KoriBlast

Plate-forme d'intégration et d'exploration de banques de données biologiques

Patrick Durand

Domaine d'activité

conception et développement d'applications et de bases de données en bioinformatique

Création: 02/2007

Soutiens: Vannes Technopole, CRITT Santé Bretagne, Crédit Mutuel de Bretagne

Prix: Boutique de Gestion, Fondation Jean Guyomarc'h

Présentation de Korilog

www.korilog.com

Offre

- plate-forme d'intégration et d'exploration de bases de données biologiques (KB)

- prestations de services en bioinformatique
  - adaptations de KoriBlast
  - conseils et développements à façon

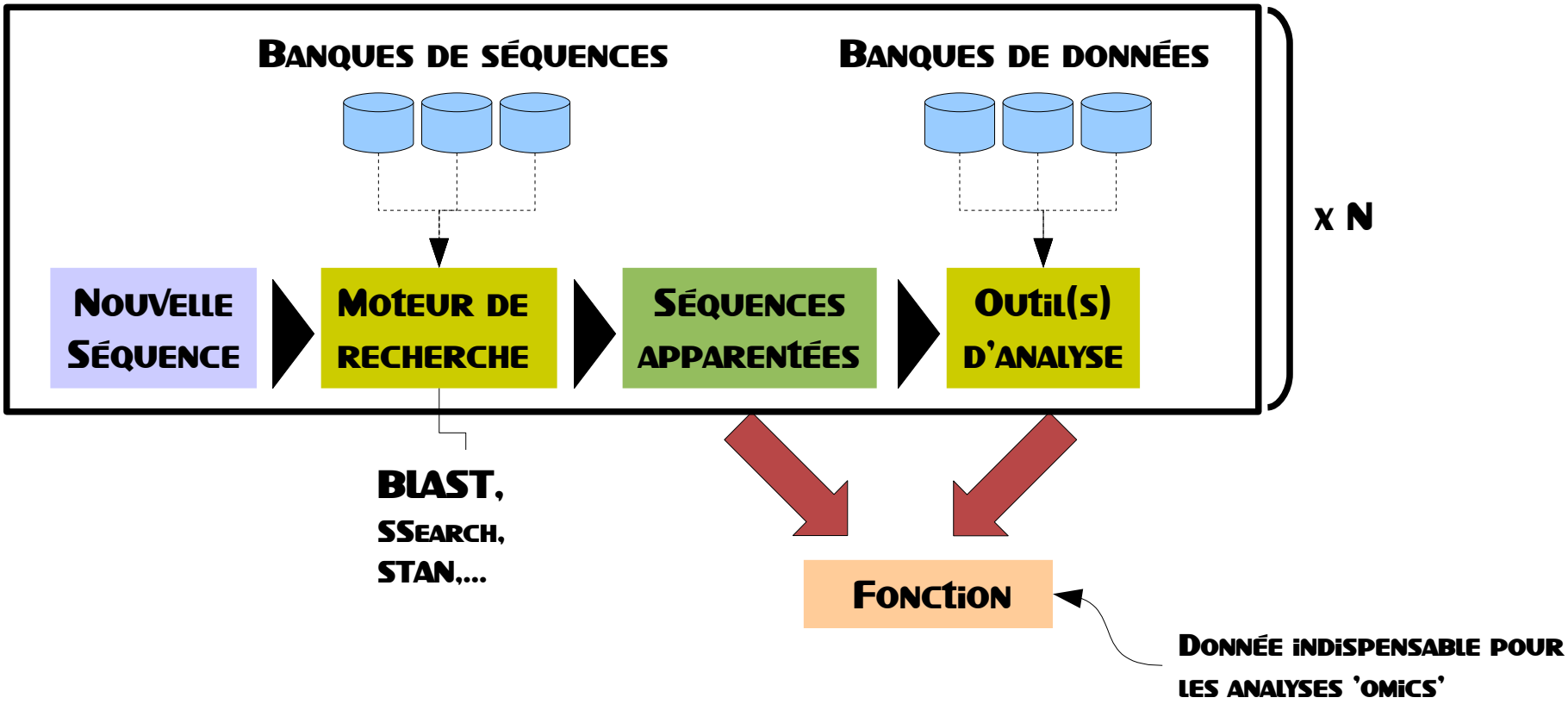
Clients

- Laboratoires de recherche publics

- industriels biotech – pharma

Korilog
bioinformatics solutions

Exploration des banques de données



Outils variés: web, ligne de commande, ...
Banques de données variées

} Lesquels ?
Comment ?

Korilog bioinformatics solutions

Analyse de séquence: en pratique...

Recherche dans les bases de séquences

Nucleotide BLAST: Search nucleotide databases using a nucleotide query - Mozilla Firefox

BLAST — Basic Local Alignment Search Tool

Home | Recent Results | Saved Strategies | Help

My NCBI — Welcome pgdurand. [Sign Out]

NCBI/BLAST/blastn suite: BLASTN programs search nucleotide databases using a nucleotide query. more... Reset page Bookmark

Enter Query Sequence

Enter accession number, gi, or FASTA sequence — Clear

```
>gi|147906581|ref|NM_001093666.1| Xenopus laevis mannosidase
GAGGGTTGAGATTATACAGTGGGTTGCTTTAAGCGTTGTGTCAGACTTCTATTCTCTTGTCT
CTAGTCAGATGGGCTGTTTATGGGCCCTGATATTGTGTCTTTTCATGATGGGATTAGAGCAG
GACGAGGTGGAAAAGTCATGACAGAAGCCAAACTTTTAGCCTGAATGGCAGATGGGAAATCC
AACGGATCTTATAAACTAAAAGGGGAAGTTCCCGGCTGTGTGCACACTGCATTAGCTGAACG
```

Query subrange — From / To

Or, upload file — Parcourir...

Job Title: mannosidase gene

Enter a descriptive title for your BLAST search

Choose Search Set

Database: Human genomic + transcript | Mouse genomic + transcript | Others (nr etc.): Reference genomic sequences (refseq_genomic)

Organism (Optional): Enter organism name or id--completions will be suggested

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Entrez Query (Optional): Enter an Entrez query to limit search

Program Selection

Optimize for: Highly similar sequences (megablast) / More dissimilar sequences (discontiguous megablast) / Somewhat similar sequences (blastn)

Choose a BLAST algorithm

BLAST — Search database refseq_genomic using Blastn (Optimize for somewhat similar sequences)

Show results in a new window

Algorithm parameters — Note: Parameter values that differ from the default are highlighted in yellow

Terminé

NCBI Blast:mannosidase gene - Mozilla Firefox

NCBI/BLAST/blastn/Formatting Results - G6D32ZT6012 [Reformat these Results] [Edit and Resubmit] [Save Search Strategies]

Job Title: mannosidase gene

BLASTN 2.2.17 (Aug-26-2007)

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: G6D32ZT6012

Database: NCBI Genomic Reference Sequences
7203 sequences; 12,028,665,686 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs
Taxonomy reports

Query= gi|147906581|ref|NM_001093666.1| Xenopus laevis mannosidase
Length=2660

Distribution of 93 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments

Color key for alignment scores: <40 | 40-50 | 50-80 | 80-200 | >=200

Query 0 500 1000 1500 2000 2500

Terminé

	Max score	Total score	Query coverage	E value
	111	599	33%	1e-20
	111	599	33%	1e-20
	111	599	33%	1e-20
	96.9	96.9	8%	2e-16
	96.9	96.9	4%	2e-16
	84.2	84.2	5%	1e-12
	84.2	132	6%	1e-12
	82.4	82.4	4%	5e-12
	78.8	78.8	4%	6e-11
	73.4	73.4	4%	2e-09
	73.4	73.4	5%	2e-09
	69.8	119	8%	3e-08
	66.2	110	6%	4e-07
	64.4	64.4	4%	1e-06
	64.4	64.4	3%	1e-06
	62.6	62.6	7%	5e-06
	60.8	60.8	2%	2e-05
	60.8	60.8	3%	2e-05
	60.8	60.8	4%	2e-05
	60.8	110	8%	2e-05
	60.8	110	8%	2e-05
	60.8	60.8	2%	2e-05
	59.0	59.0	5%	5e-05
	57.2	57.2	4%	2e-04
	57.2	57.2	3%	2e-04
	57.2	57.2	5%	2e-04
	57.2	101	4%	2e-04
	57.2	101	4%	2e-04
	55.4	55.4	1%	7e-04
	55.4	55.4	1%	7e-04
	55.4	55.4	4%	7e-04
	53.6	53.6	2%	0.002
	53.6	53.6	4%	0.002
	50.0	50.0	4%	0.028
	50.0	142	9%	0.028
	50.0	50.0	4%	0.028
	48.2	48.2	1%	0.099
	48.2	48.2	1%	0.099
	48.2	48.2	4%	0.099

```
Score =  111 bits (122),  Expect = 1e-20
Identities = 161/226 (71%), Gaps = 1/226
Strand=Plus/Minus

Query  1603      CGGCCTTTCATCTCATCAAGTCCTA
                 || |||||  ||   || ||||||||
Sbjct  99315182  CGTCCTTTTATTAGTCCAGTCCTA

Query  1663      GCTAAAAACCCATATGACAATCACT
                 || ||||||||  ||  |||| | ||
Sbjct  99315122  TCTCAAAACCCTAATAGCAATTATT

Query  1723      TGCTGGGACTGGAAGTCTTACCCTA
                 |||||| |||||||   || ||| |
Sbjct  99315062  TGCTGGAACTGGAAAGTTTTCCCAA

Query  1783      TGGCCTTCATTATCAACATTAGAGA
                 ||||| || ||     |||||||| |
Sbjct  99315002  TGGCCGTCCTTCAGTACATTAGAAA

Score = 98.7 bits (108),  Expect = 6e-17
Identities = 84/104 (80%), Gaps = 0/104 (
Strand=Plus/Minus

Query  1234      CAGTCTGTTGTTGATGCCAACATGA
                 ||||||||||| ||||| || ||||
Sbjct  99328658  CAGTCTGTTGTGGATGCTAATATGAATACTCTTCGGGTTTGGGGAGGAGGAATTTATGAG  99328599

Query  1294      AGTGATGAATTCTACAGATTGTGTGATGAACTTGGAATCATGGT  1337
                    ||||||||||   | | ||||||||||| ||||| |||||
Sbjct  99328598  CAGGATGAATTCTATGAACTCTGTGATGAACTAGGAATAATGGT  99328555

Score = 87.8 bits (96),  Expect = 1e-13
Identities = 78/98 (79%), Gaps = 0/98 (0%)
Strand=Plus/Minus

Query  658       CAGTGCTCATTTAGCTGGGACTGGGGACCTTCCTTTCCCACACAGGGTATATGGAAGGAG  717
                 || || || ||||| |||||||||| ||||||||||| || ||||| || ||||| ||
Sbjct  99371821  CAATGTTCCTTTAGTTGGGACTGGGGGCCTTCCTTTCCTACCCAGGGAATCTGGAAAGAT  99371762

Query  718       GTTACAATTGAAGCGTACAATGTGTTCCACTTGGACTA  755
                 |||| |||||||| || ||| | | ||| || ||||
Sbjct  99371761  GTTAGAATTGAAGCCTATAATATTTGTCACCTGAACTA  99371724

Score = 71.6 bits (78),  Expect = 9e-09
Identities = 114/156 (73%), Gaps = 6/156 (3%)
Strand=Plus/Minus
```


Korilog bioinformatics solutions

NCBI Sequence Viewer v2.0 - Mozilla Firefox

Fichier Édition Affichage Historique Marque-pages Outils ?

http://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?cmd=Retrieve&db=Nucleotide&list_uids=15

Démarrage | Dernières nouvelles (... | Messagerie - Wanadoo | Site du cinéma de QU... | CIC > Particuliers | Programme TNT - Vot... | EuroBio 2007 | SEPTE...

NCBI Entrez Nucleotide

My NCBI
Welcome pgdurand [Sign Out]

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search Nucleotide for Go Clear

Limits Preview/Index History Clipboard Details

Display GenBank Show 5 Send to Hide: sequence all but gene, CDS and mRNA features

Range: from begin to end Reverse complemented strand Features: + Refresh

This record may be shown in a reduced form. Use 'Hide' checkboxes for control.

1: AC_000136. Reports Homo sapiens chro...[gi:157734150] Links

Click here to see all features and the sequence of this contig record.

Comment Features Contig

```
LOCUS       AC_000136          186704410 bp    DNA     linear   CON 27-SEP-2007
DEFINITION  Homo sapiens chromosome 4, alternate assembly (based on HuRef),
            whole genome shotgun sequence.
ACCESSION   AC_000136
VERSION     AC_000136.1  GI:157734150
PROJECT     GenomeProject:20837
KEYWORDS    WGS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 186704410)
  AUTHORS   Levy,S., Sutton,G., Ng,P.C., Feuk,L., Halpern,A.L., Walenz,B.P.,
            Axelrod,N., Huang,J., Kirkness,E.F., Denisov,G., Lin,Y.,
            Macdonald,J.R., Pang,A.W., Shago,M., Stockwell,T.B., Tsiamouri,A.,
            Bafna,V., Bansal,V., Kravitz,S.A., Busam,D.A., Beeson,K.Y.,
            McIntosh,T.C., Remington,K.A., Abril,J.F., Gill,J., Borman,J.,
            Rogers,Y.H., Frazier,M.E., Scherer,S.W., Strausberg,R.L. and
            Venter,J.C.
  TITLE     The Diploid Genome Sequence of an Individual Human
  JOURNAL   (er) PLoS Biol. 5 (10), E254 (2007)
   PUBMED   17803354
COMMENT     The DNA sequence is from the whole genome assembly released by the
            J Craig Venter Institute as HuRef in May 2007 (see
            http://www.jcvi.org/research/huref/). It is included in the NCBI
            RefSeq collection as an alternative assembly to the one produced by
            the Human Genome Sequencing Consortium. The original whole genome
            shotgun project has the project accession ABBA00000000.1. The HuRef
            assembly represents a composite haploid version of the diploid
            genome sequence from a single individual. The highest scoring
```

Terminé

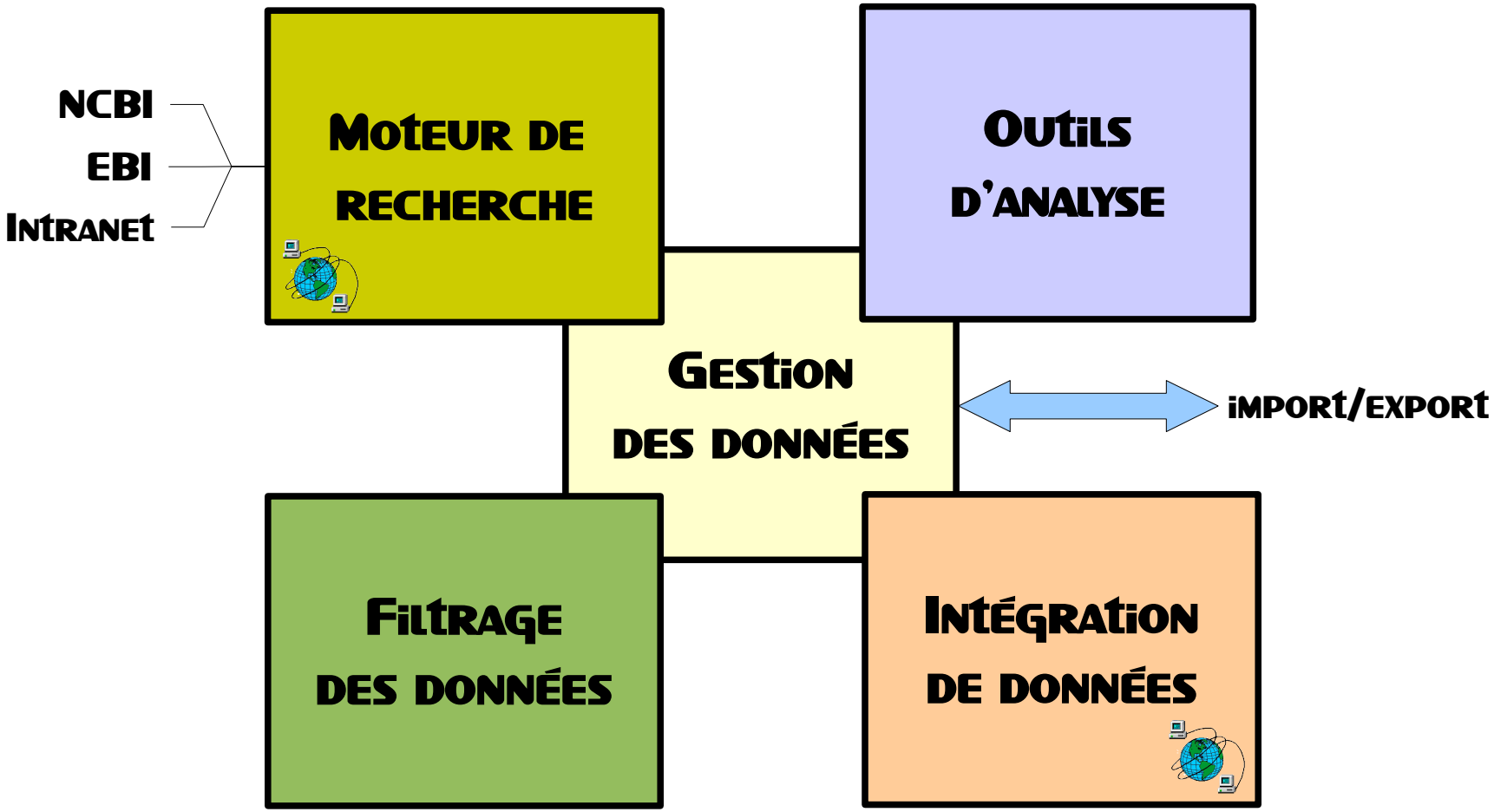
Post-traitement des résultats de BLAST

- Reconstruction d'alignements multiples (Labesse, 1996; Durand, 1997)
- calcul de scores, Classification (Martin, 2003; Rasko, 2005)
- Enrichissement en données (Worley, 1995; Dieterich, 2005)
- Requêtage (Eckman, 2004)

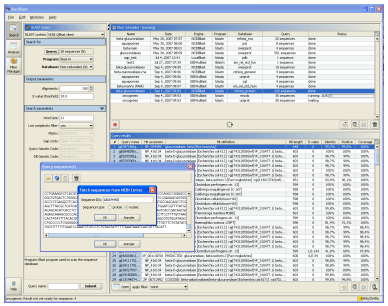
KoriBlast

plate-forme { d'intégration / d'exploration } de banques de données biologiques

- Centraliser l'accès aux outils et aux données
- Rendre l'accès aux ressources totalement transparent
- Proposer des outils adaptés
- Permettre de se concentrer sur l'analyse

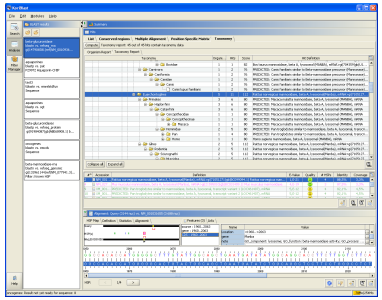

NCBI
EBI
Intranet
Moteur de recherche
Outils d'analyse
Gestion des données
import/export
Filtrage des données
Intégration de données

Java

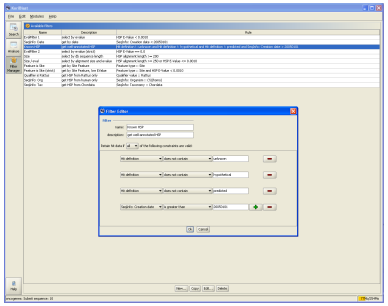


Moteur de recherche

Outils d'analyse



Gestion des données



Filtrage des données

Intégration de données

KoriBlast

File Edit Modules Help

Search
Analyse
Filter Manager

BLAST Query

BLAST system: NCBI QBlast client

Search for

Query: 35 sequences (N)

Program: Blast-N

Database: Non-redundant (N)

Output parameters

Alignments: 100

E-value threshold: 10.0

Search parameters

Word size: 11

Low complexity filter: yes

Matrix: BLOSUM 62

Gap costs: Open: 11, Ext: 1

Query Genetic Code: Standard (1)

DB Genetic Code: Standard (1)

Query sequence(s)

Fetch sequences from NCBI Entrez

Sequence IDs: AB209456

Sequence type: proteic nucleic

OK Annuler

OK Annuler

Program: Blast program used to scan the sequence database

Query name: Submit

Help

Blast Scheduler - [running]

Name	Date	Engine	Program	Database	Query	Status
beta-glucuronidase	May 30, 2007 07:57	NCBIBlast	blastn	refseq_rna	20 sequences	done
aquaporines	May 30, 2007 08:00	NCBIBlast	blastp	pat	8 sequences	done
beta-man	May 30, 2007 08:01	NCBIBlast	blastx	swissprot	4 sequences	done
glucuronidases	May 30, 2007 08:09	NCBIBlast	blastp	swissprot	501 sequences	done
aqp_test	Jul 4, 2007 12:41	LocalBlast	blastp	pdb	1 sequence	done
test3	Jul 27, 2007 07:39	EBIWuBlast	tblastn	em_rel_std_fun	1 sequence	done
beta-glucuronidases	Sep 4, 2007 09:05	NCBIBlast	blastp	swissprot	10 sequences	done
beta-mannosidase-rna	Sep 4, 2007 09:06	NCBIBlast	blastn	refseq_genomic	4 sequences	done
aquaporines	Sep 4, 2007 09:06	EBIWuBlast	blastp	uniprot	4 sequences	done
aquaporines	Sep 4, 2007 09:06	EBIWuBlast	blastp	sgt	4 sequences	done
beta-manno (RNA)	Sep 4, 2007 09:07	EBIWuBlast	blastn	em_rel_std_hum	4 sequences	done
beta-glucuronidases	Sep 4, 2007 09:09	NCBIBlast	blastp	refseq_protein	226 sequences	done
oncogenes	Sep 4, 2007 09:53	EBIWuBlast	blastn	emcds	35 sequences	running: 3/35
oncogenes	Sep 4, 2007 09:53	EBIWuBlast	blastx	uniprot	35 sequences	waiting

Query results

#	Query name	Hit accession	Hit definition	Hit length	E-value	Identity	Positive	Coverage
1	gi|387180|g...	NP_034498	glucuronidase, beta [Mus musculus]	648	0	99,7%	99,8%	100%
2	gi|584839|s...	NP_416134	beta-D-glucuronidase [Escherichia coli K12] >gi|74312058|ref|YP_310477.1| beta...	603	0	100%	100%	100%
3	gi|529330|g...	NP_416134	beta-D-glucuronidase [Escherichia coli K12] >gi|74312058|ref|YP_310477.1| beta...	603	0	98,7%	99%	100%
4	gi|529336|g...	NP_416134	beta-D-glucuronidase [Escherichia coli K12] >gi|74312058|ref|YP_310477.1| beta...	603	0	98,7%	99%	100%
			e [Escherichia coli K12] >gi|74312058|ref|YP_310477.1| beta...	603	0	98,7%	99%	100%
			e [Escherichia coli K12] >gi|74312058|ref|YP_310477.1| beta...	603	0	100%	100%	100%
			e [Escherichia coli K12] >gi|74312058|ref|YP_310477.1| beta...	603	0	98,7%	99%	100%
			nidase, beta isoform 3 [Pan troglodytes] >gi|114613742|ref|...	651	0	93,4%	96,1%	100%
			Clostridium perfringens str. 13]	599	0	100%	100%	100%
			Caldivirga maquilingensis IC-167]	558	0	100%	100%	100%
			Caldivirga maquilingensis IC-167]	558	0	100%	100%	100%
			Clostridium cellulolyticum H10]	598	0	100%	100%	100%
			Clostridium cellulolyticum H10]	598	0	100%	100%	100%
			e [Escherichia coli K12] >gi|74312058|ref|YP_310477.1| beta...	603	0	99,8%	100%	100%
			Thermotoga maritima MSB8]	563	0	100%	100%	100%
			Clostridium perfringens str. 13]	599	0	100%	100%	100%
			Haemophilus somnus 129PT]	596	0	81,4%	91,3%	100%
			e [Escherichia coli K12] >gi|74312058|ref|YP_310477.1| beta...	603	0	98,7%	99%	98,4%
			e [Escherichia coli K12] >gi|74312058|ref|YP_310477.1| beta...	603	0	98,7%	99%	98,4%
			e [Escherichia coli K12] >gi|74312058|ref|YP_310477.1| beta...	603	0	98,7%	99%	98,4%
			e [Escherichia coli K12] >gi|74312058|ref|YP_310477.1| beta...	603	0	98,7%	99%	98,4%
			e [Escherichia coli K12] >gi|74312058|ref|YP_310477.1| beta...	603	0	98,7%	99%	98,4%
			Clostridium perfringens str. 13]	599	1,E-134	41,6%	60%	97,8%
24	gi|4261801|...	XP_001138701	PREDICTED: glucuronidase, beta isoform 2 [Pan troglodytes]	600	6,E-34	100%	100%	100%
25	gi|3411175|...	NP_416134	beta-D-glucuronidase [Escherichia coli K12] >gi|74312058|ref|YP_310477.1| beta...	603	0	98,8%	99%	100%
26	gi|3411170|...	NP_416134	beta-D-glucuronidase [Escherichia coli K12] >gi|74312058|ref|YP_310477.1| beta...	603	0	98,8%	99%	100%
27	gi|38327507...	NP_416134	beta-D-glucuronidase [Escherichia coli K12] >gi|74312058|ref|YP_310477.1| beta...	603	0	100%	100%	100%
28	gi|29150589...	NP_416134	beta-D-glucuronidase [Escherichia coli K12] >gi|74312058|ref|YP_310477.1| beta...	603	0	99,8%	100%	100%
29	gi|13194574...	ZP_00712952	COG3250: Beta-galactosidase/beta-glucuronidase [Escherichia coli B171] >gi|752...	603	0	99,5%	99,8%	100%

Open apply filter: none

oncogenes: Result not yet ready for sequence: 4

43Mo/254Mo

KoriBlast

File Edit Modules Help

Search
Analyse
Filter Manager
Help

BLAST results

- beta-glucuronidase
  blastn vs. refseq_rna
  gi|147906581|ref|NM_0010936...
- aquaporines
  blastp vs. pat
  P29972 Aquaporin-CHIP
- test3
  tblastn vs. emrelstdfun
  Sequence
- aquaporines
  blastp vs. sgt
  Sequence
- beta-glucuronidases
  blastp vs. refseq_protein
  gi|91984087|gb|ABE68908.1| b...
- oncogenes
  blastn vs. emcds
  Sequence
- beta-mannosidase-rna
  blastn vs. refseq_genomic
  gi|133961144|ref|NM_077941.3|...
  Filter: Known HSP

Summary

Hits

List \ Conserved regions \ Multiple Alignment \ Position Specific Matrix \ Taxonomy

#	Accession	Definition	E-Value	Quality	# HSPs	Identity	Align. Length
1	NM_001093666	Xenopus laevis mannosidase, beta A, lysosomal (manba), mRNA>gi|50417767|gb|BC078052.1| Xenopus lae...	0		1	100%	3129
2	NM_001031655	Rattus norvegicus mannosidase, beta A, lysosomal(Manba), mRNA>gi|71051271|gb|BC099094.1| Rattus no...	1,E-21		4	88,5%	104
3	XM_697139	PREDICTED: Danio rerio similar to Mannosidase, beta A, lysosomal (LOC554712), mRNA	4,E-19		3	86,2%	116
4	NM_027288	Mus musculus mannosidase, beta A, lysosomal (Manba), mRNA>gi|21595010|gb|BC031409.1| Mus musculus ...	4,E-19		3	87,5%	104
5	NM_200159	Danio rerio mannosidase, beta A, lysosomal (manba), mRNA>gi|28278333|gb|BC045360.1| Daniorerio mann...	9,E-17		2	85,3%	116
6	XM_420666	PREDICTED: Gallus gallus mannosidase, beta A, lysosomal (MANBA), mRNA	3,E-16		4	87,4%	95
7	XM_001368674	PREDICTED: Monodelphis domestica hypothetical protein LOC100014402 (LOC100014402), mRNA	2,E-14		3	85,2%	108
8	NM_174387	Bos taurus mannosidase, beta A, lysosomal (MANBA), mRNA>gi|704359|gb|U17432.1|BTU17432 Bos taurus ...	1,E-12		4	82,7%	133
9	XM_001168983	PREDICTED: Pan troglodytes similar to mannosidase, beta A, lysosomal, transcript variant 1 (LOC461407), m...	5,E-12		4	82,1%	140
10	XM_001169005	PREDICTED: Pan troglodytes similar to mannosidase, beta A, lysosomal, transcript variant 2 (LOC461407), m...	5,E-12		4	82,1%	140
11	XM_001169032	PREDICTED: Pan troglodytes similar to mannosidase, beta A, lysosomal, transcript variant 3 (LOC461407), m...	5,E-12		4	82,1%	140
12	XM_517370	PREDICTED: Pan troglodytes similar to mannosidase, beta A, lysosomal, transcript variant 4 (LOC461407), m...	5,E-12		4	82,1%	140
13	XM_001101549	PREDICTED: Macaca mulatta mannosidase, beta A, lysosomal (MANBA), mRNA	5,E-12		4	82,1%	140
14	NM_005908	Homo sapiens mannosidase, beta A, lysosomal (MANBA), mRNA	5,E-12		4	82,1%	140
15	XM_545005	PREDICTED: Canis familiaris similar to Beta-mannosidase precursor (Mannanase) (Mannase) (LOC487883), m...	8,E-11		3	81,7%	142
16	XM_001186463	PREDICTED: Strongylocentrotus purpuratus similar to beta-mannosidase (LOC593854), mRNA	7,E-2		1	91,4%	35
17	XM_793313	PREDICTED: Strongylocentrotus purpuratus similar to beta-mannosidase (LOC593854), partial mRNA	7,E-2		1	91,4%	35
18	XM_367135	Magnaporthe grisea 70-15 hypothetical protein (MGG_07060) mRNA, complete cds	7,E-2		1	100%	23
19	XM_384855	Gibberella zeae PH-1 chromosome 2 hypothetical protein (FG04679.1) partial mRNA	7,E-2		1	100%	23
20	XM_363252	Magnaporthe grisea 70-15 hypothetical protein (MGG_01178) mRNA, complete cds	1,15		1	87,8%	41
21	XM_001386951	Pichia stipitis CBS 6054 Beta-mannosidase precursor (Mannanase) (MAN2) mRNA, complete cds	1,15		1	87,8%	41
22	XM_633030	Dictyostelium discoideum AX4 hypothetical protein (DDBDRAFT_0186566) mRNA, complete cds	1,15		1	100%	21
23	XM_535430	PREDICTED: Canis familiaris similar to fibrous sheath interacting protein 1 (LOC478256), mRNA	1,15		1	100%	21
24	XM_001433548	Paramecium tetraurelia hypothetical protein (GSPATT00035317001) mRNA, complete cds	4,53		1	100%	20
25	NM_183088	Mus musculus RIKEN cDNA 2410018M08 gene (2410018M08Rik), mRNA	4,53		1	100%	20
26	XM_001350755	Plasmodium falciparum 3D7 cell division protein FtsH, putative (PFL1925w) mRNA, complete cds	4,53		1	95,8%	24
27	XM_001033282	Tetrahymena thermophila SB210 hypothetical protein (TTHERM_00420270) mRNA, complete cds	4,53		1	95,8%	24
28	XM_001030918	Tetrahymena thermophila SB210 hypothetical protein (TTHERM_00999070) mRNA, complete cds	4,53		1	100%	20
29	XM_001210441	Aspergillus terreus NIH2624 hypothetical protein (ATEG_00355) mRNA, complete cds	4,53		1	100%	20
30	XM_001215814	Aspergillus terreus NIH2624 beta-mannosidase precursor (ATEG_06636) mRNA, complete cds	4,53		1	90,6%	32
31	XM_392850	PREDICTED: Apis mellifera similar to mannosidase, beta A, lysosomal (LOC409334), mRNA	4,53		1	85,4%	48
32	XM_001053414	PREDICTED: Rattus norvegicus similar to 3000004N20Rik protein (predicted) (RGD1307658_predicted), mRNA	4,53		1	100%	20

Fetch Features for HSP: -

Alignment: Query (3144 nuc) vs. NM_027288 (3 630 nuc)

HSP Map \ Definition \ Statistics \ Alignment

Features (5) \ Info

Query
HSP(s)
NM_027288

source : 1223..1266
gene : 1223..1266
CDS : 1223..1266
exon : 1223..1243
exon : 1244..1266

Name	Value
Location	<1223..>1266
gene	Manba
note	GO_component: lysosome; GO_function: cation binding; GO_function: catalytic activit...

1320 1330 1340 1350

TGTGATGAACTTGGAATCATGGTCTGGCAGGACTTTATGTTTGC

TGTGATGAACTTGGGATAATGGTGTGGCAGGACTTTATGTTTGC

1230 1240 1250 1260

HSP: < 2/3 >

oncogenes: Result not yet ready for sequence: 6

55Mo/254Mo

ANALYSE TAXONOMIQUE

KoriBlast

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BLAST results

- beta-glucuronidase blastn vs. refseq_rna gi|147906581|ref|NM_0010936...
- aquaporines blastp vs. pat P29972 Aquaporin-CHIP
- test3 tblastn vs. emrelstdfun Sequence
- aquaporines blastp vs. sgt Sequence
- beta-glucuronidases blastp vs. refseq_protein gi|91984087|gb|ABE68908.1| b...
- oncogenes blastn vs. emcds Sequence
- beta-mannosidase-rna blastn vs. refseq_genomic gi|133961144|ref|NM_077941.3|... Filter: Known HSP

Summary

Hits

List | Conserved regions | Multiple Alignment | Position Specific Matrix | Taxonomy

Compute | Taxonomy report: 45 out of 45 hits contain taxonomy data

Organism Report | Taxonomy Report

Taxonomy	Organi...	Hits	Score	Hit Definition
Bovidae	1	1	82	Bos taurus mannosidase, beta A, lysosomal (MANBA), mRNA>gi|704359|gb|U1...
Carnivora	1	2	76	PREDICTED: Canis familiaris similar to Beta-mannosidase precursor (Mannanase)...
Caniformia	1	2	76	PREDICTED: Canis familiaris similar to Beta-mannosidase precursor (Mannanase)...
Canidae	1	2	76	PREDICTED: Canis familiaris similar to Beta-mannosidase precursor (Mannanase)...
Canis	1	2	76	PREDICTED: Canis familiaris similar to Beta-mannosidase precursor (Mannanase)...
Canis lupus familiaris	1	2	76	PREDICTED: Canis familiaris similar to Beta-mannosidase precursor (Mannanase)...
Euarchontoglires	5	11	112	Rattus norvegicus mannosidase, beta A, lysosomal(Manba), mRNA>gi|7105127...
Primates	3	6	80	PREDICTED: Macaca mulatta mannosidase, beta A, lysosomal (MANBA), mRNA
Haplorrhini	3	6	80	PREDICTED: Macaca mulatta mannosidase, beta A, lysosomal (MANBA), mRNA
Catarrhini	3	6	80	PREDICTED: Macaca mulatta mannosidase, beta A, lysosomal (MANBA), mRNA
Cercopithecidae	1	1	80	PREDICTED: Macaca mulatta mannosidase, beta A, lysosomal (MANBA), mRNA
Cercopithecinae	1	1	80	PREDICTED: Macaca mulatta mannosidase, beta A, lysosomal (MANBA), mRNA
Macaca	1	1	80	PREDICTED: Macaca mulatta mannosidase, beta A, lysosomal (MANBA), mRNA
Hominidae	2	5	80	PREDICTED: Pan troglodytes similar to mannosidase, beta A, lysosomal, transcri...
Pan	1	4	80	PREDICTED: Pan troglodytes similar to mannosidase, beta A, lysosomal, transcri...
Homo	1	1	80	Homo sapiens mannosidase, beta A, lysosomal (MANBA), mRNA
Glires	2	5	112	Rattus norvegicus mannosidase, beta A, lysosomal(Manba), mRNA>gi|7105127...
Rodentia	2	5	112	Rattus norvegicus mannosidase, beta A, lysosomal(Manba), mRNA>gi|7105127...
Sciurognathi	2	5	112	Rattus norvegicus mannosidase, beta A, lysosomal(Manba), mRNA>gi|7105127...
Muroidea	2	5	112	Rattus norvegicus mannosidase, beta A, lysosomal(Manba), mRNA>gi|7105127...

Collapse all | Expand all

#	Accession	Definition	E-Value	Quality	# HSPs	Identity	Coverage
2	NM_001...	Rattus norvegicus mannosidase, beta A, lysosomal(Manba), mRNA>gi|71051271|gb|BC099094.1| Rattus norvegicus man...	1,E-21		4	88,5%	3,3%
4	NM_027...	Mus musculus mannosidase, beta A, lysosomal (Manba), mRNA>gi|21595010|gb|BC031409.1| Mus musculus mannosidase...	4,E-19		3	87,5%	3,3%
9	XM_001...	PREDICTED: Pan troglodytes similar to mannosidase, beta A, lysosomal, transcript variant 1 (LOC461407), mRNA	5,E-12		4	82,1%	4,5%
10	XM_001...	PREDICTED: Pan troglodytes similar to mannosidase, beta A, lysosomal, transcript variant 2 (LOC461407), mRNA	5,E-12		4	82,1%	4,5%

Alignment: Query (3144 nuc) vs. NM_001031655 (3 688 nuc)

HSP Map | Definition | Statistics | Alignment

Features (3) | Info

Query
HSP(s)
NM_001031655

source : 1960..2063
gene : 1960..2063
CDS : 1960..2063

Name	Value
Location	<1960..>2063
gene	Manba
note	GO_component: lysosome; GO_function: beta-mannosidase activity; GO_process: ...

2050 2060 2070 2080 2090 2100 2110

GGCCACACCATGGGGGCTTTGTATTGGCAGCTGAATGATATATGGCAGGCACCTTCTTGGTCTTCA

GGCCACACCATGGGGGCACTGTACTGGCAGCTGAATGATATCTGGCAGGCTCCTTCCTGGGCCTCT

1960 1970 1980 1990 2000 2010 2020

HSP: < 1/4 >

oncogenes: Result not yet ready for sequence: 8

78Mo/254Mo

Etude des régions conservées

KoriBlast

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BLAST results

- beta-glucuronidase
  blastn vs. refseq_rna
  gi|147906581|ref|NM_0010936...
- aquaporines
  blastp vs. pat
  P29972 Aquaporin-CHIP
- test3
  tblastn vs. emrelstdfun
  Sequence
- aquaporines
  blastp vs. sgt
  Sequence
- beta-glucuronidases
  blastp vs. refseq_protein
  gi|91984087|gb|ABE68908.1| b...
- oncogenes
  blastn vs. emcds
  Sequence
- beta-mannosidase-rna
  blastn vs. refseq_genomic
  gi|133961144|ref|NM_077941.3|...
  Filter: Known HSP

Summary

Hits

List | Conserved regions | Multiple Alignment | Position Specific Matrix | Taxonomy

#	Hit	HSP	E-Value
1	NM_001...	1-1	0
2	NM_001...	1-4	1,E-21
3	XM_697139	1-3	4,E-19
4	NM_027...	1-3	4,E-19
5	NM_200...	1-2	9,E-17
6	XM_420666	1-4	3,E-16
7	XM_0013...	1-3	2,E-14
8	NM_174...	1-4	1,E-12
9	XM_0011...	1-4	5,E-12
10	XM_0011...	1-4	5,E-12
11	XM_0011...	1-4	5,E-12
12	XM_517370	1-4	5,E-12
13	XM_0011...	1-4	5,E-12
14	NM_005...	1-4	5,E-12
15	XM_545005	1-3	8,E-11
16	XM_0011...	1-1	7,E-2
17	XM_793313	1-1	7,E-2
18	XM_367135	1-1	7,E-2

Sort by: Hit order Display: Cluster HSPs Header: Identities Features: CDS

Alignment: Query (3144 nuc) vs. NM_027288 (3 630 nuc)

HSP Map | Definition | Statistics | Alignment

Query
HSP(s)
NM_027288

Features (5) | Info

- source : 1223..1266
- gene : 1223..1266
- CDS : 1223..1266
- exon : 1223..1243
- exon : 1244..1266

Name	Value
Location	<1223..>1266
gene	Manba
note	GO_component: lysosome; GO_function: cation binding; GO_function: catalytic activit...

1320 1330 1340 1350

TGTGATGAACTTGGGAATCATGGTCTGGCAGGACTTTATGTTTGC

TGTGATGAACTTGGGATAATGGTGTGGCAGGACTTTATGTTTGC

1230 1240 1250 1260

HSP: < 2/3 >

oncogenes: Result not yet ready for sequence: 7

65Mo/254Mo

KoriBlast

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Available filters

Name	Description	Rule
EvalFilter 1	select by evalue	HSP E-Value < 0.0010
SeqInfo: Date	get by date	SeqInfo: Creation date < 20050101
Known HSP	get well-annotated HSP	Hit definition !: unknown and Hit definition !: hypothetical and Hit definition !: predicted and SeqInfo: Creation date > 20050101
EvalFilter 2	select by evalue (strict)	HSP E-Value == 0.0
Size	select by db sequence length	HSP alignment length >= 200
Size / eval	select by alignment size and evalue	HSP alignment length >= 250 or HSP E-Value <= 0.0010
Feature is Site	get by Site Feature	Feature type :: Site
Feature is Site (strict)	get by Site Feature, low EValue	Feature type :: Site and HSP E-Value < 0.0010
Qualifier is Rattus	get HSP from Rattus only	Qualifier value :: Rattus
SeqInfo: Org	get HSP from human only	SeqInfo: Organism :: (?i)(homo)
SeqInfo: Tax	get HSP from Chordata	SeqInfo: Taxonomy :: Chordata

Filter Editor

Filter

name: Known HSP

description: get well-annotated HSP

Retain hit data if all of the following constraints are valid:

Hit definition | does not contain | unknown

Hit definition | does not contain | hypothetical

Hit definition | does not contain | predicted

SeqInfo: Creation date | is greater than | 20050101

Ok Cancel

Help

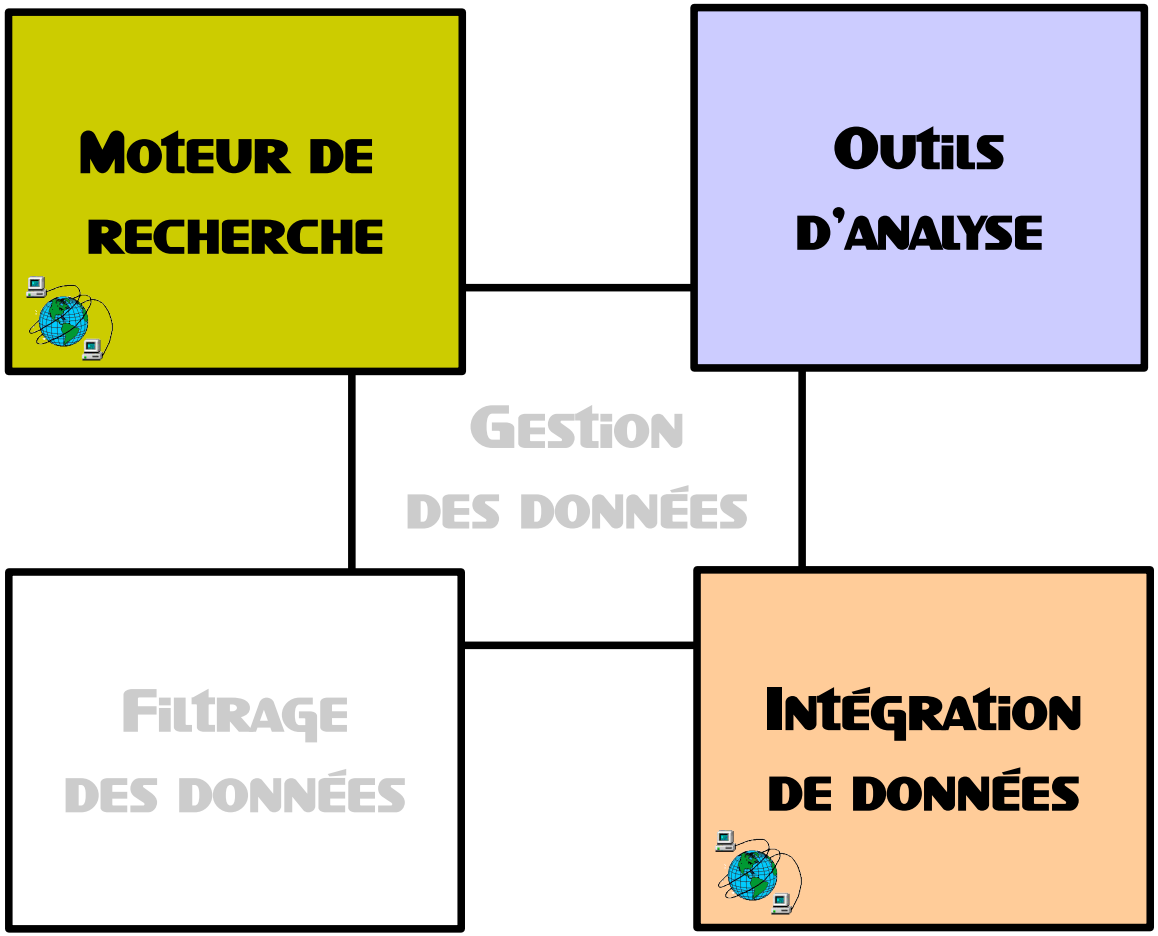
New... Copy Edit... Delete

oncogenes: Submit sequence: 10

77Mo/254Mo

- Exemples d'utilisations:
  - *'analyse dans la dentelle'*:
    - etude de site actif (fonction/structure),
    - analyse de mutations
    - analyse taxonomique
  - *'travail en gros'* :
    - recherche de contaminants (séquençage)
    - annotation de génomes

- Répondre à des besoins spécifiques



- Adapter KoriBlast pour utiliser des méthodes d'analyses particulières
- Configurer KoriBlast pour exploiter des banques de données propriétaires

MERCi...

... QUESTiONS ?