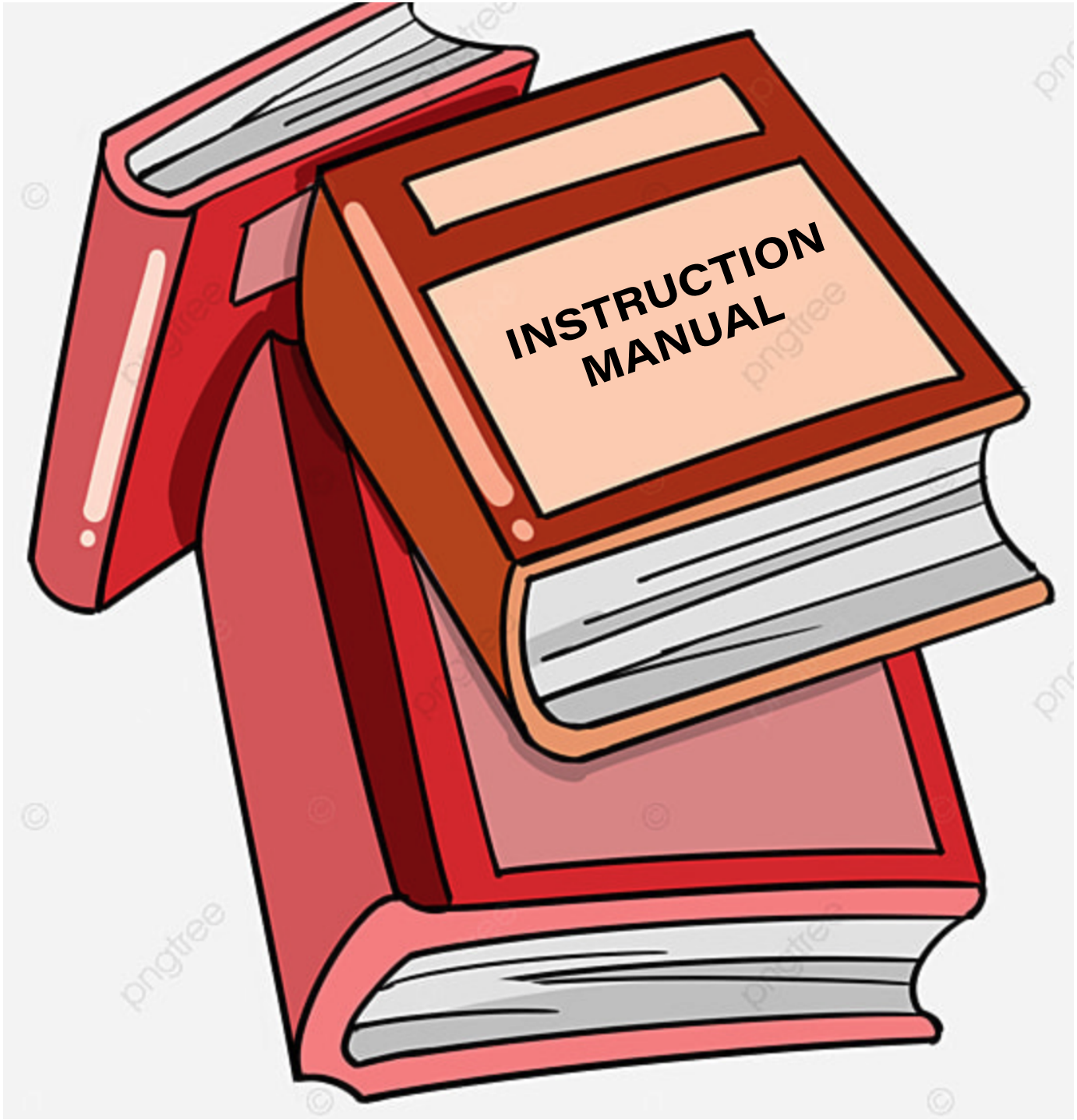
Eric Nawrocki

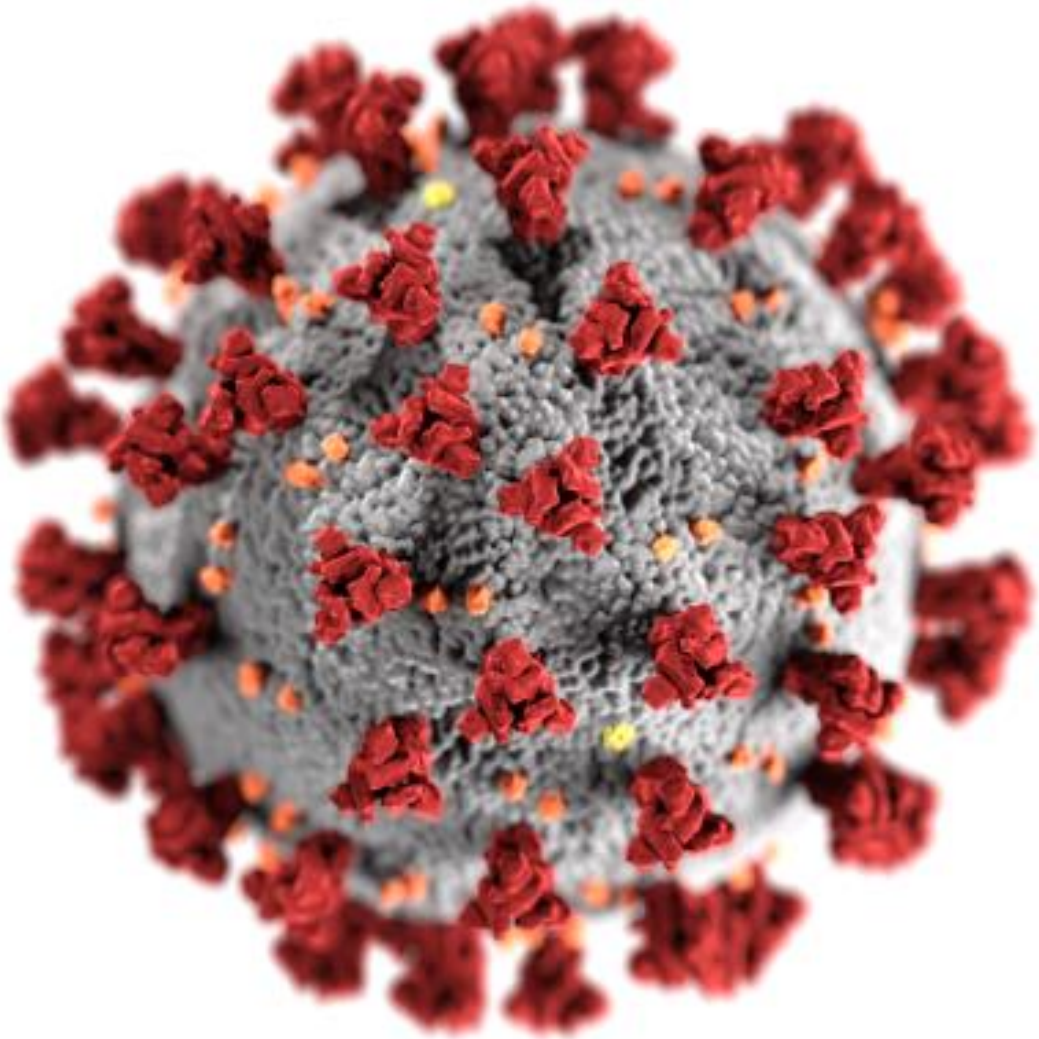
Scientist - National Library of Medicine

Career day advice from my daughter:

"Bring candy"

Library: scientific books and journals


INSTRUCTION
MANUAL



DEC. 25, 2023

PERSON OF THE YEAR | TAYLOR SWIFT

INSTRUCTIONS
classroomclipart.com

What language stores the information of life?

What is the alphabet of DNA?

- A, C, G, and T are the four bases (nucleotides) of DNA

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- DNA is made up of two linked strands in a twisted ladder shape

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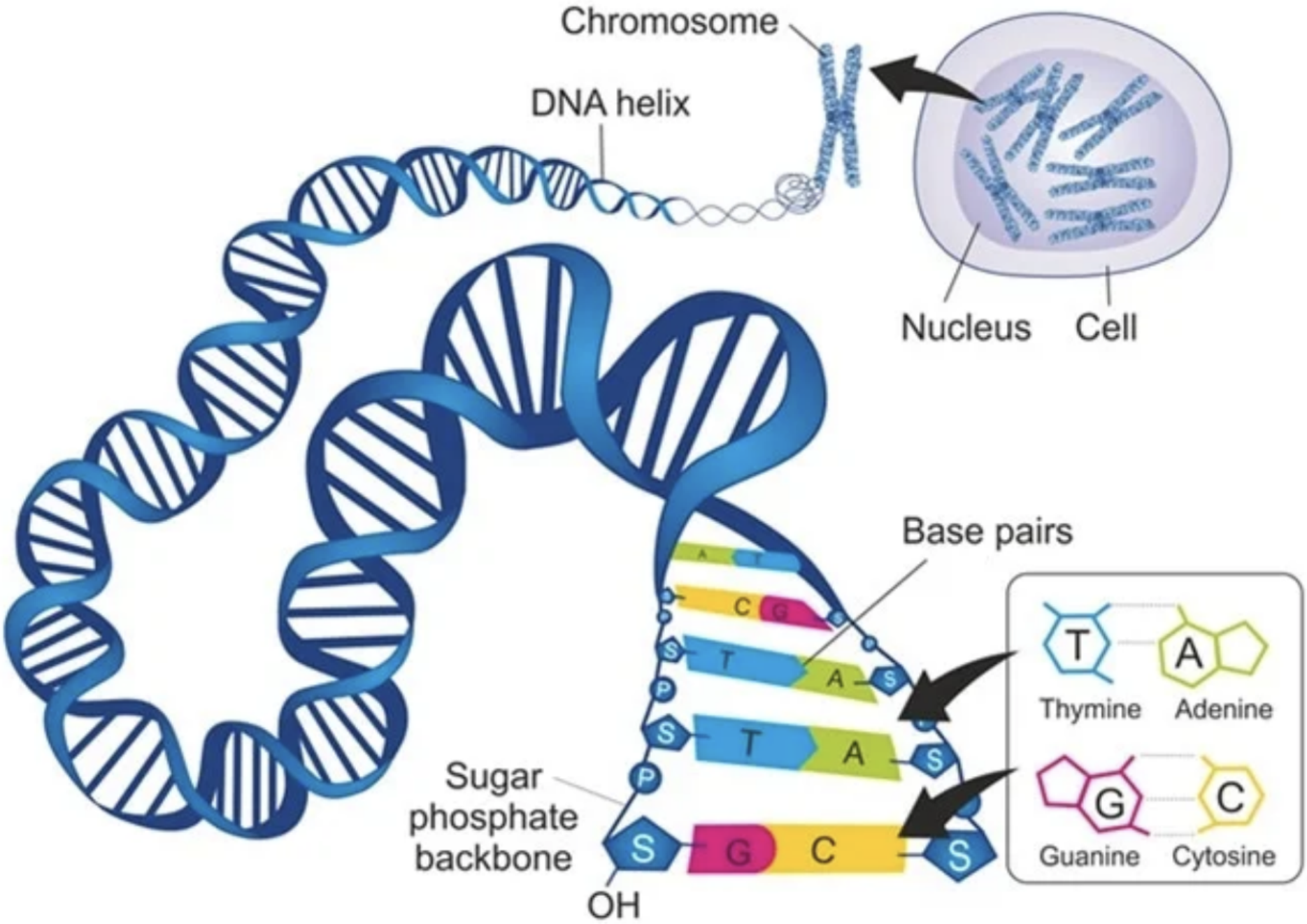
- A, C, G, and T are the four bases (nucleotides) of DNA
- DNA is made up of two linked strands in a twisted ladder shape
- One base on each strand pairs with a base on the other strand
- Which bases form pairs?


Chromosome
DNA helix
Nucleus
Cell
Base pairs
Sugar
phosphate
backbone
OH
T
A
Thymine
Adenine
G
C
Guanine
Cytosine

A C G T

GTAACCGTAAATAATAAACTTTTGAAGTCTAAGCTCATCATATCTATTCA
TCCTTTGGATTCAAGACATTTTTTAAAAAATGCGCAATCACTATAAACCA
TATCGATTAATGCGAATAACTATATTTCTAGAACCTAGAAAAATCATTCC
CACATCTTGAGAAAAACTTCCCCTAAATTGCTAGCGTGCATCTAACACGT
GACTTCTTTAATCTAACTTGGTAAAGTGCTGGTCTTTGCGTCCTCGTAGC
TCAGCAGGATAGAGCGGTTGCCTCCTAAGCAGCAGGCCATGCGTTCGAAT
CGCATCGAGGACGATTTTTTGCCTTTAACTCCTAAAGTACTAATTTGCTT
GTATCTGTGGTTTACGTATTTTAGCGATATTCTGTTTTGGTTTCTGAAAA
CTAGGTCCAGAAAGAAAATTATGAACTCCCTCGGCGATGCCTTTCGCTAC
ATGCATACGATAGCGAGCATCTTGCAGGGCCGCACGTTCACGACTATTGG
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ACAACAAAGTTCGCAGTTTTCAAACCTCGAGACTTCAAAATGCCATTTTT
TTCCATAGCAGCTAAAATGTTTTTTCCCAGTACTTCTGACATGCGATTCC
TAGTCGGAGATCCGACCTTACCATTATAAAAATATACTTCGGTGCCAAAG
GCTGCTGCGTTTGAAGAATGATTACAGTGGATGCTGATAAAGACATCCCC
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CAGAAGATCGGGTTAGCTGAGGTTTATAACCCATCCGCTTTAAGTAACTT
TGAACCGTCAAAGCAAGAGACAGGGTCAGGGACTTCTCTTCATAATGAAG
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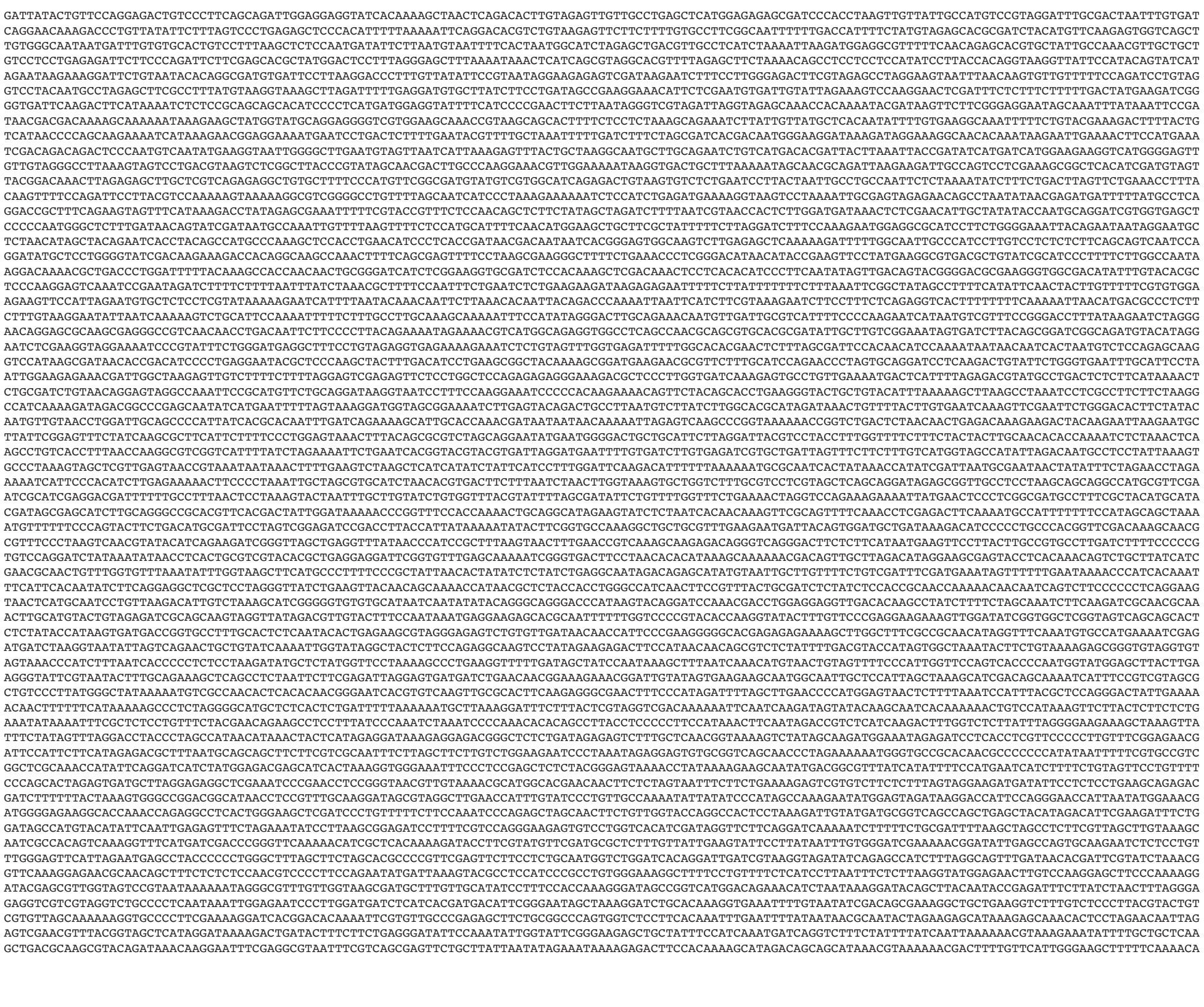
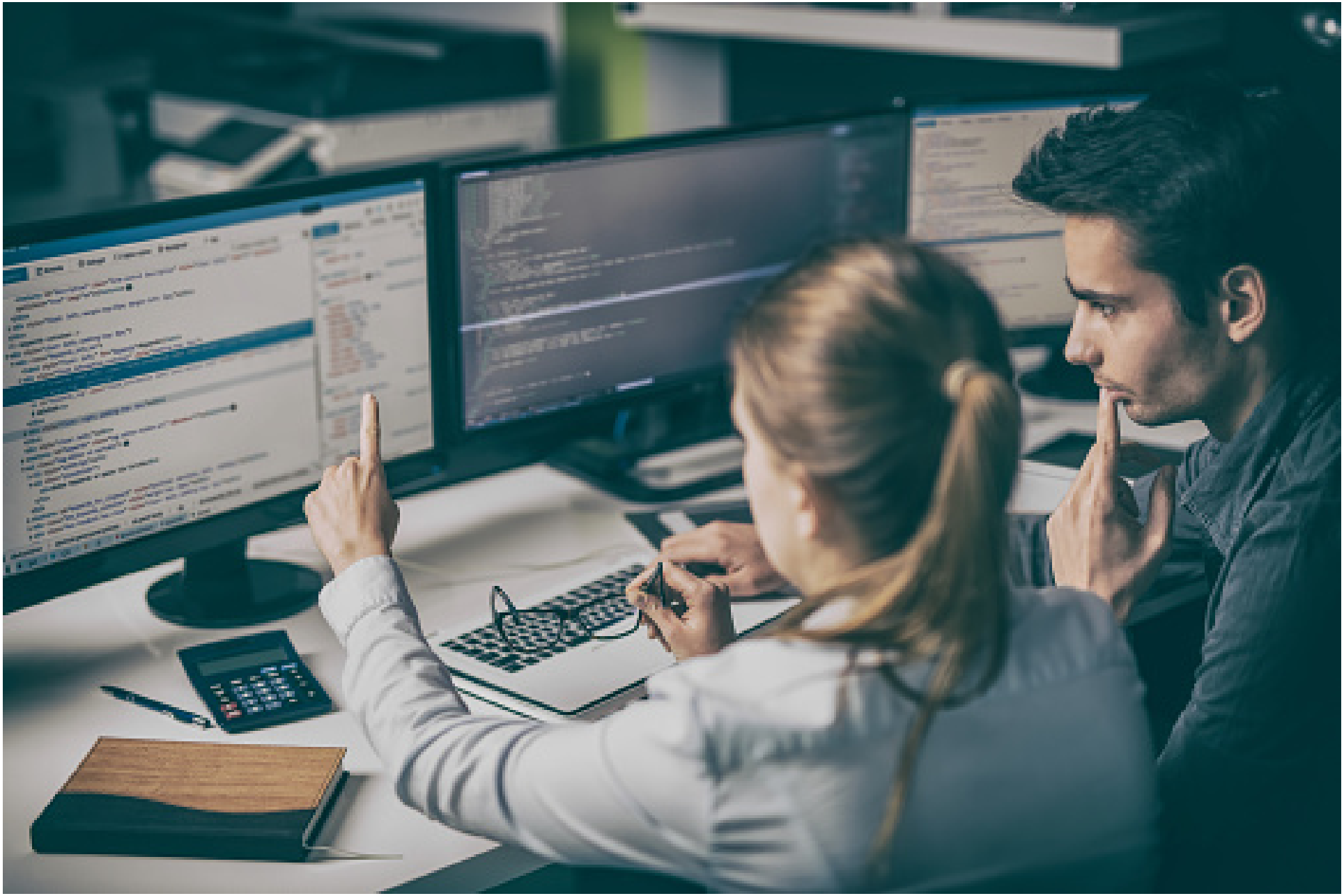




the field of bioinformatics

Dictionary

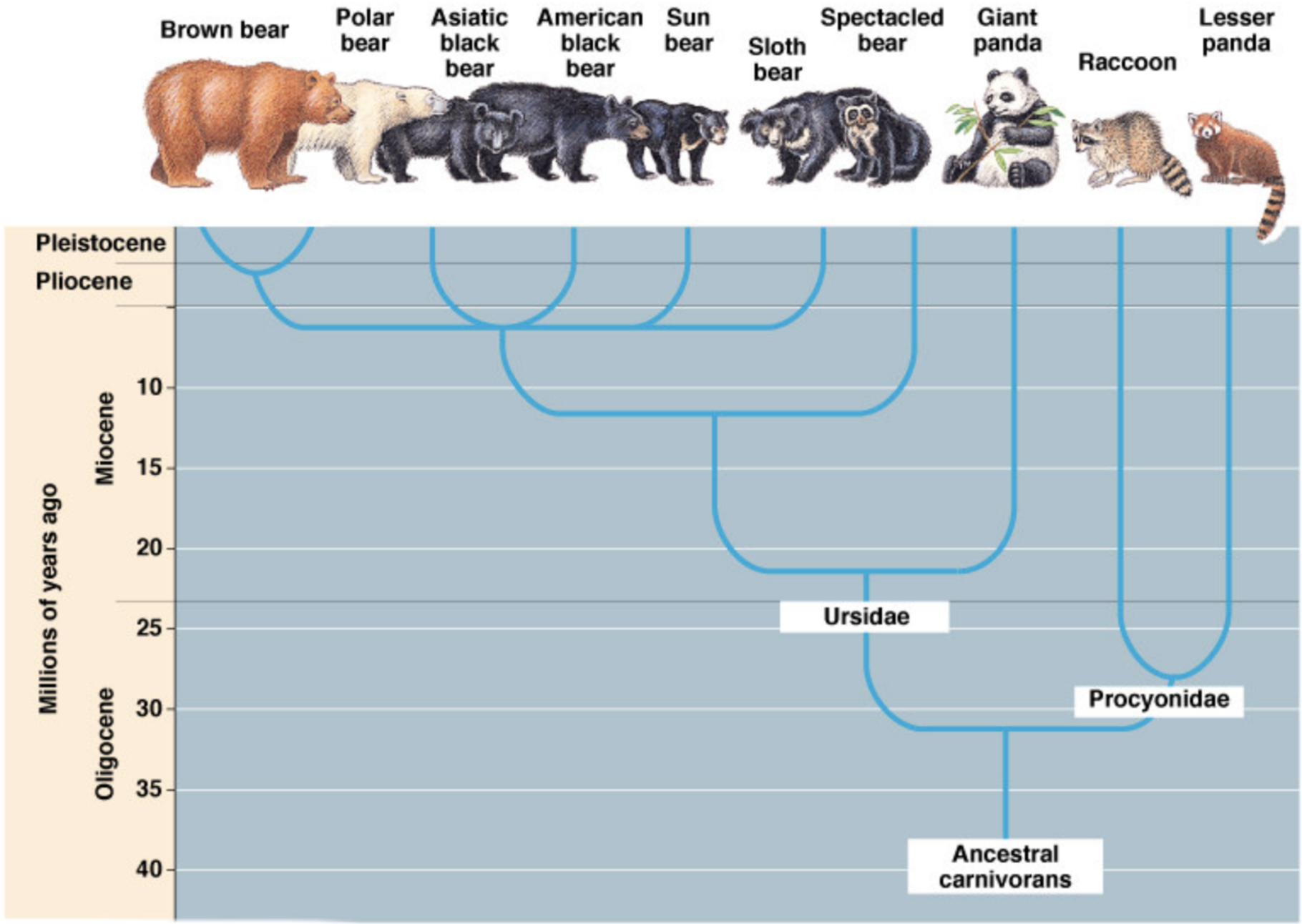
Definitions from Oxford Languages · Learn more

bi·o·in·for·mat·ics

/ˌbīōˌinfərˈmadiks/

noun

the science of collecting and analyzing complex biological data such as genetic codes.


Brown bear
Polar bear
Asiatic black bear
American black bear
Sun bear
Sloth bear
Spectacled bear
Giant panda
Raccoon
Lesser panda
Pleistocene
Pliocene
Miocene
Oligocene
Millions of years ago
10
15
20
25
30
35
40
Ursidae
Procyonidae
Ancestral carnivorans

GTAACCGTAAATAATAAACTTTTGAAGTCTAAGCTCATCATATCTATTCA
TCCTTTGGATTCAAGACATTTTTTAAAAAATGCGCAATCACTATAAACCA
TATCGATTAATGCGAATAACTATATTTCTAGAACCTAGAAAAATCATTCC
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TAGTCGGAGATCCGACCTTACCATTATAAAAATATACTTCGGTGCCAAAG
GCTGCTGCGTTTGAAGAATGATTACAGTGGATGCTGATAAAGACATCCCC
CTGCCCACGGTTCGACAAAGCAACGCGTTTCCCTAAGTCAACGTATACAT
CAGAAGATCGGGTTAGCTGAGGTTTATAACCCATCCGCTTTAAGTAACTT
TGAACCGTCAAAGCAAGAGACAGGGTCAGGGACTTCTCTTCATAATGAAG
TTCCTTACTTGCCGTGCCTTGATCTTTTCCCCCGTGTCCAGGATCTATAA
ATATAACCTCACTGCGTCGTACACGCTGAGGAGGATTCGGTGTTTGAGCA


GTAACCGTAAATAATAAACTTTTGAAGTCTAAGCTCATCATATCTATTCA
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ATGCATACGATAGCGAGCATCTTGCAGGGCCGCACGTTCACGACTATTGG
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ACAACAAAG
TTCCATAGC
TAGTCGGAG
GCCATTTTT
TGCGATTCC
GTGCCAAAG
genes are important
subsequences of genomes
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CTGCCCACGGTTCGACAAAGCAACGCGTTTCCCTAAGTCAACGTATACAT
CAGAAGATCGGGTTAGCTGAGGTTTATAACCCATCCGCTTTAAGTAACTT
TGAACCGTCAAAGCAAGAGACAGGGTCAGGGACTTCTCTTCATAATGAAG
TTCCTTACTTGCCGTGCCTTGATCTTTTCCCCCGTGTCCAGGATCTATAA
ATATAACCTCACTGCGTCGTACACGCTGAGGAGGATTCGGTGTTTGAGCA

human GCTTTCGCTGC

```
jellyfish GGCTTCGGCCC
fly       GCCTTCGTAGC
cow       GCATTCGTTGC
mouse     GCTTTCGCTTC
human     GCTTTCGCTGC
chicken   GTATTCGTTAC
snake     GTGTTCGCGAC
croc      GTTTTCGAGAC
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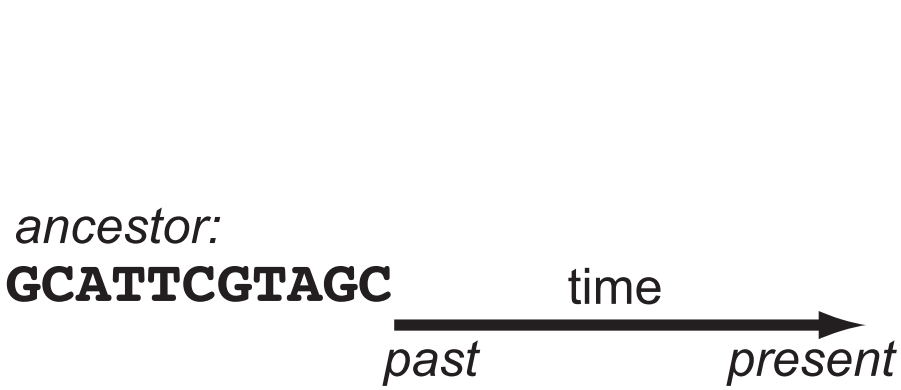
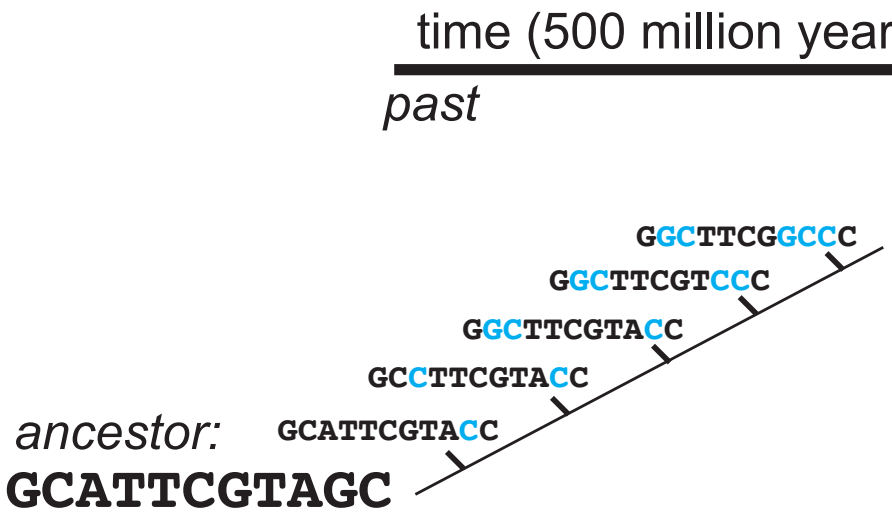
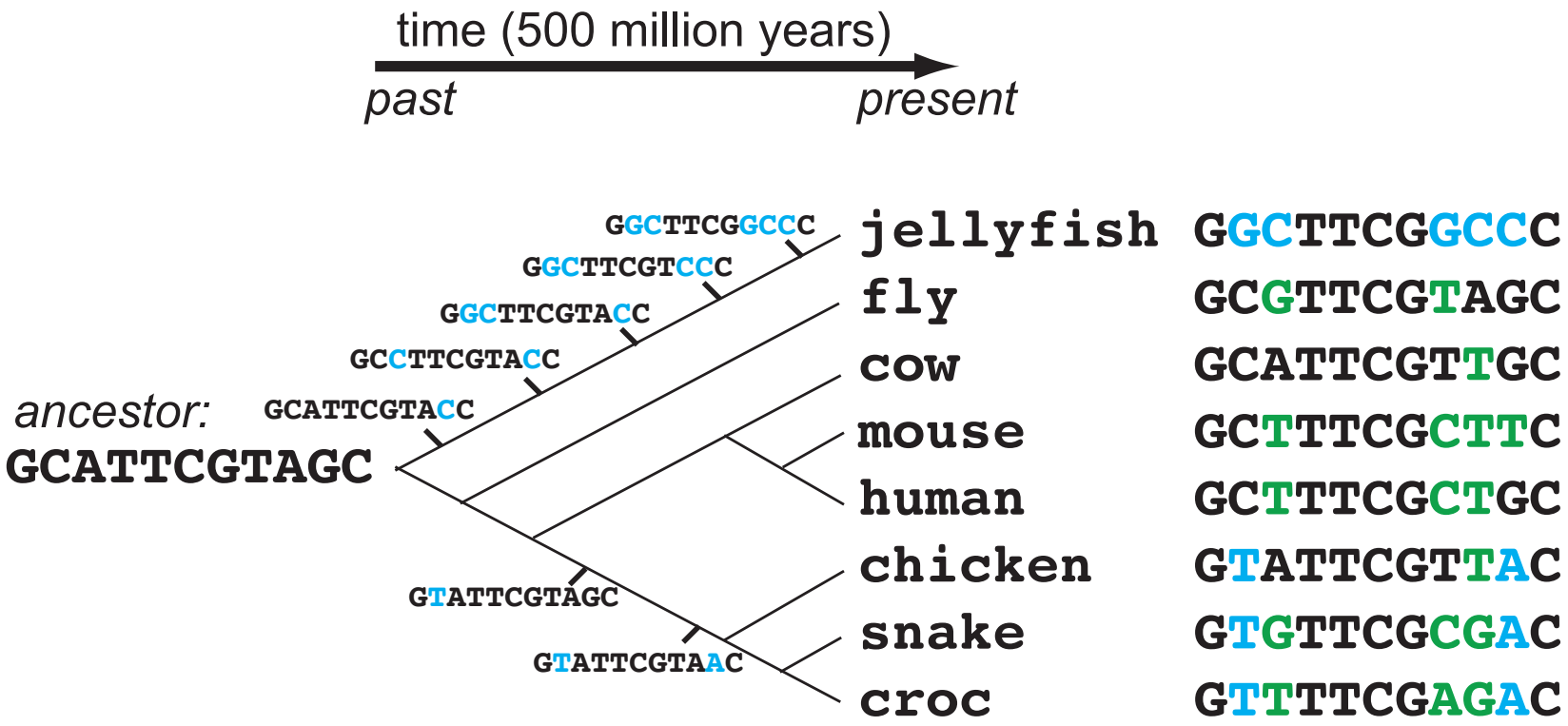



```
jellyfish GGCTTCGGCCC
fly       GCCTTCGTAGC
cow       GCATTCGTTGC
mouse     GCTTTCGCTTC
human     GCTTTCGCTGC
chicken   GTATTCGTTAC
snake     GTGTTCGCGAC
croc      GTTTTCGAGAC
```



jellyfish	GGCTTCGGCCC
fly	GCGTTCGTAGC
cow	GCATTCGTTGC
mouse	GCTTTCGCTTC
human	GCTTTCGCTGC
chicken	GTATTCGTTAC
snake	GTGTTCGCGAC
croc	GTTTTCGAGAC


time (500 million years)
past
present
ancestor:
GCATTCGTAGC
GGCTTCGGCCC
GGCTTCGTCCC
GGCTTCGTACC
GCCTTCGTACC
GCATTCGTACC
GTATTCGTAGC
GTATTCGTAAC
jellyfish GGCTTCGGCCC
fly GCGTTCGTAGC
cow GCATTCGTTGC
mouse GCTTTCGCTTC
human GCTTTCGCTGC
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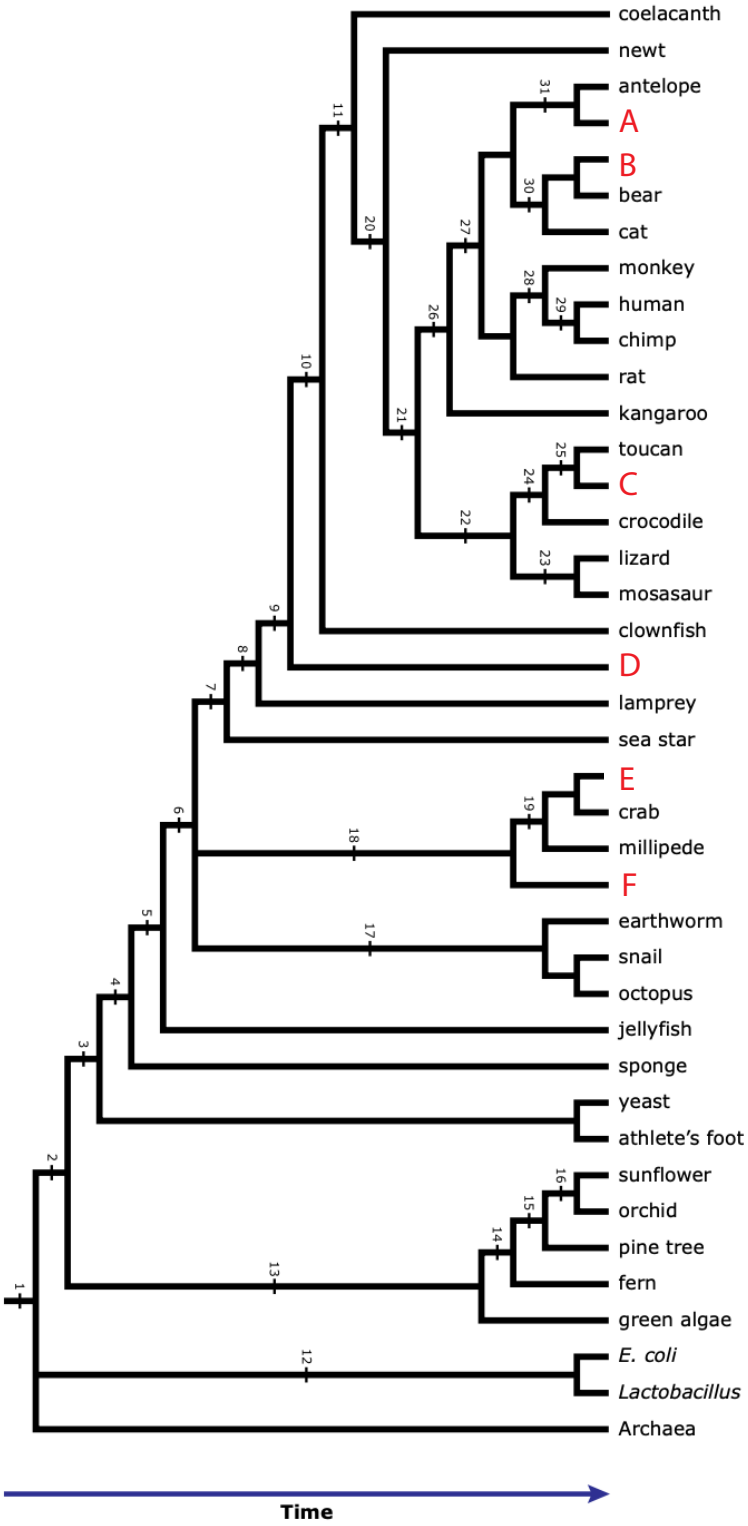
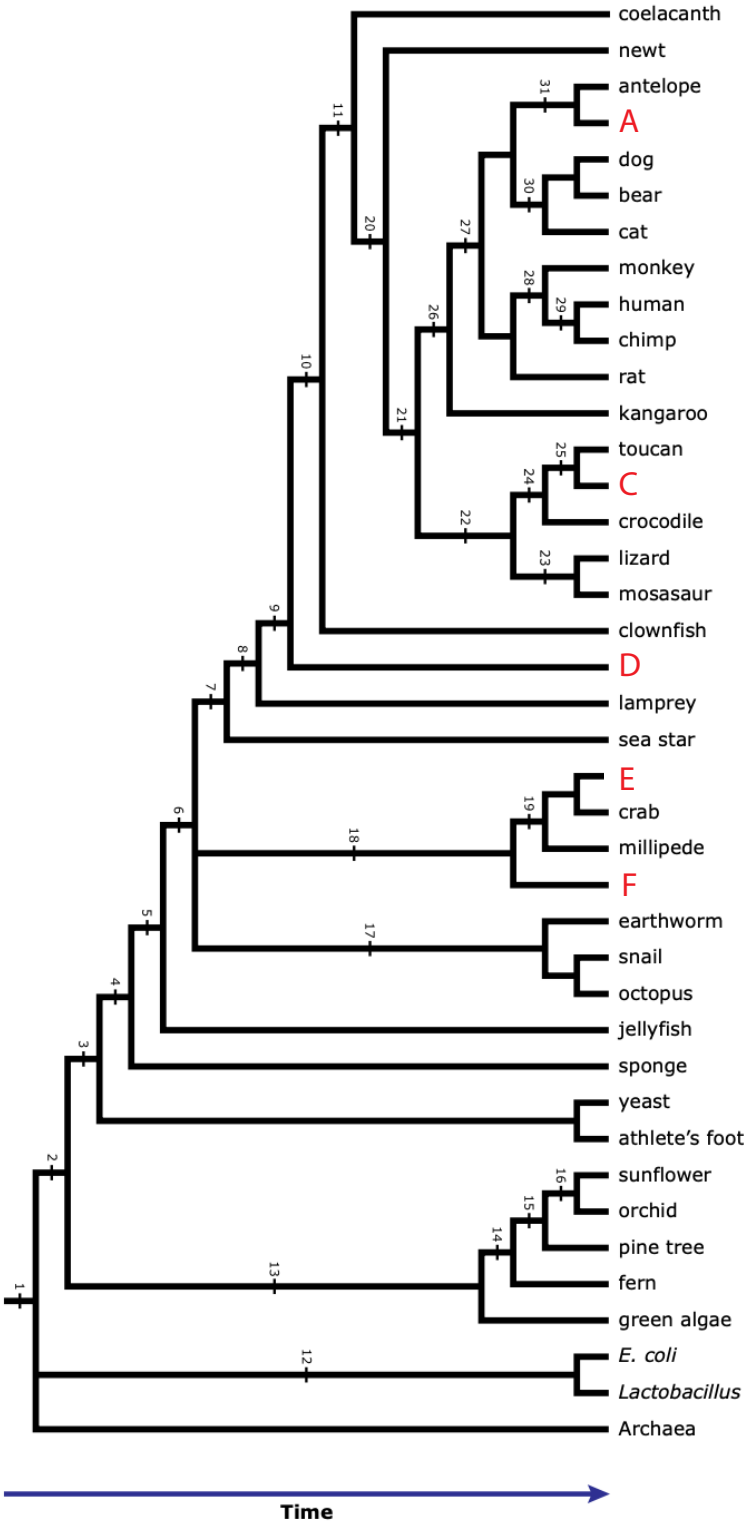
snake GTGTTCGCGAC
croc GTTTTCGAGAC



Where do the following organisms fit in the tree?

- dog?
- spider?
- T. rex?
- butterfly?
- whale?
- shark?



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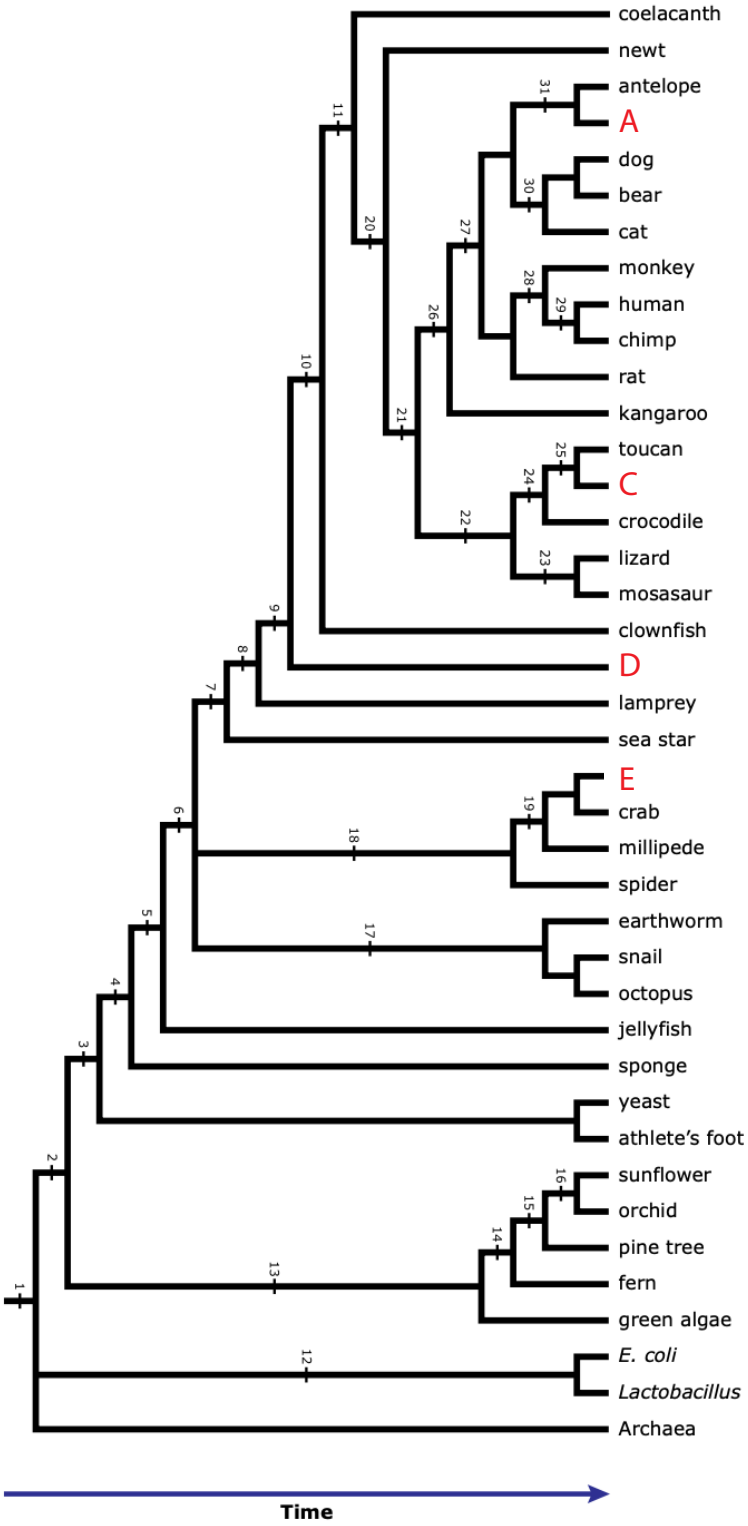

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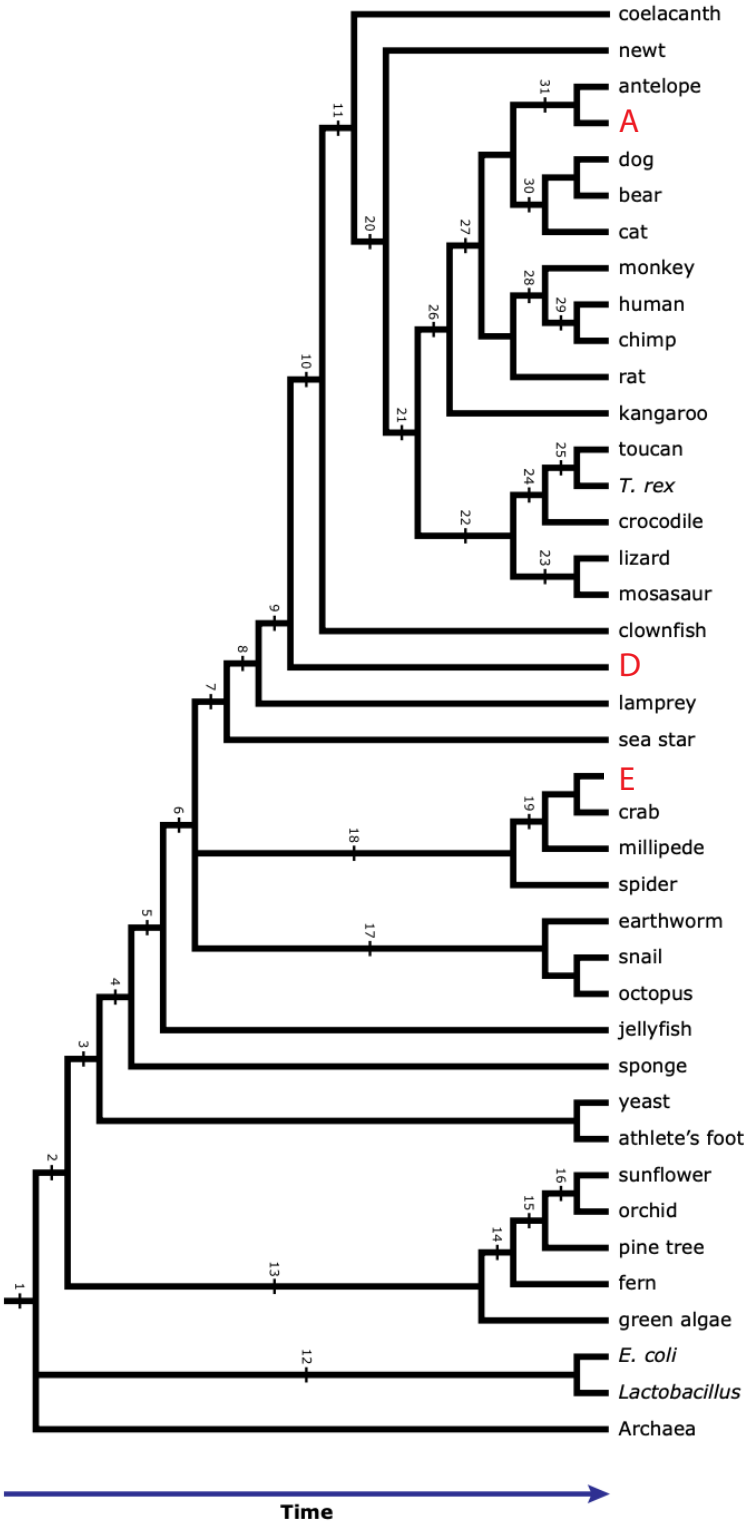

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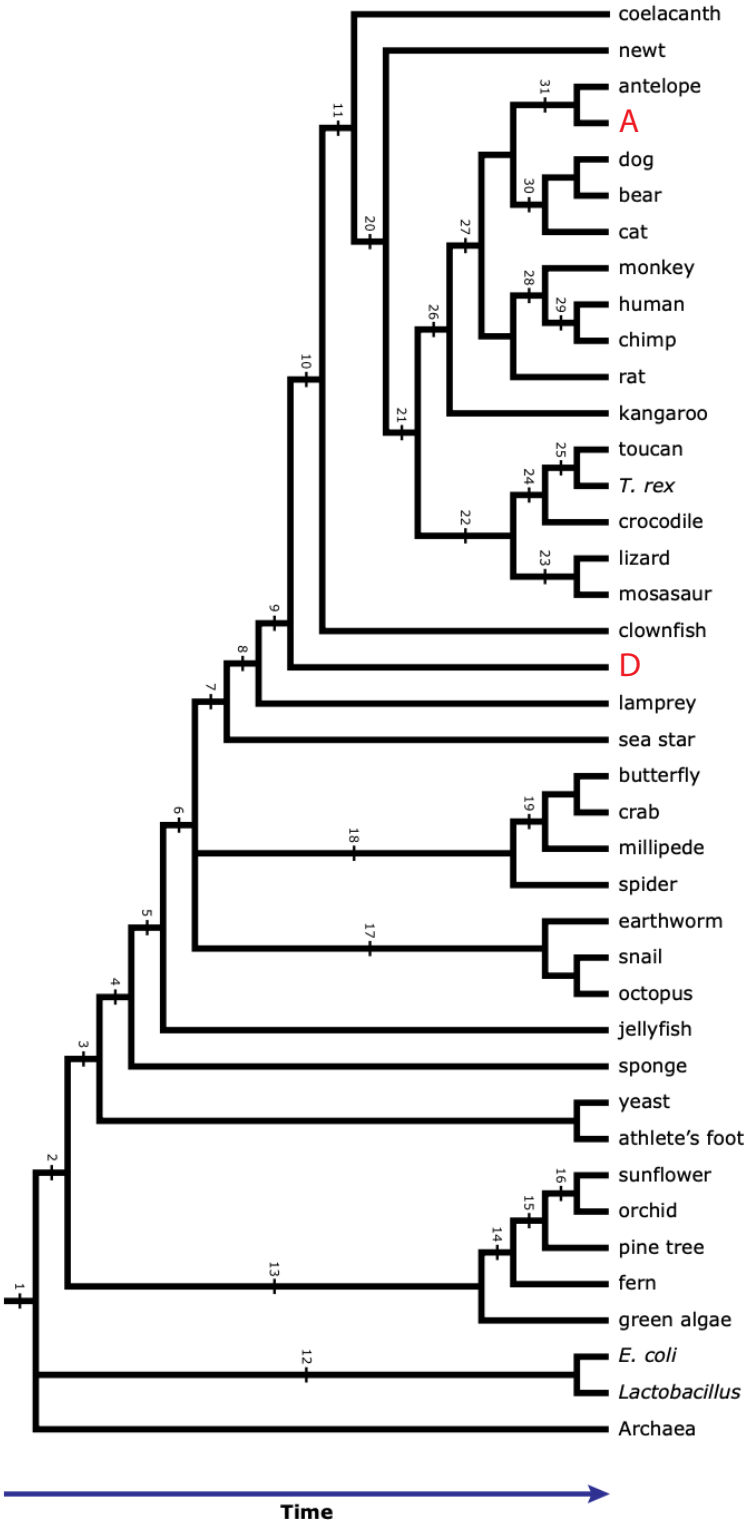

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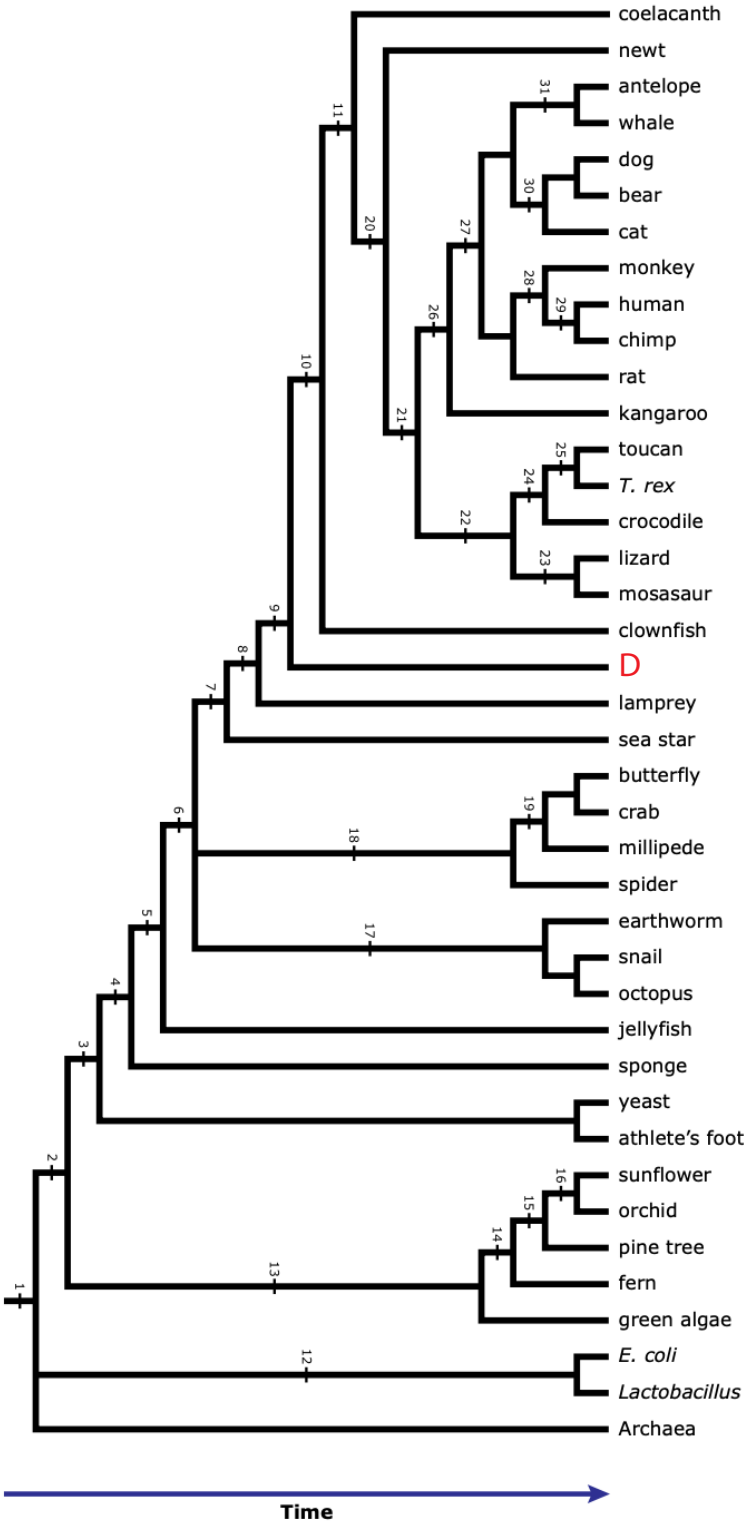

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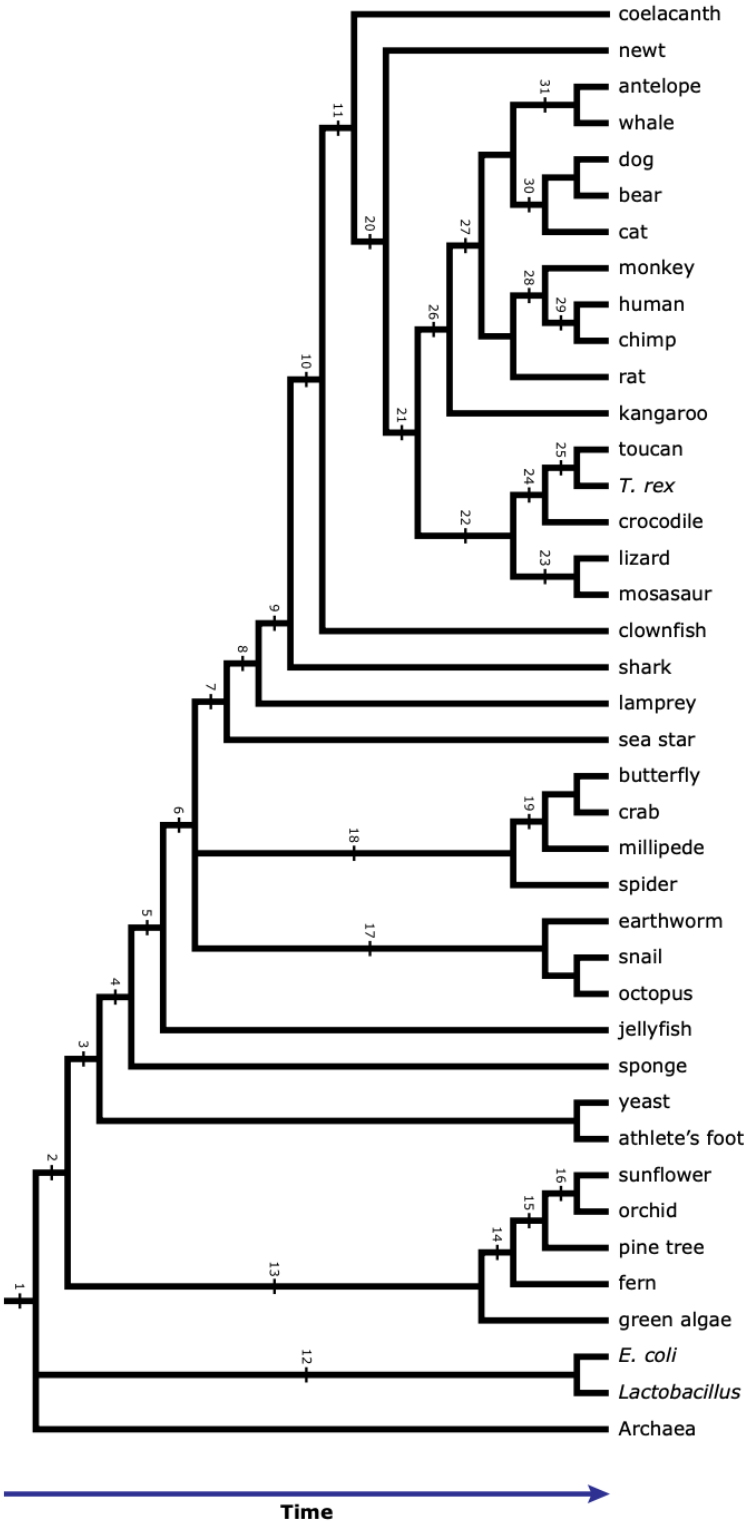

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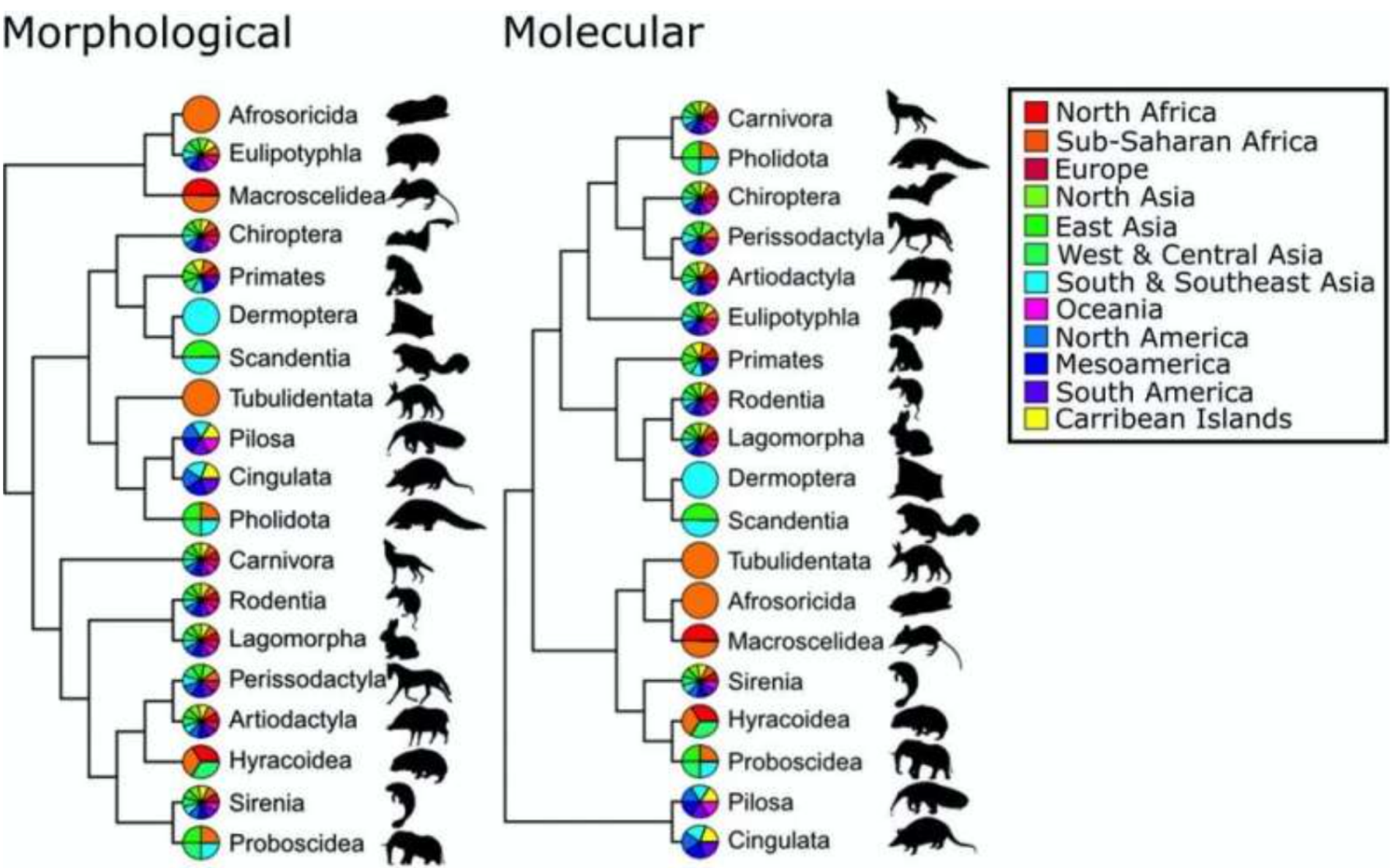
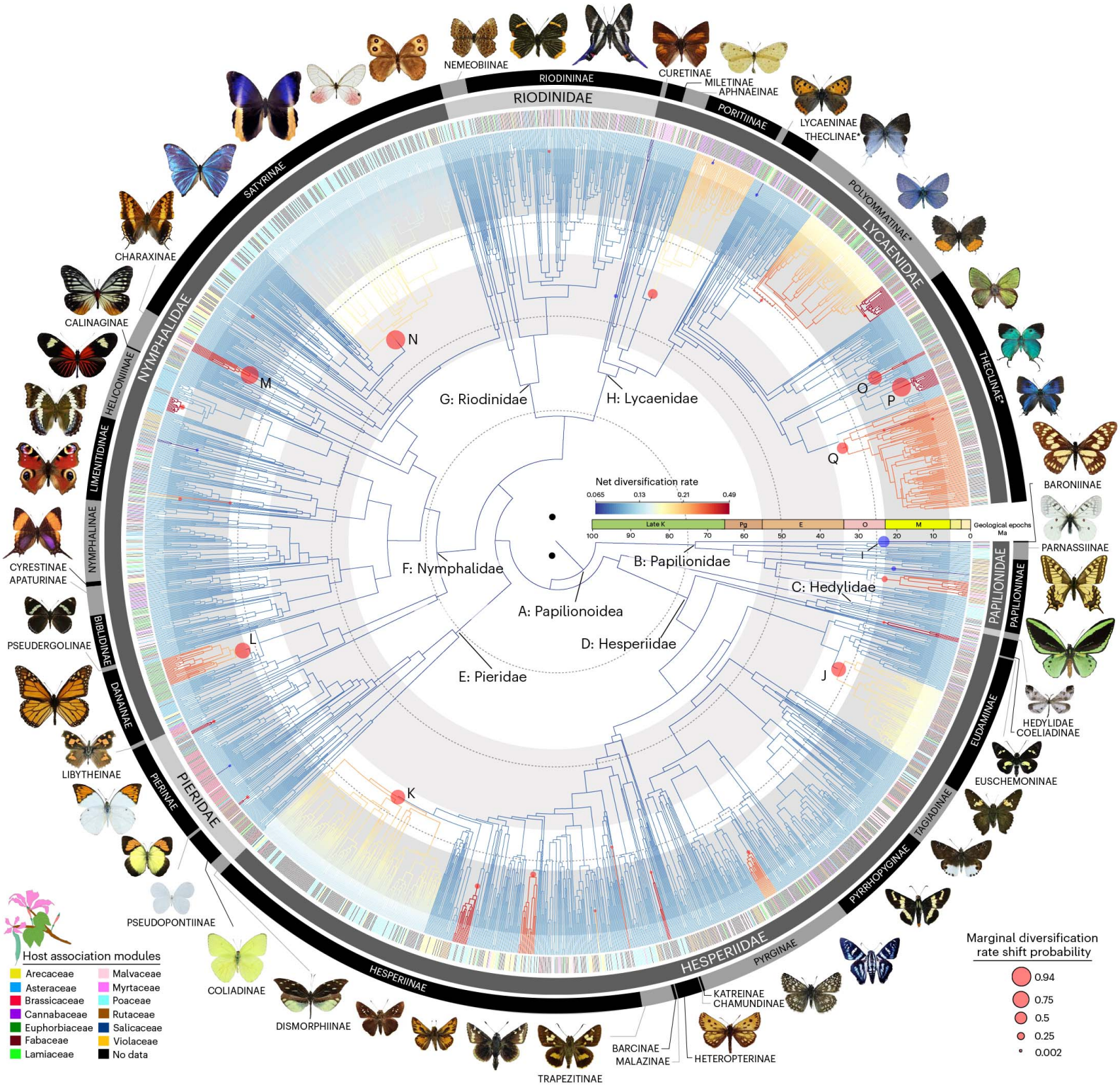
Evolutionary tree of life: modern science is showing how we got so much wrong

by Matthew Wills, The Conversation

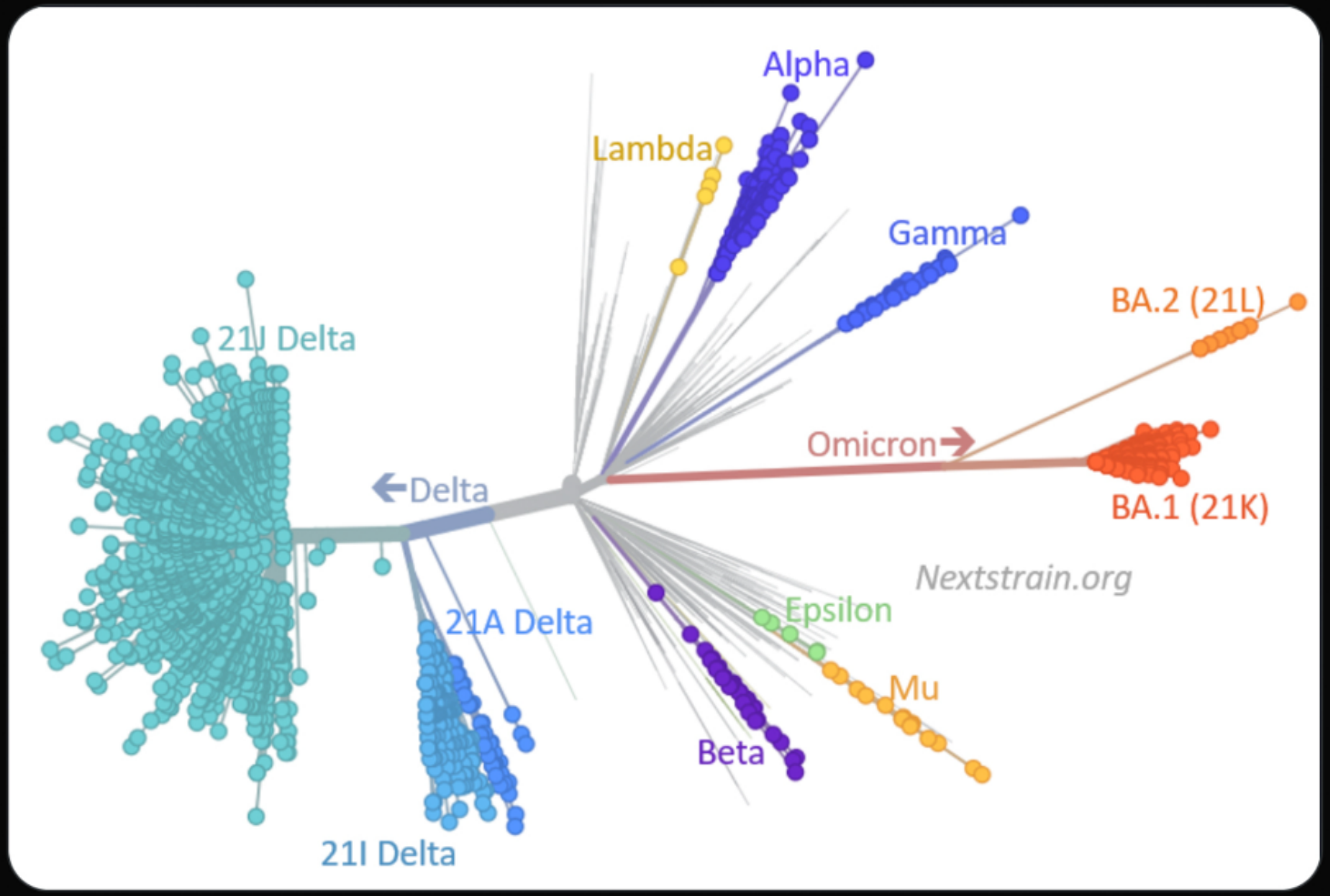



NEMEOBIINAE
RIODININAE
RIODINIDAE
CURETINAE
MILETINAE
APHNAEINAE
PORITIINAE
LYCAENINAE
THECLINAE*
POLYOMMATINAE*
LYCAENIDAE
THECLINAE*
BARONIINAE
PARNASSIINAE
PAPILIONIDAE
PAPILIONINAE
HEDYLIDAE
COELIADINAE
EUDAMINAE
EUSCHEMONINAE
TAGIADINAE
PYRRHOPYGINAE
HESPERIIDAE
PYRGINAE
KATREINAE
CHAMUNDINAE
HETEROPTERINAE
BARCINAE
MALAZINAE
TRAPEZITINAE
HESPERIINAE
DISMORPHIINAE
COLIADINAE
PSEUDOPONTIINAE
PIERIDAE
PIERINAE
DANAINAE
LIBYTHEINAE
BIBLIDINAE
PSEUDERGOLINAE
NYMPHALINAE
CYRESTINAE
APATURINAE
LIMENITIDINAE
HELICONIINAE
NYMPHALIDAE
CALINAGINAE
CHARAXINAE
SATYRINAE
Net diversification rate
0.065
0.13
0.21
0.49
Late K
Pg
E
O
M
Geological epochs
Ma
100
90
80
70
60
50
40
30
20
10
0
G: Riodinidae
H: Lycaenidae
F: Nymphalidae
B: Papilionidae
A: Papilionoidea
C: Hedylidae
D: Hesperiidae
E: Pieridae
N
M
O
P
Q
L
J
K
Host association modules
Arecaceae
Asteraceae
Brassicaceae
Cannabaceae
Euphorbiaceae
Fabaceae
Lamiaceae
Malvaceae
Myrtaceae
Poaceae
Rutaceae
Salicaceae
Violaceae
No data
Marginal diversification rate shift probability
0.94
0.75
0.5
0.25
0.002

Dr Emma Hodcroft @firefoxx66 · Jan 27

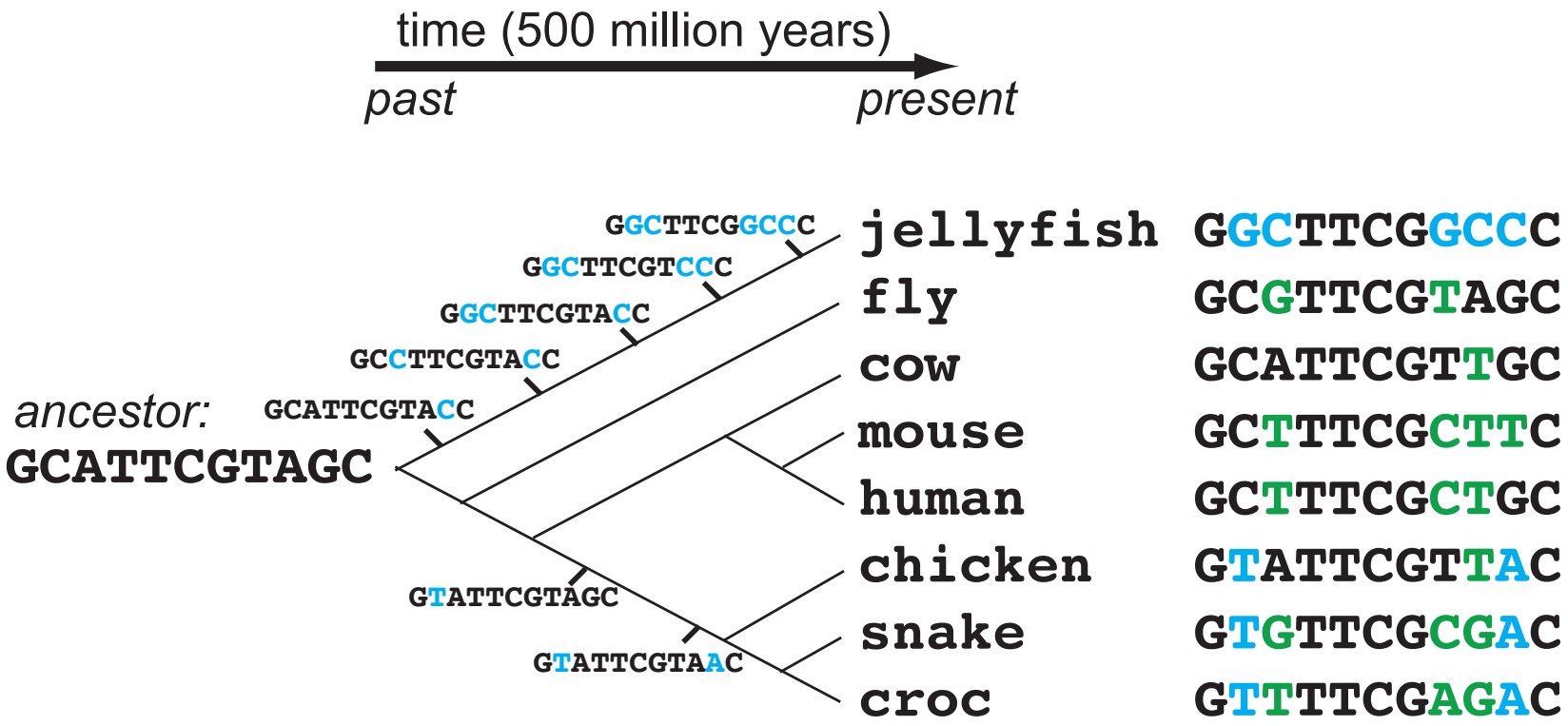
This filtered @Nextstrain build gives a nice visual display of how distant the Omicron family is from everything else, & how different BA.1 (21K) & BA.2 (21L) are from each other. Distance is in mutations.

nextstrain.org/ncov/gisaid/gl...



59 1.4K 3K

1,999 × 1,763


time (500 million years)
past
present
ancestor:
GCATTCGTAGC
GGCTTCGGCCC
GGCTTCGTCCC
GGCTTCGTACC
GCCTTCGTACC
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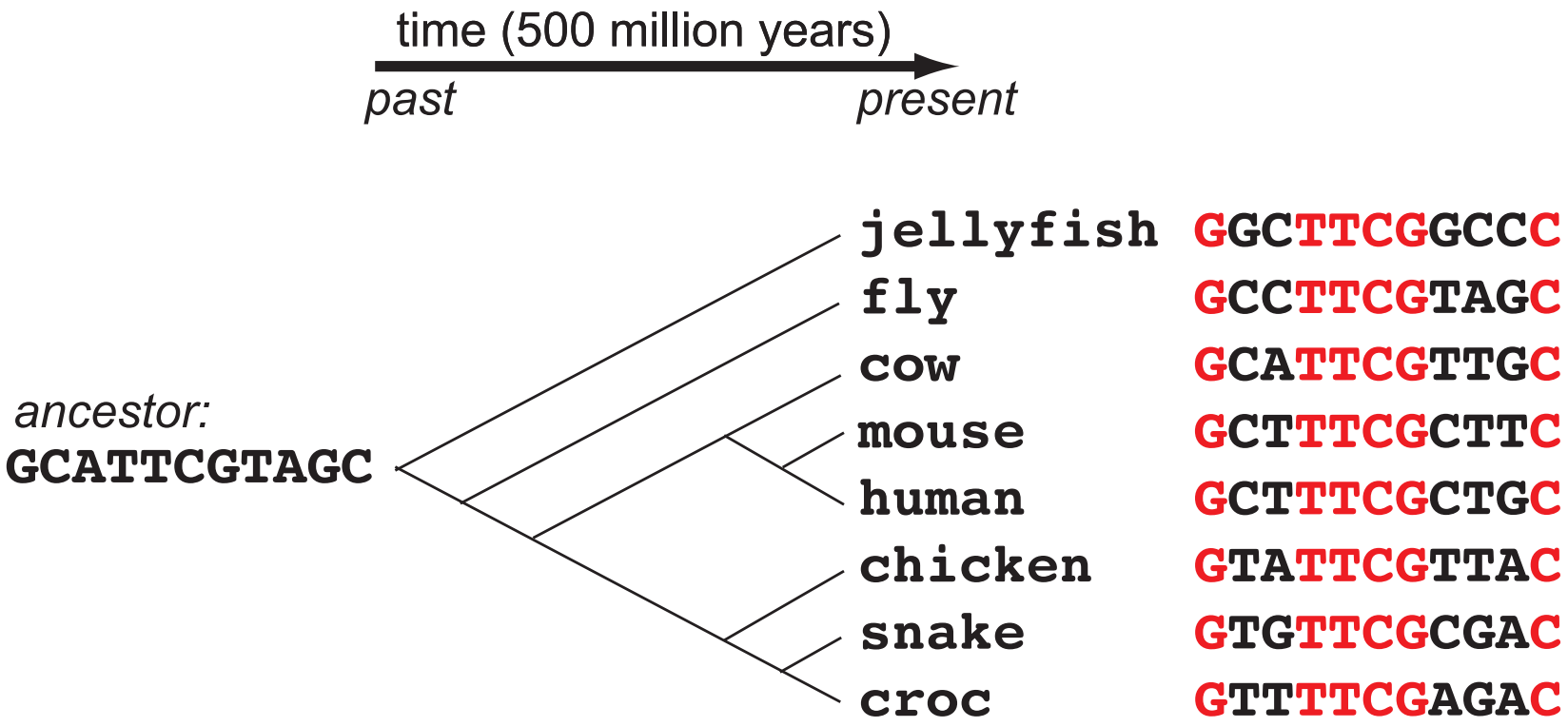
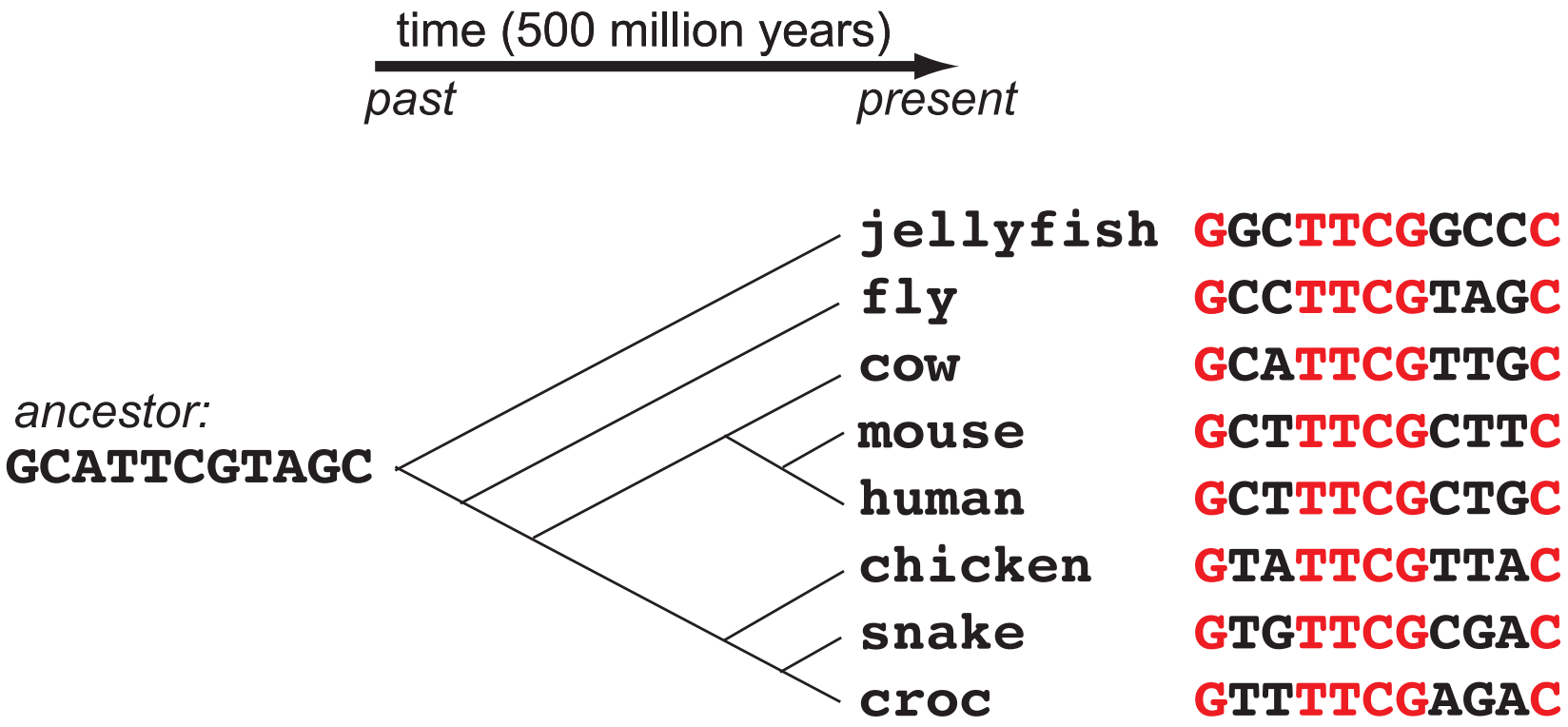
GTATTCGTAGC
GTATTCGTAAC
jellyfish GGCTTCGGCCC
fly GCGTTCGTAGC
cow GCATTCGTTGC
mouse GCTTTCGCTTC
human GCTTTCGCTGC
chicken GTATTCGTTAC
snake GTGTTCGCGAC
croc GTTTTCGAGAC


time (500 million years)
past
present
ancestor:
GCATTCGTAGC
jellyfish GGCTTCGGCCC
fly GCCTTCGTAGC
cow GCATTCGTTGC
mouse GCTTTCGCTTC
human GCTTTCGCTGC
chicken GTATTCGTTAC
snake GTGTTCGCGAC
croc GTTTTCGAGAC

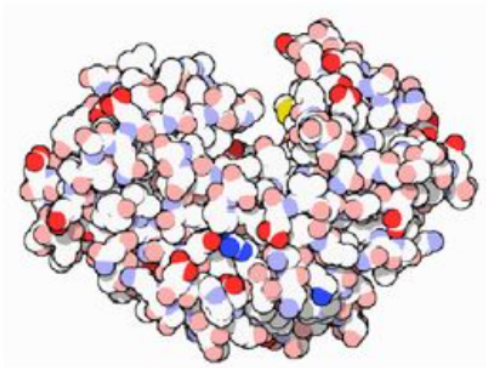


Important sequences are conserved throughout evolution

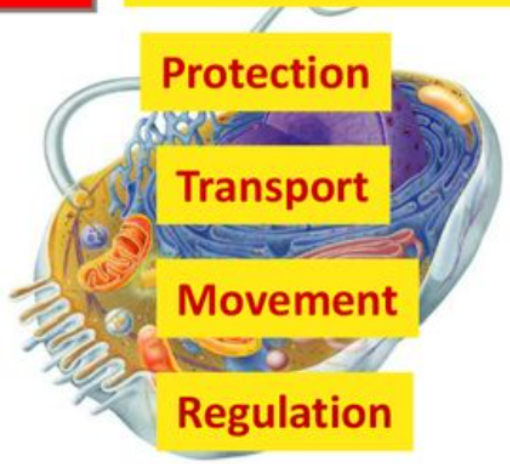
Proteins are the workhorses of the cell.

Proteins do all the work!

ATGCGTTCGAATCG
CATCGAGGACGATT
TTTTGCCTTTAA



one gene encodes
one protein

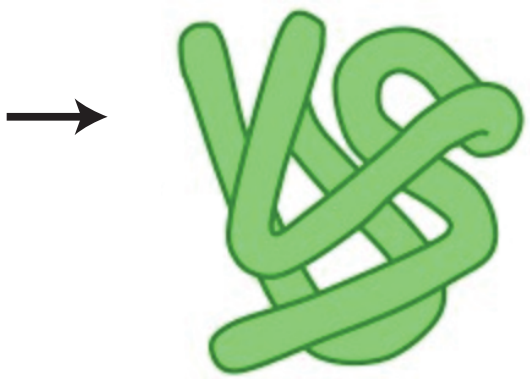


- Chemical reactions
- Protection
- Transport
- Movement
- Regulation
- Communication
- Structure

DNA → **PROTEINS** → **CELLS**

One gene sequence contains the "instructions" for one protein

human ATGCGTTCGAATCGCATCGAGGACGATTTTTTGCCTTTAA



Knowing what parts of the sequence are conserved tells researchers what to focus on

```
      ****          ******          *******
   fly ATGCCTACGAATCGCAT-GGAAACCATTTTTTGCCGTCAA
   cow ATGCGTTCGAATCGCATCGAGGACGATTTTTTGCCTTTAA
 mouse ATGCCTCCGAATCGCAT-GAGGACCATTTTTTGTCTAGAG
 human ATGCGTTCGAATCGCATCGAGGACGATTTTTTGCCTTTAA
chicken ATGCTCTGGA-TCGCAT-CTCTTTAATTTTTTGC-TGTAA
 snake ATGCAGTC-AATCGCATCTGGTACGATTTTTTGTCCTTTC
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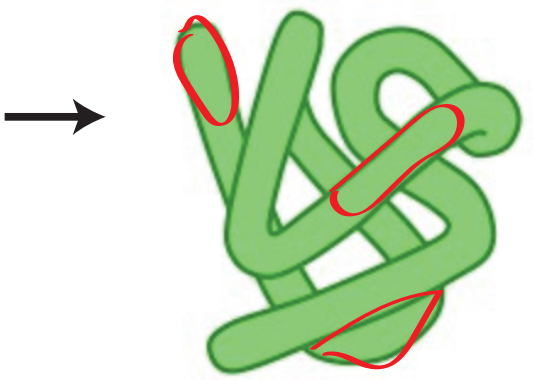

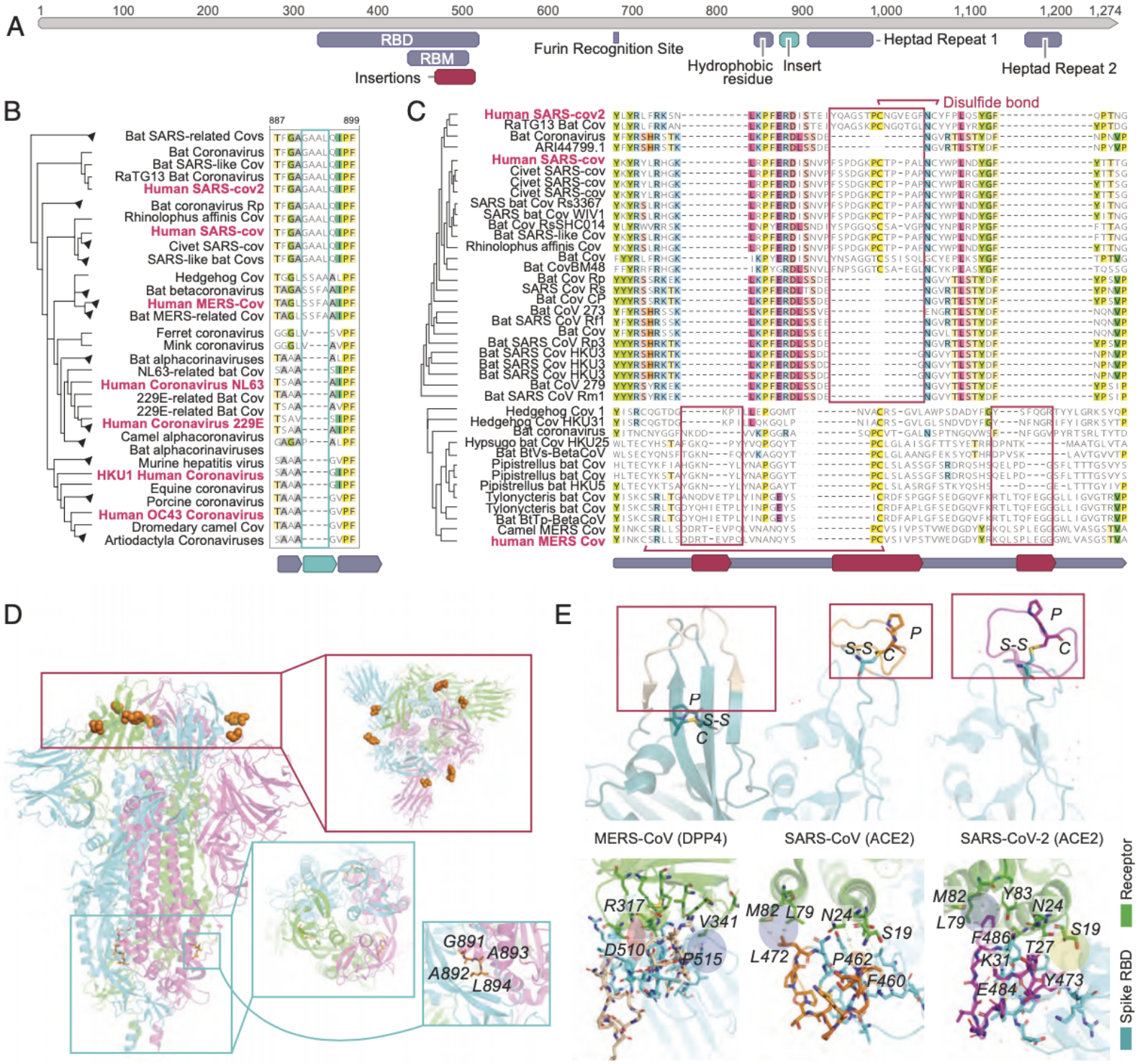
A
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100
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1,274
RBD
RBM
Insertions
Furin Recognition Site
Hydrophobic residue
Insert
Heptad Repeat 1
Heptad Repeat 2
B
887
899
Bat SARS-related Covs
Bat Coronavirus
Bat SARS-like Cov
RaTG13 Bat Coronavirus
Human SARS-cov2
Bat coronavirus Rp
Rhinolophus affinis Cov
Human SARS-cov
Civet SARS-cov
SARS-like bat Covs
Hedgehog Cov
Bat betacoronavirus
Human MERS-Cov
Bat MERS-related Cov
Ferret coronavirus
Mink coronavirus
Bat alphacorinaviruses
NL63-related bat Cov
Human Coronavirus NL63
229E-related Bat Cov
229E-related Bat Cov
Human Coronavirus 229E
Camel alphacoronavirus
Bat alphacoronaviruses
Murine hepatitis virus
HKU1 Human Coronavirus
Equine coronavirus
Porcine coronavirus
Human OC43 Coronavirus
Dromedary camel Cov
Artiodactyla Coronaviruses
C
Disulfide bond
Human SARS-cov2
RaTG13 Bat Cov
Bat Coronavirus
ARI44799.1
Human SARS-cov
Civet SARS-cov
Civet SARS-cov
Civet SARS-cov
SARS bat Cov Rs3367
SARS bat Cov WIV1
Bat Cov RsSHC014
Bat SARS-like Cov
Rhinolophus affinis Cov
Bat Cov
Bat CovBM48
Bat Cov Rp
SARS Cov Rs
Bat Cov CP
Bat CoV 273
Bat SARS CoV Rf1
Bat Cov
Bat SARS CoV Rp3
Bat SARS Cov HKU3
Bat SARS Cov HKU3
Bat SARS Cov HKU3
Bat CoV 279
Bat SARS CoV Rm1
Hedgehog Cov 1
Hedgehog Cov HKU31
Bat coronavirus
Hypsugo bat Cov HKU25
Bat BtVs-BetaCoV
Pipistrellus bat Cov
Pipistrellus bat Cov
Pipistrellus bat HKU5
Tylonycteris bat Cov
Tylonycteris bat Cov
Bat BtTp-BetaCoV
Camel MERS Cov
human MERS Cov
D
E
P
S-S
C
MERS-CoV (DPP4)
SARS-CoV (ACE2)
SARS-CoV-2 (ACE2)
R317
V341
D510
P515
M82
L79
N24
S19
L472
P462
F460
Y83
F486
T27
K31
E484
Y473
Receptor
Spike RBD

What do I actually do all day?

I write code

```
File Edit Options Buffers Tools C Help
/* serial_loop():
 *
 * Read the sequence file one window of CM_MAX_RESIDUE_COUNT
 * residues (or one sequence, if seqlen < CM_MAX_RESIDUE_COUNT)
 * at a time. Search the top strand of the window, then revcomp it and
 * search the bottom strand.
 */
static int
serial_loop(WORKER_INFO *info, ESL_SQFILE *dbfp, int64_t *srcL)
{
  int       status;
  int       wstatus;
  int       prv_pli_ntophits;    /* number of top hits before each cm_Pipeline() */
  int64_t   seq_idx = 0;
  ESL_SQ   *dbsq    = esl_sq_CreateDigital(info->cm->abc);

  wstatus = esl_sqio_ReadWindow(dbfp, info->pli->maxW, CM_MAX_RESIDUE_COUNT, dbsq);
  seq_idx++;

  while(wstatus == eslEOD) { /* this block is only necessary to chew up zero-length sequences */
    info->pli->nseqs++;
    esl_sq_Reuse(dbsq);
    wstatus = esl_sqio_ReadWindow(dbfp, info->pli->maxW, CM_MAX_RESIDUE_COUNT, dbsq);
    seq_idx++;
  }

  /*printf("SER just read seq %ld (%40s) %10ld..%10ld\n", seq_idx, dbsq->name, dbsq->start, dbsq->end);*/
  while (wstatus == eslOK ) {
    /* if this is the first window for this sequence, set dbsq->L */
    if(dbsq->start == 1) dbsq->L = srcL[seq_idx-1];

    cm_pli_NewSeq(info->pli, dbsq, seq_idx-1);

    if (info->pli->do_top) {
      prv_pli_ntophits = info->th->N;
      if((status = cm_Pipeline(info->pli, info->cm->offset, info->om, info->bg, info->p7_evparam, info->msvdata, dbsq, info->th, FALSE, /* FALSE: not in reverse complement */
                               NULL, &(info->gm), &(info->Rgm), &(info->Lgm), &(info->Tgm), &(info->cm))) != eslOK) cm_Fail("cm_pipeline() failed unexpected with status code %d\n%s\n", status, i\
nfo->pli->errbuf);
      cm_pipeline_Reuse(info->pli); /* prepare for next search */

      /* subtract overlapping residues from previous window */
      if(dbsq->C > 0) cm_pli_AdjustNresForOverlaps(info->pli, dbsq->C, FALSE); /* 'FALSE': we're not on bottom strand */

      /* modify hit positions to account for the position of the window in the full sequence */
      cm_tophits_UpdateHitPositions(info->th, prv_pli_ntophits, dbsq->start, FALSE);
    }

    /* reverse complement */
    if (info->pli->do_bot && dbsq->abc->complement != NULL) {
-UU-:----F1  cmsearch.c<src>   28% (796,0)    (C/*l Abbrev) ----------------------------------------------------------------------------------------------------------------
```

and develop and publish software

OPEN ACCESS Freely available online

PLoS COMPUTATIONAL BIOLOGY

Query-Dependent Banding (QDB) for Faster RNA Similarity Searches

Eric P. Nawrocki, Sean R. Eddy*

Howard Hughes Medical Institute, Janelia Farm Research Campus, Ashburn, Virginia, United States of America

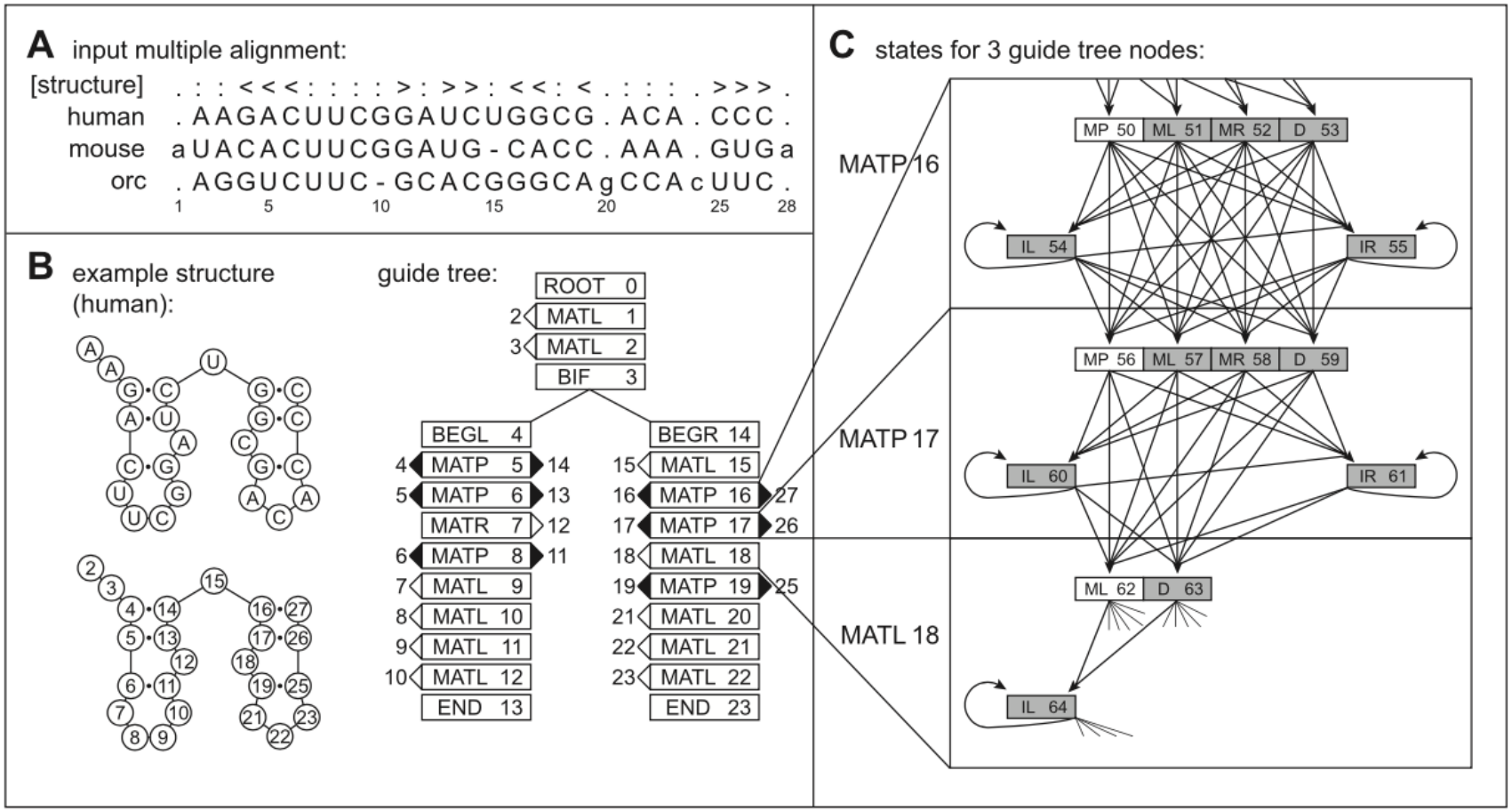
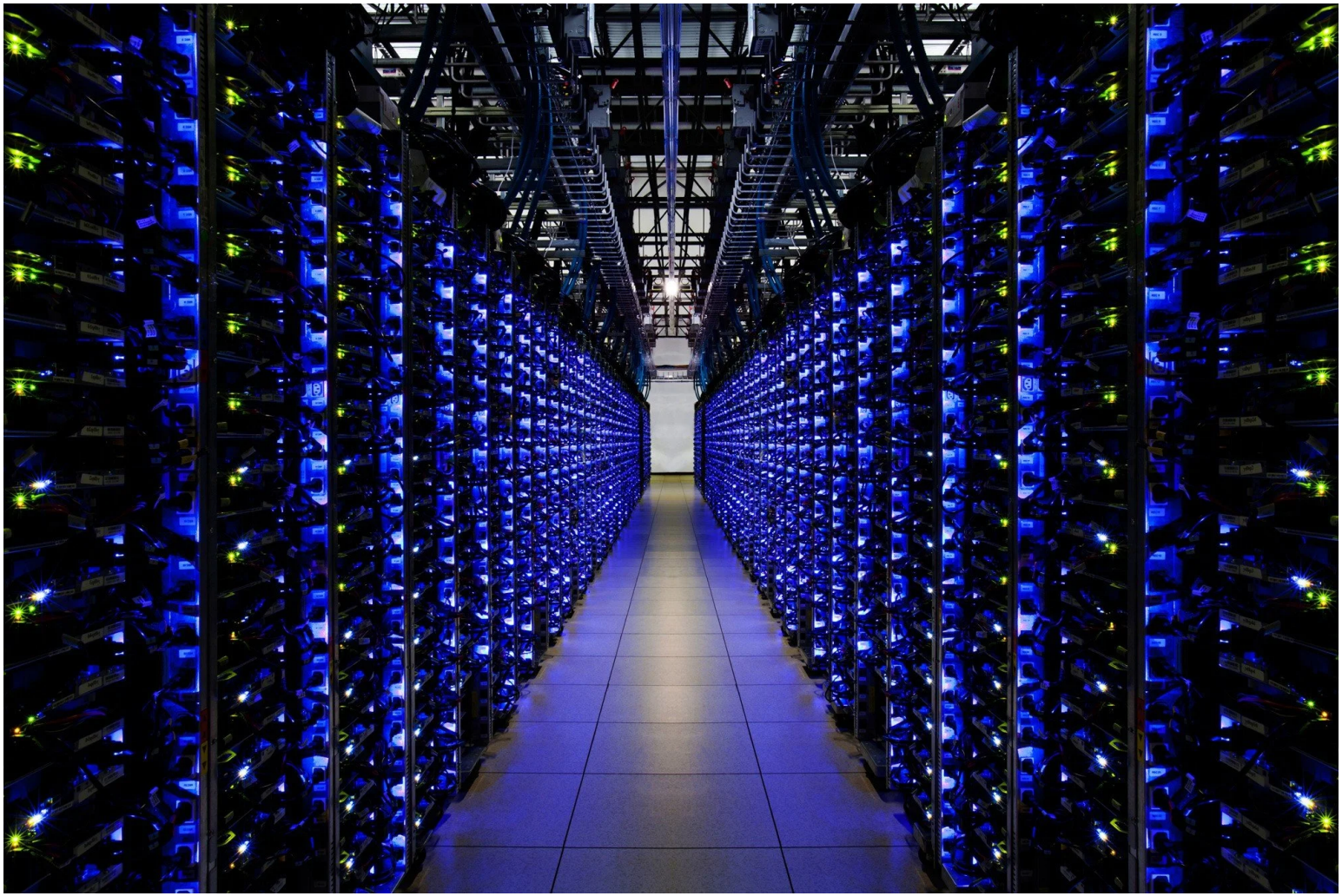


Figure 1. An Example RNA Family and Corresponding CM



Education

- College - University of Maryland
  - biology
  - computer science
- Graduate school - Washington University in St. Louis
  - Ph.D. in computational biology

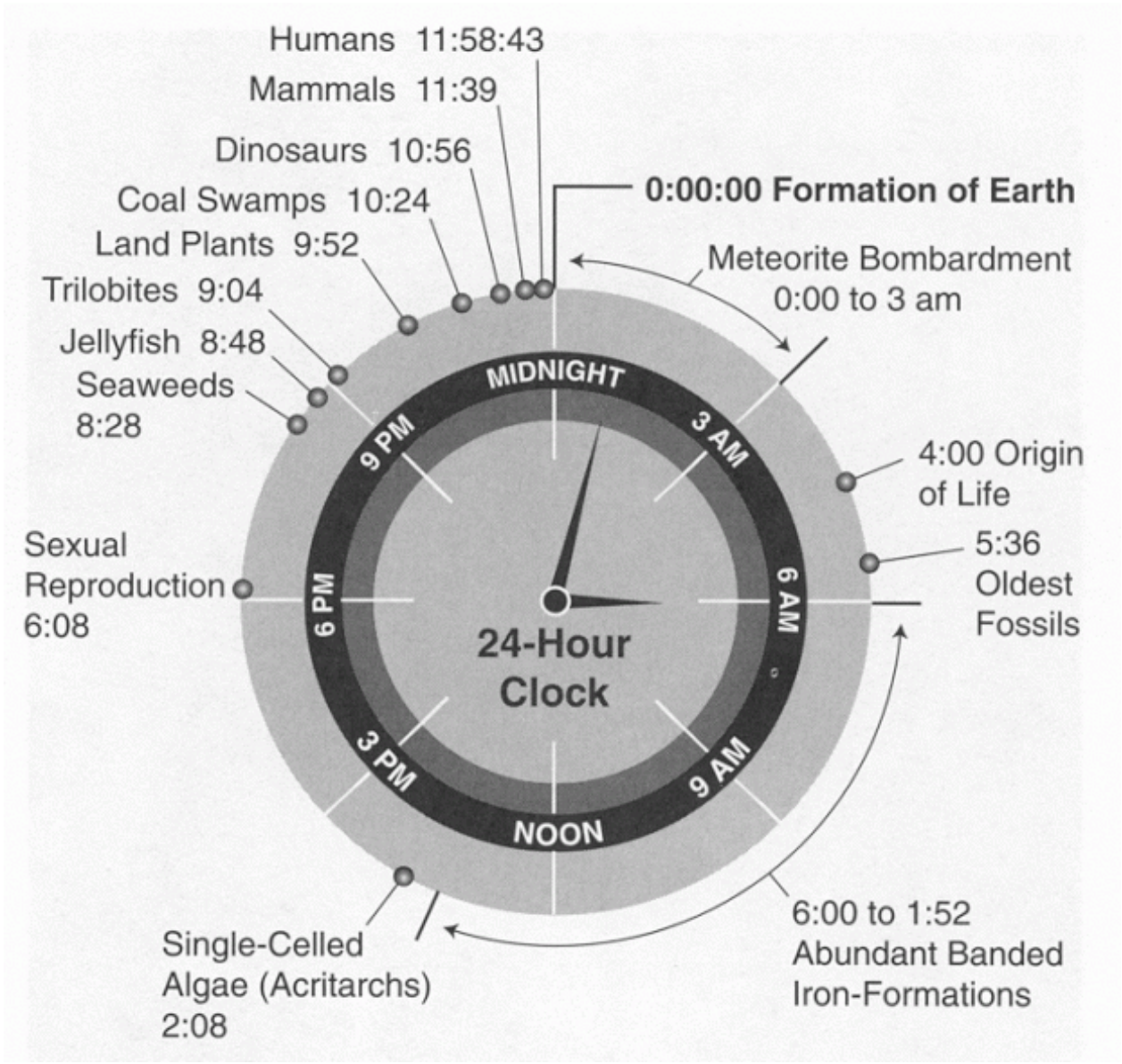
Biology careers

- Research
  - government (NIH)
  - academia - professor or research assistant
- Industry
  - pharmaceutical company
  - biotech company
- Medicine
  - doctor
  - nurse
  - veterinarian

Science research job perks

- get paid to go to graduate school (at least for biology)
- very flexible; you can be your own boss
- get to follow your own interests
- conferences and collaborations are international
  - Spain (6 times)
  - England (5 times)
  - Sweden
  - Denmark

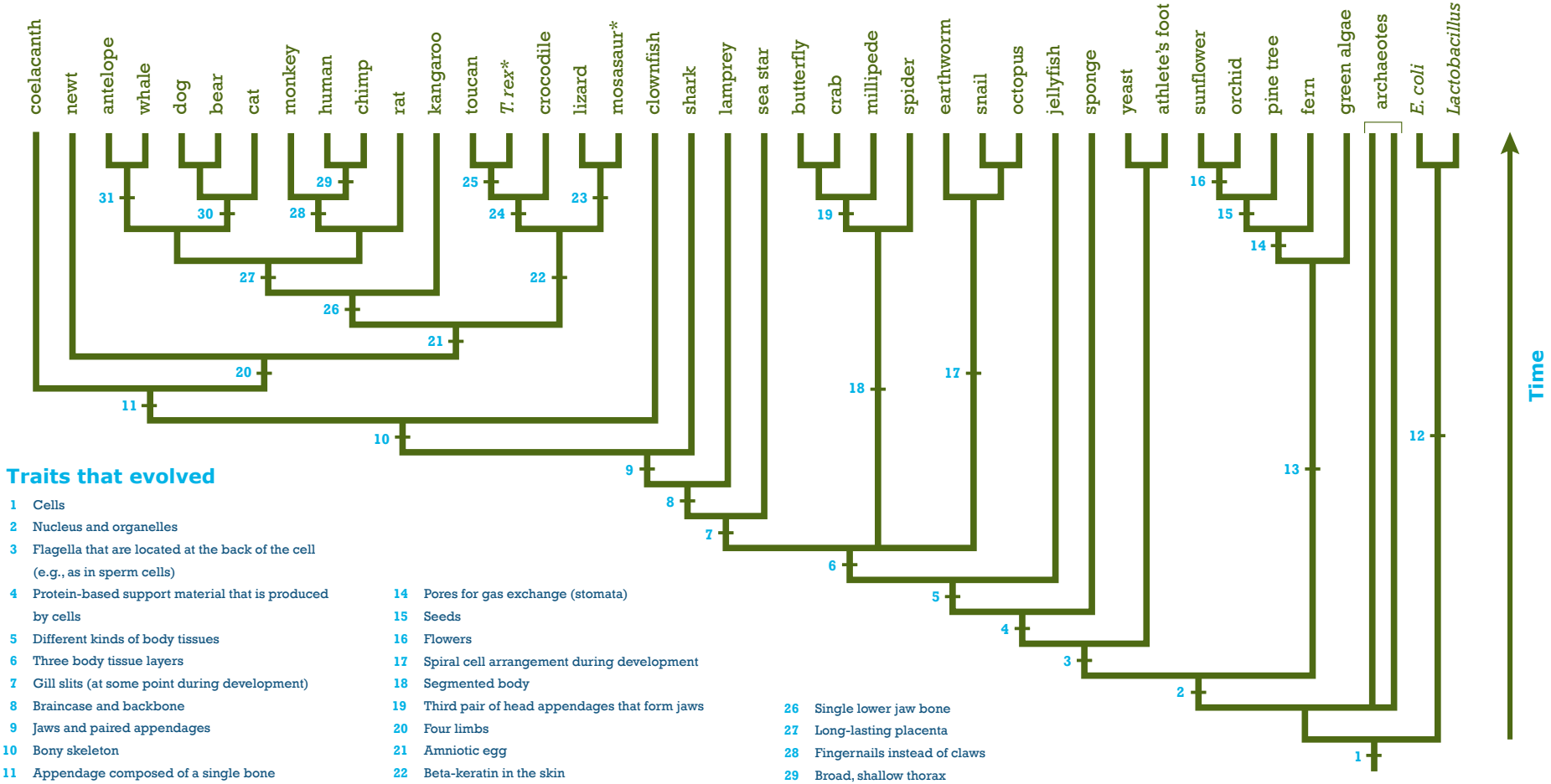

THANK YOU


Humans 11:58:43
Mammals 11:39
Dinosaurs 10:56
Coal Swamps 10:24
Land Plants 9:52
Trilobites 9:04
Jellyfish 8:48
Seaweeds 8:28
0:00:00 Formation of Earth
Meteorite Bombardment 0:00 to 3 am
4:00 Origin of Life
5:36 Oldest Fossils
6:00 to 1:52 Abundant Banded Iron-Formations
Single-Celled Algae (Acritarchs) 2:08
Sexual Reproduction 6:08
MIDNIGHT
3 AM
6 AM
9 AM
NOON
3 PM
6 PM
9 PM
24-Hour Clock

The Tree of Life

Find your favorite organisms and follow the tree to find their common ancestor.

Visit **The Tree Room** at **www.treeroom.org** to learn more about evolutionary trees.



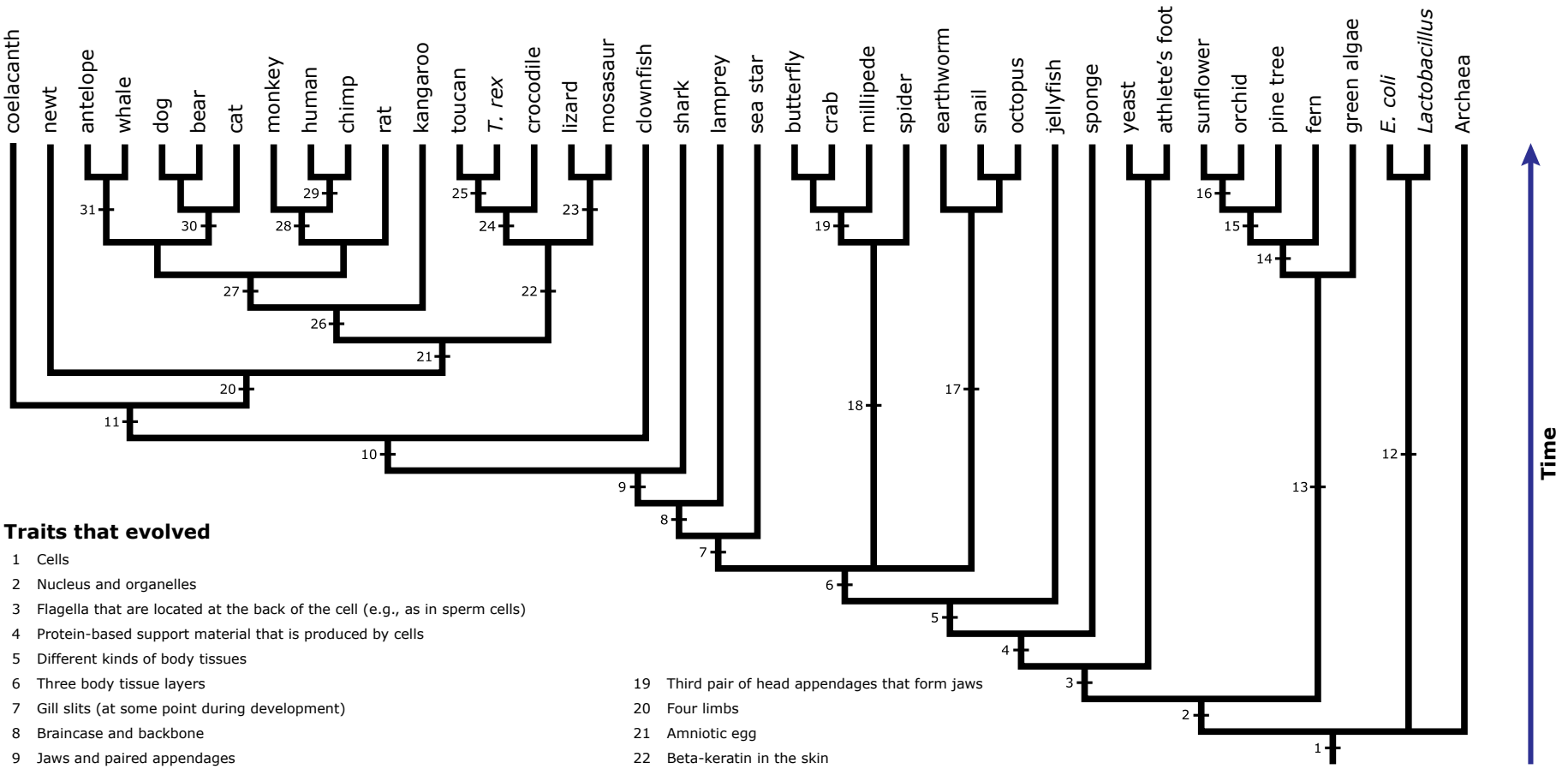
Traits that evolved

1 Cells
2 Nucleus and organelles
3 Flagella that are located at the back of the cell (e.g., as in sperm cells)
4 Protein-based support material that is produced by cells
5 Different kinds of body tissues
6 Three body tissue layers
7 Gill slits (at some point during development)
8 Braincase and backbone
9 Jaws and paired appendages
10 Bony skeleton
11 Appendage composed of a single bone (humerus) that articulates with the shoulder
12 Hollow flagella on cells
13 Cell wall made of cellulose
14 Pores for gas exchange (stomata)
15 Seeds
16 Flowers
17 Spiral cell arrangement during development
18 Segmented body
19 Third pair of head appendages that form jaws
20 Four limbs
21 Amniotic egg
22 Beta-keratin in the skin
23 Flexible bones at back of skull (cranial kinesis)
24 Bump on the rear of the ankle bone (calcaneus)
25 Wishbone or furcula (fused clavicle bones)
26 Single lower jaw bone
27 Long-lasting placenta
28 Fingernails instead of claws
29 Broad, shallow thorax
30 Specialized slicing teeth (large upper fourth premolar and lower first molar)
31 Double pulley ankle bone (astragalus)

**extinct*

Modified from The Wellcome Tree of Life
http://www.wellcometreeoflife.org/interactive

The Tree of Life



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