# Utilization of Computer Programs and Molecular Biology in Documentation of Egyptian clover

Abd alaziz.T. Bondok<sup>1</sup>, Shereen M. ElNahrawy<sup>1</sup>, and Ahamed Fouid<sup>2</sup>

#### ABSTRACT

Egyptian clover varieties are part of a very important agricultural family, second only to cereals. In this paper, the materials under the present investigation consisted of three biological datasets, containing different protein characteristics annotated from interpro, prints and quick Godatabasesthey were selected and have been applied to data from XML flat files into a local database of size 10MB in oracle tool which is used throughout the experiments Shimaa A. Badawy(2013).Moreover, in the present study, a new program was designed and applied which showed high flexibility and efficient of mining the hierarchy (Molecular Biology data of *T. alexandrinum* L.). In addition describe protein characteristics including family of protein, finger print of protein of *Trifoliumalexandrinum* L.

Keywords: Molecular biology, computer programs, documentation, *Trifoliumalexandrinum* L., hierarchy databases, sequences, framgments, protein.

#### **INTRODUCTION**

The genus *Trifolium* comprises approximately 290 species. While, *T. repens, T. Pratense, T. nigrescens*, etc., are important constitutents of temperate pastures, *T. alexandrinum* and *T. resupinatum* are cultivated as winter annual fodder in the tropical and sub-tropical belt. *Trifoliumalexandrinum*, commonly known as berseem or Egyptian clover is an important winter annual fodder legume cultivated in Egypt Khaled Y.Abdel-Halim (2014).

In the present study an attempt was carried out have tried to develop methods of the Egyptian clover documentation through working on two levels:

- Moleclar biology data.

- Databases of computer programs.

Databases are the heart of computer programs essentially they are electronic filing cabinets that offer a convenient and efficient method of storing vast amounts of information. There are many different databases types, depending on the nature of the information being stored (e.g, sequences, structures, etc.). The number of different databases is growing very rapidly. During the year 2000, 55 new databases were created, bringing the total at the end of the year to 2811. Documentation contains data related to molecular biology characteristics and data bases of computer programs characteristics related to Egyptian Clover.

The Reasons for doing documentation on the Egyptian cloverare to:

- Avoiding genetic erosion which has also been caused by the replacement of domestic cultivars of Egyptian clover by improved cultivars with a narrow genetic base (Hawkes, 1983).

Moreover, Gene Banks will have the fact that genetic variability allows populations to adapt to environmental changes is valied for all organisms including Egyptian clover, .....etc and microflora where the evaluation course is quite variable. The evolutionary process that maintained this diversity in the past is unable to surve in the present technological era. The present abundance of genetic diversity which still survives is being threatened by a combination of population pressures, adverse economic conditions and the interaction among these factors and subsequently further deterioration of genetic resources (Egyptian Clovercultivars).

The science of genetics in general and precisely the conservation genetics should play a sizable part to minimize the effect of these risks (Abdel Salam et al., 1994).

In Egypt, The population is rapidly increasing and at the same time these is a big gap between the food and feed needs and the available production of the crops. This due to the limited natural recourses especially the water resources. The visible way to narrow this gap is through vertical development of our agricultural system. High yielding varieties of various crops are playing very efficient roles in increasing the agricultural production vertically.Our objective in current research paper was developing high yielding cultivars of Egyptian clover

To develop varieties so, this is a need to use of huge information in molecular biology and computer science area to make databases on DNA hierarchy and amino acids sequences levels in Egyptian clover varieties to create a new varieties in a short time.

<sup>&</sup>lt;sup>1</sup>Forage crops Res. Department, field Crops Res. institute, ARC, Giza, Egypt.

<sup>&</sup>lt;sup>2</sup>Faculty of computer and information, Ain Shams univ., Cairo, Egypt.

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#### The aims of the present study were:

- Designed and applied new database for mining the hierarchy related to Egyptian Clover. This database will enable to describe protein attributes including family of protein and its fingerprint related to Egyptian clover.
- Determination of best programs which might be be used efficiently in documentation of Egyptian clover germplasm.
- In future goal, update of the breeding methods of Egyptian clover speciesemploying computer programs.

#### MATERIALS AND METHODS

#### Plant material:

Plant material of Egyptian clover was obtained from the Forage Crops Res. Depart. Field Crops Res. Institute, ARC, Giza Egypt.

#### **SDS – PAGE electrophoresis:**

Total protein content was determined in grounded fine powder seeds of each sample by the mothd described by Bradford (1976) using bovine serum albumin (96%, Sigma Chemical Co, St. Louis, MO, USA), as standard, then total soluble proteins were extracted with extraction buffer. Fifty  $\mu$ 1 of the extract were mixed with 50 of SDS, 5% v/v  $\beta$  mecaptothanol, 7% v/v glycerol and 0.03% bromphenol blue and boiled for 7min in a boiling water bath. 14  $\mu$ 1 of the sample was loaded on to each well.

Electrophoresis SDS-PAGE was carried out according to the procedures of Laemmli (Laemmli, 1970) in 1.5 mm thick gels with 14% (w/v) separating gel and 4% (w/v) stacking gel in a vertical

electrophoress unit (Cleaver Scientific, England). SDS – PAGE was carried out at 75 volt for 3 hours. After electrophoresis, the gels were over night stained using 0.1% (w/v) Coomassie Brilliant Blue R-250. Then, distained using a 10%(v/v) acetic acid solution until a clear background was achieved. A page ruler pertained protein ladder (thermo – Fisher Scientific) was used as protein molecular weight marker.

Gel documentation system (Geldoc – It<sup>e</sup> imaging system, uvp, England), was applied for data scoring and documentation. Total lab analysis software (Total Lab TL120,V2008)was employed for constructingbinary matrix for SDS PAGE data according to presence or absence of a band of each sample which remarked as I or O.

#### **DATA BASE LOADER**

The main issue now is how to get available biological data on to a local database in order to perform different kinds of computation.

In fact, the three discussed databases, above, are available in XML flat files to down load via the web, interpro, prints and quick go. The whole process is illustrated in Fig (1). First, XML flat files are parsed by a Java or  $C^{++}$ .

Parser program to extract table definitions tages and data. Second extracted data is loaded into oracle database, using a DBLoaderhttp://www.ailab25.engr.uconn.edu: in order to produce a local biological database, called BioDB. Note that one has to determine if he wants to process all data or part of it, database loader application in the present study is performed to the molecular biology data.



Fig. 1. Preprocessing to create local database (BioDB)

#### Inter pro database:

Inter pro is one of the database with signature diagnostic for protein families, domains, repeats, or functional sites, which amalgamates the efforts of proslte, prints, Pfam (Bat man et al., 2000), and pro dom (Corpet et al., 2000) database projects.

#### Prints database:

Prints database has been the international project to cooperate with prosite, pfam, and pro Dom databases. This database houses a collection, of fingerprint information for protein families, fingerprints are groups of motifs (i.e., specific protein sequences fragments) that could be inferred by aligning similar sequences (Attwood et al., 2002).

#### **Quick Godatabase:**

Quick go contains information about the gene ontology produced by the gene ontology(Go) consortium (Ashburner, et al, 2000). The gene ontology components of IPR000276. Gene ontology part of biological process of IPR 000276 is shown. Each gene ontologycomponents has itsown go entryid, in the from of go xxxx with x as digits.

#### **RESULTS AND DISCUSSIONS**

#### **Molecular Biology Data**

#### **Biological data:**

Biological data of *Trifoliumalexandrinum* is an informative -rich domain, where data needs to be analyzed. Biological data of *Trifolumalexandrinum* has been chosen for two reasons: the first one is its built-in hierarchy in most of the databases available as will be illustrated in details in the next section: The other reason is the use of biological data is timely as the information community is in great need for using data mining techniques to predict, for example gene, functions by analyzing data cumulated from diversified sources and protein functions as well in the present study used three available databases.



Fig. 2. Three used biological databases

#### - Interpro database:

Interproof Trifolumalexandrinum is one of the databases with signatures diagnostic for protein families. domains, repeats, or functional sites (Apweileret al 2000) which amalgamates the efforts of PROSITE (Hoffman et al, 1999), PRINTS' (Attwood et Pfam(Batmanet al, 2002), al, 2000), and ProDom(Corpetet al, 2000) database projects. It is a vital tool for the computation of functional classification of newly determined sequences of Trifoliumalexandrinum that lack biochemical characterization. Interproof Trifoliumalexandrinum has rationalize been developed to protein'family characterization and inherit functional insights in order functionalities. to discover new Interproof *T.alexandrinum* provides interface for both text-and sequence-based searches. Overlapping domains, signatures or profiles describing common domains or protein families were merged into a single Interpro entry with a unique accession number (which takes the form IPRxxxx, where x is a digit). An example of an Interpro of T. alexandrinum search results is shown in Fig. (3) Other links of protein family signatures are also provided, such as Pfam database (PF00001), PRINTS database (PR00237), and PROSITE (PS00237). The type of ID is specificed whether it is a protein family domain repeat, or functional site, where it is a family type in the current case.

Figure (3) also illustrates family tree if there exists one, whether it is a-family or a domain type. Hierarchical information in the interproof *Trifolumalexandrinum* database includes both is- $a^1$  (parent -child) and contains found -in information for example, in 'is-a' relationship if there exists an edge between two nodes we can say that one of them is a parent of the other.

#### - PRINTS database:

PRINTS of Trifolumalexandrinum database contains information about the Pfam, and ProDom databases. This database houses a collection of fingerprint information for protein families (Attwood et al, 2002). Fingerprints of Trifolumalexandrinum are groups of motifs (i.e., specific protein sequences fragments) that could be inferred by aligning similar sequences. Those motifs characterize aligned family and provide specific diagnostic signature. Fingerprints are more powerful than single motif approaches. The technique used to collect fingerprints is to discriminate patterns in a hierarchical form, i.e., protein sequences. Such a hierarchical approach has been used to, resolve Gprotein-Coupled -Receptors (GPCRs) super families into their constituent families and receptors subtypes and to classify a variety of channel proteins, transporters, and enzymes. Fig. (4) shows the results for family ID IPR000276 fingerprint at PRINTS. Each fingerprint of *Trifolumalexandrinum* entry has its own PRINTs entry ID< called accession number, which is PR00237 in this cases.

#### - QuickGO Database:

QuickGOof *Trifolumalexandrinum* contains information about the Gene ontology, produced by the gene Ontology (GO) Consortium (Ashburner*et al* 2000)/ The Gene ontology components of IPR000276 are shown in Fig. (6)where they are linked to interpro database. In Fig.(5) (a), Gene Ontology part of Biological process.IPR000276 is shown. Each Gene Ontologyof *Trifolumalexandrinum* component has its own Go-entry id, in the form of GO-XXXXX with x as digits. Representation of hierarchical knowledge has widely seen as an important aspect in the design of a formal ontology. Gene Ontology structure is represented as a directed-Acyclic Graph (DAG) that represents a network rather than a tree. Each node can be a child or a parent; a child may have more than one parent. There are two types of parents in a hierarchical structure that a node can have; is -arelationship or 'partof relationship. A node can have more than one parent of one type 'is-a'/'part-of relationship or a mixed of both and part-of relationships,

Access. Number		Macthes: 6914 proteins					
	Number	Rhodopsin-like GPCR superfamily					
Signatures of protein	Signatures	PF0001:7tm -1					
families		PR00237:GPCRRHODOPSN PS'00237:GproteinJR Recep-					
		F1-1					
		PS50262:Gprotein recap FI-2.					
	Туре	Family					
Part of children tree of	Children	IPR00025;Melatonin Receptors					
GPCR superfamily	_	IPR00174; interleuk in-8 Receptor					
	Erocess	G;Protein coupled receptor protein					
J		signaling pathway (GO:0007186)					
Gene ontology production	Function	Rhodopsin-like receptor activity (GO.005164)					
	Component	Integral to membrane (GO:0016021)					
	Database	Blocks:BL00.237					
	- Links						

#### Fig. 3. Interporof T. alexandrinumExamples of IPR000276 Search results

		Gpcrrhodopsn (view relation] [view alignment] [view
		structure]
No. of	Accession	PR00237
motifs	No of moieties	7
	Creation Date	12-JUL-2010
included in the	Title	Rhodopsin-lik'e superfamily signature (GPCR)
fingerprint,		
Literature	Database References	Interpro:IPR000276JBLOCKS:BL002 37:Pfam:PF00O01
references		
where	'Literature References	1.ATTWOOD,T.K. AND
discussion		FINDLAYJ.B.C.
about		Fingerprinting G protein-coupled
motifs		receptors
appears		PROTEIN ENG.7(2) 195 -203 (1994)
		G protein-coupled receptors (GPCRs) constitute a vast protein
		family that encompasses a wide range of functions.
Part of IDs of	Documentation	G protein-coupled receptors (GPCRs) constitute a vast protein
protein Matches for		family that encompasses a wide range of functions.

Fig. 4. Shows the result for family IDIPR 000276 finger print at PRINTS of T.alexandrinum

The is-a' relationship or 'part-of relationship, node can have more than one parent of one type is-a'/part-of relationship refers to 'when a child is an instance of the parent.and the 'pat of relationship. These types of relationships of *Trifolumalexandrinum* are available for the three, extensions of gene product; the molecular function, the biological processes and the cellular component. For example, in Fig. (5) a tree term, which has a (P) in front of it, means this term' is a part of the above term. However, a tree term, which has an (I) in front of it, means this term is a child of the term above it. Fig. (6)illustrates a part of the biological process of IPRG000276; a biological process is a part of the Gene ontology, but a cellular process is a biological process and a cell communication is a cellular process, etc. In Fig. (5), which shows the description of molecular function IPR000276, molecular function is a part of the Gene ontology, but signal transducer activity is a molecular function. Finally, each item described in the tree of biological process, molecular function, or cellular component, may have other children, which applies to the same rules as their parents.

#### **Tables Created at BioDB:**

BioDBof *Trifolumalexandrinum* contains a database schema from annotating information of the three databases as illustrated in Fig. (7), which consist of 6 Tables as follows:

	1 0	GO':0007186
	Name	G-protein coupled receptor protein signaling pathway
Parent tree	Tree	Gene ontology (GO:0003673) (P) Biological process (GO:0008150) (1): Cellular process (1) Cell communication (1) signal transduction
	Child terms	<ul> <li>Signal transduction during conjugaton with cellular fusion.</li> <li>Signal transduction during conjugation without cellular fusion</li> </ul>
Part of child terms	Interpro Mappings	<ul> <li>Psin</li> <li>Chemokine receptor</li> <li>G-Protein, Gamma Subunit</li> </ul>

## Fig. 5. Part of Quick GO of *T.alexandrinum* reference for biological process of IPR000276 (GO:0007186) (HTTP://WWW.geneontology.org)

GO;0001584	
Rhodopsin-like receptor activity	Name
Gene ontology (GO:0003673)	Tree
(P) Molecular function (GO: 0008150)	
(1): signal transducer activity	
(1) Receptor activity	
(1) transmembrane receptor activity	
(I) G-protein coupled receptor Activity	
(I) Rhodopsin-like receptor Activity	
- Nucelotide receptor activity	Child terms
- Viral receptor activity	
- Amine receptor activity	
- Opsin	Interpro Mappings
- Histamine H4 receptor	
- Perojpsin	

Fig. 6. Part of QuickGO reference for molecular function of IPR000276 (GO: 0001584)



Fig. 7. BioDatabaseof TrifolumalexandrinumSchema used in experiments

#### A- Interpro Table of Trifolumalexandrinum:

Which includes Interpro entry ID, (primary key), type of the entry (family, domain, etc), parent list/child list (the relationship used to indicate true protein family/subfamily relationships), contains list the relationship used to indicate domain composition. Some domains can be found in more than one type of protein or family of proteins, but is not a SUBTYPE in the family.

#### **B-** INTERPRO-GO Tableof Trifolumalexandrinum:

That includes Interpro entry ID. Interpro entry may have multiple Gene ontology (GO) annotations, hence the possible duplications of Interpro-ID in this table. Not all Interpro entries are annot-ated by GO. Another attribute in Interpro,-GO also includes GO-ID, which may be associated with multiple Interpro entries as different proteins may share similar functions. For example, in Table (1) Interpro-id IPR000003 has three molecular functions; DNA binding (GO:0003677), Ligand-depen-dent nucle-ar receptor and GO-category describes functional classification of the entry, where Gene Ontology (GO) terms are described in' three **Molecular biology**  categories: Molecular function, Cellular Component, Biological Process. FinaUy, "GO-description gives Brief annotation about the function of the interpro entry. An example of the outcome of INTER-PRO-GO table is given in Table (1).

#### C- FINGERPINT tableof Trifolumalexandrinum:

In table (2) lists protein fingerprint fields from PROSITE, PFAM, PRODOM, and PRINTS to each Interpro entry. It includes Inte-rpro-id, Fprint-code, Fprint -name2, F print-name3, Fprint-type and printlinks. Fprint' code resembles the entries in each fingerprint database. F print -name2 defines the accession number at the PRINTS database. Fprintname3 is .the given name for this particular fingerprint at PRINTS; Fprint-type is the type of the composition of the fingerprint (the number of motifs in the fingerprint): Fprintlinks contains 8 different databases of fingerprint. Table (2), illustrates an example of TrifolumalexandrinumofAttributes of FINGERPRINT table, such as Inte-rpror-ID is IPR000482 its Fprintcode is BRECEPTR Fprint -name is PR00651, Fprinttype is compound (8) and Fprint-like is PR00251.

 Table 1. Example of Attributes of INTERPRO-GO table

ROW	INTERPROID	GO ID	GO CATEGORY	GO DESCRIPTION
1	IPR000001			
2	IPR000002			
3	IPR000003	0003677	Molecular function	DNA binding
4	IPR000005	0003700	Molecular function	Transcription factor activity
5	IPR000006	0046872	Molecular function	Metal ion binding
6	IPR000007			
7	IPR000008			
8	IPR000009	0000159	Cellular component	Protein phosphatase type 2A complex
9	IPR000010	0004869	Molecular function	Cysteine protease inhibitor activity
10	IPR000011	0006464	Biological process	Protein modification
11	IPR000012	0005554	Molecular function	Molecular function unknown
12	IPR000013	0005576	Cellular component	Extracellular region
13	IPR000014	0004871	Molecular function	Single transducer activity
14	IPR000015	0005215	Molecular function	Transporter activity
15	IPR000018	0007186	<b>Biological process</b>	G- protein coupled receptor protein
				signalling pathway
16	IPR000020	0005576	Cellular component	Extracellular region
17	IPR000021	0016021	Cellular component	Membrane
18	IPR000022	0016874	Molecular function	Ligase activity
19	IPR000023	0003872	Molecular function	6- photosphofructokinase activity

ROW         Finger pint code         Finger pint print         Finger print name print         Finger print type         interpro- type         Print links type           1         11SGLOB         PR00439         11-S seed storage protein family signature         COMPOUN         IPR000459           2         1433ZETA         PR00305         14-3-3 protein family signature signature         D(6)         PR000308           3         2CENDOP         PR00150         2C endopeptidase (C24)         COMPOUN         IPR000317         PR0017           4         2FENDOP         PR00159         2Fe-4S ferredoxin         COMPOUN         IPR000677         PR00439           5         2SGLOBU         PR00352         3Fe-4S ferredoxin         COMPOUN         IPR001080         LIN           6         3FE4SFRD         PR00352         3Fe-4S ferredoxin         COMPOUN         IPR001080         LIN           7         4DISULPH         PR000353         4fe-4s ferredoxin         COMPOUN         IPR01400         ISGLOBU           8         4FE4SFRD         PR00512         5-hydroxtryptamine 1D cOMPOUN         IPR00140         PR00251           9         SHTHBREC         PR00513         5-hydroxtryptamine 1D comPount         COMPOUN         IPR002147         PR00251 <th>Table 2</th> <th>. Example o</th> <th>f Attribute</th> <th>s of Fingerprint table</th> <th></th> <th></th> <th></th>	Table 2	. Example o	f Attribute	s of Fingerprint table			
	ROW	Finger pint	Finger	Finger print name	Finger print	interpro	Print links
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ULIN         protein family signature         D(7)           2         1433ZETA         PRO0305         14-3-3 protein zeta signature         COMPOUN         IPR000308           3         2CFNDOP         PRO0916         2C endopeptidase (C24) cysteine protease family signature         COMPOUN         IPR000317         PR0017           4         2FENDOP         PRO0519         2Fe-45         COMPOUN         IPR000564         SRSVCYSP           5         2SGLOBU         PRO0551         2-Sglobulin family signature         COMPOUN         IPR000677         PR00439           0XINN         signature         D(9)         IPR001080         IISGLOBU           7         4DISULPH         PR00032         3Fe-45         COMPOUN         IPR001450           0XINN         signature         D(2)         IPR001450         Signature         D(2)           9         SHTIBREC         PR00513         5-hydroxytryptamine 1         COMPOUN         IPR002147         PR00251           10         SHTIBREC         PR00513         5-hydroxytryptamine 1D         COMPOUN         IPR002147         PR00251           11         SHTIBREC         PR00514         5-hydroxytryptamine 1D         COMPOUN         IPR002147         PR00251	1	11SGLOB	PR00439	11-S seed storage	COMPOUN	IPR000459	
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TASEcysteine protease family signatureD(4)SRSVCYSP TASE42FENDOPPRO01592Fe-48 ferredoxin signatureCOMPOUN D(2)IPR00056452SGLOBUPRO05512-Sglobulin family signatureCOMPOUN D(9)IPR000677PR0043963FE4SFRDPR003523Fe-4S ferredoxin signatureCOMPOUN D(3)IPR001080ISGLOBU LIN63FE4SFRDPR003523Fe-4S ferredoxin signatureCOMPOUN D(4)IPR001080ISGLOBU LIN74DISULPHPR0003534fe-4s ferredoxin signatureCOMPOUN D(4)IPR00145084FE4SFRDPR005125-hydroxytryptamine 1 compositionCOMPOUN LINIPR0025195HTIBRECPR005125-hydroxytryptamine 1D receptor signatureCOMPOUN D(5)IPR002147 BACTRLOP SIN105HTIPRECPR005145-hydroxytryptamine 1D receptor signatureCOMPOUN D(5)IPR00251 BACTRLOP SIN115HTIPRECPR005165-hydroxytryptamine 1D receptor signatureCOMPOUN D(7)IPR000450 BACTRLOP SIN125HT2AREPR005165-hydroxytryptamine 1F receptor signatureCOMPOUN D(7)IPR000455 BACTRLOP SIN135H12BRECPR005165-hydroxytryptamine 2A receptor signatureCOMPOUN D(8)IPR000455 SIN145H12BRECPR005175-hydroxytryptamine 2B receptor signatureCOMPOUN D(8)IPR000377 SIN155H12RECPR005185-hy	3	2CENDOP	PROO916	2C endopeptidase (C24)	COMPOUN	IPROOO317	PR0017
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4         2FENDOP         PRO0159         2Fe-45 ferredoxin signature         COMPOUN         IPR000564           5         2SGLOBU         PRO051         2-Sglobulin family signature         COMPOUN         IPR000677         PRO0439           6         3FE45FRD         PRO0352         3Fe-4S ferredoxin signature         COMPOUN         IPR001080         LIN           7         4DISULPH         PR00033         4fe-4s ferredoxin signature         COMPOUN         IPR00221         CORE         CORE         signature         D(3)         D(4)         EVENDO1450         SIN           9         SHTIBREC         PR00512         S-hydroxytryptamine 1 A receptor signature         COMPOUN         IPR00217         PR00251           9         SHTIDREC         PR00513         S-hydroxytryptamine 1D COMPOUN         COMPOUN         IPR002147         PR00251           10         SHTIDREC         PR00513         S-hydroxytryptamine 1D receptor signature         COMPOUN         IPR000505         PR00251           11         SHTIPREC         PR00515         S-hydroxytryptamine 1D receptor signature         COMPOUN         IPR000450         PR00251           12         SHT2ARE         PR00515         S-hydroxytryptamine 2A receptor signature         COMPOUN         IPR00455         P				signature			TASE
TASEsignatureD(2)52SGLOBUPRO0512-Sglobulin familyCOMPOUNIPR000677PRO0439LINsignatureD(9)IISGLOBULIN63FE4SFRDPRO03523Fe-4S feredoxinCOMPOUNIPR001080OXINNsignatureD(3)D(3)174DISULPHPR00034-disulphide coreCOMPOUNIPR00221COREsignatureD(4)COMPOUNIPR00145084FE4SFRDPR003534fe-4s ferredoxinCOMPOUNIPR001450OXINsignatureD(2)IPR001450SIN9SHTIBRECPR005125-hydroxytryptamine 1COMPOUNIPR002147PR00251FEPTRA receptor signatureD(5)BACTRLOPSIN10SHTIPRECPR005145-hydroxytryptamine 1DCOMPOUNIPR00250PR00251EPTRcceptor signatureD(5)BACTRLOPSIN11SHTIFRECPR005155-hydroxytryptamine 1DCOMPOUNIPR000505PR0025112SHT2AREPR005155-hydroxytryptamine 2ACOMPOUNIPR000450PR0025113SH12BRECPR005155-hydroxytryptamine 2ACOMPOUNIPR000450PR0025114SH12BRECPR005155-hydroxytryptamine 2ACOMPOUNIPR000452PR0025115SH12BRECPR005155-hydroxytryptamine 2BCOMPOUNIPR000377PR0025116SH12RECPR005175-hydroxytryptamine 2C<	4	2FENDOP	PROO159	2Fe-4S ferredoxin	COMPOUN	IPR000564	
5       2SGLOBU       PRO0551       2-Sglobulin family signature       COMPOUN       IPR00437       PR00439         6       3FE4SFRD       PR00352       3Fe-4S ferredoxin       COMPOUN       IPR001080       LIN         6       3FE4SFRD       PR00352       3Fe-4S ferredoxin       COMPOUN       IPR002221       LIN         7       4DISULPH       PR00033       4fe-4s ferredoxin       COMPOUN       IPR001450       D(3)         8       4FE4SFRD       PR00512       5-hydroxytryptamine 1       COMPOUN       IPR002147       PR00251         9       SHTIBREC       PR00513       5-hydroxytryptamine 1D       COMPOUN       IPR002147       PR00251         10       SHTIDREC       PR00513       5-hydroxytryptamine 1D       COMPOUN       IPR002147       PR00251         11       SHTIFREC       PR00514       5-hydroxytryptamine 1D       COMPOUN       IPR000505       PR00251         12       SHT2ARE       PR00515       5-hydroxytryptamine 1P       COMPOUN       IPR00450       PR00251         12       SHT2ARE       PR00515       5-hydroxytryptamine 2A       COMPOUN       IPR00455       PR00251         13       SHI2BREC       PR00515       5-hydroxytryptamine 2A       COMPOUN		TASE		signature	D(2)		
LINsignatureD(9)11SGLOBU LIN63FE4SFRDPRO03523Fe-4S ferredoxinCOMPOUNIPR00108074DISULPHPR000034-disulphide coreCOMPOUNIPR00222174DISULPHPR000034-disulphide coreCOMPOUNIPR00222184FE4SFRDPR003534fe-4s ferredoxinCOMPOUNIPR00145095HTIBRECPR005125-hydroxytryptamine 1COMPOUNIPR000610PR0025195HTIBRECPR005135-hydroxytryptamine 1DCOMPOUNIPR002147PR00251105HTIDRECPR005135-hydroxytryptamine 1DCOMPOUNIPR002147PR00251115HTIFRECPR005155-hydroxytryptamine 1DCOMPOUNIPR002505PR00251115HTIFRECPR005155-hydroxytryptamine 1DCOMPOUNIPR000450PR00251125HT2AREPR005155-hydroxytryptamine 1FCOMPOUNIPR000455PR00251125H12BRECPR005165-hydroxytryptamine 2ACOMPOUNIPR000455PR00251135H12BRECPR005165-hydroxytryptamine 2BCOMPOUNIPR000452PR00251145H12BRECPR005175-hydroxytryptamine 2CCOMPOUNIPR000377PR00251155HT2RECPR005175-hydroxytryptamine 2DD(8)BACTRLOPSIN165HT4RECPR005185-hydroxytryptamine 2ACOMPOUNIPR00150PR00251165HT2RECPR005185-h	5	2SGLOBU	PROO551	2-Sglobulin family	COMPOUN	IPR000677	PROO439
LIN         LIN           6         3FE4SFRD         PRO0352         3Fe-4S ferredoxin         COMPOUN         IPR001080           7         4DISULPH         PR00033         4-disulphide core         COMPOUN         IPR002221           CORE         signature         D(4)         IPR001450         COMPOUN         IPR00250           8         4FE45FRD         PR00512         5-hydroxytryptamine 1         COMPOUN         IPR000610         PR00251           9         SHTIBREC         PR00513         5-hydroxytryptamine 1D         COMPOUN         IPR002147         PR00251           10         SHTIDREC         PR00513         5-hydroxytryptamine 1D         COMPOUN         IPR002147         PR00251           11         SHTIFREC         PR00514         5-hydroxytryptamine 1D         COMPOUN         IPR00450         PR00251           12         SHT2ARE         PR00515         5-hydroxytryptamine 1F         COMPOUN         IPR00450         PR00251           13         SHI2BREC         PR00515         5-hydroxytryptamine 2A         COMPOUN         IPR00455         PR00251           14         SHI2BREC         PR00515         5-hydroxytryptamine 2B         COMPOUN         IPR000455         PR00251		LIN		signature	D(9)		11SGLOBU
6         3FE4SFRD OXINN         PRO0352         3Fe-4S ferredoxin signature         COMPOUN D(3)         IPR001080           7         4DISULPH         PR00003         4-disulphide core signature         COMPOUN         IPR002221           8         4FE4SFRD         PR00353         4fe-4s ferredoxin signature         COMPOUN         IPR001450           9         5HTIBREC         PR00512         5-hydroxytryptamine 1         COMPOUN         IPR00010         PR00251           9         5HTIBREC         PR00513         5-hydroxytryptamine 1D         COMPOUN         IPR002147         PR00251           10         5HTIDREC         PR00513         5-hydroxytryptamine 1D         COMPOUN         IPR002147         PR00251           11         5HTIFREC         PR00515         5-hydroxytryptamine 1D         COMPOUN         IPR000450         PR00251           12         SHT2ARE         PR00516         5-hydroxytryptamine 1F         COMPOUN         IPR00450         PR00251           13         SHI2BREC         PR00516         5-hydroxytryptamine 2A         COMPOUN         IPR00455         PR00251           14         5HI2BREC         PR00515         5-hydroxytryptamine 2A         COMPOUN         IPR00455         PR00251           13							LIN
OXINNsignatureD(3)74DISULPHPR000034-disulphide coreCOMPOUNIPR002221COREsignatureD(4)84FE4SFRDPR003534fe-4s ferredoxinCOMPOUNIPR001450OXINsignatureD(2)9SHTIBRECPR005125-hydroxytryptamine 1COMPOUNIPR000610PR00251EPTRA receptor signatureD(7)BACTRLOPSIN10SHTIDRECPR005135-hydroxytryptamine 1DCOMPOUNIPR002147PR00251EPTRreceptor signatureD(5)BACTRLOPSIN11SHTIFRECPR005145-hydroxytryptamine 1DCOMPOUNIPR00505PR00251EPTRreceptor signatureD(5)BACTRLOPSIN12SHT2AREPR005155-hydroxytryptamine 1FCOMPOUNIPR00450PR00251CEPTRreceptor signatureD(7)BACTRLOPSIN13SHI2BRECPR005165-hydroxytryptamine 2ACOMPOUNIPR00455PR0025114SH12BRECPR006515-hydroxytryptamine 2BCOMPOUNIPR000377PR0025115SHT2RECPR005175-hydroxytryptamine 2CCOMPOUNIPR000377PR0025116SHT4RECPR0159COMPOUND(3)COMPOUNIPR001307PR0025117SHT5AREPR005185-hydroxytryptamine 5ACOMPOUNIPR001307PR0025116SHT4RECPR0159COMPOUND(3)COMPOUN <t< td=""><td>6</td><td>3FE4SFRD</td><td>PROO352</td><td>3Fe-4S ferredoxin</td><td>COMPOUN</td><td>IPR001080</td><td></td></t<>	6	3FE4SFRD	PROO352	3Fe-4S ferredoxin	COMPOUN	IPR001080	
7       4DISULPH CORE       PR00003       4-disulphide core signature       COMPOUN D(4)       IPR002221         8       4FE4SFRD       PR00353       4fe-4s ferredoxin signature       COMPOUN       IPR001450         9       5HTIBREC       PR00512       5-hydroxytryptamine 1       COMPOUN       IPR00210       PR00251         9       5HTIBREC       PR00513       5-hydroxytryptamine 1D       COMPOUN       IPR002147       PR00251         10       5HTIBREC       PR00513       5-hydroxytryptamine 1D       COMPOUN       IPR002147       PR00251         11       5HTIFREC       PR00514       5-hydroxytryptamine 1D       COMPOUN       IPR000505       PR00251         12       5HT2ARE       PR00515       5-hydroxytryptamine 1F       COMPOUN       IPR000450       PR00251         13       5H12BREC       PR00516       5-hydroxytryptamine 2A       COMPOUN       IPR000455       PR00251         14       5H12BREC       PR00517       5-hydroxytryptamine 2B       COMPOUN       IPR000377       PR00251         15       SHT2REC       PR00517       5-hydroxytryptamine 2C       COMPOUN       IPR00377       PR00251         14       5H12BREC       PR00517       5-hydroxytryptamine 2C       COMPOUN		OXINN		signature	D(3)		
COREsignatureD(4)84FE4SFRDPR003534fe-4s ferredoxinCOMPOUNIPR001450OXINsignatureD(2)995HTIBRECPR005125-hydroxytryptamine 1COMPOUNIPR000610PR0025195HTIDRECPR005135-hydroxytryptamine 1DCOMPOUNIPR002147PR00251105HTIDRECPR005135-hydroxytryptamine 1DCOMPOUNIPR002147PR00251115HTIFRECPR005145-hydroxytryptamine 1DCOMPOUNIPR000505PR00251115HTIFRECPR005155-hydroxytryptamine 1FCOMPOUNIPR000450PR00251125HT2AREPR005155-hydroxytryptamine 1FCOMPOUNIPR000450PR00251135H12BRECPR005165-hydroxytryptamine 2ACOMPOUNIPR000455PR00251145H12BRECPR005175-hydroxytryptamine 2BCOMPOUNIPR000482PR00251155HT2RECPR005175-hydroxytryptamine 2CCOMPOUNIPR000377PR00251165HT4RECPR0159COMPOUND(3)COMPOUNIPR001307PR00251165HT4RECPR0159COMPOUND(3)COMPOUNIPR001307PR00251175HT5AREPR005185-hydroxytryptamine 5ACOMPOUNIPR001307PR00251185HT5BREPR005185-hydroxytryptamine 5ACOMPOUNIPR001307PR00251185HT5BREPR005185-hydroxytryptamine 5ACOMPOUNIPR	7	4DISULPH	PR00003	4-disulphide core	COMPOUN	IPR002221	
8         4FEASFRD OXIN         PR00353 signature         4fe-4s ferredoxin D(2)         COMPOUN D(2)         IPR001450 D(2)           9         5HTIBREC EPTR         PR00512         5-hydroxytryptamine 1 A receptor signature         COMPOUN D(7)         IPR000610         PR00251           10         5HTIDREC         PR00513         5-hydroxytryptamine 1D receptor signature         COMPOUN         IPR002147         PR00251           11         5HTIFREC EPTR         PR00514         5-hydroxytryptamine 1D receptor signature         COMPOUN         IPR000505         PR00251           12         5HT2ARE CEPTR         PR00515         5-hydroxytryptamine 1F receptor signature         COMPOUN         IPR000450         PR00251           13         5H12BREC EPIR         PR00516         5-hydroxytryptamine 2A receptor signature         COMPOUN         IPR000455         PR00251           14         5H12BREC EPIR         PR00516         5-hydroxytryptamine 2B receptor signature         COMPOUN         IPR000482         PR00251           15         5HT2REC EPIR         PR00517         5-hydroxytryptamine 2C receptor signature         COMPOUN         IPR000482         PR00251           16         5HT2REC EPTR         PR01059         COMPOUND(3)         COMPOUN         IPR001397         PR00251           1		CORE		signature	D(4)		
OXINsignatureD(2)9SHTIBRECPR005125-hydroxytryptamine 1COMPOUNIPR000610PR00251EPTRA receptor signatureD(7)BACTRLOPSIN10SHTIDRECPR005135-hydroxytryptamine 1DCOMPOUNIPR002147PR00251EPTRreceptor signatureD(5)BACTRLOPSIN11SHTIFRECPR005145-hydroxytryptamine 1DCOMPOUNIPR000505PR00251EPTRreceptor signatureD(5)BACTRLOPSIN12SHT2AREPR005155-hydroxytryptamine 1FCOMPOUNIPR000450PR00251CEPTRreceptor signatureD(7)BACTRLOPSIN13SHI2BRECPR005165-hydroxytryptamine 2ACOMPOUNIPR000455PR00251EPIRreceptor signatureD(7)BACTRLOPSIN14SHI2BRECPR005165-hydroxytryptamine 2BCOMPOUNIPR000482PR00251EPIRreceptor signatureD(8)BACTRLOPSIN15SHT2RECPR0159COMPOUND(3)COMPOUNIPR000377PR0025116SHT4RECPR0159COMPOUND(3)COMPOUNIPR001397PR0025117SHT5AREPR005185-hydroxytryptamine 5ACOMPOUNIPR001397PR0025118SHT5BREPR005185-hydroxytryptamine 5BCOMPOUNIPR000431PR0025118SHT5BREPR005195-hydroxytryptamine 5BCOMPOUNIPR00431PR00251	8	4FE4SFRD	PR00353	4fe-4s ferredoxin	COMPOUN	IPR001450	
9       5HTIBREC       PR00512       5-hydroxytryptamine 1       COMPOUN       IPR000610       PR00251         10       5HTIDREC       PR00513       5-hydroxytryptamine 1D       COMPOUN       IPR002147       PR00251         10       5HTIDREC       PR00513       5-hydroxytryptamine 1D       COMPOUN       IPR002147       PR00251         11       SHTIFREC       PR00514       5-hydroxytryptamine 1D       COMPOUN       IPR000505       PR00251         12       SHT2ARE       PR00515       5-hydroxytryptamine 1F       COMPOUN       IPR000450       PR00251         13       SH12BREC       PR00516       5-hydroxytryptamine 2A       COMPOUN       IPR000455       PR00251         14       SH12BREC       PR00651       5-hydroxytryptamine 2B       COMPOUN       IPR000482       PR00251         15       SH12REC       PR00517       5-hydroxytryptamine 2C       COMPOUN       IPR000482       PR00251         15       SH12BREC       PR00517       5-hydroxytryptamine 2C       COMPOUN       IPR000377       PR00251         15       SH12BREC       PR00518       5-hydroxytryptamine 2C       COMPOUN       IPR000377       PR00251         16       SHT4REC       PR00518       5-hydroxytryptamine 5A <td></td> <td>OXIN</td> <td></td> <td>signature</td> <td>D(2)</td> <td></td> <td></td>		OXIN		signature	D(2)		
EPTRA receptor signatureD(7)BACTRLOP SIN10SHTIDRECPR005135-hydroxytryptamine 1DCOMPOUNIPR002147PR00251EPTRreceptor signatureD(5)BACTRLOPSIN11SHTIFRECPR005145-hydroxytryptamine 1DCOMPOUNIPR000505PR00251EPTRreceptor signatureD(5)IPR000505PR00251SIN12SHT2AREPR005155-hydroxytryptamine 1FCOMPOUNIPR000450PR00251CEPTRreceptor signatureD(7)BACTRLOPSIN13SH12BRECPR005165-hydroxytryptamine 2ACOMPOUNIPR000455PR0025114SH12BRECPR006515-hydroxytryptamine 2BCOMPOUNIPR000482PR0025115SHT2RECPR005175-hydroxytryptamine 2CCOMPOUNIPR000377PR0025116SHT4RECPR005185-hydroxytryptamine 5ACOMPOUNIPR001307PR0025116SHT4RECPR005185-hydroxytryptamine 5ACOMPOUNIPR001397PR0025117SHT5AREPR005185-hydroxytryptamine 5BCOMPOUNIPR001397PR0025118SHT5BREPR005195-hydroxytryptamine 5BCOMPOUNIPR001397PR0025118SHT5BREPR005195-hydroxytryptamine 5BCOMPOUNIPR00431PR0025118SHT5BREPR05195-hydroxytryptamine 5BCOMPOUNIPR00431PR0025118SHT5BREPR05195-hydroxytr	9	5HTIBREC	PR00512	5-hydroxytryptamine 1	COMPOUN	IPR000610	PR00251
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10       SHTIDREC       PR00513       5-hydroxytryptamine 1D receptor signature       COMPOUN       IPR002147       PR00251 BACTRLOP         11       SHTIFREC       PR00514       5-hydroxytryptamine 1D receptor signature       COMPOUN       IPR000505       PR00251         12       SHT2ARE CEPTR       PR00515       5-hydroxytryptamine 1F receptor signature       COMPOUN       IPR000450       PR00251         13       SH12BREC       PR00516       5-hydroxytryptamine 2A receptor signature       COMPOUN       IPR000455       PR00251         14       SH12BREC       PR00651       5-hydroxytryptamine 2B receptor signature       COMPOUN       IPR000482       PR00251         15       SH12BREC       PR00517       5-hydroxytryptamine 2B receptor signature       COMPOUN       IPR000482       PR00251         16       SHT2REC       PR01059       COMPOUND(3)       COMPOUN       IPR00150       PR00251         16       SHT4REC       PR01059       COMPOUND(3)       COMPOUN       IPR001397       PR00251         17       SHT5ARE       PR00518       5-hydroxytryptamine 5A receptor signature       COMPOUN       IPR001397       PR00251         17       SHT5ARE CEPTR       PR00518       5-hydroxytryptamine 5A receptor signature       COMPOUN       IPR0013							SIN
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#### D-Interpro-examples table of Trifolumalexandrinum:

This table collects a representative list of the kind of proteins matching the entry. The list shows the diversity of the matches in terms of function and/or taxonomic range for each InterPro entry. The proteins are from either SWISSPROT or TREMBL. INTERPRO-EXAMPLS, table contains four attributes of *Trifoliumalexandrinum*:Interpro-ID, Match-pid, match-pd, -and Match-pname; Interpro-ID, is the Interpro entry ID, where Match-pdb contains IDS for matched proteins. Match-pids can be used to protein sequences from protein table. Match-pdb describes two protein databases that contain the matching protein entries. Finally, match-pname is the names of the matching protein entries.

#### **E-Quick Go table:**

In table (1) consists of four attributes: Go-id, Go – Isarelation, and go – Partofrelation. Go – id is the Goentry id, where Go – Isarelation shows if there exist a parent – child relationship between this go – id and other Go – ID – finally, Go – Partofrelation shows whether this go – id is Go; a part of other Go-IDS or not for example if Go – ID is 0004872 the Go– isarelation is Go :000481 and Go– Partofrelation would have a null value.

#### **F-Motif Table:**

This table contains three attributes print - code, match - proteins, and Motifseq3, where it includes the matched proteins for a specific fingerprint code. For example, in Table (3), Finger - Print code 115Globulin has a number of matching proteins such as Gluz -Trifolum and Gu12 - Trifolum Motifs sequences are shown in the same table too as well.

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### Databases

- : (Databases)
- 1- Interpro Databases.
- 2- Prints Databases.
- 3- Quick Go Databases.

#### Genetic Erosion

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