

ΠΡΑΚΤΙΚΗ ΕΦΑΡΜΟΓΗ

Αντιστοιχία αλληλουχιών ανά ζεύγη - FASTA

Ανοίξτε το Internet Explorer και πληκτρολογήστε τη διεύθυνση:

<http://www.uniprot.org/> για την πρόσβαση στην βάση δεδομένων SWISS-PROT που περιέχει αλληλουχίες πρωτεϊνών. Μετά πληκτρολογήστε στο πλαίσιο παρακάτω: adrenergic receptor alpha 1A – human, και επιλέξτε “Search”.

The mission of UniProt is to provide the scientific community with a comprehensive, high-quality and freely accessible resource of protein sequence and functional information.

UniProtKB
UniProt Knowledgebase
Swiss-Prot (561,911)
Manually annotated and reviewed.
Records with information extracted from literature and curator-evaluated computational analysis.

TrEMBL
(177,754,527)
Automatically annotated and not reviewed.
Records that await full manual annotation.

UniRef
Sequence clusters

UniParc
Sequence archive

Proteomes
Proteome sets

Supporting data

Literature citations

Cross-ref. databases

Taxonomy

Diseases

Subcellular locations

Keywords

New UniProt portal for the latest SARS-CoV-2 coronavirus protein entries and receptors, updated independent of the general UniProt release cycle.
[View SARS-CoV-2 Proteins and Receptors](#)

News

Forthcoming changes
Planned changes for UniProt

UniProt release 2020_01
Coronavirus SARS-CoV-2 in UniProtKB | Changes to UniProt release cycle

UniProt release 2019_11
Thicker than water | Functional annotation of different gene products | Changes to FT and CC text format | Cross-references to RNAct | Pr...

VODAFONE_WIFI_108
Πρόσβαση στο Internet

https://www.uniprot.org/uniprot/?query=+adrenergic+receptor&sort=score

UniProtKB adrenergic receptor Advanced Search

BLAST Align Retrieve/ID mapping Peptide search Help Contact

UniProtKB results

UniProtKB consists of two sections:

- Reviewed (Swiss-Prot) - Manually annotated**
Records with information extracted from literature and curator-evaluated computational analysis.
- Unreviewed (TrEMBL) - Computationally analyzed**
Records that await full manual annotation.

The UniProt Knowledgebase (UniProtKB) is the central hub for the collection of functional information on proteins, with accurate, consistent and rich annotation. In addition to capturing the core data mandatory for each UniProtKB entry (mainly, the amino acid sequence, protein name or description, taxonomic data and citation information), as much annotation information as possible is added.

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1 to 25 of 5,078 Show 25

Filter by:

	Entry	Entry name	Protein names	Gene names	Organism	Length	Columns
P35348	ADA1A_HUMAN	Alpha-1A adrenergic receptor	ADRA1A ADRA1C	Homo sapiens (Human)	466		
P25100	ADA1D_HUMAN	Alpha-1D adrenergic receptor	ADRA1D ADRA1A	Homo sapiens (Human)	572		
P08913	ADA2A_HUMAN	Alpha-2A adrenergic receptor	ADRA2A ADRA2R, ADRAR	Homo sapiens (Human)	450		
P18089	ADA2B_HUMAN	Alpha-2B adrenergic receptor	ADRA2B ADRA2L1, ADRA2RL1	Homo sapiens (Human)	450		
P18825	ADA2C_HUMAN	Alpha-2C adrenergic receptor	ADRA2C ADRA2L2, ADRA2RL2	Homo sapiens (Human)	462		
P22086	ADA2C_RAT	Alpha-2C adrenergic receptor	Adra2c	Rattus norvegicus (Rat)	458		
Q01337	ADA2C_MOUSE	Alpha-2C adrenergic receptor	Adra2c	Mus musculus (Mouse)	458		
P22909	ADA2A_RAT	Alpha-2A adrenergic receptor	Adra2a	Rattus norvegicus (Rat)	450		
P43140	ADA1A_RAT	Alpha-1A adrenergic receptor	Adra1a Adra1c	Rattus norvegicus (Rat)	466		

gene ontology (4,881) P07718 ADA1A_MOUSE Alpha-1A adrenergic receptor Adra1a Adra1c Mus musculus (Mouse) 466

We'd like to inform you that we have updated our Privacy Notice to comply with Europe's new General Data Protection Regulation (GDPR) that applies since 25 May 2018.

protein family (3,364) P23944 ADA1D_RAT Alpha-1D adrenergic receptor Adra1d Adra1a Rattus norvegicus (Rat) 561

Do not show this banner again

Στη συνέχεια, δίνεται μια λίστα σχετικών πρωτεΐνων. Η ζητούμενη πρωτεΐνη είναι η ADA1A_HUMAN, οπότε επιλέξτε αυτό το όνομα.

FASTA/SEARCH/GGSEARCH... adrenergic receptor alpha ... +

www.uniprot.org/uniprot/?query=adrenergic+receptor+alpha+1A+-+human&sort=score

Πιο συχνά αναγνωσμέ... Σεκινώντας Θεση ειδικοτήτας αμα... Suggested Sites Web Slice Gallery

UniProtKB adrenergic receptor alpha 1a human Advanced Search

BLAST Align Retrieve/ID mapping Help Contact

Results

Quote terms: "adrenergic receptor"

About UniProtKB Basket

Filter by:

- Reviewed (30) Swiss-Prot
- Unreviewed (17) TrEMBL

Popular organisms:

- Human (22)
- Rat (5)
- Bovine (2)
- Mouse (1)
- RABBIT (2)
- Other organisms

Go

Search terms

Entry	Entry name	Protein names	Gene names	Organism	Length
P35348	ADA1A_HUMAN	Alpha-1A adrenergic receptor	ADRA1A, ADRA1C	Homo sapiens (Human)	466
P25100	ADA1D_HUMAN	Alpha-1D adrenergic receptor	ADRA1D, ADRA1A	Homo sapiens (Human)	572
P23944	ADA1D_RAT	Alpha-1D adrenergic receptor	Adra1d, Adra1a	Rattus norvegicus (Rat)	561
P08908	5HT1A_HUMAN	5-hydroxytryptamine receptor 1A	HTR1A, ADRB2RL1, ADRBRL1	Homo sapiens (Human)	422
P35368	ADA1B_HUMAN	Alpha-1B adrenergic receptor	ADRA1B	Homo sapiens (Human)	520
P15823	ADA1B_RAT	Alpha-1B adrenergic receptor	Adra1b	Rattus norvegicus (Rat)	515
P12371	FCERA_RAT	High affinity immunoglobulin epsilon...	Fcer1a, Fce1a	Rattus norvegicus (Rat)	245
P20489	FCERA_MOUSE	High affinity immunoglobulin	Fcer1a, Fce1a	Mus musculus (Mouse)	250

Μετά δίνονται οι πληροφορίες γι' αυτήν την πρωτεΐνη. Επιλέξτε “FASTA format”.

https://www.uniprot.org/uniprot/P35348

UniProtKB - P35348 (ADA1A_HUMAN)

Display

Entry Protein Alpha-1A adrenergic receptor

Publications Gene ADRA1A

Feature viewer Organism Homo sapiens (Human)

Feature table Status Reviewed - Annotation score: 5 - Experimental evidence at protein level¹

None

Function

This alpha-adrenergic receptor mediates its action by association with G proteins that activate a phosphatidylinositol-calcium second messenger system. Its effect is mediated by G(q) and G(11) proteins. Nuclear ADRA1A-ADRA1B heterooligomers regulate phenylephrine(PE)-stimulated ERK signaling in cardiac myocytes. [View 2 Publications](#)

Names & Taxonomy

Subcellular location

Pathology & Biotech

PTM / Processing

Expression

Interaction

Structure

Family & Domains

Sequences (9+)

Similar proteins

Cross-references

Entry information

Miscellaneous

Function¹

GO - Molecular function¹

- adrenergic receptor activity [Source: GO_Central](#)
- alpha1-adrenergic receptor activity [Source: BHF-UCL](#)
- protein heterodimerization activity [Source: UniProtKB](#)

[View the complete GO annotation on QuickGO ...](#)

GO - Biological process¹

- activation of phospholipase C activity [Source: BHF-UCL](#)
- adenylate cyclase-activating adrenergic receptor signaling pathway [Source: GO_Central](#)
- adenylate cyclase-modulating G protein-coupled receptor signaling pathway [Source: GO_Central](#)
- adult heart development [Source: Ensembl](#)
- aging [Source: BHF-UCL](#)
- apoptotic process [Source: ProtInc](#)
- calcium ion transport into cytosol [Source: BHF-UCL](#)
- cell-cell signaling [Source: ProtInc](#)
- cell growth involved in cardiac muscle cell development [Source: Ensembl](#)
- G protein-coupled receptor signaling pathway [Source: Reactome](#)
- intracellular signal transduction [Source: ProtInc](#)
- micturition [Source: Ensembl](#)
- negative regulation of autophagy [Source: Ensembl](#)
- negative regulation of cell population proliferation [Source: ProtInc](#)
- negative regulation of heart rate involved in baroreceptor response to increased systemic arterial blood pressure [Source: Ensembl](#)
- negative regulation of Rho protein signal transduction [Source: BHF-UCL](#)

Help Contact [Basket](#)

Fasta/Search/GGSEAR... x ADRA1A - Alpha-1A adren... x ADRA1A - Alpha-1A adren... x +

www.uniprot.org/uniprot/P35348

Πιο συχνά αναγνωραμέ... Μ Ξεκινώντας Θεση ειδικοτητας αιμα... Suggested Sites Web Slice Gallery

Display None

PS50262: G_PROTEIN_RECEP_F1_2, 1 hit.
[Graphical view]

Sequences (9)ⁱ

Sequence statusⁱ: Complete.

This entry describes 9 isoformsⁱ produced by alternative splicing. [Align](#)

Isoform 1 (identifier: P35348-1) [UniParc] [FASTA](#) [Add to Basket](#)

Also known as: Alpha 1c-1, Alpha(1A-1)

Sequence data in FASTA format

This isoform has been chosen as the 'canonical' sequence. All positional information in this entry refers to it. This is also the sequence that appears in the downloadable versions of the entry.

Length: 466
Mass (Da): 51,487
Last modified: November 1, 1995 - v2
Checksum: ⁱ 1A50487531DECDF0

BLAST GO

10 20 30 40 50
MVFLSGNASD SSNCTQPPAP VNISKAILLG VILGGLILFG VLGNILVILS
60 70 80 90 100
VACHRHLHSV THYYIVNLAV ADLLLTSTVL PFSAIFEVLG YWAFGRVFCN
110 120 130 140 150
IWAADVVLCC TASIMGLCII SIDRYIGVSY PLRYPTIVTQ RRGLMALLCV
160 170 180 190 200
WALSLVISIG PLFGWRQPAP EDETCIQINE EPGYVLFSAL GSFYLPLAII
210 220 230 240 250
LVMYCRVYVV AKRESRLKS GLKTDKSDSE QVTLRRIHRKN APAGGSGMAS
260 270 280 290 300
AKTKTHFSVR LLKFSREKKA AKTLGIVVGC FVLCWLPPFL VMPIGSFFPD
310 320 330 340 350

Τότε δίνεται η αλληλουχία της πρωτεΐνης, οπότε την επιλέγουμε και την αντιγράφουμε για να την επικολλήσουμε μέσα στο πρόγραμμα FASTA.

The screenshot shows a web browser window with three tabs open:

- FASTA/SEARCH/GGSEARCH...
- http://www.uniprot.org/uniprot/P35348.fasta
- ADRA1A - Alpha-1A adrenergic receptor

The main content area displays the protein sequence:

```
>sp|P35348|ADA1A_HUMAN Alpha-1A adrenergic receptor OS=Homo sapiens GN=ADRA1A PE=1 SV=2
MVFLSGNASDSSNCTQPPAPVNISKAILLGVILGGILIFGVLGNIILVILSVACHRHLHSV
THYYIVNLAVADLLTSTVLPSAIFEVLYWAFGRVFCNIIWAADVLCCTASIMGLCII
SIDRYIGVSYPRLYPTIVTQRRLMALLCVWALSLVISIGPLFGWRQPAPEDETICQINE
EPGYVLFSAALGSFYPLAIILVMYCRVVVAKRESRGILKSGLKTDKSDSEQVTLRIHRKN
APAGGGSGMASAKTKTHFSVRLLKFSREKKAAKTLGIVVGCFLCWLPFFLVMPIGSFFPD
FKPKSETVFKIVFWLGYINSCINPIIYPCSSQEFFKAQFQNVLRIQCLCRKQSSKHALGYTL
HPPSQAVEGQHKDMVRIPVGSRFTYRISKIDGVCEWKFSSMPRGSAIRITVSKDQSSCT
TARVRSKSFLQVCCCVGPSTPSLDKNHQVPTIKVHTISLSENGEEV
```

Για πρόσβαση στο FASTA, ανοίξτε το Internet Explorer και πληκτρολογήστε
“[http://www.ebi.ac.uk/Tools/ssss/fasta/..](http://www.ebi.ac.uk/Tools/ssss/fasta/)

The screenshot shows the EMBL-EBI homepage with a dark header bar. On the left, there's a navigation menu with links to 'EMBL-EBI', 'Services', 'Research', 'Training', 'Industry', 'About us', and a search icon. On the right, it displays the 'EMBL-EBI Hinxton' logo. Below the header, a large teal section features the word 'FASTA' in white. A horizontal menu bar below this contains links for 'Protein', 'Nucleotide', 'Genomes', 'Proteomes', 'Whole Genome Shotgun', 'Web services', 'Help & Documentation', 'Bioinformatics Tools FAQ', 'Feedback', and 'Share'. The main content area shows a breadcrumb trail: 'Tools > Sequence Similarity Searching > FASTA'. The title 'Protein Similarity Search' is prominently displayed in large teal text.

Protein Similarity Search

This tool provides sequence similarity searching against protein databases using the FASTA suite of programs. FASTA provides a heuristic search with a protein query. FASTX and FASTY translate a DNA query. Optimal searches are available with SSEARCH (local), GGSEARCH (global) and GLSEARCH (global query, local database).

STEP 1 - Select your databases

PROTEIN DATABASES

1 Database Selected

Clear Selection

- UniProt Knowledgebase (The UniProt Knowledgebase includes UniProtKB/Swiss-Prot and UniProtKB/TrEMBL)
- UniProtKB/Swiss-Prot (The manually annotated section of UniProtKB)

Στη συνέχεια, στο πλαίσιο παρακάτω επικολλήστε την αντιγραμμένη σειρά που θέλετε να αντιστοιχίσετε και προσδιορίστε τις διάφορες παραμέτρους.

The screenshot shows a web browser window with three tabs open: "FASTA/SSEARCH/GGSEARCH...", "http://www.uniprot.org/uniprot/P35348.fasta", and "ADRA1A - Alpha-1A adren...". The main content area is the EBI FASTA search tool. It has three main sections:

- STEP 2 - Enter your input sequence:** A text input field containing the protein sequence: "THYYIVNLAVADLLTSTVLPFSAlFEVLGYWAFGRVFCNIWAADVVLCCATASIMGLCII SIDRYIGVSYPLRYPVTIVTQRRGLMALLCVWALSVISIGPLFGWRQPAPEDETICQINE EPGYVLFSAALGSFYLPAlAIlVMYCRVYVAKRESRGLKSGLKTDSSEQVTLRIHRKN APAGGSGMASAKTKTHFSVRLLKFREKKAAKTLGIVVGCFLCWLPFLVMPIGSFPD FKPSSETVKIVFWLGYNNSCINPIIYPCSSQEFKKAFQNVLRIQCLCRKQSSKHALGYTL HPPSQAVEGQHKDMVRIPVGSRFTYRISKTDGVCEWKFFSSMPRGSRARITVSKDQSSCT TARVRSKSFLQVCCCVCVPSTPSLDKNHQVPTIKVHTISLSENGEEV". Below the input field is a note: "or Upload a file: Αναζήτηση... Δεν επιλέχθηκε αρχείο."
- STEP 3 - Set your parameters:** A section titled "PROGRAM" with a dropdown menu set to "FASTA". A note below says: "The default settings will fulfill the needs of most users and, for that reason, are not visible." There is a link "More options..." "(Click here, if you want to view or change the default settings.)"
- STEP 4 - Submit your job:** A section with a checkbox "Be notified by email (Tick this box if you want to be notified by email when the results are available)" and a "Submit" button.

At the bottom, there is a note: "If you plan to use these services during a course please contact us."

Μετά κάντε κλικ στο “Submit” και περιμένετε για μερικά δευτερόλεπτα.

Job running: fasta-I201502... <http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?CMD=Search&QUERY=P35348.fasta> ADRA1A - Alpha-1A adren...

www.ebi.ac.uk/Tools/services/web/toolresult.ebi?jobId=fasta-I20150224-215052-0338-9295396-oy&context=protein

fasta

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FASTA

Protein Nucleotide Genomes Proteomes Whole Genome Shotgun Web services Help & Documentation Share Feedback

Tools > Sequence Similarity Searching > FASTA

Your job is currently running... please be patient

The result of your job will appear in this browser window.

Job ID: [fasta-I20150224-215052-0338-9295396-oy](#)

Please note the following

- o You may press Shift+Refresh or Reload on your browser at any time to check if results are ready.
- o You may bookmark this page to view your results later if you wish.
- o Results are stored for 7 days.

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Τα αποτελέσματα (output) παρέχουν μια λίστα όλων των αλληλουχιών που είναι όμοιες με την ζητούμενη αλληλουχία. Οι αλληλουχίες προέρχονται από τη βάση δεδομένων SWISS-PROT. Το μήκος, ομοιότητα και το E-value για κάθε σύγκριση δίνεται. Αν ενδιαφέρεστε να συγκρίνετε μόνο τις σειρές ADA1A_HUMAN και A1AA_RAT, μην επιλέγεται (unmark) όλα τα πλαίσια κάτω από το “Alignment” εκτός από το ADA1A_RAT. Μετά επιλέξτε το “Show Alignments”.

The screenshot shows the EBI FASTA search results page. The top navigation bar includes tabs for "Summary Table < FASTA < ...", "http://www.ebi.ac.uk/P35348.fasta", and "ADRA1A - Alpha-1A adren...". The main content area displays the results for job "fasta-l20150224-215052-0338-9295396-oy". The "Summary Table" tab is selected. The results table has columns for Align., DB-ID, Source, Length, Score, Identities %, Positives %, and E(). The table lists four alignments:

Align.	DB-ID	Source	Length	Score	Identities %	Positives %	E()
<input checked="" type="checkbox"/> 1	SP:ADA1A_HUMAN	Alpha-1A adrenergic receptor OS=Homo sapiens GN=ADRA1A PE=1 SV=2 Cross-references and related information in: ▶ Gene expression ▶ Small molecules ▶ Nucleotide sequences ▶ Genomes ▶ Samples & ontologies ▶ Molecular interactions ▶ Protein families ▶ Literature ▶ Reactions, pathways & diseases ▶ Protein sequences	466	3143	100.0	100.0	5.7E-189
<input checked="" type="checkbox"/> 2	SP:ADA1A_RABIT	Alpha-1A adrenergic receptor OS=Oryctolagus cuniculus GN=ADRA1A PE=2 SV=1 Cross-references and related information in: ▶ Small molecules ▶ Nucleotide sequences ▶ Genomes ▶ Samples & ontologies ▶ Protein families ▶ Literature ▶ Protein sequences	466	2985	94.0	98.3	4.2E-179
<input checked="" type="checkbox"/> 3	SP:ADA1A_CAVPO	Alpha-1A adrenergic receptor OS=Cavia porcellus GN=ADRA1A PE=2 SV=2 Cross-references and related information in: ▶ Small molecules ▶ Nucleotide sequences ▶ Samples & ontologies ▶ Protein families ▶ Literature ▶ Protein sequences	466	2982	94.4	97.9	6.5E-179
<input checked="" type="checkbox"/> 4	SP:ADA1A_BOVIN	Alpha-1A adrenergic receptor OS=Bos taurus GN=ADRA1A PE=2 SV=1	466	2944	92.1	98.3	1.5E-176

On the left sidebar, there are sections for "Selection:" (with "Select All", "Invert", "Clear" buttons), "Annotations:" (with "Show", "Hide" buttons), "Alignments:" (with "Show", "Hide" buttons), "Entries:" (with "Download" button), and "Tools:" (with "Launch" button). The "Annotations:" section is currently expanded, showing cross-references to gene expression, small molecules, nucleotide sequences, genomes, samples & ontologies, molecular interactions, protein families, literature, reactions, pathways & diseases, and protein sequences.

Τότε εμφανίζονται οι αντιστοιχίες.

Summary Table < FASTA <... x http://www.ebi.ac.uk/Tools/services/web/toolresult.cgi?jobId=fasta-l20150224-215052-0338-9295396-oy&context=protein ADRA1A - Alpha-1A adren... x +

Πιο συχνά αναγνωραμέ... Μ Ξεκινώντας Θεση ειδικοτήτας αιμα... Suggested Sites Web Slice Gallery

C g fasta

Annotations: Show Hide

Alignments: Show Hide

Entries: Download in fasta format

Tools: Launch Clustal Omega

Cross-references and related information in:

- Gene expression
- Small molecules
- Nucleotide sequences
- Genomes
- Samples & ontologies
- Molecular interactions
- Protein families
- Literature
- Reactions, pathways & diseases
- Protein sequences

>>SP:ADA1A_HUMAN P35348 Alpha-1A adrenergic receptor OS=Homo
sapiens GN=ADRA1A PE=1 SV=2 (466 aa)
initn: 3143 initl: 3143 opt: 3143 Z-score: 3528.1 bits: 662.1 E(547599): 5.7e-189
Smith-Waterman score: 3143; 100.0% identity (100.0% similar) in 466 aa overlap (1-466:1-466)

10	20	30	40	50	60		
EMBOS	MVFLSGNASDSSNCTQPPAPVNISKAILLGVLGLLFGVLGNILVILSVACHRHLHSV		
SP:ADA	MVFLSGNASDSSNCTQPPAPVNISKAILLGVLGLLFGVLGNILVILSVACHRHLHSV	10	20	30	40	50	60
	
70	80	90	100	110	120		
EMBOS	THYYIVNLAVADLLLSTVLPFSAAIFEVLYWAFGRVFCNIWAADVLCCTASIMGLCII		
SP:ADA	THYYIVNLAVADLLLSTVLPFSAAIFEVLYWAFGRVFCNIWAADVLCCTASIMGLCII	70	80	90	100	110	120
	
130	140	150	160	170	180		
EMBOS	SIDRYIGVSYPLRYPTIVTQRQLMALLCVWALSIVISIGPLFGWRQPAPEDETICQINE		
SP:ADA	SIDRYIGVSYPLRYPTIVTQRQLMALLCVWALSIVISIGPLFGWRQPAPEDETICQINE	130	140	150	160	170	180
	
190	200	210	220	230	240		
EMBOS	EPGYVLFSAALGSFYLPALIILVMYCRVYVAKRESRGLKSGLKDSDSEQVTLRIHRKN		
SP:ADA	EPGYVLFSAALGSFYLPALIILVMYCRVYVAKRESRGLKSGLKDSDSEQVTLRIHRKN	190	200	210	220	230	240
	
250	260	270	280	290	300		
EMBOS	APAGGSGMASAKTKTHFSVRLLKFSREKKAAKTLGIVVGCFLCWLPFFLVMPIGSFFPD		
SP:ADA	APAGGSGMASAKTKTHFSVRLLKFSREKKAAKTLGIVVGCFLCWLPFFLVMPIGSFFPD	250	260	270	280	290	300
	
310	320	330	340	350	360		
EMBOS	FKPSETVFKIVFWLGYLNNSCINPIIYPCSSQEFKKAFQNVLRIQCLCRKQSSKHALGYTL		
SP:ADA	FKPSETVFKIVFWLGYLNNSCINPIIYPCSSQEFKKAFQNVLRIQCLCRKQSSKHALGYTL	310	320	330	340	350	360
	

Summary Table < FASTA < ... x http://www.ebi.ac.uk/Tools/services/web/toolresult.cgi?jobId=fasta-l20150224-215052-0338-9295396-oy&context=protein ADRA1A - Alpha-1A adren... +

www.ebi.ac.uk/Tools/services/web/toolresult.cgi?jobId=fasta-l20150224-215052-0338-9295396-oy&context=protein

g fasta

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[Small molecules](#) [Nucleotide sequences](#) [Genomes](#) [Samples & ontologies](#) [Protein families](#)

[Literature](#) [Protein sequences](#)

>>SP:ADRA1A_RABIT 002824 Alpha-1A adrenergic receptor
OS=Oryctolagus cuniculus GN=ADRA1A PE=2 SV=1 (466 aa)
initn: 2985 initl: 2985 opt: 2985 Z-score: 3350.9 bits: 629.3 E(547599): 4.2e-179
Smith-Waterman score: 2985; 94.0% identity (98.3% similar) in 466 aa overlap (1-466:1-466)

	10	20	30	40	50	60	
EMBOS	MVFLSGNASDSSNCTQPPAPVNISKAILLGVLGLLIFGVVLGNILVILSVACHRHLSV	:	:	:	:	:	
SP:ADA	MVFLSGNASDSSNCTHPPAPVNISKAILLGVLGLLIFGVVLGNILVILSVACHRHLSV	10	20	30	40	50	60
	70	80	90	100	110	120	
EMBOS	THYYIVNLAVADLLLTSTVLPFSAlFEVLGYWAFGRVFCNIWAADVVLCCATASIMGLCII	:	:	:	:	:	
SP:ADA	THYYIVNLAVADLLLTSTVLPFSAlFEILGYWAFGRVFCNIWAADVVLCCATASISLCVI	70	80	90	100	110	120
	130	140	150	160	170	180	
EMBOS	SIDRYIGVSYPLRYPTIVTQRRLGMLALLCVWALSLVISIGPLFGWRQPAPEDETICQINE	:	:	:	:	:	
SP:ADA	SIDRYIGVSYPLRYPTIVTQRRLGALLCVWFSLVISVGPLFGWRQPAPDDETICQINE	130	140	150	160	170	180
	190	200	210	220	230	240	
EMBOS	EPMGVVLFSALGSFYLPPLAIILVMYCRVYVVAKRESRGLKSGLTKDSSEQVTLRHKRN	:	:	:	:	:	
SP:ADA	EPMGVVLFSALGSFYVPLTIIILAMYCRVYVVAKRESRGLKSGLTKDSSEQVTLRHKRN	190	200	210	220	230	240
	250	260	270	280	290	300	
EMBOS	APAGGSGMASAKTKTHFSVRLLKFSREKKAAKTLGIVVGCFVLCWLPPFLVMPIGSFDPD	:	:	:	:	:	
SP:ADA	APAGGSGVVASAKNKTHFSVRLLKFSREKKAAKTLGIVVGCFVLCWLPPFLVMPIGSFDPD	250	260	270	280	290	300
	310	320	330	340	350	360	
EMBOS	FKPSETVFKIVFWLGYNLNSCINPIIYPCSSQEFKKAFQNVLRIQCLCRQSSKHALGYTL	:	:	:	:	:	
SP:ADA	FKPPETVFKIVFWLGYNLNSCINPIIYPCSSQEFKKAFQNVLKIQCLRRQSSKHALGYTL	310	320	330	340	350	360
	370	380	390	400	410	420	
EMBOS	IPRDSQIIEQSKWIKMPLIPIQGCPETEYVQSKTECQKTEHVVVEFSCMPBPGSARITHVKWDQSCST	:	:	:	:	:	

ΠΡΑΚΤΙΚΗ ΕΦΑΡΜΟΓΗ

BLAST

Ανοίξτε το Internet Explorer και πληκτρολογήστε τη διεύθυνση:

<http://blast.ncbi.nlm.nih.gov/Blast.cgi>. Μετά επιλέξτε “protein blast”

The screenshot shows the NCBI BLAST homepage. At the top, there's a banner for "BLAST+ 2.9.0 is here!" with a link to "More BLAST news...". Below the banner, there are three main search tools: "Nucleotide BLAST" (nucleotide > nucleotide), "blastx" (translated nucleotide > protein), and "tblastn" (protein > translated nucleotide). To the right, there's a "Protein BLAST" section (protein > protein). Below these, there's a "BLAST Genomes" search bar with dropdown options for "Human", "Mouse", "Rat", and "Microbes", and a "Search" button. At the bottom, there are sections for "Standalone and API BLAST" (with links to "Download BLAST" and "Use BLAST API"), and "Specialized searches" (with a link to "Use BLAST in the cloud").

https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome

NIH U.S. National Library of Medicine NCBI National Center for Biotechnology Information Sign in to NCBI

BLAST® » blastp suite

Standard Protein BLAST

blast blastp blastx tblastn tblastx

Enter Query Sequence
Enter accession number(s), g(s), or FASTA sequence(s) Clear Query subrange From To

Or, upload file Επιλογή αρχείου Δεν επλέχθηκε.. ανέντα αρχείο.

Job Title Enter a descriptive title for your BLAST search

Align two or more sequences

Choose Search Set

Database Non-redundant protein sequences (nr)

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

Optional Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Exclude Models (XM/XP) Non-redundant RefSeq proteins (WP) Uncultured/environmental sample sequences

Entrez Query You Create custom database

Optional Enter an Entrez query to limit search

Program Selection

Algorithm Quick BLASTP (Accelerated protein-protein BLAST)
 blastp (protein-protein BLAST)
 PSI-BLAST (Position-Specific Iterated BLAST)
 PHI-BLAST (Pattern Hit Initiated BLAST)
 DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)
Choose a BLAST algorithm

BLAST Search database Non-redundant protein sequences (nr) using Blastp (protein-protein BLAST)
 Show results in a new window

+ Algorithm parameters

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Επιλέγουμε την αλληλουχία ADA1_HUMAN σε FASTA μορφή και την επικολλούμε

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BLAST ® > blastp suite Home Recent Results Saved Strategies Help

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Standard Protein BLAST

blastn blastp blastx tblastn tblastx

Enter Query Sequence

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

From
To

Or, upload file Δεν επιλέχθηκε αρχείο.

Job Title
Enter a descriptive title for your BLAST search

Align two or more sequences

BLAST results will be displayed in a new format by default
You can always switch back to the Traditional Results page. 

Choose Search Set

Database: UniProtKB/Swiss-Prot(swissprot)

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

Exclude: Models (XM/XP) Non-redundant RefSeq proteins (WP) Uncultured/environmental sample sequences

Program Selection

Algorithm: blastp (protein-protein BLAST) PSI-BLAST (Position-Specific Iterated BLAST)

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Και επιλέγουμε BLAST

The screenshot shows the NCBI BLAST search interface. At the top, the URL is https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&PAGE_TYPE=BlastSearch&LINK_L. The database dropdown is set to UniProtKB/Swiss-Prot(swissprot). In the Program Selection section, the algorithm is set to blastp (protein-protein BLAST). A large red circle highlights the 'BLAST' button at the bottom left of the main search area. Below the search button, there is a note: 'Search database swissprot using Blastp (protein-protein BLAST)' and an option to 'Show results in a new window'. The footer contains links for Support center, Mailing list, NIH, USA.gov, and VODAFONE_WIFI_108.

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Align two or more sequences

Choose Search Set

Database: UniProtKB/Swiss-Prot(swissprot)

Organism: Enter organism name or id—completions will be suggested

Exclude: Models (XMP), Non-redundant RefSeq proteins (WP), Uncultured/environmental sample sequences

Program Selection

Algorithm: blastp (protein-protein BLAST)

Search database swissprot using Blastp (protein-protein BLAST)

Note: Parameter values that differ from the default are highlighted in yellow and marked with ♦ sign

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NCBI
National Center for Biotechnology Information, U.S. National Library of Medicine
8600 Rockville Pike, Bethesda MD, 20894 USA

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BLAST® > blastp suite > RID-91F4TMMMO16 Home Recent Results Saved Strategies Help

[Formatting options]

Job Title: Protein Sequence

Request ID	91F4TMMMO16
Status	Searching
Submitted at	Fri Apr 10 14:36:09 2020
Current time	Fri Apr 10 14:36:12 2020
Time since submission	00:00:02

This page will be automatically updated in 2 seconds

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Support center Mailing list

NCBI
National Center for Biotechnology Information, U.S. National Library of Medicine
8600 Rockville Pike, Bethesda MD, 20894 USA

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BLAST® » blastp suite » results for RID-91F4TMM016

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< Edit Search Save Search Search Summary ▾

Job Title Protein Sequence
RID 91F4TMM016 Search expires on 04-12 02:36 am Download All ▾
Program BLASTP Citation
Database swissprot See details ▾
Query ID Icl|Query_46622
Description None
Molecule type amino acid
Query Length 466
Other reports Distance tree of results Multiple alignment MSA viewer ?

How to read this report? BLAST Help Videos Back to Traditional Results Page

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

Descriptions Graphic Summary Alignments Taxonomy

Sequences producing significant alignments Download Manage Columns Show 100 ? VODAFONE_WIFI_108 Πρόσβαση στο Internet

Η αντιστοίχιση της αλληλουχίας μας....

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Descriptions Graphic Summary Alignments Taxonomy

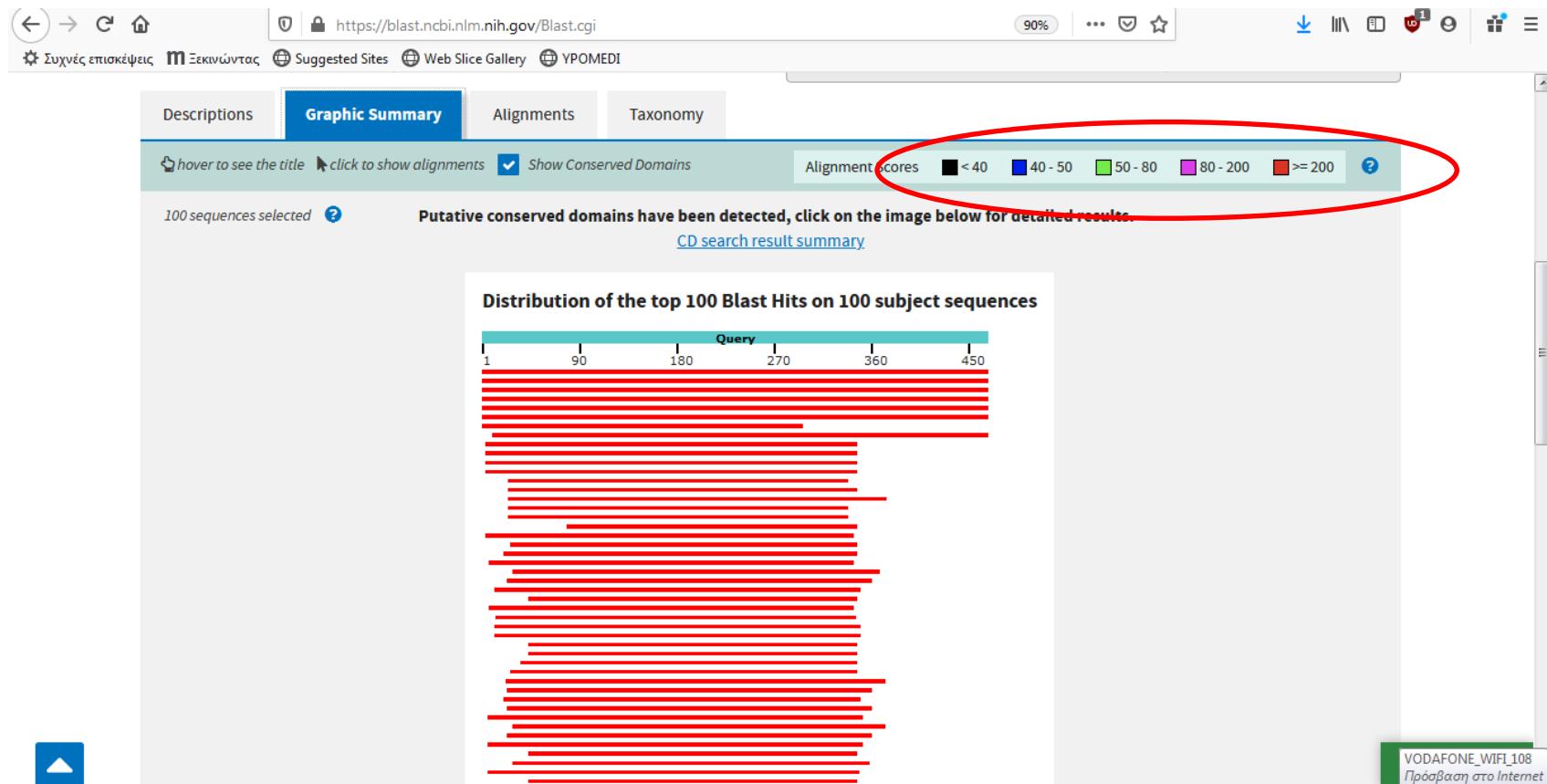
Sequences producing significant alignments Download Manage Columns Show 100 ?

select all 100 sequences selected

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input checked="" type="checkbox"/>	RecName: Full=Alpha-1A adrenergic receptor; AltName: Full=Alpha-1A adrenoreceptor; Short=Alpha-1A adrenoceptor; AltName: Full=Alpr	956	956	100%	0.0	100.00%	P35348.2
<input checked="" type="checkbox"/>	RecName: Full=Alpha-1A adrenergic receptor; AltName: Full=Alpha-1A adrenoreceptor; Short=Alpha-1A adrenoceptor; AltName: Full=Alpr	907	907	100%	0.0	94.42%	Q9WU25.2
<input checked="" type="checkbox"/>	RecName: Full=Alpha-1A adrenergic receptor; AltName: Full=Alpha-1A adrenoreceptor; Short=Alpha-1A adrenoceptor; AltName: Full=Alpr	906	906	100%	0.0	93.99%	Q02824.1
<input checked="" type="checkbox"/>	RecName: Full=Alpha-1A adrenergic receptor; AltName: Full=Alpha-1A adrenoreceptor; Short=Alpha-1A adrenoceptor; AltName: Full=Alpr	894	894	100%	0.0	92.70%	P43140.1
<input checked="" type="checkbox"/>	RecName: Full=Alpha-1A adrenergic receptor; AltName: Full=Alpha-1A adrenoreceptor; Short=Alpha-1A adrenoceptor; AltName: Full=Alpr	892	892	100%	0.0	92.06%	P18130.1
<input checked="" type="checkbox"/>	RecName: Full=Alpha-1A adrenergic receptor; AltName: Full=Alpha-1A adrenoreceptor; Short=Alpha-1A adrenoceptor; AltName: Full=Alpr	881	881	100%	0.0	91.85%	P97718.3
<input checked="" type="checkbox"/>	RecName: Full=Alpha-1A adrenergic receptor; AltName: Full=Alpha-1A adrenoreceptor; Short=Alpha-1A adrenoceptor; AltName: Full=Alpr	581	581	63%	0.0	95.93%	Q77621.1
<input checked="" type="checkbox"/>	RecName: Full=Alpha-1A adrenergic receptor; AltName: Full=Alpha-1A adrenoreceptor; Short=Alpha-1A adrenoceptor; AltName: Full=MAF	557	557	98%	0.0	59.96%	Q91175.1
<input checked="" type="checkbox"/>	RecName: Full=Alpha-1B adrenergic receptor; AltName: Full=Alpha-1B adrenoreceptor; Short=Alpha-1B adrenoceptor [Mesocricetus auratus]	455	455	73%	6e-156	62.25%	P18841.1
<input checked="" type="checkbox"/>	RecName: Full=Alpha-1B adrenergic receptor; AltName: Full=Alpha-1B adrenoreceptor; Short=Alpha-1B adrenoceptor [Rattus norvegicus]	454	454	73%	8e-156	62.25%	P15823.2
<input checked="" type="checkbox"/>	RecName: Full=Alpha-1B adrenergic receptor; AltName: Full=Alpha-1B adrenoreceptor; Short=Alpha-1B adrenoceptor [Homo sapiens]	454	454	73%	2e-155	62.54%	P35368.3
<input checked="" type="checkbox"/>	RecName: Full=Alpha-1B adrenergic receptor; AltName: Full=Alpha-1B adrenoreceptor; Short=Alpha-1B adrenoceptor [Mus musculus]	445	445	73%	4e-152	61.96%	P97717.2
<input checked="" type="checkbox"/>	RecName: Full=Alpha-1D adrenergic receptor; AltName: Full=Alpha-1A adrenergic receptor; AltName: Full=Alpha-1D adrenoreceptor; Sh	429	429	67%	4e-145	61.88%	P25100.2
<input checked="" type="checkbox"/>	RecName: Full=Alpha-1D adrenergic receptor; AltName: Full=Alpha-1D adrenoreceptor; Short=Alpha-1D adrenoceptor [Sus scrofa]	421	421	69%	6e-142	60.91%	Q9TTM9.1
<input checked="" type="checkbox"/>	RecName: Full=Alpha-1D adrenergic receptor; AltName: Full=Alpha-1D adrenoreceptor; Short=Alpha-1D adrenoceptor [Oryctolagus cuniculus]	415	415	75%	2e-139	57.87%	Q02666.1
<input checked="" type="checkbox"/>	RecName: Full=Alpha-1D adrenergic receptor; AltName: Full=Alpha-1A adrenergic receptor; AltName: Full=Alpha-1D adrenoreceptor; Sh	408	408	67%	7e-137	60.00%	P23944.2

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Επιλέγοντας Graphic Summary



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Other reports Distance tree of results Multiple alignment MSA viewer ? Filter Reset

Descriptions Graphic Summary Alignments Taxonomy

Alignment view Pairwise Download

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RecName: Full=Alpha-1A adrenergic receptor; AltName: Full=Alpha-1A adrenoreceptor; Short=Alpha-1A adrenoceptor; AltName: Full=Alpha-1C adrenergic receptor; AltName: Full=Alpha-adrenergic receptor 1c [Homo sapiens]

Sequence ID: P35348.2 Length: 466 Number of Matches: 1

Range 1: 1 to 466 GenPept Graphics ▾ Next Match ▾ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
956 bits(2472)	0.0	Compositional matrix adjust.	466/466(100%)	466/466(100%)	0/466(0%)

Query 1 MVFLSGN ASDSSNCT QPPAP VNISKAI LLGV ILFG VLGN ILVIL SVAC RRHL HSV 60
Sbjct 1 MVFLSGN ASDSSNCT QPPAP VNISKAI LLGV ILFG VLGN ILVIL SVAC RRHL HSV 60

Query 61 THYYIVNL AVADLLL TSVLPF SAI FEV LGW AFGRV FCNI IAA DVLC CTAS IMGL CII 120
Sbjct 61 THYYIVNL AVADLLL TSVLPF SAI FEV LGW AFGRV FCNI IAA DVLC CTAS IMGL CII 120

Query 121 SIDRYIG VSYPL RYPTI VTQ RRG L MALL C VWA LS L VIS I G P L F G W R Q P A P E D E T I C Q I N E 180
Sbjct 121 SIDRYIG VSYPL RYPTI VTQ RRG L MALL C VWA LS L VIS I G P L F G W R Q P A P E D E T I C Q I N E 180

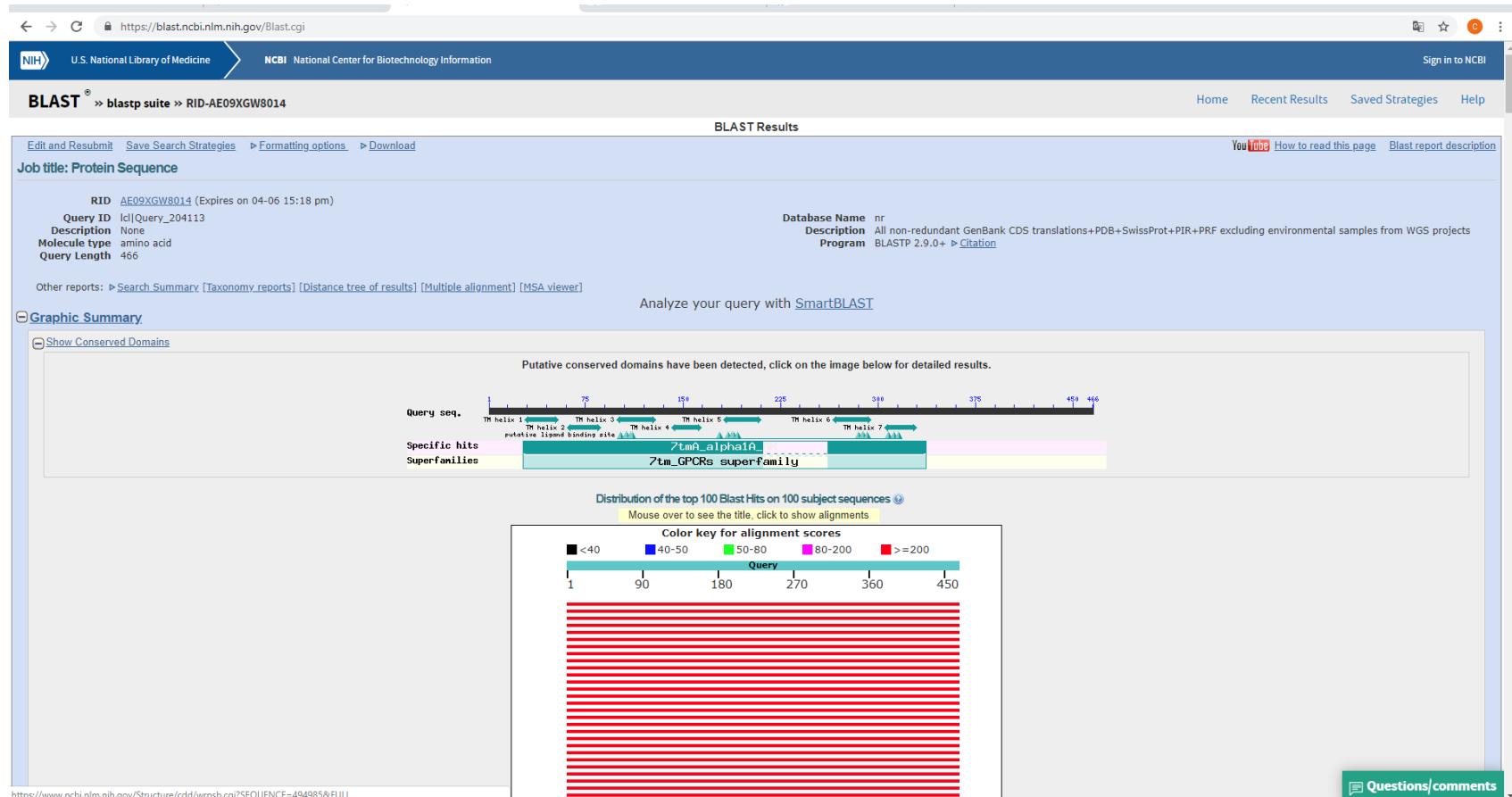
Query 181 EPGYVLF SALGS FYL PLA II LV MYCRV YVVA KRES RGL K SG L K TD K SD SE QV TL RI HR KN 240
Sbjct 181 EPGYVLF SALGS FYL PLA II LV MYCRV YVVA KRES RGL K SG L K TD K SD SE QV TL RI HR KN 240

Query 241 APAGGSGMASAKT KTHFSVRLL KFSREKKA AKT L GIVVGCFVL C WL PFFL VMPIGS FFPD 300
Sbjct 241 APAGGSGMASAKT KTHFSVRLL KFSREKKA AKT L GIVVGCFVL C WL PFFL VMPIGS FFPD 300

Related Information Gene - associated gene details

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Αν κάνουμε κλικ πάνω στην εικόνα αυτή



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Descriptions Graphic Summary Alignments **Taxonomy**

Reports Lineage Organism Taxonomy

100 sequences selected ?

Organism	Blast Name	Score	Number of Hits	Description
Bilateria	animals	101		
. Euteleostomi	vertebrates	97		
. . Tetrapoda	vertebrates	88		
. . . Amniota	vertebrates	83		
. . . . Theria	mammals	82		
. Boreoeutheria	placentals	80		
. Euarchontoglires	placentals	56		
. Catarrhini	primates	19		
. Homininae	primates	17		
. Homo sapiens	primates	956	12	Homo sapiens hits
. Gorilla gorilla gorilla	primates	221	2	Gorilla gorilla gorilla hits
. Pan troglodytes	primates	221	3	Pan troglodytes hits
. Macaca mulatta	primates	212	2	Macaca mulatta hits
. Cavia porcellus	rodents	907	7	Cavia porcellus hits
. Oryctolagus cuniculus	rabbits & hares	906	4	Oryctolagus cuniculus hits
. Rattus norvegicus	rodents	894	11	Rattus norvegicus hits
. Mus musculus	rodents	881	10	Mus musculus hits
. Mesocricetus auratus	rodents	455	2	Mesocricetus auratus hits
. Tscherskia triton	rodents	220	1	Tscherskia triton hits
. Nannospalax ehrenbergi	rodents	214	1	Nannospalax ehrenbergi hits

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