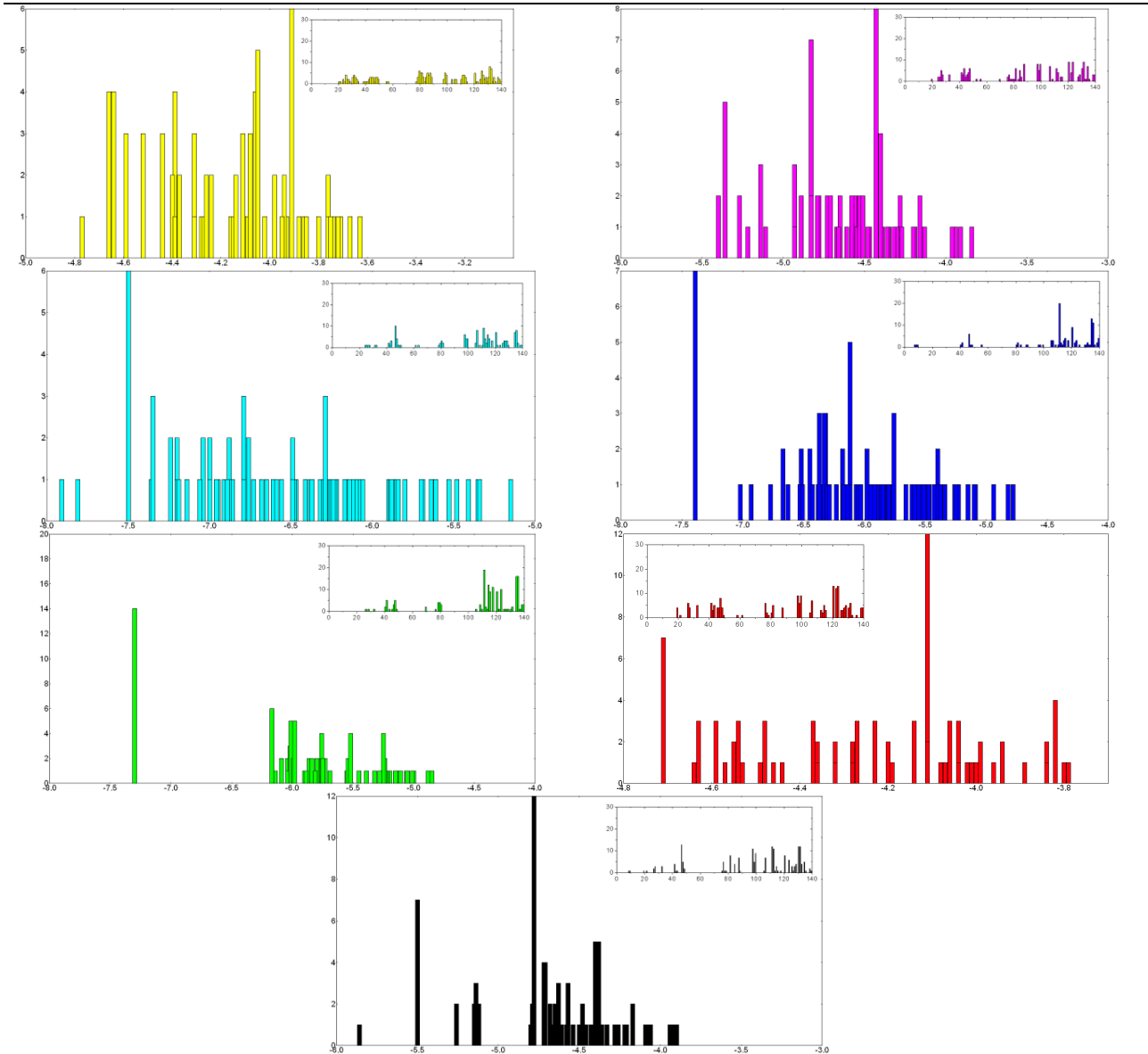
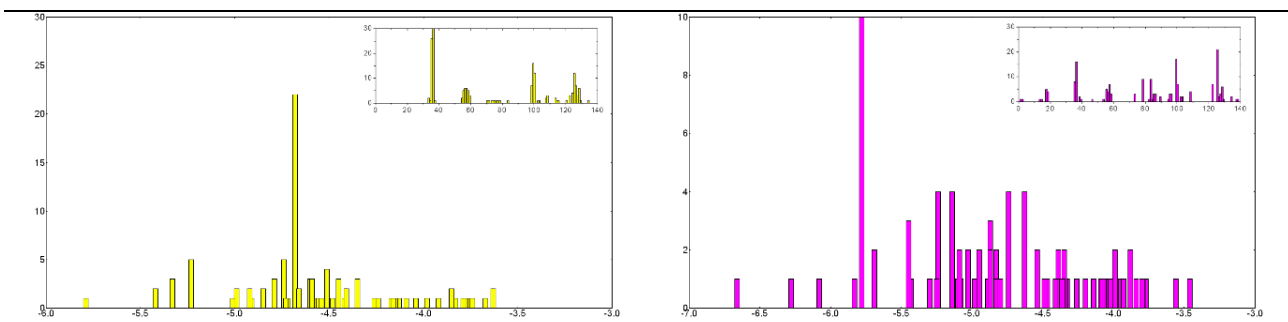
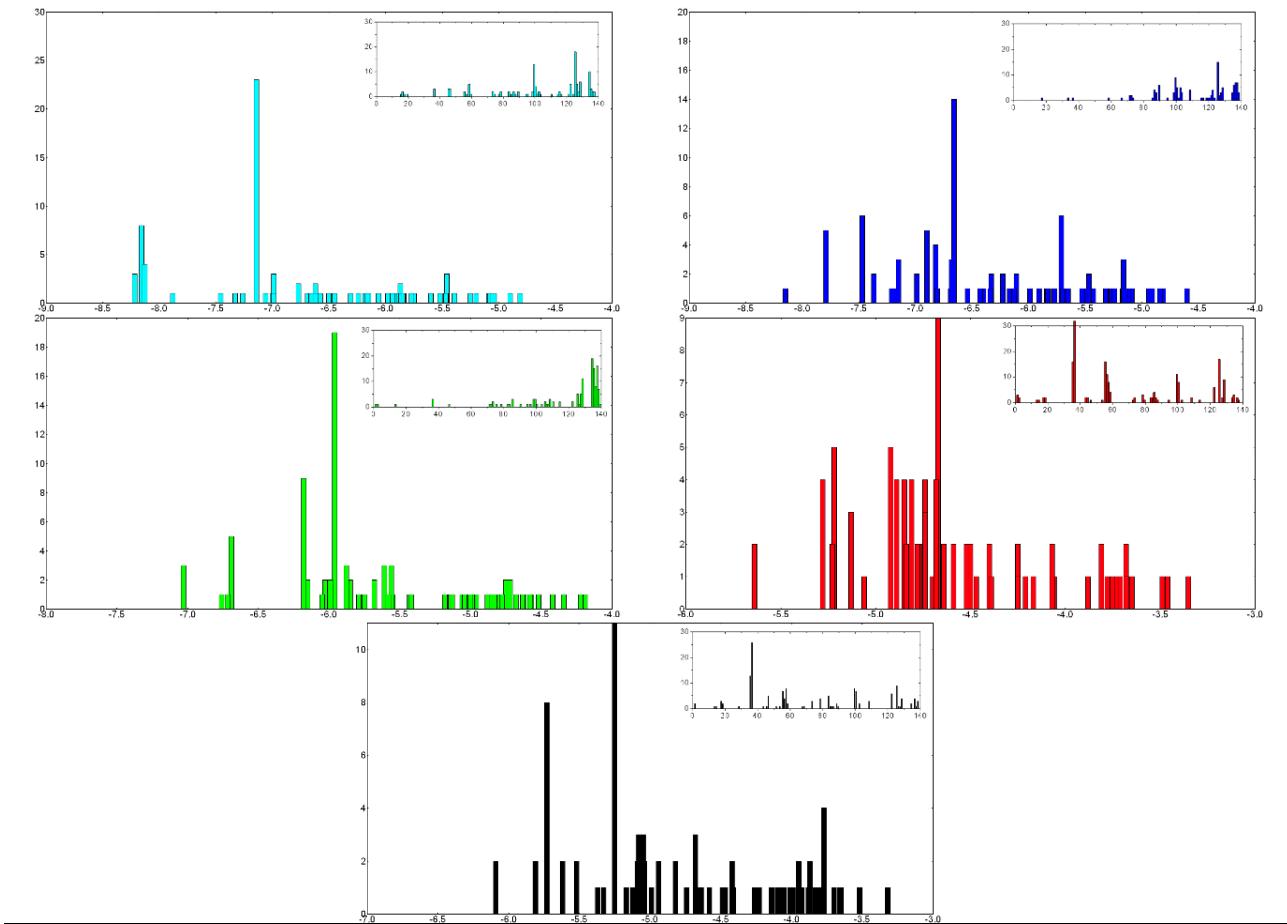


## Cluster 1

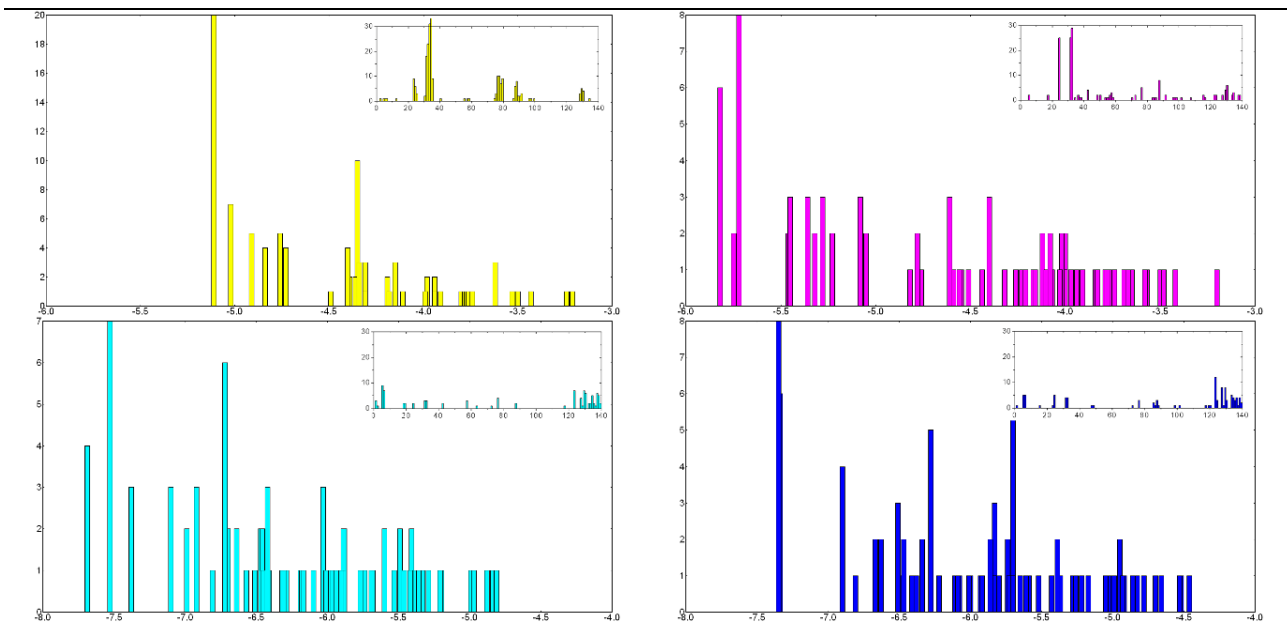


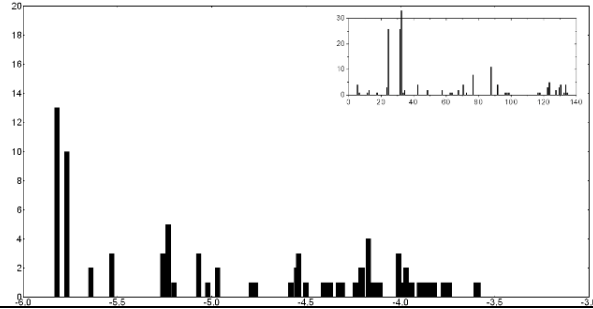
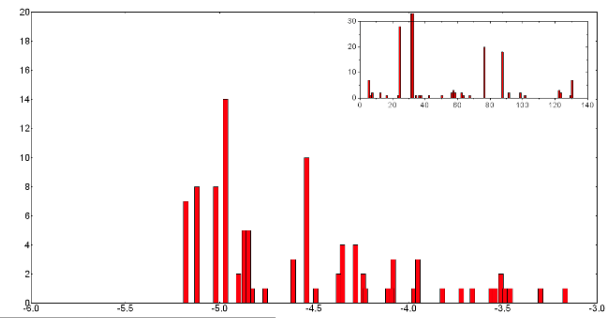
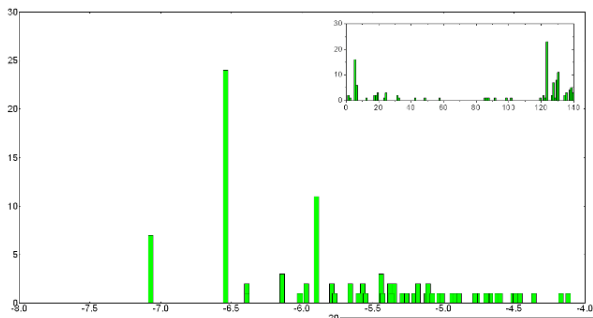
## Cluster 2



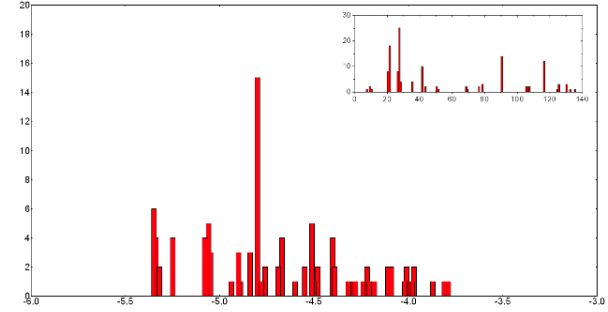
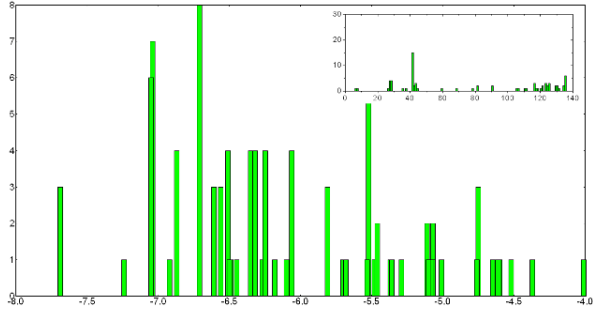
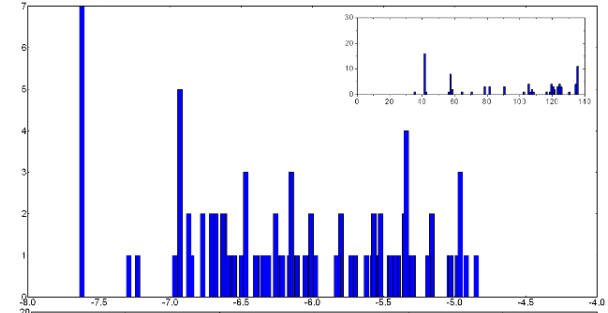
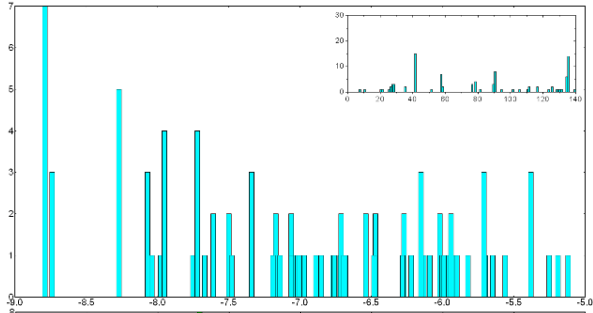
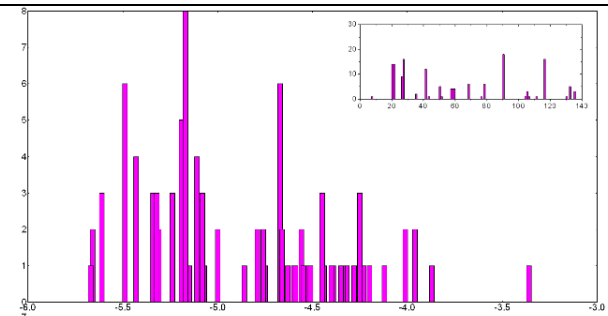
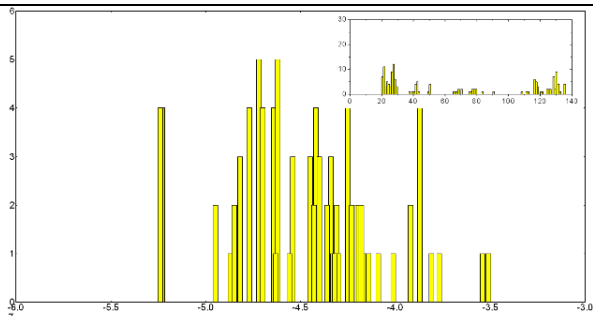


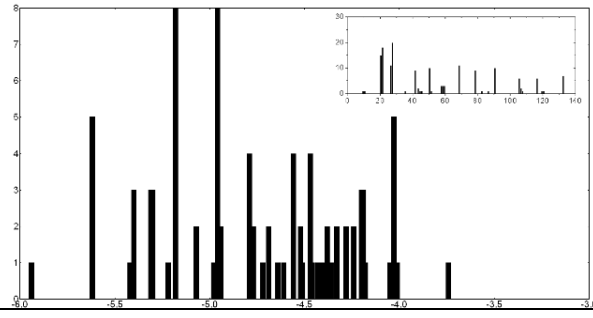
Cluster 3



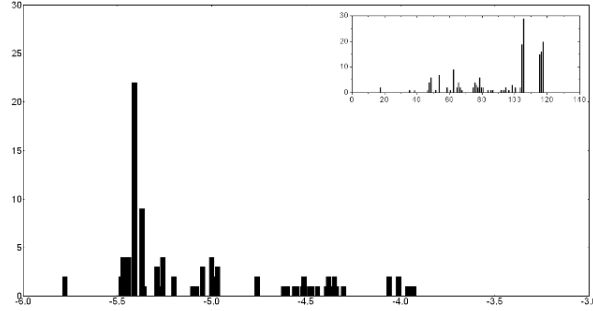
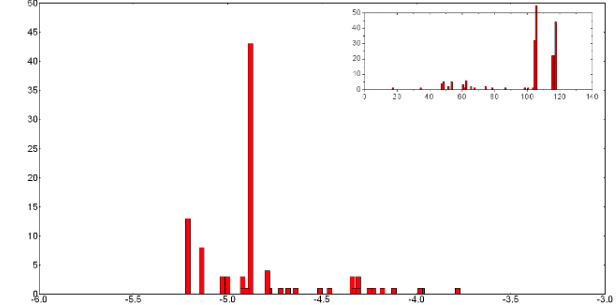
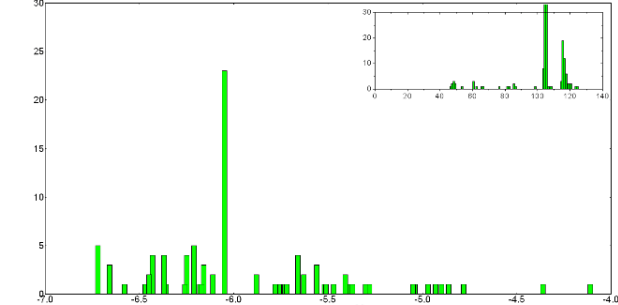
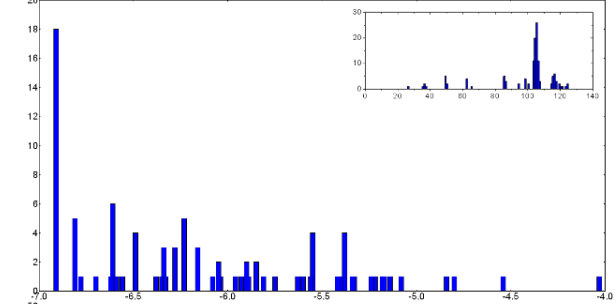
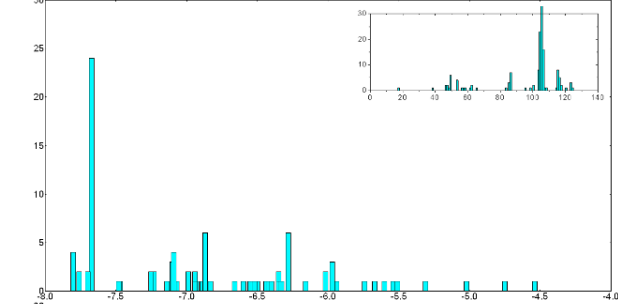
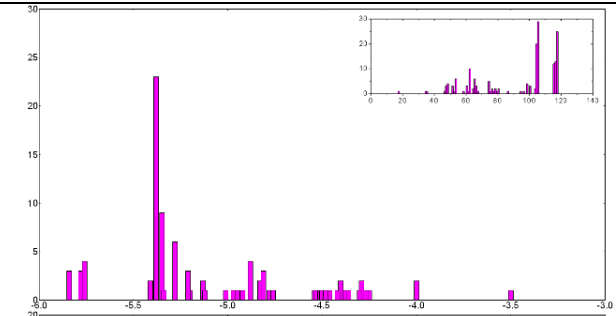
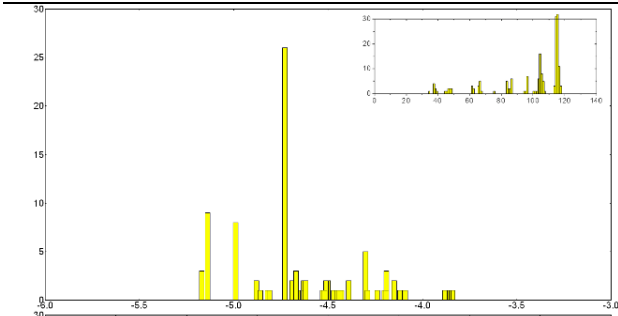


### Cluster 4

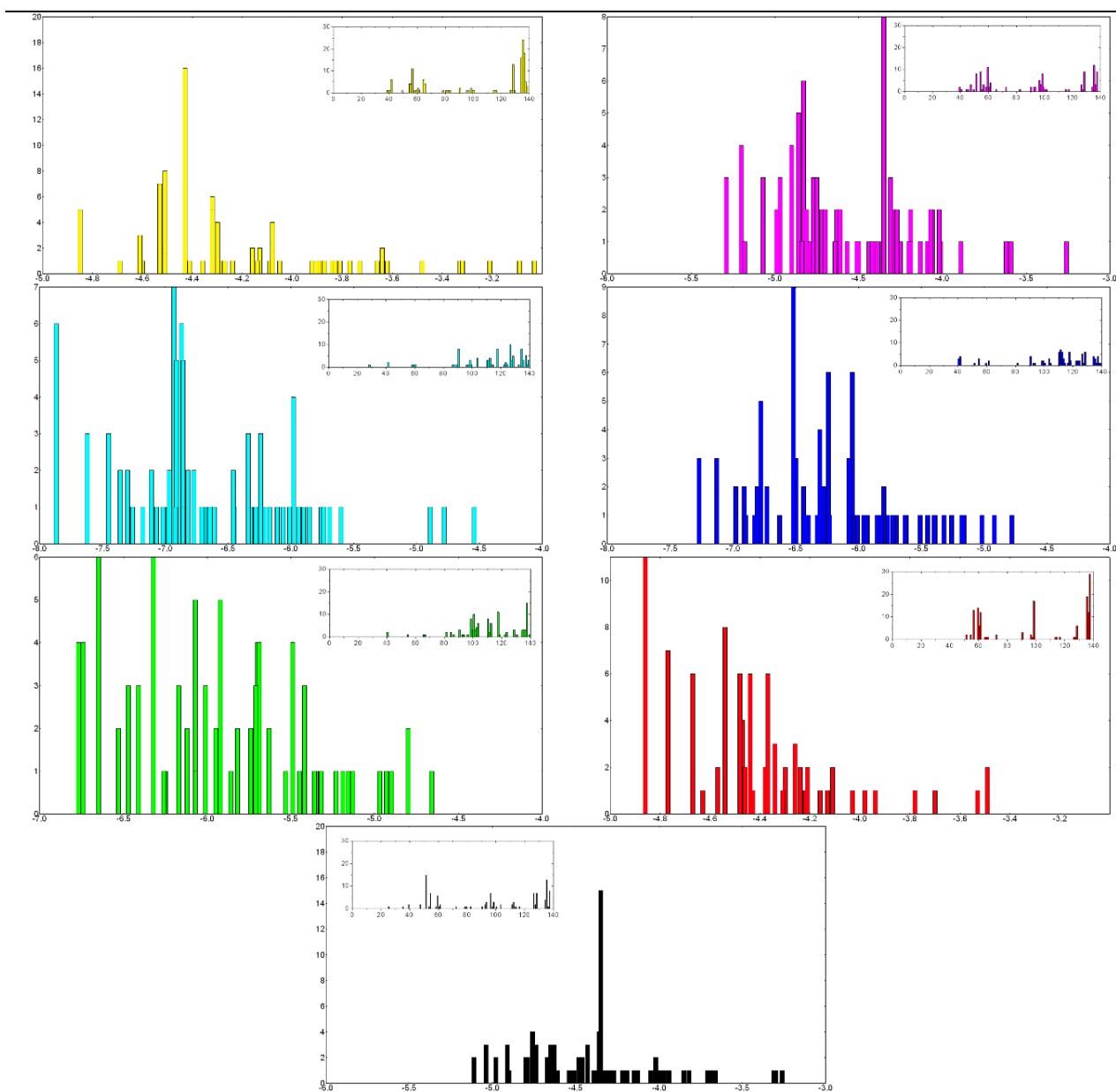




Cluster 5



## Cluster 6



**Figure S2. Molecular docking:** Results for the 100 runs for each of the 6 AS representatives conformations with DCH (yellow), DHI (pink), DOP (light blue), DOP-H (blue), DQ (green), IQ (red) and LEUK (black) (54 complexes). Clustering of the docking results, as implemented in AUTODOCK, plotted as a function of the AUTODOCK scoring function (in Kcal/mol). Inset: The number of hits (defined in Tab. 2SI) between AS and the respective ligand.