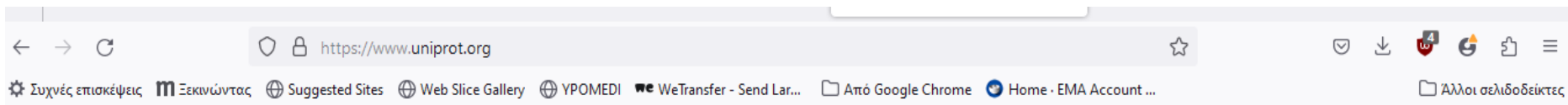


ΠΡΑΚΤΙΚΗ ΕΦΑΡΜΟΓΗ

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”.



Find your protein

UniProtKB ▾

Advanced | List Search

Examples: `Insulin`, `APP`, `Human`, `P05067`, `organism_id:9606`

UniProt is the world's leading high-quality, comprehensive and freely accessible resource of protein sequence and functional information. [Cite UniProt](#)™



UniProt invites you to participate in a survey on the use and value of UniProt. [Please click on the link provided to complete the survey](#) ↗ .

Proteins

Species

Protein Clusters

Sequence

Status

- Reviewed (Swiss-Prot) (47)
- Unreviewed (TrEMBL) (1,607)

Popular organisms

- Human (12)
- Rat (11)
- Mouse (10)
- Bovine (9)
- Zebrafish (5)

Taxonomy

Filter by taxonomy

Group by

Taxonomy

Select how you would like to view your results

Cards
 Table

Q9P7E8 - APP1_SCHPO

Protein app1 - Schizosaccharomyces pombe [strain 972 / ATCC 24843] (Pombe yeast) - Evidence at protein level - Annotation score: 100

1 domain - 1 active site - 4 isoforms - 7 reviewed publications

Q9P7E8 - APP1_YEAST

Phosphatidate phosphatase APP1 - Saccharomyces cerevisiae [strain ATCC 204508 / S288c] (Baker's yeast) - EC:3.1.3.41 - Gene APP1 - 587 amino acids - Evidence at protein level - Annotation score: 100

12 interactions - 50 reviewed publications

Q9P7E8 - APP1_SCHPO

Protein app1 - Schizosaccharomyces pombe [strain 972 / ATCC 24843] (Pombe yeast) - Evidence at structural level - Annotation score: 100

2 domains - 2 reviewed publications

Q92624 - APP2_HUMAN

Anyoloid protein-binding protein 2 - Homo sapiens (Human) - Gene: APPBP2 (KIAA0228, NAT1) - 585 amino acids - Evidence at protein level - Annotation score: 100

1 reviewed variant - 108 interactions - 9 reviewed publications

Entry	Entry Name	Protein Names	Gene Names	Organism	Length
Q9P7E8	APP1_YEAST	Phosphatidate phosphatase APP1...	APP1...	Saccharomyces cerevisiae [strain ATCC 204508 / S288c] (Baker's yeast)	587 AA
Q9P7E8	APP1_SCHPO	Protein app1	app1...	Schizosaccharomyces pombe [strain 972 / ATCC 24843] (Pombe yeast)	857 AA
Q92624	APP2_HUMAN	Anyoloid protein-binding protein 2...	APPBP2...	Homo sapiens (Human)	585 AA
Q44750	XPP1_CAEEL	Xao-Pro aminopeptidase app-1	app-1...	Caenorhabditis elegans	616 AA
P05067	AA1_HUMAN	Anyoloid beta precursor protein...	APP1...	Homo sapiens (Human)	770 AA
P51972	FA2H1_AKAPH	Basic phospholipase A2 APP-049...		Aphelionella plusioides plusioides (Eastern cottontail)	123 AA
Q12564	LEA1_HUMAN	MEBOB-activating enzyme E2 regulatory subunit 1	NAE1...	Homo sapiens (Human)	534 AA

View results

Entry	Entry Name	Protein Names	Gene Names	Organism	Length
Q9P7E8	APP1_YEAST	Phosphatidate phosphatase APP1...	APP1...	Saccharomyces cerevisiae [strain ATCC 204508 / S288c] (Baker's yeast)	587 AA
Q9P7E8	APP1_SCHPO	Protein app1	app1...	Schizosaccharomyces pombe [strain 972 / ATCC 24843] (Pombe yeast)	857 AA
Q92624	APP2_HUMAN	Anyoloid protein-binding protein 2...	APPBP2...	Homo sapiens (Human)	585 AA
Q44750	XPP1_CAEEL	Xao-Pro aminopeptidase app-1	app-1...	Caenorhabditis elegans	616 AA
P05067	AA1_HUMAN	Anyoloid beta precursor protein...	APP1...	Homo sapiens (Human)	770 AA
P51972	FA2H1_AKAPH	Basic phospholipase A2 APP-049...		Aphelionella plusioides plusioides (Eastern cottontail)	123 AA
Q12564	LEA1_HUMAN	MEBOB-activating enzyme E2 regulatory subunit 1	NAE1...	Homo sapiens (Human)	534 AA
Q002824	ADA1A_RABIT	Alpha-1A adrenergic receptor...	ADRA1A, ADRA1C	Oryctolagus cuniculus (Rabbit)	466 AA

Feedback

Help

status

Reviewed (Swiss-Prot) (47)

Unreviewed (TrEMBL) (1,607)

Popular organisms

Human (12)

Rat (11)

Mouse (10)

Bovine (9)

Zebrafish (5)

Taxonomy

[filter by taxonomy](#)

Group by

Taxonomy

UniProtKB 1,654 results

[BLAST](#) [Align](#) [Map IDs](#) [Download](#) [Add](#) View: [Cards](#) [Table](#) [Customize columns](#) [Share](#)

Entry	Entry Name	Protein Names	Gene Names	Organism	Length
<input type="checkbox"/> P35348	ADA1A_HUMAN	Alpha-1A adrenergic receptor[...]	ADRA1A , ADRA1C	Homo sapiens (Human)	466 AA
<input type="checkbox"/> P18130	ADA1A_BOVIN	Alpha-1A adrenergic receptor[...]	ADRA1A , ADRA1C	Bos taurus (Bovine)	466 AA
<input type="checkbox"/> P43140	ADA1A_RAT	Alpha-1A adrenergic receptor[...]	Adra1a , Adra1c	Rattus norvegicus (Rat)	466 AA
<input type="checkbox"/> P97718	ADA1A_MOUSE	Alpha-1A adrenergic receptor[...]	Adra1a , Adra1c	Mus musculus (Mouse)	466 AA
<input type="checkbox"/> P25100	ADA1D_HUMAN	Alpha-1D adrenergic receptor[...]	ADRA1D , ADRA1A	Homo sapiens (Human)	572 AA
<input type="checkbox"/> O02824	ADA1A_RABIT	Alpha-1A adrenergic receptor[...]	ADRA1A , ADRA1C	Oryctolagus cuniculus (Rabbit)	466 AA

[Feedback](#)

[Help](#)

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

The screenshot shows the UniProt website interface. At the top, there is a navigation bar with the UniProt logo and various search options: BLAST, Align, Peptide search, ID mapping, SPARQL, and UniProtKB. A search bar contains the text "Advanced | List Search". Below the navigation bar, the main content area displays the entry for "P35348 - ADA1A_HUMAN".

Function

Names & Taxonomy

- Proteinⁱ | Alpha-1A adrenergic receptor
- Geneⁱ | ADRA1A
- Statusⁱ | UniProtKB reviewed (Swiss-Prot)
- Organismⁱ | Homo sapiens (Human)

Amino acids | 466 (go to sequence)

Protein existenceⁱ | Evidence at protein level

Annotation scoreⁱ | (5/5)

Subcellular Location

Disease & Variants

PTM/Processing

Expression

Interaction

Structure

Family & Domains

Sequence & Isoforms

Similar Proteins

Entry | Variant viewer **630** | Feature viewer | Genomic coordinates | Publications | External links | History

BLAST | Align | Download | Add | Add a publication | Entry feedback

Functionⁱ

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 G₁₁ proteins. Nuclear ADRA1A-ADRA1B heterooligomers regulate phenylephrine(PE)-stimulated ERK signaling in cardiac myocytes. **2 Publications**

GO annotationsⁱ

Access the complete set of GO annotations on QuickGO

9:22 AM

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

The screenshot shows the UniProt website interface. The browser address bar displays <https://www.uniprot.org/uniprotkb/P35348/entry>. The UniProt logo and navigation menu are visible at the top. The main content area is titled "Entry SynVariant viewer 630" and includes tabs for "Feature viewer", "Genomic coordinates", "Publications", "External links", and "History".

Function

Names & Taxonomy

- Subcellular Location
- Disease & Variants
- PTM/Processing
- Expression
- Interaction
- Structure
- Family & Domains
- Sequence & Isoforms
- Similar Proteins

Organism names

Taxonomic identifierⁱ	9606 NCBI ↗
Organismⁱ	Homo sapiens (Human)
Taxonomic lineageⁱ	cellular organisms > Eukaryota (eucaryotes) > Opisthokonta > Metazoa (metazoans) > Eumetazoa > Bilateria > Deuterostomia > Chordata (chordates) > Craniata > Vertebrata (vertebrates) > Gnathostomata (jawed vertebrates) > Teleostomi > Euteleostomi (bony vertebrates) > Sarcopterygii > Dipnotetrapodomorpha > Tetrapoda (tetrapods) > Amniota (amniotes) > Mammalia (mammals) > Theria > Eutheria (placentals) > Boreoeutheria > Euarchontoglires > Primates > Haplorrhini > Simiiformes > Catarrhini > Hominoidea (apes) > Hominidae (great apes) > Homininae > Homo

Accessions

Primary accession	P35348
Secondary accessions	A8K0I3 B0ZBD1

9:24 AM

- Function
- Names & Taxonomy
- Subcellular Location
- Disease & Variants
- PTM/Processing
- Expression
- Interaction
- Structure
- Family & Domains
- Sequence & Isoforms
- Similar Proteins

accession: Entry **Variant viewer** ⁶³⁰ Feature viewer Genomic coordinates Publications External links History
Secondary A8K0I3

accessions	B0ZBD1 B0ZBD2 B0ZBD4 B0ZBD5 More accessions
------------	---

Proteomes ⁱ	
Identifier	UP000005640
Component ⁱ	Chromosome 8

Organism-specific databases			
AGR	HGNC:277	VEuPathDB	HostDB:ENSG00000120907
HGNC	HGNC:277 ADRA1A	neXtProt	NX_P35348
MIM	104221 gene		

Feedback

Help



https://www.uniprot.org/uniprotkb/P35348/entry#sequences



Συχνές επισκέψεις Μεκινώντας Suggested Sites Web Slice Gallery YPOMEDI WeTransfer - Send Lar... Από Google Chrome Home - EMA Account ...

Άλλοι σελίδοδε



BLAST Align Peptide search ID mapping SPARQL UniProtKB

Advanced | List

Search



Function

Names & Taxonomy

Subcellular Location

Disease & Variants

PTM/Processing

Expression

Interaction

Structure

Family & Domains

Sequence & Isoforms

Similar Proteins

Entry

Sequence status: Variant viewer 630

Feature viewer

Genomic coordinates

Publications

External links

History

This entry describes 9 isoformsⁱ produced by **Alternative splicing**.

P35348-1

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.

Name 1

Synonyms Alpha 1c-1, Alpha(1A-1)

See also sequence in **UniParc** or sequence clusters in **UniRef**

Tools Download Add Highlight Copy sequence

Length 466

Mass (Da) 51,487

Last updated 1995-11-01 v2

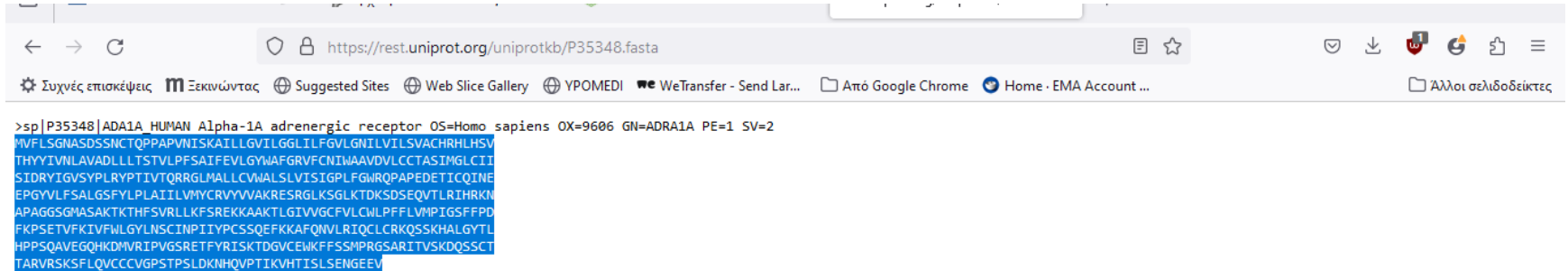
Checksumⁱ 1A50487531DECDF0

MVFLSGNASD	SSNCTQPPAP	VNISKAILLG	VILGGLILFG	VLGNILVILS	VACHRHLSV	THYYIVNLAV	ADLLLTSTVL	PFSAIFEVLG
YWAFGRVFCN	IWAADVLC	TASIMGLCII	SIDRYIGVSY	PLRYPTIVTQ	RRGLMALLCV	WALSIVISIG	PLFGWRQPAP	EDETICQINE

Feedback

Help

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



```
>sp|P35348|ADA1A_HUMAN Alpha-1A adrenergic receptor OS=Homo sapiens OX=9606 GN=ADRA1A PE=1 SV=2
MVFLSGNASDSSNCTQPPAPVNIKAILLGVILGGLILFGVLGNILVILSVACHRHLSV
THYYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAADVLCCTASIMGLCTI
SIDRYIGVSYPLRYPTIVTQRRGLMALLCVMALSLVVISIGPLFGWRQPAPEDETICQINE
EPGYVLF SALGSFYLP LAIILWYCRVWVWAKRESRGLKSGLKTDKSDSEQVTLRIHRKM
APAGSGMASAKTKTHFSVRLKFSREKKAAKTLGIVVGCFLCWL PFFLWMPIGSFFPD
FKPSETVFKIVFWLGYLNSCINPIIYPCSSQEFKAFQNVLRIQCLCRKQSSKHALGYTL
HPPSQAVEGQHKDMVRIPVGSRETFYRISKTDGVCWEKFFSSMPRGSARITVSKDQSSCT
TARVRSKSF LQVCCVGPSTPSLDKNHQPVTIKVHTISLSENGEEV
```


Για πρόσβαση στο FASTA, ανοίξτε το Internet Explorer και πληκτρολογήστε
“http://www.ebi.ac.uk/Tools/sss/fasta/..

The screenshot shows the EMBL-EBI FASTA Sequence Similarity Search (SSS) web interface. At the top, there is a navigation bar with links for EMBL-EBI home, Services, Research, Training, and About us, along with a search icon and the EMBL-EBI logo. Below the navigation bar is a large banner with a blue and green background featuring binary code and abstract patterns. The banner contains the text "FASTA" in large bold letters and "Sequence Similarity Search (SSS)" below it. Underneath the banner, there are links for Job Dispatcher, Help & Privacy, Your Jobs, Protein, and Nucleotide, and a Feedback button. The main content area contains a paragraph describing the tool: "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)." Below this text is a section titled "Databases" with an information icon and "(Protein)" below it. To the right of this section is a form titled "Protein DATABASES" containing a "Clear selection" button and the text "1 Database selected".

← → ↻ <https://www.ebi.ac.uk/jdispatcher/sss/fasta> ☆

Συχνές επισκέψεις **m** Εκκινώντας Suggested Sites Web Slice Gallery YPOMEDI WeTransfer - Send Lar... Από Google Chrome Home - EMA Account ... Άλλοι σελιδοδείκτες

Input sequence ⓘ

Sequence type

Protein DNA RNA

Paste your sequence here - or use the example sequence

```
MVFLSGNASDSSNCTOPPAPVNISKAILLGVILGGLIFGVLGNILVILSVACHRHLSV
THYYIVNLAVALLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAAVDVLCCTASIMGLCII
SIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSIVISIGPLFGWROPAPEDETICQINE
EPGYVLFSAIGSFYPLAAILVMYCRVYVVAKRERGLKSGDKTDKSDSEQVTLRIHRKN
APAGGSGMASAKTKTHFSVRLKFSREKKAATLGIVVGCFLCWLPPFLVMPIGSFFPD
FKPSETVFKIVFWLGYLNSCINPIIYPCSSOEFKAFONVLRIOCLCRKOSKHALGYTL
HPPSOAVEGOHKDMVRIPVGSRETFYRISKTDGVCEWKFFSSMPRGSARITVSKDOSSCT
TARVRSKSFQVCCVGPSTPSLDKNHQVPTIKVHTISLSENGEEV|
```

[Περίληψη...](#) Δεν επιλέχθηκε αρχείο. [Use the example](#) [Clear sequence](#) [More example inputs](#)

Program ⓘ

FASTA FASTX FASTY SSEARCH GGSEARCH GLSEARCH TFASTX TFASTY

Κρατάμε τις επιλεγμένες (default) παραμέτρους, αλλά θα μπορούσαμε να αλλάξουμε όποιαδήποτε παράμετρο

The screenshot shows a web browser window with the URL <https://www.ebi.ac.uk/jdispatcher/sss/fasta>. The browser's address bar and tabs are visible at the top. Below the browser, the page content is organized into sections:

- Program**: A row of radio buttons for selecting the analysis program. The 'FASTA' option is selected.
- Parameters**: A grid of dropdown menus for configuring various parameters. Each parameter has an information icon (i) to its right.

Parameter	Value
MATRIX	BLOSUM50
GAP OPEN	-10
GAP EXTEND	-2
KTUP	2
EXPECTATION UPPER LIMIT	10
EXPECTATION LOWER LIMIT	0
DNA STRAND	N/A
HISTOGRAM	no
FILTER	none
STATISTICAL ESTIMATES	Regress
SCORES	50
ALIGNMENTS	50
SEQUENCE RANGE	START-END
DATABASE RANGE	START-END
MULTI HSPS	no
ANNOTATION FEATURES	

SCORE REPORT FORMAT ⓘ

[Less options ^](#)

Submit

Title

If you use this service, please consider citing the following publication: [Search and sequence analysis tools services from EMBL-EBI in 2022](#). More information about this bioinformatics application can be found in its [bio.tools](#) record.

Please read the provided [Help & Privacy](#) before seeking help from our support staff. If you have any



https://www.ebi.ac.uk/jdispatcher/sss/fasta



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Άλλοι σελιδοδείκτες

Parameters

Submit

YOUR JOB IS SUBMITTED... please be patient!

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

Job ID: [fasta-I20240412-073632-0848-36948228-p1m](#)

SUBMITTED



▼ Please note the following

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

https://www.ebi.ac.uk/jdispatcher/sss/fasta/summary?jobId=

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_OS, μην επιλέγεται (unmark) όλα τα πλαίσια κάτω από το “Alignment” εκτός από το ADA1A_OS. Μετά επιλέξτε το “Show Alignments”.

FASTA
Sequence Similarity Search (SSS)

Job Dispatcher Help & Privacy Your Jobs Protein Nucleotide Feedback

Results for Job ID: fasta-I20240412-073632-0848-36948228-p1m

Summary Table Tool Output Visual Output Functional Predictions Result Files Submission Details

50 results found Items per page: 50 1 – 50 of 50

Organisms

- Homo sapiens (34)
- Mus musculus (2)
- Bos taurus (2)
- Cavia porcellus (2)
- Oryctolagus cuniculus (2)
- Rattus norvegicus (2)

<input checked="" type="checkbox"/>	Align	DB:ID	Source	Length	Score(Bits)	Identities(%)	Positives(%)	E()
<input checked="" type="checkbox"/>	1	SP:P35348	Alpha-1A adrenergic receptor OS=Homo sapiens OX=9606 GN=ADRA1A PE=1 SV=2 View Cross-references [13] ▶ Gene expression ▶ Bioactive molecules ▶ Nucleotide sequences ▶ Macromolecular structures ▶ Genomes & metagenomes ▶ Literature ▶ Samples & ontologies ▶ Protein families ▶ Molecular interactions ▶ Diseases ▶ Protein expression data ▶ Reactions & pathways ▶ Protein sequences	466	626.1	100.0	100.0	9.6e-178
<input checked="" type="checkbox"/>	2	SP:P35348	Alpha-1A adrenergic receptor OS=Homo sapiens	466	626.1	100.0	100.0	9.6e-178

Τότε εμφανίζονται οι αντιστοιχίες.

Browser tabs: MailEnable Web Mail::DOXANI, Αρχική Σελίδα :: Εισόδος, FASTA < EMBL-EBI, rest.uniprot.org/uniprotkb/P35348.f

Address bar: <https://www.ebi.ac.uk/jdispatcher/sss/fasta/summary?jobId=fasta-l20240412-073632-0848-36948228-p> 80%

Navigation: Συχνές επισκέψεις, Ξεκινώντας, Suggested Sites, Web Slice Gallery, YPOMEDI, WeTransfer - Send Lar..., Από Google Chrome, Home · EMA Account ...

Cavia porcellus (2)
 Oryctolagus cuniculus (2)
 Rattus norvegicus (2)
 Canis lupus familiaris (2)
More

Apply to selection
 Annotation
 Alignment
Download as FASTA

Apply to selection

[Gene expression](#) ▶ [Bioactive molecules](#) ▶ [Nucleotide sequences](#)
[Macromolecular structures](#) ▶ [Genomes & metagenomes](#)
[Literature](#) ▶ [Samples & ontologies](#) ▶ [Protein families](#)
[Molecular interactions](#) ▶ [Diseases](#) ▶ [Protein expression data](#)
[Reactions & pathways](#) ▶ [Protein sequences](#)

>SP:P35348 ADA1A_HUMAN Alpha-1A adrenergic receptor OS=Homo sapiens OX=9606 GN=ADRA1A PE=1 SV=2 (466 aa)
 initn: 3143 init1: 3143 opt: 3143 Z-score: 3333.3 bits: 626.1 E(1307104): 9.6e-178
 Smith-Waterman score: 3143; 100.0% identity (100.0% similar) in 466 aa overlap (1-466:1-466)

```

          10      20      30      40      50      60
EMBOSS MVFLSGNASDSSNCTQPPAPVNIKAILLGVILGGLILFGVLGNILVILSVACHRHLHSV
          .....
SP:P35  MVFLSGNASDSSNCTQPPAPVNIKAILLGVILGGLILFGVLGNILVILSVACHRHLHSV
          10      20      30      40      50      60

          70      80      90      100     110     120
EMBOSS THYIYVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAADVLCCTASIMGLCII
          .....
SP:P35  THYIYVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAADVLCCTASIMGLCII
          70      80      90      100     110     120

          130     140     150     160     170     180
EMBOSS SIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLSVISIGPLFGWRQPAPEDETICQINE
          .....
SP:P35  SIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLSVISIGPLFGWRQPAPEDETICQINE
          130     140     150     160     170     180
        
```

<input type="checkbox"/>	2	SP:P35348	Alpha-1A adrenergic receptor OS=Homo sapiens OX=9606 GN=ADRA1A PE=1 SV=2 View Cross-references [13] <small>▶ Gene expression ▶ Bioactive molecules ▶ Nucleotide sequences</small>	466	626.1	100.0	100.0	9.6e-178
--------------------------	---	---------------------------	---	-----	-------	-------	-------	----------

fasta-l20240412-073632-0848-36948228-p1m-entries-fasta - Σημειωματάριο

Αρχείο Επεξεργασία Μορφή Προβολή Βοήθεια
 >UNIPROT:ADA1A_RABIT O02824 Alpha-1A adrenergic receptor (Alpha-1A adrenoceptor) (Alpha-1A adrenoceptor) (Alpha-1C adrene
 MVFLSGNASDSSNCTPPAPVNIKAIILGVILGGLILFGVLGNILVILSVACHRHLSV
 THYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAADVLCCTASIIISLCVI
 SIDRYIGVSYPLRYPTIVTQRRGLRALLCVWAFSLVISVGPLFGWRQPAPDDEETICQINE
 EPGYVLFALGSAFYVPLTIIILAMYCRVYVAKRESRGLKSGLKTDKSDSEQVTLRIHRKN
 APAGGSGVASAKNKTTHFSVRLKFSREKKAAKTLGIVVGCFLCWLPPFLVMPIGSFFPD
 FKPPETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAQNVLKIQLRRKQSSKHALGYTL
 HAPSQALEGQHKDMVRIPVGSGETFYKISKTDGVCWKFSSMPRGSARITVPKQDSACT
 TARVRSKSLQVCCVGPSTPNPGENHQVPTIKIHTISLSENGEEV
 >sp|P35348-8|ADA1A_HUMAN Isoform 8 of Alpha-1A adrenergic receptor OS=Homo sapiens OX=9606 GN=ADRA1A
 MVFLSGNASDSSNCTPPAPVNIKAIILGVILGGLILFGVLGNILVILSVACHRHLSV
 THYYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAADVLCCTASIMGLCII
 SIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLSVIGPLFGWRQPAPEDEETICQINE
 EPGYVLFALGSAFYPLPLAIIILVYCRVYVAKRESRGLKSGLKTDKSDSEQVTLRIHRKN
 APAGGSGMASAKTKTHFSVRLKFSREKKAAKTLGIVVGCFLCWLPPFLVMPIDEVSLC
 HQAGVQWHDLGSQQPPPGFKRFSCLSLPSWDYRDVPPGRRHQALIFVFLVETGFHHV
 GQDDLDTLS
 >sp|P35348-8|ADA1A_HUMAN Isoform 8 of Alpha-1A adrenergic receptor OS=Homo sapiens OX=9606 GN=ADRA1A
 MVFLSGNASDSSNCTPPAPVNIKAIILGVILGGLILFGVLGNILVILSVACHRHLSV
 THYYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNIWAADVLCCTASIMGLCII
 SIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLSVIGPLFGWRQPAPEDEETICQINE
 EPGYVLFALGSAFYPLPLAIIILVYCRVYVAKRESRGLKSGLKTDKSDSEQVTLRIHRKN
 APAGGSGMASAKTKTHFSVRLKFSREKKAAKTLGIVVGCFLCWLPPFLVMPIDEVSLC
 HQAGVQWHDLGSQQPPPGFKRFSCLSLPSWDYRDVPPGRRHQALIFVFLVETGFHHV

	100.0	9.6e-178
	98.3	2e-168
	98.3	2e-168
	97.9	2.9e-168

Ln	Col 1	100%	Unix (LF)	UTF-8	
5	SP:Q9WU25	Alpha-1A adrenergic receptor OS=Cavia porcellus OX=10141 GN=ADRA1A PE=2 SV=2	466	594.6	94.4

View Cross-references [7]

- Bioactive molecules
- Nucleotide sequences
- Literature
- Samples & ontologies
- Protein families
- Protein sequences
- Genomes & metagenomes

Apply to selection

Visual Output

Download (PNG)



Functional Predictions

Download (PNG)



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 BLAST website in a browser. The address bar displays <https://blast.ncbi.nlm.nih.gov/Blast.cgi>. The page header includes the NIH logo and the text "National Library of Medicine National Center for Biotechnology Information". A "Log in" button is visible in the top right. Below the header, the "BLAST" logo is followed by navigation links: "Home", "Recent Results", "Saved Strategies", and "Help".

The main content area features a section titled "Basic Local Alignment Search Tool". It describes BLAST as a tool that finds regions of similarity between biological sequences. A "Learn more" link is provided. To the right of this section is a "NEWS" box with the following text: "BLAST+ 2.15.0 is here! We have included two exciting new features in the latest BLAST+ release. Tue, 28 Nov 2023. More BLAST news..."

Below the "Basic Local Alignment Search Tool" section is a "Web BLAST" section. It contains three main components:

- Nucleotide BLAST**: A green box with a DNA double helix graphic. Text: "nucleotide ► nucleotide".
- blastx**: A blue arrow-shaped box pointing right. Text: "translated nucleotide ► protein".
- tblastn**: A blue arrow-shaped box pointing left. Text: "protein ► translated nucleotide".
- Protein BLAST**: A blue box with a protein ribbon graphic. Text: "protein ► protein".

MailEnable Web Mail: DOXANIC x Αρχική Σελίδα :: Είσοδος x FASTA < EMBL-EBI x Protein BLAST: search protein d x

https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&PAGE_TYPE=BlastSearch&LINK_LOC=blasthom 90%

Συχνές επισκέψεις Μ Εκκινώντας Suggested Sites Web Slice Gallery YPOMEDI WeTransfer - Send Lar... Από Google Chrome Home · EMA Account ... Άλλοι σελιδοδείκτες

An official website of the United States government [Here's how you know](#)

NIH National Library of Medicine
National Center for Biotechnology Information Log in

BLAST® » **blastp suite** Home Recent Results Saved Strategies Help

blastn **blastp** blastx tblastn tblastx **Standard Protein BLAST**

BLASTP programs search protein databases using a protein query. more... Reset page Bookmark

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) Clear Query subrange

From To

Or, upload file Περιήγηση... Δεν επιλέχθηκε αρχείο. ?

Job Title
Enter a descriptive title for your BLAST search ?

Align two or more sequences ?

Choose Search Set

Databases Standard databases (nr etc.): New Experimental databases Try experimental clustered nr database
For more info see [What is clustered nr?](#)

Compare Select to compare standard and experimental database ?

Standard

Database ?

9:46 AM

Επιλέγουμε την αλληλουχία ADA1_HUMAN σε FASTA μορφή και την επικολλούμε

BLAST [®] >> blastp suite Home Recent Results Saved Strategies Help

COVID-19 is an emerging, rapidly evolving situation.
Get the latest public health information from CDC: <https://www.coronavirus.gov>.
Get the latest research from NIH: <https://www.nih.gov/coronavirus>.

Standard Protein BLAST

blastn **blastp** blastx tblastn tblastx

BLASTP programs search protein databases using a protein query. [more...](#) [Reset page](#) [Bookmark](#)

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

Choose Search Set

Database

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

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

Program Selection

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

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

VODAFONE_WIFI_108
Πρόσβαση στο Internet

Και επιλέγουμε BLAST

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

Enter a descriptive title for your BLAST search

Align two or more sequences

Choose Search Set

Databases

Standard databases (nr etc.) **New** Experimental databases [Try experimental clustered nr database](#)
For more info see [What is clustered nr?](#)

Standard

Database **+** UniProtKB/Swiss-Prot (swissprot)

Organism Optional
Enter organism name or id—completions will be suggested exclude [Add organism](#)
Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

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

Compare Select to compare standard and experimental database

Program Selection

Algorithm

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 swissprot using Blastp (protein-protein BLAST)
 Show results in a new window

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

+ Algorithm parameters

Log in

BLAST® » **blastp suite** » **RID-1HP83SYY013**

[Home](#) [Recent Results](#) [Saved Strategies](#) [Help](#)

Format Request Status

[\[Formatting options\]](#)

Job Title: Protein Sequence

Request ID	1HP83SYY013
Status	Searching
Submitted at	Fri Apr 12 02:47:31 2024
Current time	Fri Apr 12 02:47:48 2024
Time since submission	00:00:17

This page will be automatically updated in 2 seconds

FOLLOW NCBI



Log in

[Edit Search](#) Save Search Search Summary ▾

[How to read this report?](#) [BLAST Help Videos](#) [Back to Traditional Results Page](#)

Job Title	Protein Sequence
RID	1HP83SY013 Search expires on 04-13 14:47 pm Download All ▾
Program	BLASTP Citation ▾
Database	nr See details ▾
Query ID	lcl Query_9614096
Description	unnamed protein product
Molecule type	amino acid
Query Length	466
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 to **E value** to **Query Coverage** to

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

Descriptions Graphic Summary Alignments Taxonomy

Sequences producing significant alignments Download ▾ Select columns ▾ Show 100 ▾ [?](#)

Η αντιστοίχιση της αλληλουχίας μας...

Browser tabs: MailEnable Web Mail::DOXA... Αρχική Σελίδα :: Εισοδος FASTA < EMBL-EBI NCBI Blast:Protein Sequence rest.uniprot.org/uniprotkb/P3534...

Address bar: <https://blast.ncbi.nlm.nih.gov/Blast.cgi> 90%

Navigation: Συχνές επισκέψεις, Έκτιμώντας, Suggested Sites, Web Slice Gallery, YPOMEDI, WeTransfer - Send Lar..., Από Google Chrome, Home · EMA Account ... Άλλοι σελιδοδείκτες

select all 100 sequences selected

GenPept Graphics Distance tree of results Multiple alignment MSA Viewer

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> alpha-1A adrenergic receptor isoform 1 (Homo sapiens)	Homo sapiens	956	956	100%	0.0	100.00%	466	NP_000671.2
<input checked="" type="checkbox"/> alpha-1A adrenergic receptor isoform X1 (Pan paniscus)	Pan paniscus	952	952	100%	0.0	99.79%	466	XP_008975445.1
<input checked="" type="checkbox"/> alpha-1A adrenergic receptor isoform X1 (Gorilla gorilla gorilla)	Gorilla gorilla g...	952	952	100%	0.0	99.57%	466	XP_055204251.1
<input checked="" type="checkbox"/> Adrenergic, alpha-1A-, receptor (Homo sapiens)	Homo sapiens	952	952	100%	0.0	99.57%	466	AAH95512.1
<input checked="" type="checkbox"/> alpha1C adrenergic receptor (Homo sapiens)	Homo sapiens	951	951	100%	0.0	99.57%	466	BAA04960.1
<input checked="" type="checkbox"/> alpha adrenergic receptor subtype alpha 1c (human, heart, Peptide, 466 aa) (Homo sapiens)	Homo sapiens	949	949	100%	0.0	99.57%	466	AAB31165.1
<input checked="" type="checkbox"/> alpha1C adrenergic receptor (Homo sapiens)	Homo sapiens	946	946	100%	0.0	99.14%	466	AAA93114.1
<input checked="" type="checkbox"/> adrenergic receptor alpha-1a (Homo sapiens)	Homo sapiens	946	946	100%	0.0	98.93%	466	AAK77197.1
<input checked="" type="checkbox"/> alpha-1A adrenergic receptor isoform X1 (Aotus nancymaae)	Aotus nancymaae	944	944	100%	0.0	98.71%	466	XP_064224789.1
<input checked="" type="checkbox"/> alpha-1A adrenergic receptor isoform X2 (Pongo pygmaeus)	Pongo pygmaeus	944	944	100%	0.0	98.93%	466	XP_054354523.1
<input checked="" type="checkbox"/> alpha-1A adrenergic receptor isoform X1 (Sapajus apella)	Sapajus apella	942	942	100%	0.0	98.50%	466	XP_032144476.1
<input checked="" type="checkbox"/> alpha-1A adrenergic receptor isoform X1 (Nomascus leucogenys)	Nomascus leuc...	940	940	100%	0.0	98.28%	466	XP_012363809.1
<input checked="" type="checkbox"/> alpha-1A adrenergic receptor isoform X1 (Callithrix jacchus)	Callithrix jacchus	940	940	100%	0.0	98.50%	466	XP_008977331.1
<input checked="" type="checkbox"/> alpha-1A adrenergic receptor isoform X1 (Papio anubis)	Papio anubis	940	940	100%	0.0	98.50%	466	XP_003902622.1
<input checked="" type="checkbox"/> alpha-1A adrenergic receptor isoform X1 (Trachypithecus francoisi)	Trachypithecus ...	940	940	100%	0.0	98.28%	466	XP_033085140.1
<input checked="" type="checkbox"/> alpha-1A adrenergic receptor isoform X1 (Cebus imitator)	Cebus imitator	939	939	100%	0.0	98.28%	466	XP_017395880.1
<input checked="" type="checkbox"/> alpha-1A adrenergic receptor (Hylobates moloch)	Hylobates moloch	939	939	100%	0.0	98.28%	466	XP_031999438.1
<input checked="" type="checkbox"/> alpha-1A adrenergic receptor (Macaca mulatta)	Macaca mulatta	939	939	100%	0.0	98.28%	466	NP_001108205.1
<input checked="" type="checkbox"/> alpha-1A adrenergic receptor isoform X1 (Rhinopithecus roxellana)	Rhinopithecus r...	938	938	100%	0.0	98.28%	466	XP_010376433.1

Taskbar: Αναζήτηση, 14°C Ηλιοφάνεια, 9:48 AM 4/12/2024

Επιλέγοντας Graphic Summary

Descriptions **Graphic Summary** Alignments Taxonomy

[hover to see the title](#) [click to show alignments](#) Show Conserved Domains Alignment scores ■ < 40 ■ 40 - 50 ■ 50 - 80 ■ 80 - 200 ■ >= 200 ?

100 sequences selected ? **Putative conserved domains have been detected, click on the image below for detailed results.**
[CD search result summary](#)

Distribution of the top 100 Blast Hits on 100 subject sequences

Query
1 90 180 270 360 450

VODAFONE_WIFI_108
Πρόσβαση στο Internet

Other reports: [Distance tree of results](#) [Multiple alignment](#) [MSA viewer](#) ?

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

Descriptions | **Graphic Summary** | **Alignments** | Taxonomy

Alignment view: **Pairwise**

[Download](#)

[Download](#) [GenPept](#) [Graphics](#) [Next](#) [Previous](#) [Descriptions](#)

RecName: Full=Alpha-1A adrenergic receptor; AltName: Full=Alpha-1A adrenoceptor; 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](#)

Related Information
[Gene](#) - associated gene details

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		MVFLSGNASDSSNCTQPPAPVNI			60
Sbjct 1		MVFLSGNASDSSNCTQPPAPVNI			60
Query 61		THYYIVNLAVADLLLTSTVLPFSAI			120
Sbjct 61		THYYIVNLAVADLLLTSTVLPFSAI			120
Query 121		SIDRYIGVSYPLRYPTIVTQRRGLM			180
Sbjct 121		SIDRYIGVSYPLRYPTIVTQRRGLM			180
Query 181		EPGYVLFSAALGSPYLPFLAII			240
Sbjct 181		EPGYVLFSAALGSPYLPFLAII			240
Query 241		APAGSSGMASAKTKTHFSVRL			300
Sbjct 241		APAGSSGMASAKTKTHFSVRL			300

Αν κάνουμε κλικ πάνω στην εικόνα αυτή

The screenshot displays a web browser window with the URL https://www.ncbi.nlm.nih.gov/Structure/fcn3d/full.html?from=blast&blast_rep_id=NP_000671&query_id=Query_9614096. The browser's address bar shows the target protein as NP_000671 (ALPHA-1A ADRENERGIC RECEPTOR (P35348)).

The main content area features a 3D ribbon diagram of the protein structure, colored by pLDDT. A legend in the bottom-left corner explains the color coding:

- Very high (pLDDT > 90): Blue
- Confident (90 > pLDDT > 70): Light Blue
- Low (70 > pLDDT > 50): Yellow
- Very low (pLDDT < 50): Orange

The right-hand side of the interface contains a 'Sequences and Annotations' panel. It includes a 'Summary' tab and a 'Details' tab. Under 'Annotations', several options are checked, including 'Conserved Domains', 'Functional Sites', and 'PTM (UniProt)'. Below this, there are buttons for 'Selection: Name: seq_1', 'Save', and 'Clear'.

The 'Proteins' section shows a sequence alignment for 'Protein P35348_A' and 'Query: Query_9614096'. The alignment is as follows:

```
Protein P35348_A 1 MVFLSGNASDSSNCTQPPAPVNI SKA ILLGVILGGLILFGVLGN
BLAST, E: 0.0 MVFLSGNASDSSNCTQPPAPVNI SKA ILLGVILGGLILFGVLGN
Query: Query_9614096 1 MVFLSGNASDSSNCTQPPAPVNI SKA ILLGVILGGLILFGVLGN
```

Below the alignment, domain and feature annotations are listed:

- domain: 7tmA_a... 261 Res
- feat: TM helix 1 27 Res
- feat: TM helix 2 27 Res
- feat: TM helix 3 31 Res
- feat: TM helix 4 24 Res
- feat: TM helix 5 26 Res

The bottom of the image shows the Windows taskbar with the search bar containing 'Αναζήτηση', several application icons, and system tray information including '14°C Ηλιόφάνεια', 'ENG', and the time '9:50 AM 4/12/2024'.

Navigation tabs: Descriptions, Graphic Summary, Alignments, **Taxonomy** (circled in red)

Sub-navigation tabs: 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
Tscherkia triton	rodents	220	1	Tscherkia triton hits
Nannospalax ehrenbergi	rodents	214	1	Nannospalax ehrenbergi hits