

# Анализ белковых последовательностей: Swiss-Prot



Swiss-Prot – одна из первых баз данных белковых последовательностей, “gold standard” белковой аннотации.

Аннотация выполнена вручную группой профессиональных экспертов на основе экспериментальной информации, описанной в научных статьях.

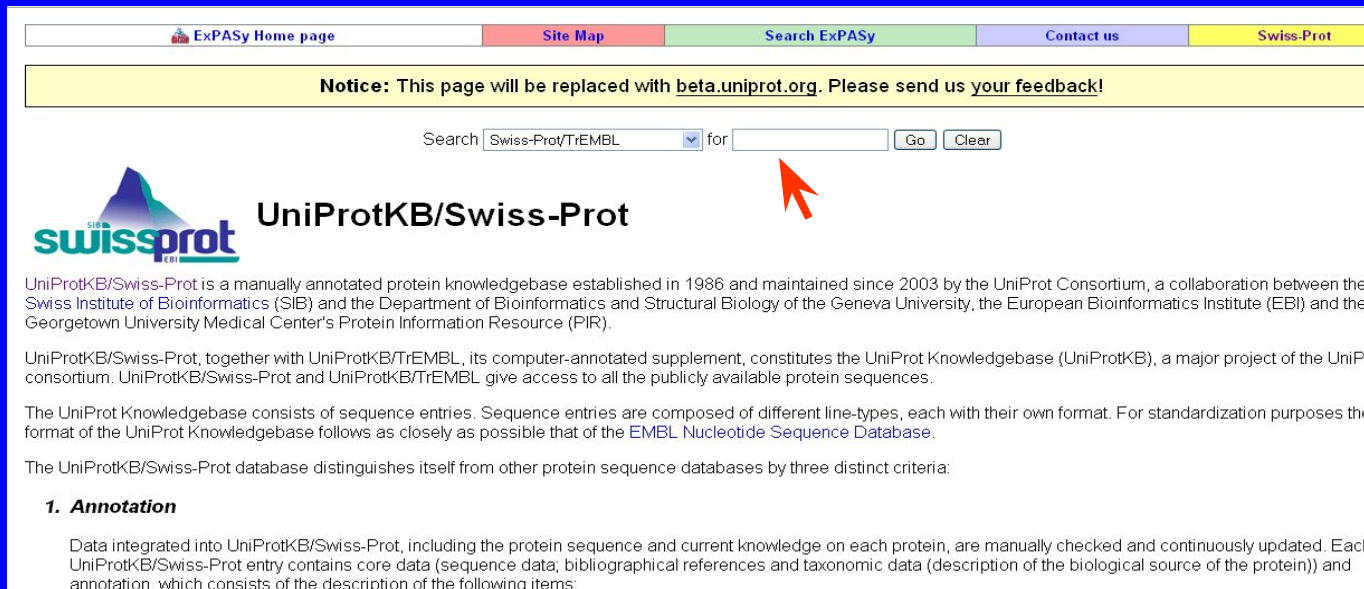
Организована в 1986 году –  
SIB+EBI+PIR+GU = prof. Amos Bairoch

На сегодняшний день – Release 56.2 -  
**398181** последовательностей

# UniProt DB

UniProt = Swiss-Prot + TrEMBL (Translated EMBL sequence database)

TrEMBL – Release 39.2 - 6534543 sequences



The screenshot shows the UniProtKB/Swiss-Prot website interface. At the top, there is a navigation bar with links for "ExPASy Home page", "Site Map", "Search ExPASy", "Contact us", and "Swiss-Prot". Below this is a yellow notice box stating: "Notice: This page will be replaced with [beta.uniprot.org](https://beta.uniprot.org). Please send us your feedback!".

Below the notice is a search bar with a dropdown menu set to "Swiss-Prot/TrEMBL" and a search input field. A red arrow points to the search input field. There are "Go" and "Clear" buttons next to the search bar.

The main content area features the UniProtKB/Swiss-Prot logo, which includes the text "SIB swissprot EBI". To the right of the logo is the text "UniProtKB/Swiss-Prot".

Below the logo and text, there is a paragraph of text: "UniProtKB/Swiss-Prot is a manually annotated protein knowledgebase established in 1986 and maintained since 2003 by the UniProt Consortium, a collaboration between the Swiss Institute of Bioinformatics (SIB) and the Department of Bioinformatics and Structural Biology of the Geneva University, the European Bioinformatics Institute (EBI) and the Georgetown University Medical Center's Protein Information Resource (PIR)."

Another paragraph follows: "UniProtKB/Swiss-Prot, together with UniProtKB/TrEMBL, its computer-annotated supplement, constitutes the UniProt Knowledgebase (UniProtKB), a major project of the UniProt consortium. UniProtKB/Swiss-Prot and UniProtKB/TrEMBL give access to all the publicly available protein sequences."

The next paragraph states: "The UniProt Knowledgebase consists of sequence entries. Sequence entries are composed of different line-types, each with their own format. For standardization purposes the format of the UniProt Knowledgebase follows as closely as possible that of the EMBL Nucleotide Sequence Database."

The final paragraph reads: "The UniProtKB/Swiss-Prot database distinguishes itself from other protein sequence databases by three distinct criteria:"

**1. Annotation**

Data integrated into UniProtKB/Swiss-Prot, including the protein sequence and current knowledge on each protein, are manually checked and continuously updated. Each UniProtKB/Swiss-Prot entry contains core data (sequence data; bibliographical references and taxonomic data (description of the biological source of the protein)) and annotation, which consists of the description of the following items:

# Поиск белка в Swiss-Prot (по названию)

Search in UniProt Knowledgebase (Swiss-Prot and TrEMBL) for: Na(+)/K(+) ATPase - Mozilla Firefox

Файл Правка Вид Журнал Закладки Инструменты Справка

http://www.expasy.org/cgi-bin/sprot-search-de?%20Na(%2B)%2F(%2B)%20ATPase

Customize Links Free Hotmail Windows Marketplace Windows Media Windows

Swiss-Prot - Поиск в Google Search in UniProt Knowledgebas... UniProtKB

ExPASy Home page Site Map Search ExPASy Contact us Swiss-Prot

Hosted by SIB Switzerland | Mirror sites: Australia | Brazil | Canada | China | Korea |

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Search  for

## Search in UniProt Knowledgebase (Swiss-Prot and TrEMBL) for: Na(+)/K(+) ATPase

UniProtKB/Swiss-Prot Release 54.3 of 02-Oct-2007  
UniProtKB/TrEMBL Release 37.3 of 02-Oct-2007

- Number of sequences found in UniProt Knowledgebase (Swiss-Prot(42) and TrEMBL(0): **42**
- Note that the selected sequences can be saved to a file to be later retrieved; to do so, go to the bottom of this page.
- For more directed searches, you can use the Sequence Retrieval System SRS.

**Search in UniProtKB/Swiss-Prot: There are matches to 42 out of 285335 entries**

AT1A1\_ANGAN (Q92030)  
Sodium/potassium-transporting ATPase subunit alpha-1 precursor (EC 3.6.3.9) (Sodium pump subunit alpha-1) (Na(+)/K(+) ATPase alpha-1 subunit). {GENE: Name=atp1a1} - Anguilla anguilla (European freshwater eel)

AT1A1\_BOVIN (Q08DA1)  
Sodium/potassium-transporting ATPase subunit alpha-1 precursor (EC 3.6.3.9) (Sodium pump subunit alpha-1) (Na(+)/K(+) ATPase alpha-1 subunit). {GENE: Name=ATP1A1} - Bos taurus (Bovine)

AT1A1\_BUFMA (P30714)  
Sodium/potassium-transporting ATPase subunit alpha-1 precursor (EC 3.6.3.9) (Sodium pump subunit alpha-1) (Na(+)/K(+) ATPase alpha-1 subunit). {GENE: Name=ATP1A1} - Bufo marinus (Giant toad) (Cane toad)

AT1A1\_CANFA (P50997)  
Sodium/potassium-transporting ATPase subunit alpha-1 precursor (EC 3.6.3.9) (Sodium pump subunit alpha-1) (Na(+)/K(+) ATPase alpha-1 subunit). {GENE: Name=ATP1A1} - Canis familiaris (Dog)

# Advances search



## UniProt Knowledgebase (Swiss-Prot and TrEMBL) Advanced Search

This search program uses SRS to perform queries. Simpler forms are available to search by description or by full text. Available connectors within a field are "&" (and), "|" (or) and "!" (but not). You can prefix your search terms by ! to specify "not" (this is not possible in SRS). Example queries:

- To retrieve all AP1 complex proteins from mouse (AP1S1, AP1G1, etc. but not MIAP1, IQGAP1, ...), specify *Gene Name: ap1\**, *Organism: Mus*, and deselect "Append and prefix \* to query terms".
- To retrieve the three human beta-adrenergic receptor proteins in UniProtKB/Swiss-Prot, but not the beta-adrenergic receptor kinases, specify *Description: beta&adrenergic&receptor!kinase*, *Organism: Homo sapiens*, and select "Append and prefix \* to query terms".

Search  UniProtKB/Swiss-Prot  UniProtKB/TrEMBL

Description

AND

AND Organism

Append and prefix \* to query terms

view of  results

This tool can be used to create links to UniProtKB by using the URL of the results page.

*The gory details:*

- **The description line** is indexed as a series of words. If no wildcard (\*) is present at the start of the query, it will only match entries where the query is the start of the

# Результаты

## UniProtKB/Swiss-Prot description: ATPase

### Description and organism

There are 114 UniProtKB/Swiss-Prot entries with the description *ATPase* and from taxon *Homo sapiens*. The following is a list of the first 100 entries, sorted by entry name (ID

### Entries in UniProtKB/Swiss-Prot (114):

Send selected sequences to



	Entry name	AC	Gene names	Description	Organisms	Len
<input type="checkbox"/>	ADRM1_HUMAN	Q16186	ADRM1, GP110	<b>Protein ADRM1</b> (Adhesion-regulating molecule 1) (110 kDa cell membrane glycoprotein) (Gp110) (Proteasome regulatory particle non-ATPase 13) (hRpn13)	Homo sapiens (Human)	407
<input type="checkbox"/>	AHSA1_HUMAN	O95433	AHSA1, C14orf3, HSPC322	<b>Activator of 90 kDa heat shock protein ATPase homolog 1</b> (AHA1) (p38)	Homo sapiens (Human)	338
<input type="checkbox"/>	ARSA1_HUMAN	O43681	ASNA1	<b>Arsenical pump-driving ATPase</b> (EC 3.6.3.16) (Arsenite-translocating ATPase) (Arsenical resistance ATPase) (Arsenite-transporting ATPase) (ARSA) (ASNA-I)	Homo sapiens (Human)	348
<input type="checkbox"/>	AT10A_HUMAN	O60312	ATP10A, ATP10C, ATPVC, KIAA0566	<b>Probable phospholipid-transporting ATPase VA</b> (EC 3.6.3.1) (ATPVA) (Aminophospholipid translocase VA)	Homo sapiens (Human)	149
<input type="checkbox"/>	AT10B_HUMAN	O94823	ATP10B, ATPVB, KIAA0715	<b>Probable phospholipid-transporting ATPase VB</b> (EC 3.6.3.1)	Homo sapiens (Human)	146
<input type="checkbox"/>	AT10D_HUMAN	Q9P241	ATP10D, KIAA1487	<b>Probable phospholipid-transporting ATPase VD</b> (EC 3.6.3.1) (ATPVD)	Homo sapiens (Human)	142
<input type="checkbox"/>	AT11A_HUMAN	P98196	ATP11A, ATPIH, ATPIS, KIAA1021	<b>Probable phospholipid-transporting ATPase IH</b> (EC 3.6.3.1) (ATPase class I type 11A) (ATPase IS)	Homo sapiens (Human)	113



# Выборка гомологичных белков

## UniProtKB/Swiss-Prot description: dUTPase

### Description

There are 212 UniProtKB/Swiss-Prot entries with the description *dUTPase*. The following is a list of the first 100 entries, sorted by entry name (ID).

### Entries in UniProtKB/Swiss-Prot (212):

Send selected sequences to

Entry name	AC			Organisms	Len	
<input type="checkbox"/>	DUT_ACIAD	Q6FDR0		<b>Deoxyuridine 5'-triphosphate nucleotidohydrolase</b> (EC 3.6.1.23) (dUTPase) (dUTP pyrophosphatase)	Acinetobacter sp. (strain ADP1)	150
<input type="checkbox"/>	DUT_ADEG1	Q89662		<b>Deoxyuridine 5'-triphosphate nucleotidohydrolase</b> (EC 3.6.1.23) (dUTPase) (dUTP pyrophosphatase)	Avian adenovirus gal1 (strain Phelps) (FAdV-1) (Fowl adenovirus 1)	178
<input type="checkbox"/>	DUT_ADEG8	Q9YYS0		<b>Deoxyuridine 5'-triphosphate nucleotidohydrolase</b> (EC 3.6.1.23) (dUTPase) (dUTP pyrophosphatase)	Avian adenovirus 8 (strain ATCC A-2A) (FAdV-8) (Fowl adenovirus 8)	163
<input type="checkbox"/>	DUT_AERPE	Q9YG32	<b>dut</b> , <i>APE_0069.1</i>	<b>Probable deoxyuridine 5'-triphosphate nucleotidohydrolase</b> (EC 3.6.1.23) (dUTPase) (dUTP pyrophosphatase)	Aeropyrum pernix	159
<input type="checkbox"/>	DUT_AGRT5	Q8UII1	<b>dut</b> , <i>Atu0314</i> , <i>AGR_C_548</i>	<b>Deoxyuridine 5'-triphosphate nucleotidohydrolase</b> (EC 3.6.1.23) (dUTPase) (dUTP pyrophosphatase)	Agrobacterium tumefaciens (strain C58 / ATCC 33970)	156
<input type="checkbox"/>	DUT_ANAMM	Q5PAE6	<b>dut</b> , <i>AMB05</i>	<b>Deoxyuridine 5'-triphosphate nucleotidohydrolase</b> (EC 3.6.1.23) (dUTPase) (dUTP pyrophosphatase)	Anaplasma marginale (strain St. Maries)	147
<input type="checkbox"/>	DUT_ANTLO	Q6E4Q0	<b>DUT1</b>	<b>Deoxyuridine 5'-triphosphate nucleotidohydrolase</b> (EC 3.6.1.23) (dUTPase) (dUTP pyrophosphatase)	Antonospora locustae (Nosema locustae)	143
<input type="checkbox"/>	DUT_AQUAE	O66592	<b>dut</b> , <i>aq_220</i>	<b>Deoxyuridine 5'-triphosphate nucleotidohydrolase</b> (EC 3.6.1.23) (dUTPase) (dUTP pyrophosphatase)	Aquifex aeolicus	150
<input type="checkbox"/>	DUT_ARCFU	O29157	<b>dut</b> , <i>AF_1108</i>	<b>Probable deoxyuridine 5'-triphosphate nucleotidohydrolase</b> (EC 3.6.1.23) (dUTPase) (dUTP pyrophosphatase)	Archaeoglobus fulgidus	168
<input type="checkbox"/>	DUT_ASHGO	Q74ZF0	<b>DUT1</b> , <i>AGR249C</i>	<b>Deoxyuridine 5'-triphosphate nucleotidohydrolase</b> (EC 3.6.1.23) (dUTPase) (dUTP pyrophosphatase)	Ashbya gossypii (Yeast) (Eremothecium gossypii)	153
<input type="checkbox"/>	DUT_AZOSE	Q5P7Z9	<b>dut</b> , <i>AZOSEA04400</i> , <i>ebA837</i>	<b>Deoxyuridine 5'-triphosphate nucleotidohydrolase</b> (EC 3.6.1.23) (dUTPase) (dUTP pyrophosphatase)	Azoarcus sp. (strain EbN1) (Aromatoleum aromaticum (strain EbN1))	149
<input type="checkbox"/>	DUT_BACFN	Q5LIH9	<b>dut</b> , <i>BF0272</i>	<b>Deoxyuridine 5'-triphosphate nucleotidohydrolase</b> (EC 3.6.1.23) (dUTPase) (dUTP pyrophosphatase)	Bacteroides fragilis (strain ATCC 25285 / NCTC 9343)	144

# Сохранить в FASTA формате

```
Swiss-Prot - Поиск в Google http://www.expa.../cgi-bin/wgetz
>DUT_ACIAD
MKVQVKILDQRLGQEWPLPSYATTGSAGLDRACLDEAIQIEPGQTVLIKTMAIYIHDT
NFAGLILPRSLGKHGKIVLGNLVGLIDSDYQGELMISVWNRGQNTFFLEPGERLAQTVL
VPVIAQAEFEQVEEFVATDRGAGGFGHTGQK
>DUT_ADEG1
MDPFGSSSVPCSTSDLPEPKLYFVRLSPHAVPPVRATHGAAGYDLFSAYDIKVPARGRA
LVPTDLVVFQPPGCGYRIAPRSLAAKFFIDVGAGVIDPDYRGNVSVVLFNFSESSFNIR
RGDRVAQLILERIMPELSELTQLGETDRGASGFGSTGMGAVDNRQSVLEWLTGSR
>DUT_ADEG8
MSFDSGCPPTPPVKLLFKKHSFPAVTPQRATSGAAGYDLCSADVVVPPKRSRSLIPTDLS
FQFPRGVYRIAPRSLAVKFFIDVGAGVIDSDYRGIIVSVLLFNFSDHNFVNRGDRIAQ
LILERHLTPDLEERSGLDETARGAAGFGSTGGFDTGVCPSFS
>DUT_AERPE
MFLSGRDLVLLGVVKHNSGAIQPAQVDSLVSIEIADAGFLGEEKIMPKGDRIQCEY
GVCELEPGAYRLRFNEVVSIPPQHVGFCEPRSSLLRMGCYLGCAVWDPGYTGRQAMLLV
ANPHGLRLEMGSRIAQLVVARVEGPLTSLYKGDYQGEGL
>DUT_AGR75
MTVQNDNRPLRLVRLANGADLELPSYETRGAAGMDLRAAVPADEPLNLQGERALVPTG
FIFEVPPQGYEAQIRPRSLAIKNGITCLNSPGTVDSYRGEVKVILANLQDDFTIERGM
RIAQHVIAPVVTQVTVSEVTETSETARGAGGFSTGV
>DUT_ANAMM
MLKVKILRLASGYGLPLPSYATPKSAGLDLYAAVDSKLVVHPGGRCVAVKTGVALELPGY
EAQIRSRSLAANFGICVLNAPGTIDSDYRGETTVVLSNFGSEYVVISRGDRVAQMVIAP
VERVEEVEVNSITATSRGEGGFSTGT
>DUT_ANTLO
MSEIITVKRLFSDAKIPVRHSEGAAYDLYAYEDTVVAPNERKVIATGVRIITVPLSCQGT
IYSRSLALKYCIEIFGVNIGPGETKDIVVDIYNHGKMPFNVAKGDRIAQIVFKLFGGD
LHEVSELSDTKRSGCGWSTGIS
>DUT_AQUAE
MSKVILKIKRPLPHAQDLPLPSYATPHSSGLDLRAAIEKPLKIKPFERVL IPTGLILEIPE
GYEGQVPRSLAWKKGLTVLNAPGTIDADYRGEVKVILVNLGNEEVVIERGERIAQLVI
APVQRVEVVEVEEVSQTRGEGGFSTGTE
>DUT_ARCFU
MAVLSGDEIRKLIQKEGLIRDYVDLETDQIQPNFGDCTLRVYRLRGCGRVDFDNSRREL
ELEEVEFRDWWYLPKGVYRAKLEVVRLGNDIMAIARPRSTLIRCGANVLTAVWDAGYEG
RSEVSIIVVHNDYGIWLSRNARIQLVFI RLSSPTKGYEGVYKGENIDS
>DUT_ASHG0
MTDQPAKKVHSAPTLKVQLRSENAIAPTSGSAAAAGYDIYASQDCVIPGRGQGLVATDVS
FTVPVGTYRIAPRSLAVKHGIQTGAGVVDRTYTGVEVKIVLFNHSDRDYAVKRGDRVAQ
```

# Стандартная запись Swiss-Prot

Search  for

## UniProtKB/Swiss-Prot entry **Q9CIT4**

[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#) [\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

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### Entry information

Entry name	ACMA_LACLA
Primary accession number	<b>Q9CIT4</b>
Secondary accession numbers	None
Integrated into Swiss-Prot on	August 14, 2001
Sequence was last modified on	June 1, 2001 (Sequence version 1)
Annotations were last modified on	October 2, 2007 (Entry version 45)

### Name and origin of the protein

Protein name	<b>Probable N-acetylmuramidase [Precursor]</b>
Synonyms	<b>EC 3.2.1.17</b> <b>Peptidoglycan hydrolase</b> <b>Autolysin</b> <b>Lysozyme</b>
Gene name	<b>Name: acmA</b> OrderedLocusNames: LL0272
From	Lactococcus lactis subsp. lactis (Streptococcus lactis) [TaxID: 1360] [HAMAP proteome]
Taxonomy	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
Protein existence	3: Inferred from homology;

### References

[1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
**STRAIN=IL 1403**;  
DOI=10.1101/gr.1697R; PubMed=11337471 [NCBI, ExPASy, EBI, Israel, Japan]  
Bolotin A., Wincker P., Mauger S., Jaillon O., Malmme K., Weissenbach J., Ehrlich S.D., Sorokin A.;  
"The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis IL 1403.";  
Genome Res. 11:731-753(2001).

### Comments

- **FUNCTION:** Required for cell separation during growth (*By similarity*).
- **CATALYTIC ACTIVITY:** Hydrolysis of 1,4-beta-linkages between N-acetylmuramic acid and N-acetyl-D-glucosamine residues in a peptidoglycan and between



# Стандартные поля: entry, name, origin

## UniProtKB/Swiss-Prot entry P00533

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[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#) [\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

*Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.*

### Entry information

Entry name	EGFR_HUMAN
Primary accession number	P00533
Secondary accession numbers	O00688 O00732 P06268 Q14225 Q92795 Q9BZS2 Q9GZX1 Q9H2C9 Q9H3C9 Q9UMD7 Q9UMD8 Q9UMG5
Integrated into Swiss-Prot on	July 21, 1986
Sequence was last modified on	November 1, 1997 (Sequence version 2)
Annotations were last modified on	October 2, 2007 (Entry version 121)

### Name and origin of the protein

Protein name	Epidermal growth factor receptor [Precursor]
Synonyms	EC 2.7.10.1 Receptor tyrosine-protein kinase ErbB-1
Gene name	Name: EGFR Synonyms: ERBB1
From	Homo sapiens (Human) [TaxID: 9606]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.
Protein existence	1: Evidence at protein level;

### References

[1] NUCLEOTIDE SEQUENCE (MPN1) (ISOFORM 1)

Название записи, уникальный идентификатор (ID), предыдущие идентификаторы соответствующей записи, даты первой и последней модификаций, распространенное название белка и его синонимы (ЕС номер для ферментов), название гена, организм и его таксономия, уровень подтверждения

# NiceZyme (ферменты)

## NiceZyme View of ENZYME: EC 2.7.10.1

### Official Name

Receptor protein-tyrosine kinase.

### Alternative Name(s)

Receptor protein tyrosine kinase.

### Reaction catalysed

ATP + a [protein]-L-tyrosine <=> ADP + a [protein]-L-tyrosine phosphate

### Comment(s)


- The receptor protein-tyrosine kinases, which can be defined as having a transmembrane domain, are a large and diverse multigene family found only in metazoans.
- In the human genome, 58 receptor-type protein-tyrosine kinases have been identified and these are distributed into 20 subfamilies.
- Formerly EC 2.7.1.112.

### Cross-references

PROSITE	PDOC00100
BRENDA	2.7.10.1
PUMA2	2.7.10.1
PRIAM enzyme-specific profiles	2.7.10.1
KEGG Ligand Database for Enzyme Nomenclature	2.7.10.1
IUBMB Enzyme Nomenclature	2.7.10.1
IntEnz	2.7.10.1
MEDLINE	Find literature relating to 2.7.10.1
MetaCyc	2.7.10.1

P13368, 7LESS_DROME;	P20806, 7LESS_DROVI;	Q9UH73, ALK_HUMAN;
P97793, ALK_MOUSE;	Q9VBW3, CAD96_DROME;	P79750, CSF11_FUGRU;
Q8UVR8, CSF12_FUGRU;	Q9I8N6, CSF1R_DANRE;	P13369, CSF1R_FELCA;
P07333, CSF1R_HUMAN;	P09581, CSF1R_MOUSE;	Q00495, CSF1R_RAT;
Q08345, DDR1_HUMAN;	Q03146, DDR1_MOUSE;	Q7YR43, DDR1_PANTR;
Q63474, DDR1_RAT;	Q16832, DDR2_HUMAN;	Q62371, DDR2_MOUSE;
P13387, EGFR_CHICK;	P04412, EGFR_DROME;	P00533, EGFR_HUMAN;
P55245, EGFR_MACMU;	Q01279, EGFR_MOUSE;	Q10656, EGL15_CAEEL;
Q13148, EPA4A_DANRE;	Q91845, EPA4A_XENLA;	Q91694, EPA4B_XENLA;
Q91571, EPB1A_XENLA;	Q91736, EPB1B_XENLA;	P21709, EPHA1_HUMAN;
Q60750, EPHA1_MOUSE;	P29317, EPHA2_HUMAN;	Q1KL86, EPHA2_MACFA;
Q03145, EPHA2_MOUSE;	P29318, EPHA3_CHICK;	Q13146, EPHA3_DANRE;
P29320, EPHA3_HUMAN;	P29319, EPHA3_MOUSE;	Q08680, EPHA3_RAT;
Q07496, EPHA4_CHICK;	P54764, EPHA4_HUMAN;	Q03137, EPHA4_MOUSE;
P54755, EPHA5_CHICK;	P54756, EPHA5_HUMAN;	Q60629, EPHA5_MOUSE;
P54757, EPHA5_RAT;	Q9UF33, EPHA6_HUMAN;	Q62413, EPHA6_MOUSE;
P54758, EPHA6_RAT;	Q9UF34, EPHA6_MOUSE;	Q16295, EPHA6_HUMAN;

# Taxonomy Browser



UniProt Taxonomy Browser



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Enter search term:  Match: complete word Query:  Include all synonyms and misspellings

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Eukaryota
Viroids
Viruses

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## Homo sapiens (Human)

Lineage	Taxonomy identifier	9606	External information
<ul style="list-style-type: none"> <li>• <a href="#">Eukaryota</a></li> <li>• <a href="#">Metazoa</a></li> <li>• <a href="#">Chordata</a></li> <li>• <a href="#">Craniata</a></li> <li>• <a href="#">Vertebrata</a></li> <li>• <a href="#">Euteleostomi</a></li> <li>• <a href="#">Mammalia</a></li> <li>• <a href="#">Eutheria</a></li> <li>• <a href="#">Euarchontoglires</a></li> <li>• <a href="#">Primates</a></li> <li>• <a href="#">Haplorrhini</a></li> <li>• <a href="#">Catarrhini</a></li> <li>• <a href="#">Hominidae</a></li> <li>• <a href="#">Homo</a></li> </ul>	Organism identification code	HUMAN	  <p style="font-size: small; margin-top: 10px;"> <a href="http://www.mnh.si.edu/anthro/humanorigins/ha/sap.htm">http://www.mnh.si.edu/anthro/humanorigins/ha/sap.htm</a>  <a href="http://www.ebi.ac.uk/integr8/QuickSearch.do?action=doOrgSearch&amp;organismName=homo-">http://www.ebi.ac.uk/integr8/QuickSearch.do?action=doOrgSearch&amp;organismName=homo-</a> </p>
	Scientific name	Homo sapiens	
	Common name	Human	
	Synonym	-	
	Other NCBI synonyms	man	
	Rank	species	
	Number of UniProtKB/Swiss-Prot entries	<a href="#">17483</a>	
	Number of UniProtKB/TrEMBL entries	<a href="#">53589</a>	

**Taxonomy navigation**

Up taxonomy tree	Down taxonomy tree
<a href="#">Homo</a>	♦ <a href="#">Homo sapiens neanderthalensis</a>

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 Source of data : [Swiss-Prot](#) [NCBI taxonomy for this taxon](#)

UniProt
[Swiss-Prot@ExPASy](#)
[Swiss-Prot@EBI](#)
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# Ссылки на статьи, использованные для аннотации

UniProtKB/Swiss-Prot entry P00533 [EGFR\_HUMAN] Epidermal growth factor receptor - Mozilla Firefox

http://www.expasy.org/uniprot/P00533

Protein existence 1: Evidence at protein level;

### References

- NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).  
DOI=10.1038/309418a0; PubMed=6328312 [NCBI, ExPASy, EBI, Israel, Japan]  
Ullrich A., Coussens L., Hayflick J.S., Dull T., Gray A., Tam A.W., Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J., Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.;  
"Human epidermal growth factor receptor cDNA sequence and aberrant expression of the amplified gene in A431 epidermoid carcinoma cells.";  
Nature 309:418-425(1984).
- NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).  
TISSUE=Placenta;  
DOI=10.1002/mrd.1080410205; PubMed=7654368 [NCBI, ExPASy, EBI, Israel, Japan]  
Ilekis J.V., Stark B.C., Scoccia B.;  
"Possible role of variant RNA transcripts in the regulation of epidermal growth factor receptor expression in human placenta.";  
Mol. Reprod. Dev. 41:149-156(1995).
- NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA] (ISOFORM 2).  
TISSUE=Placenta;  
DOI=10.1093/nar/24.20.4050; PubMed=8918811 [NCBI, ExPASy, EBI, Israel, Japan]  
Reiter J.L., Maihle N.J.;  
"A 1.8 kb alternative transcript from the human epidermal growth factor receptor gene encodes a truncated form of the receptor.";  
Nucleic Acids Res. 24:4050-4056(1996).
- NUCLEOTIDE SEQUENCE (ISOFORM 2).  
TISSUE=Placenta;  
DOI=10.1006/gyno.1996.4526; PubMed=9103388 [NCBI, ExPASy, EBI, Israel, Japan]  
Ilekis J.V., Gariti J., Niederberger C., Scoccia B.;  
"Expression of a truncated epidermal growth factor receptor-like protein (TEGFR) in ovarian cancer.";  
Gynecol. Oncol. 65:36-41(1997).
- NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA] (ISOFORMS 3 AND 4).  
TISSUE=Placenta;  
DOI=10.1006/geno.2000.6341; PubMed=11161793 [NCBI, ExPASy, EBI, Israel, Japan]  
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J., Schehl Sinclair C., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.D., Magnuson T.R., James C.D., Maihle N.J.;  
"Comparative genomic sequence analysis and isolation of human and mouse alternative EGFR transcripts encoding truncated receptor isoforms.";  
Genomics 71:1-20(2001).
- NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS GLN-98; ARG-266; LYS-521; ILE-674; GLY-962 AND PRO-988.  
Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.;  
"NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";  
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
- NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 575-687.  
Reiter J.L., Threadgill D.W., Danielsen A.J., Schehl C.M., Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R., Maihle N.J.;  
"Human and mouse alternative EGFR transcripts encoding only the extracellular domain of the receptor.";  
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

Горюбо

start 5 Firefox Total Comm... Microsoft P... test\_seq - ... report.zip - ... ABBYY Lingvo Windows M... Hardcopy EN 22:44

# Комментарии

## Comments

- **FUNCTION:** Receptor for EGF, but also for other members of the EGF family, as TGF-alpha, amphiregulin, betacellulin, heparin-binding EGF-like growth factor, GP30 and vaccinia virus growth factor. Is involved in the control of cell growth and differentiation.
- **FUNCTION:** Isoform 2/truncated isoform may act as an antagonist.
- **CATALYTIC ACTIVITY:** ATP + a [protein]-L-tyrosine = ADP + a [protein]-L-tyrosine phosphate.
- **SUBUNIT:** Binds RIPK1. CBL interacts with the autophosphorylated C-terminal tail of the EGF receptor. Part of a complex with ERBB2 and either PIK3C2A or PIK3C2B. The autophosphorylated form interacts with PIK3C2B, maybe indirectly. Interacts with PELP1.
- **INTERACTION:**  
Self; NbExp=1; IntAct=EBI-297353, EBI-297353;  
Q29376:- (xeno); NbExp=1; IntAct=EBI-297353, EBI-1256881;  
Q53FG0:-; NbExp=2; IntAct=EBI-297353, EBI-913954;  
P62157:CALM (xeno); NbExp=1; IntAct=EBI-297353, EBI-397403;  
P62158:CALM1; NbExp=1; IntAct=EBI-297353, EBI-397435;  
P62161:Calm1 (xeno); NbExp=2; IntAct=EBI-297353, EBI-397530;  
P62204:Calm1 (xeno); NbExp=1; IntAct=EBI-297353, EBI-397460;  
P22681:CBL; NbExp=1; IntAct=EBI-297353, EBI-518228;  
P22682:Cbl (xeno); NbExp=1; IntAct=EBI-297353, EBI-640919;  
P13987:CD59; NbExp=1; IntAct=EBI-297353, EBI-297972;  
P01133:EGF; NbExp=2; IntAct=EBI-297353, EBI-640857;  
P04626:ERBB2; NbExp=2; IntAct=EBI-297353, EBI-641062;  
P21860:ERBB3; NbExp=2; IntAct=EBI-297353, EBI-720706;  
Q15303:ERBB4; NbExp=2; IntAct=EBI-297353, EBI-80371;  
P62993:GRB2; NbExp=2; IntAct=EBI-297353, EBI-401755;  
O00750:PIK3C2B; NbExp=4; IntAct=EBI-297353, EBI-641107;  
P98083:Shc1 (xeno); NbExp=1; IntAct=EBI-297353, EBI-300201;  
P63104:YWHAZ; NbExp=1; IntAct=EBI-297353, EBI-347088;
- **SUBCELLULAR LOCATION:** Cell membrane; Single-pass type I membrane protein. Isoform 2: Secreted.
- **ALTERNATIVE PRODUCTS:** 4 named isoforms [FASTA] produced by alternative splicing.

<b>Name</b>	<b>1</b>
Synonyms	p170
Isoform ID	P00533-1
This is the isoform sequence displayed in this entry.	

<b>Name</b>	<b>2</b>
Synonyms	p60, Truncated, TEGFR
Isoform ID	P00533-2
Features which should be applied to build the isoform sequence: <a href="#">VSP_002887</a> , <a href="#">VSP_002888</a> .	

<b>Name</b>	<b>3</b>
Synonyms	p110
Isoform ID	P00533-3



# Продолжение

- **SUBCELLULAR LOCATION:** Cell membrane; Single-pass type I membrane protein. Isoform 2: Secreted.
- **ALTERNATIVE PRODUCTS:** 4 named isoforms [FASTA] produced by alternative splicing.

<b>Name</b>	1
Synonyms	p170
Isoform ID	P00533-1
This is the isoform sequence displayed in this entry.	

<b>Name</b>	2
Synonyms	p60, Truncated, TEGFR
Isoform ID	P00533-2
Features which should be applied to build the isoform sequence: VSP_002887, VSP_002888.	

<b>Name</b>	3
Synonyms	p110
Isoform ID	P00533-3
Features which should be applied to build the isoform sequence: VSP_002889, VSP_002890.	

<b>Name</b>	4
Isoform ID	P00533-4
Features which should be applied to build the isoform sequence: VSP_002891, VSP_002892.	

- **TISSUE SPECIFICITY:** Expressed in placenta. Isoform 2 is also expressed in ovarian cancers.
- **PTM:** Phosphorylation of Ser-695 is partial and occurs only if Thr-693 is phosphorylated.
- **PTM:** Monoubiquitinated and polyubiquitinated upon EGF stimulation; which does not affect tyrosine kinase activity or signaling capacity but may play a role in lysosomal targeting. Polyubiquitin linkage is mainly through 'Lys-63', but linkage through 'Lys-48', 'Lys-11' and 'Lys-29' also occur.
- **DISEASE:** Defects in EGFR are associated with lung cancer [MIM:211980].
- **MISCELLANEOUS:** Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complex, induction of the tyrosine kinase activity, stimulation cell DNA synthesis, and cell proliferation.
- **SIMILARITY:** Belongs to the protein kinase superfamily. Tyr protein kinase family. EGF receptor subfamily.
- **SIMILARITY:** Contains 1 protein kinase domain.
- **WEB RESOURCE:** Name=GeneReviews; URL="<http://www.genetests.org/query?gene=EGFR>";.
- **WEB RESOURCE:** Name=Wikipedia; Note=EGFR entry; URL="[http://en.wikipedia.org/wiki/Epidermal\\_growth\\_factor\\_receptor](http://en.wikipedia.org/wiki/Epidermal_growth_factor_receptor)";.

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## Cross-references

### Sequence databases

X00588; CAA25240.1; -; mRNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
U95089; AAB53063.1; -; mRNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]

# Возможные разделы Комментариев

Topic	Description
ALLERGEN	Information relevant to allergenic proteins
ALTERNATIVE PRODUCTS	Description of the existence of related protein sequence(s) produced by alternative splicing of the same gene, alternative promoter usage, ribosomal frameshifting or by the use of alternative initiation codons; see 3.21.15
BIOPHYSICOCHEMICAL PROPERTIES	Description of the information relevant to biophysical and physicochemical data and information on pH dependence, temperature dependence, kinetic parameters, redox potentials, and maximal absorption; see 3.21.8
BIOTECHNOLOGY	Description of the use of a specific protein in a biotechnological process
CATALYTIC ACTIVITY	Description of the reaction(s) catalyzed by an enzyme [1]
CAUTION	Warning about possible errors and/or grounds for confusion
COFACTOR	Description of any non-protein substance required by an enzyme for its catalytic activity
DEVELOPMENTAL STAGE	Description of the developmentally-specific expression of mRNA or protein
DISEASE	Description of the disease(s) associated with a deficiency of a protein
DOMAIN	Description of the domain structure of a protein
ENZYME REGULATION	Description of an enzyme regulatory mechanism
FUNCTION	General description of the function(s) of a protein
INDUCTION	Description of the compound(s) or condition(s) that regulate gene expression
INTERACTION	Conveys information relevant to binary protein-protein interaction 3.21.12
MASS SPECTROMETRY	Reports the exact molecular weight of a protein or part of a protein as determined by mass spectrometric methods; see 3.21.23
MISCELLANEOUS	Any comment which does not belong to any of the other defined topics
PATHWAY	Description of the metabolic pathway(s) with which a protein is associated
PHARMACEUTICAL	Description of the use of a protein as a pharmaceutical drug
POLYMORPHISM	Description of polymorphism(s)
PTM	Description of any chemical alternation of a polypeptide (proteolytic cleavage, amino acid modifications including crosslinks). This topic complements information given in the feature table or indicates polypeptide modifications for which position-specific data is not available.
RNA EDITING	Description of any type of RNA editing that leads to one or more amino acid changes
SEQUENCE CAUTION	Description of protein sequence reports that differ from the sequence that is shown in UniProtKB due to conflicts that are not described in FT CONFLICT lines, such as frameshifts, erroneous gene model predictions, etc. See 3.21.34
SIMILARITY	Description of the similaritie(s) (sequence or structural) of a protein with other proteins
SUBCELLULAR LOCATION	Description of the subcellular location of the mature protein
SUBUNIT	Description of the quaternary structure of a protein and any kind of interactions with other proteins or protein complexes; except for receptor-ligand interactions, which are described in the topic FUNCTION.
TISSUE SPECIFICITY	Description of the tissue-specific expression of mRNA or protein
TOXIC DOSE	Description of the lethal dose (LD), paralytic dose (PD) or effective dose of a protein
WEB RESOURCE	Description of a cross-reference to a network database/resource for a specific protein; see 3.21.36

# Cross-References

Cross-references		
Sequence databases		
EMBL	X00588; CAA25240.1; -; mRNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	U95089; AAB53063.1; -; mRNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	U48722; AAC50802.1; -; mRNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	U48723; AAC50804.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	U48724; AAC50796.1; -; Genomic_RNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	U48725; AAC50797.1; -; Genomic_RNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	U48726; AAC50798.1; -; Genomic_RNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	U48727; AAC50799.1; -; Genomic_RNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	U48728; AAC50800.1; -; Genomic_RNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	U48729; AAC50801.1; -; Genomic_RNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF288738; AAG35786.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF288738; AAG35787.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF288738; AAG35788.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF288738; AAG35789.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF288738; AAG35790.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AY588246; AAS83109.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF277897; AAK01080.1; -; mRNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF125253; AAG43240.1; -; mRNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF125539; AAG43243.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AF125538; AAG43243.1; JOINED; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
X06370; CAA29668.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]	
X00663; CAA25282.1; -; mRNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]	
M38425; AAA63171.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]	
M11234; AAA52370.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]	
PIR	A00641; GQHUE.	
RefSeq	NP_005219.2; -.	
	NP_958439.1; -.	
	NP_958440.1; -.	
	NP_958441.1; -.	
UniGene	Hs.488293	
3D structure databases		
	1DNQ; Model; A=25-336.	[ExPASy / RCSB / EBI]
	1DNR; Model; A=337-645.	[ExPASy / RCSB / EBI]
	1IVO; X-ray; A/B=25-646.	[ExPASy / RCSB / EBI]
	1M14; X-ray; A=695-1022.	[ExPASy / RCSB / EBI]
	1M17; X-ray; A=695-1022.	[ExPASy / RCSB / EBI]
	1MOX; X-ray; A/B=25-525.	[ExPASy / RCSB / EBI]



# Cross-References

UniGene	Hs.488293
<b>3D structure databases</b>	
PDB	1DNQ; Model; A=25-336. [ExpASy / RCSB / EBI] 1DNR; Model; A=337-645. [ExpASy / RCSB / EBI] 1IVO; X-ray; A/B=25-646. [ExpASy / RCSB / EBI] 1M14; X-ray; A=695-1022. [ExpASy / RCSB / EBI] 1M17; X-ray; A=695-1022. [ExpASy / RCSB / EBI] 1MOX; X-ray; A/B=25-525. [ExpASy / RCSB / EBI] 1NQL; X-ray; A=25-642. [ExpASy / RCSB / EBI] 1XKK; X-ray; A=695-1022. [ExpASy / RCSB / EBI] 1Z9I; NMR; A=669-721. [ExpASy / RCSB / EBI] 2EXP; Model; A=311-326. [ExpASy / RCSB / EBI] 2GS2; X-ray; A=696-1022. [ExpASy / RCSB / EBI] 2GS7; X-ray; A/B=696-1022. [ExpASy / RCSB / EBI] Detailed list of linked structures.
DisProt	DP00309; -.
ModBase	P00533.
<b>Protein-protein interaction databases</b>	
DIP	DIP:405N; -.
IntAct	P00533; -.
<b>PTM databases</b>	
GlycoSuiteDB	P00533; -.
<b>Enzyme and pathway databases</b>	
Reactome	REACT_9417; Signaling by EGFR.
<b>Polymorphism databases</b>	
NIEHS-SNPs	EGFR.
<b>2D gel databases</b>	
SWISS-2DPAGE	P00533; HUMAN.
<b>Organism-specific databases</b>	
HGNC	HGNC:3236; EGFR.
GeneCards	EGFR.
GeneLynx	EGFR; Homo sapiens.
GenAtlas	EGFR.
HPA	CAB000035; -. HPA001200; -.
MIM	131550; gene. [NCBI / EBI] 211980; phenotype. [NCBI / EBI]
Orphanet	360; Glioblastoma.
PharmGKB	PA7360; -.


регистрация



# 3D-Structure (список структур)

## PDB structures for UniProtKB entry **P00533** (EGFR\_HUMAN)

Epidermal growth factor receptor precursor (EC 2.7.10.1) (Receptor tyrosine-protein kinase ErbB-1).

PDB	Swiss-Prot entries	Compound name (Submission date)
 1DNQ	EGFR_HUMAN (P00533)	MOL_ID: 1; MOLECULE: EPIDERMAL GROWTH FACTOR RECEPTOR; CHAIN: A; FRAGMENT: L1 AND S1 DOMAINS; EC: 2.7.1.112; ENGINEERED: YES [2.60 Å] (16-DEC-99)
 1DNR	EGFR_HUMAN (P00533)	MOL_ID: 1; MOLECULE: EPIDERMAL GROWTH FACTOR RECEPTOR; CHAIN: A; FRAGMENT: L2 AND S2 DOMAINS; EC: 2.7.1.112; ENGINEERED: YES [2.60 Å] (16-DEC-99)
 1IVO	EGFR_HUMAN (P00533) EGF_HUMAN (P01133)	MOL_ID: 1; MOLECULE: EPIDERMAL GROWTH FACTOR RECEPTOR; CHAIN: A, B; FRAGMENT: EXTRACELLULAR DOMAINS I, II AND IV; EC: 2.7.1.112; ENGINEERED: YES; MOL_ID: 2; MOLECULE: EPIDERMAL GROWTH FACTOR; CHAIN: C, D; FRAGMENT RESIDUES 1-53; SYNONYM: EGF; ENGINEERED: YES [3.30 Å] (28-MAR-02)
 1M14	EGFR_HUMAN (P00533)	MOL_ID: 1; MOLECULE: EPIDERMAL GROWTH FACTOR RECEPTOR; CHAIN: A; FRAGMENT: TYROSINE KINASE DOMAIN (RESIDUES 671-998); SYNONYM: RECEPTOR PROTEIN-TYROSINE KINASE ERBB-1; EC: 2.7.1.112; ENGINEERED: YES; MUTATION: YES [2.60 Å] (17-JUN-02)
 1M17	EGFR_HUMAN (P00533)	MOL_ID: 1; MOLECULE: EPIDERMAL GROWTH FACTOR RECEPTOR; CHAIN: A; FRAGMENT: TYROSINE KINASE DOMAIN (RESIDUES 671-998); SYNONYM: RECEPTOR PROTEIN-TYROSINE KINASE ERBB-1; EC: 2.7.1.112; ENGINEERED: YES [2.60 Å] (17-JUN-02)
 1MOX	EGFR_HUMAN (P00533) TGFA_HUMAN (P01135)	MOL_ID: 1; MOLECULE: EPIDERMAL GROWTH FACTOR RECEPTOR; CHAIN: A, B; FRAGMENT: EXTRACELLULAR FRAGMENT EC: 2.7.1.112; ENGINEERED: YES; MOL_ID: 2; MOLECULE: TRANSFORMING GROWTH FACTOR ALPHA; CHAIN: C, D; ENGINEERED: YES [2.50 Å] (10-SEP-02)
 1NQL	EGFR_HUMAN (P00533) EGF_HUMAN (P01133)	MOL_ID: 1; MOLECULE: EPIDERMAL GROWTH FACTOR RECEPTOR; CHAIN: A; FRAGMENT: EXTRACELLULAR DOMAIN; ENGINEERED: YES; MOL_ID: 2; MOLECULE: EPIDERMAL GROWTH FACTOR; CHAIN: B; SYNONYM: EGF, [CONTAINS: EPIDERMAL GROWTH FACTOR UROGASTRONE, ]; ENGINEERED: YES [2.80 Å] (21-JAN-03)
 1XKK	EGFR_HUMAN (P00533)	MOL_ID: 1; MOLECULE: EPIDERMAL GROWTH FACTOR RECEPTOR; CHAIN: A; FRAGMENT: EGFR KINASE DOMAIN; SYNONYM: RECEPTOR PROTEIN-TYROSINE KINASE ERBB-1; EC: 2.7.1.112; ENGINEERED: YES [2.40 Å] (29-SEP-04)
 129I	EGFR_HUMAN (P00533)	MOL_ID: 1; MOLECULE: EPIDERMAL GROWTH FACTOR RECEPTOR; CHAIN: A; FRAGMENT: SEQUENCE DATABASE RESIDUES 669-721; SYNONYM: RECEPTOR TYROSINE-PROTEIN KINASE ERBB-1; EC: 2.7.1.112; ENGINEERED: YES [NMR, 25 STRUCTURES] (02-APR-05)
 2EXP	EGFR_HUMAN (P00533) HVM6I_MOUSE (P18532)	MOL_ID: 1; MOLECULE: LIGHT CHAIN FROM FV FRAGMENT OF MONOCLONAL ANTIBODY 806; CHAIN: L; MOL_ID: 2; MOLECULE: HEAVY CHAIN FROM FV FRAGMENT OF MONOCLONAL ANTIBODY 806; CHAIN: H; MOL_ID: 3; MOLECULE: EPIDERMAL GROWTH FACTOR RECEPTOR; CHAIN: A; SYNONYM: RECEPTOR TYROSINE-PROTEIN KINASE ERBB-1; EC: 2.7.1.112 (08-NOV-05)
 2GS2	EGFR_HUMAN (P00533)	MOL_ID: 1; MOLECULE: EPIDERMAL GROWTH FACTOR RECEPTOR; CHAIN: A; FRAGMENT: KINASE DOMAIN; SYNONYM: RECEPTOR TYROSINE-PROTEIN KINASE ERBB-1; EC: 2.7.1.112; ENGINEERED: YES [2.80 Å] (25-APR-08)



# Reactome

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Find everything with ALL of the words in Homo sapiens

## EGFR autophosphorylation [Homo sapiens]

**Reactionmap**

**Diagram**

**Details**

open to selected event open all close all

- Signaling by EGFR
  - Pro-EGF is cleaved to form mature EGF
  - EGFR binds EGF ligand
  - EGFR dimerization
  - EGFR autophosphorylation [Homo sapiens]**
  - Phosphorylation of EGFR by SRC kinase

EGFR autophosphorylation	
Stable identifier	REACT_9388.1
Authored	Castagnoli, L, 2006-10-10
Reviewed	Muthuswamy, S, 2007-02-16

The cytoplasmic domain of EGFR contains tyrosine, serine and threonine phosphorylation sites. Dimerization of EGFR activates its intrinsic protein kinase activity resulting in autophosphorylation of 5 of these sites (Y992, Y1068, Y1086, Y1148 and Y1173). Tyrosine autophosphorylation is crucial for normal receptor signalling and provides specific binding sites for cytosolic target proteins involved in signal transmission.

extracellular  
membrane  
cytosol

Input (present at start of reaction)	EGF:EGFR dimer [plasma membrane] ATP [cytosol] <b>CCP</b> x 10
--------------------------------------	---

# Полиморфизмы

[Return to NIEHS SNPs Home](#)  
[Return to A-Z Finished Genes Directory](#)



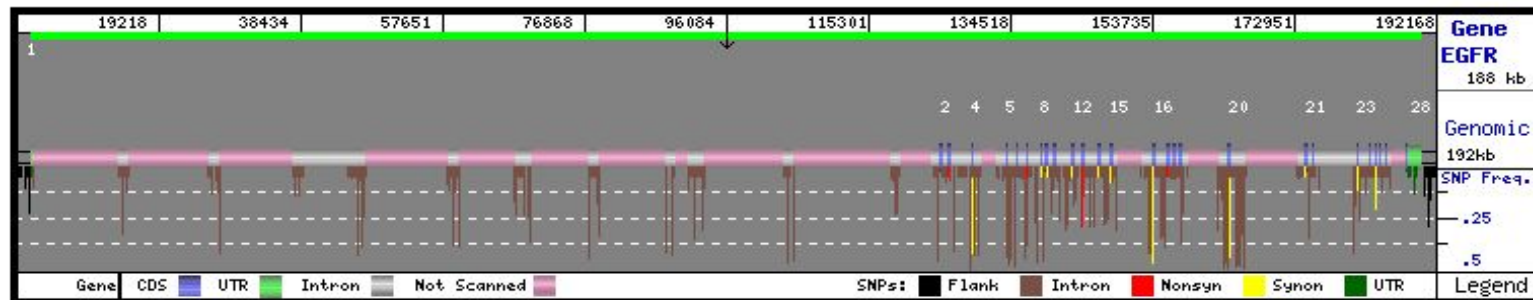
National Institute of Environmental Health Sciences  
Environmental Genome Project  
**NIEHS SNPs**

## **EGFR:epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)**

Chromosomal Location: 7p12

Go to [EGFR Genotyping Data](#)

GeneSNPs Image



### IMAGE CONTROLS

View

Full Gene

Scroll by:

1000 bp

Scroll  
Direction



Repeats

Hide Repeats

### SNP CONTROLS

SNP  
Views

All SNPs

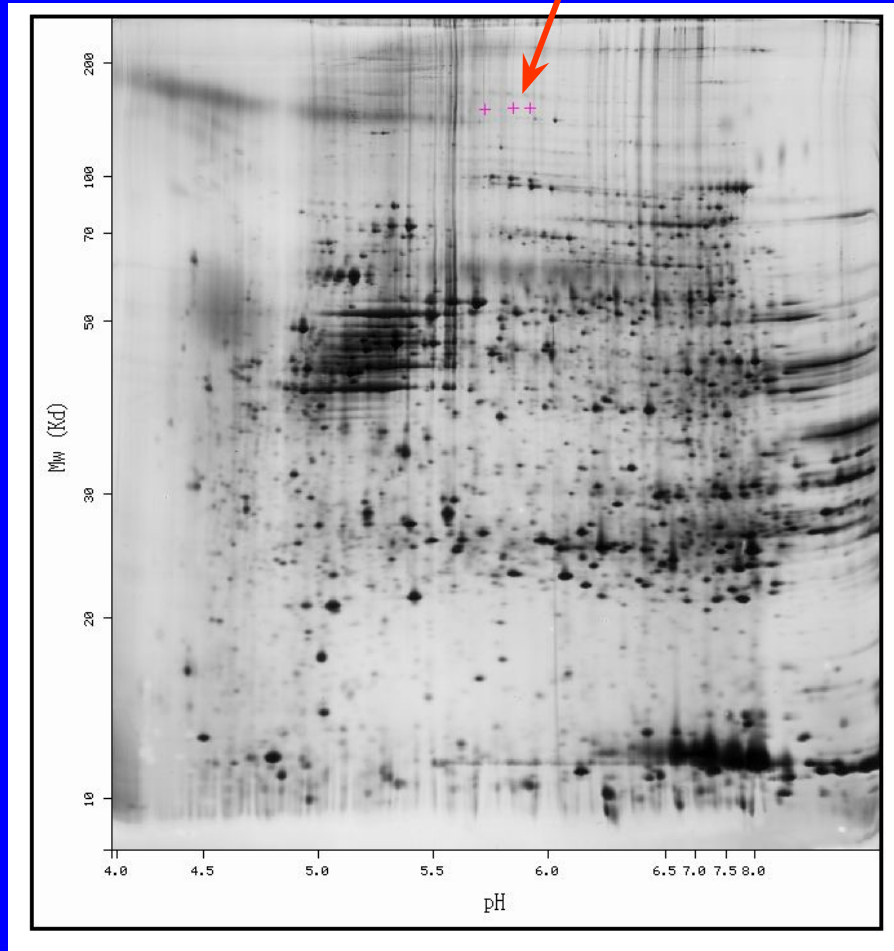
Frequency

High Freq

Reset

# 2D GEL

+ кырсор

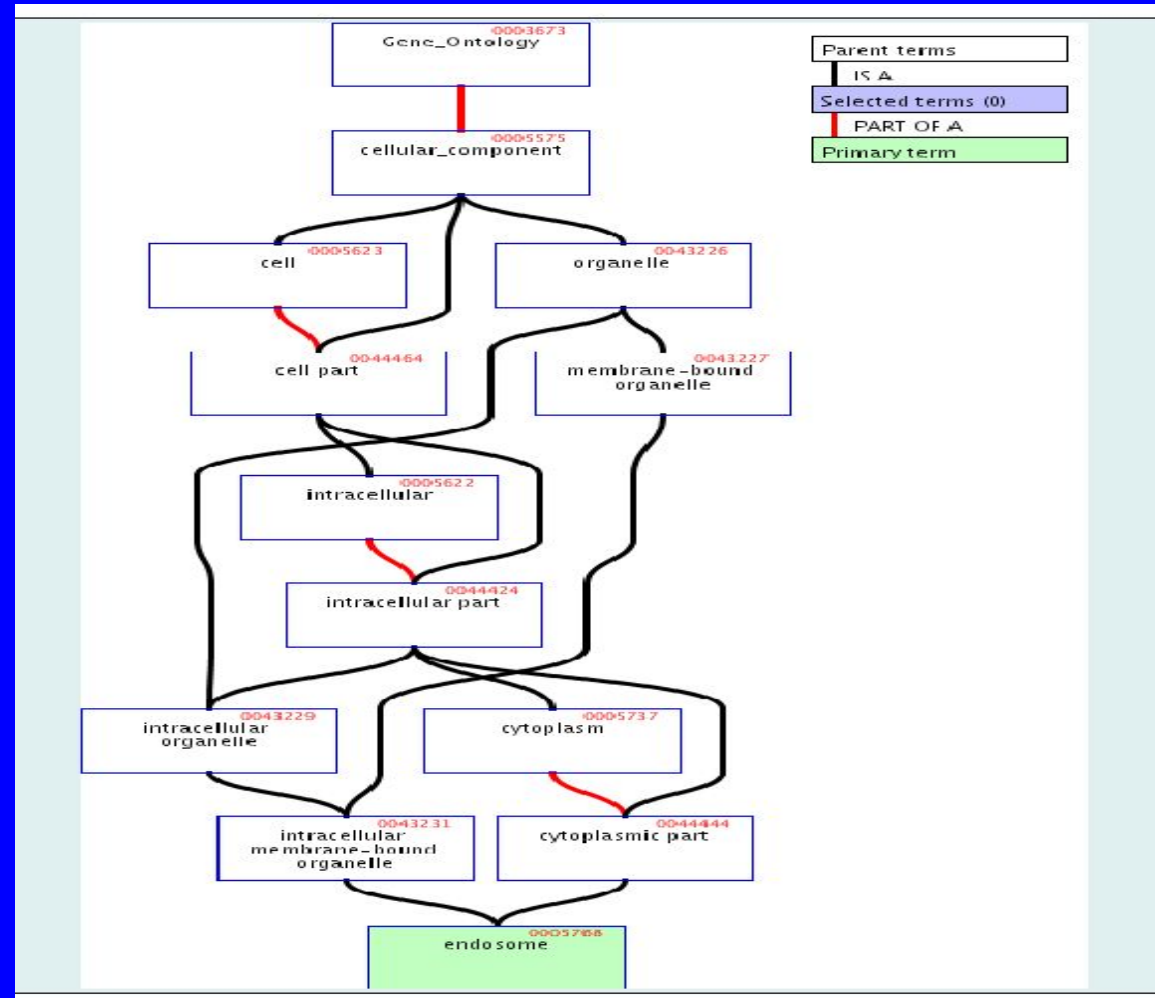


# Cross-References

HOVERGEN [Family Alignment Tree]	
<b>Gene expression databases</b>	
CleanEx	HGNC:3236; EGFR.
ArrayExpress	P00533; -.
GermOnline	ENSG00000146648; Homo sapiens.
<b>Ontologies</b>	
GO	<p>GO:0005768; Cellular component: endosome (<i>inferred from direct assay from UniProtKB</i>).</p> <p>GO:0005615; Cellular component: extracellular space (<i>non-traceable author statement from UniProtKB</i>).</p> <p>GO:0005634; Cellular component: nucleus (<i>inferred from direct assay from UniProtKB</i>).</p> <p>GO:0005886; Cellular component: plasma membrane (<i>inferred from direct assay from HGNC</i>).</p> <p>GO:0051015; Molecular function: actin filament binding (<i>inferred from direct assay from UniProtKB</i>).</p> <p>GO:0003690; Molecular function: double-stranded DNA binding (<i>non-traceable author statement from UniProtKB</i>).</p> <p>GO:0005006; Molecular function: epidermal growth factor receptor activity (<i>inferred from direct assay from UniProtKB</i>).</p> <p>GO:0042802; Molecular function: identical protein binding (<i>inferred from physical interaction from IntAct</i>).</p> <p>GO:0004710; Molecular function: MAP/ERK kinase kinase activity (<i>non-traceable author statement from UniProtKB</i>).</p> <p>GO:0046982; Molecular function: protein heterodimerization activity (<i>inferred from direct assay from UniProtKB</i>).</p> <p>GO:0043006; Biological process: calcium-dependent phospholipase A2 activation (<i>traceable author statement from UniProtKB</i>).</p> <p>GO:0016337; Biological process: cell-cell adhesion (<i>inferred from mutant phenotype from UniProtKB</i>).</p> <p>GO:0007173; Biological process: epidermal growth factor receptor signaling pathway (<i>inferred from direct assay from UniProtKB</i>).</p> <p>GO:0001503; Biological process: ossification (<i>non-traceable author statement from UniProtKB</i>).</p> <p>GO:0007202; Biological process: phospholipase C activation (<i>traceable author statement from UniProtKB</i>).</p> <p>GO:0030335; Biological process: positive regulation of cell migration (<i>inferred from mutant phenotype from UniProtKB</i>).</p> <p>GO:0050679; Biological process: positive regulation of epithelial cell proliferation (<i>inferred from direct assay from UniProtKB</i>).</p> <p>GO:0043406; Biological process: positive regulation of MAP kinase activity (<i>inferred from direct assay from UniProtKB</i>).</p> <p>GO:0045429; Biological process: positive regulation of nitric oxide biosynthetic process (<i>inferred from direct assay from UniProtKB</i>).</p> <p>GO:0042327; Biological process: positive regulation of phosphorylation (<i>inferred from direct assay from UniProtKB</i>).</p> <p>GO:0051205; Biological process: protein insertion into membrane (<i>traceable author statement from UniProtKB</i>).</p> <p>GO:0050999; Biological process: regulation of nitric-oxide synthase activity (<i>inferred from direct assay from UniProtKB</i>).</p> <p>GO:0050730; Biological process: regulation of peptidyl-tyrosine phosphorylation (<i>inferred from mutant phenotype from UniProtKB</i>).</p> <p>GO:0006950; Biological process: response to stress (<i>non-traceable author statement from UniProtKB</i>).</p> <p>QuickGo view.</p>
<b>Family and domain databases</b>	
InterPro	<p>IPR000494; EGF_rcpt_L.</p> <p>IPR006211; Furin-like.</p> <p>IPR006212; Furin_repeat.</p> <p>IPR000719; Prot_kinase_core.</p> <p>IPR001245; Tyr_pkinase.</p> <p>IPR008266; Tyr_pkinase_AS.</p> <p>Graphical view of domain structure.</p>

# GO terms

Определение термина, синонимы, родительские (Hierarchy) и дочерние термины, ключевые слова, дата последней модификации





# Cross-References, Keywords

InterPro	IPR000719; Prot_kinase_core. IPR001245; Tyr_pkinase. IPR008266; Tyr_pkinase_AS. Graphical view of domain structure.
Pfam	PF00757; Furin-like; 1. PF07714; Pkinase_Tyr; 1. PF01030; Recep_L_domain; 2. Pfam graphical view of domain structure.
PRINTS	PR00109; TYRKINASE.
ProDom	PD000001; Prot_kinase; 1. [Domain structure / List of seq. sharing at least 1 domain]
SMART	SM00261; FU; 3. SM00219; TyrKc; 1. SMART graphical view of domain structure.
PROSITE	PS00107; PROTEIN_KINASE_ATP; 1. PS50011; PROTEIN_KINASE_DOM; 1. PS00109; PROTEIN_KINASE_TYR; 1. PROSITE graphical view of domain structure (profiles).
BLOCKS	P00533.
<b>Proteomic databases</b>	
PeptideAtlas	P00533; -.
<b>Genome annotation databases</b>	
Ensembl	ENSG00000146648; Homo sapiens. [Contig view]
GenelD	1956; -.
KEGG	hsa:1956; -.
<b>Other</b>	
DrugBank	BTD00071; Cetuximab. APRD00951; Erlotinib. APRD00997; Gefitinib.
LinkHub	P00533; -.
SOURCE	EGFR; Homo sapiens.
ProtoNet	P00533.
UniRef	View cluster of proteins with at least 50% / 90% / 100% identity.
<b>Keywords</b>	
3D-structure; Alternative splicing; Anti-oncogene; ATP-binding; Cell cycle; Direct protein sequencing; Disease mutation; Glycoprotein; Kinase; Membrane; Nucleotide-binding; Phosphorylation; Polymorphism; Receptor; Repeat; Secreted; Signal; Transferase; Transmembrane; Tyrosine-protein kinase; Ubl conjugation	
<b>Features</b>	

# KEGG

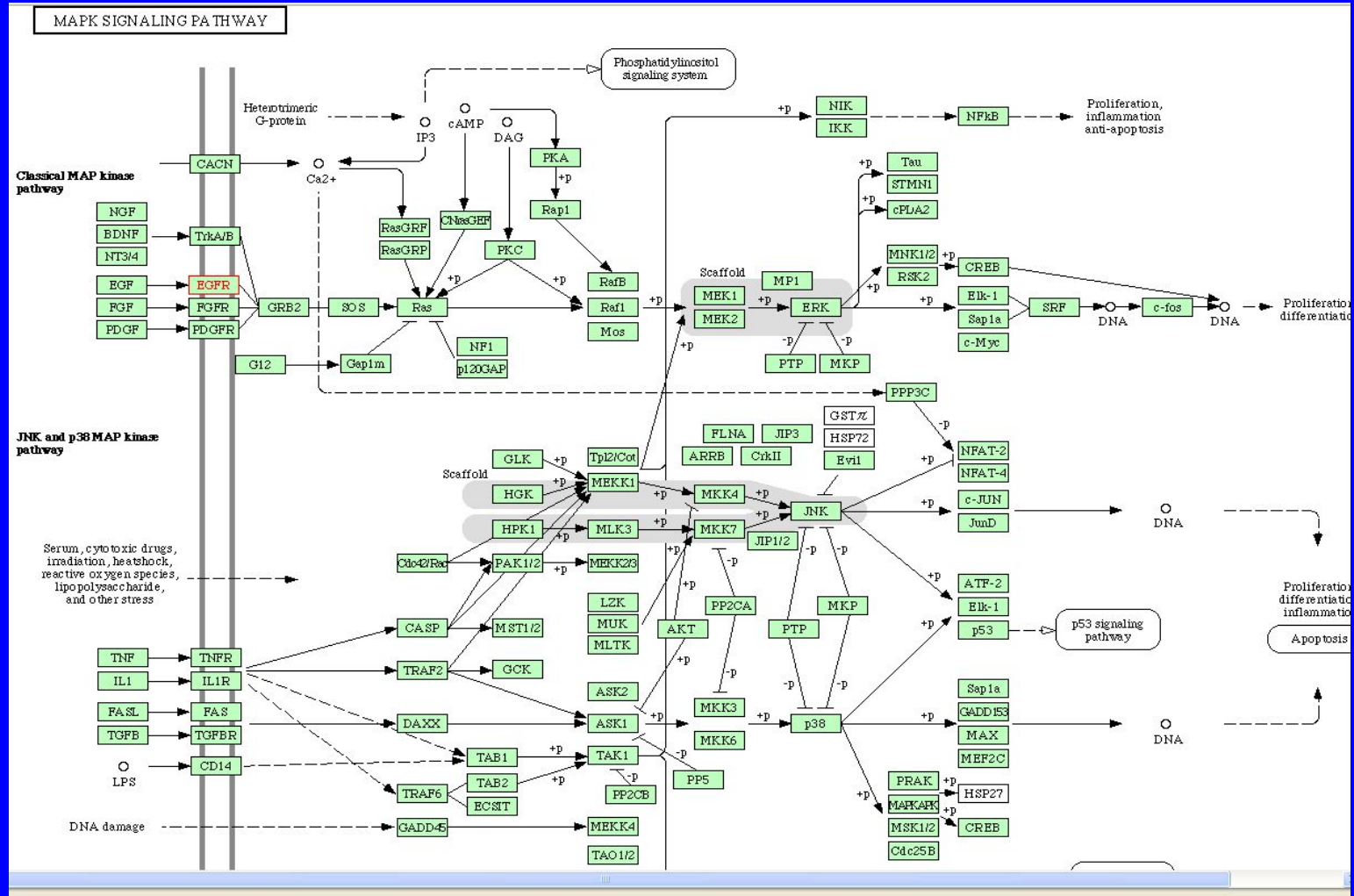


Homo sapiens (human): 1956

[Help](#)

<b>Entry</b>	1956	CDS	H.sapiens
<b>Gene name</b>	EGFR, ERBB		
<b>Definition</b>	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) [EC:2.7.10.1]		
<b>Orthology</b>	KO: K04361 epidermal growth factor receptor		
<b>Pathway</b>	PATH: hsa04010 MAPK signaling pathway PATH: hsa04012 ErbB signaling pathway PATH: hsa04020 Calcium signaling pathway PATH: hsa04060 Cytokine-cytokine receptor interaction PATH: hsa04320 Dorsal-ventral axis formation PATH: hsa04510 Focal adhesion PATH: hsa04520 Adherens junction PATH: hsa04540 Gap junction PATH: hsa04810 Regulation of actin cytoskeleton PATH: hsa04912 GnRH signaling pathway PATH: hsa05120 Epithelial cell signaling in Helicobacter pylori infection PATH: hsa05210 Colorectal cancer PATH: hsa05212 Pancreatic cancer PATH: hsa05213 Endometrial cancer PATH: hsa05214 Glioma PATH: hsa05215 Prostate cancer PATH: hsa05218 Melanoma PATH: hsa05219 Bladder cancer PATH: hsa05223 Non-small cell lung cancer		
<b>Class</b>	<a href="#">BRITE hierarchy</a>		
<b>SSDB</b>	<a href="#">Ortholog</a> <a href="#">Paralog</a> <a href="#">Gene cluster</a>		
<b>Motif</b>	Pfam: Recep_L_domain Furin-like Keratin_B2 Pkinase_Tyr Pkinase PROSITE: PROTEIN_KINASE_ATP PROTEIN_KINASE_TYR CYS_RICH PROTEIN_KINASE_DOM <a href="#">Motif</a>		
<b>Other DBs</b>	OMIM: 131550 NCBI-GI: 29725609 NCBI-GeneID: 1956 HGNC: 3236 HPRD: 00579 Ensembl: ENSG00000146648 UniProt: P00533		
<b>LinkDB</b>	<a href="#">All DBs</a>		

# KEGG (pathway viewer)



# DrugBank

DrugBank: Cetuximab - Mozilla Firefox

Файл Правка Вид Журнал Закладки Инструменты Справка

http://redpoll.pharmacy.ualberta.ca/drugbank/cgi-bin/getCard.cgi?CARD=BTD00071.txt

Customize Links Free Hotmail Windows Marketplace Windows Media Windows

Swiss-Prot - Поиск... UniProtKB/Swiss-Pr... MAPK signaling pat... Entrez Gene: EGF... DrugBank: Cetux... ProtoNet: The Req... UniRef90 Entry - U... UniProt Knowledge...

## DrugBank

Home Browse PharmaBrowse ChemQuery Text Query SeqSearch Data Extractor Download

Search DrugBank for:  Search

DrugBank  
Cetuximab  
(BTD00071)

Show Similar Structure(s) for Approved Drugs

Creation Date	2005/6/28 0:11:12 GMT
Last Update	Feb 01, 2007
Accession Number	BTD00071
Generic Name	Cetuximab
Synonyms	1. Anti EGFR 2. Ig gamma-1 chain C region
Brand Names	Erbix (ImClone Systems Inc)
Description	Epidermal growth factor receptor binding FAB. Cetuximab is composed of the Fv (variable; antigen-binding) regions of the 225 murine EGFR monoclonal antibody specific for the N-terminal portion of human EGFR with human IgG1 heavy and kappa light chain constant (framework) regions.
Chemical IUPAC Name	Humanized anti-EGF receptor (EGFR) antibody
Chemical Formula	C <sub>6484</sub> H <sub>110042</sub> N <sub>1732</sub> O <sub>2023</sub> S <sub>36</sub>
	> Cetuximab  > Anti-EGFR heavy chain 1 QVQLKQSGPGLVQPSSQLSIITCTVSGFSLTNYGVHVRQSPGKGLEVLGVIWSGGNTDYN TPFTSRISLNKDNSKSNQVFFKHNLSQNDTAIYYCARALTYDYEFAYVGGTLVTVSA STKGFSPFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSQVHTFPAVLQSSG LYSLSSVFTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSPKSCDKHTCCPPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTPREEQ YNSTRYRVSVLTVHLQDMLNGKEYVCKVSNKALPAPIEKTISKAKGPREPQVYTLPPSR

Горюбо

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# Keywords

## UniProt Knowledgebase keyword: Alternative splicing

### Description

Protein for which at least two isoforms exist due to distinct pre-mRNA splicing events.

### Hierarchy

Coding sequence diversity ▾ Alternative splicing

### Entries in UniProtKB/Swiss-Prot (13153):

Send selected sequences to

Entry name	AC	Gene names	Description	Organisms	Length
<input type="checkbox"/> 12S1_ARATH	P15455	<b>CRA1</b> , <i>At5g44120</i> , <i>MLN1.4</i>	<b>12S seed storage protein CRA1 precursor</b> [Contains: 12S seed storage protein CRA1 alpha chain (12S seed storage protein CRA1 acidic chain); 12S seed storage protein CRA1 beta chain (12S seed storage protein CRA1 basic chain)]	Arabidopsis thaliana (Mouse-ear cress)	472
<input type="checkbox"/> 14310_ARATH	P48347	<b>GRF10</b> , <i>At1g22300</i> , <i>T16E15.8</i>	<b>14-3-3-like protein GF14 epsilon</b> (General regulatory factor 10)	Arabidopsis thaliana (Mouse-ear cress)	254
<input type="checkbox"/> 14333_ARATH	P42644	<b>GRF3</b> , <i>RCI1</i> , <i>At5g38480</i> , <i>MX110.21</i>	<b>14-3-3-like protein GF14 psi</b> (General regulatory factor 3) (14-3-3-like protein RCI1)	Arabidopsis thaliana (Mouse-ear cress)	255
<input type="checkbox"/> 14336_ARATH	P48349	<b>GRF6</b> , <i>AFT1</i> , <i>RCI2</i> , <i>At5g10450</i> , <i>F12B17_200</i>	<b>14-3-3-like protein GF14 lambda</b> (General regulatory factor 6) (14-3-3-like protein RCI2) (14-3-3-like protein AFT1)	Arabidopsis thaliana (Mouse-ear cress)	248
<input type="checkbox"/> 14338_ARATH	P48348	<b>GRF8</b> , <i>At5g65430</i> , <i>MNA5.16</i>	<b>14-3-3-like protein GF14 kappa</b> (General regulatory factor 8)	Arabidopsis thaliana (Mouse-ear cress)	248
<input type="checkbox"/> 14339_ARATH	Q96299	<b>GRF9</b> , <i>At2g42590</i> , <i>F14N22.14</i>	<b>14-3-3-like protein GF14 mu</b> (General regulatory factor 9)	Arabidopsis thaliana (Mouse-ear cress)	263
<input type="checkbox"/> 1433E_DROME	P92177	<b>14-3-3epsilon</b> , <i>14-3-3e</i> , <i>SR3-9</i> , <i>CG31196</i>	<b>14-3-3 protein epsilon</b> (Suppressor of Ras1 3-9)	Drosophila melanogaster (Fruit fly)	262
<input type="checkbox"/> 1433S_HUMAN	P31947	<b>SFN</b> , <i>HME1</i>	<b>14-3-3 protein sigma</b> (Stratifin) (Epithelial cell marker protein 1)	Homo sapiens (Human)	248
<input type="checkbox"/> 1433T_MOUSE	P68254	<b>Ywhaq</b>	<b>14-3-3 protein theta</b> (14-3-3 protein tau)	Mus musculus (Mouse)	245

# Словарь ключевых слов

http://www.expasy.org - List of UniProtKB/Swiss-Prot keywords - Mozilla Firefox

The definition of the keywords and categories usage as well as other information is provided in the following format:

Line code	Content	Occurrence in an entry
ID	Identifier (keyword)	Once; starts a keyword entry
IC	Identifier (category)	Once; starts a category entry
AC	Accession (KW-xxxx)	Once
DE	Definition	Once or more
SY	Synonyms	Optional; once or more
GO	Gene ontology (GO) mapping	Optional; once or more
HI	Hierarchy	Optional; once or more
WW	Relevant WWW site	Optional; once or more
CA	Category	Once per keyword entry; absent in category entries
//	Terminator	Once; ends an entry

---

ID 2Fe-2S.  
AC KW-0001  
DE Protein which contains at least one 2Fe-2S iron-sulfur cluster: 2 iron atoms complexed to 2 inorganic sulfides and 4 sulfur atoms of cysteines from the protein.  
GO GO:0051537; 2 iron, 2 sulfur cluster binding  
HI Ligand: Iron; Iron-sulfur; 2Fe-2S.  
HI Ligand: Metal-binding; 2Fe-2S.  
CA Ligand.  
//  
ID 3D-structure.  
AC KW-0002  
DE Protein, or part of a protein, whose three-dimensional structure has been resolved experimentally (for example by X-ray crystallography or NMR spectroscopy) and whose coordinates are available in the PDB database. Can also be used for theoretical models.  
HI Technical term: 3D-structure.  
CA Technical term.  
//  
ID 3Fe-4S.  
AC KW-0003  
DE Protein which contains at least one 3Fe-4S iron-sulfur cluster: 3 iron atoms complexed to 4 inorganic sulfides and 3 sulfur atoms of cysteines from the protein. In a number of iron-sulfur proteins, the 4Fe-4S cluster can be reversibly converted by oxidation and loss of one iron ion to a 3Fe-4S cluster.  
GO GO:0051538; 3 iron, 4 sulfur cluster binding  
HI Ligand: Iron; Iron-sulfur; 3Fe-4S.  
HI Ligand: Metal-binding; 3Fe-4S.  
CA Ligand.  
//  
ID 4Fe-4S.  
AC KW-0004  
DE Protein which contains at least one 4Fe-4S iron-sulfur cluster: 4 iron atoms complexed to 4 inorganic sulfides and 4 sulfur atoms of cysteines from the protein. In a number of iron-sulfur proteins, the 4Fe-4S cluster can be reversibly converted by oxidation and loss of one iron ion to a 3Fe-4S cluster.  
GO GO:0051539; 4 iron, 4 sulfur cluster binding

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# Feature Table

Features					
Feature table viewer			Feature aligner		
Key	From	To	Length	Description	FTId
SIGNAL	1	24	24		
CHAIN	25	1210	1186	Epidermal growth factor receptor.	PRO_000001
TOPO_DOM	25	645	621	Extracellular <i>(Potential)</i> .	
TRANSMEM	646	668	23	<i>Potential</i> .	
TOPO_DOM	669	1210	542	Cytoplasmic <i>(Potential)</i> .	
REPEAT	75	300	226	Approximate.	
REPEAT	390	600	211	Approximate.	
DOMAIN	712	979	268	Protein kinase.	
NP_BIND	718	726	9	ATP <i>(By similarity)</i> .	
COMPBIAS	1025	1071	47	Ser-rich.	
ACT_SITE	837	837		Proton acceptor <i>(By similarity)</i> .	
BINDING	745	745		ATP <i>(By similarity)</i> .	
SITE	1016	1016	1	Important for interaction with PIK3C2B.	
MOD_RES	678	678		Phosphothreonine; by PKC.	
MOD_RES	693	693		Phosphothreonine.	
MOD_RES	695	695		Phosphoserine.	
MOD_RES	978	978		Phosphotyrosine.	
MOD_RES	991	991		Phosphoserine.	
MOD_RES	995	995		Phosphoserine.	
MOD_RES	998	998		Phosphotyrosine.	
MOD_RES	1026	1026		Phosphoserine.	
MOD_RES	1064	1064		Phosphoserine.	
MOD_RES	1069	1069		Phosphotyrosine.	
MOD_RES	1070	1070		Phosphoserine.	
MOD_RES	1071	1071		Phosphoserine.	
MOD_RES	1092	1092		Phosphotyrosine; by autocatalysis.	
MOD_RES	1110	1110		Phosphotyrosine; by autocatalysis.	
MOD_RES	1138	1138		Phosphotyrosine.	
MOD_RES	1166	1166		Phosphoserine.	
MOD_RES	1172	1172		Phosphotyrosine; by autocatalysis.	
MOD_RES	1197	1197		Phosphotyrosine; by autocatalysis.	
CARBOHYD	56	56		N-linked (GlcNAc...) (complex); atypical; partial [GlycoSuiteDB].	CAR_000227
CARBOHYD	128	128		N-linked (GlcNAc...).	
CARBOHYD	175	175		N-linked (GlcNAc...).	
CARBOHYD	196	196		N-linked (GlcNAc...).	
CARBOHYD	352	352		N-linked (GlcNAc...).	

# Координаты в Feature table

## UniProtKB/Swiss-Prot: P00533 (EGFR\_HUMAN)

The section of the sequence P00533 (EGFR\_HUMAN) you have selected corresponds to:

SIGNAL 1 24

In one-letter code:

```
      1      11      21      31      41      51
1  MRPSGTAGAA LLALLAALCP ASRALEEKKV CQGTSNKLTO LGTFEDHFLS LQRMFNANCEV 60
61  VLGNIIEITYV QRNYDLSFLK TIQEVAGYVL IALNTVERIP LENLQIIRGN MYYENSYALA 120
121 VLSNYDANKT GLKELPMRNL QEILHGAVRF SNNPALCNVE SIQWRDIVSS DFLSNMSMDF 180
181 QNHLGSCQKC DPSCPNGSCW GAGEENCQKL TKIICAQQCS GRCRGKSPSD CCHNQCAAGC 240
241 TGPRESDECLV CRKFRDEATC KDTCPPLMLY NPTTYQMDVN PEGKYSFGAT CVKKCPRNYV 300
301 VTDHGSCVRA CGADSYEMEE DGVRKCKKCE GPCRKVCNGI GIGEFKDSLS INATNIKHKFK 360
361 NCTSISGDLH LLPVAFRGDS FTHTPPLDPQ ELDILKTVE ITGFLLIQAW PENRTDLHAF 420
421 ENLEIIRGRT KQHGGQFSLAV VSLNITSLGL RSLKEISDGD VIISGNKNLC YANTINWKKL 480
481 FGTSGQKTKI ISNRGENSCK ATGOVCHALC SPEGCWGPEP RDCVSCRNVS RGRECVDKCN 540
541 LLEGEPREFV ENSECIQCHP ECLPQAMNIT CTGRGPDNCI QCAHYIDGPH CVKTCPAGVM 600
601 GENNTLVWKY ADAGHVCHLC HPNCTYGCCTG PGLEGCPNTG PKIPSIATGM VGALLLLLVV 660
661 ALGIGLFMRR RHIVRKRTL RLLQERELVE PLTPSGEAPN QALLRILKET EFKKIKVLGS 720
721 GAFGTVYKGL WIPEGEKVKI PVAIKELREA TSPKANKEIL DEAYVMASVD NPHVCRLGI 780
781 CLTSTVQLIT QLMPPFGLLD YVREHKDNIG SQYLLNWCVQ IAKGMNYLED RRLVHRDLAA 840
841 RNVLVKTPQH VKITDFGLAK LLGAEKEYH AEGGKVPKW MALESILHRI YTHQSDVWSY 900
901 GVTVWELMTF GSKPYDGIPA SEISSILEKG ERLPQPPICT IDVYMIMVKC WMIDADSRPK 960
961 FRELIIFFSK MARDPQRYLV IQGDERMHLP SPTDSNFYRA LMDEEDMDV VDADEYLIPQ 1020
1021 QGFFSSPSTS RTPLLSSLSA TSMNSTVACI DRNGLQSCPI KEDSFLQRY S DPTGALTED 1080
1081 SIDDTFLPVP EYINQSVPKR PAGSVQNPVY HNQPLNPAPS RDPHYQDPHS TAVGNPEYLN 1140
1141 TVQPTCVNST FDSPAHAQK GSHQISLDNP DYQQDFFPKE AKPNGIFKGS TAENAEYLRV 1200
1201 APQSSEFIGA
```

In three-letter code:

```
      1      2      3      4      5      6      7      8      9     10     11     12     13     14     15
1  Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu 15
16 Ala Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val 30
31 Cys Gln Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu 45
46 Asp His Phe Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val 60
```



# Feature table, продолжение

DISULFID	595	617			
DISULFID	620	628			
DISULFID	624	636			
CROSSLNK	716	716		Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin).	
CROSSLNK	737	737		Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin).	
CROSSLNK	754	754		Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin).	
CROSSLNK	867	867		Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin).	
CROSSLNK	929	929		Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin).	
CROSSLNK	970	970		Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin).	
VAR_SEQ	404	405		FL -> LS (in isoform 2).	VSP_002887
VAR_SEQ	406	1210		Missing (in isoform 2).	VSP_002888
VAR_SEQ	628	705		CTGPGLEGCPITNGPKIPSIATGMVGAALLLVVALGIGLF MRRRHIVRKRTRLRRLQERELVEPLTPSGEAPNQALLR -> PGNESLKAMLFCLFKLSSCNQSNQSGVSHQSGSPAQAQESC LGWIPSLLPSEFQLGWGGCSHLHAWPSASVIITASSCH (in isoform 3).	VSP_002889
VAR_SEQ	628	628		C -> S (in isoform 4).	VSP_002891
VAR_SEQ	629	1210		Missing (in isoform 4).	VSP_002892
VAR_SEQ	706	1210		Missing (in isoform 3).	VSP_002890
VARIANT	98	98	1	R -> Q (in dbSNP:rs17289589 [NCBI]).	VAR_019293
VARIANT	266	266	1	P -> R (in dbSNP:rs17336639 [NCBI]).	VAR_019294
VARIANT	521	521	1	R -> K (in dbSNP:rs11543848 [NCBI]).	VAR_019295
VARIANT	674	674	1	V -> I (in dbSNP:rs17337079 [NCBI]).	VAR_019296
VARIANT	709	709	1	E -> A (in lung cancer).	VAR_026084
VARIANT	709	709	1	E -> K (in lung cancer).	VAR_026085
VARIANT	719	719	1	G -> A (in lung cancer).	VAR_026086
VARIANT	719	719	1	G -> C (in lung cancer; dbSNP:rs28929495 [NCBI]).	VAR_026087
VARIANT	719	719	1	G -> D (in lung cancer).	VAR_026088
VARIANT	719	719	1	G -> S (in lung cancer; somatic mutation).	VAR_019297
VARIANT	724	724	1	G -> S (in lung cancer).	VAR_026089
VARIANT	734	734	1	E -> K (in lung cancer).	VAR_026090
VARIANT	746	750	5	Missing (in lung cancer).	VAR_026092

# Feature Table, продолжение

```

MUTAGEN 1110 1110 Y->F: NO change in interaction with PIK3C2B.
MUTAGEN 1172 1172 Y->F: No change in interaction with PIK3C2B.
MUTAGEN 1197 1197 Y->F: No change in interaction with PIK3C2B. 65% decrease in interaction with PIK3C2B; when associated
with F-1016. Abolishes interaction with PIK3C2B; when associated with F-1092 and F-1016.

CONFLICT 540 540 N -> K (in Ref. 1).

STRAND 40 43 4
HELIX 44 55 12
STRAND 59 63 5
STRAND 65 67 3
HELIX 77 81 5
STRAND 84 87 4
STRAND 89 93 5
HELIX 101 103 3
TURN 114 116 3
STRAND 117 122 6
STRAND 145 152 8
HELIX 159 161 3
TURN 164 167 4
TURN 173 175 3
    
```

Только экспериментальные

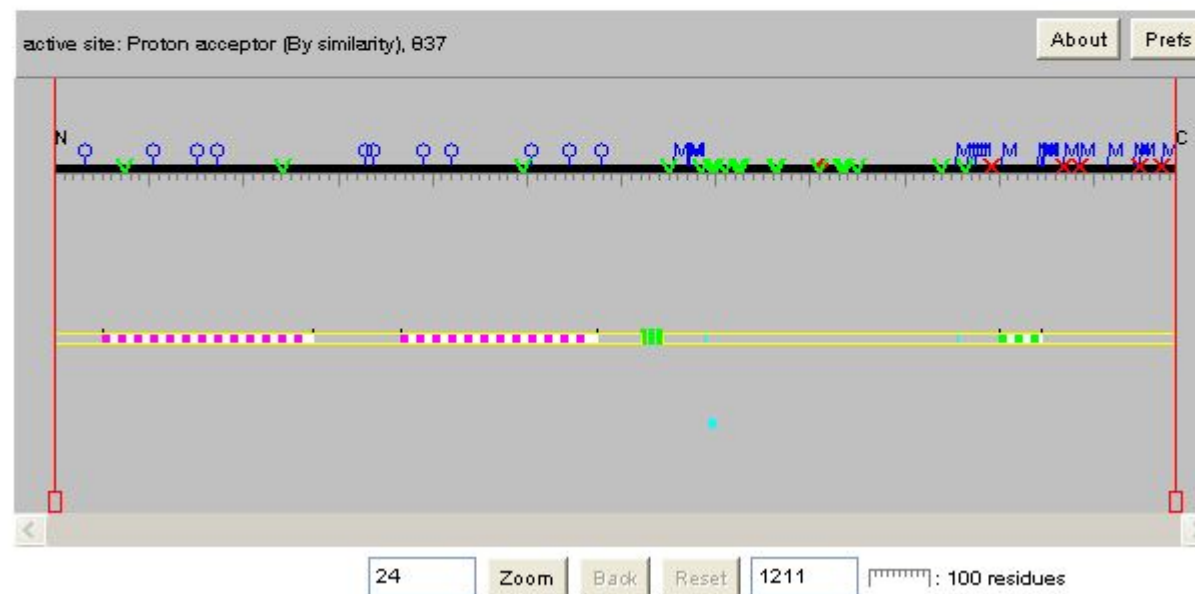
DSSP code	DSSP definition	Swiss-Prot assignment
H	Alpha-helix	HELIX
G	3(10) helix	HELIX
I	Pi-helix	HELIX
E	Hydrogen-bonded beta-strand (extended strand)	STRAND
B	Residue in an isolated beta-bridge	STRAND
T	H-bonded turn (3-turn, 4-turn or 5-turn)	TURN
S	Bend (five-residue bend centered at residue i)	Not specified

# Feature Table viewer (Sequence Element viewer)

For reference to the SEView applet, see *In Silico Biology*, Vol. 1 (1998).

[Click here](#) for a description of represented protein features.

**Note to Mac users:** There seems to be a bug in many versions (4.x) of Netscape Communicator. Please try with Explorer or upgrade your version of Netscape.





# Feature aligner

## Feature aligner

Selected features of [P00533](#) (EGFR\_HUMAN) Epidermal growth factor receptor precursor (EC 2.7.10.1) (Receptor tyrosine-protein kinase ErbB-1) [Homo sapiens (Human)].

	Key	Position	Length	Description
<input type="checkbox"/>	CHAIN	<a href="#">25-1210</a>	1186	<b>Epidermal growth factor receptor</b> LEEKKVCQGT SNKLTQLGTF EDHFLSLQRM FNNCEVVLGN LEITYVQRNY DLSFLKTIQE VAGYVLIALN TVERIPIENL QIIRGNMYYE NSYALAVLSN YDANKTGLK LPMRNLQEIL HGAVRFSNMP ALCNVESIQW RDIVSSDFLS NMSMDFQNH GSCQKCDPSC PNGSCWGAGE ENCQKLTKII CAQQCSGRGR GKSPSDCCHN QCAAAGCTGP ESDCLVCRKF RDEATCKDTC PPLMLYNPTT YQMDVNPEGK YSFGATCVKK CPRNYVVDH GSCVRACGAD SYEMEEEDGVR KCKKCEGPCR KVCNGIGIGE FKDSLINA NIKHFKNCTS ISGDLHLIPV AFRGDSFTHT PPLDPQELDI LKTVKEITGF LLIQAWPENR TDLHAFENLE IIRGRTKQH QFSLAVVSLN ITSLGLRSLK EISDGDVII GNKNLCYANT INWKKLFGTS GQRTKIISNR GENSCKATGQ VCHALCSPEG CUGPEPRDCV SCRNVSRGRE CVDKCNLLEG EPREFVENSE CIQCHPECLP QAMNITCTG GPDNCIQCAH YIDGPHCVKT CPAGVMGENN TLVWKYADAG HVCHLCHPNC TYGCTGPGLE GCPTNGPKIP SIATGMVVAL LLLLVLVALGI GLFMRRRHIV RKRTRRLL ERELVEPLTP SGEAPNQAALL RILKETEFKK IKVLGSGAFG TVYKGLWIPE GEKVKIPVAI KELREATSPK ANKEILDEAY VMAVDNPHV CRLGLGICLTS TVQLITQLM FGCLLDYVRE HKDNIGSQYL LNWCVQIARG MNYLEDRLV HRDLAARNVL VKTPQHVKIT DFGLAKLLGA EEKEYHAEGG KVPKUMALE SILHRIYTHQ SDVWSYGVV WELMTFGSKP YDGIPASEIS SILEKGERLP OPPICTIDVY MIHVKCMWID ADSRPKFREL IIEFSKMARD PQRYLVIQGD ERMHLPSPDT SNFYRALMDE EDMDDVVDA EYLIPQQGFF SSPSTSRTP LSSLSATSMN STVACIDRNG LQSCPIKEDS FLQRYSSDPT GALTEDSIDD TFLPVPEYIN QSVPKRPAGS VQNPVYHNQP LNPAPSRDP YQDPHSTAVG NPEYLNTPQP TCVNSTFDSF AHWAQKGSQH ISLDNPDYQQ DFFPKKAPKN GIFKGSTAEN AEYLRVAPQS SEFIGA
<input type="checkbox"/>	TOPO_DOM	<a href="#">25-645</a>	621	<b>Extracellular (Potential)</b> LEEKKVCQGT SNKLTQLGTF EDHFLSLQRM FNNCEVVLGN LEITYVQRNY DLSFLKTIQE VAGYVLIALN TVERIPIENL QIIRGNMYYE NSYALAVLSN YDANKTGLK LPMRNLQEIL HGAVRFSNMP ALCNVESIQW RDIVSSDFLS NMSMDFQNH GSCQKCDPSC PNGSCWGAGE ENCQKLTKII CAQQCSGRGR GKSPSDCCHN QCAAAGCTGP ESDCLVCRKF RDEATCKDTC PPLMLYNPTT YQMDVNPEGK YSFGATCVKK CPRNYVVDH GSCVRACGAD SYEMEEEDGVR KCKKCEGPCR KVCNGIGIGE FKDSLINA NIKHFKNCTS ISGDLHLIPV AFRGDSFTHT PPLDPQELDI LKTVKEITGF LLIQAWPENR TDLHAFENLE IIRGRTKQH QFSLAVVSLN ITSLGLRSLK EISDGDVII GNKNLCYANT INWKKLFGTS GQRTKIISNR GENSCKATGQ VCHALCSPEG CUGPEPRDCV SCRNVSRGRE CVDKCNLLEG EPREFVENSE CIQCHPECLP QAMNITCTG GPDNCIQCAH YIDGPHCVKT CPAGVMGENN TLVWKYADAG HVCHLCHPNC TYGCTGPGLE GCPTNGPKIP S
<input type="checkbox"/>	TRANSMEM	<a href="#">646-668</a>	23	<b>(Potential)</b> IATGMVVAL LLLLVLVALGI LFM
<input type="checkbox"/>	TOPO_DOM	<a href="#">669-1210</a>	542	<b>Cytoplasmic (Potential)</b> RRRHIVRKR LRRLLQEREL VEPLTPSGEA PNQALLRILK ETEFKKIKVL GSGAFGTVYK GLWPEGEKV KIPVAIKELR EATSPKANKE ILDEAYVMAS VDNPHVCRL GICLTSTVQL ITQLMPFGCL LDYVREHKDN IGSQYLLNWC VQIAGKMNVL EDRRLVHRDL AARNVLVKTP QHVKITDFGL AKLLGAEKEE YHAEGGKVP KUMALESIL RIYTHQSDVW SYGVTWELM TFGSKPYDGI PASEISSILE KGERLPQPI CTIDVYMIMV KCWMIDADSR PKFRELIIEF SKMARDPQRY LVIQGDERMH LPSPTDSNF RALMDEEDMD DVVDDEYLI PQQGFSSPS TSRTPLSSSL SATSMNSTVA CIDRNLQSC PIKEDSFLQR YSSDPTGALT EDSIDDTFLP VPEYINQSVV KRPAGSVQN VYHNQPLNPA PSRDPHYQDP HSTAVGNPEY LNTVQPTCVN STFDSPAHWA QKGSQHSISLD NPDYQQDFFF KEAKPNGIFK GSTAENAEYL RVAPOSSEFI GA
<input type="checkbox"/>	REPEAT	<a href="#">75-300</a>	226	<b>Approximate</b> DLSFLKTIQE VAGYVLIALN TVERIPIENL QIIRGNMYYE NSYALAVLSN YDANKTGLKE LPMRNLQEIL HGAVRFSNMP ALCNVESIQW RDIVSSDFLS NMSMDFQNH GSCQKCDPSC PNGSCWGAGE ENCQKLTKII CAQQCSGRGR GKSPSDCCHN QCAAAGCTGPR ESDCLVCRKF RDEATCKDTC PPLMLYNPTT YQMDVNPEGK YSFGATCVK CPRNVV
<input type="checkbox"/>	REPEAT	<a href="#">390-600</a>	211	<b>Approximate</b> QELDILKTVK EITGFLLIQA WPNRNTDLHA FENLEIIRGR TKQHGFSLA VVSLNITSLG LRLSKEISDG DVIISGNKNL CYANTINWKK LFGTSGQKTK IISNRGENS KATGQVCHAL CSPEGCWPE PRDCVSCRNV SRGRECVDKC NLLEGEPPREF VENSECIQCH PECLPQAMNI TCTGRGPDNC IQCAHYIDGP HCVKTCAPAGV H
<input type="checkbox"/>	DOMAIN	<a href="#">712-979</a>	268	<b>Protein kinase</b> FKKIRVLGSG AFGTVYKGLW IPEGEKVKIP VAIKELREAT SPRANKEILD EAYVMASVDN PHVCRLLGIC LTSTVQLITQ LMPFGCLLDY VREHKDNIGS QYLLNWCVQ AKGMNYLEDR RLVHRDLAAR NVLVKTPQHV KITDFGLAKL LGAEKEYEHA EGGKVPKUM ALESILHRIY THQSDVWSYG VTVWELMTFG SKPYDGIPAS EISSILEKG RLPQPPICTI DVYIMVWKCW MIDADSRPKF RELIIEFSKM ARDPQRYL

Можно построить множественное выравнивание подмножества этих элементов (ClustalW) или скопировать их в FASTA формате



# Sequence

## Sequence information

Length: **1210 AA** [This is the length of the unprocessed precursor]

Molecular weight: **134277 Da** [This is the MW of the unprocessed precursor]

CRC64: **D8A2A50B4EFB6ED2** [This is a checksum on the sequence]

```
10      20      30      40      50      60
MRPSGTAGAA LLALLAALCP ASRALEEKKV CQGTSNKLTV LGTFEDHFLS LQRMFMNCEV

70      80      90      100     110     120
VLGNLEITYV QRNYDLSFLK TIOEVAGYVL IALNTVERIF LENLQIIRGN MYYENSYALA

130     140     150     160     170     180
VLSNYDANKT GLKELPMRNL QEILHGAVRF SNNPALCNVE SIQWRDIVSS DFLSNMSMDF

190     200     210     220     230     240
QNHGSCQKCK DPSCPNGSCW GAGEENCQKL TKIICAQCCS GRCRGRKSPSD CCHNQCAAGC

250     260     270     280     290     300
TGPRESDECLV CRKFRDEATC KDTCPLMLY NPTTYQMDVN PEGKYSFGAT CVKKCPNRYV

310     320     330     340     350     360
VTDHGSCVRA CGADSYEMEE DGVRKCKKCE GPCRKVCNGI GIGEFKDSL S INATNIKHFK

370     380     390     400     410     420
NCTSIGDLH ILPVAFRGDS FTHTPPLDPQ ELDILKTVKE ITGFLLIQAW PENRTDLHAF

430     440     450     460     470     480
ENLEIIRGRT KQHGFSLAV VSLNITSLGL RSLKEISDGD VIISGNKNLC YANTINWKKL

490     500     510     520     530     540
FGTSGQRTKI ISNRGENSCK ATGQVCHALC SPEGCWGPEF RDCVSCRNVS RGRECVDKCN

550     560     570     580     590     600
LLEGEPREFV ENSECIQCHP ECLPQAMNIT CTGRGPDNCI QCAHYIDGPH CVKTCPAGVM

610     620     630     640     650     660
GENNTLVWKY ADAGHVCHLC HPNCTYGCTG PGLEGCPING PKIPSIATGM VGALLLLLVV

670     680     690     700     710     720
ALGIGLFMR R RHIVRKRTRL RLLQERELVE PLTPSGEAPN QALLRILKET EFKKIKVLGS

730     740     750     760     770     780
GAFGTVYKGL WIPEGEKVKI PVAIKELREA TSPKANKEIL DEATVMASVD NPHVCRLLGI

790     800     810     820     830     840
CLTSTVQLIT QLMFPGCLLD YVREHKDNIG SQYLLNWCVQ IAKGMNYLED RRLVHRDLAA

850     860     870     880     890     900
RNVLVKTPQH VKITDFGLAK LLGAEKEYH AEGGKVIKW MALESILHRI YTHQSDVUSY

910     920     930     940     950     960
RNVLVKTPQH VKITDFGLAK LLGAEKEYH AEGGKVIKW MALESILHRI YTHQSDVUSY
```

<http://www.expasy.org/cgi-bin/aligner?P00533>

# Sequence, продолжение

```
970      980      990      1000      1010      1020
FRELIIIEFSK HARDPQRYLV IQGDERMHLP SPTDSNFYRA LMDEEDMDDV VDADEYLIPQ

1030      1040      1050      1060      1070      1080
QGFFSSPSTS RTPLLSSLSA TSNNSTVACI DRNGLQSCPI KEDSFLQRYV SDPTGALTED

1090      1100      1110      1120      1130      1140
SIDDTFLPVP EYINQSVPKR PAGSVQNPVY HNOPLNPAPV RDPHYQDPHS TAVGNPEYLN

1150      1160      1170      1180      1190      1200
TVQPTCVNST FDSPAHWAQK GSHQISLDNP DYQQDFFPKE AKPNGIFKGS TAENAEYLRV

1210
APOSSEFIGA
```

[P00533 in FASTA format](#)

[View entry in original UniProtKB/Swiss-Prot format](#)

[View entry in raw text format \(no links\)](#)

[Report form for errors/updates in this UniProtKB/Swiss-Prot entry](#)

**BLAST**

BLAST submission on ExPASy/SIB  
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter,  
Dotlet (Java)



ScanProsite, MotifScan



Submit a homology modeling request to SWISS-MODEL

**NPS@**

NPSA Sequence analysis tools

# FASTA format

```
Swiss-Prot - Поиск в Google http://www.exp...rot/P00533.fas UniProtKB/Swiss-F
>P00533|EGFR_HUMAN Epidermal growth factor receptor - Homo sapiens (Human).
MRPSGTAGAALLLALLAALCPASRALEEKVKVCGQTSNKLTLQGLTFEDHFSLQRMFNCEV
VLGNLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIPLLENLQIIRGNMYYENSYALA
VLSNYDANKTGLKELPMRNLQEILHGAVRFSNNPALCNVESIQWRDIVSSDFLSNMSMDF
QNHLSGCQKCDPSCPNGSCWGAAGEENCQKLTKIICAQQCSGRRCRGKSPSDCCHNQCAAGC
TGPRESDECLVCRKFRDEATCKDTCPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYV
VTDHGSCVRACGADSYEMEEDGVRKCKKCEGPCRKVCNGIGIGEFKDSLSINATNIKHFK
NCTSIGDLHLIPVAFRGDSFTHTPPLDPQELDILKTVKEITGFLLIQAWPENRTDLHAF
ENLEIIRGRTKQHGFSLAVVSLNITSLGLRSLKEISDGDVVISGNKNLCYANTINWKKL
FGTSGQKTKIISNRGENSCKATGQVCHALCSPEGCWGPEPRDCVSCRNVSRGRECVDKCN
LLEGEPRFVENSEC IQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPHCVKTCPPAGVM
GENNTLVWKYADAGHVCHLCHPNCTYGCTGPGLEGCTNGPKIPSIATGMVGAALLLLLVV
ALGIGLFMRRRHIVRKRTRLRRLQERELVEPLTPSGEAPNQALLRILKETEFKKIKVLGS
GAFGTVYKGLWIPEGEKVKIPVAIKELREATSPKANKEILDEAYVMASVDNPHVCRLGI
CLTSTVQLITQLMPFGCLLDYVREHKDNIGSQYLLNWCVQIAKGMNYLEDRLVHRDLAA
RNVLVKTPQHVKITDFGLAKLLGAEKEYHAEGGKVP IKWMALESILHRIYTHQSDVWSY
GVTVWELMTFGSKPYDGIPASEISSILEKGERLPQPP ICTIDVYIMIMVKCWMIDADSRPK
FRELIIIEFSKMARDPQRYLVIQGDERMHLPSPTDSNFYRALMDEEDMDDVVDADAYLIPQ
QGFFSSPSTSRPTLLSLSATSNNSTVACIDRNLQSCP IKEDSFLQRYSSDPTGALTED
SIDDTFLPVPEYINQSVKRPAGSVQNPVYHNQPLNPAISRDPHYQDPHSTAVGNPEYLN
TVQPTCVNSTFDSPAHWAKGSHQISLDNPDYQQDFFPKEAKPNGIFKGSTAENAEYLRV
APQSSEFIGA
```

Программа FASTA (1988, WR Pearson & DJ Lipman):

>(the definition line)\_уникальный\_ID + короткое описание  
ПОСЛЕДОВАТЕЛЬНОСТЬ БЕЛКА (ИЛИ ДНК) В ОДНОБУКВЕННОМ  
КОДЕ

RAW format – без definition line

# NiceProt view

## UniProtKB/Swiss-Prot: P00533

*NiceProt* - a user-friendly view of this UniProtKB/Swiss-Prot entry

ID EGFR\_HUMAN Reviewed: 1210 AA.  
AC P00533; O00688; O00732; P06268; Q14225; Q92795; Q9BZS2; Q9GZX1;  
AC Q9H2C9; Q9H3C9; Q9UMD7; Q9UMD8; Q9UMG5;  
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.  
DT 01-NOV-1997, sequence version 2.  
DT 02-OCT-2007, entry version 121.  
DE Epidermal growth factor receptor precursor (EC 2.7.10.1) (Receptor  
DE tyrosine-protein kinase ErbB-1).  
GN Name=EGFR; Synonyms=ERBB1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).  
RX MEDLINE=84219729; PubMed=6328312 [NCBI, ExpASY, EBI, Israel, Japan]; DOI=10.1038/309418a0;  
RA Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W.,  
RA Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J.,  
RA Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.;  
RT "Human epidermal growth factor receptor cDNA sequence and aberrant  
RT expression of the amplified gene in A431 epidermoid carcinoma cells.";  
RL Nature 309:418-425(1984).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).  
RC TISSUE=Placenta;  
RX MEDLINE=95382957; PubMed=7654368 [NCBI, ExpASY, EBI, Israel, Japan]; DOI=10.1002/mrd.1080410205;  
RA Ileki J.V., Stark B.C., Scoccia B.;  
RT "Possible role of variant RNA transcripts in the regulation of  
RT epidermal growth factor receptor expression in human placenta.";  
RL Mol. Reprod. Dev. 41:149-156(1995).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA] (ISOFORM 2).  
RC TISSUE=Placenta;  
RX MEDLINE=97078686; PubMed=8918811 [NCBI, ExpASY, EBI, Israel, Japan]; DOI=10.1093/nar/24.20.4050;  
RA Reiter J.L., Maihle N.J.;  
RT "A 1.8 kb alternative transcript from the human epidermal growth  
RT factor receptor gene encodes a truncated form of the receptor.";  
RL Nucleic Acids Res. 24:4050-4056(1996).  
RN [4]  
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).  
RC TISSUE=Placenta;  
RX MEDLINE=97256547; PubMed=9103388 [NCBI, ExpASY, EBI, Israel, Japan]; DOI=10.1006/gyno.1996.4526;