Similarità, omologia e identità fra sequenze proteiche

Identità grado di corrispondenza esatta fra due sequenze proteiche allineate (tenendo anche conto di **GAP**). (gap = lacuna)

$I \geq 25\%$ implica simili funzioni $18 \leq I \geq 25$ (grey area) possibile similarità

(NB 2 sequenze casuali con > 100 residui possono avere un'identità > 25%)

Similarità grado di somiglianza generale fra due sequenze (tiene conto di **gap** e AA simili)

Omologia discendenza da *una sequenza ancestrale comune*

identità vs. similarità

identity → **exact match** fra due sequenze nucleotidiche o peptidiche (considerando gaps)

similarity → **assomiglianza** fra due sequenze **maggiore di quella possibilmente casuale**.

Metodi per confronto di sequenze basati su identità r similarità

- L'**allineamento di sequenze** è un metodo *bioinformatico* per confrontare due o più sequenze amminoacidiche o nucleotidiche.

```
METQGKKLKRNHGPPGLFVDRTYNSTWKKSVLGQILW
  ||:|||:|   | ||||:|||||:|||||    ||||||
            MESQGKRLIVNNGPPGIFVDRTFNSTWKYIKLGQILW
```

- Permette di **individuare regioni identiche o simili** che potrebbero avere **relazioni filogenetiche** (evolutive) e/o **funzionali** e **strutturali**.

- Questo metodo è anche molto utile per determinare se una sequenza di interesse è presente nelle **database di sequenze conosciute**, oppure se esiste una sequenza simile in un altro organismo.

Query sequence

```
METQGKKLKRNHGPPGLFVDRTYNSTWKKSVLGQILW
```

Database

```
MHSSIVLATVLFVAIASASKTRELCMKSLEHAKVGTSKEAKQDGIDL
YKHMFEHYPAMKKYFKHRENYTPADVQKDPFFIKQGQNILLACHV
LCATYDDRETFDAYVGELMARHERDHVKVPNDVWNHFWEHFIEF
LGSK

TTLDEPTKHAWQEIGKEFSHEISHHGRHSVRDHCMNSLEYIAIGDK
EHQKQNGIDLYKHMFEHYPHMRKAFKGRENFTKEDVQKDAFFVN
KDTRFCWPFVCCDSSYDDEPTFDYFVDALMDRHIKDDIHLPQEQ
WHEFWK

LFAEYLNEKSHQHLTEAEKHAWSTIGEDFAHEADKHAKAEKDHHE
GEHKEEHHKLGGGENAMKAAVPLFYKKVLADERVKHFFKNTDMDH
QTKQQTDFLTMLLGGPNHYKGKNMT

EAHKGMNLQNLHFDAIIENLAATLKELGVTDAVINEAAKVIEHTRK
DMLGKTINIIKATVPVLKEHGVTITTTFYKNLFAKHPEVRPLFDMGR
QESLEQPKALAMTVLAAAQNIEN

LPAILPAVKKIAVKHCQAGVAAAHYPIVGQELLGAIKEVLGDAATD
DILDAWGKAYGVIADVFIQVEADLYAQAVEQELLGAIKEVLGDAAT
DDILDAWGKAYGVIADVFIQVEADLAQAVE

EPTKHAWQEIGKEFSHEISHHGRHSVRDHCMNSLEYIAIGDKEHQ
KQNGIDLYKHMFEHYPHMRKAFKGRENFTKEDVQKDAFFVNKDT
RFCWPFVCCDSSYDDEPTFDYFVDALMDRHIKDDIHLPQEQW
```

Best alignment

```
METQGKKLKRNHGPPGLFVDRTYNSTWKKSVLGQILW   query
||:|||:|   | ||||:|||||:|||||    ||||||
MESQGKRLIVNNGPPGIFVDRTFNSTWKYIKLGQILW   subject
```

Identità e similarità di sequenza vs omologia – il ruolo dei GAP

Come si determina la similarità – fattori genotipici e fenotipici

1st letter	Second Letter: U	Second Letter: C	Second Letter: A	Second Letter: G	3rd letter
U	UUU Phe UUC UUA Leu UUG	UCU UCC Ser UCA UCG	UAU Tyr UAC UAA Stop UAG Stop	UGU Cys UGC UGA Stop UGG Trp	U C A G
C	CUU CUC Leu CUA CUG	CCU CCC Pro CCA CCG	CAU His CAC CAA Gln CAG	CGU CGC Arg CGA CGG	U C A G
A	AUU AUC Ile AUA AUG Met	ACU ACC Thr ACA ACG	AAU Asn AAC AAA Lys AAG	AGU Ser AGC AGA Arg AGG	U C A G
G	GUU GUC Val GUA GUG	GCU GCC Ala GCA GCG	GAU Asp GAC GAA Glu GAG	GGU GGC Gly GGA GGG	U C A G

Major forms of mutation are:

Point mutation

Silent (**synonimous**) substitutions - change nucleotide sequence (genotype) but not the amino acid sequence (phenotype)

Nonsilent (**nonsynonymous, missense**) substitutions - change AA seq

(**nonsense**) substitutions - AA → stop

Insertion/deletion (indel) – addition/removal of **whole triplet**

Lys (K) → Arg (R)

probabilità Gen Fen

AAA CGA CGC
AAG CGU CGG
AGA AGG ☑ ☑

Phe (F) → Trp (W)
→ Tyr (Y)

UUU UGG ☒ ~☑
UUC UAU ☑ ~☑
UAC ☑ ~☑

Phe (F) → Gly (G)

UUU → GGU GGC ☒ ☒
UUC GGA GGG

Ile (I) → Lys (K)

AUU → AAA ☑ ☒
AUC AUG
AUA

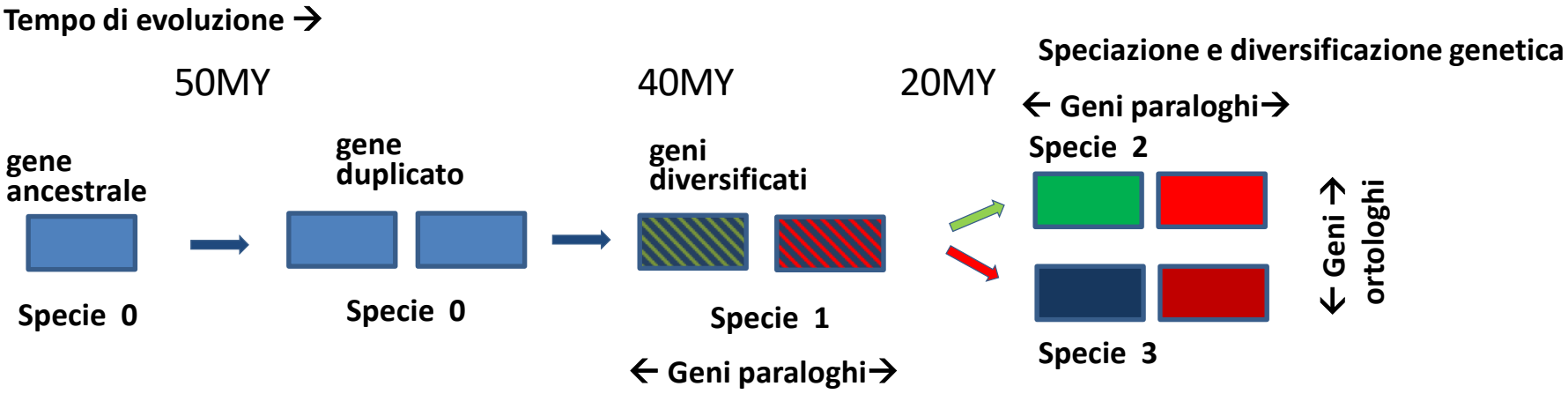
Metodi per misurare la similarità di sequenza

Sequenze proteiche

Distanze "genetiche" basandosi su modelli di come si evolvono le sequenze amminoacidiche

- matrici *"Point Accepted Mutation"* (PAM) (anni 1970)
- matrici BLOSUM (*Blocks Substitution Matrix*)

Gene duplication (fattore complicante) un organismo può avere due o più sequenze geniche derivate da un unico gene ancestrale che si è duplicato (geni paraloghi).



Paralogo: geni nello stesso organismo che derivano da un **gene duplicato e poi diverisficato** (le proteine codificate possono avere funzioni diverse avendo seguito un percorso evolutivo diverso)

Ortologo: dovuto a speciazione - gene in diverse specie che deriva da **uno dei due geni duplicate, che continua a diversificarsi in nuove specie** (in genere la proteina codificata mantiene strutture e funzione simili nelle diverse specie)

"Pairwise alignment" and "Substitution matrix"

```
PSHLQYHERTHTGEKPYECHQCGQATFKKCSLLQRHKRTHTGEKPYE-CGQCGKAFAQ-
HSHLQCHKRTHTGEKPYECNQCGKA-FSQHGLLQRHKRTHTGEKPYMNVINMVKPLHNS
****  *:**********:***:* *.:  .****************      :   *.: :
```

BLOSUM (**BLO**cks **SU**bstitution **M**atrix). Matrici statistiche di <u>frequenza intrinseca dei residui</u> e <u>probabilità che un residuo si trasformi in un altro</u> (fra le 210 possibili paia di sostituzioni per i 20 amino acidi proteinogenici).

BLOSUM62 → matrice per protein fino al 62% di identità

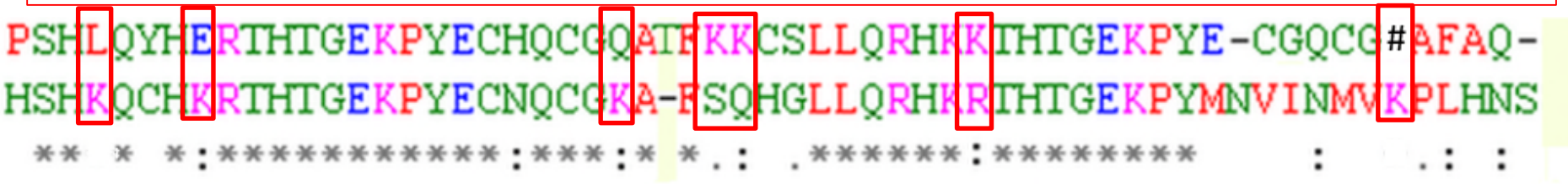
Più alto il mumero di matrice più simili sono le protein confrontate

BLOSUM 62

	C	S	T	P	A	G	N	D	E	Q	H	R	K	M	I	L	V	F	Y	W	
C	9																				C
S	-1	4																			S
T	-1	1	5																		T
P	-3	-1	-1	7																	P
A	0	1	0	-1	4																A
G	-3	0	-2	-2	0	6															G
N	-3	1	0	-2	-2	0	6														N
D	-3	0	-1	-1	-2	-1	1	6													D
E	-4	0	-1	-1	-1	-2	0	2	5												E
Q	-3	0	-1	-1	-1	-2	0	0	2	5											Q
H	-3	-1	-2	-2	-2	-2	1	-1	0	0	8										H
R	-3	-1	-1	-2	-1	-2	0	-2	0	1	0	5									R
K	-3	0	-1	-1	-1	-2	0	-1	1	1	-1	2	5								K
M	-1	-1	-1	-2	-1	-3	-2	-3	-2	0	-2	-1	-1	5							M
I	-1	-2	-1	-3	-1	-4	-3	-3	-3	-3	-3	-3	-3	1	4						I
L	-1	-2	-1	-3	-1	-4	-3	-4	-3	-2	-3	-2	-2	2	2	4					L
V	-1	-2	0	-2	0	-3	-3	-3	-2	-2	-3	-3	-2	1	3	1	4				V
F	-2	-2	-2	-4	-2	-3	-3	-3	-3	-3	-1	-3	-3	0	0	0	-1	6			F
Y	-2	-2	-2	-3	-2	-3	-2	-3	-2	-1	2	-2	-2	-1	-1	-1	-1	3	7		Y
W	-2	-3	-2	-4	-3	-2	-4	-4	-3	-2	-2	-3	-3	-1	-3	-2	-3	1	2	11	W
	C	S	T	P	A	G	N	D	E	Q	H	R	K	M	I	L	V	F	Y	W	

> 3 = *
≥ 1 = :
0 = .
< 0 =

“Pairwise alignment” and “Substitution matrix”



PAM (**Point Accepted Mutation) Matrix**: Probabilità che un residuo amminoacidico si trasformi in un altro mediante i normali processi di mutazione, tenendo conto anche di sostituzioni multiple in una posizione.

PAM30 basata sul confronto di sequenze con
3O mutazioni / 100 residui

PAM70 basata sul confronto di sequenze con
7O mutazioni / 100 residui

Più alto il numero PAM
più distanti evolutivamente
sono le sequenze confrontate

(# = STOP)

PAM 250

	G	A	V	L	I	P	S	T	D	E	N	Q	K	R	H	F	Y	W	M	C	B	Z	X	*	
G	5																								G
A	1	2																							A
V	-1	0	4																						V
L	-4	-2	2	6																					L
I	-3	-1	4	2	5																				I
P	0	1	-1	-3	-2	6																			P
S	1	1	-1	-3	-1	1	2																		S
T	0	1	0	-2	0	0	1	3																	T
D	1	0	-2	-4	-2	-1	0	0	4																D
E	0	0	-2	-3	-2	-1	0	0	3	4															E
N	0	0	-2	-3	-2	0	1	0	2	1	2														N
Q	-1	0	-2	-2	-2	0	-1	-1	2	2	1	4													Q
K	-2	-1	-2	-3	-2	-1	0	0	0	0	1	1	5												K
R	-3	-2	-2	-3	-2	0	0	-1	-1	-1	0	1	3	6											R
H	-2	-1	-2	-2	-2	0	-1	-1	1	1	2	3	0	2	6										H
F	-5	-3	-1	2	1	-5	-3	-3	-6	-5	-3	-5	-5	-4	-2	9									F
Y	-5	-3	-2	-1	-1	-5	-3	-3	-4	-4	-2	-4	-4	-4	0	7	10								Y
W	-7	-6	-6	-2	-5	-6	-2	-5	-7	-7	-4	-5	-3	-2	-3	0	0	17							W
M	-3	-1	2	4	2	-2	-2	-1	-3	-2	-2	-1	0	0	-2	0	-2	-4	6						M
C	-3	-2	-2	-6	-2	-3	0	-2	-5	-5	-4	-5	-5	-4	-3	-4	0	-8	-5	12					C
B	0	0	-2	-3	-2	-1	0	0	3	3	2	1	1	-1	1	-4	-3	-5	-2	-4	3				B
Z	0	0	-2	-3	-2	0	0	-1	3	3	1	3	0	0	2	-5	-4	-6	-2	-5	2	3			Z
X	-1	0	-1	-1	-1	-1	0	0	-1	-1	0	-1	-1	-1	-1	-2	-2	-4	-1	-3	-1	-1	-1		X
*	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	1	*
	G	A	V	L	I	P	S	T	D	E	N	Q	K	R	H	F	Y	W	M	C	B	Z	X	*	

Score, Bit-score, E-value

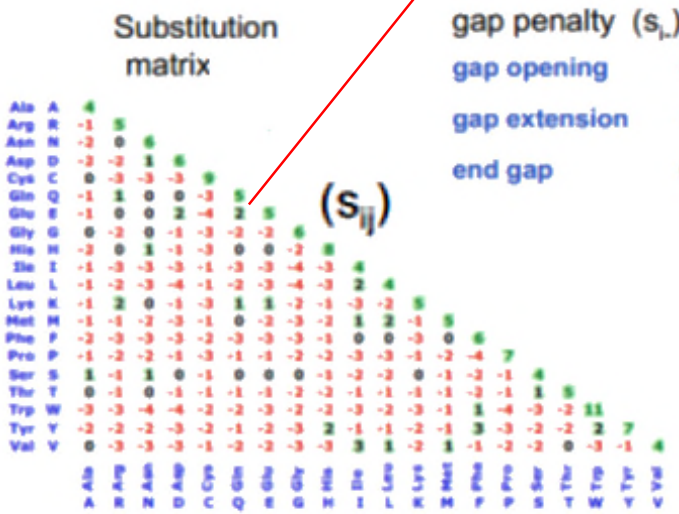
Score: A number used to assess the biological relevance of a finding.

In the context of sequence alignments, a score is a numerical value that describes the overall quality of an alignment. Higher numbers correspond to higher similarity. The score scale depends on the scoring system used (substitution matrix, gap penalty).

Example:

	R	L	A	S	V	-	E	T	D	M	W	T	P	L	T	L	R	Q	H
	.	|	.	|	:		:	|	.	:			.	|	.	.	|		
	T	L	T	S	L	A	Q	T	T	L	-	-	K	A	H	L	G	T	H
S_{ij}	−1	+4	+0	+4	+1	−4	+2	+5	−1	+2	−4	−1	−1	−1	−2	+4	−2	−1	+8	= 12

$$S = \sum_{i=1}^{L} s_{r_{1,i} r_{2,i}}$$



gap penalty (s_i)

gap opening	-4
gap extension	-1
end gap	0

SCORE - punteggio grezzo

Bit-SCORE - punteggio normalizzato

E-value - probabilità che lo score sia dovuto a identità/similarità casuali

Sequence alignment tools

GLOBAL ALIGNMENT confronta l'intera sequenza di una proteina (query) con le sequenze presenti in una banca dati (lento ma più preciso)

LOCAL ALIGNMENT confronta una piccolo parte della sequenza con le sequenze presenti in una banca dati. Poi estende dai lati della sequenza locale (veloce ma meno preciso, adatto a metodi euristici)

MULTIPLE ALIGNMENT confronta sequenze multiple, portando anche ad una relazione filogenetica tra le sequenze

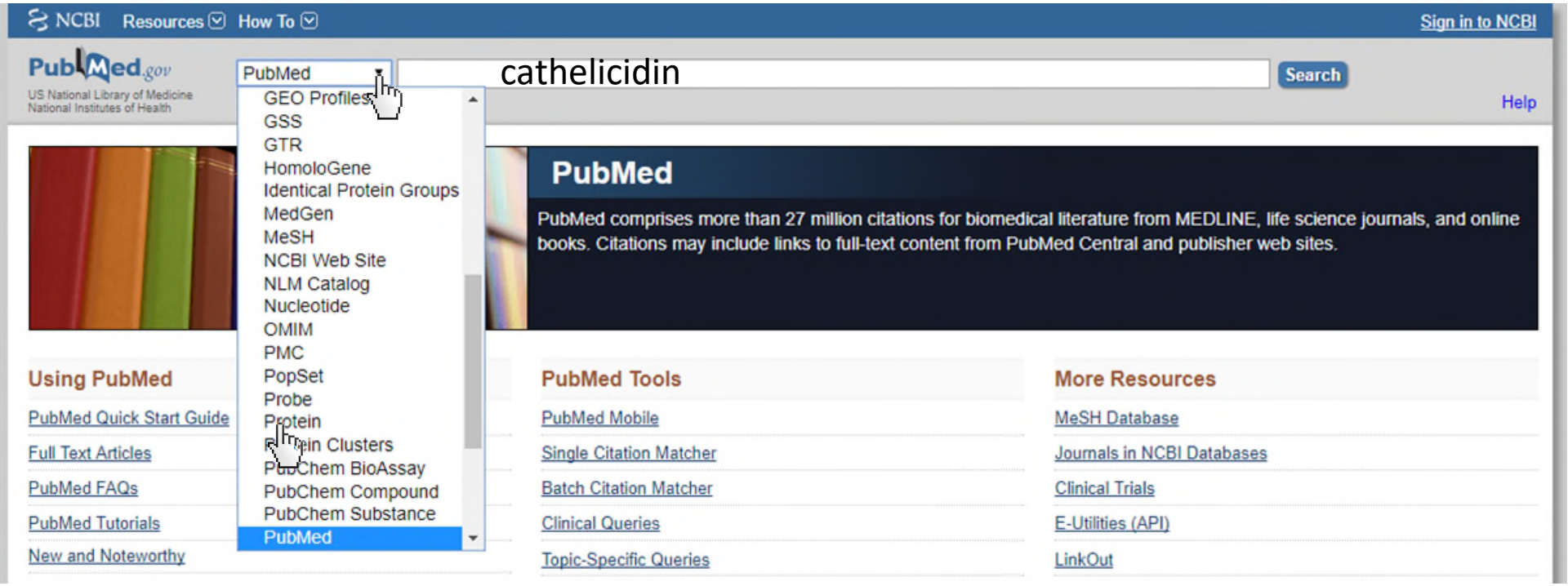
BLAST **(metodo euristico) (Basic Local Alignment Search Tool)** confronta una sequenza proteica o nucleotidica nota (query sequence) con tutte le sequenze presenti in una banca dati e trova quelle più simili. Usa matrici di similarità fra AA per decidere il grado di similarità. Usa brevi sequenze, tipicamente di 3 AA o 11 nucleotide per allineamenti locali (https://blast.ncbi.nlm.nih.gov/Blast.cgi)

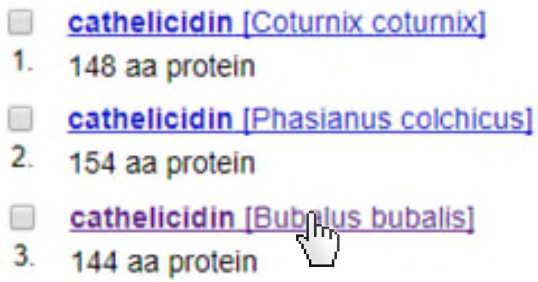
FASTA **(altro metodo euristico)** usa un approccio aprossimativo per determinare il grado di similarità, sempre in base a matrici di similarità fra amminoacidi (https://www.ebi.ac.uk/Tools/sss/fasta/)

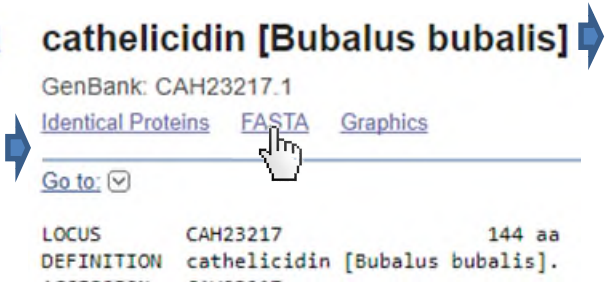
CLUSTAL (Cluster analysisis) programma per l'allineamento di sequenze multiple (https://www.ebi.ac.uk/Tools/msa/clustalo/)

Scegliamo una sequenza proteica

1) Google [Pubmed]

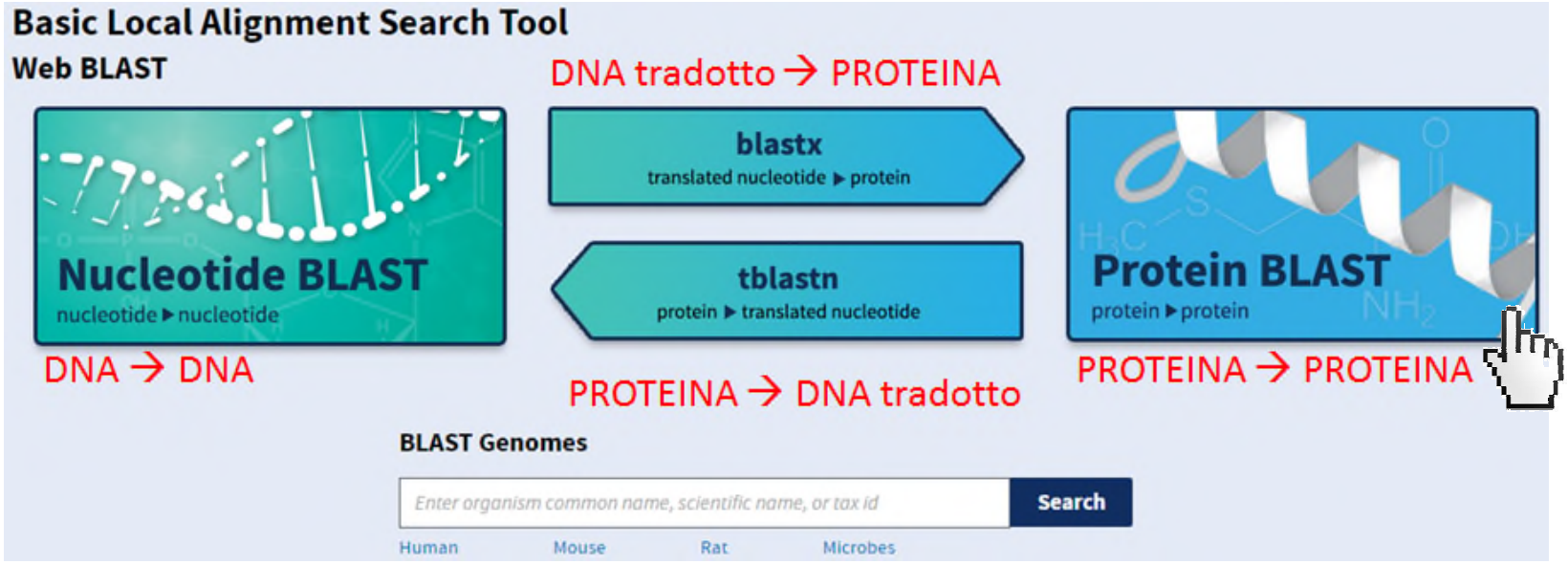


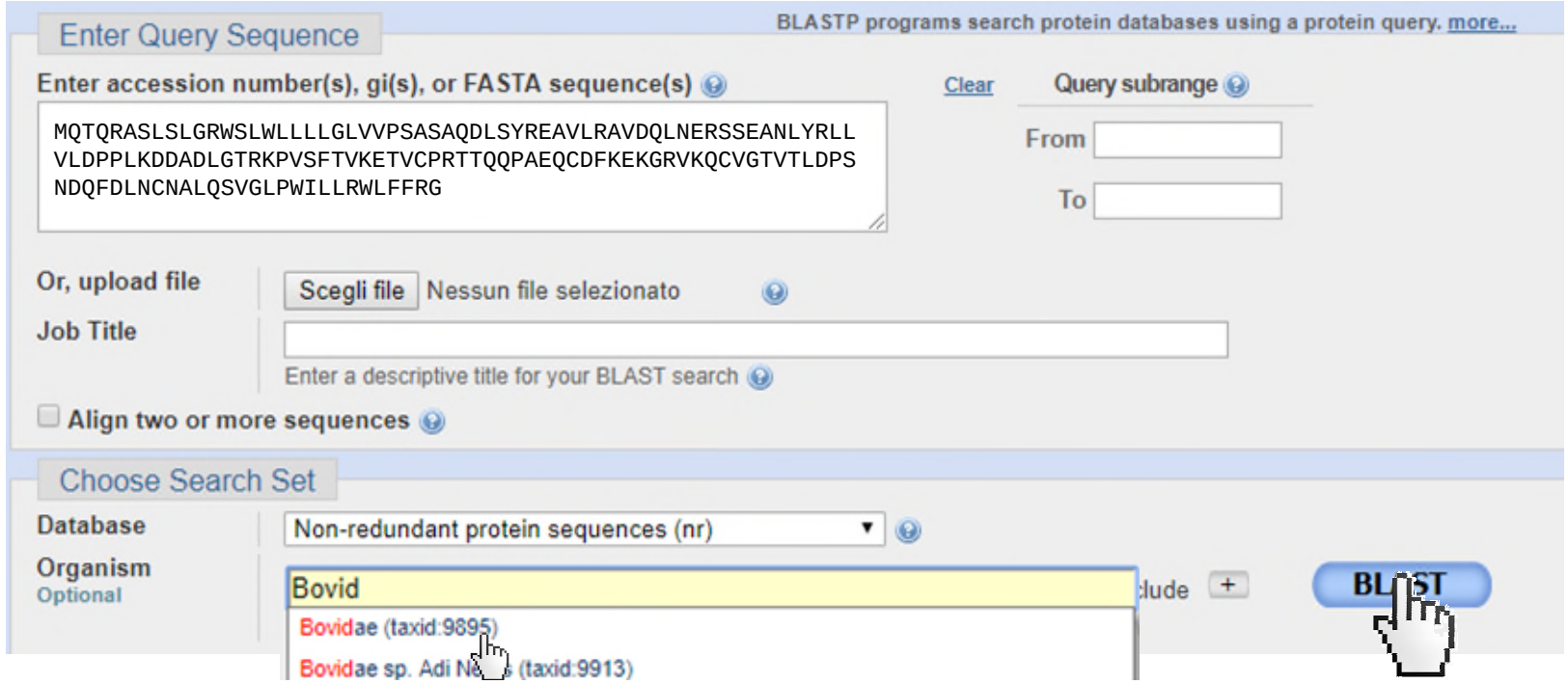




Seleziona e copia

BLAST (https://blast.ncbi.nlm.nih.gov/Blast.cgi)





‹ Edit Search | Save Search | Search Summary

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

Your search is limited to records that include: Bovidae (taxid:9895)

Job Title	**Protein Sequence**
RID	XHTT4PVN01N *Search expires on 12-16 23:41 pm* Download All
Program	BLASTP Citation
Database	nr See details
Query ID	lcl|Query_89537
Description	None
Molecule type	amino acid
Query Length	144
Other reports	Distance tree of results Multiple alignment MSA viewer

Filter Results

Organism *only top 20 will appear* exclude

Type common name, binomial, taxid or group name

+ Add organism

Percent Identity to

E value to

Query Coverage to

Filter Reset

Descriptions | Graphic Summary | Alignments | Taxonomy

Sequences producing significant alignments Download | New Select columns | Show 100

select all *100 sequences selected* GenPept Graphics Distance tree of results Multiple alignment

Description	Common Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
cathelicidin-4-like isoform X1 [Bubalus bubalis]	water buffalo	291	291	100%	3e-102	100.00%	144	XP_025127734.1
cathelicidin 4 [Bubalus bubalis]	water buffalo	290	290	100%	8e-102	99.31%	144	AIZ93856.1
cathelicidin 4 [Bubalus bubalis]	water buffalo	290	290	100%	1e-101	98.61%	144	AIZ93859.1
cathelicidin 4 [Bubalus bubalis]	water buffalo	288	288	100%	9e-101	98.61%	144	AIZ93860.1
cathelicidin 4 [Bubalus bubalis]	water buffalo	285	285	100%	1e-99	97.22%	144	AIZ93889.1
cathelicidin 4 [Bubalus bubalis]	water buffalo	285	285	100%	1e-99	97.22%	144	AIZ93858.1
cathelicidin 4 [Bubalus bubalis]	water buffalo	285	285	100%	1e-99	97.92%	144	AIZ93901.1
cathelicidin 4 [Bubalus bubalis]	water buffalo	285	285	100%	1e-99	97.92%	144	AIZ93891.1
cathelicidin 4 [Bubalus bubalis]	water buffalo	259	259	100%	9e-90	93.75%	144	AIZ93880.1

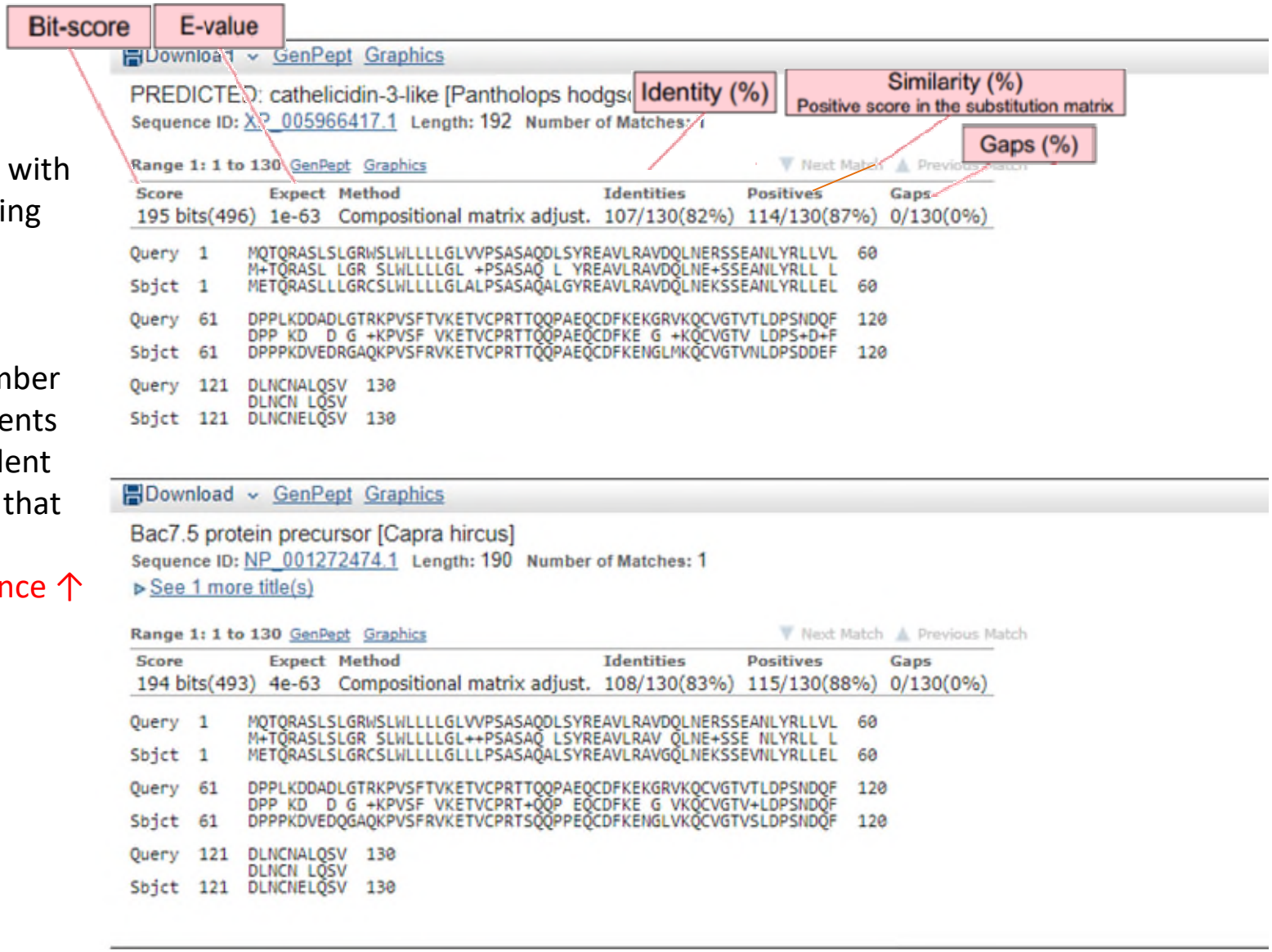
bit score

S score normalized with respect to the scoring System

E value

represents the number of different alignments with scores equivalent to or better than S that Occur by chance.

E value ↓ significance ↑



CLUSTALL (https://www.ebi.ac.uk/Tools/msa/clustalo/)

Allineamento e confronto di sequenze multiple

In PUBMED seleziona la banca dati [Protein] e cerca “cathelicidin homo sapiens” (uomo)

Scegli e apri una scheda (entry) e poi all’interno selezionare la sequenza in formato FASTA e copia tutto

>NP_004336.3 cathelicidin antimicrobial peptide preproprotein [Homo sapiens]
MGTMKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVS
FTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKRFALLGDFFRKSKEKIGKEFKRIVQRIKD
FLRNLVPRTES (copia tutto in una file di testo)

Poi fai lo stesso per pig, rabbit, dog, bovine

```
>NP_004336.3 cathelicidin antimicrobial peptide preproprotein [Homo sapiens]
MGTMKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCM
GTVTLNQARGSFDISCDKDNKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES
>CAA73261.1 cathelicidin [Bos taurus]
METQRASFSLGRSSLWLLLLGLVVPSASAQDLSYREAVLRAVDQFNERSSEANLYRLLELDPPPEQDVEHPGARKPVSFTVKETVCPRTTPQPPEQCDFKENGLVKQCVGTV
TRYWIRGDFDITCNNIQSAGLFRRLRDSIRRGQQKILEKARRIGERIKDIFRG
>NP_999615.1 antibacterial protein PR-39 precursor [Sus scrofa]
METQRASLCLGRWSLWLLLLGLVVPSASTQALSYREAVLRAVDRLNEQSSEANLYRLLELDQPPKADEDP
GTPKPVSFTVKETVCPRPTQRPPELCDFKENGRVKQCVGTVTLNPSNDPLDISCNEIQSVRRRPRPPYLP
RPRPPPFFPPRLPPRIPPGFPPRFPPRFPGKR
>NP_001075774.1 antimicrobial protein CAP18 precursor [Oryctolagus cuniculus]
METHKHGPSLAWWSLLLLLLGLLMPPAIAQDLTYREAVLRAVDAFNQQSSEANLYRLLSMDPQQLEDAKP
YTPQPVSFTVKETECPRTTWKLPEQCDFKEDGLVKRCVGTVTRYQAWDSFDIRCNRAQESPEPTGLRKRL
RKFRNKIKEKLKKIGQKIQGFVPKLAPRTDY
```

Apri CLUSTAL OMEGA e incolla tutte le sequenze nella finestra

Multiple Sequence Alignment

Clustal Omega is a new multiple sequence alignment program that uses seeded guide trees and HMM profile-profile techniques to generate alignments between **three or more** sequences. For the alignment of two sequences please instead use our pairwise sequence alignment tools.

Important note: This tool can align up to 4000 sequences or a maximum file size of 4 MB.

STEP 1 - Enter your input sequences

Enter or paste a set of

PROTEIN

sequences in any supported format:

```
>CAA73261.1 cathelicidin [Bos taurus]
METQRASFSLGRSSLWLLLLGLVVPSASAQDLSYREAVLRAVDQFNERSSEANLYRLLELDPPPEQDVEHPGARKPVSFTVKETVCPRTTPQPPEQ
CDFKENGLVKQCVGTVTRYWIRGDFDITCNNIQSAGLFRRLRDSIRRGQQKILEKARRIGERIKDIFRG
>NP_004336.3 cathelicidin antimicrobial peptide preproprotein [Homo sapiens]
MGTMKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQS
PEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES
```

Or, upload a file: Scegli file Nessun file selezionato

STEP 2 - Set your parameters

OUTPUT FORMAT

Clustal w/o numbers

The default settings will fulfill the needs of most users.

More options... *(Click here, if you want to view or change the default settings.)*

STEP 3 - Submit your job

Be notified by email *(Tick this box if you want to be notified by email when the results are available)*

Submit

Results for job clustalo-I20171122-114750-0238-29794709-pg

Alignments | Result Summary | Phylogenetic Tree | Submission Details

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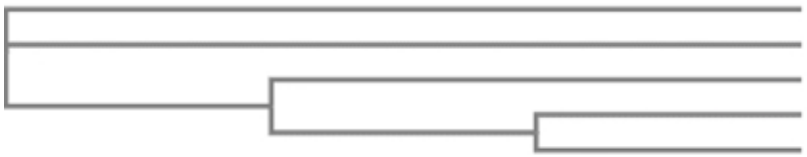
```
CLUSTAL O(1.2.4) multiple sequence alignment


NP_004336.3         MGTMKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYR
NP_001075774.1      ---METHKHGPSLAWWSLLLLLLGLLMPPA-IAQDLTYREAVLRAVDAFNQQSSEANLYR
AAR26245.1          ---METQKDSPSLGRWSLLLLLLGLVITPA-ASRALSYREAVLRAVNGFNQRSSEENLYR
CAA73261.1          ---METQRASFSLGRSSLWLLLLGLVVPSA-SAQDLSYREAVLRAVDQFNERSSEANLYR
P49932.1            ---METQRASLCLGRWSLWLLLLALVVPSA-SAQALSYREAVLRAVDRLNEQSSEANLYR
                       *:*:: . .*.  ** ****.*::  *  :: *:*:******:: :*::**: ****

NP_004336.3         LLDLDPRPTMD-GDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQ
NP_001075774.1      LLSMDPQQLED-AKPYTPQPVSFTVKETECPRTTWKLPEQCDFKEDGLVKRCVGTVTRYQ
AAR26245.1          LLQLNSQPKGD-EDPNIPKPVSFTVKETVCPKTTQQPLEQCGFKDNGLVKQCEGTVILDE
CAA73261.1          LLELDPPPEQDVEHPGARKPVSFTVKETVCPRTTPQPPEQCDFKENGLVKQCVGTVTRYW
P49932.1            LLELDQPPKAD-EDPGTPKPVSFTVKETVCPRPTWRPPELCDFKENGRVKQCVGTVTLDQ
                    **.::     *  .*   :********* **: * :  * *.**.:* **:* ***

NP_004336.3         ARGSFDISCDKDN--KRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES-
NP_001075774.1      AWDSFDIRCNRAQESPEPTGLRKRLRKFRNKIKEKLKKIGQKIQGFVPKLAPRTDY-
AAR26245.1          DTGYFDLNCDSILQVKKIDRLKELITTGGQKIGEKIRRIGQRIKDFFKNLQPREEKS
CAA73261.1          IRGDFDITCNNIQSAGLFRRLRDSIRRGQQKILEKARRIGERIKDIFRG--------
P49932.1            IKDPLDITCNEIQSVGLLSRLRDFLSDRGRRLGEKIERIGQKIKDLSEFFQS-----
                      . :*: *:          * . :    .:: :: .:* ::*:.:
```



NP_004336.3 0.18524 Human Euarchontoglires
NP_001075774.1 0.23488 Rabbit Euarchontoglires
AAR26245.1 0.21227 Dog Laurasiatheria
CAA73261.1 0.12484 Cow Laurasiatheria
P49932.1 0.16784 Pig Laurasiatheria

TRADURRE DNA IN PROTEINA

Translate tool

https://web.expasy.org/translate/

Translate is a tool which allows the translation of a nucleotide (DNA/RNA) sequence to a protein sequence.

DNA or RNA sequence

Please enter a DNA or RNA sequence - numbers and blanks are ignored

```
ATGGGGACCATGAAGACCCAAAGGGATGGCCACTCCCTGGGGCGGTGGTCACTGGTGCTCCTGCTGCTGGG
CCTGGTGATGCCTCTGGCCATCATTGCCCAGGTCCTCAGCTACAAGGAAGCTGTGCTTCGTGCTATAGATG
GCATCAACCAGCGGTCCTCGGATGCTAACCTCTACCGCCTCCTGGACCTGGACCCCAGGCCCACGATGGAT
GGGGACCCAGACACGCCAAAGCCTGTGAGCTTCACAGTGAAGGAGACAGTGTGCCCCAGGACGACACAGCA
CGGAAATCTAAAGAGAAGATTGGCAAAGAGTTTAAAAGAATTGTCCAGAGAATCAAGGATTTTTTGCGGAA
TCTTGTACCCAGGACAGAGTCCTAG
```

Paste DNA sequence in window

Output format

- ○ Verbose: Met, Stop, spaces between residues
- ◉ Compact: M, -, no spaces
- ○ Includes nucleotide sequence
- ○ Includes nucleotide sequence, no spaces

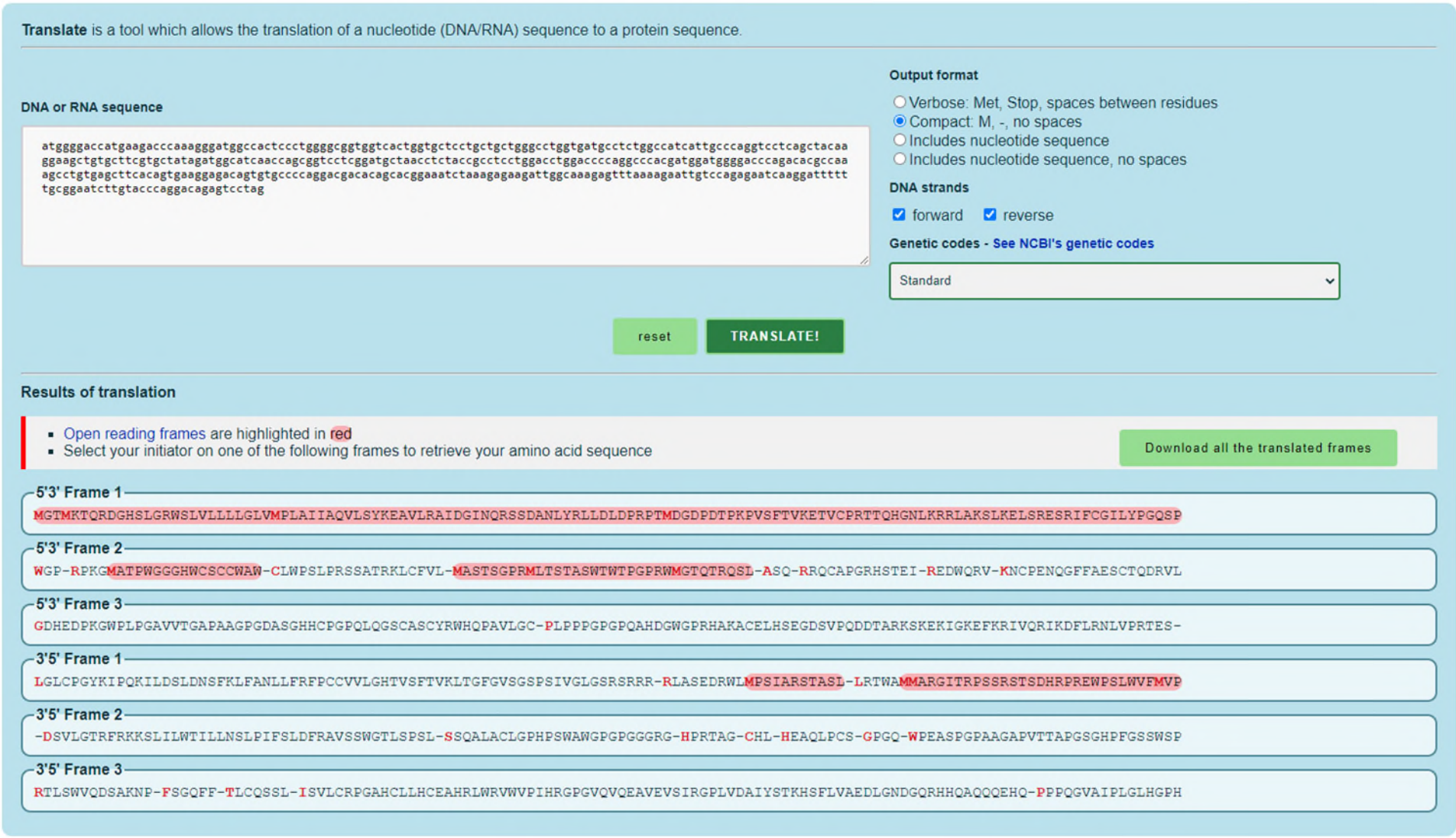
DNA strands

☑ forward ☑ reverse

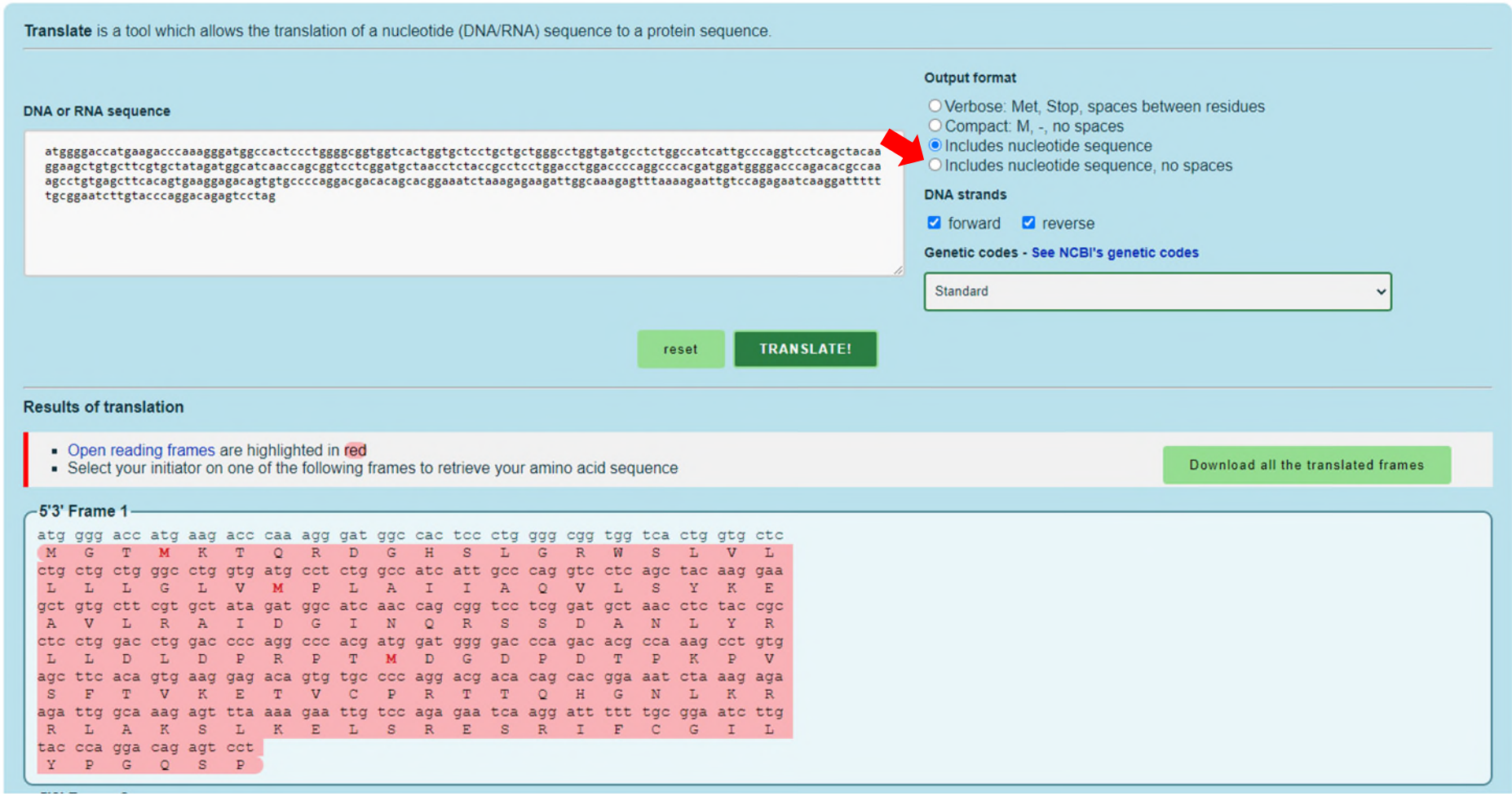
Genetic codes - See NCBI's genetic codes

Standard

reset TRANSLATE!



TRE cornici di letura per il filamento 1 (5’ → 3’) e tre cornici di lettura per il filamento complementare (3’ <__ 5’)



Si può anche vedere la sequenza proteica allineata a quella nucleotidica