

# Support de cours Motifs et Profils Domaines fonctionnels



# Motifs et profils

**Définition** : zone d'une séquence nucléique ou protéique présentant une conservation quand on compare plusieurs séquences.

- correspondent en général à des zones fonctionnelles
- ADN et ARN : aussi appelé **signal**, ces zones interviennent souvent dans des systèmes de régulation, ex :
  - -10 et -35 des promoteurs chez les procaryotes, jonction d'épissage,
  - boîte CRE (catabolite repression element) : après mise en évidence de certains gènes soumis à la répression catabolique chez *B. subtilis*, l'identification du signal permet de rechercher dans le génome complet les boîtes CRE et donc les gènes qui pourraient être soumis à la répression catabolique.
- différents des signaux reconnus par les enzymes de restrictions qui reconnaissent des séquences exactes, ex: GAATTC pour ECOR1.
- Les motifs et profils présentent une certaine **variabilité** (souvent impliquée dans la variabilité de la régulation par une reconnaissance plus ou moins forte des partenaires)

**Comment représenter cette variabilité ?**

- séquence consensus
- matrice de poids

# Représentation : Séquence consensus

## Exemples des boîtes CRE:

<i>acsA</i>	TGAAAGCGTTACCA
<i>acuA</i>	TGAAAACGCTTTAT
<i>amyE</i>	TGTAAGCGTTAACA
<i>gntR</i>	TGAAAGCGGTACCA
<i>hutP</i>	TGAAACCGCTTCCA
<i>licS</i>	AGAAAACGCTTTCA
<i>xylA</i>	TGGAAGCGTAAACA
<i>xylA</i>	TGAAAGCGCAAACA
<i>xylA</i>	AGTAAGCGTTTACA
<i>ackA</i>	TGTAAGCGTTATCA
consensus	<b>TGAAAGCGNTAACA</b>
	<b>T TC</b>

# Motif dans les séquences de Maltose Binding Proteins

YvfK_Bs	PT <b>P</b> NIPEMNEIW
YvfK_Bs	PT <b>P</b> NIPEMAEVW
MalX_Sp	PL <b>P</b> NISQMSAVW
MalE_Sc	PR <b>P</b> ALPEYSSLW
MalE_Tm	PM <b>P</b> NVPEMAPVW
MalE_Dr	PM <b>P</b> NIPEMGAVW
CymE_Ko	AM <b>P</b> SIPEMGYLW
MalE_Ea	IM <b>P</b> NI PQMSAFW
MalE_Sy	IM <b>P</b> NI PQMSAFW
MalE_Ec	IM <b>P</b> NI PQMSAFW

**Signature PROSITE :**

**[PAI]-[TLRM]-P-[NAS]-[ILV]-[PS]-[EQ]-[MY]-[NASG]-[EASPY]-[ILVF]-W**

# Représentation : Matrice de poids

**Exemples de 242 séquences de promoteurs (-10) chez *E. coli* :**

**Matrices du nombre d'occurrences de chaque base  $b$  à chaque position  $i$  ( $n_{b,i}$ ) du motif -10 (6 positions) :**

Pos.	1	2	3	4	5	6
A	9	214	63	142	118	8
C	22	7	26	31	52	13
G	18	2	29	38	29	5
T	193	19	124	31	43	216

# Représentation : Matrice de poids

**Exemples de 242 séquences de promoteurs (-10) chez *E. coli* :**

**Matrices des fréquences de chaque base  $b$  à chaque position  $i$  ( $f_{b,i}$ ) du motif -10 (6 positions) :**

Pos .	1	2	3	4	5	6
A	0.04	0.88	0.26	0.59	0.49	0.03
C	0.09	0.03	0.11	0.13	0.22	0.05
G	0.07	0.01	0.12	0.16	0.12	0.02
T	0.80	0.08	0.51	0.13	0.18	0.89

Avec

$$f_{b,i} = n_{b,i} / n_{tot}$$

$n_{tot}$  : nombre total de séquences analysées

# Représentation : Matrice de poids (Position Weight Matrix, PWM)

Exemples de 242 séquences de promoteurs (-10) chez *E. coli* :

Normalisation de la matrice : log matrice  $\log_2(f_{b,i}/P_b)$

$f_{b,i}$  = fréquence observée de la base  $b$  à la position  $i$  dans toutes les séquences

$P_b$  = fréquence de cette base dans l'ensemble du génome

Pos .	1	2	3	4	5	6
A	-2.76	1.88	0.06	1.23	0.96	-2.92
C	-1.46	-3.11	-1.22	-1.00	-0.22	-2.21
G	-1.76	-5.00	-1.06	-0.67	-1.06	-3.58
T	1.67	-1.66	1.04	-1.00	-0.49	1.84

Le rapport  $f_{b,i}/P_b$  est une mesure de l'écart entre fréquence observée et attendue.

## Utilisation d'une matrice de poids sur une séquence

Pos.	1	2	3	4	5	6
A	-28	18	1	12	10	-29
C	-15	-31	-12	-10	-2	-22
G	-18	-50	-11	-7	-11	-36
T	17	-17	10	-10	-5	18

**A** CTATAATCG

$$\text{Score1} = -15 - 17 + 1 - 10 + 10 - 29 = -60$$

**AC** TATAATCG

$$\text{Score2} = 17 + 18 + 10 + 12 + 10 + 18 = 85$$

**ACT** ATAATCG

$$\text{Score3} = -28 - 17 + 1 + 12 - 5 - 22 = -59$$



## Exemples de fonction pour le calcul du score

Soit  $l$  le nombre de positions dans le motif,  $f_{b,i}$  la fréquence de la base  $b$  observée à la position  $i$  dans la séquence analysée et  $f_{max,i}$  la fréquence de la base la plus fréquente à la position  $i$  dans la matrice de poids :

$$S = \frac{\sum_{i=1}^l f_{b,i}}{\sum_{i=1}^l f_{max,i}}$$

La valeur du score  $S$  va varier entre 0 et 1, quelque soit la longueur du motif étudié et la matrice de poids établie.  
On retient la séquence comme motif putatif si  $S \geq$  seuil.

$$D = \sum_{i=1}^l \ln\left(\frac{f_{max,i} + 0.5}{f_{b,i} + 0.5}\right)$$

$D$  est un indice de disimilarité établi par Berg and Von Hippel. Plus la valeur de  $D$  sera élevée, plus la séquence analysée est éloignée de la séquence consensus. On ajoute 0.5 pour éviter la division par 0 quand  $f_{b,i}$  est nulle.

On retient la séquence comme motif putatif si  $D \leq$  seuil.

# Théorie de l'information

Shannon et Weaver (1949).

La valeur de l'information  $I$  à la position  $j$  d'un signal est donnée par :

$$I(j) = \sum_i f_{ij} \log_2 f_{ij} - \sum_i P_i \log_2 P_i$$

où :

$P_i$  ( $i = 1$  à  $4$ ) est la fréquence de la base  $i$  dans l'ensemble du génome (probabilité théorique)

$f_{ij}$  est la fréquence observée de la base  $i$  à la position  $j$  d'un signal sur un ensemble d'exemples.

Les  $P_i$  étant estimées à 0.25 pour chacune des 4 bases on a :

$$\sum_i P_i \log_2 P_i = -2$$

donc

$$I(j) = \sum_i f_{ij} \log_2 f_{ij} + 2$$

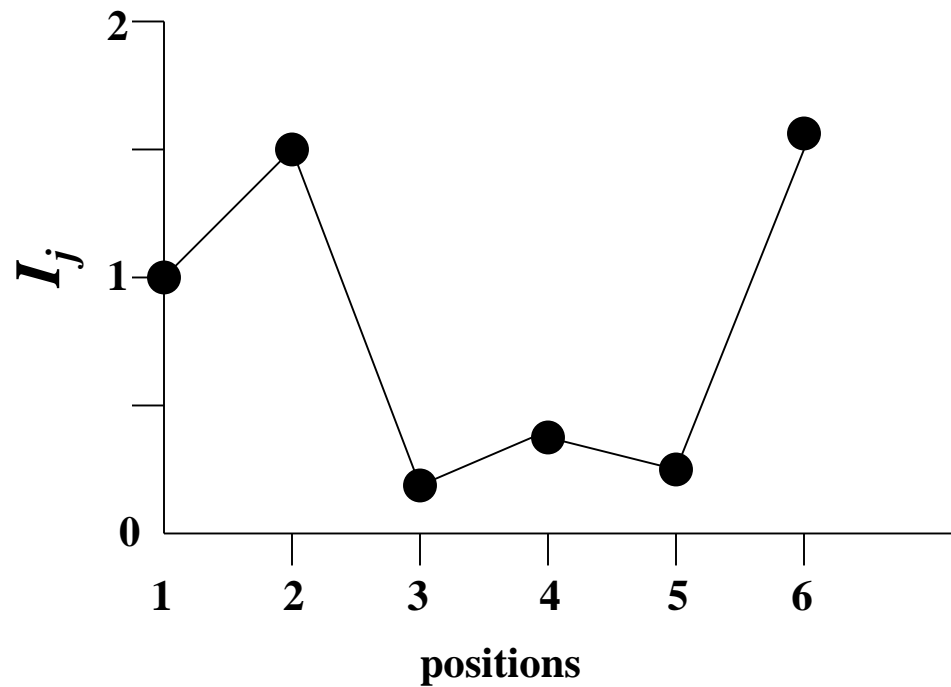
Les positions du signal qui contiendront de l'information seront celles qui auront une composition très biaisées par rapport à ce qui est attendu.

Si à une position  $j$  du signal, présence d'une seule base invariante  $i$  alors  $f_{ij} = 1$  et  $\log_2 f_{ij} = 0$   
donc

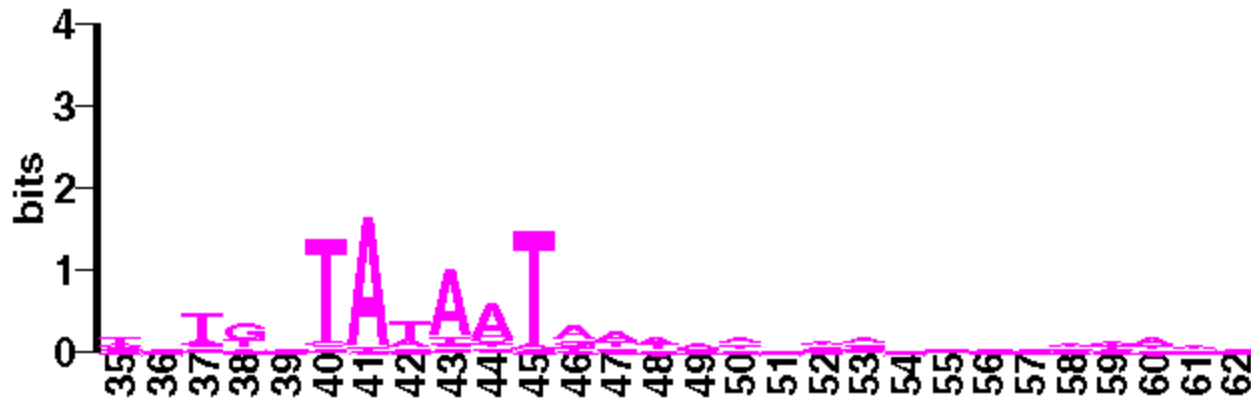
$f_{ij} \log_2 f_{ij} = 0$  et les fréquences observées des autres bases sont nulles. On aura

$$I(j) = 2 \text{ information maximale}$$

# Valeurs de l'information $I_j$ à chaque position $j$ du motif -10 des promoteurs d'*E. coli*.



### Compilation of *Bacillus subtilis* sigma A-dependent promoter elements



# Domaines fonctionnels

Deux définitions des domaines : domaines structuraux et domaines fonctionnels. Ils constituent des parties de la protéines. Un domaine structural est une partie de la chaîne polypeptidique qui se replie indépendamment. Un domaine fonctionnel est une région de la protéine qui présente une conservation de séquence mise en évidence par alignement multiple auquel on peut associer une fonction. Il forme une « brique » qui a pu être recombinaison dans différents arrangements pour moduler l'expression des protéines au cours de l'évolution.

Les deux classifications des domaines fonctionnels et structuraux coïncident assez souvent.

Les domaines fonctionnels peuvent contenir des motifs (ou pattern) fonctionnels. La différence est souvent liée à leur taille, plus petite pour les motifs.

# Exemple de coïncidence entre domaines fonctionnels et structuraux

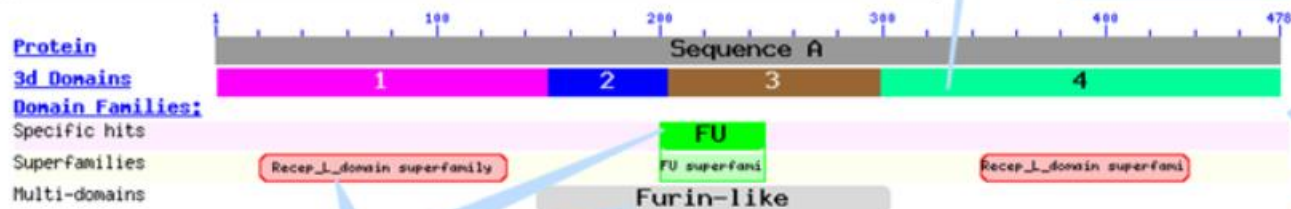
Type 1 Insulin-like Growth Factor Receptor (1IGR),  
colored by domain



**3D domains** are compact structural units identified by purely geometric criteria. Each 3D domain is shown in the same color in both the structure view window and the 3D domains bar graph that shows the span of each domain on the protein chain.

**Conserved domains** shown here as **Domain Families**, are recurring units in molecular evolution and appear in protein sequences as conserved blocks of amino acid residues that have distinct functions. Conserved domains serve as building blocks and can be recombined in different arrangements to make proteins with different functions, and often correspond to the 3D domains of a protein structure.

Follow the links in the text below this graphic for additional details and interactive views of the protein structure, conserved domains, and small molecules.



In the live view of the structure record (1IGR, accessible from the text beneath this graphic), click on a conserved domain to view information about its function and the multiple sequence alignment from which the domain model was developed, and to link to other protein sequences that contain the domain.

ProSite consiste en un ensemble d'entrées décrivant les domaines protéiques et les motifs caractéristiques de fonctions ou de familles protéiques.

Une entrée Prosite est constituée de deux parties :

- une fiche qui fournit une description des domaines et des motifs fonctionnels et renseigne sur la fonction associée au domaine ou motif. Cette fiche a un préfixe PDOC (exemple : PDOC00185)
- Une fiche décrivant le motif ou le domaine qui a un préfixe PS (exemple PS50893)

This form allows you to scan proteins for matches against the PROSITE collection of motifs as well as against your own patterns.

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

- Option 1 - Submit PROTEIN sequences to scan them against the PROSITE collection of motifs.
- Option 2 - Submit MOTIFS to scan them against a PROTEIN sequence database.
- Option 3 - Submit PROTEIN sequences and MOTIFS to scan them against each other.

Reset

STEP 1 - Submit PROTEIN sequences [help]

Submit PROTEIN sequences (max. 10) [Examples](#)

Submit a PROTEIN database (max. 16MB) for repeated scans (The data will be stored on our server for 1 month).

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

Supported input:

- UniProtKB accessions e.g. P98073 or Identifiers e.g. ENTK\_HUMAN
- PDB Identifiers e.g. 4DGJ
- Sequences in FASTA format

Séquence(s) à analyser (max 10)

STEP 2 - Select options [help]

Exclude motifs with a high probability of occurrence from the scan

Exclude profiles from the scan

Run the scan at high sensitivity (show weak matches for profiles)

Exclure de l'analyse les motifs avec une forte probabilité d'occurence

STEP 3 - Select output options and submit your job

Output format: Graphical view

Retrieve complete sequences:  if you choose this option, not all output formats are available.

Receive your results by email

**START THE SCAN** Reset

```
ID ASN_GLYCOSYLATION; PATTERN.  
AC PS00001;  
DE N-glycosylation site.  
PA N-{P}-[ST]-{P}
```



This form allows you to scan proteins for matches against the PROSITE collection of motifs as well as against your own patterns.

- Option 1 - Submit PROTEIN sequences to scan them against the PROSITE collection of motifs.
- Option 2 - Submit MOTIFS to scan them against a PROTEIN sequence database.
- Option 3 - Submit PROTEIN sequences and MOTIFS to scan them against each other.

Reset

STEP 1 - Enter a MOTIF or a combination of MOTIFS [Examples](#) [\[help\]](#)

Enter a PROSITE accession or identifier or your own pattern or a combination

Supported input:

- A PROSITE accession e.g. PSS0240 or Identifier e.g. TRYPSIN\_DOM
- Your own pattern e.g. P-x(2)-G-E-S-G(2)-[AS]

» More

Options « [\[help\]](#)

- Minimal number of hits per matched sequences:
- Profile option
  - Run the scan at a high sensitivity (show weak matches for profiles)
- Pattern options
  - Number of X characters in a scanned sequence that can be matched by a conserved position in a pattern:
  - Match mode:

Motif ou combinaison de motifs à rechercher. Soit un numéro d'accèsion dans ProSite, soit votre propre motif (format ProSite)

STEP2 - Select a PROTEIN sequence database [\[help\]](#)

- UniProtKB
  - Swiss-Prot  Include splice variants
  - TrEMBL
- PDB
- Your protein database
- Randomized UniProtKB/Swiss-Prot

Exclude fragments (concerns UniProtKB only)

» Filters [\[help\]](#)

Choix de la banque de séquences protéiques à analyser

STEP 3 - Select output options and submit your job

Output format:

Maximum number of displayed matches:  If you select 100'000, results are returned by email and not all output formats are available.

Retrieve complete sequences:  if you choose this option, a maximum of 1'000 matched sequences can be displayed and not all output formats are available.

Receive your results by email

**START THE SCAN**

# Domaines et motifs fonctionnels par l'exemple



ScanProsite tool

Analyse de la séquence protéique ComA de *Streptococcus pneumoniae* souche R6

This form allows you to scan proteins for matches against the PROSITE collection of motifs as well as against your own patterns.

- Option 1 - Submit PROTEIN sequences to scan them against the PROSITE collection of motifs.
- Option 2 - Submit MOTIFS to scan them against a PROTEIN sequence database.
- Option 3 - Submit PROTEIN sequences and MOTIFS to scan them against each other.

Reset

## STEP 1 - Submit PROTEIN sequences [help]

- Submit PROTEIN sequences (max. 10) [Examples](#)
- Submit a PROTEIN database (max. 16MB) for repeated scans (The data will be stored on our server for 1 month).

```
>SpneA01.COMA|
MKFGKRHYRPOVDQMDCGVASLAMVFGYYGSYYFLAHLRELAKTMDGTTALGLVKVAEE
IGFETRAIKADMILFDLPDLTFPFVAHVLEKQKLLHYVVTGQDKDSIHIADFPDGVKLI
KLPRERFEEEWIGVTLFMAPSPDYKPKHEQRNGLLSFIPILVKQRGLIANIVLATLLVTV
INIVGSSVYLOSIIDTYVDPQMRSTLGIISIGLVIVVYLQOILSYAQEYLLLVLGQRLSID
VILSYIKHVFHLMSEFFATRRTGEIVSRETDANSIIDALASTILSIFLDVSTVVIISIVL
FSQNTNLFMTLLALFYTYVIFAFMKPFERKQNRDTMEANAVLSSSIIEDINGIETIKSL
TSESQRVQKIDKEFVDYLKKSFTYSRAESQQKALKKVAHLLLNVCILWMCVAVLMDGKMS
LQQLITVNTLLVYFNPLENIINLQTKLQTAQVANNRLNEVYLVASEFEEKKTVEDLSIM
KGDMTFKQVHYKYGYGRDVLSDINLIVPQGSKVAEFGISGSGKITLAKMMVNEYDPSQGE
ISLGGVNLNQIDKKALRQYINVLPOQPVVFNQTLLENLLGAKEGTQRDILRAVELASL
RSDTFRMIMYQYETFRNCACTSCCGQRIARATLFRAPITFRDPTSETDITTEPRT
```

Supported input:

- UniProtKB accessions e.g. P98073 or identifiers e.g. ENTK\_HUMAN
- PDB identifiers e.g. 4DGJ
- Sequences in FASTA format

## STEP 2 - Select options [help]

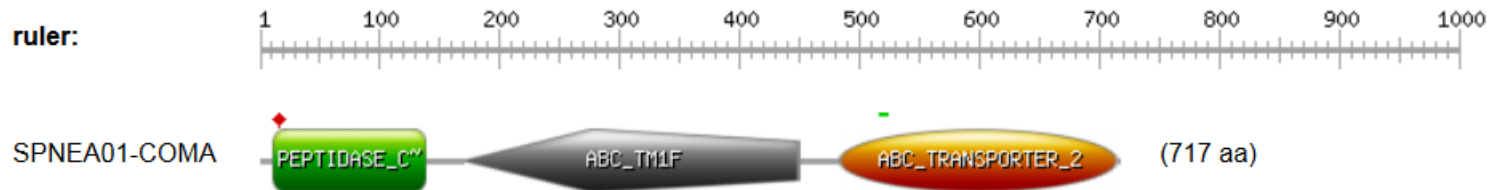
- Exclude motifs with a high probability of occurrence from the scan
- Exclude profiles from the scan
- Run the scan at high sensitivity (show weak matches for profiles)

# Domaines et motifs fonctionnels par l'exemple

## Domaines fonctionnels identifiés dans la séquence ComA de *S. pneumoniae*

hits by profiles: [3 hits (by 3 distinct profiles) on 1 sequence]

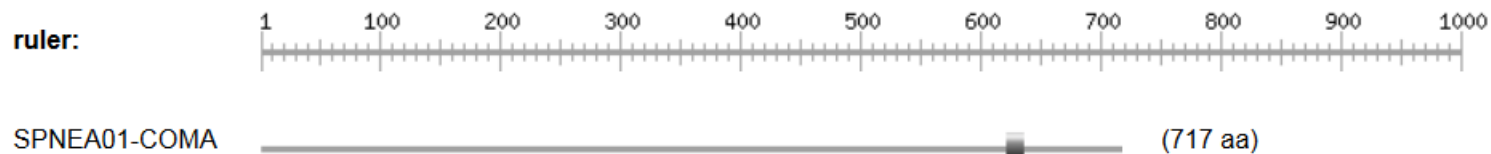
Upper case represents match positions, lower case insert positions, and the '-' symbol represents deletions relative to the matching profile.



## Motif fonctionnel identifié dans la séquence ComA de *S. pneumoniae*

hits by patterns: [1 hit (by 1 pattern) on 1 sequence]

Hits by [PS00211](#) ABC\_TRANSPORTER\_1 ABC transporters family signature :



622 - 636: [confidence level: (0)] ISGGQRQRIALARAL

# Mesure du pouvoir prédictif d'une méthode

4 paramètres importants :

- pourcentage de vrais positifs (VP, True positive)
- pourcentage de faux positifs (FP, False positive)
- pourcentage de vrais négatifs (VN, True negative)
- pourcentage de faux négatifs (FN, False negative)

		Réalité	
		Groupe 1	Groupe 2
prédiction	Groupe 1	% vrais positifs	% faux positifs
	Groupe 2	% faux négatifs	% vrais négatifs

Groupe 1 : exemples

Groupe 2 : contre-exemples

# Entrée ProSite associées au domaine fonctionnel ABC\_TRANSPORTER\_2

ABC\_TRANSPORTER\_2, [PS50893](#); ATP-binding cassette, ABC transporter-type domain profile (MATRIX)

- Sequences in UniProtKB/Swiss-Prot known to belong to this class: 3998
  - detected by PS50893: 3983 (true positives)
  - undetected by PS50893: 15 (5 false negatives and 10 'partials')
- Other sequence(s) in UniProtKB/Swiss-Prot detected by PS50893:  
NONE.
- [Domain architecture view of Swiss-Prot proteins matching PS50893](#)



- 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 PS50893](#)
- [Retrieve a list of all UniProtKB \(Swiss-Prot + TrEMBL\) entries matching PS50893](#)
- [Scan UniProtKB \(Swiss-Prot and/or TrEMBL\) entries against PS50893](#)
- [View ligand binding statistics of PS50893](#)
- [Matching PDB structures: 1B0U 1F3O 1G29 1G6H ... \[ALL\]](#)

# Extrait de la matrice (profil) ProSite associées au domaine fonctionnel ABC\_TRANSPORTER\_2

Matrix / Profile  
[info]

```
/GENERAL_SPEC: ALPHABET='ABCDEFGHIJKLMNPQRSTVWYZ'; LENGTH=240;
/DISJOINT: DEFINITION=PROTECT; N1=6; N2=235;
/NORMALIZATION: MODE=1; FUNCTION=LINEAR; R1=5.7291522; R2=0.0066693; TEXT='NScore';
/NORMALIZATION: MODE=-1; FUNCTION=LINEAR; R1=27511.1894531; R2=19.6396694; TEXT='Heuristic 5.0%';
/CUT_OFF: LEVEL=0; SCORE=431; H_SCORE=35976; N_SCORE=8.6; MODE=1; TEXT='!';
/CUT_OFF: LEVEL=-1; SCORE=116; H_SCORE=29789; N_SCORE=6.5; MODE=1; TEXT='?';
/DEFAULT: M0=-8; D=-20; I=-20; B0=*; B1=*; E0=*; E1=*; MI=-105; MD=-105; IM=-105; DM=-105;

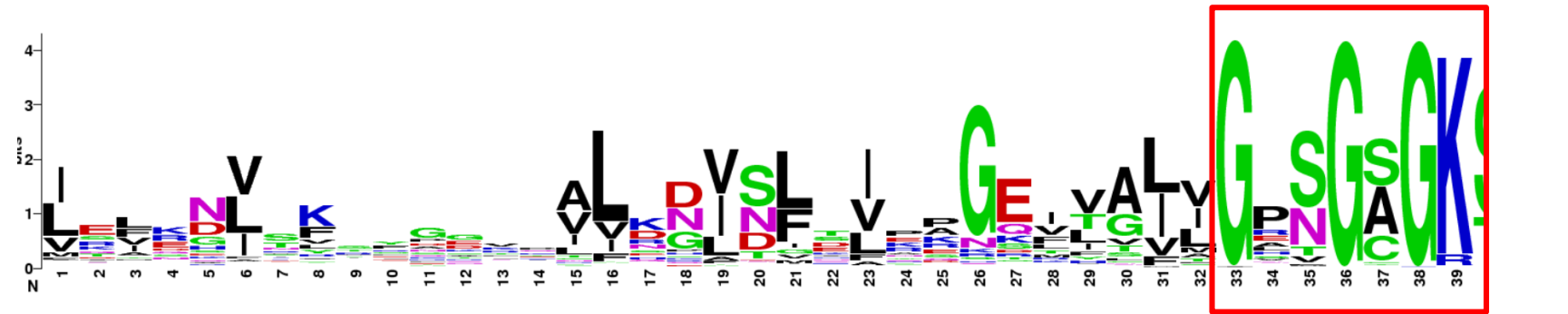
      A  B  C  D  E  F  G  H  I  K  L  M  N  P  Q  R  S  T  V  W  Y  Z
/I:      B0=0; B1=0; BI=-105; BD=-105;
/M: SY='I'; M= -6,-30,-18,-32,-26, 4,-32,-26, 29,-26, 29, 16,-28,-28,-24,-22,-20, -6, 29,-24, -4,-26;
/M: SY='R'; M=-16, -4,-30, -4, 6,-26,-20, 19,-28, 22,-22, -6, 2,-16, 21, 38, -8,-12,-24,-22, -5, 10;
/M: SY='L'; M=-10,-10,-18,-11,-14, 8,-25,-18, 2,-19, 11, 0,-13,-22,-20,-16, -9, 4, 5,-22, -2,-16;
/M: SY='E'; M=-10, 1,-27, 5, 12,-24,-23, -9, -8, 3,-12, -6, -4,-12, 9, -3, -6, -8, -7,-27,-12, 10;
/M: SY='D'; M=-12, 38,-23, 41, 10,-30, -5, 2,-30, -2,-30,-25, 32,-13, 0, -7, 10, -2,-27,-40,-20, 5;
/M: SY='V'; M= -5,-30,-17,-32,-27, 3,-32,-27, 31,-25, 25, 15,-28,-28,-25,-22,-19, -5, 33,-25, -5,-27;
/M: SY='F'; M= -8,-18,-21,-21,-17, 7,-20, -4, -6,-17, -9, -6,-13,-22,-16,-14, -3, 1, 0, 3, 6,-16;
/M: SY='K'; M=-13,-10,-27,-14, -4, 8,-23,-13,-20, 22,-16, -7, -7,-17, -7, 13,-13,-10,-13,-10, 4, -4;
/M: SY='T'; M= 3,-12,-17,-15,-12, -5,-17, -8, -6, -5,-10, -6, -9,-19, -8, -1, 4, 6, 1,-15, 6,-12;
/I:      I=-5; MI=0; MD=-27; IM=0; DM=-27;
/M: SY='F'; M=-17,-20,-25,-22, -9, 28,-27, -8, -6,-11, 6, -1,-15,-24,-15, 0,-17,-10, -7, -3, 19,-12;
/M: SY='G'; M= -5,-12,-30, -9, -6,-23, 25,-17,-25,-16,-15,-13, -9, 1,-13,-17, -7,-15,-23,-23,-24,-10;
/M: SY='E'; M= -9, 5,-30, 11, 15,-28, 8,-10,-24, -7,-20,-16, 1,-11, -2,-12, -3,-13,-22,-27,-20, 6;
/M: SY='V'; M= -9,-20,-18,-26,-22, 12,-28, -6, 10,-20, 3, 4,-15,-24,-21,-17, -8, 2, 16,-20, 4,-22;
/M: SY='E'; M=-10,-10,-27, -8, 3,-12,-23, -9,-12, 2, -7, -6,-11, 2, -3, -3, -9, -1,-13,-18, -1, -1;
/M: SY='A'; M= 25,-20,-10,-25,-20,-10,-15,-25, 10,-15, 0, 0,-20,-20,-20,-20, 0, 0, 25,-25,-15,-20;
/M: SY='L'; M= -8,-30,-18,-30,-22, 8,-30,-22, 22,-28, 44, 18,-30,-30,-22,-20,-27, -8, 16,-22, -2,-22;
/M: SY='K'; M=-14, 9,-30, 13, 12,-32,-18, -3,-30, 29,-27,-13, 4,-12, 17, 24, -6,-10,-24,-24,-12, 14;
/M: SY='G'; M= -6, 10,-29, 12, 2,-30, 33,-10,-36, -9,-28,-22, 11,-15, -8,-13, 1,-14,-30,-28,-25, -3;
/M: SY='V'; M= -5,-28,-17,-32,-27, 2,-30,-24, 30,-22, 20, 21,-27,-27,-22,-20,-17, -5, 33,-25, -5,-25;
/M: SY='S'; M= 2, 12,-13, 4, -2,-18, -4, -6,-18, -7,-26,-18, 23,-13, -2, -7, 27, 19,-14,-38,-18, -2;
/M: SY='F'; M=-13,-30,-22,-36,-26, 32,-32,-22, 20,-30, 30, 13,-24,-28,-27,-22,-24,-10, 11,-10, 10,-26;
/M: SY='E'; M= -4, 7,-21, 4, 12,-24,-13, -5,-21, 7,-23,-14, 10,-10, 12, 3, 12, 9,-19,-30,-15, 12;
/M: SY='V'; M= 3,-27,-18,-31,-25, -1,-28,-27, 28,-23, 17, 12,-24,-24,-22,-23,-14, -5, 29,-24, -7,-25;
/M: SY='T'; M=-13, 7,-28, 4, 13,-25,-16, -1,-28, 26,-25,-14, 13,-14, 10, 32, -4, -8,-24,-26,-14, 10;
/M: SY='K'; M= -4, 2,-29, 7, 12,-28,-15, -9,-27, 14,-24,-16, -2, 8, 3, 10, -4, -8,-22,-26,-18, 6;
/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=-14, 23,-30, 35, 39,-35,-16, 2,-32, 6,-24,-20, 7, -5, 19, -2, 0,-10,-30,-32,-18, 29;
/M: SY='V'; M= -7,-30,-15,-33,-28, 25,-30,-25, 20,-25, 17, 9,-27,-30,-31,-20,-16, -5, 29,-17, 3,-28;
/M: SY='T'; M= -5,-17,-16,-24,-19, -2,-26,-20, 14,-18, 12, 13,-15,-19,-14,-16, -5, 15, 14,-25, -5,-17;
/M: SY='A'; M= 16,-15,-15,-20,-12,-10,-13,-19, 3,-17, 2, -2,-10,-16,-11,-19, 5, 2, 4,-26,-13,-12;
/M: SY='I'; M= -8,-30,-23,-35,-27, 3,-35,-27, 37,-28, 28, 18,-25,-25,-22,-25,-22, -8, 27,-22, -2,-27;
/I:      I=-6; MD=-32;
```

# Entrée ProSite associées au motif fonctionnel ABC\_TRANSPORTER\_1

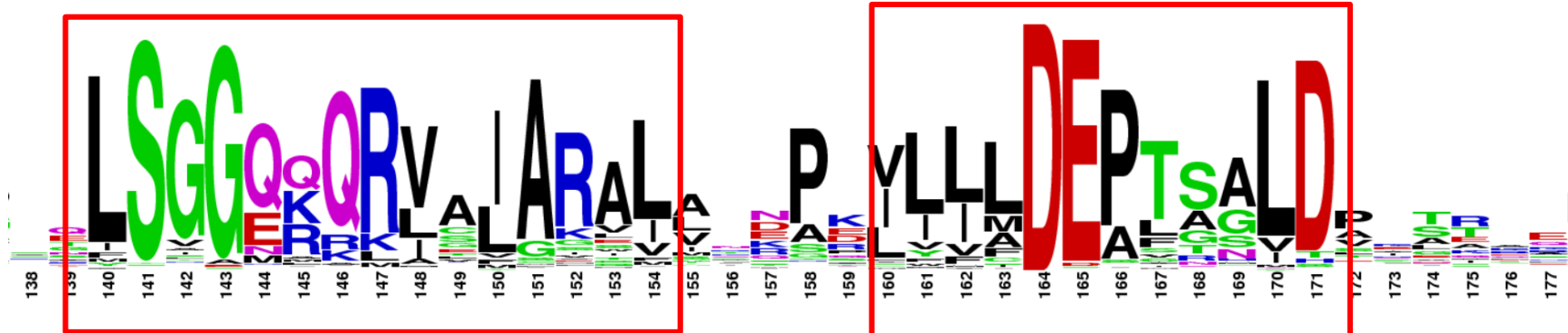
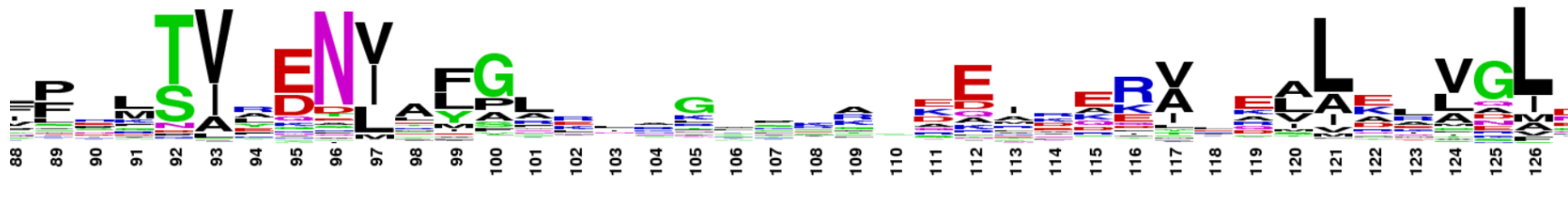
ABC\_TRANSPORTER\_1, [PS00211](#); ABC transporters family signature (PATTERN)

- Consensus pattern:  
[LIVMFYC]-[SA]-[SAPGLVFKQH]-G-[DENQMW]-[KRQASPCLIMFW]-[KRNQSTAVM]-[KRACLVM]-[LIVMFYPAN]-{PHY}-  
[LIVMFW]-[SAGCLIVP]-{FYWHP}-{KRHP}-[LIVMFYWSTA]
- Sequences in UniProtKB/Swiss-Prot known to belong to this class: 4003
  - detected by PS00211: [3668](#) (true positives)
  - undetected by PS00211: 335 ([327](#) false negatives and 8 'partials')
- Other sequence(s) in UniProtKB/Swiss-Prot detected by PS00211:  
[201](#) 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 PS00211](#)
- [Retrieve a list of all UniProtKB \(Swiss-Prot + TrEMBL\) entries matching PS00211](#)
- [Scan UniProtKB \(Swiss-Prot and/or TrEMBL\) entries against PS00211](#)
- [View ligand binding statistics of PS00211](#)
- [Matching PDB structures: 1B0U 1F3O 1G29 1G6H ... \[ALL\]](#)

# Extrait du logo du domaine fonctionnel ABC\_TRANSPORTER\_2 de ProSite



Motif Walker A



Motif ABC transporters  
family signature

Motif Walker B



# Banque de données Pfam : banque de domaines fonctionnels

La banque de données Pfam est une large collection de familles de protéines représentées par des alignements multiples et des modèles de Markov cachés.

Les protéines sont généralement composée d'une ou plusieurs régions fonctionnelles, appelées domaines. Différentes combinaisons de domaines donnent naissance aux différentes protéines trouvées dans la nature. L'identification des domaines présents dans une protéine permet donc d'avoir des idées sur sa fonction.

2 sections dans Pfam:

Pfam-A : entrées de très grande qualité produite par des experts

Pfam-B : entrées produites par une procédure automatisée.

# Page d'entrée de Pfam

<http://pfam.xfam.org/>



[HOME](#) | [SEARCH](#) | [BROWSE](#) | [FTP](#) | [HELP](#) | [ABOUT](#)



## Pfam 30.0 (June 2016, 16306 entries)

The Pfam database is a large collection of protein families, each represented by **multiple sequence alignments** and **hidden Markov models (HMMs)**. [More...](#)

### QUICK LINKS

[SEQUENCE SEARCH](#)

[VIEW A PFAM ENTRY](#)

[VIEW A CLAN](#)

[VIEW A SEQUENCE](#)

[VIEW A STRUCTURE](#)

[KEYWORD SEARCH](#)

[JUMP TO](#)

### YOU CAN FIND DATA IN PFAM IN VARIOUS WAYS...

Analyze your protein sequence for Pfam matches

View Pfam annotation and alignments

See groups of related entries

Look at the domain organisation of a protein sequence

Find the domains on a PDB structure

Query Pfam by keywords

Enter any type of accession or ID to jump to the page for a Pfam entry or clan, UniProt sequence, PDB structure, etc.

Or view the [help](#) pages for more information

Analyser le contenu en domaines d'une séquence protéique

# Analyse de la séquence protéique ComA de *Streptococcus pneumoniae* souche R6



## Sequence search results

[Show](#) the detailed description of this results page.

We found 3 Pfam-A matches to your search sequence (**all** significant)



[Show](#) the search options and sequence that you submitted.

[Return](#) to the search form to look for Pfam domains on a new sequence.

## Significant Pfam-A Matches


[Show](#) or [hide](#) all alignments.

Family	Description	Entry type	Clan	Envelope		Alignment		HMM		HMM length	Bit score	E-value	Predicted active sites	Show/hide alignment
				Start	End	Start	End	From	To					
<a href="#">Peptidase_C39</a>	Peptidase C39 family	Family	<a href="#">CL0125</a>	5	143	7	142	3	132	133	140.0	3.4e-41	n/a	<a href="#">Show</a>
<a href="#">ABC_membrane</a>	ABC transporter transmembrane region	Family	<a href="#">CL0241</a>	168	438	170	438	3	274	274	212.1	1.1e-62	n/a	<a href="#">Show</a>
<a href="#">ABC_tran</a>	ABC transporter	Domain	<a href="#">CL0023</a>	500	650	500	650	1	137	137	110.3	9.3e-32	n/a	<a href="#">Show</a>


Comments or questions on the site? Send a mail to [pfam-help@ebi.ac.uk](mailto:pfam-help@ebi.ac.uk).  
European Molecular Biology Laboratory


## Family: ABC\_tran (PF00005)

Loading page components (2 remaining)...

 1119 architectures

 228719 sequences

 14 interactions

 3422 species

 507 structures

### Summary

Domain organisation

Clan

Alignments

HMM logo

Trees

Curation & model

Species

Interactions

Structures

Jump to... 

### Summary: ABC transporter

Pfam includes annotations and additional family information from a range of different sources. These sources can be accessed via the tabs below.

[Wikipedia: ATP-binding domain of ABC transporters](#)

[Pfam](#)

[InterPro](#)

This is the Wikipedia entry entitled "[ATP-binding domain of ABC transporters](#)". [More...](#)

### ATP-binding domain of ABC transporters

In molecular biology, **ATP-binding domain of ABC transporters** is a water-soluble [domain](#) of transmembrane [ABC transporters](#).

ABC transporters belong to the [ATP-Binding Cassette superfamily](#), which uses the hydrolysis of [ATP](#) to translocate a variety of compounds across [biological membranes](#). ABC transporters are minimally constituted of two conserved regions: a highly conserved ATP binding cassette (ABC) and a less conserved transmembrane domain (TMD). These regions can be found on the same protein or on two different ones. Most ABC transporters function as a dimer and therefore are constituted of four domains, two ABC modules and two TMDs.

#### Contents [\[hide\]](#)

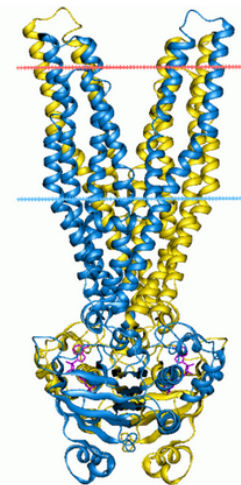
- [1 Biological function](#)
- [2 Amino acid sequence](#)
- [3 3D structure](#)
- [4 Human proteins containing this domain](#)
- [5 References](#)

### Biological function

ABC transporters are involved in the export or import of a wide variety of [substrates](#) ranging from small ions to macromolecules. The major function of ABC import systems is to provide essential nutrients to bacteria. They are found only in prokaryotes and their four constitutive domains are usually encoded by independent polypeptides (two ABC proteins and two TMD proteins). Prokaryotic importers require additional extracytoplasmic binding proteins (one or more per systems) for function. In contrast, export systems are involved in the extrusion of noxious substances, the export of extracellular toxins and the targeting of membrane components. They are found in all living organisms and in general the TMD is fused to the ABC module in a variety of combinations. Some eukaryotic exporters encode the four domains on the same polypeptide chain.

### Amino acid sequence

The ABC module (approximately two hundred amino acid residues) is known to bind and hydrolyze ATP, thereby coupling transport to ATP hydrolysis in a large number of biological processes. The cassette is duplicated in several subfamilies. Its primary sequence is highly conserved, displaying a typical



Multidrug ABC transporter SAV1866, closed state

**Identifiers**

# Différentes architectures protéiques possédant le domaine ABC\_tran (extrait)

There are 90080 sequences with the following architecture: ABC\_tran

[X6PF59\\_RETFI](#) [Reticulomyxa filosa] ATP-binding cassette protein {ECO:0000313|EMBL:ETO36694.1} (332 residues)



[Show](#) all sequences with this architecture.

There are 21754 sequences with the following architecture: ABC\_membrane, ABC\_tran

[X4ZNP7\\_9BACL](#) [Paenibacillus sabinae T27] ABC transporter ATP-binding protein {ECO:0000313|EMBL:AHV98210.1} (617 residues)



[Show](#) all sequences with this architecture.

There are 10217 sequences with the following architecture: ABC\_tran x 2

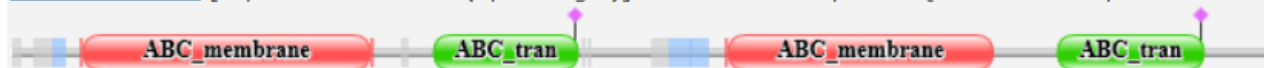
[W9SF44\\_9ROSA](#) [Morus notabilis] ABC transporter F family member 4 {ECO:0000313|EMBL:EXC49943.1} (726 residues)



[Show](#) all sequences with this architecture.

There are 8474 sequences with the following architecture: ABC\_membrane, ABC\_tran, ABC\_membrane, ABC\_tran

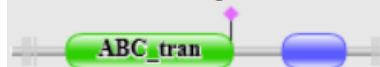
[W5N0E5\\_LEPOC](#) [Lepisosteus oculatus (Spotted gar)] Uncharacterized protein {ECO:0000313|Ensembl:ENSLOCP00000014104} (1310 residues)



[Show](#) all sequences with this architecture.

There are 8145 sequences with the following architecture: ABC\_tran, oligo\_HPY

[W8X1U8\\_CASDE](#) [Castellaniella defragrans 65Phen] Dipeptide transport ATP-binding protein DppF {ECO:0000313|EMBL:CDM26063.1} (380 residues)



[Show](#) all sequences with this architecture.

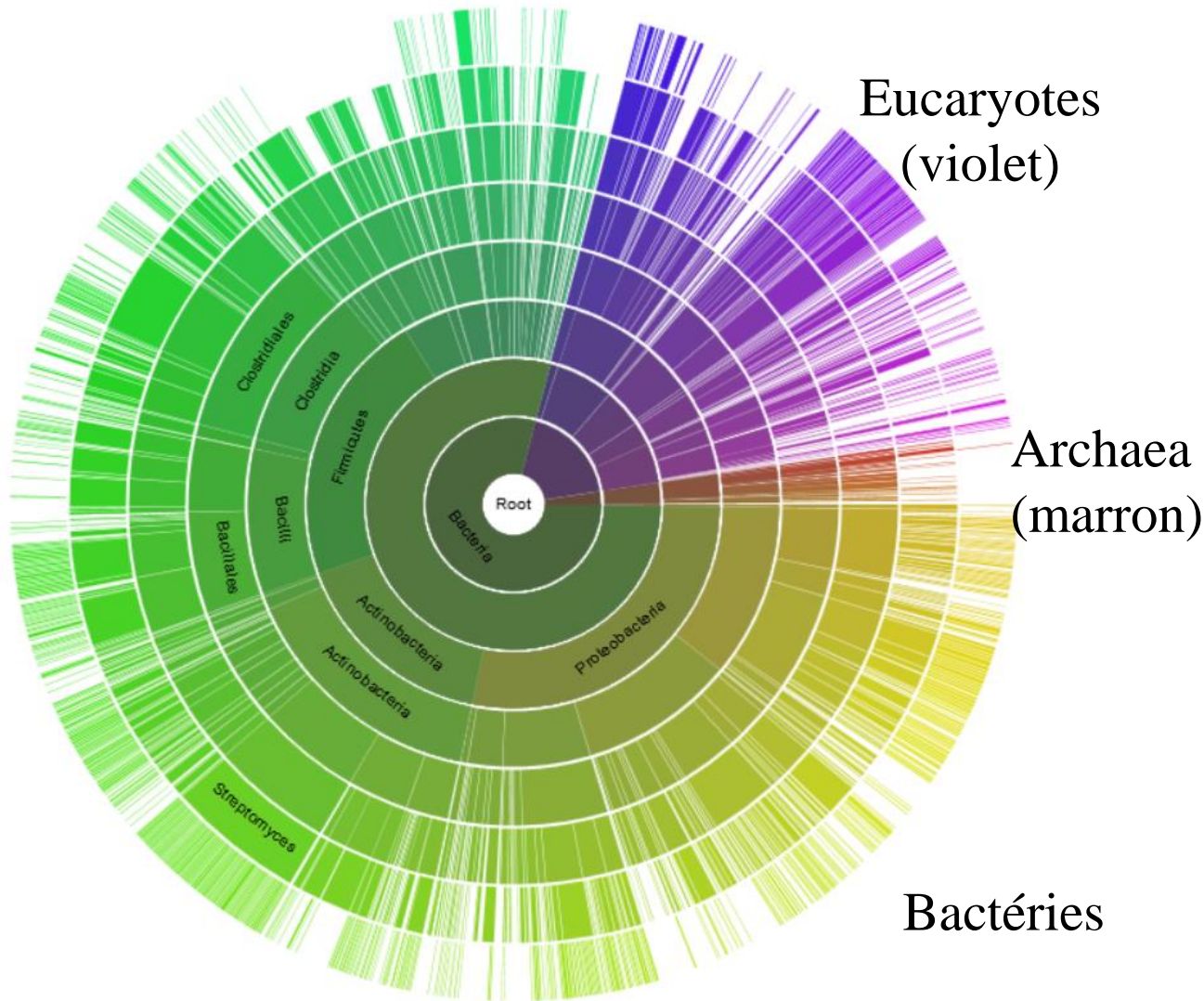
There are 7095 sequences with the following architecture: ABC\_tran, TOBE\_2

[D5RQ25\\_9PROT](#) [Roseomonas cervicalis ATCC 49957] ABC transporter, ATP-binding protein {ECO:0000313|EMBL:EFH10598.1} (347 residues)



[Show](#) all sequences with this architecture.

# Visualisation graphique simple de cette famille de protéines au sein des espèces



Arthrobacter sp. FB24

Root

- Bacteria (No kingdom)
- Actinobacteria
- Actinobacteria
- Micrococcales
- Micrococaceae
- Arthrobacter
- Arthrobacter sp. FB24

Weight segments by...









number of sequences

number of species

Change the size of the sunburst

Small  Large

Colour assignments

 Arches	 Eukaryote
 Bacteria	 Other sequences
 Viruses	 Unclassified
 Virioids	 Unclassified sequence

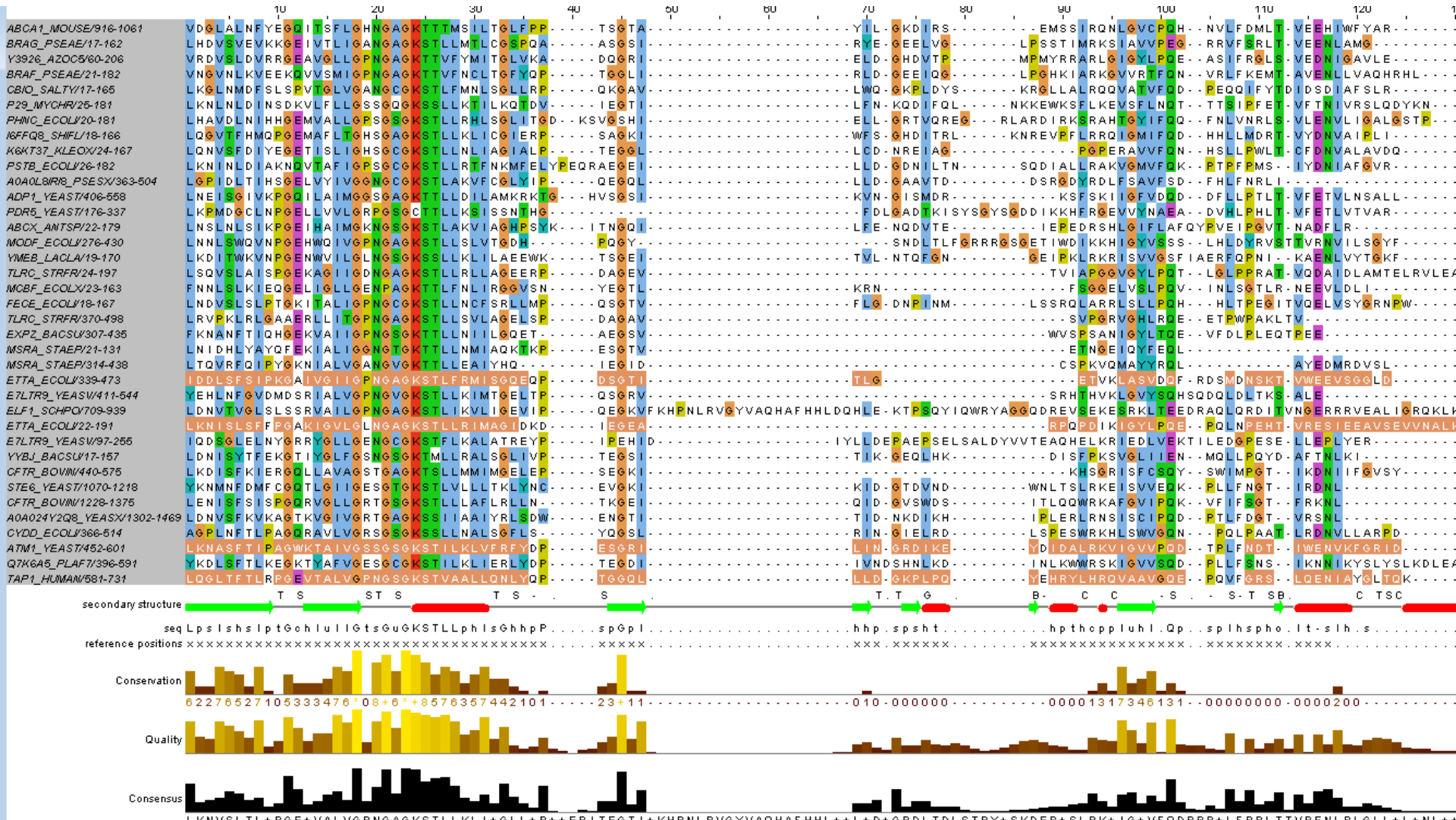
Selections

[Align](#) selected sequences to HMM

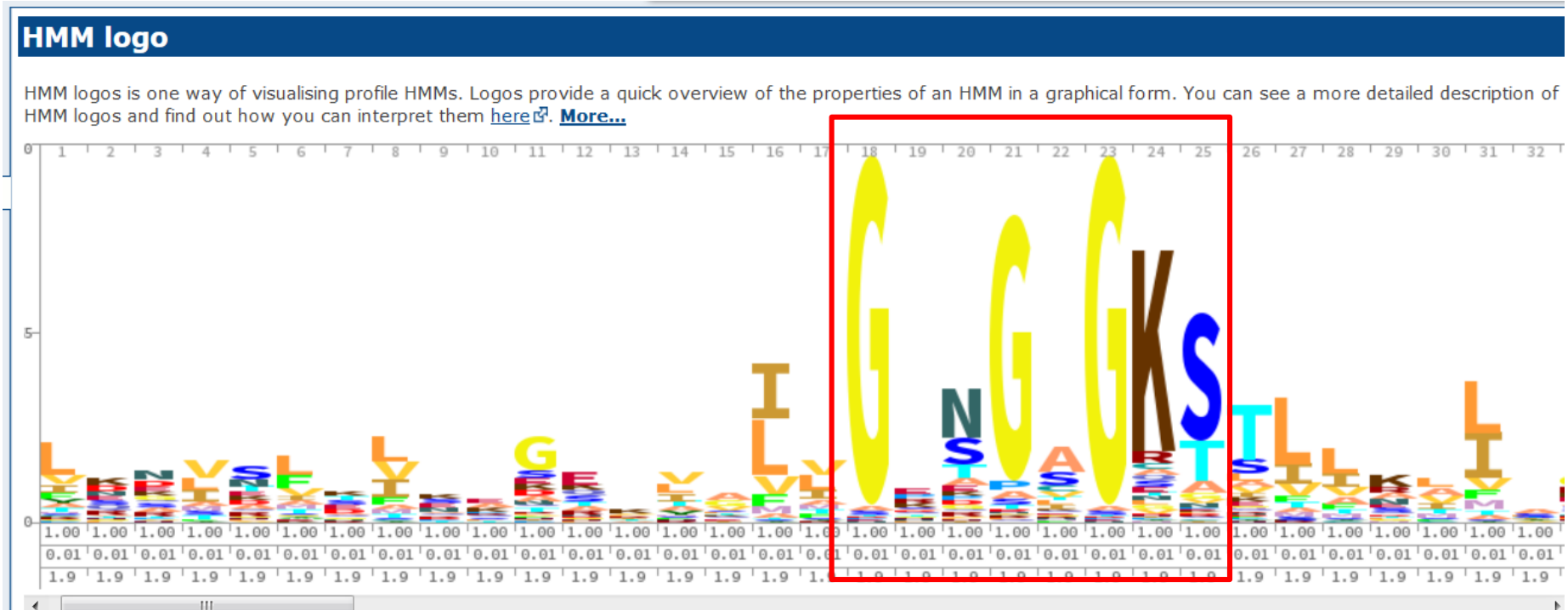
[Generate](#) a FASTA-format file

[Clear](#) selection

# Extrait de l'alignement multiple correspondant au domaine fonctionnel ABC\_tran (sous Jalview) sur les séquences « seed »



# Extrait du logo correspondant au domaine fonctionnel ABC\_tran



Correspond à la zone fortement conservée de l'alignement précédent et représente le motif Walker A de liaison de l'ATP



## InterPro

Interpro permet la classification des protéines en fonction de la présence de domaines fonctionnels, répétitions, et signaux grâce à une recherche automatisée dans plusieurs bases de données (CATH-Gene3D, HAMAP, PANTHER, Pfam, PIRSF, PRINTS, ProDom, PROSITE, SMART, SUPERFAMILY, TIGRFAMs).

# Page d'entrée d'InterPro : analyse de la séquence ComA de *S. pneumoniae*



Search InterPro...

Search

Examples: IPR020405, kinase, P51587, PF02932, GO:0007165

Home Search Release notes Download About InterPro Help Contact

By sequence By domain architecture

## InterProScan sequence search

This form allows you to scan your sequence for matches against the InterPro protein signature databases, using InterProScan tool.

Enter or paste a protein sequence in FASTA format (complete or not - e.g. PMPIGSKERPTFFEIFKTRCNKADLGPISLN), with a maximum length of 40,000 amino acid long.

Please note that you can only scan one sequence at a time.

Analyse your protein sequence

```
ESQNTNLFMTLLALPIYTVIIFAFMKPFKMNRODIMEANAVLSSSIEDINGIETKSL
TSESQRYQKIDKEEVDYLKKSFTYSRAESQQKALKVAHLLNVGILWVGAVLVMDGKMS
LGOLTYNTLVYFTNPLENINLQTKLQTAQVANNRLNEVYLVAEFEFEKKTVEDLSLM
KGDMTFKQVHYKYGYGRDVLSDINLTPQGSKVAFVGSISGSKTLAKMMVNFYDPSQGE
ISLGGVNLNQIDKKALRQYINYLPOQPYYFNGTLENLLGAKEGTTQEDILRAVELAEI
REDIERMPLNYQTELTSDGAGISGGQRORIALARALLTDAPVILDEATSSLDILTEKRI
VDNLIALDKTLFIAHRLTIAERTEKVVVLDQGGKIVEEGKHADLLAQGGFYAHLVNS
```

Advanced options

Select the applications to run: Uncheck all Select all

Member databases

Families, domains, sites & repeats

CDD  HAMAP  PANTHER  PfamA  PIRSF  PRINTS  ProDom  Prosite-Profiles  SMART  TIGRFAM  Prosite-Patterns

Structural domains

Gene3d  SFLD  SUPERFAMILY

Other sequence features

Coils  MobiDB Lite  Phobius  SignalP  TMHMM

Search | Clear Example protein sequence

### InterProScan



InterProScan is a sequence analysis application (nucleotide and protein sequences) that combines different protein signature recognition methods into one resource.

[More about InterProScan.](#)

### ? Need more help?

If you need more info on InterProScan, you can either look at the:

- Documentation page
- Online training course

or [contact us](#) directly with your question.

# Résultats de l'analyse de la séquence ComA de *S. pneumoniae*

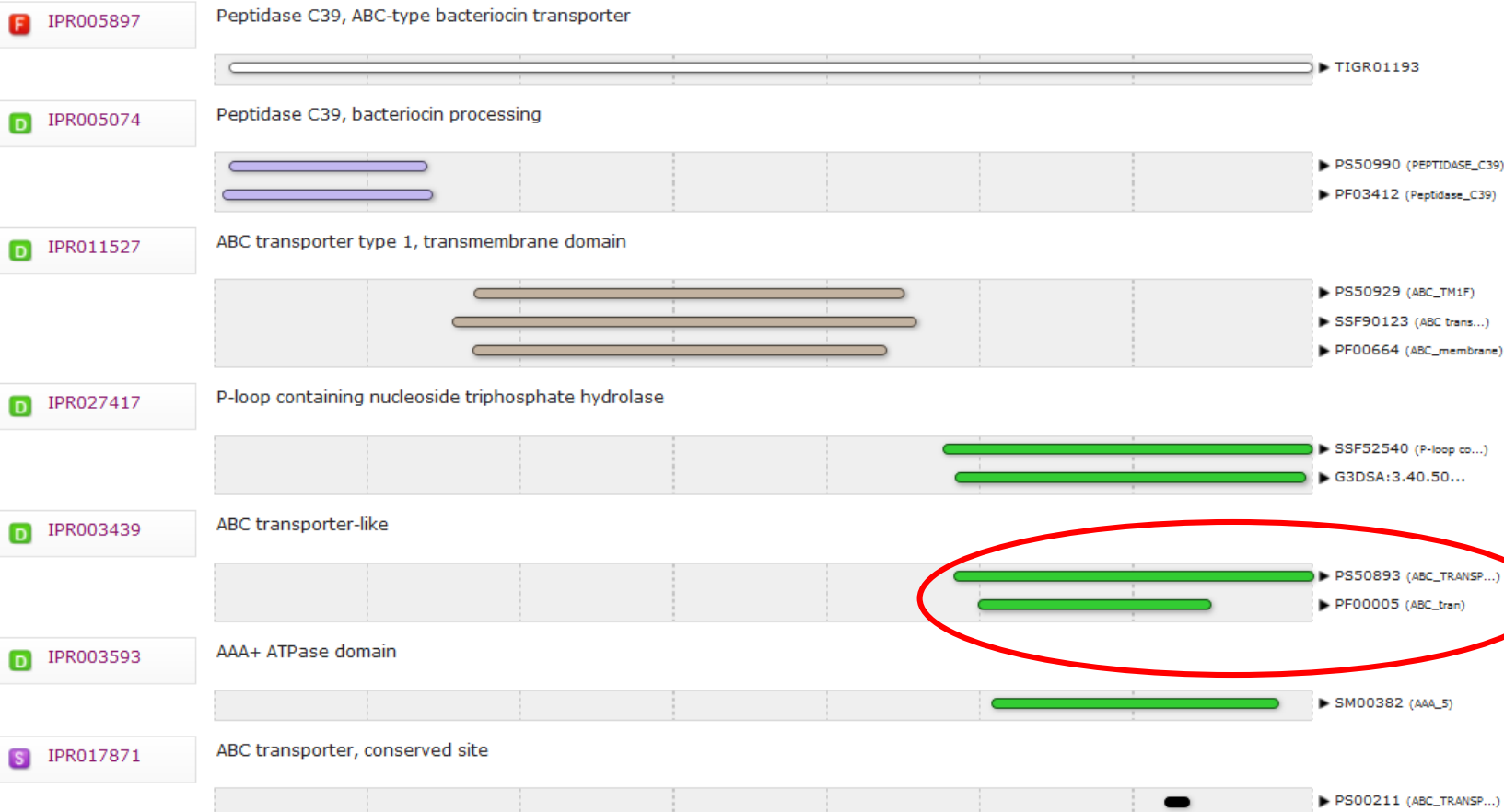
## Protein family membership

**F** Peptidase C39, ABC-type bacteriocin transporter (IPR005897)

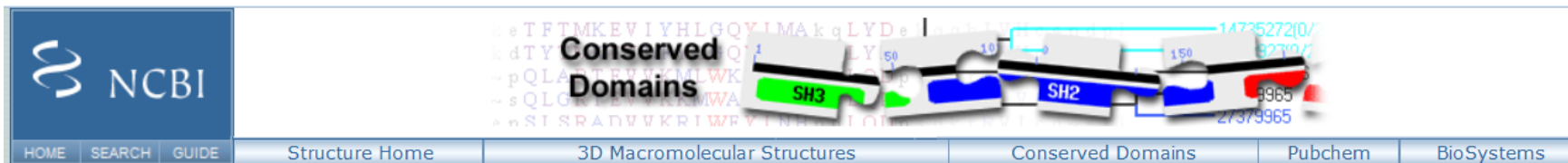
## Domains and repeats



## Detailed signature matches



# Recherche des domaines fonctionnels dans la séquence ComA de *S. pneumoniae* dans la banque « Conserved Domain Database » (CDD) maintenue au NCBI (CD\_search)



Search for Conserved Domains within a protein or coding nucleotide sequence

**NEW!** Use **Batch CD-search** to submit multiple query proteins at once!

Enter **protein** or **nucleotide** query as accession, gi, or sequence in **FASTA format** [?](#)

```
>SpneA01.COMA "Transport ATP-binding protein ComA"
MKFGKRHRYPQVDQDCGVASLAMVFGYYSYFLAHLRELAKTTMDGTTALGLVKVAEEIGFETRAIKADMTLFDLPDL
TFPFVAHVLEKGLLHYYVVTGQDKDSIHIAADPDGPKLTKLPRERFEEWTGVTLFMAPSPDYKPKHEQKNGLLSFIPI
LVKQRGLIANIVLATLLVTVINIVGSYYLQSIIDTYVPDQMRSTLGIISIGLVIVYILQQIILSYAQEYLLLVLGQRLSID
VILSYIKHVFLPMSFFATRRRTGEIVSRFTDANSIIDALASTILSIFLDVSTVVIISLVLFSQNTNLFMTLLALPIYTV
IIFAFMKPFKEMNRDTEANAVLSSSIIDINGIETIKSLTSESQRYQKIDKEFVDYLKKSFTYSRAESQQKALKKVAHL
LLNVGILWMGAVLVMDGKMSLGLITINTLLVYFTNPLENIINLQTKLQTAQVANNRLNEVYLVASEFEERKTVEDLSLM
KGDMTFKQVHYKYGYGRDVLSDINLTVPGGSKVAFVGISSGSKTTLAKMMVNFYDPSQGEISLGGVNLNQIDKKALRQYI
NYLPQQPYVFNGTILENLLLGAKEGTTQEDILRAVELAETREDIERMPLNYQTELTSDGAGISGGQRRIALARALLTDA
PVLILDEATSSLDILTTEKRIVDNLIADKTLIFIAHRLTIAERTEKVVVLDQKIVEEGKHADLLAQGGFYAHLVNS
```

Submit

Reset

## OPTIONS

Search against database [?](#): CDD v3.15 - 48963 PSSMs

Expect Value [?](#) threshold: 0.010000

Apply low-complexity filter [?](#)

Composition based statistics adjustment [?](#)

Force live search [?](#)

Rescue borderline hits  Suppress weak overlapping hits

Maximum number of hits [?](#) 500

Result mode  Concise [?](#)  Standard [?](#)  Full [?](#)

## Retrieve previous CD-search result

Request ID:   [?](#)

### References:

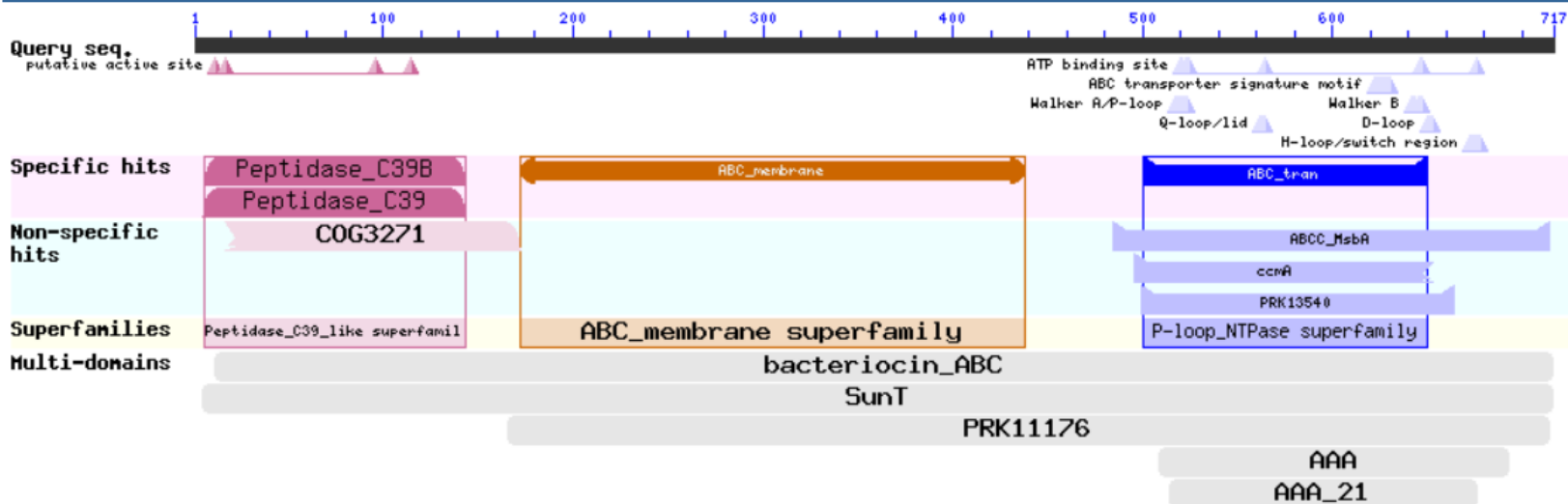
- Marchler-Bauer A et al. (2017), "CDD/SPARCLE: functional classification of proteins via subfamily domain architectures.", **Nucleic Acids Res.**45(D)200-3.
- Marchler-Bauer A et al. (2015), "CDD: NCBI's conserved domain database.", **Nucleic Acids Res.**43(D)222-6.
- Marchler-Bauer A et al. (2011), "CDD: a Conserved Domain Database for the functional annotation of proteins.", **Nucleic Acids Res.**39(D)225-9.
- Marchler-Bauer A, Bryant SH (2004), "CD-Search: protein domain annotations on the fly.", **Nucleic Acids Res.**32(W)327-331.

# Résultat de la recherche dans la banque CDD

protein containing domains Peptidase\_C39B, ABC\_membrane, and P-loop\_NTPase

## Graphical summary

Zoom to residue level [show extra options >](#)



[Search for similar domain architectures](#) ?

[Refine search](#) ?

## List of domain hits

+	Name	Accession	Description	Interval	E-value
[+]	ABCC_MsbA	cd03251	ATP-binding cassette domain of the bacterial lipid flippase and related proteins, subfamily C; ...	485-714	9.00e-79
[+]	Peptidase_C39B	cd02418	A sub-family of peptidase family C39. Peptidase family C39 mostly contains ...	6-143	1.66e-68
[+]	ABC_membrane	pfam00664	ABC transporter transmembrane region; This family represents a unit of six transmembrane ...	172-438	2.87e-64
[+]	Peptidase_C39	pfam03412	Peptidase C39 family; Lantibiotic and non-lantibiotic bacteriocins are synthesized as ...	5-143	1.20e-50
[+]	ABC_tran	pfam00005	ABC transporter; ABC transporters for a large family of proteins responsible for translocation ...	500-650	5.05e-39
[+]	ccmA	TIGR01189	heme ABC exporter, ATP-binding protein CcmA; This model describes the cyt c biogenesis protein ...	496-653	6.96e-19
[+]	PRK13540	PRK13540	cytochrome c biogenesis protein CcmA; Provisional	499-664	4.40e-10
[+]	COG3271	COG3271	Predicted double-glycine peptidase [General function prediction only];	17-172	4.87e-05
[+]	bacteriocin_ABC	TIGR01193	ABC-type bacteriocin transporter; This model describes ABC-type bacteriocin transporter. The ...	11-716	0e+00
[+]	SunT	COG2274	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase ...	5-716	0e+00
[+]	PRK11176	PRK11176	lipid transporter ATP-binding/permease protein; Provisional	166-714	9.99e-76
[+]	AAA	smart00382	ATPases associated with a variety of cellular activities; AAA - ATPases associated with a ...	509-693	8.93e-09
[+]	AAA_21	pfam13304	AAA domain, putative AbiEii toxin, Type IV TA system; Several members are annotated as being ...	514-676	1.42e-03

# Résultat détaillée de la détection du domaine fonctionnel Pfam00664

ABC transporter; ABC transporters for a large family of proteins responsible for translocation of a variety of compounds across biological membranes. ABC transporters are the largest family of proteins in many completely sequenced bacteria. ABC transporters are composed of two copies of this domain and two copies of a transmembrane domain pfam00664. These four domains may belong to a single polypeptide or belong in different polypeptide chains.

**Pssm-ID:** 278435 **Cd Length:** 150 **Bit Score:** 140.09 **E-value:** 5.05e-39

```

          10          20          30          40          50          60          70          80
          .....*.....|.....*.....|.....*.....|.....*.....|.....*.....|.....*.....|.....*.....|.....*.....|
seqsig_MKFGK_e2ea59cba8ae2f892bff9c30e69b60cc 500 LSDINLTVPQGSKVAFVGLSGSGKTLAKMMVNFYDPSQGEISLGGVNLNQIDKKALRQYINYLPPQPYVFNG-TILENL 578
Cdd:pfam00005 1 LKNVSLTLNPGEILALVGPNGAGKSTLLKLIAGLLSPTEGTILLDGGDLTDDERKSLRKEIGYVVFQDPNLFPRLTVRENL 80

          90          100          110          120          130          140          150
          .....*.....|.....*.....|.....*.....|.....*.....|.....*.....|.....*.....|.....*.....|.....
seqsig_MKFGK_e2ea59cba8ae2f892bff9c30e69b60cc 579 LLGAKEggttqEDILRAVELAEIREDIERMPINLQ--TELTSDGAGISGGQRQRIALARALLTDAPVLLIIDEATS 650
Cdd:pfam00005 81 RLGLRL---KGLSKREKDARAEALEKLGLDLldRPVGENPGTSSGGQRQVAIARALLTRPKLLLLDEPTA 150
```