# Genome Comparison based on Motif Statistics

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# Motivation : Prosite Motifs

```
AC   PS00723;
DE   Polyprenyl synthetases signature 1.
...
PA   [LIVM](2)-x-D-D-x(2,4)-D-x(4)-R-R-[GH].

...
DR   P14324, FPPS_HUMAN, T; ... P49353, FPPS_MAIZE, T;
DR   P08524, FPPS_YEAST, T; ... P08836, FPPS_CHICK, P;
...
```

Biological pertinence of motifs

with respect to target proteoms

# Content of the talk

1. Exact method
2. Approximate method
   (a) Generating function for non-self-overlapping motifs
   (b) Asymptotic Poisson distribution for rare occurrences
3. Biological application
   – Characteristic motifs in Eukaryotes, Archae-Bacteria and Bacteria

## Regular expressions

$$R = (a \cdot b \cdot a + (c^4 \cdot e)^\star \cdot b \cdot b)^\star$$

### Operators

| | |
|---|---|
| $+$ | Union |
| $\cdot$ | Concatenation |
| $\star$ | Star-operator $(A^\star = \epsilon + A + A^2 + A^3 + \ldots)$ |

## Prosite motifs

```
PA = [LIVM](2)-x-D-D-x(2,4)-D-x(4)-R-R-[GH].
```

$$PA = (L+I+V+M)^2 \cdot \Sigma \cdot D \cdot D \cdot (\Sigma^2 + \Sigma^3 + \Sigma^4) \cdot D \cdot \Sigma^4 \cdot R \cdot R \cdot (G+H)$$

$$\text{with } \Sigma = \begin{array}{l} A+R+N+D+C+Q+E+G+H+I \\ +L+K+M+F+P+S+T+W+Y+V \end{array}$$

$$\Sigma^k = \Sigma \cdot \Sigma \cdot \quad \cdots \quad \cdot \Sigma \qquad (k \text{ times})$$

# Main counting tool

$R$ given regular expression.

$X_n$ number of occurrences of words of $R$ in a text of length $n$.

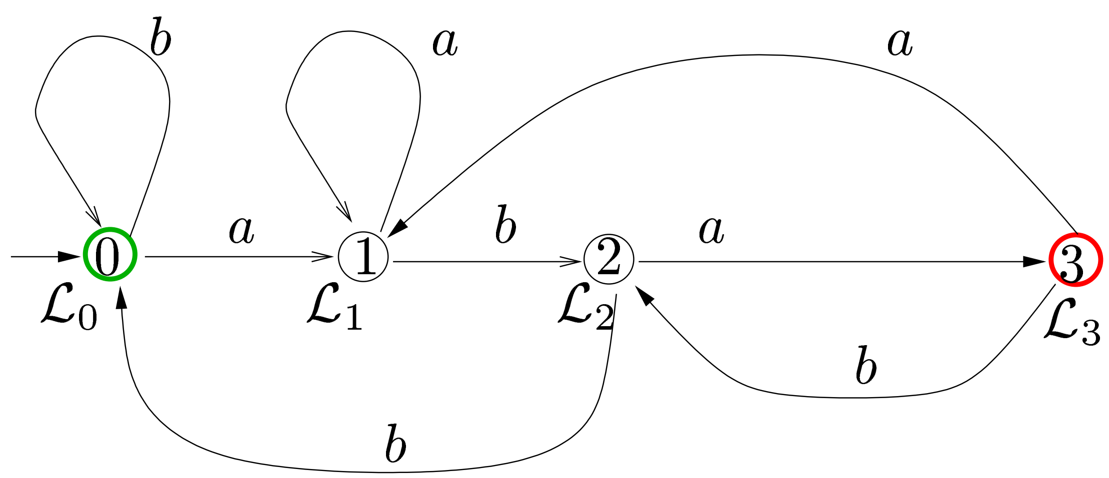
$$F(z,u) = \sum_{n,k} \Pr(X_n = k) u^k z^n = \sum_{n,k} f_{n,k} u^k z^n.$$

# Exact method

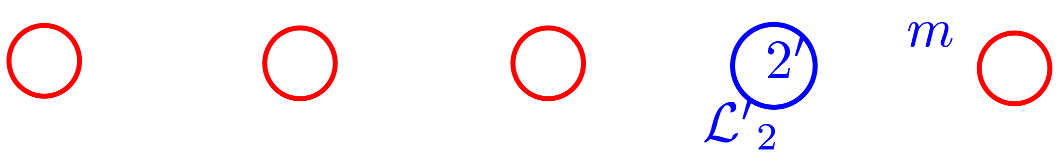
Automaton Recognizing $\Sigma^* R$

$$\Sigma = \{a, b\} \quad R = aba, \quad \Sigma^* R = \Sigma^* aba$$

$$aabbaba\bullet bbabbaba\bullet aaaba\bullet bbbb$$



marking ($\Sigma' = \Sigma \cup \{m\}$)




$aaaabambamaaabamaa$

Chomsky-Schützenberger

$$\mathcal{L}_0 = a\mathcal{L}_1 + b\mathcal{L}_0 + \epsilon, \qquad \ldots,$$

$$\mathcal{L}_2 = a\mathcal{L}'_2 + b\mathcal{L}_0 + \epsilon, \qquad \mathcal{L}'_2 = m\mathcal{L}_3,$$

$$L(a,b,m) = \frac{1 + ab(1-m)}{1 - a - b + ab(1-m) - ab^2(1-m)},$$

$$F(z,u) = L(\omega_a z, \omega_b z, u).$$

# Experimental observations

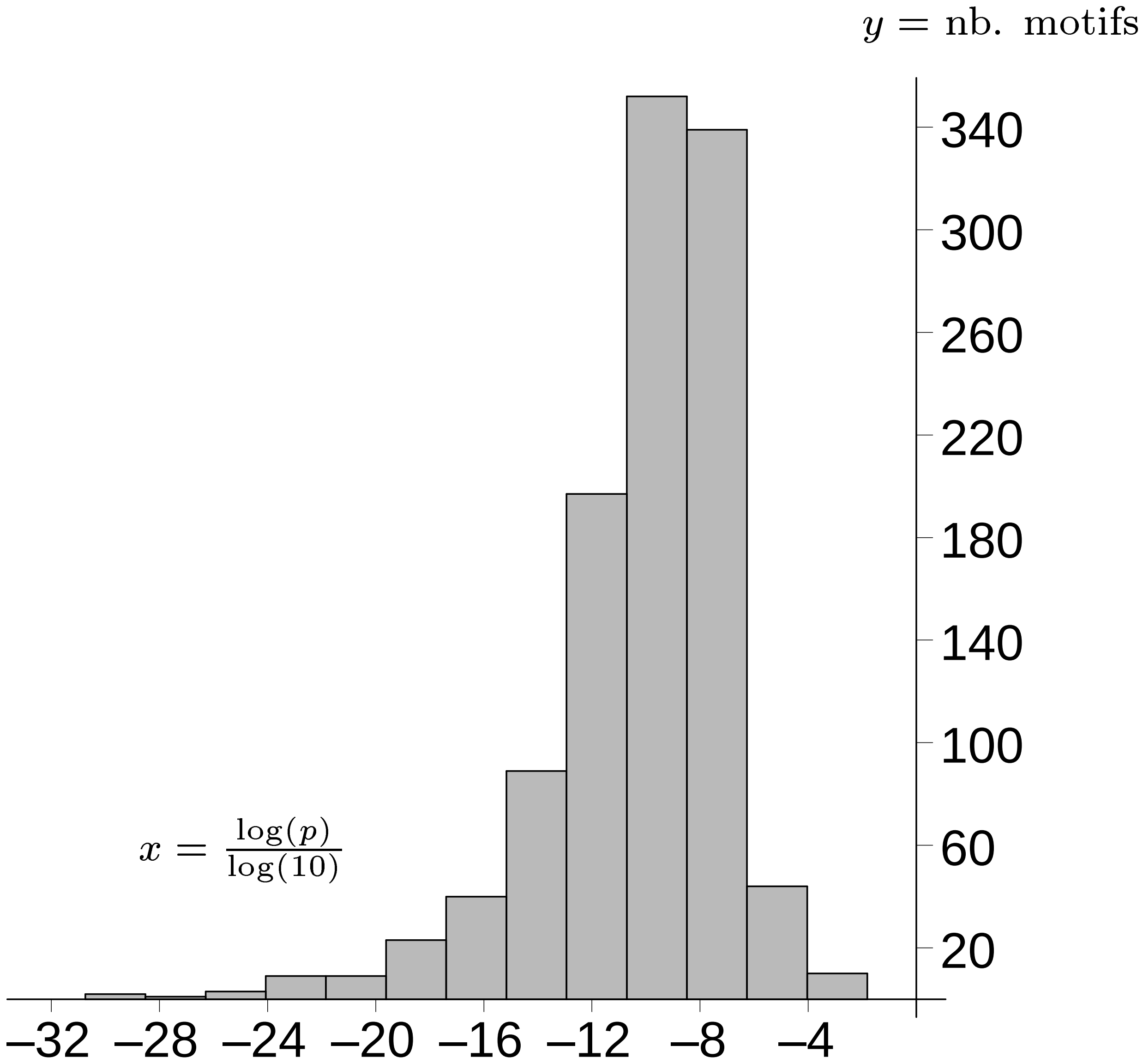



Figure 1: Histogram of probability of occurrence $p$ of a motif at a given position for the 1118 motifs exactly computed. (ProDom distribution for amino-acids)

# Approximate method

Matches for non-self-overlapping languages

$R$ non-self-overlapping, O.G.F. $R(z)$

$F(z,u) = \sum f_{n,k} u^k z^n$, O.G.F. nb. matches

$\mu_n, \sigma_n^2$ asympt. expect. and var. for nb. matches

Theorem 1:

(a) $$F(z,u) = \frac{1}{1 - z + (1-u)R(z)}$$

(b) $$\mu_n = R(1) \times n + R(1) - R'(1) + O(A^n)$$

(c) $$\sigma_n^2 = \{R(1) + R(1)^2 - 2R(1)R'(1)\} \times n + \kappa(R(1), R'(1), R''(1)) + O(A^n)$$

$$(A < 1)$$

# A non-ambiguity lemma

Warning

$A = B = C = \{a, b, ab\}$

$abab = a \cdot b \cdot ab = ab \cdot a \cdot b \in ABC$

$\Rightarrow ABC$ ambiguous

while $AB$ and $BC$ non-ambiguous

---

$R$ regular expression

$N = \Sigma^* - \Sigma^* R \Sigma^*$ lang. without occ. of $R$

Lemma:

$R$ non self-overlapping and non nested

$\Rightarrow \quad N(RN)^k$ non-ambiguous $\forall k$

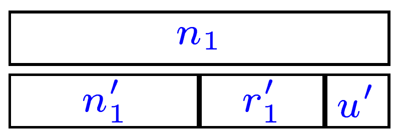
# Proof of the lemma

Let us suppose $NRN$ is ambiguous

let $w = n_1 r_1 n_2 = n'_1 r'_1 n'_2 \in NRN$, $\{n_1, n_2, n'_1, n'_2\} \subset N$, $\{r_1, r'_1\} \subset R$

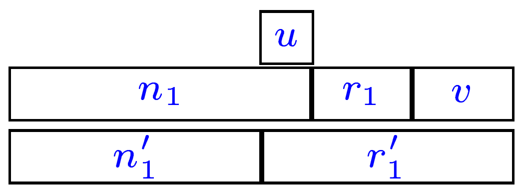
Let us suppose $|n_1| > |n'_1|$ $\quad$ ($|n_1| < |n'_1|$ is symmetrical)

$|n_1| > |n'_1 r'_1|$



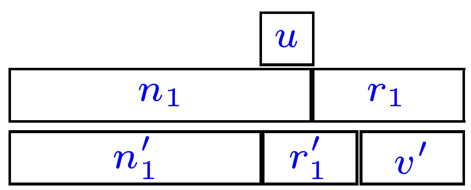

$\Rightarrow n_1 \notin N$

$|n_1 r_1| < |n'_1 r'_1|$




$\Rightarrow$ $r'_1 = u r_1 v$
$R$ nested

$|n_1 r_1| > |n'_1 r'_1|$




$\Rightarrow$ $u r_1 = r'_1 v$
$R$ overlapping

$\Rightarrow$ $n_1 = n'_1$ $\Rightarrow$ $r_1 = r'_1$ $\Rightarrow$ $n_2 = n'_2$

(elsewhere $R$ is overlapping)

$\Rightarrow$ $NRN$ non-ambiguous

$\Rightarrow$ $N(RN)^k$ $(k > 1)$ non-ambiguous (same proof)

# Proof of Theorem 1

$\phi_R$ injection $\Sigma^\star \to (\Sigma + u)^\star$

$t \to t_u = \phi_R(t)$

by inserting $u$ after each match in $t$

$\phi_R(\Sigma^\star) = \bigcup_{k\geq 0} N(RuN)^k$

$$\Rightarrow F(z,u) = \sum_{k\geq 0} N(z)(uN(z)R(z))^k = \frac{N(z)}{1 - uN(z)R(z)}$$

$$\Rightarrow F(z,1) = \frac{1}{1-z} = \frac{N(z)}{1 - N(z)R(z)}$$

$$\Rightarrow F(z,u) = \frac{1}{1 - z + (1-u)R(z)}$$

# Radius of convergence for prefix-free languages

$\mathcal{L}$ prefix-free $\quad \Leftrightarrow \quad \forall u, v \in \mathcal{L}, \quad \not\exists w, \ u = v.w$

$\mathcal{L}_k = \mathcal{L} \cup \Sigma^k$

$j > k \quad \Rightarrow \quad \mathcal{L}_j \subset \Sigma^j - \mathcal{L}_k \Sigma^{j-k}$

fix $i$

The sets $\mathcal{M}_{i,j} = \mathcal{L}_j \Sigma^{i-j}$ $(j < i)$ are disjoints

$$\bigcup_{j \leq i} \mathcal{M}_{i,j} \subset \Sigma^i, \quad \Sigma^k(1) = 1 \ (\forall k)$$

$$\Rightarrow \quad \sum_{j \leq i} M_{i,j}(1) \leq 1 \ (\forall i), \quad M_{i,j}(1) = L_j(1)$$

$$\Rightarrow \quad L(1) = \sum_{i \geq 1} L_i(1) \leq 1$$

$\tau$ radius of convergence of $L(z)$

$L(1) = \sum l_n z^n |_{z=1}$ bounded, $l_n \geq 0 \ \Rightarrow \ \tau > 1$

# Poisson law for rare occurrences

$L$ non self-overlapping, non nested, O.G.F. $L(z)$

$p_{n,k}$ prob. $k$ matches in text size $n$

Theorem 2:

(a) $\exists \rho \in \mathbb{R}^+$, $\rho < 1$, and $1 - \rho + L(\rho) = 0$

(b) for $k = O(1)$, $\exists \kappa > \rho$

$p_{n,k} = \sum_{j=1}^{k+1} (-1)^j a_j \binom{n}{j-1} \rho^{-(n+j)} + O(\kappa^{-n})$

and

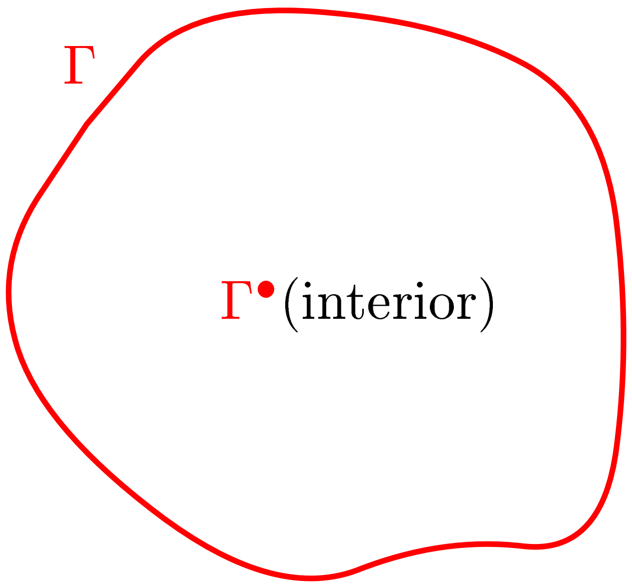
$a_{k+1} = \frac{L(\rho)^k}{\rho^{k+1}(L'(\rho)-1)^{k+1}}$

(c) asymptotically, for $k = O(1)$

$$p_{n,k} = \frac{\rho^{-n-1}}{1 - L'(\rho)} \frac{(\alpha n)^k}{k!} \left(1 + O\left(\frac{1}{n}\right)\right),$$

$$\alpha = \left(\frac{\rho^{-1} L(\rho)}{1 - L'(\rho)}\right)$$

# Rouché's Theorem




1) $f$ and $g$ differentiable in $\{\Gamma^\bullet$ - finite nb. poles$\}$

2) $0 < |f(z)| < \infty \quad$ for $z \in \Gamma$

3) $|g(z)| < |f(z)| \quad$ for $z \in \Gamma$

$\Rightarrow \quad f + g \quad$ and $\quad f$

have same number of zeroes inside $\Gamma^\bullet$

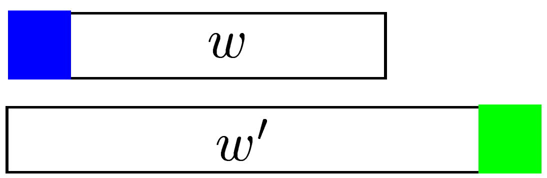
Demonstration: homotopy on

$$\frac{1}{2\pi i}\int_\Gamma \frac{f' + tg'}{f + tg}, \qquad t \in [0, 1]$$

# Proof of Theorem 2

$$F(z,u) = \frac{1}{1-z+(1-u)L(z)} = \sum_{k\geq 0} \frac{L(z)^k}{(1-z+L(z))^{k+1}} u^k$$

asymptotics come from zeroes of $1-z+L(z)$




$B = \{b, \quad b \cdot w \in L\}$

$T = \{t, \quad w' \cdot t \in L\}$

$L$ non overlapping $\quad \Rightarrow \quad T \subseteq \Sigma - B$

$b \in B, t \in T \quad \Rightarrow bbt$ and $btt \quad$ (of $B\Sigma T$) overlap

$\Rightarrow \quad L \subset B\Sigma^\star T \subseteq \Phi = B\Sigma^\star(\Sigma - B)$

$L(z) < \Phi(z) = \pi_B z \frac{1}{1-z}(1-\pi_B)z \leq \frac{z^2}{4(1-z)}$

On $\Gamma = \{|z| = 2\} \qquad |L(z)| < 1 \leq |1-z|$

Apply Rouché's Theorem with

$f = 1-z, \quad f+g = 1-z+L(z)$

$\Rightarrow 1-z+L(z)$ has only one root $\rho$ inside $\Gamma$

Perron-Frobenius $\quad \Rightarrow \quad \rho \in \mathbb{R}^+$

$L \quad$ prefix-free $\quad \Rightarrow \quad 1 < \rho < \tau$ (radius conv $(f+g)$)

# Computation of $R(z), R'(z), R(1), R'(1)$

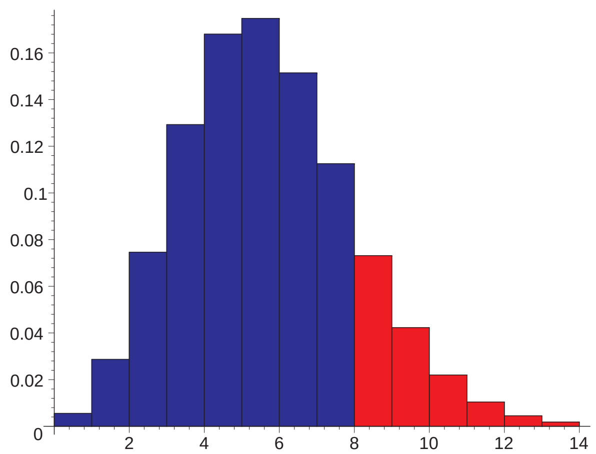
PA `[LIVM](2)-x-D-D-x(2,4)-D-x(4)-R-R-[GH]`

$R(z) = (p_L + p_I + p_V + p_M)^2 z^2 \times z \times p_D z \times p_D z \times (z^2 + z^3 + z^4) \times p_D z \times z^4 \times p_D z \times p_D z \times (p_G + p_H) z$

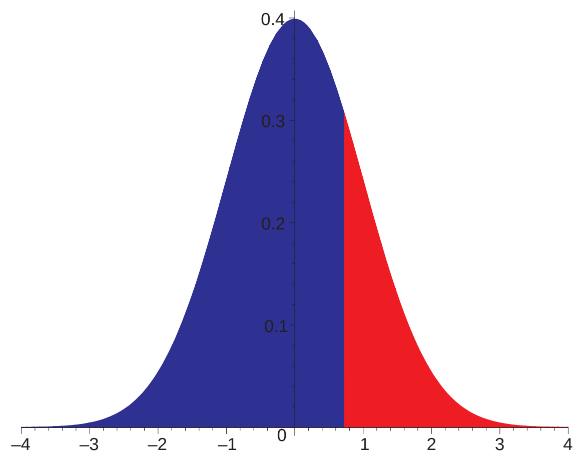
$= (p_L + p_I + p_V + p_M)^2 p_D^5 (p_G + p_H) z^{13} (z^2 + z^3 + z^4)$

$\rightarrow R'(z), R(1), R'(1)$

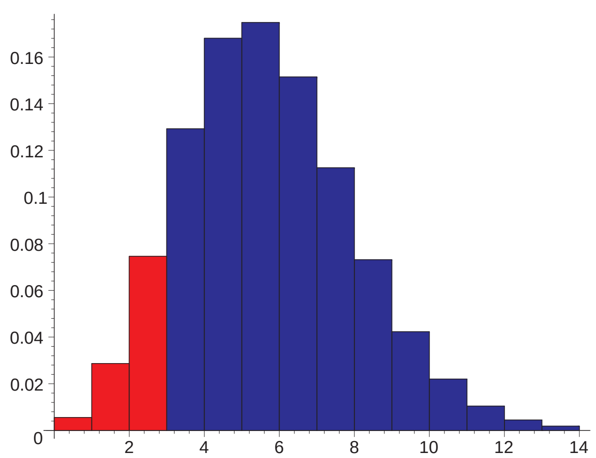
# Gaussian normalization



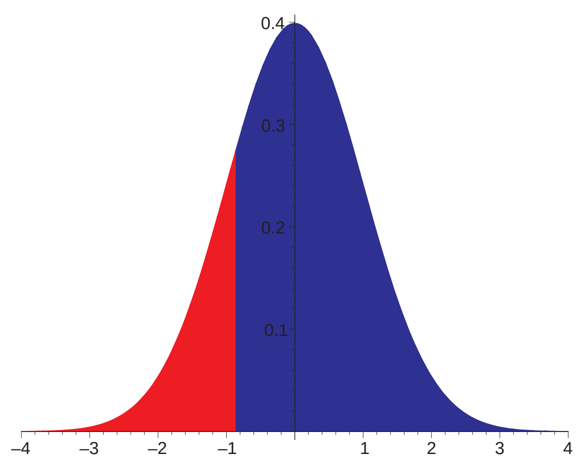

$\omega = 8$




$\gamma = +0.72$




$\omega = 2$




$\gamma = -0.81$

Poisson expectation $\mu = 5.2$

Normal distribution

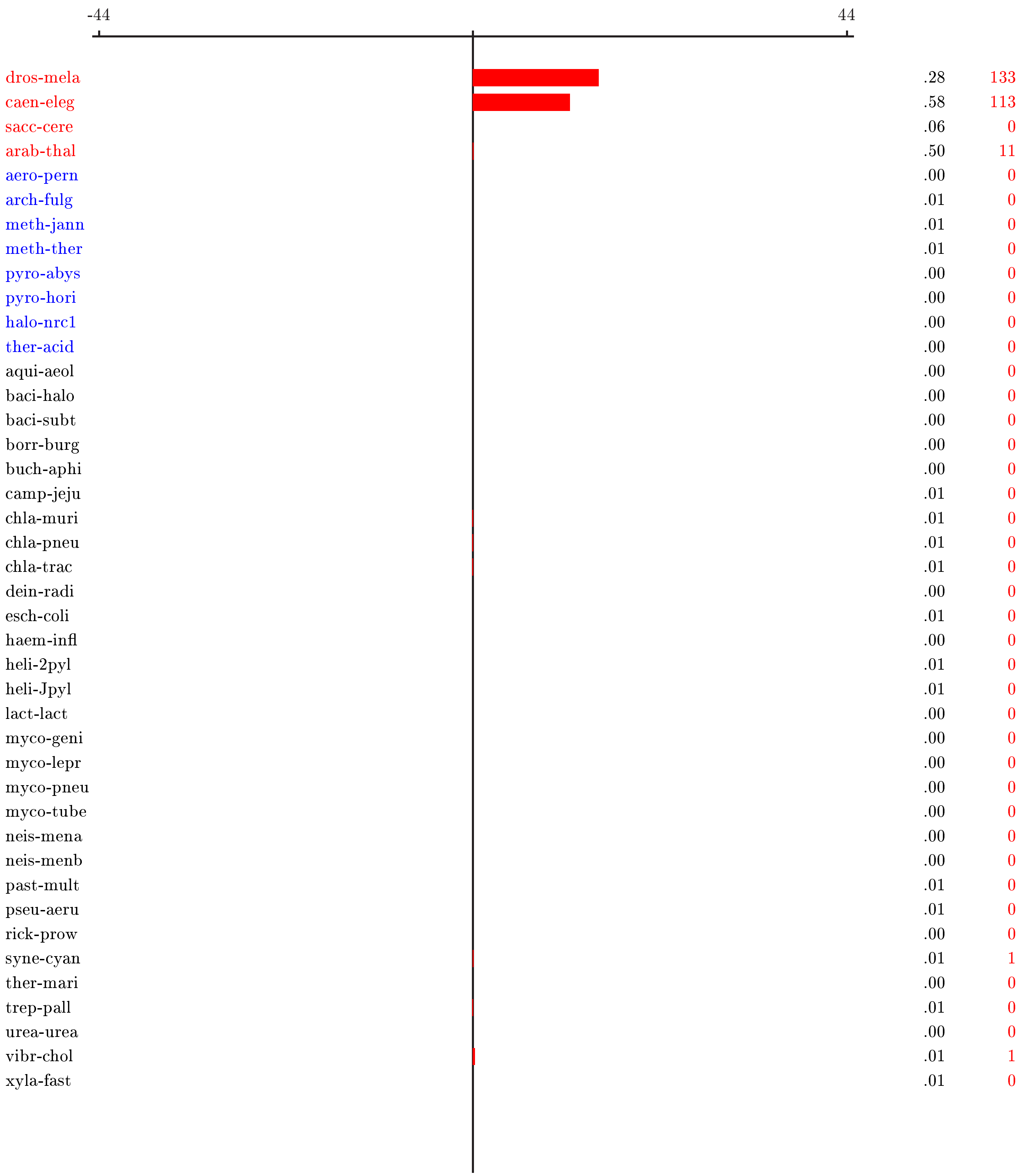
$\omega$ number of matches observed

# Comparison of 42 proteomes

| | Espèce | Longueur protéome |
|---|---|---|
| *Eukaryotes* | dros-mela | 6617803 |
| | caen-eleg | 7863058 |
| | sacc-cere | 2937205 |
| | arab-thal | 11304307 |
| *Archae-bacteria* | aero-pern | 638811 |
| | arch-fulg | 660832 |
| | meth-jann | 502362 |
| | meth-ther | 525164 |
| | pyro-abys | 535786 |
| | pyro-hori | 568584 |
| | halo-nrc1 | 624005 |
| | ther-acid | 453115 |
| *Bacteria* | aqui-aeol | 488484 |
| | baci-halo | 1169204 |
| | baci-subt | 1218487 |
| | borr-burg | 352644 |
| | buch-aphi | 187023 |
| | camp-jeju | 503501 |
| | chla-muri | 324428 |
| | chla-pneu | 361707 |
| | chla-trac | 312118 |
| | dein-radi | 951455 |
| | esch-coli | 1373785 |
| | haem-infl | 526801 |
| | heli-2pyl | 491768 |
| | heli-Jpyl | 493049 |
| | lact-lact | 655989 |
| | myco-geni | 175729 |
| | myco-lepr | 520057 |
| | myco-pneu | 237930 |
| | myco-tube | 1317198 |
| | neis-mena | 582084 |
| | neis-menb | 573863 |
| | past-mult | 667675 |
| | pseu-aeru | 1856757 |
| | rick-prow | 279044 |
| | syne-cyan | 1027015 |
| | ther-mari | 582037 |
| | trep-pall | 349913 |
| | urea-urea | 227717 |
| | vibr-chol | 1156096 |
| | xyla-fast | 744437 |

PS00010 - ASX-HYDROXYL;PATTERN. Aspartic acid and asparagine hydroxylation site.

C-x-[DN]-x(4)-[FY]-x-C-x-C



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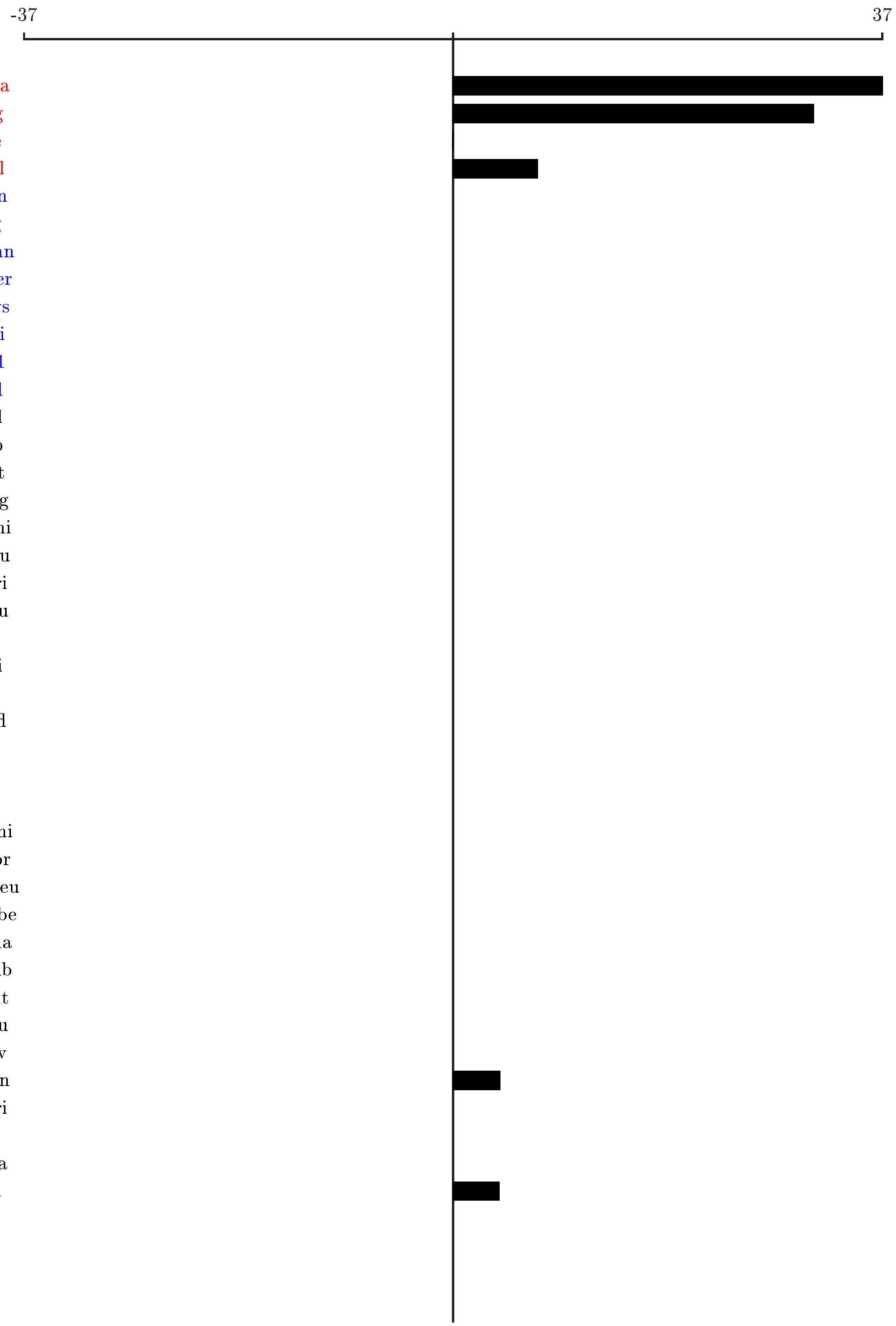
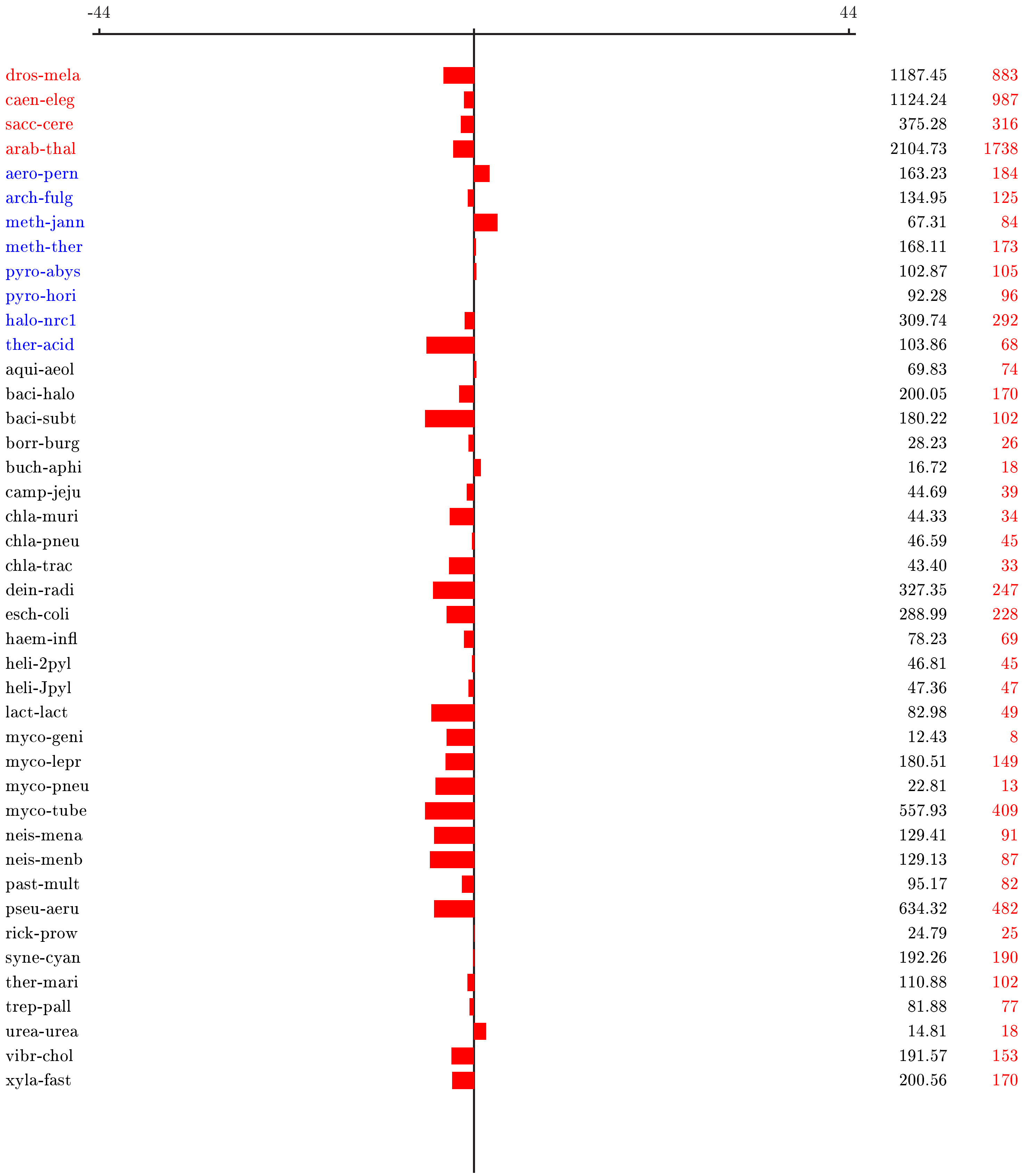



| | | |
|---|---|---|
| dros-mela | .28 | 133 |
| caen-eleg | .58 | 113 |
| sacc-cere | .06 | 0 |
| arab-thal | .50 | 11 |
| aero-pern | .00 | 0 |
| arch-fulg | .01 | 0 |
| meth-jann | .01 | 0 |
| meth-ther | .01 | 0 |
| pyro-abys | .00 | 0 |
| pyro-hori | .00 | 0 |
| halo-nrc1 | .00 | 0 |
| ther-acid | .00 | 0 |
| aqui-aeol | .00 | 0 |
| baci-halo | .00 | 0 |
| baci-subt | .00 | 0 |
| borr-burg | .00 | 0 |
| buch-aphi | .00 | 0 |
| camp-jeju | .01 | 0 |
| chla-muri | .01 | 0 |
| chla-pneu | .01 | 0 |
| chla-trac | .01 | 0 |
| dein-radi | .00 | 0 |
| esch-coli | .01 | 0 |
| haem-infl | .00 | 0 |
| heli-2pyl | .01 | 0 |
| heli-Jpyl | .01 | 0 |
| lact-lact | .00 | 0 |
| myco-geni | .00 | 0 |
| myco-lepr | .00 | 0 |
| myco-pneu | .00 | 0 |
| myco-tube | .00 | 0 |
| neis-mena | .00 | 0 |
| neis-menb | .00 | 0 |
| past-mult | .01 | 0 |
| pseu-aeru | .01 | 0 |
| rick-prow | .00 | 0 |
| syne-cyan | .01 | 1 |
| ther-mari | .00 | 0 |
| trep-pall | .01 | 0 |
| urea-urea | .00 | 0 |
| vibr-chol | .01 | 1 |
| xyla-fast | .01 | 0 |

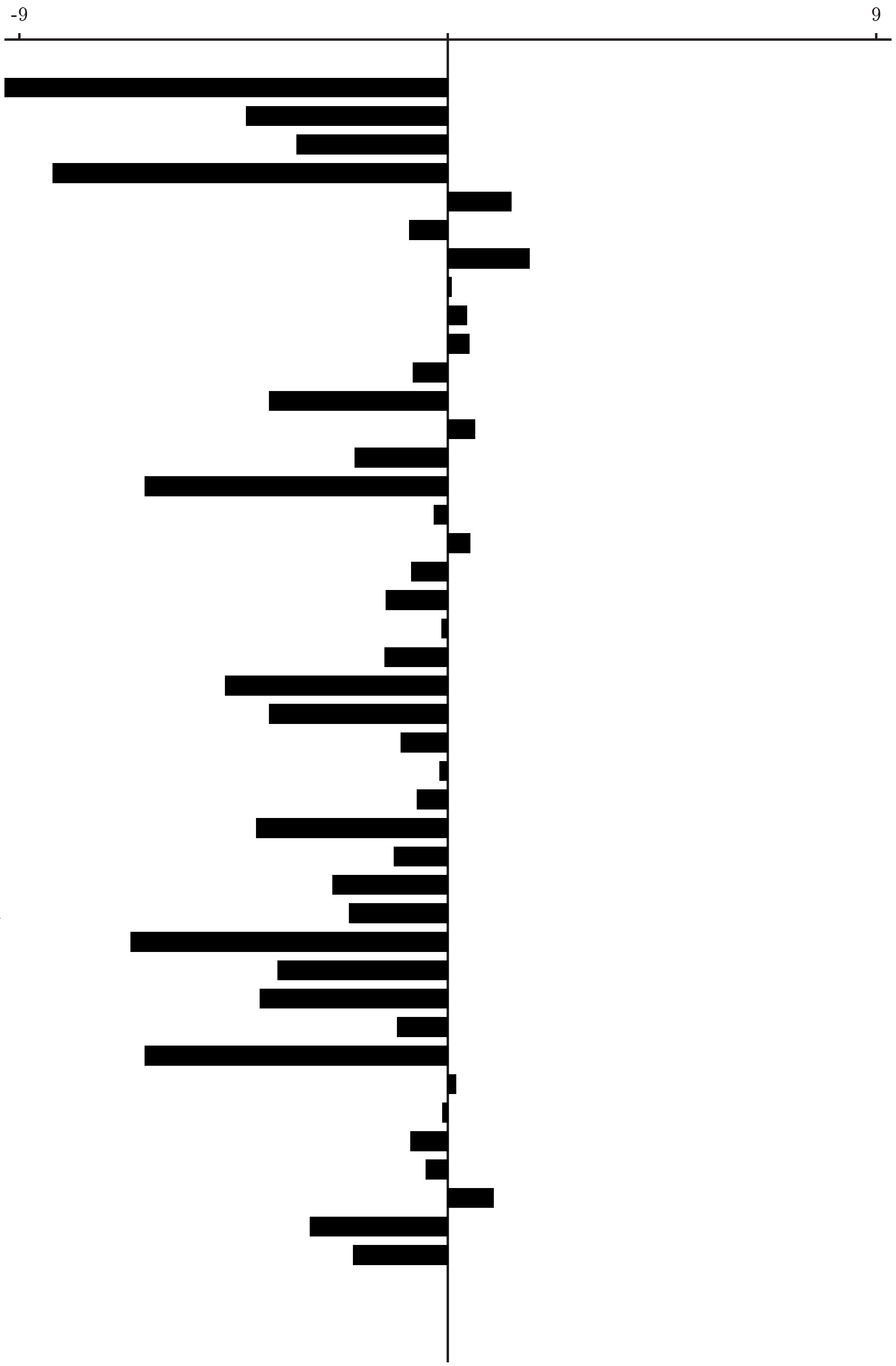
PS00016 - RGD;PATTERN. Cell attachment sequence.

R-G-D



PS00016 RGD;PATTERN. Cell attachment sequence.

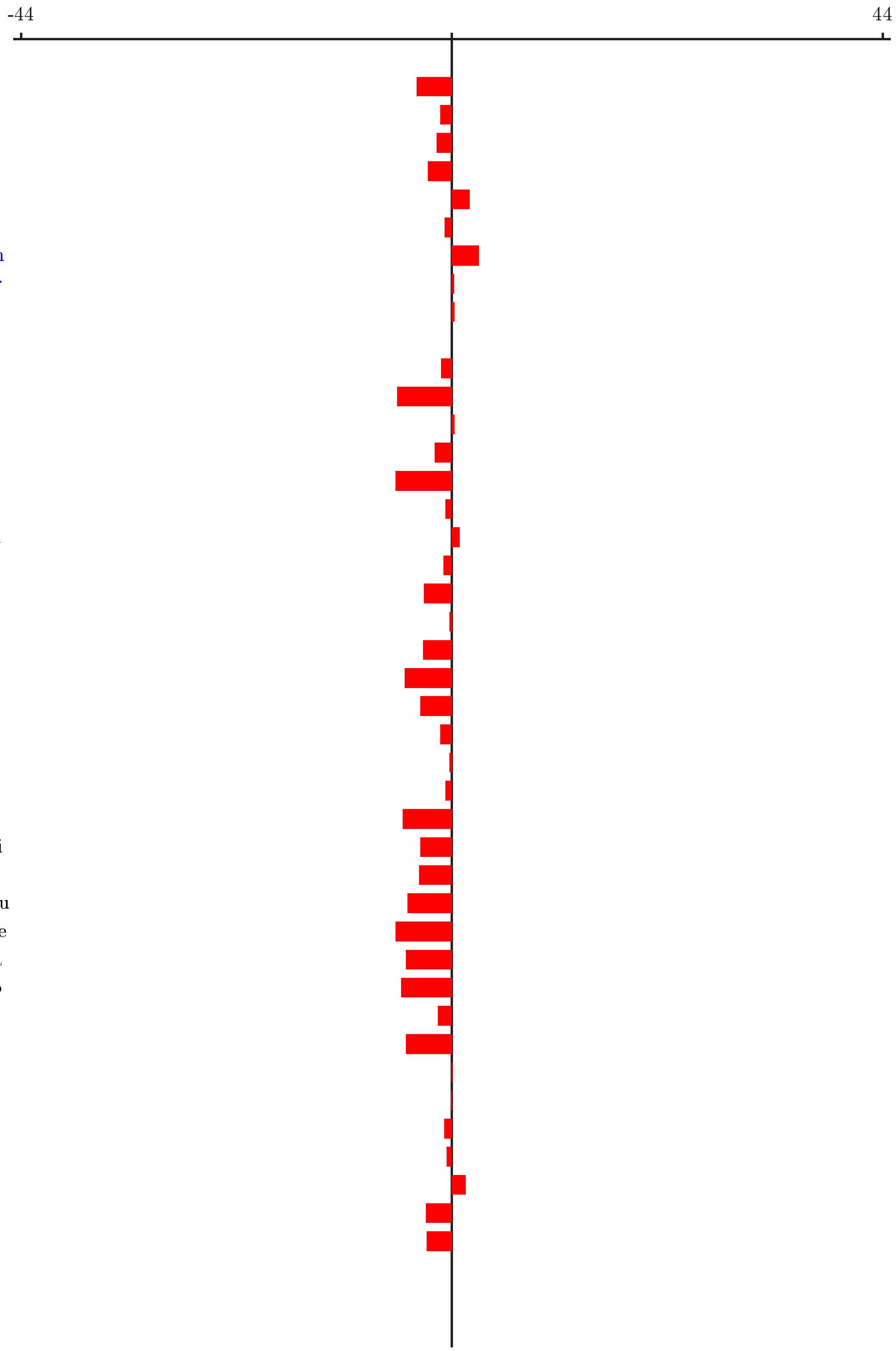
R-G-D




| | | |
|---|---|---|
| dros-mela | 1187.45 | 883 |
| caen-eleg | 1124.24 | 987 |
| sacc-cere | 375.28 | 316 |
| arab-thal | 2104.73 | 1738 |
| aero-pern | 163.23 | 184 |
| arch-fulg | 134.95 | 125 |
| meth-jann | 67.31 | 84 |
| meth-ther | 168.11 | 173 |
| pyro-abys | 102.87 | 105 |
| pyro-hori | 92.28 | 96 |
| halo-nrc1 | 309.74 | 292 |
| ther-acid | 103.86 | 68 |
| aqui-aeol | 69.83 | 74 |
| baci-halo | 200.05 | 170 |
| baci-subt | 180.22 | 102 |
| borr-burg | 28.23 | 26 |
| buch-aphi | 16.72 | 18 |
| camp-jeju | 44.69 | 39 |
| chla-muri | 44.33 | 34 |
| chla-pneu | 46.59 | 45 |
| chla-trac | 43.40 | 33 |
| dein-radi | 327.35 | 247 |
| esch-coli | 288.99 | 228 |
| haem-infl | 78.23 | 69 |
| heli-2pyl | 46.81 | 45 |
| heli-Jpyl | 47.36 | 47 |
| lact-lact | 82.98 | 49 |
| myco-geni | 12.43 | 8 |
| myco-lepr | 180.51 | 149 |
| myco-pneu | 22.81 | 13 |
| myco-tube | 557.93 | 409 |
| neis-mena | 129.41 | 91 |
| neis-menb | 129.13 | 87 |
| past-mult | 95.17 | 82 |
| pseu-aeru | 634.32 | 482 |
| rick-prow | 24.79 | 25 |
| syne-cyan | 192.26 | 190 |
| ther-mari | 110.88 | 102 |
| trep-pall | 81.88 | 77 |
| urea-urea | 14.81 | 18 |
| vibr-chol | 191.57 | 153 |
| xyla-fast | 200.56 | 170 |

PS00016 - RGD;PATTERN. Cell attachment sequence.

R-G-D

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| meth-ther | 168.11 | 173 |
| pyro-abys | 102.87 | 105 |
| pyro-hori | 92.28 | 96 |
| halo-nrc1 | 309.74 | 292 |
| ther-acid | 103.86 | 68 |
| aqui-aeol | 69.83 | 74 |
| baci-halo | 200.05 | 170 |
| baci-subt | 180.22 | 102 |
| borr-burg | 28.23 | 26 |
| buch-aphi | 16.72 | 18 |
| camp-jeju | 44.69 | 39 |
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| chla-trac | 43.40 | 33 |
| dein-radi | 327.35 | 247 |
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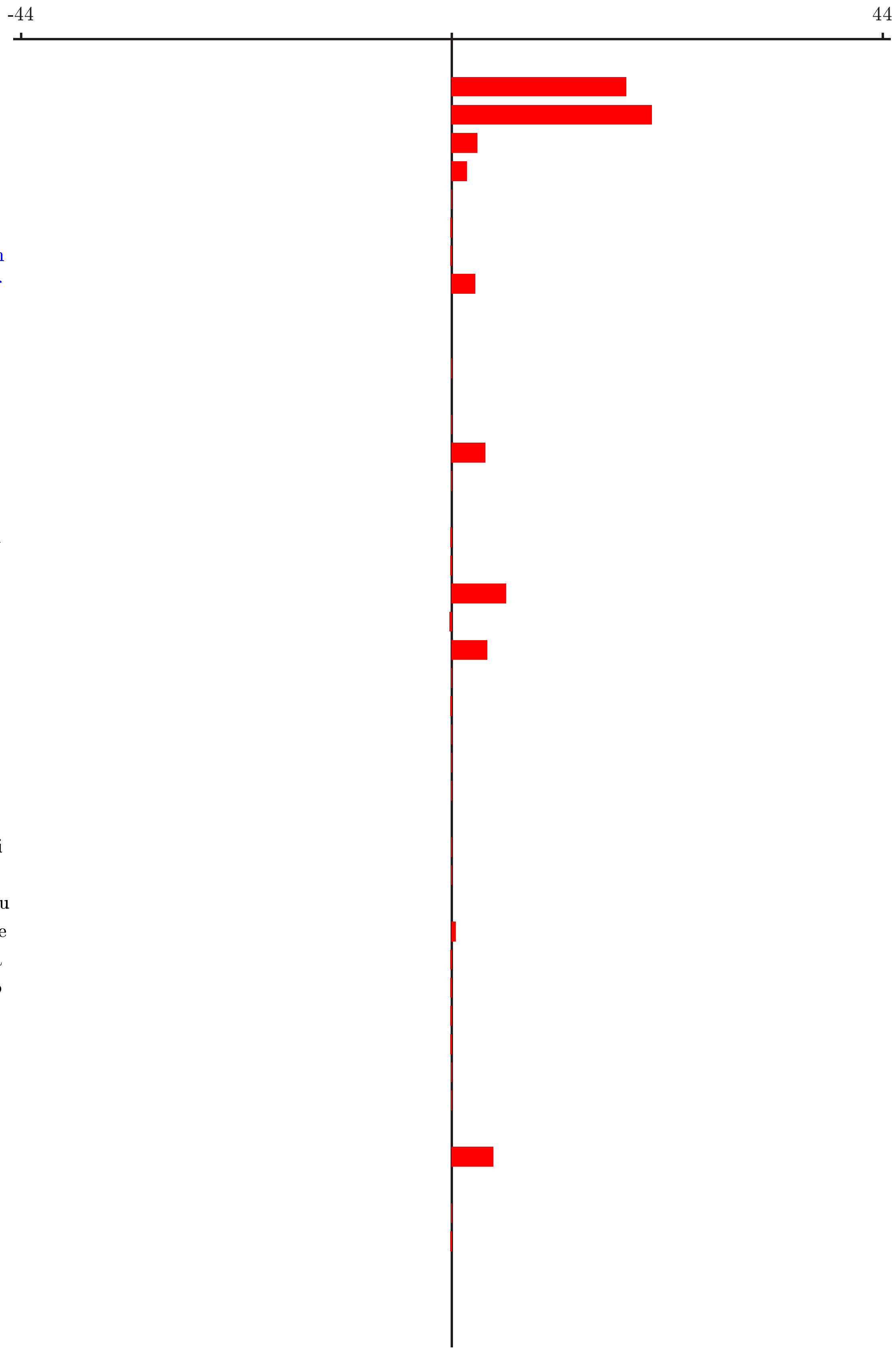
| haem-infl | 78.23 | 69 |
| heli-2pyl | 46.81 | 45 |
| heli-Jpyl | 47.36 | 47 |
| lact-lact | 82.98 | 49 |
| myco-geni | 12.43 | 8 |
| myco-lepr | 180.51 | 149 |
| myco-pneu | 22.81 | 13 |
| myco-tube | 557.93 | 409 |
| neis-mena | 129.41 | 91 |
| neis-menb | 129.13 | 87 |
| past-mult | 95.17 | 82 |
| pseu-aeru | 634.32 | 482 |
| rick-prow | 24.79 | 25 |
| syne-cyan | 192.26 | 190 |
| ther-mari | 110.88 | 102 |
| trep-pall | 81.88 | 77 |
| urea-urea | 14.81 | 18 |
| vibr-chol | 191.57 | 153 |
| xyla-fast | 200.56 | 170 |

PS00022 - EGF-1;PATTERN. EGF-like domain signature 1.

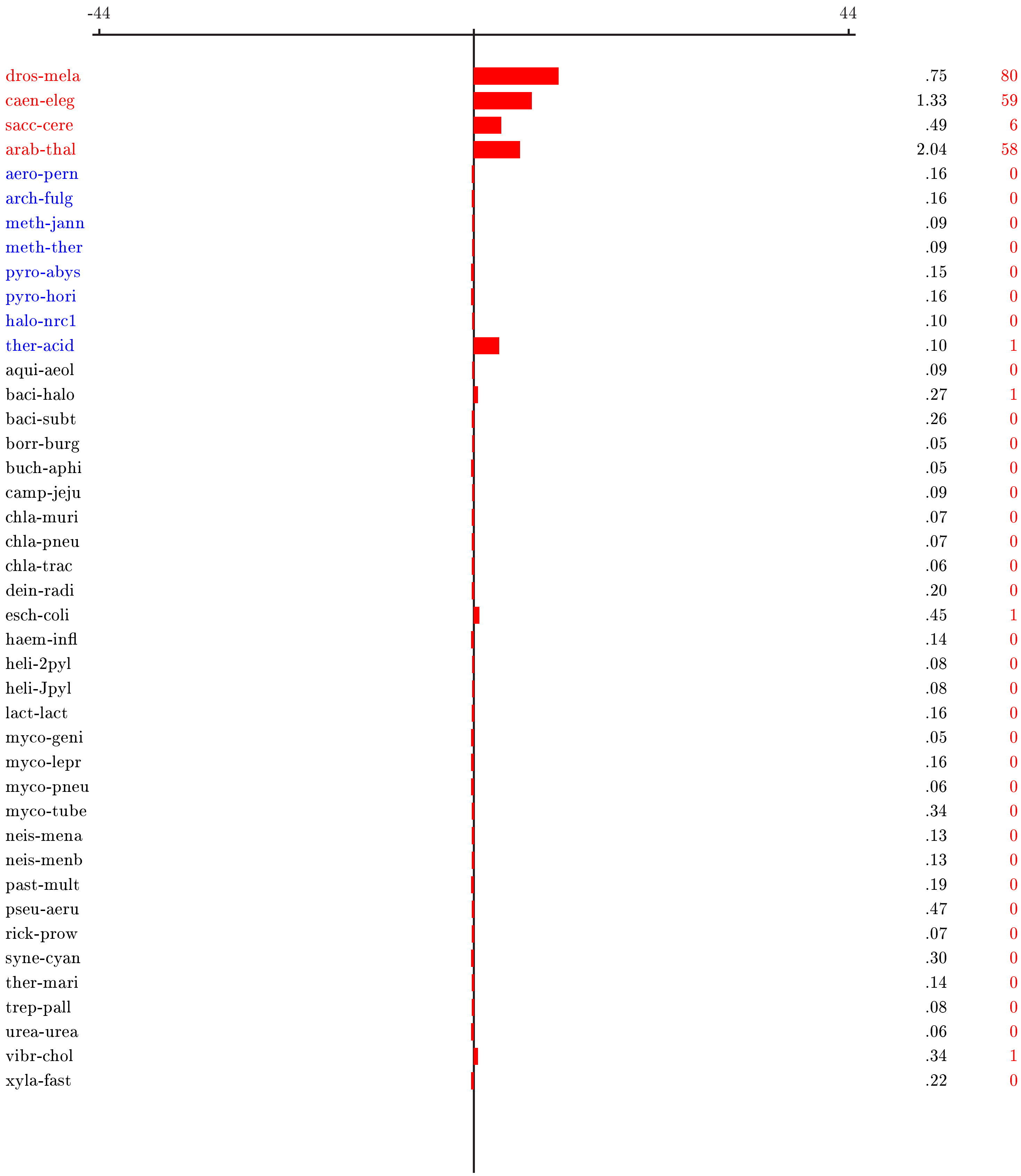
C-x-C-x(5)-G-x(2)-C




| | | |
|---|---|---|
| dros-mela | 2.71 | 280 |
| caen-eleg | 3.67 | 430 |
| sacc-cere | .32 | 4 |
| arab-thal | 4.48 | 13 |
| aero-pern | .05 | 0 |
| arch-fulg | .08 | 0 |
| meth-jann | .07 | 0 |
| meth-ther | .07 | 1 |
| pyro-abys | .01 | 0 |
| pyro-hori | .01 | 0 |
| halo-nrc1 | .02 | 0 |
| ther-acid | .01 | 0 |
| aqui-aeol | .02 | 0 |
| baci-halo | .03 | 2 |
| baci-subt | .04 | 0 |
| borr-burg | .01 | 0 |
| buch-aphi | .02 | 0 |
| camp-jeju | .05 | 0 |
| chla-muri | .09 | 2 |
| chla-pneu | .09 | 0 |
| chla-trac | .09 | 1 |
| dein-radi | .03 | 0 |
| esch-coli | .16 | 0 |
| haem-infl | .04 | 0 |
| heli-2pyl | .04 | 0 |
| heli-Jpyl | .04 | 0 |
| lact-lact | .00 | 0 |
| myco-geni | .00 | 0 |
| myco-lepr | .04 | 0 |
| myco-pneu | .01 | 0 |
| myco-tube | .09 | 1 |
| neis-mena | .05 | 0 |
| neis-menb | .05 | 0 |
| past-mult | .06 | 0 |
| pseu-aeru | .16 | 0 |
| rick-prow | .02 | 0 |
| syne-cyan | .08 | 0 |
| ther-mari | .01 | 0 |
| trep-pall | .17 | 2 |
| urea-urea | .00 | 0 |
| vibr-chol | .09 | 0 |
| xyla-fast | .10 | 0 |

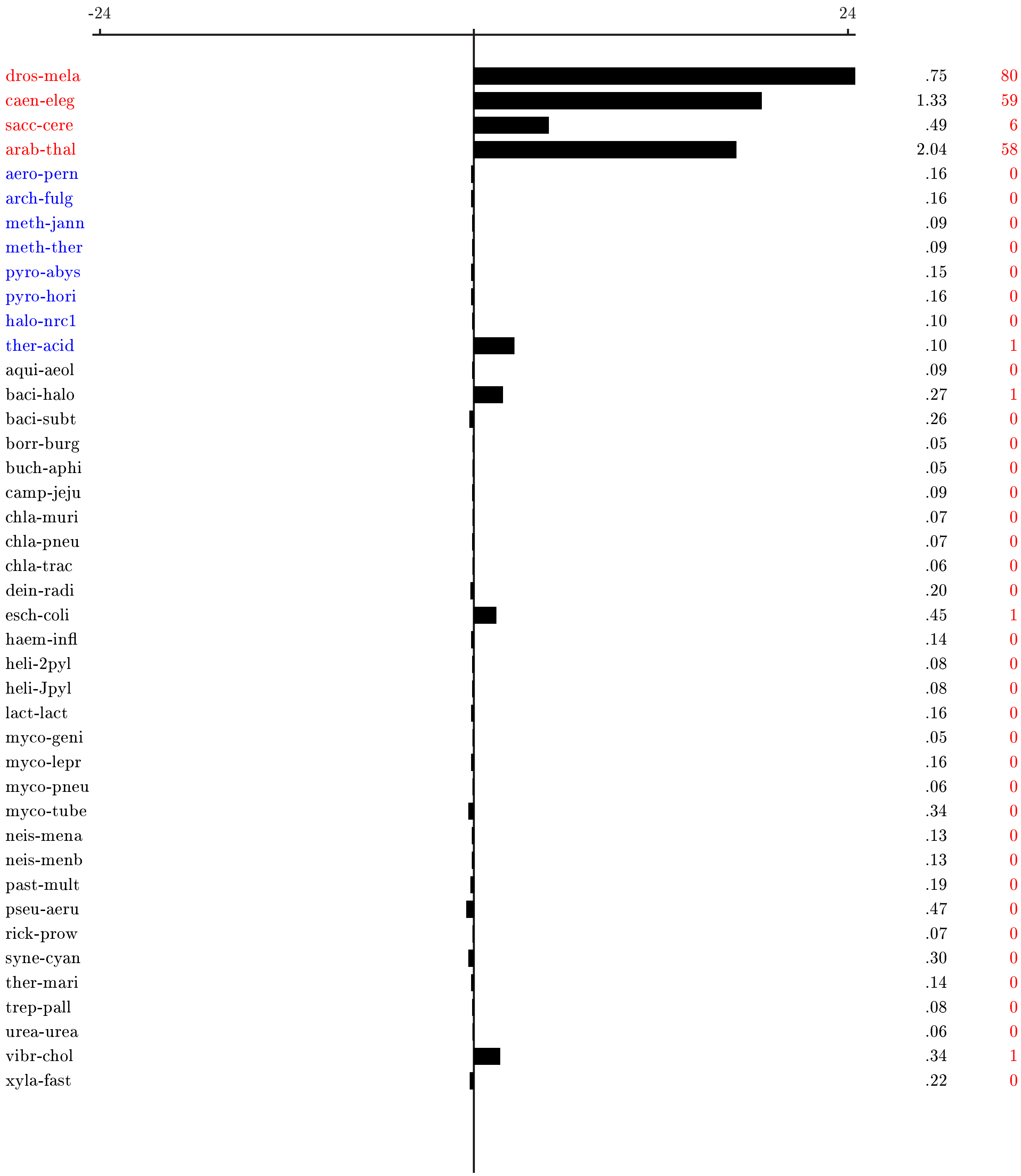
PS00027 - HOMEOBOX-1;PATTERN. 'Homeobox' domain signature.

[LIVMFYG]-[ASLVR]-x(2)-[LIVSTACN]-x-[LIVM]-x(4)-[LIV]-[RKNQESTAIY]-[LIVFSTNKH]-W-[FYVC]-x-[NDQTAH]-x(5)-[RKNAIMW]

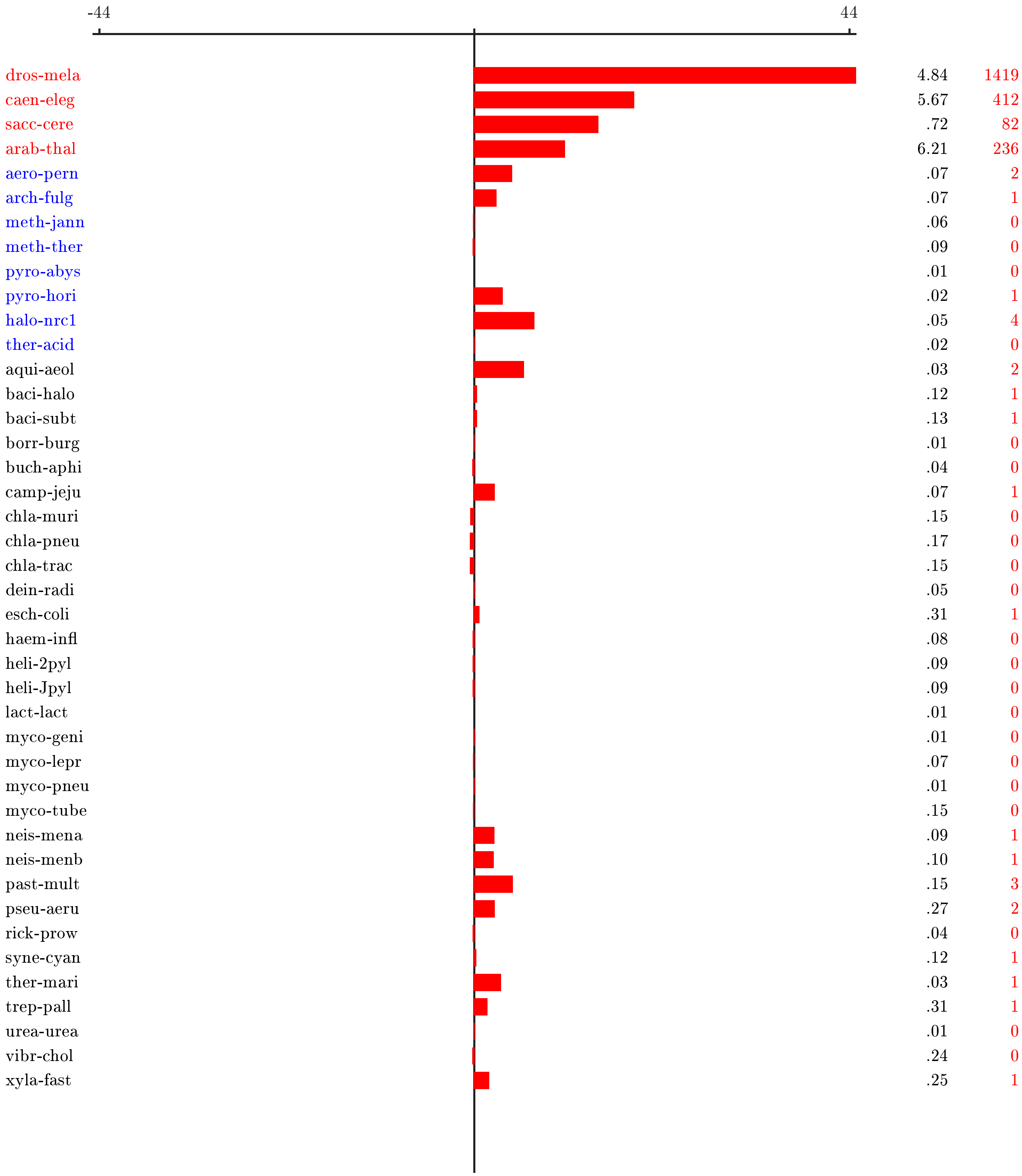


PS00027 HOMEOBOX-1;PATTERN. 'Homeobox' domain signature.

[LIVMFYG]-[ASLVR]-x(2)-[LIVSTACN]-x-[LIVM]-x(4)-[LIV]-[RKNQESTAIY]-[LIVFSTNKH]-W-[FYVC]-x-[NDQTAH]-x(5)-[RKNAIMW]

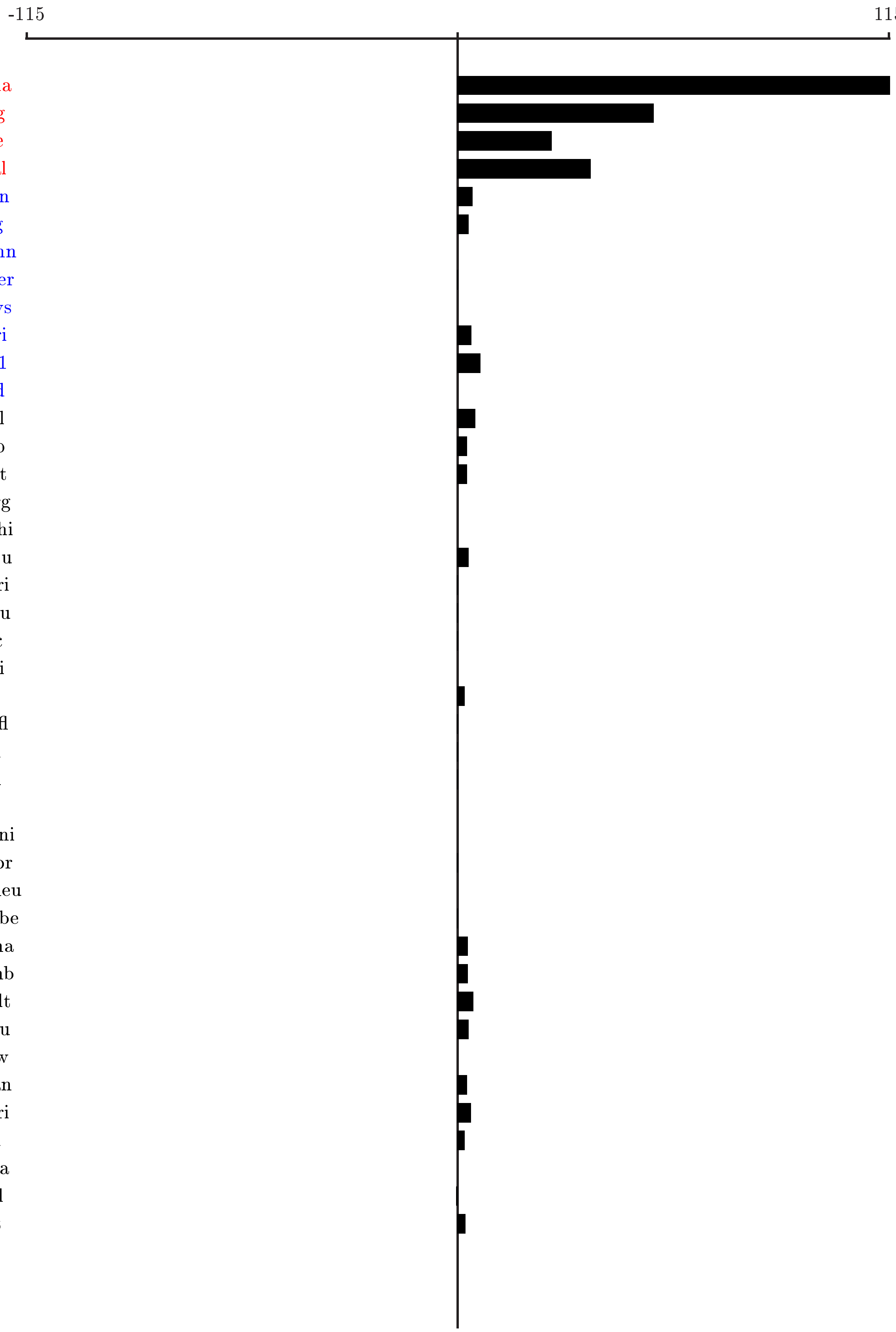


PS00028 - ZINC-FINGER-C2H2;PATTERN. Zinc finger, C2H2 type, domain.
C-x(2,4)-C-x(3)-[LIVMFYWC]-x(8)-H-x(3,5)-H



PS00028 ZINC-FINGER-C2H2;PATTERN. Zinc finger, C2H2 type, domain.

C-x(2,4)-C-x(3)-[LIVMFYWC]-x(8)-H-x(3,5)-H




| | | |
|---|---|---|
| dros-mela | 4.84 | 1419 |
| caen-eleg | 5.67 | 412 |
| sacc-cere | .72 | 82 |
| arab-thal | 6.21 | 236 |
| aero-pern | .07 | 2 |
| arch-fulg | .07 | 1 |
| meth-jann | .06 | 0 |
| meth-ther | .09 | 0 |
| pyro-abys | .01 | 0 |
| pyro-hori | .02 | 1 |
| halo-nrc1 | .05 | 4 |
| ther-acid | .02 | 0 |
| aqui-aeol | .03 | 2 |
| baci-halo | .12 | 1 |
| baci-subt | .13 | 1 |
| borr-burg | .01 | 0 |
| buch-aphi | .04 | 0 |
| camp-jeju | .07 | 1 |
| chla-muri | .15 | 0 |
| chla-pneu | .17 | 0 |
| chla-trac | .15 | 0 |
| dein-radi | .05 | 0 |
| esch-coli | .31 | 1 |
| haem-infl | .08 | 0 |
| heli-2pyl | .09 | 0 |
| heli-Jpyl | .09 | 0 |
| lact-lact | .01 | 0 |
| myco-geni | .01 | 0 |
| myco-lepr | .07 | 0 |
| myco-pneu | .01 | 0 |
| myco-tube | .15 | 0 |
| neis-mena | .09 | 1 |
| neis-menb | .10 | 1 |
| past-mult | .15 | 3 |
| pseu-aeru | .27 | 2 |
| rick-prow | .04 | 0 |
| syne-cyan | .12 | 1 |
| ther-mari | .03 | 1 |
| trep-pall | .31 | 1 |
| urea-urea | .01 | 0 |
| vibr-chol | .24 | 0 |
| xyla-fast | .25 | 1 |

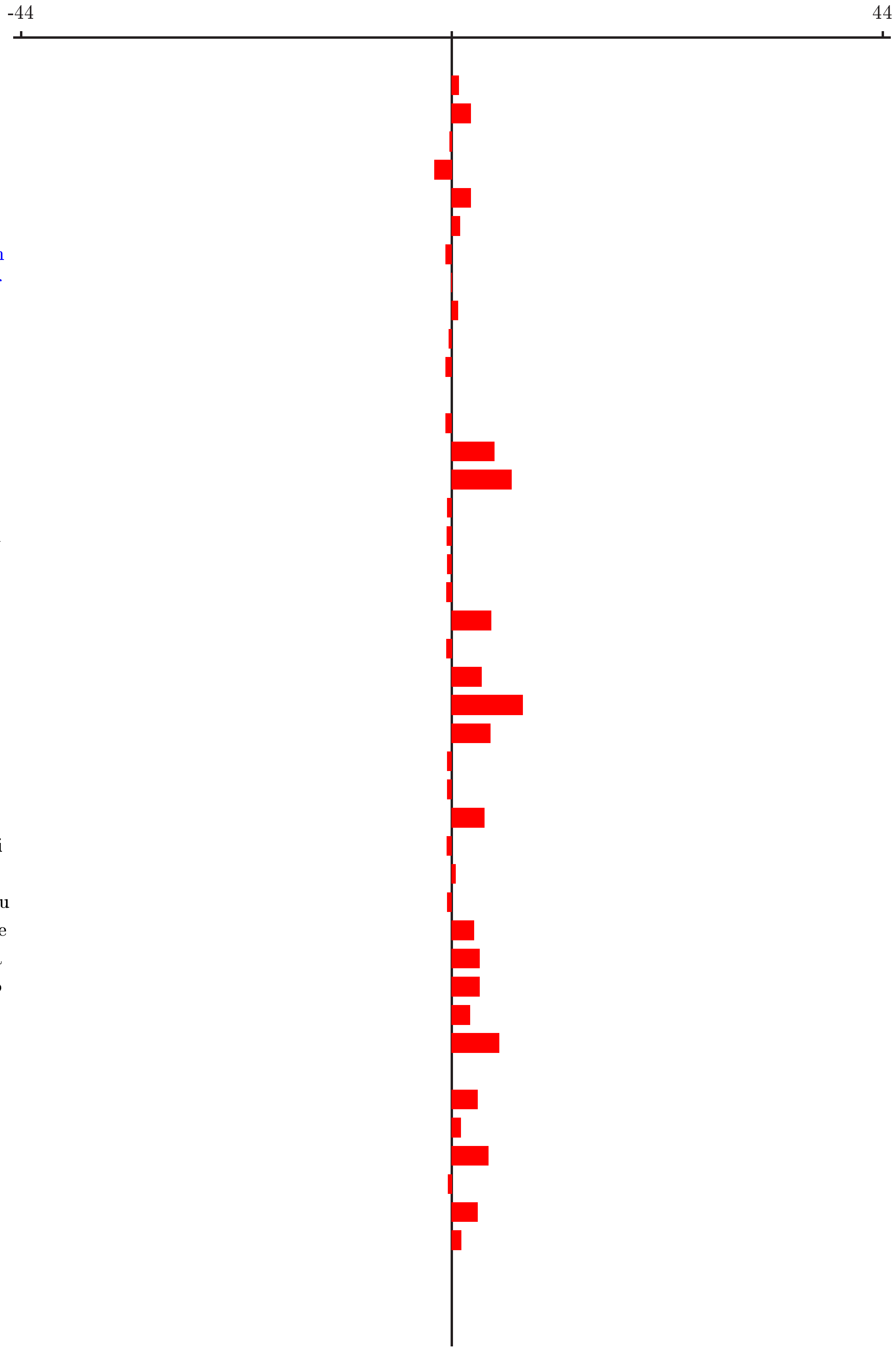
PS00039 - DEAD-ATP-HELICASE;PATTERN. AD-box subfamily ATP-dependent helicases signature.

[LIVMF](2)-D-E-A-D-[RKEN]-x-[LIVMFYGSTN]


| | | |
|---|---|---|
| dros-mela | .68 | 23 |
| caen-eleg | .92 | 23 |
| sacc-cere | .40 | 20 |
| arab-thal | 1.47 | 28 |
| aero-pern | .06 | 1 |
| arch-fulg | .16 | 2 |
| meth-jann | .13 | 1 |
| meth-ther | .14 | 2 |
| pyro-abys | .11 | 0 |
| pyro-hori | .09 | 1 |
| halo-nrc1 | .28 | 0 |
| ther-acid | .09 | 2 |
| aqui-aeol | .09 | 0 |
| baci-halo | .22 | 3 |
| baci-subt | .22 | 3 |
| borr-burg | .06 | 0 |
| buch-aphi | .02 | 1 |
| camp-jeju | .11 | 0 |
| chla-muri | .04 | 0 |
| chla-pneu | .04 | 0 |
| chla-trac | .04 | 0 |
| dein-radi | .12 | 1 |
| esch-coli | .20 | 6 |
| haem-infl | .09 | 3 |
| heli-2pyl | .08 | 0 |
| heli-Jpyl | .08 | 0 |
| lact-lact | .13 | 1 |
| myco-geni | .02 | 0 |
| myco-lepr | .09 | 2 |
| myco-pneu | .03 | 0 |
| myco-tube | .18 | 4 |
| neis-mena | .10 | 2 |
| neis-menb | .10 | 2 |
| past-mult | .10 | 3 |
| pseu-aeru | .32 | 6 |
| rick-prow | .04 | 0 |
| syne-cyan | .13 | 2 |
| ther-mari | .12 | 0 |
| trep-pall | .04 | 1 |
| urea-urea | .04 | 0 |
| vibr-chol | .17 | 10 |
| xyla-fast | .09 | 3 |

PS00043 - HTH-GNTR-FAMILY;PATTERN. Bacterial regulatory proteins, gntR family signature.

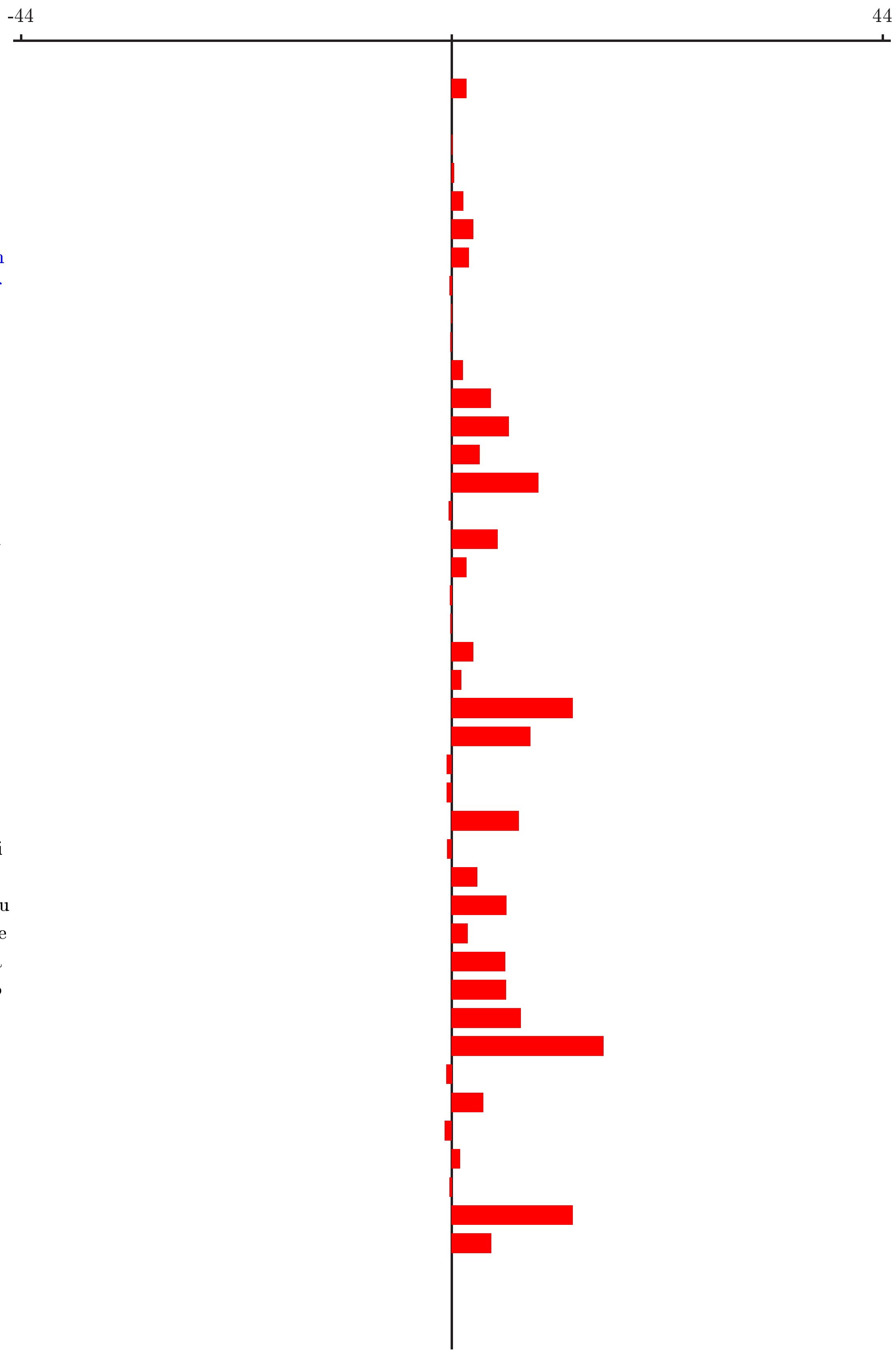
[LIVAPKR]-[PILV]-x-[EQTIVMR]-x(2)-[LIVM]-x(3)-[LIVMFYK]-x-[LIVFT]-[DNGSTK]-[RGTLV]-x-[STAIVP]-[LIVA]-x(2)-[STAGV]-[LIVMFYH]-x(2)-[LMA]




| | | |
|---|---|---|
| dros-mela | 1.41 | 2 |
| caen-eleg | 2.07 | 9 |
| sacc-cere | .74 | 0 |
| arab-thal | 3.37 | 2 |
| aero-pern | .72 | 2 |
| arch-fulg | .54 | 1 |
| meth-jann | .31 | 0 |
| meth-ther | .39 | 0 |
| pyro-abys | .52 | 1 |
| pyro-hori | .55 | 0 |
| halo-nrc1 | .40 | 0 |
| ther-acid | .32 | 0 |
| aqui-aeol | .33 | 0 |
| baci-halo | .77 | 8 |
| baci-subt | .71 | 11 |
| borr-burg | .16 | 0 |
| buch-aphi | .09 | 0 |
| camp-jeju | .23 | 0 |
| chla-muri | .19 | 0 |
| chla-pneu | .21 | 2 |
| chla-trac | .19 | 0 |
| dein-radi | .74 | 4 |
| esch-coli | .95 | 17 |
| haem-infl | .32 | 3 |
| heli-2pyl | .22 | 0 |
| heli-Jpyl | .22 | 0 |
| lact-lact | .41 | 3 |
| myco-geni | .08 | 0 |
| myco-lepr | .56 | 1 |
| myco-pneu | .10 | 0 |
| myco-tube | 1.14 | 4 |
| neis-mena | .33 | 2 |
| neis-menb | .31 | 2 |
| past-mult | .45 | 2 |
| pseu-aeru | 1.29 | 13 |
| rick-prow | .20 | 0 |
| syne-cyan | .67 | 4 |
| ther-mari | .45 | 1 |
| trep-pall | .25 | 2 |
| urea-urea | .09 | 0 |
| vibr-chol | .76 | 4 |
| xyla-fast | .54 | 1 |

PS00044 - HTH-LYSR-FAMILY;PATTERN. Bacterial regulatory proteins, lysR family signature.

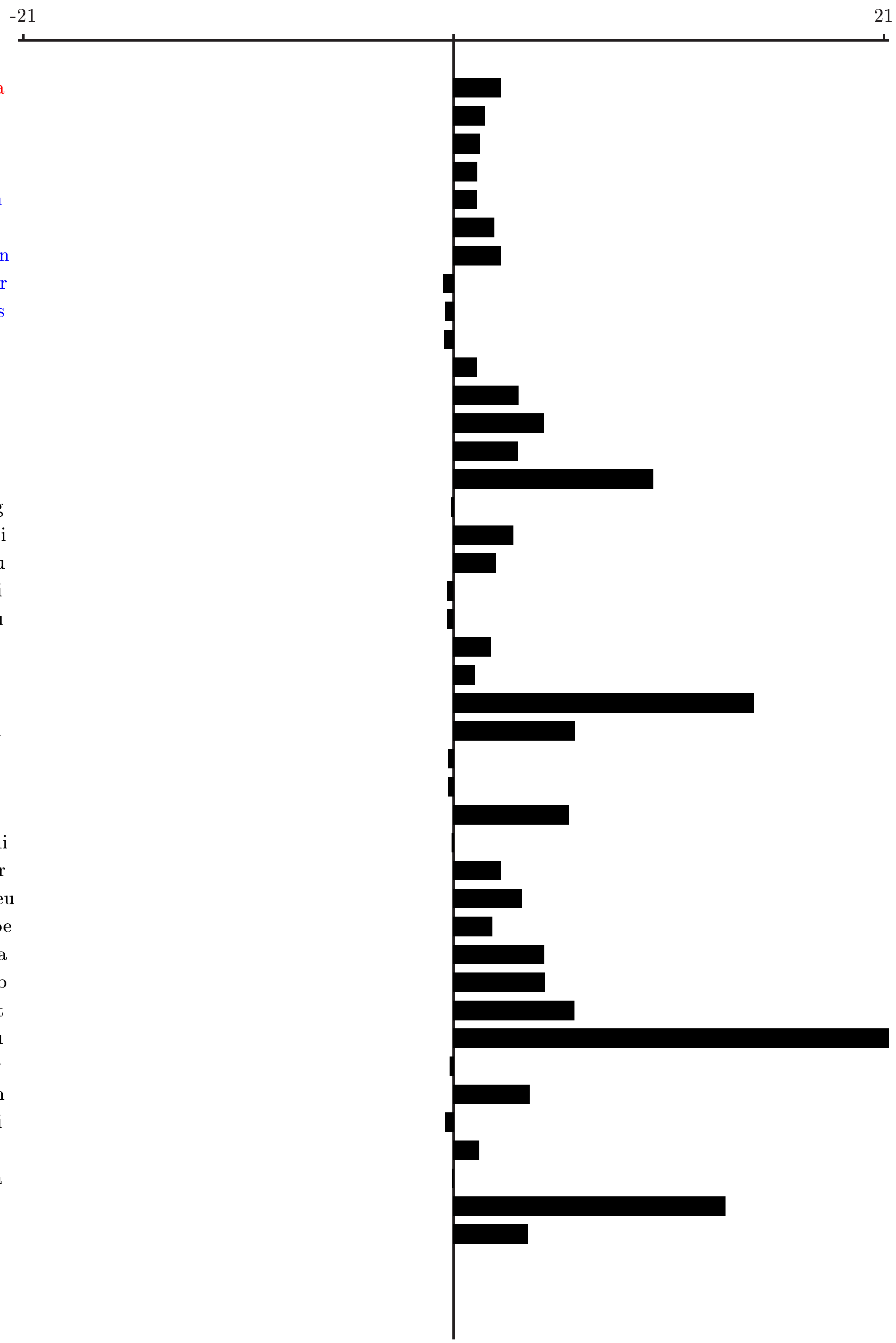
[NQKRHSTAG]-[LIVMFYTA]-x(2)-[STAGLV]-[STAG]-x(4)-[LIVMYCTQR]-[PSTANLVER]-x-[PSTAGQV]-[PSTAGNVMF]-[LIVMFA]-[STAGH]-x(2)-[LIVMF]-x(2)-[LIVMFW]-[RKEAV]-x(2)-[LIVMFYNTAE]-x(3)-[LIMVT]




| | | |
|---|---|---|
| dros-mela | 2.96 | 7 |
| caen-eleg | 3.50 | 6 |
| sacc-cere | 1.10 | 2 |
| arab-thal | 5.69 | 8 |
| aero-pern | 1.23 | 2 |
| arch-fulg | .61 | 2 |
| meth-jann | .16 | 1 |
| meth-ther | .49 | 0 |
| pyro-abys | .40 | 0 |
| pyro-hori | .45 | 0 |
| halo-nrc1 | 1.23 | 2 |
| ther-acid | .40 | 3 |
| aqui-aeol | .24 | 4 |
| baci-halo | 1.07 | 5 |
| baci-subt | .99 | 21 |
| borr-burg | .10 | 0 |
| buch-aphi | .06 | 1 |
| camp-jeju | .22 | 1 |
| chla-muri | .28 | 0 |
| chla-pneu | .28 | 0 |
| chla-trac | .28 | 1 |
| dein-radi | 2.04 | 3 |
| esch-coli | 1.73 | 45 |
| haem-infl | .46 | 8 |
| heli-2pyl | .25 | 0 |
| heli-Jpyl | .25 | 0 |
| lact-lact | .57 | 8 |
| myco-geni | .08 | 0 |
| myco-lepr | 1.33 | 4 |
| myco-pneu | .14 | 2 |
| myco-tube | 3.57 | 7 |
| neis-mena | .64 | 6 |
| neis-menb | .62 | 6 |
| past-mult | .65 | 9 |
| pseu-aeru | 2.81 | 89 |
| rick-prow | .16 | 0 |
| syne-cyan | 1.05 | 6 |
| ther-mari | .40 | 0 |
| trep-pall | .55 | 1 |
| urea-urea | .06 | 0 |
| vibr-chol | 1.33 | 36 |
| xyla-fast | 1.11 | 6 |

PS00044 HTH-LYSR-FAMILY;PATTERN. Bacterial regulatory proteins, lysR family signature.

[NQKRHSTAG]-[LIVMFYTA]-x(2)-[STAGLV]-[STAG]-x(4)-[LIVMYCTQR]-[PSTANLVER]-x-[PSTAGQV]-[PSTAGNVMF]-[LIVMFA]-[STAGH]-x(2)-[LIVMF]-x(2)-[LIVMFW]-[RKEAV]-x(2)-[LIVMFYNTAE]-x(3)-[LIMVT]




| | | |
|---|---|---|
| dros-mela | 2.96 | 7 |
| caen-eleg | 3.50 | 6 |
| sacc-cere | 1.10 | 2 |
| arab-thal | 5.69 | 8 |
| aero-pern | 1.23 | 2 |
| arch-fulg | .61 | 2 |
| meth-jann | .16 | 1 |
| meth-ther | .49 | 0 |
| pyro-abys | .40 | 0 |
| pyro-hori | .45 | 0 |
| halo-nrc1 | 1.23 | 2 |
| ther-acid | .40 | 3 |
| aqui-aeol | .24 | 4 |
| baci-halo | 1.07 | 5 |
| baci-subt | .99 | 21 |
| borr-burg | .10 | 0 |
| buch-aphi | .06 | 1 |
| camp-jeju | .22 | 1 |
| chla-muri | .28 | 0 |
| chla-pneu | .28 | 0 |
| chla-trac | .28 | 1 |
| dein-radi | 2.04 | 3 |
| esch-coli | 1.73 | 45 |
| haem-infl | .46 | 8 |
| heli-2pyl | .25 | 0 |
| heli-Jpyl | .25 | 0 |
| lact-lact | .57 | 8 |
| myco-geni | .08 | 0 |
| myco-lepr | 1.33 | 4 |
| myco-pneu | .14 | 2 |
| myco-tube | 3.57 | 7 |
| neis-mena | .64 | 6 |
| neis-menb | .62 | 6 |
| past-mult | .65 | 9 |
| pseu-aeru | 2.81 | 89 |
| rick-prow | .16 | 0 |
| syne-cyan | 1.05 | 6 |
| ther-mari | .40 | 0 |
| trep-pall | .55 | 1 |
| urea-urea | .06 | 0 |
| vibr-chol | 1.33 | 36 |
| xyla-fast | 1.11 | 6 |

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