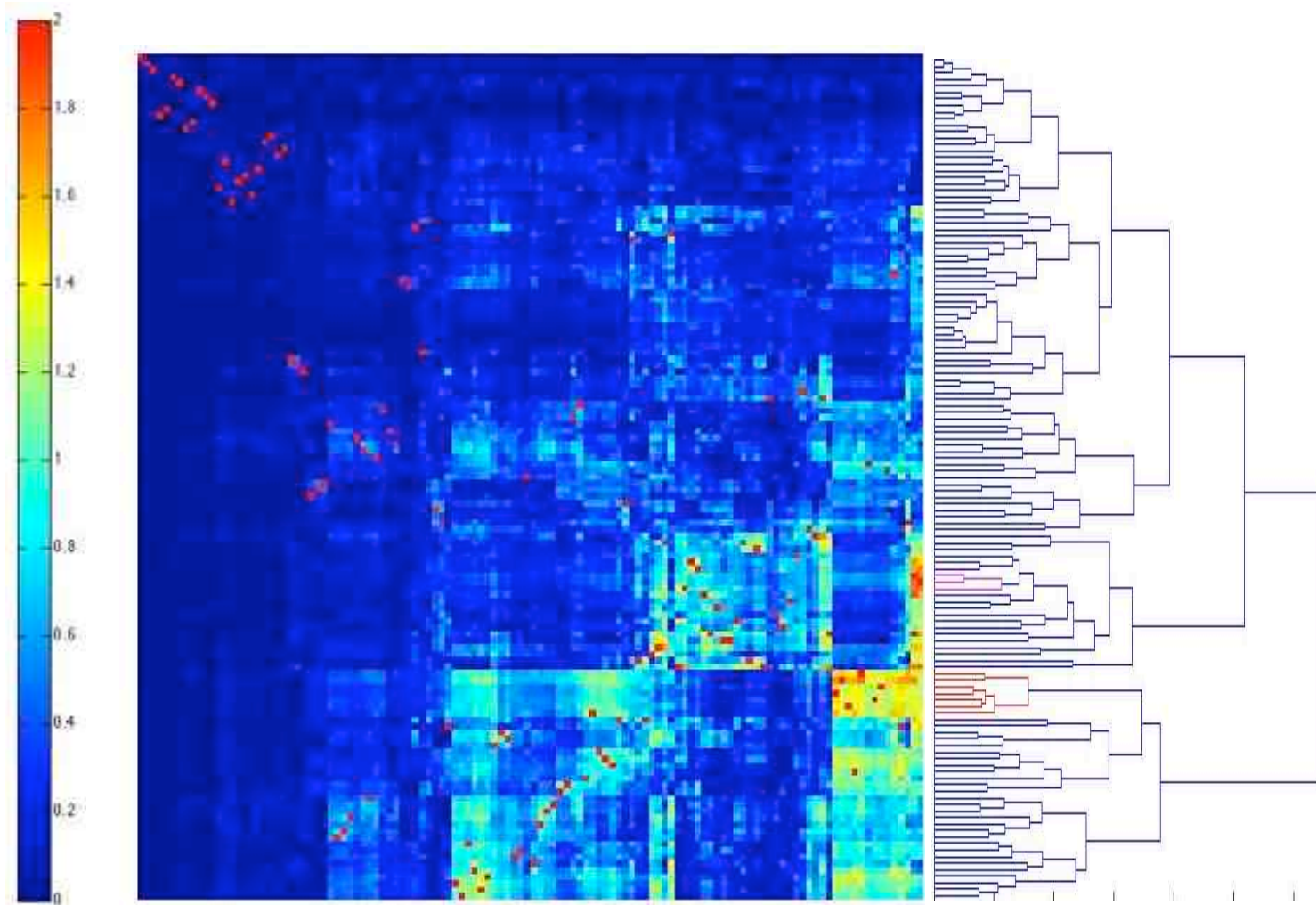


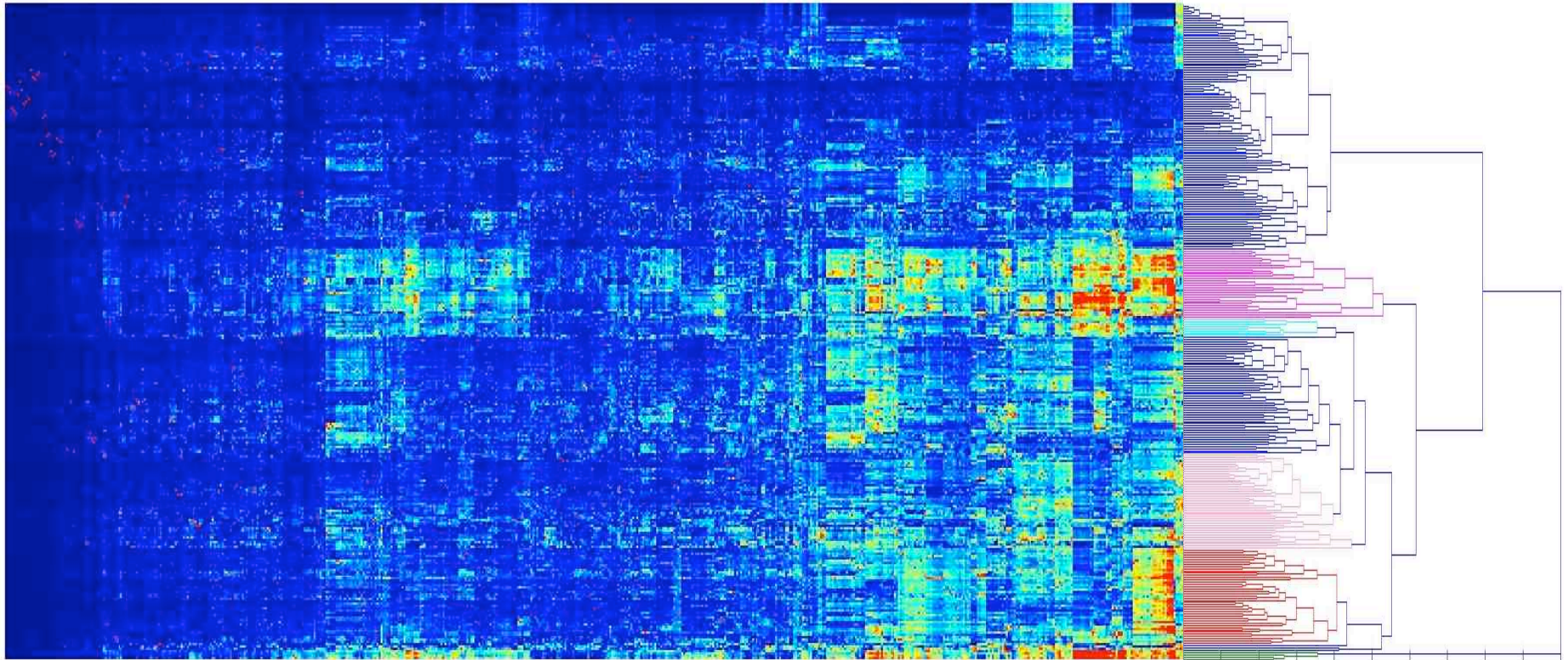
CheY a.



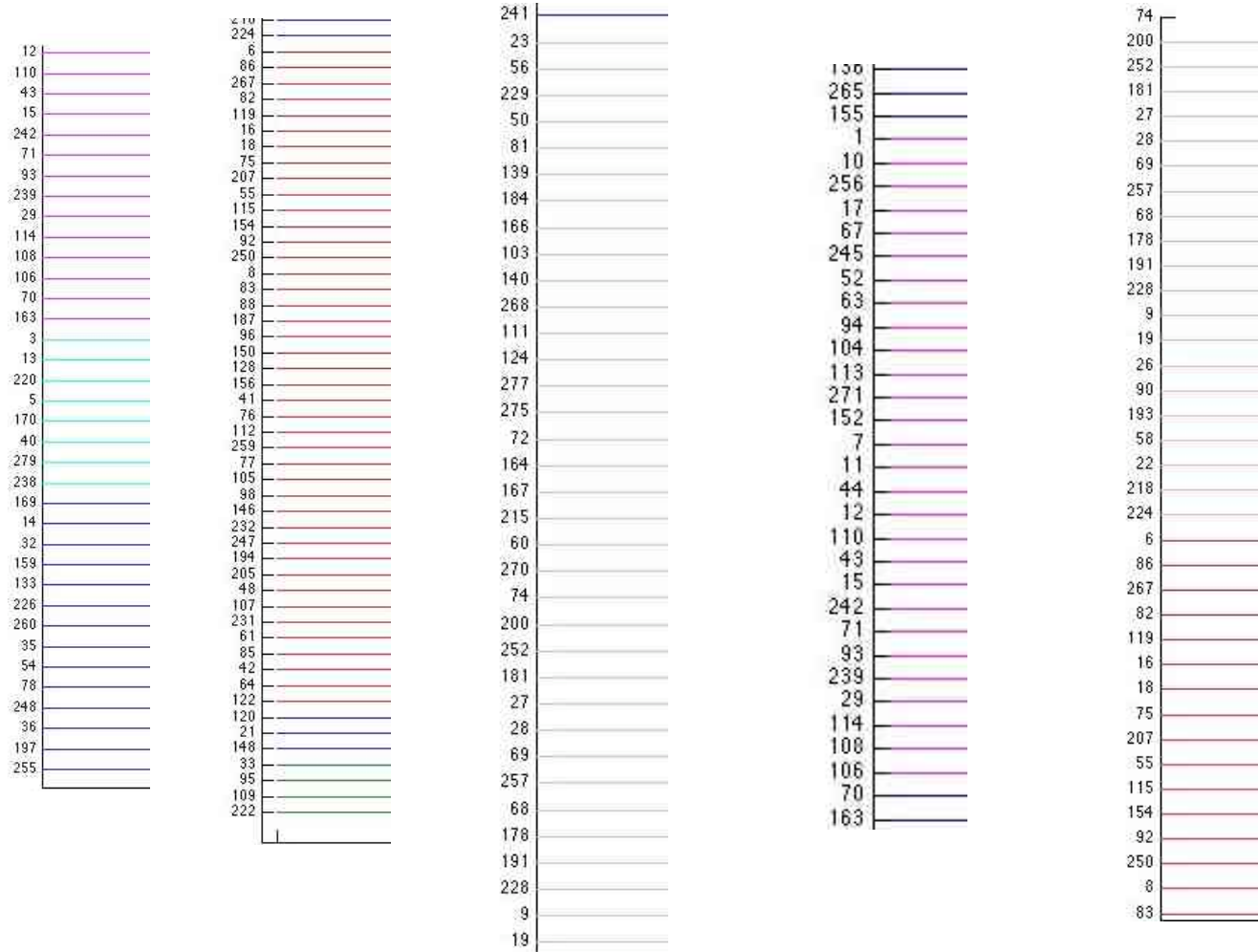
CheY b.



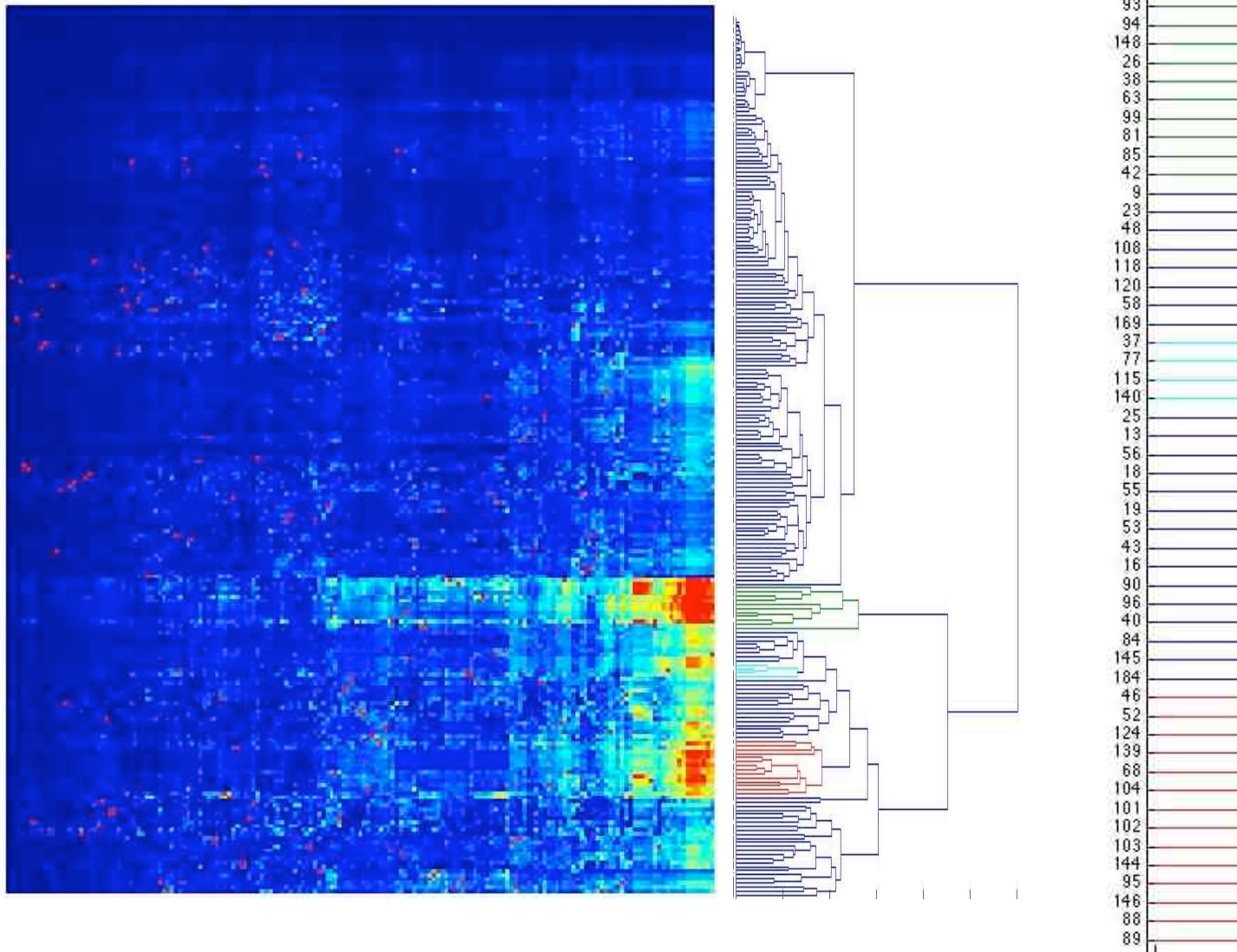
Purine repressor a.



Purine repressor b.



Tet repressor a.

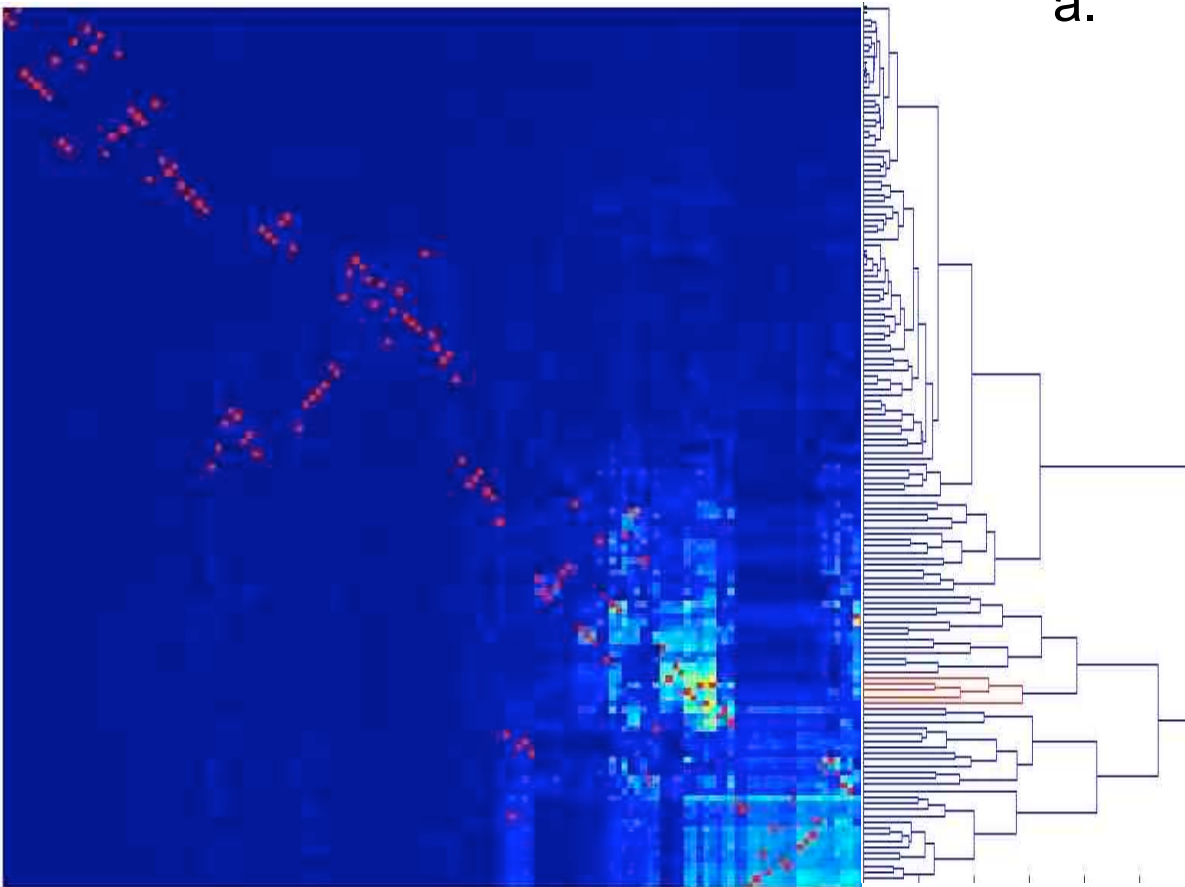


Tet repressor b.

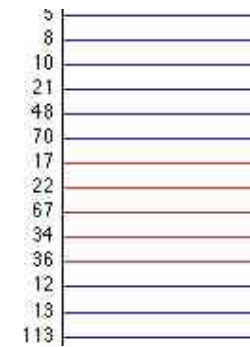


Hemoglobin, alpha subunit

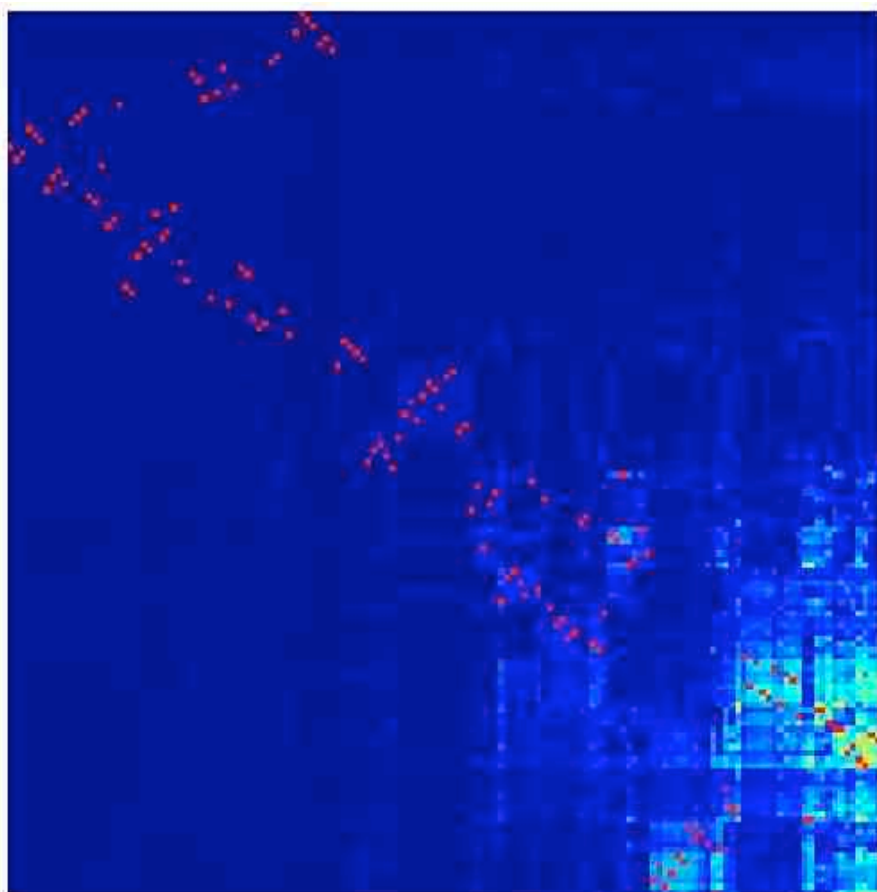
a.



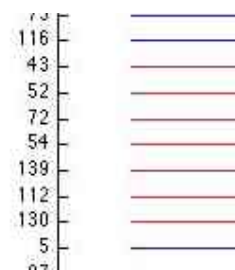
b.



Hemoglobin, beta subunit

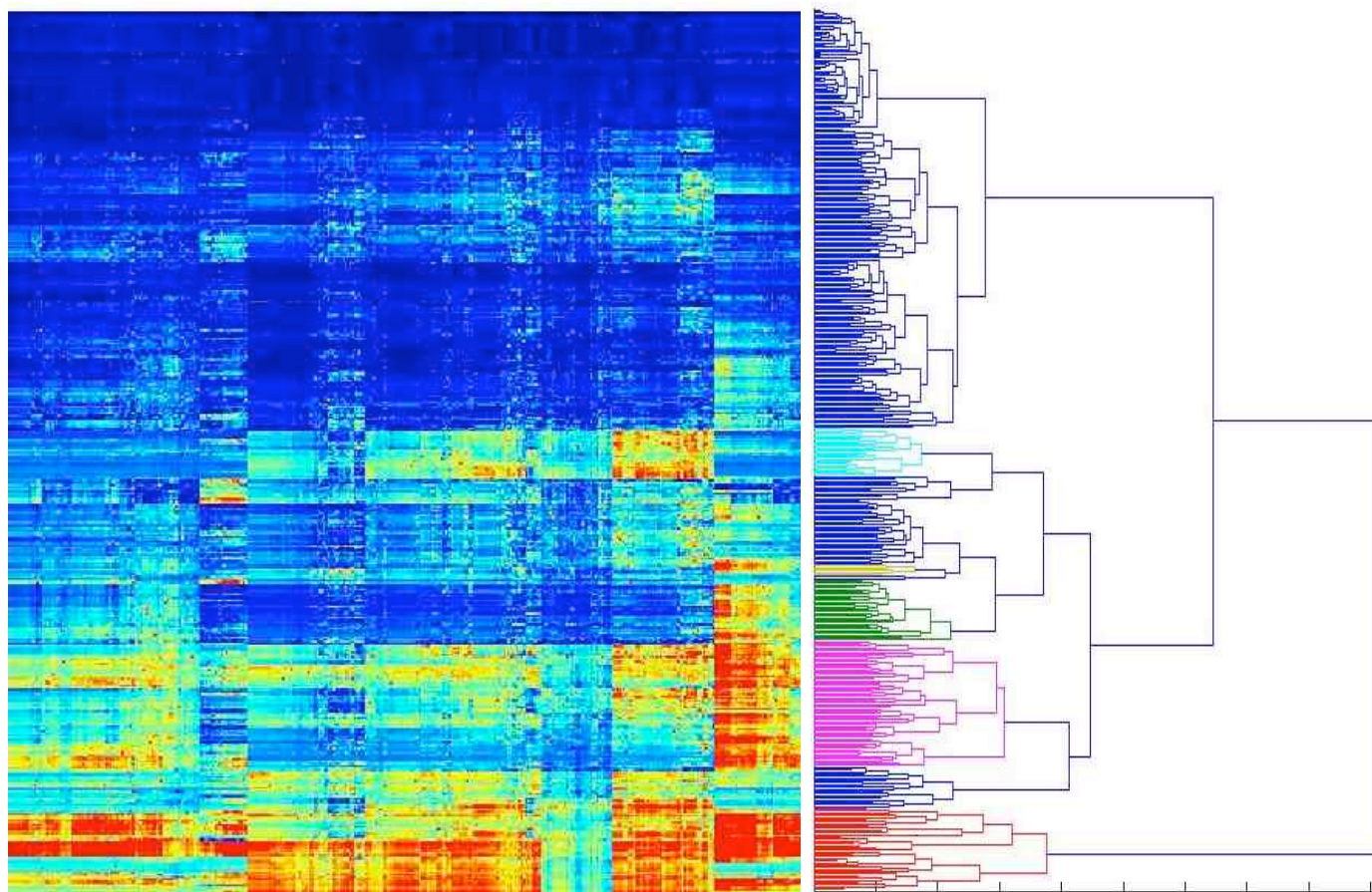


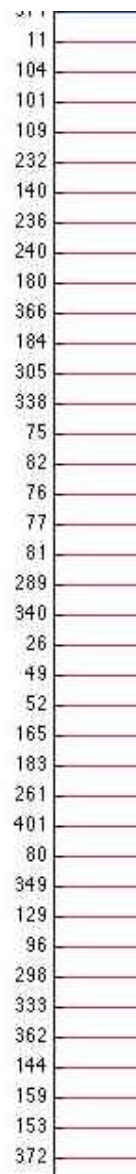
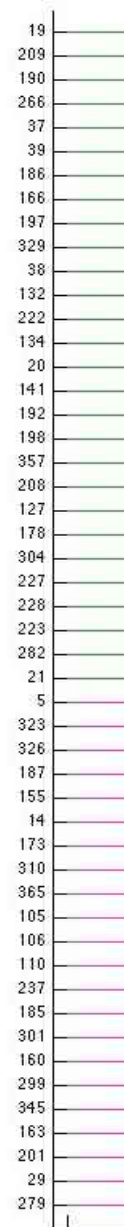
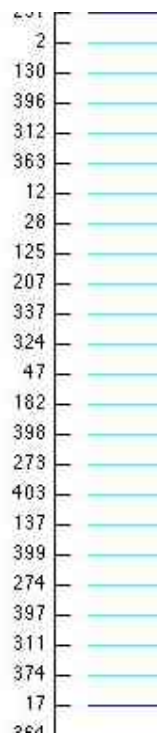
a.



b.

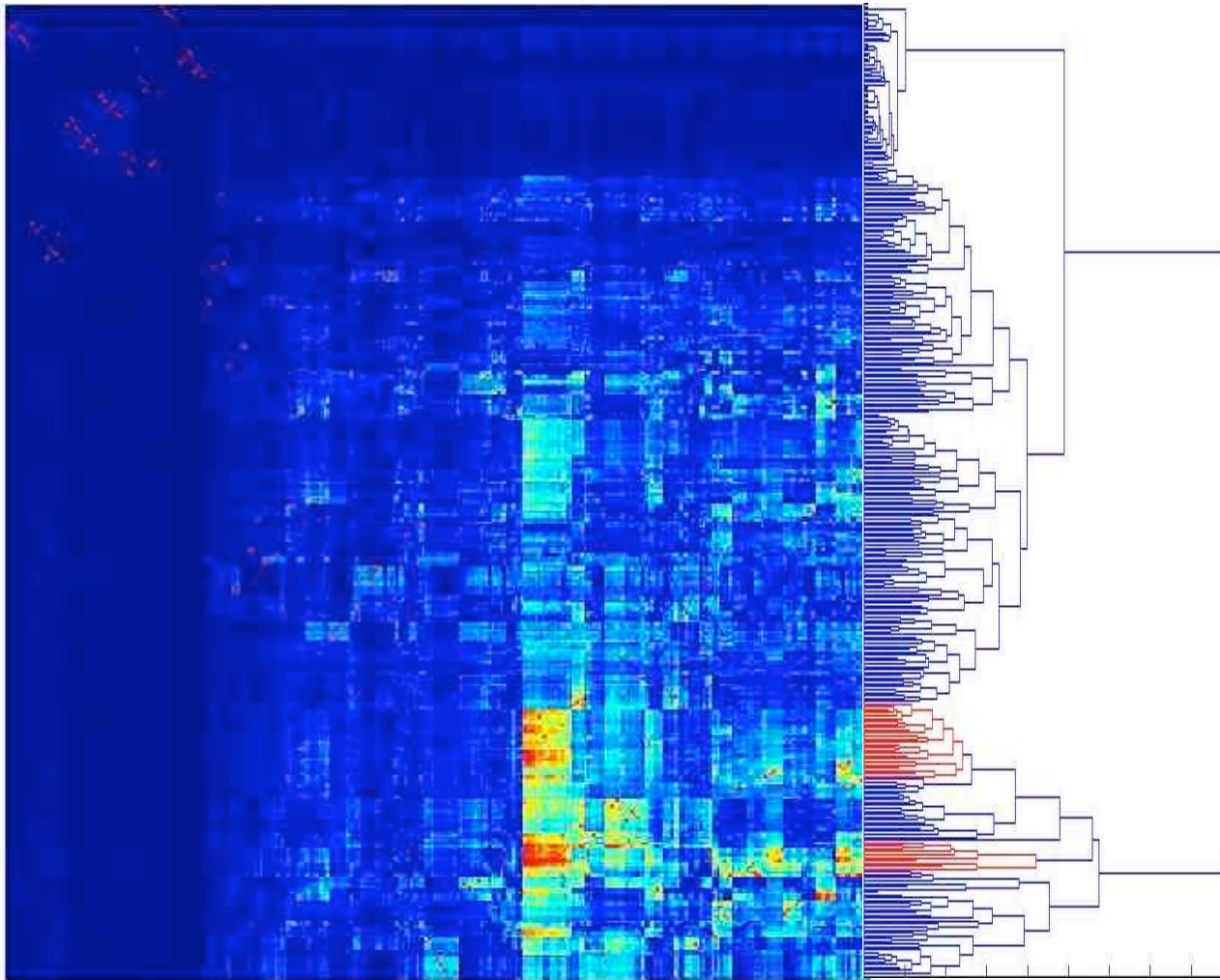
d-3-phosphoglycerate dehydrogenase a.





d-3-phosphoglycerate
dehydrogenase b.

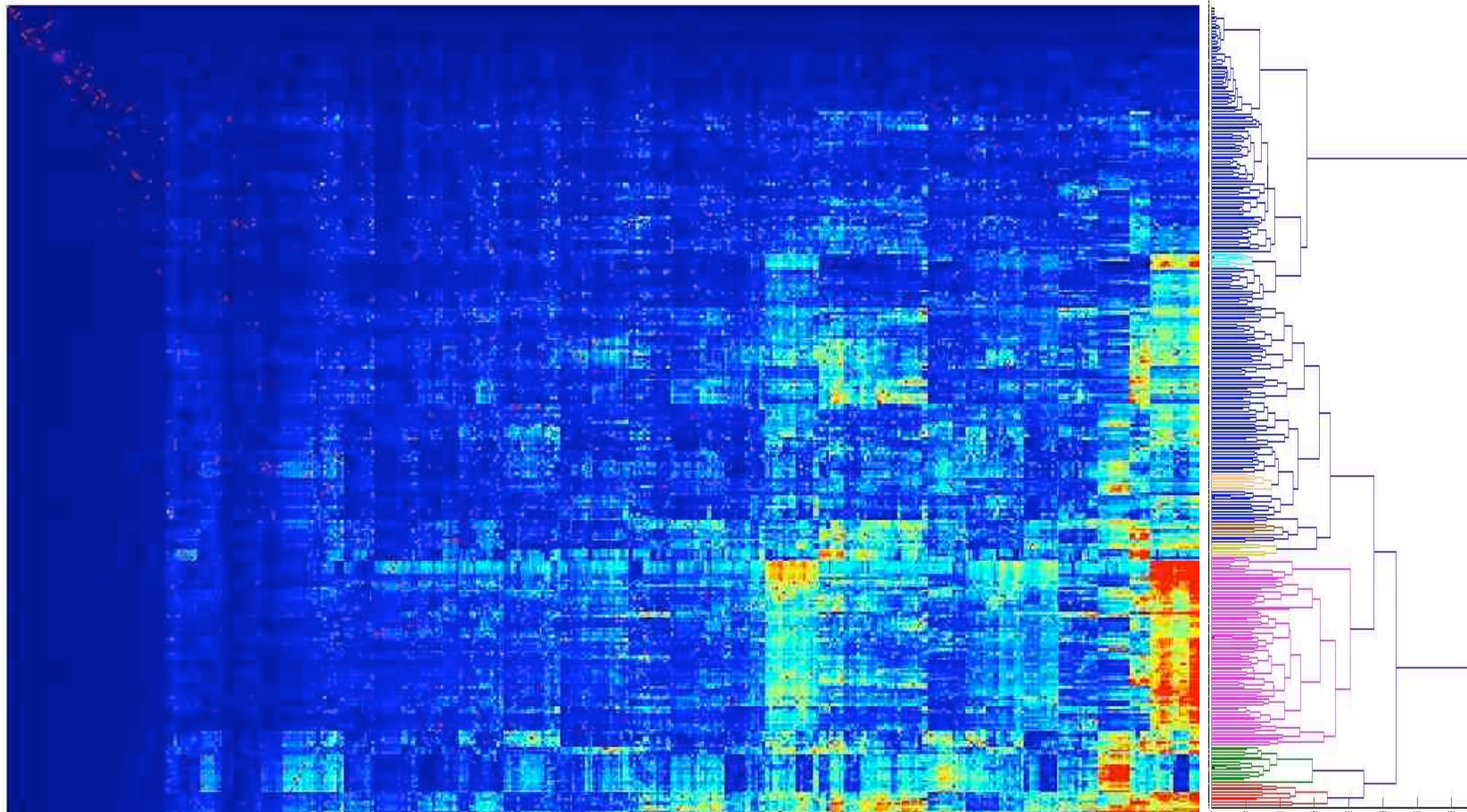
FBPase-1 a.



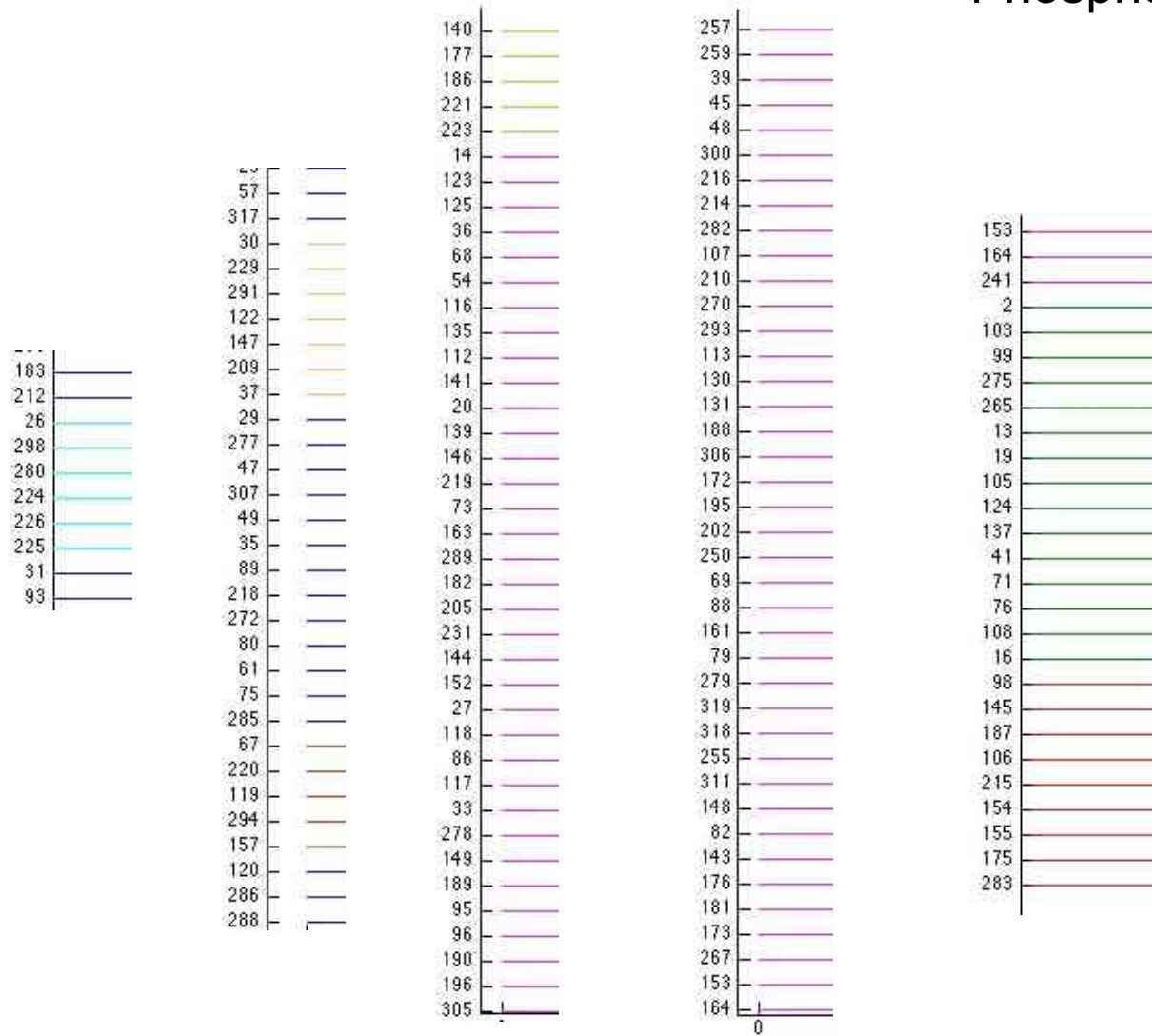
FBPase-1 b.



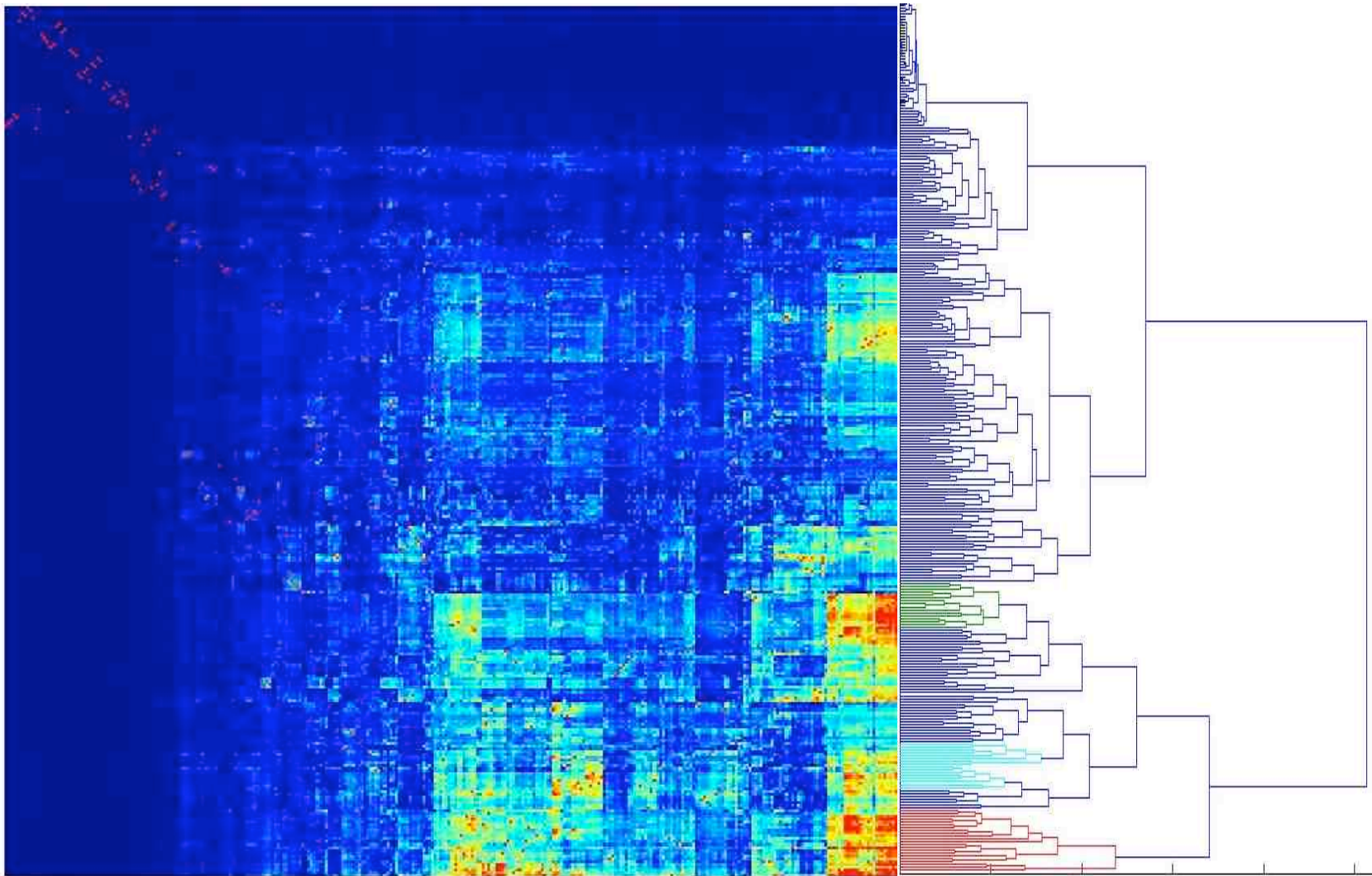
Phosphofructokinase a.



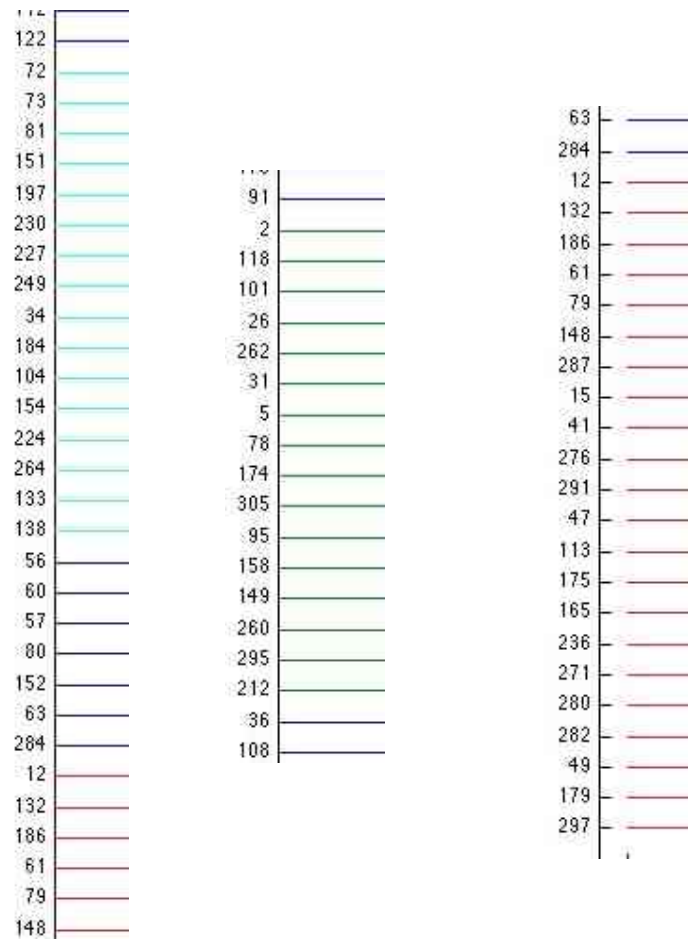
Phosphofructokinase b.



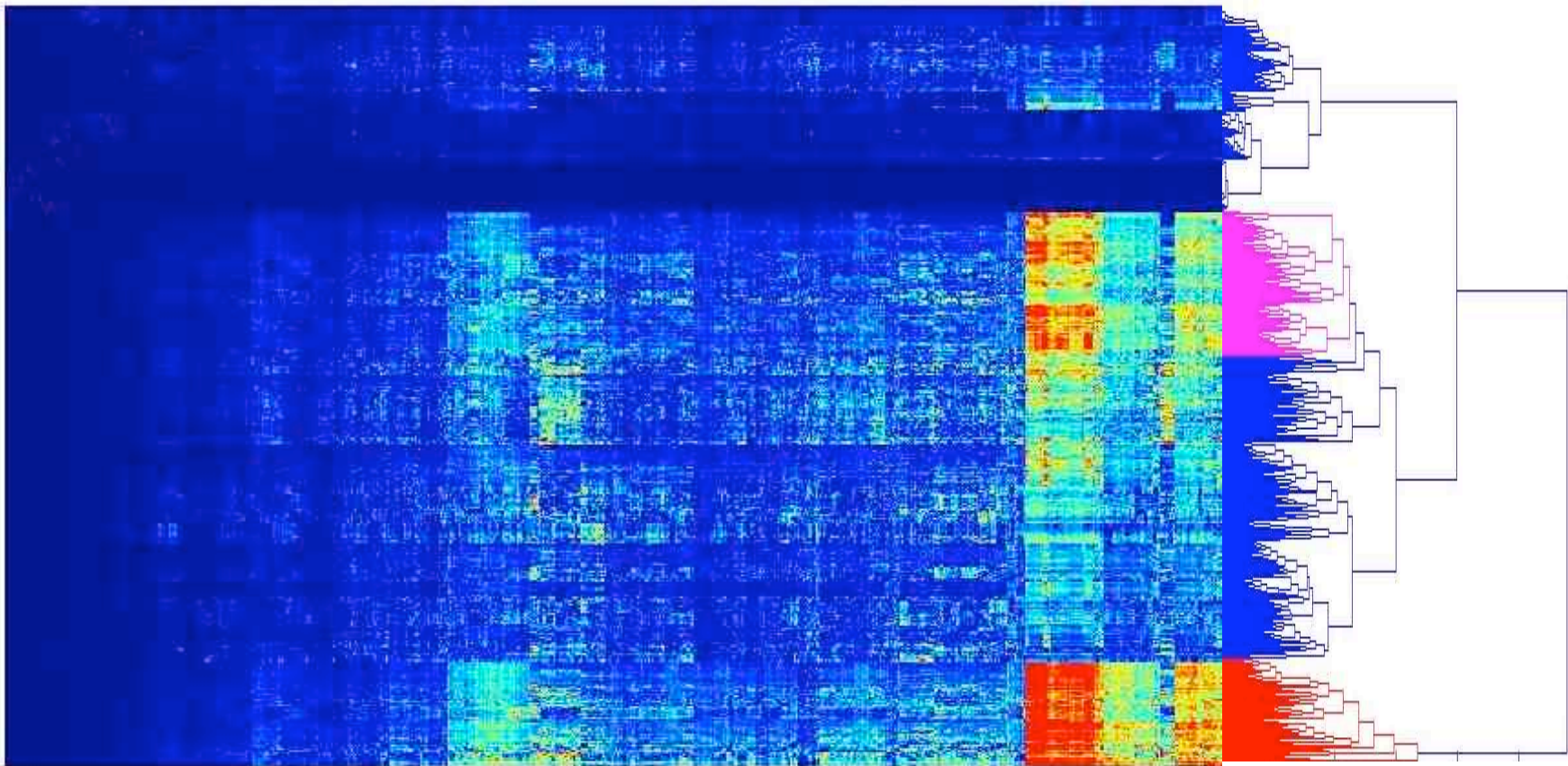
Aspartate transcarbamoylase, catalytic subunit a.



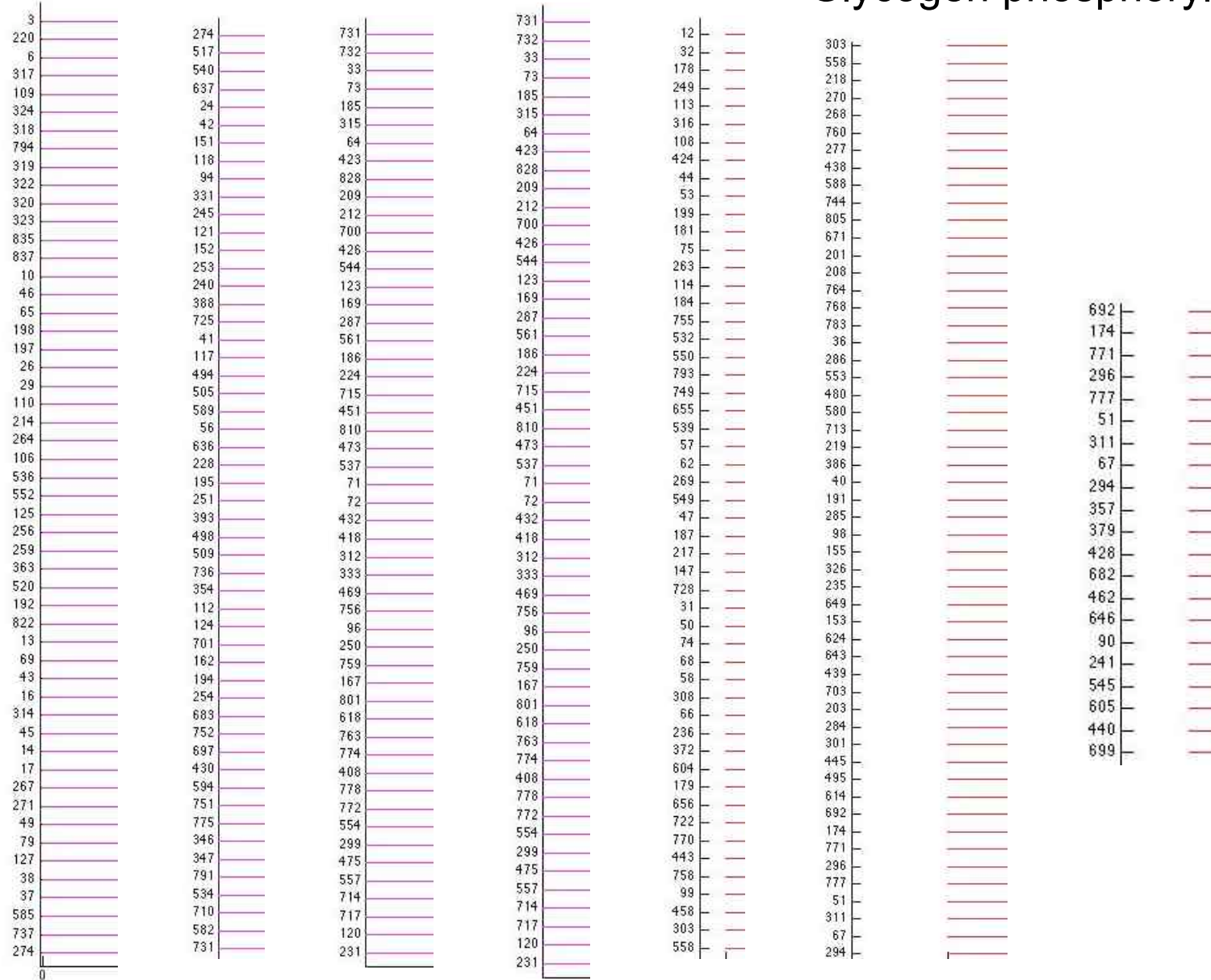
Aspartate transcarbamoylase, catalytic subunit b.



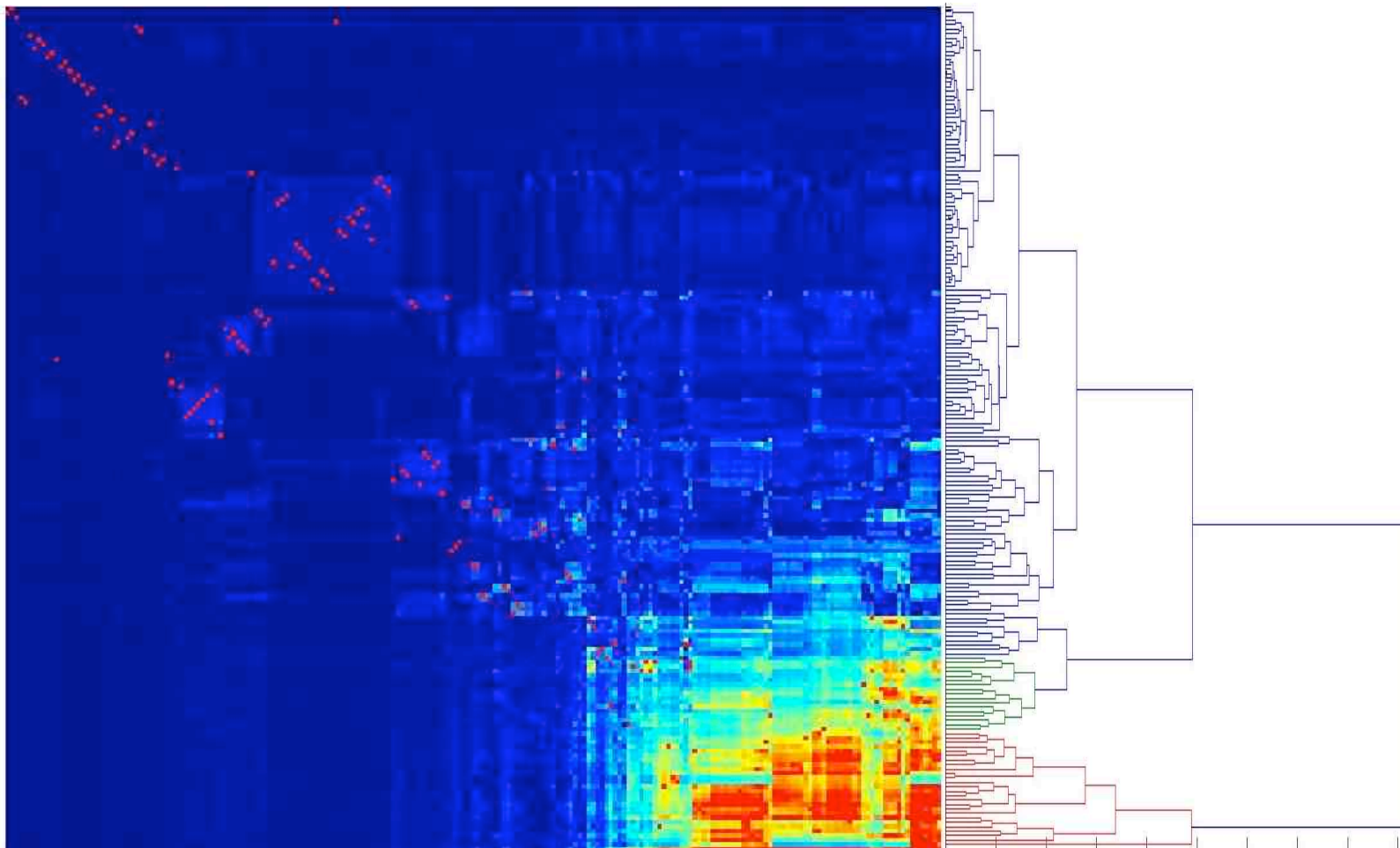
Glycogen phosphorylase a.



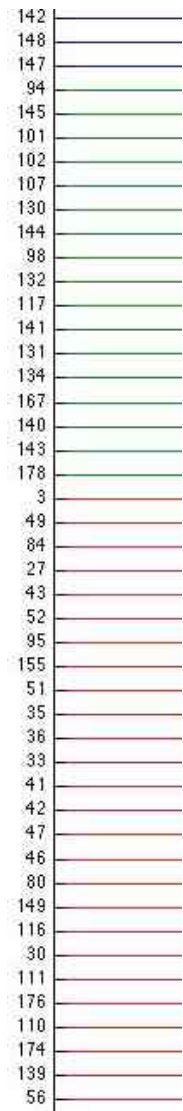
Glycogen phosphorylase b.



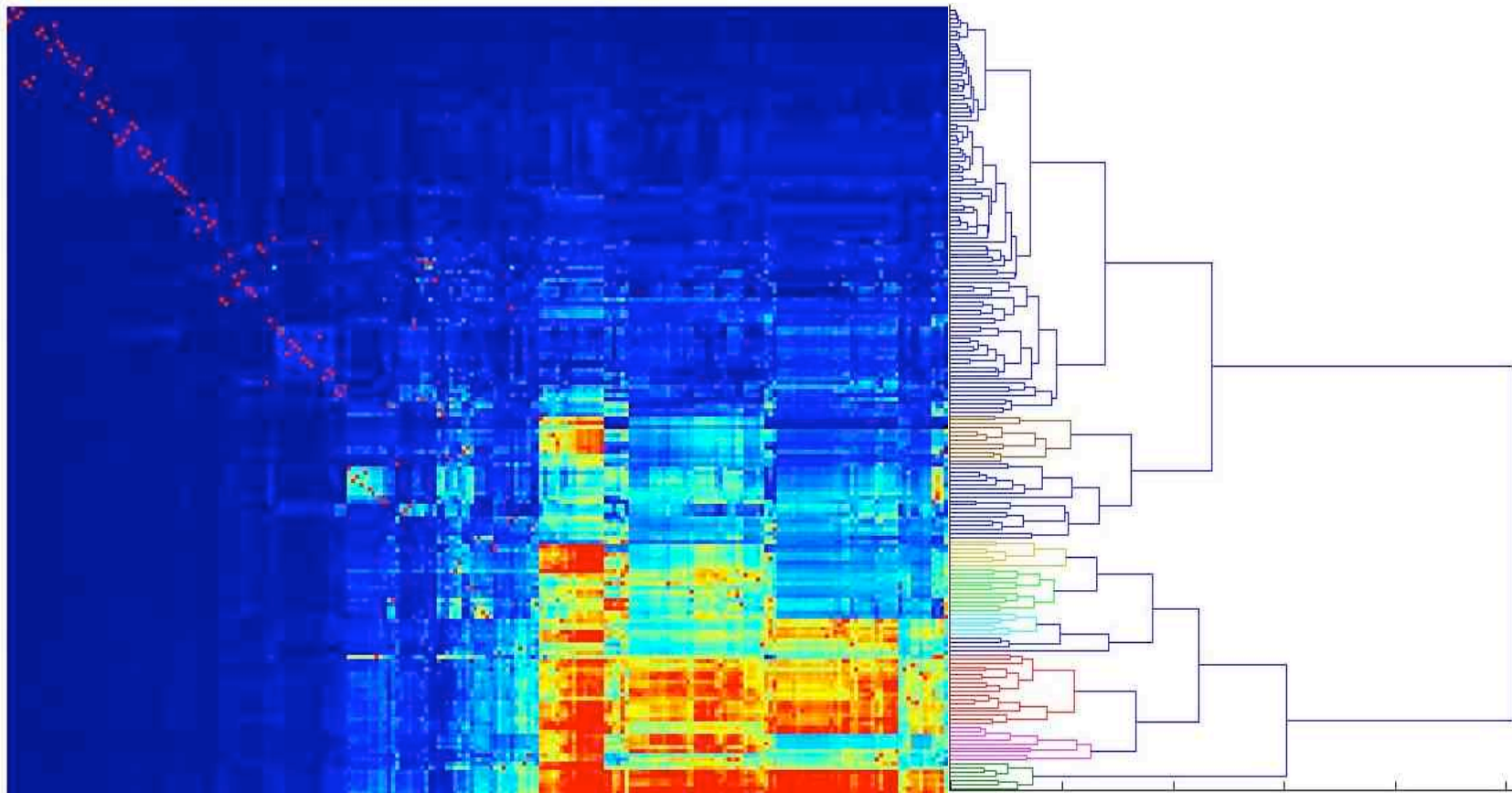
Cdc-42 a.



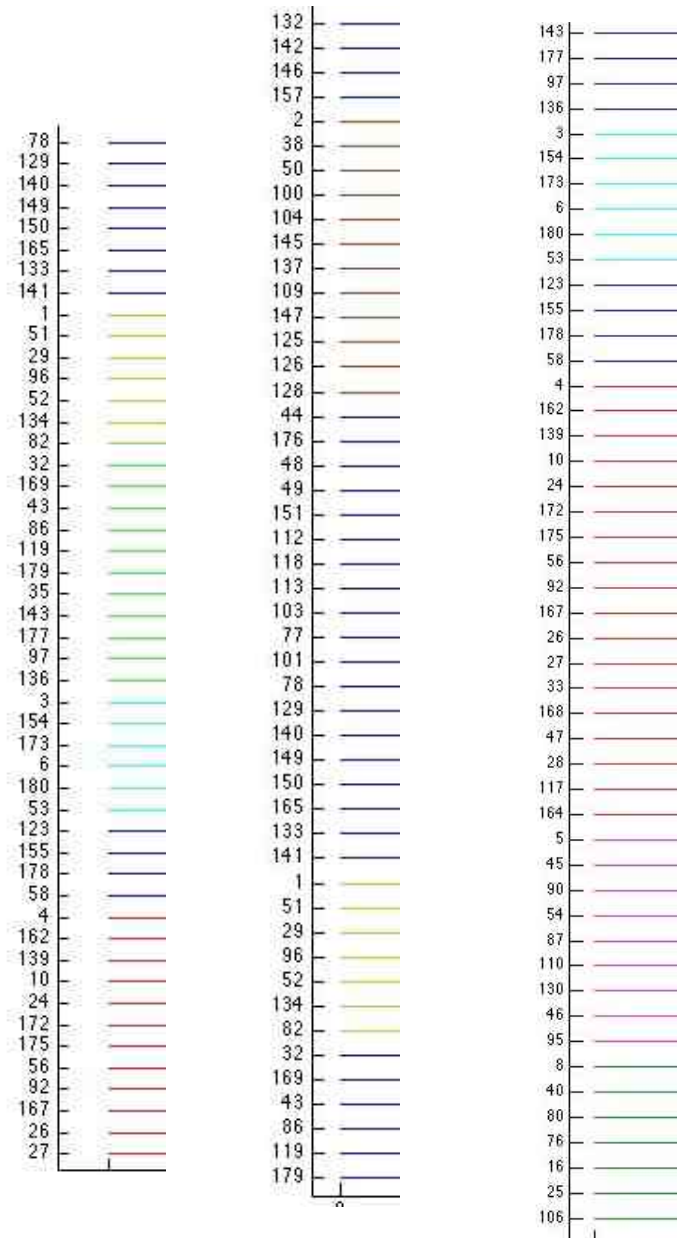
Cdc-42 b.



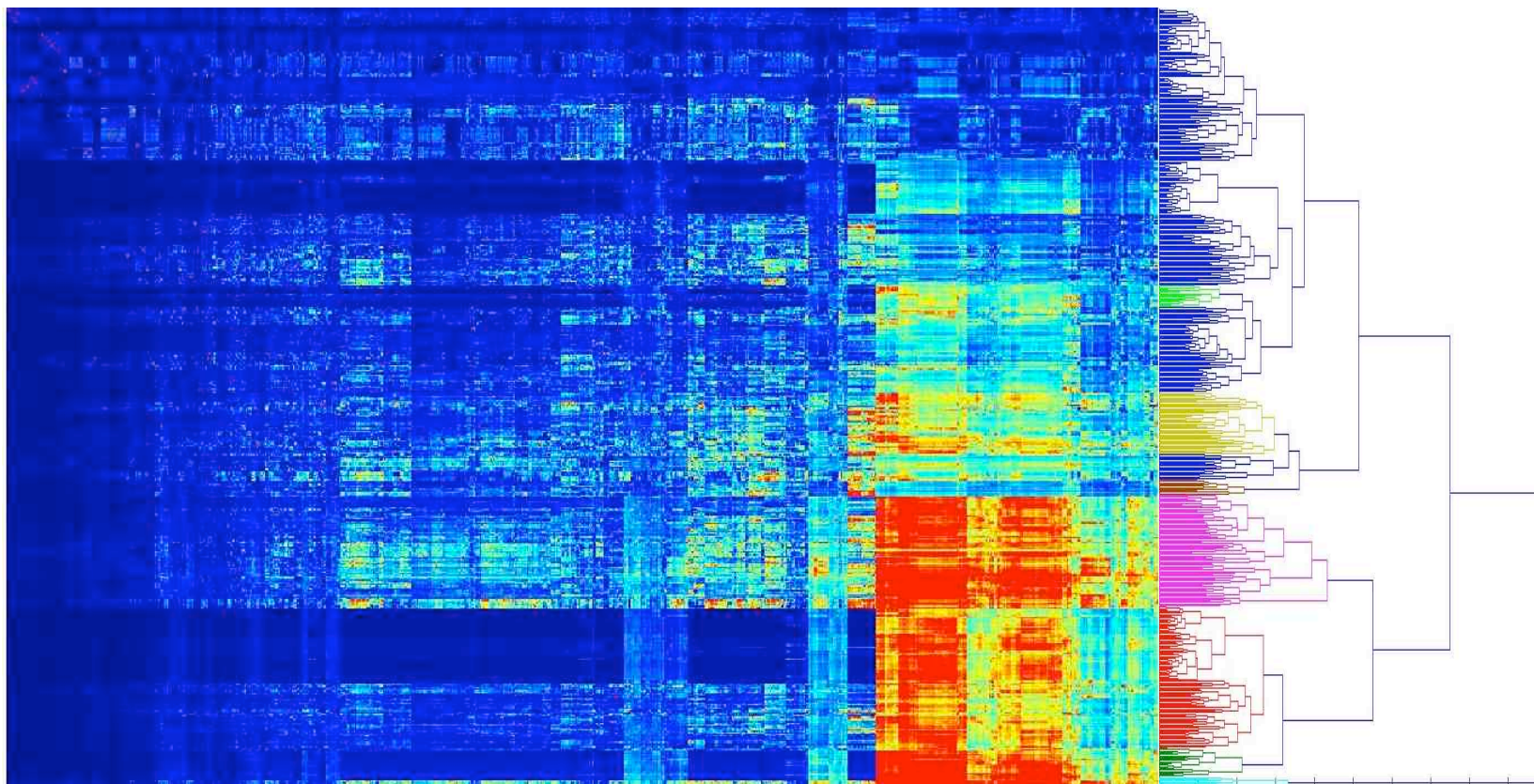
rhoA a.



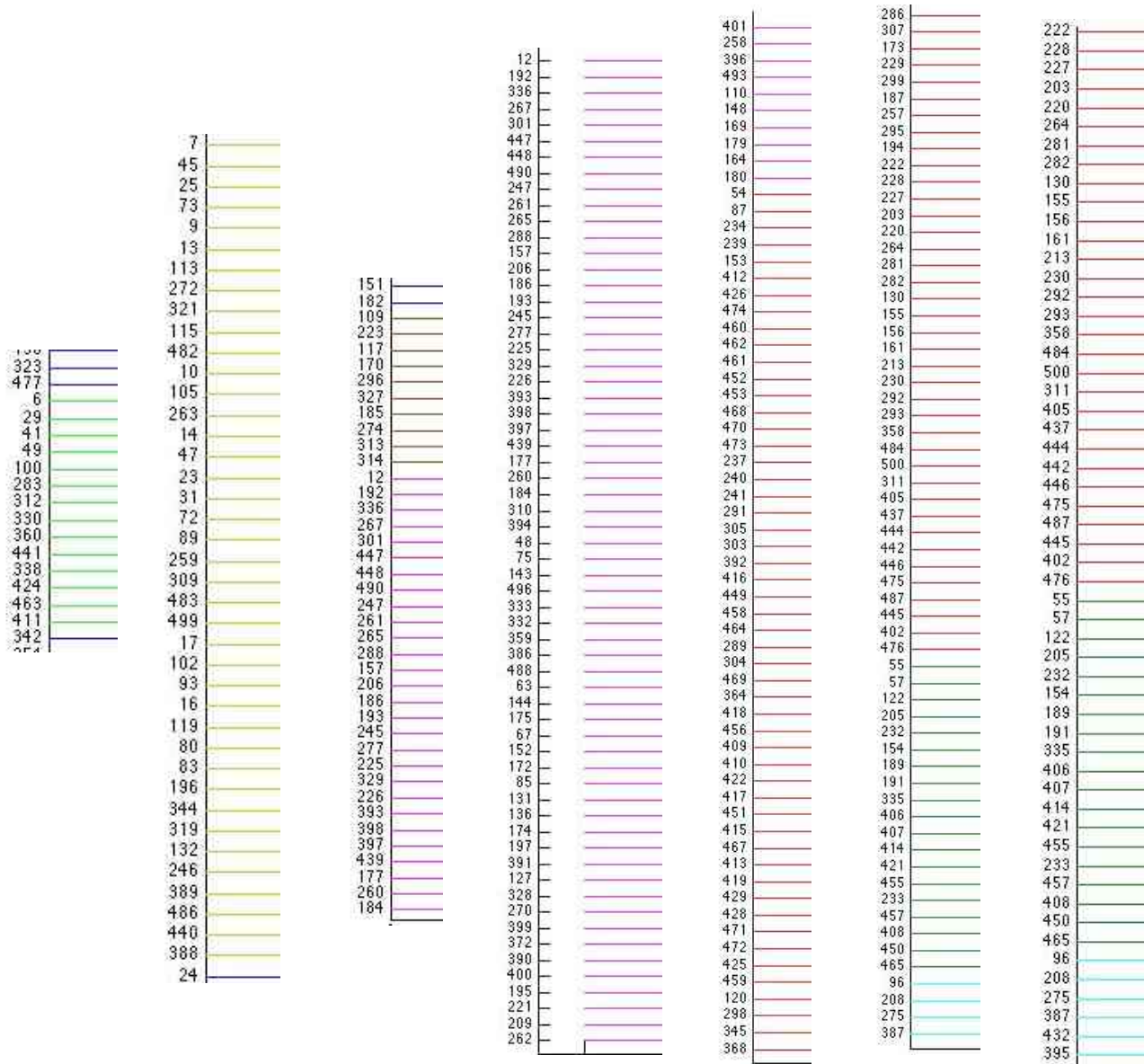
rhoA b.



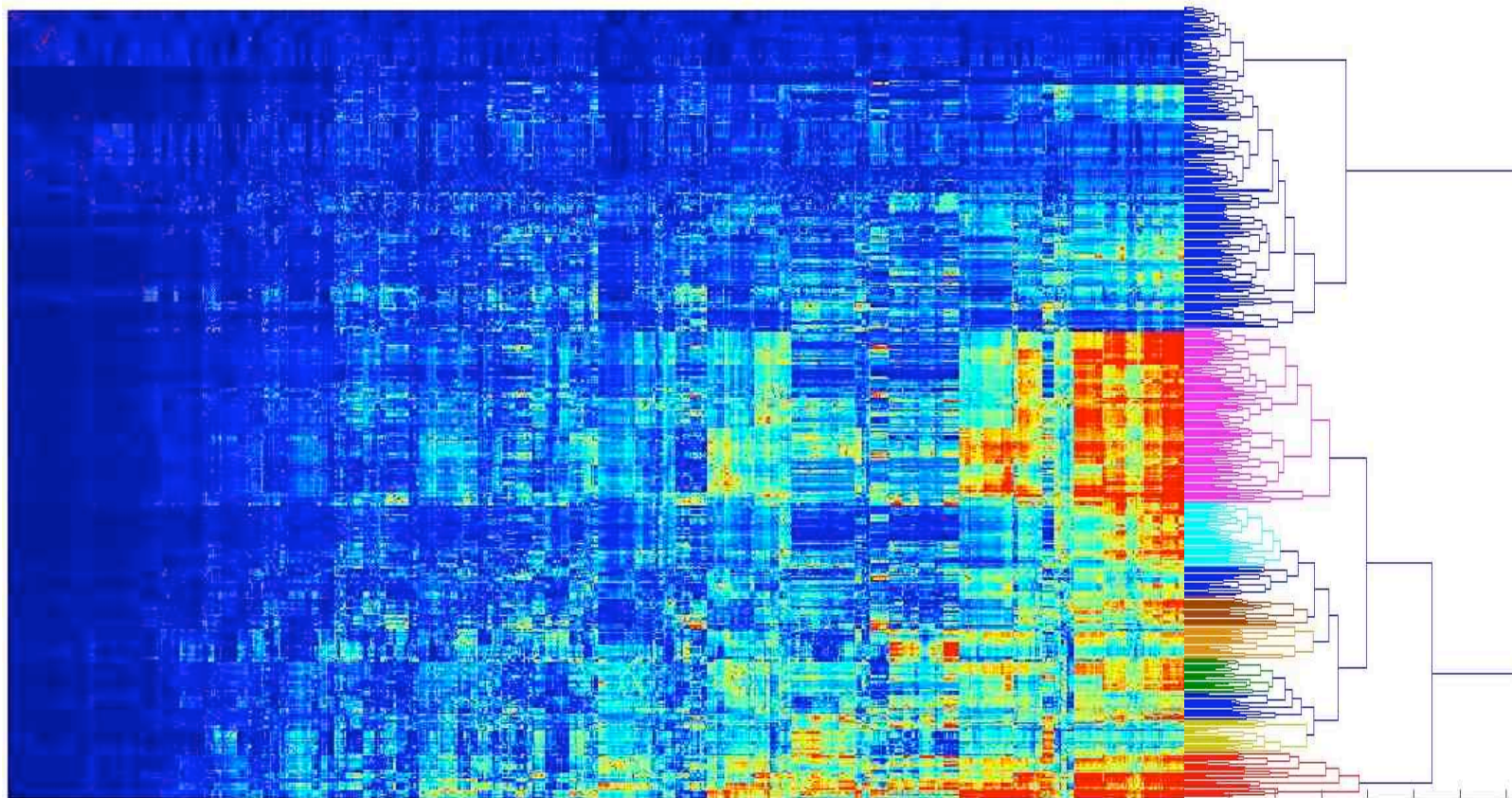
glutamate dehydrogenase a.



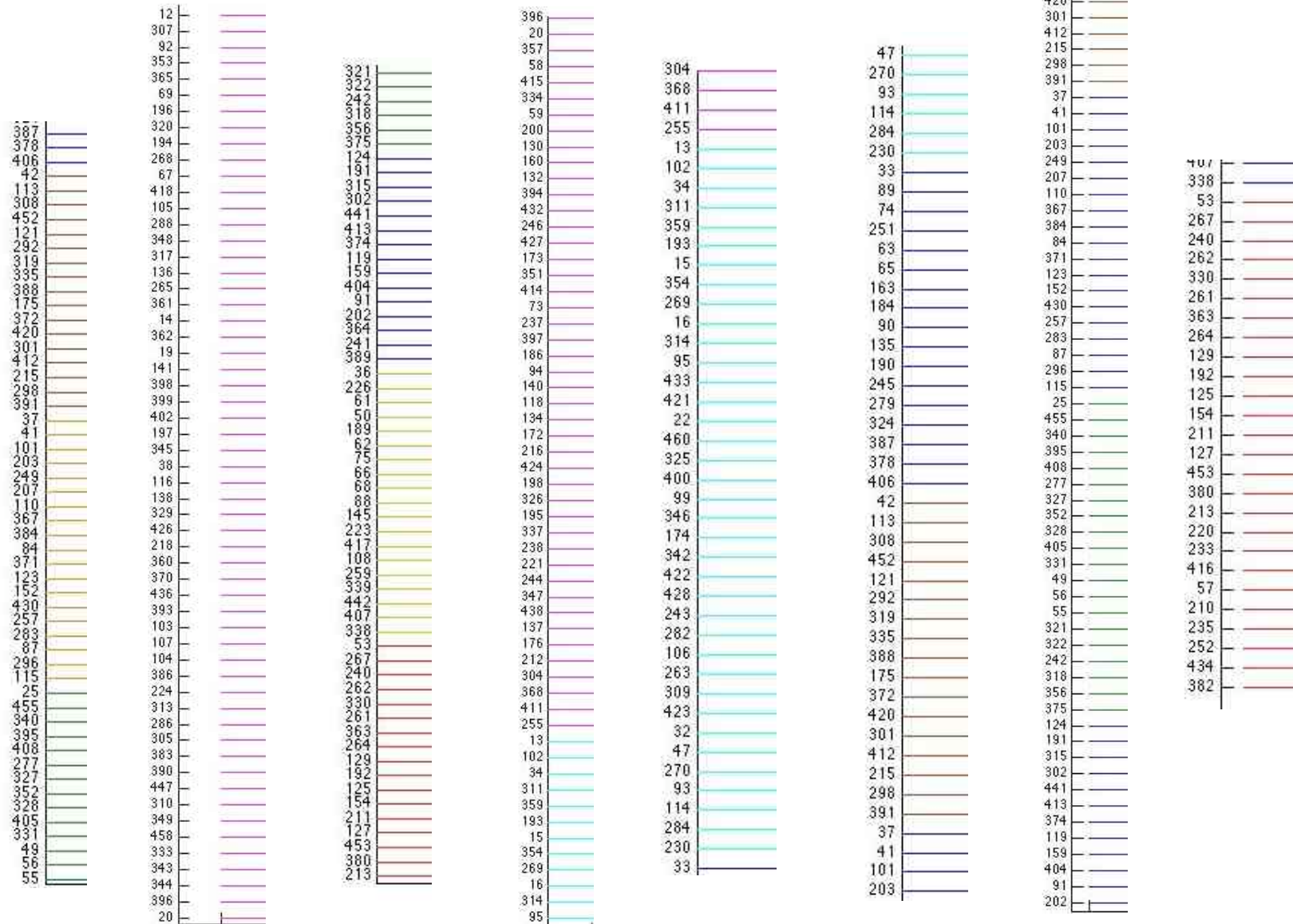
glutamate dehydrogenase b.



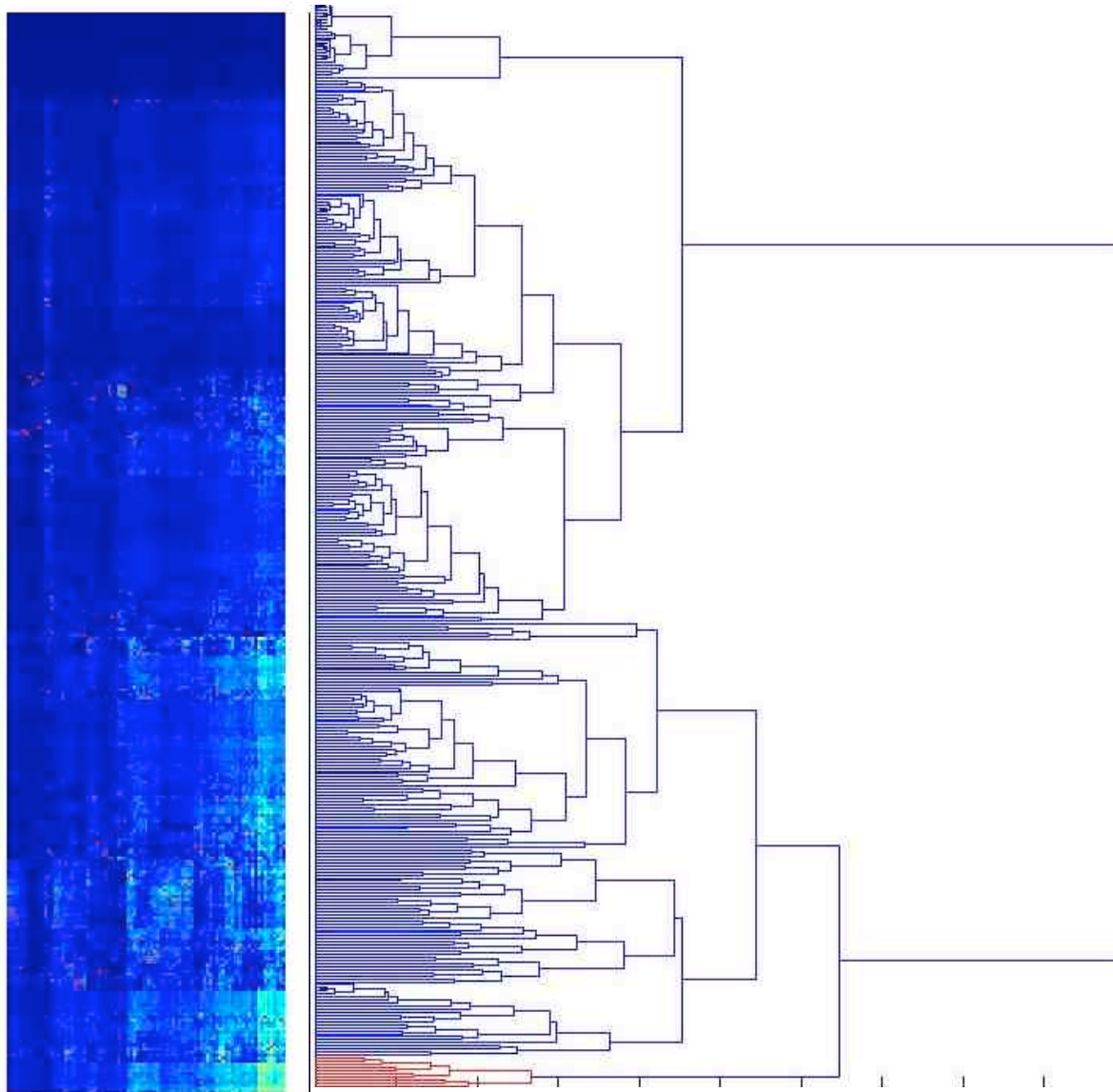
glucokinase a.



glucokinase b.



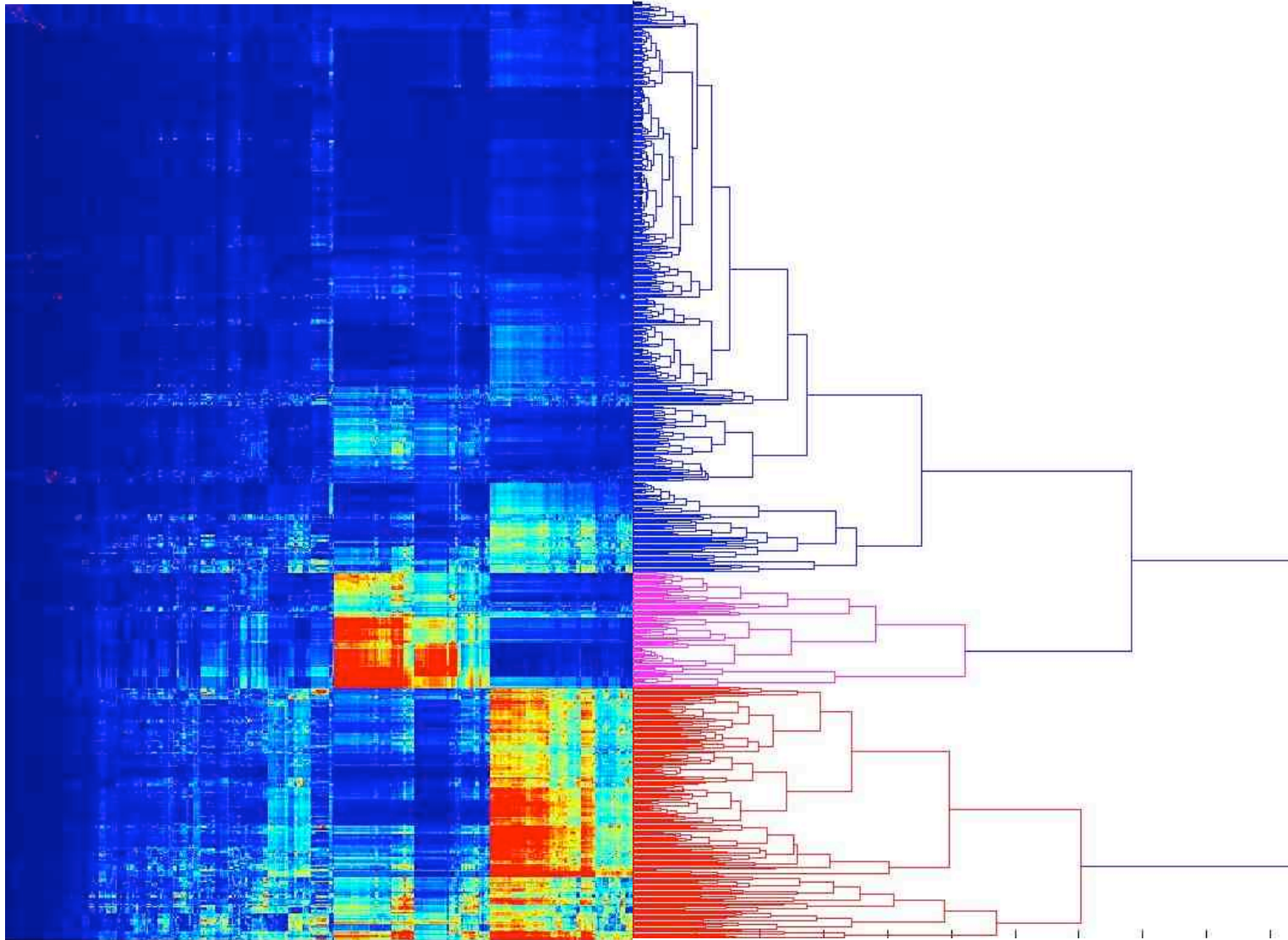
Lac repressor a.



Lac repressor b.

22	
126	
146	
113	
290	
87	
162	
125	
148	
214	

Thrombin, chain B a.



Thrombin, chain B b.

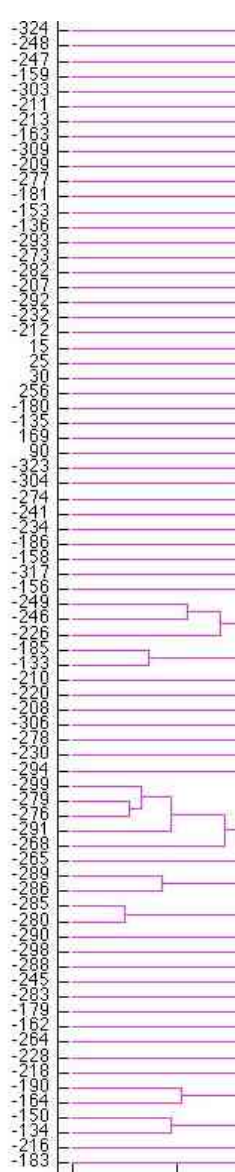


Figure S4. SCA data. Results for SCA are present for each protein from the training and independent data sets, except for myosin II where we relied on the previously published analysis by Yu et al. [F1]. a. Hierarchically clustered matrix of $\Delta\Delta G$ values and dendrogram where terminal branches correspond to residue indices of the protein sequence. Branches of the dendrogram corresponding to regions in the matrix containing clusters of high $\Delta\Delta G$ (regions with high fraction of points greater than or equal to 1.6 kT) are highlighted. The color scale is once displayed for CheY and applies to the subsequent protein systems. b. Magnification of the ends of the highlighted branches to display the residue indices, which are based on the numbering in the corresponding PDB file (except for thrombin, where negative numbers are for residues cleaved from prothrombin chain B and thrombin residues start at 1).

Supplemental References

F1. Yu H, Ma L, Yang Y, Cui Q (2007) Mechanochemical coupling in the myosin motor domain. II. Analysis of critical residues. Plos Computational Biology 3: 214-230.