Impact of Self-Induced Mutations on Skin Protein

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Abstract

The human skin is the biggest organ in the body and serves as the body's first line of defence against external aggressions thanks to its strategic placement at the boundary between the interior and exterior. It is becoming more and more obvious that mutations in numerous cutaneous-associated keratin genes cause a variety of genetic skin diseases, each of which is characterised by compromised specific cell-tissue integrity, impairing the skin's capacity to function as a proper barrier and withstand repeated physical trauma. Several other concepts, including identity, similarity, and homology, are frequently (mis)used to describe sequence comparisons. Even though they are frequently used interchangeably, their meanings are very distinct. It is necessary to find the right alignment of two sequences before computing their similarity. The ability to recognise sequence similarity allows us to save countless biological years to apply knowledge of one sequence to other comparable sequences.

Keywords: Sequence, patterns, alignment, identity, similarity, homology

Introduction

The structure but not usually the function of a protein can be impacted by changes in the amino acid sequence. A modification at some places, like conserved residues, however, can have an impact on the protein's structure as well as its functionality. This study illustrates how the initial amino acid sequence of a skin protein changes when mutations are introduced at various rates.

Subjects and samples

- a) Homo Sapiens- Homo sapiens (Latin for "wise man") is the name given to the human species. Homo sapiens is the sole living member of the genus Homo, which contains multiple extinct species.
- b) Gorilla- Gorillas are giant apes that are herbivorous and spend most of their time on the ground in the tropical forests of equatorial Africa. There are two species of gorillas, the eastern and western, and up to five subspecies within the genus gorilla.
- c) Nomascus leucogenya- (Northern White Cheeked Gibbon) is a species of <u>primates</u> in the family <u>gibbons</u>. They are listed as critically endangered by IUCN and in cites appendix i.

They are native to Asia. They are diurnal herbivores. Individuals can grow to 545 mm. Reproduction is viviparous. They have parental care (female provides care and paternal care).

- d) Pongo abelii- There are three different kinds of orangutans, and one of them is the Sumatran orangutan. Rarer than Bornean orangutans but more prevalent than the recently discovered Tapanuli orangutans, both of which may be found on Sumatra, this species is critically endangered and is located exclusively in the island's northern regions.
- e) Hylobates moloch- The silvery gibbon, or Javan gibbon, is a primate belonging to the genus Hylobatis and subfamily Hylobatidae. It can only be found on the Indonesian island of Java, which is in which it lives in the unspoiled rainforests at elevations of up to 2,450 meters.
- f) Pan troglotytes- Chimpanzees, or chimps as they are more commonly known, are a great ape species found across the tropical forests and savannahs of Africa. There are four recognized subspecies and a possible fifth.
- g) Rhinopethicus roxallana- Snub-nosed monkeys are a group of Old World monkeys and make up the entirety of the genus *Rhinopithecus*. The genus is rare and not fully researched. These monkeys are named for the short stump of a nose on their round faces, with nostrils arranged forward. They have relatively multicolored and long fur, particularly at the shoulders and backs.
- h) Rhinopethicus bieti- The black-and-white snub-nosed monkey (*Rhinopithecus bieti*), also known as the Yunnan snub-nosed monkey, is a large black and white primate that lives only in the southern Chinese province of Yunnan, where it is known to the locals as the Yunnan golden hair monkey. It is threatened by habitat loss, and is considered an endangered species. With their unique adaptations to their environment, these monkeys thrive at extreme altitudes despite the below freezing temperatures and thin air.[[]
- Macaca fascicularis- The crab-eating macaque is a species of cercopithecine primate found in Southeast Asia. It is additionally referred to as the long-tailed macaque or the cynomolgus monkey in research settings. The crab-eating macaque, a type of macaque, has coexisted with humans for a very long time.
- j) Macaca mulatta- One kind of Old World monkey is the rhesus macaque, more often known as the rhesus monkey. Six to nine recognized subspecies exist, with one group originating in China and the other in India.

Simulation Tool

Computational biologists employ numerous techniques, including similarity searches and sequence comparison. This method is commonly used by different kinds of biologists. The most popular tool for this is BLAST (basic local alignment search technique), which compares pairs of sequences to look for local similarities. The original article that developed

BLAST has received more than 12,000 citations in the 11 years after it was published, and using BLAST has become an essential technique in biology. Understanding how it functions, what it accomplishes, how to use it effectively, and how to evaluate previously published results are essential. Among the several current iterations of the BLAST algorithm, NCBI BLAST and WU-BLAST are the most recent. The National Centre for Biotechnology Information (NCBI) offers NCBI BLAST, whereas Washington University in St. Louis offers WU-BLAST. The principles, procedures, applications, and potential concerns of the NCBI version of BLAST are all discussed.

Performance parameter

- **Maximum Score** The Maximum Score represents the highest possible alignment score (bit-score) that may be achieved between the query sequence & the database segments. It has a relationship with the e-value that is inversely proportional.
- **Total Score** The term "Total Score" refers to the sum of the alignment scores for all of the sequences contained in the shared database.
- **Percent Query Coverage-** The term "Percent Query Coverage" refers to the proportion of the total length of the query that may be located in the segments that have been aligned.
- **E-value-** The e-value provides a measure of the likelihood that the similarity in sequences is not just the result of random chance.
- **Percent Identity-** The percentage of identity reveals how closely the query sequence is related to the sequences that have been aligned.

Experimental Findings

ORIGINAL AA SEQUENCE OF HUMAN SKIN PROTEIN

MCDQQKQPQFPPSCVKGSGLGAGQGSNGASVKCPVPCQTQTVCV

TGPAPCPTQTYVKYQVPCQTQTYVKCPAPCQRTYVKYPTPCQTYVKCPAPCQTTYV KC

PTPCQTYVKCPAPCQMTYIKSPAPCQTQTCYVQGASPCQSYYVQAPASGSTSQYCVT D

PCSAPCSTSYCCLAPRTFGVSPLRRWIQRPQNCNTGSSGCCENSGSSGCCGSGGCGCS CGCGSSGCCCLGIIPMRSRGPACCDHEDDCCC

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Fig 1 BLAST Window showing Original AMINO ACID Sequence of skin protein pasted in the text box

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Fig 2. Output 1 awaiting result

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	skin-specific protein 32 [Homo sapiens]	Homo sapiens	473	473	100%	1e-167	100.00%	250	NP_001019850.1	L	
	hypothetical protein KI723_012034 [Homo sapiens]	Homo sapiens	472	472	100%	3e-167	99.60%	250	KAI2519178.1		
	skin-specific protein 32 [Gorilla gorilla gorilla]	Gorilla gorilla gorilla	465	465	100%	1e-164	98.40%	250	XP_004026743.1	1	
	skin-specific protein 32 [Pan troglodytes]	Pan troglodytes	462	462	100%	3e-163	98.00%	250	XP_003308524.1	1	- 1
	skin-specific protein 32 [Nomascus leucogenys]	Nomascus leucogenys	444	444	100%	2e-156	94.80%	246	XP_003259317.1	1	- 1
	skin-specific protein 32 [Macaca mulatta]	Macaca mulatta	443	443	100%	8e-156	93.41%	258	XP_002801835.2	2	
	skin-specific protein 32 [Hylobates moloch]	Hylobates moloch	443	443	100%	1e-155	94.80%	246	XP_032010482.1	L	
	skin-specific protein 32 [Pongo abelii]	<u>Pongo abelii</u>	380	380	98%	1e-130	95.92%	250	XP_002810238.1	1	
	skin-specific protein 32 [Theropithecus gelada]	Theropithecus gelada	372	372	98%	9e-128	94.69%	250	XP_025253342.1	L	
	skin-specific protein 32 [Chlorocebus sabaeus]	Chlorocebus sabaeus	370	370	98%	6e-127	94.35%	253	XP_037853488.1	L	
	PREDICTED: skin-specific protein 32 isoform X1 [Colobus angolensis palliatus]	Colobus angolensis palliatus	370	370	98%	6e-127	94.76%	253	XP_011793318.1		
	skin-specific protein 32 [Rhinopithecus roxellana]	Rhinopithecus roxellana	370	370	98%	9e-127	94.29%	250	XP_030792113.1	-	
	PREDICTED: skin-specific protein 32 [Rhinopithecus bieti]	Rhinopithecus bieti	369	369	98%	1e-126	94.29%	250	XP_017713183.1	L	
	PREDICTED: skin-specific protein 32 [Mandrillus leucophaeus]	Mandrillus leucophaeus	368	368	98%	6e-126	93.95%	253	XP_011836309.1		
	hypothetical protein EGK_01300 [Macaca mulatta]	Macaca mulatta	367	367	96%	2e-125	90.32%	258	EHH15237.1		
	hypothetical protein EGM_19948 [Macaca fascicularis]	Macaca fascicularis	362	362	96%	9e-124	89.92%	258	EHH61820.1		*
	skin-specific protein 32 [Trachypithecus francoisi]	Trachypithecus francoisi	360	360	98%	1e-122	87.59%	271	XP_033051639.1	1	lbac
	skin-specific protein 32 [Macaca fascicularis]	Macaca fascicularis	358	358	96%	9e-122	84.21%	276	XP_045219182.1	1	Feed
	skin-specific protein 32 [Piliocolobus tephrosceles]	Piliocolobus tephrosceles	347	347	98%	3e-118	91.84%	239	XP_023070150.2	2	
	skin-specific protein 32 [Aotus nancymaae]	Aotus nancymaae	347	347	96%	7e-118	90.46%	251	XP_012318168.1	1	
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Fig 3. Output of original sequence

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1	Homo Sapiens	473	473	100%	1.00E- 167	100%
2	Gorilla gorilla	465	465	100%	1.00E- 164	99.60%
3	Pan troglotytes	462	462	100%	3.00E- 163	98%
4	Nomascus Leucogenya	444	444	100%	2.00E- 156	94.80%
5	Macaca mulatta	443	443	100%	8.00E- 156	93.41%
6	Hylobates moloch	443	443	100%	1.00E- 155	94.80%
7	Pongo abelii	380	380	98%	1.00E-	95.92%

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8	Rhinopithecus roxellana	370	370	98%	1.90E- 126	94.29%
9	Rhinopithecus bieti	369	369	98%	1.00E- 126	94.29%
10	Macaca fascicularis	358	358	96%	9.00E- 124	89.92%

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Fig 4 MUTATION 1 BLAST QUERY SENT

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Fig 5 Mutation 1 output 1 result awaited

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	skin-specific protein 32 [Homo sapiens]	Homo sapiens	466	466	100%	6e-165	98.80%	250	NP_00101	<u>9850.1</u>		
	hypothetical protein KI723_012034 [Homo sapiens]	Homo sapiens	465	465	100%	1e-164	98.40%	250	KAI25191	<u>78.1</u>		
Image: Second	skin-specific protein 32.[Gorilla.gorilla.gorilla]	Gorilla gorilla gorilla	458	458	100%	8e-162	97.20%	250	<u>XP_00402</u>	6743.1		- 1
Image:	skin-specific protein 32 [Pan troglodytes]	Pan troglodytes	455	455	100%	2e-160	96.80%	250	<u>XP_00330</u>	8524.1		- 1
Image: Second	skin-specific protein 32 [Pongo abelii]	Pongo abelii	372	372	98%	1e-127	94.69%	250	XP_00281	0238.1		- 1
	skin-specific protein 32 [Nomascus leucogenys]	Nomascus leucogenys	372	372	96%	2e-127	90.42%	246	<u>XP_00325</u>	<u>9317.1</u>		- 1
Image:	skin-specific protein 32.[Hylobates moloch]	Hylobates moloch	370	370	96%	4e-127	90.42%	246	<u>XP_03201</u>	0482.1		
Image:	skin-specific protein 32 [Theropithecus gelada]	Theropithecus gelada	365	365	98%	8e-125	93.47%	250	<u>XP_02525</u>	<u>3342.1</u>		
	skin-specific protein 32.[Chlorocebus sabaeus]	Chlorocebus sabaeus	363	363	98%	4e-124	93.15%	253	<u>XP_03785</u>	<u>3488.1</u>		
Image: A start and a start	PREDICTED: skin-specific protein 32 isoform X1 [Colobus angolensis palliatus]	Colobus angolensis palliatus	363	363	98%	5e-124	93.55%	253	<u>XP_01179</u>	<u>3318.1</u>		
Image: A start and a start	skin-specific protein 32 [Rhinopithecus roxellana]	Rhinopithecus roxellana	362	362	98%	1e-123	93.06%	250	XP_03079	2113.1		
	PREDICTED: skin-specific protein 32 [Rhinopithecus bieti]	Rhinopithecus bieti	362	362	98%	2e-123	93.06%	250	<u>XP_01771</u>	<u>3183.1</u>		
	PREDICTED: skin-specific protein 32 [Mandrillus leucophaeus]	Mandrillus leucophaeus	360	360	98%	4e-123	92.74%	253	XP_01183	<u>6309.1</u>		
Image: A start and a start	skin-specific protein 32 [Macaca mulatta]	Macaca mulatta	360	360	96%	4e-123	89.52%	258	XP_00280	1835.2		
	hypothetical protein EGK_01300 [Macaca mulatta]	Macaca mulatta	359	359	96%	2e-122	89.11%	258	EHH15237	7.1		
	hypothetical protein EGM_19948 [Macaca fascicularis]	Macaca fascicularis	355	355	96%	8e-121	88.71%	258	EHH61820	<u>).1</u>		č,
Image: Second	skin-specific protein 32.[Trachypithecus francoisi]	Trachypithecus francoisi	353	353	98%	9e-120	86.47%	271	XP_03305	1639.1		edba
Image: A start and a start	skin-specific protein 32 [Macaca fascicularis]	Macaca fascicularis	351	351	96%	6e-119	83.08%	276	<u>XP_04521</u>	<u>9182.1</u>		Fe
~	skin-specific protein 32.[Piliocolobus tephrosceles]	Piliocolobus tephrosceles	340	340	98%	2e-115	90.61%	239	<u>XP_02307</u>	0150.2		ш
	skin-specific protein 32.[Aotus nancymaae]	Aotus nancymaae	340	340	96%	7e-115	89.21%	251	<u>XP_01231</u>	<u>8168.1</u>		-
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Fig 6 Mutation 1 output 2

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1	Homo Sapiens	466	466	100%	6.00E- 165	98.80%
2	Gorilla gorilla	458	458	100%	8.00E- 162	97.20%
3	Pan troglotytes	455	455	100%	2.00E- 160	96.80%
	Nomascus				2.00E-	
4	Leucogenya	372	372	96%	127	90.42%
5	Macaca mulatta	360	360	96%	2.00E- 123	89.52%
6	Hylobates moloch	370	370	96%	4.00E- 127	90.42%
7	Pongo abelii	372	372	98%	1.00E- 127	94.69%
	Rhinopithecus				1.00E-	
8	roxellana	362	362	98%	123	93.06%
9	Rhinopithecus bieti	362	362	98%	2.00E- 123	93.06%
10	Macaca fascicularis	351	351	96%	6.00E- 119	83.08%

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Fig 7 MUTATION 2 BLAST QUERY SENT



Fig 8 MUTATION 2 OUTPUT 1 RESULT AWAITED

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hypothetical protein KI723_012034 [Homo sapiens]	Homo saplens	464 927	100% 6e-160	98.40% 250	KAI2519178.1	
skin-specific protein 32 [Gorilla.gorilla.gorilla]	<u>Gorilla gorilla gorilla</u>	457 913	100% 4e-157	97.20% 250	XP_004026743.1	
skin-specific protein 32 [Pan troglodytes]	Pan troglodytes	454 907	100% 6e-156	96.80% 250	XP_003308524.1	
skin-specific protein 32 [Pongo abelli]	Pongo abelli	371 743	98% 2e-123	94.69% 250	XP_002810238.1	
skin-specific protein 32 [Nomascus leucogenys]	Nomascus leucogenys	370 741	96% 3e-123	90.42% 246	XP_003259317.1	
skin-specific protein 32 [Hylobates moloch]	Hylobates moloch	369 739	96% 9e-123	90.42% 246	XP_032010482.1	
skin-specific protein 32 [Theropithecus gelada]	Theropithecus gelada	364 727	98% 2e-120	93.47% 250	XP_025253342.1	
skin-specific protein 32 (Rhinopithecus roxellana)	Rhinopithecus roxellana	362 723	98% 9e-120	93.06% 250	XP_030792113.1	
skin-specific protein 32.[Chlorocebus sabaeus]	Chlorocebus sabaeus	362 724	98% 1e-119	93.15% 253	XP_037853488.1	
PREDICTED: skin-specific protein 32 isoform X1 [Colobus angolensis palliatus]	Colobus angolensis palliatus	362 723	98% 1e-119	93.55% 253	XP_011793318.1	
PREDICTED: skin-specific protein 32.[Rhinopithecus bieti]	Rhinopithecus bieti	361 721	98% 2e-119	93.06% 250	XP_017713183.1	
PREDICTED: skin-specific protein 32 [Mandrillus leucophaeus]	Mandrillus leucophaeus	360 719	98% 6e-119	92.74% 253	XP_011836309.1	
skin-specific protein 32 [Macaca mulatta]	Macaca mulatta	360 719	96% 9e-119	89.52% 258	XP_002801835.2	
hypothetical protein EGK_01300 [Macaca mulatta]	Macaca mulatta	358 716	96% 4e-118	89.11% 258	EHH15237.1	č
hypothetical protein EGM_19948 [Macaca fascicularis]	Macaca fascicularis	353 707	96% 2e-116	88.71% 258	EHH61820.1	edba
skin-specific protein 32 [Trachypithecus francoisi]	Trachypithecus francoisi	352 704	98% 1e-115	86.47% 271	XP_033051639.1	Fee
skin-specific protein 32 (Macaca fascicularis)	Macaca fascicularis	350 699	96% 1e-114	83.08% 276	XP_045219182.1	
skin-specific protein 32 [Pillocolobus tephrosceles]	Piliocolobus tephrosceles	339 678	98% 5e-111	90.61% 239	XP_023070150.2	
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Fig 9 MUTATION 2 RESULT 2

Mutation 2

Sr.	Scientific nome	Max	Total	Query	E-	Percentage
No.	Scientific name	Score	Score	Cover	Value	Identity
	Homo Saniens				3.00E-	
1	rionio Supiens	465	929	100%	160	98.80%
					4.00E-	
2	Gorilla gorilla	457	913	100%	157	97.20%
	Don tradictutes				6.00E-	
3	Pan trogiotytes	454	907	100%	156	96.80%
	Nomascus				3.00E-	
4	Leucogenya	370	741	96%	123	90.42%
					9.00E-	
5	Macaca mulatta	360	719	96%	118	89.52%
	TT 1 1 / 1 1				9.00E-	
6	Hylobates moloch	369	739	96%	123	90.42%
	Danca abalii				2.00E-	
7	Poligo adelli	371	743	98%	123	94.69%
	Rhinopithecus				9.00E-	
8	roxellana	362	723	98%	120	93.06%
					2.00E-	
9	Rhinopithecus bieti	361	721	98%	119	93.06%
		l				

	Magaga fassioularis				1.00E-	
10	Macaca fascicularis	353	707	96%	114	88.71%

MUTATION 3 at position 2 replace C with P at position 11,12 replace P P with T T at position 43 replace C with G

MPDQQKQPQFTTSCVKGSGLGAGQGSNGASVKCPVPCQTQTVGV

TGPAPCPTQTYVKYQVPCQTQTYVKCPAPCQRTYVKYPTPCQTYVKCPAPCQTTYV KC

PTPCQTYVKCPAPCQMTYIKSPAPCQTQTCYVQGASPCQSYYVQAPASGSTSQYCVT D

PCSAPCSTSYCCLAPRTFGVSPLRRWIQRPQNCNTGSSGCCENSGSSGCCGSGGCGCS

CGCGSSGCCCLGIIPMRSRGPACCDHEDDCCC

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Fig 10 MUTATION 3 BLAST QUERY SENT

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Fig 11. MUTATION 3 RESULT 1

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	Description	Scientific Name	Max Score S	Total Query Score Cover	E value	Per. Ident	Acc. Len	Accession	
	skin-specific protein 32 [Homo sapiens]	Homo sapiens	461	461 100%	5e-163	98.40%	250	NP_001019850.1	
	hypothetical protein KI723_012034 [Homo sapiens]	Homo sapiens	461	461 100%	1e-162	98.00%	250	KAI2519178.1	
	skin-specific protein 32 [Gorilla gorilla gorilla]	Gorilla gorilla gorilla	454	454 100%	6e-160	96.80%	250	XP_004026743.1	
	skin-specific protein 32 [Pan troglodytes]	Pan troglodytes	450	450 100%	2e-158	96.40%	250	XP_003308524.1	
	skin-specific protein 32 [Pongo abelii]	Pongo abelii	367	367 97%	2e-125	94.65%	250	<u>XP_002810238.1</u>	
	skin-specific protein 32 [Nomascus leucogenys]	Nomascus leucogenys	366	366 96%	2e-125	90.00%	246	XP_003259317.1	
	skin-specific protein 32 [Hylobates moloch]	Hylobates moloch	365	365 95%	6e-125	90.34%	246	XP_032010482.1	
	skin-specific protein 32 [Theropithecus gelada]	Theropithecus gelada	364	364 98%	2e-124	93.47%	250	XP_025253342.1	
	skin-specific protein 32 [Chlorocebus sabaeus]	Chlorocebus sabaeus	358	358 98%	5e-122	92.74%	253	XP_037853488.1	
	PREDICTED: skin-specific protein 32 isoform X1 [Colobus angolensis palliatus]	Colobus angolensis palliatus	357	357 98%	6e-122	93.15%	253	XP_011793318.1	
	skin-specific protein 32 [Rhinopithecus roxellana]	Rhinopithecus roxellana	357	357 97%	9e-122	93.00%	250	<u>XP_030792113.1</u>	
	PREDICTED: skin-specific protein 32 [Rhinopithecus bieti]	Rhinopithecus bieti	357	357 97%	1e-121	93.00%	250	<u>XP_017713183.1</u>	
	skin-specific protein 32 [Macaca mulatta]	Macaca mulatta	356	356 96%	4e-121	89.11%	258	XP_002801835.2	
	PREDICTED: skin-specific protein 32 [Mandrillus leucophaeus]	Mandrillus leucophaeus	355	355 98%	5e-121	92.34%	253	XP_011836309.1	ack
	hypothetical protein EGK_01300 [Macaca mulatta]	Macaca mulatta	354	354 96%	1e-120	88.71%	258	EHH15237.1	edbi
	hypothetical protein EGM_19948 [Macaca fascicularis]	Macaca fascicularis	350	350 96%	9e-119	88.31%	258	<u>EHH61820.1</u>	Ē
	skin-specific protein 32 [Trachypithecus francoisi]	Trachypithecus francoisi	347	347 98%	1e-117	86.09%	271	<u>XP_033051639.1</u>	
	skin-specific protein 32 [Macaca fascicularis]	Macaca fascicularis	346	346 96%	4e-117	82.71%	276	XP_045219182.1	-
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Fig 12 MUTATION 3 RESULT 2

Sr.	Scientific nome	Max	Total	Query	E-	Percentage
No.	Scientific name	Score	Score	Cover	Value	Identity
					5.00E-	
1	Homo Sapiens	461	461	100%	163	98.40%
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2	Gorilla gorilla	454	454	100%	160	96.80%
					2.005	
3	Pan troglotytes	450	450	100%	2.00E- 158	96 40%
5			450	10070	150	20.4070
	Nomascus		_		2.00E-	
4	Leucogenya	366	366	96%	125	90.00%
	Maaaaa mulatta				4.00E-	
5		356	356	96%	121	89.11%
					6.00E-	
6	Hylobates moloch	365	365	95%	125	90.34%
					2 00F-	
7	Pongo abelii	367	367	97%	125	94.65%
	D1: :4				0.005	
0	Rhinopithecus	257	257	070/	9.00E-	02 000/
0	roxenana	557	557	97%	122	95.00%
	Rhinopithecus bieti				1.00E-	
9		357	357	97%	121	93.00%
	Magaga faggiaularia	•			9.00E-	
10	wacaca fascicularis	350	350	96%	119	88.31%

Culminated Tabular representation of Results

Max Score

Sr. No.	Output: Scientific name	Original	Mutation1	Mutation2	Mutation3
1	Homo Sapiens	473	466	465	461
2	Gorilla gorilla	465	458	457	454
3	Pan troglotytes	462	455	454	450

	Nomascus				
4	Leucogenya	444	372	370	366
5	Macaca mulatta	443	360	360	356
6	Hylobates moloch	443	370	369	365
7	Pongo abelii	380	372	371	367
	Rhinopithecus				
8	roxellana	370	362	362	357
9	Rhinopithecus bieti	369	362	361	357
10	Macaca fascicularis	358	351	353	350
	1	1			

Total Score					
Sr. No.	Output: Scientific name	Original	Mutation1	Mutation2	Mutation3
1	Homo Sapiens	473	466	929	461
2	Gorilla gorilla	465	458	913	454
3	Pan troglotytes	462	455	907	450
	Nomascus				
4	Leucogenya	444	372	741	366
5	Macaca mulatta	443	360	719	356
6	Hylobates moloch	443	370	739	365
7	Pongo abelii	380	372	743	367
	Rhinopithecus				
8	roxellana	370	362	723	357
9	Rhinopithecus bieti	369	362	721	357
10	Macaca fascicularis	358	351	707	350
		1			

Query Cover

Sr. No.	Output: Scientific name	Original	Mutation1	Mutation2	Mutation3
1	Homo Sapiens	100%	100%	100%	100%
2	Gorilla gorilla	100%	100%	100%	100%
3	Pan troglotytes	100%	100%	100%	100%
	Nomascus				
4	Leucogenya	100%	96%	96%	96%
5	Macaca mulatta	100%	96%	96%	96%
6	Hylobates moloch	100%	96%	96%	95%
7	Pongo abelii	98%	98%	98%	97%
	Rhinopithecus				
8	roxellana	98%	98%	98%	97%
9	Rhinopithecus bieti	98%	98%	98%	97%
10	Macaca fascicularis	96%	96%	96%	96%

E-Value					
Sr. No.	Output: Scientific name	Original	Mutation1	Mutation2	Mutation3
1	Homo Sapiens	1.00E- 167	6.00E- 165	3.00E- 160	5.00E- 163
2	Gorilla gorilla	1.00E- 164	8.00E- 162	4.00E- 157	6.00E- 160
3	Pan troglotytes	3.00E- 163	2.00E- 160	6.00E- 156	2.00E- 158
4	Nomascus Leucogenya	2.00E- 156	2.00E- 127	3.00E- 123	2.00E- 125
5	Macaca mulatta	8.00E- 156	2.00E- 123	9.00E- 118	4.00E- 121
6	Hylobates moloch	1.00E- 155	4.00E- 127	9.00E- 123	6.00E- 125

7	Pongo abelii	1.00E- 130	1.00E- 127	2.00E- 123	2.00E- 125
8	Rhinopithecus roxellana	1.90E- 126	1.00E- 123	9.00E- 120	9.00E- 122
9	Rhinopithecus bieti	1.00E- 126	2.00E- 123	2.00E- 119	1.00E- 121
10	Macaca fascicularis	9.00E- 124	6.00E- 119	1.00E- 114	9.00E- 119

Percentage					
Identity					
Sr. No.	Output: Scientific name	Original	Mutation1	Mutation2	Mutation3
1	Homo Sapiens	100%	98.80%	98.80%	98.40%
2	Gorilla gorilla	99.60%	97.20%	97.20%	96.80%
3	Pan troglotytes	98%	96.80%	96.80%	96.40%
	Nomascus				
4	Leucogenya	94.80%	90.42%	90.42%	90.00%
5	Macaca mulatta	93.41%	89.52%	89.52%	89.11%
6	Hylobates moloch	94.80%	90.42%	90.42%	90.34%
7	Pongo abelii	95.92%	94.69%	94.69%	94.65%
	Rhinopithecus				
8	roxellana	94.29%	93.06%	93.06%	93.00%
9	Rhinopithecus bieti	94.29%	93.06%	93.06%	93.00%
10	Macaca fascicularis	89.92%	83.08%	88.71%	88.31%

Conclusion

Researchers can now assess the genomic makeup of a broad variety of different animals thanks to the concurrent development of huge volumes of sequencing initiatives and bioinformatics tools like BLAST. This has aided bioinformatics in bridging the gap between computer science and biology, which is crucial for the further development of the field. As a

result, the analysis of genome sequence data using bioinformatics techniques has become an essential part of modern scientific research. BLAST is one of the most well-known techniques in the field of bioinformatics, and because it is available to all researchers online, it is commonly used to categorise sequences according to their functional and taxonomic characteristics. Applications include everything from testing to general expansion into sequence-based data, ranging from the analysis of raw sequence data to the assessment of genomic similarities.

Future Scope

In addition to identifying genes, classifying protein structures, making gene predictions, identifying genes, and diagnosing various illnesses that influence how genes are expressed, among other things, it is possible to analyse the evidence for evolution and to extract useful patterns in gene expression. Data mining, which is crucial for pattern identification, categorization of data, for predicting events, or for induction within genetic networks, gives the ability to analyse bioinformatics information.

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