# COMPUTATIONAL THINKING TEST USING BIOLOGICAL DATABASE

| | | | |
|---|---|---|---|
| Name | : | Major | : |
| Gender | : | Semester | : |
| Age | : | University | : |

1. A researcher wants to know the NCBI database of BRCA genes for his research data. He then opens the https://www.ncbi.nlm.nih.gov/ page by typing "BRCA gene" and clicking search. Then various gene names and their IDs appeared. The researcher selected the BRCA2 gene with ID 675 as shown in the following image (https://www.ncbi.nlm.nih.gov/gene/675).

**BRCA2** **BRCA2 DNA repair associated [ *Homo sapiens* (human) ]**

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Gene ID: 675, updated on 8-Jul-2024

**Summary**

**Official Symbol** BRCA2 provided by HGNC
**Official Full Name** BRCA2 DNA repair associated provided by HGNC
**Primary source** HGNC:HGNC:1101
**See related** Ensembl:ENSG00000139618 MIM:600185; AllianceGenome:HGNC:1101
**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** FAD; FACD; FAD1; GLM3; BRCC2; FANCD; PNCA2; FANCD1; XRCC11; BROVCA2
**Summary** Inherited mutations in BRCA1 and this gene, BRCA2, confer increased lifetime risk of developing breast or ovarian cancer. Both BRCA1 and BRCA2 are involved in maintenance of genome stability, specifically the homologous recombination pathway for double-strand DNA repair. The largest exon in both genes is exon 11, which harbors the most important and frequent mutations in breast cancer patients. The BRCA2 gene was found on chromosome 13q12.3 in human. The BRCA2 protein contains several copies of a 70 aa motif called the BRC motif, and these motifs mediate binding to the RAD51 recombinase which functions in DNA repair. BRCA2 is considered a tumor suppressor gene, as tumors with BRCA2 mutations generally exhibit loss of heterozygosity (LOH) of the wild-type allele. [provided by RefSeq, May 2020]
**Expression** Broad expression in bone marrow (RPKM 2.9), testis (RPKM 2.2) and 17 other tissues See more
**Orthologs** mouse all
NEW Try the new Gene table
Try the new Transcript table

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Genome Data Viewer
Variation Viewer (GRCh37.p13)

There are several statements related to the information in the image above:

1) BRCA2 mutation causes loss of wild-type homozygosity
2) BRCA1 and BRCA2 are at increased risk of breast cancer
3) The BRCA2 gene may inhibit cell over-proliferation
4) Exon 11, a mutated region that often occurs in breast cancer
5) BRC motif increases the negative effects of gene mutations

What information can be deciphered from the above information to help researchers understand mutations in BRCA2 ID 675 genes?

a. 1, 2, and 3
b. 3, 4, and 5
c. 2, 3, and 4
d. 2, 4, and 5

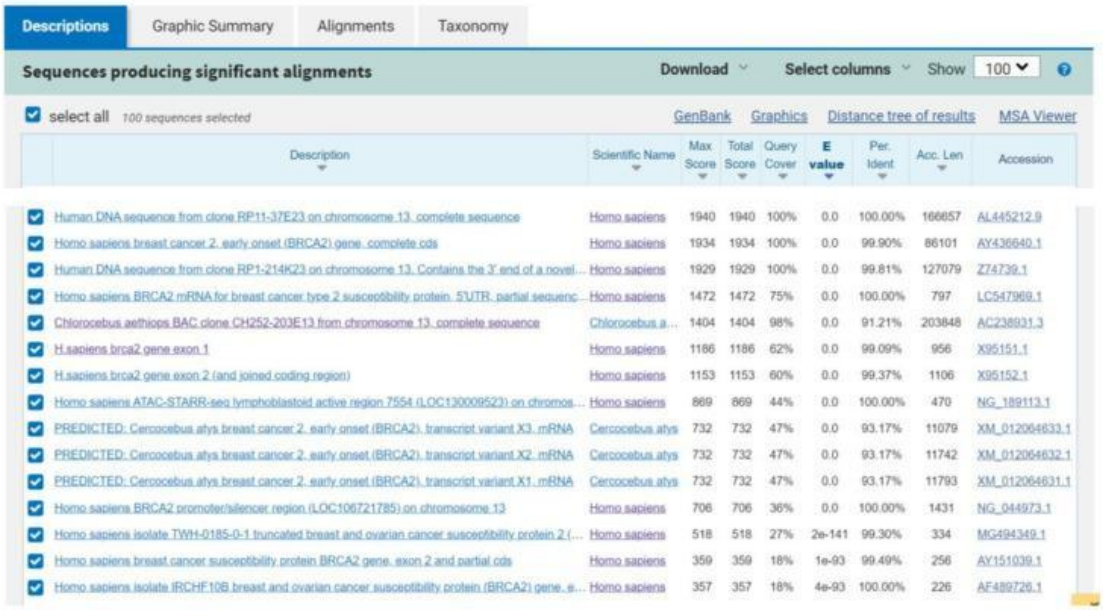
2. Still on the same page as the image above (question number 1), the researcher scrolled down the page and found the FASTA menu to find the nucleotide arrangement that makes

LIVEWORKSHEETS

up the BRCA2 ID 675 gene. The researcher then copied a number of lines of nucleotide arrangement as shown below.

```
>NC_000013.11:sample
AGAGGCGGAGCCGCTGTGGCACTGCTGCGCCTCTGCTGCGCCTCGGGTGTCTTTTGCGGCGGTGGGTCGC
CGCCGGGAGAAGCGTGAGGGGACAGATTTGTGACCGGCGCGGTTTTTGTCAGCTTACTCCGGCCAAAAAA
GAACTGCACCTCTGGAGCGGGTTAGTGGTGGTGGTAGTGGGTTGGGACGAGCGCGTCTTCCGCAGTCCCA
GTCCAGCGTGGCGGGGGAGCGCCTCACGCCCCGGGTCGCTGCCGCGGCTTCTTGCCCTTTTGTCTCTGCC
AACCCCCACCCATGCCTGAGAGAAAGGTCCTTGCCCGAAGGCAGATTTTCGCCAAGCAAATTCGAGCCCC
GCCCCTTCCCTGGGTCTCCATTTCCCGCCTCCGGCCCGGCCTTTGGGCTCCGCCTTCAGCTCAAGACTTA
ACTTCCCTCCCAGCTGTCCCAGATGACGCCATCTGAAATTTCTTGGAAACACGATCACTTTAACGGAATA
TTGCTGTTTTGGGGAAGTGTTTTACAGCTGCTGGGCACGCTGTATTTGCCTTACTTAAGCCCCTGGTAAT
TGCTGTATTCCGAAGACATGCTGATGGGAATTACCAGGCGGCGTTGGTCTCTAACTGGAGCCCTCTGTCC
CCACTAGCCACGCGTCACTGGTTAGCGTGATTGAAACTAAATCGTATGAAAATCCTCTTCTCTAGTCGCA
CTAGCCACGTTTCGAGTGCTTAATGTGGCTAGTGGCACCGGTTTGGACAGCACAGCTGTAAAATGTTCCC
ATCCTCACAGTAAGCTGTTACCGTTCCAGGAGATGGGACTGAATTAGAATTCAAACAAATTTTCCAGCGC
TTCTGAGTTTTACCTCAGTCACATAATAAGGAATGCATCCCTGTGTAAGTGCATTTTGGTCTTCTGTTTT
GCAGACTTATTTACCAAGCATTGGAGGAATATCGTAGGTAAAAATGCCTATTGGATCCAAAGAGAGGCCA
ACATTTTTTGAAATTTTTAAGACACGCTGCAACAAAGCAGGTATTGACAAATTTTATATAACTTTATAAA
```

A copy of the nucleotide array above is put into the *Nucleotide Blast* box to determine the kinship of the BRCA2 ID 675 gene with other genes. The result appears as shown in the image below.



Descriptions | Graphic Summary | Alignments | Taxonomy

Sequences producing significant alignments — Download — Select columns — Show 100

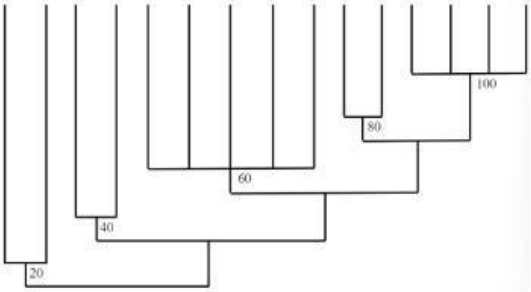
select all 100 sequences selected — GenBank — Graphics — Distance tree of results — MSA Viewer

| Description | Scientific Name | Max Score | Total Score | Query Cover | E value | Per. Ident | Acc. Len | Accession |
|---|---|---|---|---|---|---|---|---|
| Human DNA sequence from clone RP11-37E23 on chromosome 13, complete sequence | Homo sapiens | 1940 | 1940 | 100% | 0.0 | 100.00% | 166657 | AL445212.9 |
| Homo sapiens breast cancer 2, early onset (BRCA2) gene, complete cds | Homo sapiens | 1934 | 1934 | 100% | 0.0 | 99.90% | 86101 | AY436640.1 |
| Human DNA sequence from clone RP1-214K23 on chromosome 13, Contains the 3' end of a novel... | Homo sapiens | 1929 | 1929 | 100% | 0.0 | 99.81% | 127079 | Z74739.1 |
| Homo sapiens BRCA2 mRNA for breast cancer type 2 susceptibility protein, 5'UTR, partial sequenc... | Homo sapiens | 1472 | 1472 | 75% | 0.0 | 100.00% | 797 | LC547969.1 |
| Chlorocebus aethiops BAC clone CH252-203E13 from chromosome 13, complete sequence | Chlorocebus a... | 1404 | 1404 | 98% | 0.0 | 91.21% | 203848 | AC238931.3 |
| H.sapiens brca2 gene exon 1 | Homo sapiens | 1186 | 1186 | 62% | 0.0 | 99.09% | 956 | X95151.1 |
| H.sapiens brca2 gene exon 2 (and joined coding region) | Homo sapiens | 1153 | 1153 | 60% | 0.0 | 99.37% | 1106 | X95152.1 |
| Homo sapiens ATAC-STARR-seq lymphoblastoid active region 7554 (LOC130009523) on chromos... | Homo sapiens | 869 | 869 | 44% | 0.0 | 100.00% | 470 | NG_189113.1 |
| PREDICTED: Cercocebus atys breast cancer 2, early onset (BRCA2), transcript variant X3, mRNA | Cercocebus atys | 732 | 732 | 47% | 0.0 | 93.17% | 11079 | XM_012064633.1 |
| PREDICTED: Cercocebus atys breast cancer 2, early onset (BRCA2), transcript variant X2, mRNA | Cercocebus atys | 732 | 732 | 47% | 0.0 | 93.17% | 11742 | XM_012064632.1 |
| PREDICTED: Cercocebus atys breast cancer 2, early onset (BRCA2), transcript variant X1, mRNA | Cercocebus atys | 732 | 732 | 47% | 0.0 | 93.17% | 11793 | XM_012064631.1 |
| Homo sapiens BRCA2 promoter/silencer region (LOC106721785) on chromosome 13 | Homo sapiens | 706 | 706 | 36% | 0.0 | 100.00% | 1431 | NG_044973.1 |
| Homo sapiens isolate TWH-0185-0-1 truncated breast and ovarian cancer susceptibility protein 2 (... | Homo sapiens | 518 | 518 | 27% | 2e-141 | 99.30% | 334 | MG494349.1 |
| Homo sapiens breast cancer susceptibility protein BRCA2 gene, exon 2 and partial cds | Homo sapiens | 359 | 359 | 18% | 1e-93 | 99.49% | 256 | AY151039.1 |
| Homo sapiens isolate IRCHF10B breast and ovarian cancer susceptibility protein (BRCA2) gene, e... | Homo sapiens | 357 | 357 | 18% | 4e-93 | 100.00% | 226 | AF489726.1 |

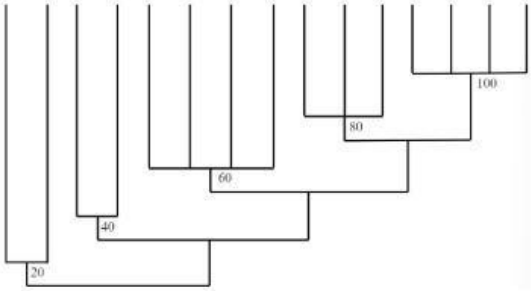
From the results obtained, the researcher plans to construct a phylogenetic tree of several samples of search results based on the percentage of each gene on the *Query cover*. Select the image below to help researchers determine the phylogenetic tree pattern from the image above!

LIVEWORKSHEETS

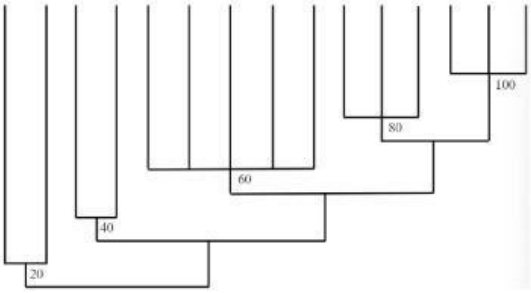
a. Picture A



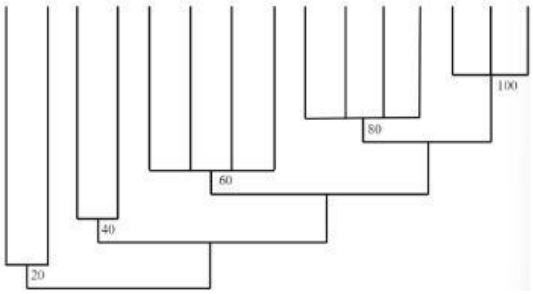

c. Picture C




b. Picture B




d. Picture D




3. From the nucleotide arrangement that the researcher copied and put into the *Nucleotide Blast* box (question number 2), data on the kinship of the BRCA2 gene ID 675 with other genes was generated. When the researcher clicked on the *Alignments* menu section, it showed a comparison of the nucleotide arrangement of the BRCA2 ID 675 gene with one of the organisms that had a similarity to it as shown in the image below.

Range 4: 62748 to 63050 GenBank Graphics ▼ Next Match ▲ Previous Match ▲ First Match

| Score | Expect | Identities | Gaps | Strand |
|---|---|---|---|---|
| 283 bits(153) | 2e-70 | 258/309(83%) | 6/309(1%) | Plus/Plus |

```
Query  1410   GCTGGGCGTGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCGGAT  1469
              |||||| | |||| ||||  |||||||||||||||||||||||||| || |||||| |||
Sbjct  62748  GCTGGGTGGGGTGTCTCATTCCTGTAATCCCAGCACTTTGGGAGGCTGAAGTGGGCAGAT  62807

Query  1470   CACTTGAGGCCAGAAGTTTGAGACCAGCCTGGCCAACATGGTGAAACCCTATCTCTACTA  1529
              |||   ||| ||| ||||  |||||||||||||||||||||||||||||| | ||||  |
Sbjct  62808  CACA--AGGTCAGGAGTTGAAGACCAGCCTGGCCAACATGGTGAAACCCTGTTTCTATGA  62865

Query  1530   AAAATACAAAAAATGTGCTGCGTGTGGTGGTGCGTGCCTGTAATCCCAGCTACACGGGAG  1589
              ||||| |||||| |  |||| | |||||||  || | |||||||||||||||  |  |||
Sbjct  62866  AAAATTCAAAAATTA-GCTGGGCGTGGTGGCACGCGTCTGTAATCCCAGCTATTCCAGAG  62924

Query  1590   GTGGAGGCAGGAGAATCGCTTGAACCCTGGAGGCAGAGGTTGCAGTGAGCCAAGATCATG  1649
              |  |||||||||||||| ||||||| || |||||||||| ||||||| |||||| ||||
Sbjct  62925  GCTGAGGCAGGAGAATTGCTTGAATCCAGGAGGCAGAGATTGCAGTAAGCCAAAATCACA  62984

Query  1650   CCACTGCACTCTAGCCTGGGCCACATAGCATGACTCTGTCTcaaaacaaacaaacaaaca  1709
              |||||||||||||||||||||| ||| |||| |||||||||||||||| ||| ||| ||| |
Sbjct  62985  CCACTGCACTCTAGCCTGGGCAACAAAGCAAGACTCTGTCTCAAAA-AAATAAATAAA-A  63042

Query  1710   aaaaacTAA  1718
              ||||| |||
Sbjct  63043  AAAAA-TAA  63050
```

The circled part is one of the types of mutations that can occur at the stage of DNA replication, analyze what type of mutation occurs in that part!

LIVEWORKSHEETS

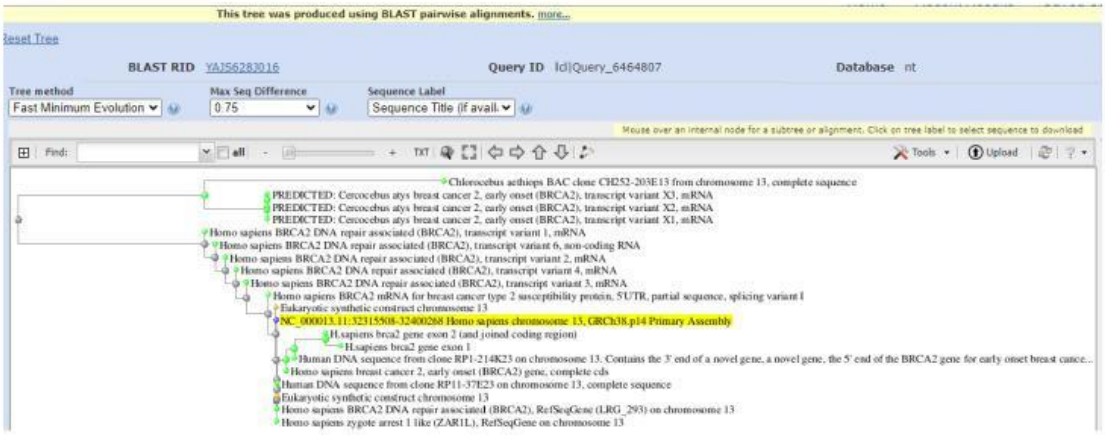
a. Transversion

b. Transition

c. Deletion

d. Insertion

4. Dimas, a researcher from BRIN, used the NCBI website to find out the kinship of the BRCA2 gene with other genes in certain organisms. On https://www.ncbi.nlm.nih.gov/gene/675 he clicks on FASTA (the array of nucleotides that make up the BRCA2 gene) and copies it. He then added the copy to the *Nucleotide Blast* menu(https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome). The results gave rise to several organisms that are closely related to the BRCA2 gene. Next, Dimas clicks on the *Distance Tree of Result* menu so that it displays the phylogenetic tree as shown in the image below.




Dimas understands the picture above and writes the results of his analysis below.

1) Write down the number of differences/analysis results for each character
2) Determine the character of each organism to be analyzed
3) Arrange phylogenetic trees according to kinship level
4) Determining the highest value (closest relatives) to the lowest
5) Analyze the differences in the character of each organism

Help Dimas arrange a systematic stage in arranging a phylogenetic tree as shown in the picture above!

a. 1, 2, 5, 4, 3

b. 2, 5, 4, 1, 3

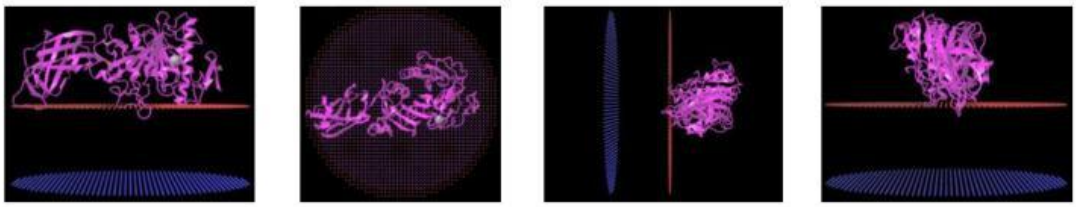
c. 2, 1, 5, 4, 3

d. 2, 5, 1, 4, 3

LIVEWORKSHEETS

5. The figure below shows the structure of Lipase Enzyme which can be accessed through the *search* menu on the NCBI website with the *structure* selection. Click search and many options appear, one of which is the image below (https://www.ncbi.nlm.nih.gov/Structure/icn3d/full.html?showanno=1&mmdbid=56257). On the menu, the *view* of the image can be changed to see other parts of the Lipase enzyme structure. If the initial *view* is changed to rotation x → rotation y → rotation z, then the change in the image can be seen in the image below.

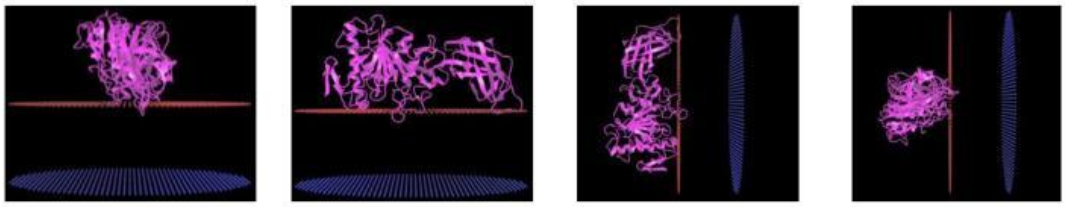
**Beginning** **X rotation** **Y rotation** **Z rotation**



If we want to change the rotation starting from z rotation to y rotation → z rotation → x rotation, what is the form of the change!

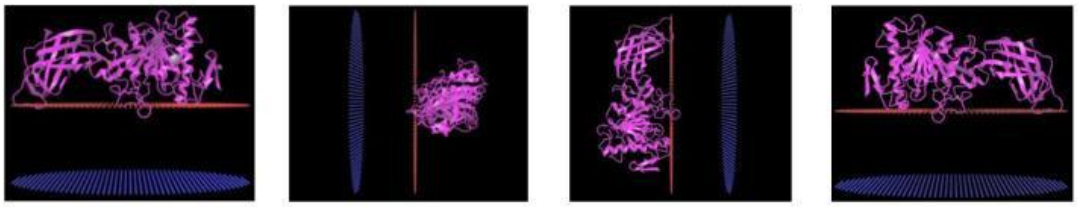
a. Picture A

**Z rotation** **Y rotation** **Z rotation** **X rotation**



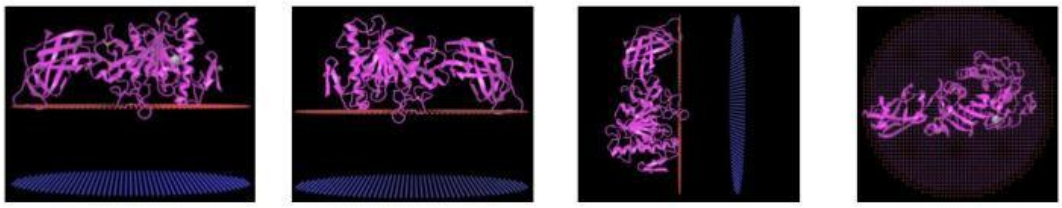
b. Picture B

**Z rotation** **Y rotation** **Z rotation** **X rotation**



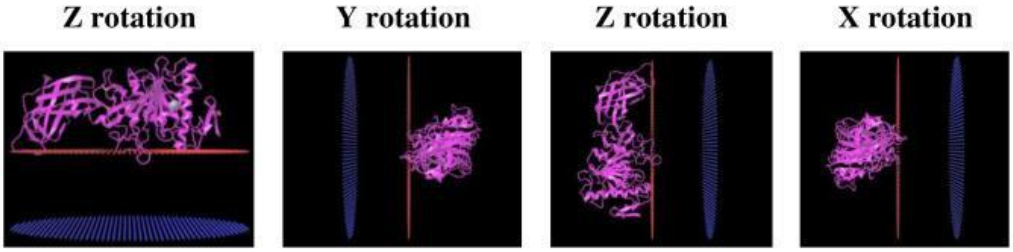
c. Picture C

**Z rotation** **Y rotation** **Z rotation** **X rotation**

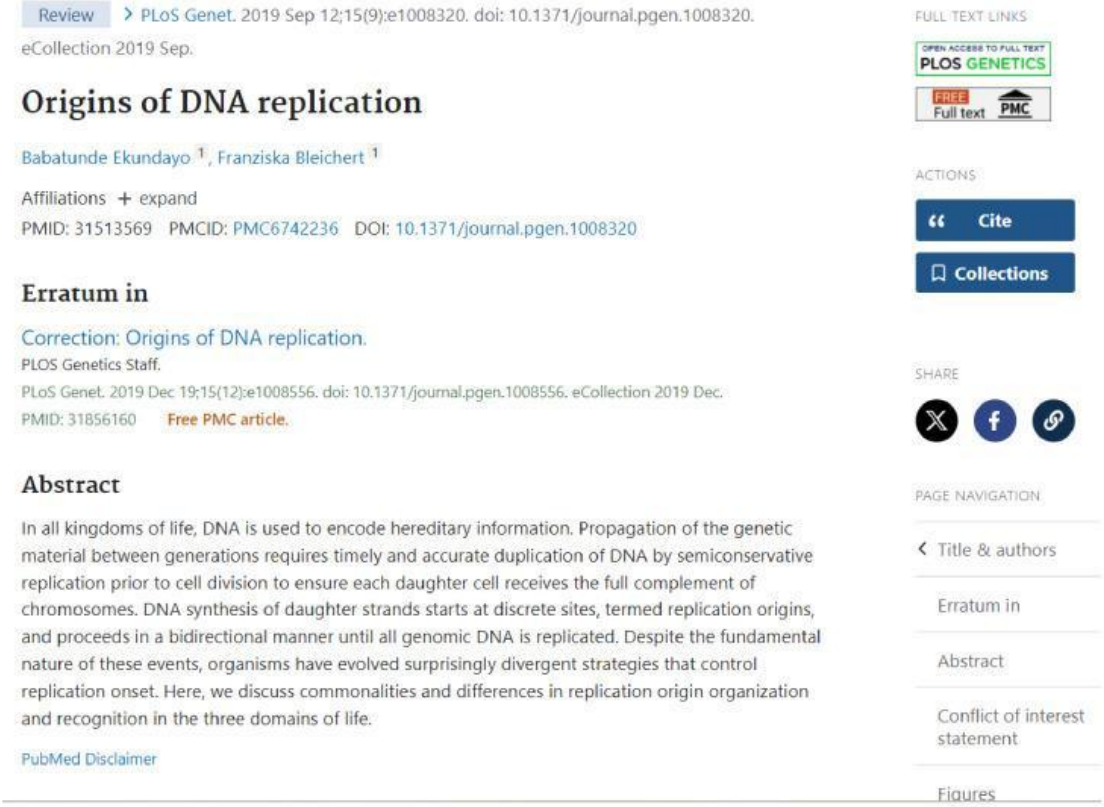


LIVEWORKSHEETS

d. Picture D




6. Indra is looking for literature on DNA replication. He opened the NCBI website which stores a database of DNA sequences and various genetic substance information and other health information. He then opens *the PubMed* (https://pubmed.ncbi.nlm.nih.gov/) menu, then types *DNA Replication* in the search field. The results show that many research articles discuss DNA replication. One of the materials that Indra reads is *Origins of DNA Replication* (https://pubmed.ncbi.nlm.nih.gov/31513569/). Indra read *the abstract* and found information that DNA replication was carried out in a semiconservative manner.



Review > PLoS Genet. 2019 Sep 12;15(9):e1008320. doi: 10.1371/journal.pgen.1008320. eCollection 2019 Sep.

**Origins of DNA replication**

Babatunde Ekundayo [1], Franziska Bleichert [1]

Affiliations + expand

PMID: 31513569 PMCID: PMC6742236 DOI: 10.1371/journal.pgen.1008320

**Erratum in**

Correction: Origins of DNA replication.
PLOS Genetics Staff.
PLoS Genet. 2019 Dec 19;15(12):e1008556. doi: 10.1371/journal.pgen.1008556. eCollection 2019 Dec.
PMID: 31856160 Free PMC article.

**Abstract**

In all kingdoms of life, DNA is used to encode hereditary information. Propagation of the genetic material between generations requires timely and accurate duplication of DNA by semiconservative replication prior to cell division to ensure each daughter cell receives the full complement of chromosomes. DNA synthesis of daughter strands starts at discrete sites, termed replication origins, and proceeds in a bidirectional manner until all genomic DNA is replicated. Despite the fundamental nature of these events, organisms have evolved surprisingly divergent strategies that control replication onset. Here, we discuss commonalities and differences in replication origin organization and recognition in the three domains of life.

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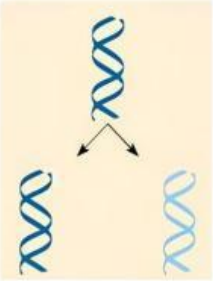
Abstract
Conflict of interest statement
Figures

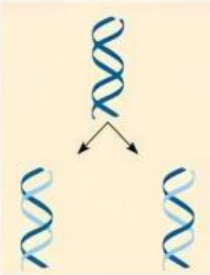
Indra's search results regarding this information show that replication per DNA will produce one new strand and one old strand. The image below that exactly states the information is ....

LIVEWORKSHEETS

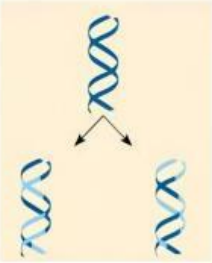
a. Picture A



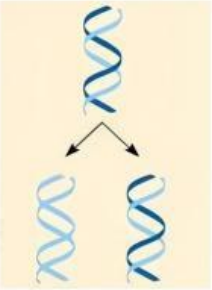
b. Picture B



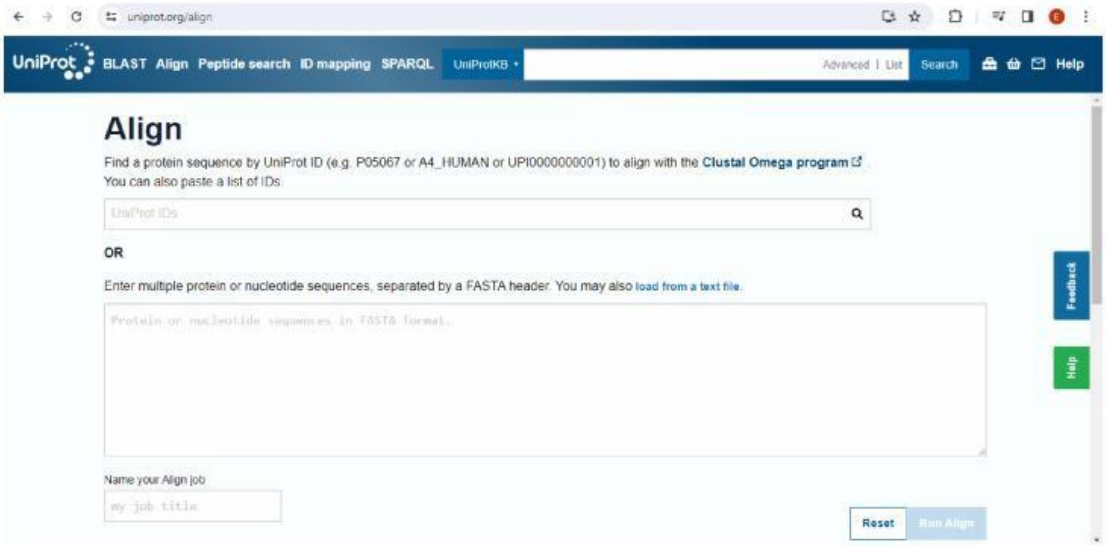
c. Picture C



d. Picture D



7. Andi has a number of DNA nucleotide arrangements. He wanted to know which parts had differences between one nucleotide and another. He then opened the UniProt website and visited the website address on *the Align* menu (https://www.uniprot.org/align) as shown in the image.




Help Andi to understand the instructions on the page so that Andi can know the difference from a number of nucleotide arrangements to be inserted. The statements below that *are not appropriate* are related to the components and what things must be considered in order to find a solution from the image above are ....

a. Inserting nucleotide arrays in the form of UniProt IDs

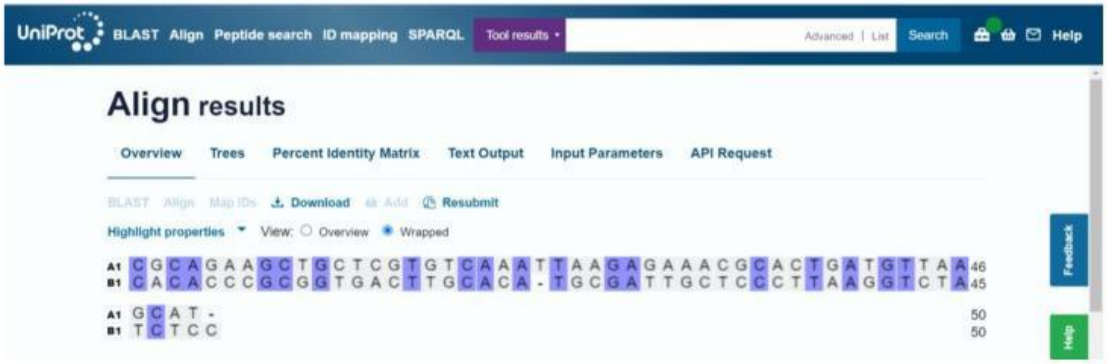
LIVEWORKSHEETS

b. Inserting multiple nucleotide arrays more than one

c. Each nucleotide array is separated by a FASTA header

d. Nucleotide IDs do not have to be compatible with the Clustal Omega program

8. From question number 7, Andi tried to enter a number of nucleotide arrangements on the *Align* page according to the instructions, so he succeeded. The figure below is the *Align results* of the nucleotide arrangement that is inserted with a total of 50 nucleotide bases.




Andi tried to analyze the pattern of the website in aligning the nucleotide arrangement that was inserted. The statement below that is appropriate regarding the pattern in Align results is ....

a. Align result marks similar nitrogenous bases, not nitrogenous base pairs

b. Align result does not mark similar nitrogenous bases, but rather marks nitrogenous base pairs

c. Align result marks similar nitrogenous bases and marks nitrogenous base pairs

d. Align result does not mark similar nitrogenous bases and does not mark nitrogenous base pairs

9. *Peptide search* is part of the UniProt menu that functions to find protein names based on the array of amino acids inserted. Intan, a student of Biology Education tried to include the following seven amino acids: Serine, Phenylalanine, Leucine, Serine, Isoleucine, Tryptophan, and Valine. The results can be seen in the image below (https://www.uniprot.org/peptide-search/PM20240304e8795ad38346422b9c77cbd85352e938/overview).

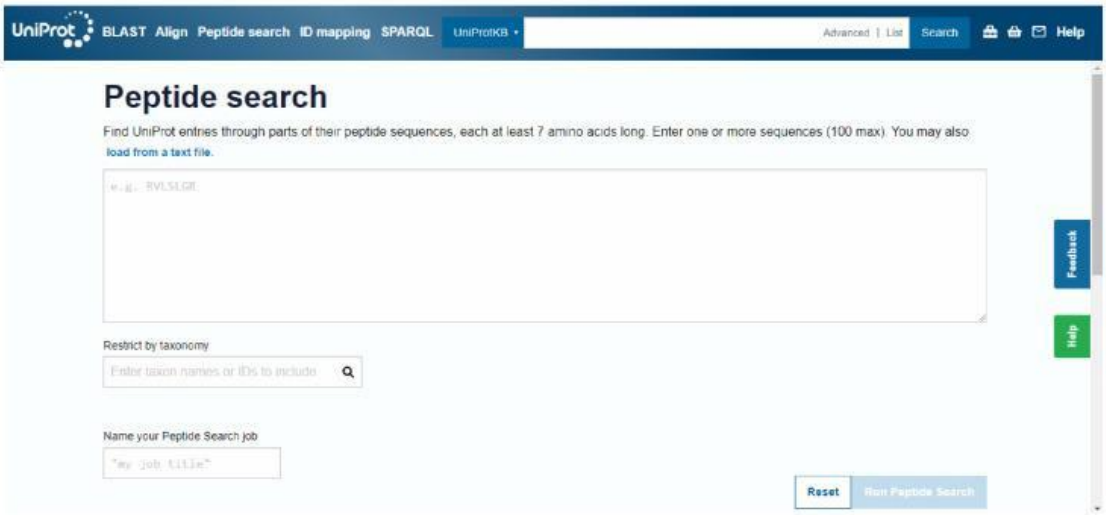
LIVEWORKSHEETS

| Match | Entry Name | Protein Names | Gene Names | Organism | Length |
|---|---|---|---|---|---|
| Positions 64-70: SPLSITV | IPSP_BOVIN | Plasma serine protease inhibitor[...] | SERPINA5 | Bos taurus (Bovine) | 404 AA |
| Positions 275-281: SPLSITV | RMD5_ARATH | Protein RMD5 homolog | RMD5, At4g37880 | Arabidopsis thaliana (Mouse-ear cress) | 388 AA |
| Positions 838-844: SPLSITV | A0A022RNK1_ERYGU | Pentacotripeptide-repeat region of PRORP domain-containing protein | MIMGU_mgv1a001284mg | Erythranthe guttata (Yellow monkey flower) (Mimulus guttatus) | 847 A |
| Positions 2004-2010: SPLSITV | A0A085W899_9BACT | histidine kinase[...] | DB31_2324 | Hyalangium minutum | 2,130 |
| Positions 497-503: SPLSITV | A0A088RJK0_9TRYP | Uncharacterized protein | LPMP_040120 | Leishmania panamensis | 596 AA |
| Positions 269-275: SPLSITV | A0A089KT78_9BACL | ROK family transcriptional regulator | R70331_05340 | Paenibacillus sp. FSL R7-0331 | 299 AA |

From the image above, there is one name for a protein that is *uncharacterized*. Analyze, the correct part of the statement based on the event is…

a. Proteins have not been identified in structure and function by UniProt
b. The sequence of amino acids inserted does not correspond to the protein
c. Proteins do not have a clear structure and their function is not yet known
d. Proteins are not yet clearly known for their function for other organisms

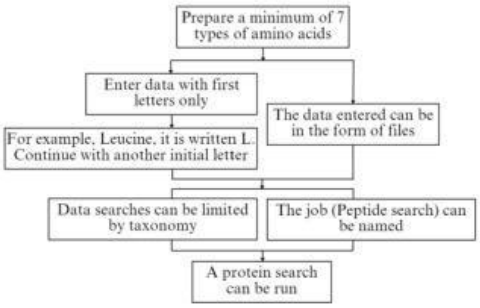
10. Just like Intan (question number 9), Nina also uses the UniProt website (https://www.uniprot.org/) to find out the name of the protein based on the type of amino acid produced from the protein synthesis process. Nina then visited the *Peptide Search menu* (https://www.uniprot.org/peptide-search), so that the page appears as shown in the image below.



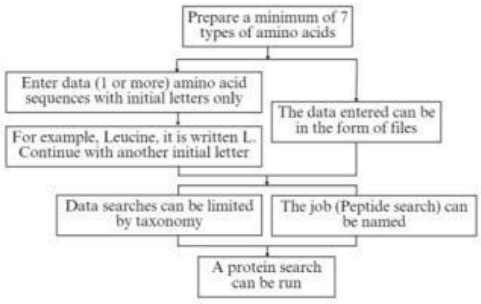

The protein synthesis stage carried out by Nina produces amino acids with the types of Serine, Phenylalanine, Leucine, Serine, Isoleucine, Tryptophan, and Valine. To find out the possible names of proteins, genes, and organisms in these amino acids, which of the following charts is appropriate related to the components and processes that must be included in the form according to the figure above!

LIVEWORKSHEETS

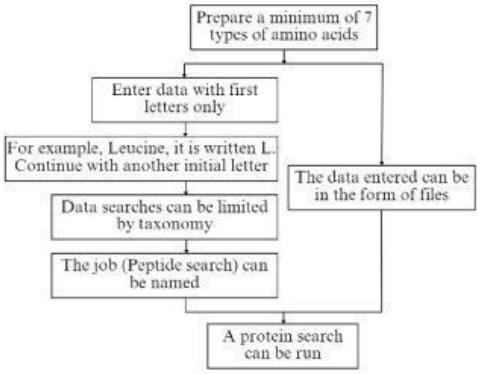
a. Chart A



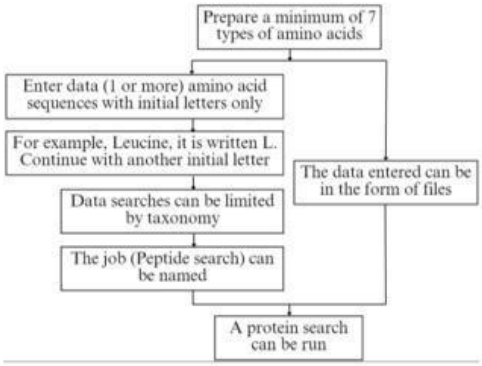

b. Chart B



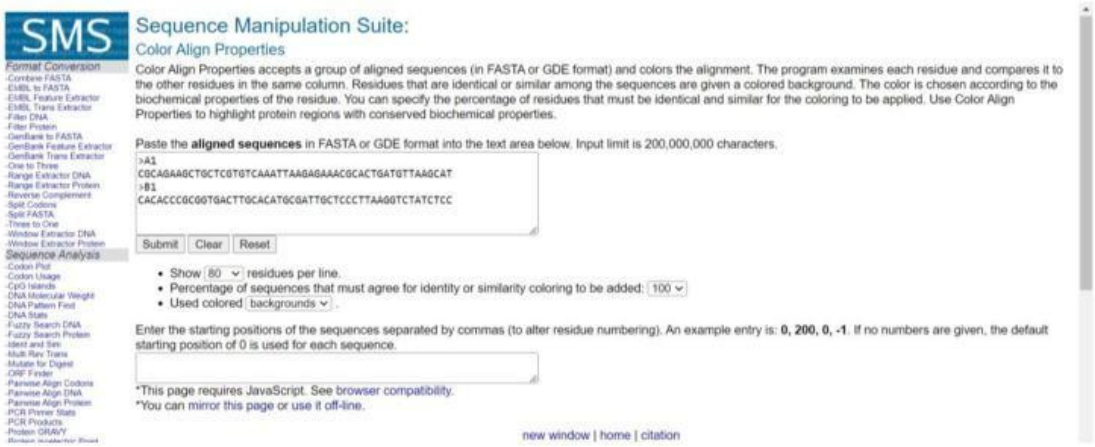

c. Chart C




d. Chart D




11. Sequence Manipulation Suite (SMS) is a collection of JavaScript programs designed to generate, format, and analyze short DNA and protein networks. One of the programs is *Color Align Properties* as shown in the image below (https://www.bioinformatics.org/sms2/color_align_cons.html). Anas, a Biology Education student, will use the website as a research medium in measuring students' computational thinking. Help Anas understand how to use the program.




There are several statements related to the Sequence Manipulation Suite program, including:

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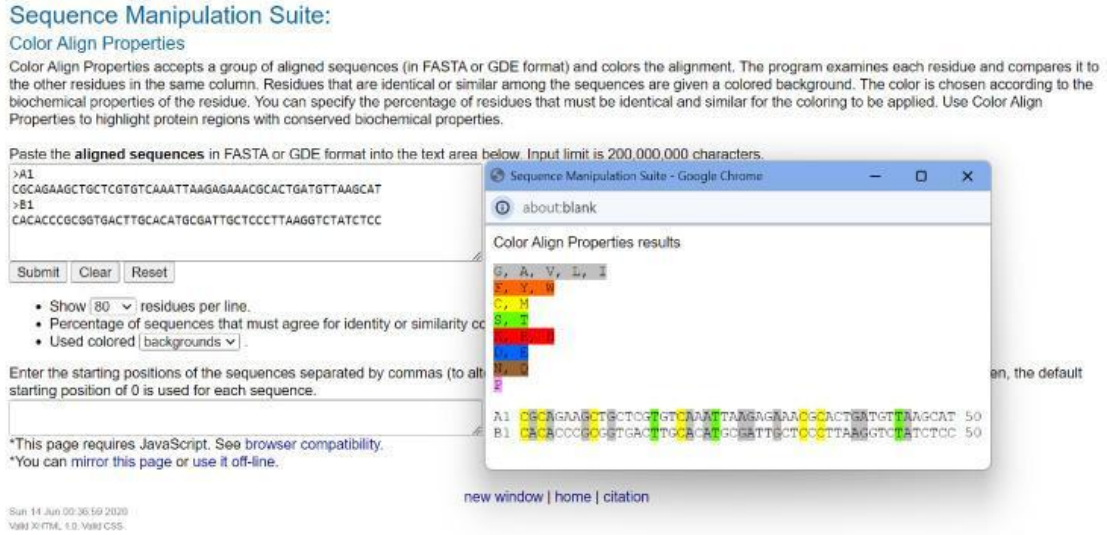
1) Sequence of nucleotide bases
2) The nucleotide base sequence format is only deep FASTA/GDE
3) Inserted DNA sequence < 2
4) Identical nucleotide bases given a colored background
5) Color Align Properties compare residues with each other (biological properties)

From the statement outlined based on the image description, what information can be used to help Anas know the use of *Color Align Properties* in SMS?

a. 2, 3, dan 5
b. 1, 3, dan 5
c. 1, 2, dan 4
d. 2, 3, dan 4

12. Thank you for helping Anas answer question number 11. Now he has successfully used *the Color Align Properties* program to see a comparison of two DNA sequence samples. The results are shown in the image below (https://www.bioinformatics.org/sms2/color_align_prop.html).




Based on the image, there are several nucleotide bases that are given and not colored. Identify the color pattern in the image, write down what nucleotide bases represent the DNA replication process!

a. A1: GGAAGATAG
b. A1: CCCTCTCCT
c. A1: GAGGAAAGAGAA
d. A1: GGAAATAGG

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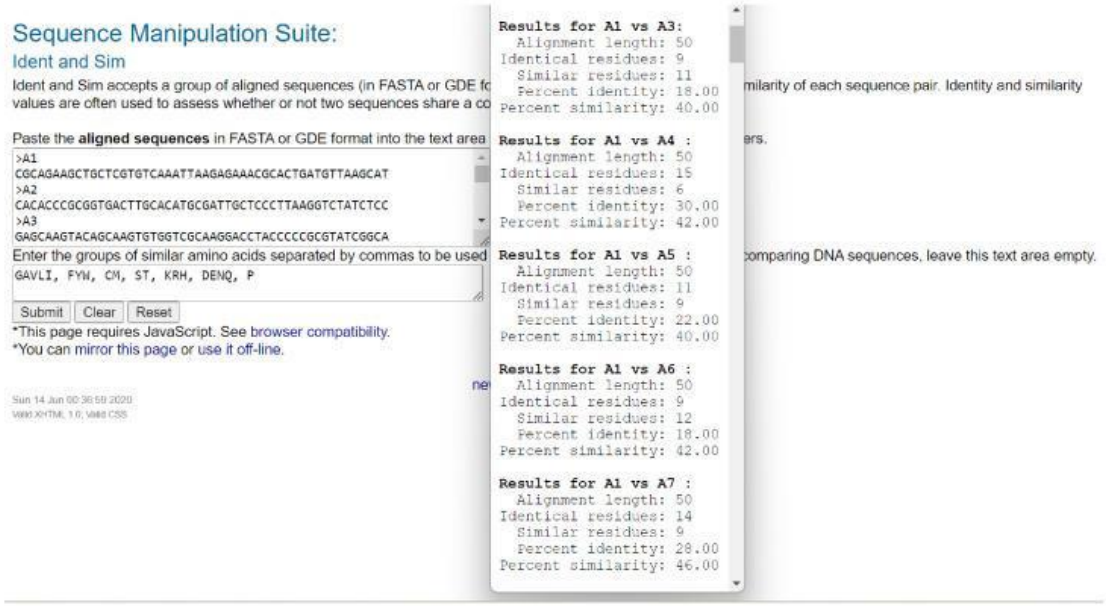
13. Another program from the Sequence Manipulation Suite (SMS) website is *Ident and Sim* (https://www.bioinformatics.org/sms2/ident_sim.html). Rani used the program to calculate the similarity of the DNA sequences that were aligned. The image below (right) is the result of several DNA sequences that Rani inserted into the program.




Analyze *the Ident and Sim results* above, which DNA groups have the closest relatives?

a. A1 vs A4

b. A1 vs A5

c. A1 vs A6

d. A1 vs A7

14. Irna did the same thing as Rani, namely taking advantage of the Ident and Sim (https://www.bioinformatics.org/sms2/ident_sim.html) to complete the final task. However, Irna did not understand how to use the program. Irna also asked Rani so that Rani gave several statements about the use of the following Ident and Sim program:

LIVEWORKSHEETS

1) Enter DNA sequence data with a limit of 20 million characters
2) Jobs can be executed by clicking *submit*
3) Enter the amino acid group separated by a comma
4) If you want to compare amino acid groups, the area above is left blank
5) The lower area is filled with amino acid groups (formed by the initial letter only)
6) Prepare multiple DNA sequences in FASTA/GDE format

As far as Irna remembers, these six statements are the way that Rani taught. However, Irna forgot the order of the process. Help Irna arrange systematic stages and sequences so that Irna can use *the Ident and Sim* program to quickly calculate the similarity of a set of DNA/amino acid sequences!

a. 1, 3, 6, 4, 5, and 2
b. 6, 1, 4, 5, 3, and 2
c. 3, 1, 6, 4, 5, and 2
d. 6, 1, 3, 4, 5, and 2

LIVEWORKSHEETS