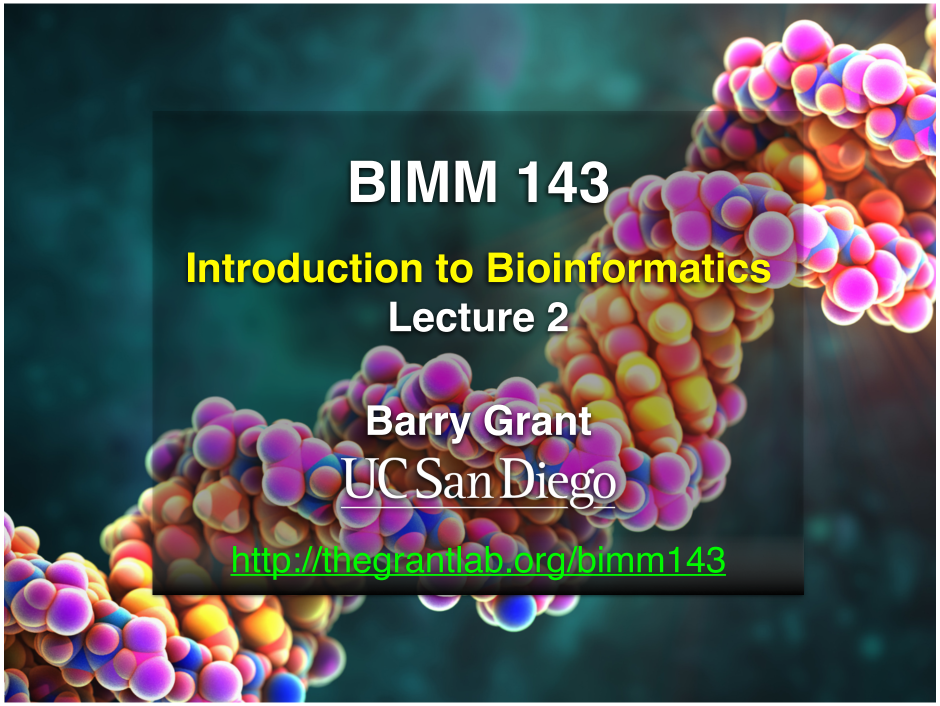


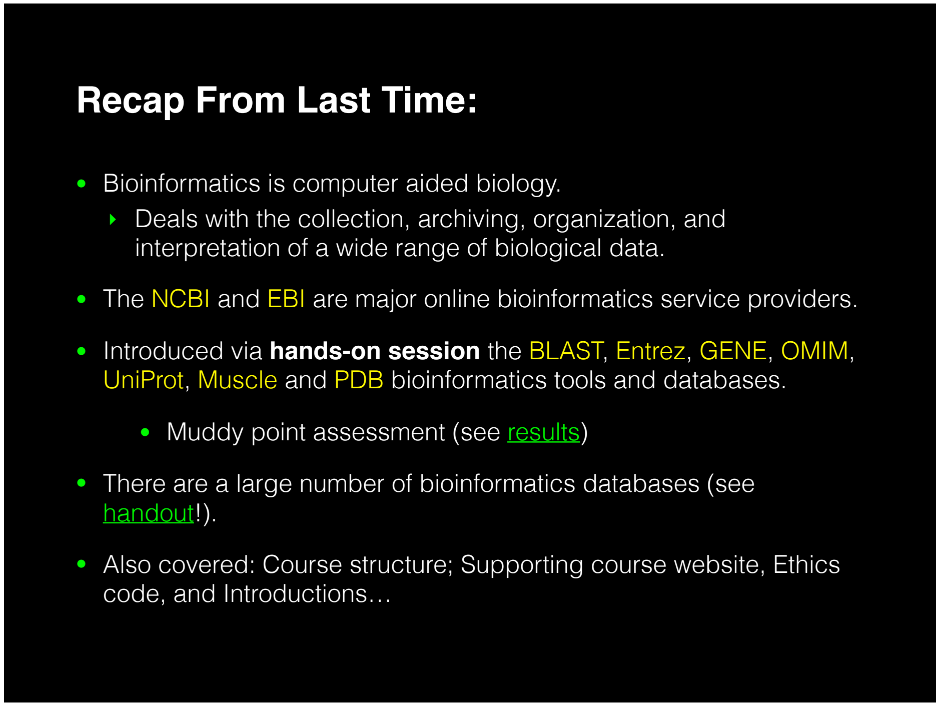
BIMM 143

Introduction to Bioinformatics
Lecture 2

Barry Grant

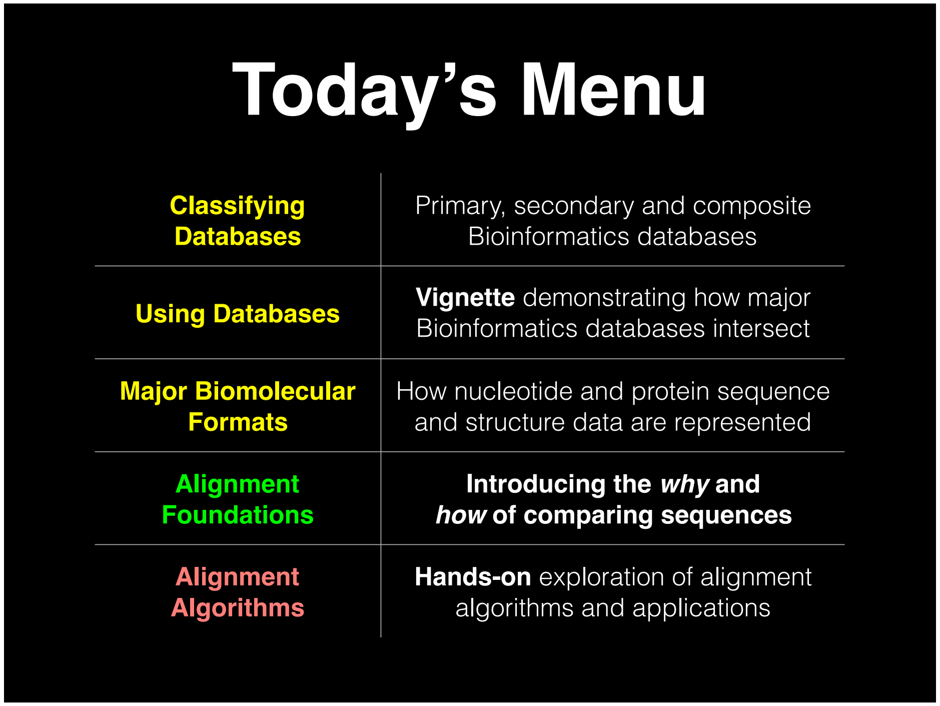
UC San Diego

http://thegrantlab.org/bimm143



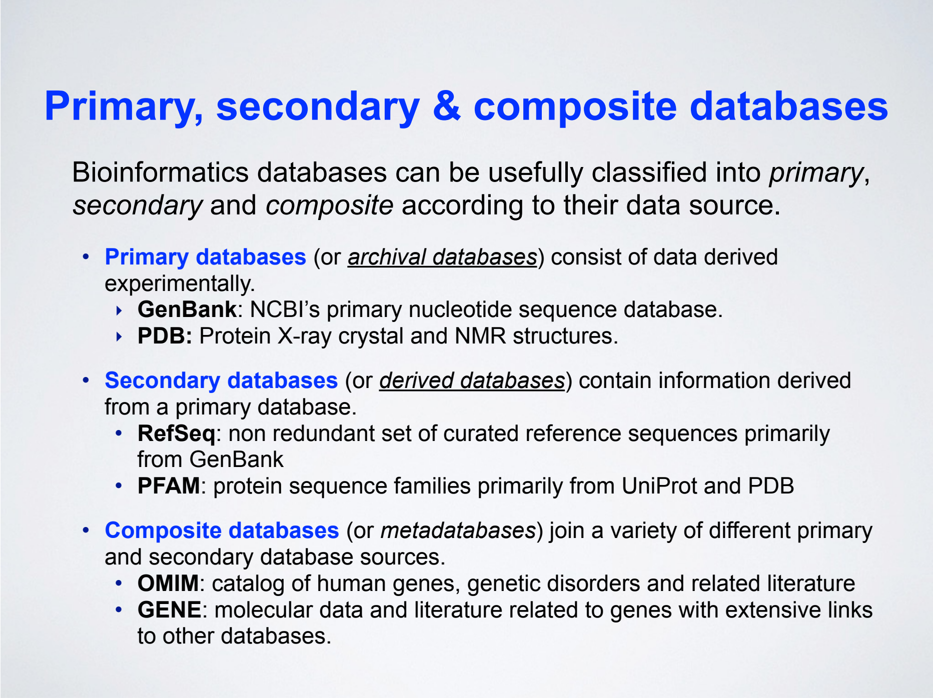
Recap From Last Time:

- Bioinformatics is computer aided biology.
  - Deals with the collection, archiving, organization, and interpretation of a wide range of biological data.
- The NCBI and EBI are major online bioinformatics service providers.
- Introduced via **hands-on session** the BLAST, Entrez, GENE, OMIM, UniProt, Muscle and PDB bioinformatics tools and databases.
  - Muddy point assessment (see results)
- There are a large number of bioinformatics databases (see handout!).
- Also covered: Course structure; Supporting course website, Ethics code, and Introductions…



Today's Menu

Classifying Databases	Primary, secondary and composite Bioinformatics databases
Using Databases	**Vignette** demonstrating how major Bioinformatics databases intersect
Major Biomolecular Formats	How nucleotide and protein sequence and structure data are represented
Alignment Foundations	**Introducing the *why* and *how* of comparing sequences**
Alignment Algorithms	**Hands-on** exploration of alignment algorithms and applications



Primary, secondary & composite databases

Bioinformatics databases can be usefully classified into *primary*, *secondary* and *composite* according to their data source.

- **Primary databases** (or *archival databases*) consist of data derived experimentally.
  - **GenBank**: NCBI's primary nucleotide sequence database.
  - **PDB:** Protein X-ray crystal and NMR structures.
- **Secondary databases** (or *derived databases*) contain information derived from a primary database.
  - **RefSeq**: non redundant set of curated reference sequences primarily from GenBank
  - **PFAM**: protein sequence families primarily from UniProt and PDB
- **Composite databases** (or *metadatabases*) join a variety of different primary and secondary database sources.
  - **OMIM**: catalog of human genes, genetic disorders and related literature
  - **GENE**: molecular data and literature related to genes with extensive links to other databases.

DATABASE VIGNETTE

You have just come out a seminar about gastric cancer and one of your co-workers asks:

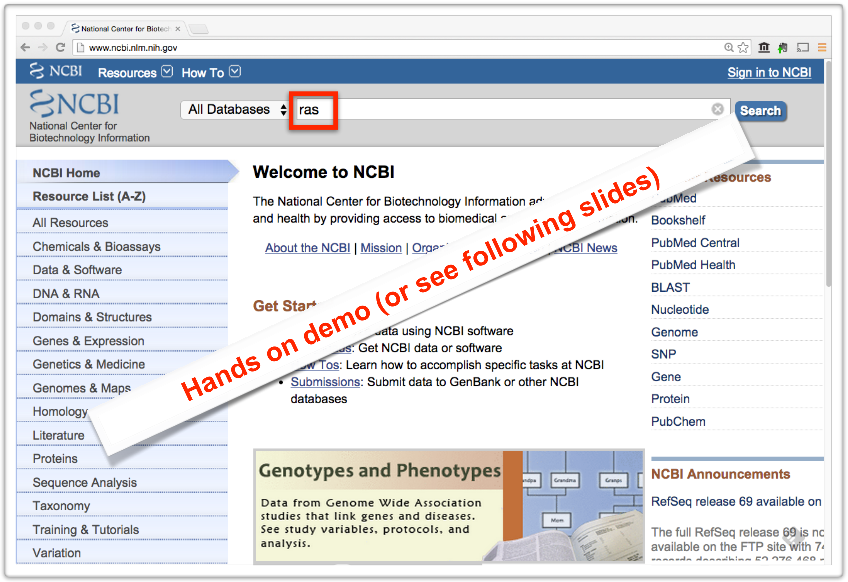
"What do you know about that 'Kras' gene the speaker kept taking about?"

You have some recollection about hearing of 'Ras' before. How would you find out more?

- Google?
- Library?
- **Bioinformatics databases at NCBI and EBI!**

http://www.ncbi.nlm.nih.gov/

http://www.ncbi.nlm.nih.gov/



Welcome to NCBI

The National Center for Biotechnology Information ad and health by providing access to biomedical ion.

Get Start

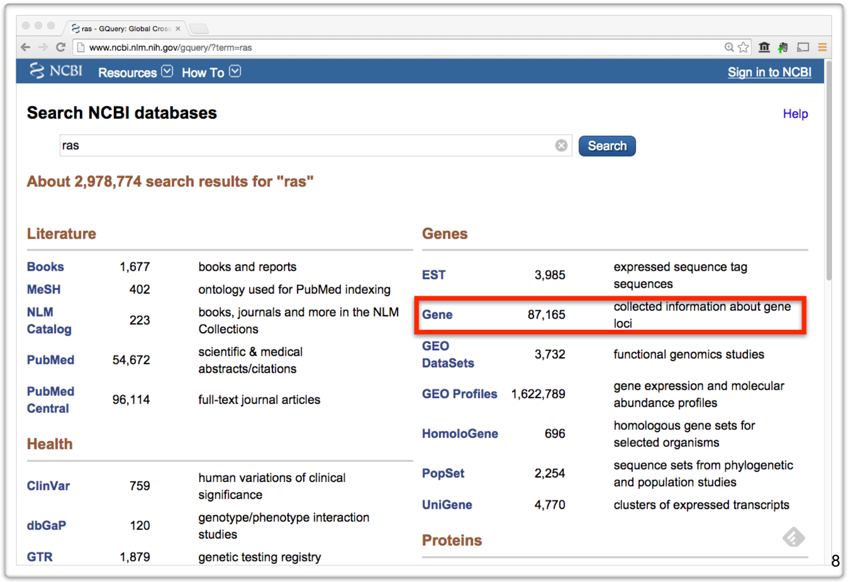
- ata using NCBI software
- s: Get NCBI data or software
- w Tos: Learn how to accomplish specific tasks at NCBI
- Submissions: Submit data to GenBank or other NCBI databases

The full RefSeq release 69 is nc available on the FTP site with 7

Hands on demo (or see following slides)

Example Vignette Questions:

- What chromosome location and what genes are in the vicinity of a given query gene? NCBI **GENE**
- What can you find out about molecular functions, biological processes, and prominent cellular locations? EBI **GO**
- What amino acid positions in the protein are responsible for ligand binding? EBI **UniProt**
- What variants of this gene are associated with gastric cancer and other human diseases? NCBI **OMIN**
- What is known about the protein family, its species distribution, number in humans and residue-wise conservation? EBI **PFAM**
- Are high resolution protein structures available to examine the details of these mutations? How might we explain their potential molecular effects? RCSB **PDB**


ras - GQuery: Global Cross
www.ncbi.nlm.nih.gov/gquery/?term=ras
NCBI
Resources
How To
Sign in to NCBI
Help
ras
Search

Search NCBI databases

About 2,978,774 search results for "ras"

Literature

Books	1,677	books and reports
MeSH	402	ontology used for PubMed indexing
NLM Catalog	223	books, journals and more in the NLM Collections
PubMed	54,672	scientific & medical abstracts/citations
PubMed Central	96,114	full-text journal articles

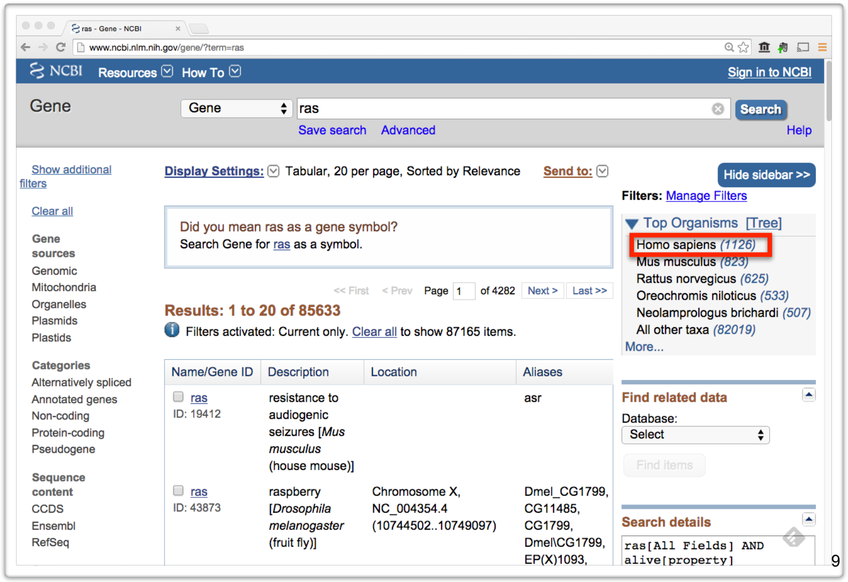
Health

ClinVar	759	human variations of clinical significance
dbGaP	120	genotype/phenotype interaction studies
GTR	1,879	genetic testing registry

Genes

EST	3,985	expressed sequence tag sequences
Gene	87,165	collected information about gene loci
GEO DataSets	3,732	functional genomics studies
GEO Profiles	1,622,789	gene expression and molecular abundance profiles
HomoloGene	696	homologous gene sets for selected organisms
PopSet	2,254	sequence sets from phylogenetic and population studies
UniGene	4,770	clusters of expressed transcripts

Proteins



ras - Gene - NCBI

www.ncbi.nlm.nih.gov/gene/?term=ras

Gene: ras

Display Settings: Tabular, 20 per page, Sorted by Relevance

Gene sources: Genomic, Mitochondria, Organelles, Plasmids, Plastids

Categories: Alternatively spliced, Annotated genes, Non-coding, Protein-coding, Pseudogene

Sequence content: CCDS, Ensembl, RefSeq

Did you mean ras as a gene symbol?
Search Gene for ras as a symbol.

<< First < Prev Page 1 of 4282 Next > Last >>

Results: 1 to 20 of 85633

Filters activated: Current only. Clear all to show 87165 items.

Name/Gene ID	Description	Location	Aliases
□ ras ID: 19412	resistance to audiogenic seizures [*Mus musculus* (house mouse)]		asr
□ ras ID: 43873	raspberry [*Drosophila melanogaster* (fruit fly)]	Chromosome X, NC_004354.4 (10744502..10749097)	Dmel_CG1799, CG11485, CG1799, Dmel\CG1799, EP(X)1093,

Filters: Manage Filters

Top Organisms [Tree]

Homo sapiens	*(1126)*
Mus musculus	*(823)*
Rattus norvegicus	*(625)*
Oreochromis niloticus	*(533)*
Neolamprologus brichardi	*(507)*
All other taxa	*(82019)*

More...

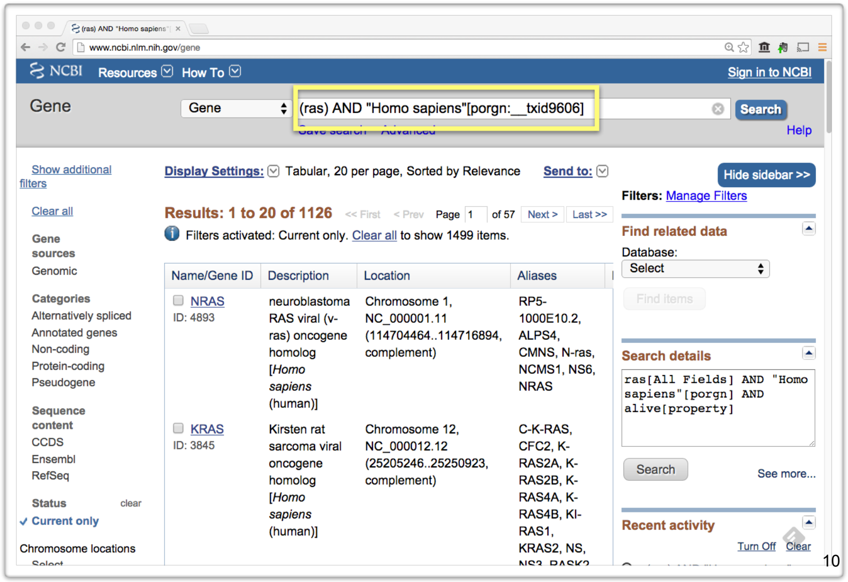
Find related data

Database: Select

Find items

Search details

```
ras[All Fields] AND
alive[property]
```



(ras) AND "Homo sapiens"[

www.ncbi.nlm.nih.gov/gene

Gene: (ras) AND "Homo sapiens"[porgn:__txid9606]

Display Settings: Tabular, 20 per page, Sorted by Relevance

Results: 1 to 20 of 1126 << First < Prev Page 1 of 57 Next > Last >>

Filters activated: Current only. Clear all to show 1499 items.

Gene sources: Genomic

Categories: Alternatively spliced, Annotated genes, Non-coding, Protein-coding, Pseudogene

Sequence content: CCDS, Ensembl, RefSeq

Status clear
✓ Current only

Chromosome locations

Name/Gene ID	Description	Location	Aliases
□ NRAS ID: 4893	neuroblastoma RAS viral (v-ras) oncogene homolog [*Homo sapiens* (human)]	Chromosome 1, NC_000001.11 (114704464..114716894, complement)	RP5-1000E10.2, ALPS4, CMNS, N-ras, NCMS1, NS6, NRAS
□ KRAS ID: 3845	Kirsten rat sarcoma viral oncogene homolog [*Homo sapiens* (human)]	Chromosome 12, NC_000012.12 (25205246..25250923, complement)	C-K-RAS, CFC2, K-RAS2A, K-RAS2B, K-RAS4A, K-RAS4B, KI-RAS1, KRAS2, NS,

Filters: Manage Filters

Find related data

Database: Select

Find items

Search details

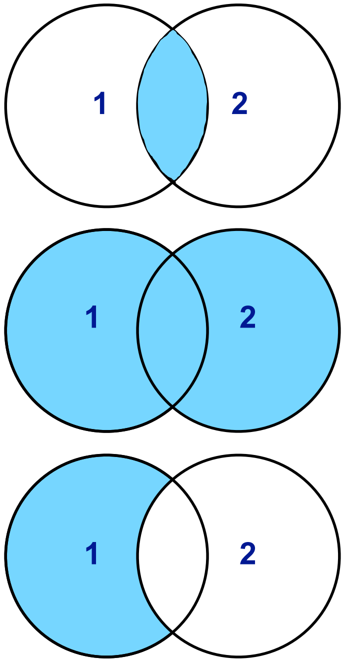
```
ras[All Fields] AND "Homo
sapiens"[porgn] AND
alive[property]
```

Search See more...

Recent activity

Turn Off Clear

1 AND 2



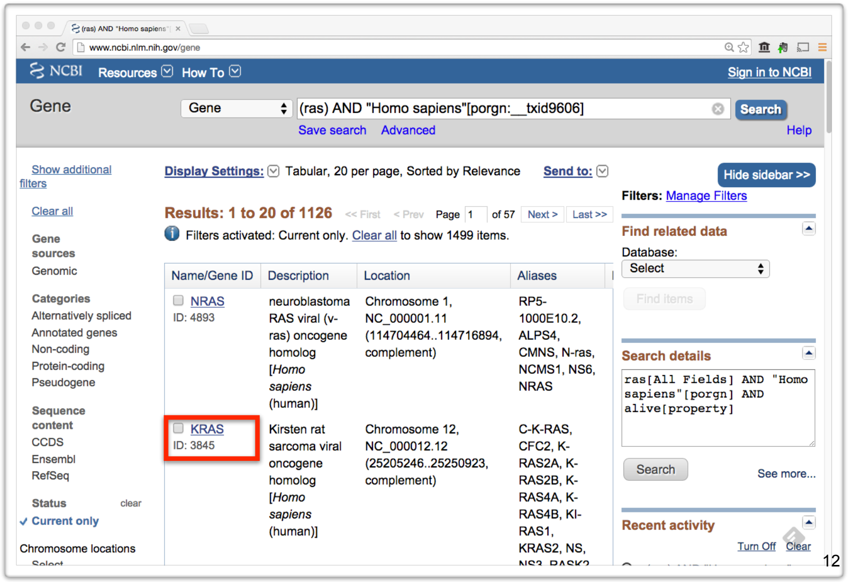
ras AND disease
(1185 results)

1 OR 2

ras OR disease
(134,872 results)

1 NOT 2

ras NOT disease
(84,448 results)



(ras) AND "Homo sapiens"[

www.ncbi.nlm.nih.gov/gene

Gene: (ras) AND "Homo sapiens"[porgn:__txid9606]

Display Settings: Tabular, 20 per page, Sorted by Relevance

Results: 1 to 20 of 1126 << First < Prev Page 1 of 57 Next > Last >>

Filters activated: Current only. Clear all to show 1499 items.

Gene sources: Genomic

Categories: Alternatively spliced, Annotated genes, Non-coding, Protein-coding, Pseudogene

Sequence content: CCDS, Ensembl, RefSeq

Status clear
✓ Current only

Chromosome locations

Name/Gene ID	Description	Location	Aliases
□ NRAS ID: 4893	neuroblastoma RAS viral (v-ras) oncogene homolog [*Homo sapiens* (human)]	Chromosome 1, NC_000001.11 (114704464..114716894, complement)	RP5-1000E10.2, ALPS4, CMNS, N-ras, NCMS1, NS6, NRAS
□ KRAS ID: 3845	Kirsten rat sarcoma viral oncogene homolog [*Homo sapiens* (human)]	Chromosome 12, NC_000012.12 (25205246..25250923, complement)	C-K-RAS, CFC2, K-RAS2A, K-RAS2B, K-RAS4A, K-RAS4B, KI-RAS1, KRAS2, NS,

Filters: Manage Filters

Find related data

Database: Select

Find items

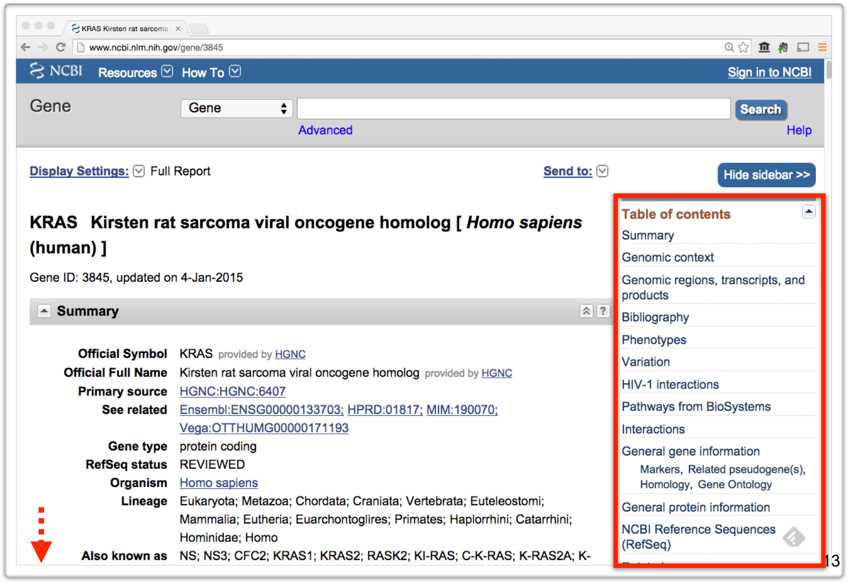
Search details

```
ras[All Fields] AND "Homo
sapiens"[porgn] AND
alive[property]
```

Search See more...

Recent activity

Turn Off Clear



Full Report

KRAS Kirsten rat sarcoma viral oncogene homolog [*Homo sapiens* (human)]

Gene ID: 3845, updated on 4-Jan-2015

Summary

Official Symbol	KRAS provided by HGNC
Official Full Name	Kirsten rat sarcoma viral oncogene homolog provided by HGNC
Primary source	HGNC:HGNC:6407
See related	Ensembl:ENSG00000133703; HPRD:01817; MIM:190070; Vega:OTTHUMG00000171193
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Homo sapiens
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo
Also known as	NS; NS3; CFC2; KRAS1; KRAS2; RASK2; KI-RAS; C-K-RAS; K-RAS2A; K-

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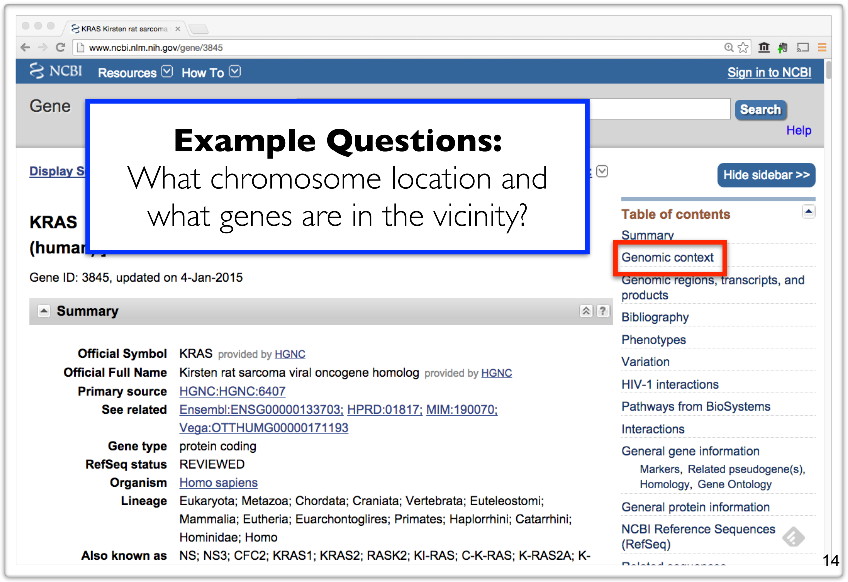
Interactions
General gene information
Markers, Related pseudogene(s), Homology, Gene Ontology
General protein information
NCBI Reference Sequences (RefSeq)



Example Questions:
What chromosome location and what genes are in the vicinity?

KRAS (human)]

Gene ID: 3845, updated on 4-Jan-2015

Summary

Official Symbol KRAS provided by HGNC
Official Full Name Kirsten rat sarcoma viral oncogene homolog provided by HGNC
Primary source HGNC:HGNC:6407
See related Ensembl:ENSG00000133703; HPRD:01817; MIM:190070; Vega:OTTHUMG00000171193
Gene type protein coding
RefSeq status REVIEWED
Organism Homo sapiens
Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo
Also known as NS; NS3; CFC2; KRAS1; KRAS2; RASK2; KI-RAS; C-K-RAS; K-RAS2A; K-

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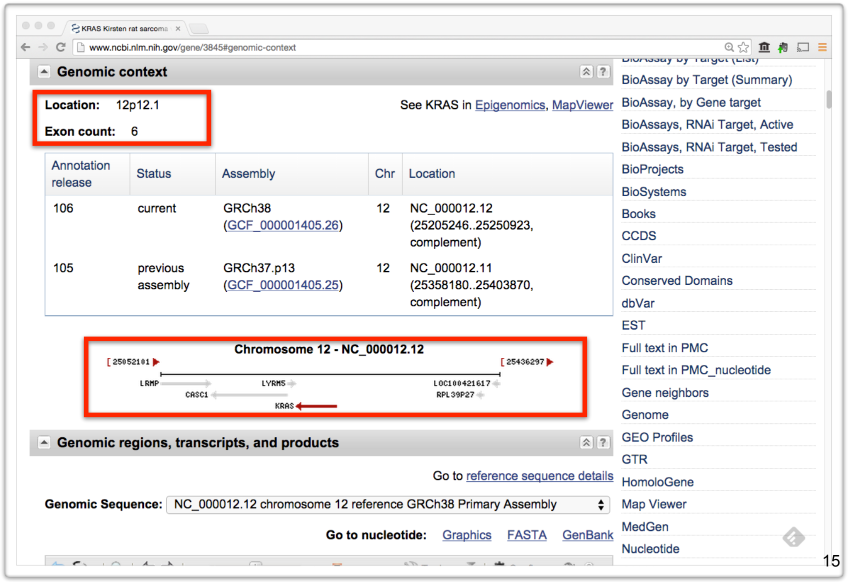


Genomic context

Location: 12p12.1

Exon count: 6

See KRAS in Epigenomics, MapViewer

Annotation release	Status	Assembly	Chr	Location
106	current	GRCh38 (GCF_000001405.26)	12	NC_000012.12 (25205246..25250923, complement)
105	previous assembly	GRCh37.p13 (GCF_000001405.25)	12	NC_000012.11 (25358180..25403870, complement)

Chromosome 12 - NC_000012.12

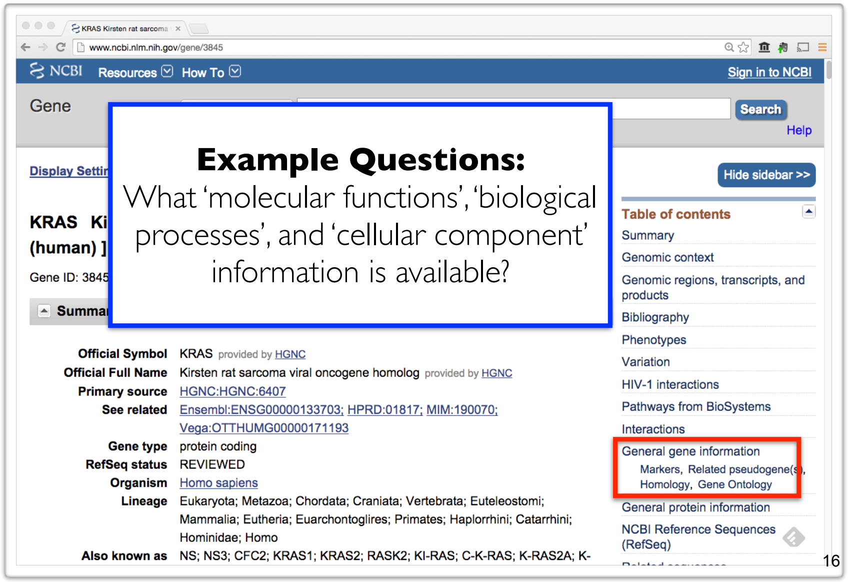
Genomic regions, transcripts, and products

Go to reference sequence details

Genomic Sequence: NC_000012.12 chromosome 12 reference GRCh38 Primary Assembly

Go to nucleotide: Graphics FASTA GenBank

BioAssay by Target (List)
BioAssay by Target (Summary)
BioAssay, by Gene target
BioAssays, RNAi Target, Active
BioAssays, RNAi Target, Tested
BioProjects
BioSystems
Books
CCDS
ClinVar
Conserved Domains
dbVar
EST
Full text in PMC
Full text in PMC_nucleotide
Gene neighbors
Genome
GEO Profiles
GTR
HomoloGene
Map Viewer
MedGen
Nucleotide



Example Questions:
What 'molecular functions', 'biological processes', and 'cellular component' information is available?

KRAS Ki (human)]

Gene ID: 3845

Summary

Official Symbol KRAS provided by HGNC
Official Full Name Kirsten rat sarcoma viral oncogene homolog provided by HGNC
Primary source HGNC:HGNC:6407
See related Ensembl:ENSG00000133703; HPRD:01817; MIM:190070; Vega:OTTHUMG00000171193
Gene type protein coding
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Organism Homo sapiens
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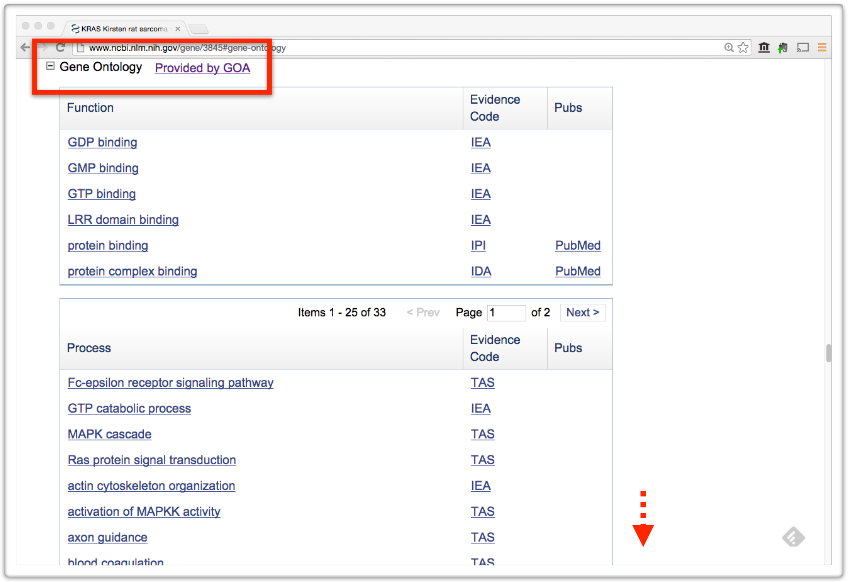


KRAS Kirsten rat sarcoma

www.ncbi.nlm.nih.gov/gene/3845#gene-ontology

⊟ Gene Ontology Provided by GOA

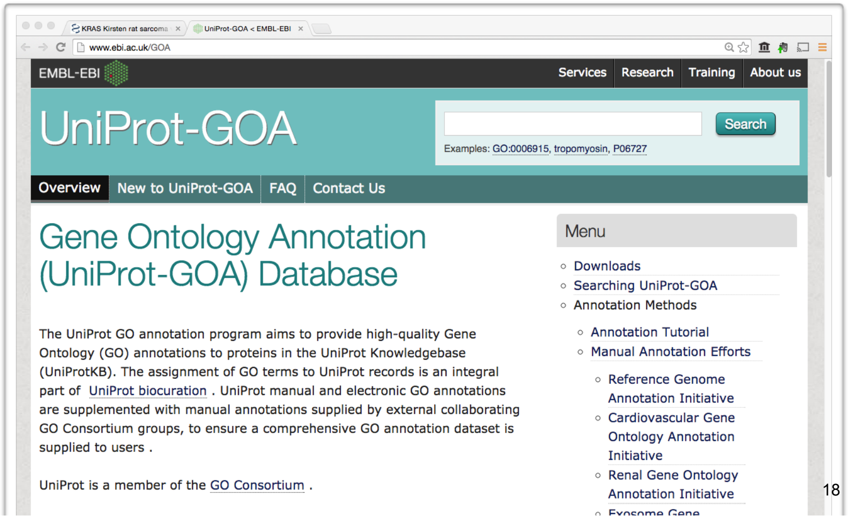
Function	Evidence Code	Pubs
GDP binding	IEA	
GMP binding	IEA	
GTP binding	IEA	
LRR domain binding	IEA	
protein binding	IPI	PubMed
protein complex binding	IDA	PubMed

Items 1 - 25 of 33 < Prev Page 1 of 2 Next >

Process	Evidence Code	Pubs
Fc-epsilon receptor signaling pathway	TAS	
GTP catabolic process	IEA	
MAPK cascade	TAS	
Ras protein signal transduction	TAS	
actin cytoskeleton organization	IEA	
activation of MAPKK activity	TAS	
axon guidance	TAS	
blood coagulation	TAS	

GO: Gene Ontology

GO provides a controlled vocabulary of terms for describing gene product characteristics and gene product annotation data



KRAS Kirsten rat sarcoma | UniProt-GOA < EMBL-EBI

www.ebi.ac.uk/GOA

EMBL-EBI | Services | Research | Training | About us

UniProt-GOA

Search

Examples: GO:0006915, tropomyosin, P06727

Overview | New to UniProt-GOA | FAQ | Contact Us

Gene Ontology Annotation (UniProt-GOA) Database

The UniProt GO annotation program aims to provide high-quality Gene Ontology (GO) annotations to proteins in the UniProt Knowledgebase (UniProtKB). The assignment of GO terms to UniProt records is an integral part of UniProt biocuration . UniProt manual and electronic GO annotations are supplemented with manual annotations supplied by external collaborating GO Consortium groups, to ensure a comprehensive GO annotation dataset is supplied to users .

UniProt is a member of the GO Consortium .

Menu

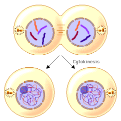
- Downloads
- Searching UniProt-GOA
- Annotation Methods
  - Annotation Tutorial
  - Manual Annotation Efforts
    - Reference Genome Annotation Initiative
    - Cardiovascular Gene Ontology Annotation Initiative
    - Renal Gene Ontology Annotation Initiative
    - Exosome Gene

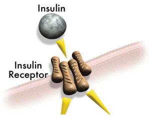
Why do we need Ontologies?

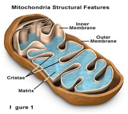
- Annotation is essential for capturing the understanding and knowledge associated with a sequence or other molecular entity
- Annotation is traditionally recorded as “free text”, which is easy to read by humans, but has a number of disadvantages, including:
  - Difficult for computers to parse
  - Quality varies from database to database
  - Terminology used varies from annotator to annotator
- Ontologies are annotations using standard vocabularies that try to address these issues
- GO is integrated with UniProt and many other databases including a number at NCBI

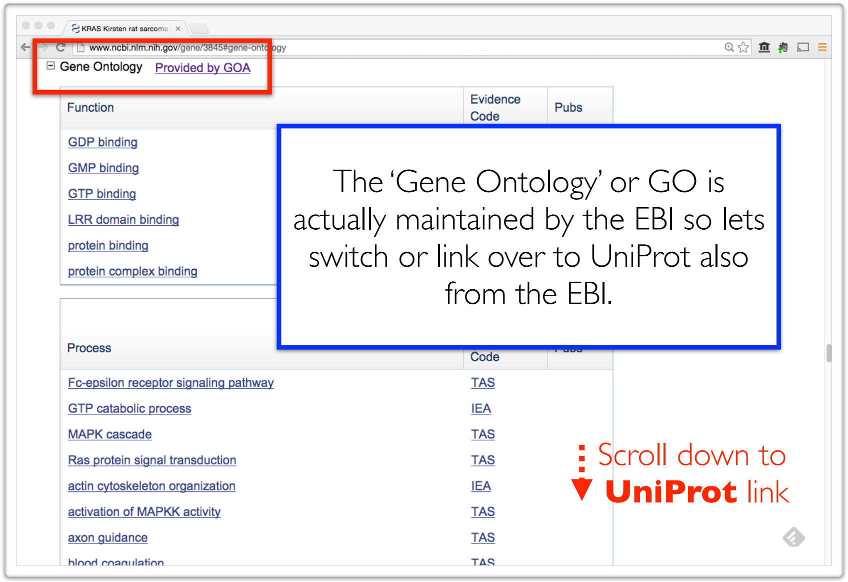
GO Ontologies

- There are three ontologies in GO:
  - **Biological <u>Process</u>**
    A commonly recognized series of events
    e.g. cell division, mitosis,
  - **Molecular <u>Function</u>**
    An elemental activity, task or job
    e.g. kinase activity, insulin binding
  - **Cellular <u>Component</u>**
    Where a gene product is located
    e.g. mitochondrion, mitochondrial membrane









⊟ Gene Ontology Provided by GOA

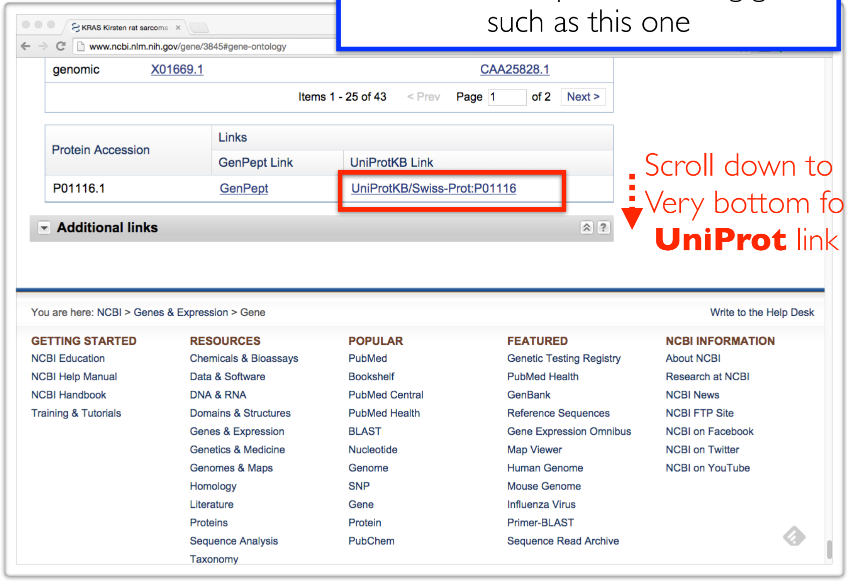
Function	Evidence Code	Pubs
GDP binding		
GMP binding		
GTP binding		
LRR domain binding		
protein binding		
protein complex binding		

Process	Evidence Code	Pubs
Fc-epsilon receptor signaling pathway	TAS	
GTP catabolic process	IEA	
MAPK cascade	TAS	
Ras protein signal transduction	TAS	
actin cytoskeleton organization	IEA	
activation of MAPKK activity	TAS	
axon guidance	TAS	
blood coagulation	TAS	

The 'Gene Ontology' or GO is actually maintained by the EBI so lets switch or link over to UniProt also from the EBI.

Scroll down to **UniProt** link

UniProt will detail much more information for protein coding genes such as this one



genomic	X01669.1	CAA25828.1

Items 1 - 25 of 43 < Prev Page 1 of 2 Next >

Protein Accession	Links	
	GenPept Link	UniProtKB Link
P01116.1	GenPept	UniProtKB/Swiss-Prot:P01116

Additional links

You are here: NCBI > Genes & Expression > Gene

Write to the Help Desk

GETTING STARTED
NCBI Education
NCBI Help Manual
NCBI Handbook
Training & Tutorials

RESOURCES
Chemicals & Bioassays
Data & Software
DNA & RNA
Domains & Structures
Genes & Expression
Genetics & Medicine
Genomes & Maps
Homology
Literature
Proteins
Sequence Analysis
Taxonomy

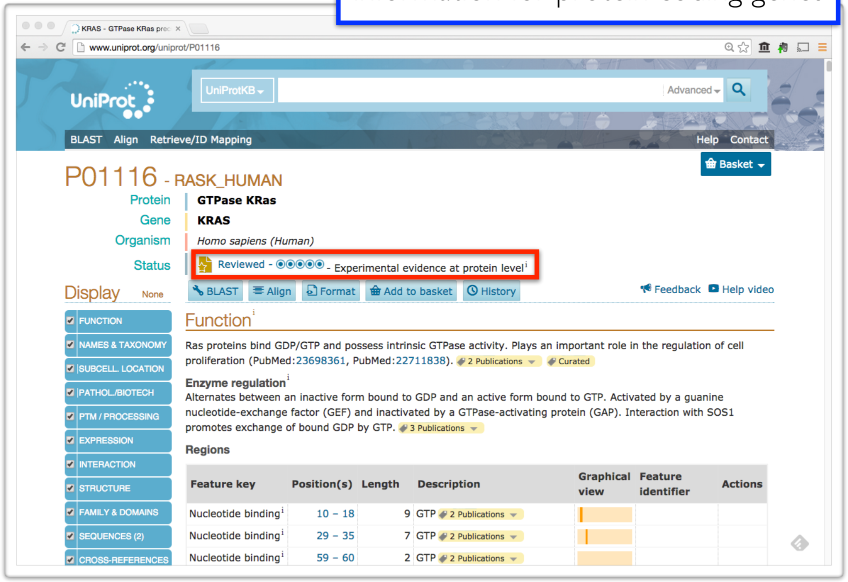
POPULAR
PubMed
Bookshelf
PubMed Central
PubMed Health
BLAST
Nucleotide
Genome
SNP
Gene
Protein
PubChem

FEATURED
Genetic Testing Registry
PubMed Health
GenBank
Reference Sequences
Gene Expression Omnibus
Map Viewer
Human Genome
Mouse Genome
Influenza Virus
Primer-BLAST
Sequence Read Archive

NCBI INFORMATION
About NCBI
Research at NCBI
NCBI News
NCBI FTP Site
NCBI on Facebook
NCBI on Twitter
NCBI on YouTube

Scroll down to Very bottom for **UniProt** link

UniProt will detail much more information for protein coding genes



P01116 - RASK_HUMAN

Protein | GTPase KRas
Gene | KRAS
Organism | *Homo sapiens (Human)*
Status | Reviewed - ◎◎◎◎◎ - Experimental evidence at protein level

Function

Ras proteins bind GDP/GTP and possess intrinsic GTPase activity. Plays an important role in the regulation of cell proliferation (PubMed:23698361, PubMed:22711838). 2 Publications Curated

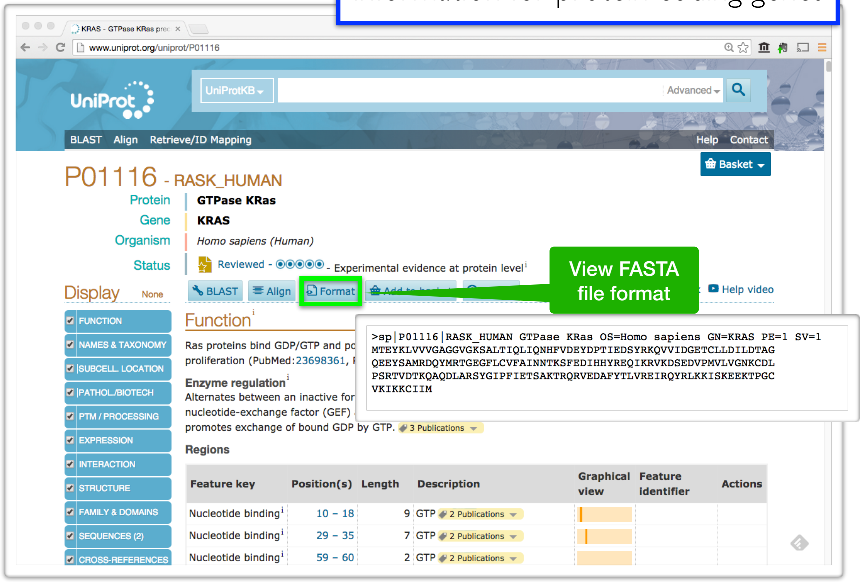
Enzyme regulation

Alternates between an inactive form bound to GDP and an active form bound to GTP. Activated by a guanine nucleotide-exchange factor (GEF) and inactivated by a GTPase-activating protein (GAP). Interaction with SOS1 promotes exchange of bound GDP by GTP. 3 Publications

Regions

Feature key	Position(s)	Length	Description	Graphical view	Feature identifier	Actions
Nucleotide binding	10 – 18	9	GTP 2 Publications			
Nucleotide binding	29 – 35	7	GTP 2 Publications			
Nucleotide binding	59 – 60	2	GTP 2 Publications			

UniProt will detail much more information for protein coding genes



P01116 - RASK_HUMAN

Protein | GTPase KRas
Gene | KRAS
Organism | *Homo sapiens (Human)*
Status | Reviewed - ◎◎◎◎◎ - Experimental evidence at protein level

View FASTA file format

```
>sp|P01116|RASK_HUMAN GTPase KRas OS=Homo sapiens GN=KRAS PE=1 SV=1
MTEYKLVVVGAGGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCLLDILDTAG
QEEYSAMRDQYMRTGEGFLCVFAINNTKSFEDIHHYREQIKRVKDSEDVPMVLVGNKCDL
PSRTVDTKQAQDLARSYGIPFIETSAKTRQRVEDAFYTLVREIRQYRLKKISKEEKTPGC
VKIKKCIIM
```

Function

Ras proteins bind GDP/GTP and pc

proliferation (PubMed:23698361, I

Enzyme regulation

Alternates between an inactive for

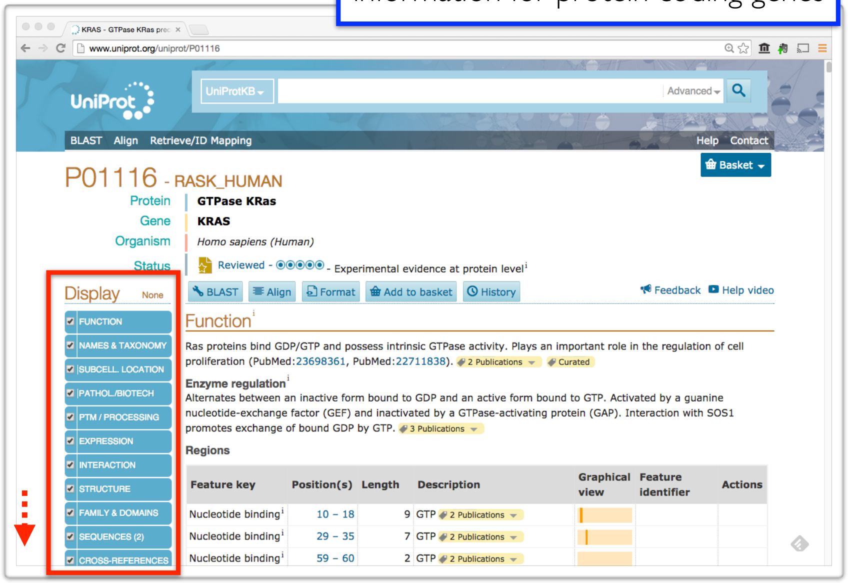
nucleotide-exchange factor (GEF)

promotes exchange of bound GDP by GTP. 3 Publications

Regions

Feature key	Position(s)	Length	Description	Graphical view	Feature identifier	Actions
Nucleotide binding	10 – 18	9	GTP 2 Publications			
Nucleotide binding	29 – 35	7	GTP 2 Publications			
Nucleotide binding	59 – 60	2	GTP 2 Publications			

UniProt will detail much more information for protein coding genes



P01116 - RASK_HUMAN

Protein	GTPase KRas
Gene	KRAS
Organism	*Homo sapiens (Human)*
Status	Reviewed - ●●●●● - Experimental evidence at protein level[i]

Function[i]

Ras proteins bind GDP/GTP and possess intrinsic GTPase activity. Plays an important role in the regulation of cell proliferation (PubMed:23698361, PubMed:22711838). 2 Publications Curated

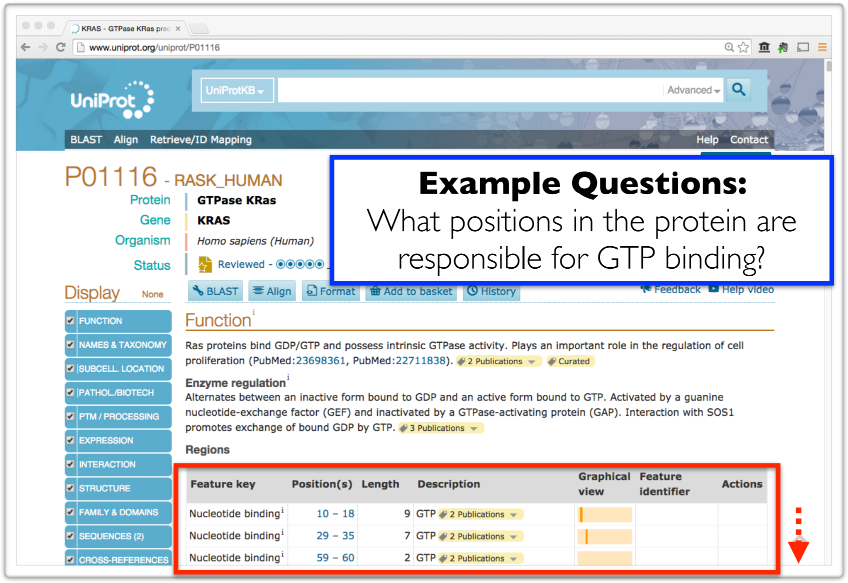
Enzyme regulation[i]

Alternates between an inactive form bound to GDP and an active form bound to GTP. Activated by a guanine nucleotide-exchange factor (GEF) and inactivated by a GTPase-activating protein (GAP). Interaction with SOS1 promotes exchange of bound GDP by GTP. 3 Publications

Regions

Feature key	Position(s)	Length	Description	Graphical view	Feature identifier	Actions
Nucleotide binding[i]	10 – 18	9	GTP 2 Publications			
Nucleotide binding[i]	29 – 35	7	GTP 2 Publications			
Nucleotide binding[i]	59 – 60	2	GTP 2 Publications			

Example Questions:
What positions in the protein are responsible for GTP binding?


P01116 - RASK_HUMAN

Protein	GTPase KRas
Gene	KRAS
Organism	*Homo sapiens (Human)*
Status	Reviewed - ●●●●●

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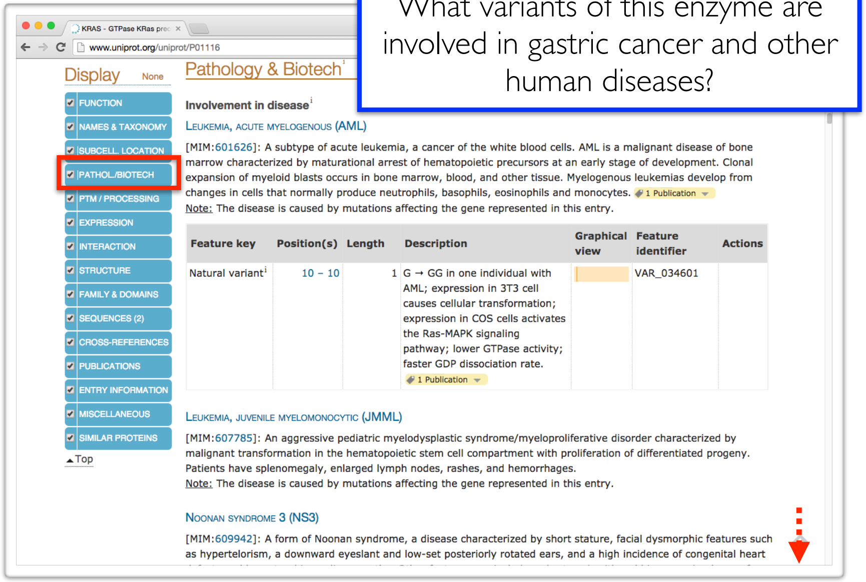
Nucleotide binding[i]	29 – 35	7	GTP 2 Publications			
Nucleotide binding[i]	59 – 60	2	GTP 2 Publications			

Example Questions:
What variants of this enzyme are involved in gastric cancer and other human diseases?



Pathology & Biotech[i]

Involvement in disease[i]

LEUKEMIA, ACUTE MYELOGENOUS (AML)

[MIM:601626]: A subtype of acute leukemia, a cancer of the white blood cells. AML is a malignant disease of bone marrow characterized by maturational arrest of hematopoietic precursors at an early stage of development. Clonal expansion of myeloid blasts occurs in bone marrow, blood, and other tissue. Myelogenous leukemias develop from changes in cells that normally produce neutrophils, basophils, eosinophils and monocytes. 1 Publication
Note: The disease is caused by mutations affecting the gene represented in this entry.

Feature key	Position(s)	Length	Description	Graphical view	Feature identifier	Actions
Natural variant[i]	10 – 10	1	G → GG in one individual with AML; expression in 3T3 cell causes cellular transformation; expression in COS cells activates the Ras-MAPK signaling pathway; lower GTPase activity; faster GDP dissociation rate. 1 Publication		VAR_034601	

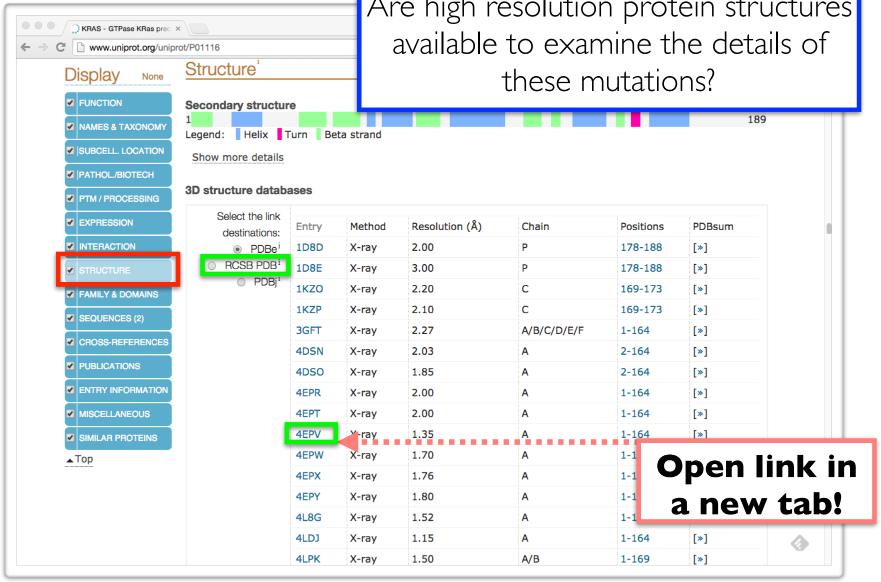
LEUKEMIA, JUVENILE MYELOMONOCYTIC (JMML)

[MIM:607785]: An aggressive pediatric myelodysplastic syndrome/myeloproliferative disorder characterized by malignant transformation in the hematopoietic stem cell compartment with proliferation of differentiated progeny. Patients have splenomegaly, enlarged lymph nodes, rashes, and hemorrhages.
Note: The disease is caused by mutations affecting the gene represented in this entry.

NOONAN SYNDROME 3 (NS3)

[MIM:609942]: A form of Noonan syndrome, a disease characterized by short stature, facial dysmorphic features such as hypertelorism, a downward eyeslant and low-set posteriorly rotated ears, and a high incidence of congenital heart

Example Questions:
Are high resolution protein structures available to examine the details of these mutations?



Structure[i]

Secondary structure

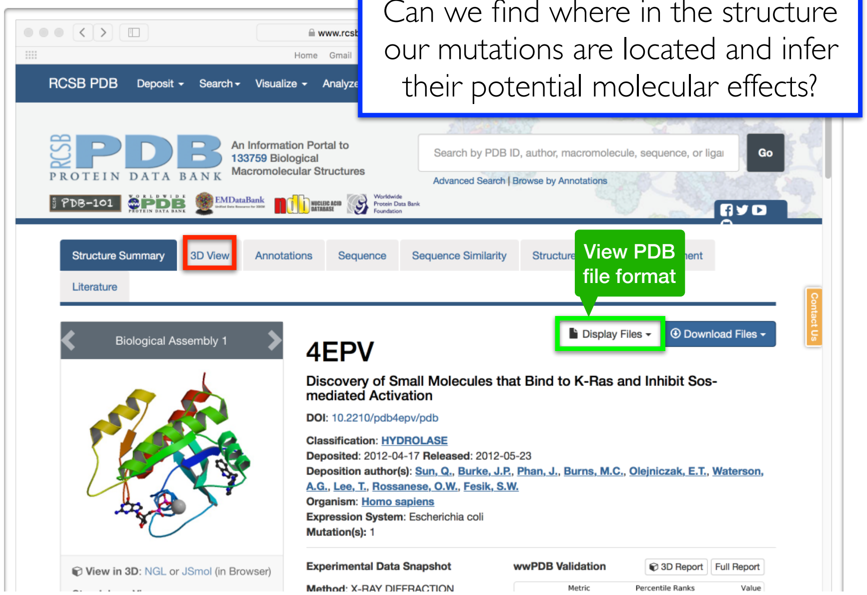
3D structure databases

Select the link destinations:
● PDBe[i]
○ RCSB PDB[i]
○ PDBj[i]

Entry	Method	Resolution (Å)	Chain	Positions	PDBsum
1D8D	X-ray	2.00	P	178-188	[»]
1D8E	X-ray	3.00	P	178-188	[»]
1KZO	X-ray	2.20	C	169-173	[»]
1KZP	X-ray	2.10	C	169-173	[»]
3GFT	X-ray	2.27	A/B/C/D/E/F	1-164	[»]
4DSN	X-ray	2.03	A	2-164	[»]
4DSO	X-ray	1.85	A	2-164	[»]
4EPR	X-ray	2.00	A	1-164	[»]
4EPT	X-ray	2.00	A	1-164	[»]
4EPV	X-ray	1.35	A	1-164	[»]
4EPW	X-ray	1.70	A	1-1	
4EPX	X-ray	1.76	A	1-1	
4EPY	X-ray	1.80	A	1-1	
4L8G	X-ray	1.52	A	1-1	
4LDJ	X-ray	1.15	A	1-164	[»]
4LPK	X-ray	1.50	A/B	1-169	[»]

Open link in a new tab!

Lets view the 3D structure:
Can we find where in the structure our mutations are located and infer their potential molecular effects?



RCSB PDB Deposit Search Visualize Analyze

PDB PROTEIN DATA BANK — An Information Portal to 133759 Biological Macromolecular Structures

Search by PDB ID, author, macromolecule, sequence, or ligai Go

Advanced Search | Browse by Annotations

Structure Summary | 3D View | Annotations | Sequence | Sequence Similarity | Structure ... ment | Literature

View PDB file format

Display Files ▾ | Download Files ▾

Biological Assembly 1

4EPV

Discovery of Small Molecules that Bind to K-Ras and Inhibit Sos-mediated Activation

DOI: 10.2210/pdb4epv/pdb

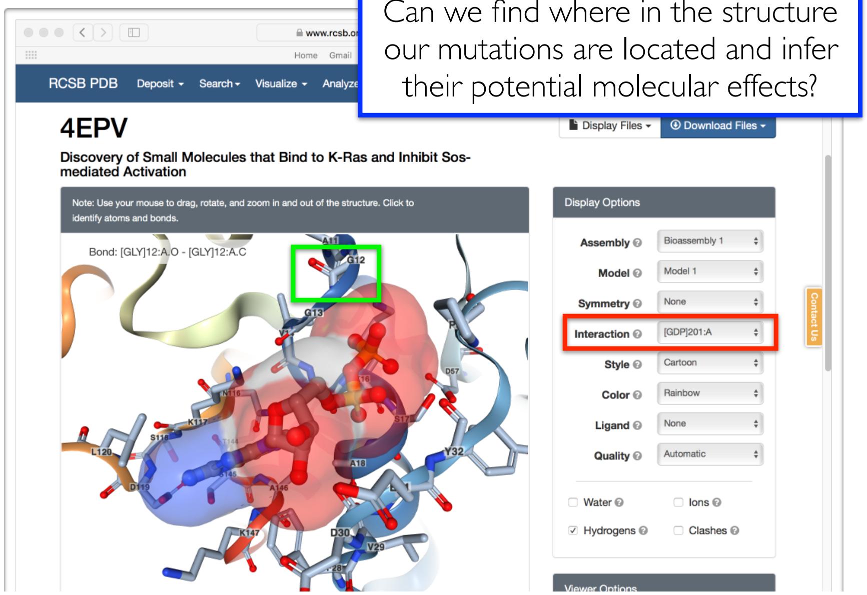
Classification: HYDROLASE
Deposited: 2012-04-17 Released: 2012-05-23
Deposition author(s): Sun, Q., Burke, J.P., Phan, J., Burns, M.C., Olejniczak, E.T., Waterson, A.G., Lee, T., Rossanese, O.W., Fesik, S.W.
Organism: Homo sapiens
Expression System: Escherichia coli
Mutation(s): 1

View in 3D: NGL or JSmol (in Browser)

Experimental Data Snapshot | wwPDB Validation | 3D Report | Full Report

Method: X-RAY DIFFRACTION

Lets view the 3D structure:
Can we find where in the structure our mutations are located and infer their potential molecular effects?



RCSB PDB Deposit Search Visualize Analyze

Display Files ▾ | Download Files ▾

4EPV

Discovery of Small Molecules that Bind to K-Ras and Inhibit Sos-mediated Activation

Note: Use your mouse to drag, rotate, and zoom in and out of the structure. Click to identify atoms and bonds.

Bond: [GLY]12:A.O - [GLY]12:A.C

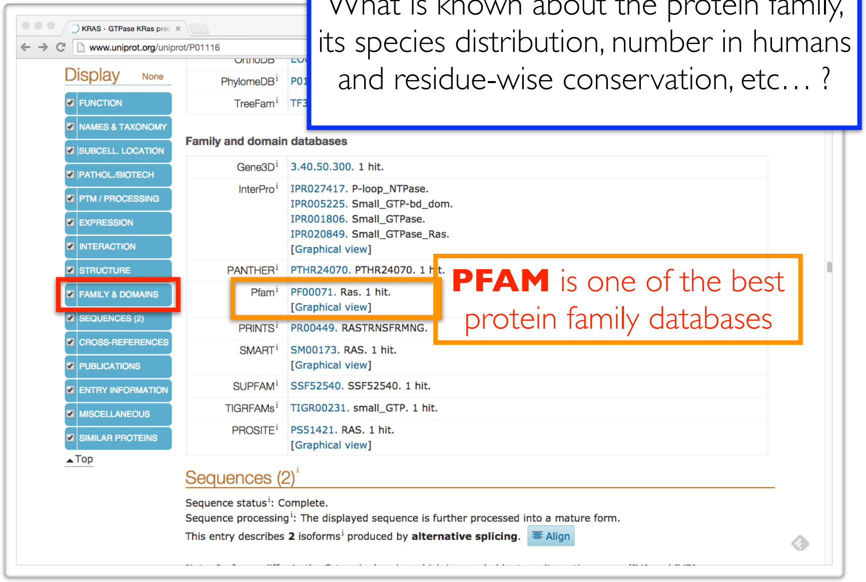
Display Options

Assembly	Bioassembly 1
Model	Model 1
Symmetry	None
Interaction	[GDP]201:A
Style	Cartoon
Color	Rainbow
Ligand	None
Quality	Automatic

☐ Water ☐ Ions
☑ Hydrogens ☐ Clashes

Viewer Options

Back to UniProt:
What is known about the protein family, its species distribution, number in humans and residue-wise conservation, etc… ?



KRAS - GTPase KRas pro
www.uniprot.org/uniprot/P01116

Display None

FUNCTION
NAMES & TAXONOMY
SUBCELL. LOCATION
PATHOL./BIOTECH
PTM / PROCESSING
EXPRESSION
INTERACTION
STRUCTURE
FAMILY & DOMAINS
SEQUENCES (2)
CROSS-REFERENCES
PUBLICATIONS
ENTRY INFORMATION
MISCELLANEOUS
SIMILAR PROTEINS
▲Top

PhylomeDB P01
TreeFam TF3

Family and domain databases

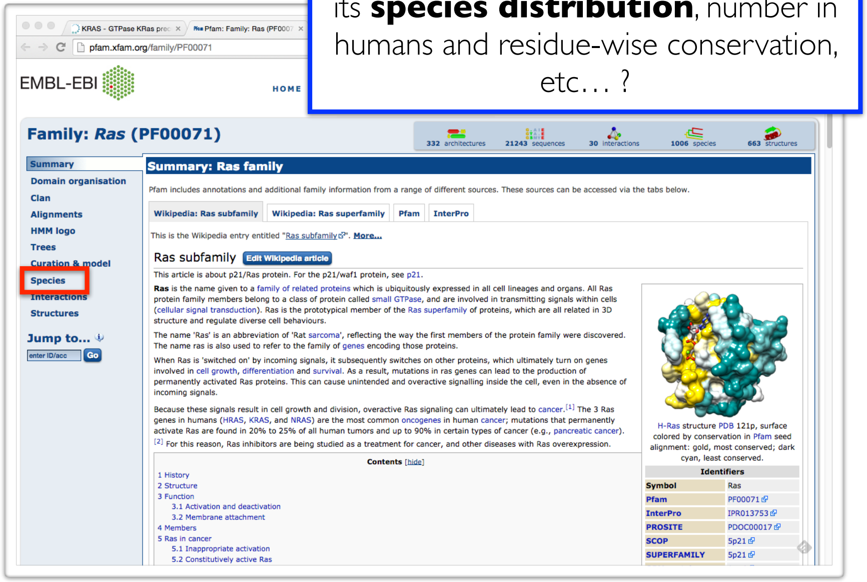
Gene3D	3.40.50.300. 1 hit.
InterPro	IPR027417. P-loop_NTPase. IPR005225. Small_GTP-bd_dom. IPR001806. Small_GTPase. IPR020849. Small_GTPase_Ras. [Graphical view]
PANTHER	PTHR24070. PTHR24070. 1 hit.
Pfam	PF00071. Ras. 1 hit. [Graphical view]
PRINTS	PR00449. RASTRNSFRMNG.
SMART	SM00173. RAS. 1 hit. [Graphical view]
SUPFAM	SSF52540. SSF52540. 1 hit.
TIGRFAMs	TIGR00231. small_GTP. 1 hit.
PROSITE	PS51421. RAS. 1 hit. [Graphical view]

PFAM is one of the best protein family databases

Sequences (2)

Sequence status: Complete.
Sequence processing: The displayed sequence is further processed into a mature form.
This entry describes 2 isoforms produced by alternative splicing. Align

Example Questions:
What is known about the protein family, its **species distribution**, number in humans and residue-wise conservation, etc… ?



KRAS - GTPase KRas pro | Pfam: Family: Ras (PF000
pfam.xfam.org/family/PF00071

EMBL-EBI HOME

Family: Ras (PF00071)

332 architectures | 21243 sequences | 30 interactions | 1006 species | 663 structures

Summary
Domain organisation
Clan
Alignments
HMM logo
Trees
Curation & model
Species
Interactions
Structures

Jump to…
enter ID/acc Go

Summary: Ras family

Pfam includes annotations and additional family information from a range of different sources. These sources can be accessed via the tabs below.

Wikipedia: Ras subfamily | Wikipedia: Ras superfamily | Pfam | InterPro

This is the Wikipedia entry entitled "Ras subfamily". More...

Ras subfamily Edit Wikipedia article

This article is about p21/Ras protein. For the p21/waf1 protein, see p21.

Ras is the name given to a family of related proteins which is ubiquitously expressed in all cell lineages and organs. All Ras protein family members belong to a class of protein called small GTPase, and are involved in transmitting signals within cells (cellular signal transduction). Ras is the prototypical member of the Ras superfamily of proteins, which are all related in 3D structure and regulate diverse cell behaviours.

The name 'Ras' is an abbreviation of 'Rat sarcoma', reflecting the way the first members of the protein family were discovered. The name ras is also used to refer to the family of genes encoding those proteins.

When Ras is 'switched on' by incoming signals, it subsequently switches on other proteins, which ultimately turn on genes involved in cell growth, differentiation and survival. As a result, mutations in ras genes can lead to the production of permanently activated Ras proteins. This can cause unintended and overactive signalling inside the cell, even in the absence of incoming signals.

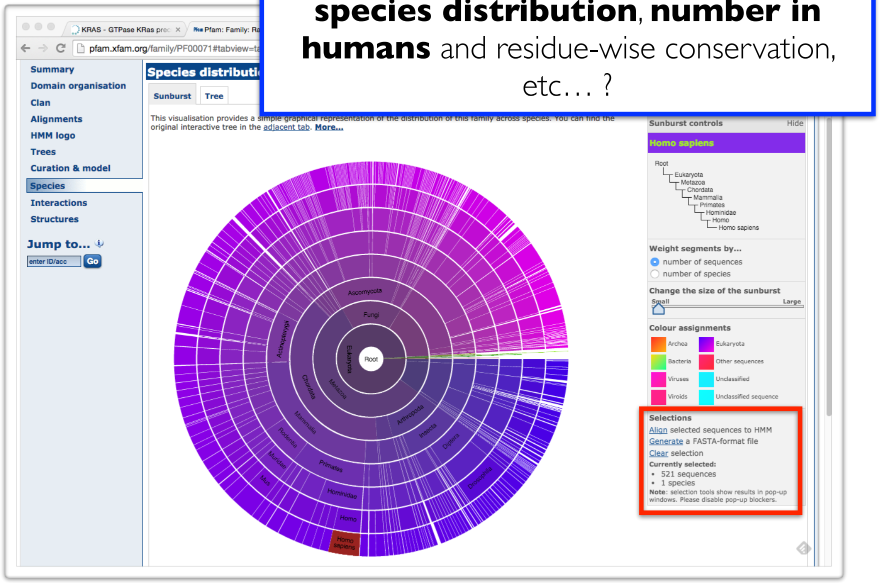
Because these signals result in cell growth and division, overactive Ras signaling can ultimately lead to cancer.[1] The 3 Ras genes in humans (HRAS, KRAS, and NRAS) are the most common oncogenes in human cancer; mutations that permanently activate Ras are found in 20% to 25% of all human tumors and up to 90% in certain types of cancer (e.g., pancreatic cancer).[2] For this reason, Ras inhibitors are being studied as a treatment for cancer, and other diseases with Ras overexpression.

Contents [hide]

1 History
2 Structure
3 Function
3.1 Activation and deactivation
3.2 Membrane attachment
4 Members
5 Ras in cancer
5.1 Inappropriate activation
5.2 Constitutively active Ras

H-Ras structure PDB 121p, surface colored by conservation in Pfam seed alignment: gold, most conserved; dark cyan, least conserved.

Identifiers	
Symbol	Ras
Pfam	PF00071
InterPro	IPR013753
PROSITE	PDOC00017
SCOP	5p21
SUPERFAMILY	5p21



Example Questions:

What is known about the protein family, its **species distribution**, **number in humans** and residue-wise conservation, etc… ?

KRAS - GTPase KRas prec × | Pfam: Family: Ra

pfam.xfam.org/family/PF00071#tabview=ta

- Summary
- Domain organisation
- Clan
- Alignments
- HMM logo
- Trees
- Curation & model
- Species
- Interactions
- Structures

Jump to… enter ID/acc Go

Species distributi

Sunburst | Tree

This visualisation provides a simple graphical representation of the distribution of this family across species. You can find the original interactive tree in the adjacent tab. More...

Sunburst controls Hide

Homo sapiens

Root
Eukaryota
Metazoa
Chordata
Mammalia
Primates
Hominidae
Homo
Homo sapiens

Weight segments by...
- ● number of sequences
- ○ number of species

Change the size of the sunburst
Small — Large

Colour assignments

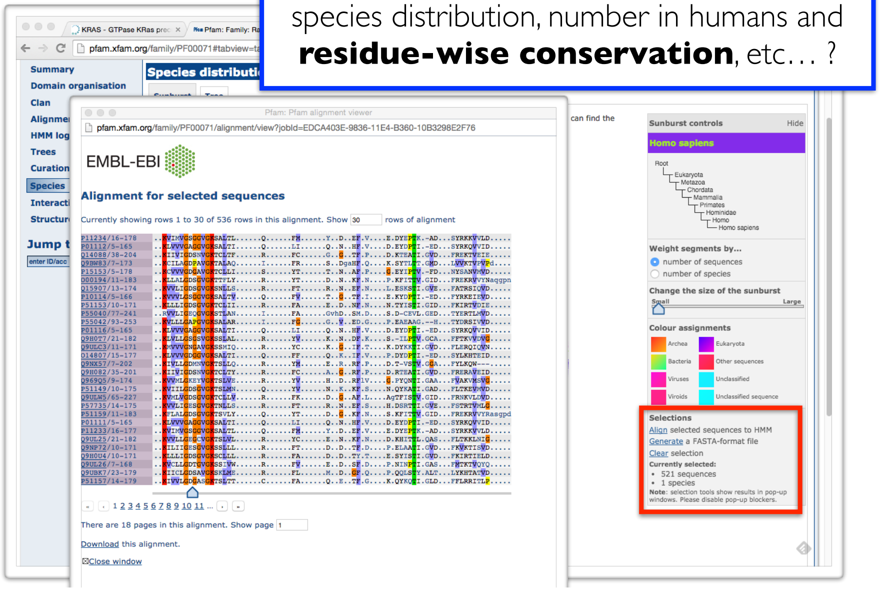
🟧	Archea	🟪	Eukaryota
🟩	Bacteria	🟥	Other sequences
🟪	Viruses	🟦	Unclassified
🟥	Viroids	🟦	Unclassified sequence

Selections

Align selected sequences to HMM
Generate a FASTA-format file
Clear selection

Currently selected:
- 521 sequences
- 1 species

Note: selection tools show results in pop-up windows. Please disable pop-up blockers.



Example Questions:

What is known about the protein family, its species distribution, number in humans and **residue-wise conservation**, etc… ?

Pfam: Pfam alignment viewer

pfam.xfam.org/family/PF00071/alignment/view?jobId=EDCA403E-9836-11E4-B360-10B3298E2F76

EMBL-EBI

Alignment for selected sequences

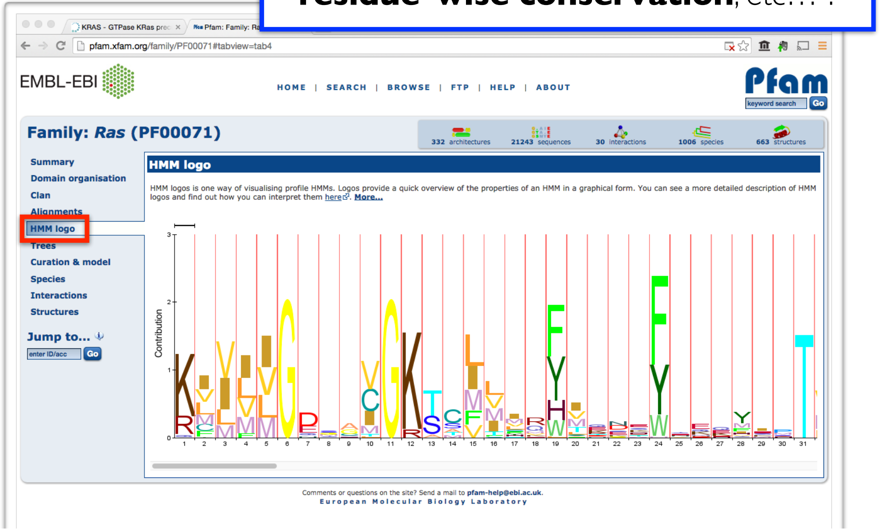
Currently showing rows 1 to 30 of 536 rows in this alignment. Show 30 rows of alignment

« ‹ 1 2 3 4 5 6 7 8 9 10 11 ... › »

There are 18 pages in this alignment. Show page 1

Download this alignment.

☒Close window



Example Questions:

What is known about the protein family, its species distribution, number in humans and **residue-wise conservation**, etc… ?

pfam.xfam.org/family/PF00071#tabview=tab4

EMBL-EBI

HOME | SEARCH | BROWSE | FTP | HELP | ABOUT

Pfam keyword search Go

Family: *Ras* (PF00071)

332 architectures | 21243 sequences | 30 interactions | 1006 species | 663 structures

- Summary
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- Clan
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- HMM logo
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- Curation & model
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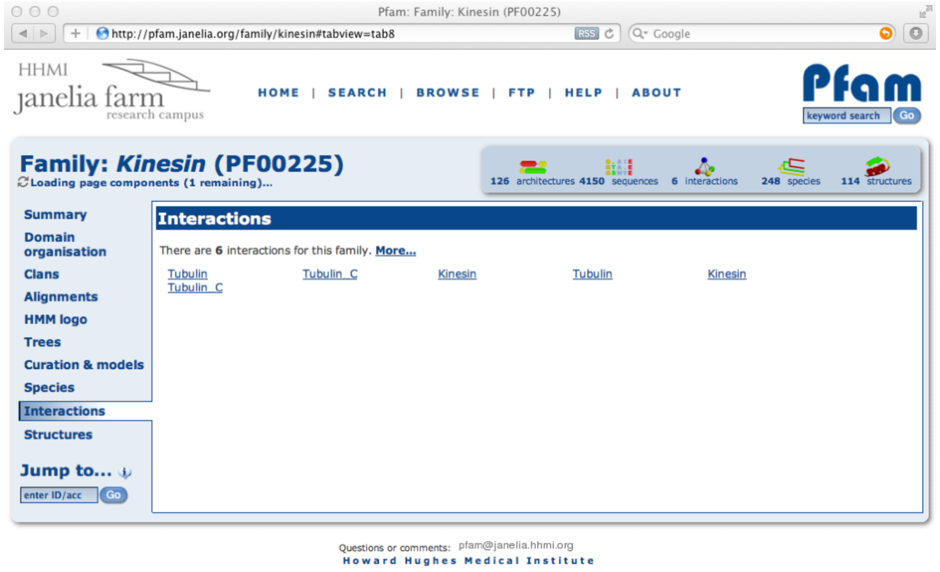
- Interactions
- Structures

Jump to… enter ID/acc Go

HMM logo

HMM logos is one way of visualising profile HMMs. Logos provide a quick overview of the properties of an HMM in a graphical form. You can see a more detailed description of HMM logos and find out how you can interpret them here. More...

Comments or questions on the site? Send a mail to pfam-help@ebi.ac.uk.
European Molecular Biology Laboratory



Pfam: Family: Kinesin (PF00225)

http://pfam.janelia.org/family/kinesin#tabview=tab8

HHMI janelia farm research campus

HOME | SEARCH | BROWSE | FTP | HELP | ABOUT

Pfam keyword search Go

Family: *Kinesin* (PF00225)

Loading page components (1 remaining)...

126 architectures | 4150 sequences | 6 interactions | 248 species | 114 structures

- Summary
- Domain organisation
- Clans
- Alignments
- HMM logo
- Trees
- Curation & models
- Species
- Interactions
- Structures

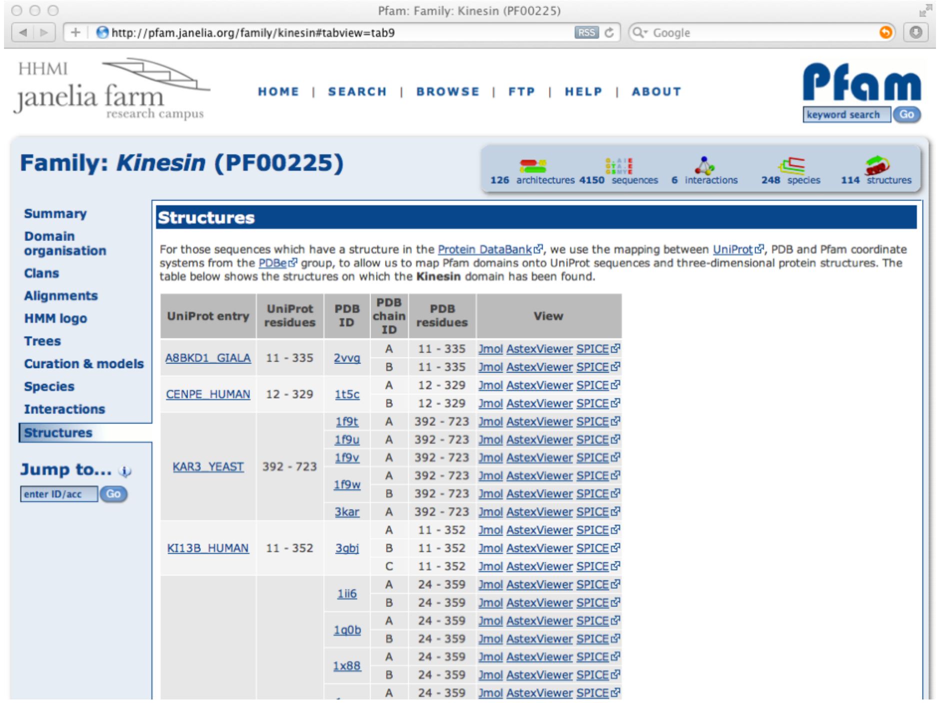
Jump to… enter ID/acc Go

Interactions

There are **6** interactions for this family. More...

Tubulin Tubulin_C	Tubulin_C	Kinesin	Tubulin	Kinesin

Questions or comments: pfam@janelia.hhmi.org
Howard Hughes Medical Institute

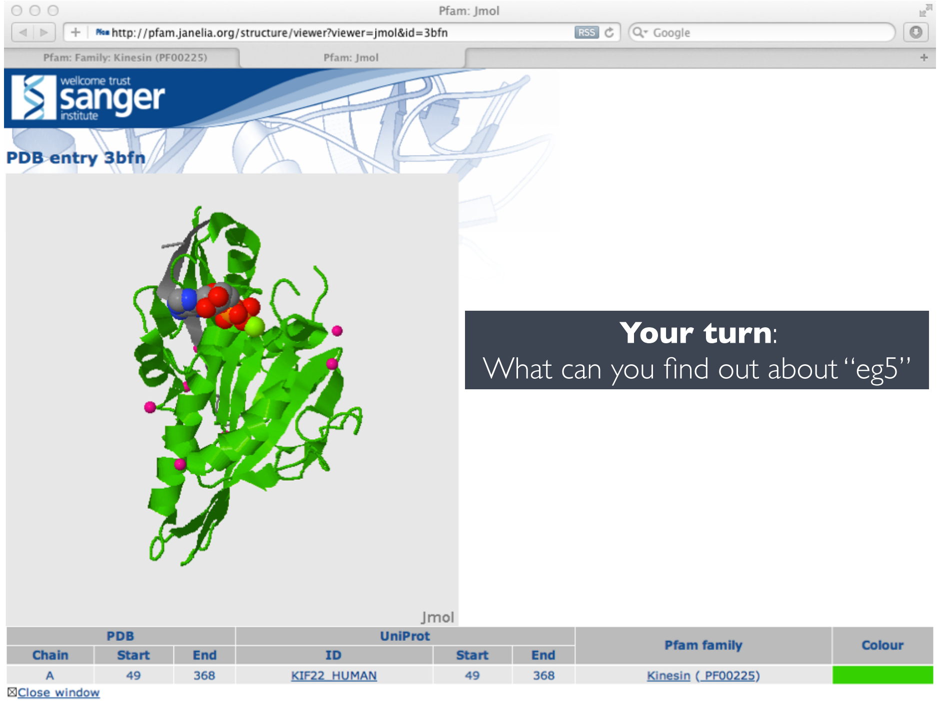


Family: *Kinesin* (PF00225)

Structures

For those sequences which have a structure in the Protein DataBank, we use the mapping between UniProt, PDB and Pfam coordinate systems from the PDBe group, to allow us to map Pfam domains onto UniProt sequences and three-dimensional protein structures. The table below shows the structures on which the **Kinesin** domain has been found.

UniProt entry	UniProt residues	PDB ID	PDB chain ID	PDB residues	View
A8BKD1_GIALA	11 - 335	2vvg	A	11 - 335	Jmol AstexViewer SPICE
			B	11 - 335	Jmol AstexViewer SPICE
CENPE_HUMAN	12 - 329	1t5c	A	12 - 329	Jmol AstexViewer SPICE
			B	12 - 329	Jmol AstexViewer SPICE
KAR3_YEAST	392 - 723	1f9t	A	392 - 723	Jmol AstexViewer SPICE
		1f9u	A	392 - 723	Jmol AstexViewer SPICE
		1f9v	A	392 - 723	Jmol AstexViewer SPICE
		1f9w	A	392 - 723	Jmol AstexViewer SPICE
			B	392 - 723	Jmol AstexViewer SPICE
		3kar	A	392 - 723	Jmol AstexViewer SPICE
KI13B_HUMAN	11 - 352	3gbj	A	11 - 352	Jmol AstexViewer SPICE
			B	11 - 352	Jmol AstexViewer SPICE
			C	11 - 352	Jmol AstexViewer SPICE
		1ii6	A	24 - 359	Jmol AstexViewer SPICE
			B	24 - 359	Jmol AstexViewer SPICE
		1q0b	A	24 - 359	Jmol AstexViewer SPICE
			B	24 - 359	Jmol AstexViewer SPICE
		1x88	A	24 - 359	Jmol AstexViewer SPICE
			B	24 - 359	Jmol AstexViewer SPICE
			A	24 - 359	Jmol AstexViewer SPICE



Pfam: Jmol
http://pfam.janelia.org/structure/viewer?viewer=jmol&id=3bfn
Google
Pfam: Family: Kinesin (PF00225)
Pfam: Jmol
wellcome trust sanger institute
Jmol

PDB entry 3bfn

PDB			UniProt			Pfam family	Colour
Chain	Start	End	ID	Start	End		
A	49	368	KIF22_HUMAN	49	368	Kinesin (PF00225)	🟩

☒Close window

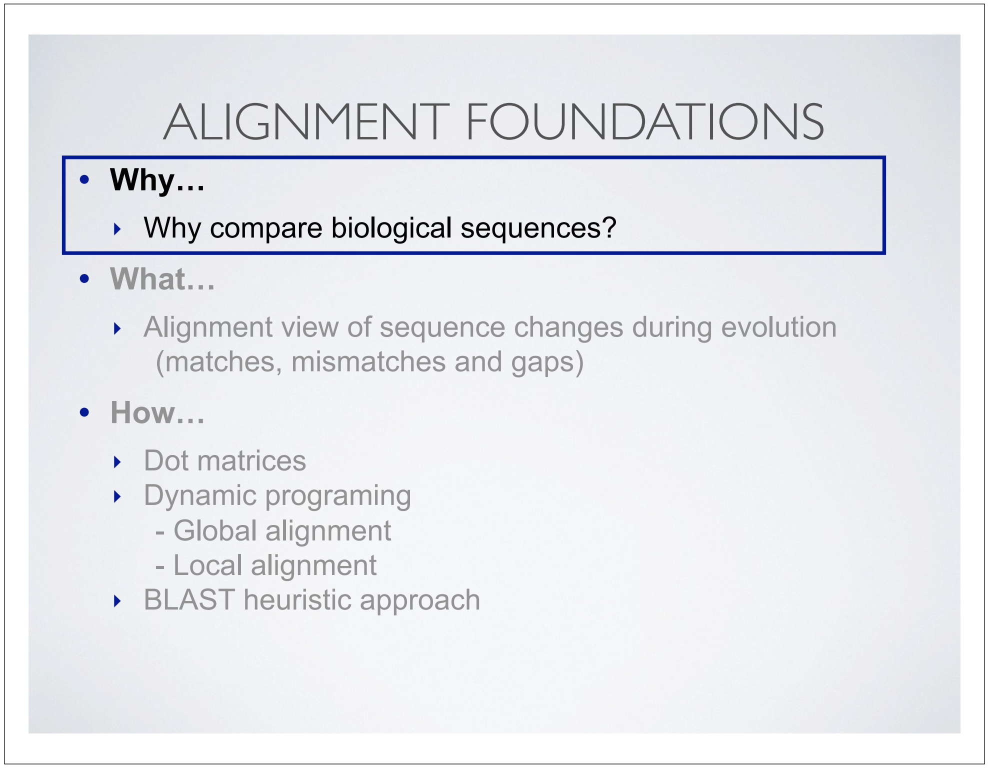
Your turn:
What can you find out about "eg5"

Today's Menu

Classifying Databases	Primary, secondary and composite Bioinformatics databases
Using Databases	**Vignette** demonstrating how major Bioinformatics databases intersect
Major Biomolecular Formats	How nucleotide and protein sequence and structure data are represented
Alignment Foundations	**Introducing the *why* and *how* of comparing sequences**
Alignment Algorithms	**Hands-on** exploration of alignment algorithms and applications

ALIGNMENT FOUNDATIONS

- **Why…**
  - Why compare biological sequences?
- **What…**
  - Alignment view of sequence changes during evolution (matches, mismatches and gaps)
- **How…**
  - Dot matrices
  - Dynamic programing
    - Global alignment
    - Local alignment
  - BLAST heuristic approach



ALIGNMENT FOUNDATIONS

- **Why…**
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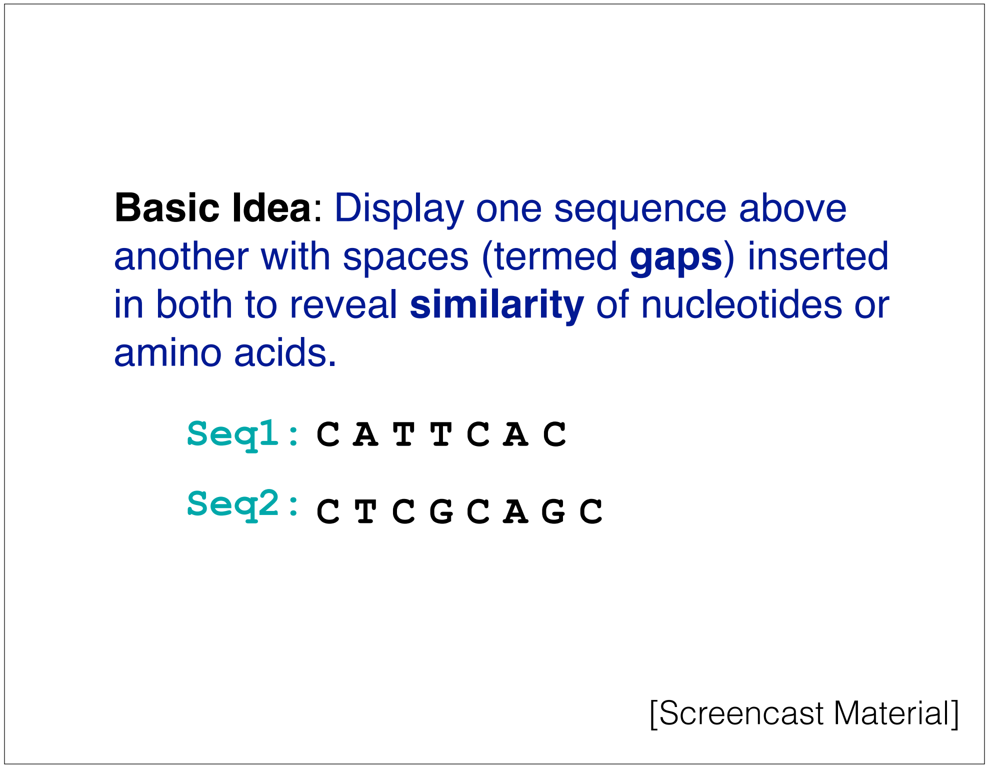
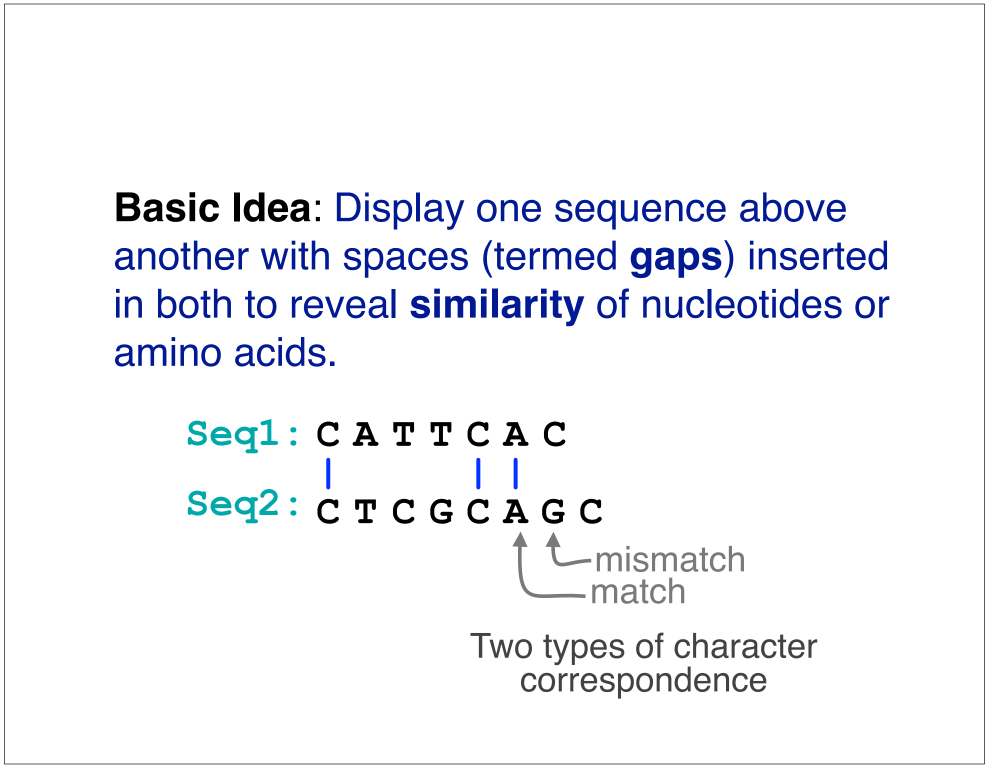


Basic Idea: Display one sequence above another with spaces (termed **gaps**) inserted in both to reveal **similarity** of nucleotides or amino acids.

```
Seq1: C A T T C A C

Seq2: C T C G C A G C
```

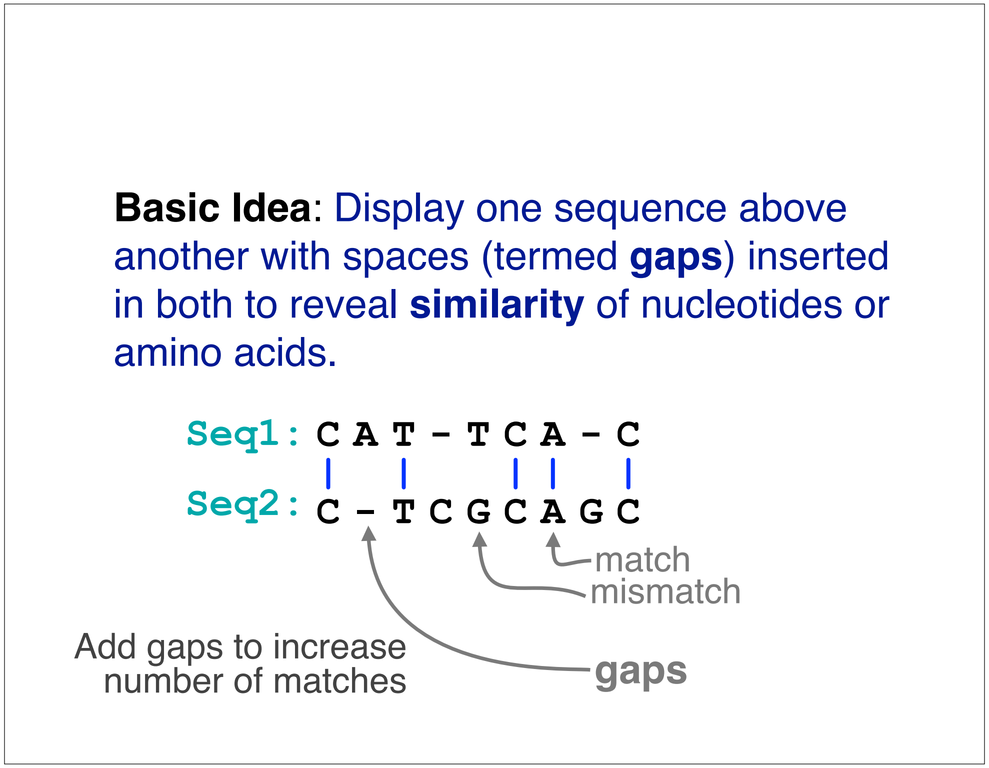
[Screencast Material]



Basic Idea: Display one sequence above another with spaces (termed **gaps**) inserted in both to reveal **similarity** of nucleotides or amino acids.

```
Seq1: C A T T C A C
      |       | |
Seq2: C T C G C A G C
```

Two types of character correspondence

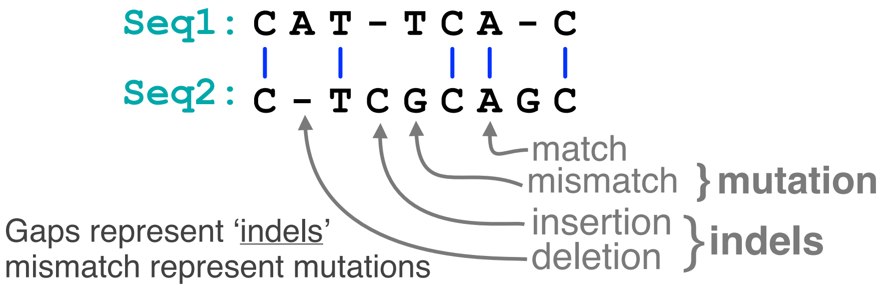


Basic Idea: Display one sequence above another with spaces (termed **gaps**) inserted in both to reveal **similarity** of nucleotides or amino acids.

```
Seq1: C A T - T C A - C
      |   |     | |   |
Seq2: C - T C G C A G C
```

Add gaps to increase number of matches

Basic Idea: Display one sequence above another with spaces (termed **gaps**) inserted in both to reveal **similarity** of nucleotides or amino acids.



```
Seq1: C A T - T C A - C
      |   |     | |   |
Seq2: C - T C G C A G C
```

Gaps represent ‘indels’
mismatch represent mutations

Why compare biological sequences?

- To obtain **functional or mechanistic insight** about a sequence by inference from another potentially better characterized sequence
- To find whether two (or more) genes or proteins are **evolutionarily related**
- To find **structurally or functionally similar regions** within sequences (e.g. catalytic sites, binding sites for other molecules, etc.)
- Many practical bioinformatics applications…

Practical applications include...

- **Similarity searching of databases**
  – Protein structure prediction, annotation, etc...
- **Assembly of sequence reads** into a longer construct such as a genomic sequence
- **Mapping sequencing reads to a known genome**
  – "Resequencing", looking for differences from reference genome - SNPs, indels (insertions or deletions)
  – Mapping transcription factor binding sites via ChIP-Seq (chromatin immuno-precipitation sequencing)
  – Pretty much all next-gen sequencing data analysis

Practical applications include...

- **Similarity searching of databases**
  – Protein structure prediction
- **Assembly of sequen** ger
  construct such ne
- **Mappi s to a known genome**
  king for differences from reference
  s, indels (insertions or deletions)
  ping transcription factor binding sites via ChIP-Seq
  (chromatin immuno-precipitation sequencing)
  – Pretty much all next-gen sequencing data analysis

N.B. Pairwise sequence alignment is arguably the most fundamental operation of bioinformatics!

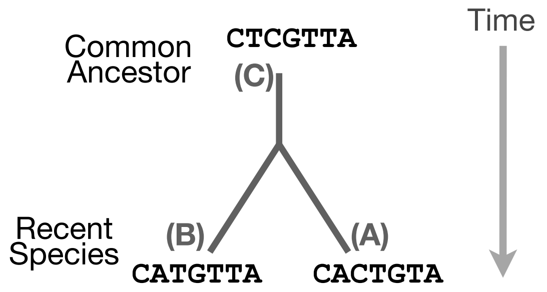
ALIGNMENT FOUNDATIONS

- **Why…**
  - Why compare biological sequences?
- **What…**
  - Alignment view of sequence changes during evolution (matches, mismatches and gaps)
- **How…**
  - Dot matrices
  - Dynamic programing
    - Global alignment
    - Local alignment
  - BLAST heuristic approach

Sequence changes during evolution

There are three major types of sequence change that can occur during evolution.

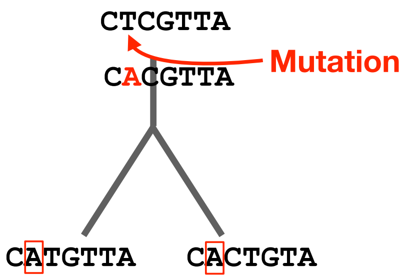
– Mutations/Substitutions
– Deletions
– Insertions



Mutations, deletions and insertions

There are three major types of sequence change that can occur during evolution.

– **Mutations/Substitutions** CTCGTTA → CACGTTA
– Deletions
– Insertions

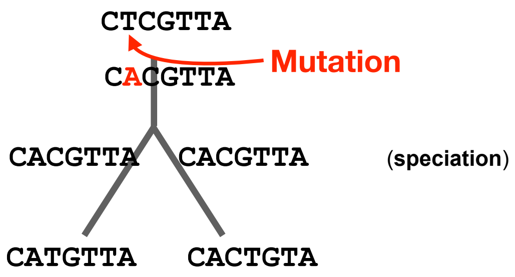


Likely occurred prior to speciation

Mutations, deletions and insertions

There are three major types of sequence change that can occur during evolution.

– Mutations/Substitutions CTCGTTA → CACGTTA
– Deletions
– Insertions



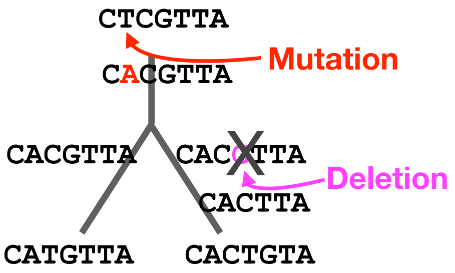
Mutations, deletions and insertions

There are three major types of sequence change that can occur during evolution.

- Mutations/Substitutions
- **Deletions**
- Insertions

CTCGTTA → CACGTTA

CACGTTA → CACTTA



Mutations, deletions and insertions

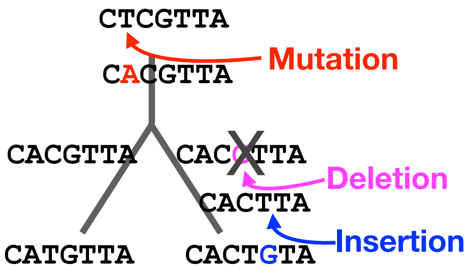
There are three major types of sequence change that can occur during evolution.

- Mutations/Substitutions
- Deletions
- **Insertions**

CTCGTTA → CACGTTA

CACGTTA → CACTTA

CACTTA → CACTGTA



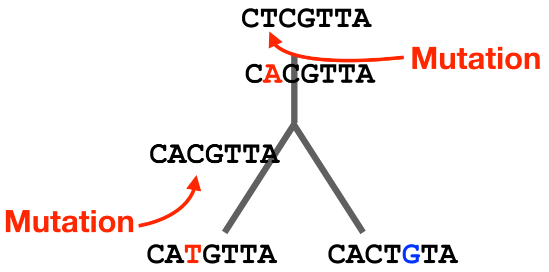
Mutations, deletions and insertions

There are three major types of sequence change that can occur during evolution.

- **Mutations/Substitutions**
- Deletions
- Insertions

CTCGTTA → CACGTTA

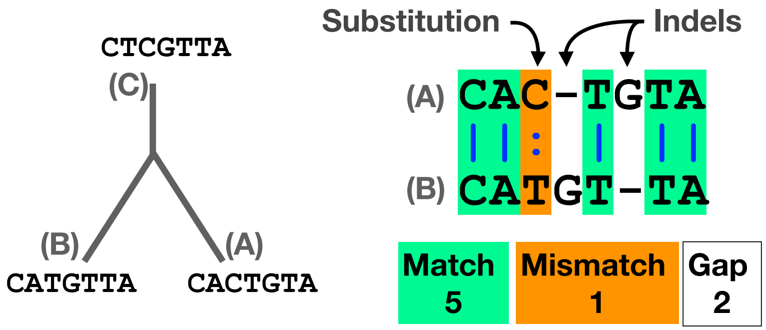
CACGTTA → CATGTTA



Alignment view

Alignments are great tools to visualize sequence similarity and evolutionary changes in homologous sequences.

- **Mismatches** represent mutations/substitutions
- **Gaps** represent insertions and deletions (indels)



Alternative alignments

- Unfortunately, finding the correct alignment is difficult if we do not know the evolutionary history of the two sequences

Q. Which of these 3 possible alignments is best?

```
1.          2.           3.
CACTGTA     CACTGT-A     CAC-TGTA
||:::||     || ||| |     ||: | ||
CATGTTA     CA-TGTTA     CATGT-TA
```

Alternative alignments

- One way to judge alignments is to compare their number of matches, insertions, deletions and mutations

🟢 4 matches
🟠 3 mismatches
○ 0 gaps

🟢 6 matches
🟠 0 mismatches
○ 2 gaps

🟢 5 matches
🟠 1 mismatches
○ 2 gaps

```
CACTGTA     CACTGT-A     CAC-TGTA
||:::||     || ||| |     ||: | ||
CATGTTA     CA-TGTTA     CATGT-TA
```

Scoring alignments

- We can assign a score for each match (+3), mismatch (+1) and indel (-1) to identify the **optimal alignment** *for this scoring scheme*

🟢 4 (+3)
🟠 3 (+1)
○ 0 (-1) = 15

🟢 6 (+3)
🟠 0 (+1)
○ 2 (-1) = 16

🟢 5 (+3)
🟠 1 (+1)
○ 2 (-1) = 14

```
CACTGTA     CACTGT-A     CAC-TGTA
||:::||     || ||| |     ||: | ||
CATGTTA     CA-TGTTA     CATGT-TA
```

Optimal alignments

- Biologists often prefer **parsimonious alignments**, where the number of postulated sequence changes is minimized.

🟢 4 matches
🟠 3 mismatches
○ 0 gaps

🟢 6 matches
🟠 0 mismatches
○ 2 gaps

🟢 5 matches
🟠 1 mismatches
○ 2 gaps

```
CACTGTA     CACTGT-A     CAC-TGTA
||:::||     || ||| |     ||: | ||
CATGTTA     CA-TGTTA     CATGT-TA
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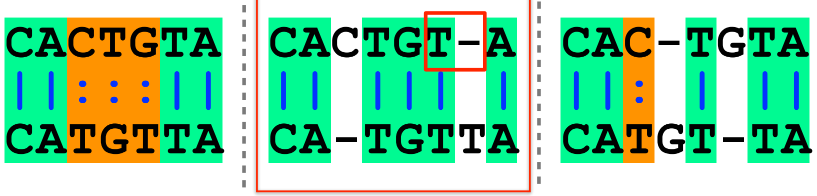
🟠 1 mismatches
○ 2 gaps



Optimal alignments

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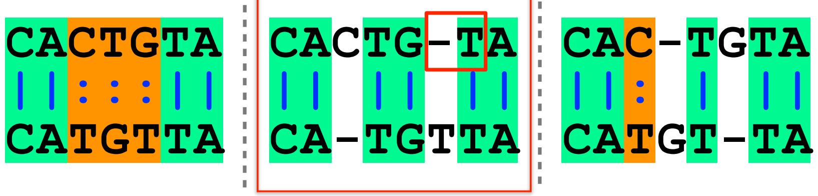
○ 0 gaps

🟢 6 matches
🟠 0 mismatches
○ 2 gaps

🟢 5 matches
🟠 1 mismatches
○ 2 gaps



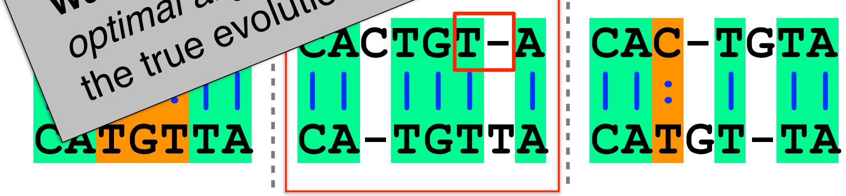
Optimal alignments

- Biologists often prefer **parsimonio** **alignments**, where the numb sequence changes is m

🟢 4 matches
🟠 3 mi

matches
🟠 1 mismatches
○ 2 gaps

Warning: There may be more than one optimal alignment and these may not reflect the true evolutionary history of our sequences!



ALIGNMENT FOUNDATIONS

- **Why…**
  - Why compare biological sequences?
- **What…**
  - Alignment view of sequence changes during evolution (matches, mismatches and gaps)
- **How…**
  - Dot matrices
  - Dynamic programing
    - Global alignment
    - Local alignment
  - BLAST heuristic approach

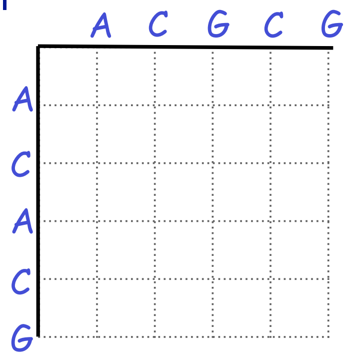
ALIGNMENT FOUNDATIONS

- **Why…**
  - Why compare biological sequences?
- **What…**
  - Alignment view of sequence changes during evolution (matches, mismatches and gaps)
- **How…**
  - Dot matrices
  - D
  - BLAST heuristic approach

How do we compute the optimal alignment between two sequences?

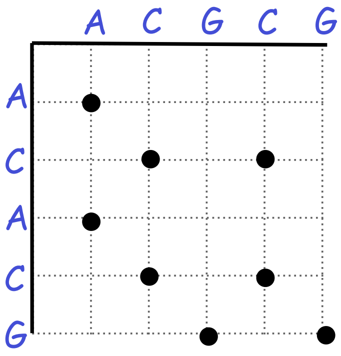
Dot plots: simple graphical approach

- Place one sequence on the vertical axis of a 2D grid (or matrix) and the other on the horizontal



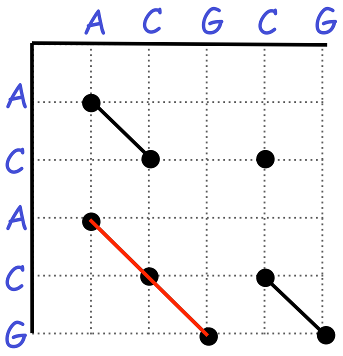
Dot plots: simple graphical approach

- Now simply put dots where the horizontal and vertical sequence values match



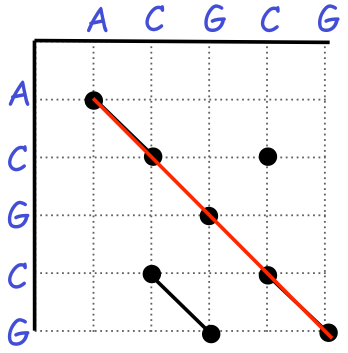
Dot plots: simple graphical approach

- Diagonal runs of dots indicate matched segments of sequence



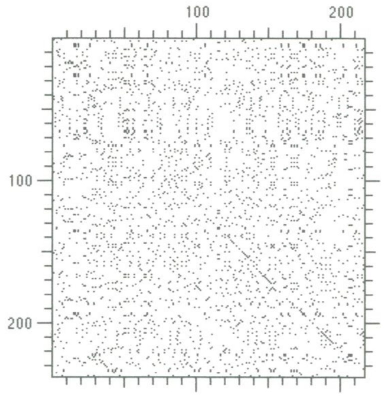
Dot plots: simple graphical approach

Q. What would the dot matrix of a two identical sequences look like?



Dot plots: simple graphical approach

- Dot matrices for long sequences can be noisy



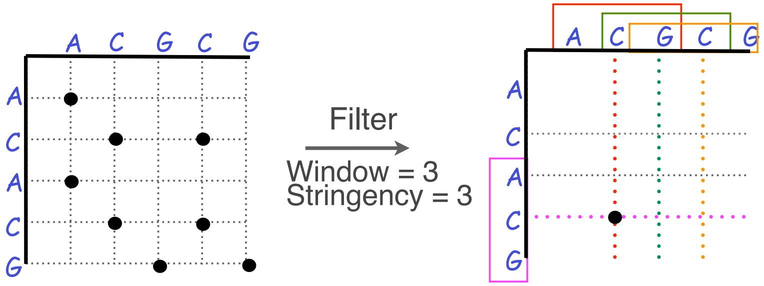
Dot plots: window size and match stringency

Solution: use a window and a threshold

– compare character by character within a window

– require certain fraction of matches within window in order to display it with a dot.

- You have to choose window size and stringency



Filter

Window = 3
Stringency = 3

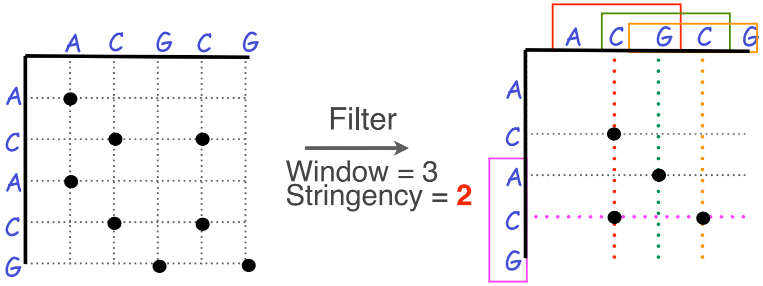
Dot plots: window size and match stringency

Solution: use a window and a threshold

– compare character by character within a window

– require certain fraction of matches within window in order to display it with a dot.

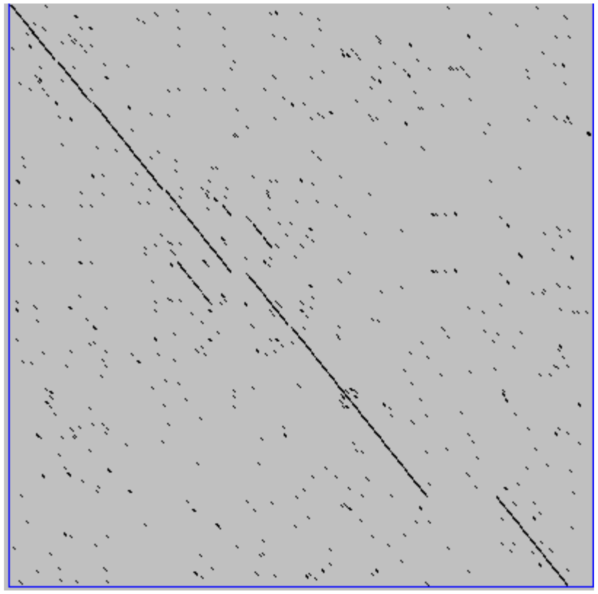
- You have to choose window size and stringency



Filter

Window = 3
Stringency = 2

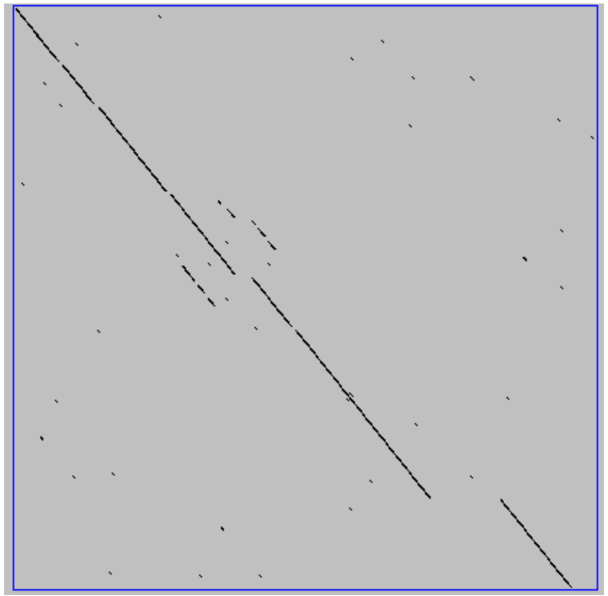
Window size = 5 bases



A dot plot simply puts a dot where two sequences match. In this example, dots are placed in the plot if 5 bases in a row match perfectly. Requiring a 5 base perfect match is a **heuristic** – only look at regions that have a certain degree of identity.

Do you expect evolutionarily related sequences to have more word matches (matches in a row over a certain length) than random or unrelated sequences?

Window size = 7 bases



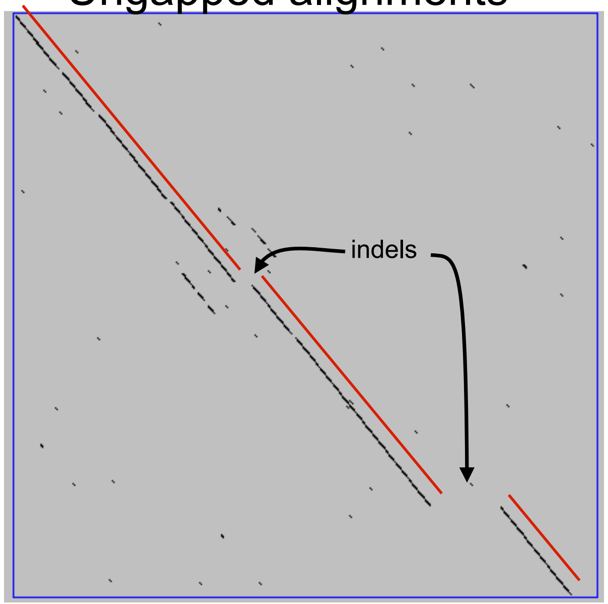
This is a dot plot of the same sequence pair. Now 7 bases in a row must match for a dot to be place. Noise is reduced.

Using windows of a certain length is very similar to using words (kmers) of N characters in the heuristic alignment search tools

Bigger window (kmer) fewer matches to consider

Web site used: http://www.vivo.colostate.edu/molkit/dnadot/

Ungapped alignments



Only **diagonals** can be followed.

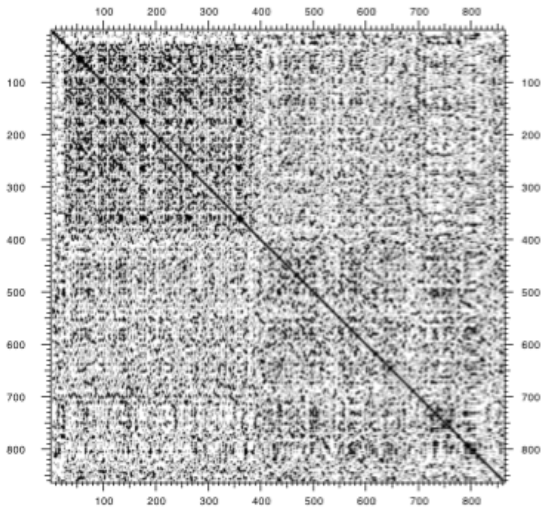
Downward or rightward paths represent **insertion** or **deletions** (gaps in one sequence or the other).

Web site used: http://www.vivo.colostate.edu/molkit/dnadot/

Uses for dot matrices

- Visually assessing the similarity of two protein or two nucleic acid sequences
- Finding local repeat sequences within a larger sequence by comparing a sequence to itself
  - Repeats appear as a set of diagonal runs stacked vertically and/or horizontally

Repeats

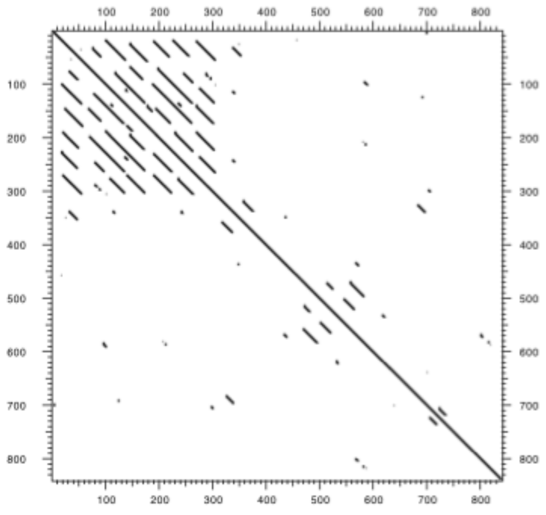


Human LDL receptor protein sequence (Genbank P01130)

W = 1
S = 1

(Figure from Mount, "Bioinformatics sequence and genome analysis")

Repeats



Human LDL receptor protein sequence (Genbank P01130)

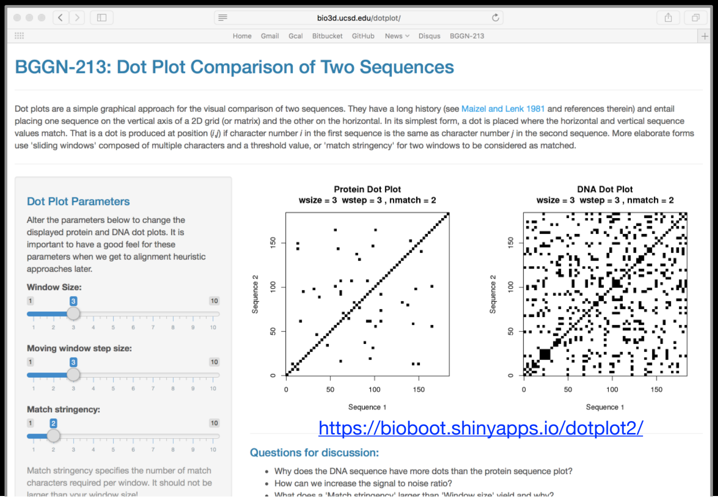
W = 23
S = 7

(Figure from Mount, "Bioinformatics sequence and genome analysis")

Your Turn!

Exploration of dot plot parameters (hands-on worksheet **Section 1**)

http://bio3d.ucsd.edu/dotplot/ https://bioboot.shinyapps.io/dotplot/



BGGN-213: Dot Plot Comparison of Two Sequences

Dot plots are a simple graphical approach for the visual comparison of two sequences. They have a long history (see Maizel and Lenk 1981 and references therein) and entail placing one sequence on the vertical axis of a 2D grid (or matrix) and the other on the horizontal. In its simplest form, a dot is placed where the horizontal and vertical sequence values match. That is a dot is produced at position (*i*,*j*) if character number *i* in the first sequence is the same as character number *j* in the second sequence. More elaborate forms use 'sliding windows' composed of multiple characters and a threshold value, or 'match stringency' for two windows to be considered as matched.

Dot Plot Parameters

Alter the parameters below to change the displayed protein and DNA dot plots. It is important to have a good feel for these parameters when we get to alignment heuristic approaches later.

Window Size: 3

Moving window step size: 3

Match stringency: 2

Match stringency specifies the number of match characters required per window. It should not be larger than your window size!

Protein Dot Plot
wsize = 3 wstep = 3 , nmatch = 2

DNA Dot Plot
wsize = 3 wstep = 3 , nmatch = 2

https://bioboot.shinyapps.io/dotplot2/

Questions for discussion:

- Why does the DNA sequence have more dots than the protein sequence plot?
- How can we increase the signal to noise ratio?
- What does a 'Match stringency' larger than 'Window size' yield and why?

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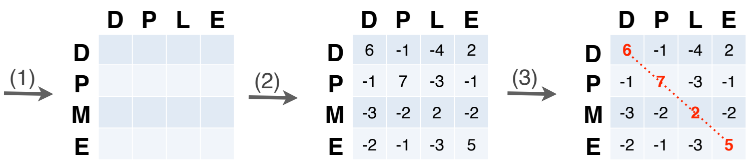
The Dynamic Programming Algorithm

- The dynamic programming algorithm can be thought of an extension to the dot plot approach
  - One sequence is placed down the side of a grid and another across the top
  - Instead of placing a dot in the grid, we **compute a score** for each position
  - Finding the optimal alignment corresponds to finding the path through the grid with the **best possible score**



	D	P	L	E
D				
P				
M				
E				

	D	P	L	E
D	6	-1	-4	2
P	-1	7	-3	-1
M	-3	-2	2	-2
E	-2	-1	-3	5

	D	P	L	E
D	6	-1	-4	2
P	-1	7	-3	-1
M	-3	-2	2	-2
E	-2	-1	-3	5

Needleman, S.B. & Wunsch, C.D. (1970) "A general method applicable to the search for similarities in the amino acid sequences of two proteins." J. Mol. Biol. 48:443-453.

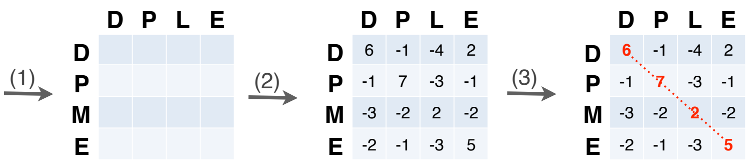
Algorithm of **Needleman and Wunsch**

- The Needleman–Wunsch approach to global sequence alignment has three basic steps:

  (1) setting up a 2D-grid (or **alignment matrix**),

  (2) **scoring the matrix**, and

  (3) identifying the **optimal path** through the matrix



	D	P	L	E
D				
P				
M				
E				

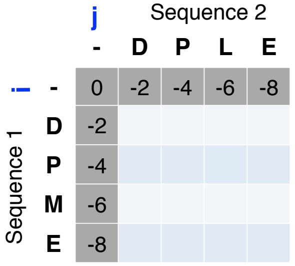
	D	P	L	E
D	6	-1	-4	2
P	-1	7	-3	-1
M	-3	-2	2	-2
E	-2	-1	-3	5

	D	P	L	E
D	6	-1	-4	2
P	-1	7	-3	-1
M	-3	-2	2	-2
E	-2	-1	-3	5

Needleman, S.B. & Wunsch, C.D. (1970) "A general method applicable to the search for similarities in the amino acid sequences of two proteins." J. Mol. Biol. 48:443-453.

Scoring the alignment matrix

- Start by filling in the first row and column – these are all indels (gaps).
  - Each step you take you will add the **gap penalty** to the score ($S_{i,j}$) accumulated in the previous cell


j
Sequence 2
i
Sequence 1

	-	D	P	L	E
-	0	-2	-4	-6	-8
D	-2				
P	-4				
M	-6				
E	-8				

Scores: match = +1, mismatch = -1, gap = -2

Scoring the alignment matrix

- Start by filling in the first row and column – these are all indels (gaps).
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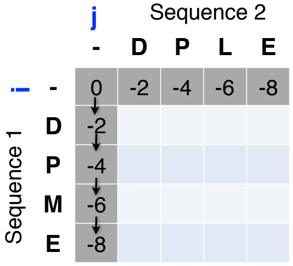

j
Sequence 2
i
Sequence 1

	-	D	P	L	E
-	0	-2	-4	-6	-8
D	-2				
P	-4				
M	-6				
E	-8				

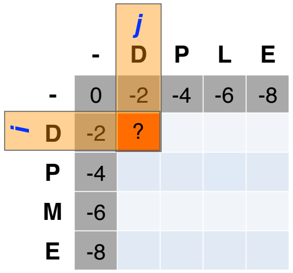
Scores: match = +1, mismatch = -1, gap = -2

$$S_{i+4} = (-2) + (-2) + (-2) + (-2)$$

```
Seq1: DPME
Seq2: ----
```

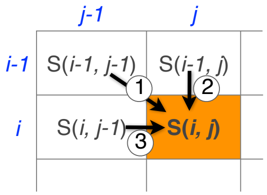
Scoring the alignment matrix

- Then go to the empty corner cell (upper left). It has filled in values in up, left and diagonal directions
  - Now can ask which of the three directions gives the highest score?
  - keep track of this score and direction



		j D	P	L	E
-	0	-2	-4	-6	-8
i D	-2	?			
P	-4				
M	-6				
E	-8				

Scores: match = +1, mismatch = -1, gap = -2



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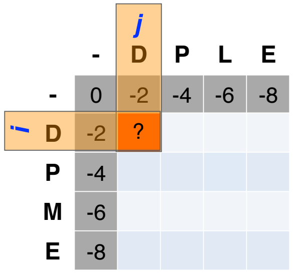


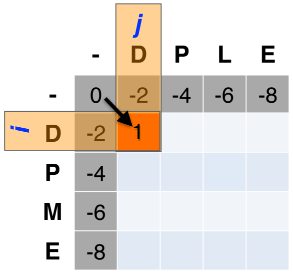
		j D	P	L	E
-	0	-2	-4	-6	-8
i D	-2	?			
P	-4				
M	-6				
E	-8				

Scores: match = +1, mismatch = -1, gap = -2

$$S(i, j) = \text{Max}\begin{cases} S(i\text{-}1, j\text{-}1) + \text{(mis)match} & \searrow \text{①} \\ S(i\text{-}1, j) + \text{gap penalty} & \downarrow \text{②} \\ S(i, j\text{-}1) + \text{gap penalty} & \rightarrow \text{③} \end{cases}$$

Scoring the alignment matrix

- Then go to the empty corner cell (upper left). It has filled in values in up, left and diagonal directions
  - Now can ask which direction gives the highest score
  - keep track of direction and score



		j D	P	L	E
-	0	-2	-4	-6	-8
i D	-2	1			
P	-4				
M	-6				
E	-8				

Scores: match = +1, mismatch = -1, gap = -2

↘ ① (0)+(+1) = +1 <= (D-D) match!

Alignment

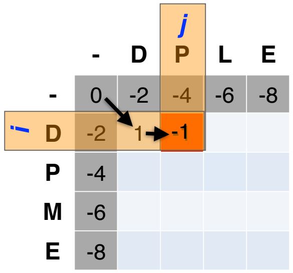
```
D
D
```

↓ ② (-2)+(-2) = -4

→ ③ (-2)+(-2) = -4

Scoring the alignment matrix

- At each step, the score in the current cell is determine by the scores in the neighboring cells
  - The maximal score and the direction that gave that score is stored (we will use these later to determine the optimal alignment)



		D	*j* P	L	E
-	0	-2	-4	-6	-8
i D	-2	1	-1		
P	-4				
M	-6				
E	-8				

Scores: match = +1, mismatch = -1, gap = -2

↘ ① (-2)+(-1) = -3 <= (D-P) mismatch!

Alignment

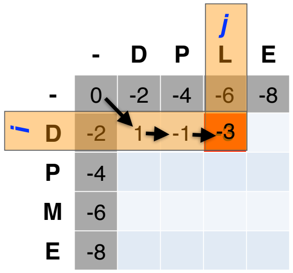
```
D-
DP
```

↓ ② (-4)+(-2) = -6

→ ③ (1)+(-2) = -1

Scoring the alignment matrix

- We will continue to store the alignment score ($S_{i,j}$) for all possible alignments in the alignment matrix.



	-	D	P	*j* L	E
-	0	-2	-4	-6	-8
i D	-2	1	-1	-3	
P	-4				
M	-6				
E	-8				

Scores: match = +1, mismatch = -1, gap = -2

↘ ① (-4)+(-1) = -5 <= (D-L) mismatch

↓ ② (-6)+(-2) = -8

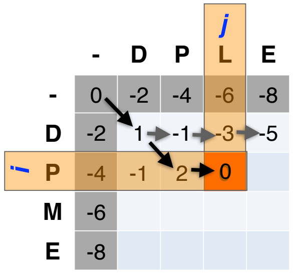
→ ③ (-1)+(-2) = -3

Alignment

```
D--
DPL
```

Scoring the alignment matrix

- For the highlighted cell, the corresponding score ($S_{i,j}$) refers to the score of the optimal alignment of the first *i* characters from sequence1, and the first *j* characters from sequence2.



	-	D	P	*j* L	E
-	0	-2	-4	-6	-8
D	-2	1	-1	-3	-5
i P	-4	-1	2	0	
M	-6				
E	-8				

Scores: match = +1, mismatch = -1, indel = -2

↘ ① (-1)+(-1) = -2

↓ ② (-3)+(-2) = -5

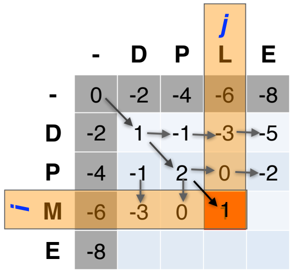
→ ③ (2)+(-2) = 0

Alignment

```
DP-
DPL
```

Scoring the alignment matrix

- At each step, the score in the current cell is determine by the scores in the neighboring cells
  - The maximal score and the direction that gave that score is stored



	-	D	P	*j* L	E
-	0	-2	-4	-6	-8
D	-2	1	-1	-3	-5
P	-4	-1	2	0	-2
i M	-6	-3	0	1	
E	-8				

Scores: match = +1, mismatch = -1, indel = -2

↘ ① (2)+(**-1**) = 0 <= mismatch

↓ ② (0)+(-2) = -2

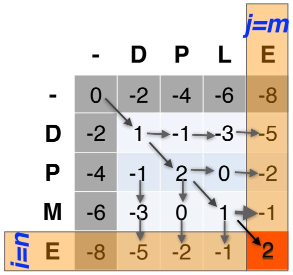
→ ③ (0)+(-2) = -2

Alignment

```
DPM
DPL
```

Scoring the alignment matrix

- The score of the best alignment of the entire sequences corresponds to $S_{n,m}$
  - (where *n* and *m* are the length of the sequences)



	-	D	P	L	*j=m* E
-	0	-2	-4	-6	-8
D	-2	1	-1	-3	-5
P	-4	-1	2	0	-2
M	-6	-3	0	1	-1
i=n E	-8	-5	-2	-1	2

Scores: match = +1, mismatch = -1, indel = -2

↘ ① (+1)+(+1) = +2

↓ ② (-1)+(-2) = -3

→ ③ (-1)+(-2) = -3

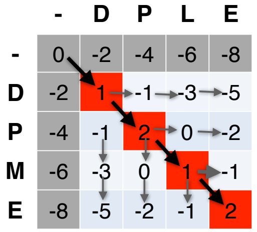
Alignment

```
DPME
DPLE
```

Scoring the alignment matrix

- To find the best alignment, we retrace the arrows starting from the bottom right cell
  - N.B. The optimal alignment score and alignment are dependent on the chosen scoring system

Scores: match = +1, mismatch = -1, indel = -2



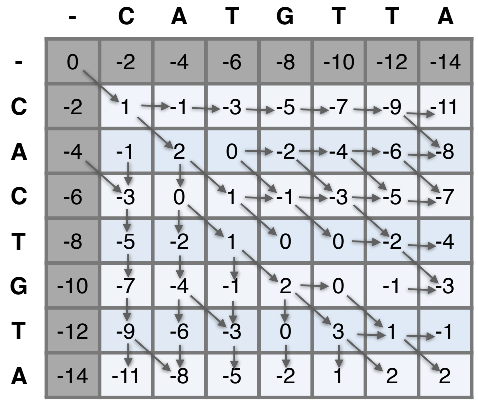
	-	D	P	L	E
-	0	-2	-4	-6	-8
D	-2	1	-1	-3	-5
P	-4	-1	2	0	-2
M	-6	-3	0	1	-1
E	-8	-5	-2	-1	2

Alignment

```
DPME
DPLE
```

Questions:

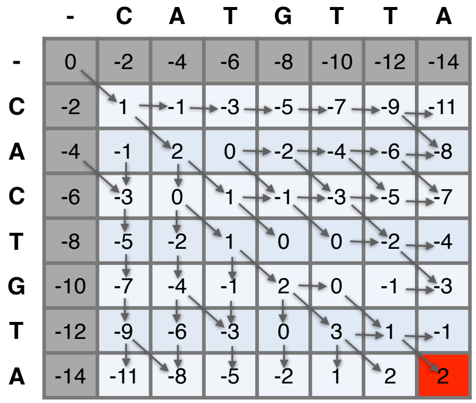
- What is the optimal score for the alignment of these sequences and how do we find the optimal alignment?



	-	C	A	T	G	T	T	A
-	0	-2	-4	-6	-8	-10	-12	-14
C	-2	1	-1	-3	-5	-7	-9	-11
A	-4	-1	2	0	-2	-4	-6	-8
C	-6	-3	0	1	-1	-3	-5	-7
T	-8	-5	-2	1	0	0	-2	-4
G	-10	-7	-4	-1	2	0	-1	-3
T	-12	-9	-6	-3	0	3	1	-1
A	-14	-11	-8	-5	-2	1	2	2

Questions:

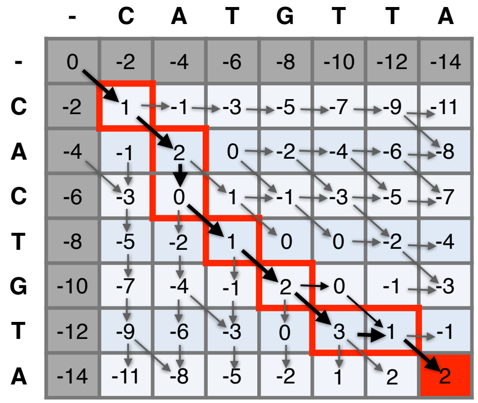
- What is the optimal score for the alignment of these sequences and how do we find the optimal alignment?



	-	C	A	T	G	T	T	A
-	0	-2	-4	-6	-8	-10	-12	-14
C	-2	1	-1	-3	-5	-7	-9	-11
A	-4	-1	2	0	-2	-4	-6	-8
C	-6	-3	0	1	-1	-3	-5	-7
T	-8	-5	-2	1	0	0	-2	-4
G	-10	-7	-4	-1	2	0	-1	-3
T	-12	-9	-6	-3	0	3	1	-1
A	-14	-11	-8	-5	-2	1	2	2

Questions:

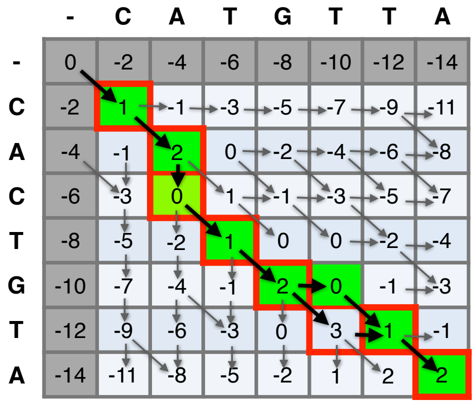
- To find the best alignment we retrace the arrows starting from the bottom right cell



	-	C	A	T	G	T	T	A
-	0	-2	-4	-6	-8	-10	-12	-14
C	-2	1	-1	-3	-5	-7	-9	-11
A	-4	-1	2	0	-2	-4	-6	-8
C	-6	-3	0	1	-1	-3	-5	-7
T	-8	-5	-2	1	0	0	-2	-4
G	-10	-7	-4	-1	2	0	-1	-3
T	-12	-9	-6	-3	0	3	1	-1
A	-14	-11	-8	-5	-2	1	2	2

More than one alignment possible

- Sometimes more than one alignment can result in the same optimal score



	-	C	A	T	G	T	T	A
-	0	-2	-4	-6	-8	-10	-12	-14
C	-2	1	-1	-3	-5	-7	-9	-11
A	-4	-1	2	0	-2	-4	-6	-8
C	-6	-3	0	1	-1	-3	-5	-7
T	-8	-5	-2	1	0	0	-2	-4
G	-10	-7	-4	-1	2	0	-1	-3
T	-12	-9	-6	-3	0	3	1	-1
A	-14	-11	-8	-5	-2	1	2	2

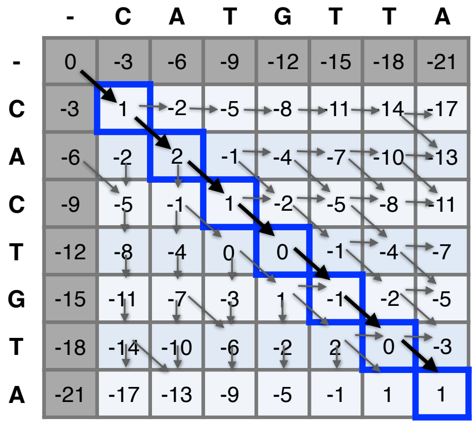
Alignment

```
CACTGT-A
CA-TGTTA

CACTG-TA
CA-TGTTA
```

The alignment and score are dependent on the scoring system

- Here we increase the gap penalty from -2 to -3



	-	C	A	T	G	T	T	A
-	0	-3	-6	-9	-12	-15	-18	-21
C	-3	1	-2	-5	-8	-11	-14	-17
A	-6	-2	2	-1	-4	-7	-10	-13
C	-9	-5	-1	1	-2	-5	-8	-11
T	-12	-8	-4	0	0	-1	-4	-7
G	-15	-11	-7	-3	1	-1	-2	-5
T	-18	-14	-10	-6	-2	2	0	-3
A	-21	-17	-13	-9	-5	-1	1	1

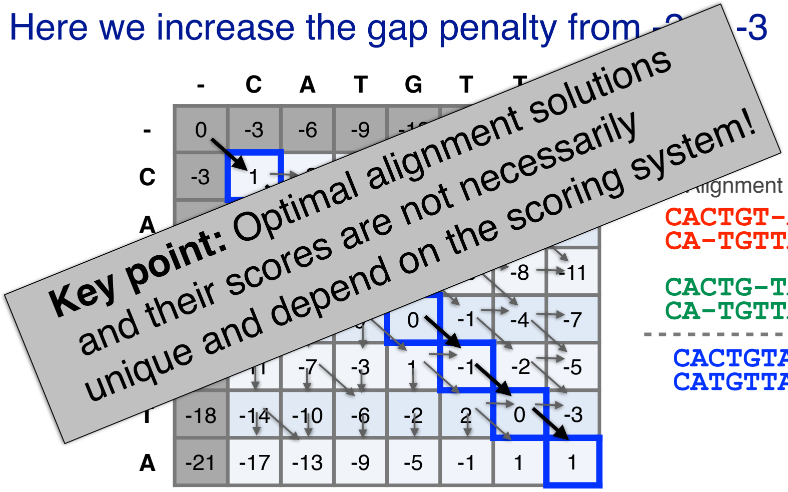
Alignment

```
CACTGT-A
CA-TGTTA

CACTG-TA
CA-TGTTA
- - - - - - - - - -
CACTGTA
CATGTTA
```

The alignment and score are dependent on the scoring system

- Here we increase the gap penalty from -2 to -3



Key point: Optimal alignment solutions and their scores are not necessarily unique and depend on the scoring system!

Alignment

```
CACTGT-A
CA-TGTTA

CACTG-TA
CA-TGTTA
- - - - - - - - - -
CACTGTA
CATGTTA
```

NW DYNAMIC PROGRAMMING

Match: +2
Mismatch: -1
Gap: -2

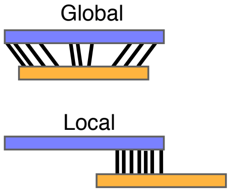
		A	G	T	T	C
	0					
A						
T						
T						
G						
C						

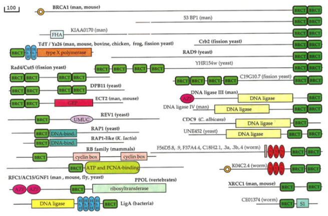
ALIGNMENT FOUNDATIONS

- **Why…**
  - Why compare biological sequences?
- **What…**
  - Alignment view of sequence changes during evolution (matches, mismatches and gaps)
- **How…**
  - Dot matrices
  - Dynamic programing
    - Global alignment
    - Local alignment
  - BLAST heuristic approach

Global *vs* local alignments

- Needleman-Wunsch is a **global alignment** algorithm
  - Resulting alignment spans the complete sequences end to end
  - This is appropriate for closely related sequences that are similar in length
- For many practical applications we require **local alignments**
  - Local alignments highlight sub-regions (*e.g.* protein domains) in the two sequences that align well





Local alignment: Definition

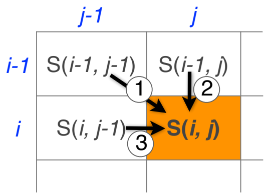
- Smith & Waterman proposed simply that a local alignment of two sequences allow arbitrary-length segments of each sequence to be aligned, with no penalty for the unaligned portions of the sequences. Otherwise, the score for a local alignment is calculated the same way as that for a global alignment

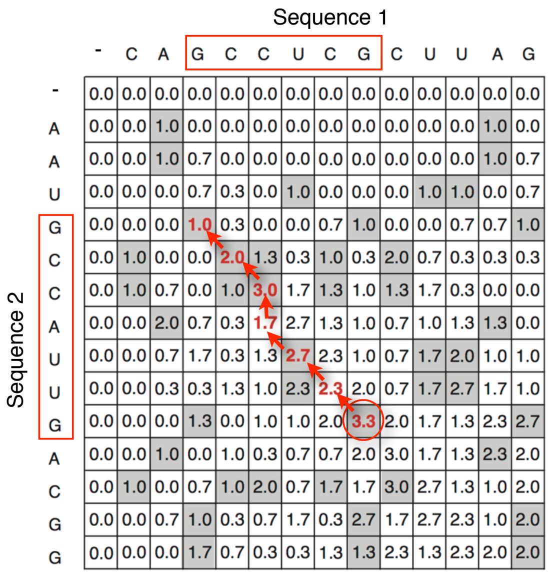
Smith, T.F. & Waterman, M.S. (1981) “Identification of common molecular subsequences.” J. Mol. Biol. 147:195-197.

The Smith-Waterman algorithm

- Three main modifications to Needleman-Wunsch:
  - Allow a node to start at 0
  - The score for a particular cell cannot be negative
    - if all other score options produce a negative value, then a zero must be inserted in the cell
  - Record the highest- scoring node, and trace back from there

$$S(i,j) = \text{Max}\begin{cases} S(i\text{-}1, j\text{-}1) + \text{(mis)match} & \searrow \; ① \\ S(i\text{-}1, j) - \text{gap penalty} & \downarrow \; ② \\ S(i, j\text{-}1) - \text{gap penalty} & \rightarrow \; ③ \\ \mathbf{0} & ④ \end{cases}$$




Sequence 1
Sequence 2

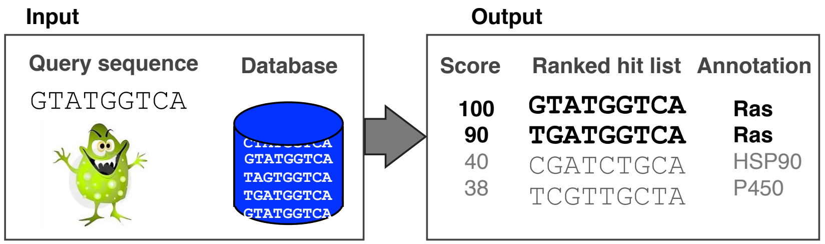
	-	C	A	G	C	C	U	C	G	C	U	U	A	G
-	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
A	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0
A	0.0	0.0	1.0	0.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.7
U	0.0	0.0	0.0	0.7	0.3	0.0	1.0	0.0	0.0	0.0	1.0	1.0	0.0	0.7
G	0.0	0.0	0.0	1.0	0.3	0.0	0.0	0.7	1.0	0.0	0.0	0.7	0.7	1.0
C	0.0	1.0	0.0	0.0	2.0	1.3	0.3	1.0	0.3	2.0	0.7	0.3	0.3	0.3
C	0.0	1.0	0.7	0.0	1.0	3.0	1.7	1.3	1.0	1.3	1.7	0.3	0.0	0.0
A	0.0	0.0	2.0	0.7	0.3	1.7	2.7	1.3	1.0	0.7	1.0	1.3	1.3	0.0
U	0.0	0.0	0.7	1.7	0.3	1.3	2.7	2.3	1.0	0.7	1.7	2.0	1.0	1.0
U	0.0	0.0	0.3	0.3	1.3	1.0	2.3	2.3	2.0	0.7	1.7	2.7	1.7	1.0
G	0.0	0.0	0.0	1.3	0.0	1.0	1.0	2.0	3.3	2.0	1.7	1.3	2.3	2.7
A	0.0	0.0	1.0	0.0	1.0	0.3	0.7	0.7	2.0	3.0	1.7	1.3	2.3	2.0
C	0.0	1.0	0.0	0.7	1.0	2.0	0.7	1.7	1.7	3.0	2.7	1.3	1.0	2.0
G	0.0	0.0	0.7	1.0	0.3	0.7	1.7	0.3	2.7	1.7	2.7	2.3	1.0	2.0
G	0.0	0.0	0.0	1.7	0.7	0.3	0.3	1.3	1.3	2.3	1.3	2.3	2.0	2.0

Local alignment

```
GCC-AUG
GCCUCGC
```

Local alignments can be used for database searching

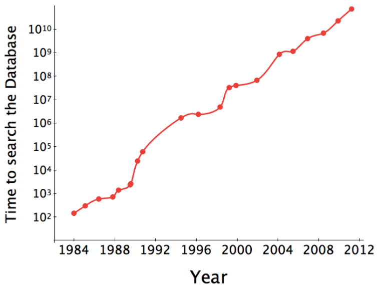
- **Goal**: Given a query sequence (Q) and a sequence database (D), find a list of sequences from D that are most similar to Q
  - **Input**: Q, D and scoring scheme
  - **Output**: Ranked list of hits



Score	Ranked hit list	Annotation
100	GTATGGTCA	Ras
90	TGATGGTCA	Ras
40	CGATCTGCA	HSP90
38	TCGTTGCTA	P450

The database search problem

- Due to the rapid growth of sequence databases, search algorithms have to be both efficient and sensitive
  - Time to search with SW is proportional to *m* x *n* (*m* is length of query, n is length of database), **too slow for large databases**!



To reduce search time **heuristic algorithms**, such as BLAST, first remove database sequences without a strong local similarity to the query sequence in a quick initial scan.

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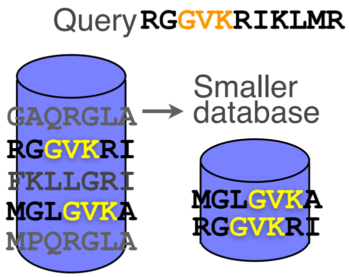


To reduce search time **heuristic algorithms**, such as BLAST, first remove database sequences without a strong local similarity to the query sequence in a quick initial scan.

ALIGNMENT FOUNDATIONS

- Why…
  - Why compare biological sequences?
- What…
  - Alignment view of sequence changes during evolution (matches, mismatches and gaps)
- **How…**
  - Dot matrices
  - Dynamic programing
    - Global alignment
    - Local alignment
  - BLAST heuristic approach

Rapid, heuristic versions of Smith–Waterman: **BLAST**

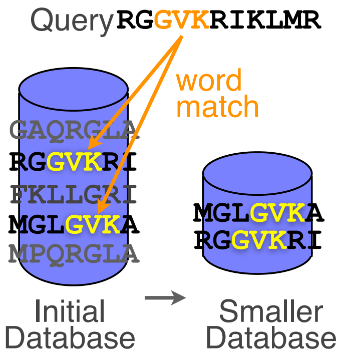
- BLAST (Basic Local Alignment Search Tool) is a simplified form of Smith-Waterman (SW) alignment that is popular because it is **fast** and **easily accessible**
  - BLAST is a heuristic approximation to SW - It examines only part of the search space
  - BLAST saves time by restricting the search by scanning database sequences for likely matches before performing more rigorous alignments
  - Sacrifices some sensitivity in exchange for speed
  - In contrast to SW, BLAST is not guaranteed to find optimal alignments

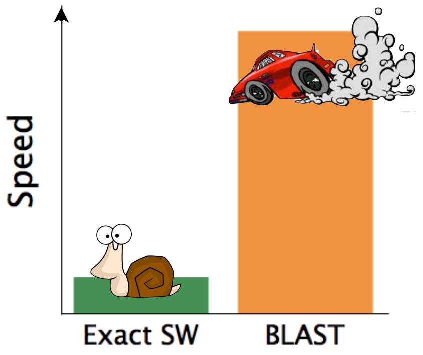
Rapid, heuristic versions of Smith–Waterman: **BLAST**

- BLAST (Basic Local Alignment Search Too simplified form of Smith-Waterman at is popular because it is **fast**
  - BLAST finds regions of al sequences
  - BLAST search by scanning d matches before performing nts
  - sensitivity in exchange for speed
  - rast to SW, BLAST is not guaranteed to find optimal alignments

“The central idea of the BLAST algorithm is to confine attention to sequence pairs that contain an initial **word pair** match” Altschul et al. (1990)

- BLAST uses this pre-screening heuristic approximation resulting in an an approach that is about 50 times faster than the Smith-Waterman





How BLAST works

- Four basic phases
  - **Phase 1**: compile a list of query word pairs (w=3)

RGGVKRI Query sequence

RGG
GGV
GVK
VKR
KRI

generate list of **w=3 words** for query

Blast

- **Phase 2**: expand word pairs to include those similar to query (defined as those above a similarity threshold to original word, i.e. match scores in substitution matrix)

RGGVKRI Query sequence

RGG RAG RIG RLG . . .
GGV GAV GTV GCV . . .
GVK GAK GIK GGK . . .
VKR VRR VHR VER . . .
KRI KKI KHI KDI . . .

extend list of words similar to query

Blast

- **Phase 3**: a database is scanned to find sequence entries that match the compiled word list

GNYGLKVISLDVE Database sequence

RGGVKRI Query sequence

RGG RAG RIG RLG . . .
GGV GAV GTV GCV . . .
GVK GLK GIK GGK . . .
VKR VRR VHR VER . . .
KRI KKI KHI KDI . . .

search for **perfect matches** in the database sequence

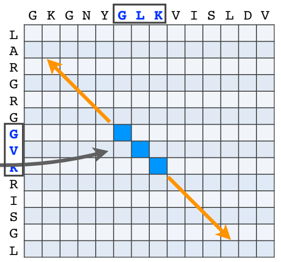
Blast

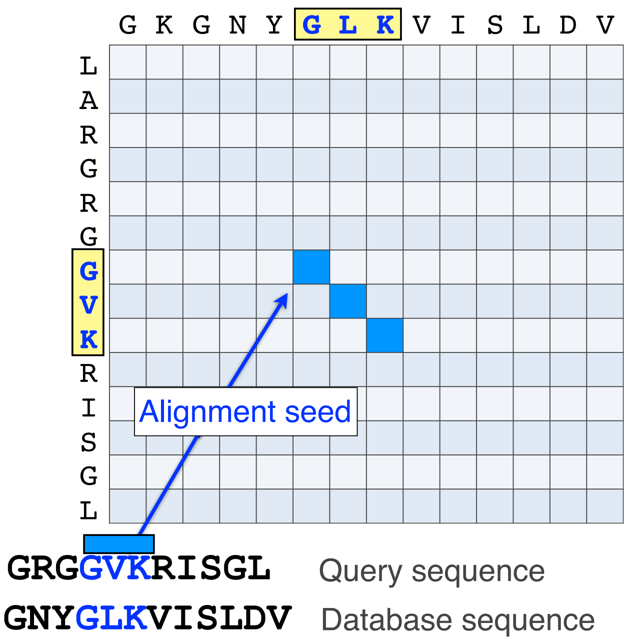
- **Phase 4**: the initial database hits are extended in both directions using dynamic programing

GNYGLKVISLDVE Database sequence

RGGVKRI Query sequence

matched word is used as a local **alignment seed**

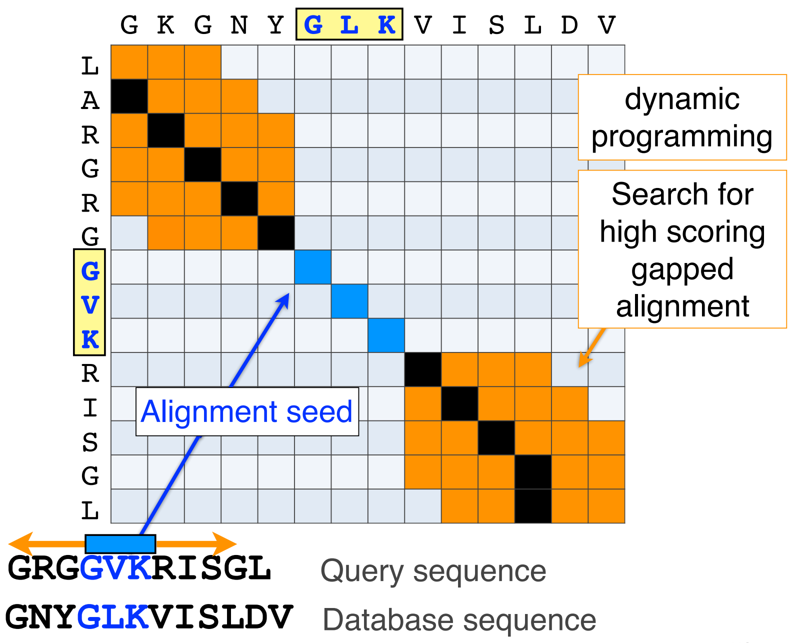




Alignment seed

GRGGVKRISGL Query sequence

GNYGLKVISLDV Database sequence



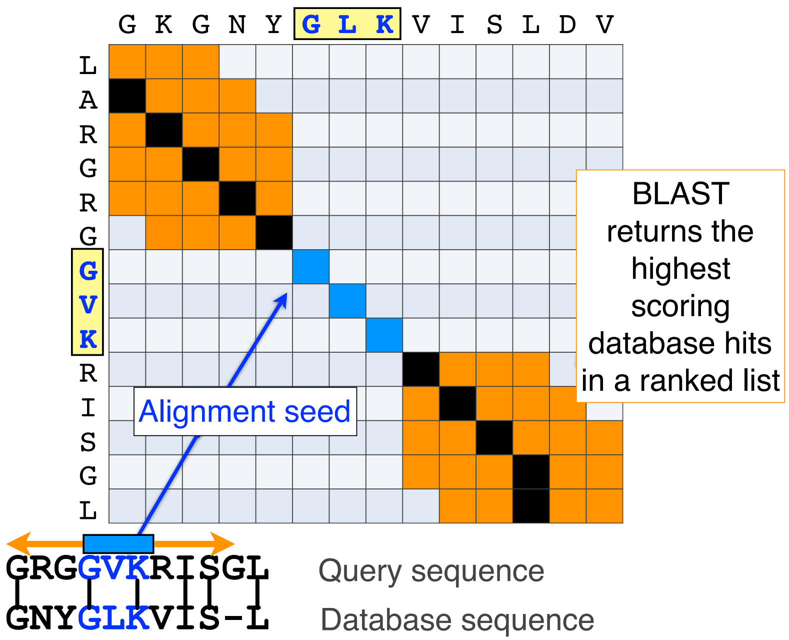
dynamic programming

Search for high scoring gapped alignment

Alignment seed

GRGGVKRISGL Query sequence

GNYGLKVISLDV Database sequence



BLAST returns the highest scoring database hits in a ranked list

Alignment seed

```
GRGGVKRISGL
|  |  ||| |
GNYGLKVIS-L
```

Query sequence

Database sequence

BLAST output

- BLAST returns the highest scoring database hits in a ranked list along with details about the target sequence and alignment statistics

Description	Max score	Query cover	E value	Max ident	Accession
kinesin-1 heavy chain [Homo sapiens]	677	100%	0	100%	NP_004512.1
Kif5b protein [Mus musculus]	676	100%	0	98%	AAA20133.1
Kinesin-14 heavy chain [Danio rerio]	595	88%	0	78%	XP_00320703
hypothetical protein EGK_18589	48.2	40%	0.03	32%	ELK35081.1
mKIAA4102 protein [Mus musculus]	42.7	38%	3.02	24%	EHH28205.1

Statistical significance of results

- An important feature of BLAST is the computation of statistical significance for each hit. This is described by the **E value** (expect value)

Description	Max score	Query cover	E value	Max ident	Accession
kinesin-1 heavy chain [Homo sapiens]	677	100%	0	100%	NP_004512.1
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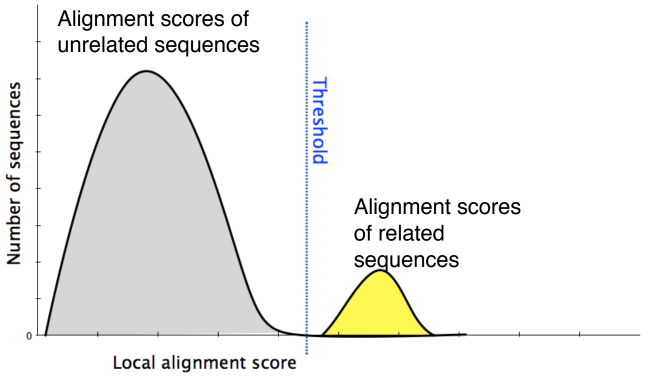
mKIAA4102 protein [Mus musculus]	42.7	38%	3.02	24%	EHH28205.1

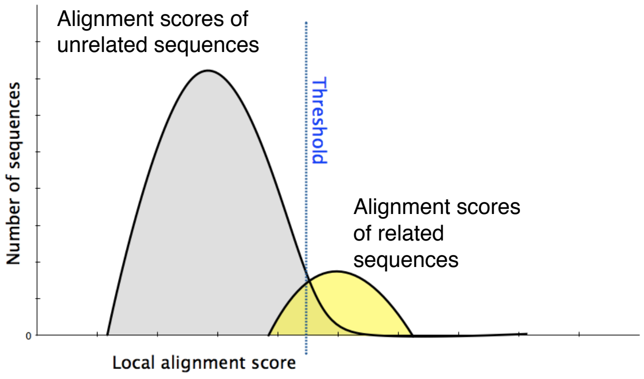
BLAST scores and E-values

- The **E value** is the **expected** number of hits that are as good or better than the observed local alignment score (with this score or better) if the query and database are **random** with respect to each other
  - *i.e.* the number of alignments expected to occur by chance with equivalent or better scores
- Typically, only hits with E value **below** a significance threshold are reported
  - This is equivalent to selecting alignments with score above a certain score threshold

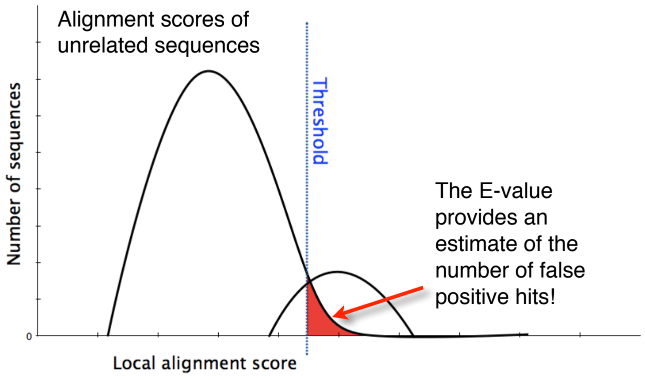
- Ideally, a threshold separates all query related sequences (yellow) from all unrelated sequences (gray)



- Unfortunately, often both score distributions overlap
  - The E value describes the expected number of hits with a score above the threshold if the query and database are unrelated

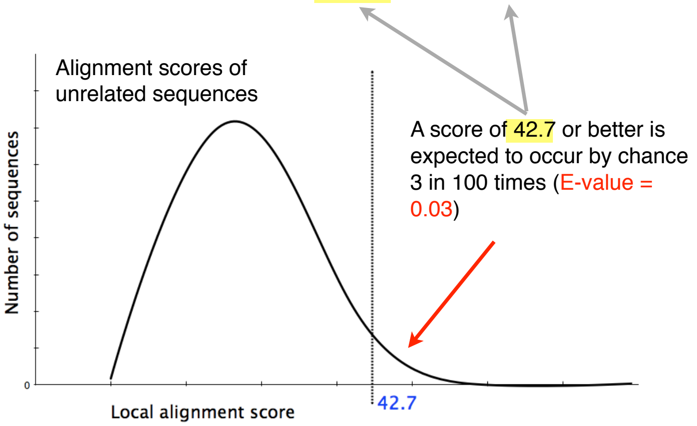


- Unfortunately, often both score distributions overlap
  - The E value describes the expected number of hits with a score above the threshold if the query and database are unrelated



The E-value provides an estimate of the number of false positive hits!

Description	Max score	Query cover	E value	Max ident	Accession
kinesin-1 heavy chain [Homo sapiens]	677	100%	0	100%	NP_004512.1
Kif5b protein [Mus musculus]	676	100%	0	98%	AAA20133.1
Kinesin-14 heavy chain [Danio rerio]	595	88%	0	78%	XP_00320703
hypothetical protein EGK_18589	42.7	40%	**0.03**	32%	ELK35081.1



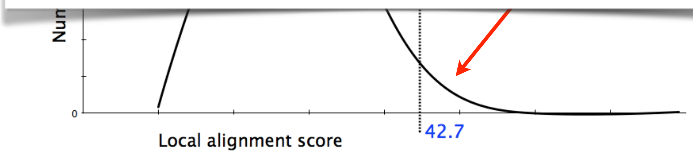
A score of 42.7 or better is expected to occur by chance 3 in 100 times (E-value = 0.03)

Description	Max score	Total score	Query cover	E value	Max ident	Accession
kinesin-1 heavy chain [Homo	677	677	100%	0	100%	NP_004512.1
Kif5b protein [Mus musculus]	676	676	100%	0	98%	AAA20133.1

In general *E* values < 0.005 are usually significant.

To find out more about *E* values see: "*The Statistics of Sequence Similarity Scores*" available in the help section of the NCBI BLAST site:

http://www.ncbi.nlm.nih.gov/blast/tutorial/Altschul-1.html

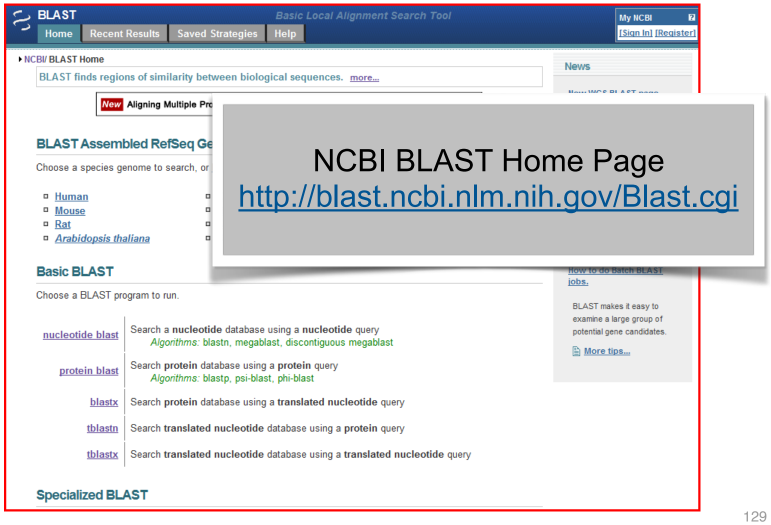


Your Turn!

Hands-on worksheet **Sections 4** & **5**

- Please do answer the last lab review question (**Q19**).
- We encourage discussion and exploration!

Practical database searching with BLAST



NCBI/ BLAST Home

BLAST finds regions of similarity between biological sequences. more...

BLAST Assembled RefSeq Ge

Choose a species genome to search, or

- Human
- Mouse
- Rat
- *Arabidopsis thaliana*

Basic BLAST

Choose a BLAST program to run.

nucleotide blast	Search a **nucleotide** database using a **nucleotide** query *Algorithms:* blastn, megablast, discontiguous megablast
protein blast	Search **protein** database using a **protein** query *Algorithms:* blastp, psi-blast, phi-blast
blastx	Search **protein** database using a **translated nucleotide** query
tblastn	Search **translated nucleotide** database using a **protein** query
tblastx	Search **translated nucleotide** database using a **translated nucleotide** query

BLAST makes it easy to examine a large group of potential gene candidates.

Specialized BLAST

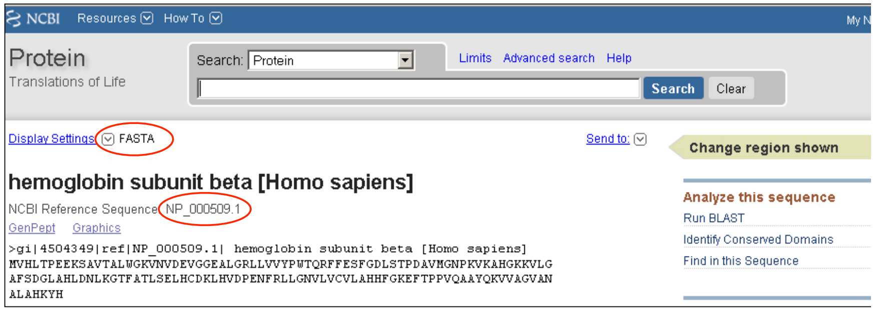
NCBI BLAST Home Page
http://blast.ncbi.nlm.nih.gov/Blast.cgi

Practical database searching with BLAST

- There are four basic components to a traditional BLAST search
  - (1) Choose the sequence (query)
  - (2) Select the BLAST program
  - (3) Choose the database to search
  - (4) Choose optional parameters
- Then click "BLAST"

Step 1: Choose your sequence

- Sequence can be input in FASTA format or as accession number



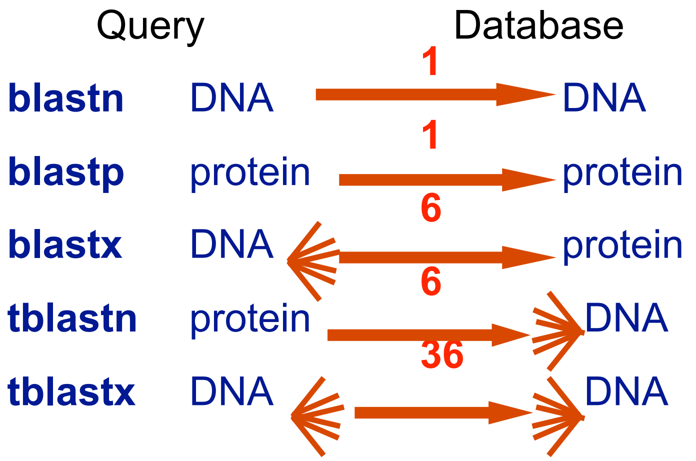
Display Settings: FASTA

hemoglobin subunit beta [Homo sapiens]

NCBI Reference Sequence NP_000509.1

```
>gi|4504349|ref|NP_000509.1| hemoglobin subunit beta [Homo sapiens]
MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPKVKAHGKKVLG
AFSDGLAHLDNLKGTFATLSELHCDKLHVDPENFRLLGNVLVCVLAHHFGKEFTPPVQAAYQKVVAGVAN
ALAHKYH
```

Step 2: Choose the BLAST program



Query Database

blastn DNA 1 DNA

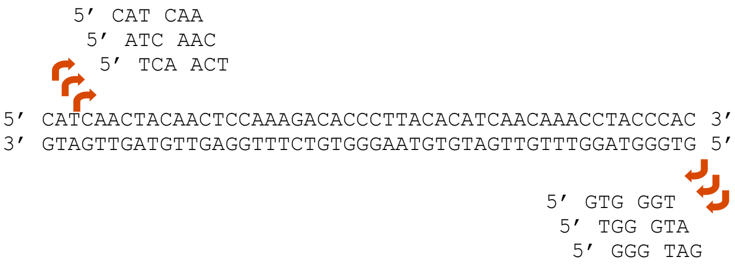
blastp protein 1 protein

blastx DNA 6 protein

tblastn protein 6 DNA

tblastx DNA 36 DNA

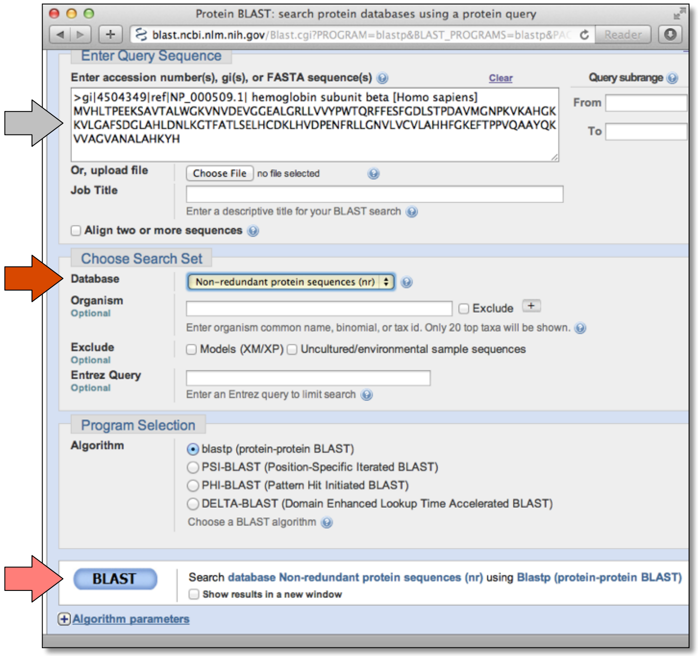
DNA potentially encodes six proteins



```
      5′ CAT CAA
        5′ ATC AAC
          5′ TCA ACT

5′ CATCAACTACAACTCCAAAGACACCCTTACACATCAACAAACCTACCCAC 3′
3′ GTAGTTGATGTTGAGGTTTCTGTGGGAATGTGTAGTTGTTTGGATGGGTG 5′

                                        5′ GTG GGT
                                          5′ TGG GTA
                                            5′ GGG TAG
```



Protein BLAST: search protein databases using a protein query

blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&BLAST_PROGRAMS=blastp&PA

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

```
>gi|4504349|ref|NP_000509.1| hemoglobin subunit beta [Homo sapiens]
MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPKVKAHGK
KVLGAFSDGLAHLDNLKGTFATLSELHCDKLHVDPENFRLLGNVLVCVLAHHFGKEFTPPVQAAYQK
VVAGVANALAHKYH
```

Query subrange: From: To:

Or, upload file: Choose File — no file selected

Job Title: Enter a descriptive title for your BLAST search

□ Align two or more sequences

Choose Search Set

Database: Non-redundant protein sequences (nr)

Organism (Optional): □ Exclude — Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Exclude (Optional): □ Models (XM/XP) □ Uncultured/environmental sample sequences

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

Program Selection

Algorithm:
- ● blastp (protein-protein BLAST)
- ○ PSI-BLAST (Position-Specific Iterated BLAST)
- ○ PHI-BLAST (Pattern Hit Initiated BLAST)
- ○ DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

Choose a BLAST algorithm

BLAST — Search database Non-redundant protein sequences (nr) using Blastp (protein-protein BLAST)

□ Show results in a new window

Algorithm parameters

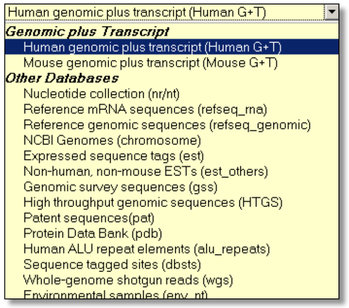
Step 3: Choose the database

nr = non-redundant (most general database)

dbest = database of expressed sequence tags

dbsts = database of sequence tag sites

gss = genomic survey sequences

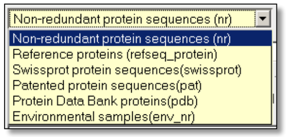


Human genomic plus transcript (Human G+T)

Genomic plus Transcript
- Human genomic plus transcript (Human G+T)
- Mouse genomic plus transcript (Mouse G+T)

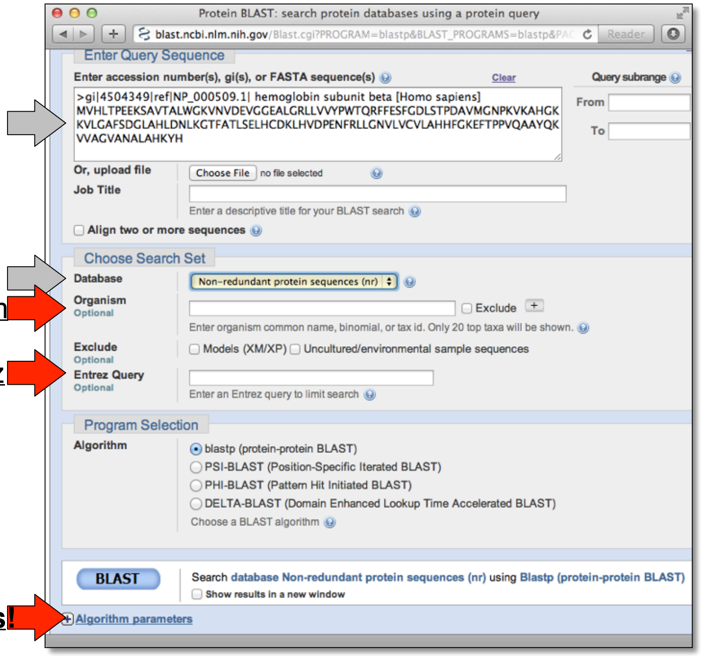
Other Databases
- Nucleotide collection (nr/nt)
- Reference mRNA sequences (refseq_rna)
- Reference genomic sequences (refseq_genomic)
- NCBI Genomes (chromosome)
- Expressed sequence tags (est)
- Non-human, non-mouse ESTs (est_others)
- Genomic survey sequences (gss)
- High throughput genomic sequences (HTGS)
- Patent sequences(pat)
- Protein Data Bank (pdb)
- Human ALU repeat elements (alu_repeats)
- Sequence tagged sites (dbsts)
- Whole-genome shotgun reads (wgs)
- Environmental samples (env_nt)

nucleotide databases



Non-redundant protein sequences (nr)
- Non-redundant protein sequences (nr)
- Reference proteins (refseq_protein)
- Swissprot protein sequences(swissprot)
- Patented protein sequences(pat)
- Protein Data Bank proteins(pdb)
- Environmental samples(env_nr)

protein databases



Protein BLAST: search protein databases using a protein query

blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&BLAST_PROGRAMS=blastp&PA

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

```
>gi|4504349|ref|NP_000509.1| hemoglobin subunit beta [Homo sapiens]
MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPKVKAHGK
KVLGAFSDGLAHLDNLKGTFATLSELHCDKLHVDPENFRLLGNVLVCVLAHHFGKEFTPPVQAAYQK
VVAGVANALAHKYH
```

Query subrange: From: To:

Or, upload file: Choose File — no file selected

Job Title: Enter a descriptive title for your BLAST search

□ Align two or more sequences

Choose Search Set

Database: Non-redundant protein sequences (nr)

Organism (Optional): □ Exclude — Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Exclude (Optional): □ Models (XM/XP) □ Uncultured/environmental sample sequences

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

Program Selection

Algorithm:
- ● blastp (protein-protein BLAST)
- ○ PSI-BLAST (Position-Specific Iterated BLAST)
- ○ PHI-BLAST (Pattern Hit Initiated BLAST)
- ○ DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

Choose a BLAST algorithm

BLAST — Search database Non-redundant protein sequences (nr) using Blastp (protein-protein BLAST)

□ Show results in a new window

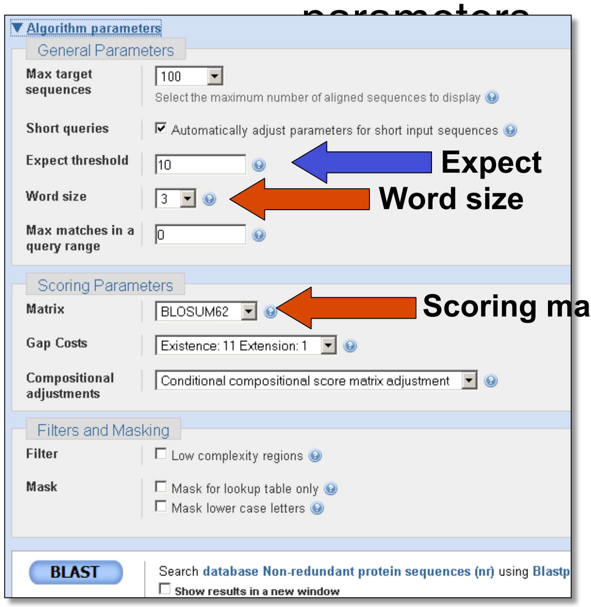
Algorithm parameters

Organism

Entrez

Settings!

Step 4a: Select optional search parameters



▼ Algorithm parameters

General Parameters

Max target sequences: 100
Select the maximum number of aligned sequences to display

Short queries: ☑ Automatically adjust parameters for short input sequences

Expect threshold: 10

Word size: 3

Max matches in a query range: 0

Scoring Parameters

Matrix: BLOSUM62

Gap Costs: Existence: 11 Extension: 1

Compositional adjustments: Conditional compositional score matrix adjustment

Filters and Masking

Filter: □ Low complexity regions

Mask: □ Mask for lookup table only
□ Mask lower case letters

BLAST

Search database Non-redundant protein sequences (nr) using Blastp

□ Show results in a new window

Expect

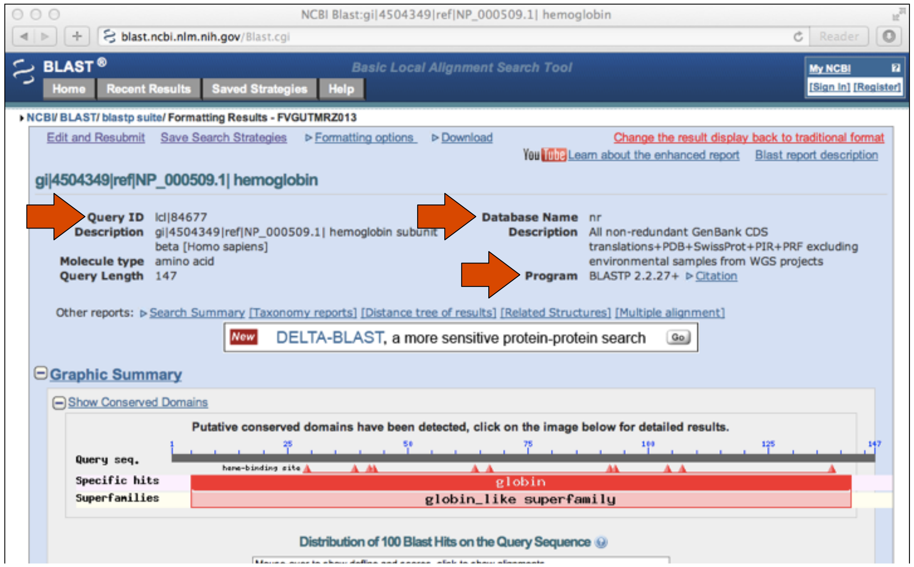
Word size

Scoring matrix

Step 4: Optional parameters

- You can...
  - choose the organism to search
  - change the substitution matrix
  - change the expect (E) value
  - change the word size
  - change the output format

Results page



NCBI Blast:gi|4504349|ref|NP_000509.1| hemoglobin

blast.ncbi.nlm.nih.gov/Blast.cgi

NCBI/ BLAST/ blastp suite/ Formatting Results - FVGUTMRZ013

Edit and Resubmit
Save Search Strategies
Formatting options
Download
Change the result display back to traditional format
YouTube Learn about the enhanced report
Blast report description

gi|4504349|ref|NP_000509.1| hemoglobin

Query ID	lcl|84677
Description	gi|4504349|ref|NP_000509.1| hemoglobin subunit beta [Homo sapiens]
Molecule type	amino acid
Query Length	147

Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program	BLASTP 2.2.27+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

New DELTA-BLAST, a more sensitive protein-protein search Go

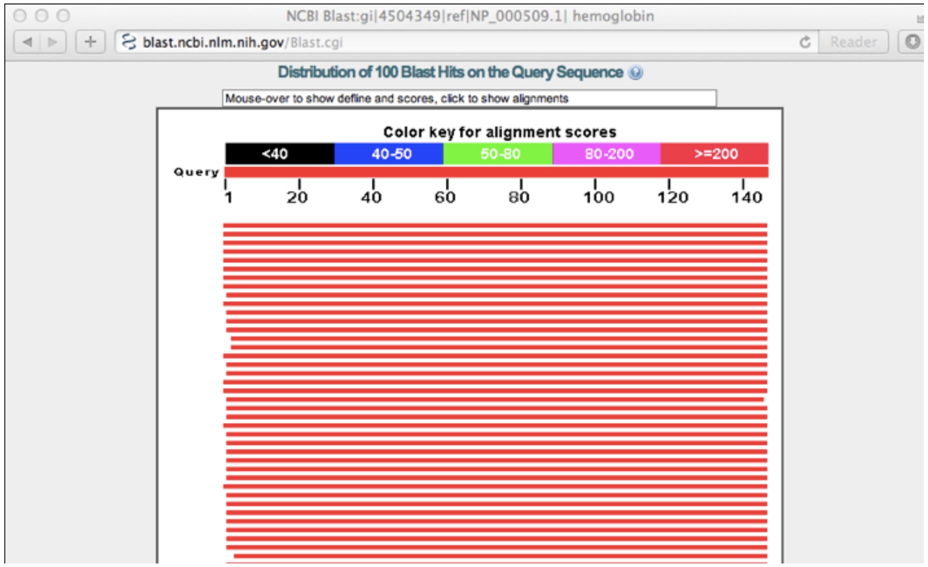
Graphic Summary

Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.

Distribution of 100 Blast Hits on the Query Sequence

Further down the results page...



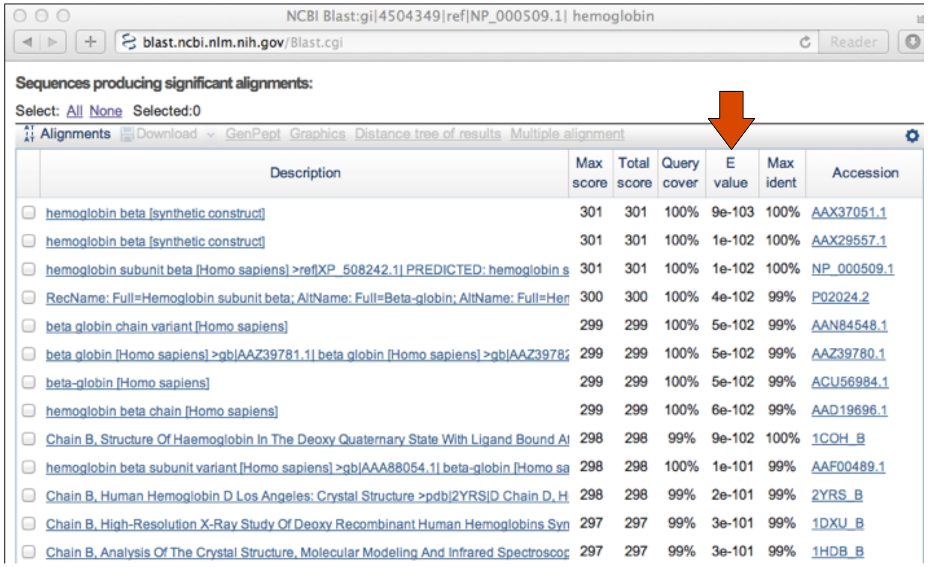
NCBI Blast:gi|4504349|ref|NP_000509.1| hemoglobin

blast.ncbi.nlm.nih.gov/Blast.cgi

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments

Further down the results page...



NCBI Blast:gi|4504349|ref|NP_000509.1| hemoglobin

blast.ncbi.nlm.nih.gov/Blast.cgi

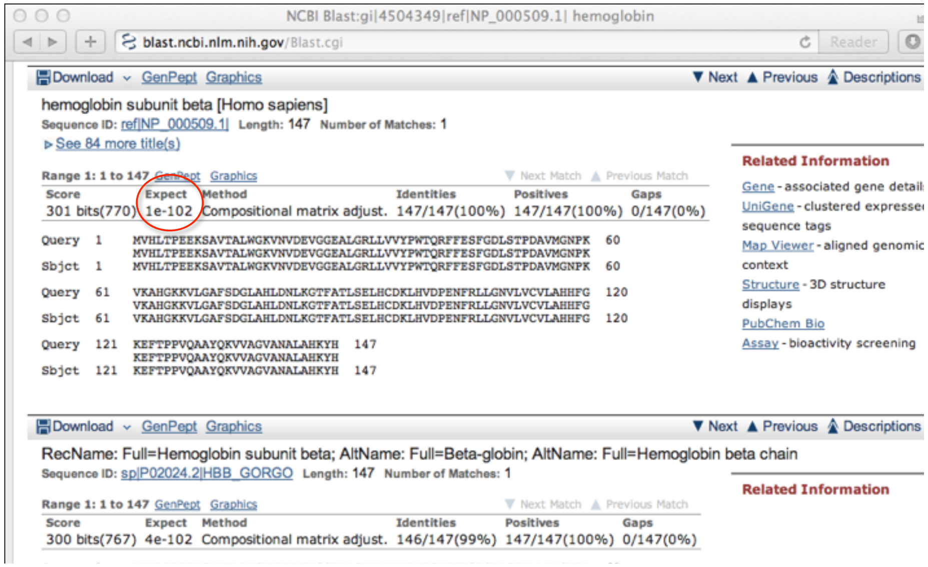
Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Max ident	Accession
□	hemoglobin beta [synthetic construct]	301	301	100%	9e-103	100%	AAX37051.1
□	hemoglobin beta [synthetic construct]	301	301	100%	1e-102	100%	AAX29557.1
□	hemoglobin subunit beta [Homo sapiens] >ref|XP_508242.1| PREDICTED: hemoglobin s	301	301	100%	1e-102	100%	NP_000509.1
□	RecName: Full=Hemoglobin subunit beta; AltName: Full=Beta-globin; AltName: Full=Hen	300	300	100%	4e-102	99%	P02024.2
□	beta globin chain variant [Homo sapiens]	299	299	100%	5e-102	99%	AAN84548.1
□	beta globin [Homo sapiens] >gb|AAZ39781.1| beta globin [Homo sapiens] >gb|AAZ3978	299	299	100%	5e-102	99%	AAZ39780.1
□	beta-globin [Homo sapiens]	299	299	100%	5e-102	99%	ACU56984.1
□	hemoglobin beta chain [Homo sapiens]	299	299	100%	6e-102	99%	AAD19696.1
□	Chain B, Structure Of Haemoglobin In The Deoxy Quaternary State With Ligand Bound At	298	298	99%	9e-102	100%	1COH_B
□	hemoglobin beta subunit variant [Homo sapiens] >gb|AAA88054.1| beta-globin [Homo sa	298	298	100%	1e-101	99%	AAF00489.1
□	Chain B, Human Hemoglobin D Los Angeles: Crystal Structure >pdb|2YRS|D Chain D, H	298	298	99%	2e-101	99%	2YRS_B
□	Chain B, High-Resolution X-Ray Study Of Deoxy Recombinant Human Hemoglobins Syn	297	297	99%	3e-101	99%	1DXU_B
□	Chain B, Analysis Of The Crystal Structure, Molecular Modeling And Infrared Spectroscop	297	297	99%	3e-101	99%	1HDB_B

Further down the results page...



NCBI Blast:gi|4504349|ref|NP_000509.1| hemoglobin

blast.ncbi.nlm.nih.gov/Blast.cgi

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

hemoglobin subunit beta [Homo sapiens]

Sequence ID: ref|NP_000509.1| Length: 147 Number of Matches: 1

▷ See 84 more title(s)

Range 1: 1 to 147 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
301 bits(770)	1e-102	Compositional matrix adjust.	147/147(100%)	147/147(100%)	0/147(0%)

```
Query  1    MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  60
            MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK
Sbjct  1    MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  60

Query  61   VKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLHVDPENFRLLGNVLVCVLAHHFG  120
            VKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLHVDPENFRLLGNVLVCVLAHHFG
Sbjct  61   VKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLHVDPENFRLLGNVLVCVLAHHFG  120

Query  121  KEFTPPVQAAYQKVVAGVANALAHKYH  147
            KEFTPPVQAAYQKVVAGVANALAHKYH
Sbjct  121  KEFTPPVQAAYQKVVAGVANALAHKYH  147
```

Related Information

Gene - associated gene detail

UniGene - clustered expresse sequence tags

Map Viewer - aligned genomic context

Structure - 3D structure displays

PubChem Bio

Assay - bioactivity screening

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

RecName: Full=Hemoglobin subunit beta; AltName: Full=Beta-globin; AltName: Full=Hemoglobin beta chain

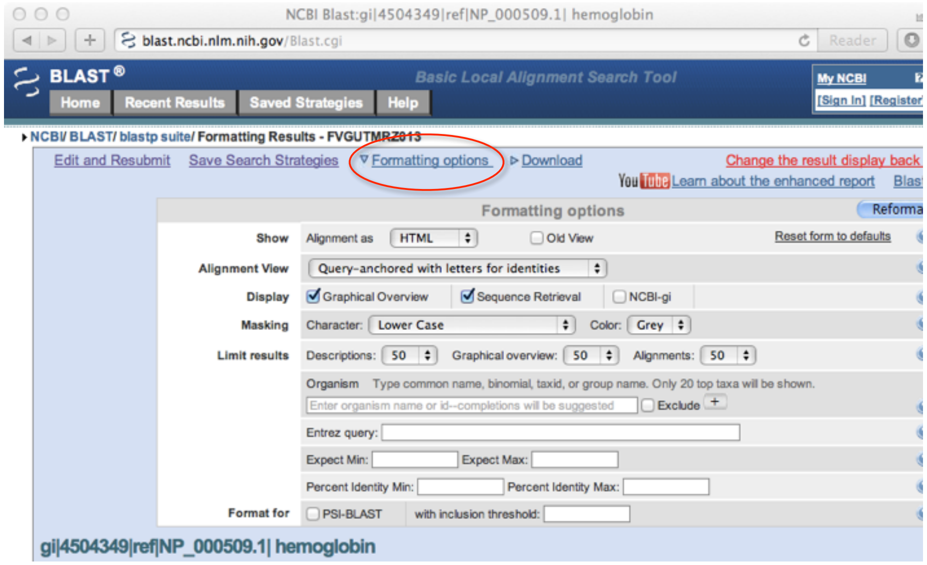
Sequence ID: sp|P02024.2|HBB_GORGO Length: 147 Number of Matches: 1

Related Information

Range 1: 1 to 147 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
300 bits(767)	4e-102	Compositional matrix adjust.	146/147(99%)	147/147(100%)	0/147(0%)

Different output formats are available



NCBI Blast:gi|4504349|ref|NP_000509.1| hemoglobin

blast.ncbi.nlm.nih.gov/Blast.cgi

BLAST® Basic Local Alignment Search Tool

Home Recent Results Saved Strategies Help

My NCBI [Sign In] [Register

▸ NCBI/ BLAST/ blastp suite/ Formatting Results - FVGUTMRZ013

Edit and Resubmit Save Search Strategies ▽ Formatting options ▷ Download Change the result display back

YouTube Learn about the enhanced report Blas

Formatting options Reforma

Show: Alignment as HTML □ Old View Reset form to defaults

Alignment View: Query-anchored with letters for identities

Display: ☑ Graphical Overview ☑ Sequence Retrieval □ NCBI-gi

Masking: Character: Lower Case Color: Grey

Limit results: Descriptions: 50 Graphical overview: 50 Alignments: 50

Organism Type common name, binomial, taxid, or group name. Only 20 top taxa will be shown.

Enter organism name or id--completions will be suggested □ Exclude +

Entrez query:

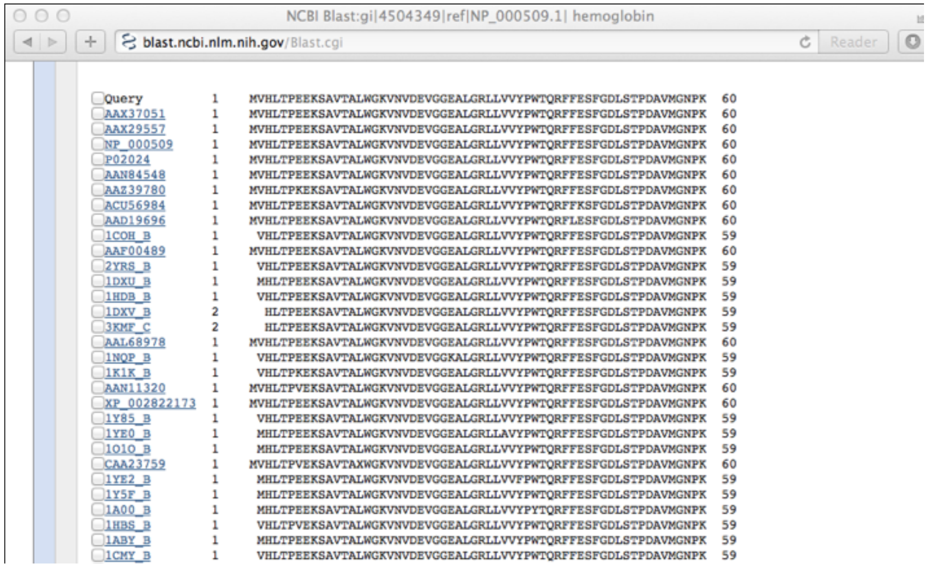
Expect Min: Expect Max:

Percent Identity Min: Percent Identity Max:

Format for: □ PSI-BLAST with inclusion threshold:

gi|4504349|ref|NP_000509.1| hemoglobin

E.g. Query anchored alignments

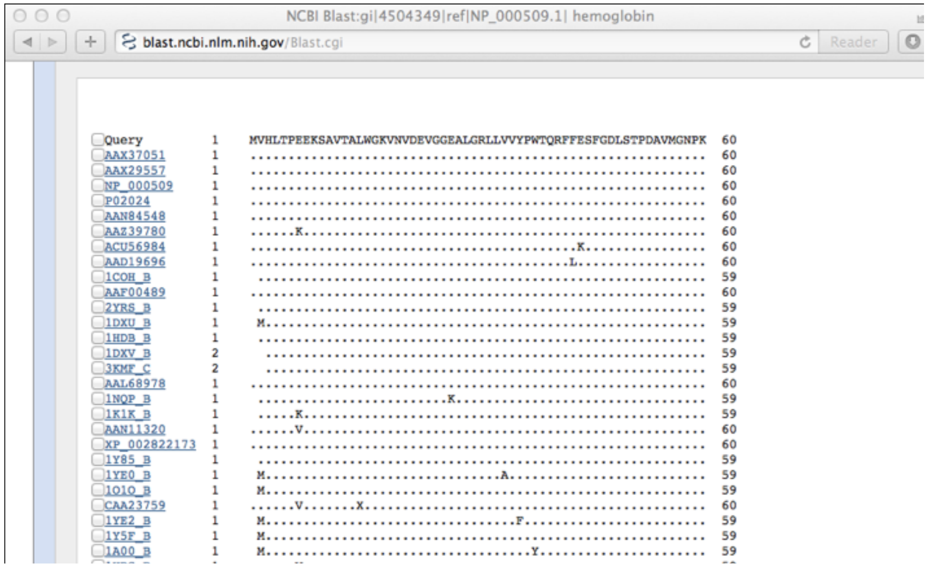


NCBI Blast:gi|4504349|ref|NP_000509.1| hemoglobin

blast.ncbi.nlm.nih.gov/Blast.cgi

```
□Query         1    MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  60
□AAX37051      1    MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  60
□AAX29557      1    MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  60
□NP_000509     1    MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  60
□P02024        1    MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  60
□AAN84548      1    MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  60
□AAZ39780      1    MVHLTPKEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  60
□ACU56984      1    MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFKSFGDLSTPDAVMGNPK  60
□AAD19696      1    MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFLESFGDLSTPDAVMGNPK  60
□1COH_B        1     VHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  59
□AAF00489      1    MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  60
□2YRS_B        1     VHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  59
□1DXU_B        1     MHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  59
□1HDB_B        1     VHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  59
□1DXV_B        2      HLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  59
□3KMF_C        2      HLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  59
□AAL68978      1    MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  60
□1NQP_B        1     VHLTPEEKSAVTALWGKVNVDEVGGKALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  59
□1K1K_B        1     VHLTPKEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  59
□AAN11320      1    MVHLTPVEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  60
□XP_002822173  1    MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  60
□1Y85_B        1     VHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  59
□1YE0_B        1     MHLTPEEKSAVTALWGKVNVDEVGGEALGRLLAVYPWTQRFFESFGDLSTPDAVMGNPK  59
□1O1O_B        1     MHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  59
□CAA23759      1    MVHLTPVEKSAVTAXWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  60
□1YE2_B        1     MHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVFPWTQRFFESFGDLSTPDAVMGNPK  59
□1Y5F_B        1     MHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  59
□1A00_B        1     MHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPYTQRFFESFGDLSTPDAVMGNPK  59
□1HBS_B        1     VHLTPVEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  59
□1ABY_B        1     MHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  59
□1CMY_B        1     VHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  59
```

... and alignments with dots for identities


NCBI Blast:gi|4504349|ref|NP_000509.1| hemoglobin
blast.ncbi.nlm.nih.gov/Blast.cgi
Reader

```
☐Query          1     MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK  60
☐AAX37051       1     ............................................................  60
☐AAX29557       1     ............................................................  60
☐NP_000509      1     ............................................................  60
☐P02024         1     ............................................................  60
☐AAN84548       1     ............................................................  60
☐AAZ39780       1     ......K.....................................................  60
☐ACU56984       1     ...........................................K................  60
☐AAD19696       1     ..........................................L.................  60
☐1COH_B         1      ...........................................................  59
☐AAF00489       1     ............................................................  60
☐2YRS_B         1      ...........................................................  59
☐1DXU_B         1      M..........................................................  59
☐1HDB_B         1      ...........................................................  59
☐1DXV_B         2       ..........................................................  59
☐3KMF_C         2       ..........................................................  59
☐AAL68978       1     ............................................................  60
☐1NQP_B         1      .........................K.................................  59
☐1K1K_B         1      .....K.....................................................  59
☐AAN11320       1     ......V.....................................................  60
☐XP_002822173   1     ............................................................  60
☐1Y85_B         1      ...........................................................  59
☐1YE0_B         1      M...............................A..........................  59
☐1O1O_B         1      M..........................................................  59
☐CAA23759       1     ......V.......X.............................................  60
☐1YE2_B         1      M.................................F........................  59
☐1Y5F_B         1      M..........................................................  59
☐1A00_B         1      M....................................Y.....................  59
```

Common problems

- Selecting the wrong version of BLAST
- Selecting the wrong database
- Too many hits returned
- Too few hits returned
- Unclear about the significance of a particular result - are these sequences homologous?

How to handle too many results

- Focus on the question you are trying to answer
  - select “refseq” database to eliminate redundant matches from “nr”
  - Limit hits by organism
  - Use just a portion of the query sequence, when appropriate
  - Adjust the expect value; lowering *E* will reduce the number of matches returned

How to handle too few results

- Many genes and proteins have no significant database matches
  - remove Entrez limits
  - raise E-value threshold
  - search different databases
  - try scoring matrices with lower BLOSUM values (or higher PAM values)
  - use a search algorithm that is more sensitive than BLAST (*e.g.* PSI-BLAST or HMMer)

Summary of key points

- Sequence alignment is a fundamental operation underlying much of bioinformatics.
- Even when optimal solutions can be obtained they are not necessarily unique or reflective of the biologically correct alignment.
- Dynamic programming is a classic approach for solving the pairwise alignment problem.
- Global and local alignment, and their major application areas.
- Heuristic approaches are necessary for large database searches and many genomic applications.

FOR NEXT CLASS…

Check out the online:

☑ **Reading**: Sean Eddy's "What is dynamic programming?"

☑ **Homework**: (1) **Quiz**, (2) **Alignment Exercise**.

Homework Grading

Both (1) quiz questions and (2) alignment exercise carry equal weights (*i.e.* 50% each).

(Homework 2) Assessment Criteria	**Points**	
Setup labeled alignment matrix	1	
Include initial column and row for GAPs	1	
All alignment matrix elements scored (i.e. filled in)	1	
Evidence for correct use of scoring scheme	1	
Direction arrows drawn between all cells	1	
Evidence of multiple arrows to a given cell if appropriate	1	D
Correct optimal score position in matrix used	1	C
Correct optimal score obtained for given scoring scheme	1	B
Traceback path(s) clearly highlighted	1	A
Correct *alignment(s)* yielding optimal score listed	1	A+