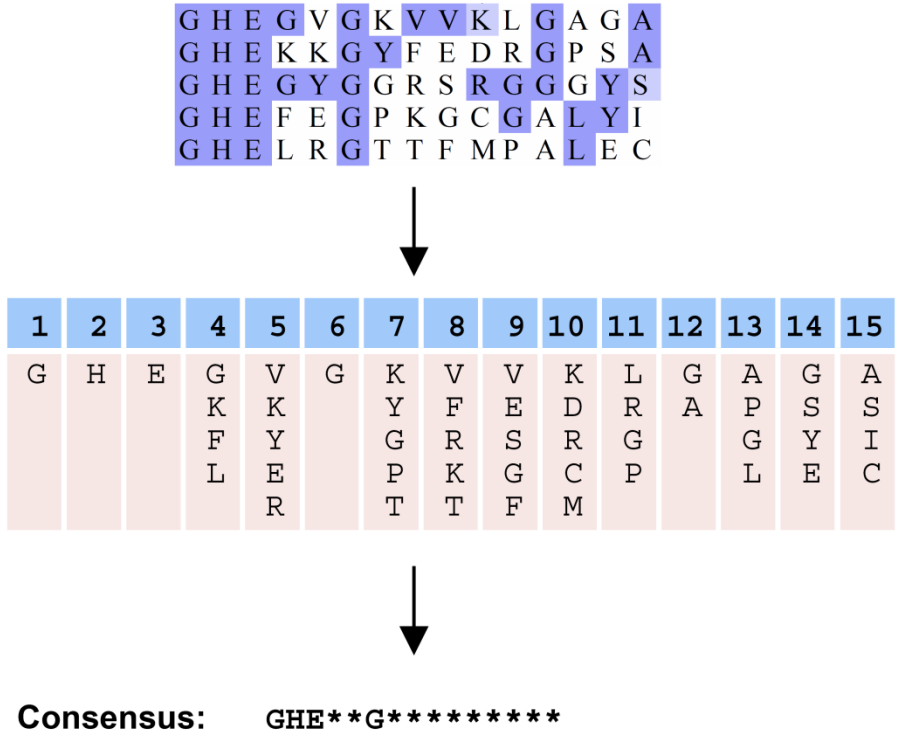
Motivos e perfis

Sequência de consenso

A partir do alinhamento múltiplo de uma família de sequências é possível determinar preferências **posicionais** para a ocorrência dos 20 aminoácidos.

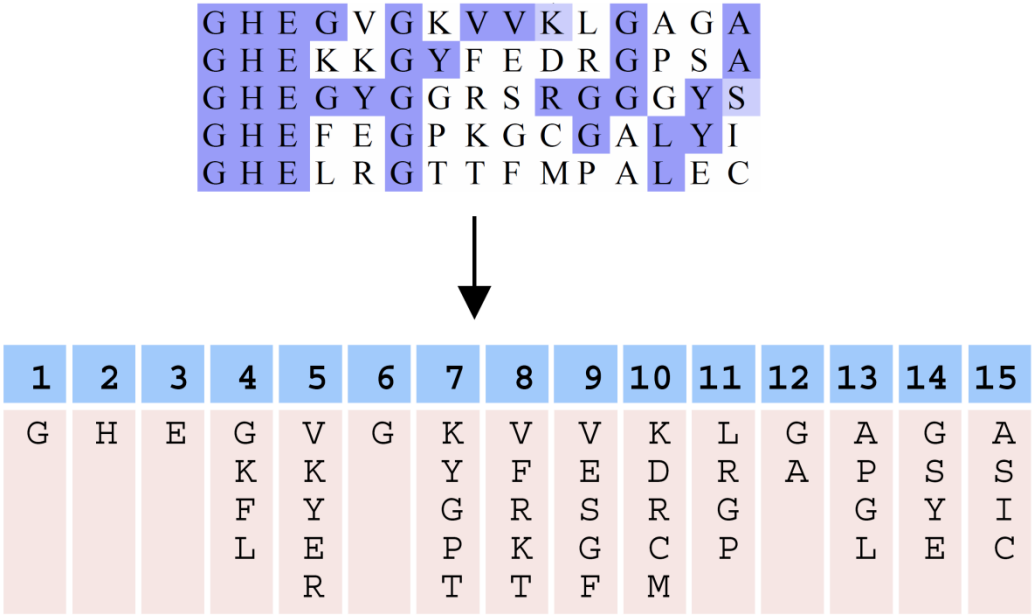
Exemplo:



Sequência de consenso: posições 100% conservadas no alinhamento.

Protocolo de alinhamentos múltiplos

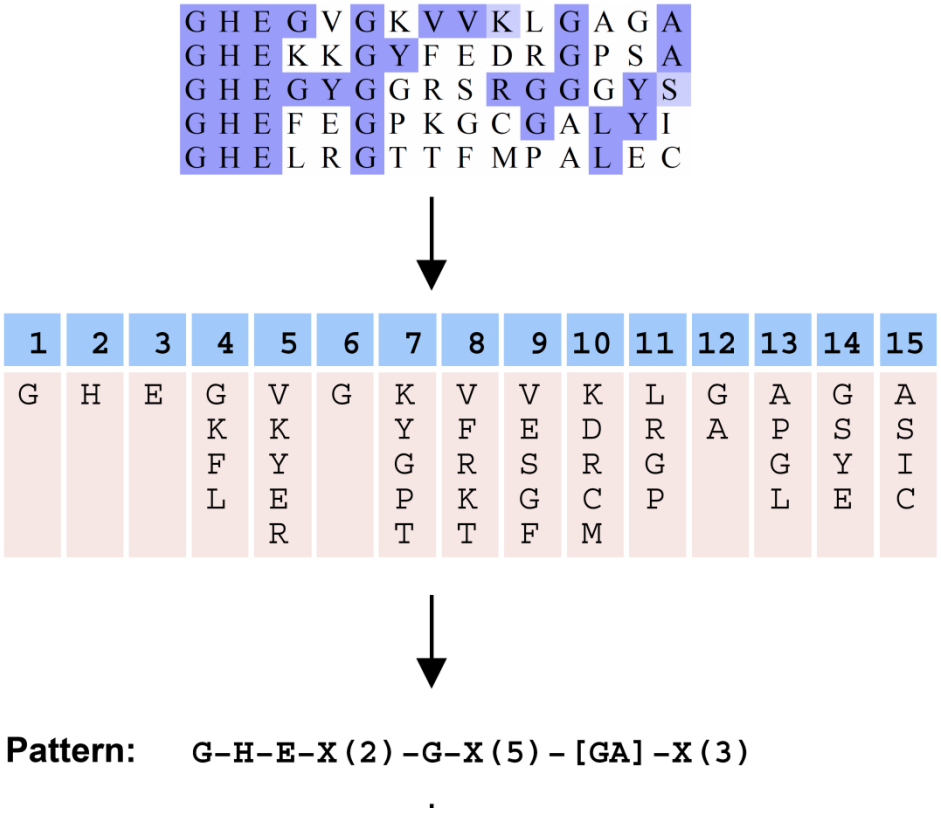
A sequência de consenso não permite descrever preferências não-integrais (<100%).



Na posição 12 podem ocorrer dois resíduos (G e A). Como representar este tipo de situação ?

Construção de Motivos

A variedade composicional do alinhamento múltiplo pode ser descrita por um **motivo**.



O **motivo** ou padrão representa de forma simbólica as características de conservação da zona alinhada. Muitos domínios funcionais apresentam motivos (ou assinaturas) característicos.

Formato dos padrões PROSITE

A sintaxe dos padrões PROSITE rege-se pelas seguintes regras:

1.Códigos IUPAC para aminóacidos (1-letter)

2.Os elementos são separados por “-”

3.“X” representa qualquer aminoácido

4.Ambiguidades representadas por “[]” (Ex. [AG] = A **ou** G)

5.Aminoácidos proibidos entre “{}” (Ex: {AG} todos os a.a. excepto A ou G)

6.Repetições são representadas por “()” (Ex: X(2) dois a.a. quaisquer, [AG](2,4) A ou G de 2 a 4 vezes

7.Para o C- e N-term (match no início ou fim) usam-se os símbolos “<“ ou “>”

Exemplo:

G-H-E-X(2)-G-X(5)-[GA]-X(3)

Exemplo de padrão PROSITE

O seguinte padrão:

<A-x-[ST](2)-x(0,1)-{V}

significa:

1. Uma Ala (A) no N-terminal,
2. Seguida de um aminoácido qualquer,
3. Seguida de uma Ser(S) ou Thr(T) duas vezes,
4. Seguida de zero ou um aminoácidos quaisquer,
5. Seguida de qualquer aminoácido menos Valina (V).

Motivos PROSITE

Padrões PROSITE que descrevem motivos de sequência primária característicos de locais de reconhecimento ou de famílias de proteínas. Associados a aspectos **funcionais** e **estruturais**.

Exemplos (usando o formato PROSITE):

• site de fosforilação das proteínas cinases:
[RK](2)-x-[ST]

• local de glicosilação:
S-G-x-G

• "Zipper" de leucina:
L-x(6)-L-x(6)-L-x(6)-L

• Família das proteases de serina, histidina do centro activo:
[LIVM]-[ST]-A-[STAG]-H-C

• Local de γ-carboxilação dependente da vitamina-K:
x(12)-E-x(3)-E-x-C-x(6)-[DEN]-x-[LIVMFY]-x(9)-[FYW]

Base de dados PROSITE

- Base de dados de famílias e domínios proteícos
- Apesar do elevado número de proteínas conhecidas, a maioria pode ser agrupada num número limitado de famílias, com base na simillaridade
- Proteínas ou domínios proteicos pertencendo a uma determinada família têm geralmente uma mesma função e um ancestral comum
- O estudo das famílias de proteínas indica que a conservação não é constante ao longo da sequência
- As zonas mais conservadas têm geralmente importância funcional
- Comparação das zonas conservadas permite derivar uma **assinatura**, ou motivo, que distingue os membros dessa família de outras proteínas
- PROSITE contem **motivos** e **perfis** para mais de 1000 famílias de proteínas
- Contem patterns (motivos) e profiles (perfis) que são formas diferentes de descrever assinaturas de uma sequência

Profiles, PWM, PSWM, P | ScanProsite | www.uniprot.org/uniprot | ExPASy - PROSITE

Paulo

prosite.expasy.org

Apps | Bookmarks | D pmartel | UALG Acad | Drug Design | Programming | Bioinformatics | Molecular Modelling | Other bookmarks

ExPASy Bioinformatics Resource Portal

PROSITE

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Home | ScanProsite | ProRule | Documents | Downloads | Links | Funding

Database of protein domains, families and functional sites

PROSITE consists of documentation entries describing protein domains, families and functional sites as well as associated patterns and profiles to identify them [More... / References / Commercial users].
PROSITE is complemented by ProRule, a collection of rules based on profiles and patterns, which increases the discriminatory power of profiles and patterns by providing additional information about functionally and/or structurally critical amino acids [More...].

Release 20.131 of 27-Oct-2016 contains 1773 documentation entries, 1309 patterns, 1172 profiles and 1193 ProRule.

Search

e.g. PDOC00022, PS50089, SH3, zinc finger

Search

Browse

- by documentation entry
- by ProRule description
- by taxonomic scope
- by number of positive hits

Quick Scan mode of ScanProsite

Quickly find matches of your protein sequences to PROSITE signatures (max. 10 sequences). [?] Examples

Enter UniProtKB accessions or identifiers or PDB identifiers or sequences in FASTA format

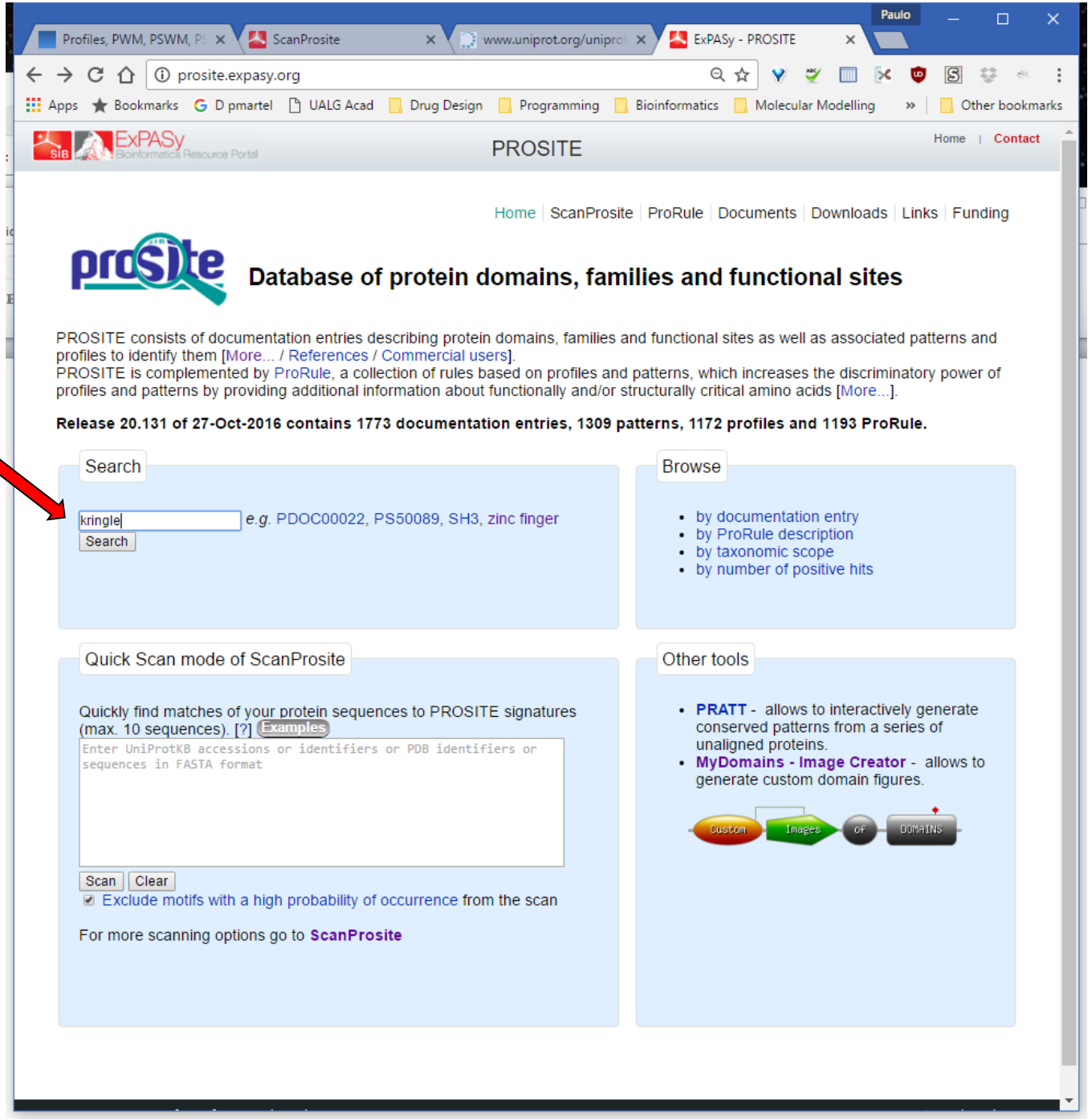
Scan | Clear

Exclude motifs with a high probability of occurrence from the scan

For more scanning options go to **ScanProsite**

Other tools

- **PRATT** - allows to interactively generate conserved patterns from a series of unaligned proteins.
- **MyDomains - Image Creator** - allows to generate custom domain figures.


Profiles, PWM, PSWM, P
ScanProsite
www.uniprot.org/uniprot
ExPASy - PROSITE
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prosite.expasy.org
Apps
Bookmarks
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Drug Design
Programming
Bioinformatics
Molecular Modelling
Other bookmarks
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kringle
e.g. PDOC00022, PS50089, SH3, zinc finger
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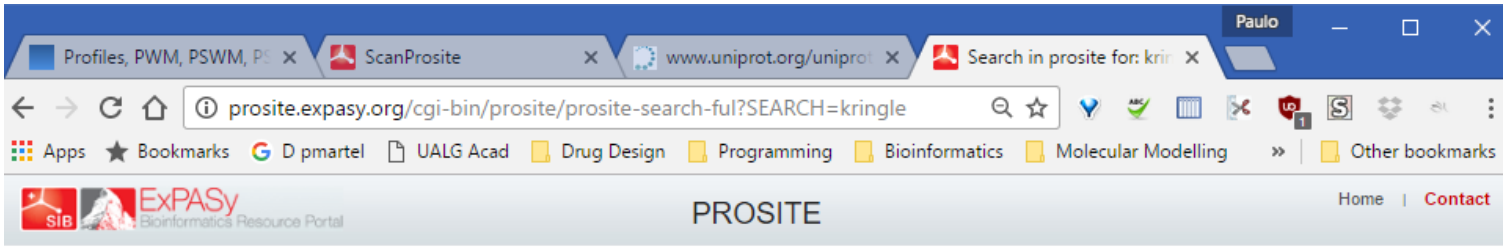
of
DOMAINS



Prosite search results

Search in PROSITE for: kringle

(Release 20.131, of 27-Oct-2016)

Enter search terms:

kringle

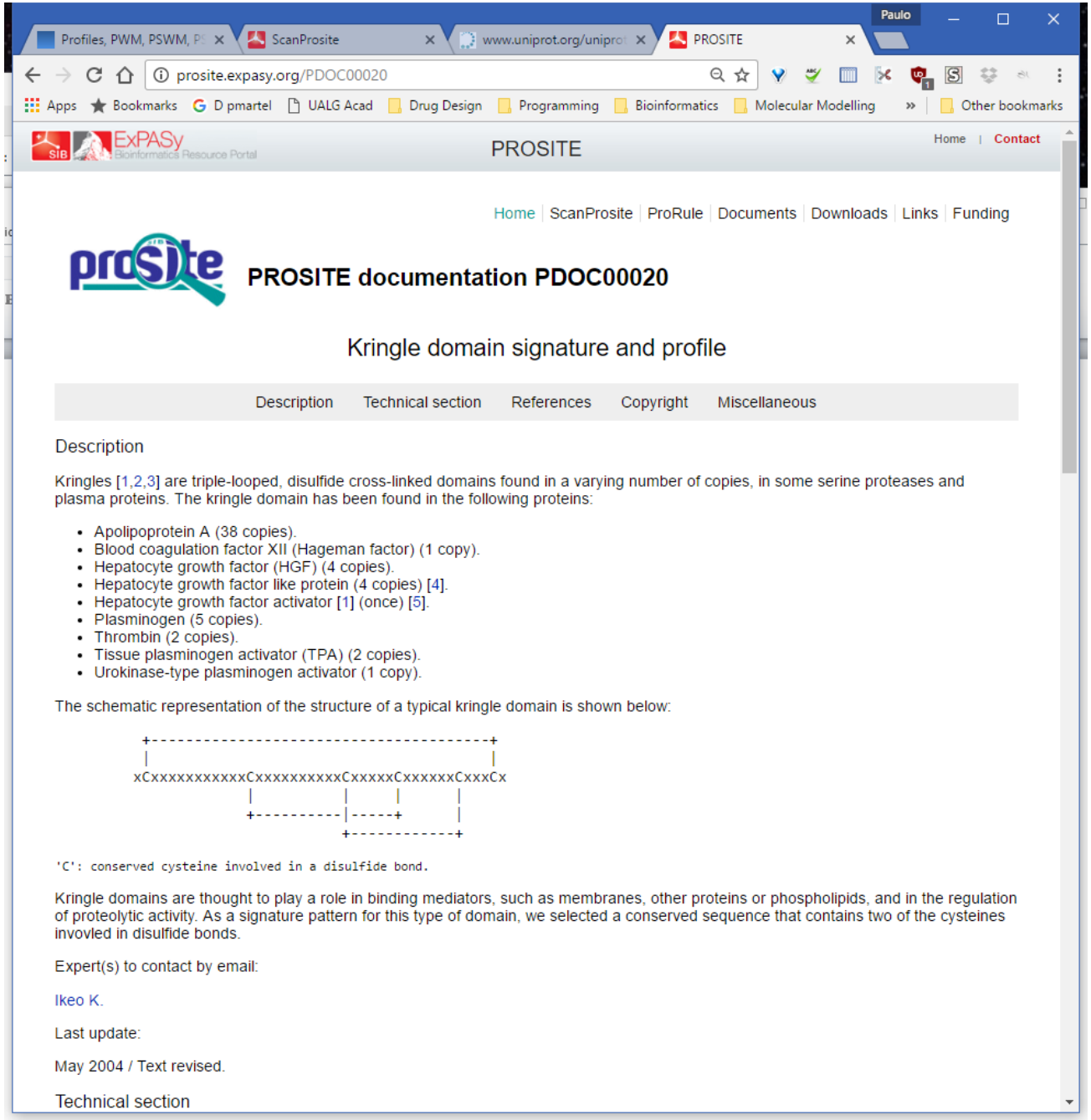
Prefix and append wildcard '*' to words.

new search clear

By default, this search engine searches for complete words only. If you did not find what you expected, and would try to do a substring match, you should perform a new search and select 'prefix and append wildcard to words'.

Number of documents in PROSITE containing the search term:4

- PDOC00537 C-type lectin domain signature and profile
- PDOC00965 Fibronectin type-I domain signature and profile
- PDOC00020 Kringle domain signature and profile
- PDOC51212 WSC domain profile


Profiles, PWM, PSWM, P
ScanProsite
www.uniprot.org/uniprot
PROSITE
Paulo
prosite.expasy.org/PDOC00020
Apps
Bookmarks
D pmartel
UALG Acad
Drug Design
Programming
Bioinformatics
Molecular Modelling
Other bookmarks
ExPASy
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PROSITE documentation PDOC00020
Kringle domain signature and profile
Description | Technical section | References | Copyright | Miscellaneous
Description
Kringles [1,2,3] are triple-looped, disulfide cross-linked domains found in a varying number of copies, in some serine proteases and plasma proteins. The kringle domain has been found in the following proteins:
Apolipoprotein A (38 copies).
Blood coagulation factor XII (Hageman factor) (1 copy).
Hepatocyte growth factor (HGF) (4 copies).
Hepatocyte growth factor like protein (4 copies) [4].
Hepatocyte growth factor activator [1] (once) [5].
Plasminogen (5 copies).
Thrombin (2 copies).
Tissue plasminogen activator (TPA) (2 copies).
Urokinase-type plasminogen activator (1 copy).
The schematic representation of the structure of a typical kringle domain is shown below:
'C': conserved cysteine involved in a disulfide bond.
Kringle domains are thought to play a role in binding mediators, such as membranes, other proteins or phospholipids, and in the regulation of proteolytic activity. As a signature pattern for this type of domain, we selected a conserved sequence that contains two of the cysteines invovled in disulfide bonds.
Expert(s) to contact by email:
Ikeo K.
Last update:
May 2004 / Text revised.
Technical section

May 2004 / Text revised.

Technical section

PROSITE methods (with tools and information) covered by this documentation:

KRINGLE_2, PS50070; Kringle domain profile (MATRIX)

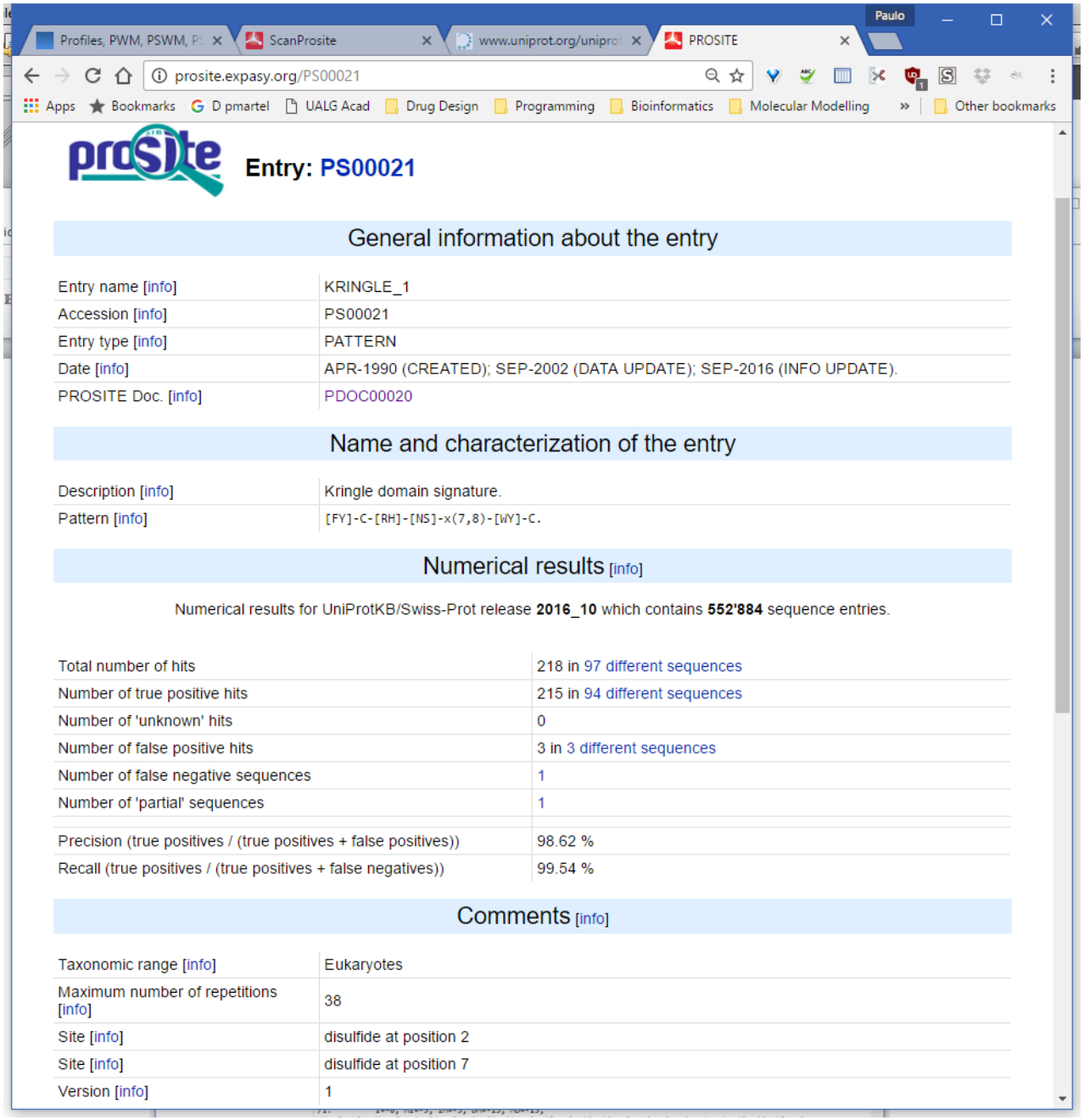
- Sequences in UniProtKB/Swiss-Prot known to belong to this class: 96
  - detected by PS50070: 95 (true positives)
  - undetected by PS50070: 1 (0 false negative and 1 'partial')
- Other sequence(s) in UniProtKB/Swiss-Prot detected by PS50070:
  NONE.
- Domain architecture view of Swiss-Prot proteins matching PS50070

- Retrieve an alignment of UniProtKB/Swiss-Prot true positive hits:
  Clustal format, color, condensed view / Clustal format, color / Clustal format, plain text / Fasta format
- Retrieve the sequence logo from the alignment
- Taxonomic distribution of all UniProtKB (Swiss-Prot + TrEMBL) entries matching PS50070
- Retrieve a list of all UniProtKB (Swiss-Prot + TrEMBL) entries matching PS50070
- Scan UniProtKB (Swiss-Prot and/or TrEMBL) entries against PS50070
- View ligand binding statistics of PS50070
- Matching PDB structures: 1A0H 1B2I 1BHT 1CEA ... [ALL]

KRINGLE_1, PS00021; Kringle domain signature (PATTERN)

- Consensus pattern:
  [FY]-C-[RH]-[NS]-x(7,8)-[WY]-C
  The 2 C's are involved in a disulfide bonds
- Sequences in UniProtKB/Swiss-Prot known to belong to this class: 96
  - detected by PS00021: 94 (true positives)
  - undetected by PS00021: 2 (1 false negative and 1 'partial')
- Other sequence(s) in UniProtKB/Swiss-Prot detected by PS00021:
  3 false positives.
- Retrieve an alignment of UniProtKB/Swiss-Prot true positive hits:
  Clustal format, color, condensed view / Clustal format, color / Clustal format, plain text / Fasta format
- Retrieve the sequence logo from the alignment
- Taxonomic distribution of all UniProtKB (Swiss-Prot + TrEMBL) entries matching PS00021
- Retrieve a list of all UniProtKB (Swiss-Prot + TrEMBL) entries matching PS00021
- Scan UniProtKB (Swiss-Prot and/or TrEMBL) entries against PS00021
- View ligand binding statistics of PS00021
- Matching PDB structures: 1A0H 1B2I 1BHT 1CEA ... [ALL]

References



Entry: PS00021

General information about the entry

Entry name [info]	KRINGLE_1
Accession [info]	PS00021
Entry type [info]	PATTERN
Date [info]	APR-1990 (CREATED); SEP-2002 (DATA UPDATE); SEP-2016 (INFO UPDATE).
PROSITE Doc. [info]	PDOC00020

Name and characterization of the entry

Description [info]	Kringle domain signature.
Pattern [info]	`[FY]-C-[RH]-[NS]-x(7,8)-[WY]-C.`

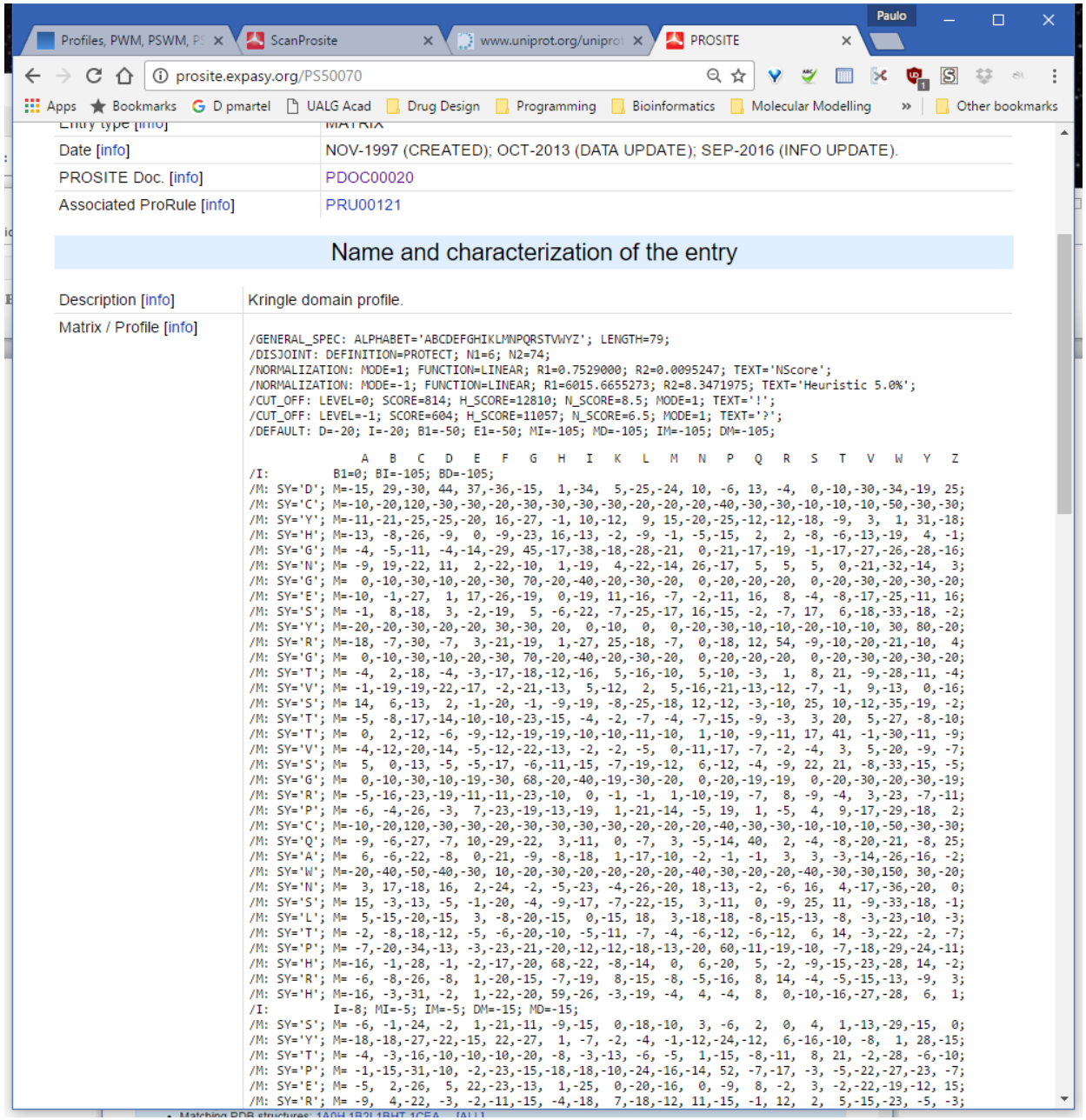
Numerical results [info]

Numerical results for UniProtKB/Swiss-Prot release **2016_10** which contains **552'884** sequence entries.

Total number of hits	218 in 97 different sequences
Number of true positive hits	215 in 94 different sequences
Number of 'unknown' hits	0
Number of false positive hits	3 in 3 different sequences
Number of false negative sequences	1
Number of 'partial' sequences	1
Precision (true positives / (true positives + false positives))	98.62 %
Recall (true positives / (true positives + false negatives))	99.54 %

Comments [info]

Taxonomic range [info]	Eukaryotes
Maximum number of repetitions [info]	38
Site [info]	disulfide at position 2
Site [info]	disulfide at position 7
Version [info]	1



Entry type [info]	MATRIX
Date [info]	NOV-1997 (CREATED); OCT-2013 (DATA UPDATE); SEP-2016 (INFO UPDATE).
PROSITE Doc. [info]	PDOC00020
Associated ProRule [info]	PRU00121

Name and characterization of the entry

Description [info]	Kringle domain profile.
Matrix / Profile [info]	

```
/GENERAL_SPEC: ALPHABET='ABCDEFGHIKLMNPQRSTVWYZ'; LENGTH=79;
/DISJOINT: DEFINITION=PROTECT; N1=6; N2=74;
/NORMALIZATION: MODE=1; FUNCTION=LINEAR; R1=0.7529000; R2=0.0095247; TEXT='NScore';
/NORMALIZATION: MODE=-1; FUNCTION=LINEAR; R1=6015.6655273; R2=8.3471975; TEXT='Heuristic 5.0%';
/CUT_OFF: LEVEL=0; SCORE=814; H_SCORE=12810; N_SCORE=8.5; MODE=1; TEXT='!';
/CUT_OFF: LEVEL=-1; SCORE=604; H_SCORE=11057; N_SCORE=6.5; MODE=1; TEXT='?';
/DEFAULT: D=-20; I=-20; B1=-50; E1=-50; MI=-105; MD=-105; IM=-105; DM=-105;

               A   B   C   D   E   F   G   H   I   K   L   M   N   P   Q   R   S   T   V   W   Y   Z
/I:         B1=0; BI=-105; BD=-105;
/M: SY='D'; M=-15, 29,-30, 44, 37,-36,-15,  1,-34,  5,-25,-24, 10, -6, 13, -4,  0,-10,-30,-34,-19, 25;
/M: SY='C'; M=-10,-20,120,-30,-30,-20,-30,-30,-30,-30,-20,-20,-20,-40,-30,-30,-10,-10,-10,-50,-30,-30;
/M: SY='Y'; M=-11,-21,-25,-25,-20, 16,-27, -1, 10,-12,  9, 15,-20,-25,-12,-12,-18, -9,  3,  1, 31,-18;
/M: SY='H'; M=-13, -8,-26, -9,  0, -9,-23, 16,-13, -2, -9, -1, -5,-15,  2,  2, -8, -6,-13,-19,  4, -1;
/M: SY='G'; M= -4, -5,-11, -4,-14,-29, 45,-17,-38,-18,-28,-21,  0,-21,-17,-19, -1,-17,-27,-26,-28,-16;
/M: SY='N'; M= -9, 19,-22, 11,  2,-22,-10,  1,-19,  4,-22,-14, 26,-17,  5,  5,  5,  0,-21,-32,-14,  3;
/M: SY='G'; M=  0,-10,-30,-10,-20,-30, 70,-20,-40,-20,-30,-20,  0,-20,-20,-20,  0,-20,-30,-20,-30,-20;
/M: SY='E'; M=-10, -1,-27,  1, 17,-26,-19,  0,-19, 11,-16, -7, -2,-11, 16,  8, -4, -8,-17,-25,-11, 16;
/M: SY='S'; M= -1,  8,-18,  3, -2,-19,  5, -6,-22, -7,-25,-17, 16,-15, -2, -7, 17,  6,-18,-33,-18, -2;
/M: SY='Y'; M=-20,-20,-30,-20,-20, 30,-30, 20,  0,-10,  0,  0,-20,-30,-10,-10,-20,-10,-10, 30, 80,-20;
/M: SY='R'; M=-18, -7,-30, -7,  3,-21,-19,  1,-27, 25,-18, -7,  0,-18, 12, 54, -9,-10,-20,-21,-10,  4;
/M: SY='G'; M=  0,-10,-30,-10,-20,-30, 70,-20,-40,-20,-30,-20,  0,-20,-20,-20,  0,-20,-30,-20,-30,-20;
/M: SY='T'; M= -4,  2,-18, -4, -3,-17,-18,-12,-16,  5,-16,-10,  5,-10, -3,  1,  8, 21, -9,-28,-11, -4;
/M: SY='V'; M= -1,-19,-19,-22,-17, -2,-21,-13,  5,-12,  2,  5,-16,-21,-13,-12, -7, -1,  9,-13,  0,-16;
/M: SY='S'; M= 14,  6,-13,  2, -1,-20, -1, -9,-19, -8,-25,-18, 12,-12, -3,-10, 25, 10,-12,-35,-19, -2;
/M: SY='T'; M= -5, -8,-17,-14,-10,-10,-23,-15, -4, -2, -7, -4, -7,-15, -9, -3,  3, 20,  5,-27, -8,-10;
/M: SY='T'; M=  0,  2,-12, -6, -9,-12,-19,-19,-10,-10,-11,-10,  1,-10, -9,-11, 17, 41, -1,-30,-11, -9;
/M: SY='V'; M= -4,-12,-20,-14, -5,-12,-22,-13, -2, -2, -5,  0,-11,-17, -7, -2, -4,  3,  5,-20, -9, -7;
/M: SY='S'; M=  5,  0,-13, -5, -5,-17, -6,-11,-15, -7,-19,-12,  6,-12, -4, -9, 22, 21, -8,-33,-15, -5;
/M: SY='G'; M=  0,-10,-30,-10,-19,-30, 68,-20,-40,-19,-30,-20,  0,-20,-19,-19,  0,-20,-30,-20,-30,-19;
/M: SY='R'; M= -5,-16,-23,-19,-11,-11,-23,-10,  0, -1, -1,  1,-10,-19, -7,  8, -9, -4,  3,-23, -7,-11;
/M: SY='P'; M= -6, -4,-26, -3,  7,-23,-19,-13,-19,  1,-21,-14, -5, 19,  1, -5,  4,  9,-17,-29,-18,  2;
/M: SY='C'; M=-10,-20,120,-30,-30,-20,-30,-30,-30,-30,-20,-20,-20,-40,-30,-30,-10,-10,-10,-50,-30,-30;
/M: SY='Q'; M= -9, -6,-27, -7, 10,-29,-22,  3,-11,  0, -7,  3, -5,-14, 40,  2, -4, -8,-20,-21, -8, 25;
/M: SY='A'; M=  6, -6,-22, -8,  0,-21, -9, -8,-18,  1,-17,-10, -2, -1, -1,  3,  3, -3,-14,-26,-16, -2;
/M: SY='W'; M=-20,-40,-50,-40,-30, 10,-20,-30,-20,-20,-20,-40,-30,-20,-20,-40,-30,-30,150, 30,-20;
/M: SY='N'; M=  3, 17,-18, 16,  2,-24, -2, -5,-23, -4,-26,-20, 18,-13, -2, -6, 16,  4,-17,-36,-20,  0;
/M: SY='S'; M= 15, -3,-13, -5, -1,-20, -4, -9,-17, -7,-22,-15,  3,-11,  0, -9, 25, 11, -9,-33,-18, -1;
/M: SY='L'; M=  5,-15,-20,-15,  3, -8,-20,-15,  0,-15, 18,  3,-18,-18, -8,-15,-13, -8, -3,-23,-10, -3;
/M: SY='T'; M= -2, -8,-18,-12, -5, -6,-20,-10, -5,-11, -7, -4, -6,-12, -6,-12,  6, 14, -3,-22, -2, -7;
/M: SY='P'; M= -7,-20,-34,-13, -3,-23,-21,-20,-12,-12,-18,-13,-20, 60,-11,-19,-10, -7,-18,-29,-24,-11;
/M: SY='H'; M=-16, -1,-28, -1, -2,-17,-20, 68,-22, -8,-14,  0,  6,-20,  5, -2, -9,-15,-23,-28, 14, -2;
/M: SY='R'; M= -6, -8,-26, -8,  1,-20,-15, -7,-19,  8,-15, -8, -5,-16,  8, 14, -4, -5,-15,-13, -9,  3;
/M: SY='H'; M=-16, -3,-31, -2,  1,-22,-20, 59,-26, -3,-19, -4,  4, -4,  8,  0,-10,-16,-27,-28,  6,  1;
/I:         I=-8; MI=-5; IM=-5; DM=-15; MD=-15;
/M: SY='S'; M= -6, -1,-24, -2,  1,-21,-11, -9,-15,  0,-18,-10,  3, -6,  2,  0,  4,  1,-13,-29,-15,  0;
/M: SY='Y'; M=-18,-18,-27,-22,-15, 22,-27,  1, -7, -2, -4, -1,-12,-24,-12,  6,-16,-10, -8,  1, 28,-15;
/M: SY='T'; M= -4, -3,-16,-10,-10,-10,-20, -8, -3,-13, -6, -5,  1,-15, -8,-11,  8, 21, -2,-28, -6,-10;
/M: SY='P'; M= -1,-15,-31,-10, -2,-23,-15,-18,-18,-10,-24,-16,-14, 52, -7,-17, -3, -5,-22,-27,-23, -7;
/M: SY='E'; M= -5,  2,-26,  5, 22,-23,-13,  1,-25,  0,-20,-16,  0, -9,  8, -2,  3, -2,-22,-19,-12, 15;
/M: SY='R'; M= -9,  4,-22, -3, -2,-11,-15, -4,-18,  7,-18,-12, 11,-15, -1, 12,  2,  5,-15,-23, -5, -3;
```

May 2004 / Text revised.

Technical section

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- Taxonomic distribution of all UniProtKB (Swiss-Prot + TrEMBL) entries matching PS50070
- Retrieve a list of all UniProtKB (Swiss-Prot + TrEMBL) entries matching PS50070
- Scan UniProtKB (Swiss-Prot and/or TrEMBL) entries against PS50070
- View ligand binding statistics of PS50070
- Matching PDB structures: 1A0H 1B2I 1BHT 1CEA ... [ALL]

KRINGLE_1, PS00021; Kringle domain signature (PATTERN)

- Consensus pattern:
  [FY]-C-[RH]-[NS]-x(7,8)-[WY]-C
  The 2 C's are involved in a disulfide bonds
- Sequences in UniProtKB/Swiss-Prot known to belong to this class: 96
  - detected by PS00021: 94 (true positives)
  - undetected by PS00021: 2 (1 false negative and 1 'partial')
- Other sequence(s) in UniProtKB/Swiss-Prot detected by PS00021:
  3 false positives.
- Retrieve an alignment of UniProtKB/Swiss-Prot true positive hits:
  Clustal format, color, condensed view / Clustal format, color / Clustal format, plain text / Fasta format
- Retrieve the sequence logo from the alignment
- Taxonomic distribution of all UniProtKB (Swiss-Prot + TrEMBL) entries matching PS00021
- Retrieve a list of all UniProtKB (Swiss-Prot + TrEMBL) entries matching PS00021
- Scan UniProtKB (Swiss-Prot and/or TrEMBL) entries against PS00021
- View ligand binding statistics of PS00021
- Matching PDB structures: 1A0H 1B2I 1BHT 1CEA ... [ALL]

References

PROSITE

prosite.expasy.org/cgi-bin/prosite/sequence_logo.cgi?ac=PS00021

Apps | Bookmarks | D pmartel | UALG Acad | Drug Design | Programming | Bioinformatics | Molecular Modelling | Science | Enzymology | To watch and read | Misc | GW2 | Other bookmarks

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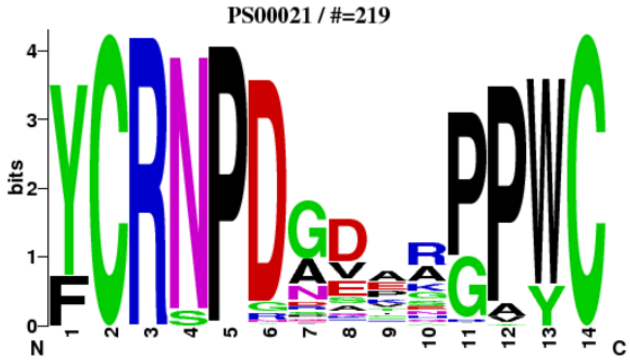
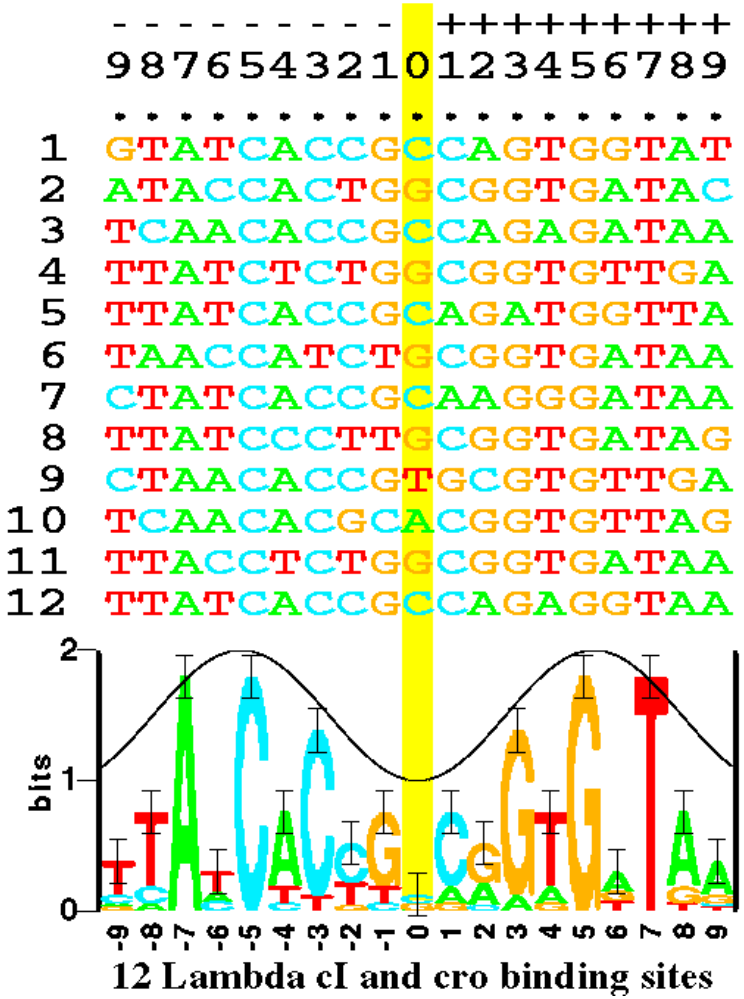
Sequence logo for PS00021



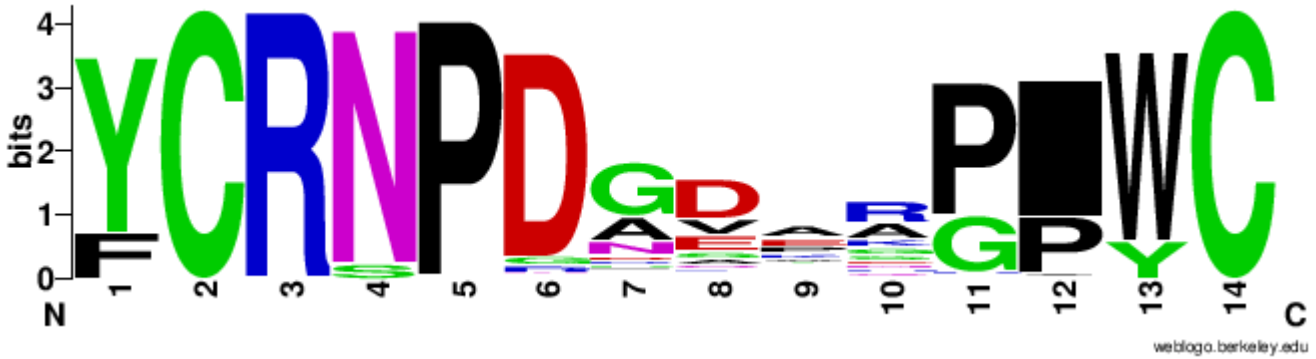
Number of UniProtKB/Swiss-Prot true positive hits used to build the logo:219.
Go to UniProtKB/Swiss-Prot true positive sequences.
Go to the list of all PROSITE motifs.
Go to the sequence logo help document.

[FY]-C-[RH]-[NS]-x(7,8)-[WY]-C



http://weblogo.berkeley.edu/

Logo *versus* padrão PROSITE



[FY]-C-[RH]-[NS]-x(7,8)-[WY]-C

ExPASy - PROSITE

prosite.expasy.org

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Database of protein domains, families and functional sites

PROSITE consists of documentation entries describing protein domains, families and functional sites as well as associated patterns and profiles to identify them [More... / References / Commercial users].
PROSITE is complemented by ProRule, a collection of rules based on profiles and patterns, which increases the discriminatory power of profiles and patterns by providing additional information about functionally and/or structurally critical amino acids [More...].

Release 20.131 of 27-Oct-2016 contains 1773 documentation entries, 1309 patterns, 1172 profiles and 1193 ProRule.

Search

e.g. PDOC00022, PS50089, SH3, zinc finger

Search

Browse

- by documentation entry
- by ProRule description
- by taxonomic scope
- by number of positive hits

Quick Scan mode of ScanProsite

Quickly find matches of your protein sequences to PROSITE signatures (max. 10 sequences). [?] Examples

P00748

P00748 – Factor de coagulação F12

Scan | Clear

Exclude motifs with a high probability of occurrence from the scan

For more scanning options go to **ScanProsite**

Other tools

- **PRATT** - allows to interactively generate conserved patterns from a series of unaligned proteins.
- **MyDomains - Image Creator** - allows to generate custom domain figures.

Profiles, PWM, PSWM, PS | ScanProsite | www.uniprot.org/uniprot | PROSITE | ScanProsite | Paulo

prosite.expasy.org/cgi-bin/prosite/ScanView.cgi?scanfile=156895430889.scan.gz

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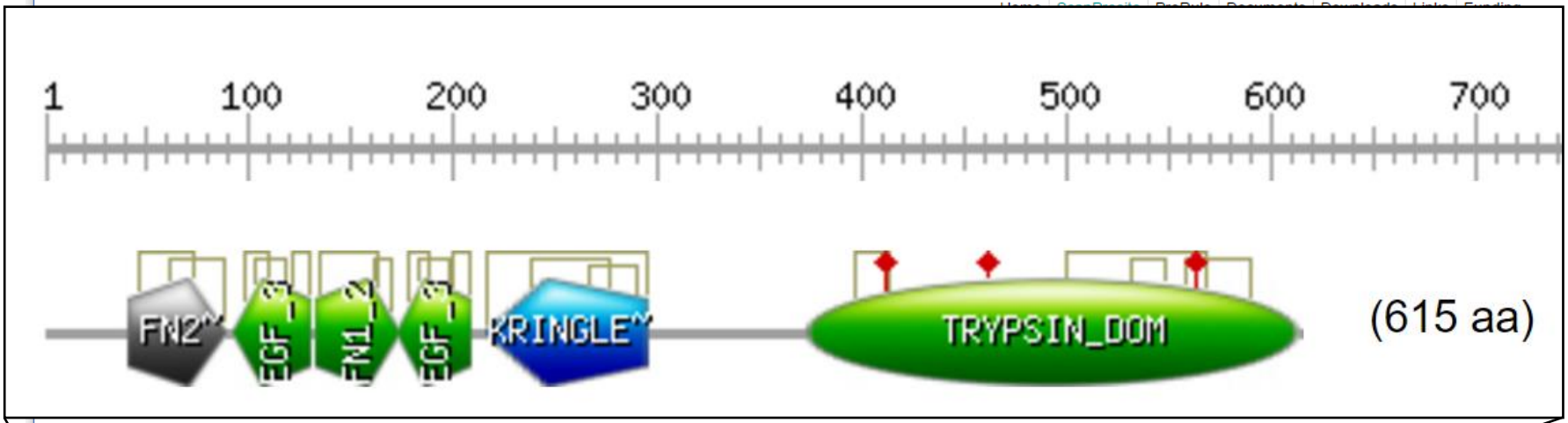


Legend:

disulfide bridge | active site | other 'ranges' | other sites

Please note that the graphical representations of domains displayed hereafter are for illustrative purposes only, and that their colors and shapes are not intended to indicate homology or shared function.
For more information about how these graphical representations are constructed, go to http://prosite.expasy.org/mydomains/.

hits by profiles: [6 hits (by 5 distinct profiles) on 1 sequence]

Upper case represents match positions, lower case insert positions, and the '-' symbol represents deletions relative to the matching profile.

ruler: 1 100 200 300 400 500 600 700 800 900 1000

sp-P00748-FA12_HUMAN (sp-P00748-FA12_HUMAN) (615 aa)

PS51092 **FN2_2** *Fibronectin type-II collagen-binding domain profile* :

42 - 90: **score** = 19.967

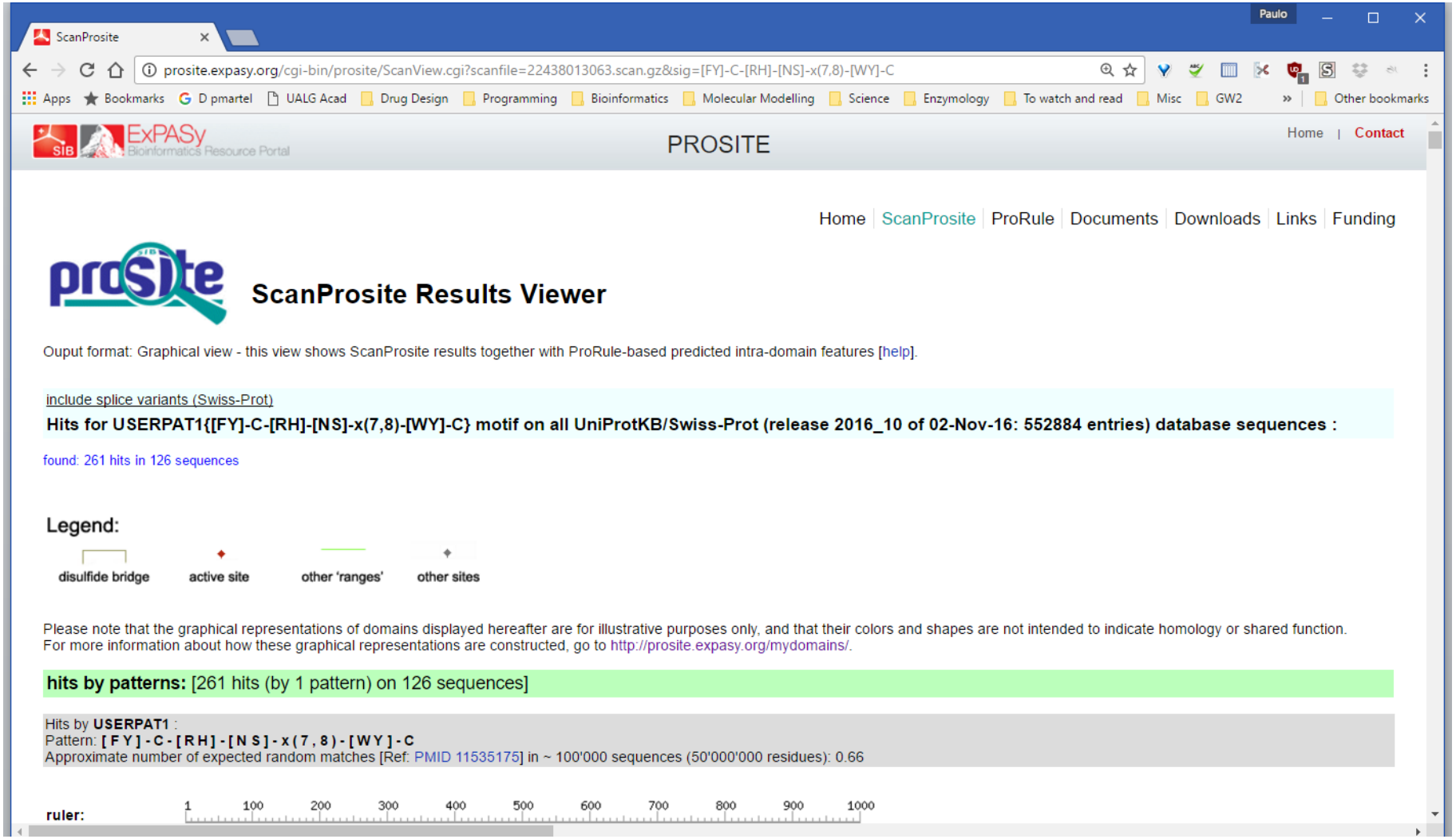
VTGEPCHFPFQYHRQLYHKCTHKGRPGPQPWCATTPNFDQDQRWGYCLE

Predicted features:

DOMAIN	42	90	Fibronectin type-II	[condition: none]
DISULFID	47	73		[condition: C-x*-C]

Pesquisa de motivos com Prosite

http://prosite.expasy.org/scanprosite/


ScanProsite
Paulo
prosite.expasy.org/cgi-bin/prosite/ScanView.cgi?scanfile=22438013063.scan.gz&sig=[FY]-C-[RH]-[NS]-x(7,8)-[WY]-C
Apps
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Ouput format: Graphical view - this view shows ScanProsite results together with ProRule-based predicted intra-domain features [help].
include splice variants (Swiss-Prot)
Hits for USERPAT1{[FY]-C-[RH]-[NS]-x(7,8)-[WY]-C} motif on all UniProtKB/Swiss-Prot (release 2016_10 of 02-Nov-16: 552884 entries) database sequences :
found: 261 hits in 126 sequences
Legend:
disulfide bridge
active site
other 'ranges'
other sites
Please note that the graphical representations of domains displayed hereafter are for illustrative purposes only, and that their colors and shapes are not intended to indicate homology or shared function.
For more information about how these graphical representations are constructed, go to http://prosite.expasy.org/mydomains/.
hits by patterns: [261 hits (by 1 pattern) on 126 sequences]
Hits by USERPAT1 :
Pattern: [FY]-C-[RH]-[NS]-x(7,8)-[WY]-C
Approximate number of expected random matches [Ref: PMID 11535175] in ~ 100'000 sequences (50'000'000 residues): 0.66
ruler:
1 100 200 300 400 500 600 700 800 900 1000

ScanProsite

prosite.expasy.org/cgi-bin/prosite/ScanView.cgi?scanfile=22438013063.scan.gz&sig=[FY]-C-[RH]-[NS]-x(7,8)-[WY]-C

Please note that the graphical representations of domains displayed hereafter are for illustrative purposes only, and that their colors and shapes are not intended to indicate homology or shared function.
For more information about how these graphical representations are constructed, go to http://prosite.expasy.org/mydomains/.

hits by patterns: [261 hits (by 1 pattern) on 126 sequences]

Hits by **USERPAT1** :
Pattern: **[FY]-C-[RH]-[NS]-x(7,8)-[WY]-C**
Approximate number of expected random matches [Ref: PMID 11535175] in ~ 100'000 sequences (50'000'000 residues): 0.66

ruler: 1 100 200 300 400 500 600 700 800 900 1000

P08519
(APOA_HUMAN)

Apolipoprotein(a) (Apo(a)) (Lp(a)) (EC 3.4.21.-). *Homo sapiens (Human)*

76 - 88:	YCRNpdavaap.YC
190 - 202:	YCRNpdavaap.YC
304 - 316:	YCRNpdavaap.YC
418 - 430:	YCRNpdavaap.YC
532 - 544:	YCRNpdavaap.YC
646 - 658:	YCRNpdavaap.YC
760 - 772:	YCRNpdavaap.YC
874 - 886:	YCRNpdavaap.YC
988 - 1000:	YCRNpdavaap.YC
1102 - 1114:	YCRNpdavaap.YC
1216 - 1228:	YCRNpdavaap.YC

Exemplo de entrada na base PROSITE (motivo)

```
ID   CUTINASE_1; PATTERN.
AC   PS00155;
DT   APR-1990 (CREATED); NOV-1997 (DATA UPDATE); MAR-2005 (INFO UPDATE).
DE   Cutinase, serine active site.
PA   P-x-[STA]-x-[LIV]-[IVT]-x-[GS]-G-Y-S-[QL]-G.
NR   /RELEASE=46.4,178022;
NR   /TOTAL=20(20); /POSITIVE=20(20); /UNKNOWN=0(0); /FALSE_POS=0(0);
NR   /FALSE_NEG=0; /PARTIAL=0;
CC   /TAXO-RANGE=??EP?; /MAX-REPEAT=1;
CC   /SITE=11,active_site;
DR   P63880, CUT1_MYCBO , T; P63879, CUT1_MYCTU , T; P63882, CUT2_MYCBO , T;
DR   P63881, CUT2_MYCTU , T; P0A537, CUT3_MYCBO , T; P0A536, CUT3_MYCTU , T;
DR   P00590, CUTI1_FUSSO, T; Q96UT0, CUTI2_FUSSO, T; Q96US9, CUTI3_FUSSO, T;
DR   P41744, CUTI_ALTBR , T; P29292, CUTI_ASCRA , T; P52956, CUTI_ASPOR , T;
DR   Q00298, CUTI_BOTCI , T; P10951, CUTI_COLCA , T; P11373, CUTI_COLGL , T;
DR   Q8X1P1, CUTI_ERYGR , T; Q99174, CUTI_FUSSC , T; P30272, CUTI_MAGGR , T;
DR   Q8TGB8, CUTI_MONFR , T; Q9Y7G8, CUTI_PYRBR , T;
3D   1AGY; 1CEX; 1CUA; 1CUB; 1CUC; 1CUD; 1CUE; 1CUF; 1CUG; 1CUH; 1CUS; 1CUU;
3D   1CUV; 1CUW; 1CUY; 1CUZ; 1FFA; 1FFB; 1FFC; 1FFD; 1FFE; 1OXM; 1XZA; 1XZB;
3D   1XZC; 1XZD; 1XZE; 1XZF; 1XZG; 1XZH; 1XZJ; 1XZK; 1XZL; 1XZM; 2CUT;
DO   PDOC00140;
//
```

http://www.expasy.org/prosite

Exemplo de entrada na base PROSITE (perfil)

```
ID   HSP20; MATRIX.
AC   PS01031;
DT   JUN-1994 (CREATED); DEC-2001 (DATA UPDATE); MAR-2005 (INFO UPDATE).
DE   Heat shock hsp20 proteins family profile.
MA   /GENERAL_SPEC: ALPHABET='ABCDEFGHIKLMNPQRSTVWYZ'; LENGTH=88;
MA   /DISJOINT: DEFINITION=PROTECT; N1=6; N2=83;
MA   /NORMALIZATION: MODE=1; FUNCTION=LINEAR; R1=-0.7971325; R2=0.0157729; TEXT='-LogE';
MA   /CUT_OFF: LEVEL=0; SCORE=590; N_SCORE=8.5; MODE=1; TEXT='!';
MA   /CUT_OFF: LEVEL=-1; SCORE=463; N_SCORE=6.5; MODE=1; TEXT='?';
MA   /DEFAULT: M0=-8; D=-20; I=-20; B1=-50; E1=-50; MI=-105; MD=-105; IM=-105; DM=-105;
MA   /I: B1=0; BI=-105; BD=-105;
MA   /M: SY='D'; M=-10,26,-29,38,34,-34,-14,-2,-33,7,-24,-23,8,-6,8,-4,0,-9,-27,-33,-19,21;
MA   /M: SY='I'; M=-8,-31,-23,-35,-28,7,-32,-27,27,-24,15,13,-27,-26,-24,-23,-20,-9,25,-4,2,-27;
MA   /M: SY='R'; M=-11,-12,-26,-12,-1,-13,-23,-1,-8,1,-7,-3,-8,-11,-2,8,-9,-6,-8,-22,-3,-4;
MA   /M: SY='E'; M=-11,17,-27,23,29,-24,-15,-3,-27,1,-22,-20,9,-1,6,-6,3,-4,-25,-32,-17,17;
MA   /M: SY='D'; M=-7,10,-23,11,2,-25,0,-6,-26,-4,-23,-18,7,-6,-5,-8,7,7,-20,-31,-17,-2;
MA   /I: I=-4; MD=-22;
MA   /M: SY='D'; M=-8,17,-27,25,19,-30,-13,-5,-28,6,-25,-20,7,3,4,-1,0,-7,-24,-30,-19,10; D=-4;
MA   /I: I=-4; MI=0; MD=-22; IM=0; DM=-22;
MA   /M: SY='D'; M=-11,20,-25,24,16,-29,-12,-1,-27,14,-25,-16,14,-9,10,5,1,-6,-23,-28,-14,13; D=-4;
MA   /I: I=-4; DM=-22;
..
... Some lines omitted..
..
MA   /M: SY='K'; M=-9,-5,-25,-6,0,-22,-21,-12,-17,30,-21,-6,-3,-16,1,23,-9,-7,-6,-23,-11,0;
MA   /I: E1=0; IE=-105; DE=-105;
NR   /RELEASE=46.4,178022;
NR   /TOTAL=195(194); /POSITIVE=190(189); /UNKNOWN=5(5); /FALSE_POS=0(0);
NR   /FALSE_NEG=1; /PARTIAL=8;
CC   /MATRIX_TYPE=protein_domain;
CC   /SCALING_DB=reversed;
CC   /AUTHOR=P_Bucher;
CC   /TAXO-RANGE=A?EP?; /MAX-REPEAT=2;
CC   /FT_KEY=DOMAIN; /FT_DESC=HSP20;
DR   P0A5B8, 14KD_MYCBO , T; P0A5B7, 14KD_MYCTU , T; P46729, 18K1_MYCAV , T;
DR   P46730, 18K1_MYCIT , T; P46731, 18K2_MYCAV , T; P46732, 18K2_MYCIT , T;
DR   P12809, 18KD_MYCLE , T; P80485, ASP1_STRTR , T; O30851, ASP2_STRTR , T;
..
... Some lines omitted..
```

Perfis (profiles)

Um **perfil** é uma descrição do padrão subjacente a um alinhamento múltiplo e reflecte a probabilidade de ocorrência de cada tipo de resíduo numa dada posição. Tem várias aplicações:

• Permite uma maior precisão no alinhamento de sequências distantes da mesma família

• Os padrões emergentes são úteis para a **classificação** de sub-famílias dentro de um conjunto de sequências homólogas.

• O alinhamento de uma sequência a um perfil é geralmente mais fiável e melhora o processo de **modelação estrutural** por homologia

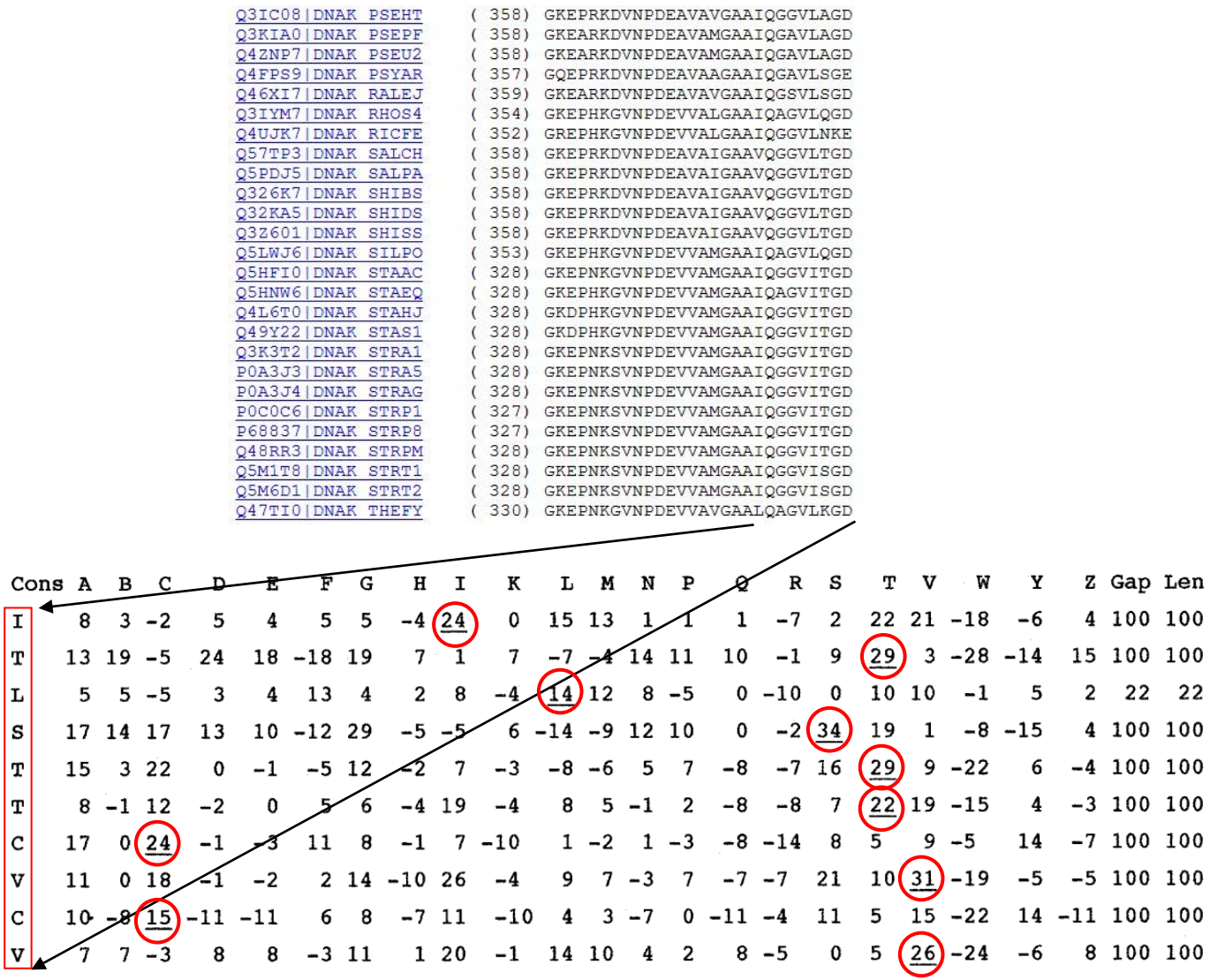
• Os perfis permite **pesquisas de elevada sensibilidade** para a detecção de parentes distantes de uma dada família de proteínas

O alinhamento de uma sequência a um perfil é condicionado pela sua natureza e pelo seu grau de conservação. Assim, resíduos altamente conservados no perfil terão um score mais alto, e resíduos pouco conservados um score mais baixo. Este processo impõe uma tendência para alinhar em primeiro lugar as *zonas mais conservadas*.

Geração de perfis a partir de alinhamentos múltiplos

```
Q3IC08|DNAK_PSEHT    ( 358) GKEPRKDVNPDEAVAVGAAIQGGVLAGD
Q3KIA0|DNAK_PSEPF    ( 358) GKEARKDVNPDEAVAMGAAIQGAVLAGD
Q4ZNP7|DNAK_PSEU2    ( 358) GKEARKDVNPDEAVAMGAAIQGAVLAGD
Q4FPS9|DNAK_PSYAR    ( 357) GQEPRKDVNPDEAVAAGAAIQGAVLSGE
Q46XI7|DNAK_RALEJ    ( 359) GKEARKDVNPDEAVAVGAAIQGSVLSGD
Q3IYM7|DNAK_RHOS4    ( 354) GKEPHKGVNPDEVVALGAAIQAGVLQGD
Q4UJK7|DNAK_RICFE    ( 352) GREPHKGVNPDEVVALGAAIQGGVLNKE
Q57TP3|DNAK_SALCH    ( 358) GKEPRKDVNPDEAVAIGAAVQGGVLTGD
Q5PDJ5|DNAK_SALPA    ( 358) GKEPRKDVNPDEAVAIGAAVQGGVLTGD
Q326K7|DNAK_SHIBS    ( 358) GKEPRKDVNPDEAVAIGAAVQGGVLTGD
Q32KA5|DNAK_SHIDS    ( 358) GKEPRKDVNPDEAVAIGAAVQGGVLTGD
Q3Z601|DNAK_SHISS    ( 358) GKEPRKDVNPDEAVAIGAAVQGGVLTGD
Q5LWJ6|DNAK_SILPO    ( 353) GKEPHKGVNPDEVVAMGAAIQAGVLQGD
Q5HFI0|DNAK_STAAC    ( 328) GKEPNKGVNPDEVVAMGAAIQGGVITGD
Q5HNW6|DNAK_STAEQ    ( 328) GKEPHKGVNPDEVVAMGAAIQAGVITGD
Q4L6T0|DNAK_STAHJ    ( 328) GKDPHKGVNPDEVVAMGAAIQGGVITGD
Q49Y22|DNAK_STAS1    ( 328) GKDPHKGVNPDEVVAMGAAIQGGVITGD
Q3K3T2|DNAK_STRA1    ( 328) GKEPNKSVNPDEVVAMGAAIQGGVITGD
P0A3J3|DNAK_STRA5    ( 328) GKEPNKSVNPDEVVAMGAAIQGGVITGD
P0A3J4|DNAK_STRAG    ( 328) GKEPNKSVNPDEVVAMGAAIQGGVITGD
P0C0C6|DNAK_STRP1    ( 327) GKEPNKSVNPDEVVAMGAAIQGGVITGD
P68837|DNAK_STRP8    ( 327) GKEPNKSVNPDEVVAMGAAIQGGVITGD
Q48RR3|DNAK_STRPM    ( 328) GKEPNKSVNPDEVVAMGAAIQGGVITGD
Q5M1T8|DNAK_STRT1    ( 328) GKEPNKSVNPDEVVAMGAAIQGGVISGD
Q5M6D1|DNAK_STRT2    ( 328) GKEPNKSVNPDEVVAMGAAIQGGVISGD
Q47TI0|DNAK_THEFY    ( 330) GKEPNKGVNPDEVVAVGAALQAGVLKGD
```

Cons	A	B	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y	Z	Gap	Len
I	8	3	-2	5	4	5	5	-4	24	0	15	13	1	1	1	-7	2	22	21	-18	-6	4	100	100
T	13	19	-5	24	18	-18	19	7	1	7	-7	-4	14	11	10	-1	9	29	3	-28	-14	15	100	100
L	5	5	-5	3	4	13	4	2	8	-4	14	12	8	-5	0	-10	0	10	10	-1	5	2	22	22
S	17	14	17	13	10	-12	29	-5	-5	6	-14	-9	12	10	0	-2	34	19	1	-8	-15	4	100	100
T	15	3	22	0	-1	-5	12	-2	7	-3	-8	-6	5	7	-8	-7	16	29	9	-22	6	-4	100	100
T	8	-1	12	-2	0	5	6	-4	19	-4	8	5	-1	2	-8	-8	7	22	19	-15	4	-3	100	100
C	17	0	24	-1	-3	11	8	-1	7	-10	1	-2	1	-3	-8	-14	8	5	9	-5	14	-7	100	100
V	11	0	18	-1	-2	2	14	-10	26	-4	9	7	-3	7	-7	-7	21	10	31	-19	-5	-5	100	100
C	10	-8	15	-11	-11	6	8	-7	11	-10	4	3	-7	0	-11	-4	11	5	15	-22	14	-11	100	100
V	7	7	-3	8	8	-3	11	1	20	-1	14	10	4	2	8	-5	0	5	26	-24	-6	8	100	100



Cons	A	B	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y	Z	Gap	Len
I	8	3	-2	5	4	5	5	-4	24	0	15	13	1	1	1	-7	2	22	21	-18	-6	4	100	100
T	13	19	-5	24	18	-18	19	7	1	7	-7	-4	14	11	10	-1	9	29	3	-28	-14	15	100	100
L	5	5	-5	3	4	13	4	2	8	-4	14	12	8	-5	0	-10	0	10	10	-1	5	2	22	22
S	17	14	17	13	10	-12	29	-5	-5	6	-14	-9	12	10	0	-2	34	19	1	-8	-15	4	100	100
T	15	3	22	0	-1	-5	12	-2	7	-3	-8	-6	5	7	-8	-7	16	29	9	-22	6	-4	100	100
T	8	-1	12	-2	0	5	6	-4	19	-4	8	5	-1	2	-8	-8	7	22	19	-15	4	-3	100	100
C	17	0	24	-1	-3	11	8	-1	7	-10	1	-2	1	-3	-8	-14	8	5	9	-5	14	-7	100	100
V	11	0	18	-1	-2	2	14	-10	26	-4	9	7	-3	7	-7	-7	21	10	31	-19	-5	-5	100	100
C	10	-8	15	-11	-11	6	8	-7	11	-10	4	3	-7	0	-11	-4	11	5	15	-22	14	-11	100	100
V	7	7	-3	8	8	-3	11	1	20	-1	14	10	4	2	8	-5	0	5	26	-24	-6	8	100	100

PIR
Protein Information Resource
A UniProt CONSORTIUM MEMBER

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HOME / Search / *Pattern Search*

http://pir.georgetown.edu/pirwww/search/pattern.shtml

Pattern Search Forms ?

Search a query pattern against a UniProt database

1. Select a database: (•) **UniProtKB** (or restricted by organism/taxon group)
( ) **UniRef100**

2. Insert a user-defined pattern below:

x(12)-E-x(3)-E-x-C-x(6)-[DEN]-x-[LIVMFY]-x(9)-[FYW]

Or, alternatively, enter a valid PROSITE code for a query pattern:

Submit Reset

Example: PS00888 (annotated output)

Search your query sequence against the PROSITE database

Insert a query sequence below using the single letter amino acid code:

Or, alternatively, enter a UniProtKB identifier:

Submit Reset

Example: O05689 (annotated output)

Matrizes PSSM

Matrizes PSSM

- PSSM (**P**osition **S**pecific **S**coring **M**atrix) é um tipo de matriz cujos scores por aminoácido são dependentes da **posição do aminoácido** na sequência.
- As matrizes PSSM são semelhantes a **perfis** e permitem armazenar informação para uma determinada **assinatura** ou motivo de uma família de proteínas.
- Os valores de uma matriz PSSM são calculados a partir regiões conservadas de alinhamentos de sequências.
- As matrizes PSSM permitem detectar padrões e similaridades fracas
- Os scores produzidos por uma matriz PSSM refletem as particularidades da família de proteínas a partir da qual foram construídas (valore totalmente diferente de matrizes BLOSUM ou PAM)

Criação de uma matriz PSSM

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
A	0	0	0	0	0	0	0	0	0	0	0	2	1	0	2
C	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
D	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E	0	0	5	0	1	0	0	0	1	0	0	0	0	1	0
F	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0
G	5	0	0	2	0	5	1	0	1	0	2	3	1	1	0
H	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0
I	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
K	0	0	0	1	1	0	1	1	0	1	0	0	0	0	0
L	0	0	0	1	0	0	0	0	0	0	1	0	2	0	0
M	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0
Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
R	0	0	0	0	1	0	0	1	0	1	1	0	0	0	0
S	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0
T	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
V	0	0	0	0	1	0	0	1	1	0	0	0	0	0	0
W	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Y	0	0	0	0	1	0	1	0	0	0	0	0	0	1	0

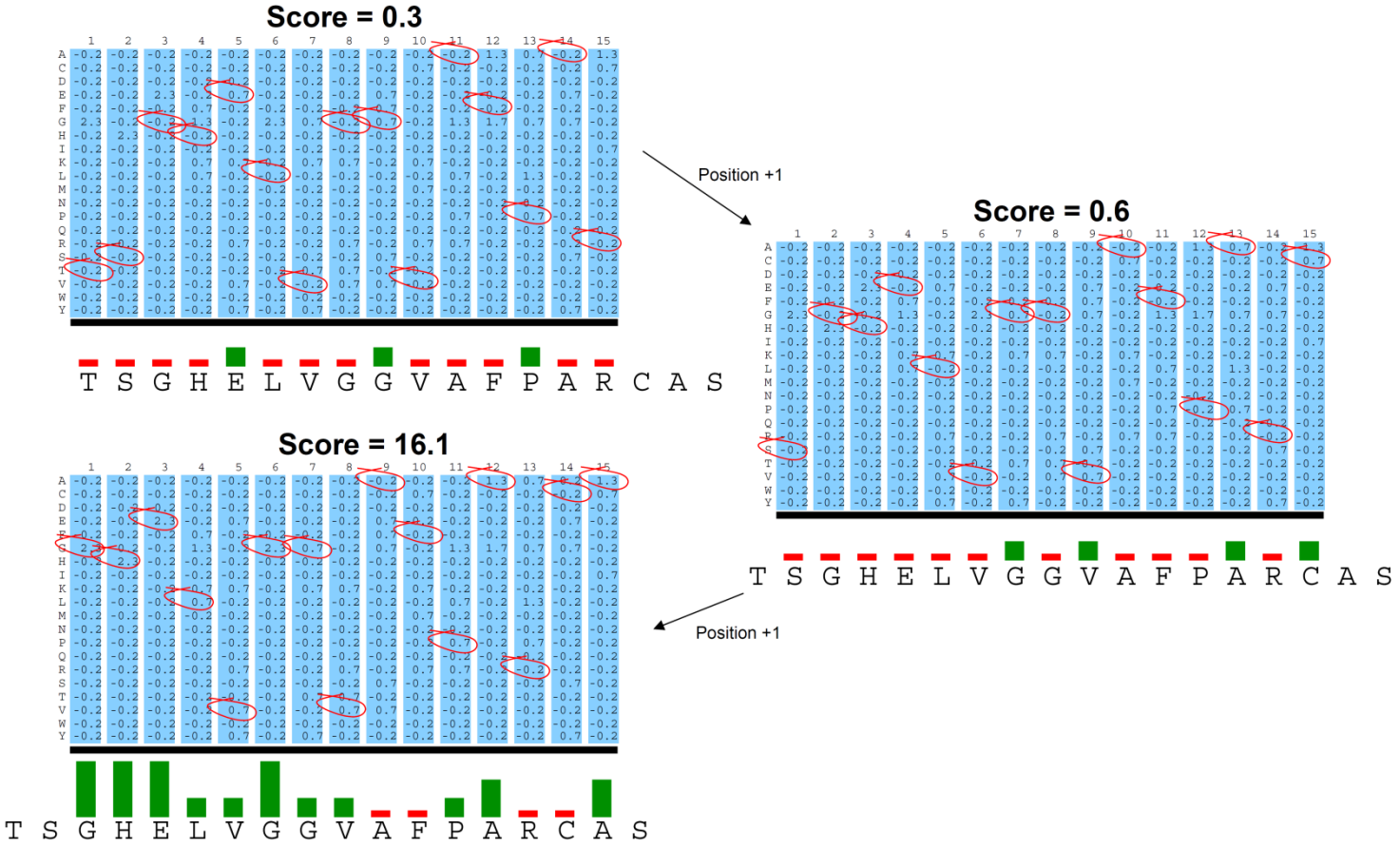
As frequências de ocorrência de cada aminoácido são contadas para cada **posição** do alinhamento. As contagens são normalizadas e convertidas numa matriz *log odds* semelhante a uma matriz de score.

Criação de uma matriz PSSM

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
A	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	1.3	0.7	-0.2	1.3
C	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	0.7	-0.2	-0.2	-0.2	-0.2	0.7
D	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2
E	-0.2	-0.2	2.3	-0.2	0.7	-0.2	-0.2	-0.2	0.7	-0.2	-0.2	-0.2	-0.2	0.7	-0.2
F	-0.2	-0.2	-0.2	0.7	-0.2	-0.2	-0.2	-0.2	0.7	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2
G	2.3	-0.2	-0.2	1.3	-0.2	2.3	0.7	-0.2	0.7	-0.2	1.3	1.7	0.7	0.7	-0.2
H	-0.2	2.3	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2
I	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	0.7
K	-0.2	-0.2	-0.2	0.7	0.7	-0.2	0.7	0.7	-0.2	0.7	-0.2	-0.2	-0.2	-0.2	-0.2
L	-0.2	-0.2	-0.2	0.7	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	0.7	-0.2	1.3	-0.2	-0.2
M	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	0.7	-0.2	-0.2	-0.2	-0.2	-0.2
N	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2
P	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	0.7	-0.2	0.7	-0.2	-0.2
Q	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2
R	-0.2	-0.2	-0.2	-0.2	0.7	-0.2	-0.2	0.7	-0.2	0.7	0.7	-0.2	-0.2	-0.2	-0.2
S	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	0.7	-0.2	-0.2	-0.2	-0.2	0.7	-0.2
T	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	0.7	0.7	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2
V	-0.2	-0.2	-0.2	-0.2	0.7	-0.2	-0.2	0.7	0.7	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2
W	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2
Y	-0.2	-0.2	-0.2	-0.2	0.7	-0.2	0.7	-0.2	-0.2	-0.2	-0.2	-0.2	-0.2	0.7	-0.2

Matriz PSSM calculada a partir do exemplo do slide anterior.

Uso de matriz PSSM



A matriz PSSM “desliza” sobre a sequência em análise, produzindo um score para cada posição. O score máximo indicará a posição do padrão codificado pela matriz PSSM.

Geração de PSSMs com **pssmsearch**

Q3IC08|DNAK_PSEHT	GKEPRKDVNPDEAVAVGAAIQGGVLAGD
Q3KIA0|DNAK_PSEPF	GKEARKDVNPDEAVAMGAAIQGAVLAGD
Q4ZNP7|DNAK_PSEU2	GKEARKDVNPDEAVAMGAAIQGAVLAGD
Q4FPS9|DNAK_PSYAR	GQEPRKDVNPDEAVAAGAAIQGAVLSGE
Q46XI7|DNAK_RALEJ	GKEARKDVNPDEAVAVGAAIQGSVLSGD
Q3IYM7|DNAK_RHOS4	GKEPHKGVNPDEVVALGAAIQAGVLQGD
Q4UJK7|DNAK_RICFE	GREPHKGVNPDEVVALGAAIQGGVLNKE
Q57TP3|DNAK_SALCH	GKEPRKDVNPDEAVAIGAAVQGGVLTGD
Q5PDJ5|DNAK_SALPA	GKEPRKDVNPDEAVAIGAAVQGGVLTGD
Q326K7|DNAK_SHIBS	GKEPRKDVNPDEAVAIGAAVQGGVLTGD
Q32KA5|DNAK_SHIDS	GKEPRKDVNPDEAVAIGAAVQGGVLTGD
Q3Z601|DNAK_SHISS	GKEPRKDVNPDEAVAIGAAVQGGVLTGD
Q5LWJ6|DNAK_SILPO	GKEPHKGVNPDEVVAMGAAIQAGVLQGD
Q5HFI0|DNAK_STAAC	GKEPNKGVNPDEVVAMGAAIQGGVITGD
Q5HNW6|DNAK_STAEQ	GKEPHKGVNPDEVVAMGAAIQAGVITGD
Q4L6T0|DNAK_STAHJ	GKEPHKGVNPDEVVAMGAAIQGGVITGD
Q49Y22|DNAK_STAS1	GKDPHKGVNPDEVVAMGAAIQGGVITGD
Q3K3T2|DNAK_STRA1	GKEPNKSVNPDEVVAMGAAIQGGVITGD
P0A3J3|DNAK_STRA5	GKEPNKSVNPDEVVAMGAAIQGGVITGD
P0A3J4|DNAK_STRAG	GKEPNKSVNPDEVVAMGAAIQGGVITGD
P0C0C6|DNAK_STRP1	GKEPNKSVNPDEVVAMGAAIQGGVITGD
P68837|DNAK_STRP8	GKEPNKSVNPDEVVAMGAAIQGGVITGD
Q48RR3|DNAK_STRPM	GKEPNKSVNPDEVVAMGAAIQGGVITGD
Q5M1T8|DNAK_STRT1	GKEPNKSVNPDEVVAMGAAIQGGVISGD
Q5M6D1|DNAK_STRT2	GKEPNKSVNPDEVVAMGAAIQGGVISGD
Q47TI0|DNAK_THEFY	GKEPNKGVNPDEVVAVGAALQAGVLKGD

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
C	-3.72	-4.52	-5.29	-3.46	-4.45	-4.52	-3.36	-1.32	-4.02	-4.13	-5.14	-5.32	-1.02	-1.32	-0.70	-1.86	-3.72	-0.70	-0.70	-1.82	-4.33	-3.02	-2.96	-1.32	-1.93	-1.66	-3.77	-5.15
P	-3.19	-1.70	-1.74	8.77	-3.10	-1.59	-2.22	-3.55	-3.07	10.62	-2.28	-1.71	-2.46	-3.55	-1.29	-3.59	-3.19	-1.29	-1.29	-4.04	-1.99	-2.79	-2.72	-3.55	-4.18	-1.59	-3.03	-2.18
Q	-2.69	2.08	2.41	-1.83	0.70	1.71	-1.05	-3.33	-0.17	-1.94	-0.59	2.58	-2.35	-3.33	-1.28	-1.74	-2.69	-1.28	-1.28	-3.95	7.87	-2.39	-2.27	-3.33	-3.53	0.58	-2.11	0.03
N	-0.72	-0.37	-0.25	-2.87	3.10	-0.39	0.81	-4.31	8.71	-2.98	1.70	-0.49	-3.37	-4.31	-2.33	-3.70	-0.72	-2.33	-2.33	-4.73	-0.13	-0.92	-0.79	-4.31	-4.90	0.82	-0.68	1.48
T	-2.39	-1.12	-1.36	-1.40	-1.30	-1.10	-0.58	-0.24	-0.24	-1.64	-1.66	-1.35	-0.17	-0.24	-0.18	-0.97	-2.39	-0.18	-0.18	-1.04	-1.11	-1.90	-1.63	-0.24	-1.55	2.43	-2.26	-1.60
S	-0.53	-0.45	-0.31	-0.75	-0.46	-0.42	1.34	-2.53	0.70	-1.26	-0.52	-0.31	-0.42	-2.53	1.50	-2.23	-0.53	1.50	1.50	-3.36	-0.28	-0.09	0.38	-2.53	-3.58	1.36	-0.51	-0.47
G	8.13	-2.41	-3.04	-2.53	-2.22	-2.34	2.89	-4.69	-0.78	-3.17	-2.04	-3.15	-2.07	-4.69	0.12	-3.98	8.13	0.12	0.12	-5.37	-2.71	6.37	5.89	-4.69	-5.41	-1.47	7.12	-2.16
A	0.12	-1.24	-1.43	0.61	-2.27	-1.19	-0.24	-0.43	-2.39	-1.27	-2.68	-1.35	2.54	-0.43	5.94	-0.20	0.12	5.94	5.94	-1.75	-1.30	1.55	1.35	-0.43	-2.14	0.66	0.05	-2.45
V	-4.65	-3.39	-3.69	-2.89	-4.11	-3.40	-3.94	6.22	-4.33	-3.49	-4.68	-3.63	3.42	6.22	-0.39	1.40	-4.65	-0.39	-0.39	3.17	-3.31	-3.54	-3.55	6.22	2.23	-1.04	-4.52	-4.50
I	-5.49	-4.01	-4.70	-3.72	-4.61	-3.99	-4.53	3.53	-4.82	-4.08	-4.65	-4.72	2.14	3.53	-2.02	1.79	-5.49	-2.02	-2.02	5.09	-4.14	-4.65	-4.64	3.53	3.55	-2.06	-5.34	-4.64
L	-5.35	-3.58	-4.28	-3.88	-3.97	-3.67	-4.79	0.98	-5.06	-4.22	-5.35	-4.22	0.03	0.98	-2.23	1.59	-5.35	-2.23	-2.23	1.76	-3.22	-4.62	-4.61	0.98	3.71	-2.47	-5.18	-5.16
M	-3.98	-1.97	-3.08	-3.28	-2.48	-2.09	-3.61	0.84	-3.28	-3.67	-4.56	-2.99	0.12	0.84	-1.46	3.60	-3.98	-1.46	-1.46	1.45	-0.74	-3.42	-3.38	0.84	2.32	-1.40	-3.78	-4.29
F	-4.60	-4.53	-4.74	-4.94	-3.46	-4.58	-4.45	-1.38	-4.50	-5.29	-5.18	-4.72	-2.00	-1.38	-3.31	-0.35	-4.60	-3.31	-3.31	-0.49	-4.71	-4.33	-4.30	-1.38	0.18	-3.44	-4.59	-5.09
Y	-4.50	-2.68	-3.11	-4.03	-0.68	-2.76	-3.88	-1.90	-3.18	-4.31	-4.57	-3.02	-2.14	-1.90	-2.66	-1.74	-4.50	-2.66	-2.66	-2.02	-2.19	-4.11	-4.04	-1.90	-1.79	-2.46	-4.33	-4.30
W	-3.71	-4.24	-4.32	-5.10	-4.24	-4.40	-4.59	-4.25	-5.52	-5.37	-6.23	-4.20	-4.01	-4.25	-3.77	-2.78	-3.71	-3.77	-3.77	-3.86	-2.95	-3.70	-3.71	-4.25	-2.95	-3.75	-3.75	-5.87
H	-3.06	-0.96	-0.36	-3.08	4.06	-1.17	-2.00	-4.66	0.66	-3.21	-1.76	-0.27	-3.61	-4.66	-2.46	-3.15	-3.06	-2.46	-2.46	-4.76	0.51	-2.93	-2.84	-4.66	-4.38	-1.53	-2.87	-1.50
K	-2.32	5.33	0.90	-1.48	1.16	6.82	-1.24	-3.43	-0.43	-1.56	-1.16	1.02	-2.34	-3.43	-1.17	-2.61	-2.32	-1.17	-1.17	-3.89	1.71	-2.08	-1.99	-3.43	-3.77	0.20	-0.32	-0.76
R	-3.44	2.99	-0.39	-2.97	3.16	2.92	-2.34	-3.77	-0.81	-3.14	-2.46	-0.27	-3.01	-3.77	-2.16	-2.75	-3.44	-2.16	-2.16	-4.28	1.29	-3.17	-3.06	-3.77	-3.66	-0.82	-2.41	-2.06
D	-2.01	-1.17	2.87	-2.26	-0.40	-1.14	3.33	-4.70	1.67	-2.23	8.58	2.08	-3.72	-4.70	-2.65	-4.50	-2.01	-2.65	-2.65	-4.70	-0.59	-2.08	-1.97	-4.70	-5.03	-0.96	-1.92	6.99
E	-3.16	1.05	6.30	-1.64	-0.33	0.99	0.26	-3.69	-0.56	-1.70	2.04	7.19	-2.57	-3.69	-1.36	-3.33	-3.16	-1.36	-1.36	-4.54	2.55	-2.78	-2.63	-3.69	-4.41	-0.43	-2.63	2.84

http://slim.icr.ac.uk/pssmsearch/

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
C	-3.72	-4.52	-5.29	-3.46	-4.45	-4.52	-3.36	-1.32	-4.02	-4.13	-5.14	-5.32	-1.02	-1.32	-0.70	-1.86	-3.72	-0.70	-0.70	-1.82	-4.33	-3.02	-2.96	-1.32	-1.93	-1.66	-3.77	-5.15
P	-3.19	-1.70	-1.74	8.77	-3.10	-1.59	-2.22	-3.55	-3.07	10.62	-2.28	-1.71	-2.46	-3.55	-1.29	-3.59	-3.19	-1.29	-1.29	-4.04	-1.99	-2.79	-2.72	-3.55	-4.18	-1.59	-3.03	-2.18
Q	-2.69	2.08	2.41	-1.83	0.70	1.71	-1.05	-3.33	-0.17	-1.94	-0.59	2.58	-2.35	-3.33	-1.28	-1.74	-2.69	-1.28	-1.28	-3.95	7.87	-2.39	-2.27	-3.33	-3.53	0.58	-2.11	0.03
N	-0.72	-0.37	-0.25	-2.87	3.10	-0.39	0.81	-4.31	8.71	-2.98	1.70	-0.49	-3.37	-4.31	-2.33	-3.70	-0.72	-2.33	-2.33	-4.73	-0.13	-0.92	-0.79	-4.31	-4.90	0.82	-0.68	1.48
T	-2.39	-1.12	-1.36	-1.40	-1.30	-1.10	-0.58	-0.24	-0.24	-1.64	-1.66	-1.35	-0.17	-0.24	-0.18	-0.97	-2.39	-0.18	-0.18	-1.04	-1.11	-1.90	-1.63	-0.24	-1.55	2.43	-2.26	-1.60
S	-0.53	-0.45	-0.31	-0.75	-0.46	-0.42	1.34	-2.53	0.70	-1.26	-0.52	-0.31	-0.42	-2.53	1.50	-2.23	-0.53	1.50	1.50	-3.36	-0.28	-0.09	0.38	-2.53	-3.58	1.36	-0.51	-0.47
G	8.13	-2.41	-3.04	-2.53	-2.22	-2.34	2.89	-4.69	-0.78	-3.17	-2.04	-3.15	-2.07	-4.69	0.12	-3.98	8.13	0.12	0.12	-5.37	-2.71	6.37	5.89	-4.69	-5.41	-1.47	7.12	-2.16
A	0.12	-1.24	-1.43	0.61	-2.27	-1.19	-0.24	-0.43	-2.39	-1.27	-2.68	-1.35	2.54	-0.43	5.94	-0.20	0.12	5.94	5.94	-1.75	-1.30	1.55	1.35	-0.43	-2.14	0.66	0.05	-2.45
V	-4.65	-3.39	-3.69	-2.89	-4.11	-3.40	-3.94	6.22	-4.33	-3.49	-4.68	-3.63	3.42	6.22	-0.39	1.40	-4.65	-0.39	-0.39	3.17	-3.31	-3.54	-3.55	6.22	2.23	-1.04	-4.52	-4.50
I	-5.49	-4.01	-4.70	-3.72	-4.61	-3.99	-4.53	3.53	-4.82	-4.08	-4.65	-4.72	2.14	3.53	-2.02	1.79	-5.49	-2.02	-2.02	5.09	-4.14	-4.65	-4.64	3.53	3.55	-2.06	-5.34	-4.64
L	-5.35	-3.58	-4.28	-3.88	-3.97	-3.67	-4.79	0.98	-5.06	-4.22	-5.35	-4.22	0.03	0.98	-2.23	1.59	-5.35	-2.23	-2.23	1.76	-3.22	-4.62	-4.61	0.98	3.71	-2.47	-5.18	-5.16
M	-3.98	-1.97	-3.08	-3.28	-2.48	-2.09	-3.61	0.84	-3.28	-3.67	-4.56	-2.99	0.12	0.84	-1.46	3.60	-3.98	-1.46	-1.46	1.45	-0.74	-3.42	-3.38	0.84	2.32	-1.40	-3.78	-4.29
F	-4.60	-4.53	-4.74	-4.94	-3.46	-4.58	-4.45	-1.38	-4.50	-5.29	-5.18	-4.72	-2.00	-1.38	-3.31	-0.35	-4.60	-3.31	-3.31	-0.49	-4.71	-4.33	-4.30	-1.38	0.18	-3.44	-4.59	-5.09
Y	-4.50	-2.68	-3.11	-4.03	-0.68	-2.76	-3.88	-1.90	-3.18	-4.31	-4.57	-3.02	-2.14	-1.90	-2.66	-1.74	-4.50	-2.66	-2.66	-2.02	-2.19	-4.11	-4.04	-1.90	-1.79	-2.46	-4.33	-4.30
W	-3.71	-4.24	-4.32	-5.10	-4.24	-4.40	-4.59	-4.25	-5.52	-5.37	-6.23	-4.20	-4.01	-4.25	-3.77	-2.78	-3.71	-3.77	-3.77	-3.86	-2.95	-3.70	-3.71	-4.25	-2.95	-3.75	-3.75	-5.87
H	-3.06	-0.96	-0.36	-3.08	4.06	-1.17	-2.00	-4.66	0.66	-3.21	-1.76	-0.27	-3.61	-4.66	-2.46	-3.15	-3.06	-2.46	-2.46	-4.76	0.51	-2.93	-2.84	-4.66	-4.38	-1.53	-2.87	-1.50
K	-2.32	5.33	0.90	-1.48	1.16	6.82	-1.24	-3.43	-0.43	-1.56	-1.16	1.02	-2.34	-3.43	-1.17	-2.61	-2.32	-1.17	-1.17	-3.89	1.71	-2.08	-1.99	-3.43	-3.77	0.20	-0.32	-0.76
R	-3.44	2.99	-0.39	-2.97	3.16	2.92	-2.34	-3.77	-0.81	-3.14	-2.46	-0.27	-3.01	-3.77	-2.16	-2.75	-3.44	-2.16	-2.16	-4.28	1.29	-3.17	-3.06	-3.77	-3.66	-0.82	-2.41	-2.06
D	-2.01	-1.17	2.87	-2.26	-0.40	-1.14	3.33	-4.70	1.67	-2.23	8.58	2.08	-3.72	-4.70	-2.65	-4.50	-2.01	-2.65	-2.65	-4.70	-0.59	-2.08	-1.97	-4.70	-5.03	-0.96	-1.92	6.99
E	-3.16	1.05	6.30	-1.64	-0.33	0.99	0.26	-3.69	-0.56	-1.70	2.04	7.19	-2.57	-3.69	-1.36	-3.33	-3.16	-1.36	-1.36	-4.54	2.55	-2.78	-2.63	-3.69	-4.41	-0.43	-2.63	2.84

http://slim.icr.ac.uk/pssmsearch/

PSI-BLAST

PSI-BLAST

A variante PSI (**P**osition **S**pecific **I**terated) do programa BLAST combina um modelo PSSM com uma esquema de penalidades afins para *gaps.*

- Princípio do algoritmo:
  1. Fazer uma pesquisa BLAST standard contra uma base de dados usando uma matriz de alinhamento standard (por exemplo BLOSUM62).
  2. Um modelo PSSM é construído automaticamente a partir do alinhamento múltiplo dos "hits" de score mais elevado (E-value inferior ao valor do parâmetro *PSI-BLAST Thresold*) .
  3. O modelo PSSM é usado em vez da matriz de score original para realizar uma nova pesquisa BLAST. Como resultado, poderão ser adicionadas novas sequências de E-value inferior ao valor de *PSI-BLAST Thresold.*
  4. O novo conjunto de sequências obtido em 3. é usado para construir um novo alinhamento múltiplo e, a partir deste, uma nova matriz PSSM
  5. Os passos 3. e 4. são repetidos enquanto sejam adicionadas, em cada iteração, novas sequências à lista de hits.
  6. Considera-se que o algoritmo convergiu quando não são adicionadas mais sequências à nova iteração.

Bases de dados de motivos e domínios

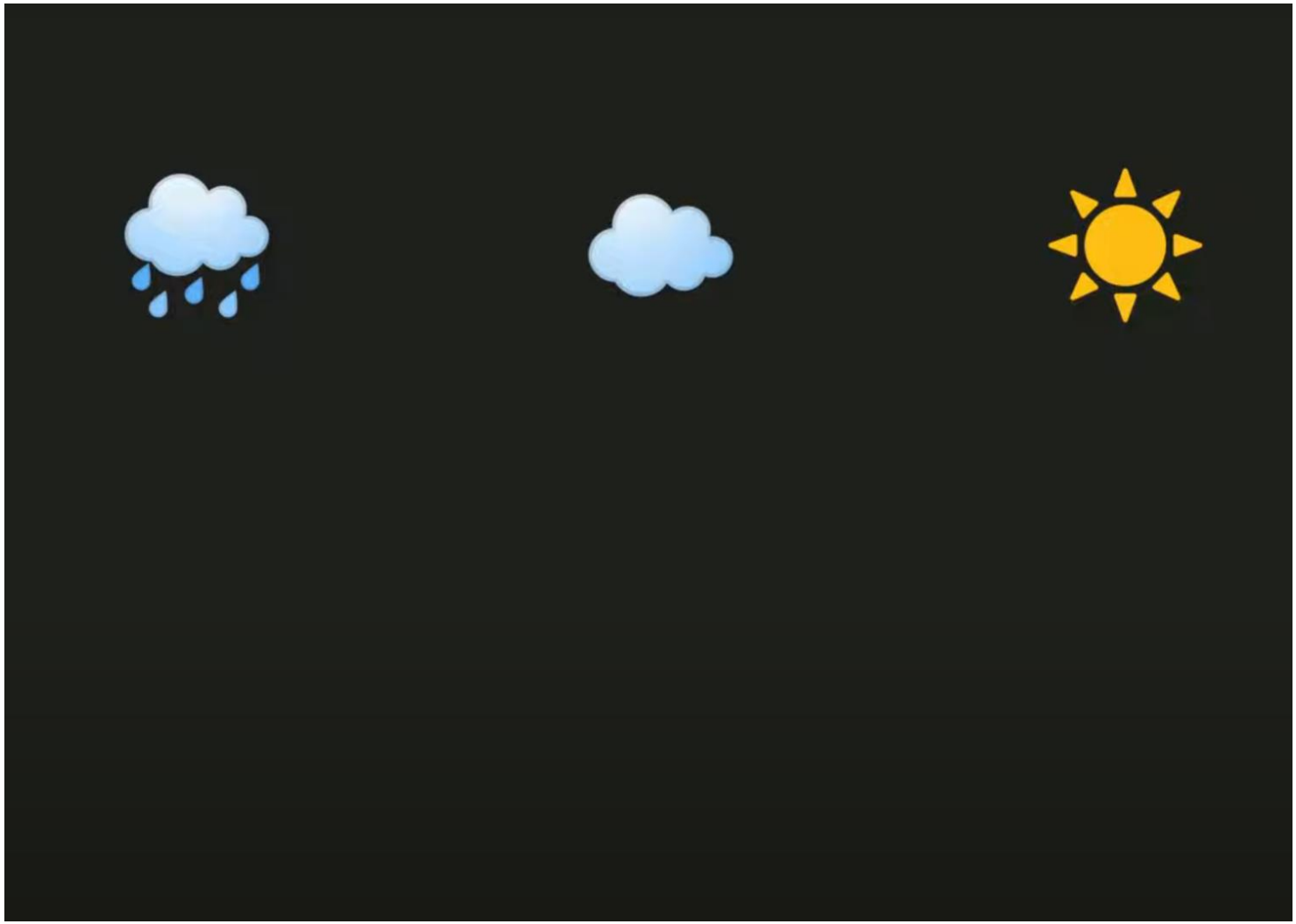
- **PROSITE**
  http://www.expasy.ch/prosite
- **PRINTS**
  http://www.bioinf.man.ac.uk/dbbrowser/PRINTS
- **PFAM**
  http://www.sanger.ac.uk/Software/Pfam
- **PRODOM**
  http://prodom.prabi.fr
- **SMART**
  http://smart.embl-heidelberg.de

Pesquisa em múltiplas bases de dados:

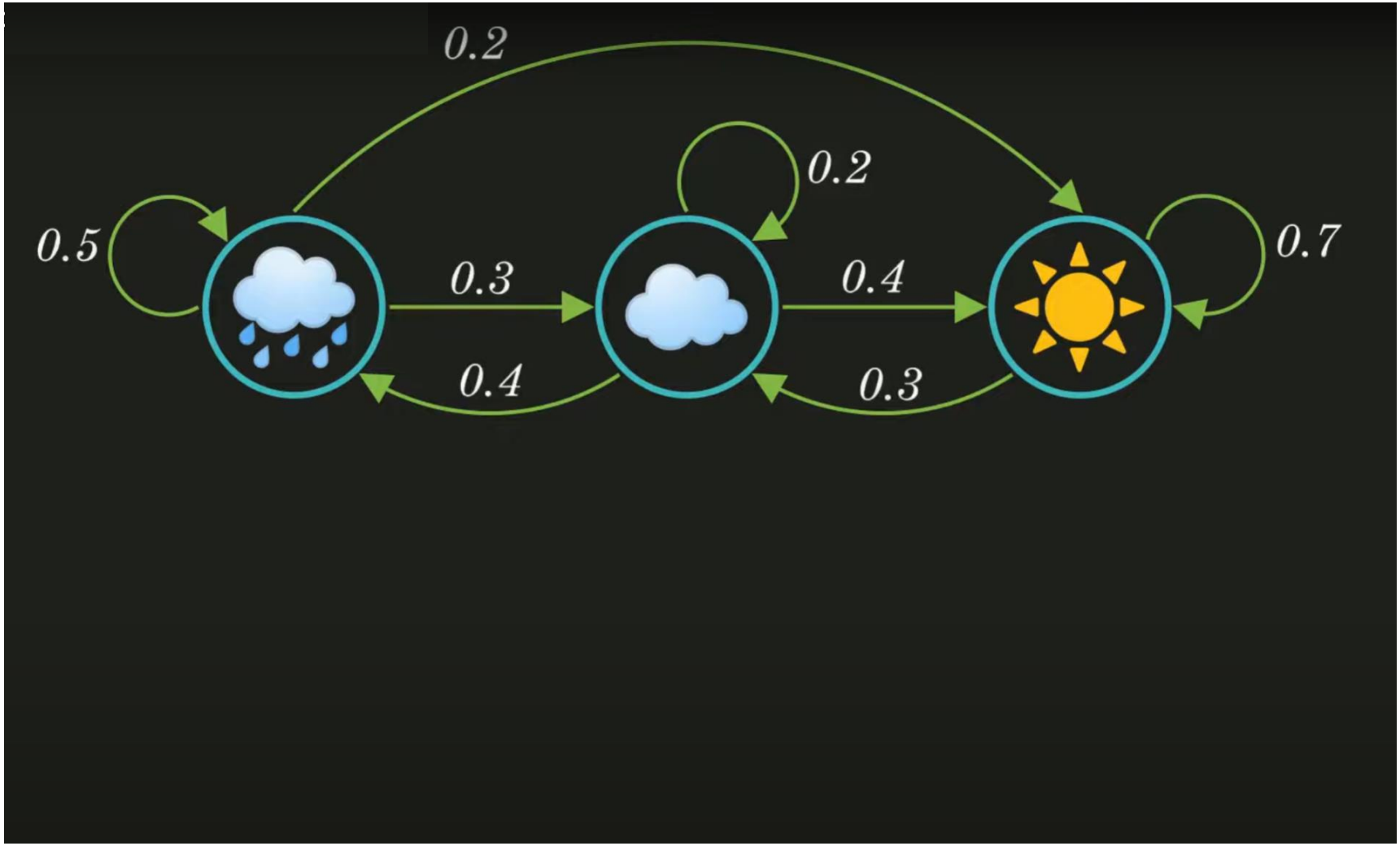
INTERPRO
http://www.ebi.ac.uk/interpro

Hidden Markov Models (HMMs)

- Modelos estocásticos que representam a estrutura de uma sequência em termos de distribuições de probabilidade de transição entre diferentes estados.
- As variáveis observáveis são determinadas pelos estados do sistema, estes tipicamente ocultos.
- Através da análise de uma ou mais sequências, é possível estimar os parâmetros internos de um dado modelo.
- Conhecidos os parâmetros, é possível estimar a probabilidade de um modelo produzir uma certa sequência.
- Permitem obter representações probabilísticas de conjuntos de sequências que capturam as preferências posicionais da composição aminoacídica.
- Permitem a construção de alinhamentos múltiplos
- Os HMMs são um dos métodos mais sensíveis para deteção de similaridades fracas entre sequências.



https://youtu.be/RWkHJnFj5rY



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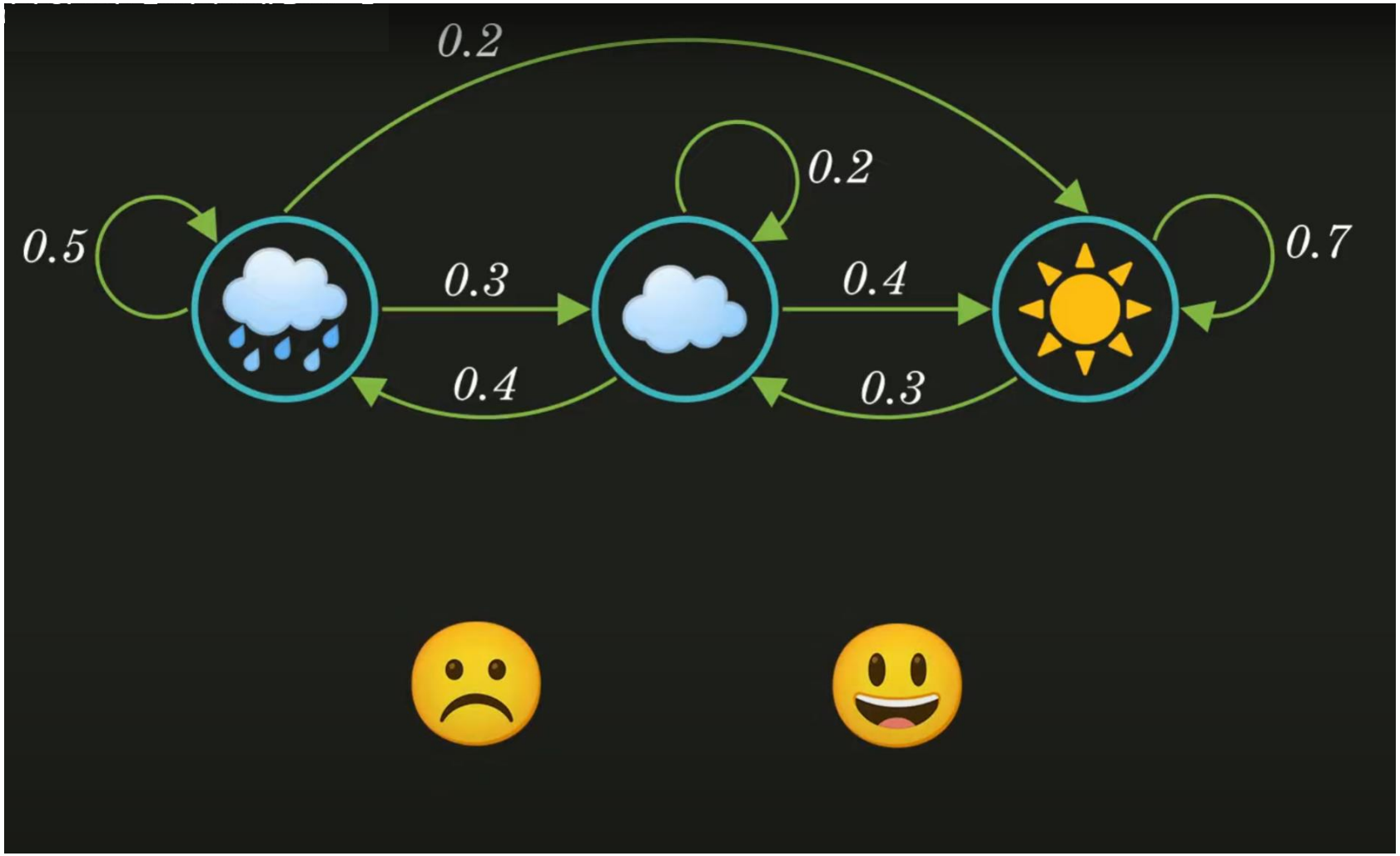

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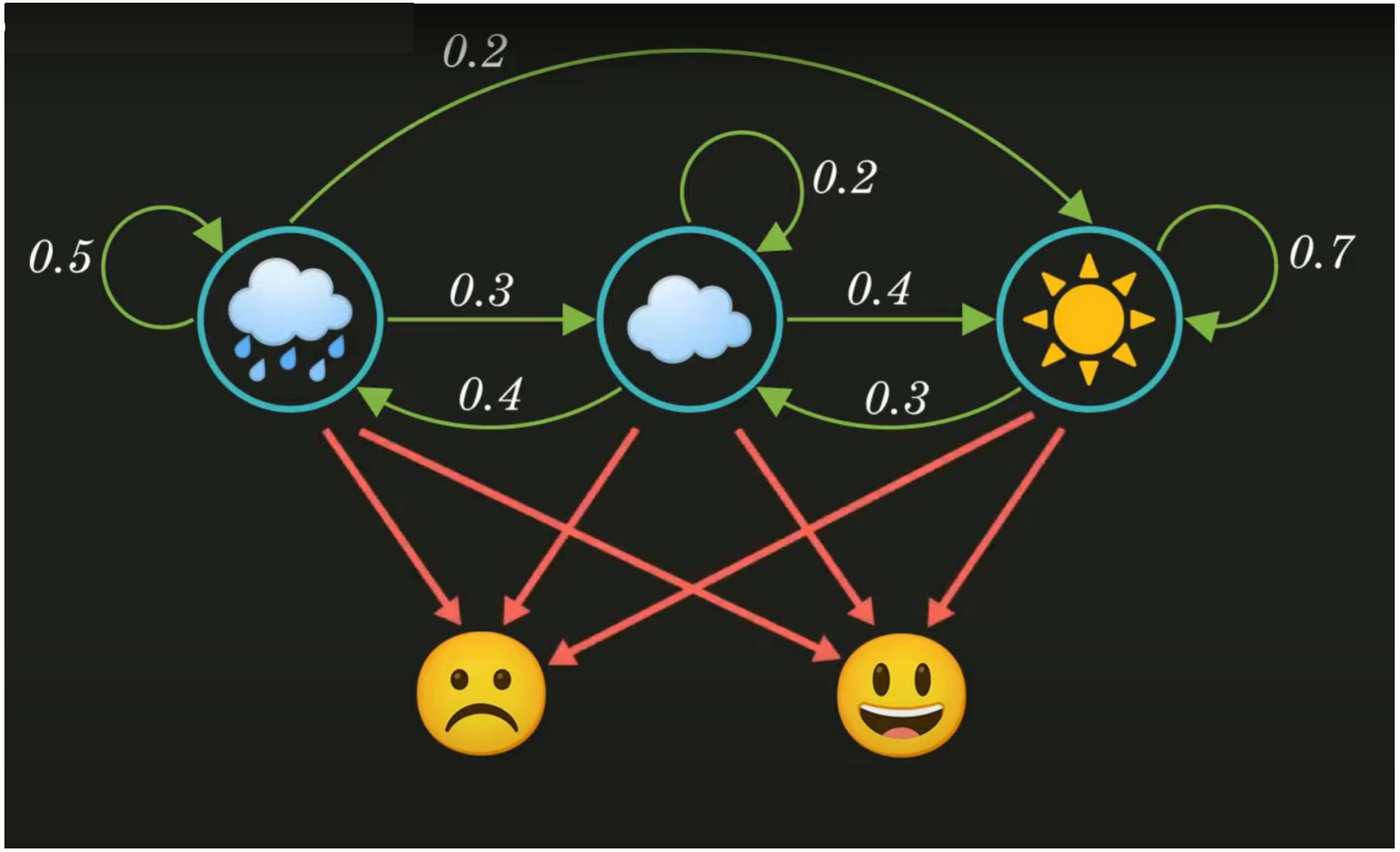

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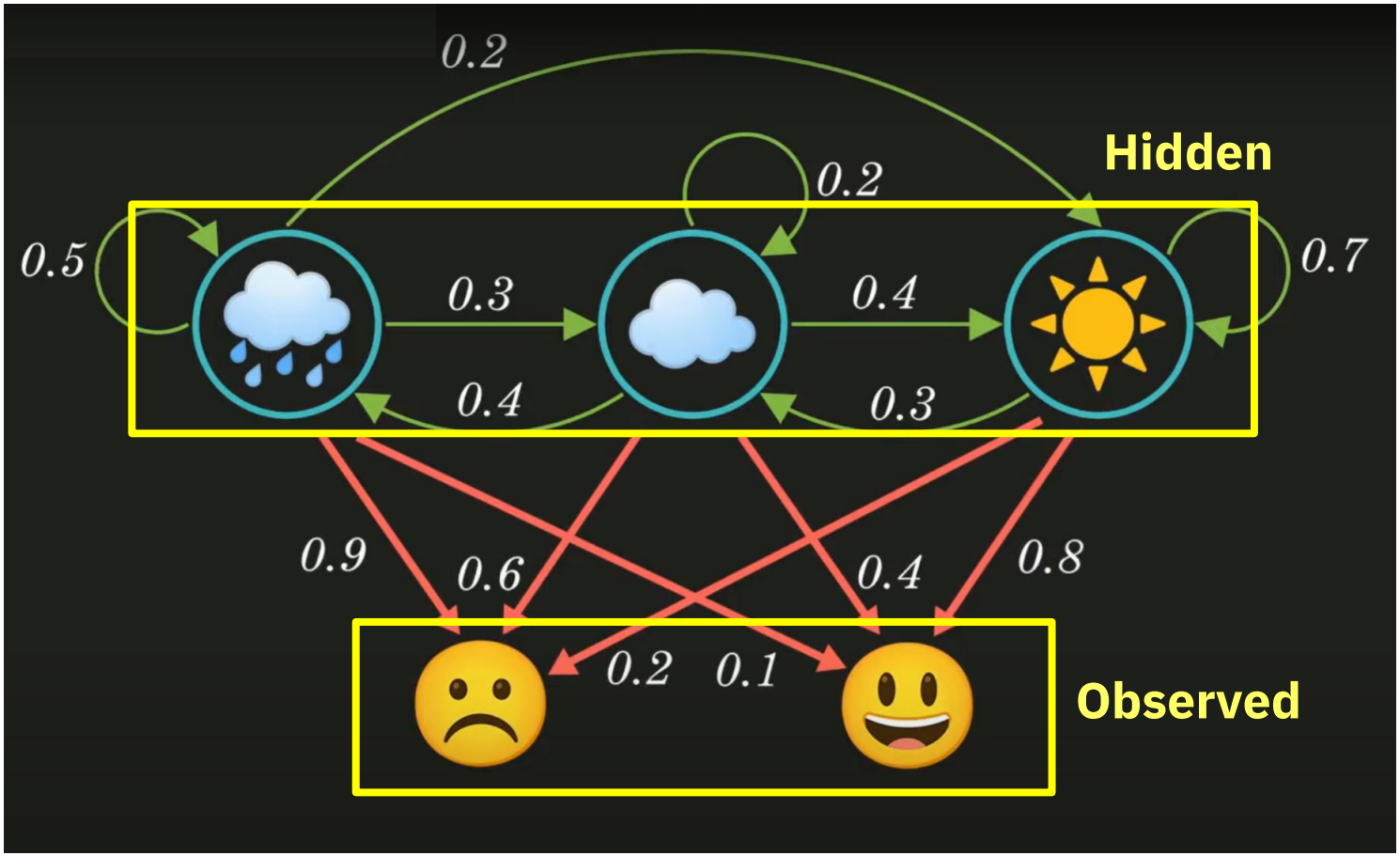

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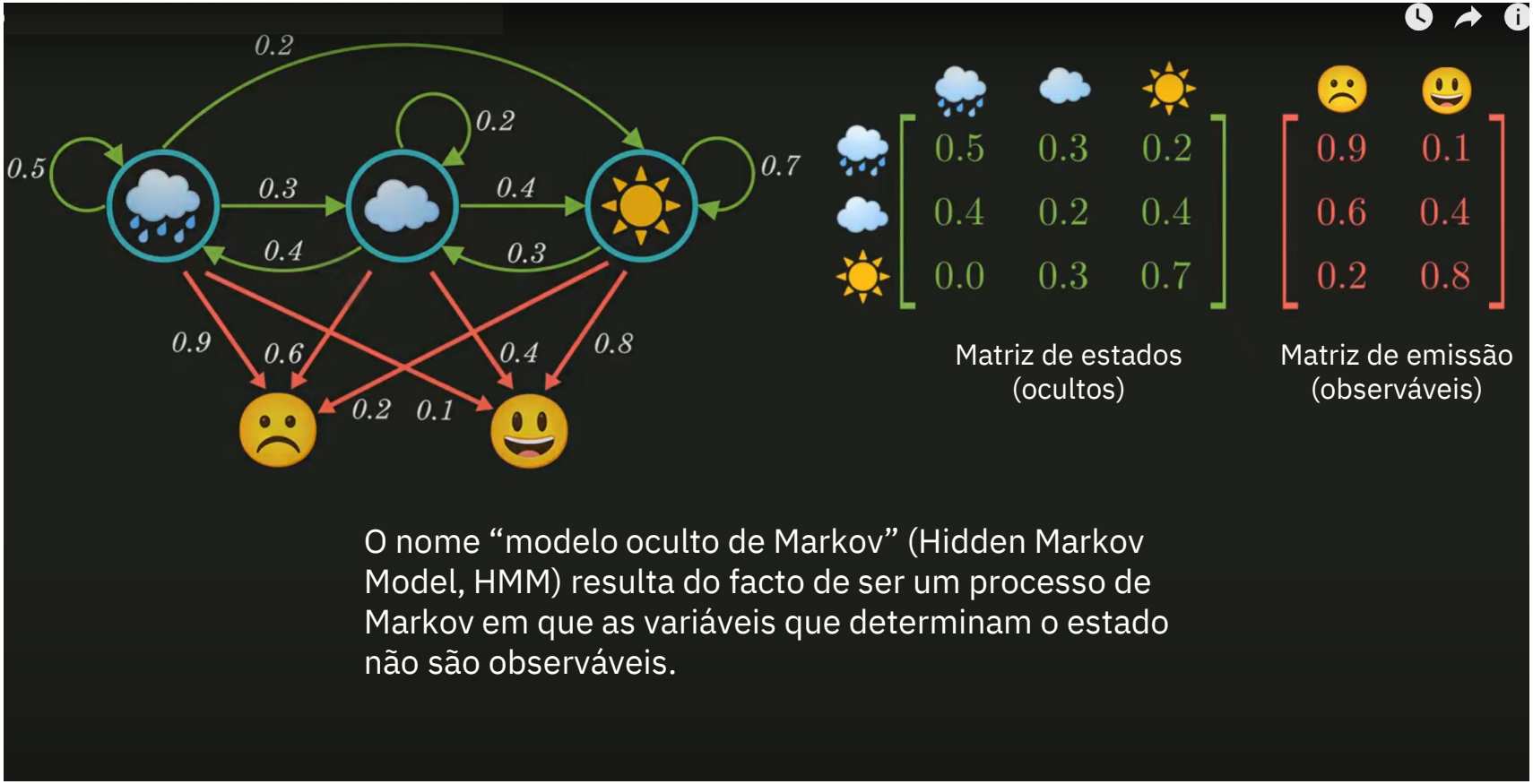

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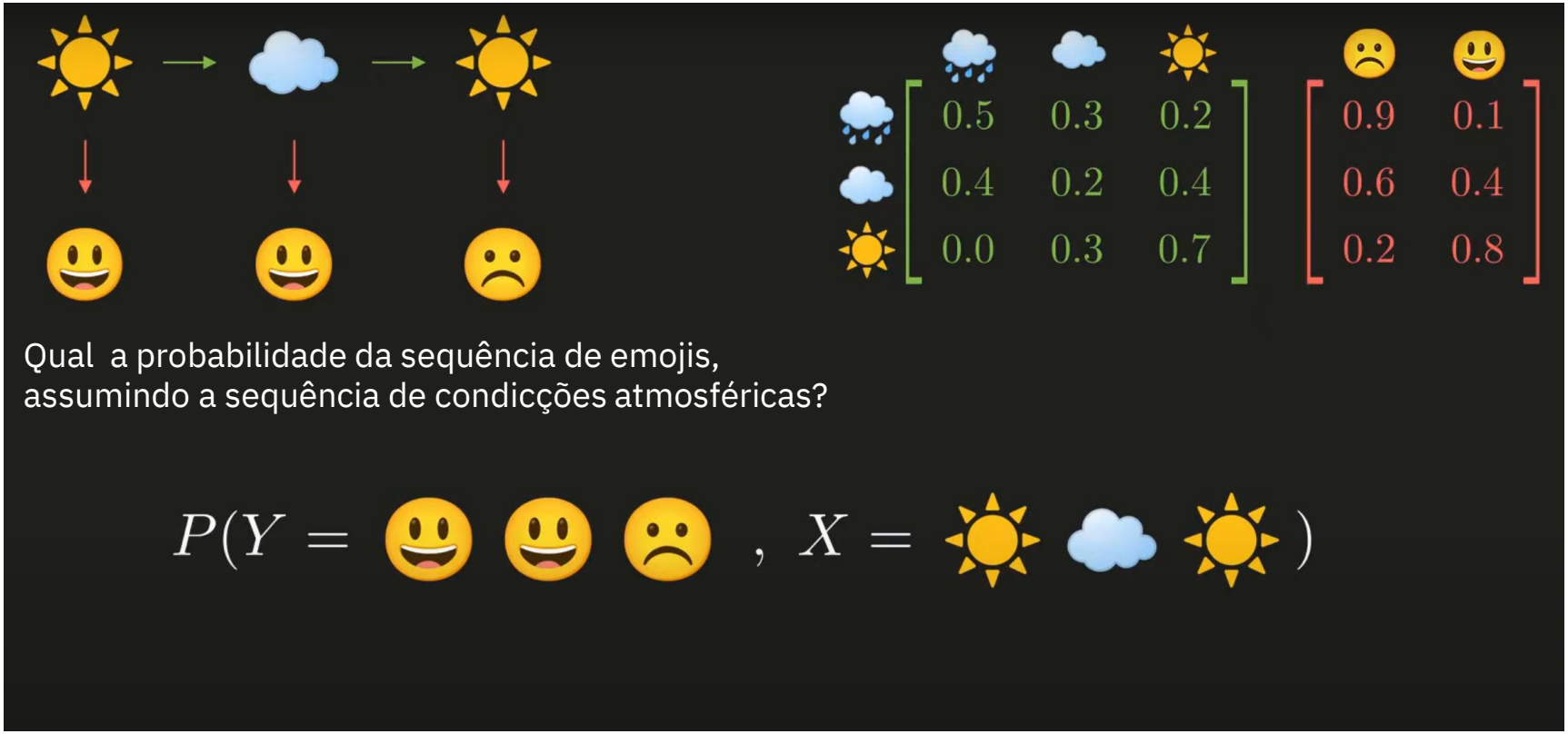

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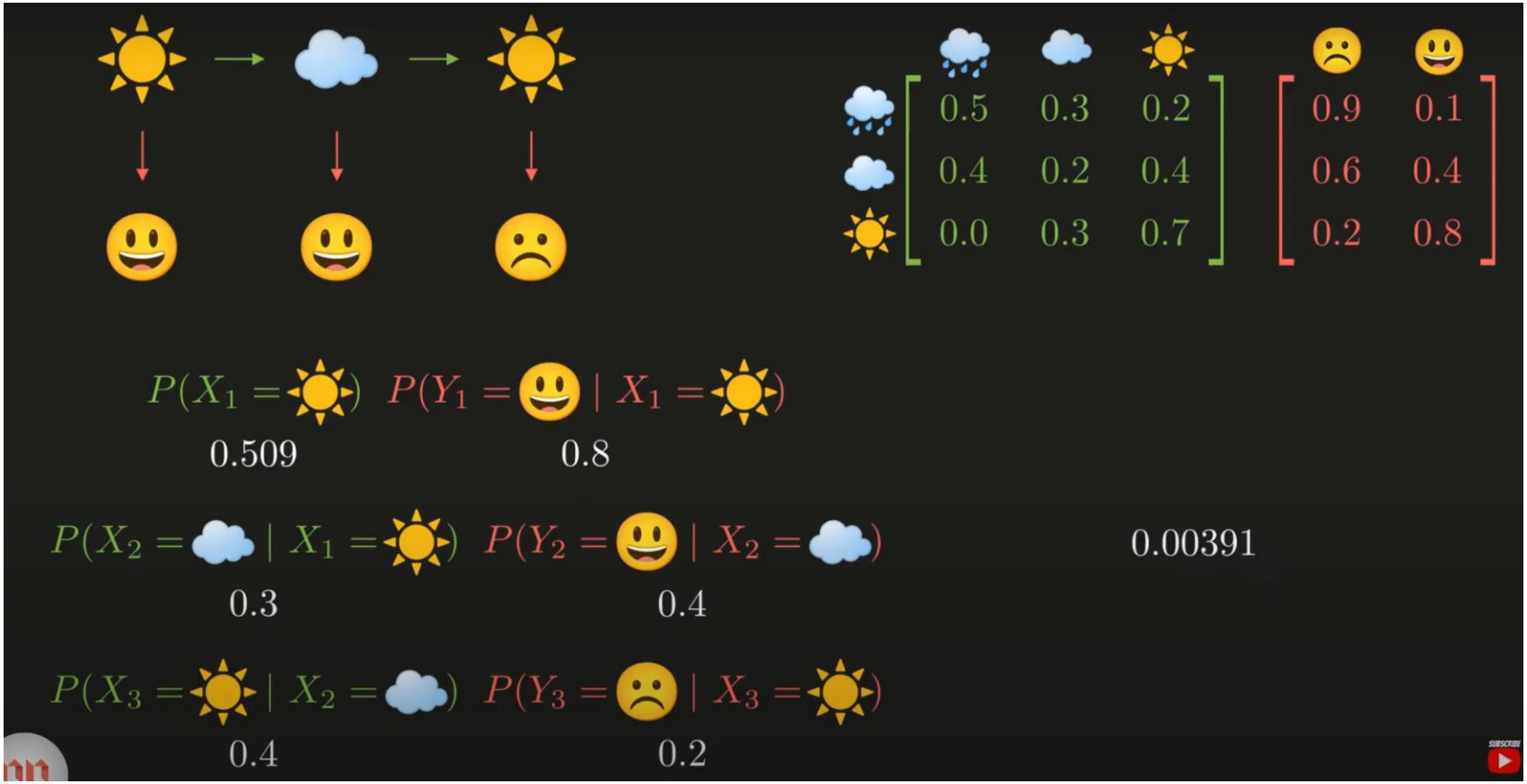

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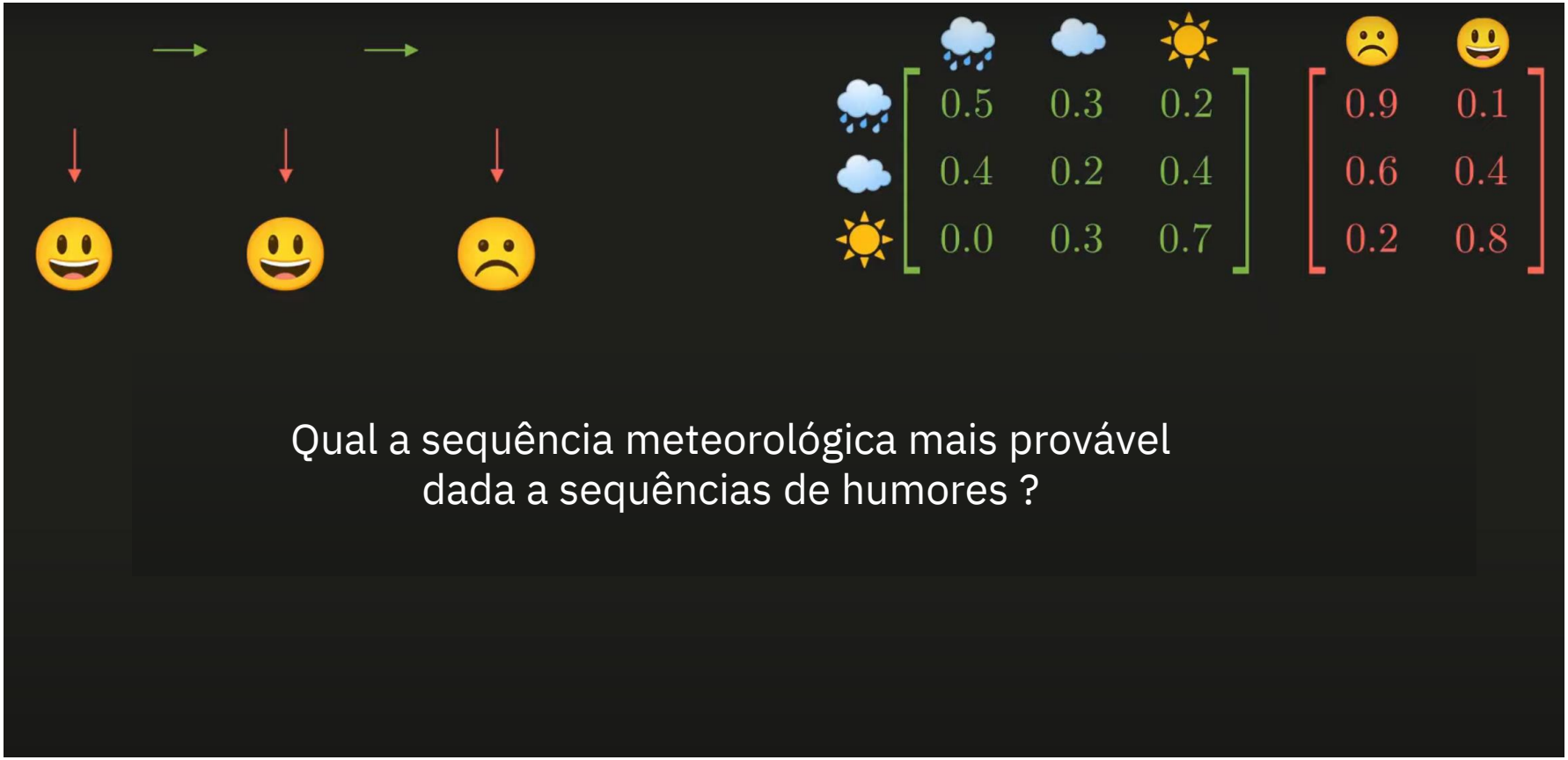
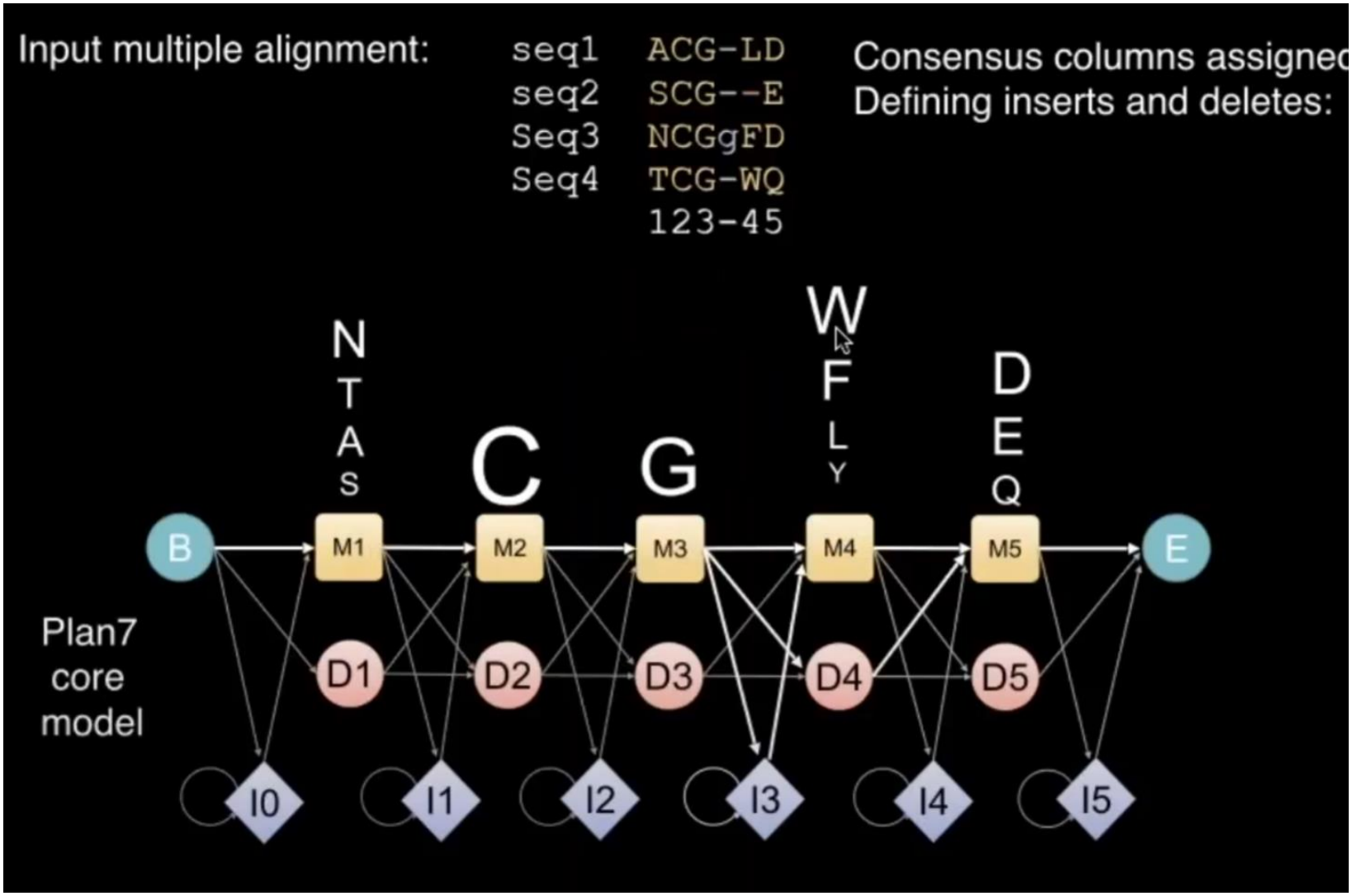


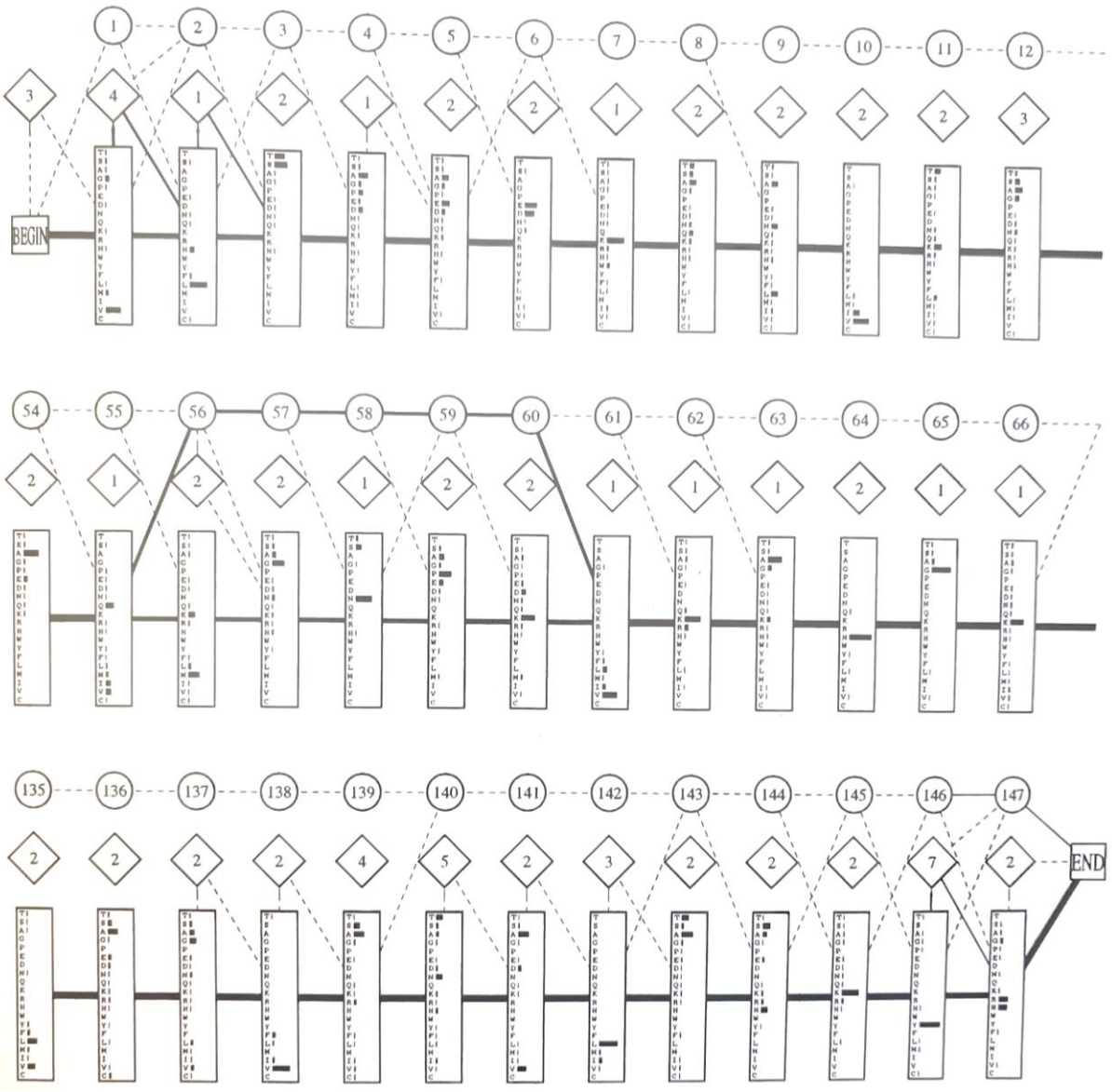
https://youtu.be/RWkHJnFj5rY

https://youtu.be/RWkHJnFj5rY

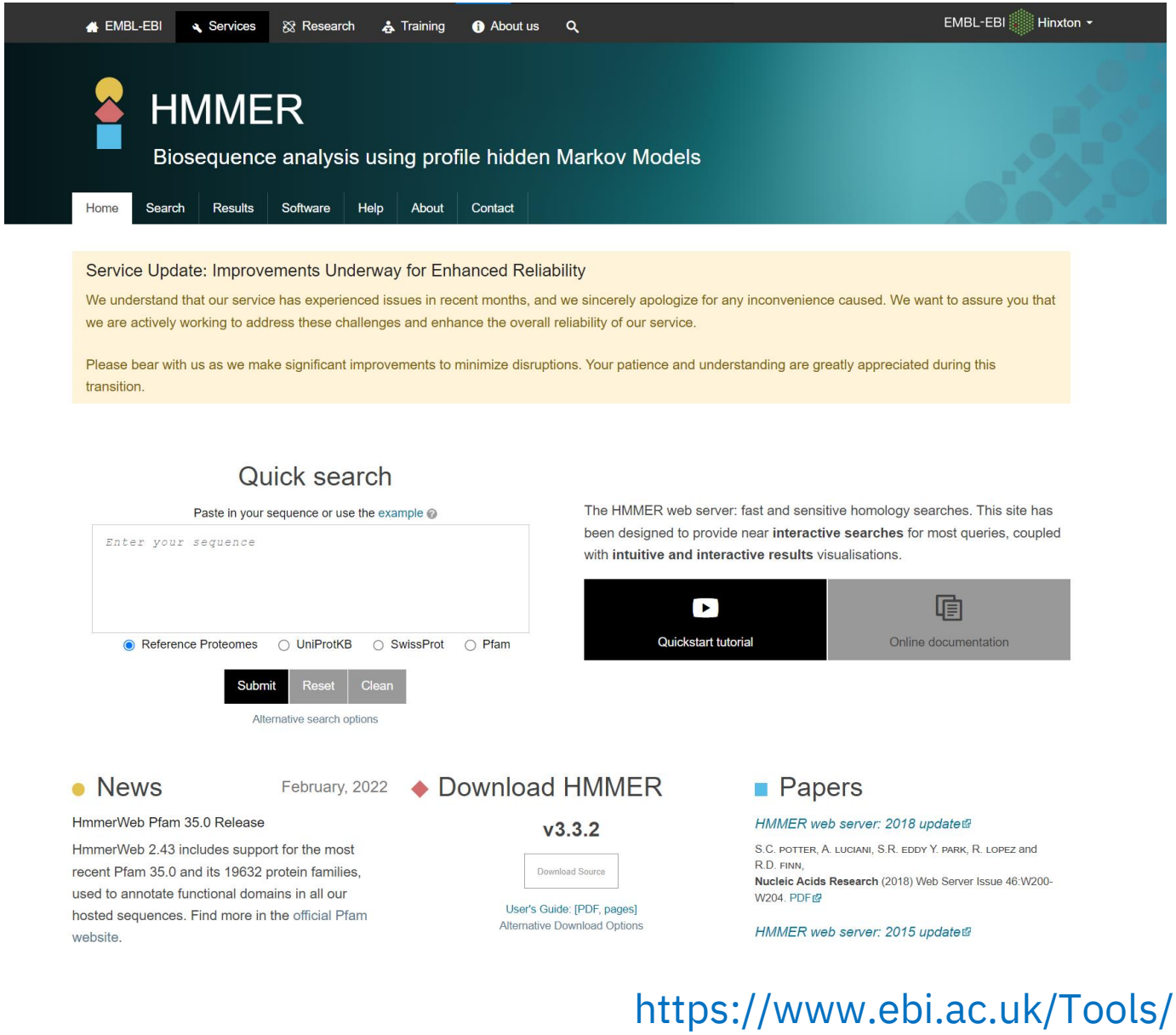
Representação HMM de um alinhamento



Perfil HMM das globlulinas



HMMER@EBI

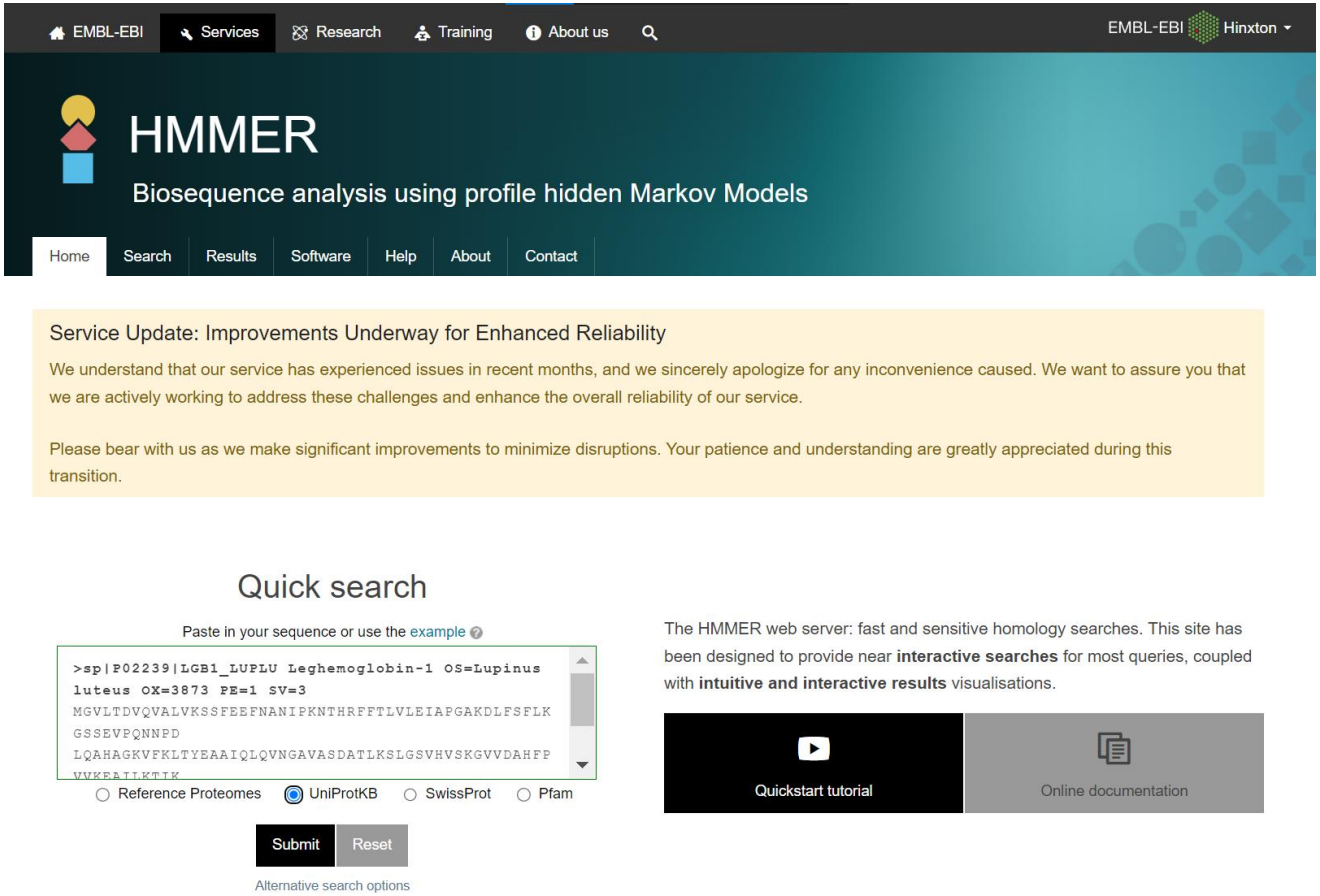


https://www.ebi.ac.uk/Tools/hmmer/

Ferramentas de HMMER

- **phmmer** – sequência de proteína contra uma base de dados de sequências de proteína (pouco mais sensível que uma pesquisa normal com BLAST)
- **hmmscan** – sequência de proteína contra uma livraria de perfis de HMM (pfam, TIGRFAM, Gene3D, Superfamily, PIRSF, TreeFam)
- **hmmsearch** – alinhamento múltiplo ou perfil HMM contra uma base de dados de sequências de proteínas
- **jackhammer** – pesquisa iterativa iniciada com uma única sequência, perfil HMM ou alinhamento múltiplo. Cada nova interação usa as sequências encontradas para refinar o perfil HMM.

HMMER@EBI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Quick search
Paste in your sequence or use the example
>sp|P02239|LGB1_LUPLU Leghemoglobin-1 OS=Lupinus luteus OX=3873 PE=1 SV=3
MGVLTDVQVALVKSSFEEFNANIPKNTHRFFTLVLEIAPGAKDLFSFLK
GSSEVPQNNPD
LQAHAGKVFKLTYEAAIQLQVNGAVASDATLKSLGSVHVSKGVVDAHFP
Reference Proteomes
UniProtKB
SwissProt
Pfam
Submit
Reset
Alternative search options
The HMMER web server: fast and sensitive homology searches. This site has been designed to provide near interactive searches for most queries, coupled with intuitive and interactive results visualisations.
Quickstart tutorial
Online documentation
News
February, 2022
HmmerWeb Pfam 35.0 Release
HmmerWeb 2.43 includes support for the most recent Pfam 35.0 and its 19632 protein families, used to annotate functional domains in all our hosted sequences. Find more in the official Pfam website.
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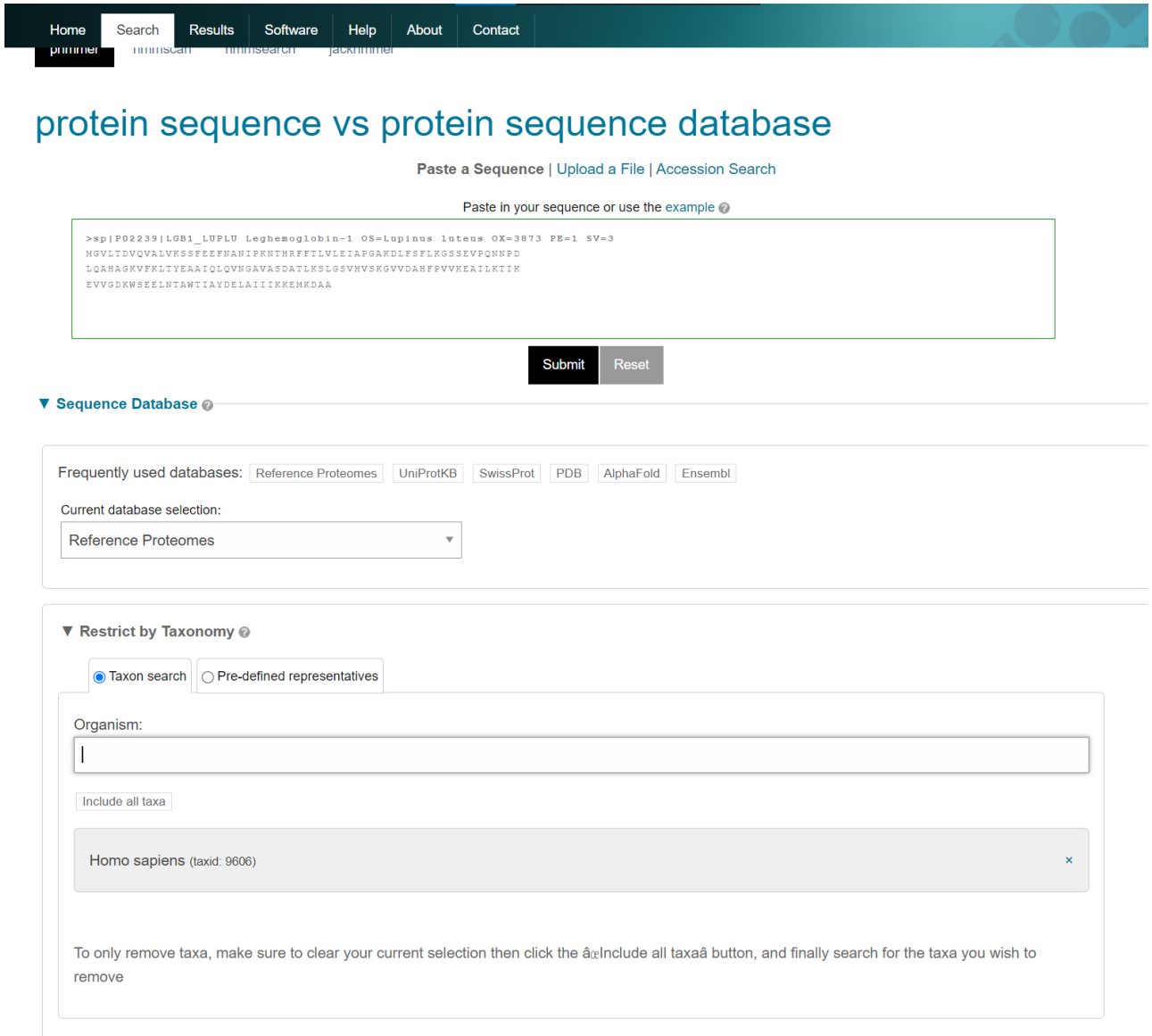
v3.3.2
Download Source
User's Guide: [PDF, pages]
Alternative Download Options
Papers
HMMER web server: 2018 update
S.C. POTTER, A. LUCIANI, S.R. EDDY Y. PARK, R. LOPEZ and R.D. FINN,
Nucleic Acids Research (2018) Web Server Issue 46:W200-W204. PDF
HMMER web server: 2015 update

phhmer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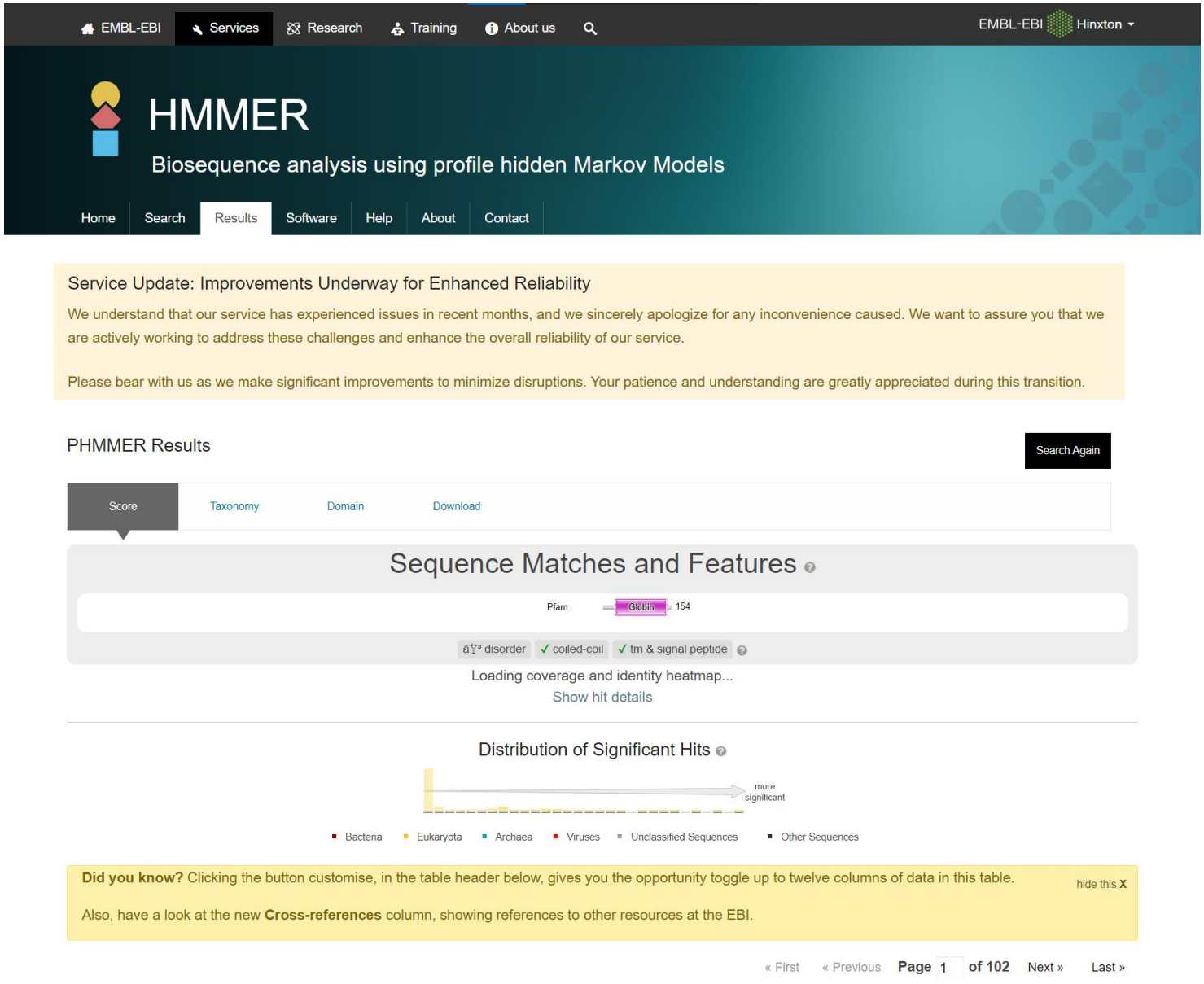
protein sequence vs protein sequence database
Paste a Sequence | Upload a File | Accession Search
Paste in your sequence or use the example
>sp|P02239|LGB1_LUPLU Leghemoglobin-1 OS=Lupinus luteus OX=3873 PE=1 SV=3
MGVLTDVQVALVKSSFEEFNANIPKNTHRFFTLVLEIAPGAKDLFSFLKGSSEVPQNNPD
LQAHAGKVFKLTYEAAIQLQVNGAVASDATLKSLGSVHVSKGVVDAHFPVVKEAILKTIK
EVVGDKWSEELNTAWTIAYDELAIIIKKEMKDAA
Submit
Reset
▼ Sequence Database
Frequently used databases: Reference Proteomes UniProtKB SwissProt PDB AlphaFold Ensembl
Current database selection:
Reference Proteomes
▼ Restrict by Taxonomy
Taxon search
Pre-defined representatives
Organism:
Include all taxa
Homo sapiens (taxid: 9606)
To only remove taxa, make sure to clear your current selection then click the âIncludeall taxaâ button, and finally search for the taxa you wish to remove

phhmer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PHMMER Results
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Taxonomy
Domain
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Sequence Matches and Features
Pfam
Globin
154
â Ÿ³ disorder
✓ coiled-coil
✓ tm & signal peptide
Loading coverage and identity heatmap...
Show hit details
Distribution of Significant Hits
more significant
Bacteria
Eukaryota
Archaea
Viruses
Unclassified Sequences
Other Sequences
Did you know? Clicking the button customise, in the table header below, gives you the opportunity toggle up to twelve columns of data in this table.
hide this X
Also, have a look at the new Cross-references column, showing references to other resources at the EBI.
« First
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Page 1 of 102
Next »
Last »

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Show hit details

Distribution of Significant Hits

Bacteria Eukaryota Archaea Viruses Unclassified Sequences Other Sequences

« First « Previous **Page** 1 **of 102** Next » Last »

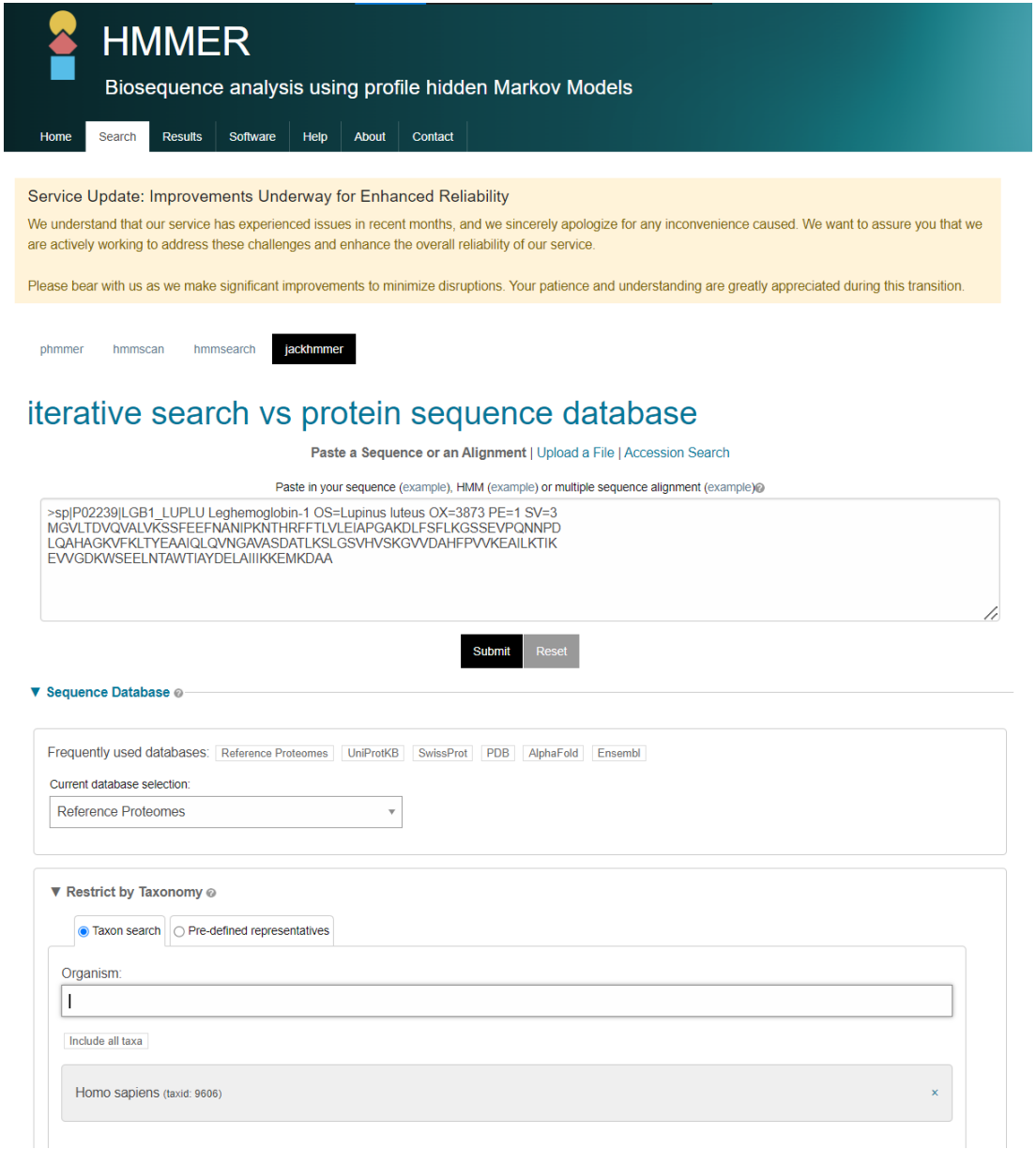
Significant Query Matches (4036) in *uniprotkb* (v.2021_04) **Customise**

	Target	Species	E-value
>	A0A833QD73_9POAL	Carex littledalei	8.3e-112
>	A0A443PME4_9MAGN	Cinnamomum micranthum f. kanehirae	6.2e-104
>	A0A443PMG7_9MAGN	Cinnamomum micranthum f. kanehirae	2.1e-103
>	A0A7M7G143_STRPU	Strongylocentrotus purpuratus	1.5e-96
>	A0A0D9Z4F0_9ORYZ	Oryza glumipatula	2.9e-95
>	LGB1_LUPLU	Lupinus luteus	2.7e-94
>	A0A7M7HNK1_STRPU	Strongylocentrotus purpuratus	2.7e-89
>	A0A7M7LT58_STRPU	Strongylocentrotus purpuratus	6.1e-89
>	A0A833RM36_9POAL	Carex littledalei	5.9e-85
>	A0A833QA41_9POAL	Carex littledalei	3.6e-84
>	A0A394DEX3_LUPAN	Lupinus angustifolius	2.1e-83
>	A0A6A4P2K0_LUPAL	Lupinus albus	1.4e-82
>	A0A0D3FFX0_9ORYZ	Oryza barthii	2.3e-82
>	A0A7M7HLE9_STRPU	Strongylocentrotus purpuratus	8.8e-82
>	A0A7M7HID4_STRPU	Strongylocentrotus purpuratus	9.6e-82
>	LGB2_LUPLU	Lupinus luteus	6.2e-81
>	Q6LBG6_LUPLU	Lupinus luteus	1.9e-79

(show all) alignments Your search took: 6.44 secs showing rows 1 - 100 of 10125

> A0A1J7GNZ5_LUPAN Lupinus angustifolius 2.2e-78

jackhmmer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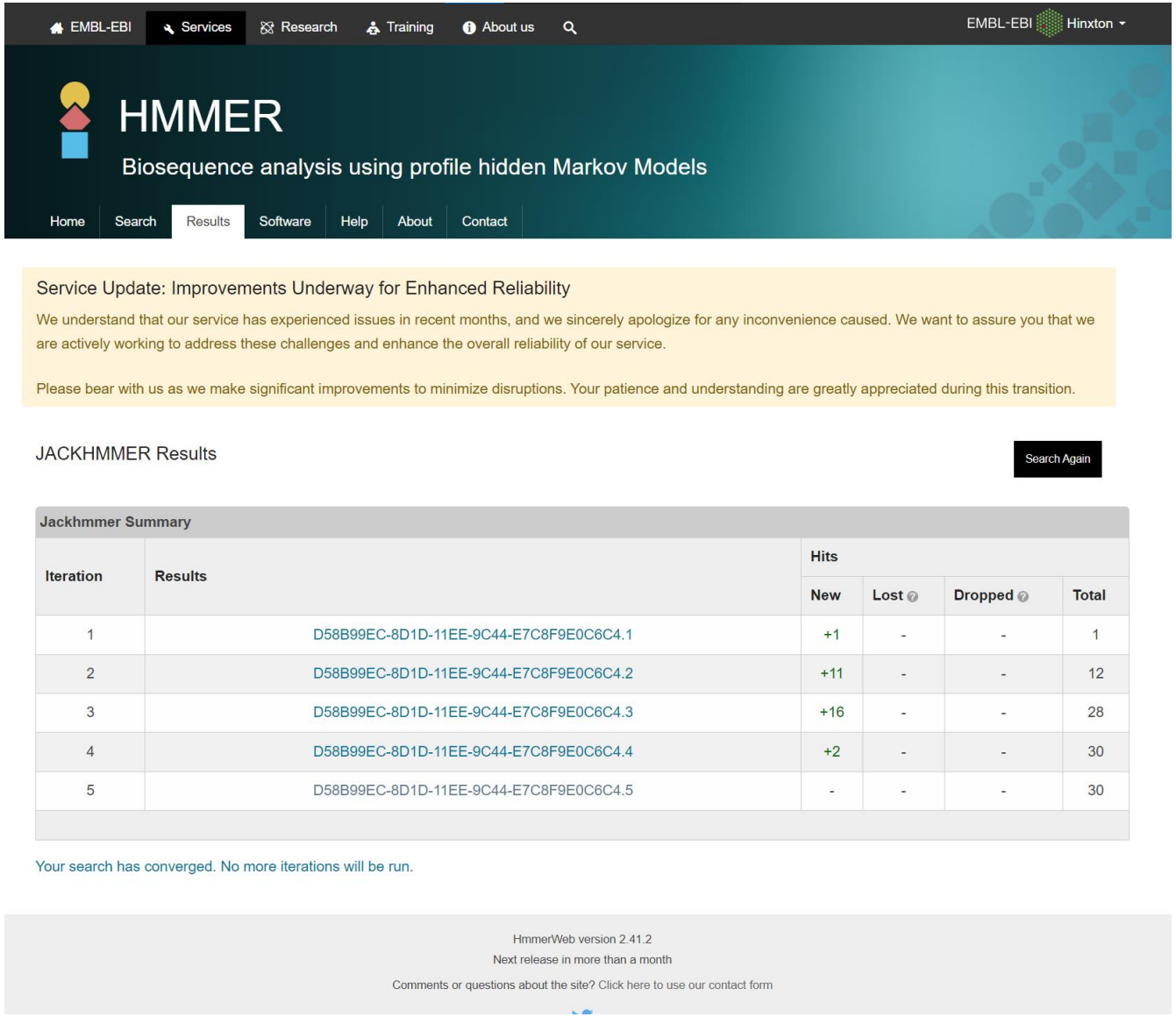
hmmscan
hmmsearch
jackhmmer
iterative search vs protein sequence database
Paste a Sequence or an Alignment | Upload a File | Accession Search
Paste in your sequence (example), HMM (example) or multiple sequence alignment (example)
>sp|P02239|LGB1_LUPLU Leghemoglobin-1 OS=Lupinus luteus OX=3873 PE=1 SV=3
MGVLTDVQVALVKSSFEEFNANIPKNTHRFFTLVLEIAPGAKDLFSFLKGSSEVPQNNPD
LQAHAGKVFKLTYEAAIQLQVNGAVASDATLKSLGSVHVSKGVVDAHFPVVKEAILKTIK
EVVGDKWSEELNTAWTIAYDELAIIIKKEMKDAA
Submit
Reset
▼ Sequence Database
Frequently used databases: Reference Proteomes UniProtKB SwissProt PDB AlphaFold Ensembl
Current database selection:
Reference Proteomes
▼ Restrict by Taxonomy
Taxon search
Pre-defined representatives
Organism:
Include all taxa
Homo sapiens (taxid: 9606)

jackhmmer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Results
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Help
About
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JACKHMMER Results
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Jackhmmer Summary
Iteration
Results
Hits
New
Lost
Dropped
Total
1 D58B99EC-8D1D-11EE-9C44-E7C8F9E0C6C4.1 +1 - - 1
2 D58B99EC-8D1D-11EE-9C44-E7C8F9E0C6C4.2 +11 - - 12
3 D58B99EC-8D1D-11EE-9C44-E7C8F9E0C6C4.3 +16 - - 28
4 D58B99EC-8D1D-11EE-9C44-E7C8F9E0C6C4.4 +2 - - 30
5 D58B99EC-8D1D-11EE-9C44-E7C8F9E0C6C4.5 - - - 30
Your search has converged. No more iterations will be run.
HmmerWeb version 2.41.2
Next release in more than a month
Comments or questions about the site? Click here to use our contact form

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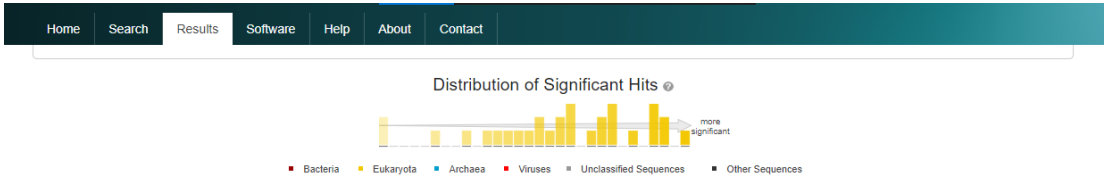

Significant Query Matches (30) in *uniprotrefprot* (v.2021_04) **Customise**

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>	A0A2R8Y7X9_HUMAN	Homo sapiens	9.0e-61	
>	HBG1_HUMAN	Homo sapiens	2.4e-56	
>	HBG2_HUMAN	Homo sapiens	3.4e-56	
>	HBD_HUMAN	Homo sapiens	1.4e-54	
>	HBE_HUMAN	Homo sapiens	3.3e-54	
>	HBB_HUMAN	Homo sapiens	5.7e-54	
>	CYGB_HUMAN	Homo sapiens	1.8e-50	
>	HBA_HUMAN	Homo sapiens	3.4e-47	
>	HBAZ_HUMAN	Homo sapiens	3.4e-47	
>	MYG_HUMAN	Homo sapiens	6.3e-46	
>	B0QYF8_HUMAN	Homo sapiens	3.2e-45	
>	HBAT_HUMAN	Homo sapiens	9.7e-44	
>	HBM_HUMAN	Homo sapiens	3.2e-42	
>	NGB_HUMAN	Homo sapiens	5.9e-39	
>	E9PFT6_HUMAN	Homo sapiens	6.5e-39	
>	A0A2R8Y7R2_HUMAN	Homo sapiens	1.2e-37	
>	E9PEW8_HUMAN	Homo sapiens	2.5e-37	
>	K7EMC7_HUMAN	Homo sapiens	1.5e-35	
>	G3V1N2_HUMAN	Homo sapiens	1.1e-33	
>	E9PBW4_HUMAN	Homo sapiens	4.5e-33	
>	F2Z2F1_HUMAN	Homo sapiens	8.3e-32	
>	K7EIM9_HUMAN	Homo sapiens	2.2e-30	
>	F8W6P5_HUMAN	Homo sapiens	6.7e-29	
>	A0A2R8Y7C0_HUMAN	Homo sapiens	1.9e-27	