Základy praktické Bioinformatiky

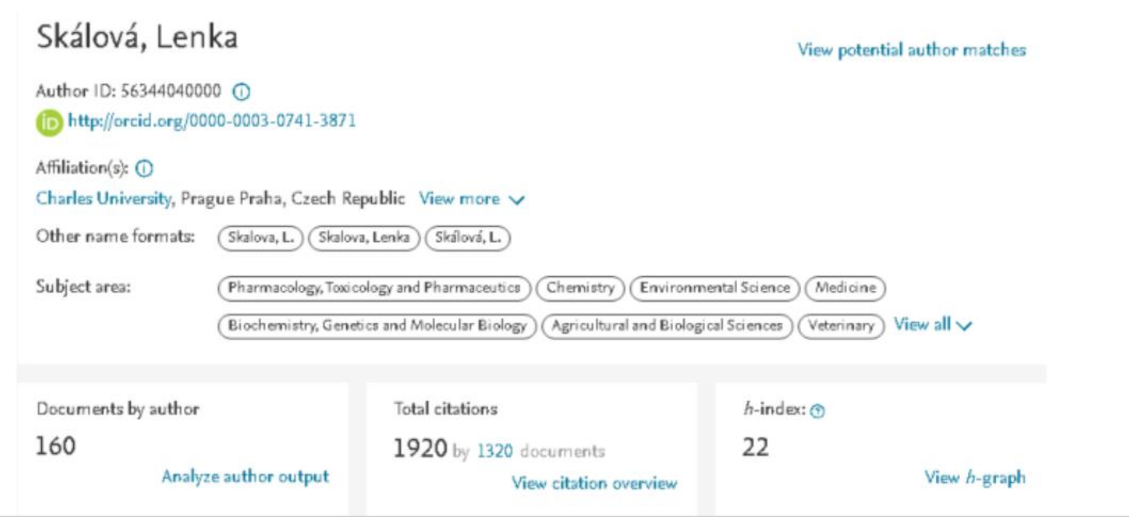
PETRA MATOUŠKOVÁ

2023/2024

2/10

H-index (může se lišit)

Scopus



Skálová, Lenka

View potential author matches

Author ID: 56344040000 ⓘ

http://orcid.org/0000-0003-0741-3871

Affiliation(s): ⓘ

Charles University, Prague Praha, Czech Republic View more

Other name formats: Skalova, L. | Skalova, Lenka | Skálová, L.

Subject area: Pharmacology, Toxicology and Pharmaceutics | Chemistry | Environmental Science | Medicine | Biochemistry, Genetics and Molecular Biology | Agricultural and Biological Sciences | Veterinary | View all

Documents by author
160
Analyze author output

Total citations
1920 by 1320 documents
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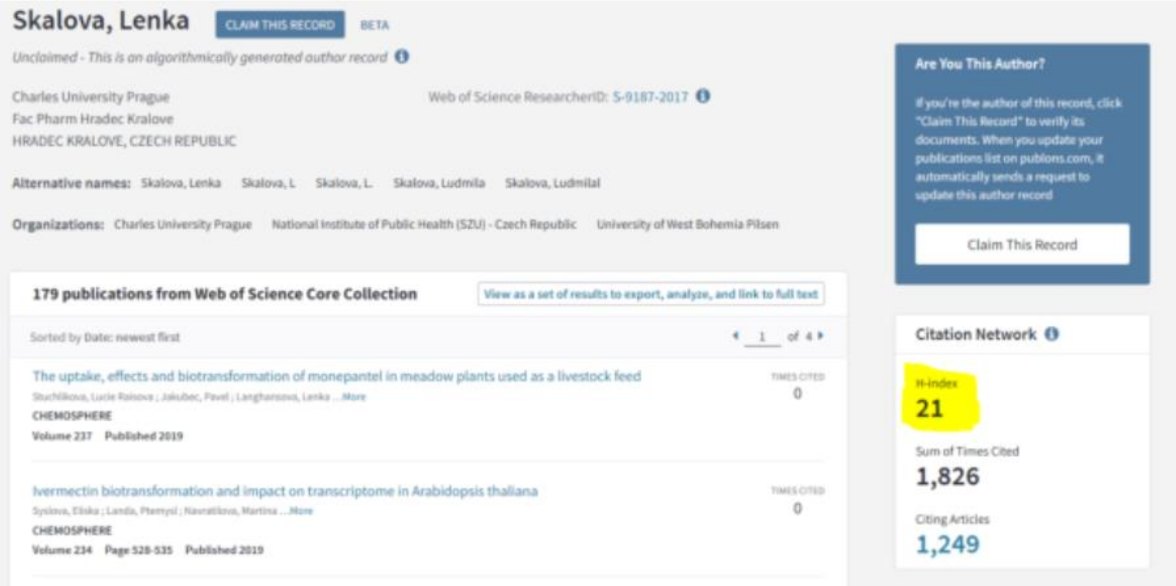
h-index: ⓘ
22
View *h*-graph

WoS



Skalova, Lenka CLAIM THIS RECORD BETA

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Charles University Prague
Fac Pharm Hradec Kralove
HRADEC KRALOVE, CZECH REPUBLIC

Web of Science ResearcherID: S-9187-2017

Alternative names: Skalova, Lenka | Skalova, L | Skalova, L. | Skalova, Ludmila | Skalova, Ludmilal

Organizations: Charles University Prague | National Institute of Public Health (SZU) - Czech Republic | University of West Bohemia Pilsen

179 publications from Web of Science Core Collection

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Sorted by Date: newest first | 1 of 4

The uptake, effects and biotransformation of monepantel in meadow plants used as a livestock feed
Stuchlikova, Lucie Raisova ; Jakubec, Pavel ; Langhansova, Lenka ...More
CHEMOSPHERE
Volume 237 Published 2019
TIMES CITED 0

Ivermectin biotransformation and impact on transcriptome in Arabidopsis thaliana
Syslova, Eliska ; Landa, Premysl ; Navratilova, Martina ...More
CHEMOSPHERE
Volume 234 Page 528-535 Published 2019
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1,826

Citing Articles
1,249

Základy praktické bioinformatiky

Téma 2/10

Proteinová bioinformatika I

Cíle:

Student bude schopen vyhledat a stáhnout požadovanou sekvenci proteinu. Na základě sekvence bude schopen určit (nalézt nebo spočítat) fyzikálně-biochemické vlastnosti proteinu.

Rešeršní projekt: NQO1

Vyhledejte dostupné informace o NQO1, získejte co nejvíce literárních, sekvenčních, případně i strukturních a dalších údajů o tomto genu/proteinu.

Nalezněte podobné sekvence a porovnejte je na proteinové úrovni.

- **NAD(P)H:chinonoxidoreduktasa / reference**

„Proteinová bioinformatika I“

Vyhledávání AMK sekvencí

Analýza vlastností sekvencí (aminokyselinové složení, molekulová hmotnost, isoelektrický bod…)

Štěpení proteasami

Analýza hydrofobních segmentů, transmembránových úseků

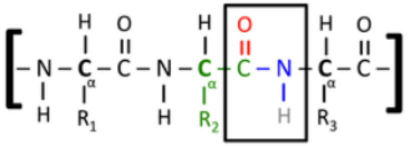
Predikce sekundární struktury

3D-struktura, vizualizace

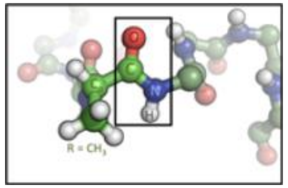
Vyhledání a porovnání podobných sekvencí

Evoluční příbuznost sekvencí

…



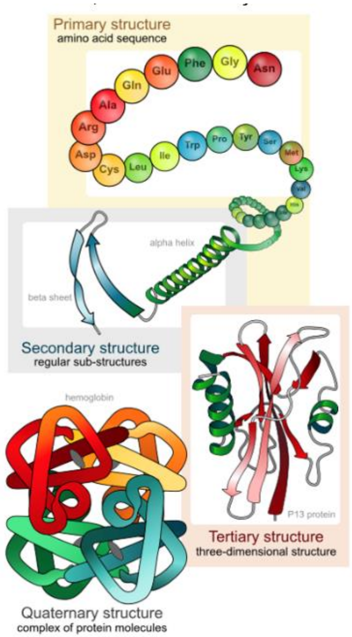
Proteiny

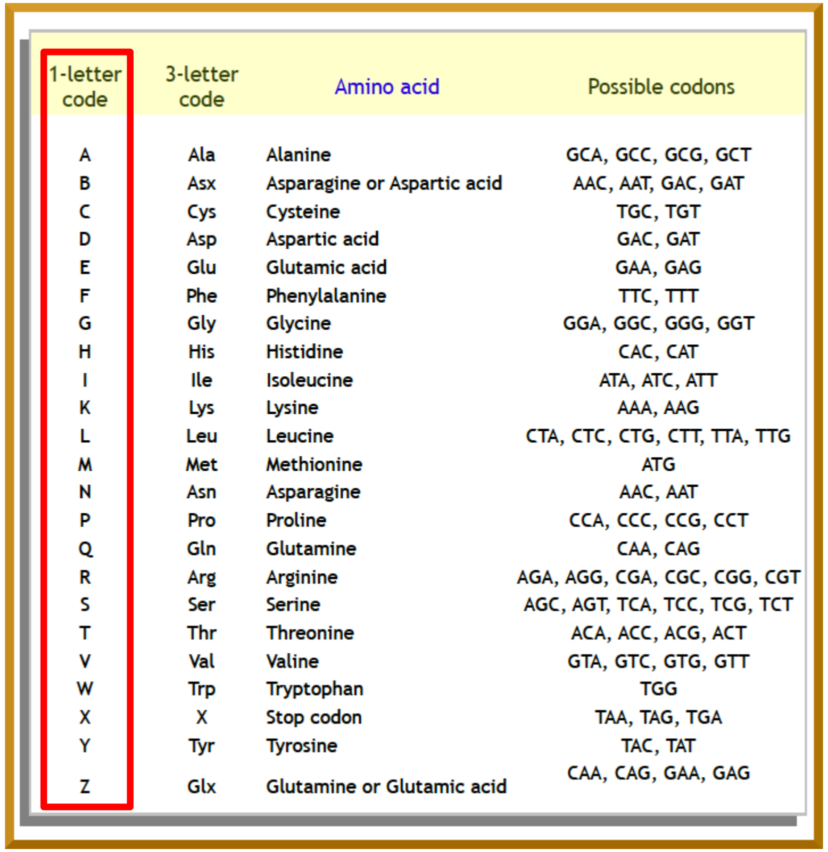


20 Aminokyselin – primární struktura:

(Frederick Sanger-1958 Nobelova cena za sekvenování insulinu)

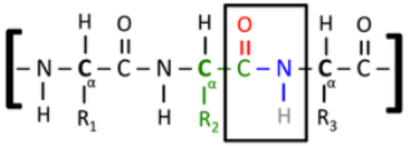
Sekundární struktura
Terciární struktura
Kvartérní struktura



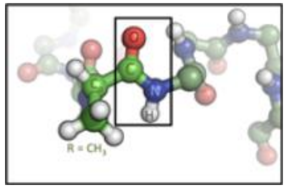


1-letter code	3-letter code	Amino acid	Possible codons
A	Ala	Alanine	GCA, GCC, GCG, GCT
B	Asx	Asparagine or Aspartic acid	AAC, AAT, GAC, GAT
C	Cys	Cysteine	TGC, TGT
D	Asp	Aspartic acid	GAC, GAT
E	Glu	Glutamic acid	GAA, GAG
F	Phe	Phenylalanine	TTC, TTT
G	Gly	Glycine	GGA, GGC, GGG, GGT
H	His	Histidine	CAC, CAT
I	Ile	Isoleucine	ATA, ATC, ATT
K	Lys	Lysine	AAA, AAG
L	Leu	Leucine	CTA, CTC, CTG, CTT, TTA, TTG
M	Met	Methionine	ATG
N	Asn	Asparagine	AAC, AAT
P	Pro	Proline	CCA, CCC, CCG, CCT
Q	Gln	Glutamine	CAA, CAG
R	Arg	Arginine	AGA, AGG, CGA, CGC, CGG, CGT
S	Ser	Serine	AGC, AGT, TCA, TCC, TCG, TCT
T	Thr	Threonine	ACA, ACC, ACG, ACT
V	Val	Valine	GTA, GTC, GTG, GTT
W	Trp	Tryptophan	TGG
X	X	Stop codon	TAA, TAG, TGA
Y	Tyr	Tyrosine	TAC, TAT
Z	Glx	Glutamine or Glutamic acid	CAA, CAG, GAA, GAG

SEKVENCE ⇨ STRUKTURA ⇨ FUNKCE

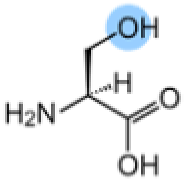


Proteiny

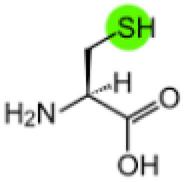


20 Aminokyselin – primární struktura:

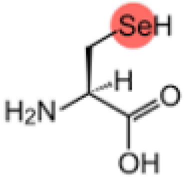
J	Xle	Isoleucine/Leucine
O	Pyl	Pyrrolysine
U	Sec	Selenocysteine
X	Xaa	Any residue



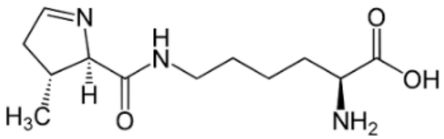
Serine (Ser)



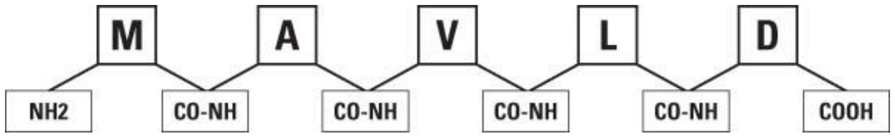
Cysteine (Cys)

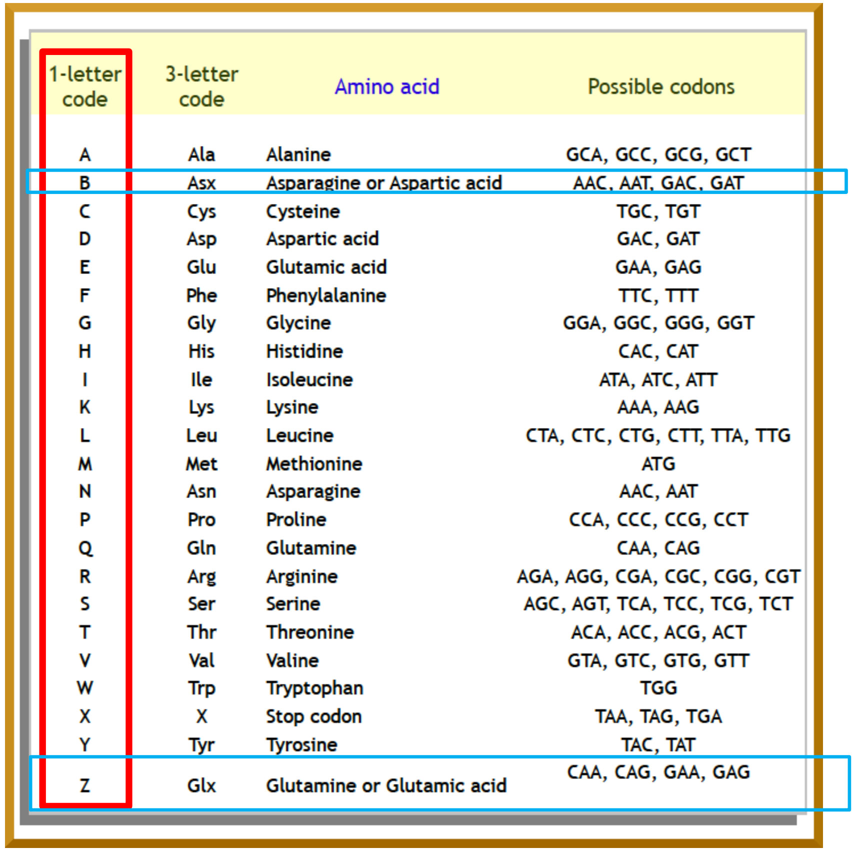


Selenocysteine (Sec)



N-konec → C-konec





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E	Glu	Glutamic acid	GAA, GAG
F	Phe	Phenylalanine	TTC, TTT
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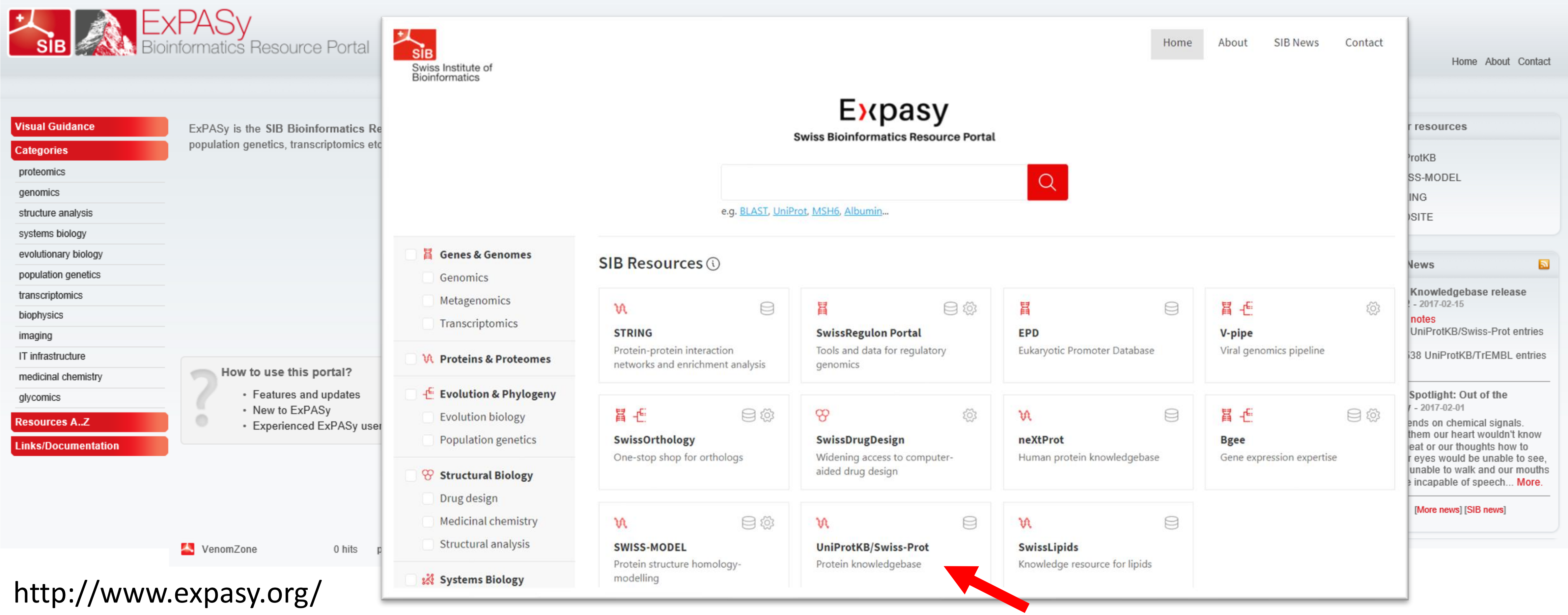
H	His	Histidine	CAC, CAT
I	Ile	Isoleucine	ATA, ATC, ATT
K	Lys	Lysine	AAA, AAG
L	Leu	Leucine	CTA, CTC, CTG, CTT, TTA, TTG
M	Met	Methionine	ATG
N	Asn	Asparagine	AAC, AAT
P	Pro	Proline	CCA, CCC, CCG, CCT
Q	Gln	Glutamine	CAA, CAG
R	Arg	Arginine	AGA, AGG, CGA, CGC, CGG, CGT
S	Ser	Serine	AGC, AGT, TCA, TCC, TCG, TCT
T	Thr	Threonine	ACA, ACC, ACG, ACT
V	Val	Valine	GTA, GTC, GTG, GTT
W	Trp	Tryptophan	TGG
X	X	Stop codon	TAA, TAG, TGA
Y	Tyr	Tyrosine	TAC, TAT
Z	Glx	Glutamine or Glutamic acid	CAA, CAG, GAA, GAG

Databáze

PRIMÁRNÍ	**SEKUNDÁRNÍ**
Ukládání primárních dat (sekvence, struktury…)	Shromažďování, analýza a propojování dat
Přímé vkládání	Primární databáze, literatura (po analýze a interpretaci primárních dat)
Genbank, DDBJ, ENA Protein Data Bank GEO…	SwissProt, InterPro, Ensembl, OMIM, STRING…

Proteinové databáze: UniProt


ExPASy
Bioinformatics Resource Portal

Visual Guidance
Categories
- proteomics
- genomics
- structure analysis
- systems biology
- evolutionary biology
- population genetics
- transcriptomics
- biophysics
- imaging
- IT infrastructure
- medicinal chemistry
- glycomics

Resources A..Z
Links/Documentation

ExPASy is the SIB Bioinformatics Re
population genetics, transcriptomics etc

How to use this portal?
- Features and updates
- New to ExPASy
- Experienced ExPASy user

VenomZone 0 hits

Swiss Institute of Bioinformatics

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Swiss Bioinformatics Resource Portal

e.g. BLAST, UniProt, MSH6, Albumin...

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☐ Genomics
☐ Metagenomics
☐ Transcriptomics
☐ **Proteins & Proteomes**
☐ **Evolution & Phylogeny**
☐ Evolution biology
☐ Population genetics
☐ **Structural Biology**
☐ Drug design
☐ Medicinal chemistry
☐ Structural analysis
☐ **Systems Biology**

SIB Resources

STRING Protein-protein interaction networks and enrichment analysis	**SwissRegulon Portal** Tools and data for regulatory genomics	**EPD** Eukaryotic Promoter Database	**V-pipe** Viral genomics pipeline
SwissOrthology One-stop shop for orthologs	**SwissDrugDesign** Widening access to computer-aided drug design	**neXtProt** Human protein knowledgebase	**Bgee** Gene expression expertise
SWISS-MODEL Protein structure homology-modelling	**UniProtKB/Swiss-Prot** Protein knowledgebase	**SwissLipids** Knowledge resource for lipids	

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SITE

News
Knowledgebase release
- 2017-02-15
notes
UniProtKB/Swiss-Prot entries
38 UniProtKB/TrEMBL entries

Spotlight: Out of the
- 2017-02-01
ends on chemical signals.
them our heart wouldn't know
eat or our thoughts how to
r eyes would be unable to see,
unable to walk and our mouths
incapable of speech... More.

[More news] [SIB news]

http://www.expasy.org/

Možnosti databáze UniProt

http://www.uniprot.org/

Vyhledávání sekvencí, vlastnosti sekvencí

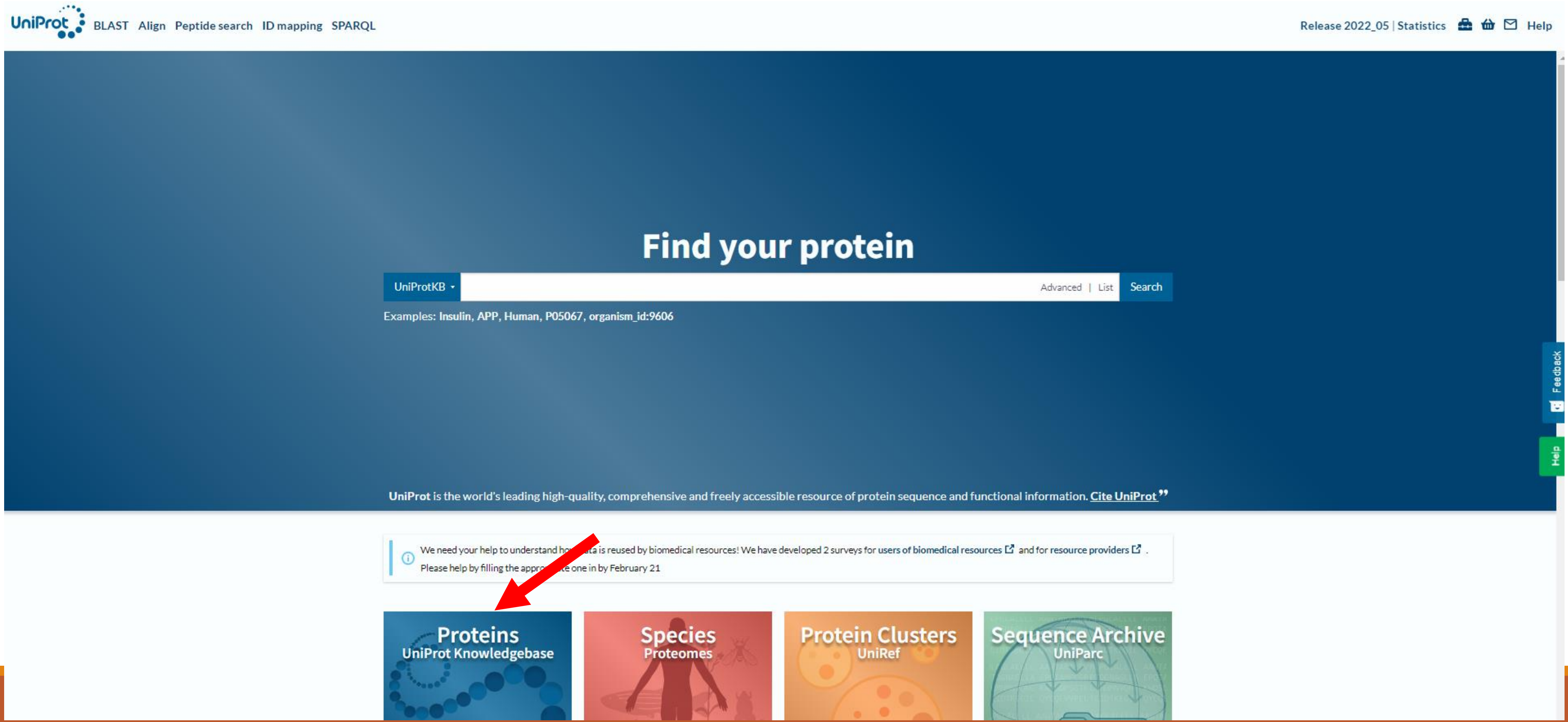
Funkce proteinů, interakce, dráhy

Propojení s nemocemi, mutace

Propojení do dalších databází

Proteinové databáze: UniProt

http://www.uniprot.org/



Find your protein

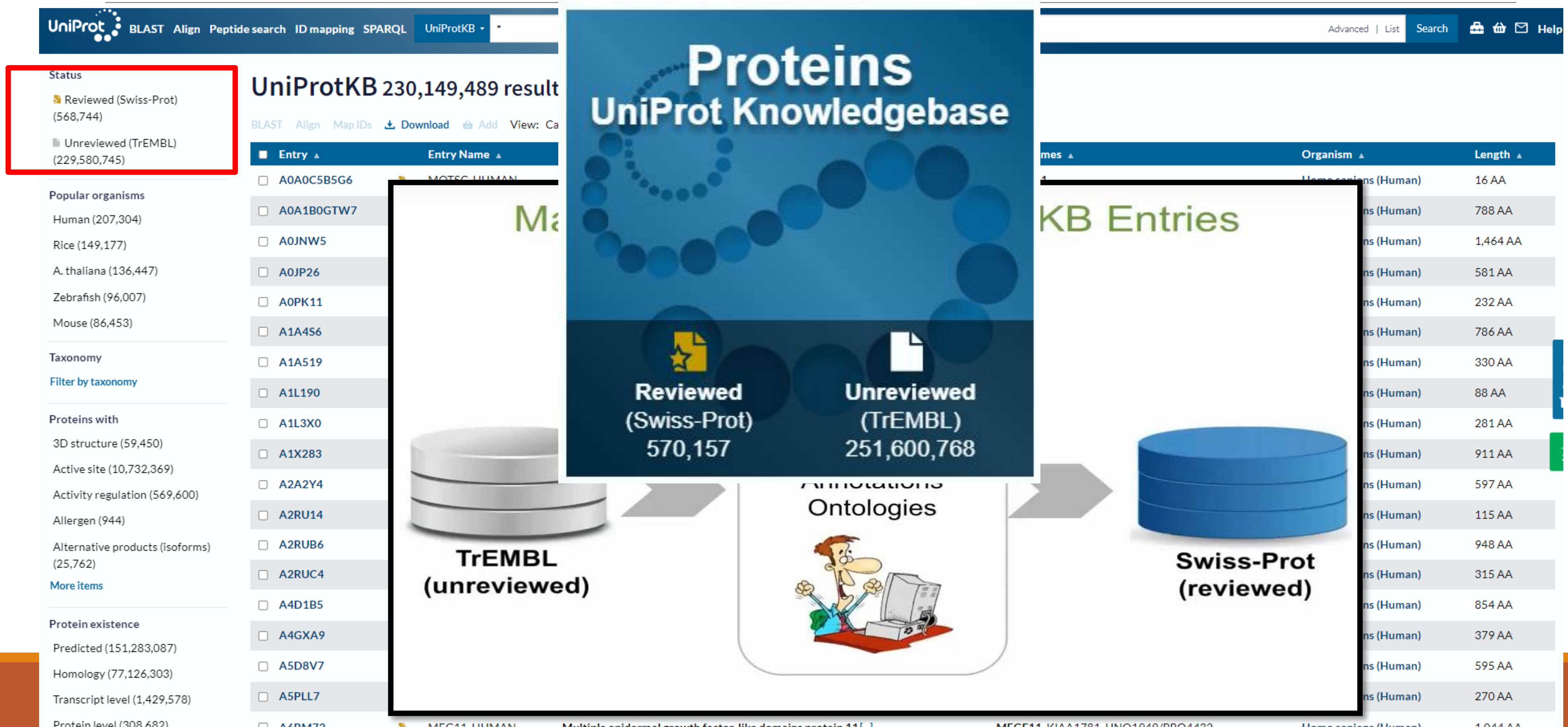
Examples: Insulin, APP, Human, P05067, organism_id:9606

UniProt is the world's leading high-quality, comprehensive and freely accessible resource of protein sequence and functional information. Cite UniProt

We need your help to understand ho… …a is reused by biomedical resources! We have developed 2 surveys for users of biomedical resources and for resource providers . Please help by filling the appro… …e one in by February 21

Proteinové databáze: UniProt

http://www.uniprot.org/



Status

Reviewed (Swiss-Prot) (568,744)

Unreviewed (TrEMBL) (229,580,745)

Popular organisms

- Human (207,304)
- Rice (149,177)
- A. thaliana (136,447)
- Zebrafish (96,007)
- Mouse (86,453)

Taxonomy

Filter by taxonomy

Proteins with

- 3D structure (59,450)
- Active site (10,732,369)
- Activity regulation (569,600)
- Allergen (944)
- Alternative products (isoforms) (25,762)

More items

Protein existence

- Predicted (151,283,087)
- Homology (77,126,303)
- Transcript level (1,429,578)
- Protein level (308,682)

UniProtKB 230,149,489 result

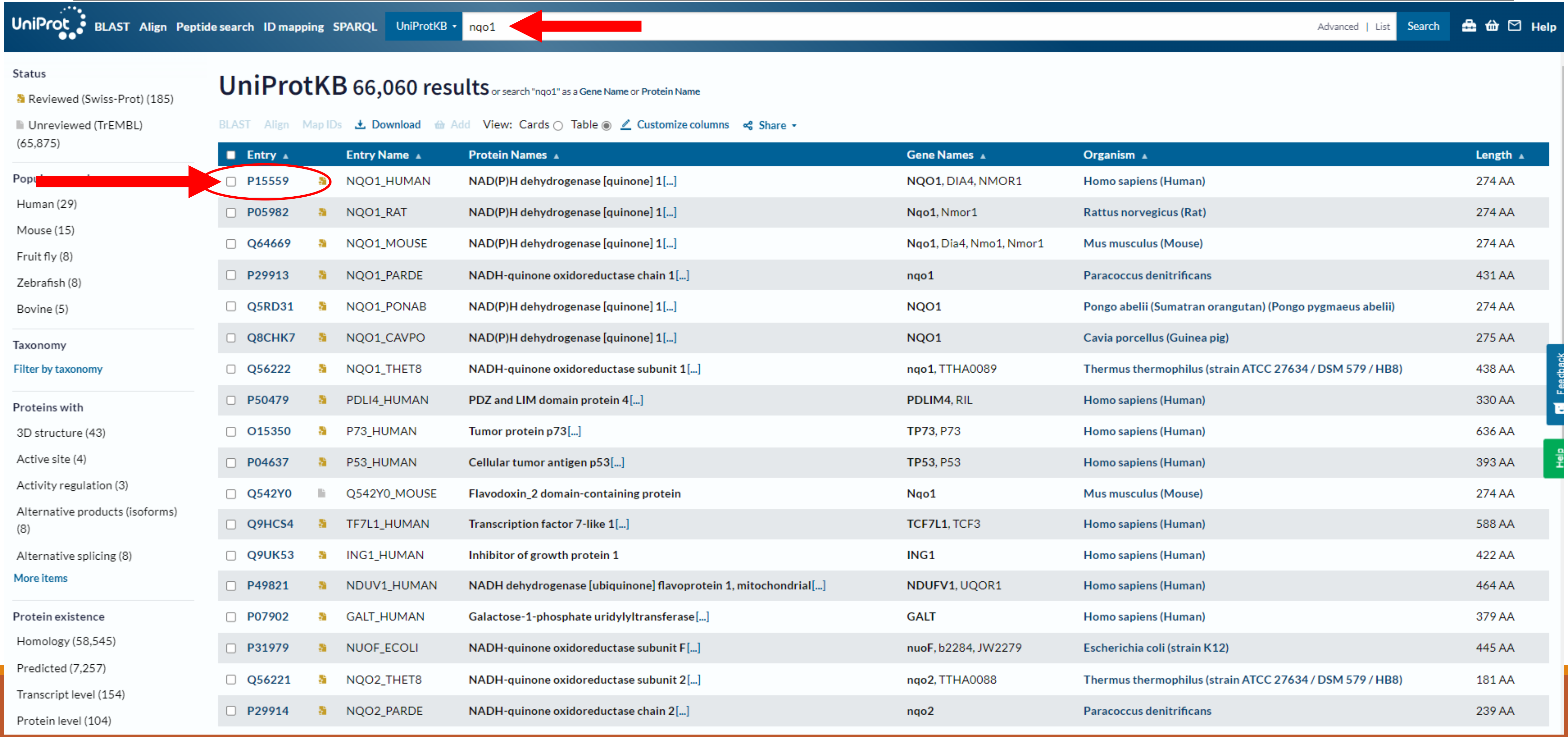
Entry	Entry Name	mes	Organism	Length
A0A0C5B5G6	MOTSC_HUMAN		Homo sapiens (Human)	16 AA
A0A1B0GTW7			ns (Human)	788 AA
A0JNW5			ns (Human)	1,464 AA
A0JP26			ns (Human)	581 AA
A0PK11			ns (Human)	232 AA
A1A4S6			ns (Human)	786 AA
A1A519			ns (Human)	330 AA
A1L190			ns (Human)	88 AA
A1L3X0			ns (Human)	281 AA
A1X283			ns (Human)	911 AA
A2A2Y4			ns (Human)	597 AA
A2RU14			ns (Human)	115 AA
A2RUB6			ns (Human)	948 AA
A2RUC4			ns (Human)	315 AA
A4D1B5			ns (Human)	854 AA
A4GXA9			ns (Human)	379 AA
A5D8V7			ns (Human)	595 AA
A5PLL7			ns (Human)	270 AA
A6BM72	MEG11_HUMAN	Multiple epidermal growth factor-like domains protein 11 [...] MEGF11 KIAA1781 UNQ1949/PRO4432	Homo sapiens (Human)	1,044 AA

Reviewed (Swiss-Prot) 570,157

Unreviewed (TrEMBL) 251,600,768

Proteinové databáze: UniProt

http://www.uniprot.org/



Status

Reviewed (Swiss-Prot) (185)

Unreviewed (TrEMBL) (65,875)

Popu

Human (29)

Mouse (15)

Fruit fly (8)

Zebrafish (8)

Bovine (5)

Taxonomy

Filter by taxonomy

Proteins with

3D structure (43)

Active site (4)

Activity regulation (3)

Alternative products (isoforms) (8)

Alternative splicing (8)

More items

Protein existence

Homology (58,545)

Predicted (7,257)

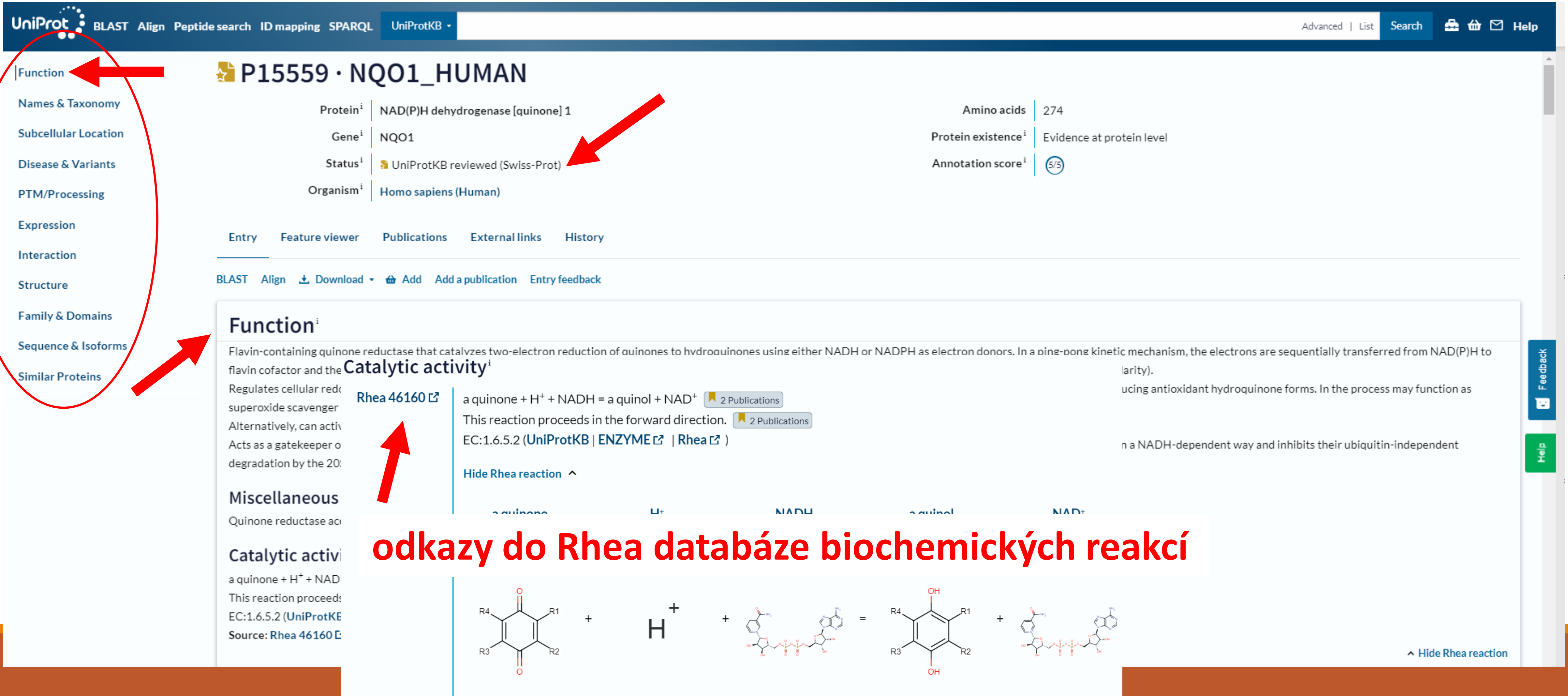
Transcript level (154)

Protein level (104)

UniProtKB 66,060 results or search "nqo1" as a Gene Name or Protein Name

Entry	Entry Name	Protein Names	Gene Names	Organism	Length
P15559	NQO1_HUMAN	NAD(P)H dehydrogenase [quinone] 1[...]	NQO1, DIA4, NMOR1	Homo sapiens (Human)	274 AA
P05982	NQO1_RAT	NAD(P)H dehydrogenase [quinone] 1[...]	Nqo1, Nmor1	Rattus norvegicus (Rat)	274 AA
Q64669	NQO1_MOUSE	NAD(P)H dehydrogenase [quinone] 1[...]	Nqo1, Dia4, Nmo1, Nmor1	Mus musculus (Mouse)	274 AA
P29913	NQO1_PARDE	NADH-quinone oxidoreductase chain 1[...]	nqo1	Paracoccus denitrificans	431 AA
Q5RD31	NQO1_PONAB	NAD(P)H dehydrogenase [quinone] 1[...]	NQO1	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)	274 AA
Q8CHK7	NQO1_CAVPO	NAD(P)H dehydrogenase [quinone] 1[...]	NQO1	Cavia porcellus (Guinea pig)	275 AA
Q56222	NQO1_THET8	NADH-quinone oxidoreductase subunit 1[...]	nqo1, TTHA0089	Thermus thermophilus (strain ATCC 27634 / DSM 579 / HB8)	438 AA
P50479	PDLI4_HUMAN	PDZ and LIM domain protein 4[...]	PDLIM4, RIL	Homo sapiens (Human)	330 AA
O15350	P73_HUMAN	Tumor protein p73[...]	TP73, P73	Homo sapiens (Human)	636 AA
P04637	P53_HUMAN	Cellular tumor antigen p53[...]	TP53, P53	Homo sapiens (Human)	393 AA
Q542Y0	Q542Y0_MOUSE	Flavodoxin_2 domain-containing protein	Nqo1	Mus musculus (Mouse)	274 AA
Q9HCS4	TF7L1_HUMAN	Transcription factor 7-like 1[...]	TCF7L1, TCF3	Homo sapiens (Human)	588 AA
Q9UK53	ING1_HUMAN	Inhibitor of growth protein 1	ING1	Homo sapiens (Human)	422 AA
P49821	NDUV1_HUMAN	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial[...]	NDUFV1, UQOR1	Homo sapiens (Human)	464 AA
P07902	GALT_HUMAN	Galactose-1-phosphate uridylyltransferase[...]	GALT	Homo sapiens (Human)	379 AA
P31979	NUOF_ECOLI	NADH-quinone oxidoreductase subunit F[...]	nuoF, b2284, JW2279	Escherichia coli (strain K12)	445 AA
Q56221	NQO2_THET8	NADH-quinone oxidoreductase subunit 2[...]	nqo2, TTHA0088	Thermus thermophilus (strain ATCC 27634 / DSM 579 / HB8)	181 AA
P29914	NQO2_PARDE	NADH-quinone oxidoreductase chain 2[...]	nqo2	Paracoccus denitrificans	239 AA

Proteinové databáze: UniProt



P15559 · NQO1_HUMAN

Protein: NAD(P)H dehydrogenase [quinone] 1

Gene: NQO1

Status: UniProtKB reviewed (Swiss-Prot)

Organism: Homo sapiens (Human)

Amino acids: 274

Protein existence: Evidence at protein level

Annotation score: 5/5

Function

Flavin-containing quinone reductase that catalyzes two-electron reduction of quinones to hydroquinones using either NADH or NADPH as electron donors. In a ping-pong kinetic mechanism, the electrons are sequentially transferred from NAD(P)H to flavin cofactor and the … arity).

Regulates cellular red… ucing antioxidant hydroquinone forms. In the process may function as superoxide scavenger…

Alternatively, can acti…

Acts as a gatekeeper o… n a NADH-dependent way and inhibits their ubiquitin-independent degradation by the 20…

Miscellaneous

Quinone reductase ac…

Catalytic activi…

a quinone + H^+ + NAD…

This reaction proceed…

EC:1.6.5.2 (UniProtKE…

Source: Rhea 46160

Catalytic activity

Rhea 46160

a quinone + H^+ + NADH = a quinol + NAD^+ 2 Publications

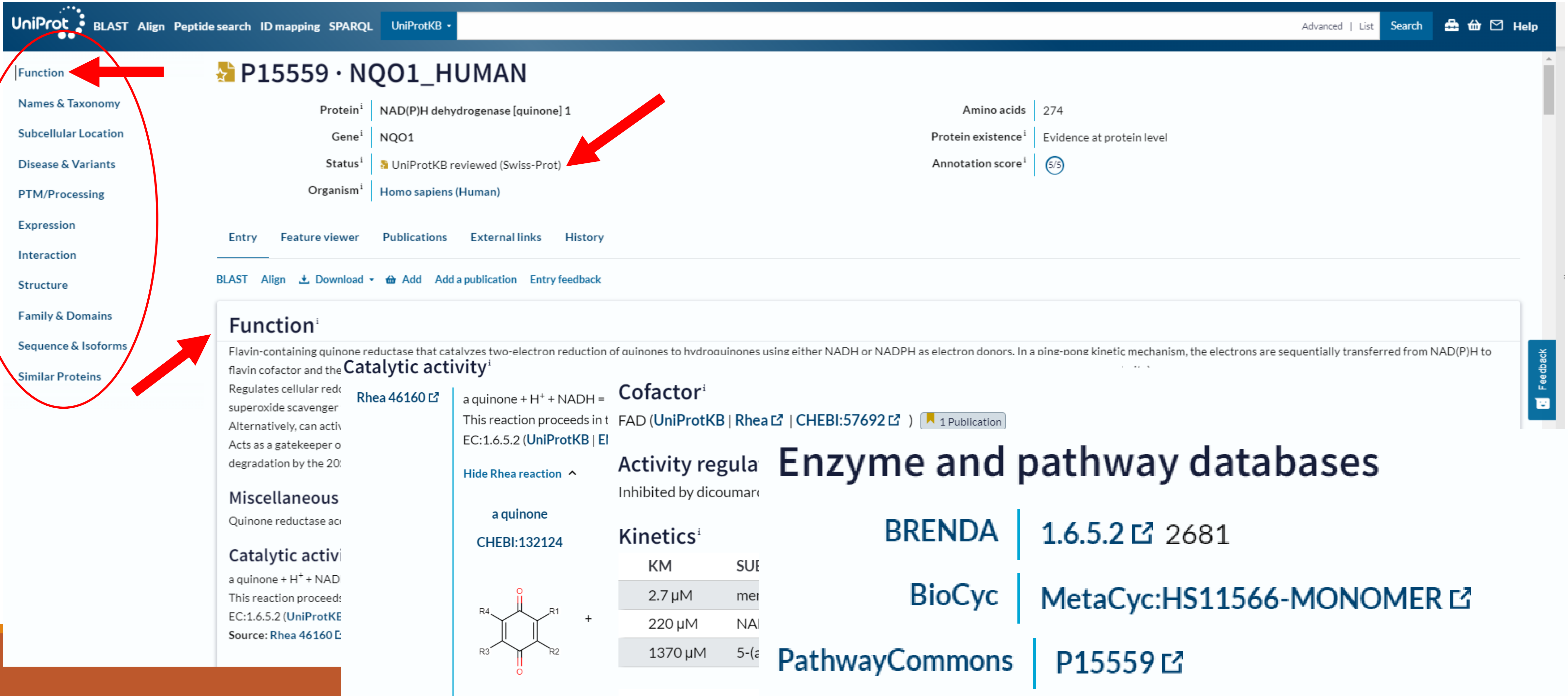
This reaction proceeds in the forward direction. 2 Publications

EC:1.6.5.2 (UniProtKB | ENZYME | Rhea)

Hide Rhea reaction

odkazy do Rhea databáze biochemických reakcí

Proteinové databáze: UniProt



P15559 · NQO1_HUMAN

Protein: NAD(P)H dehydrogenase [quinone] 1
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Regulates cellular red
superoxide scavenger
Alternatively, can acti
Acts as a gatekeeper o
degradation by the 20

Miscellaneous

Quinone reductase ac

Catalytic activi

a quinone + H⁺ + NAD
This reaction proceed
EC:1.6.5.2 (UniProtKE
Source: Rhea 46160

Catalytic activity

Rhea 46160

a quinone + H^+ + NADH =
This reaction proceeds in t
EC:1.6.5.2 (UniProtKB | El

Hide Rhea reaction

a quinone
CHEBI:132124

Cofactor

FAD (UniProtKB | Rhea | CHEBI:57692) 1 Publication

Activity regula

Inhibited by dicoumar

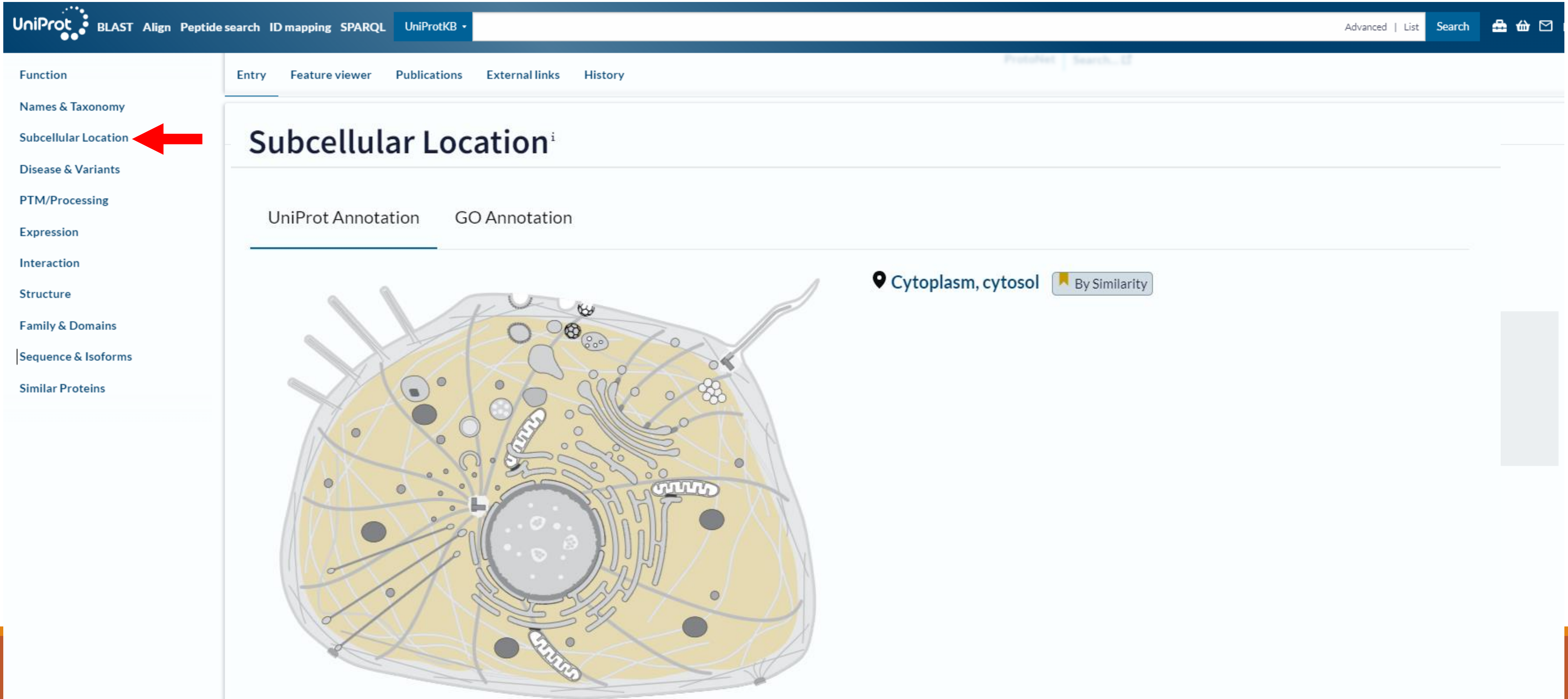
Kinetics

KM	SUE
2.7 μM	mer
220 μM	NAI
1370 μM	5-(a

Enzyme and pathway databases

BRENDA	1.6.5.2 2681
BioCyc	MetaCyc:HS11566-MONOMER
PathwayCommons	P15559

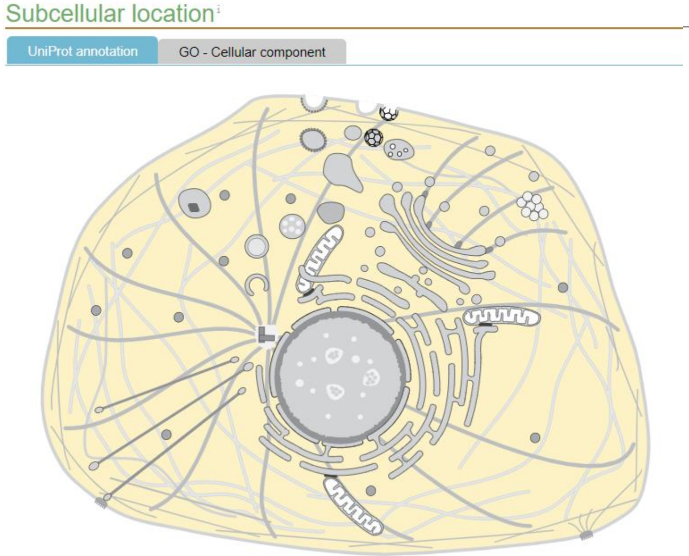
Proteinové databáze: UniProt

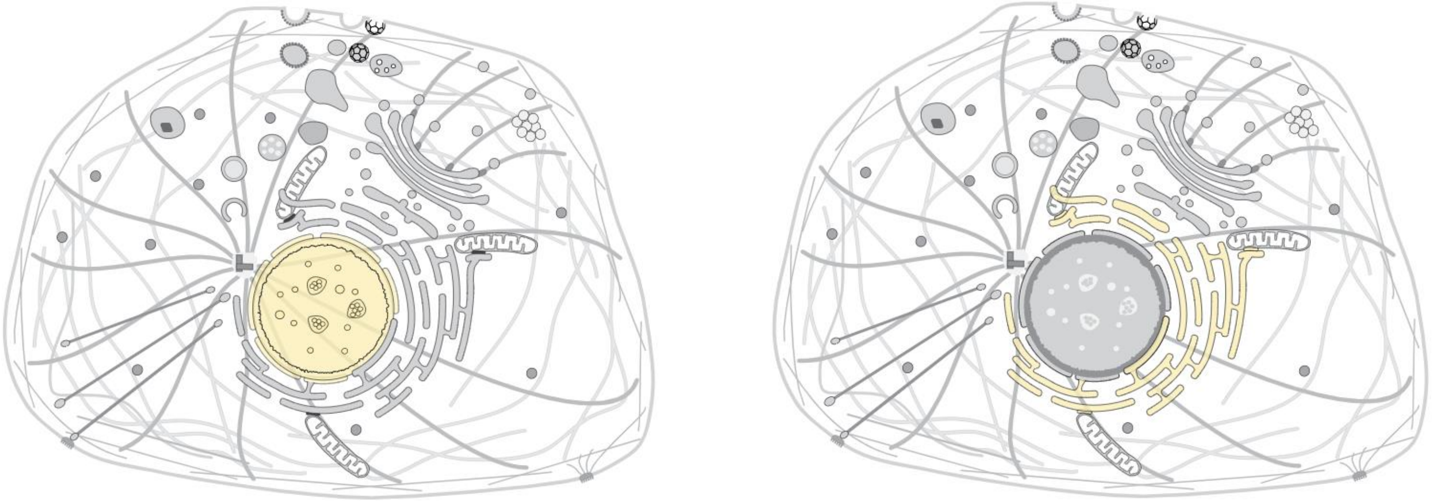


Subcellular Location

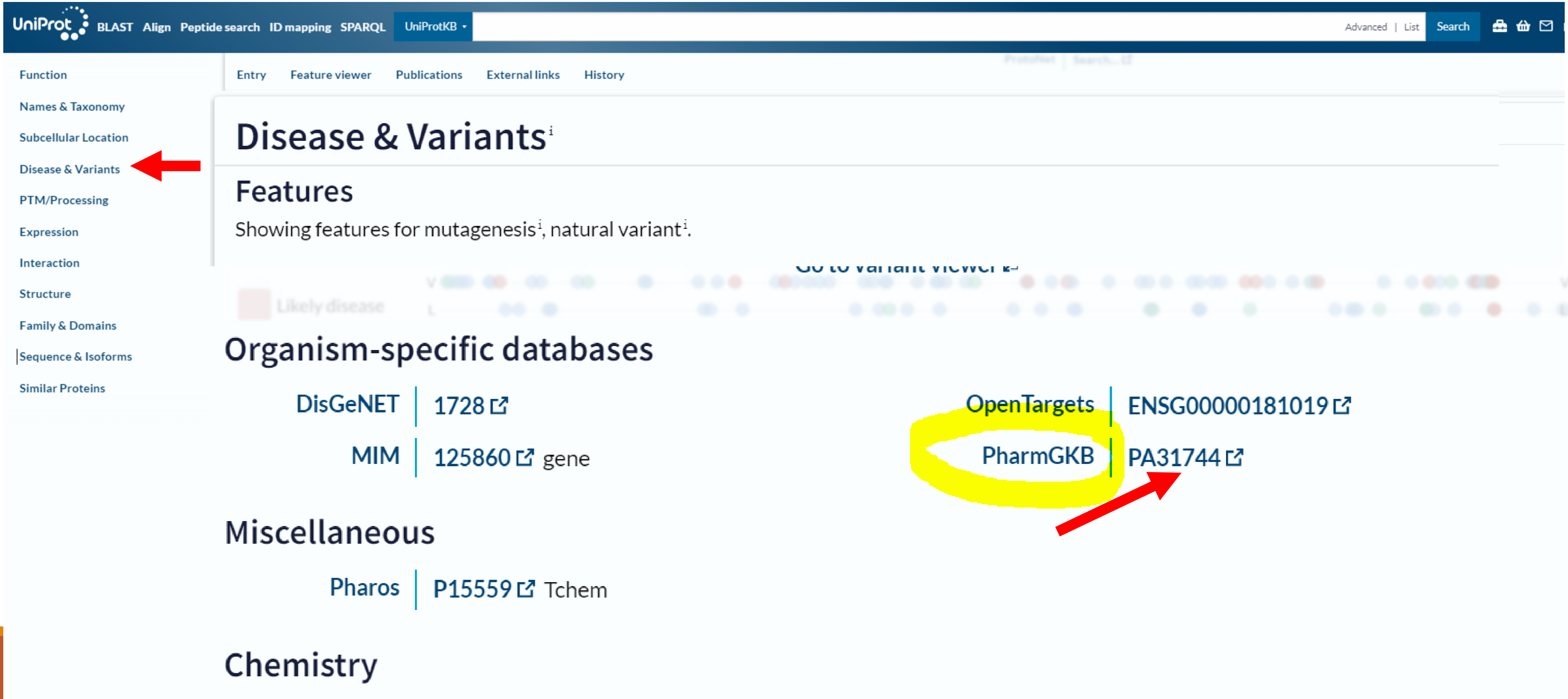
Cytoplasm, cytosol By Similarity

UNIPROT / subcelulární lokalizace





Proteinové databáze: UniProt



Disease & Variants

Features

Showing features for mutagenesis, natural variant.

Organism-specific databases

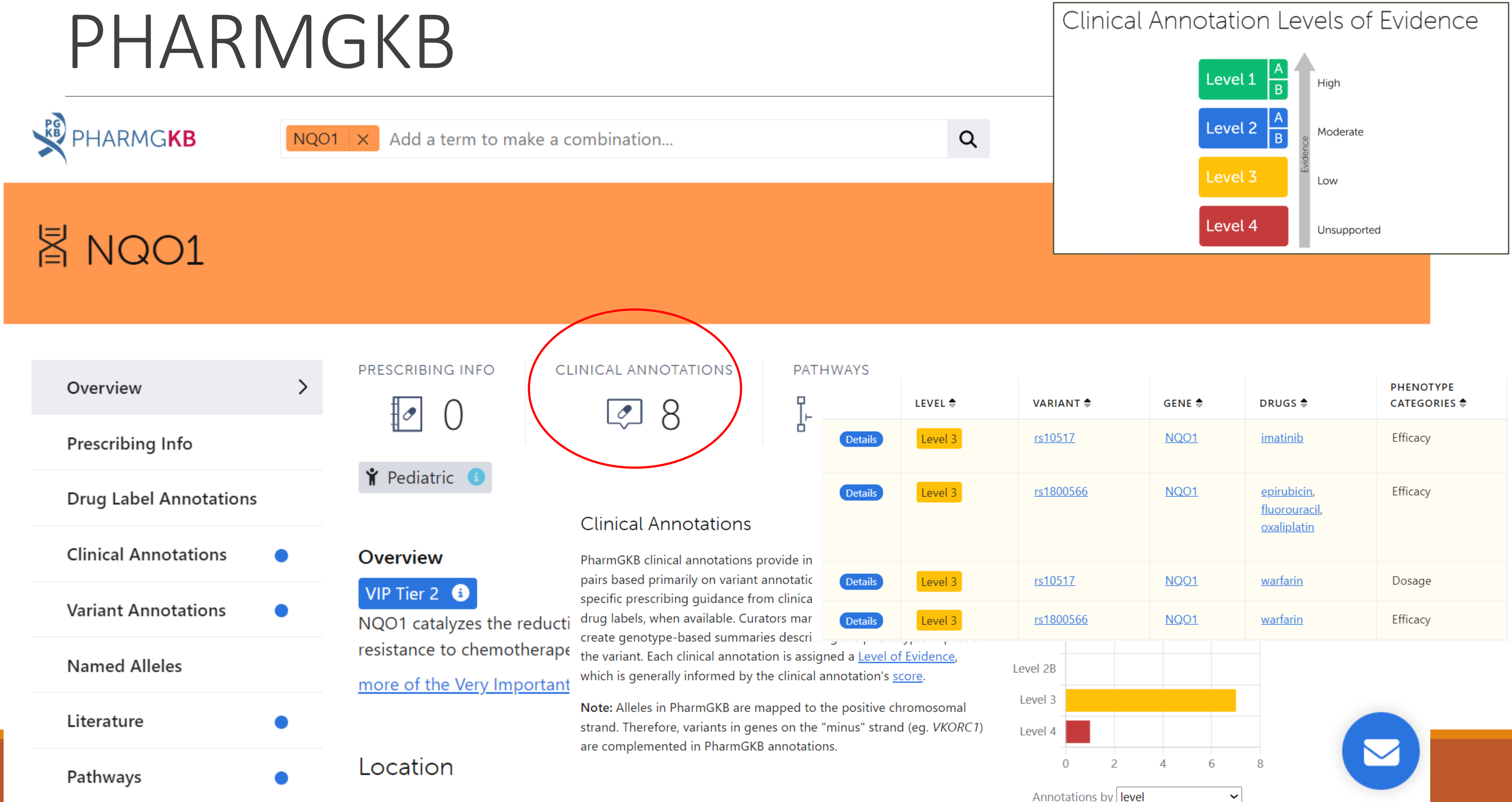
DisGeNET	1728	OpenTargets	ENSG00000181019
MIM	125860 gene	PharmGKB	PA31744

Miscellaneous

Pharos	P15559 Tchem

Chemistry

PHARMGKB



Clinical Annotation Levels of Evidence

NQO1

PRESCRIBING INFO 0

CLINICAL ANNOTATIONS 8

PATHWAYS

	LEVEL	VARIANT	GENE	DRUGS	PHENOTYPE CATEGORIES
Details	Level 3	rs10517	NQO1	imatinib	Efficacy
Details	Level 3	rs1800566	NQO1	epirubicin, fluorouracil, oxaliplatin	Efficacy
Details	Level 3	rs10517	NQO1	warfarin	Dosage
Details	Level 3	rs1800566	NQO1	warfarin	Efficacy

Overview

VIP Tier 2

NQO1 catalyzes the reducti
resistance to chemotherape
more of the Very Important

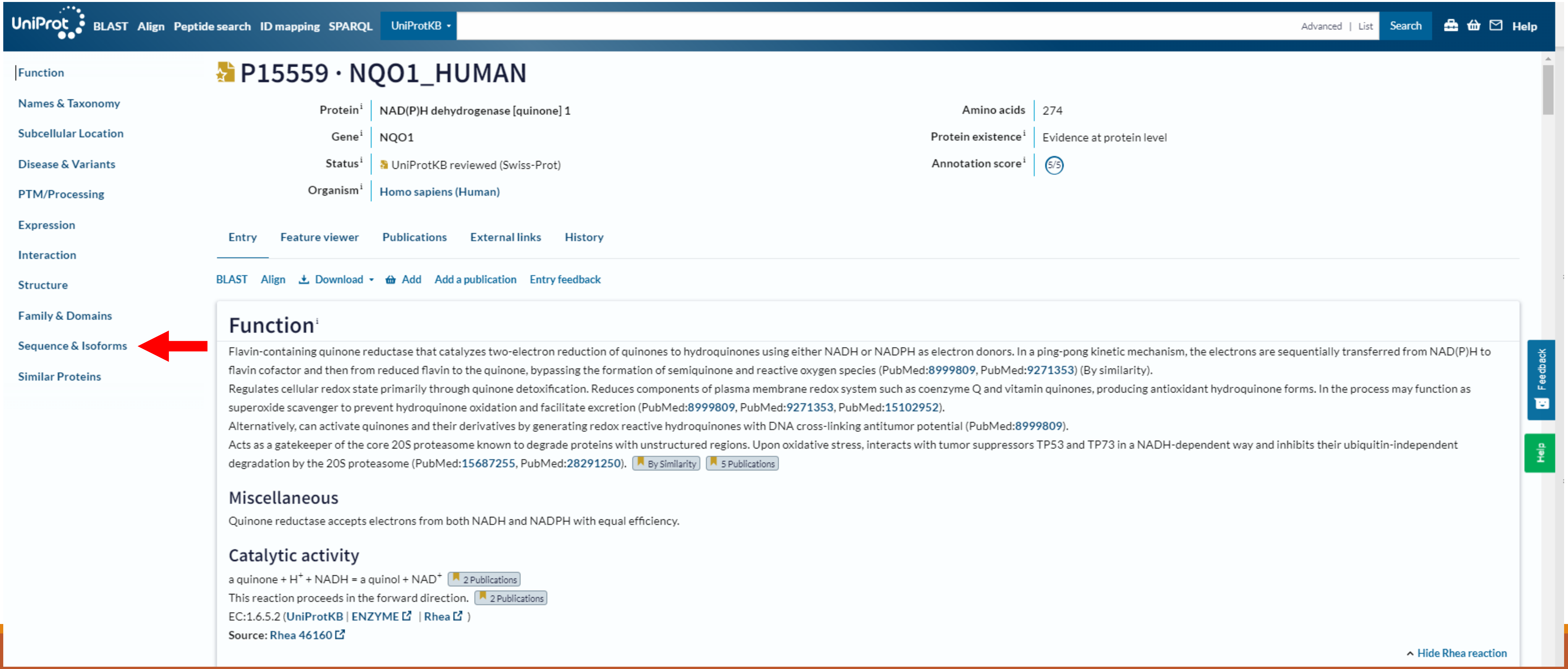
Clinical Annotations

PharmGKB clinical annotations provide in
pairs based primarily on variant annotatic
specific prescribing guidance from clinica
drug labels, when available. Curators mar
create genotype-based summaries descri
the variant. Each clinical annotation is assigned a Level of Evidence, which is generally informed by the clinical annotation's score.

Note: Alleles in PharmGKB are mapped to the positive chromosomal strand. Therefore, variants in genes on the "minus" strand (eg. *VKORC1*) are complemented in PharmGKB annotations.

Location

Proteinové databáze: UniProt



P15559 · NQO1_HUMAN

Protein NAD(P)H dehydrogenase [quinone] 1
Gene NQO1
Status UniProtKB reviewed (Swiss-Prot)
Organism Homo sapiens (Human)
Amino acids 274
Protein existence Evidence at protein level
Annotation score 5/5

Function

Flavin-containing quinone reductase that catalyzes two-electron reduction of quinones to hydroquinones using either NADH or NADPH as electron donors. In a ping-pong kinetic mechanism, the electrons are sequentially transferred from NAD(P)H to flavin cofactor and then from reduced flavin to the quinone, bypassing the formation of semiquinone and reactive oxygen species (PubMed:8999809, PubMed:9271353) (By similarity).
Regulates cellular redox state primarily through quinone detoxification. Reduces components of plasma membrane redox system such as coenzyme Q and vitamin quinones, producing antioxidant hydroquinone forms. In the process may function as superoxide scavenger to prevent hydroquinone oxidation and facilitate excretion (PubMed:8999809, PubMed:9271353, PubMed:15102952).
Alternatively, can activate quinones and their derivatives by generating redox reactive hydroquinones with DNA cross-linking antitumor potential (PubMed:8999809).
Acts as a gatekeeper of the core 20S proteasome known to degrade proteins with unstructured regions. Upon oxidative stress, interacts with tumor suppressors TP53 and TP73 in a NADH-dependent way and inhibits their ubiquitin-independent degradation by the 20S proteasome (PubMed:15687255, PubMed:28291250). By Similarity 5 Publications

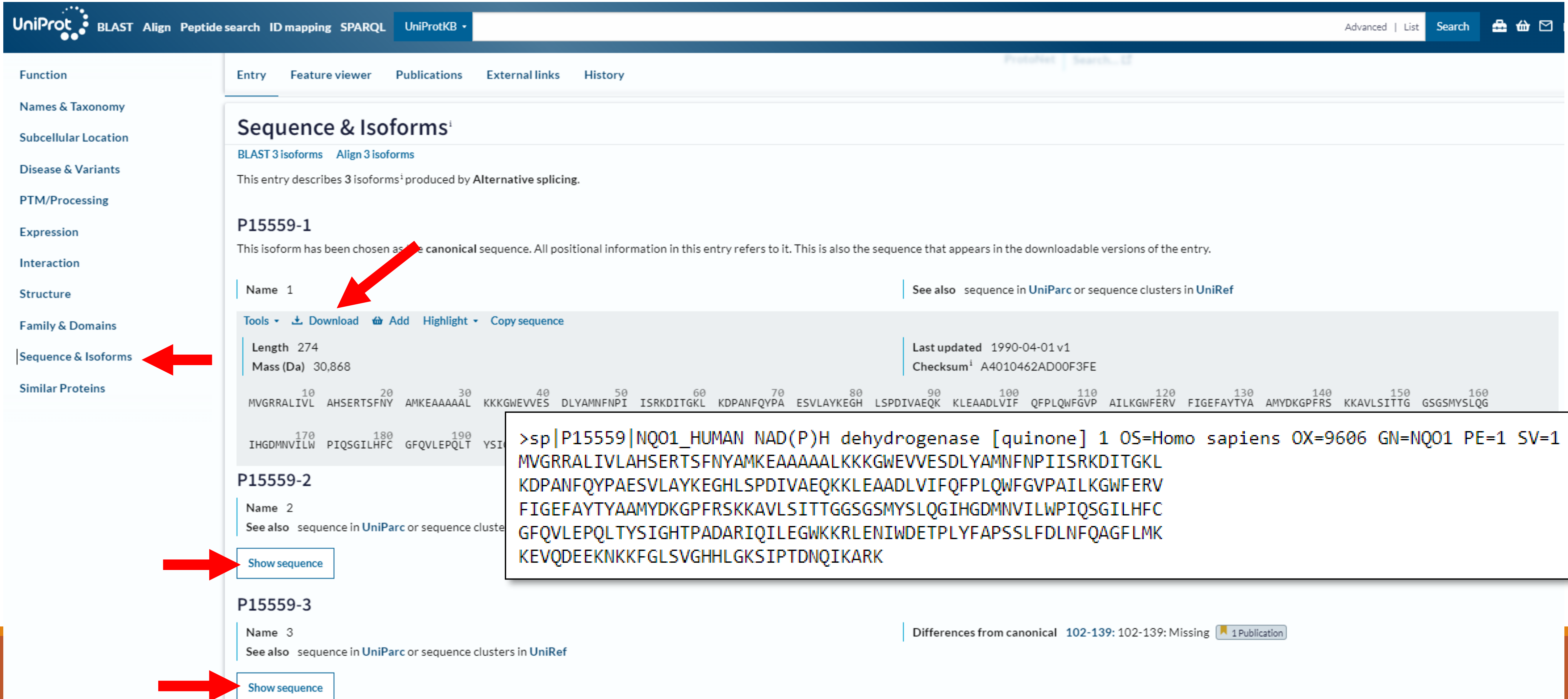
Miscellaneous

Quinone reductase accepts electrons from both NADH and NADPH with equal efficiency.

Catalytic activity

a quinone + H^+ + NADH = a quinol + NAD^+ 2 Publications
This reaction proceeds in the forward direction. 2 Publications
EC:1.6.5.2 (UniProtKB | ENZYME | Rhea)
Source: Rhea 46160

Proteinové databáze: UniProt



Sequence & Isoforms

BLAST 3 isoforms   Align 3 isoforms

This entry describes **3** isoforms produced by **Alternative splicing**.

P15559-1

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

See also sequence in UniParc or sequence clusters in UniRef

Length 274
Mass (Da) 30,868

Last updated 1990-04-01 v1
Checksum A4010462AD00F3FE

```
        10         20         30         40         50         60         70         80         90        100        110        120        130        140        150        160
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       170        180        190
IHGDMNVILW PIQSGILHFC GFQVLEPQLT YSI
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```
>sp|P15559|NQO1_HUMAN NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens OX=9606 GN=NQO1 PE=1 SV=1
MVGRRALIVLAHSERTSFNYAMKEAAAAALKKKGWEVVESDLYAMNFNPIISRKDITGKL
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FIGEFAYTYAAMYDKGPFRSKKAVLSITTGGSGSMYSLQGIHGDMNVILWPIQSGILHFC
GFQVLEPQLTYSIGHTPADARIQILEGWKKRLENIWDETPLYFAPSSLFDLNFQAGFLMK
KEVQDEEKNKKFGLSVGHHLGKSIPTDNQIKARK
```

P15559-2

Name 2

See also sequence in UniParc or sequence cluste

P15559-3

Name 3

See also sequence in UniParc or sequence clusters in UniRef

Differences from canonical 102-139: 102-139: Missing 1 Publication

FASTA (a RAW) formát

název odvozen:

FASTA = populární program pro porovnávání sekvencí a prohledávání databází

W.R. Pearson a D.J. Lipman 1988

následující formát sekvence:

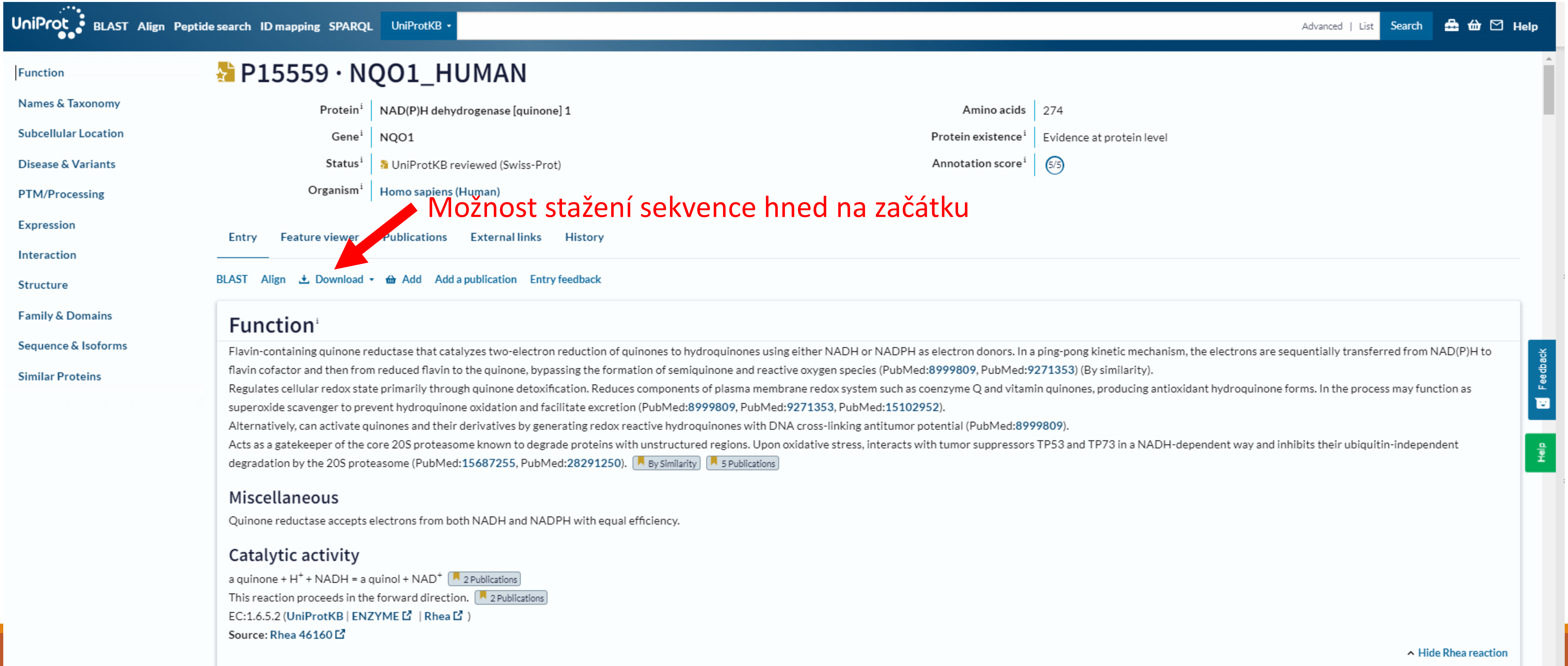
```
>NQO1_homo
MVGRRALIVLAHSERTSFNYAMKEAAAAA
LKKKGWEVVESDLYAMNFNPIISRKDITG
KLKDPANFQYPA
```

```
MVGRRALIVLAHSERTSFNYAMKEAAAAA
LKKKGWEVVESDLYAMNFNPIISRKDITG
KLKDPANFQYPA
```

1. „definiční“ řádek (hlavička) začíná **>** a obsahuje unikátní identifikátor, následovaný krátkým popisem (nemusí být).

2. řádek – vlastní sekvence (DNA/protein- v jedno-písmenném kódování) až po další symbol >, určující začátek další sekvence.

Proteinové databáze: UniProt



Možnost stažení sekvence hned na začátku

P15559 · NQO1_HUMAN

Protein	NAD(P)H dehydrogenase [quinone] 1	Amino acids	274
Gene	NQO1	Protein existence	Evidence at protein level
Status	UniProtKB reviewed (Swiss-Prot)	Annotation score	5/5
Organism	Homo sapiens (Human)		

Function

Flavin-containing quinone reductase that catalyzes two-electron reduction of quinones to hydroquinones using either NADH or NADPH as electron donors. In a ping-pong kinetic mechanism, the electrons are sequentially transferred from NAD(P)H to flavin cofactor and then from reduced flavin to the quinone, bypassing the formation of semiquinone and reactive oxygen species (PubMed:8999809, PubMed:9271353) (By similarity).
Regulates cellular redox state primarily through quinone detoxification. Reduces components of plasma membrane redox system such as coenzyme Q and vitamin quinones, producing antioxidant hydroquinone forms. In the process may function as superoxide scavenger to prevent hydroquinone oxidation and facilitate excretion (PubMed:8999809, PubMed:9271353, PubMed:15102952).
Alternatively, can activate quinones and their derivatives by generating redox reactive hydroquinones with DNA cross-linking antitumor potential (PubMed:8999809).
Acts as a gatekeeper of the core 20S proteasome known to degrade proteins with unstructured regions. Upon oxidative stress, interacts with tumor suppressors TP53 and TP73 in a NADH-dependent way and inhibits their ubiquitin-independent degradation by the 20S proteasome (PubMed:15687255, PubMed:28291250). By Similarity 5 Publications

Miscellaneous

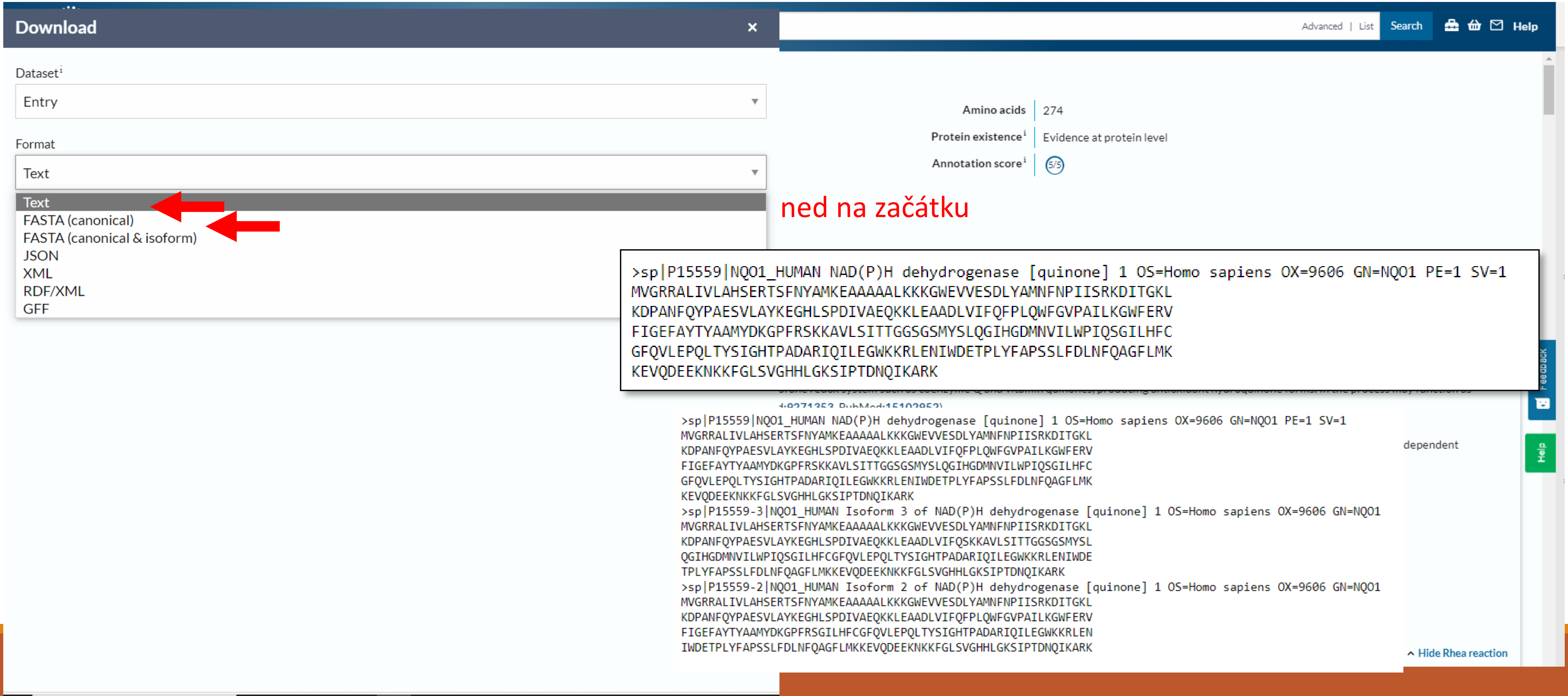
Quinone reductase accepts electrons from both NADH and NADPH with equal efficiency.

Catalytic activity

a quinone + H^+ + NADH = a quinol + NAD^+ 2 Publications
This reaction proceeds in the forward direction. 2 Publications
EC:1.6.5.2 (UniProtKB | ENZYME | Rhea)
Source: Rhea 46160

Hide Rhea reaction

Proteinové databáze: UniProt



Dataset: Entry

Format: Text

Amino acids: 274

Protein existence: Evidence at protein level

Annotation score: 5/5

ned na začátku

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```

```
>sp|P15559|NQO1_HUMAN NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens OX=9606 GN=NQO1 PE=1 SV=1
MVGRRALIVLAHSERTSFNYAMKEAAAAALKKKGWEVVESDLYAMNFNPIISRKDITGKL
KDPANFQYPAESVLAYKEGHLSPDIVAEQKKLEAADLVIFQFPLQWFGVPAILKGWFERV
FIGEFAYTYAAMYDKGPFRSKKAVLSITTGGSGSMYSLQGIHGDMNVILWPIQSGILHFC
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KEVQDEEKNKKFGLSVGHHLGKSIPTDNQIKARK
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>sp|P15559-2|NQO1_HUMAN Isoform 2 of NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens OX=9606 GN=NQO1
MVGRRALIVLAHSERTSFNYAMKEAAAAALKKKGWEVVESDLYAMNFNPIISRKDITGKL
KDPANFQYPAESVLAYKEGHLSPDIVAEQKKLEAADLVIFQFPLQWFGVPAILKGWFERV
FIGEFAYTYAAMYDKGPFRSGILHFCGFQVLEPQLTYSIGHTPADARIQILEGWKKRLEN
IWDETPLYFAPSSLFDLNFQAGFLMKKEVQDEEKNKKFGLSVGHHLGKSIPTDNQIKARK
```

dependent

Procvičování v UniProt

Najděte si „svou vlastní“ sekvenci

-podívejte se na: lokalizaci, počet isoforem…

- uložte si FASTA formát

Procvičování v UniProt

Najděte přístupový kód lidského cytochromu P450 isoformy 3A4 (CYP3A4)

Jakou má funkci a kde je lokalizován enzym Q9C0B1?

Jakou má funkci enzym O95251 a kolik má isoforem?

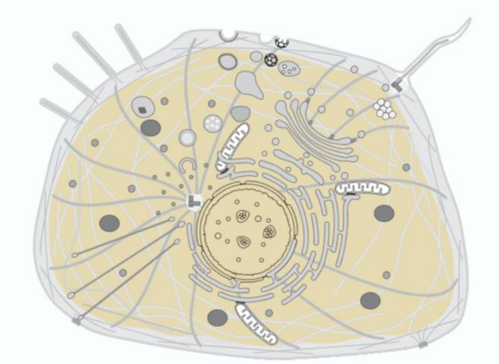
Procvičování v UniProt

Najděte přístupový kód lidského cytochromu P450 isoformy 3A4 (CYP3A4)

P08684

Jakou má funkci a kde je lokalizován enzym Q9C0B1?

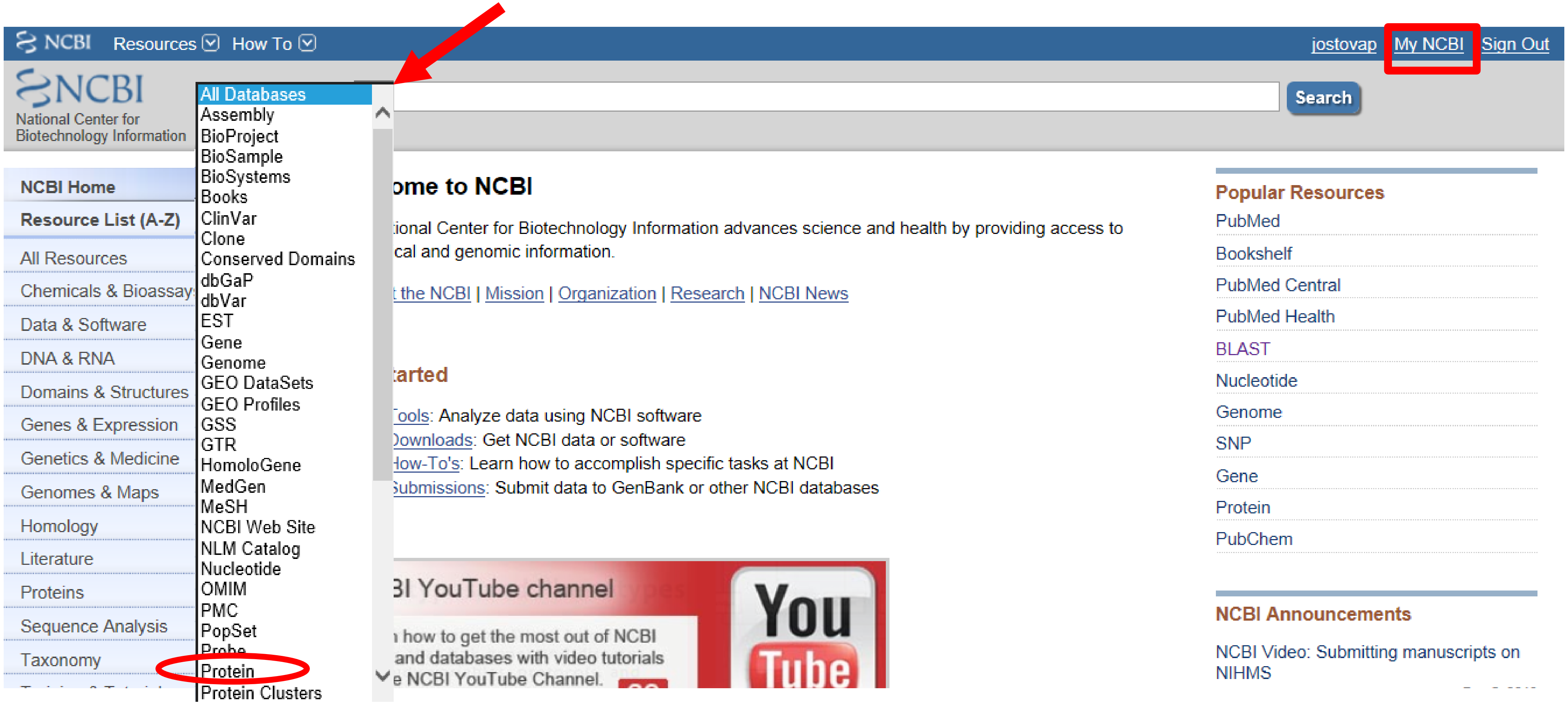
Alpha-ketoglutarate-dependent dioxygenase FTO



Jakou má funkci enzym O95251 a kolik má isoforem?

Histone acetyltransferase KAT7, 5 isoforem

Proteinové databáze: NCBI



ome to NCBI

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cal and genomic information.

the NCBI | Mission | Organization | Research | NCBI News

arted

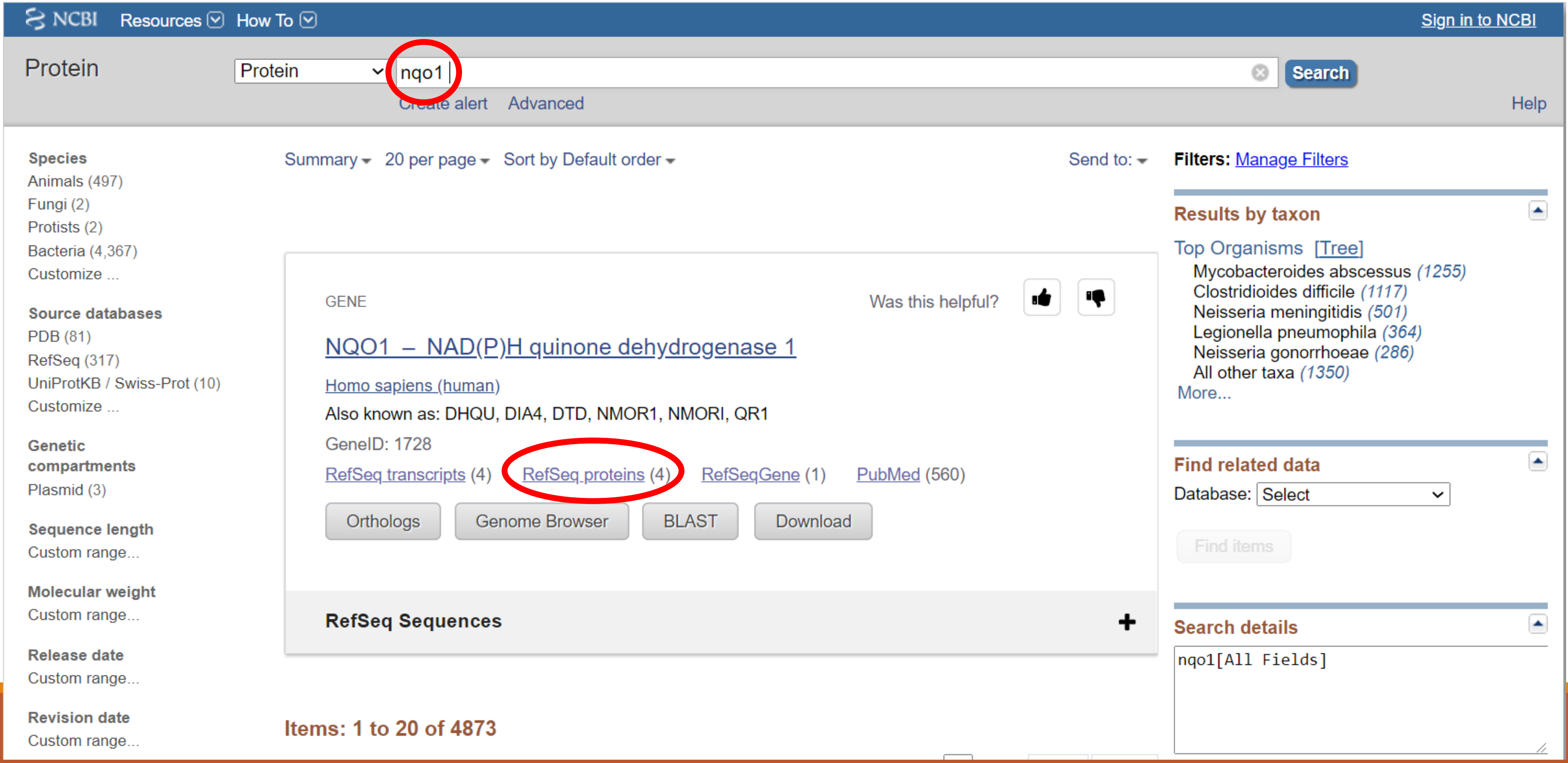
ools: Analyze data using NCBI software
ownloads: Get NCBI data or software
ow-To's: Learn how to accomplish specific tasks at NCBI
ubmissions: Submit data to GenBank or other NCBI databases

BI YouTube channel

how to get the most out of NCBI
and databases with video tutorials
e NCBI YouTube Channel.

NCBI Video: Submitting manuscripts on NIHMS

Proteinové databáze: NCBI



Protein: nqo1

GENE

NQO1 – NAD(P)H quinone dehydrogenase 1

Homo sapiens (human)

Also known as: DHQU, DIA4, DTD, NMOR1, NMORI, QR1

GeneID: 1728

RefSeq transcripts (4) RefSeq proteins (4) RefSeqGene (1) PubMed (560)

Items: 1 to 20 of 4873

Top Organisms:

- Mycobacteroides abscessus *(1255)*
- Clostridioides difficile *(1117)*
- Neisseria meningitidis *(501)*
- Legionella pneumophila *(364)*
- Neisseria gonorrhoeae *(286)*
- All other taxa *(1350)*

Search details:

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nqo1[All Fields]
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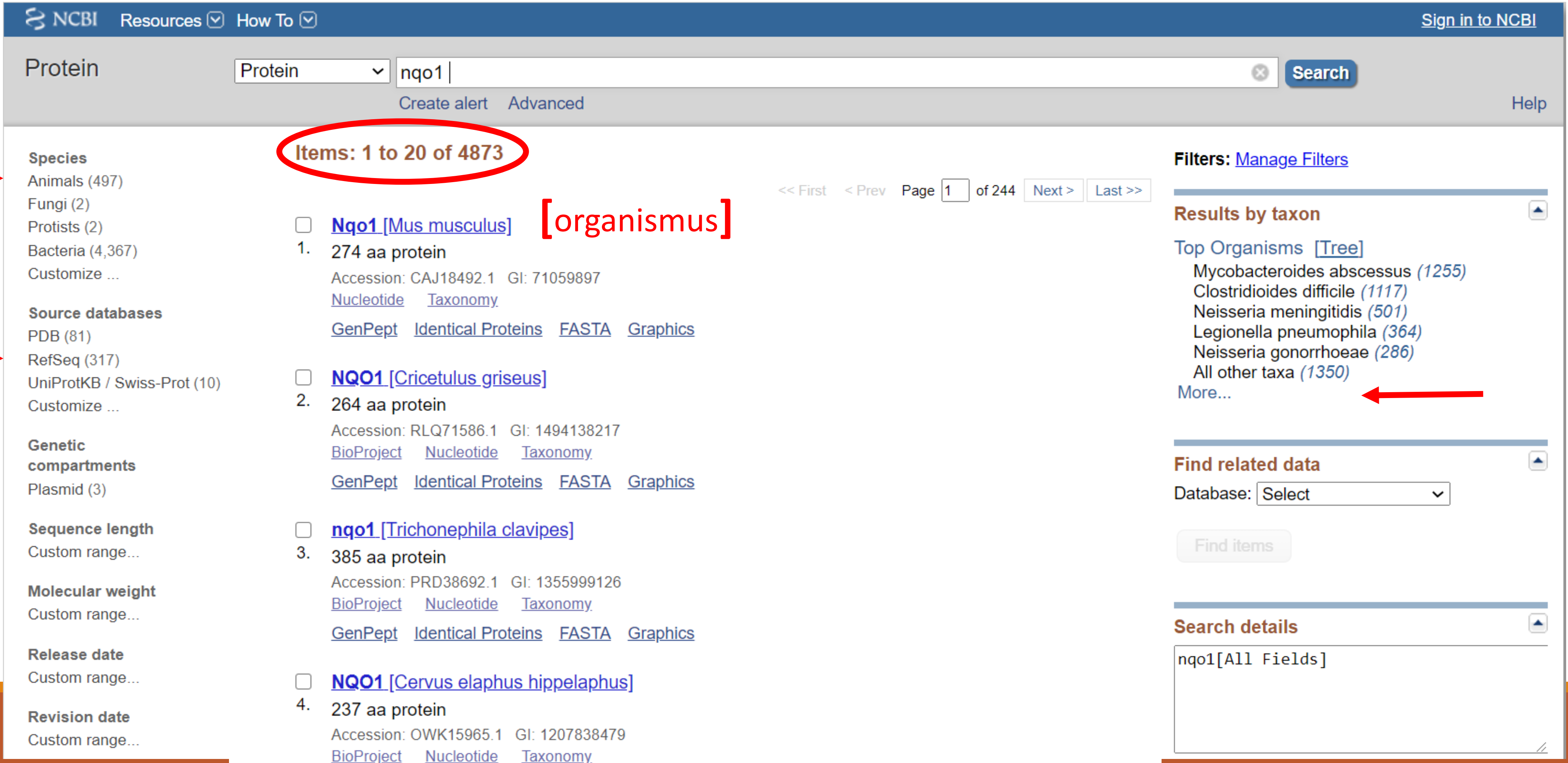
Proteinové databáze: NCBI



nqo1

Species
Animals (497)
Fungi (2)
Protists (2)
Bacteria (4,367)
Customize ...

Source databases
PDB (81)
RefSeq (317)
UniProtKB / Swiss-Prot (10)
Customize ...

Genetic compartments
Plasmid (3)

Sequence length
Custom range...

Molecular weight
Custom range...

Release date
Custom range...

Revision date
Custom range...

Items: 1 to 20 of 4873

<< First < Prev Page 1 of 244 Next > Last >>

[organismus]

☐ 1. **Nqo1** [Mus musculus]
274 aa protein
Accession: CAJ18492.1 GI: 71059897
Nucleotide Taxonomy
GenPept Identical Proteins FASTA Graphics

☐ 2. **NQO1** [Cricetulus griseus]
264 aa protein
Accession: RLQ71586.1 GI: 1494138217
BioProject Nucleotide Taxonomy
GenPept Identical Proteins FASTA Graphics

☐ 3. **nqo1** [Trichonephila clavipes]
385 aa protein
Accession: PRD38692.1 GI: 1355999126
BioProject Nucleotide Taxonomy
GenPept Identical Proteins FASTA Graphics

☐ 4. **NQO1** [Cervus elaphus hippelaphus]
237 aa protein
Accession: OWK15965.1 GI: 1207838479
BioProject Nucleotide Taxonomy

Filters: Manage Filters

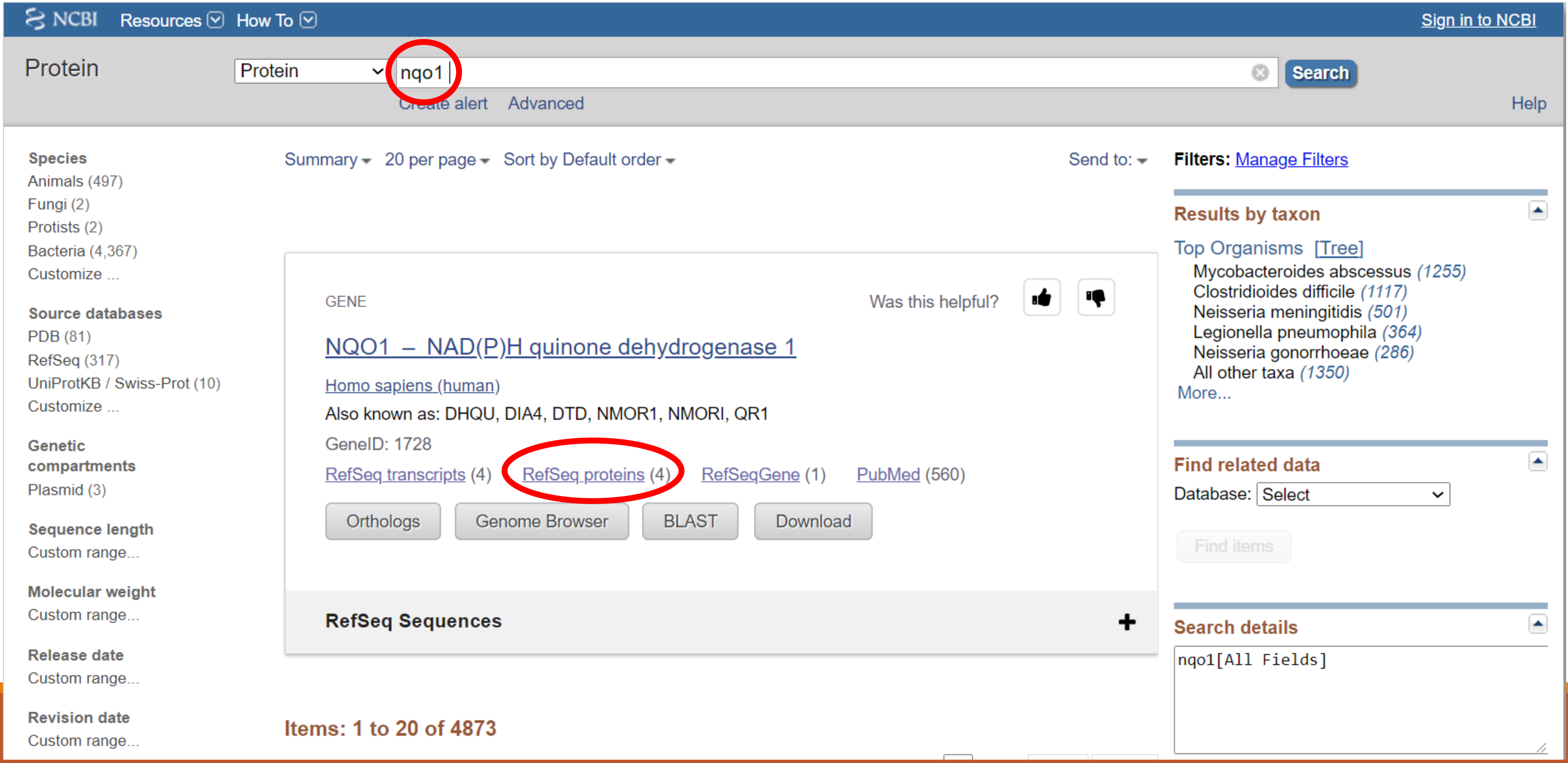
Results by taxon

Top Organisms [Tree]
Mycobacteroides abscessus *(1255)*
Clostridioides difficile *(1117)*
Neisseria meningitidis *(501)*
Legionella pneumophila *(364)*
Neisseria gonorrhoeae *(286)*
All other taxa *(1350)*
More...

Find related data
Database: Select
Find items

Search details
nqo1[All Fields]

Proteinové databáze: NCBI



Search: nqo1

Species
Animals (497)
Fungi (2)
Protists (2)
Bacteria (4,367)
Customize ...

Source databases
PDB (81)
RefSeq (317)
UniProtKB / Swiss-Prot (10)
Customize ...

Genetic compartments
Plasmid (3)

Sequence length
Custom range...

Molecular weight
Custom range...

Release date
Custom range...

Revision date
Custom range...

GENE

NQO1 – NAD(P)H quinone dehydrogenase 1

Homo sapiens (human)

Also known as: DHQU, DIA4, DTD, NMOR1, NMORI, QR1

GeneID: 1728

RefSeq transcripts (4) RefSeq proteins (4) RefSeqGene (1) PubMed (560)

Items: 1 to 20 of 4873

Filters: Manage Filters

Results by taxon

Top Organisms [Tree]
Mycobacteroides abscessus *(1255)*
Clostridioides difficile *(1117)*
Neisseria meningitidis *(501)*
Legionella pneumophila *(364)*
Neisseria gonorrhoeae *(286)*
All other taxa *(1350)*
More...

Find related data

Database: Select

Search details

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nqo1[All Fields]
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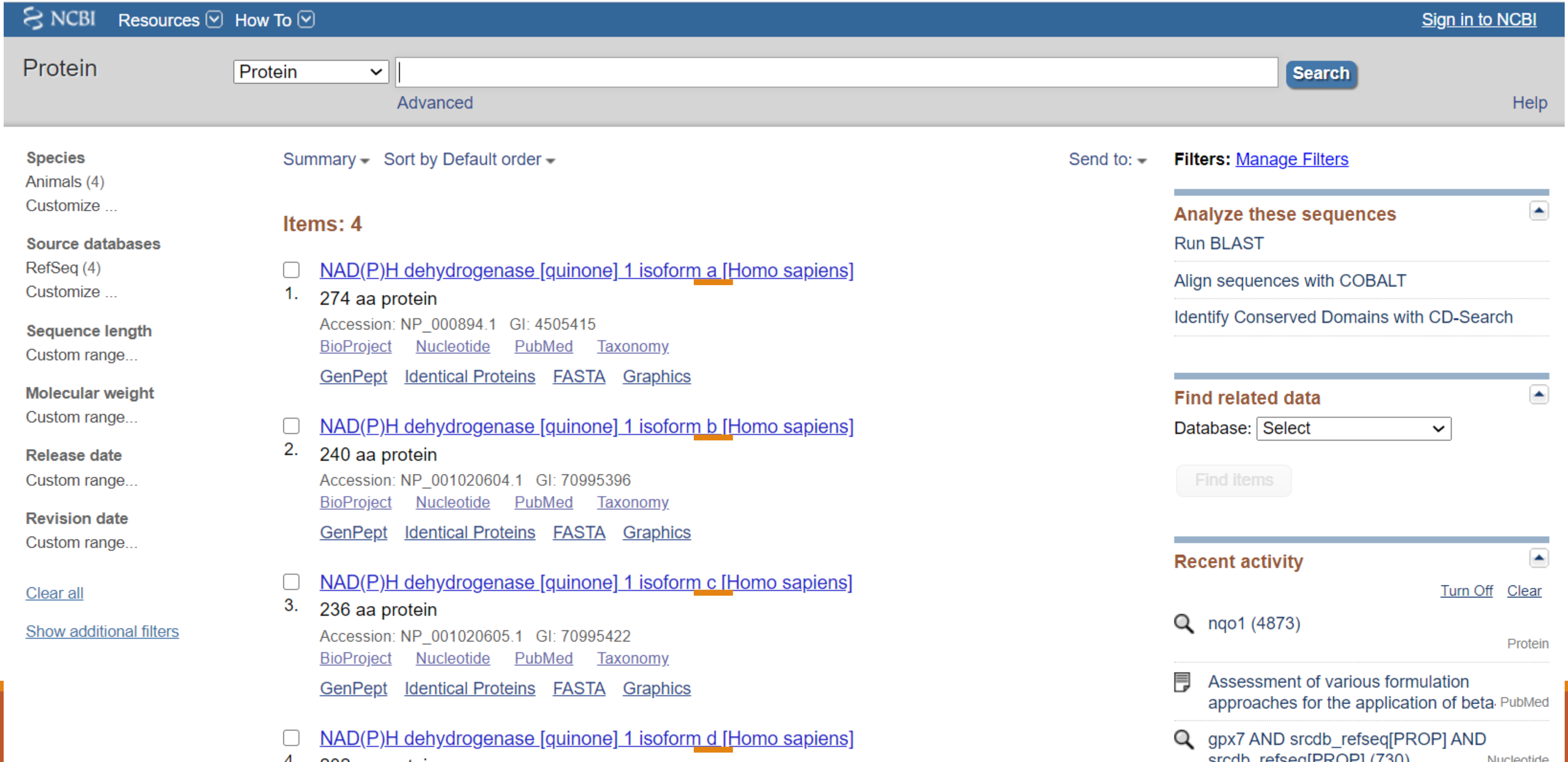
Proteinové databáze: NCBI



Species
Animals (4)
Customize ...

Source databases
RefSeq (4)
Customize ...

Sequence length
Custom range...

Molecular weight
Custom range...

Release date
Custom range...

Revision date
Custom range...

Clear all

Show additional filters

Items: 4

☐ 1. NAD(P)H dehydrogenase [quinone] 1 isoform a [Homo sapiens]
274 aa protein
Accession: NP_000894.1 GI: 4505415
BioProject Nucleotide PubMed Taxonomy
GenPept Identical Proteins FASTA Graphics

☐ 2. NAD(P)H dehydrogenase [quinone] 1 isoform b [Homo sapiens]
240 aa protein
Accession: NP_001020604.1 GI: 70995396
BioProject Nucleotide PubMed Taxonomy
GenPept Identical Proteins FASTA Graphics

☐ 3. NAD(P)H dehydrogenase [quinone] 1 isoform c [Homo sapiens]
236 aa protein
Accession: NP_001020605.1 GI: 70995422
BioProject Nucleotide PubMed Taxonomy
GenPept Identical Proteins FASTA Graphics

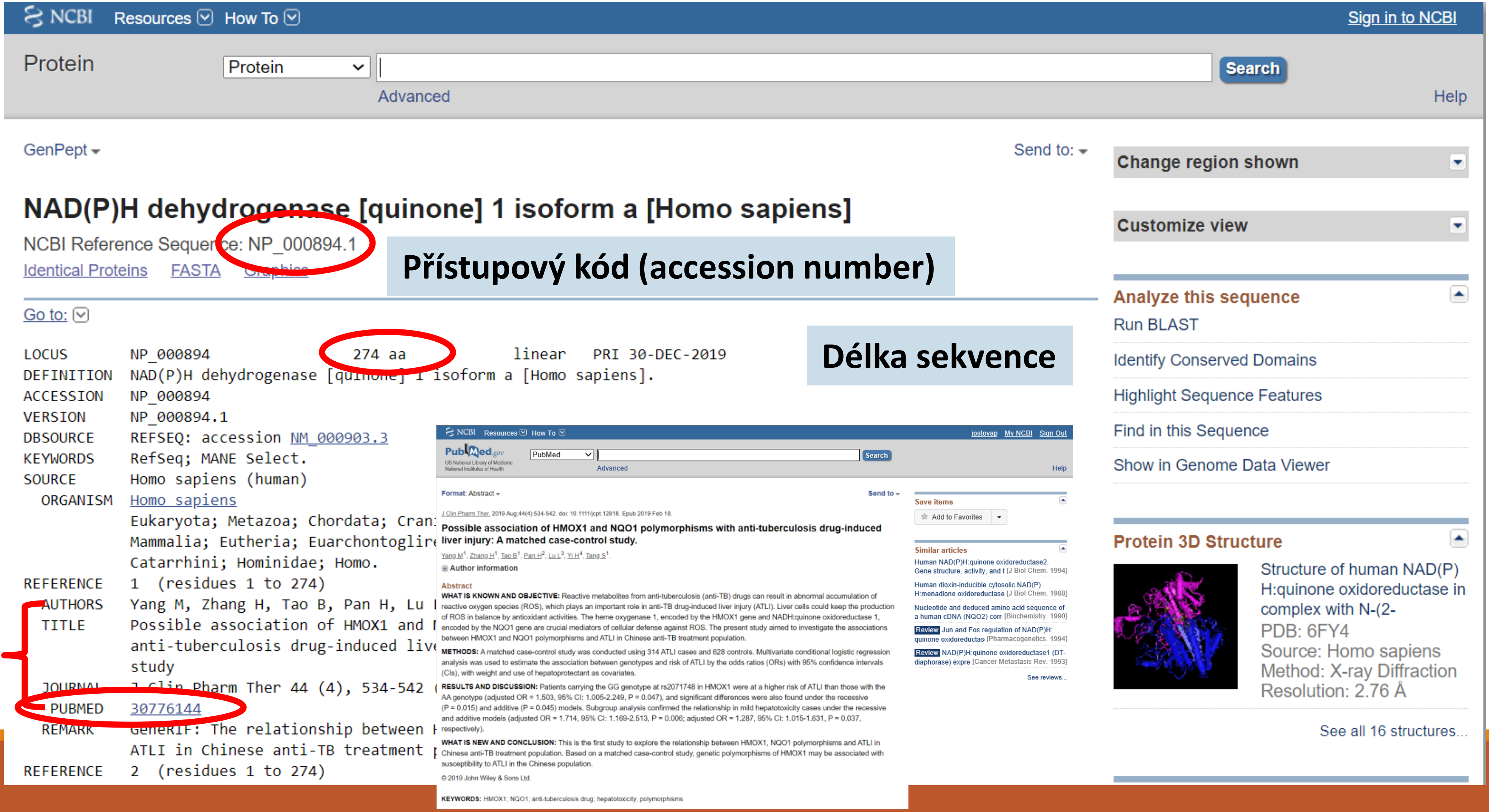
☐ 4. NAD(P)H dehydrogenase [quinone] 1 isoform d [Homo sapiens]

Analyze these sequences
Run BLAST
Align sequences with COBALT
Identify Conserved Domains with CD-Search

Find related data
Database: Select
Find items

Recent activity
Turn Off Clear
nqo1 (4873) Protein
Assessment of various formulation approaches for the application of beta PubMed
gpx7 AND srcdb_refseq[PROP] AND srcdb_refseq[PROP] (730) Nucleotide

Proteinové databáze: NCBI



NAD(P)H dehydrogenase [quinone] 1 isoform a [Homo sapiens]

NCBI Reference Sequence: NP_000894.1

Identical Proteins FASTA Graphics

Go to:

Přístupový kód (accession number)

Délka sekvence

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LOCUS       NP_000894                274 aa            linear   PRI 30-DEC-2019
DEFINITION  NAD(P)H dehydrogenase [quinone] 1 isoform a [Homo sapiens].
ACCESSION   NP_000894
VERSION     NP_000894.1
DBSOURCE    REFSEQ: accession NM_000903.3
KEYWORDS    RefSeq; MANE Select.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Cran
            Mammalia; Eutheria; Euarchontoglir
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 274)
  AUTHORS   Yang M, Zhang H, Tao B, Pan H, Lu
  TITLE     Possible association of HMOX1 and
            anti-tuberculosis drug-induced liv
            study
  JOURNAL   J Clin Pharm Ther 44 (4), 534-542
   PUBMED   30776144
  REMARK    GeneRIF: The relationship between
            ATLI in Chinese anti-TB treatment
REFERENCE   2  (residues 1 to 274)
```

Structure of human NAD(P) H:quinone oxidoreductase in complex with N-(2-
PDB: 6FY4
Source: Homo sapiens
Method: X-ray Diffraction
Resolution: 2.76 Å

J Clin Pharm Ther. 2019 Aug;44(4):534-542. doi: 10.1111/jcpt.12818. Epub 2019 Feb 18.

Possible association of HMOX1 and NQO1 polymorphisms with anti-tuberculosis drug-induced liver injury: A matched case-control study.

Yang M[1], Zhang H[1], Tao B[1], Pan H[2], Lu L[3], Yi H[4], Tang S[1].

Author information

Abstract

WHAT IS KNOWN AND OBJECTIVE: Reactive metabolites from anti-tuberculosis (anti-TB) drugs can result in abnormal accumulation of reactive oxygen species (ROS), which plays an important role in anti-TB drug-induced liver injury (ATLI). Liver cells could keep the production of ROS in balance by antioxidant activities. The heme oxygenase 1, encoded by the HMOX1 gene and NADH:quinone oxidoreductase 1, encoded by the NQO1 gene are crucial mediators of cellular defense against ROS. The present study aimed to investigate the associations between HMOX1 and NQO1 polymorphisms and ATLI in Chinese anti-TB treatment population.

METHODS: A matched case-control study was conducted using 314 ATLI cases and 628 controls. Multivariate conditional logistic regression analysis was used to estimate the association between genotypes and risk of ATLI by the odds ratios (ORs) with 95% confidence intervals (CIs), with weight and use of hepatoprotectant as covariates.

RESULTS AND DISCUSSION: Patients carrying the GG genotype at rs2071748 in HMOX1 were at a higher risk of ATLI than those with the AA genotype (adjusted OR = 1.503, 95% CI: 1.005-2.249, P = 0.047), and significant differences were also found under the recessive (P = 0.015) and additive (P = 0.045) models. Subgroup analysis confirmed the relationship in mild hepatotoxicity cases under the recessive and additive models (adjusted OR = 1.714, 95% CI: 1.169-2.513, P = 0.006; adjusted OR = 1.287, 95% CI: 1.015-1.631, P = 0.037, respectively).

WHAT IS NEW AND CONCLUSION: This is the first study to explore the relationship between HMOX1, NQO1 polymorphisms and ATLI in Chinese anti-TB treatment population. Based on a matched case-control study, genetic polymorphisms of HMOX1 may be associated with susceptibility to ATLI in the Chinese population.

© 2019 John Wiley & Sons Ltd.

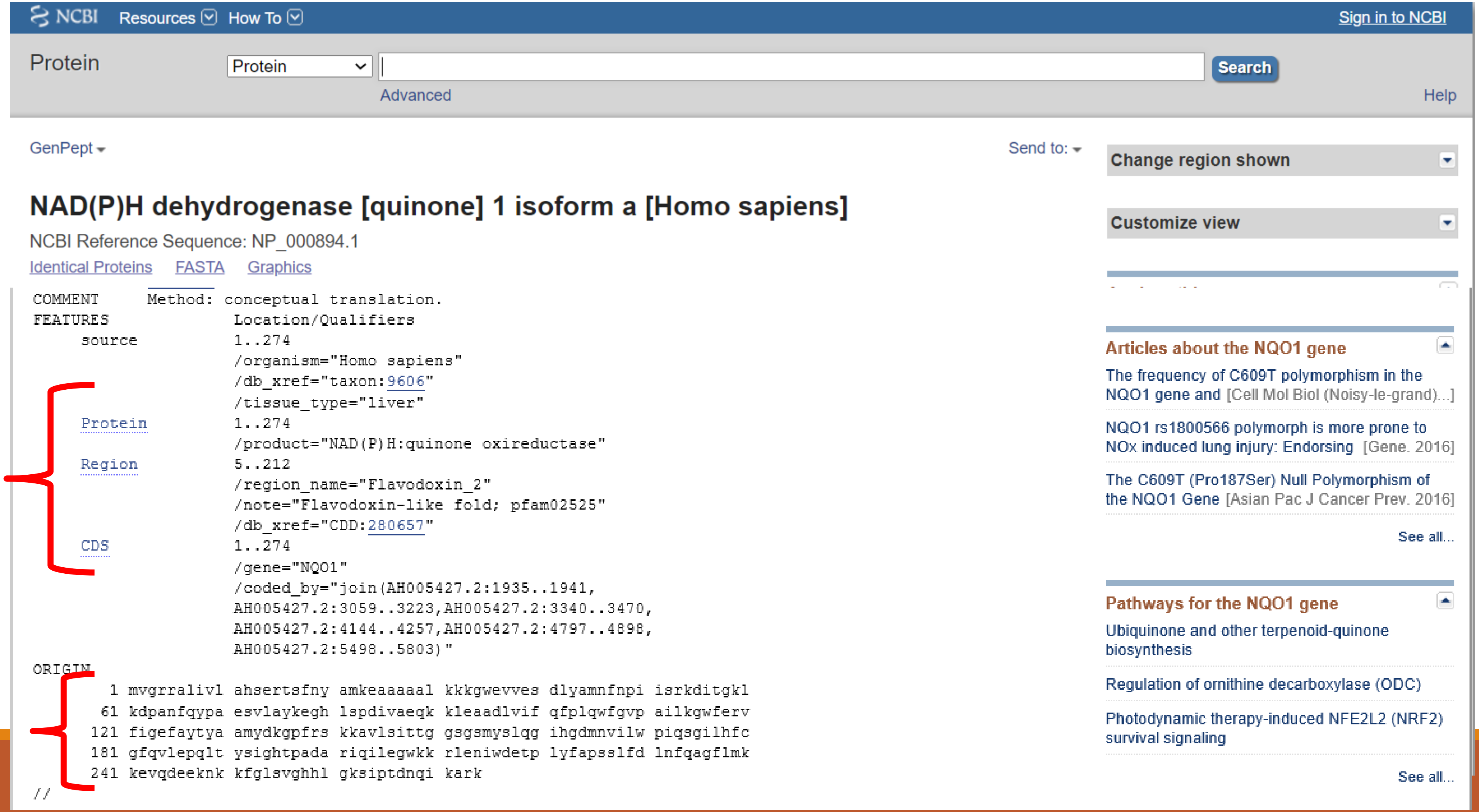
KEYWORDS: HMOX1; NQO1; anti-tuberculosis drug; hepatotoxicity; polymorphisms

Similar articles

- Human NAD(P)H:quinone oxidoreductase2. Gene structure, activity, and t [J Biol Chem. 1994]
- Human dioxin-inducible cytosolic NAD(P) H:menadione oxidoreductase [J Biol Chem. 1988]
- Nucleotide and deduced amino acid sequence of a human cDNA (NQO2) corr [Biochemistry. 1990]
- Review Jun and Fos regulation of NAD(P)H: quinone oxidoreductas [Pharmacogenetics. 1994]
- Review NAD(P)H:quinone oxidoreductase1 (DT-diaphorase) expre [Cancer Metastasis Rev. 1993]

See reviews...

Proteinové databáze: NCBI



NAD(P)H dehydrogenase [quinone] 1 isoform a [Homo sapiens]

NCBI Reference Sequence: NP_000894.1

Identical Proteins FASTA Graphics

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COMMENT     Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..274
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                     /db_xref="taxon:9606"
                     /tissue_type="liver"
     Protein         1..274
                     /product="NAD(P)H:quinone oxireductase"
     Region          5..212
                     /region_name="Flavodoxin_2"
                     /note="Flavodoxin-like fold; pfam02525"
                     /db_xref="CDD:280657"
     CDS             1..274
                     /gene="NQO1"
                     /coded_by="join(AH005427.2:1935..1941,
                     AH005427.2:3059..3223,AH005427.2:3340..3470,
                     AH005427.2:4144..4257,AH005427.2:4797..4898,
                     AH005427.2:5498..5803)"
ORIGIN
        1 mvgrralivl ahsertsfny amkeaaaaal kkkgwevves dlyamnfnpi isrkditgkl
       61 kdpanfqypa esvlaykegh lspdivaeqk kleaadlvif qfplqwfgvp ailkgwferv
      121 figefaytya amydkgpfrs kkavlsittg gsgsmyslqg ihgdmnvilw piqsgilhfc
      181 gfqvlepqlt ysightpada riqilegwkk rleniwdetp lyfapsslfd lnfqagflmk
      241 kevqdeeknk kfglsvghhl gksiptdnqi kark
//
```

Articles about the NQO1 gene

The frequency of C609T polymorphism in the NQO1 gene and [Cell Mol Biol (Noisy-le-grand)...]

NQO1 rs1800566 polymorph is more prone to NOx induced lung injury: Endorsing [Gene. 2016]

The C609T (Pro187Ser) Null Polymorphism of the NQO1 Gene [Asian Pac J Cancer Prev. 2016]

See all...

Pathways for the NQO1 gene

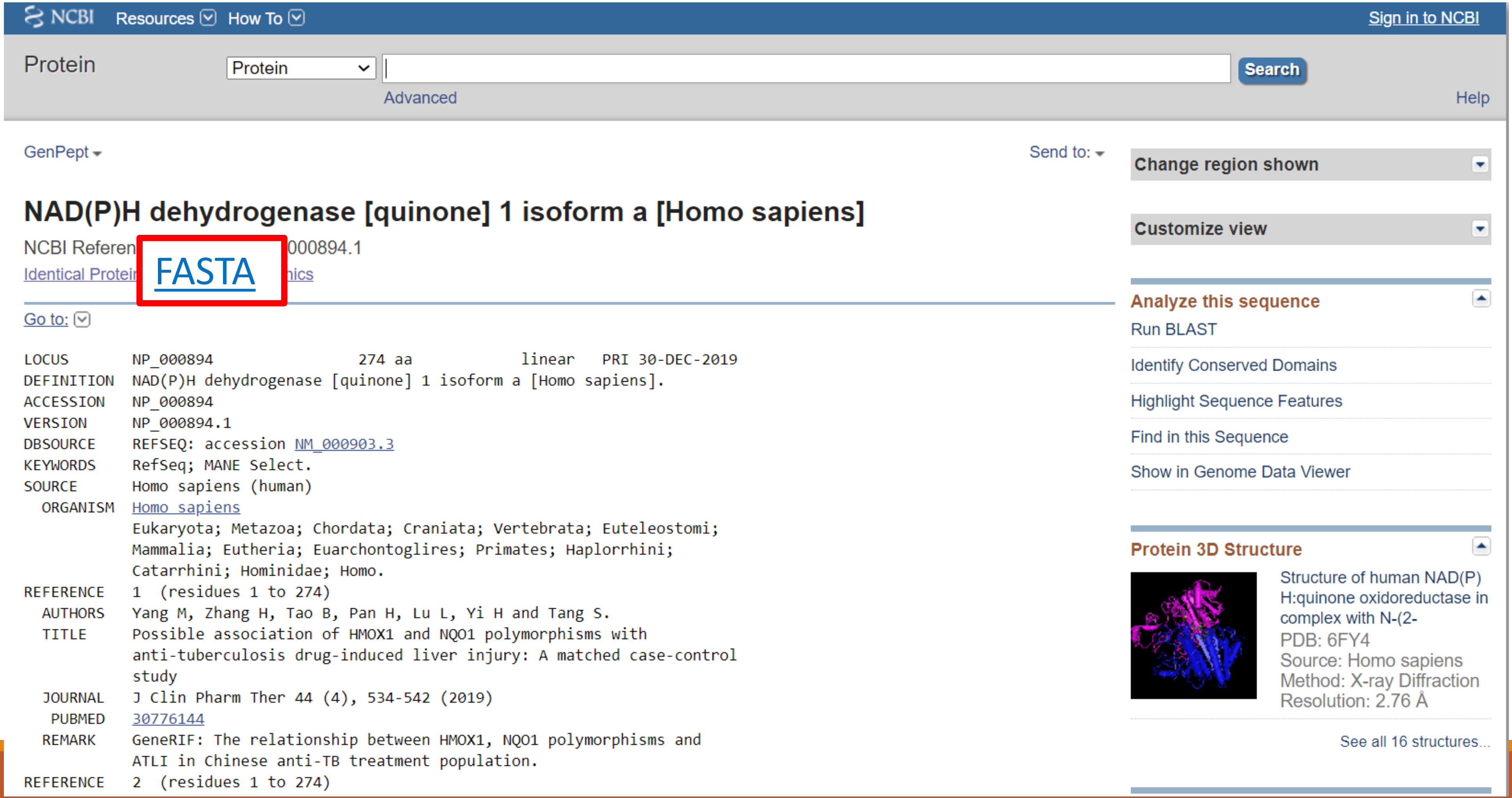
Ubiquinone and other terpenoid-quinone biosynthesis

Regulation of ornithine decarboxylase (ODC)

Photodynamic therapy-induced NFE2L2 (NRF2) survival signaling

See all...

Proteinové databáze: NCBI



NAD(P)H dehydrogenase [quinone] 1 isoform a [Homo sapiens]

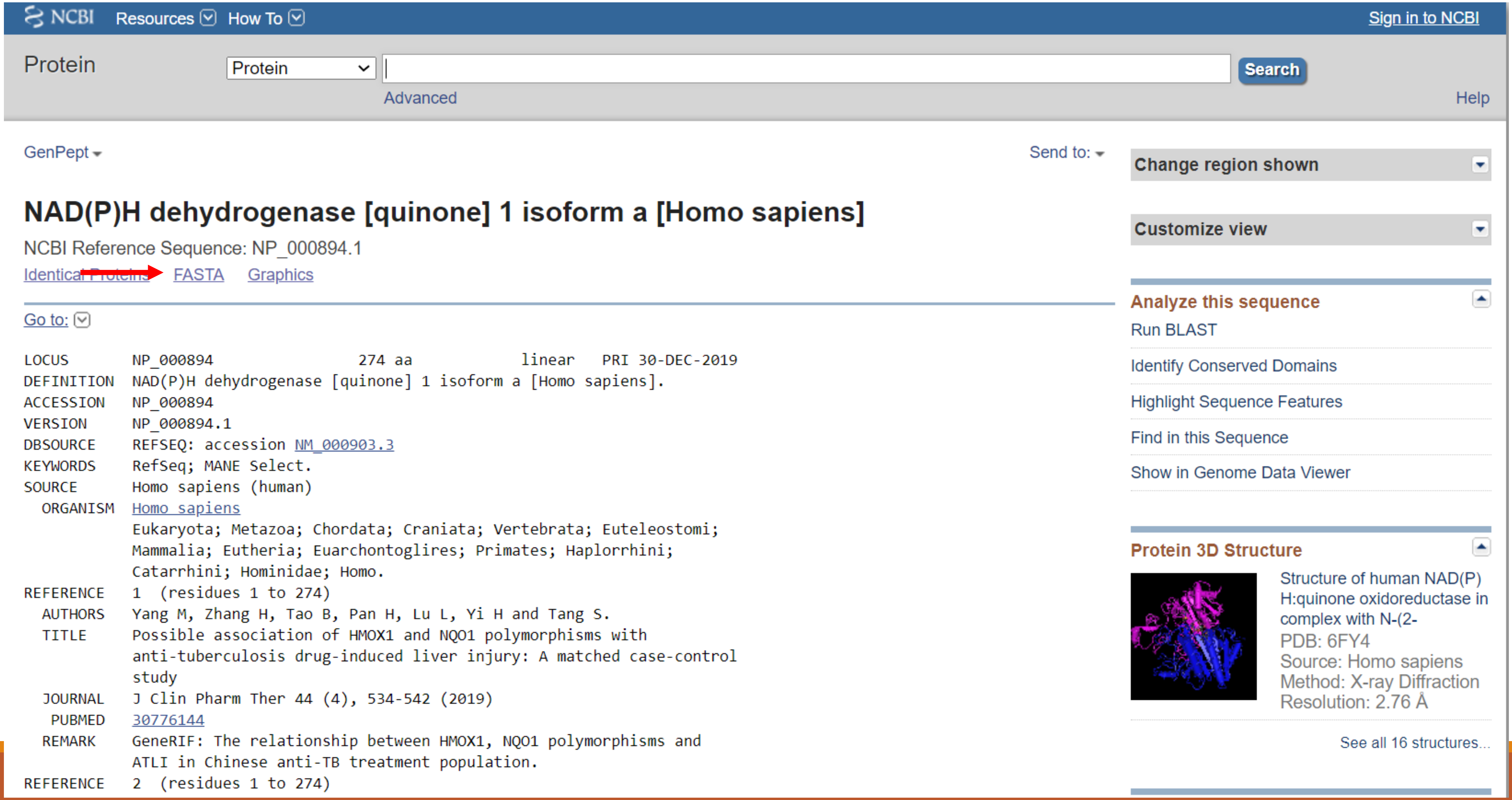
NCBI Referen 000894.1

Identical Protei ics

```
LOCUS       NP_000894                274 aa            linear   PRI 30-DEC-2019
DEFINITION  NAD(P)H dehydrogenase [quinone] 1 isoform a [Homo sapiens].
ACCESSION   NP_000894
VERSION     NP_000894.1
DBSOURCE    REFSEQ: accession NM_000903.3
KEYWORDS    RefSeq; MANE Select.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 274)
  AUTHORS   Yang M, Zhang H, Tao B, Pan H, Lu L, Yi H and Tang S.
  TITLE     Possible association of HMOX1 and NQO1 polymorphisms with
            anti-tuberculosis drug-induced liver injury: A matched case-control
            study
  JOURNAL   J Clin Pharm Ther 44 (4), 534-542 (2019)
   PUBMED   30776144
  REMARK    GeneRIF: The relationship between HMOX1, NQO1 polymorphisms and
            ATLI in Chinese anti-TB treatment population.
REFERENCE   2  (residues 1 to 274)
```

Structure of human NAD(P)H:quinone oxidoreductase in complex with N-(2-
PDB: 6FY4
Source: Homo sapiens
Method: X-ray Diffraction
Resolution: 2.76 Å

Proteinové databáze: NCBI



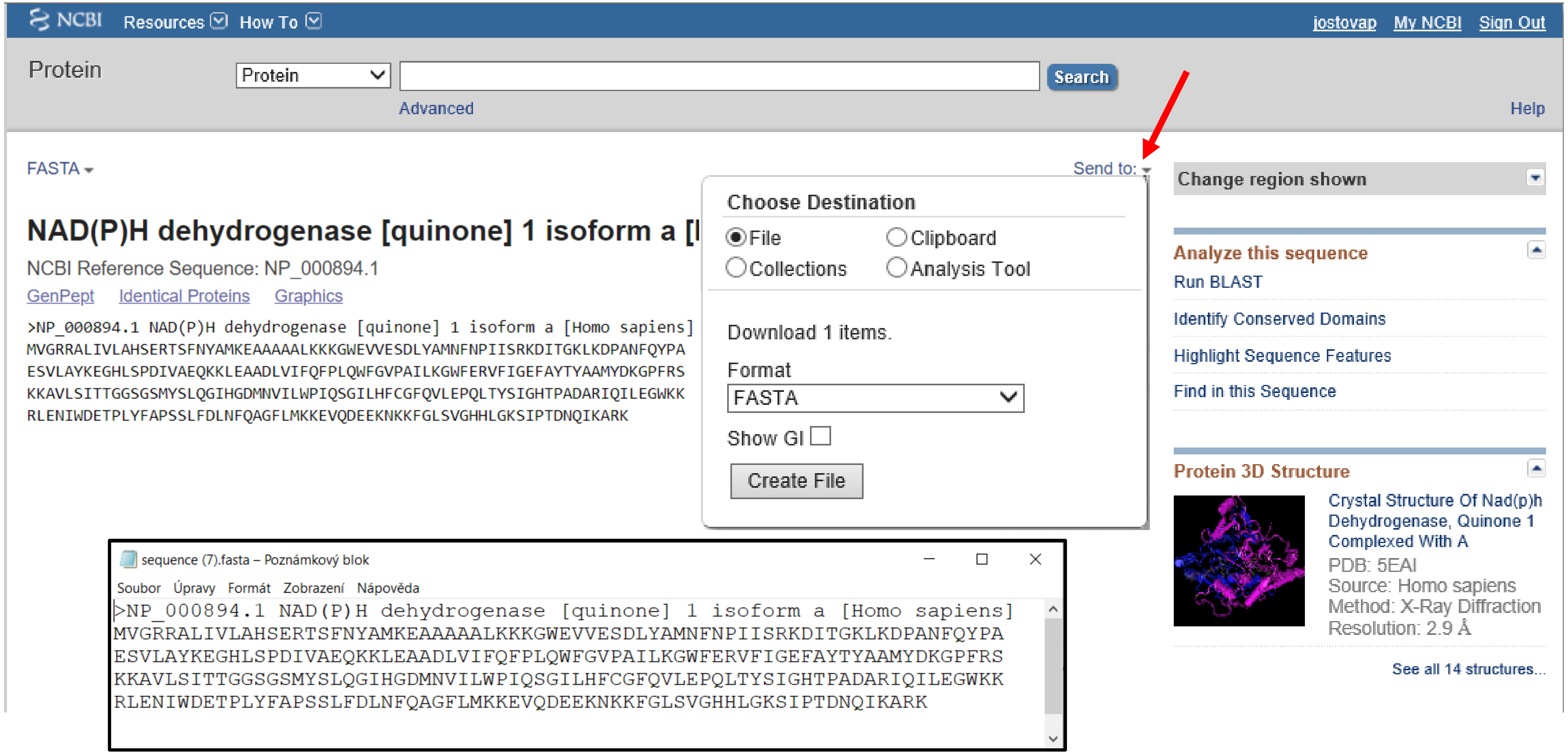
NAD(P)H dehydrogenase [quinone] 1 isoform a [Homo sapiens]

NCBI Reference Sequence: NP_000894.1

```
LOCUS       NP_000894                274 aa            linear   PRI 30-DEC-2019
DEFINITION  NAD(P)H dehydrogenase [quinone] 1 isoform a [Homo sapiens].
ACCESSION   NP_000894
VERSION     NP_000894.1
DBSOURCE    REFSEQ: accession NM_000903.3
KEYWORDS    RefSeq; MANE Select.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 274)
  AUTHORS   Yang M, Zhang H, Tao B, Pan H, Lu L, Yi H and Tang S.
  TITLE     Possible association of HMOX1 and NQO1 polymorphisms with
            anti-tuberculosis drug-induced liver injury: A matched case-control
            study
  JOURNAL   J Clin Pharm Ther 44 (4), 534-542 (2019)
   PUBMED   30776144
  REMARK    GeneRIF: The relationship between HMOX1, NQO1 polymorphisms and
            ATLI in Chinese anti-TB treatment population.
REFERENCE   2  (residues 1 to 274)
```

Structure of human NAD(P) H:quinone oxidoreductase in complex with N-(2-
PDB: 6FY4
Source: Homo sapiens
Method: X-ray Diffraction
Resolution: 2.76 Å

Proteinové databáze: NCBI



Protein ▾

NAD(P)H dehydrogenase [quinone] 1 isoform a [

NCBI Reference Sequence: NP_000894.1

```
>NP_000894.1 NAD(P)H dehydrogenase [quinone] 1 isoform a [Homo sapiens]
MVGRRALIVLAHSERTSFNYAMKEAAAAALKKKGWEVVESDLYAMNFNPIISRKDITGKLKDPANFQYPA
ESVLAYKEGHLSPDIVAEQKKLEAADLVIFQFPLQWFGVPAILKGWFERVFIGEFAYTYAAMYDKGPFRS
KKAVLSITTGGSGSMYSLQGIHGDMNVILWPIQSGILHFCGFQVLEPQLTYSIGHTPADARIQILEGWKK
RLENIWDETPLYFAPSSLFDLNFQAGFLMKKEVQDEEKNKKFGLSVGHHLGKSIPTDNQIKARK
```

Choose Destination

● File ○ Clipboard

○ Collections ○ Analysis Tool

Download 1 items.

Format: FASTA ▾

Show GI ☐

Create File

Crystal Structure Of Nad(p)h Dehydrogenase, Quinone 1 Complexed With A

PDB: 5EAI

Source: Homo sapiens

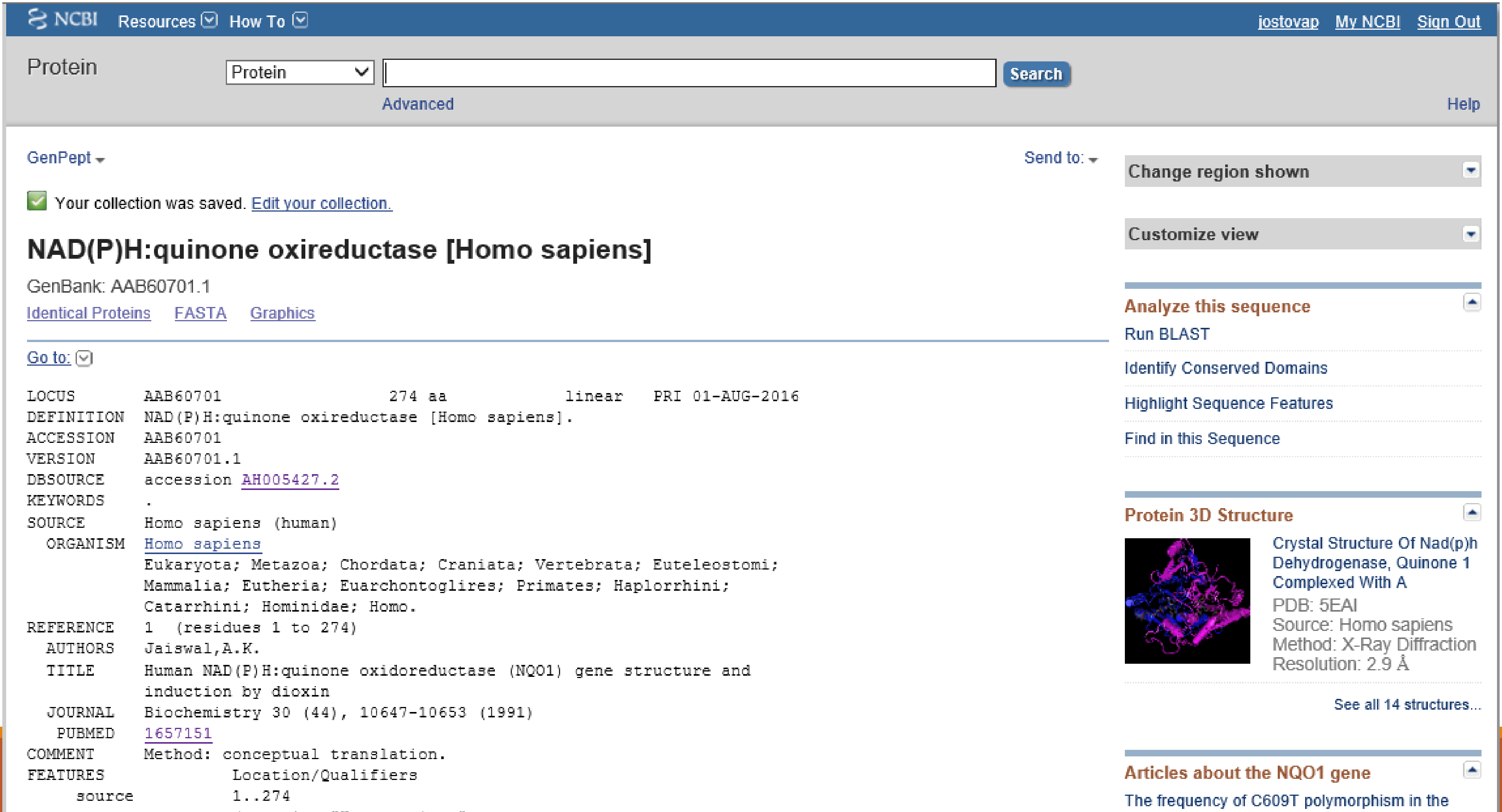
Method: X-Ray Diffraction

Resolution: 2.9 Å

sequence (7).fasta – Poznámkový blok

```
>NP_000894.1 NAD(P)H dehydrogenase [quinone] 1 isoform a [Homo sapiens]
MVGRRALIVLAHSERTSFNYAMKEAAAAALKKKGWEVVESDLYAMNFNPIISRKDITGKLKDPANFQYPA
ESVLAYKEGHLSPDIVAEQKKLEAADLVIFQFPLQWFGVPAILKGWFERVFIGEFAYTYAAMYDKGPFRS
KKAVLSITTGGSGSMYSLQGIHGDMNVILWPIQSGILHFCGFQVLEPQLTYSIGHTPADARIQILEGWKK
RLENIWDETPLYFAPSSLFDLNFQAGFLMKKEVQDEEKNKKFGLSVGHHLGKSIPTDNQIKARK
```

Proteinové databáze: NCBI → **My NCBI**



☑ Your collection was saved. Edit your collection.

NAD(P)H:quinone oxireductase [Homo sapiens]

GenBank: AAB60701.1

```
LOCUS       AAB60701                 274 aa            linear   PRI 01-AUG-2016
DEFINITION  NAD(P)H:quinone oxireductase [Homo sapiens].
ACCESSION   AAB60701
VERSION     AAB60701.1
DBSOURCE    accession AH005427.2
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 274)
  AUTHORS   Jaiswal,A.K.
  TITLE     Human NAD(P)H:quinone oxidoreductase (NQO1) gene structure and
            induction by dioxin
  JOURNAL   Biochemistry 30 (44), 10647-10653 (1991)
   PUBMED   1657151
COMMENT     Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..274
```

Analyze this sequence

Run BLAST

Identify Conserved Domains

Highlight Sequence Features

Find in this Sequence

Protein 3D Structure

Crystal Structure Of Nad(p)h Dehydrogenase, Quinone 1 Complexed With A

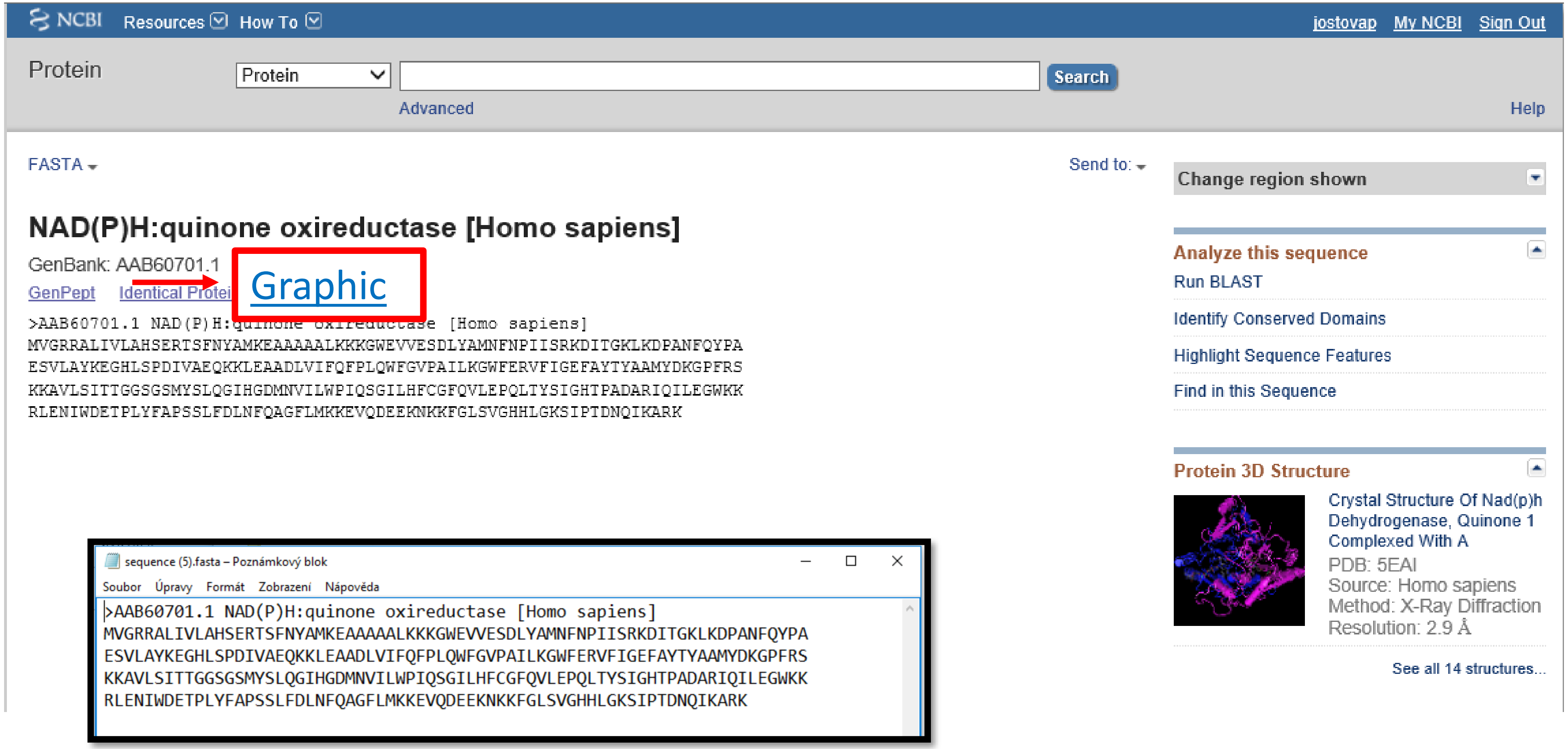
PDB: 5EAI
Source: Homo sapiens
Method: X-Ray Diffraction
Resolution: 2.9 Å

See all 14 structures...

Articles about the NQO1 gene

The frequency of C609T polymorphism in the

Proteinové databáze: NCBI



NAD(P)H:quinone oxireductase [Homo sapiens]

GenBank: AAB60701.1

GenPept Identical Protei

Graphic

```
>AAB60701.1 NAD(P)H:quinone oxireductase [Homo sapiens]
MVGRRALIVLAHSERTSFNYAMKEAAAAALKKKGWEVVESDLYAMNFNPIISRKDITGKLKDPANFQYPA
ESVLAYKEGHLSPDIVAEQKKLEAADLVIFQFPLQWFGVPAILKGWFERVFIGEFAYTYAAMYDKGPFRS
KKAVLSITTGGSGSMYSLQGIHGDMNVILWPIQSGILHFCGFQVLEPQLTYSIGHTPADARIQILEGWKK
RLENIWDETPLYFAPSSLFDLNFQAGFLMKKEVQDEEKNKKFGLSVGHHLGKSIPTDNQIKARK
```

Crystal Structure Of Nad(p)h Dehydrogenase, Quinone 1 Complexed With A

PDB: 5EAI

Source: Homo sapiens

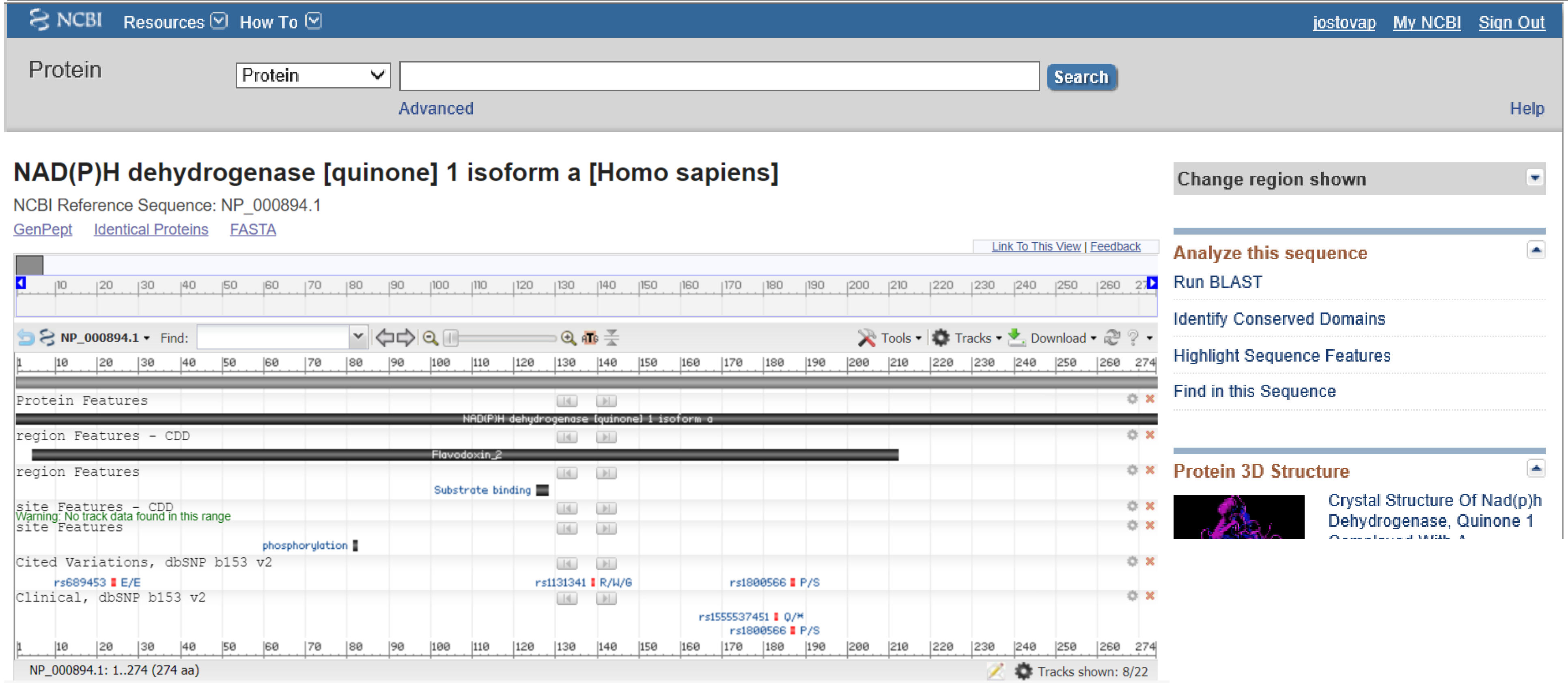
Method: X-Ray Diffraction

Resolution: 2.9 Å

sequence (5).fasta – Poznámkový blok

```
>AAB60701.1 NAD(P)H:quinone oxireductase [Homo sapiens]
MVGRRALIVLAHSERTSFNYAMKEAAAAALKKKGWEVVESDLYAMNFNPIISRKDITGKLKDPANFQYPA
ESVLAYKEGHLSPDIVAEQKKLEAADLVIFQFPLQWFGVPAILKGWFERVFIGEFAYTYAAMYDKGPFRS
KKAVLSITTGGSGSMYSLQGIHGDMNVILWPIQSGILHFCGFQVLEPQLTYSIGHTPADARIQILEGWKK
RLENIWDETPLYFAPSSLFDLNFQAGFLMKKEVQDEEKNKKFGLSVGHHLGKSIPTDNQIKARK
```

Proteinové databáze: NCBI



NAD(P)H dehydrogenase [quinone] 1 isoform a [Homo sapiens]

NCBI Reference Sequence: NP_000894.1

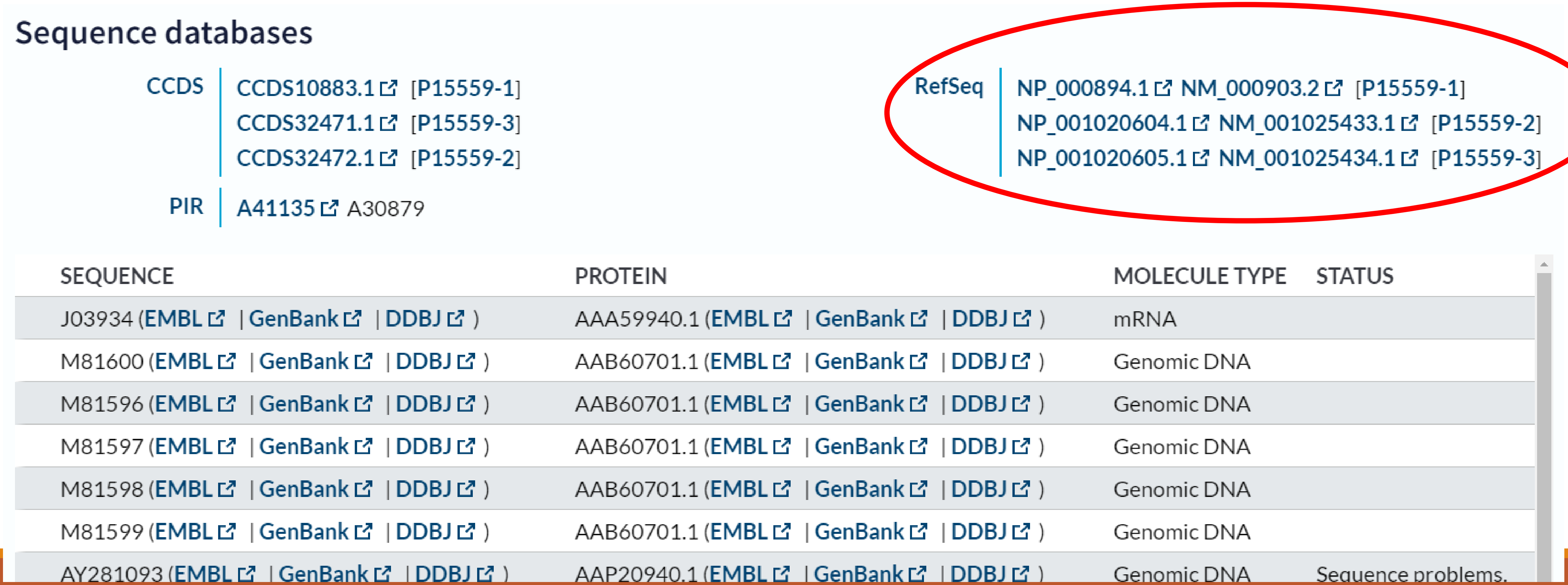
NP_000894.1: 1..274 (274 aa)

Warning: No track data found in this range

Tracks shown: 8/22

Proteinové databáze: UNIPROT →NCBI

Sequence & Isoforms - posunout se níže na:



Sequence databases

CCDS	CCDS10883.1 [P15559-1] CCDS32471.1 [P15559-3] CCDS32472.1 [P15559-2]
PIR	A41135 A30879
RefSeq	NP_000894.1 NM_000903.2 [P15559-1] NP_001020604.1 NM_001025433.1 [P15559-2] NP_001020605.1 NM_001025434.1 [P15559-3]

SEQUENCE	PROTEIN	MOLECULE TYPE	STATUS
J03934 (EMBL | GenBank | DDBJ)	AAA59940.1 (EMBL | GenBank | DDBJ)	mRNA	
M81600 (EMBL | GenBank | DDBJ)	AAB60701.1 (EMBL | GenBank | DDBJ)	Genomic DNA	
M81596 (EMBL | GenBank | DDBJ)	AAB60701.1 (EMBL | GenBank | DDBJ)	Genomic DNA	
M81597 (EMBL | GenBank | DDBJ)	AAB60701.1 (EMBL | GenBank | DDBJ)	Genomic DNA	
M81598 (EMBL | GenBank | DDBJ)	AAB60701.1 (EMBL | GenBank | DDBJ)	Genomic DNA	
M81599 (EMBL | GenBank | DDBJ)	AAB60701.1 (EMBL | GenBank | DDBJ)	Genomic DNA	
AY281093 (EMBL | GenBank | DDBJ)	AAP20940.1 (EMBL | GenBank | DDBJ)	Genomic DNA	Sequence problems.

Vyzkoušejte si NCBI proteinovou databázi

Najděte si „svou vlastní“ sekvenci

-vyzkoušejte hledat „přímo“ v NCBI
-vyzkoušejte „projít“ skrz „Sequence databases“ a „Refseq“ v Uniprot databázi

„Proteinová bioinformatika“

Vyhledávání AMK sekvencí

Analýza vlastností sekvencí (aminokyselinové složení, molekulová hmotnost, isoelektrický bod…)

Štěpení proteasami

Analýza hydrofobních segmentů, transmembránových úseků

Predikce sekundární struktury

3D-struktura, vizualizace

Vyhledání a porovnání podobných sekvencí

Evoluční příbuznost sekvencí

…

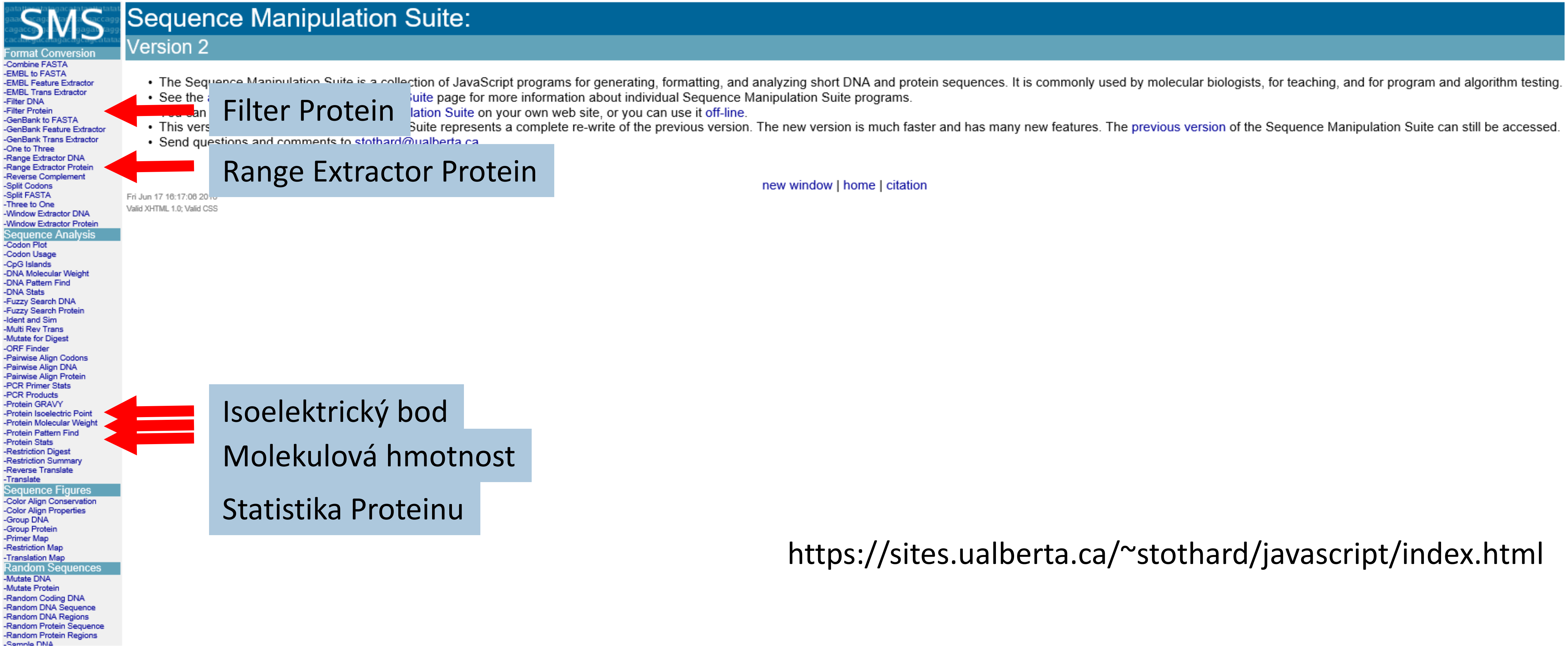
Analýza vlastností proteinu/sekvence

Molekulární hmotnost

Isoelektrický bod

Složení AMK

Analýza vlastností proteinu/sekvence



SMS

Format Conversion
- -Combine FASTA
- -EMBL to FASTA
- -EMBL Feature Extractor
- -EMBL Trans Extractor
- -Filter DNA
- -Filter Protein
- -GenBank to FASTA
- -GenBank Feature Extractor
- -GenBank Trans Extractor
- -One to Three
- -Range Extractor DNA
- -Range Extractor Protein
- -Reverse Complement
- -Split Codons
- -Split FASTA
- -Three to One
- -Window Extractor DNA
- -Window Extractor Protein

Sequence Analysis
- -Codon Plot
- -Codon Usage
- -CpG Islands
- -DNA Molecular Weight
- -DNA Pattern Find
- -DNA Stats
- -Fuzzy Search DNA
- -Fuzzy Search Protein
- -Ident and Sim
- -Multi Rev Trans
- -Mutate for Digest
- -ORF Finder
- -Pairwise Align Codons
- -Pairwise Align DNA
- -Pairwise Align Protein
- -PCR Primer Stats
- -PCR Products
- -Protein GRAVY
- -Protein Isoelectric Point
- -Protein Molecular Weight
- -Protein Pattern Find
- -Protein Stats
- -Restriction Digest
- -Restriction Summary
- -Reverse Translate
- -Translate

Sequence Figures
- -Color Align Conservation
- -Color Align Properties
- -Group DNA
- -Group Protein
- -Primer Map
- -Restriction Map
- -Translation Map

Random Sequences
- -Mutate DNA
- -Mutate Protein
- -Random Coding DNA
- -Random DNA Sequence
- -Random DNA Regions
- -Random Protein Sequence
- -Random Protein Regions
- -Sample DNA

Sequence Manipulation Suite:

Version 2

- The Sequence Manipulation Suite is a collection of JavaScript programs for generating, formatting, and analyzing short DNA and protein sequences. It is commonly used by molecular biologists, for teaching, and for program and algorithm testing.
- See the uite page for more information about individual Sequence Manipulation Suite programs.
- lation Suite on your own web site, or you can use it off-line.
- This vers Suite represents a complete re-write of the previous version. The new version is much faster and has many new features. The previous version of the Sequence Manipulation Suite can still be accessed.
- Send questions and comments to stothard@ualberta.ca

new window | home | citation

Fri Jun 17 16:17:06 201
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Filter Protein

Range Extractor Protein

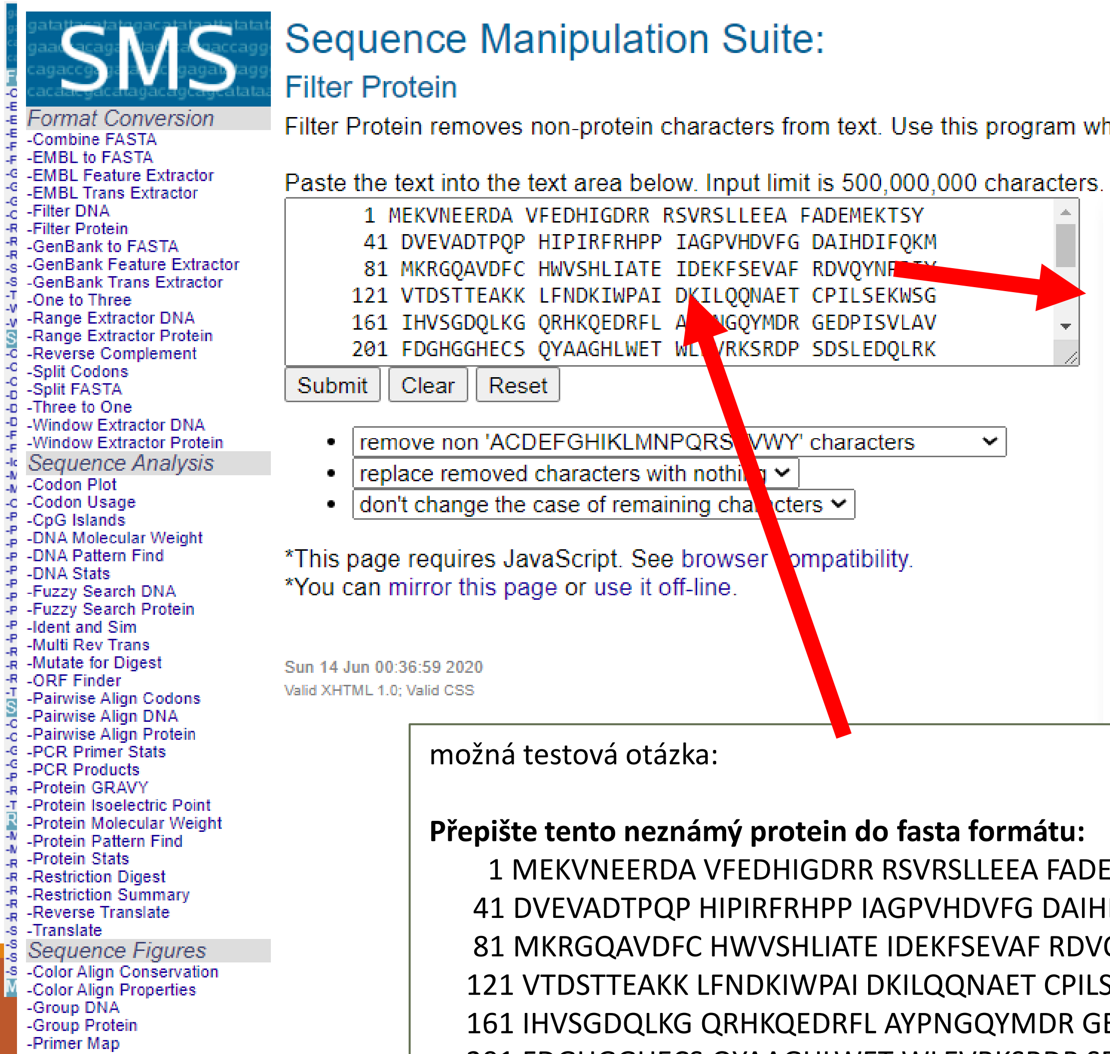
Isoelektrický bod

Molekulová hmotnost

Statistika Proteinu

https://sites.ualberta.ca/~stothard/javascript/index.html

Analýza vlastností proteinu/sekvence



Sequence Manipulation Suite:

Filter Protein

Filter Protein removes non-protein characters from text. Use this program when you wish to remove digits and blank spaces from a sequence to make it suitable for other applications.

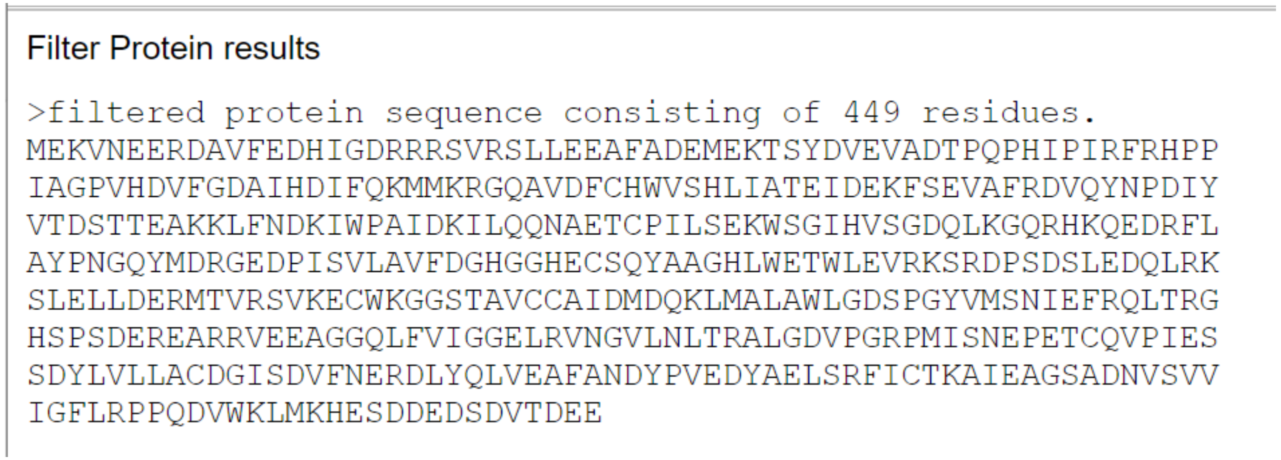
Paste the text into the text area below. Input limit is 500,000,000 characters.

```
      1 MEKVNEERDA VFEDHIGDRR RSVRSLLEEA FADEMEKTSY
     41 DVEVADTPQP HIPIRFRHPP IAGPVHDVFG DAIHDIFQKM
     81 MKRGQAVDFC HWVSHLIATE IDEKFSEVAF RDVQYNPDIY
    121 VTDSTTEAKK LFNDKIWPAI DKILQQNAET CPILSEKWSG
    161 IHVSGDQLKG QRHKQEDRFL AYPNGQYMDR GEDPISVLAV
    201 FDGHGGHECS QYAAGHLWET WLEVRKSRDP SDSLEDQLRK
```

- remove non 'ACDEFGHIKLMNPQRSTVWY' characters
- replace removed characters with nothing
- don't change the case of remaining characters

*This page requires JavaScript. See browser compatibility.
*You can mirror this page or use it off-line.

Sun 14 Jun 00:36:59 2020
Valid XHTML 1.0; Valid CSS



Filter Protein results

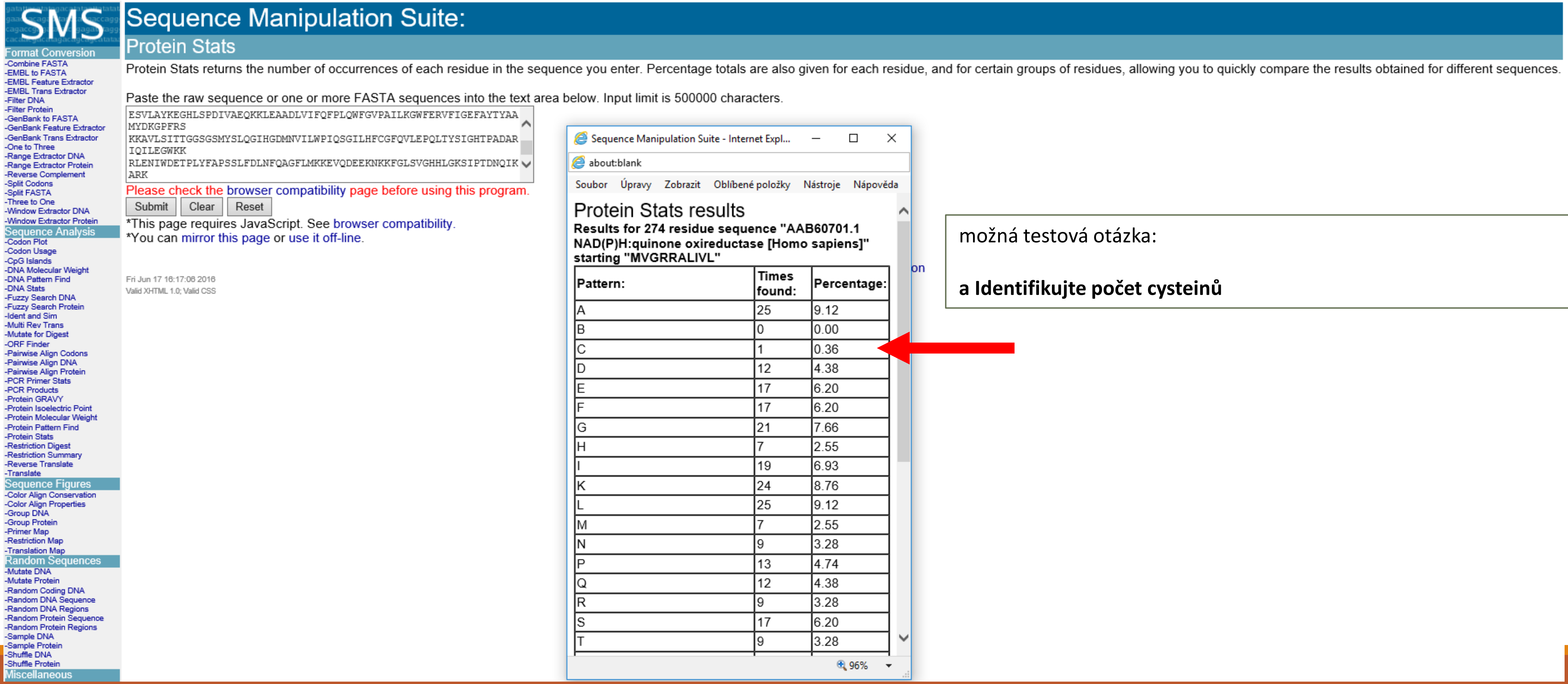
```
>filtered protein sequence consisting of 449 residues.
MEKVNEERDAVFEDHIGDRRRSVRSLLEEAFADEMEKTSYDVEVADTPQPHIPIRFRHPP
IAGPVHDVFGDAIHDIFQKMMKRGQAVDFCHWVSHLIATEIDEKFSEVAFRDVQYNPDIY
VTDSTTEAKKLFNDKIWPAIDKILQQNAETCPILSEKWSGIHVSGDQLKGQRHKQEDRFL
AYPNGQYMDRGEDPISVLAVFDGHGGHECSQYAAGHLWETWLEVRKSRDPSDSLEDQLRK
SLELLDERMTVRSVKECWKGGSTAVCCAIDMDQKLMALAWLGDSPGYVMSNIEFRQLTRG
HSPSDEREARRVEEAGGQLFVIGGELRVNGVLNLTRALGDVPGRPMISNEPETCQVPIES
SDYLVLLACDGISDVFNERDLYQLVEAFANDYPVEDYAELSRFICTKAIEAGSADNVSVV
IGFLRPPQDVWKLMKHESDDEDSDVTDEE
```

možná testová otázka:

Přepište tento neznámý protein do fasta formátu:

```
  1 MEKVNEERDA VFEDHIGDRR RSVRSLLEEA FADEMEKTSY
 41 DVEVADTPQP HIPIRFRHPP IAGPVHDVFG DAIHDIFQKM
 81 MKRGQAVDFC HWVSHLIATE IDEKFSEVAF RDVQYNPDIY
121 VTDSTTEAKK LFNDKIWPAI DKILQQNAET CPILSEKWSG
161 IHVSGDQLKG QRHKQEDRFL AYPNGQYMDR GEDPISVLAV
```

Analýza vlastností proteinu/sekvence



Sequence Manipulation Suite:

Protein Stats

Protein Stats returns the number of occurrences of each residue in the sequence you enter. Percentage totals are also given for each residue, and for certain groups of residues, allowing you to quickly compare the results obtained for different sequences.

Paste the raw sequence or one or more FASTA sequences into the text area below. Input limit is 500000 characters.

```
ESVLAYKEGHLSPDIVAEQKKLEAADLVIFQFPLQWFGVPAILKGWFERVFIGEFAYTYAA
MYDKGPFRS
KKAVLSITTGGSGSMYSLQGIHGDMNVILWPIQSGILHFCGFQVLEPQLTYSIGHTPADAR
IQILEGWKK
RLENIWDETPLYFAPSSLFDLNFQAGFLMKKEVQDEEKNKKFGLSVGHHLGKSIPTDNQIK
ARK
```

Please check the browser compatibility page before using this program.

*This page requires JavaScript. See browser compatibility.
*You can mirror this page or use it off-line.

Fri Jun 17 16:17:06 2016
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Protein Stats results

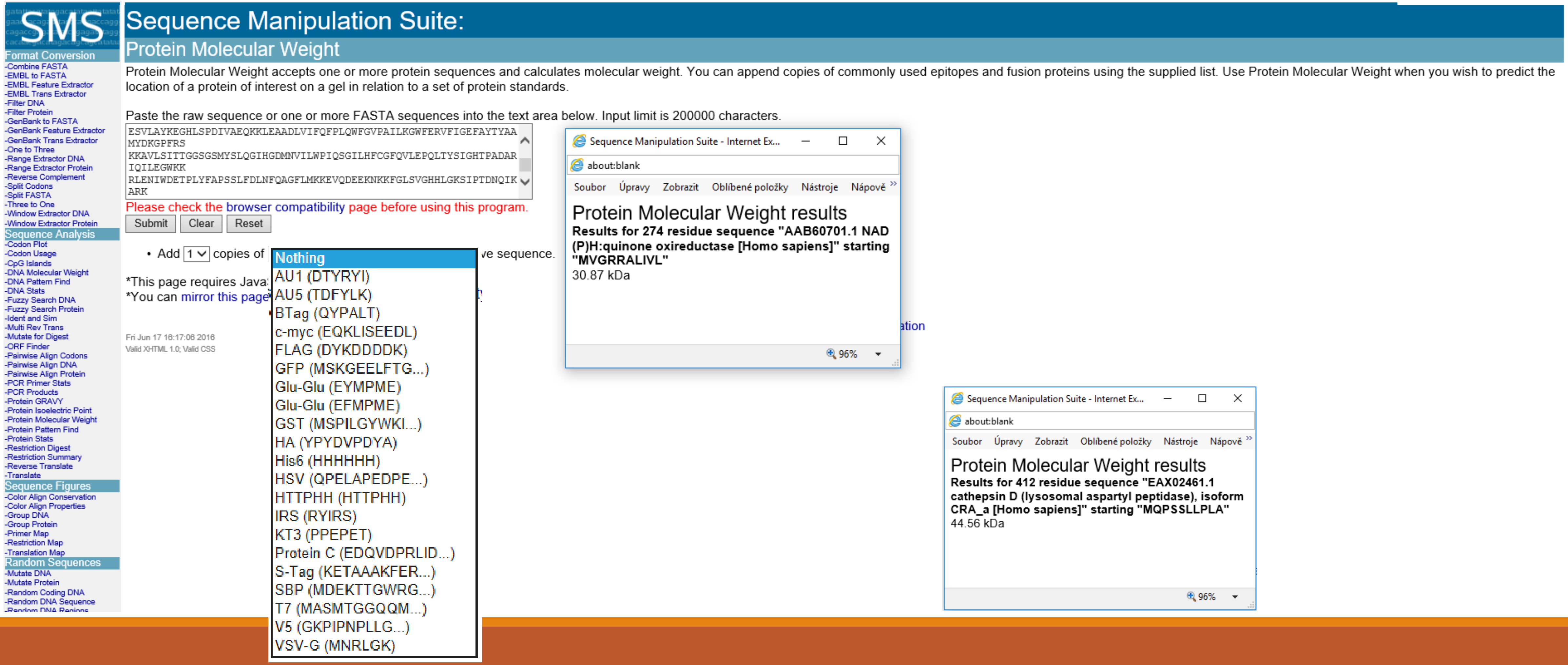
Results for 274 residue sequence "AAB60701.1 NAD(P)H:quinone oxireductase [Homo sapiens]" starting "MVGRRALIVL"

Pattern:	Times found:	Percentage:
A	25	9.12
B	0	0.00
C	1	0.36
D	12	4.38
E	17	6.20
F	17	6.20
G	21	7.66
H	7	2.55
I	19	6.93
K	24	8.76
L	25	9.12
M	7	2.55
N	9	3.28
P	13	4.74
Q	12	4.38
R	9	3.28
S	17	6.20
T	9	3.28

možná testová otázka:

a Identifikujte počet cysteinů

Analýza vlastností proteinu/sekvence



Sequence Manipulation Suite:

Protein Molecular Weight

Protein Molecular Weight accepts one or more protein sequences and calculates molecular weight. You can append copies of commonly used epitopes and fusion proteins using the supplied list. Use Protein Molecular Weight when you wish to predict the location of a protein of interest on a gel in relation to a set of protein standards.

Paste the raw sequence or one or more FASTA sequences into the text area below. Input limit is 200000 characters.

```
ESVLAYKEGHLSPDIVAEQKKLEAADLVIFQFPLQWFGVPAILKGWFERVFIGEFAYTYAA
MYDKGPFRS
KKAVLSITTGGSGSMYSLQGIHGDMNVILWPIQSGILHFCGFQVLEPQLTYSIGHTPADAR
IQILEGWKK
RLENIWDETPLYFAPSSLFDLNFQAGFLMKKEVQDEEKNKKFGLSVGHHLGKSIPTDNQIK
ARK
```

Please check the browser compatibility page before using this program.

- Add 1 copies of Nothing ve sequence.

*This page requires Java

*You can mirror this page

ation

Fri Jun 17 16:17:06 2016
Valid XHTML 1.0; Valid CSS

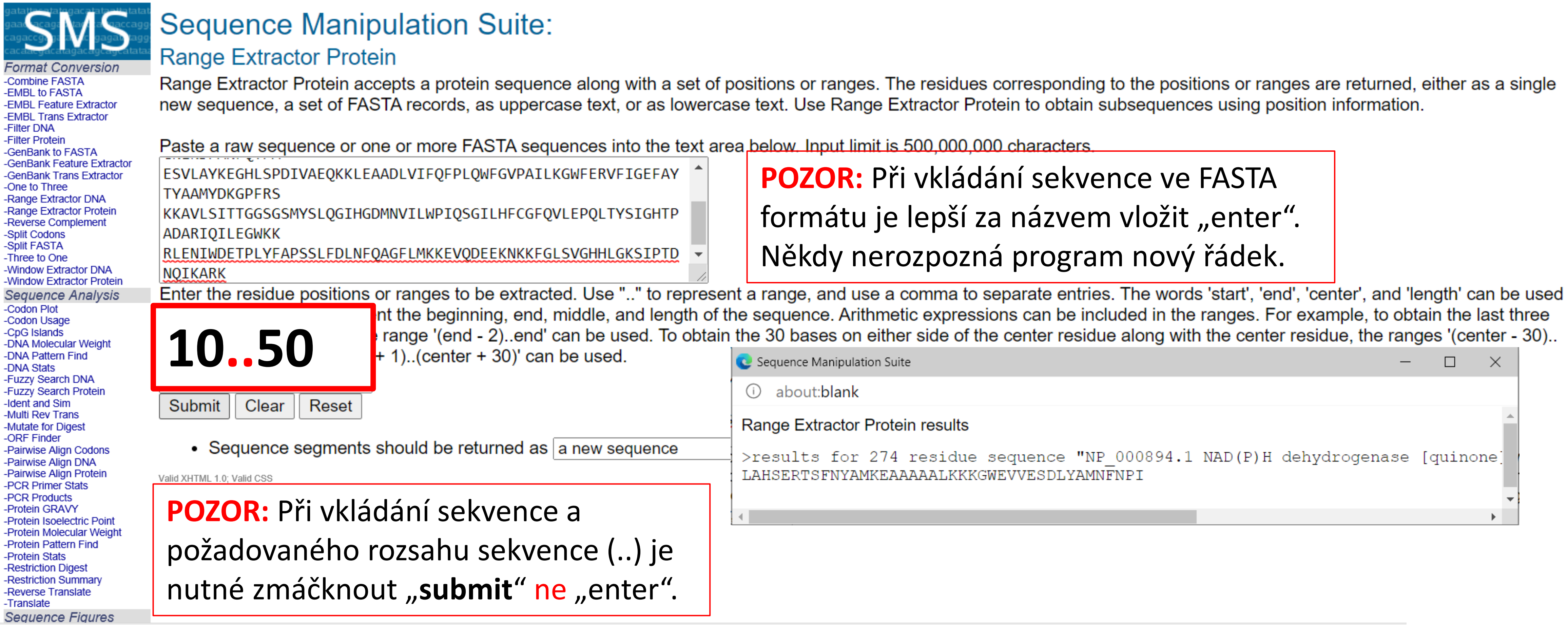
Protein Molecular Weight results

Results for 274 residue sequence "AAB60701.1 NAD (P)H:quinone oxireductase [Homo sapiens]" starting "MVGRRALIVL"
30.87 kDa

Protein Molecular Weight results

Results for 412 residue sequence "EAX02461.1 cathepsin D (lysosomal aspartyl peptidase), isoform CRA_a [Homo sapiens]" starting "MQPSSLLPLA"
44.56 kDa

Analýza vlastností proteinu/sekvence



Sequence Manipulation Suite:

Range Extractor Protein

Range Extractor Protein accepts a protein sequence along with a set of positions or ranges. The residues corresponding to the positions or ranges are returned, either as a single new sequence, a set of FASTA records, as uppercase text, or as lowercase text. Use Range Extractor Protein to obtain subsequences using position information.

Paste a raw sequence or one or more FASTA sequences into the text area below. Input limit is 500,000,000 characters.

```
ESVLAYKEGHLSPDIVAEQKKLEAADLVIFQFPLQWFGVPAILKGWFERVFIGEFAY
TYAAMYDKGPFRS
KKAVLSITTGGSGSMYSLQGIHGDMNVILWPIQSGILHFCGFQVLEPQLTYSIGHTP
ADARIQILEGWKK
RLENIWDETPLYFAPSSLFDLNFQAGFLMKKEVQDEEKNKKFGLSVGHHLGKSIPTD
NQIKARK
```

Enter the residue positions or ranges to be extracted. Use ".." to represent a range, and use a comma to separate entries. The words 'start', 'end', 'center', and 'length' can be used …nt the beginning, end, middle, and length of the sequence. Arithmetic expressions can be included in the ranges. For example, to obtain the last three … range '(end - 2)..end' can be used. To obtain the 30 bases on either side of the center residue along with the center residue, the ranges '(center - 30).. … + 1)..(center + 30)' can be used.

10..50

- Sequence segments should be returned as: a new sequence

Range Extractor Protein results

```
>results for 274 residue sequence "NP_000894.1 NAD(P)H dehydrogenase [quinone]
LAHSERTSFNYAMKEAAAAALKKKGWEVVESDLYAMNFNPI
```

POZOR: Při vkládání sekvence ve FASTA formátu je lepší za názvem vložit „enter“. Někdy nerozpozná program nový řádek.

POZOR: Při vkládání sekvence a požadovaného rozsahu sekvence (..) je nutné zmáčknout „**submit**“ ne „enter“.

Vyzkoušejte si SMS suite

Analyzujte si „svou vlastní“ sekvenci

- kolik má váš protein prolinů?
- identifikujte 100. aminokyselinu
- jaká bude molekulová hmotnost vašeho proteinu s histidinovou kotvou (6xHis)?

„Proteinová bioinformatika“

Vyhledávání AMK sekvencí

Analýza vlastností sekvencí (aminokyselinové složení, molekulová hmotnost, isoelektrický bod…)

Štěpení proteasami

Analýza hydrofobních segmentů, transmembránových úseků

Predikce sekundární struktury

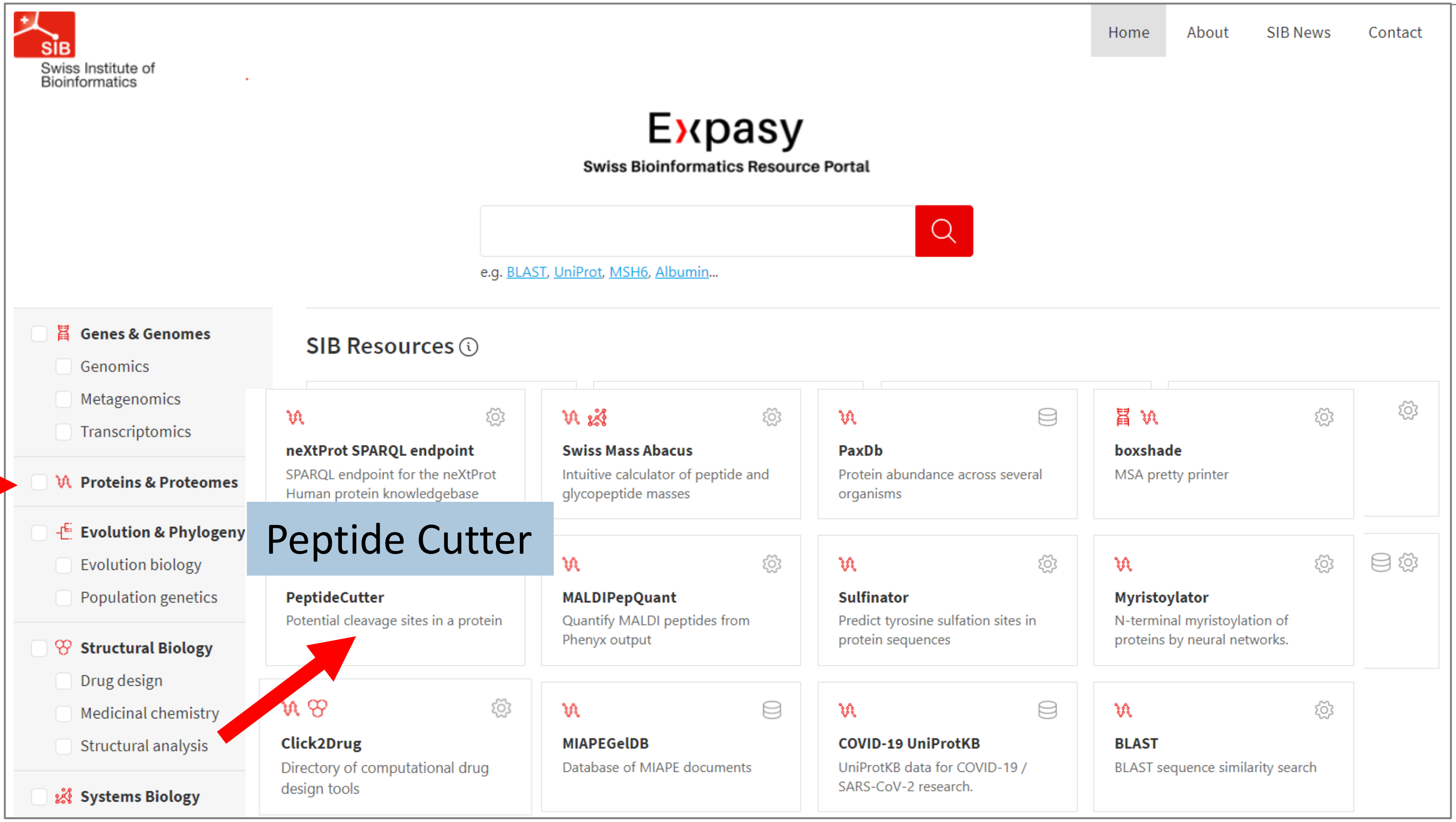
3D-struktura, vizualizace

Vyhledání a porovnání podobných sekvencí

Evoluční příbuznost sekvencí

…

Štěpení proteasami



SIB Swiss Institute of Bioinformatics

Home About SIB News Contact

Expasy

Swiss Bioinformatics Resource Portal

e.g. BLAST, UniProt, MSH6, Albumin...

☐ **Genes & Genomes**
- ☐ Genomics
- ☐ Metagenomics
- ☐ Transcriptomics

☐ **Proteins & Proteomes**

☐ **Evolution & Phylogeny**
- ☐ Evolution biology
- ☐ Population genetics

☐ **Structural Biology**
- ☐ Drug design
- ☐ Medicinal chemistry
- ☐ Structural analysis

☐ **Systems Biology**

SIB Resources

neXtProt SPARQL endpoint
SPARQL endpoint for the neXtProt Human protein knowledgebase

Swiss Mass Abacus
Intuitive calculator of peptide and glycopeptide masses

PaxDb
Protein abundance across several organisms

boxshade
MSA pretty printer

PeptideCutter
Potential cleavage sites in a protein

MALDIPepQuant
Quantify MALDI peptides from Phenyx output

Sulfinator
Predict tyrosine sulfation sites in protein sequences

Myristoylator
N-terminal myristoylation of proteins by neural networks.

Click2Drug
Directory of computational drug design tools

MIAPEGelDB
Database of MIAPE documents

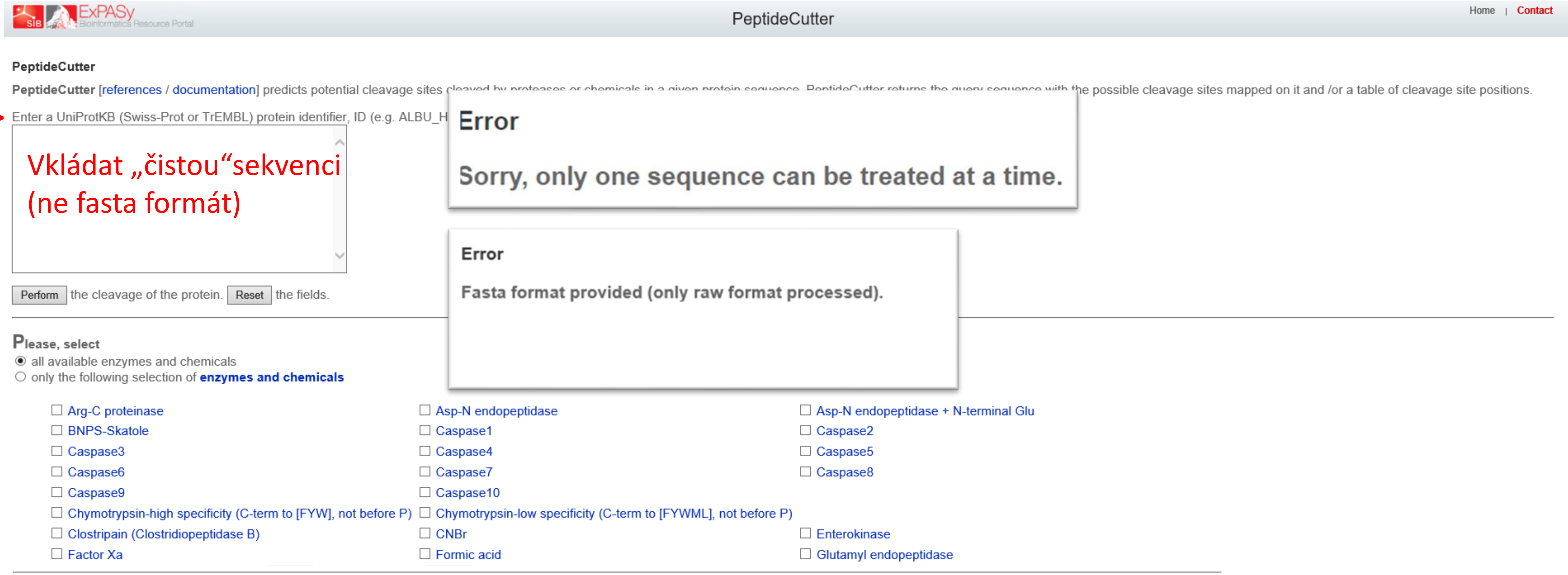
COVID-19 UniProtKB
UniProtKB data for COVID-19 / SARS-CoV-2 research.

BLAST
BLAST sequence similarity search

Peptide Cutter

http://web.expasy.org/peptide_cutter/

Štěpení proteasami



PeptideCutter

PeptideCutter [references / documentation] predicts potential cleavage sites cleaved by proteases or chemicals in a given protein sequence. PeptideCutter returns the query sequence with the possible cleavage sites mapped on it and /or a table of cleavage site positions.

Enter a UniProtKB (Swiss-Prot or TrEMBL) protein identifier, ID (e.g. ALBU_H

Vkládat „čistou“sekvenci (ne fasta formát)

Error

Sorry, only one sequence can be treated at a time.

Error

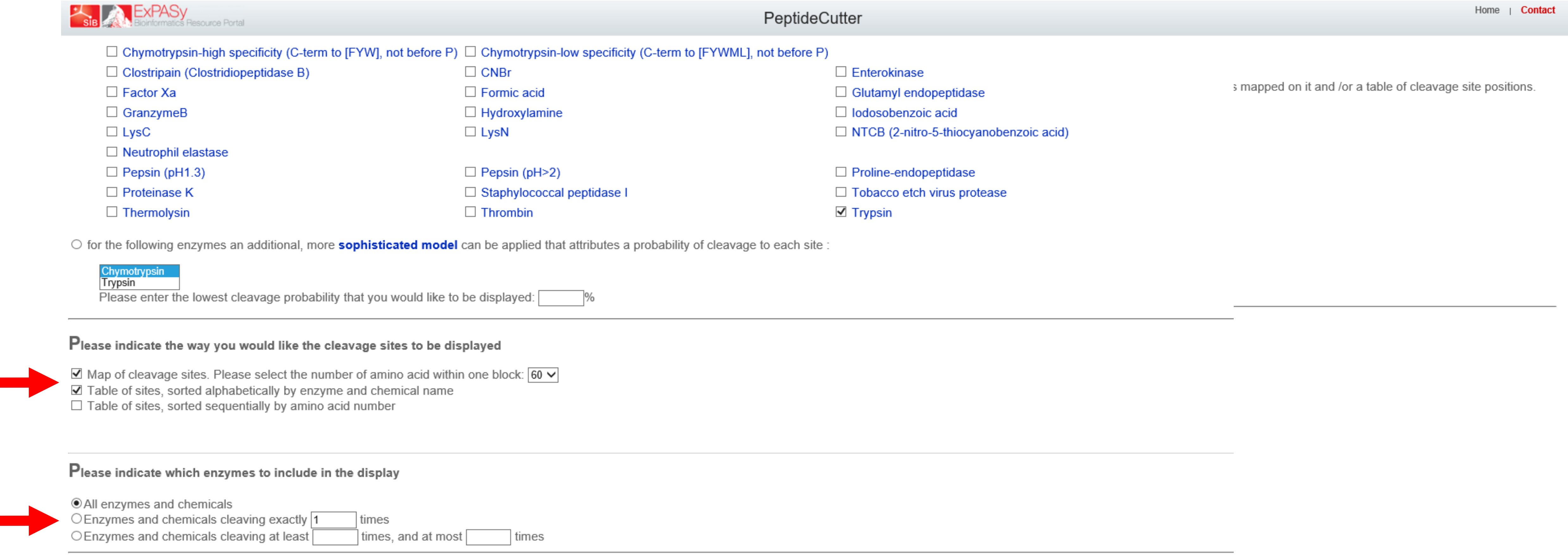
Fasta format provided (only raw format processed).

Please, select

● all available enzymes and chemicals
○ only the following selection of **enzymes and chemicals**

☐ Arg-C proteinase
☐ Asp-N endopeptidase
☐ Asp-N endopeptidase + N-terminal Glu
☐ BNPS-Skatole
☐ Caspase1
☐ Caspase2
☐ Caspase3
☐ Caspase4
☐ Caspase5
☐ Caspase6
☐ Caspase7
☐ Caspase8
☐ Caspase9
☐ Caspase10
☐ Chymotrypsin-high specificity (C-term to [FYW], not before P)
☐ Chymotrypsin-low specificity (C-term to [FYWML], not before P)
☐ Clostripain (Clostridiopeptidase B)
☐ CNBr
☐ Enterokinase
☐ Factor Xa
☐ Formic acid
☐ Glutamyl endopeptidase

Štěpení proteasami



PeptideCutter

☐ Chymotrypsin-high specificity (C-term to [FYW], not before P)
☐ Clostripain (Clostridiopeptidase B)
☐ Factor Xa
☐ GranzymeB
☐ LysC
☐ Neutrophil elastase
☐ Pepsin (pH1.3)
☐ Proteinase K
☐ Thermolysin

☐ Chymotrypsin-low specificity (C-term to [FYWML], not before P)
☐ CNBr
☐ Formic acid
☐ Hydroxylamine
☐ LysN
☐ Pepsin (pH>2)
☐ Staphylococcal peptidase I
☐ Thrombin

☐ Enterokinase
☐ Glutamyl endopeptidase
☐ Iodosobenzoic acid
☐ NTCB (2-nitro-5-thiocyanobenzoic acid)
☐ Proline-endopeptidase
☐ Tobacco etch virus protease
☑ Trypsin

mapped on it and /or a table of cleavage site positions.

○ for the following enzymes an additional, more **sophisticated model** can be applied that attributes a probability of cleavage to each site :

Chymotrypsin
Trypsin

Please enter the lowest cleavage probability that you would like to be displayed: ____ %

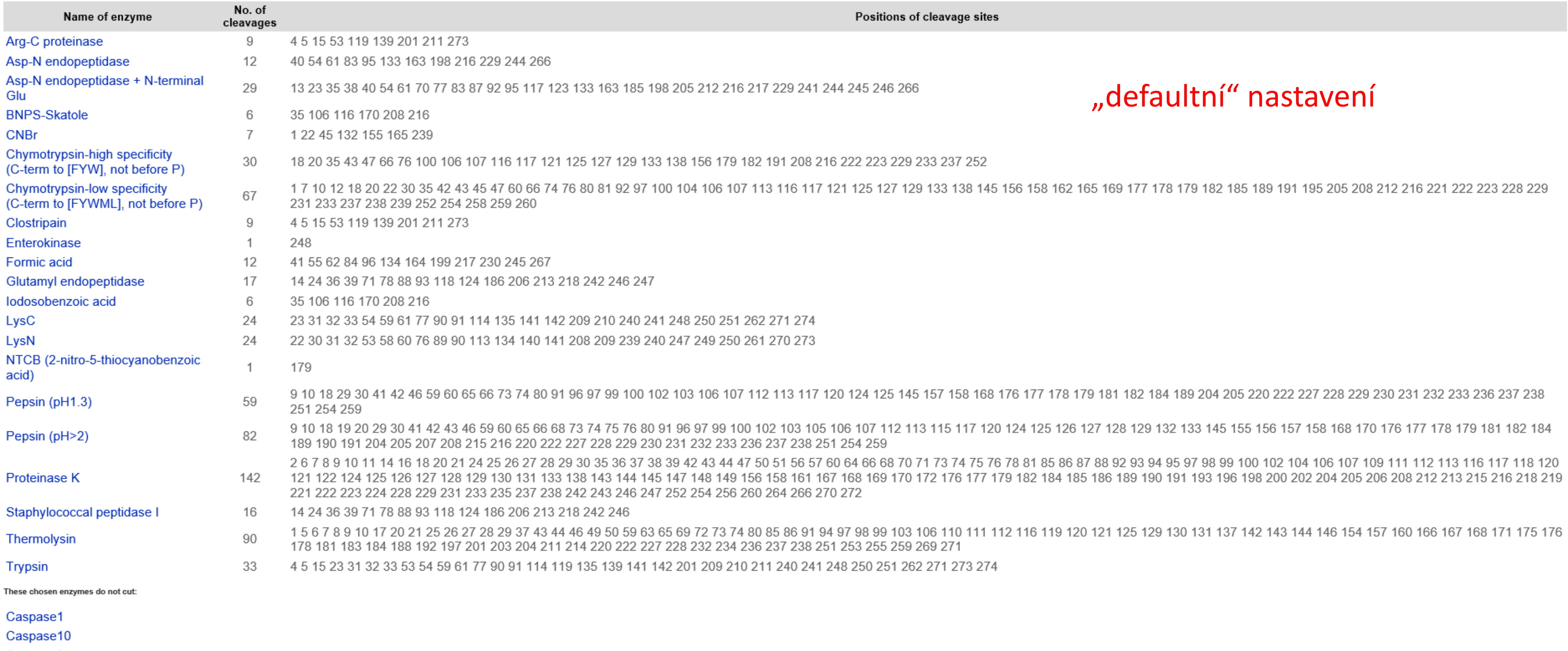
Please indicate the way you would like the cleavage sites to be displayed

☑ Map of cleavage sites. Please select the number of amino acid within one block: 60
☑ Table of sites, sorted alphabetically by enzyme and chemical name
☐ Table of sites, sorted sequentially by amino acid number

Please indicate which enzymes to include in the display

● All enzymes and chemicals
○ Enzymes and chemicals cleaving exactly 1 times
○ Enzymes and chemicals cleaving at least ____ times, and at most ____ times

Štěpení proteasami-PeptideCutter



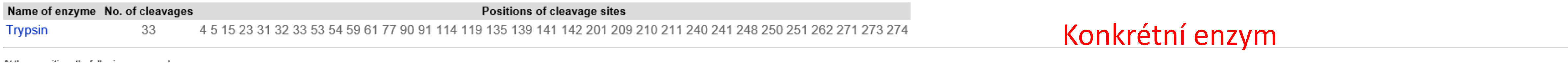
„defaultní“ nastavení

Name of enzyme	No. of cleavages	Positions of cleavage sites
Arg-C proteinase	9	4 5 15 53 119 139 201 211 273
Asp-N endopeptidase	12	40 54 61 83 95 133 163 198 216 229 244 266
Asp-N endopeptidase + N-terminal Glu	29	13 23 35 38 40 54 61 70 77 83 87 92 95 117 123 133 163 185 198 205 212 216 217 229 241 244 245 246 266
BNPS-Skatole	6	35 106 116 170 208 216
CNBr	7	1 22 45 132 155 165 239
Chymotrypsin-high specificity (C-term to [FYW], not before P)	30	18 20 35 43 47 66 76 100 106 107 116 117 121 125 127 129 133 138 156 179 182 191 208 216 222 223 229 233 237 252
Chymotrypsin-low specificity (C-term to [FYWML], not before P)	67	1 7 10 12 18 20 22 30 35 42 43 45 47 60 66 74 76 80 81 92 97 100 104 106 107 113 116 117 121 125 127 129 133 138 145 156 158 162 165 169 177 178 179 182 185 189 191 195 205 208 212 216 221 222 223 228 229 231 233 237 238 239 252 254 258 259 260
Clostripain	9	4 5 15 53 119 139 201 211 273
Enterokinase	1	248
Formic acid	12	41 55 62 84 96 134 164 199 217 230 245 267
Glutamyl endopeptidase	17	14 24 36 39 71 78 88 93 118 124 186 206 213 218 242 246 247
Iodosobenzoic acid	6	35 106 116 170 208 216
LysC	24	23 31 32 33 54 59 61 77 90 91 114 135 141 142 209 210 240 241 248 250 251 262 271 274
LysN	24	22 30 31 32 53 58 60 76 89 90 113 134 140 141 208 209 239 240 247 249 250 261 270 273
NTCB (2-nitro-5-thiocyanobenzoic acid)	1	179
Pepsin (pH1.3)	59	9 10 18 29 30 41 42 46 59 60 65 66 73 74 80 91 96 97 99 100 102 103 106 107 112 113 117 120 124 125 145 157 158 168 176 177 178 179 181 182 184 189 204 205 220 222 227 228 229 230 231 232 233 236 237 238 251 254 259
Pepsin (pH>2)	82	9 10 18 19 20 29 30 41 42 43 46 59 60 65 66 68 73 74 75 76 80 91 96 97 99 100 102 103 105 106 107 112 113 115 117 120 124 125 126 127 128 129 132 133 145 155 156 157 158 168 170 176 177 178 179 181 182 184 189 190 191 204 205 207 208 215 216 220 222 227 228 229 230 231 232 233 236 237 238 251 254 259
Proteinase K	142	2 6 7 8 9 10 11 14 16 18 20 21 24 25 26 27 28 29 30 35 36 37 38 39 42 43 44 47 50 51 56 57 60 64 66 68 70 71 73 74 75 76 78 81 85 86 87 88 92 93 94 95 97 98 99 100 102 104 106 107 109 111 112 113 116 117 118 120 121 122 124 125 126 127 128 129 130 131 133 138 143 144 145 147 148 149 156 158 161 167 168 169 170 172 176 177 179 182 184 185 186 189 190 191 193 196 198 200 202 204 205 206 208 212 213 215 216 218 219 221 222 223 224 228 229 231 233 235 237 238 242 243 246 247 252 254 256 260 264 266 270 272
Staphylococcal peptidase I	16	14 24 36 39 71 78 88 93 118 124 186 206 213 218 242 246
Thermolysin	90	1 5 6 7 8 9 10 17 20 21 25 26 27 28 29 37 43 44 46 49 50 59 63 65 69 72 73 74 80 85 86 91 94 97 98 99 103 106 110 111 112 116 119 120 121 125 129 130 131 137 142 143 144 146 154 157 160 166 167 168 171 175 176 178 181 183 184 188 192 197 201 203 204 211 214 220 222 227 228 232 234 236 237 238 251 253 255 259 269 271
Trypsin	33	4 5 15 23 31 32 33 53 54 59 61 77 90 91 114 119 135 139 141 142 201 209 210 211 240 241 248 250 251 262 271 273 274

These chosen enzymes do not cut:

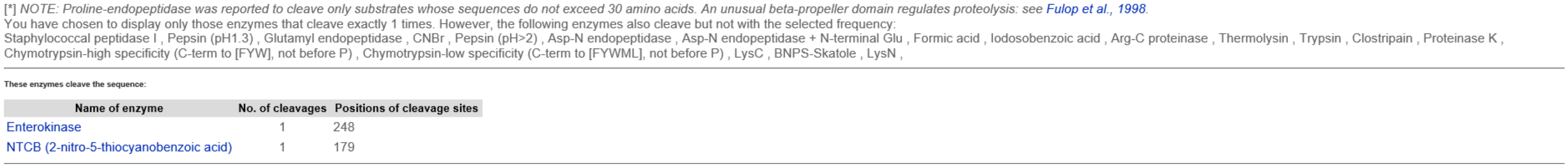
Caspase1
Caspase10

Štěpení proteasami-PeptideCutter



Name of enzyme	No. of cleavages	Positions of cleavage sites
Trypsin	33	4 5 15 23 31 32 33 53 54 59 61 77 90 91 114 119 135 139 141 142 201 209 210 211 240 241 248 250 251 262 271 273 274

Konkrétní enzym



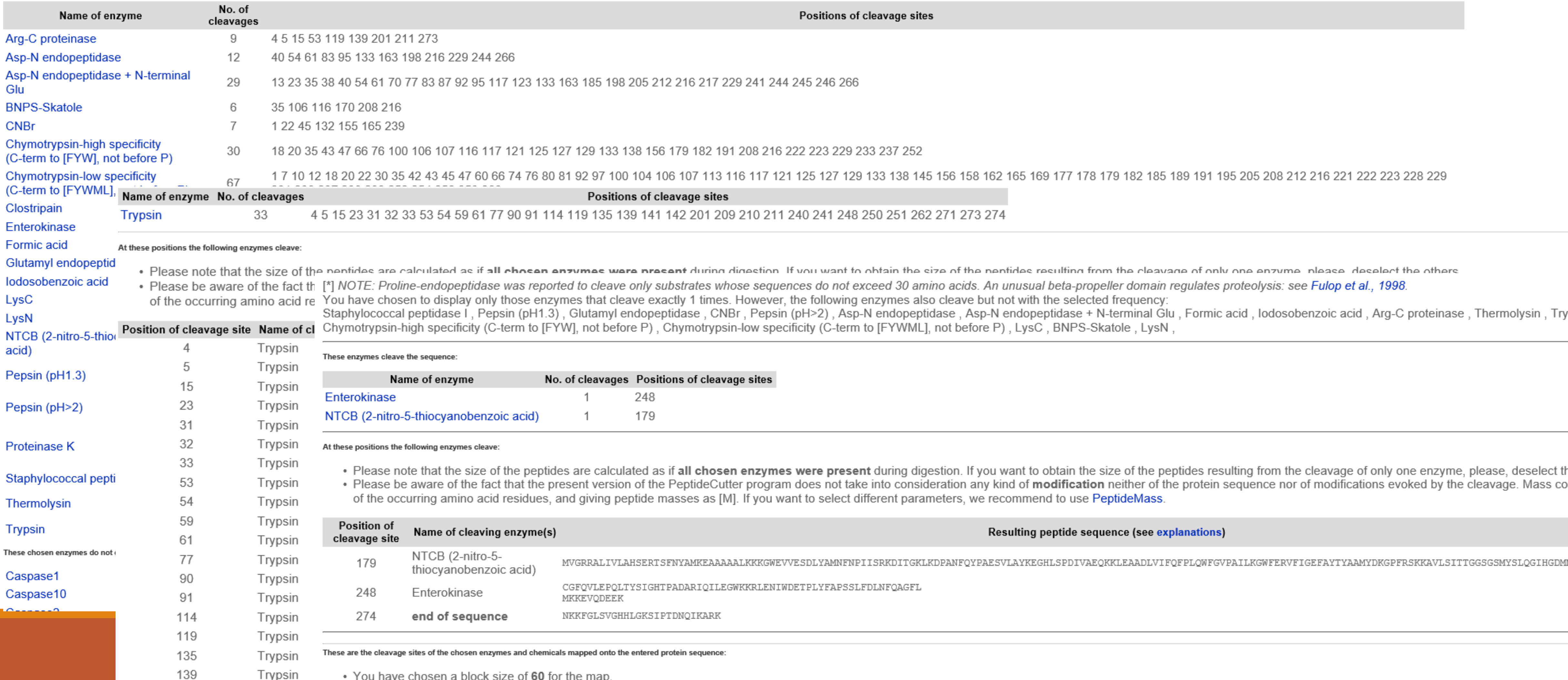
[*] *NOTE: Proline-endopeptidase was reported to cleave only substrates whose sequences do not exceed 30 amino acids. An unusual beta-propeller domain regulates proteolysis: see Fulop et al., 1998.*
You have chosen to display only those enzymes that cleave exactly 1 times. However, the following enzymes also cleave but not with the selected frequency:
Staphylococcal peptidase I , Pepsin (pH1.3) , Glutamyl endopeptidase , CNBr , Pepsin (pH>2) , Asp-N endopeptidase , Asp-N endopeptidase + N-terminal Glu , Formic acid , Iodosobenzoic acid , Arg-C proteinase , Thermolysin , Trypsin , Clostripain , Proteinase K , Chymotrypsin-high specificity (C-term to [FYW], not before P) , Chymotrypsin-low specificity (C-term to [FYWML], not before P) , LysC , BNPS-Skatole , LysN ,

These enzymes cleave the sequence:

Name of enzyme	No. of cleavages	Positions of cleavage sites
Enterokinase	1	248
NTCB (2-nitro-5-thiocyanobenzoic acid)	1	179

Co štěpí přesně jednou?

Štěpení proteasami-PeptideCutter



Name of enzyme	No. of cleavages	Positions of cleavage sites
Arg-C proteinase	9	4 5 15 53 119 139 201 211 273
Asp-N endopeptidase	12	40 54 61 83 95 133 163 198 216 229 244 266
Asp-N endopeptidase + N-terminal Glu	29	13 23 35 38 40 54 61 70 77 83 87 92 95 117 123 133 163 185 198 205 212 216 217 229 241 244 245 246 266
BNPS-Skatole	6	35 106 116 170 208 216
CNBr	7	1 22 45 132 155 165 239
Chymotrypsin-high specificity (C-term to [FYW], not before P)	30	18 20 35 43 47 66 76 100 106 107 116 117 121 125 127 129 133 138 156 179 182 191 208 216 222 223 229 233 237 252
Chymotrypsin-low specificity (C-term to [FYWML],	67	1 7 10 12 18 20 22 30 35 42 43 45 47 60 66 74 76 80 81 92 97 100 104 106 107 113 116 117 121 125 127 129 133 138 145 156 158 162 165 169 177 178 179 182 185 189 191 195 205 208 212 216 221 222 223 228 229
Clostripain		
Enterokinase		
Formic acid		
Glutamyl endopeptid		
Iodosobenzoic acid		
LysC		
LysN		
NTCB (2-nitro-5-thio acid)		
Pepsin (pH1.3)		
Pepsin (pH>2)		
Proteinase K		
Staphylococcal pepti		
Thermolysin		
Trypsin		

These chosen enzymes do not

Caspase1
Caspase10

Name of enzyme	No. of cleavages	Positions of cleavage sites
Trypsin	33	4 5 15 23 31 32 33 53 54 59 61 77 90 91 114 119 135 139 141 142 201 209 210 211 240 241 248 250 251 262 271 273 274

At these positions the following enzymes cleave:

- Please note that the size of the peptides are calculated as if **all chosen enzymes were present** during digestion. If you want to obtain the size of the peptides resulting from the cleavage of only one enzyme, please, deselect the others
- Please be aware of the fact th of the occurring amino acid re

Position of cleavage site	Name of cl
4	Trypsin
5	Trypsin
15	Trypsin
23	Trypsin
31	Trypsin
32	Trypsin
33	Trypsin
53	Trypsin
54	Trypsin
59	Trypsin
61	Trypsin
77	Trypsin
90	Trypsin
91	Trypsin
114	Trypsin
119	Trypsin
135	Trypsin
139	Trypsin

[*] *NOTE: Proline-endopeptidase was reported to cleave only substrates whose sequences do not exceed 30 amino acids. An unusual beta-propeller domain regulates proteolysis: see Fulop et al., 1998.*

You have chosen to display only those enzymes that cleave exactly 1 times. However, the following enzymes also cleave but not with the selected frequency:
Staphylococcal peptidase I , Pepsin (pH1.3) , Glutamyl endopeptidase , CNBr , Pepsin (pH>2) , Asp-N endopeptidase , Asp-N endopeptidase + N-terminal Glu , Formic acid , Iodosobenzoic acid , Arg-C proteinase , Thermolysin , Try
Chymotrypsin-high specificity (C-term to [FYW], not before P) , Chymotrypsin-low specificity (C-term to [FYWML], not before P) , LysC , BNPS-Skatole , LysN ,

These enzymes cleave the sequence:

Name of enzyme	No. of cleavages	Positions of cleavage sites
Enterokinase	1	248
NTCB (2-nitro-5-thiocyanobenzoic acid)	1	179

At these positions the following enzymes cleave:

- Please note that the size of the peptides are calculated as if **all chosen enzymes were present** during digestion. If you want to obtain the size of the peptides resulting from the cleavage of only one enzyme, please, deselect th
- Please be aware of the fact that the present version of the PeptideCutter program does not take into consideration any kind of **modification** neither of the protein sequence nor of modifications evoked by the cleavage. Mass co of the occurring amino acid residues, and giving peptide masses as [M]. If you want to select different parameters, we recommend to use PeptideMass.

Position of cleavage site	Name of cleaving enzyme(s)	Resulting peptide sequence (see explanations)
179	NTCB (2-nitro-5-thiocyanobenzoic acid)	MVGRRALIVLAHSERTSFNYAMKEAAAAALKKKGWEVVESDLYAMNFNPIISRKDITGKLKDPANFQYPAESVLAYKEGHLSPDIVAEQKKLEAADLVIFQFPLQWFGVPAILKGWFERVFIGEFAYTYAAMYDKGPFRSKKAVLSITTGGSGSMYSLQGIHGDM
248	Enterokinase	CGFQVLEPQLTYSIGHTPADARIQILEGWKKRLENIWDETPLYFAPSSLFDLNFQAGFL MKKEVQDEEK
274	**end of sequence**	NKKFGLSVGHHLGKSIPTDNQIKARK

These are the cleavage sites of the chosen enzymes and chemicals mapped onto the entered protein sequence:

- You have chosen a block size of **60** for the map.

Štěpení proteasami-PeptideCutter

Hledání nejdelšího peptidu po štěpení jedním enzymem

PeptideCutter

PeptideCutter [references / documentation] predicts potential cleavage sites cleaved by proteases or chemicals in a given protein sequence. PeptideCutter returns the query sequence with the possible cleavage sites mapped on it and /or a table of cleavage site positions.

Enter a UniProtKB (Swiss-Prot or TrEMBL) protein identifier, ID (e.g. ALBU_HUMAN), or accession number, AC (e.g. P04406), **or** an amino acid sequence (e.g. 'SERVELAT'):

```
MAARRALIVLAHSEKTSFNYAMKEAAVEALKKRGWEVLESDLYAMNFNPIIS
RNDITGEL
KDSKNFQYPSESSLAYKEGRLSPDIVAEHKKLEAADLVIFQFPLQWFGVPAI
LKGWFERV
LVAGFAYTYAAMYDNGPFQNKKTLLSITTGGSGSMYSLQGVHGDMNVILWPI
QSGILRFC
GFQVLEPQLVYSIGHTPPDARMQILEGWKKRLETVWEETPLYFAPSSLFDLN
FQAGFLMK
KEVQEEQKKNKFGLSVGHHLGKSIPADNQIKARK
```

the cleavage of the protein. the fields.

Please, select

○ all available enzymes and chemicals
● only the following selection of **enzymes and chemicals**

☐ Arg-C proteinase
☐ Asp-N endopeptidase
☐ Asp-N endopeptidase + N-terminal Glu
☐ BNPS-Skatole
☐ Caspase1
☐ Caspase2
☐ Caspase3
☐ Caspase4
☐ Caspase5
☐ Caspase6
☐ Caspase7
☐ Caspase8
☐ Caspase9
☐ Caspase10
☐ Chymotrypsin-high specificity (C-term to [FYW], not before P)
☐ Chymotrypsin-low specificity (C-term to [FYWML], not before P)
☐ Clostripain (Clostridiopeptidase B)
☐ CNBr
☐ Enterokinase
☐ Factor Xa
☐ Formic acid
☐ Glutamyl endopeptidase
☐ GranzymeB
☐ Hydroxylamine
☐ Iodosobenzoic acid
☐ LysC
☐ LysN
☐ NTCB (2-nitro-5-thiocyanobenzoic acid)
☐ Neutrophil elastase
☐ Pepsin (pH1.3)
☐ Pepsin (pH>2)
☐ Proline-endopeptidase
☐ Proteinase K
☐ Staphylococcal peptidase I
☐ Tobacco etch virus protease
☐ Thermolysin
☐ Thrombin
☑ Trypsin

Please indicate the way you would like the cleavage sites to be displayed

☑ Map of cleavage sites. Please select the number of amino acid within one block: 60
☑ Table of sites, sorted alphabetically by enzyme and chemical name
☑ Table of sites, sorted sequentially by amino acid number

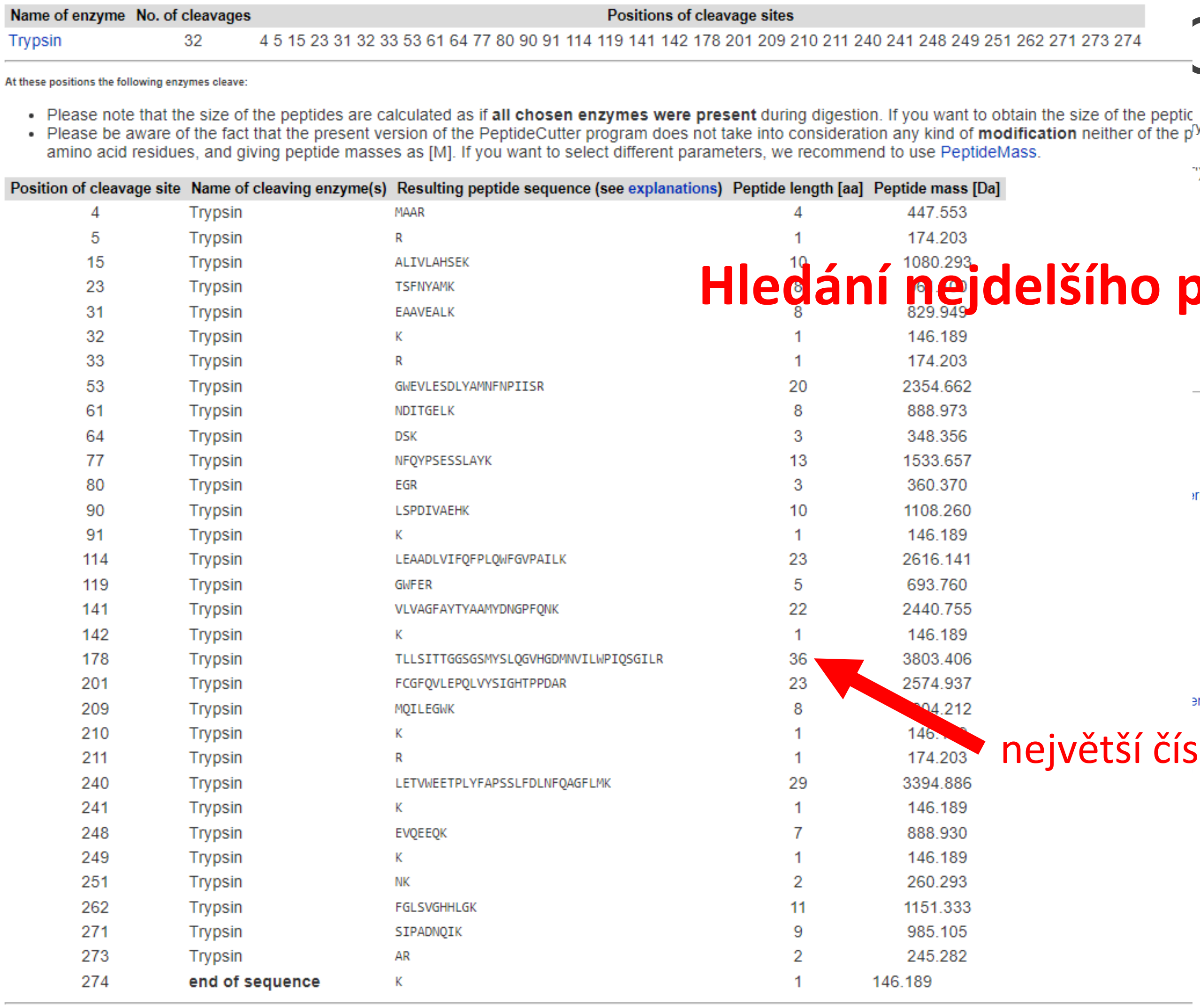
ptideCutter

ry sequence with the possible cleavage sites mapped on it and /or a table of cleavage site

"):

rminal Glu

nzoic acid)



Name of enzyme	No. of cleavages	Positions of cleavage sites
Trypsin	32	4 5 15 23 31 32 33 53 61 64 77 80 90 91 114 119 141 142 178 201 209 210 211 240 241 248 249 251 262 271 273 274

At these positions the following enzymes cleave:

- Please note that the size of the peptides are calculated as if **all chosen enzymes were present** during digestion. If you want to obtain the size of the peptic
- Please be aware of the fact that the present version of the PeptideCutter program does not take into consideration any kind of **modification** neither of the p amino acid residues, and giving peptide masses as [M]. If you want to select different parameters, we recommend to use PeptideMass.

Position of cleavage site	Name of cleaving enzyme(s)	Resulting peptide sequence (see explanations)	Peptide length [aa]	Peptide mass [Da]
4	Trypsin	MAAR	4	447.553
5	Trypsin	R	1	174.203
15	Trypsin	ALIVLAHSEK	10	1080.293
23	Trypsin	TSFNYAMK	8	[illegible]
31	Trypsin	EAAVEALK	8	829.949
32	Trypsin	K	1	146.189
33	Trypsin	R	1	174.203
53	Trypsin	GWEVLESDLYAMNFNPIISR	20	2354.662
61	Trypsin	NDITGELK	8	888.973
64	Trypsin	DSK	3	348.356
77	Trypsin	NFQYPSESSLAYK	13	1533.657
80	Trypsin	EGR	3	360.370
90	Trypsin	LSPDIVAEHK	10	1108.260
91	Trypsin	K	1	146.189
114	Trypsin	LEAADLVIFQFPLQWFGVPAILK	23	2616.141
119	Trypsin	GWFER	5	693.760
141	Trypsin	VLVAGFAYTYAAMYDNGPFQNK	22	2440.755
142	Trypsin	K	1	146.189
178	Trypsin	TLLSITTGGSGSMYSLQGVHGDMNVILWPIQSGILR	36	3803.406
201	Trypsin	FCGFQVLEPQLVYSIGHTPPDAR	23	2574.937
209	Trypsin	MQILEGWK	8	[illegible]
210	Trypsin	K	1	[illegible]
211	Trypsin	R	1	174.203
240	Trypsin	LETVWEETPLYFAPSSLFDLNFQAGFLMK	29	3394.886
241	Trypsin	K	1	146.189
248	Trypsin	EVQEEQK	7	888.930
249	Trypsin	K	1	146.189
251	Trypsin	NK	2	260.293
262	Trypsin	FGLSVGHHLGK	11	1151.333
271	Trypsin	SIPADNQIK	9	985.105
273	Trypsin	AR	2	245.282
274	**end of sequence**	K	1	146.189

Hledání nejdelšího peptidu po štěpení

největší číslo

Vyzkoušejte si PeptideCutter

Analyzujte si „svou vlastní“ sekvenci

- Štěpí nějaký enzym pouze jedenkrát? (-vyzkoušejte štěpení všemi (default nastavení)
  (nebo: Vyberte pouze enzym, který štěpí jedenkrát.)
- Jak dlouhý je nejdelší vzniklý peptid po štěpení trypsinem? (omezte štěpení pouze na Trypsin, zaškrtněte si tabulku s „počtem aminokyselin“)

„Proteinová bioinformatika“

Vyhledávání AMK sekvencí

Analýza vlastností sekvencí (aminokyselinové složení, molekulová hmotnost, isoelektrický bod…)

Štěpení proteasami

Analýza hydrofobních segmentů, transmembránových úseků

Predikce sekundární struktury

3D-struktura, vizualizace

Vyhledání a porovnání podobných sekvencí

Evoluční příbuznost sekvencí

…

shrnutí I - Rešeršní projekt: NQO1

Vyhledejte dostupné informace o NQO1, získejte co nejvíce literárních, sekvenčních, případně i strukturních a dalších údajů o tomto genu/proteinu.

Nalezněte podobné sekvence a porovnejte je na proteinové úrovni.

- **NAD(P)H:chinonoxidoreduktasa / reference**
- **Protein: NP_000894, P15559 / 274 AMK; 30,8 kDa; trypsin štěpí 33x (59AMK nejdelší peptid)…**

DÚ2: Vyhledávání proteinů

Pracujte s „vaším“ genem/proteinem/enzymem (př. NQO1)

1) Vyhledejte „referenční“ NCBI a UniProt přístupové kódy

2) Najděte a uložte si „FASTA“ formát sekvence a uložte si ji (jako text-ne jako výstřižek)

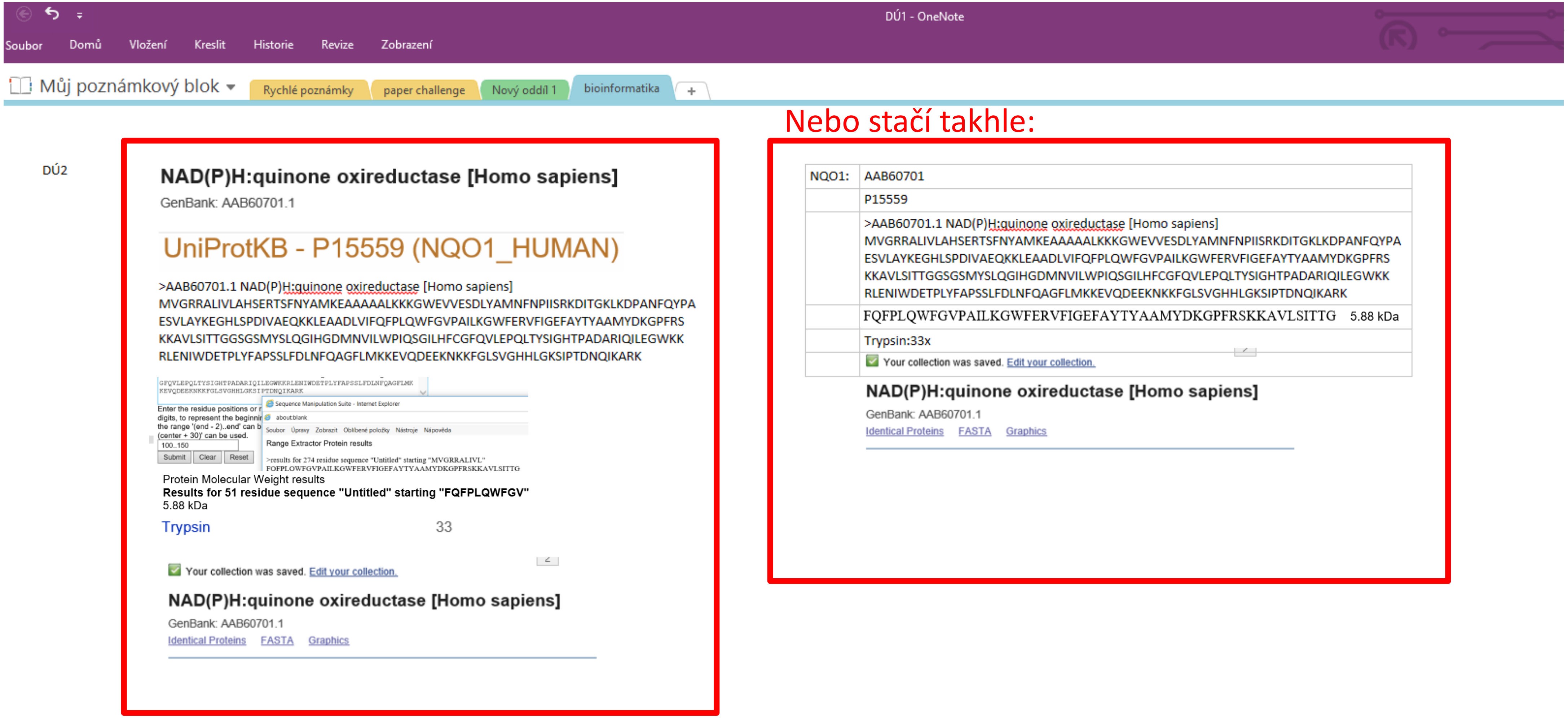
3) Vyberte část proteinu od **10. do 50.** aminokyseliny

4) Spočítejte molekulovou hmotnost tohoto úseku proteinu

5) Zjistěte kolikrát bude vaše **celá** sekvence štěpena trypsinem

- vše zpracujte do bloku OneNote, Word, Pdf

Literární rešerše: DÚ2-příklad řešení



DÚ2

NAD(P)H:quinone oxireductase [Homo sapiens]

GenBank: AAB60701.1

UniProtKB - P15559 (NQO1_HUMAN)

>AAB60701.1 NAD(P)H:quinone oxireductase [Homo sapiens]
MVGRRALIVLAHSERTSFNYAMKEAAAAALKKKGWEVVESDLYAMNFNPIISRKDITGKLKDPANFQYPA
ESVLAYKEGHLSPDIVAEQKKLEAADLVIFQFPLQWFGVPAILKGWFERVFIGEFAYTYAAMYDKGPFRS
KKAVLSITTGGSGSMYSLQGIHGDMNVILWPIQSGILHFCGFQVLEPQLTYSIGHTPADARIQILEGWKK
RLENIWDETPLYFAPSSLFDLNFQAGFLMKKEVQDEEKNKKFGLSVGHHLGKSIPTDNQIKARK

```
GFQVLEPQLTYSIGHTPADARIQILEGWKKRLENIWDETPLYFAPSSLFDLNFQAGFLMK
KEVQDEEKNKKFGLSVGHHLGKSIPTDNQIKARK
```

Enter the residue positions or r
digits, to represent the beginnir
the range '(end - 2)..end' can b
(center + 30)' can be used.

100..150

Range Extractor Protein results

```
>results for 274 residue sequence "Untitled" starting "MVGRRALIVL"
FQFPLQWFGVPAILKGWFERVFIGEFAYTYAAMYDKGPFRSKKAVLSITTG
```

Protein Molecular Weight results
Results for 51 residue sequence "Untitled" starting "FQFPLQWFGV"
5.88 kDa

Trypsin 33

✅ Your collection was saved. Edit your collection.

NAD(P)H:quinone oxireductase [Homo sapiens]

GenBank: AAB60701.1

Identical Proteins FASTA Graphics

Nebo stačí takhle:

NQO1:	AAB60701
	P15559
	>AAB60701.1 NAD(P)H:quinone oxireductase [Homo sapiens] MVGRRALIVLAHSERTSFNYAMKEAAAAALKKKGWEVVESDLYAMNFNPIISRKDITGKLKDPANFQYPA ESVLAYKEGHLSPDIVAEQKKLEAADLVIFQFPLQWFGVPAILKGWFERVFIGEFAYTYAAMYDKGPFRS KKAVLSITTGGSGSMYSLQGIHGDMNVILWPIQSGILHFCGFQVLEPQLTYSIGHTPADARIQILEGWKK RLENIWDETPLYFAPSSLFDLNFQAGFLMKKEVQDEEKNKKFGLSVGHHLGKSIPTDNQIKARK
	FQFPLQWFGVPAILKGWFERVFIGEFAYTYAAMYDKGPFRSKKAVLSITTG 5.88 kDa
	Trypsin:33x
	✅ Your collection was saved. Edit your collection.

NAD(P)H:quinone oxireductase [Homo sapiens]

GenBank: AAB60701.1

Identical Proteins FASTA Graphics