OMA 2011: orthology inference among 1000 complete genomes

Adrian M. Altenhoff^{1,2}, Adrian Schneider³, Gaston H. Gonnet^{1,2} and Christophe Dessimoz^{1,2,*}

¹ETH Zurich, Computer Science, Universitätstr. 6, 8092 Zurich, Switzerland, ²Swiss Institute of Bioinformatics, Universitätstr. 6, 8092 Zurich, Switzerland and ³University of Edinburgh, Institute of Evolutionary Biology, West Mains Rd, Edinburgh, EH9 3JT, UK

Received August 13, 2010; Revised October 1, 2010; Accepted November 13, 2010

ABSTRACT

OMA (Orthologous MAtrix) is a database that identifies orthologs among publicly available, complete genomes. Initiated in 2004, the project is at its 11th release. It now includes 1000 genomes, making it one of the largest resources of its kind. Here, we describe recent developments in terms of species covered; the algorithmic pipeline—in particular regarding the treatment of alternative splicing, and new features of the web (OMA Browser) and programming interface (SOAP API). In the second part, we review the various representations provided by OMA and their typical applications. The database is publicly accessible at http:// omabrowser.org.

INTRODUCTION

Entire genomes are being sequenced faster than ever, yet making sense out of the resulting sequences remains a challenge. Fortunately, there is no need to start *ab initio* with each new genome, as much knowledge can be transferred from evolutionarily related species better characterized. In this context, a central notion is that of *orthologs*, pairs of genes that started diverging through speciation (1). Since by definition, orthologs were the same gene in their last common ancestor, it is commonly assumed that they have kept a similar function [e.g. (2)].

The interest for orthology has given rise to the development of several specialized databases, such as COG/KOG (3), InParanoid (4), OrthoMCL (5), YGOB (6), Roundup (7), Homologene (8), Ensembl Compara (9), HOGENOM (10), EggNog (11), MBGD (12), OrthoDB (13), PhyloDB (14) and PHOG (15).

Since 2004, we have been developing the orthology database OMA (Orthologous MAtrix), with the goal of analyzing all genomes that are publicly available (16).

OMA is based on an algorithm that compares genes on the basis of evolutionary distances, considers distance inference uncertainty and accounts for differential gene losses (17). In an extensive assessment of 11 databases and methods, we showed that the orthologs inferred by OMA show high accuracy in terms of Fitch's phylogeny-based definition and high conservation in terms of functional annotations (18). Results can be downloaded as raw data, consulted interactively using a web interface or accessed through the programming interfaces SOAP and DAS (19).

Recently, we have released the 11th revision of OMA, which includes ortholog predictions among 1000 genomes. This new milestone is an opportunity to inform the community of OMA's latest developments. In the first part of this article, we reflect on the growth of OMA, describe algorithmic refinements and introduce new features of the web and programming interface. In the second part, we discuss the various types of representations and typical use cases. Finally, we conclude with thoughts on the future of OMA and of orthology databases in general.

RECENT DEVELOPMENTS AND NEW FUNCTIONS

Species analyzed

Between 2005 and 2010, OMA was updated 11 times, steadily increasing the number of genomes under analysis from 150 to 1000 genomes (Figure 1). This linear growth is noteworthy, because most orthology inference methods have a computational cost at least quadratic in the number of species. In OMA, we could compensate this computational burden through a combination of hardware and software improvements, and especially the 10-fold speed-up obtained from vectorizing the computation of Smith–Waterman sequence alignments (20).

The 11th release includes 827 bacteria, 103 eukaryotes and 70 archaea. The distribution of species among the

© The Author(s) 2010. Published by Oxford University Press.

^{*}To whom correspondence should be addressed. Tel: +41 44 6327472; Fax: +41 44 6321374; Email: cdessimoz@inf.ethz.ch

This is an Open Access article distributed under the terms of the Creative Commons Attribution Non-Commercial License (http://creativecommons.org/licenses/ by-nc/2.5), which permits unrestricted non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

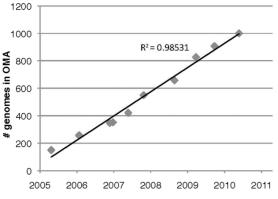


Figure 1. Growth of the OMA database since its first release.

main taxonomic ranks is depicted in Figure 2. Our primary sources for complete and annotated genomes included into OMA are GenomeReviews (21), Ensembl (22), EnsemblGenomes (23) and JGI (http://www.jgi .doe.gov). Thus, we rely on the quality and completeness standards of these databases. In addition, we also update genomes that have significantly changed since they were added to OMA. For instance, in the 10th release, 88 genomes (8.8%) were updated. The priority order of new and updated genomes is influenced by the needs of our users, whom we encourage to give us feedback.

Algorithmic refinements

Since publication of the algorithm of OMA (17), our main algorithmic improvement has been in how we handle splice variants. In eukaryotic genomes, genes often have many splice variants, also called alternative splicings. In the version of the human genome currently in OMA (Ensembl v.55), genes have up to 44 annotated splice variants. This poses a challenge for ortholog prediction algorithms based on protein sequences, because orthology is defined at gene level. Thus, although all proteins produced from a particular gene should reflect its evolutionary history, problems arise when inconsistent splice variants are compared across species.

In previous works, alternative splicings have been handled in mainly three ways. Most commonly, a reference splice variant is selected, usually the longest one, and used exclusively in all computations (4,13). In Ensembl Compara, the reference ('canonical') variant is further required to be a *bona fide* transcript, and not a processed pseudogene, the result of non-sense mediated decay, or other such aberration (A. Vilella, personal communication). A potential problem with this first approach is that the reference variant might not necessarily match across all species. This problem is addressed in the second approach, which consists in keeping all splicing variants for the first part of the analysis, explicitly identifying the corresponding variants across species and choosing a representative one on this basis (25). But this idea entails markedly higher time complexity, and to our knowledge has only been applied to genome pairs. Finally, the third approach consists in considering for each gene the concatenation of all exons. This notion ('metascript'),

proposed in the context of a study on the selective pressure of protein-coding genes (26), has yet to be adopted by orthology databases (whose authors are perhaps reluctant to base all computations on artificial constructs).

In OMA, the way splicing variants are treated uses a combination of the first and second approaches above. First, not all splicing variants are integrated into the OMA sequence database. The longest variant is always retained, but shorter variants are only kept if they differ at least in 10% of their sequence from all longer variants retained. This way, most exons of a given gene will be part of some OMA sequence, while at the same time the total numbers of sequences is kept low. During the all-against-all pairwise alignment phase of OMA, these splicing variants are treated independently and are aligned against all other sequences (and splicing variants) in all other genomes. Later, for the formation of stable pairs, the pairs of putative orthologs, and all subsequent steps of the algorithm, only one splicing variant is used to represent a given gene. This is particularly important in OMA because such variants would be indistinguishable from paralogs, and paralogs are used as potential witnesses of non-orthology in the verification phase (27). At this stage, ideally, one would have to find the optimal combination of variants to keep for each gene, such that a maximal number of orthologs can be found. But as alluded above, the testing of the many combinations is excessively costly and thus a heuristic has to be employed. Thus, for each gene with alternative splicings, we select the variant for which the highest number of significant matches in all other genomes has been recorded in the all-against-all step. This is based on the assumption that a protein involved in more significant matches is also likely to form a higher number of orthologous pairs. For instance, with gene T22D3_HUMAN, the algorithm selects as reference splicing variant the same one as SwissProt's canonical sequence, which happens not to be the longest transcript. In total, out of the 36603 genes with alternate splicings, a non-longest transcript was selected 12752 cases (34%). This proportion varies among the different genomes and is lowest for human (19%) and mouse (21%) and is highest for the pufferfish (54%). The impact on orthology inference is more difficult to assess, but we observe that the new procedure leads to more orthologous pairs inferred, and to larger OMA groups on average.

Hierarchical groups of orthologs

Starting with the 11th release (November 2010), we are adding a new type of orthologous grouping in OMA. Previously, our main type of groups were 'OMA groups', which are constructed with the objective that every pair of genes be orthologous. As we discuss in the next section, however, there are inherent limitations to this type of grouping strategy. As alternative to OMA groups, we now offer 'hierarchical groups of orthologs', groups of genes that descend from a single common ancestral gene within a given taxonomic range. This type of groups are at the core of several other orthology databases, most notably COG/KOG (3), OrthoDB (13) and EggNOG

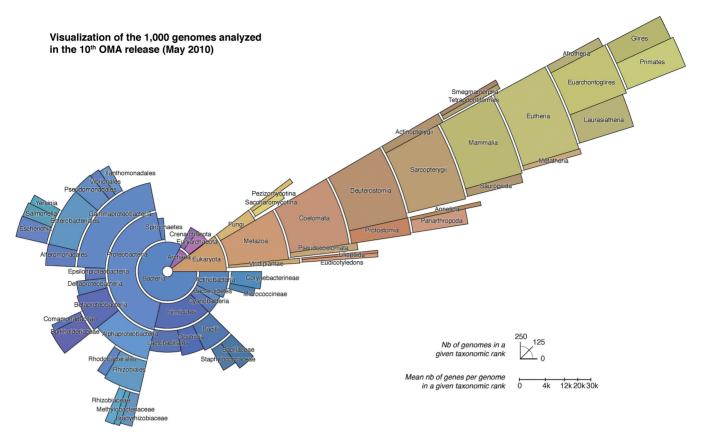


Figure 2. Visualization of the 1000 genomes included in the 10th release of OMA. Lineage assignments are based on NCBI Taxonomy database (24). Note that the radial scale (mean number of genes/genome) is not cumulative, i.e. it refers to the height of individual "band sectors".

(11). We infer such groups from our pairwise orthology predictions and the NCBI taxonomy database (24) using the following idea. It can be easily shown that, with correct and complete pairwise orthology relations, hierarchical groups correspond to connected components in the orthology graph of the relevant species (the graph consists of genes as vertices, and orthology relations as edges). In practice, however, orthology graphs are rarely correct and complete. Missing edges are often not problematic, because the connected components tend to be strongly connected. Spurious edges, however, can lead to erroneous merging of distinct groups. To limit this problem, we identify and remove weak connections between clusters using a min-cut algorithm (28). We discuss applications of hierarchical groups in the last part of the article.

Web interface and API

We added new functionalities to the web and programming interfaces of OMA. First, given that one of the main interests in orthology is to determine the function of sequences, we have substantially improved the integration of Gene Ontology (GO) annotations to OMA. With each new OMA release, we retrieve the latest annotations from the GO consortium (29) and from the GOA database (30), and map them to all relevant sequences in OMA. The annotations are displayed on both protein-centric and OMA group views of the web interface. For all annotations, we now provide evidence codes and references/links to relevant PubMed articles or inference methods.

Second, whenever a gene has several splicing variants, all of them are listed under the 'Information' section. For variants other than the reference one, there is a link under 'Ortholog' to the splicing variant from which the orthology relationships have been computed.

Third, we have developed a new representation, which we call 'genome pair view', to provide a list of all orthologs between any two species. The function is accessible from the 'Download' section and the landing page of the OMA Browser. We discuss typical uses of this format in the next section.

Fourth, protein sequence search has been extended to support approximate sequence matching. The search algorithm is based on a seed-and-extend approach, with seeds of nine residues. Hence, at least nine consecutive characters need to match exactly for a sequence to be found. As a result, our system finds approximate queries almost instantaneously.

And fifth, we have added new functions to the SOAP programming interface to list the various identifiers supported in OMA (e.g. Swiss-Prot, Ensembl and GenBank) and perform conversions among them. For instance, it is now possible to retrieve the OMA identifiers corresponding to a list of Swiss-Prot gene names in a single function call. Using the same mechanism, it is also possible to retrieve Gene Ontology functional annotations

corresponding to a list of proteins identified by any unique identifier supported in OMA. To help users getting started, we provide example clients in Python and Perl programming language (linked from http://omabrowser .org/API.html).

TYPES OF GROUPS AND THEIR APPLICATIONS

The primary product of the OMA pipeline is a list of high-confidence pairs of orthologous genes. This list is available for download, but is for most users too cumbersome to process and too general for typical applications. Thus, we also combine these pairwise relations into four types of groups. The existence of these different representations—and in general of multiple and at times conflicting definitions of orthologous groups—can be confusing for many users. In this section, we review the four types of groups provided in OMA, and discuss their advantages, limitations and applications (Figure 3).

The most straightforward type of groups is the 'proteincentric view'. In this representation, the OMA Browser provides the user with a list of genes orthologous to a specific gene. This view is appropriate for analyses centered on a single or only few genes of interest, e.g. to predict their function. More typical uses are provided in Table 1.

For analyses involving mainly pairs of genomes, the 'genome pair view' accessible in the 'Download' section of the OMA Browser is the most appropriate: it provides a list of all pairs of orthologs between any two genomes specified by the user.

The third type of groups, 'OMA groups', consists in groups of genes in which all pairs are orthologs. In a graph representation with genes as nodes and orthology relations as edge, OMA groups correspond to fully connected subgraphs. Due to this definition, each OMA group includes at most one sequence per species, and, save for inference errors, the gene trees obtained from them should be congruent to the tree of the corresponding species. Indeed, the primary application of OMA groups is to provide input data for phylogenetic inference. In other applications, OMA group are often less appropriate. For example, evolutionary histories involving a duplication will, by definition, require at least two groups. Similarly, spuriously missed (i.e. false negative) orthologous predictions will also result in group fragmentation. And finally, because each protein belongs to one group at most, this representation only captures a subset of all inferred pairs of orthologs.

The last type of groups, 'hierarchical groups', consists in groups of genes that have descended from a common ancestral gene within a specific taxonomic range. Thus, by definition, hierarchical groups include both orthologs and in-paralogs with respect to the last common ancestor of the taxonomic range. In term of the underlying gene trees, hierarchical groups correspond to the leaves of subtrees rooted in the speciation events that define the taxonomic clade in question. By exploring groups across several levels, it is (at least in principle) possible to pinpoint the timing of particular duplication events. Hence, hierarchical groups can convey phylogenetic signal in ways that pairwise orthology/paralogy relations cannot.

CONCLUSIONS AND OUTLOOK

After 7 years of existence and trillions of alignments using over 5 million CPU hours, the OMA database now identifies orthologs among 1000 complete genomes. Recently, we have improved the way we handle alternative splicings, extended our integration of Gene Ontology functional annotations on the web interface, and added new functions to the SOAP programming interface. Furthermore, we have reviewed here how the four grouping strategies provided by OMA can be used for various typical analyses.

As for future developments, we see three areas of high potential for improvement. First, the orthology/paralogy dichotomy only considers speciation and gene duplication events. Thus, this leaves out other important evolutionary mechanisms, such as gene fusion and fission, domain shuffling, hybridization or lateral gene transfer. This

Table 1. Typical applications of orthologs and their most suitable representation of orthology

Application	Appropriate orthology type	Comments
Propagate functional annotations between two genomes	Genome pair view, filtered to 1:1 orthologs	According to current models, 1:1 orthologs are likely to have a similar function.
Identify all orthologs of a gene in a given set of organisms	Protein-centric view	This includes in-paralogs in the target genomes lineages with respect to the speciation event with the query genome
Allign two whole genomes	Genome pair view	Orthologous genes are anchor points.
Align protein-protein interaction networks between two genomes	Genome pair view	Orthologs can be used to restrict the alignment search space. Thus, only conserved parts are used as anchors.
Identify all genes in vertebrates that descended from the ancestral β-hemoglobin Identify orthologs to infer a species tree	Hierarchical group of human β-hemoglobin with 'Vertebrata' as taxonomic rangeOMA groups with high-coverage of the species of interest	 This also retrieves γ-hemoglobin and ε-hemoglobin, which are thought to have diverged within the vertebrates (31). Since, barring classification error, all sequence pairs within an OMA group are orthologs, the corresponding gene tree is expected to follow the species tree.

				(b)			
	mabrowser.org/cgi-bin/gate	Entry HUMAN21428 vay.pl?f=DisplayEntry&p1=374549&p2=ortholo	gs C (Qr Coogle)	IP + Ohttp://omabrov	ser.org/cgi-bin/gateway.c	OMA Browser - Orthologs between	C Q+ Coogle
Entry HUMAN21428	49	(Search)	, n	OMA trowser - Orthologs betwee		Search	
		ence O Group Entry			word O Protein	Sequence O Group O Entry	
Entry HUMAN	21428			Genome P	air Viev	v	
Information	Orthologs (74)	Groupings		Genome		•	
	11000 DE	Sie 4.9		Download orth	ologs be	tween two speci	es
Pairwise orthologs (🗣 download (fasta)	Use the following form	to download the	e list of all predicted orthol	ogs between a pair of genomes of interest.
:1 Orthologs (?)	E Pan troglo		PANTR01925 PONAB16627	orthologs are sometime	es 1:many or m	any:many relations, this d	ownload will return more orthologs than what
	(E) Macaca m		MACMU24682	covered by the OMA g	oups. The resu	It is returned as a tab-sep	parated text file, each line corresponding to c
	E] Callithrix j	acchus	CALJA04306	orthologous relation. The	ne columns are	the two IDs, the type of o	rthology (1:1, 1:n, m:1 or m:n) and (if availab
	(E) Tarsius sy		TARSY09118 MICMU07389	the OMA group contain	ing both seque	nces.	
	E Microcebu		CAVPO17286	Homo sapiens			
	E Dipodomy		DIPOR11143	Mus musculus			
	E Mus musc		MOUSE21140	3 			
	E Rattus nor		RATNO01164 TUPGB08815	Preferred IDs format:			
	E] Tupaia bel E] Procavia c	angen anensis	TUPGB08815 PROCA09976	UniProt/SwissProt IDs +	Get Pairs!		
	E Loxodonta		LOXAF12835				
	E Echinops	telfairi	ECHTE03053				
	(E) Canis fami		CANFA10000				
	E Felis catus E Tursiops t		FELCA10639 TURTR04981				
	E) Bos taurus		BOVIN01504				
	E] Lama guar	nicoe pacos	LAMPA01664				
	E] Pteropus		PTEVA10126				
	E Myotis luc		MYOLU01045 ERIEU05157				
	E Sorex arar		SORAR03646				
	E] Equus cab	allus	HORSE15436				
	E Dasypus r		DASNO12071				
		his domestica mchus anatinus	MONDO06336 ORNAN10673				
)				(d)			
• 1P + • http://or		Group 223720: xay.pftp1=2237204-DisplayGroup	¢)(\$ coops)		1.8080/cgi-bin/gateway.p	Croup HUMAN21428 Mamm M—DisplayTRCroup6p1=03745498p2=Mam	
) P + @ http://or Croup 223720 Croup 223720 Croup 223720 Croup 223720	mabrowser.org/cgi-bin/gatew	vay.pRp1=223720&f=DisplayGroup	6) (Gr Coope		5	Pf=DisplayTRGroup&p1=0374549&p2=Marr	nalla malia C Qr Google
Group 223720 223720 Crowref Keyword	nabrowser.org/cgi-bin/gates	vay.pRp1=223720&f=DisplayGroup	6) (Gr Coope	Croup HUMAN2 1428 Marmalia Oman Drower (Okaya Marmalia Oman Drower (Okaya Marmalia Keyword (Open	tein Sequence 🔾 Group	IY−DisplayTRGroup&p1=0374549&p2=Marr Geerch) ⊕ Entry	nala C) (Qr Coogle
Group 223720 Group 223720 Group 223720 Growsef Crewood Keyword	nabrowstr.org/cgi-bin/gates Protein Sequence @ Gr 20	vay.pRp1=223720&f=DisplayGroup	6) (Gr Googen *	Croup HUMAN21428 Mammalia	tein Sequence () Group	IY−DisplayTRGroup&p1=0374549&p2=Marr Geerch) ⊕ Entry	nalia malia G Qe Coogle
P + O http://or Croup 223720 Croup 223720 Croup 223720 Croup Croup Croup Croup Croup As 33 members erprint: NEPEIGE	mbrowser.org/cgl-bin/gates O Protein Sequence @ Gr 20 7: A1 :33 [12]uhayota	vay offo1-2217204/-DisplayGroup		Cong HIMAX21428 Manuala Cong HIMAX21428 Manuala Cong HIMAX21428 Manuala Drowver Kiswood Pro Hierachical Group of	tein Sequence () Group HUMAN21428 Jukaryota	IY−DisplayTRGroup&p1=0374549&p2=Marr Geerch) ⊕ Entry	nalia malia C Qe Coogle Dountood: * Index, *
Crosp 223720 Crosp 223720 Crosp 223720 Crosp 223720 Crosp 223720 Crosp 22372 Crosp 2237 Crosp 237 Crosp 237 Crop	nibrower.org/cpi-bin/gates Protein Sequence @ Gr 20 r A1 r S3 [[]pharyota 20ose Groups I Phyleth	(seen) (seen) op Enty Profile (Ontology	Downlad, * fass, * davie,	A CONTRACT AND ADDRESS AN	tein Sequence () Group HUMAN21428 Jukaryota	IY−DisplayTRGroup&p1=0374549&p2=Marr Geerch) ⊕ Entry	mula C Q Coope Developed: # Note, #
Croup 22720 223720 223720 Croup 22720 Croup 22720 Croup Carlos Croup Carlos Cro	nabrowser.org/cgi-bin/gates Protein Sequence @ Ge 20 r A1 :33 [Epulanyses Close Groups I Phyleth HUMAN21428	e Profile I Ontology KK1A1_HUMANs/		A T T T T T T T T T T T T T T T T T	tein Sequence O Group HUMAN21428 Jakaryote	M=Dipley/RGroupsol=0374588692-Mem (Secon) 8 Enty 8 at Mammalia level	matia C Q Qe Google Download: * Inste, * Accola dhylmographa (NGP) (1, 5, 1, 1, 1, 2)(Achyle and Academy)(A Accola dhylmographa (NGP) (1, 5, 1, 1, 1, 2)(Achyle and Academy)(A Academy (1, 1, 1, 1)) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1, 1) (1,
Croup 223720 23270 C Keyword A Group 22374 tase family 1 member print: NEPEIGE in List 1 Alignment 1 mo sepiens troglodytes	nibrower.org/cpi-bin/gates Protein Sequence @ Gr 20 r A1 r S3 [[]pharyota 20ose Groups I Phyleth	KIAI_HUMAN/ KIAI_HUMAN/ KIAI_HUMAN/ KIAI_HUMAN/	Downlad, * fass, * davie,	Comp MMM22428 Memolia Comp MMM2248 Comp MMM2248 Comp MMM24 Comp MM24 Co	ten Sequence () Group HUMAN2142E gataryota 999 HUMAN21428 GORGO12659 PANTRO1925	************************************	entia C Q Cooper Deventade & Inter- Actoria delynologoreas (NADP-) (EC 1.1.1.2)/Actingle enclarations actuates lenging (EC 1.1.1.2)/Actingle enclarations Actoria delynologoreas (NADP-) (EC 1.1.1.2)/Actingle enclarations actuates lenging (E
Croup 223720 223720 Carlot 2 223720 Carlot 2 Carlot	nabrowser.org/cgi-bin/gates Potein Sequence @ Gr 20 133 [Educytes HUMAN21428 PANTHO 1925 PONTHO 1925 PONTHO 1925 PONTHO 1925	King (1) - 237724/- DisplayEncep Server) Error Creation Creat	Dewelded: * finsk, # dawle Acoho dalvjorgense (MD*-1020 L1.1 z/Mohy in mountae)/Mobiert maticate lanks / fill posture / 12 z/Mohy in mountae)/Mobiert Puteline unchanacterized poten DAT2p409/2011.	A State	ten Bequence () Group HUMAN21428 ()utaryota Butaryota GORG012659 PANTR01255 PONAB16827	Mr-Dipler/TiCroupsig1=03/3518852=Merr (Sec) Sat Mammalia level AK1A1_HUMAN# Elensyrappin Elensyrappin AK1A1_HUMAN# Elensyrappin Elensyrappin	matia C Q Q Coope
Creup 223720 223730 Creating and a second	O Protein Sequence @ Ge O Protein Sequence @ Ge O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O O		Downlad: * fast, * down Acoho delychoprese (NDP-) EC 11 20/06-byte mulcitate laft) meter X1 300-byte mulcitate laft) meter X1 300-byte Plastire uncharacterized protein DKI2p609/2011. - - - - - - - - - - - - - -	Comparison of the second	teen Bequence () Group HUMAN2142E pakeyota BORO012659 PANTR01825 PONAB16827 MACMU24682	***-01984/*162reus631-0374548652-sker ************************************	matia C C Cooper Deventional: To the second of the second
Creup 223720 223730 Creative Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Cont	nabrowster.org/cgl-bin/gates Protein Sequence @ Ge 20 7 A1 33 [pickayeta HUMAN21428 PANTR0122 PANTR0122 CALAD0306 TARSY00118		Dewelded: * finsk, # dawle Acoho dalvjorgense (MD*-1020 L1.1 z/Mohy in mountae)/Mobiert maticate lanks / fill posture / 12 z/Mohy in mountae)/Mobiert Puteline unchanacterized poten DAT2p409/2011.	Construction C	ten Bequence () Group HUMAN2142E gotaryola GORGO12659 PANTRO1925 PANTRO1925 CALIAO4308	***-019/07/16/20up/81-03/131388/2-Marr ***-019/07/16/20up/81-03/131388/2-Marr ************************************	entia C C Cooper Described: * Inter- Actival dehydrogenes (NDP-) (5C 1.1.1.2)(Actival) en documento matchices family Actival dehydrogenes (NDP-) (5C 1.1.1.2)(Actival) en documento Actival dehydrogenes (NDP-) (5C 1.1.1.2)(Actival) en document
Coup 223720 223720 Course Coup 22372 tase family 1 member print: NEPEricit in List I Alignment I no sapiens sapiens togo pymasos abelii sae mulati lithrix jacchus alus syriothi roobus member	Altrower org/cg-bin/gates Protein Sequence @ Gr 20 20 21 23 20 21 23 21 23 21 23 21 23 21 23 21 24 24 24 24 24 24 24 24 24 24 24 24 24	yey g/tbj-2337244-0bg4bg6ixeg (term) go ① Entry KX1A1_XUMANs? KX1A1_XUMANs? ENSPTRPR0000001585 ENSIMUPR00000025806 ENSIMUPR0000005857e ENSIMUPR0000001531e	Downlad: * fast, * down Acoho delychoprese (NDP-) EC 11 20/06-byte mulcitate laft) meter X1 300-byte mulcitate laft) meter X1 300-byte Plastire uncharacterized protein DKI2p609/2011. - - - - - - - - - - - - - -	Construction C	teen Bequence () Group HUMAN2142E pakeyota BORO012659 PANTR01825 PONAB16827 MACMU24682	Important Important	matia C C Cooper Deventional: To the second of the second
Consp 223720 237320 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520 247520	Patern Seyence @ Ge Patern Seyence @ Ge 20 r A1 33 [phanyots HUMAN21428 PANTR0125 PANTR0125 PANTR0125 CALAD0306 TARSY00118 MCMU26882 CALAD0306 TARSY00118		Devended: * Tank, * Source Andred delyclogenese (MDP-1) EC 1.1.1.2004/shydre reducter/Mido-kete enductasa lanky in ensute AVI (Baurss Lin-PorKBieweit # Port Acc 19460) Publice unchanacterized protein (MPZ-MB201). Andred and Source Lin-PorKBieweit # Port Acc 19460) Control Lin-PorKBieweit # Port Acc 194600 .	Construction C	tem Bequence O Group HUMAN21422E basyots bayy HUMAN21428 GORGO12859 PANATRO1255 PANATRO12559 PANATRO12559 CALIAC4308 CALIAC4308 CALIAC4309118 MICMU07389 OTOGA10461	Important Important	matia C C Cooper Deventional: To the second of the second
Craup 223720 223730 A Group 22377 Charles San John San Bannhein print: NEPEIGE in List I Alignment I I no sapiens toglodyte go pygmacs abelii ase mulata isito sprichs toglodytes sito sprichs coobus minus totoglodytes coobus minus totoglodytes coobus minus	Altrower org/cg-bin/gates Protein Sequence @ Gr 20 20 21 23 20 21 23 21 23 21 23 21 23 21 23 21 24 24 24 24 24 24 24 24 24 24 24 24 24	yey g/tbj-2337244-0bg4bg6ixeg (term) go ① Entry KX1A1_XUMANs? KX1A1_XUMANs? ENSPTRPR0000001585 ENSIMUPR00000025806 ENSIMUPR0000005857e ENSIMUPR0000001531e	Devended: * Tank, * Source Andred delyclogenese (MDP-1) EC 1.1.1.2004/shydre reducter/Mido-kete enductasa lanky in ensute AVI (Baurss Lin-PorKBieweit # Port Acc 19460) Publice unchanacterized protein (MPZ-MB201). Andred and Source Lin-PorKBieweit # Port Acc 19460) Control Lin-PorKBieweit # Port Acc 194600 .	A Construction of the second of the sec	tem Sequence Group HUMAN21428 GORGO12659 PANTR0125 PANTR0125 PANTR01262 CALJA04306 TARSY09118 MICMU07389 MICMU07389 OCGA10461 RABIT00210 RABIT00210	***-019/07/16/20up/821-03/21518852-344/r ***-019/07/16/20up/821-03/21518852-344/r ************************************	matia C C Cooper Deventional: To the second of the second
Crueg 223720 223720 Creating Control 223720 A Group 22372 A tase family 1 member way has 3 members in List 1 Alignment 1 no appies in Cable 1 no	Poter Segunce @ G Poter Segunce @ G 20 20 20 20 20 20 20 20 20 20		Devended: * Tank, * Source Andred delyclogenese (MDP-1) EC 1.1.1.2004/shydre reducter/Mido-kete enductasa lanky in ensute AVI (Baurss Lin-PorKBieweit # Port Acc 19460) Publice unchanacterized protein (MPZ-MB201). Andred and Source Lin-PorKBieweit # Port Acc 19460) Control Lin-PorKBieweit # Port Acc 194600 .	Construction	tem Bequence O Group HUMAN21422E basyots bayy HUMAN21428 GORGO12859 PANATRO1255 PANATRO12559 PANATRO12559 CALIAC4308 CALIAC4308 CALIAC4309118 MICMU07389 OTOGA10461	Phe-Dipelar/TRCroupsol=03/2458852-blant Image: State of the sta	entia C C Cooper Described: * Inter- Actival dehydrogenes (NDP-) (5C 1.1.1.2)(Actival) en documento matchices family Actival dehydrogenes (NDP-) (5C 1.1.1.2)(Actival) en documento Actival dehydrogenes (NDP-) (5C 1.1.1.2)(Actival) en document
Crue 223720 223730 Keyned A Group 2237 intes family 1 meruba print: NEPEIGE in Liet I Algoment I no spiese se mulati se mulati se mulati se spiese site spichts is porellus domys entil	Abrowser org/cgbin/gates Protein Sequence @ Ge 20 20 21 23 23 23 23 23 24 24 24 24 24 24 24 24 24 24	yey g/tbj-2337244-0bg4bg/ineg (mem) wo ① Entry Profile F Ontoiogy AK1A1_HUMAN# ENSPTRPA000000188# ENSPTRPA000000188# ENSPTRPA000000188# ENSPTRPA0000001831# ENSURATION ENSURATION	Devented: ** fanty, ** down Andred adhydrogenaer, MXDP-1 (CC 11.1 gX/Adhydr makutaer/Mido-bate motacaa lamly 11 mmiter A1) (Source Lin-PoRAI Source PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAccc PretAcc PretAccc PretAcc PretAcc PretAcc	Control Section C		Phe-Dipelar/TRGroupsol=03/2458852-bland Image: State of the sta	entia C C Cooper Described: * Inter- Actival dehydrogenes (NDP-) (5C 1.1.1.2)(Actival) en documento matchices family Actival dehydrogenes (NDP-) (5C 1.1.1.2)(Actival) en documento Actival dehydrogenes (NDP-) (5C 1.1.1.2)(Actival) en document
Case 22279 22703 22703 22703 22703 20704 A Group 2237 A Group 223	Platein Sequence @ Ga Platein Sequence @ Ga 20 20 21 23 21 23 21 20 20 20 20 20 20 20 20 20 20		Devented: ** fanty, ** down Andred adhydrogenaer, MXDP-1 (CC 11.1 gX/Adhydr makutaer/Mido-bate motacaa lamly 11 mmiter A1) (Source Lin-PoRAI Source PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAccc PretAcc PretAccc PretAcc PretAcc PretAcc	Control C	Нет Веринос © Group Нимализателе Нимализате	Imperior Transmission	entia C C Cooper Described: * Inter- Actival dehydrogenes (NDP-) (5C 1.1.1.2)(Actival) en documento matchices family Actival dehydrogenes (NDP-) (5C 1.1.1.2)(Actival) en documento Actival dehydrogenes (NDP-) (5C 1.1.1.2)(Actival) en document
Conservation of the second sec	Paterio Seyence @ Ge Paterio Seyence @ Ge 20 r A1 33 [Class Groups I Phylett HUMAN21428 PANTRO1825 PANTRO1825 PANTRO1825 CALIDAUS68 CALIDAUS68 DIPOR11143 MCUS521140 BATNCO1164		Exercise: * finite, * device Andred adhydrogenese (MDP) (20 11.1 20/Abdryde reductes()/Abd-Abdr endicates femty 1 member A11 (Source UnitroXXII Search Andred Abdr Abdr di dhydrogenese (MDP) (20 11.1 20/Abdryde reductes()/Abd-Abdr endicates femty 1 member A11 (Source UnitroXXII Search Abdr) Abdr di dhydrogenese (MDP) (20 11.1 20/Abdryde reductes()/Abd-Abdr endicates femty 1 member A11 (Source UnitroXXII Search Abdr) (20 11.1 20/Abdryde reductes()/Abd-Abdr endicates femty 1 member A11 (Source UnitroXXII Search Abdr) (20 11.1 20/Abdryde reductes()/Abd-Abdr endicates femty 1 member A11 (Source UnitroXXII Search Abdr) (20 11.1 20/Abdryde reductes()/Abd-Abdr endicates femty 1 member A11 (Source UnitroXXII Search Abdr) (20 11.1 20/Abdryde reductes()/Abd-Abdr endicates femty 1 member A11 (Source UnitroXXII Search Abdr) (20 11.1 20/Abdryde reductes()/Abd-Abdr endicates femty 1 member A11 (Source UnitroXXII Search Abdr) (20 11.1 20/Abdryde reductes()/Abd-Abdr endicates femty 1 member A11 (Source UnitroXXII Search Abdr) (20 11.1 20/Abdryde reductes()/Abd-Abdr endicates femty 1 member A11 (Source UnitroXXII Search Abdr) (20 11.1 20/Abdryde reductes()/Abd-Abdr endicates femty 1 member A11 (Source UnitroXXII Search Abdr) (20 11.1 20/Abdryde reductes()/Abd-Abdr endicates femty 1 member A11 (Source UnitroXXII Search Abdr) (20 11.1 20/Abdryde reductes()/Abd-Abdr endicates femty 1 member A11 (Source UnitroXXII Search Abdr) (20 11.1 20/Abdryde reductes()/Abd-Abdr endicates femty 1 member A11 (Source UnitroXXII Search Abdr) (20 11.1 20/Abdr)	Constant and a series and	Нимали (Санарания) Нимали (Санарания) Нимали (Санарания) Нимали (Санарания) Нимали (Санарания) Нимали (Санарания) Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накурона Накур	ACLAL_HUMAN# ACLAL_HUMAN# Comparing the second secon	metia C C Cooper.
Case 32278 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 21728 2172	Albrowser org/cgi-bin/gates Protein Sequence @ Gr 20 20 20 20 20 20 20 20 20 20		Exercise: * Instruct * Exercise Acobol dehydrogensells (MDP+1) EC 1.11. 2(Mohr)en modurasi/Maio-beter market An () Exercise (MOP-1) EC 1.11. 2(Mohr)en modurasi/Maio-beter market understandig optimic MAT2-6409/2001. Acobol dehydrogensells (MAT) () EC 1.11. 2(Mohr)en modurate/(Maio-beter modulates introl 1, member Al () EC/0.11. 2(Mohr)en modurate/(Maio- Acobol dehydrogenses (MAT) () EC 1.11. 2(Mat) ()	Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control	Нет Вершино С Владе Нимала21428 Нимала21428 Докруго Нимала21428 Докруго Нимала21428 Докруго Половодов	Important Important	metia C C Cooper.
Comparison of the second	Paterio Seguro 6 Gr Paterio Seguro 6 Gr 20 20 21 23 20 20 20 20 20 20 20 20 20 20		Devented: ** fanty, ** down Andred adhydrogenaer, MXDP-1 (CC 11.1 gX/Adhydr makutaer/Mido-bate motacaa lamly 11 mmiter A1) (Source Lin-PoRAI Source PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAcc PretAccc PretAcc PretAccc PretAcc PretAcc PretAcc	Construction C	нел Вершика © Влад. НШМАЛК21428 Врануски: 1997 НИМАЛК21428 СОСНИТСКА СОСНИТСКА ПОСИТОВО СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТОВА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТСКА СОСНИТОВА СОСНИТСКА СОСНИТСКА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СОСНИТОВА СО	Important Important	metia C C Cooper.
Constantion of the second seco	Patern Seyance @ Ge Patern Seyance @ Ge 20 r A1 33 [Enterprise] FURMAN21428 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR01225 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANTR0125 PANT		Exercise: * Instruct * Exercise Acobol dehydrogensells (MDP+1) EC 1.11. 2(Mohr)en modurasi/Maio-beter market An () Exercise (MOP-1) EC 1.11. 2(Mohr)en modurasi/Maio-beter market understandig optimic MAT2-6409/2001. Acobol dehydrogensells (MAT) () EC 1.11. 2(Mohr)en modurate/(Maio-beter modulates introl 1, member Al () EC/0.11. 2(Mohr)en modurate/(Maio- Acobol dehydrogenses (MAT) () EC 1.11. 2(Mat) ()	Constant and a series	нет Вершика () Влоде НШМАН21428 ракуска 1997 НИМАН21428 ООРООТСЯВ ООРООТСЯВ ООРООТСЯВ НАМАНИЗАТИ САЦИАНЗА САЦИАНЗА СТСАЛ4961 ТАВЗОРИ18 МСМИ2488 СТСАЛ4961 СТСАЛ4961 СТСАЛ4961 СТСАЛ4961 СТСАЛ4961 ССНРПАЗАЯ САЦИАНЗА СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРПАЗАЯ СОСНРЛАВАЯ СОСНРЛАВАЯ СОСНРЛАВАЯ СОСНРАЛАВАЯ СОСЛНА СОСНРЛАВАЯ СОСНРОВА СОСНРОВА СОСНРОВАЯ СОСНРЛАВАЯ СОСЛНИ		metia C C Cooper.
Cess 22278 Cess 22278 Cess 22728 Cess 2728 Cess 272	Abrowser org/cgi-bin/gates Protein Sequence @ Gr 20 20 20 20 20 20 20 20 20 20		Accide daily-daignesse (ALDP-) (EC 1.1.2)/Addresse in motional (Alde-Anti- anticata lanks) if memice AII (Baures Lindreck VIII) (Alde-Anti- metricata lanks) if memice AII (Baures Lindreck VIII) (Alde-Anti- metricata lanks) if memice AII (Baures Lindreck VIII) (Alde-Anti- anticata lanks) if memice AII (Baures Lindreck VIII) (Alde-Anti- anticata Lindreck VIII) (Baures Lindreck VIII) (Alde-Anti- metricata lanks) if memice AII (Baures Lindreck) (Baures VIII) (Alde-Anti- metricata lanks) if memice AII (Baures Lindreck) (Baures VIII) (Baures VIII) (Baures Lindreck Lindreck VIII) (CI 1.1.2) (Alder) in moticata) (Baures Lindreck VIII) (CI 1.1.2) (Alder) in moticata) (Baures) (CI 1.2) (Alder) in moticata) (Baures) (CI 1.2) (Constant and a second a second and a second a seco	Нет Вершино С Владе Нимализателе Нимализателе Нимализателе Нимализателе Поредования	Important Important	metia
Compared and a second a seco	Potein Seyance @ Ge Potein Seyance @ Ge 20 20 7.41 33 [picksyste] HUMAN21428 HUMAN21428 PANTR0125 PONAB16627 MACMU26882 CALA04306 TARSY0118 MCMU27883 OCHPR08167 TARSY0118 MCMU27883 OCHPR08167 TARSY0118 MCMU2788 DIPOR11143 MOUSE21140 RATR001164 TUPG808615 DIXA116283 CANF010154 TUPG808615 DIXA1164 TUPG808615 DIXA1164 TUPG808615 DIXA1164 TUPG808615 TUPG80815 TUPG808 TUPG808 TUPG80		Accide daily-daignesse (ALDP-) (EC 1.1.2)/Addresse in motional (Alde-Anti- anticata lanks) if memice AII (Baures Lindreck VIII) (Alde-Anti- metricata lanks) if memice AII (Baures Lindreck VIII) (Alde-Anti- metricata lanks) if memice AII (Baures Lindreck VIII) (Alde-Anti- anticata lanks) if memice AII (Baures Lindreck VIII) (Alde-Anti- anticata Lindreck VIII) (Baures Lindreck VIII) (Alde-Anti- metricata lanks) if memice AII (Baures Lindreck) (Baures VIII) (Alde-Anti- metricata lanks) if memice AII (Baures Lindreck) (Baures VIII) (Baures VIII) (Baures Lindreck Lindreck VIII) (CI 1.1.2) (Alder) in moticata) (Baures Lindreck VIII) (CI 1.1.2) (Alder) in moticata) (Baures) (CI 1.2) (Alder) in moticata) (Baures) (CI 1.2) (Constantial activity Constantial Consta	Нел Вершика © Владе НИМАН21428 Декрупка НИМАН21428 Докума НИМАН21428 Докума НИМАН21428 Докума Докума НИМАН21428 Докума Докума НИМАН21428 Докума	***-Ospelar/TiCroupsel=0373548852*-blar ************************************	metia
Course 223720 Course	Abrowser. ang/opi-bin/gates Protein Sequence @ Ge 20 133 [Epidenyete] Elises Groups I Phyletit HUMAN21428 PANTR01225 PONTB1025 TARSY00118 MCCNU7289 TARSY00118 MCCNU7289 TARSY00118 MCCNU7289 TARSY00118 MCCNU7289 TARSY011143 MCDU5221140 RATNO01126 DIPOR11143 MCDU5221140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO0140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140		Exercise: * Instruct * Exercise Acobol dehydrogenesis (MDP+) (EC 11.1 2/Mohry in inductas)(Mob-kets mature A1) (Exercise ModP+) (EC 11.1 2/Mohry in inductas)(Mob-kets mature A1) (Exercise ModP+) (EXERCISE) Acobol dehydrogenesis (Border A1) Bornes Laford A1) (Exercise Mohry A1) Acobol dehydrogenesis (Border A1) Source Laford A1) Acobol dehydrogenesis (Border A1) Source Laford A1) Acobol dehydrogenesis (Border B1) Acobol dehydrogenesis (Constant and a second a secon	Нет Вершино С Владе Нимализателе Нимализателе Нимализателе Нимализателе Поредования	Important Important	Imitia Imitia<
Course 223728 Course 223728 Course 223728 Sarata Course 22378 Sarata Course 23378	Plotein Seguro () California Plotein Seguro () California 20 20 7 A1 33 [Disaryota 20 20 20 20 20 20 20 20 20 20		Accide daily-daignesse (ALDP-) (EC 1.1.2)/Addresse in motional (Alde-Anti- anticata lanks) if memice AII (Baures Linit-MCAI Baues And Alde Priddez) Accide daily-daignesse (ALDP-) (EC 1.1.2)/Addresse in motional (Alde-Anti- anticata lanks) if memice AII (Baures Linit-MCAI Baues And Alde Priddez) Accide daily-daignesse (BADP-) (EC 1.1.2)/Addresse in motional (Alde-Anti- motional service) and the Alder Alder Alder Anti- motional service (PADP-) (EC 1.1.2)/Addresse in motional (Alde-Anti- motional service) and the Alder Alder Alder Alder Anti- motional service (PADP-) (EC 1.1.2)/Addresse in Motional (Baues Inductional service) (PADP-) (EC 1.1.2)/Addresse in motional (Alde-Anti- motional service) (PADP-) (EC 1.1.2)/Addresse in Motional (Baues Inductional service) (PADP-) (EC 1.1.2)/Addresse in Motional (Baues Inductional Service) (PADP-) (EC 1.1.2)/Address	Constantial activity Constantial	селя Вершика © Владе НОМАЛК21428 Доларких НОМАЛК21428 ОСПОСТОВИНИИ НОМАЛК21428 ОСПОСТОВИНИИ ПОЛИКОИТОВИ ОСПОСТОВИНИИ ПАЛКООТОВИ ОСПОСТОВИНИИ ПАЛКООТОВИ ОСПОСТОВИНИИ ПОЛИКОИТОВИ ПОЛИКОИТОВИ ПОЛИКОИТОВИ ПОЛИКОИТОВИ ПОЛИКОИТОВИ ПОЛИКОИТОВИ ПОЛИКОИТОВИ ПОЛИКОИТОВИ ПОЛИКОИТОВИ ПОЛИКОИТОВИ ПОЛИКОИТОВИ ПОЛИКОИТОВИ ПОЛИКОИТОВИ ПОЛИКОИТОВИ ПОЛИКОИТОВИ ПОЛИКОИТОВИ ПОЛИКОИТОВИ ПОЛИКОИТОВИ ПОЛИКОИТОВИ	Important Important	Imitia Imitia<
Cese 32278 Cese 32278 Cese 32778 Cese 3278 Cese 3278	Abrowser. ang/opi-bin/gates Protein Sequence @ Ge 20 133 [Epidenyete] Elises Groups I Phyletit HUMAN21428 PANTR01225 PONTB1025 TARSY00118 MCCNU7289 TARSY00118 MCCNU7289 TARSY00118 MCCNU7289 TARSY00118 MCCNU7289 TARSY011143 MCDU5221140 RATNO01126 DIPOR11143 MCDU5221140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO0140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO01140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140 RATNO0140		Accide daily-daignesse (ALDP-) (EC 1.1.2)/Addresse in motional (Alde-Anti- anticata lanks) if memice AII (Baures Linit-MCAI Baues And Alde Priddez) Accide daily-daignesse (ALDP-) (EC 1.1.2)/Addresse in motional (Alde-Anti- anticata lanks) if memice AII (Baures Linit-MCAI Baues And Alde Priddez) Accide daily-daignesse (BADP-) (EC 1.1.2)/Addresse in motional (Alde-Anti- motional service) and the Alder Alder Alder Anti- motional service (PADP-) (EC 1.1.2)/Addresse in motional (Alde-Anti- motional service) and the Alder Alder Alder Alder Anti- motional service (PADP-) (EC 1.1.2)/Addresse in Motional (Baues Inductional service) (PADP-) (EC 1.1.2)/Addresse in motional (Alde-Anti- motional service) (PADP-) (EC 1.1.2)/Addresse in Motional (Baues Inductional service) (PADP-) (EC 1.1.2)/Addresse in Motional (Baues Inductional Service) (PADP-) (EC 1.1.2)/Address	Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial Constantial C	Нел Вершика © Владе НИМАН21428 Декрупка НИМАН21428 Докума НИМАН21428 Докума НИМАН21428 Докума Докума НИМАН21428 Докума Докума НИМАН21428 Докума Докума Докума НИМАН21428 Докума		metia C Operange Accord adhysiogeness (NADP-) (EC 1.1.1.2)/Achysios exclusion/ medicines lenny 1 member AN (Source Label Activity) (Activity) and Activity medicines lenny 1 member AN (Source Label Activity) (Activity) and Activity medicines lenny 1 member AN (Source Label Activity) (Activity) (Activity
Cess 2279 Cess 2279 Cess 2279 Cess 2779 Cess 2779	Allowest org/cgi-bin/gate Protein Sequence @ Gr 20 20 20 20 20 20 20 20 20 20 20 20 20	avg.afbs1-2337284-0bg4bgCinegi Clean ac ac<	Processors ** ***** *************************	Constanting and a second a	Humanization Brouge Humanization Brouge Humanization Brouge Balance Brouge Humanization Brouge Humanization Brouge Humanization Brouge Autoritistic Caludotistic Parating Caludotistic Caludotistic Caludotistic Caludotistic Caludotistic Concentration Caludotistic Procontine Caludotistic Concentratistic Caludotistic Concentratistic Caludotistic Procontine Caludotistic Concentratistic Caludotistic Concentratistic Caludotistic Concentratistic Caludotistic C		metia
Crosp 223720 Crosp 223720 Crosp 223720 Crosp 223720 Crosp 223720 Crosp 22372 Crosp 2237 Crosp 237 Crosp 237 Crop	Paterin Seyance @ Ge Paterin Seyance @ Ge 20 21 22 23 23 24 24 24 24 25 26 26 26 26 27 20 20 20 20 20 20 20 20 20 20		Accide daily-daignesse (ALDP-) (EC 1.1.2)/Addresse in motional (Alde-Anti- anticata lanks) if memice AII (Baures Linit-MCAI Baues And Alde Priddez) Accide daily-daignesse (ALDP-) (EC 1.1.2)/Addresse in motional (Alde-Anti- anticata lanks) if memice AII (Baures Linit-MCAI Baues And Alde Priddez) Accide daily-daignesse (BADP-) (EC 1.1.2)/Addresse in motional (Alde-Anti- motional service) and the Alder Alder Alder Anti- motional service (PADP-) (EC 1.1.2)/Addresse in motional (Alde-Anti- motional service) and the Alder Alder Alder Alder Anti- motional service (PADP-) (EC 1.1.2)/Addresse in Motional (Baues Inductional service) (PADP-) (EC 1.1.2)/Addresse in motional (Alde-Anti- motional service) (PADP-) (EC 1.1.2)/Addresse in Motional (Baues Inductional service) (PADP-) (EC 1.1.2)/Addresse in Motional (Baues Inductional Service) (PADP-) (EC 1.1.2)/Address	Constantial and a constantial and constantial and constantial and a constantial and a constantial	Кел Вершика © Владе НИМАЛК21428 Давирика НИМАЛК21428 Доворска НИМАЛК21428 Доворска ПОЛКА1428 Доворска ПОЛКА1428 Доворска ПОЛКА1428 Доворска ПОЛКА1428 ПОЛКА14 ПОЛКА14 ПОЛКА14 ПОЛКА14 ПОЛКА14 ПОЛКА14 ПОЛКА14 ПОЛКА14	Important Important	meta C C+ Cospet Activital dehydrogenesa (NACP+) (C = 1.1.1.2) C = Cospet C = Cospet Activital dehydrogenesa (NACP+) (C = 1.1.1.2) C = Cospet C = Cospet Pathie extremely C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet C = Cospet </td

Figure 3. The four types of ortholog grouping provided in OMA. (a) protein-centric view reports orthologs to a gene of reference; (b) genome pair view lists all orthologs between two species; (c) OMA group view displays sets of genes in which all pairs of genes are orthologs and (d) hierarchical groups, groups of genes that descend from a single common ancestral gene within a given taxonomic range.

latter phenomenon is particularly relevant in prokaryotes, where lateral gene transfer has long been recognized as a major evolutionary force. Second, orthology and paralogy are pairwise relations, and are thus ill-suited to expressing the evolutionary relationship of more than two genes at a time. Instead, gene trees labeled with relevant evolutionary events (speciation, duplication, LGT, etc.) constitute a better representation of the evolutionary relationships. As was suggested previously (32), we believe that in the medium term, gene trees will supersede pairwise orthology/paralogy predictions in most databases. And third, the growth in newly sequenced genomes will further accelerate in the foreseeable future. To cope with this increase, orthology inference algorithms will have to become more efficient. We are currently looking at ways to bypass part of the all-against-all phase by propagating orthology predictions across related organisms, but other approaches will need to be explored as well if we are to someday predict orthology among 10 000 genomes.

ACKNOWLEDGEMENTS

We thank all users of OMA and in particular those who have provided comments and suggestions. We also thank the attendees of the PhyloSIB 2010 meeting for the stimulating discussions in the session 'Scaling up to orthology prediction of 10 000 genomes'. Finally, we are grateful to Manuel Gil, Elke Shaper, Adam Szalkowski and the anonymous referees for their feedback on the article.

FUNDING

Funding for open access charge: The publication charges are funded through the lab's ordinary budget.

Conflict of interest statement. None declared.

REFERENCES

- Fitch,W.M. (1970) Distinguishing homologous from analogous proteins. Syst. Zool., 19, 99–113.
- Koonin, E.V. (2005) Orthologs, paralogs, and evolutionary genomics. Annu. Rev. Genet., 39, 309–38.
- Tatusov,R.L., Fedorova,N.D., Jackson,J.D., Jacobs,A.R., Kiryutin,B., Koonin,E.V., Krylov,D.M., Mazumder,R., Mekhedov,S.L., Nikolskaya,A.N. *et al.* (2003) The cog database: an updated version includes eukaryotes. *BMC Bioinformatics*, 4, Article no. 41.
- Ostlund,G., Schmitt,T., Forslund,K., Köstler,T., Messina,D.N., Roopra,S., Frings,O. and Sonnhammer,E.L.L. (2010) Inparanoid 7: new algorithms and tools for eukaryotic orthology analysis. *Nucleic Acids Res.*, 38, D196–D203.
- Li,L., Stoeckert,C.J.J. and Roos,D.S. (2003) Orthomcl: identification of ortholog groups for eukaryotic genomes. *Genome Res.*, 13, 2178–2189.
- 6. Byrne,K.P. and Wolfe,K.H. (2005) The yeast gene order browser: combining curated homology and syntenic context reveals gene fate in polyploid species. *Genome Res.*, **15**, 1456–1461.
- DeLuca, T.F., Wu, I.-H., Pu, J., Monaghan, T., Peshkin, L., Singh, S. and Wall, D.P. (2006) Roundup: a multi-genome repository of orthologs and evolutionary distances. *Bioinformatics*, 22, 2044–2046.
- Wheeler, D.L., Barrett, T., Benson, D.A., Bryant, S.H., Canese, K., Chetvernin, V., Church, D.M., DiCuccio, M., Edgar, R., Federhen, S. *et al.* (2007) Database resources of the national center for biotechnology information. *Nucleic Acids Res.*, 35, D5–D12.
- Vilella,A.J.J., Severin,J., Ureta-Vidal,A., Durbin,R., Heng,L. and Birney,E. (2009) Ensemblecompara genetrees: analysis of complete, duplication aware phylogenetic trees in vertebrates. *Genome Res.*, 19, 327–335.
- Penel,S., Arigon,A.-M., Dufayard,J.-F., Sertier,A.-S., Daubin,V., Duret,L., Gouy,M. and Perrière,G. (2009) Databases of homologous gene families for comparative genomics. *BMC Bioinformatics*, 10(Suppl. 6), S3.
- Muller, J., Szklarczyk, D., Julien, P., Letunic, I., Roth, A., Kuhn, M., Powell, S., von Mering, C., Doerks, T., Jensen, L.J. *et al.* (2010) eggnog v2.0: extending the evolutionary genealogy of genes with enhanced non-supervised orthologous groups, species and functional annotations. *Nucleic Acids Res.*, 38, D190–D195.
- Uchiyama, I., Higuchi, T. and Kawai, M. (2010) Mbgd update 2010: toward a comprehensive resource for exploring microbial genome diversity. *Nucleic Acids Res.*, 38, D361–D365.
- Kriventseva, E.V., Rahman, N., Espinosa, O. and Zdobnov, E.M. (2008) Orthodb: the hierarchical catalog of eukaryotic orthologs. *Nucleic Acids Res.*, 36, D271–D275.
- Huerta-Cepas, J., Bueno, A., Dopazo, J. and Gabaldón, T. (2008) Phylomedb: a database for genome-wide collections of gene phylogenies. *Nucleic Acids Res.*, 36, D491–D496.

- Datta,R.S., Meacham,C., Samad,B., Neyer,C. and Sjölander,K. (2009) Berkeley phog: phylofacts orthology group prediction web server. *Nucleic Acids Res.*, 37, W84–W89.
- 16. Dessimoz, C., Cannarozzi, G., Gil, M., Margadant, D., Roth, A., Schneider, A. and Gonnet, G. (2005) OMA, a comprehensive, automated project for the identification of orthologs from complete genome data: introduction and first achievements. In McLysath, A. and Huson, D.H. (eds), *RECOMB 2005 Workshop on Comparative Genomics*. Springer-Verlag, Berlin/ Heidelberg, Vol. LNBI 3678 of Lecture Notes in Bioinformatics, pp. 61–72.
- Roth,A.C., Gonnet,G.H. and Dessimoz,C. (2008) The algorithm of OMA for large-scale orthology inference. *BMC Bioinformatics*, 9, 518.
- Altenhoff, A.M. and Dessimoz, C. (2009) Phylogenetic and functional assessment of orthologs inference projects and methods. *PLoS Comput. Biol.*, 5, e1000262.
- Schneider, A., Dessimoz, C. and Gonnet, G.H. (2007) OMA Browser — exploring orthologous relations across 352 complete genomes. *Bioinformatics*, 23, 2180–2182.
- Szalkowski, A., Ledergerber, C., Krähenbühl, P. and Dessimoz, C. (2008) Swps3 - fast multi-threaded vectorized smith-waterman for ibm cell/b.e. and x86/sse2. *BMC Res. Notes*, 1, 107.
- Kersey, P., Bower, L., Morris, L., Horne, A., Petryszak, R., Kanz, C., Kanapin, A., Das, U., Michoud, K., Phan, I. *et al.* (2005) Integr8 and genome reviews: integrated views of complete genomes and proteomes. *Nucleic Acids Res.*, 33, D297–D302.
- 22. Flicek, P., Aken, B.L., Ballester, B., Beal, K., Bragin, E., Brent, S., Chen, Y., Clapham, P., Coates, G., Fairley, S. et al. (2010) Ensembl's 10th year. Nucleic Acids Res., 38, D557–D562.
- Kersey, P.J., Lawson, D., Birney, E., Derwent, P.S., Haimel, M., Herrero, J., Keenan, S., Kerhornou, A., Koscielny, G., Kähäri, A. *et al.* (2010) Ensembl genomes: extending ensembl across the taxonomic space. *Nucleic Acids Res.*, 38, D563–D569.
- 24. Sayers,E.W., Barrett,T., Benson,D.A., Bryant,S.H., Canese,K., Chetvernin,V., Church,D.M., DiCuccio,M., Edgar,R., Federhen,S. *et al.* (2009) Database resources of the national center for biotechnology information. *Nucleic Acids Res.*, 37, D5–D15.
- Goodstadt, L. and Ponting, C.P. (2006) Phylogenetic reconstruction of orthology, paralogy, and conserved syntemy for dog and human. *PLoS Comput. Biol.*, 2, e133.
- Hoffman, M.M. and Birney, E. (2007) Estimating the neutral rate of nucleotide substitution using introns. *Mol. Biol. Evol.*, 24, 522–531.
- Dessimoz, C., Boeckmann, B., Roth, A.C.J. and Gonnet, G.H. (2006) Detecting non-orthology in the cogs database and other approaches grouping orthologs using genome-specific best hits. *Nucleic Acids Res.*, 34, 3309–3316.
- Karger, D.R. (1994) Random sampling in cut, flow, and network design problems. *Proceedings of the twenty-sixth annual ACM* symposium on Theory of computing. ACM, New York, NY, USA, pp. 648–657.
- Harris, M.A., Clark, J., Ireland, A., Lomax, J., Ashburner, M., Foulger, R., Eilbeck, K., Lewis, S., Marshall, B., Mungall, C. et al. (2004) The Gene Ontology (GO) database and informatics resource. *Nucleic Acids Res.*, 32, 258–261.
- Barrell,D., Dimmer,E., Huntley,R.P., Binns,D., O'Donovan,C. and Apweiler,R. (2009) The goa database in 2009–an integrated gene ontology annotation resource. *Nucleic Acids Res.*, 37, D396–D403.
- Aguileta,G., Bielawski,J.P. and Yang,Z. (2006) Proposed standard nomenclature for the alpha- and beta-globin gene families. *Genes Genet. Syst.*, 81, 367–371.
- 32. Gabaldón, T. (2008) Large-scale assignment of orthology: back to phylogenetics? *Genome Biol.*, **9**, 235.