruiting in *Coprinus cinereus*. *Mycol. Res.* **93**: 543-546.
- Bourne, A.M., Chiu, S.W. and Moore, D. (1996). Experimental approaches to the study of pattern formation in *Coprinus cinereus*. In Chiu, S.W. and Moore, D. Ed. Patterns in Fungal Development. Cambridge University Press, Cambridge, UK, pp. 126-155.
- Casselton, L.A. (2002). Mate recognition in fungi. *Heredity* **88**, 142-147.
- Cavalier-Smith, T. and Chao, E.E. (1995). The opalozoan *Apusomonas* is related to the common ancestor of animals, fungi and choanoflagellates. *Proc. Roy. Soc., London Ser. B*, **261**:1-6.

- Chiu, S.W. (1996). Nuclear changes during fungal development. In: *Patterns in Fungal Development* (S.W. Chiu and D. Moore, eds). Pp. 105-125. Cambridge: Cambridge University Press.
- Chiu, S.W. and Moore, D. (1988a). Evidence for developmental commitment in the differentiating fruit body of *Coprinus cinereus*. *Trans. Br. Mycol. Soc.* **90**:247-253.
- Chiu, S.W. and Moore, D. (1988b). Ammonium ions and glutamine inhibit sporulation of *Coprinus cinereus* basidia assayed *in vitro*. *Cell Biol. Int. Repts* **12**:519-526.
- Chiu, S.W. and Moore, D. (1990). Sporulation in *Coprinus cinereus*: use of an *in vitro* assay to establish the major landmarks in differentiation. *Mycological Research* **94**, 249-253.
- Chiu, S.W. and Moore, D. (1993). Cell form, function and lineage in the hymenia of *Coprinus cinereus* and *Volvariella bombycina*. *Mycol. Res.* **97**:221-226.
- Chiu, S.W., Chan, Y.H., Law, S.C., Cheung, K.T. and Moore, D. (1998). Cadmium and manganese in contrast to calcium reduce yield and nutritional value of the edible mushroom *Pleurotus pulmonarius*. *Mycol. Res.* **102**:449-457.
- Harris, M.A., Clark, J., Ireland, A., Lomax, J., Ashburner, M., Foulger, R., Eilbeck, K., Lewis, S., Marshall, B., Mungall, C., Richter, J., Rubin, G.M., Blake, J.A., Bult, C., Dolan, M., Drabkin, H., Eppig, J.T., Hill, D.P., Ni, L., Ringwald, M., Balakrishnan, R., Cherry, J.M., Christie, K.R., Costanzo, M.C., Dwight, S.S., Engel, S., Fisk, D.G., Hirschman, J.E., Hong, E.L., Nash, R.S., Sethuraman, A., Theesfeld, C.L., Botstein, D., Dolinski, K., Feierbach, B., Berardini, T., Mundodi, S., Rhee, S.Y., Apweiler, R., Barrell, D., Camon, E., Dimmer, E., Lee, V., Chisholm, R., Gaudet, P., Kibbe, W., Kishore, R., Schwarz, E.M., Sternberg, P., Gwinn, M., Hannick, L., Wortman, J., Berriman, M., Wood, V., de la, Cruz N., Tonellato, P., Jaiswal, P., Seigfried, T. and White, R. (2004). The Gene Ontology (GO) database and informatics resource. *Nucleic Acids Res.* **32**:D258-D261.
- Horner, J. and Moore, D. (1987). Cystidial morphogenetic field in the hymenium of *Coprinus cinereus*. *Trans. Br. Mycol. Soc.* **88**:479-488.
- Huala, E., Dickerman, A.W., Garcia-Hernandez, M., Weems, D., Reiser, L., LaFond, F., Hanley, D., Kiphart, D., Zhuang, M., Huang, W., Mueller, L.A., Bhattacharyya, D., Bhaya, D., Sobral, B.W., Beavis, W., Meinke, D.W., Town, C.D., Somerville, C. and Rhee, S.Y. (2001). The *Arabidopsis* Information Resource (TAIR): a comprehensive database and web-based information retrieval, analysis, and visualization system for a model plant. *Nucleic Acids Res.* **29**:102-105.
- Kosarev, P., Mayer, K.F.X. and Hardtke, C. (2002). Evaluation and classification of RING-finger domains encoded by the *Arabidopsis* genome. *Genome Biol.* **3** (4): research0016.1-0016.12 (online at <http://genomebiology.com/2002/3/4/research/0016>).
- Kreppel, L., Fey, P., Gaudet, P., Just, E., Kibbe, W.A., Chisholm, R.L. and Kimmel, A.R. (2004). dictyBase: a new *Dictyostelium discoideum* genome database. *Nucleic Acids Res.* **32**:D332-D333.
- Matsuzawa, S., Takayama, S., Froesch, B.A., Zapata, J.M. and Reed, J.C. (1998). p53-inducible human homologue of *Drosophila* seven in absentia (Siah) inhibits cell growth: suppression by BAG-1. *EMBO J.* **17**:2736-2747.
- Meinhardt, H. and Gierer, A. (1974). Applications of a theory of biological pattern formation based on lateral inhibition. *J. Cell Sci.* **15**:321-346.
- Meinhardt, H. and Gierer, A. (1980). Generation and regeneration of sequence of structures during morphogenesis. *J. Theor. Biol.* **85**:429-450.
- Meinhardt, H. (1984). Models of pattern formation and their application to plant development. In Barlow, P.W. and Carr, D.J. Ed. *Positional Controls in Plant Development*. Cambridge University Press, Cambridge, UK, pp. 1-32.

- Meinhardt, H. (1998). *The Algorithmic Beauty of Sea Shells*. Springer-Verlag, New York, Heidelberg, Berlin, pp. 236.
- Meškauskas, A., Lehmann-Horn, F. and Jurkat-Rott, K. (2004). Sight: automating genomic data-mining without programming skills. *Bioinformatics* **20**:1718-1720.
- Moore, D. (1988). Recent developments in morphogenetic studies of higher fungi. *Mushroom J. Tropics* **8**:109-128.
- Moore, D. (1998). *Fungal Morphogenesis*. Cambridge University Press, New York. Pp. 469.
- Moore, D. (2005) Principles of mushroom developmental biology. *Int. J. Med. Mushrooms* **7**:79-102.
- Moore, D., Chiu, S.W., Umar, M.H. and Sánchez, C. (1998). In the midst of death we are in life: further advances in the study of higher fungi. *Bot. J. Scotland* **50**:121-135.
- Moore, D., Walsh, C. and Robson, G.D. (2005). A search for developmental gene sequences in the genomes of filamentous fungi. In Arora, D.K. and Berka, R. Ed. *Applied Mycology and Biotechnology*, Vol. 6, Genes, Genomics and Bioinformatics, Elsevier Science, Amsterdam. Pp. 169-188.
- Pringle, A. and Taylor, J.W. (2002). The fitness of filamentous fungi. *Trends in Microbiol.* **10**:474-481.
- Rosin, I.V. and Moore, D. (1985). Differentiation of the hymenium in *Coprinus cinereus*. *Trans. Br. Mycol. Soc.* **84**:621-628.
- Trinci, A.P.J., Wiebe, M.G. and Robson, G.D. (1994). The mycelium as an integrated entity. In Wessels, J.G.H. and Meinhardt, F. Ed, *The Mycota vol. I*, Springer-Verlag, Berlin and Heidelberg. Pp. 175-193.
- Twigger, S., Lu, J., Shimoyama, M., Chen, D., Pasko, D., Long, H., Ginster, J., Chen, C.F., Nigam, R., Kwitek, A., Eppig, J., Maltais, L., Maglott, D., Schuler, G., Jacob, H. and Tonellato, P.J. (2002). Rat Genome Database (RGD): mapping disease onto the genome. *Nucleic Acids Res.* **30**:125-128.
- Umar, M.H. and Van Griensven, L.J.L.D. (1997a). Morphological studies on the life span, developmental stages, senescence and death of *Agaricus bisporus*. *Mycol. Res.* **101**: 1409-1422.
- Umar, M.H., and Van Griensven L.J.L.D. (1997b). Morphogenetic cell death in developing primordia of *Agaricus bisporus*. *Mycologia* **89**:274-277.
- Umar, M.H., and Van Griensven L.J.L.D. (1998). The role of morphogenetic cell death in the histogenesis of the mycelial cord of *Agaricus bisporus* and in the development of macrofungi. *Mycol. Res.* **102**:719-735.
- Venter, J.C., Adams, M.D., Martin-Gallardo, A., McCombie, W.R. and Fields, C. (1992). Genome sequence analysis: scientific objectives and practical strategies. *Trends Biotechnol.* **10**: 8-11.
- Watling, R. and Moore, D. (1994). Moulding moulds into mushrooms: shape and form in the higher fungi. In Ingram, D.S. and Hudson, A. Ed. *Shape and Form in Plants and Fungi*, Academic Press, London. Pp. 270-290.
- Wheeler, D.L., Barrett, T., Benson, D.A., Bryant, S.H., Canese, K., Church, D.M., DiCuccio, M., Edgar, R., Federhen, S., Helmsberg, W., Kenton, D.L., Khovayko, O., Lipman, D. J., Madden, T.L., Maglott, D.R., Ostell, J., Pontius, J.U., Pruitt, K.D., Schuler, G.D., Schriml, L.M., Sequeira, E., Sherry, S.T., Sirotkin, K., Starchenko, G., Suzek, T.O., Tatusov, R., Tatusova, T.A., Wagner, L. and Yaschenko, E. (2005). Database resources of the National Center for Biotechnology Information. *Nucleic Acids Res.* **33** Database Issue:D39-D45.
- Wheeler, D.L., Church, D.M., Federhen, S., Lash, A.E., Madden, T.L., Pontius, J.U., Schuler, G.D., Schriml, L.M., Sequeira, E., Tatusova, T.A. and Wagner, L. (2003). Database resources of the National Center for Biotechnology. *Nucleic Acids Res.* **31**:28-33.

Supplementary table (not included in the original publication). Animal-only similarities found

Entries under 'genome hit' show *E*-value as returned by the sequence comparison software: a reference to the specific database entry and brief descriptive annotation. No hits were returned to these plant sequences by searches of Metazoan or Fungal genomes.

NOTE that small *E*-values are shown as exponential functions, i.e. $1.217\text{E-}29 = 1.217 \times 10^{-29}$

AmiGO description and hyperlinks USE Link2	Metazoan genome hit	Viridiplantae genome hit	Fungi genome hit
Link1 Link2 >UNIPROT Q9NZ56 symbol:FMN2: human Formin 2 [fragments].	1.6872E-23, 51459134 human Formin 2 (predicted).	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q05315 symbol:LPPL: human eosinophil lysophospholipase.	1.57917E-21, 187274 Charcot-Leyden crystal protein [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P06454 symbol:THYA: human prothymosin alpha.	1.33862E-20, 55250213 LOC495667 protein [<i>Xenopus laevis</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O43308 symbol:O43308: human KIAA0425 protein [fragment].	6.00084E-21, 40788254 unidentified KIAA0425 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q16760 symbol:KDGD: human delta diacylglycerol kinase.	4.59468E-21, 25777598 diacylglycerol kinase, delta 130kDa isoform 2 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 human 3B3 protein [fragment]	6.44308E-14, Animal_dna Human pre-T/NK cell associated protein (3B3) mRNA, 3' end.	no hits returned	no hits returned
Link1 Link2 >UNIPROT P43694 symbol:GAT4: human transcription factor GATA-4.	1.20913E-21, 33188461 GATA binding protein 4 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P22932 symbol:RRG2: human retinoic acid receptor gamma-2.	1.29355E-23, 297146 retinoic acid receptor gamma 2 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >tr Q9WU66: mouse secreted frizzled-related protein.	6.44453E-31, 31560421 secreted frizzled-related sequence protein 5 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O00292 symbol:TGF4: human transforming growth factor beta 4 precursor.	6.41984E-23, 27436881 endometrial bleeding associated factor preproprotein [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P04141 symbol:CSF2: human granulocyte-macrophage colony-stimulating factor precursor.	1.57885E-21, 3002476 CSF1 [<i>Homo sapiens</i>].	no hits returned	no hits returned

Link1 Link2 >UNIPROT O60447 symbol:O60447: human EVI-5 homolog.	2.97819E-20, 52630438 ecotropic viral integration site 5 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P25942 symbol:TNR5: human tumour necrosis factor receptor superfamily member 5 precursor.	1.99567E-24, 23312371 CD40 antigen isoform 2 precursor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P19883 symbol:FSA: human follistatin precursor.	3.75869E-23, 7242222 follistatin isoform FST344 precursor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P09016 symbol:HXD4: human homeobox protein Hox-D4.	2.60298E-24, 23397672 homeobox D4 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P26951 symbol:IL3R: human interleukin-3 receptor alpha chain precursor.	4.15572E-22, 54781361 interleukin 3 receptor, alpha (low affinity) [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P05111 symbol:IHA: human inhibin alpha chain precursor.	7.83735E-21, 4504697 inhibin alpha subunit precursor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q03167 symbol:TGR3: human TGF-beta receptor type III precursor.	3.52269E-21, 4507471 transforming growth factor, beta receptor III (betaglycan, 300kDa) [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9UBN7 symbol:HDA6: Histone deacetylase 6.	6.00084E-21, 13543430 HDAC6 protein [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >CG14307-PK: <i>Drosophila melanogaster</i> gene fruitless (transcription factor activity).	1.68686E-23, 45446541 gene product from transcript CG14307-RK of <i>D. melanogaster</i> .	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q8BPE6: mouse Hoxa4.	8.9463E-25, 46275810 homeobox protein A4 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P56177 symbol:DLX1: Human homeobox protein DLX-1.	5.79883E-24, 38093375 predicted protein: similar to DLX-1 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9UJU5 symbol:FXD3: human Forkhead box protein D3 (transcription repressor).	9.25797E-22, 6912372 forkhead box D3 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9NZR4 symbol:VSX1: human visual system homeobox 1.	1.58126E-21, 40806216 visual system homeobox 1 protein isoform b [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q14526 symbol:HIC1: human hypermethylated in cancer 1 protein (transcription repressor).	1.43162E-14, 34873170 predicted protein: similar to hypermethylated in cancer 1 [<i>Rattus norvegicus</i>].	no hits returned	no hits returned

Link1 Link2 >CG5370-PA: <i>Drosophila melanogaster</i> gene Death caspase-1.	2.43582E-22, 7291604 CG5370 gene product (dcp-1) from transcript CG5370-RA of <i>D.</i> <i>melanogaster</i> .	no hits returned	no hits returned
Link1 Link2 >UNIPROT P02340 symbol:P53: mouse tumour suppressor p53.	3.18192E-22, 6755881 transformation related protein 53 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >MGI MGI:96173 symbol:Hoxa13: mouse homeo box A13 gene.	7.83735E-21, 51094974 homeo box A13 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P25791 symbol:RHM2: human rhombotin-2 (LIM-only protein 2).	8.38458E-23, 23272668 LMO2 protein [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P56524 symbol:HDA4: human histone deacetylase 4.	1.57917E-21, 5174481 histone deacetylase 4 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P31273 symbol:HXC8: human homeobox protein Hox-C8.	2.20355E-23, 12056969 homeo box C8 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 Japanese rice fish progonadoliberin II precursor.	3.30261E-40, 34098706 Japanese rice fish progonadoliberin II precursor.	no hits returned	no hits returned
Link1 Link2 >UNIPROT O60565 symbol:O60565: human gremlin-1 precursor (cytokine).	2.69366E-21, 55641811 predicted protein: similar to cysteine knot superfamily 1, BMP antagonist 1; proliferation- inducing gene 2 [<i>Pan trogodytes</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O15537 symbol:XLR1: human retinoschisin precursor.	3.40409E-24, 10835083 X- linked juvenile retinoschisin protein [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P56705 symbol:WNT4: human Wnt-4 protein precursor.	2.98213E-20, 37183012 Wnt4 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P01138 symbol:NGF: human beta-nerve growth factor precursor.	3.18192E-22, 4505391 nerve growth factor, beta polypeptide [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P54852 symbol:EMP3: human epithelial membrane protein-3.	6.41135E-23, 4503563 epithelial membrane protein 3 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q99583 symbol:MNT: human MAX binding protein MNT (transcription repressor).	8.6652E-20, 9945318 MAX binding protein [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P17482 symbol:HXB9: human homeobox protein Hox-B9.	1.4283E-22, 15029508 Homeobox protein Hox-B9 [<i>Homo sapiens</i>].	no hits returned	no hits returned

Link1 Link2 >CG14029-PA: <i>Drosophila melanogaster</i> gene vrille.	2.43954E-22, 7296965 CG14029-PA, isoform A (gene <i>vri</i>) [<i>Drosophila melanogaster</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q12952 symbol:FXL1: human forkhead box protein L1.	7.08858E-22, 22779860 forkhead box L1 [<i>Homo</i> <i>sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >MGI MGI:108360 symbol:Enah: mouse homolog of the <i>Drosophila</i> enabled gene.	3.75869E-23, 37887218 MENA protein [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P78504 symbol:JAG1: human Jagged-1 precursor.	1.33685E-20, 4557679 jagged 1 precursor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9H1B4 symbol:NXF5: human nuclear RNA export factor 5.	2.60298E-24, 15487664 nuclear RNA export factor 5 isoform c [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q8K4G1 symbol:LTB4: mouse latent transforming growth factor beta binding protein 4 precursor.	3.51803E-21, 32189330 mouse latent transforming growth factor beta binding protein 4 precursor.	no hits returned	no hits returned
Link1 Link2 >UNIPROT P35555 symbol:FBN1: human fibrillin-1 precursor.	6.00084E-21, 24430141 fibrillin 1 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q09553 symbol:GAS1: <i>Caenorhabditis</i> <i>elegans</i> growth-arrest-specific protein 1 homolog precursor.	1.20913E-21, 25150480 <i>Caenorhabditis elegans</i> growth- arrest-specific protein 1 homolog precursor.	no hits returned	no hits returned
Link1 Link2 >UNIPROT P54257 symbol:HAP1: human Huntingtin- associated protein 1.	3.75869E-23, 10433320 unnamed protein product [<i>Homo</i> <i>sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O14905 symbol:WN9B: human Wnt-9b protein precursor.	2.06519E-21, 37181546 WNT9B [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9UKU9 symbol:ANL2: human angiotensin- related protein 2 precursor.	1.29158E-23, 37181668 NL1 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q01196 symbol:RUN1: human runt-related transcription factor 1.	1.02494E-20, 49574546 runt- related transcription factor 1 isoform b [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P25391 symbol:LMA1: human laminin alpha-1 chain precursor.	3.18192E-22, 38788416 laminin, alpha 1 precursor [<i>Homo</i> <i>sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O15146 symbol:MUSK: human muscle, skeletal receptor tyrosine protein kinase precursor.	1.74598E-20, 55632049 predicated protein: similar to muscle, skeletal, receptor tyrosine kinase; receptor tyrosine kinase MuSK [<i>Pan troglodytes</i>].	no hits returned	no hits returned

Link1 Link2 >MGI[MGI:103581 symbol:Musk: mouse muscle, skeletal receptor tyrosine protein kinase.	2.97819E-20, 13592003 muscle, skeletal, receptor tyrosine kinase [<i>Rattus norvegicus</i>].	no hits returned	no hits returned
Link1 Link2 >CG8208-PA: <i>Drosophila melanogaster</i> gene MBD-like (methyl-CpG-binding-domain-like-protein).	2.06246E-21, 23170814 CG8208-PA, isoform A (mbd-like gene)[<i>Drosophila melanogaster</i>].	no hits returned	no hits returned
Link1 Link2 >MGI[MGI:2136761 symbol:Fzd10: mouse frizzled homolog 10.	5.79883E-24, 28202015 frizzled 10 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P21741 symbol:MK: human midkine precursor.	1.09361E-22, 4505135 midkine [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P40205 symbol:NCYM: human N-cym protein.	8.9463E-25, 477439 DNA-binding transcription activator homolog N-cym - human.	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9P2N4 symbol:ATS9: human ADAMTS-9 precursor.	1.74562E-20, 55666917 predicated protein: similar to a disintegrin and metalloproteinase with thrombospondin motifs 9 isoform 1 preproprotein [<i>Pan troglodytes</i>].	no hits returned	no hits returned
Link1 Link2 >tr Q6NVE6 Plexin A2: mouse plexin A2.	2.29212E-28, 33859839 plexin A2 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P36955 symbol:PEDF: human pigment epithelium-derived factor precursor.	1.4283E-22, 1144299 pigment epithelium-derived factor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >tr P70208 Plexin 3: mouse plexin A3.	3.90976E-28, 6679391 plexin A3 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P51805 symbol:PXA3: human plexin A3 precursor.	6.00084E-21, 8923793 plexin A3 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >tr P97299: mouse secreted frizzled-related sequence protein 2.	1.58734E-29, 6677895 secreted frizzled-related sequence protein 2 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P01137 symbol:TGF1: human transforming growth factor beta 1 precursor.	7.84773E-21, 30583329 transforming growth factor, beta 1 (Camurati-Engelmann disease) [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >tr P70206: mouse plexin A1.	6.66905E-28, 6679389 plexin A1 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q06430 symbol:BGIB: human N-acetylglucosaminide beta-1,6-N-acetylglucosaminyl-transferase.	7.83575E-21, 4503963 glucosaminyl (N-acetyl) transferase 2 isoform B [<i>Homo sapiens</i>].	no hits returned	no hits returned

Link1 Link2 >UNIPROT P13497 symbol:BMP1: human bone morphogenetic protein 1 precursor.	1.42801E-22, 4502421 bone morphogenetic protein 1 isoform 1, precursor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O35516 symbol:NTC2: mouse Neurogenic locus Notch homolog protein 2 precursor.	1.80262E-25, 33859592 Notch gene homolog 2 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O75474 symbol:FRT2: human GSK-3 binding protein FRAT2 (regulates the Wnt signaling pathway).	1.02359E-20, 16507243 GSK-3 binding protein FRAT2 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q08629 symbol:TIC1: human Testican-1 precursor.	1.86789E-22, 4759164 sparc/osteonectin, cwcv and kazal-like domains proteoglycan precursor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q04721 symbol:NTC2: human Neurogenic locus Notch homolog protein 2 precursor.	1.38022E-25, 24041035 notch 2 preproprotein [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9QW30 symbol:NTC2: rat Neurogenic locus Notch homolog protein 2 precursor.	2.35429E-25, 13242247 notch gene homolog 2 [<i>Rattus norvegicus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P57058 symbol:HUNK: human hormonally up-regulated neu tumor-associated kinase.	1.4283E-22, 55656971 predicted protein: similar to hormonally upregulated Neu-associated kinase [<i>Pan troglodytes</i>].	no hits returned	no hits returned
Link1 Link2 >FB FBgn0004364 symbol:18w: <i>Drosophila melanogaster</i> gene 18 wheeler (transmembrane receptor).	3.51731E-21, 7302422 18w gene product from CG8896-PA [<i>Drosophila melanogaster</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O75603 symbol:GCM2: human chorion-specific transcription factor GCMb.	9.8913E-24, 55625856 predicted protein: glial cells missing homolog 2 [<i>Pan troglodytes</i>].	no hits returned	no hits returned
Link1 Link2 >tr Q9CZW3: mouse wingless-related MMTV integration site 2.	1.30025E-31, 38322763 wingless-type MMTV integration site family member 2 precursor [<i>Rattus norvegicus</i>].	no hits returned	no hits returned
Link1 Link2 >tr Q8BMF6: mouse semaphorin 3D.	2.9936E-28, 31560069 semaphorin 3D [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O43603 symbol:GALS: human Galanin receptor type 2.	5.42754E-22, 4503905 galanin receptor 2 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P09630 symbol:HXC6: human Homeobox protein Hox-C6.	1.09361E-22, 21362259 homeo box C6 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 : human psychosine receptor	0.0, 33695104 G protein-coupled receptor 65 [<i>Homo sapiens</i>].	no hits returned	no hits returned

Link1 Link2 >UNIPROT Q9NSA3 symbol:ICAT: human beta-catenin-interacting protein 1.	1.02359E-20, 9910390 catenin, beta interacting protein 1 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P26436 symbol:ASPX: human acrosomal protein SP-10 precursor.	5.99963E-21, 4501879 acrosomal vesicle protein 1 isoform a precursor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P35368 symbol:A1AB: human alpha-1B adrenergic receptor.	8.37179E-23, 4501959 alpha-1B-adrenergic receptor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9BQE5 symbol:APL2: human apolipoprotein-L2.	7.08714E-22, 13562090 apolipoprotein L2 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q12950 symbol:FXD4: human forkhead box protein D4.	7.83735E-21, 55665349 forkhead box D4 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 : Zebrafish Wnt-2 protein precursor.	0.0, 18859561 wingless-type MMTV integration site family member 2 [<i>Danio rerio</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P09544 symbol:WNT2: human Wnt-2 protein precursor.	1.52803E-24, 51095112 wingless-type MMTV integration site family member 2 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P32243 symbol:OTX2: human homeobox protein OTX2.	5.42754E-22, 27699029 predicated protein similar to orthodenticle 2 isoform b [<i>Rattus norvegicus</i>].	no hits returned	no hits returned
Link1 Link2 >DDB0214993: countin, a cell-counting factor in <i>Dictyostelium discoideum</i> .	4.51717E-8, Animal.dna <i>Mus musculus</i> BAC clone RP23-244N5 from 15, complete sequence.	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q08117 symbol:GRG: human GRG protein.	1.4283E-22, 5706731 amino-terminal enhancer of split isoform b [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P31311 symbol:HXAB: mouse homeobox protein Hox-A11.	9.8913E-24, 6754226 homeobox protein A11 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O43186 symbol:CRX: human cone-rod homeobox protein.	1.86504E-22, 31565779 CRX protein [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P54849 symbol:EMP1: human epithelial membrane protein-1.	3.51803E-21, 4503559 epithelial membrane protein 1 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9NZK5 symbol:CES1: human cat eye syndrome critical region protein 1 precursor.	1.74562E-20, 29029550 cat eye syndrome critical region protein 1 isoform a precursor	no hits returned	no hits returned

	[<i>Homo sapiens</i>].		
Link1 Link2 >UNIPROT P54851 symbol:EMP2: human epithelial membrane protein-2.	4.909E-23, 4503561 epithelial membrane protein 2 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >tr Q8CAH7: mouse secreted frizzled-related sequence protein 4.	2.07314E-29, 7710094 secreted frizzled-related sequence protein 4 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q99801 symbol:NK31: human homeobox protein Nkx-3.1.	1.57917E-21, 19923352 NK3 transcription factor related, locus 1 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q93097 symbol:WN2B: human Wnt-2b protein precursor.	2.98213E-20, 13518021 wingless-type MMTV integration site family, member 2B isoform WNT-2B2 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P57082 symbol:TBX4: human T-box transcription factor TBX4.	3.52269E-21, 18129690 T-box 4 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q15113 symbol:PCO1: human procollagen C-proteinase enhancer protein precursor.	4.15572E-22, 21619971 Procollagen C-endopeptidase enhancer [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q14004 symbol:CDL5: human cell division cycle 2-like protein kinase 5.	3.51731E-21, 55628472 predicated protein: similar to KIAA1791 protein [<i>Pan troglodytes</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q06141 symbol:PAP1: human pancreatitis-associated protein 1 precursor.	2.43631E-22, 21070995 pancreatitis-associated protein precursor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9Y6F9 symbol:WNT6: human Wnt-6 protein precursor.	8.38458E-23, 16507239 wingless-type MMTV integration site family, member 6 precursor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P57682 symbol:KLF3: human Kruppel-like factor 3.	6.41135E-23, 12644533 human Kruppel-like factor 3.	no hits returned	no hits returned
Link1 Link2 >tr O88424 : mouse integrin beta 2-like.	2.7076E-29, 6680492 integrin beta 2-like [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q96HE4 symbol:Q96HE4: human ST6GAL2 protein.	2.06519E-21, 26190610 beta-galactoside alpha-2,6-sialyltransferase II [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >FB FBgn0038498 symbol:beat-IIa: <i>Drosophila melanogaster</i> beaten path IIa gene.	4.908E-23, 28381329 CG14334 gene product from transcript CG14334-RA of <i>D. melanogaster</i> .	no hits returned	no hits returned

Link1 Link2 >UNIPROT O60663 symbol:LMXB: human LIM homeobox transcription factor 1 beta.	2.20355E-23, 4505007 LIM homeobox transcription factor 1, beta [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >MGI MGI:2446084 symbol:Wnt9a: mouse wingless-type MMTV integration site 9A.	3.89479E-20, 21314846 wingless-type MMTV integration site 9A [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O14904 symbol:WN9A: human Wnt-9a protein precursor.	1.02494E-20, 15082261 wingless-type MMTV integration site family, member 9A [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P09466 symbol:PAEP: human glycodelin precursor.	9.25797E-22, 55958591 progestagen-associated endometrial protein [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P08887 symbol:IL6A: human interleukin-6 receptor alpha chain precursor.	6.00084E-21, 4504673 interleukin 6 receptor isoform 1 precursor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P15018 symbol:LIF:human leukemia inhibitory factor precursor.	2.87793E-23, 4504991 leukemia inhibitory factor (cholinergic differentiation factor) [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q99865 symbol:SPN3: human spindlin-like protein 3.	3.52269E-21, 54291727 spindlin family, member 2 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >tr Q8BMF7: mouse Lefty-2, left-right determination factor 2.	1.48541E-27, 42490977 Left-right determination factor 2 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q8IUG7 symbol:Q8IUG7: human alpha 2,6-sialyltransferase.	8.38458E-23, 26190610 beta-galactoside alpha-2,6-sialyltransferase II [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q8BUU4 symbol:Q8BUU4: mouse hypothetical glycosyltransferase family 29 containing protein	3.75869E-23, 27370242 beta-galactoside alpha-2,6-sialyltransferase II [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P01148 symbol:GON1: human progonadoliberin I precursor.	4.909E-23, 1070543 gonadoliberin precursor [validated] - human.	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q15303 symbol:ERB4: human receptor tyrosine-protein kinase erbB-4 precursor.	2.69366E-21, 4885215 v-erb-a erythroblastic leukemia viral oncogene homolog 4 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >tr Q8VEA3: mouse homeo box B2.	3.19839E-30, 19527250 homeo box B2 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q15583	2.98213E-20, 28178849 TG-	no hits returned	no hits returned

symbol: TGIF: human homeobox 5'-TG-3' interacting factor.	interacting factor isoform c [<i>Homo sapiens</i>].		
Link1 Link2 >UNIPROT O95789 symbol: Z258: human Zinc finger protein 258.	1.4283E-22, 6005978 zinc finger protein 258 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P29746 symbol: BNB: bangles and beads protein (<i>Drosophila melanogaster</i>).	2.69311E-21, 22832525 CG7088-PD, isoform D – bmb gene [<i>Drosophila melanogaster</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q02535 symbol: ID3: human DNA-binding protein inhibitor ID-3.	1.09361E-22, 3219578 inhibitor of DNA binding 3, dominant negative helix-loop-helix protein [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q02363 symbol: ID2: human DNA-binding protein inhibitor ID-2.	2.06246E-21, 31982933 inhibitor of DNA binding 2 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 mouse peroxisome proliferator-activated receptor binding protein homolog.	0.0, 26344245 unnamed protein product [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P11308 symbol: ERG: human transcriptional regulator ERG.	2.06246E-21, 19526802 avian erythroblastosis virus E-26 (v-ets) oncogene related [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P09017 symbol: HXC4: human homeobox protein Hox-C4.	6.84994E-25, 7305149 homeobox C4 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 : human transcription factor ESE-3A.	1.73712E-169, 4838432 transcription factor ESE-3A [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P15907 symbol: SIA1: human CMP-N-acetylneuraminase-beta-galactosamide-alpha-2,6-sialyltransferase.	1.43019E-22, 4506949 sialyltransferase 1 isoform a [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9HBU1 symbol: BRX1: human homeobox protein BarH-like 1.	1.74562E-20, 14194481 Homeobox protein BarH-like 1 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 : flounder progonadoliberin I precursor	2.47941E-51, 18253180 seabream-type gonadotropin-releasing hormone precursor [<i>Verasper moseri</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P56706 symbol: WN7B: human Wnt-7b protein precursor.	1.86789E-22, 17505193 wingless-type MMTV integration site family, member 7B precursor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P98174 symbol: FGD1: human faciogenital dysplasia 1 protein.	3.39959E-24, 24797153 faciogenital dysplasia protein [<i>Homo sapiens</i>].	no hits returned	no hits returned

Link1 Link2 >tr Q8R1J4: mouse Sfrp1 protein (secreted frizzled-related sequence protein 1).	7.3735E-27, 19353578 Secreted frizzled-related sequence protein 1 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P13725 symbol:ONCM: human oncostatin M precursor.	1.93041E-19, 10092621 oncostatin M precursor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P01588 symbol:EPO: human erythropoietin precursor.	1.86542E-22, 30172717 unknown [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P06213 symbol:INSR: human insulin receptor precursor.	1.20913E-21, 4557884 insulin receptor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O95238 symbol:O95238: human Ets transcription factor PDEF.	1.57917E-21, 6912580 SAM pointed domain containing ets transcription factor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P55075 symbol:FGF8: human fibroblast growth factor-8 precursor.	2.69366E-21, 15147348 fibroblast growth factor 8 isoform E precursor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O00548 symbol:DLL1: human Delta-like protein 1 precursor.	3.18192E-22, 37182902 DLL1 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P97677 symbol:DLL1: rat Delta-like protein 1 precursor.	9.25797E-22, 39754753 delta like-1 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >MGI MGI:99614 symbol:Mst1r: mouse macrophage stimulating 1 receptor (c-met-related tyrosine kinase).	4.59468E-21, 6677765 macrophage stimulating 1 receptor [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q14586 symbol:Z267: human Zinc finger protein 267.	1.58126E-21, 8163824 krueppel-like zinc finger protein HZF2 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9UL17 symbol:TX21: human T-box transcription factor TBX21.	1.52803E-24, 7019549 T-box 21 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P34707 symbol:SKN1: <i>Caenorhabditis</i> Skinhead-1 protein (specifies fate of ventral blastomeres in the early embryo).	3.52269E-21, 25148068 SKiNhead SKN-1 (70.7 kD) (skn-1) [<i>Caenorhabditis elegans</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9Y2B6 symbol:Q9Y2B6: human nuclear migration protein nudC.	2.43954E-22, 4587127 unique gene expressed in fibroblasts of periodontal ligament [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P07332 symbol:FES: human proto-oncogene	1.86542E-22, 55642669 predicted protein similar to	no hits returned	no hits returned

tyrosine-protein kinase Fes/Fps.	proto-oncogene tyrosine-protein kinase FES/FPS (C-FES) [<i>Pan troglodytes</i>].		
Link1 Link2 >UNIPROT Q13535 symbol:Q13535: human serine-protein kinase ATR.	2.69366E-21, 4502325 ataxia telangiectasia and Rad3 related protein [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O00508 symbol:O00508: human latent TGF-beta binding protein-4.	2.69366E-21, 4505037 latent transforming growth factor beta binding protein 4 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9Y2P7 symbol:Z256: human Zinc finger protein 256.	2.06519E-21, 30582545 zinc finger protein 256 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P13611 symbol:PGCV: human versican core protein precursor	1.4283E-22, 37663 unnamed protein product [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q07820 symbol:MCL1: human induced myeloid leukemia cell differentiation protein Mcl-1.	1.57917E-21, 33519458 myeloid cell leukemia sequence 1 isoform 2 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q14774 symbol:HLX1: human homeobox protein HLX1.	3.75869E-23, 11386181 H2.0-like homeo box 1 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q01664 symbol:TAP4: human transcription factor AP-4.	5.43472E-22, 3152675 AP-4 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >tr Q9QZC2: mouse plexin C1 (cell surface receptor).	3.30981E-27, 9055376 plexin C1 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P55771 symbol:PAX9: human paired box protein Pax-9.	1.57917E-21, 7242167 paired box gene 9 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q92766 symbol:RRE1: human RAS-responsive element binding protein 1.	1.09506E-22, 51173735 ras responsive element binding protein 1 isoform 2 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P14138 symbol:ET3: human endothelin-3 precursor.	3.18192E-22, 46370062 endothelin 3 isoform 3 preproprotein [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P12757 symbol:SKIL: human SKI-like protein.	7.09797E-22, 4885599 SKI-like [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O60353 symbol:FZD6: human Frizzled 6 precursor.	3.39959E-24, 34734079 frizzled 6 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P29317 symbol:EPA2: human ephrin type-A	3.18192E-22, 32967311 ephrin receptor EphA2 [<i>Homo sapiens</i>].	no hits returned	no hits returned

receptor 2 precursor.			
Link1 Link2 >UNIPROT P40225 symbol:TPO: human thrombopoietin precursor.	3.89479E-20, 4507493 thrombopoietin isoform 1 precursor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q16534 symbol:HLF: human hepatic leukemia factor	8.37349E-23, 4504421 hepatic leukemia factor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q16587 symbol:ZNF74: human Zinc finger protein 74.	6.00879E-21, 33871364 ZNF74 protein [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >tr Q8C8B0: mouse cartilage homeo protein 1.	1.75466E-28, 27369774 cartilage homeo protein 1 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9UJV9 symbol:ABS: human DEAD-box protein abstrakt homolog.	2.06204E-21, 55625482 hypothetical protein XP_518135 [<i>Pan troglodytes</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P19622 symbol:HME2: human homeobox protein engrailed-2.	4.15572E-22, 37674425 unknown [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >tr Q91VN6: mouse DEAD (Asp-Glu-Ala-Asp) box polypeptide 41.	4.32188E-27, 21536246 DEAD (Asp-Glu-Ala-Asp) box polypeptide 41 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9HBU2 symbol:Q9HBU2: human LIM- homeobox transcription factor LHX3.	2.69723E-21, 7657303 LIM homeobox protein 3 isoform b [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 : Zebrafish Wnt-5 protein precursor.	0.0, 18859567 wingless-type MMTV integration site family, member 5a [<i>Danio rerio</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9V574 symbol:L2K1: <i>Drosophila</i> Lethal(2)k10201 protein.	2.97819E-20, 28381061 CG13951-PA [<i>Drosophila melanogaster</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P51826 symbol:LAF4: human lymphoid nuclear protein related to AF4.	1.4283E-22, 4504939 lymphoid nuclear protein related to AF4 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9UBV4 symbol:WN16: human Wnt-16 protein precursor.	4.9155E-23, 17402916 wingless- type MMTV integration site family, member 16 isoform 1 precursor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >MGI MGI:2136018 symbol:Wnt16: mouse wingless- related MMTV integration site 16.	3.76367E-23, 31560011 wingless-related MMTV integration site 16 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q14202 symbol:Z261: human Zinc finger protein 261.	4.44589E-24, 15278179 ZNF261 protein [<i>Homo sapiens</i>].	no hits returned	no hits returned

Link1 Link2 >UNIPROT P49639 symbol:HX A1: human homeobox protein Hox-A1.	8.37349E-23, 41350071 unknown [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q02548 symbol:PAX5: human paired box protein Pax-5.	1.4283E-22, 38885391 BSAP [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9UGP4 symbol:LIMD: human LIM domains containing protein 1.	5.42754E-22, 7657307 LIM domains containing 1 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q92576 symbol:PHF3: human PHD finger protein 3.	1.20913E-21, 7662018 PHD finger protein 3 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P35453 symbol:HXDD: human homeobox protein Hox-D13.	1.02359E-20, 9625000 homeo box D13 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O88879 symbol:APAF: mouse apoptotic protease activating factor 1.	5.99963E-21, 28278781 Apaf1 protein [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O43610 symbol:SPY3: human Sprouty homolog 3.	9.27024E-22, 27501452 sprouty homolog 3 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 : African cichlid progonadoliberin II precursor.	3.25564E-43, 28201250 African cichlid progonadoliberin II precursor.	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9GZY0 symbol:NXF2: human Nuclear RNA export factor 2.	3.0748E-25, 14277694 nuclear RNA export factor 2 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P35452 symbol:HXDC: human Homeobox protein Hox-D12.	3.18192E-22, 8777658 transcription factor HOXD12 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 : flounder progonadoliberin II precursor	8.56748E-44, 18253178 chicken-II type gonadotropin- releasing hormone precursor [<i>Verasper moseri</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q01726 symbol:MSHR: human melanocyte stimulating hormone receptor.	5.08002E-20, 30582781 tubulin, beta, 4 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P31269 symbol:HX A9: human homeobox protein Hox-A9.	5.42754E-22, 23097236 homeobox protein A9 isoform a [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P13631 symbol:RRG1: human retinoic acid receptor gamma-1.	8.38458E-23, 4506423 retinoic acid receptor, gamma [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O95202 symbol:O95202: human leucine zipper-EF-hand containing	3.75869E-23, 6912482 leucine zipper-EF-hand containing transmembrane protein 1 [<i>Homo</i>	no hits returned	no hits returned

transmembrane protein 1, mitochondrial precursor.	<i>sapiens</i>].		
Link1 Link2 : <i>Drosophila melanogaster</i> gene thread (ubiquitin-protein ligase activity).	1.57917E-21, 23093361 CG12284-PC, isoform C [<i>Drosophila melanogaster</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q14641 symbol:INL4: human early placenta insulin-like peptide precursor.	1.86542E-22, 4504711 insulin-like 4 precursor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q10589 symbol:BST2: human bone marrow stromal antigen 2.	7.83575E-21, 4757876 bone marrow stromal cell antigen 2 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >tr Q9DC11: mouse plexin domain containing 2.	2.44892E-30, 31543855 tumor endothelial marker 7-related precursor [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q8NHV9 symbol:PEP1: human paired-like homeobox protein PEPP-1.	3.18192E-22, 23943886 paired-like homeobox protein OTEX [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9NP84 symbol:FN14: human tumour necrosis factor receptor superfamily member Fn14 precursor.	1.57917E-21, 7706186 type I transmembrane protein Fn14 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q01974 symbol:ROR2: human tyrosine-protein kinase transmembrane receptor ROR2 precursor.	2.06519E-21, 19743898 receptor tyrosine kinase-like orphan receptor 2 precursor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >tr Q8R143: mouse pituitary tumour-transforming 1 interacting protein.	5.45563E-30, 22122339 pituitary tumor-transforming gene 1 protein-interacting protein [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P24347 symbol:MM11: human stromelysin-3 precursor.	2.43631E-22, 5174581 matrix metalloproteinase 11 preproprotein [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O00526 symbol:UPK2: human uroplakin-2 precursor	3.29713E-19, 38385727 uroplakin II [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q92583 symbol:SY17: human small inducible cytokine A17 precursor.	4.16122E-22, 55643989 hypothetical protein XP_523377 [<i>Pan troglodytes</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O75094 symbol:SLT3: human slit homolog 3 protein precursor.	4.16122E-22, 37182886 SLIT3 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P01033 symbol:TIM1: human metalloproteinase inhibitor 1 precursor.	3.76367E-23, 13937969 TIMP1 protein [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P70661 symbol:NGN3: mouse neurogenin	1.4283E-22, 3913130 mouse	no hits returned	no hits returned

3.	neurogenin 3.		
Link1 Link2 >UNIPROT O35305 symbol:TR11: mouse tumour necrosis factor receptor superfamily member 11A precursor.	4.9155E-23, 17380323 mouse tumour necrosis factor receptor superfamily member 11A precursor.	no hits returned	no hits returned
Link1 Link2 : mouse Neurog3.	2.20921E-122, 31560622 neurogenin 3 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q00994 symbol:NADE: human p75NTR-associated cell death executor.	7.5735E-24, 7657044 nerve growth factor receptor (TNFRSF16) associated protein 1 isoform b [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q13461 symbol:FXE3: human forkhead box protein E3.	1.4283E-22, 11386197 forkhead box E3 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O75629 symbol:O75629: human CREG1 protein precursor.	7.83735E-21, 37183260 CREG [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >tr Q9D7A3: mouse RIKEN cDNA 2310020H19 gene (Zn finger protein).	2.29166E-28, 21313494 RIKEN cDNA 2310020H19 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >tr Q8R3P8: mouse RIKEN cDNA 2810428C21 gene (Zn finger protein).	5.10528E-28, 23943840 hypothetical protein LOC69942 [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P56279 symbol:TCLA: human T-cell leukemia/lymphoma protein 1A.	9.9044E-24, 11415028 T-cell lymphoma-1 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P05230 symbol:FGF1: human Heparin-binding growth factor 1 precursor.	2.87793E-23, 15055545 fibroblast growth factor 1 (acidic) isoform 3 precursor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O95935 symbol:TX18: human T-box transcription factor TBX18.	5.08675E-20, 51465420 predicted T-box 18 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O15541 symbol:Z183: human Zinc finger protein 183.	1.09506E-22, 30583189 zinc finger protein 183 (RING finger, C3HC4 type) [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 : human SUFU, suppressor of fused homolog.	0.0, 5739507 suppressor of fused [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q92859 symbol:NEO1: human neogenin precursor.	3.51803E-21, 4505375 neogenin homolog 1 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O96005 symbol:O96005: human cleft lip and palate transmembrane protein 1.	2.06246E-21, 13436080 CLPTM1 protein [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q05195 symbol:MAD: human MAD protein	4.59468E-21, 4505069 MAX dimerization protein 1 [<i>Homo</i>	no hits returned	no hits returned

(antagonizes MYC transcriptional activity).	<i>sapiens</i>].		
Link1 Link2 >UNIPROT Q10588 symbol:BST1: human ADP-ribosyl cyclase 2 precursor (synthesizes cyclic ADP-ribose, a second messenger that elicits calcium release from intracellular stores).	6.63336E-20, 4757874 bone marrow stromal cell antigen 1 precursor [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O00590 symbol:CKD6: human chemokine binding protein 2.	7.08714E-22, 18088707 CCBP2 protein [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9JM05 symbol:PIA4: mouse protein inhibitor of activated STAT protein 4.	3.88963E-20, 24850133 protein inhibitor of activated STAT, 4 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q99835 symbol:SMO: human smoothed homolog precursor.	6.00879E-21, 51094856 smoothed homolog (<i>Drosophila</i>) [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 : human Ets-related transcription factor.	0.0, 5565859 epithelium-restricted Ets protein ESX [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q9UIW2: human NOV/plexin-A1 protein [fragment].	9.9044E-24, 6010217 NOV/plexin-A1 protein [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >tr Q8K4U6: mouse orthodenticle homolog 3 (<i>Drosophila</i>).	2.29212E-28, 21623544 PaxB [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q14548 symbol:Q14548: human HOX2.8 protein [fragment].	4.89269E-14, Animal.dna <i>Homo sapiens</i> homeobox protein (HOX 2.8) mRNA, partial cds.	no hits returned	no hits returned
Link1 Link2 >tr Q69ZA1 MKIAA1791: mouse CDC215 (cell division cycle 2-like 5 (cholinesterase-related cell division controller).	1.02868E-28, 50511115 mKIAA1791 protein [<i>Mus musculus</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P20930 symbol:FILA: human filaggrin precursor [fragment].	4.15572E-22, 51458780 predicted filaggrin [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT Q01212 symbol:Q01212: human profilaggrin [fragment].	7.08858E-22, 55588198 hypothetical protein XP_513808 [<i>Pan troglodytes</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT P20962 symbol:THYP: human parathymosin.	2.52453E-19, 46276863 parathymosin [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >MGI MGI:1202907 symbol:Csrp2: mouse cysteine and glycine-rich protein 2.	8.09159E-26, 15215096 Cysteine and glycine-rich protein 2 [<i>Mus musculus</i>].	no hits returned	no hits returned

Link1 Link2 >UNIPROT Q96JF0 symbol:Q96JF0: human KIAA1877 protein [fragment].	2.88174E-23, 14017971 KIAA1877 protein [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 >UNIPROT O43638 symbol:FREA: human forkhead- related transcription factor 10.	1.4283E-22, 28973785 forkhead-like 18 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link : Rat GATA binding protein 4.	0.0, 25282465 GATA binding protein 4 [<i>Rattus norvegicus</i>].	no hits returned	no hits returned
Link1 Link2 : human protein O- mannosyl-transferase 1.	0.0, 5257133 protein O- mannosyl-transferase 1 [<i>Homo sapiens</i>].	no hits returned	no hits returned
Link1 Link2 : chick progonadoliberin I precursor	3.06851E-46, 311612 chicken gonadotrophin releasing hormone-I [<i>Gallus gallus</i>].	no hits returned	no hits returned