

# Projet REGULON

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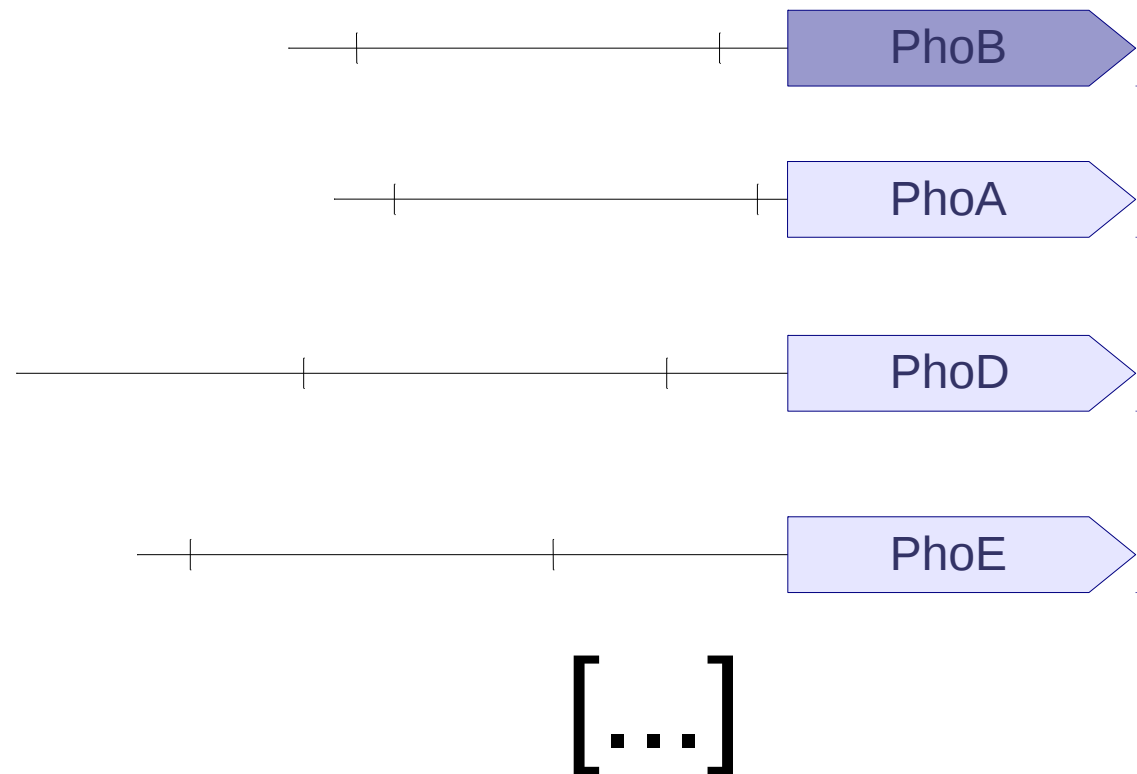
Mélissa Cardon – Nika Abdollahi

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14 décembre 2016  
M2 BIM – GENOM  
UPMC

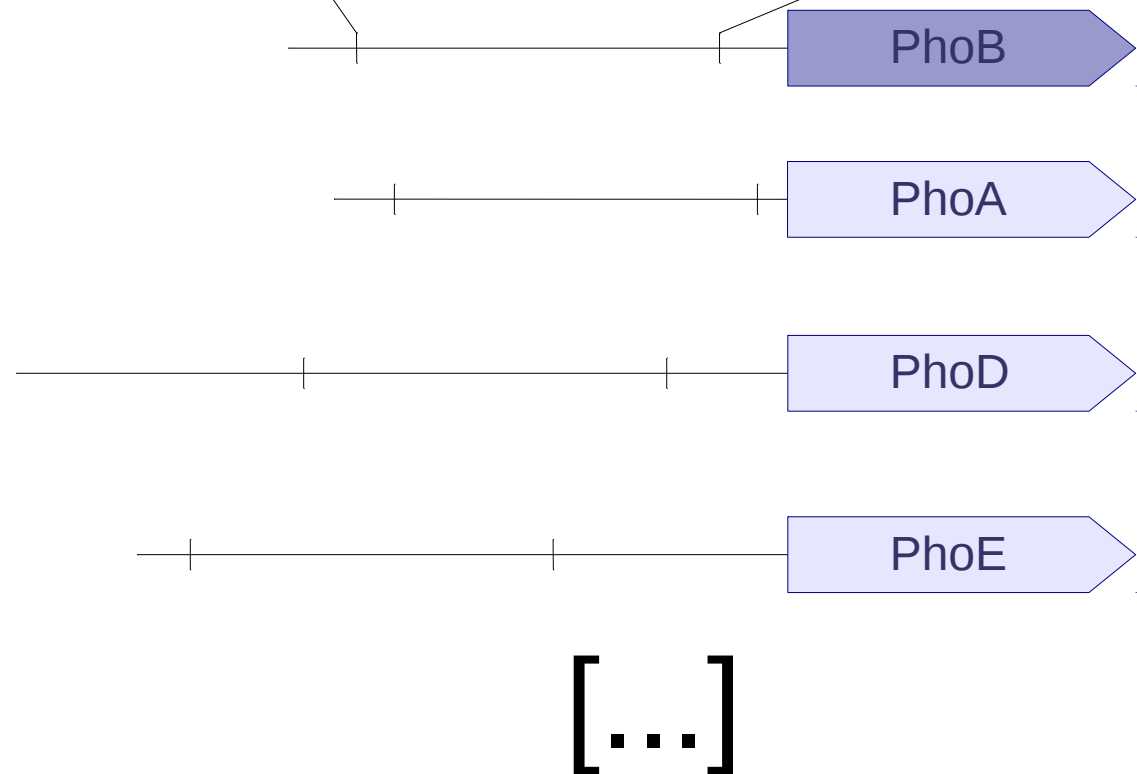
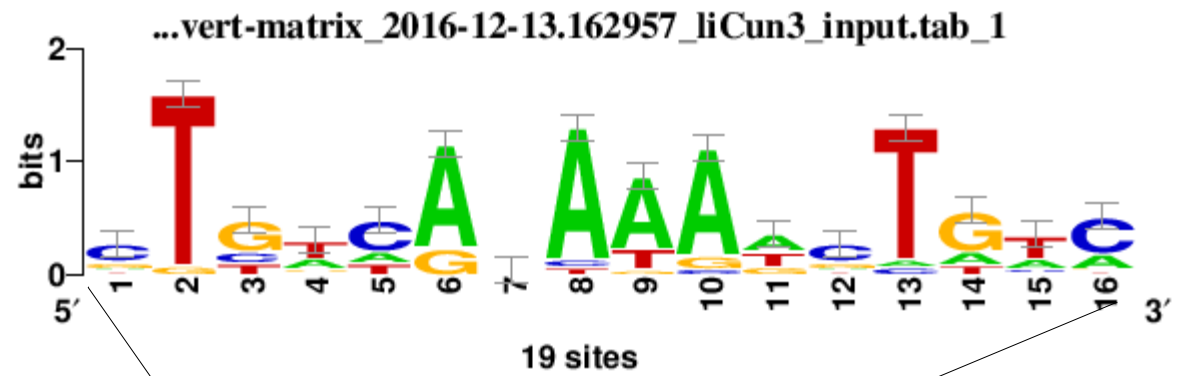
# Régulon Pho

Pst-PhoR

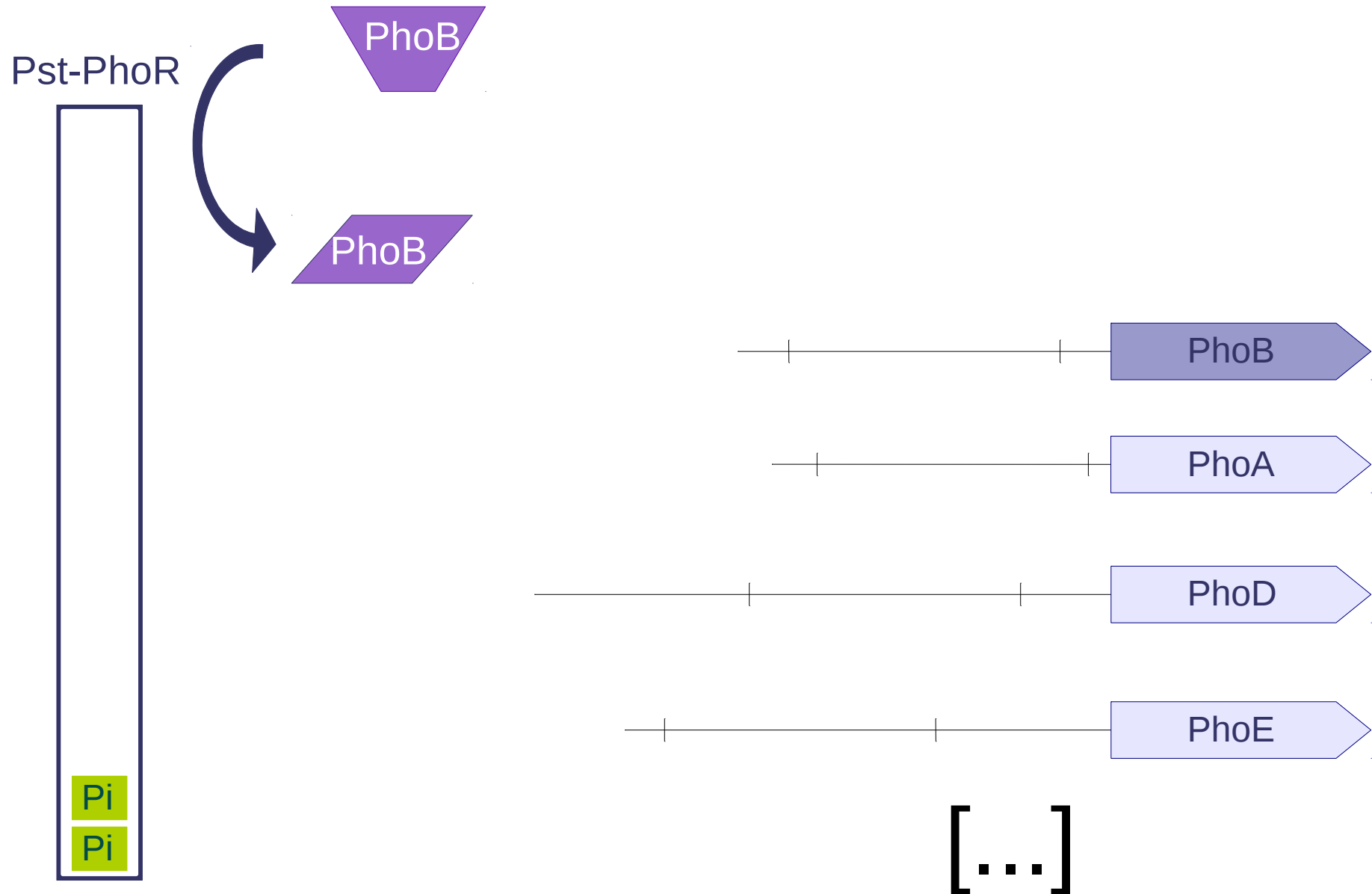


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Pst-PhoR

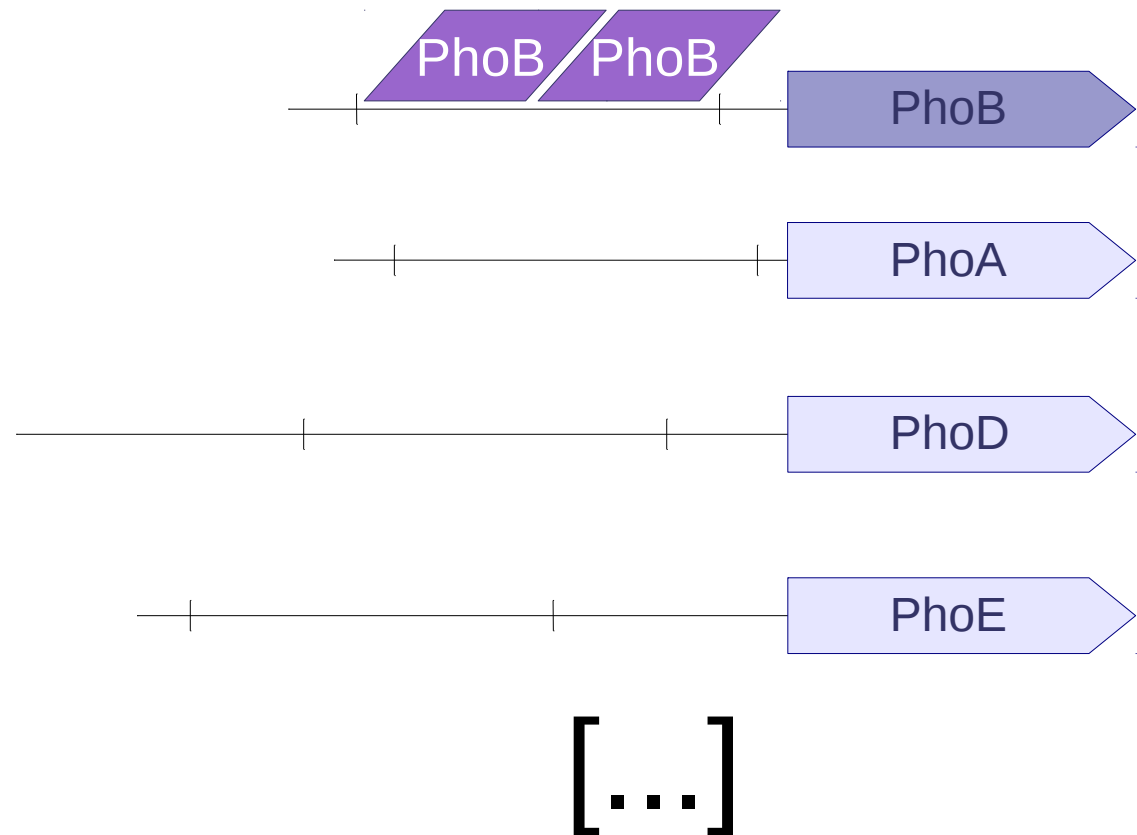


# Régulon Pho

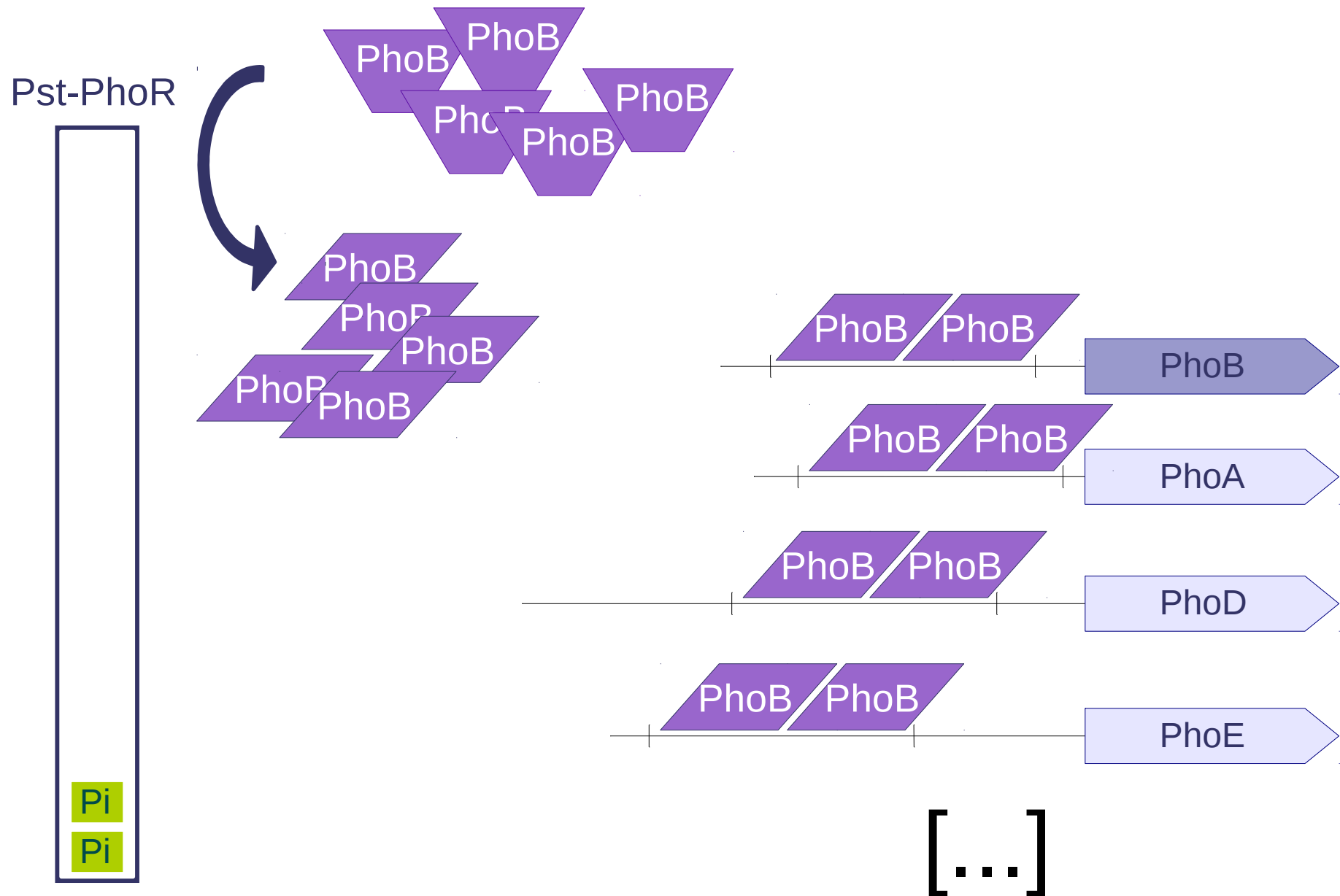


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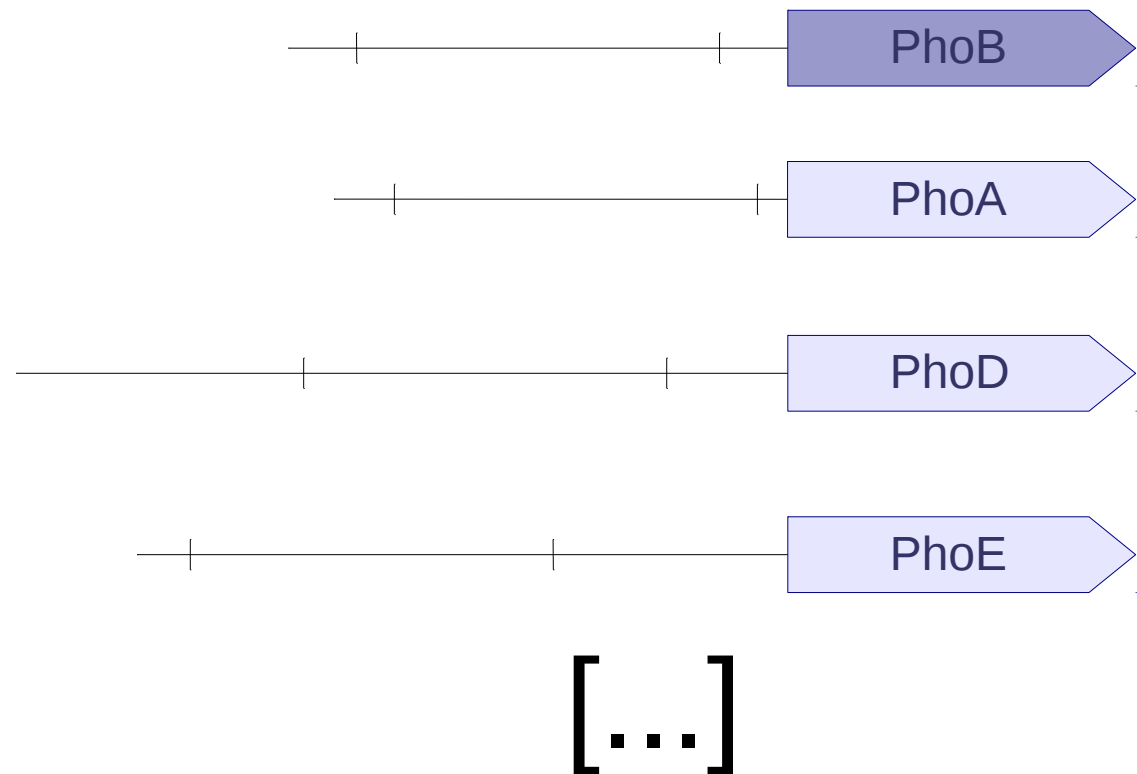
Pst-PhoR



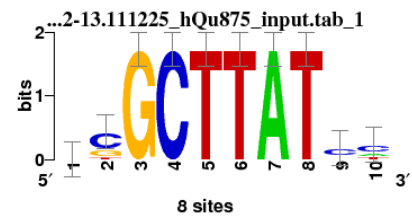
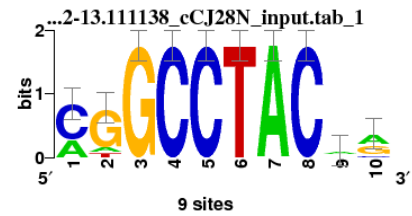
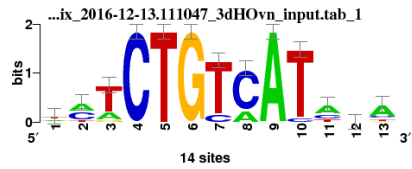
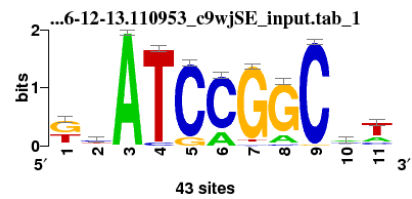
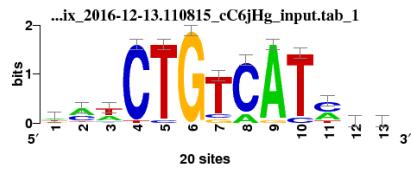
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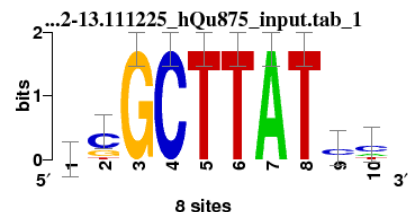
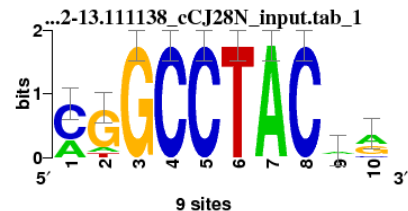
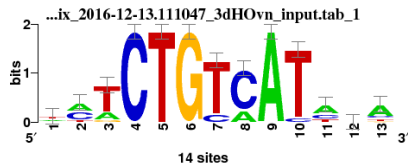
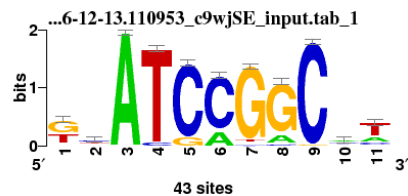
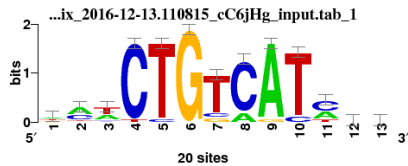
## Base de données (86 FT)





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- Alignement Local Smith-Waterman
- Plusieurs métriques :



Pearson correlation  
coefficient (PCC)

$$PCC(X, Y) = \frac{\sum_{b=A}^T (f_X(b) - \bar{f}_X) \cdot (f_Y(b) - \bar{f}_Y)}{\sqrt{\sum_{b=A}^T (f_X(b) - \bar{f}_X)^2 \cdot \sum_{b=A}^T (f_Y(b) - \bar{f}_Y)^2}}$$

Chi-square (pCS)  
(1-p-value of)

$$\chi^2_3(X, Y) = \sum_{K=\{X,Y\}} \sum_{b=A}^T \frac{(n_K(b) - n_K^e(b))^2}{n_K^e(b)}$$

Average  
Kullback-Leibler (AKL)

$$AKL(X, Y) = 10 - \frac{\sum_{b=A}^T f_X(b) \cdot \log \frac{f_X(b)}{f_Y(b)} + \sum_{b=A}^T f_Y(b) \cdot \log \frac{f_Y(b)}{f_X(b)}}{2}$$

Sum of squared  
distances (SSD)

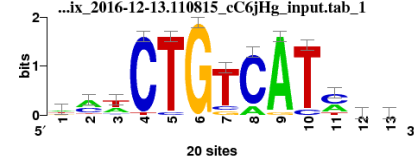
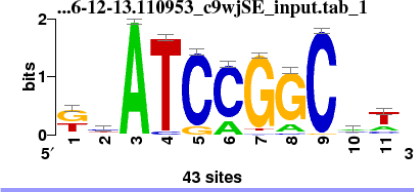
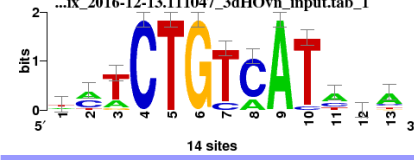
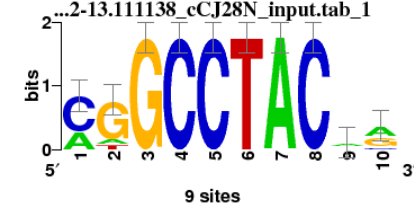
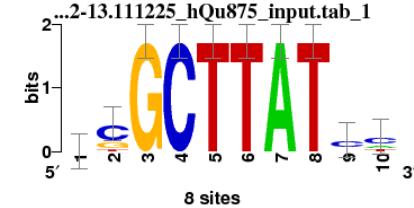
$$SSD(X, Y) = 2 - \sum_{b=A}^T (f_X(b) - f_Y(b))^2$$

Average log-likelihood  
ratio (ALLR)

$$ALLR(X, Y) = \frac{\sum_{b=A}^T n_X(b) \cdot \log \frac{f_Y(b)}{p_{ref}(b)} + \sum_{b=A}^T n_Y(b) \cdot \log \frac{f_X(b)}{p_{ref}(b)}}{\sum_{b=A}^T (n_X(b) + n_Y(b))}$$

ALLR with lower limit  
(ALLR\_LL)

Same as above, but a lower limit of -2 is  
imposed on the score (see text)

	PCC	SSD	AKL
 <p>...ix_2016-12-13.110815_cC6jHg_input.tab_1</p> <p>bits</p> <p>20 sites</p>	<b>PhoB</b> SlyA NarP RscB TorR ...	<b>CysB</b> OmpR ArgP CRP ArcA ...	<b>OmpR</b> XylR ArcA Fis PhoP ...
		PhoB : 57/86	PhoB : 42/86
 <p>...6-12-13.110953_c9wjSE_input.tab_1</p> <p>bits</p> <p>43 sites</p>	<b>SlyA</b> RelBReIE HipB MetR IclR ...	<b>FlhDC</b> CysB AraC HipB Dan ...	<b>PhoP</b> AscG Lrp RcsAB HNS ...
	PhoB : 38/86	PhoB : 52/86	PhoB : 27/86
 <p>...ix_2016-12-13.111047_3dHOvn_input.tab_1</p> <p>bits</p> <p>14 sites</p>	<b>PhoB</b> RcsB TorR HNS RelBReIE ...	<b>PhoB</b> CysB OmpR ArgP ArcA ...	<b>OmpR</b> CysB CRP ArcA XylR ...
			PhoB : 73/86
 <p>...2-13.111138_cCJ28N_input.tab_1</p> <p>bits</p> <p>9 sites</p>	<b>IHF</b> AsnC RstA NarP NanR ...	<b>NanR</b> EvgA NarP ModE NtrC ...	<b>EvgA</b> DeoR NtrC GadW SoxS ...
	PhoB : 62/86	PhoB : 38/86	PhoB : 53/86
 <p>...2-13.111225_hQu875_input.tab_1</p> <p>bits</p> <p>8 sites</p>	<b>ExuR</b> <b>NanR</b> RelBReIE DgsA HipB ...	<b>Nac</b> ModE ArgP GntR DnaA ...	<b>GntR</b> ModE Fur Nac Fis ...
	PhoB : 50/86	PhoB : 57/86	PhoB : 75/86

# Analyse de signaux

Base de données (304 PSSMs)



Matrice d'affinite



Methode de clustering : Affinity propagation

# Analyse de signaux

16 clusters

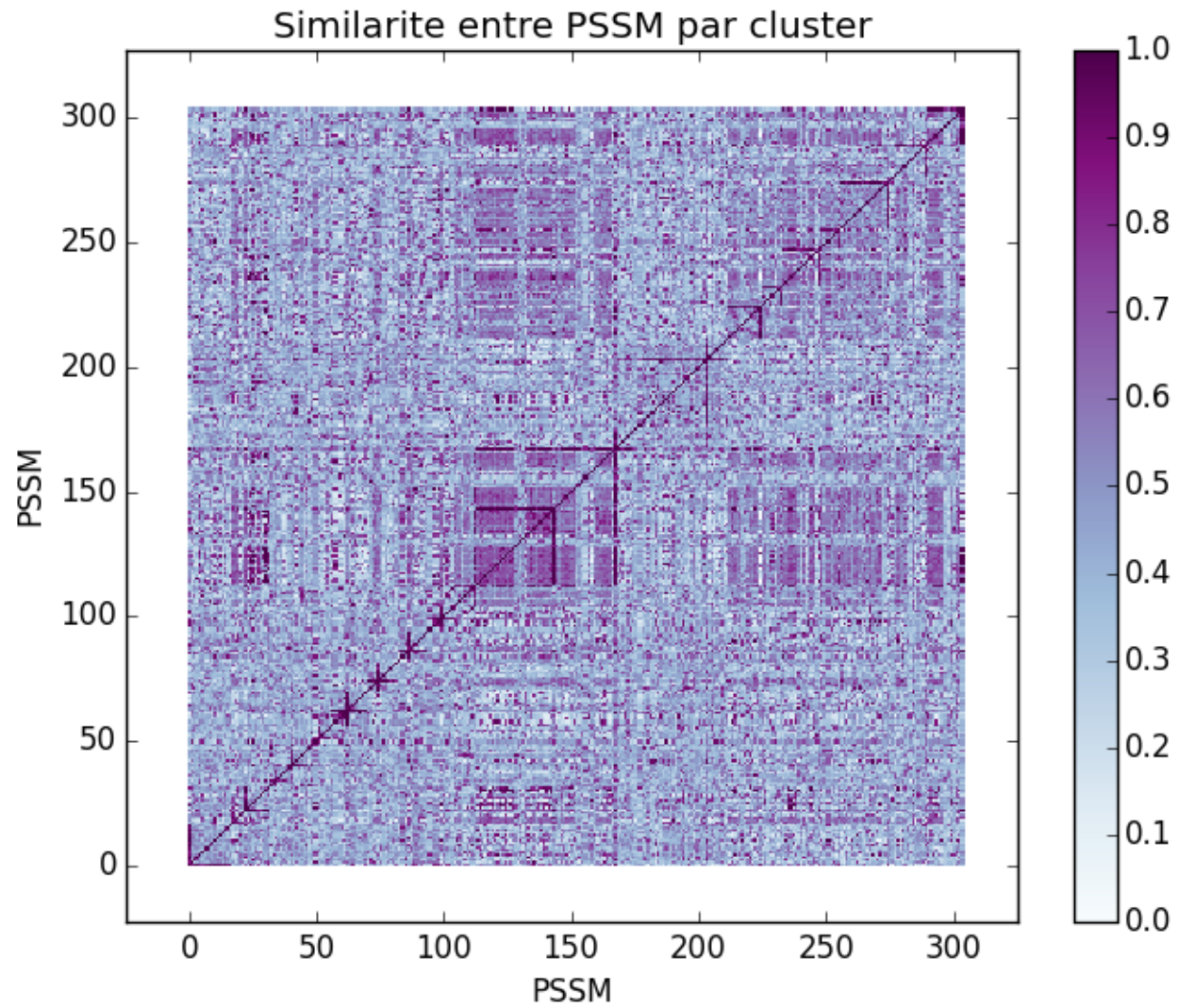


PhoB dans le meme cluster que  
PhoA, PhoX, PhoD, ArgR, Lrp, IHF, GadE, GcvA

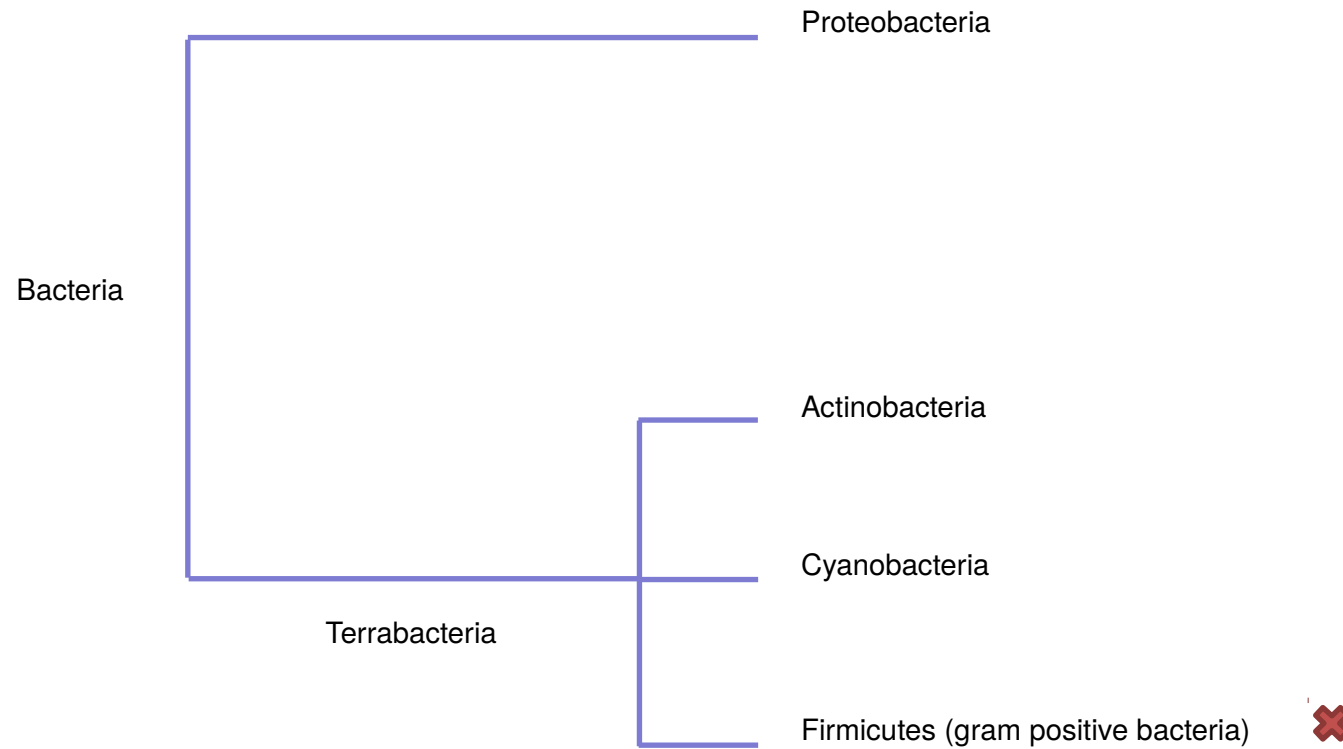
Séquences régulatrices  
-Actinobacteria  
-Cyanobacteria  
-Proteobacteria

Motifs facteurs de transcription *E. Coli*

# Similarite de signaux



# Conservation de signaux



Merci de votre attention