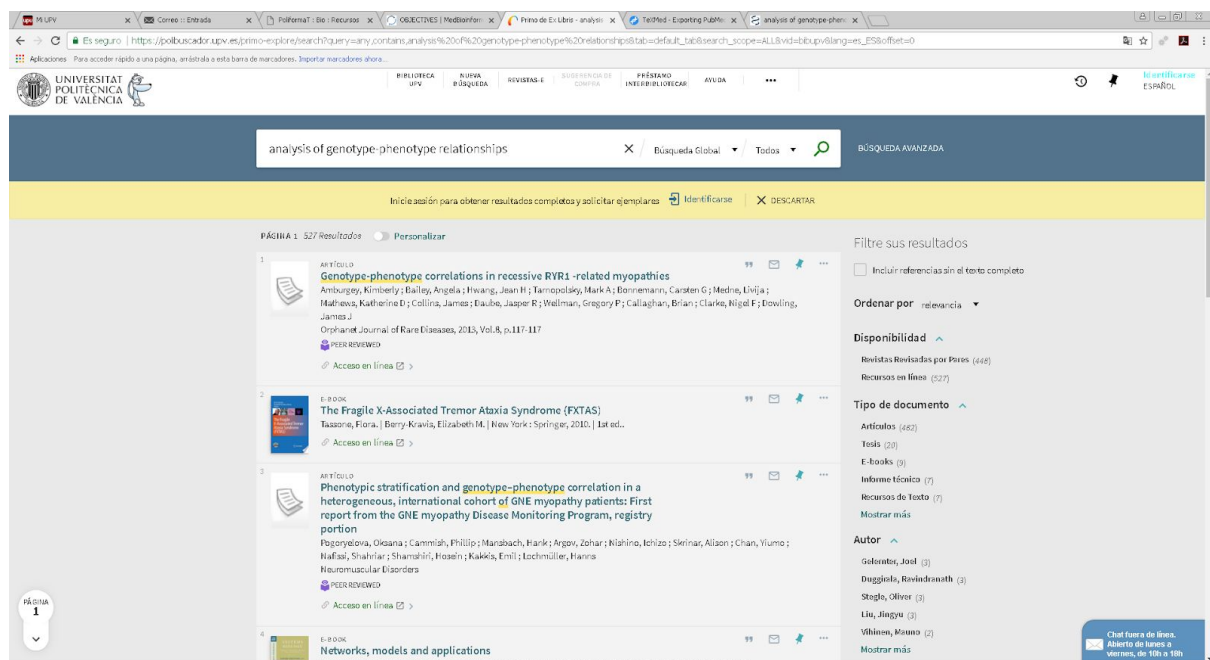
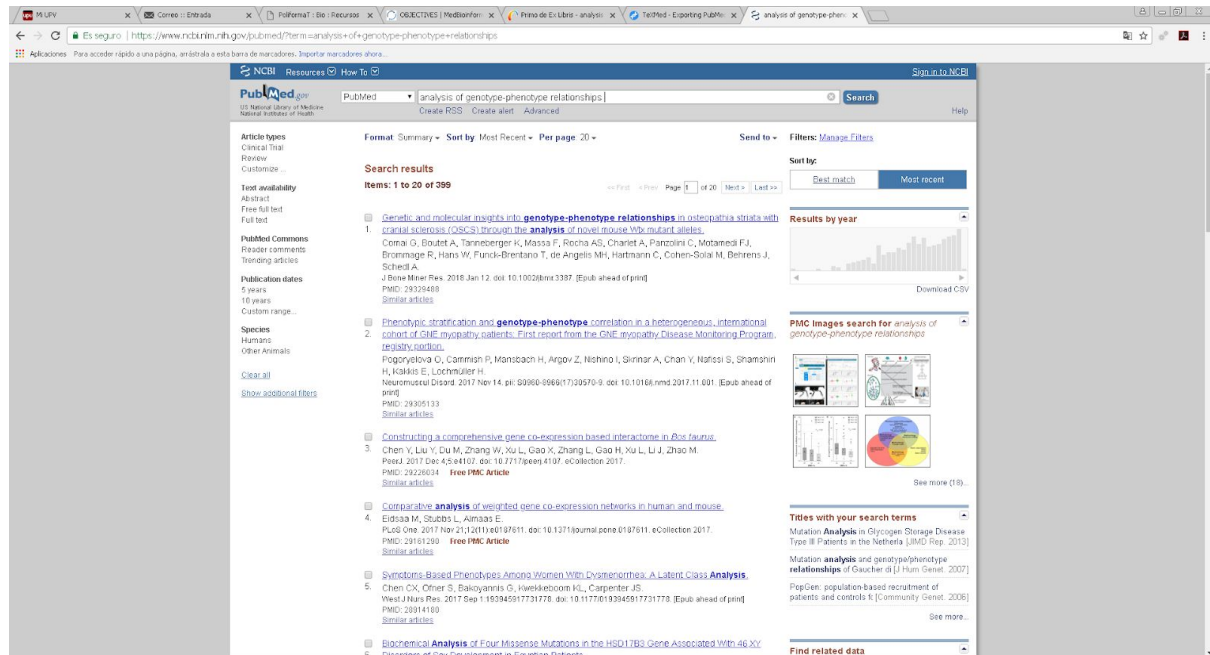


PRÁCTICA 2 BIOINFORMÁTICA

EJERCICIO 1.-

1.1.



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1.3.

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BIOLÓGICA UPV VÍDEO BÚSQUEDA REVISTAS E SUBSECCIONES DE COMPRENSIÓ PRÉMIOS INTERBIBLIOTECARIOS AYUDA

molecular diagnosis

Inicie sesión para obtener resultados completos y añadir ejemplares

PÁGINA 1 303,298 Resultados Personalizar

1. E-BOOK
Next generation sequencing based clinical molecular diagnosis of human genetic disorders
Wong, Leo Jun C.,
Acceso en línea [link](#)
2. E-BOOK
Vascular tumors and developmental malformations: pathogenic mechanisms and molecular diagnosis
North, Paula E.; North, Paula E.; Sander, Tara.; 1st ed. 2016.,
Acceso en línea [link](#)
3. ARTÍCULO
RVP1 gene as a target for molecular diagnosis of histoplasmosis
Brilhante, Raimunda Sâmia Nogueira.; Cuedes, Glaucia Morgana de Melo.; Riello, Giovanna Barbosa.; Ribeiro, Joyce Fonteles.; Alencar, Lucas Pereira.; Banderia, Silvana Pracianno.; Castelo-Branco, Debora Souza Collares Maia.; Oliveira, Jonathan Sales.; Freire, Janaina Maria Maia.; Mesquita, Jacó Ricardo Lima de.; Camargo, Zolito Pires de.; Cordeiro, Rossana de Aguiar.; Rocha, Marcos Fábio Caldeira.; Sidiro, José Julio Costa.
Journal of Microbiological Methods, November 2016, Vol.139, pp.112-114
PES REVISADO
Acceso en línea [link](#)
4. ARTÍCULO
Molecular diagnosis of bacterial vaginosis: Does adjustment for total bacterial load or human cellular content improve diagnostic performance?
Plummer, E.L.; Garland, S.M.; Bradshaw, C.S.; Law, M.G.; Vodacek, J.A.; Hocking, J.S.; Fairley, C.K.; Talbot, S.N.
Journal of Microbiological Methods, February 2017, Vol.133, pp.68-88

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Disponibilidad

Revistas Revisadas por Pares (288,822)

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Ejemplares (3)

Biblioteca

Bib. Agroingeniería (3)

Biblioteca Central (1)

Tipo de documento

Artículos (293,297)

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Autor

Chen, Chih-Ping (222)

Chih-Ping Chen (222)

Chat fuera de línea. Abierto de lunes a viernes, de 10h a 18h

1.4. Estos artículos nos otorgarán la información necesaria para comprender, interpretar y explicar algunos de los conceptos que aparecen en nuestro trabajo, algunos de los cuales son ajenos a nuestro entender.

1.5.

15LUV x Correo: Entrada x Poliformat: Bio | Recursos x OBJECTOS | MedBentom: x Prímo de Ex Libris - análisis x TeXMed - Exporting PubMed x analysis of genotype phen: x

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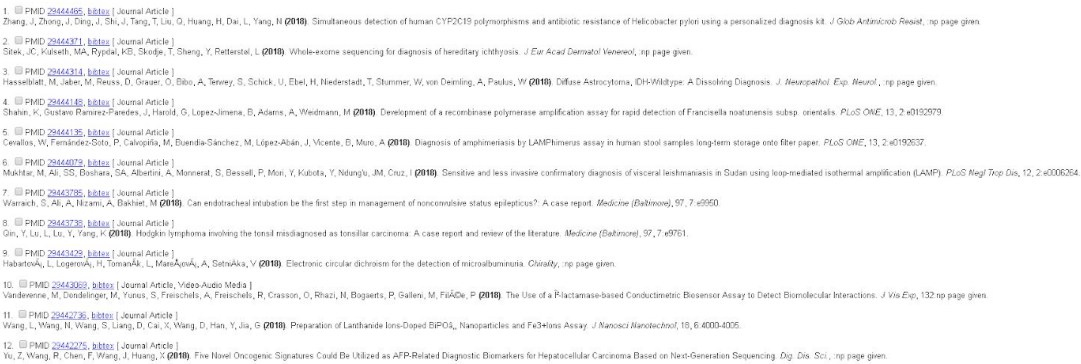
Received 250 references

☐ incl. abstract ☐ link article ids (requires unzippackage(hypertext))

- ☐ PMID [29326488](#), [bibtex](#) [Journal Article]
Comai, G, Boutelet, A, Tanneberger, K, Massa, F, Rocha, AS, Charlet, A, Piarzoli, C, Metamedi, FJ, Brenneise, R, Hars, W, Funck-Brentano, T, de Angelis, MH, Hartmann, C, Cohen-Solal, M, Behrens, J, Schedl, A (2018) Genetic and molecular insights into genotype-phenotype relationships in osteopathia striata with cranial sclerosis (OSCS) through the analysis of novel mouse Wts mutant alleles. *J. Bone Miner. Res.*, no page given.
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2.11. Un homólogo es una secuencia similar a otra de dos o más proteínas o ácidos nucleicos.

2.12. Hemoglobina Beta

EJERCICIO 3.-

3.2. Es unico

3.3. Ser humano

3.4. 13116

3.5. CYP4A11

3.6. cytochrome P450

3.7. 693..13116

3.8. La proteína empieza en la posición 1004 con los nucleótidos ATG, que en el ARN serían AUG que corresponde al aminoácido llamado Metionina (Met) cuya característica es que es el aminoácido que inicia la traducción o biosíntesis de la proteína.

3.9.(2). Es único.

3.9.(3). Caenorhabditis elegans.

3.9.(4). 1191

3.9.(5). apn-1

3.9.(6). DNA-(apurinic or apyrimidinic site) lyase

3.9.(7). 1..1191

3.9.(8). La proteína empieza en la posición 1 con los nucleótidos ATG, que en el ARN serían AUG que corresponde al aminoácido llamado Metionina (Met) cuya característica es que es el aminoácido que inicia la traducción o biosíntesis de la proteína.

3.10. Nos indica que es una subsecuencia RefSeq revisada por expertos.

EJERCICIO 4.-

4.1.

BLAST

Align

Download

Add to basket

Columns

	Entry	Entry name		Protein names	Gene names	Organism
	Q10002	APN1_CAEEL		DNA-(apurinic or apyrimidinic site)...	apn-1 T05H10.2	Caenorhabditis elegans

4.2. Sí, este es su ficha: <http://www.uniprot.org/uniprot/Q10002>

4.3. Sí, es exactamente la misma secuencia.

4.4. EMBL, GenBank, DDBJ, PIR, RefSeq, UniGene, ProteinModelPortal, SMR, ModBase, MobiDB, STRING, EPC, PaxDb, PeptideAtlas, Structural Biology Knowledgebase, EnsemblMetazoa, GeneID, KEGG, UCSC, CTD, WormBase, eggNOG, GeneTree, HOGENOM, InParanoid, KO, OMA, OrthoDB, PhylomeDB, PRO, Bgee, CDD, HAMAP, InterPro, PANTHER, Pfam, SMART, SUPGAM, TIGRFAMs, PROSITE, ProtoNet

4.5. Encabezado en negrita:

>sp|Q10002|APN1_CAEEL DNA-(apurinic or apyrimidinic site) lyase OS=Caenorhabditis elegans

GN=apn-1 PE=2 SV=2

MANKKVTFREDVKSPAIRKLKQKLTPKIKKGRGKIQKHQKTLQKMKEEEESENQSPGT
TVEETLTEENISTDKEETSKLENKPKKTRKTSGETIAQKKSRETVGVVEVLKTSEGSSKML
GFHVSAAGGLEQAIYNARAEGCRSFAMFVRNQRTWNHKKPMSEEVVENWWKAVRETNFPLD
QIVPHGSYLMNAGSPEAEKLEKSRLAMLDECQRAEKLGITMYNFHPGSTVGKCEKEECMT
TIAETIDFVVEKTENIILVLETMAGQGNSIGGTFEELKFIDKVKVKS RVGVCIDTCHIF
AGGYDIRTQKAYEEVMKNFGEVVGWNYLKAIHINDSKGDVGSKLDRHEHIGQGKIGKAAF
ELLMNDNRDLGIPMILETPEGKYPEEMMIMYNMDKR

EJERCICIO 5.-

5.1. Su único dominio es: <http://www.ebi.ac.uk/interpro/entry/IPR013022>

5.2. Pfam es una base de datos que contiene familias de proteínas, cada una representada por alineamientos de secuencias múltiples y modelos ocultos de Markov.

5.3.

Interpro: [Xylose isomerase-like, TIM barrel domain](#) (IPR013022)

Pfam: AP_endonuc_2 (PF01261)