1. Select one or more structures from the pocketome (here the SAM binding site of the RNA methyltransferase NSUN4 [PDB code 4FP9])

2. Click display
3. Scroll-down for a bird’s eye view of the structurally closest pockets mapped on phylogenetic trees of epigenetic target classes

4. Click on a tree for more details

Legend

ND: no data available
- structure distance < 0.5
- structure distance < 0.75
- structure distance < 1
- structure distance < 1.5
- structure distance >= 1.5
5. Scroll-down to inspect values of structural distances on the selected tree

(In this example, we can see that the cofactor binding site of the RNA methyltransferase NSUN4 (selected in step #1) is closer to cofactor sites of Rossman fold methyltransferases (tree on the right), in particular DOT1L and PRMT5, than SET domain methyltransferases (tree on the left).)

Legend

ND: no data available
- structure distance < 0.5
- structure distance < 0.75
- structure distance < 1
- structure distance < 1.5
- structure distance >= 1.5