

Исходные данные:
Белок: P00395

UniProt

UniProtKB

BLAST Align Retrieve/ID mapping Peptide search SPARQL

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UniProtKB - P00395 (COX1_HUMAN)

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Protein

Gene

Organism

Status

Cytochrome c oxidase subunit 1

MT-CO1

Homo sapiens (Human)

Reviewed - Annotation score: - Experimental evidence at protein level

Function

Names & Taxonomy

Subcellular location

Pathology & Biotech

FTM / Processing

Expression

Interaction

Structure

Family & Domains

Sequence

Similar proteins

Function

Component of the cytochrome c oxidase, the last enzyme in the mitochondrial electron transport chain which drives oxidative phosphorylation. The respiratory chain contains 3 multisubunit complexes succinate dehydrogenase (complex II, CII), ubiquinol-cytochrome c oxidoreductase (cytochrome b-c1 complex, complex III, CIII) and cytochrome c oxidase (complex IV, CIV), that cooperate to transfer electrons derived from NADH and succinate to molecular oxygen, creating an electrochemical gradient over the inner membrane that drives transmembrane transport and the ATP synthase. Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Electrons originating from reduced cytochrome c in the intermembrane space (IMS) are transferred via the dinuclear copper center (Cu(A)) of subunit 2 and heme A of subunit 1 to the active site in subunit 1, a binuclear center (BNC) formed by heme A3 and copper B (Cu(B)). The BNC reduces molecular oxygen to 2 water molecules using 4 electrons from cytochrome c in the IMS and 4 protons from the mitochondrial matrix.

Catalytic activity

4 [Fe(II)-cytochrome c] + 8 H⁺(in) + O₂ = 4 [Fe(III)-cytochrome c] + 4 H⁺(out) + 2 H₂O

EC:7.1.1.9

This reaction proceeds in the forward direction.

Source: Rhea.

Fe(II)cytochrome c

H⁺(in)

O₂

Fe(III)cytochrome c

H⁺(out)

Запускаю Блэст

Job status: RUNNING

Running **blastp** job against **UNIPROTKB_REFPROTSWISSPROT** for 10s

Job information

Query sequence	<pre>>sp P00395 COX1_HUMAN Cytochrome c oxidase subunit 1 OS=Homo sapiens OX=9606 GN=MT-CO1 PE=1 SV=1 MFADRMFLFSTNHKIDIGTLVLLFGAWAGVLGTALLSLLIRAEIGQPGNLLGNDHIYNNIVITA HAFVMIFFFHNPIMIGGFGHMLVPIUNIGAPDMAFRPMNMISFHLPPSLLLLASAMVEA GAGTGMTVYYPPLAGNYSHPGASVDLTIFSLHLAGVSSILGAINFITTTIINPKPPAMTQYQ TPLFWISVLITAVLLLSLPVLAAGITMILLTDRLNLTTFDPAAGGDPILYQHLFWFFGH PEVYILTLPGFGMISHIVTYYSKGKEPFYNGHVMWAMISIGFLGFIVMAHHFTVGNDDVD TRAYTSATMIIAIPGKVFSHLATLHGSNWKWSAAVLWALGFILFTVGGTLGIVLAN SSLDIVLHDTYYVAHPHYVLSMGAVFAINGGFIHWFPLFSGYTLDDQTYAKIHFTIMFIG VILTFPQHFLGLSGMPRRYSOYPDAYTTWNLSSVGSFISLTAVMLMIFHIEAFASKR KVLNVEEPSMNLMLYGCPPPYHTFEPPVYVNS</pre>
Job identifier	B20220223F248CABF64506F29A91F8037F07B67D102FF8E4 (jobs are stored for 7 days)
Program	blastp
Matrix	blosum62
Threshold	10
Filtered	false
Gapped	true
Maximum number of hits reported	250

Tools

Core data

Supporting data

Information

Job information

Query sequence	<pre>>sp P00395 COX1_HUMAN Cytochrome c oxidase subunit 1 OS=Homo sapiens OX=9606 GN=MT-CO1 PE=1 SV=1 MFADRWLFSTNHKDIGTLYLLFGAWAGVLGTALSLIRAE LGQGNLLGNDHIYNVIVTA HAFVMIFFMVMPTMIGGFGNVLPLMIGAPDMAFPRMNMMSFWLLPPSLLLLLASAMVEA GAGTGWTVYPPLAGNYSHPGASVDLTIFSLHLAGVSSILGAINFITTIINMKPPAMTQYQ TPLFWWSVLITAVLLLLSLPVLAAGITMLLTDRLNLTTFDPAAGGDPIYQHLFWFFGH PEVYILILPGFGMISHIVTYYSKGKPEFGYMGVMWAMMSIGFLGFIWAHMMFTVGMDDV TRAYFTSATMIIAIP TGKVFSLATLHGSNMKWSAAVLWALGFIFLFTVGGLTGIVLAN SSLDIVLHDTYYVAHFHYVLSMGAVFAIMGGFIHWFPLFSGYTLDDQTYAKIHFTIMFIG VNLTFPQHFLGLSGMPRRYSYDPDAYTTWNILSSVGSFISLTAVMLMIFMIWEAFASKR KVLHVEEPSMNLWLYGCPPPYHTFEPPVYMK5</pre>
Date of job execution	2022-02-23
Job identifier	B20220223F248CABF64506F29A91F8037F07B67D102FF8E4 (jobs are stored for 7 days)
Running time	115.5 seconds
Scheduled time	92.6 seconds
Program	blastp (blastp BLASTP 2.9.0+)
Database	uniprotkb_refprotswissprot (Protein) generated for BLAST on Nov 17, 2021
Sequences	64,899,224 sequences consisting of 25,452,742,688 letters
Matrix	blosum62
Threshold	10
Filtered	false
Gapped	true
Maximum number of hits reported	250

Результаты:

BLAST

Filter by: Reviewed (108) Swiss-Prot, Unreviewed (142) TrEMBL, With 3D structure (3), Popular organisms: Human (1), Mouse (1), Zebrafish (1), A. thaliana (2), Rat (1), All (250)

Map to: UniProtKB, UniRef, UniParc, View by: Results table

Identity % scale: 100 to 0

Overview

Entry	Protein names	Match Int.	Identity
P00395	Cytochrome c oxidase subunit 1 (Homo sapiens)	100	100.0%
Q9T9W1	Cytochrome c oxidase subunit 1 (Pan troglodytes)	98	98.8%
Q9T9X0	Cytochrome c oxidase subunit 1 (Pan paniscus)	98	98.8%
G3SHV8	Cytochrome c oxidase subunit 1 (Gorilla gorilla gorilla)	98	98.4%

Alignments

Entry	Alignment overview	Info	Status
P00395	COX1_HUMAN - Cytochrome c oxidase subunit 1 Homo sapiens (Human) - View alignment	E-value: 0.0 Score: 2,732 Ident.: 100.0%	

То есть нашлось 250 совпадений

Лучшие находки : 1ая - P00395 с Identity = 100%

2ая находка Q9T9W1 с Identity = 98.8%

Для logo: (нашел сам себя, никто такое не запрещал)

Данные из Swiss-Prot

Protein

Cytochrome c oxidase subunit 1

Gene

MT-CO1

Organism

Homo sapiens (Human)

UniProtKB - P00395 (COX1_HUMAN)

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Status

Cytochrome c oxidase subunit 1

MT-CO1

Homo sapiens (Human)

Reviewed - Annotation score: ★★★★★ - Experimental evidence at protein level¹

Function

Names & Taxonomy

Subcellular location

Pathology & Biotech

PTM / Processing

Expression

Interaction

Structure

Family & Domains

Sequence

None

Function¹

Component of the cytochrome c oxidase, the last enzyme in the mitochondrial electron transport chain which drives oxidative phosphorylation. The respiratory chain contains 3 multisubunit complexes succinate dehydrogenase (complex II, CII), ubiquinol-cytochrome c oxidoreductase (cytochrome b-c1 complex, complex III, CIII) and cytochrome c oxidase (complex IV, CIV), that cooperate to transfer electrons derived from NADH and succinate to molecular oxygen, creating an electrochemical gradient over the inner membrane that drives transmembrane transport and the ATP synthase. Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Electrons originating from reduced cytochrome c in the intermembrane space (IMS) are transferred via the dinuclear copper A center (CU(A)) of subunit 2 and heme A of subunit 1 to the active site in subunit 1, a binuclear center (BNC) formed by heme A3 and copper B (CU(B)). The BNC reduces molecular oxygen to 2 water molecules using 4 electrons from cytochrome c in the IMS and 4 protons from the mitochondrial matrix.

By similarity

Catalytic activity¹

4 [Fe(II)cytochrome c] + 8 H⁺(in) + O₂ = 4 [Fe(III)cytochrome c] + 4 H⁺(out) + 2 H₂O

By similarity

EC:7.1.1.9

By similarity

This reaction proceeds in the forward direction.

By similarity

Source: Rhea. < Hide

- E-value: 0.0
- Score: 2732
- Ident.: 100.0%
- Positives : 100.0%
- Query Length: 513
- Match Length: 513

<input type="checkbox"/>	P00395	COX1_HUMAN - Cytochrome c oxidase subunit 1 Homo sapiens (Human) - View alignment	E-value: 0.0 Score: 2,732 Ident.: 100.0%		
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Покрытие :

P00395	COX1_HUMAN	1	MFADRWLFSTNHKDIGTLYLLFGAWAGVLGTALSLLIRAE	60
P00395	COX1_HUMAN	1	MFADRWLFSTNHKDIGTLYLLFGAWAGVLGTALSLLIRAE	60
P00395	COX1_HUMAN	61	HAFVMIFFMVMPIMIGGFGNWLVP	120
P00395	COX1_HUMAN	61	HAFVMIFFMVMPIMIGGFGNWLVP	120
P00395	COX1_HUMAN	121	GAGTGWTVYPPLAGNYSHPGASVDLTIFSLHLAGVSSILGAINFITTIINMKPPAMTQYQ	180
P00395	COX1_HUMAN	121	GAGTGWTVYPPLAGNYSHPGASVDLTIFSLHLAGVSSILGAINFITTIINMKPPAMTQYQ	180
P00395	COX1_HUMAN	181	TPLFVWSVLITAVLLLLSLPVLAA	240
P00395	COX1_HUMAN	181	TPLFVWSVLITAVLLLLSLPVLAA	240
P00395	COX1_HUMAN	241	PEVYILILPGFGMISHIVTYYS	300
P00395	COX1_HUMAN	241	PEVYILILPGFGMISHIVTYYS	300
P00395	COX1_HUMAN	301	TRAYFTSATMIIAIP	360
P00395	COX1_HUMAN	301	TRAYFTSATMIIAIP	360
P00395	COX1_HUMAN	361	SSLDIVLHDTYVVVAHFHYVLSMGAVFAIMGGFIHWFFLFSGYTLDQTYAKIHFTIMFIG	420
P00395	COX1_HUMAN	361	SSLDIVLHDTYVVVAHFHYVLSMGAVFAIMGGFIHWFFLFSGYTLDQTYAKIHFTIMFIG	420
P00395	COX1_HUMAN	421	VNLTFPPQHFLGLSGMPRRYS	480
P00395	COX1_HUMAN	421	VNLTFPPQHFLGLSGMPRRYS	480
P00395	COX1_HUMAN	481	KVLMVEEPSMNLEWLYGCPPPYHTFEEFVYMK	513
P00395	COX1_HUMAN	481	KVLMVEEPSMNLEWLYGCPPPYHTFEEFVYMK	513

Для 2ого:

UniProtKB - Q9T9W1 (COX1_PANTR)

Display

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Protein

Gene

Organism

Status

Cytochrome c oxidase subunit 1

MT-CO1

Pan troglodytes (Chimpanzee)

Reviewed - Annotation score: - Protein inferred from homologyⁱ

Functionⁱ

Component of the cytochrome c oxidase, the last enzyme in the mitochondrial electron transport chain which drives oxidative phosphorylation. The respiratory chain contains 3 multisubunit complexes succinate dehydrogenase (complex II, CII), ubiquinol-cytochrome c oxidoreductase (cytochrome b-c1 complex, complex III, CIII) and cytochrome c oxidase (complex IV, CIV), that cooperate to transfer electrons derived from NADH and succinate to molecular oxygen, creating an electrochemical gradient over the inner membrane that drives transmembrane transport and the ATP synthase. Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Electrons originating from reduced cytochrome c in the intermembrane space (IMS) are transferred via the dinuclear copper A center (CU(A)) of subunit 2 and heme A of subunit 1 to the active site in subunit 1, a binuclear center (BNC) formed by heme A3 and copper B (CU(B)). The BNC reduces molecular oxygen to 2 water molecules using 4 electrons from cytochrome c in the IMS and 4 protons from the mitochondrial matrix.

By similarity

Catalytic activityⁱ

4 [Fe(II)cytochrome c] + 8 H⁺(in) + O₂ = 4 [Fe(III)cytochrome c] + 4 H⁺(out) + 2 H₂O

EC:7.1.1.9

By similarity

This reaction proceeds in the forward

By similarity

direction.

Source: Rhea.

Hide

Protein
Cytochrome c oxidase subunit 1

Gene
MT-CO1

Organism
Pan troglodytes (Chimpanzee)

<input type="checkbox"/>	Q9T9W1	COX1_PANTR - Cytochrome c oxidase subunit 1 - Pan troglodytes ... - View alignment	E-value: 0.0 Score: 2,707 Ident.: 98.8%		
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- E-value: 0.0
- Score: 2707
- Ident.: 98.8%
- Positives : 99.2%
- Query Length: 513
- Match Length: 513

Покрытие :

P00395	COX1_HUMAN	1	MFADRWLFSTNNHKDIGTLYLLFGAWAGVLGTALSLIRAEELGQPGNLLGNDHIYNVIVTA	60
Q9T9W1	COX1_PANTR	1	MF DRWLFSTNNHKDIGTLYLLFGAWAGVLGTALSLIRAEELGQPGNLLGNDHIYNVIVTA	60
P00395	COX1_HUMAN	61	HAFVMIFFMVMPIMIGGFGNWLVPMLIGAPDMAFPRMNNMSFWLLPPSLLLLLASAMVEA	120
Q9T9W1	COX1_PANTR	61	HAFVMIFFMVMPIMIGGFGNWLVPMLIGAPDMAFPRMNNMSFWLLPPSLLLLLASAMVEA	120
P00395	COX1_HUMAN	121	GAGTGWTVYPPLAGNYSHPGASVDLTIFSLHLAGVSSILGAINFITTIIINMKPPAMTQYQ	180
Q9T9W1	COX1_PANTR	121	GAGTGWTVYPPLAGNYSHPGASVDLTIFSLHLAGVSSILGAINFITTIIINMKPPAMTQYQ	180
P00395	COX1_HUMAN	181	TPLFVWSVLITAVLLLLSLFVLAAGITMLLTDRNLNTTFFDPAGGGDPILYQHLFWFFGH	240
Q9T9W1	COX1_PANTR	181	TPLFVWSVLITAVLLLLSLFVLAAGITMLLTDRNLNTTFFDPAGGGDPILYQHLFWFFGH	240
P00395	COX1_HUMAN	241	PEVYILILPGFGMISHIVTYYSGKKEPFGYMGVMWAMMSIGFLGFIVWAHMFVGMVDVD	300
Q9T9W1	COX1_PANTR	241	PEVYILILPGFGMISHIVTYYSGKKEPFGYMGVMWAMMSIGFLGFIVWAHMFVGMVDVD	300
P00395	COX1_HUMAN	301	TRAYFTSATMIIAIPRGVVFVSWLATLHGSNMKWSAAVLWALGFIFLFTVGGTIGIVLAN	360
Q9T9W1	COX1_PANTR	301	TRAYFTSATMIIAIPRGVVFVSWLATLHGSNMKWSAAVLWALGFIFLFTVGGTIGIVLAN	360
P00395	COX1_HUMAN	361	SSLDIVLHDTYYVVAHFHYVLSMGAVFAIMGGFIHWFFLFSGYTLDQTYAKIHFTIMFIG	420
Q9T9W1	COX1_PANTR	361	SSLDIVLHDTYYVVAHFHYVLSMGAVFAIMGGFIHWFFLFSGYTLDQTYAKI F IMFIG	420
P00395	COX1_HUMAN	421	VNLTFFFPQHFLGLSGMPRRYSYDPDAYTTWNILSSVGSFISLTAVMLMIFMIWEAFASKR	480
Q9T9W1	COX1_PANTR	421	VNLTFFFPQHFLGLSGMPRRYSYDPDAYTTWNILSSVGSFISLTAVMLMIFMIWEAFASKR	480
P00395	COX1_HUMAN	481	KVLMVEEPSMNLEWLYGCPPPYHTFEPPVYMK	513
Q9T9W1	COX1_PANTR	481	KVLMVEEPSNLEWLYGCPPPYHTFEPPVYMK	513

*По цифрам справа можно посчитать несовпадения-гепы

Все находки имеют Е-значение = 0.0, сотых не видно. Я думаю, что в данном случае лимит стоит на максимальным числом находок, но 250 является максимально допустимым (там где я запускала- а точнее не изменяемым). *Запускала я из <https://www.uniprot.org/blast/uniprot/B20220223F248CABF64506F29A91F8037F07B67D102FF8E4> (UNIPROT)

Поменяем параметры в Blastp:

General Parameters

Max target sequences	<div>1000</div> <div>Select the maximum number of aligned sequences to display ?</div>
Short queries	<div><input checked="" type="checkbox"/> Automatically adjust parameters for short input sequences ?</div>
Expect threshold	<div>10</div> <div>?</div>
Word size	<div>6</div> <div>?</div>
Max matches in a query range	<div>0</div> <div>?</div>

Scoring Parameters

Matrix	<div>BLOSUM62</div> <div>?</div>
Gap Costs	<div>Existence: 11 Extension: 1</div> <div>?</div>
Compositional adjustments	<div>Conditional compositional score matrix adjustment</div> <div>?</div>

Filters and Masking


Filter	<div><input checked="" type="checkbox"/> Low complexity regions ?</div>
Mask	<div><input type="checkbox"/> Mask for lookup table only ?</div> <div><input type="checkbox"/> Mask lower case letters ?</div>

Я оставила таким же threshold, и увеличила кол-во таргетных последовательностей(чтобы проверить предположение выше)

<https://blast.ncbi.nlm.nih.gov/Blast.cgi>

Действительно, нашлось еще больше последовательностей, но все тоже с E-значением = 0.0

Фильтр по E-значению выдал пустой результат


Your results are filtered to match records with expect value between 0.01 and 10.

Job Title	sp P00395 COX1_HUMAN Cytochrome c oxidase...		
RID	1D2E4JEV016	Search expires on 02-25 02:23 am	Download All
Program	Citation		
Database	nr	See details	
Query ID	lcl Query_78983		
Description	sp P00395 COX1_HUMAN Cytochrome c oxidase subunit ...		
Molecule type	amino acid		
Query Length	513		
Other reports	?		

Filter Results

Percent Identity

to

E value


to

Query Coverage

to

Filter

Reset


No significant similarity found. For reasons why, [click here](#)

Поменяю параметры еще раз:

General Parameters

Max target sequences

5000

Select the maximum number of aligned sequences to display ?

Short queries

☒ Automatically adjust parameters for short input sequences ?

Expect threshold

10

Expected number of chance matches in a random model. [more...](#) [YouTube](#) [Expect value tutorial](#)

Word size

6

?

Max matches in a query range

0

?

Scoring Parameters

Matrix

BLOSUM62

?

Gap Costs

Existence: 11 Extension: 1

?

Compositional adjustments

Conditional compositional score matrix adjustment

?

Filters and Masking

Filter

☐ Low complexity regions ?

Mask

☐ Mask for lookup table only ?

☐ Mask lower case letters ?

Таким образом я попытаюсь получить меньше результатов, но возможно с увеличенным Е-значением

Мой компьютер завис:

< Edit Search

Save Search

Search Summary

How to read this report?

BLAST Help Videos

Back to Traditional Results Page

Job Title

sp|P00395|COX1_HUMAN Cytochrome c oxidase...

RID

1D2SSU22013 Search expires on 02-25 02:29 am Download All

Program

BLASTP Citation

Database

nr See details

Query ID

Id|Query_80918

Description

sp|P00395|COX1_HUMAN Cytochrome c oxidase subunit 1 OS

Molecule type

amino acid

Query Length

513

Other reports

Distance tree of results Multiple alignment MSA viewer

Filter Results

Organism

only top 20 will appear

☐ exclude

Type common name, binomial, taxid or group name

Add organism

Percent Identity

E value

Query Coverage

to to to

Filter

Reset

Compare these results against the new Clustered nr database ?

BLAST

Descriptions

Graphic Summary

Sequences producing significant alignments

Download

Manage Columns

Show

5000

☐ select all 0 sequences selected

GenPept

Graphics

Distance tree of results

Multiple alignment

MSA Viewer

	Description	Scientific Name	Common Name	Taxid	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input type="checkbox"/>	cytochrome c oxidase subunit I (Homo sapiens)	Homo s...	human	9606	1027	1027	100%	0.0	100.00%	516	ACA22152.1
<input type="checkbox"/>	cytochrome c oxidase subunit I (Homo sapiens)	Homo s...	human	9606	1027	1027	100%	0.0	100.00%	516	AAK17768.1

Теория не сработало, нашлось таки 5000 мэтчей

Sequences producing significant alignments

☒ select all 5000 sequences selected

Фильтрация по Е-значению снова не принесла желаемого результата

i Your results are filtered to match records with expect value between 0.001 and 10.

Job Title	sp P00395 COX1_HUMAN Cytochrome c oxidase...
RID	1D2SSU22013 Search expires on 02-25 02:29 am Download All ▼
Program	? Citation ▼
Database	nr See details ▼
Query ID	lcl Query_80918
Description	sp P00395 COX1_HUMAN Cytochrome c oxidase subunit ...
Molecule type	amino acid
Query Length	513
Other reports	?

Filter Results

Percent Identity	E value	Query Coverage
<input type="text"/> to <input type="text"/>	<input type="text"/> 0.001 to <input type="text"/>	<input type="text"/> to <input type="text"/>
Filter		Reset

A No significant similarity found. For reasons why, [click here](#)

то есть все метчи имеют Е-значение = 0.0

Теперь поменяю длину слова

General Parameters

Max target sequences

5000
Select the maximum number of aligned sequences to display

Short queries

☒ Automatically adjust parameters for short input sequences

Expect threshold

10
Expected number of chance matches in a random model. [more...](#) [YouTube](#) [Expect value tutorial](#)

Word size

2

Max matches in a query range

0

Scoring Parameters

Matrix

BLOSUM62

Gap Costs

Existence: 11 Extension: 1

Compositional adjustments

Conditional compositional score matrix adjustment

Filters and Masking

Filter

☐ Low complexity regions

Mask

☐ Mask for lookup table only
☐ Mask lower case letters

BLAST

Search **database nr** using **Blastp (protein-protein BLAST)**
☒ Show results in a new window

Я сломала Блaст

There was a problem with the search. Please, contact [Help Desk](#) and include RID 1D3ASZC3016.
CPU usage limit was exceeded. You may need to change your search strategy. Helpful changes include reducing the number of queries, choosing a smaller database and setting an organism limit. You may also need to adjust the Algorithm parameters in the bottom section of the form. Choose a smaller number of target sequences, set a smaller Expect cut-off, use a larger word-size and turn on species specific repeats.

Job Title

sp|P00395|COX1_HUMAN Cytochrome c oxidase...

RID

1D3ASZC3016 Search expires on 02-25 02:39 am [Download All](#)

Program

[Citation](#)

Database

nr [See details](#)

Query ID

Id|Query_87002

Description

sp|P00395|COX1_HUMAN Cytochrome c oxidase subunit ...

Molecule type

amino acid

Query Length

513

Other reports

[?](#)

Filter Results

Percent Identity

to

E value

to

Query Coverage

to

Filter

Reset

No significant similarity found. For reasons why, [click here](#)

По итогу опять получили 5000 метчей

фильтр по E-значению опять дал 0 результатов

Е-значение от 0.000000001 до 0.001

 No significant similarity found. For reasons why, [click here](#)

i Your results are filtered to match records with expect value between 1e-12 and 0.001.

Job Title	sp P00395 COX1_HUMAN Cytochrome c oxidase...
RID	1D3GV5EW013 <small>Search expires on 02-25 02:42 am</small> Download All ▼
Program	? Citation ▼
Database	nr See details ▼
Query ID	Id Query_65435
Description	sp P00395 COX1_HUMAN Cytochrome c oxidase subunit ...
Molecule type	amino acid
Query Length	513
Other reports	?

Filter Results

Percent Identity

to

E value

1e-12 to 0.001

Query Coverage

to

[Filter](#) [Reset](#)

A No significant similarity found. For reasons why, [click here](#)

Тем ни менее из отличий с заданием №1 могу отметить, что появились результаты с более высоким совпадением как 99%

<input type="checkbox"/>	cytochrome c oxidase subunit I [Homo sapiens]	Homo s...	human	9606	1027	1027	100%	0.0	100.00%	516	ACA22152.1
<input type="checkbox"/>	cytochrome c oxidase subunit I [Homo sapiens]	Homo s...	human	9606	1027	1027	100%	0.0	100.00%	516	AAK17768.1
<input type="checkbox"/>	cytochrome c oxidase subunit I [Homo sapiens]	Homo s...	human	9606	1026	1026	100%	0.0	100.00%	514	ABB78366.1
<input type="checkbox"/>	cytochrome c oxidase subunit I [Homo sapiens]	Homo s...	human	9606	1026	1026	100%	0.0	100.00%	516	AQU28739.1
<input type="checkbox"/>	cytochrome c oxidase subunit I [Homo sapiens neanderthalensis]	Homo s...	Neande...	63221	1026	1026	100%	0.0	100.00%	513	YP_002124304.1
<input type="checkbox"/>	cytochrome c oxidase subunit I [Homo sapiens]	Homo s...	human	9606	1026	1026	100%	0.0	100.00%	516	ARK17627.1
<input type="checkbox"/>	cytochrome c oxidase subunit I [Homo sapiens]	Homo s...	human	9606	1026	1026	100%	0.0	100.00%	514	ASF85330.1
<input type="checkbox"/>	cytochrome c oxidase subunit I [Homo sapiens]	Homo s...	human	9606	1026	1026	100%	0.0	99.81%	513	ABS58164.1
<input type="checkbox"/>	cytochrome c oxidase subunit I [Homo sapiens]	Homo s...	human	9606	1026	1026	100%	0.0	99.81%	513	AAR94669.1
<input type="checkbox"/>	cytochrome c oxidase subunit I [Homo sapiens]	Homo s...	human	9606	1026	1026	100%	0.0	99.81%	513	AAX53752.1
<input type="checkbox"/>	cytochrome c oxidase subunit I [Homo sapiens]	Homo s...	human	9606	1026	1026	100%	0.0	99.81%	513	AGW61601.1
<input type="checkbox"/>	cytochrome c oxidase subunit I [Homo sapiens]	Homo s...	human	9606	1026	1026	100%	0.0	100.00%	516	ACI04331.1
<input type="checkbox"/>	cytochrome c oxidase subunit I [Homo sapiens]	Homo s...	human	9606	1026	1026	100%	0.0	99.81%	513	ACD78178.1
<input type="checkbox"/>	cytochrome c oxidase subunit I [Homo sapiens]	Homo s...	human	9606	1026	1026	100%	0.0	99.81%	513	AAZ01530.1

cytochrome c oxidase subunit I [Homo sapiens]

Sequence ID: [ABS58164.1](#) Length: 513 Number of Matches: 1

[See 2 more title\(s\)](#) ▼ [See all Identical Proteins\(IPG\)](#)

Range 1: 1 to 513 [GenPept](#) [Graphics](#)

▼ [Next Match](#) ▲ [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps
1026 bits(2653)	0.0	Compositional matrix adjust.	512/513(99%)	513/513(100%)	0/513(0%)
Query 1	MFADRWLFSTNHKDIGTLYLLFGAWAGVLGTALSL LIRAE LGQPGNLLGNDHIYNVIVTA				60
Sbjct 1	MFADRWLFSTNHKDIGTLYLLFGAWAGVLGTALSL LIRAE LGQPGNLLGNDHIYNVIVTA				60
Query 61	HAFVMIFFMVMPIMIGGFGNMLVPLMIGAPDMAFPRMNMMSFWL LPPSLLLLASAMVEA				120
Sbjct 61	HAFVMIFFMVMPIMIGGFGNMLVPLMIGAPDMAFPRMNMMSFWL LPPSLLLLASAMVEA				120
Query 121	GAGTGWTVYPPLAGNYSHPGASVDLTIFSLHLAGVSSILGAINFITTIINMKPPAMTQYQ				180
Sbjct 121	GAGTGWTVYPPLAGNYSHPGASVDLTIFSLHLAGVSSILGAINFITTIINMKPPAMTQYQ				180
Query 181	TPLFVMSVLITAVLLLLSLPVLAAAGITMLLTDRNLNTTFFDPAAGGDPILYQHLFWFFGH				240
Sbjct 181	TPLFVMSVLITAVLLLLSLPVLAAAGITMLLTDRNLNTTFFDPAAGGDPILYQHLFWFFGH				240
Query 241	PEVYILILPGFGMISHIVTYYSKKKEPFGYMGMVWAMMSIGFLGFIVNAHHMFTVGMVDV				300
Sbjct 241	PEVYILILPGFGMISHIVTYYSKKKEPFGYMGMVWAMMSIGFLGFIVNAHHMFTVGMVDV				300
Query 301	TRAYFTSATMIIAIP TGKVF SWLATLHGSNMKWSAAVLWALGFI FLFTVGGLTGIVLAN				360
Sbjct 301	TRAYFTSATMIIAIP TGKVF SWLATLHGSNMKWSAAVLWALGFI FLFTVGGLTGIVLAN				360
Query 361	SSLDIVLHDITYYVAHFHYVLSMGAVFAIMGGFIHWFPLFSGYTLDQTYAKIHTIFIMFIG				420
Sbjct 361	SSLDIVLHDITYYVAHFHYVLSMGAVFAIMGGFIHWFPLFSGYTLDQTYAKIHTIFIMFIG				420
Query 421	VNLTFPQHFLGLSGMPRRYSYDPDAYTTWNILSSVGSFISLTAVMLMIFMIWEAFASKR				480
Sbjct 421	VNLTFPQHFLGLSGMPRRYSYDPDAYTTWNILSSVGSFISLTAVMLMIFMIWEAFASKR				480
Query 481	KVLMVEEPSMNLEWLYGCPPPYHTFEFPVYMK		513		
Sbjct 481	KVLMVEEPSMNLEWLYGCPPPYHTFEFPVYMK		513		

Related Information

[Identical Proteins](#) - Identical proteins to ABS58164.1

Score	Expect	Method	Identities	Positives	Gaps
1026 bits(2653)	0.0	Compositional matrix adjust.	512/513(99%)	513/513(100%)	0/513(0%)

НЕТ ВОЗМОЖНОСТИ ВЫБРАТЬ Е-ЗНАЧЕНИЕ != 0.0

Ссылки для проверки:

<https://www.uniprot.org/blast/uniprot/B20220223F248CABF64506F29A91F8037F07B67D102FF8E4>

Мой белок

<https://www.uniprot.org/blast/uniprot/B20220223F248CABF64506F29A91F8037F07B67D102FF8E4?alignment=1>

1ое совпадение

<https://www.uniprot.org/uniprot/P00395>

2ое совпадение

<https://www.uniprot.org/uniprot/Q9T9W1>