Introduction to Bioinformatics

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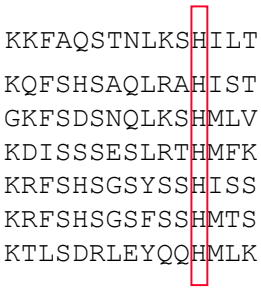
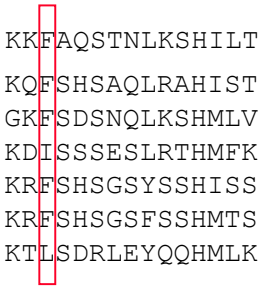
Sequence patterns

```
KKFAQSTNLKSHILT
KQFSHSAQLRAHIST
GKFSDSNQLKSHMLV
KDISSSESLRTHMFK
KRFSHSGSYSSHISS
KRFSHSGSFSSHMTS
KTLSDRLEYQQHMLK
```

Sequence patterns



Sequence patterns



Regular Expressions

Operation	Regular Expression	Example
Concatenation	DLIV	DLIV
Alternation	D[LIV]K	DLK
Replication	DL(2,5)K	DLLK

Regular Expressions

Patterns described in a standard way are known as *regular expressions*

x	ANY		
[ ]	OR	[ILV]	I or L or V
{ }	NOT	{DE}	not D or E
( )	repetitions	x(2,3)	x-x or x-x-x
-	separator		
<	N-terminal		
>	C-terminal		
.	END		

Regular Expressions

[AC]-x-V-x(4)-{ED}.

[Ala or Cys]-any-Val-any-any-any-any-{any but Glu or Asp}

```
...LKHVAYVFQALIYWIK...
...AVEMAGVKYLQVQHGS...
...LYTGAIVTNNDGPYMA...
...KEYKCKVEKELTDICN...
```

PROSITE Database

Current version contains 1079 documentation entries that describe 1459 different patterns, rules and profiles/matrices

[ST]-x(2)-[DE]
Casein kinase II phosphorylation site

[AG]-x(4)-G-K-[ST]
ATP/GTP-binding site motif A (P-loop)

Y-x-[NQH]-K-[DE]-[IVA]-F-[LM]-R-[ED]
Heat shock hsp90 proteins family signature

http://www.expasy.ch/prosite

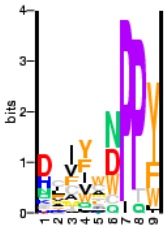
PROSITE Database

Blocks Database

Blocks are multiply aligned ungapped segments corresponding to the most highly conserved regions of proteins

N-6 Adenine-specific DNA methylases proteins
width=9 seqs=78

```
DMA_VIBCH|Q08318  (85)  SCTQWWPPF 77
HEMK_MYCLE|P45832 (181) DLFVAQPTL 100
MT57_ECOLI|P25240 (111) DGALGNPPF 13
MTC1_CHVN1|Q01511 (172) NFVFLDPPY 8
MTC1_COREQ|P42828 (71)  QLSFSCPPF 49
MTH2_HAEHA|P00473 (32)  KIAFFDPQY 52
MTH3_HAEIN|P43871 (23)  HAIISDIPY 73
MTM1_MICAM|P50190 (306) AAVLTNPPF 14
MTM2_MORBO|P23192 (25)  QLAVIDPPY 10
MTMU_MYCSP|P43641 (37)  QVIYADPPW 13
MTR1_RHOSH|P14751 (60)  QLIICDPPY 8
.....................................
```



http://www.blocks.fhcrc.org/

Pfam Database

Pfam is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains

Zinc finger, C2H2 type

```
TYY1_HUMAN/383-407   YVCPF.DGCN...KKFAQSTNLKSHILT...H
ZG52_XENLA/61-83     YTCT...QCN...KQFSHSAQLRAHIST...H
KRUP_DROME/306-328   YTCE...ICD...GKFSDSNQLKSHMLV...H
YKQ8_CAEEL/78-102    YKCT...VCR...KDISSSESLRTHMFKQ.HH
DEFI_CHICK/268-292   YECP...NCK...KRFSHSGSYSSHISSK.KC
ZFH1_DROME/389-413   FGCD...NCG...KRFSHSGSFSSHMTSK.KC
YL57_CAEEL/42-65     YLCY...YCG...KTLSDRLEYQQHMLK..VH
ZFA_MOUSE/542-564    FKCD...ICL...LTFSDTKEVQQHALV...H
BASO_HUMAN/719-742   FQCD...ICK...KTFKNACSVKIHHKN..MH
HUNB_DROME/297-319   FQCD...KCS...YTCVNKSMLNSHRKS...H
SFP1_YEAST/598-623   FKCPV.IGCE...KTYKNQNGLKYHRLH..GH
ZG29_XENLA/62-84     FVCT...VCG...KTYKYKHGLNTHLHS...H
```

http://pfam.wustl.edu/

Other Motif Databases

PRINTS : a compendium of protein fingerprints. A fingerprint is a group of conserved motifs used to characterise a protein family
http://bioinf.man.ac.uk/dbbrowser/PRINTS/

DOMO : a protein domain database
http://www.infobiogen.fr/~gracy/domo/home.htm

ProDom : a protein domain database
http://protein.toulouse.inra.fr/prodom.html

InterPro Database

InterPro : integrated resource for the commonly used signature databases - Pfam, PRINTS, PROSITE, ProDom and SWISS-PROT + TrEMBL.

Current release of InterPro (3.2) contains 3939 entries, representing 1009 domains, 2850 families, 65 repeats and 15 post-translational modification sites.

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

InterPro Database