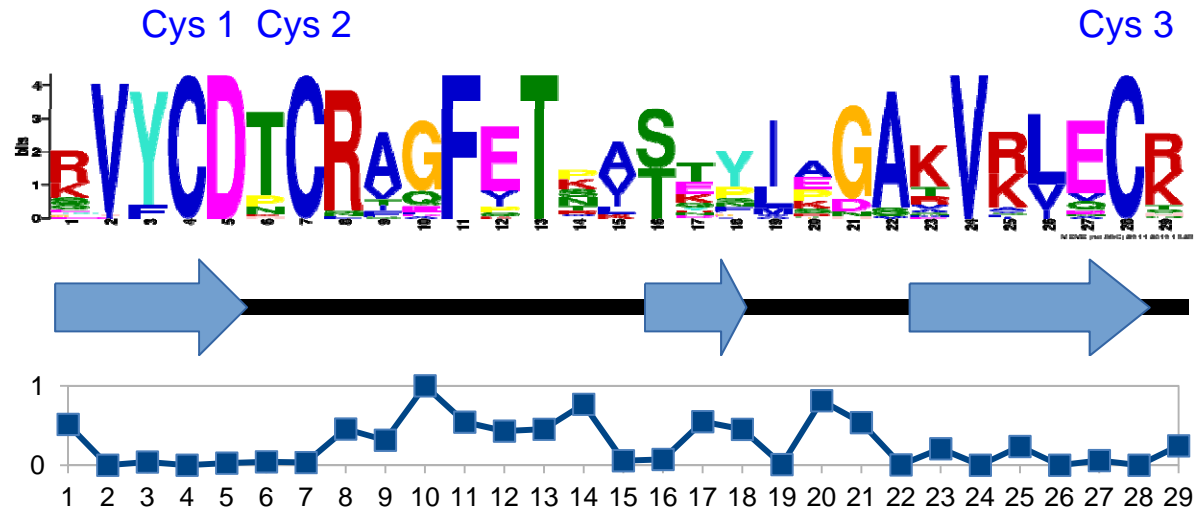


Supplementary file 12. Solvent accessibility and secondary structure for each residue and alignment of this information with the conserved sequence profiles of PAC domains for each clade.

The conserved motifs are described in Figures 7 and 8.

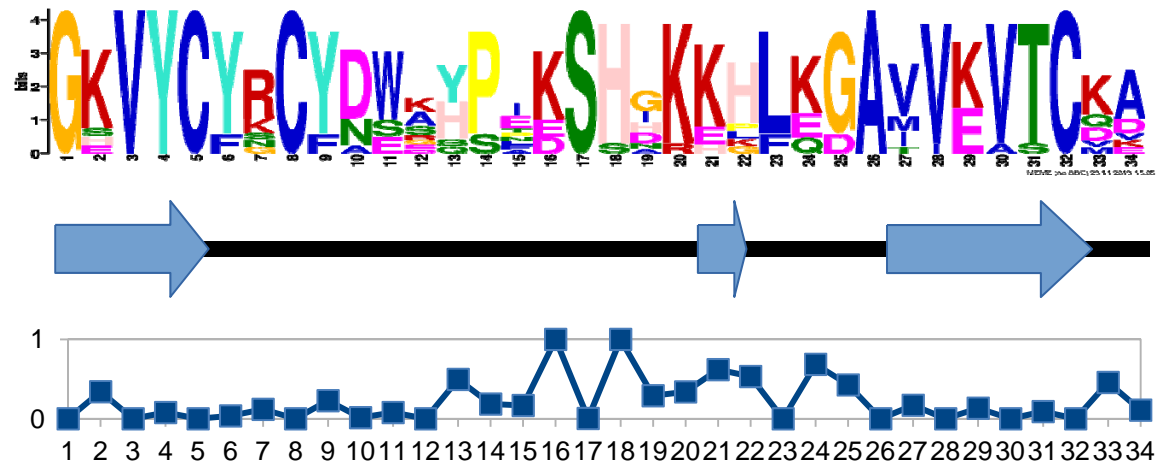
Clade A

46/49 sequences
4.7 e-809



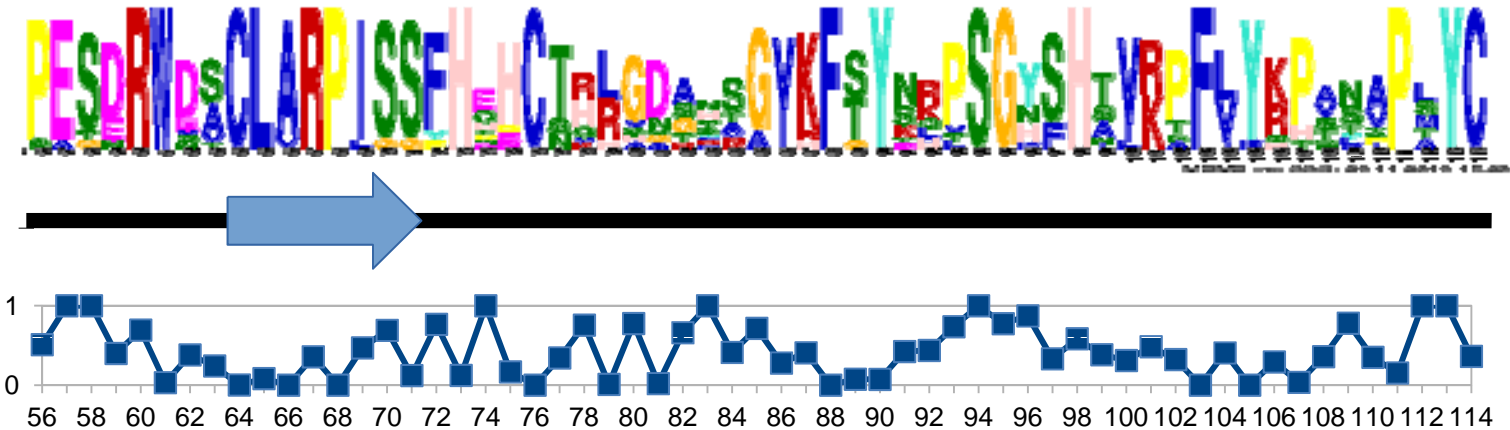
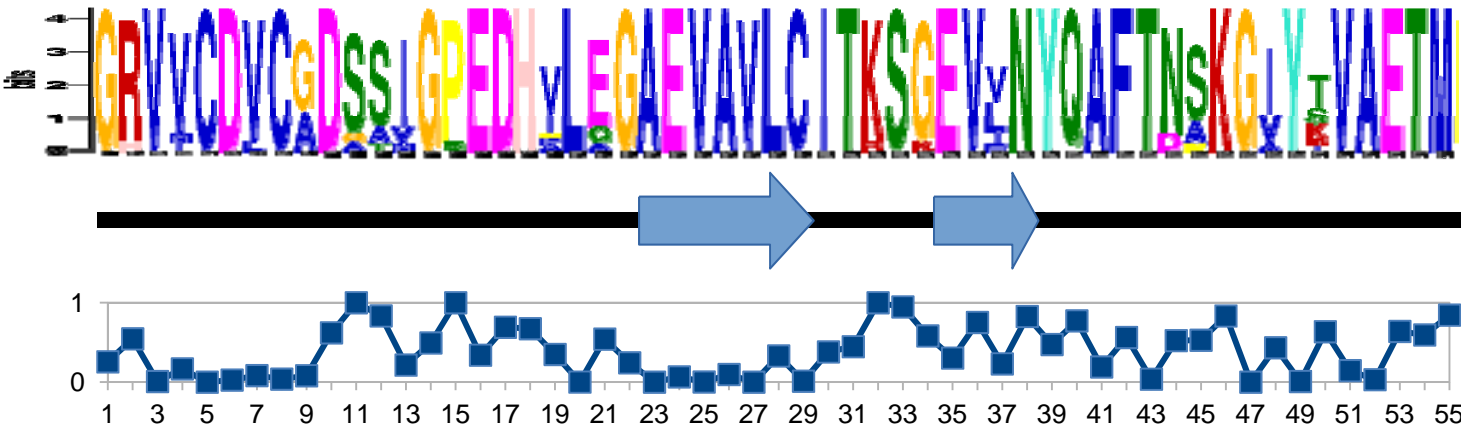
Clade B

12/12 sequences
7.8 e-176



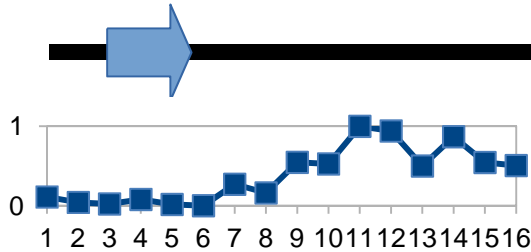
Clade C (highly conserved PAC domains)

14/14 sequences
4.5 e-1085



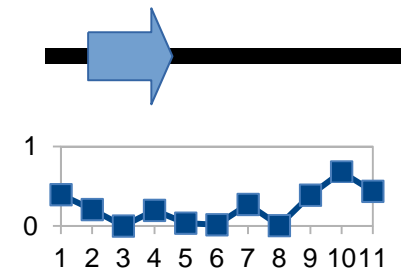
Clade D

11/11 sequences
5.2 e-090



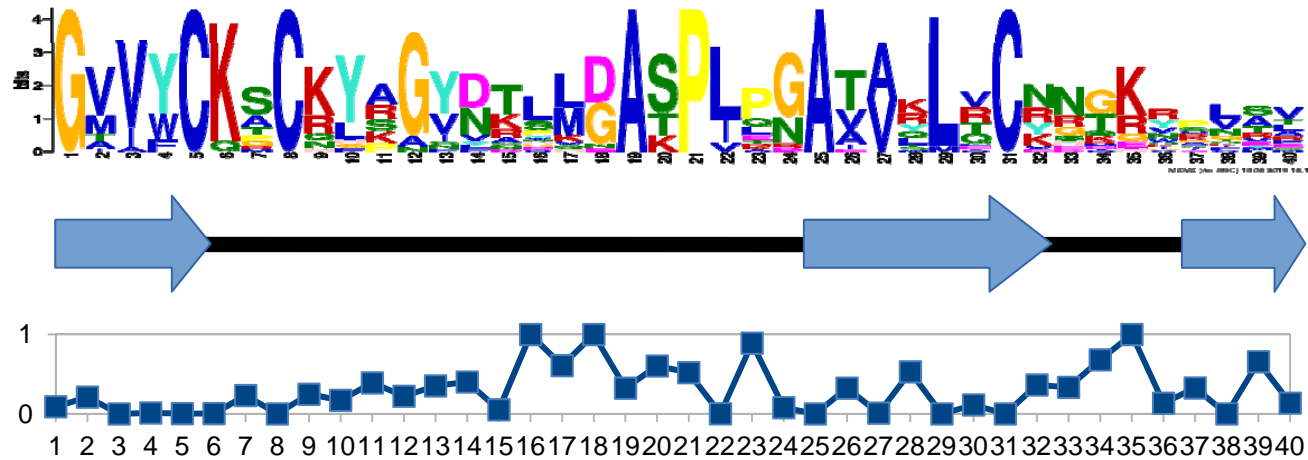
Clade E

19/19 sequences
6.0 e-112



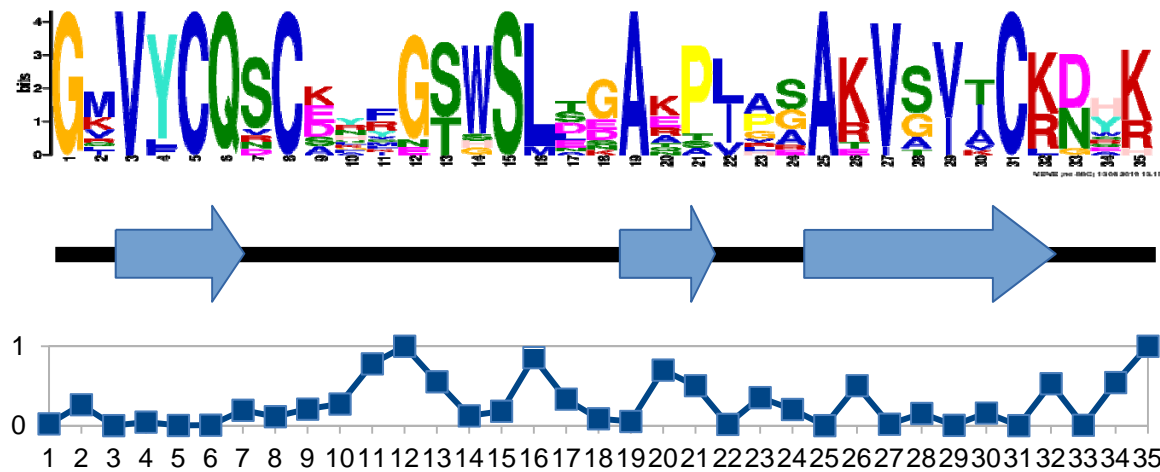
Clade G

23/24 sequences
1.6 e-355



Clade H

14/16 sequences
4.7 e-223



Clade I

8/8 sequences

3.8 e-124

