

Lecture 07

molecular sequences



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Lecture 07 outline

Last time: shell scripts

This time: molecular sequences

Topics

- sequence data
- GenBank
- BLAST

A ***molecular sequence*** is a string of characters from a molecular alphabet.

Examples: *DNA, RNA, amino acid sequences*

Sequences are key to understanding:

- disease mechanism
- gene expression
- developmental biology
- heredity and ancestry
- protein and cell function
- biodiversity patterns

sequence length is
18 base pairs (bp)



...ATGCGACGATGGATACCATAG...



DNA alphabet:
A, C, G, T

fourth position
is in state C

...ATGCGACGATGGATACCATAG...



transcription

...AUGCGACGAUGGAAUACCAUAG...

RNA alphabet:
A, C, G, U

...ATGCGACGATGGATACCATAG...

start
codon



transcription

stop
codon

...[AUG]CGACGAUGGAUACCA[UAG]...



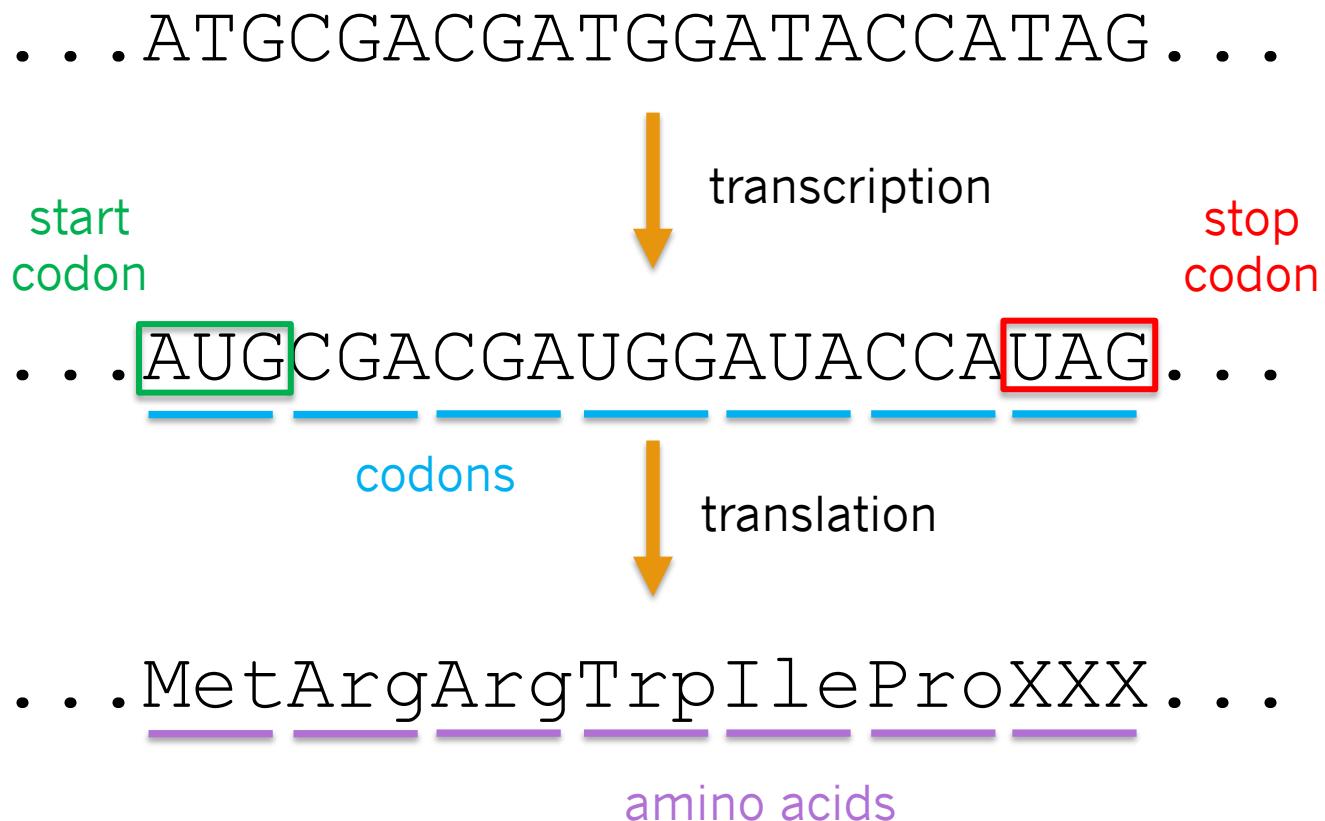
codons

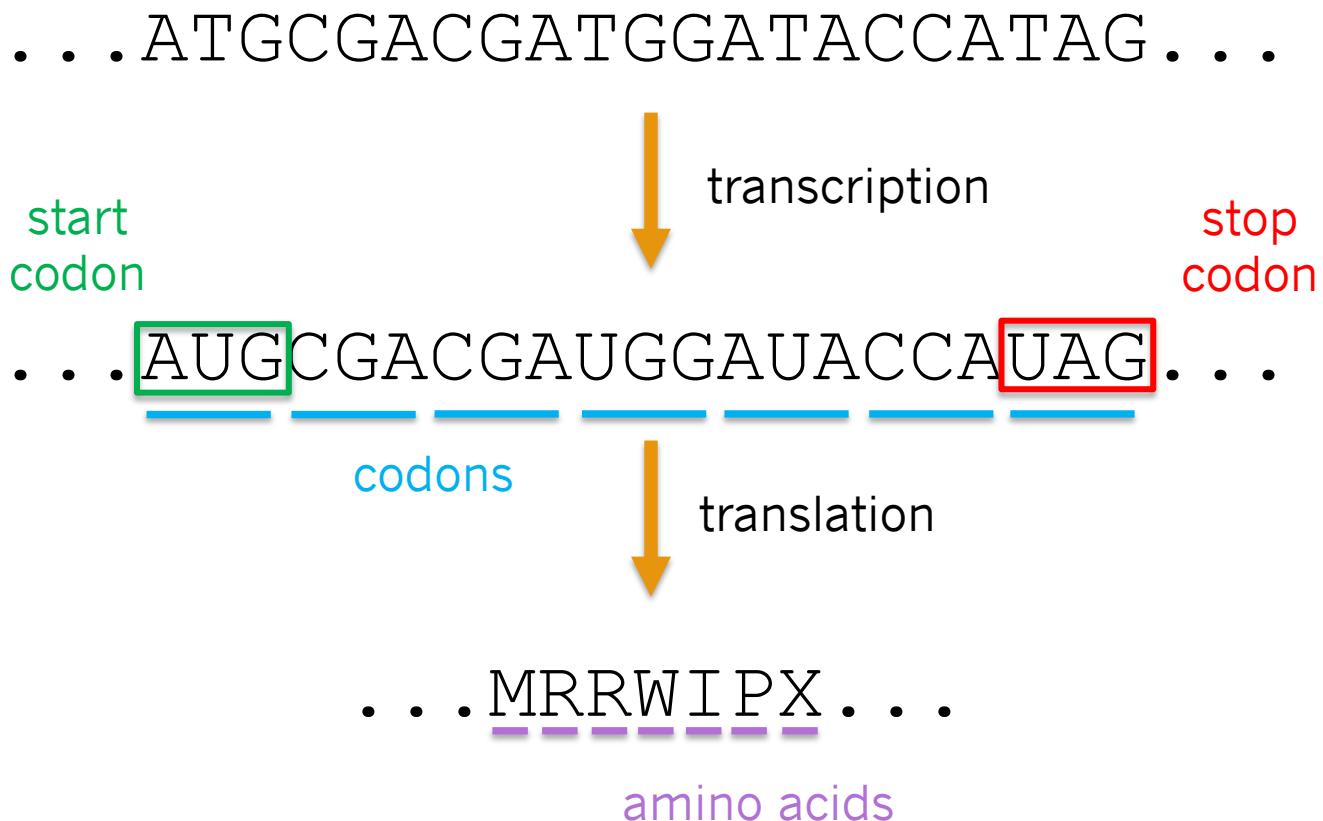
Standard genetic code

		Second letter								
		U	C	A	G					
First letter	U	UUU UUC UUA UUG	Phenylalanine (Phe)	UCU UCC UCA UCG	Serine (Ser)	UAU UAC UAA UAG	Tyrosine (Tyr)	UGU UGC UGA UGG	Cysteine (Cys)	U C
	C	CUU CUC CUA CUG	Leucine (Leu)	CCU CCC CCA CCG	Proline (Pro)	CAU CAC CAA CAG	Histidine (His)	CGU CGC CGA CGG	Stop	A G
	A	AUU AUC AUA AUG	Isoleucine (Ile)	ACU ACC ACA ACG	Threonine (Thr)	AAU AAC AAA AAG	Asparagine (Asn)	AGU AGC AGA AGG	Arginine (Arg)	U C
	G	GUU GUC GUA GUG	Methionine (Met)	GCU GCC GCA GCG	Alanine (Ala)	GAU GAC GAA GAG	Aspartic acid (Asp)	GGU GGC GGA GGG	Serine (Ser)	A G

Standard genetic code

		Second letter											
		U	C	A	G								
First letter	U	UUU UUC UUA UUG	UCU UCC UCA UCG	UAU UAC	Tyrosine (Tyr)	UGU UGC	Cysteine (Cys)						
	C	CUU CUC CUA CUG	CCU CCC CCA CCG	CAU CAC CAA CAG	Histidine (His)	CGU CGC CGA CGG	Stop						
	A	AUU AUC AUU AUG	Isoleucine (Ile)	ACU ACC ACA ACG	Threonine (Thr)	AAU AAC	Glutamine (Gln)						
						AAA AAG	Lysine (Lys)						
	G	GUU GUC GUA GUG	Valine (Val)	GCU GCC GCA GCG	Alanine (Ala)	GAU GAC GAA GAG	Aspartic acid (Asp) Glutamic acid (Glu)						
start codon		GUU, GUC, GUA, GUG all encode Valine				AAA and AAG encode Lysine							
stop codons													
U C A G													





NCBI GenBank

The screenshot shows the NCBI GenBank homepage. At the top, there's a navigation bar with links for NCBI, Resources, How To, and Sign in to NCBI. Below the navigation is a search bar with "GenBank" selected and a dropdown menu set to "Nucleotide". A search button is visible next to the search bar. Underneath the search bar is a horizontal menu with categories: GenBank, Submit, Genomes, WGS, Metagenomes, TPA, TSA, INSDC, Other. A prominent orange banner overlays this menu. The banner contains a black exclamation mark icon, the text "COVID-19 Information", and a close button (an 'X'). Below this, there are two rows of links: "Public health information (CDC) | Research information (NIH)" and "SARS-CoV-2 data (NCBI) | Prevention and treatment information (HHS) | Español".

GenBank Overview

What is GenBank?

GenBank® is the NIH genetic sequence database, an annotated collection of all publicly available DNA sequences ([Nucleic Acids Research, 2013 Jan;41\(D1\):D36-42](#)). GenBank is part of the [International Nucleotide Sequence Database Collaboration](#), which comprises the DNA DataBank of Japan (DDBJ), the European Nucleotide Archive (ENA), and GenBank at NCBI. These three organizations exchange data on a daily basis.

A GenBank release occurs every two months and is available from the [ftp site](#). The [release notes](#) for the current version of GenBank provide detailed information about the release and notifications of upcoming changes to GenBank. Release notes for [previous GenBank releases](#) are also available. GenBank growth [statistics](#) for both the traditional GenBank divisions and the WGS division are available from each release.

An [annotated sample GenBank record](#) for a *Saccharomyces cerevisiae* gene demonstrates many of the features of the GenBank flat file format.

GenBank Resources

[GenBank Home](#)

[Submission Types](#)

[Submission Tools](#)

[Search GenBank](#)

[Update GenBank Records](#)

<https://www.ncbi.nlm.nih.gov/genbank/>

GenBank sequences

GenBank publicly hosts (Aug '22)

- 239,915,786 sequences
- 1,492,800,704,497 bases

NCBI sequences are used extensively

- identifying anonymous sequences
- inferring gene function
- searching for drug targets
- expanding datasets
- met-analyses

Homo sapiens isolate C15542T cytochrome b (cytb) gene, partial cds; mitochondrial

GenBank: JN034136.1

[FASTA](#) [Graphics](#) [PopSet](#)

Go to:

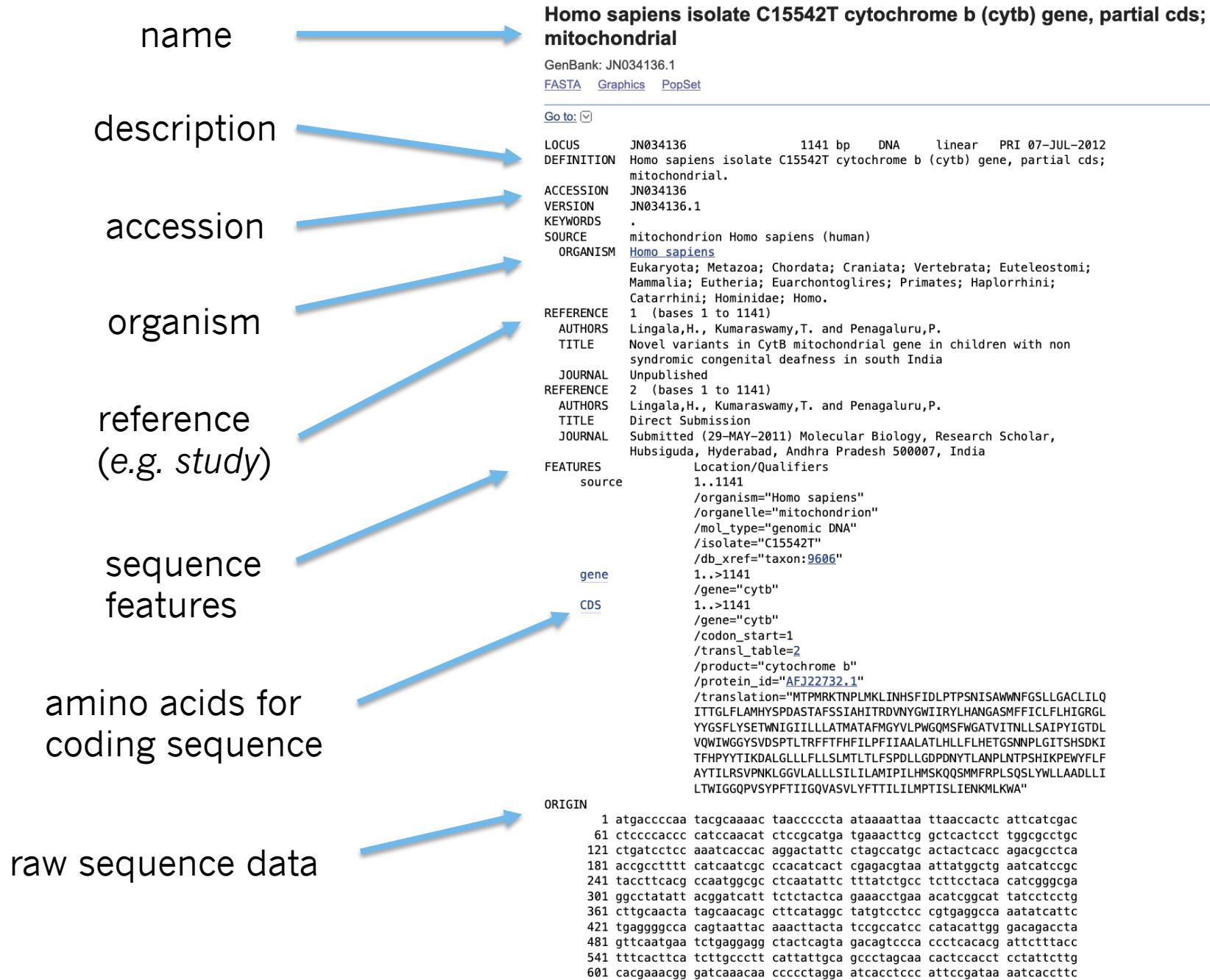
LOCUS JN034136 1141 bp DNA linear PRI 07-JUL-2012
DEFINITION Homo sapiens isolate C15542T cytochrome b (cytb) gene, partial cds; mitochondrial.
ACCESSION JN034136
VERSION JN034136.1
KEYWORDS .
SOURCE mitochondrion Homo sapiens (human)
ORGANISM [Homo sapiens](#)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1141)
AUTHORS Lingala,H., Kumaraswamy,T. and Penagaluru,P.
TITLE Novel variants in CytB mitochondrial gene in children with non syndromic congenital deafness in south India
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1141)
AUTHORS Lingala,H., Kumaraswamy,T. and Penagaluru,P.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2011) Molecular Biology, Research Scholar,
Hubsiguda, Hyderabad, Andhra Pradesh 500007, India

FEATURES	Location/Qualifiers
source	1..1141 /organism="Homo sapiens" /organelle="mitochondrion" /mol_type="genomic DNA" /isolate="C15542T" /db_xref="taxon: 9606 "
gene	1..>1141 /gene="cytb"
CDS	1..>1141 /gene="cytb" /codon_start=1 /transl_table= 2 /product="cytochrome b" /protein_id=" AFJ22732.1 " /translation="MTPMRKTNPLMKLINHSFIDLPTPSNISAWWNFGSLLGACLILQ ITTGLFLAMHYSPDASTAFSSIAHITRDVNYGWIIRYLHANGASMFFICLFLHIGRGL YYGSFLYSETWNIGIILLLATMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTDL VQWIWGGYSVDSPTLTRFFTfhFILPFIIAALATLHLLFLHETGSNNPLGITSHSDKI TFHPYYTIKDALGLLFLLSLMTLTLFSPDLDGDPDNYTLANPLNTPSHIKPEWYFLF AYTILRSVPNKLGGVLALLSILILAMIPILHMSKQQSMMFRPLSQSLYWLLAADLLI LTWIGGQPVSYPFTIIGQVASVLYFTTILILMPTISLIENKMLKWA"

ORIGIN

1 atgaccccaa tacgcaaaac taacccccta ataaaattaa ttaaccactc attcatcgac
61 ctccccaccc catccaacat ctccgcata tgaaacttcg gctcactcct tggcgccctgc
121 ctgatcctcc aaatcaccac aggactattc ctagccatgc actactcacc agacgcctca
181 accgcctttt catcaatcgc ccacatcact cgagacgtaa attatggctg aatcatccgc
241 taccttcacg ccaatggcgc ctcaatattc tttatctgcc tcttcctaca catcggcga
301 ggcctatatt acggatcatt tctctactca gaaacctgaa acatcggcat tatcctcctg
361 cttgcaacta tagcaacagc cttcataggc tatgtcctcc cgtgaggcca aatatcattc
421 tgaggggcca cagtaattac aaacttacta tccgccatcc catacattgg gacagaccta
481 gttcaatgaa tctgaggagg ctactcagta gacagtccca ccctcacacg attcttacc
541 tttcacttca tcttgccctt cattattgca gccctagcaa cactccaccc cctattcttg
601 cacgaaacgg gatcaaacaa ccccctagga atcacccccc attccgataaa aatcaccc
661 cacccttact acacaatcaa agacgcccctc ggcttacttc tcttccttct ctccttaatg
721 acattaacac tattctcacc agacccctta ggcgacccag acaattatac cctagccaac
781 cccttaaaca ccccttccca catcaagccc gaatgatatt tcctattcgc ctacacaatt
841 ctccgatccg tccctaacaa actaggaggc gtccttgccc tattactatc catcctcattc
901 ctagcaataa tccccatcct ccatatatcc aaacaacaaa gcataatatt tcgcccacta
961 agccaatcac tttattgact cctagccgca gacccctca ttctaacctg aatcggagga
1021 caaccagtaa gctacccttt taccatcatt ggacaagtag catccgtact atacttcaca
1081 acaatcctaa tcctaataacc aactatctcc ctaattgaaa acaaaaactact caaatgggcc
1141 t

//



Genome collections

Viruses > Riboviria > Orthornavirae > Kitrinoviricota > Alsuviricetes > Martellivirales > Togaviridae >

Alphavirus - 34 complete genomes

Retrieve sequences: -- Select data set from the list --

* The list view for each taxonomy node shows only the next level of sublineages.
 * Unclassified/unassigned names are written in copper

Species [33] unclassified Alphavirus [1]

Genome	Accession	RefSeq type	Source information	Segm	Length	Protein	Neighbors	Host	Created	Updated
Aura virus	NC_003900	complete		-	11824 nt	3	1		02/09/1999	08/13/2018
Barmah Forest virus	NC_001786	complete	strain:BH2193	-	11488 nt	4	35	human, invertebrates, vertebrates	01/14/1997	08/13/2018
Bebaru virus	NC_016962	complete		-	11877 nt	3	-		03/09/2012	08/13/2018
Caaingua virus	NC_055569	complete	isolate:MS681	-	12096 nt	2	-	invertebrates	06/01/2021	06/07/2021
Cabassou virus	NC_038670	complete	strain:CaAr 508	-	11385 nt	2	-		08/24/2018	08/24/2018
Chikungunya virus	NC_004162	complete	strain:S27-African prototype	-	11826 nt	2	922	human, invertebrates, vertebrates	09/06/2002	10/29/2018
Eastern equine encephalitis virus	NC_003899	complete	strain:ssp. North American variant	-	11675 nt	4	453	human, invertebrates, vertebrates	12/16/1991	08/13/2018
Elat virus	NC_018615	complete	isolate:EO329	-	11634 nt	3	1	invertebrates	09/20/2012	08/13/2018
Everglades virus	NC_038671	complete	strain:Everglades Fe3-7c	-	11395 nt	2	-		08/24/2018	08/24/2018
Fort Morgan virus	NC_013528	complete	isolate:CM4-146	-	11381 nt	3	1	invertebrates, vertebrates	11/25/2009	08/13/2018
Getah virus	NC_006558	complete	isolate:swine	-	11597 nt	3	46	invertebrates, vertebrates	12/17/2004	08/13/2018
Highlands J virus	NC_012561	complete	isolate:585-01	-	11526 nt	3	9	invertebrates, vertebrates	04/15/2009	08/13/2018
Madariaga virus	NC_023812	complete	strain:MADV/Cebus apella/BRA/BEAN5122/1956	-	11624 nt	2	29	human, invertebrates, vertebrates	03/20/2014	08/13/2018
Mayaro virus	NC_003417	complete		-	11411 nt	4	41	invertebrates, vertebrates	02/22/2002	08/13/2018
Middelburg virus	NC_024887	complete	isolate:ArB-8422	-	11550 nt	2	11	invertebrates, vertebrates	09/17/2014	08/13/2018
Mosso das Pedras virus	NC_038857	complete	strain:78V-3531	-	11465 nt	2	-		08/24/2018	08/24/2018
Mucambo virus	NC_038672	complete	strain:Mucambo BeAn 8	-	11391 nt	2	1	invertebrates	08/24/2018	08/24/2018
Ndumu virus	NC_016959	complete		-	11688 nt	4	1	invertebrates, vertebrates	03/09/2012	08/13/2018
Onyong-nyong virus	NC_001512	complete		-	11835 nt	3	3	human, invertebrates	08/02/1993	08/13/2018
Pixuna virus	NC_038673	complete	strain:Pixuna BeAr 35645	-	11344 nt	2	-	vertebrates	08/24/2018	08/24/2018

BLAST: Basic Local Alignment Search Tool

What if the identity of your sequence is unknown?

Matches a ***query sequence*** against any number of ***target*** sequences in a database (e.g. GenBank)

Simple, versatile, and fast

Used to

- identify species
- identify gene function
- locate domains in gene
- locate gene in genome
- expand datasets
- filter out noisy data
- perform meta-analysis

BLAST searches

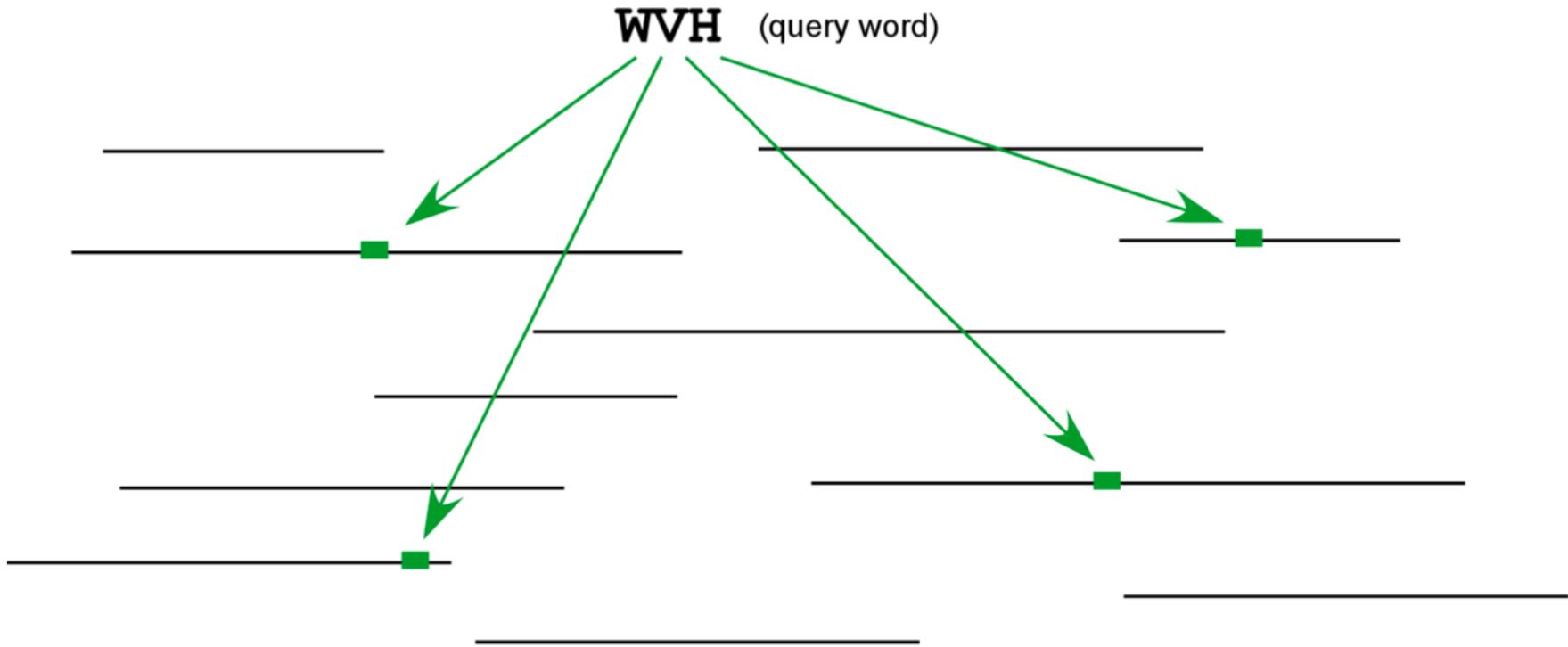
- For example, the search sequence word "WVH" might score above threshold with these indexed sequences:

Indexed word	Score
WVH	23
WIH	22
WVY	17
WIY	16

- Target sequences around each indexed word hit are retrieved and match is extended in both directions:

...VFEWVHLLP... your sequence
 ← WIY → database (many sites)

Schematic of indexed matches



Result - instead of aligning these 3 amino acids to everything, they are aligned only with the tiny fraction of sequence regions that are good candidates for a valid alignment.

Extension and scoring

	Match Score:	Total Score:
... QSVFEWVHLLPGA WIY ..	16	16
... QSVFEWVHLLPGA WIYQ ..	-3	13
... QSVFEWVHLLPGA WIYQK ..	-2	11
... QSVFEWVHLLPGA WIYQKA ..	-1	10

NCBI BLAST interface

Input your
query sequence
as text



BLAST® » blastn suite

Standard Nucleotide BLAST

Enter Query Sequence

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

Query subrange

Or, upload file No file selected.

Job Title

Enter a descriptive title for your BLAST search

Align two or more sequences

New columns added to the Description Table
Click 'Select Columns' or 'Manage Columns'.

Choose Search Set

Database Standard databases (nr etc.) rRNA/ITS databases Genomic + transcript databases Betacoronavirus
Nucleotide collection (nr/nt)

Organism Optional Enter organism name or id—completions will be suggested exclude

Exclude Optional Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown Models (XM/XP) Uncultured/environmental sample sequences

Limit to Optional Sequences from type material

Entrez Query Optional Enter an Entrez query to limit search

Program Selection

Optimize for Highly similar sequences (megablast) More dissimilar sequences (discontiguous megablast) Somewhat similar sequences (blastn)
Choose a BLAST algorithm

BLAST Show results in a new window

Perform BLAST
against
subject sequences



https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE_TYPE=BlastSearch
gene from Kerfeld and Scott (PLoS Biology 2011)

“BLAST hits”

Sequence name
e.g. species/gene ID

Download
sequences

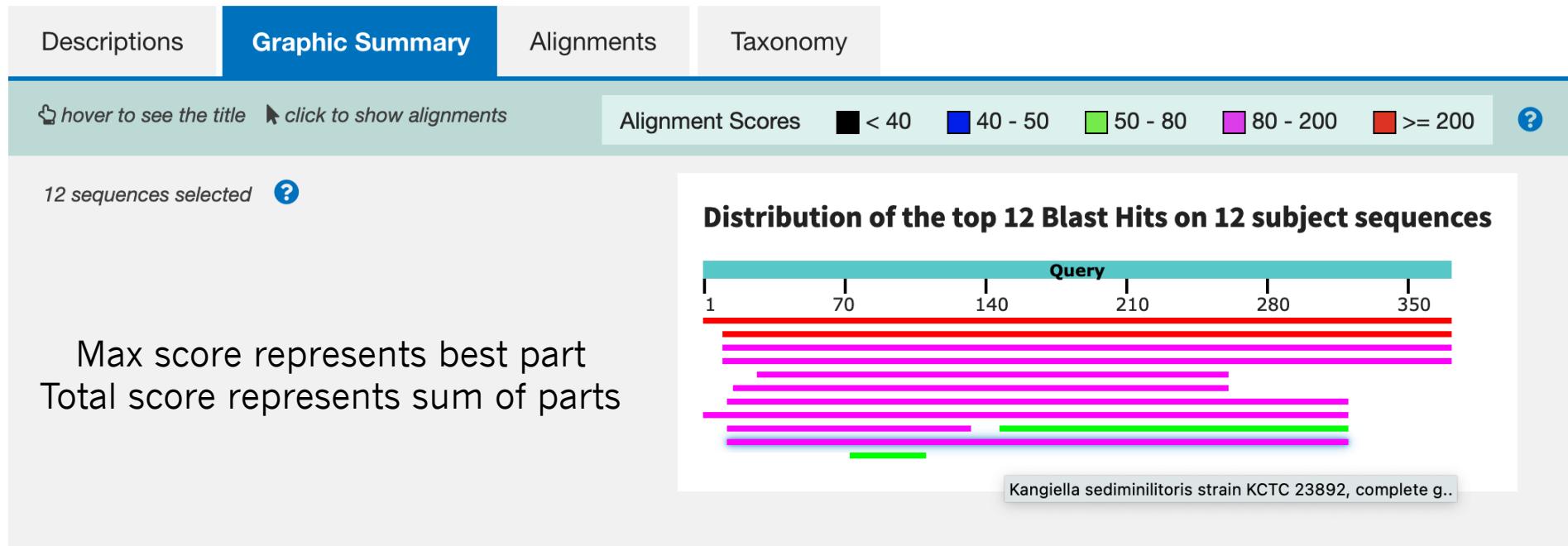
Expect value
lower = more significant

% identical
characters
in alignment

Descriptions		Graphic Summary	Alignments	Taxonomy	Sequences producing significant alignments								
		Download									New Select columns	Show 100	?
		GenBank Graphics Distance tree of results									New MSA Viewer		
		Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession			
<input checked="" type="checkbox"/>		Thiomicrospira crunogena XCL-2, complete genome	Hydrogenovibrio crunogen...	688	688	100%	0.0	100.00%	2427734	CP000109.2			
<input checked="" type="checkbox"/>		Hydrogenovibrio crunogenus strain SP-41 chromosome, complete genome	Hydrogenovibrio crunogen...	632	632	100%	6e-177	97.31%	2453259	CP032096.1			
<input checked="" type="checkbox"/>		Hydrogenovibrio thermophilus strain JR-2 chromosome, complete genome	Hydrogenovibrio thermophil...	427	427	100%	3e-115	87.40%	2612894	CP035033.1			
<input checked="" type="checkbox"/>		Thiomicrospira sp. S5 chromosome, complete genome	Thiomicrospira sp. S5	427	427	100%	3e-115	87.40%	2770466	CP014470.1			
<input checked="" type="checkbox"/>		Hydrogenovibrio marinus MH-110 DNA, complete genome	Hydrogenovibrio marinus	374	374	100%	4e-99	84.96%	2491293	AP020335.1			
<input checked="" type="checkbox"/>		Thiosulfatimonas sediminis aks77 DNA, complete genome	Thiosulfatimonas sediminis	272	272	97%	2e-68	80.49%	2722826	AP021889.1			
<input checked="" type="checkbox"/>		Thiomicrobacter aquaedulcis DNA, complete genome	Thiomicrobacter aquaedul...	250	250	97%	7e-62	79.45%	2440205	AP018722.1			
<input checked="" type="checkbox"/>		Shewanella dokdonensis strain DSM 23626 chromosome, complete genome	Shewanella dokdonensis	198	198	82%	3e-46	78.53%	4127406	CP074572.1			
<input checked="" type="checkbox"/>		Flocculibacter collagenilyticus strain SM1988 chromosome	Flocculibacter collagenilyticus	196	196	91%	9e-46	77.33%	3973578	CP059888.1			
<input checked="" type="checkbox"/>		Shewanella sp. FJAT-54481 chromosome, complete genome	Shewanella sp. FJAT-54481	187	187	87%	6e-43	77.20%	3812587	CP073587.1			
<input checked="" type="checkbox"/>		Amphritea japonica ATCC BAA-1530 DNA, complete genome	Amphritea japonica ATCC ...	174	174	83%	4e-39	77.29%	3833046	AP014545.1			
<input checked="" type="checkbox"/>		Legionella pneumophila subsp. fraseri strain F-4198 chromosome, complete genome	Legionella pneumophila su...	171	171	97%	6e-38	75.73%	3461540	CP021279.1			
<input checked="" type="checkbox"/>		Legionella pneumophila subsp. fraseri strain D-4058 chromosome, complete genome	Legionella pneumophila su...	171	171	97%	6e-38	75.73%	3548205	CP021277.1			
<input checked="" type="checkbox"/>		Legionella pneumophila subsp. franciscana strain D-5027 chromosome, complete genome	Legionella pneumophila su...	171	171	97%	6e-38	75.73%	3471650	CP021264.1			

BLAST alignment score
higher = better match

Graphic summary of BLAST scores



Scores determined by alignment costs
for match/mismatch/indel reconciliation
(covered in a later lab)

BLAST generates a summary for each subject sequence

Sulfurovum indicum strain ST-419 chromosome, complete genome

Sequence ID: [CP063164.1](#) Length: 2209694 Number of Matches: 1

Range 1: 2058656 to 2058979 [GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand	
102 bits(55)	2e-17	241/330(73%)	15/330(4%)	Plus/Minus	
Query 1		ATGGCAATTACAAAAGACGATATTTAGAAGCAGTTGCTAACATGTCAGTAATGGAAGTT		60	
Sbjct 2058979		ATGGCAACAACAAAAGAAGATGTATTAGAATTATTCTAACCTTCAGTACTTGAGCTT		2058920	
Query 61		GTTGAACCTGTTGAAGCAATGGAAGAGAAGTTGGTGTCTCA---GCAGCAGTTGCG		117	
Sbjct 2058919		TCTGAGCTTGTAAAAGAATTGAGAAAGAAAAATTGGTGTAACTGCACAAGCTACAGTAGTT		2058860	
Query 118		GTTGCAGGTCTGCAGGTGATGCTGGCGCTGCTGGTGAAGAACAAACAGAGTTGACGTT		177	
Sbjct 2058859		GCAGCTGGTGCTGCCGGTGGTGCCTGCTGAAGCTGCTGAAGAGCAGACAGATTCAACGTT		2058800	
Query 178		GT-CTTGACTGGTGCTGGTACAACAAAGT-TGCAGCAATCAAAGCCGTTGTGGCGCA-		234	
Sbjct 2058799		GTTCTT-ACAGACGCTGGTGCAGAAAGATCAACAA-CATAAAGTTGTAAGAGCAGTC		2058743	
Query 235		ACTGGTCTTGGGCTTAAAGAAGCGAAAAGTGAGTTGAAAGTG-CACCAT-TACGCTT		291	
Sbjct 2058742		ACAGGTCTGGACTTAAAGAAGCGAAAGCTGCTGTTG-AAGAGACTCCATCTTA-CTT		2058686	
Query 292		AAAGAGGGTGTCTAAAGAAGAAGCAGAA 321			
Sbjct 2058685		AAAGAGGGTGTCTAAAGAAGAAGCTGAA 2058656			

Query sequence position

Subject sequence position

Poor alignment
(gaps, mismatches = lower score)

Perfect alignment
(more matches = higher score)

arrays

an **array variable** contains multiple values
that are individually accessed by index

```
#!/bin/sh
# populate array
LETTERS[0]="A"
LETTERS[1]="B"
LETTERS[2]="C"
# INCORRECT: access array, show element 0
echo $LETTERS
# INCORRECT: access array, add "[1]" text
echo ${LETTERS[1]}
# CORRECT: access element 1
echo ${LETTERS[1]}
```

array1.sh

```
$ ./array1.sh
A
A[1]
B
```

running array1.sh

```
#!/bin/sh
# create array
NUMBERS=(1 2 3 4)
echo ${NUMBERS[2]} # 3
echo ${NUMBERS[9]} # empty (no entry)
# assign new array values
NUMBERS[2]="three"
NUMBERS[9]="ten"
echo ${NUMBERS[2]} # "three"
echo ${NUMBERS[9]} # "ten" (new entry)
```

array2.sh

```
$ ./array2.sh
3
three
ten
```

running array2.sh

more with arrays

```
#!/bin/sh
# arg1 is directory
DIR=$1
# make array with `ls` command subst.
FILES=( $(ls ${DIR}) )
# print individual array elements
echo "Individual elements"
echo "${FILES[0]}"
echo "${FILES[1]}"
# print entire array
echo "Entire array"
echo "${FILES[@]}
```

array3.sh

```
$ ls tmp
file1.txt file2.txt file3.txt
$ ./array3.sh tmp
Individual elements
file1.txt
file2.txt
Entire array
file1.txt file2.txt file3.txt
```

running array3.sh

```
#!/bin/sh
# all args are stored in $@ array
for i in "$@"; do
  if [[ -f ${i} ]]; then
    echo "Copying ${i} to ${i}.bak"
    cp ${i} ${i}.bak
  fi
done
```

```
$ ls tmp
file1.txt file2.txt file3.txt
$ ./array4.sh tmp/*.txt
Copying tmp/file1.txt to tmp/file1.txt.bak
Copying tmp/file2.txt to tmp/file2.txt.bak
Copying tmp/file3.txt to tmp/file3.txt.bak
$ ls tmp
file1.txt  file1.txt.bak  file2.txt
file2.txt.bak  file3.txt  file3.txt.bak
```

running array4.sh

for-loops with files

two approaches to loop over lines in a file;
set the ***input field separator*** (IFS) to split by line

```
#!/bin/bash
FILE=$1          # arg1: input file
SAVE_IFS=${IFS}    # restore IFS when done
IFS=$'\n'        # set '\n' for IFS
LINES=$(cat ${FILE}) # extract text from FILE
for LINE in ${LINES} # for each line (split by IFS)
do
    echo ${LINE}      # print LINE to stdout
done
IFS=${SAVE_IFS}      # done! restore IFS
```

forloop1.sh is simpler, but less portable

```
$ ./forloop1.sh file.txt
Knock, knock!
Who's there?
```

running *forloop1.sh*

```
#!/bin/bash
FILE=$1          # arg1: input file
# while : loop until stop condition (EOF)
# IFS= : IFS set to null ('\n')
# read : split input by IFS + advance file position
# -r : do not treat '\' as special char
# LINE : store each token in LINE
while IFS= read -r LINE
do
    echo ${LINE}      # begin code block
done < ${FILE}      # input redirect to while/done
```

forloop2.sh is more complex, but more portable

```
$ ./forloop2.sh file.txt
Knock, knock!
Who's there?
```

running *forloop2.sh*

xargs

xargs (extended arguments) converts input into arguments for another command

```
$ # find all .txt files
$ find data -name "*.txt"
data/file1.txt
data/docs/file2.txt
data/secrets/password.txt
$ # word count of `find` output
$ find data -name "*.txt" | wc
    3 3 61
$ # word count against each found file
$ find data -name "*.txt" | xargs wc
0 0 0 data/file1.txt
0 0 0 data/docs/file2.txt
0 0 0 data/secrets/password.txt
0 0 0 total
```

```
$ # argument file
$ cat files.txt
example/file1.txt
example/file2.txt
example/file3.txt
$ # target files to remove
$ ls example/
file1.txt file2.txt file3.txt
$ # use argument file lines for rm
$ xargs -a files.txt rm
$ # files deleted
$ ls example/
```

```
$ ls
a.txt b.txt
$ echo "a.txt a.txt.tmp b.txt b.txt.tmp" | xargs cp
cp: target 'b.txt.tmp' is not a directory
$ echo "a.txt a.txt.tmp b.txt b.txt.tmp" | xargs -n2
a.txt a.txt.tmp
b.txt b.txt.tmp
$ echo "a.txt a.txt.tmp b.txt b.txt.tmp" | xargs -n2 cp
$ ls
a.txt a.txt.tmp b.txt b.txt.tmp
```

Overview for Lab 07