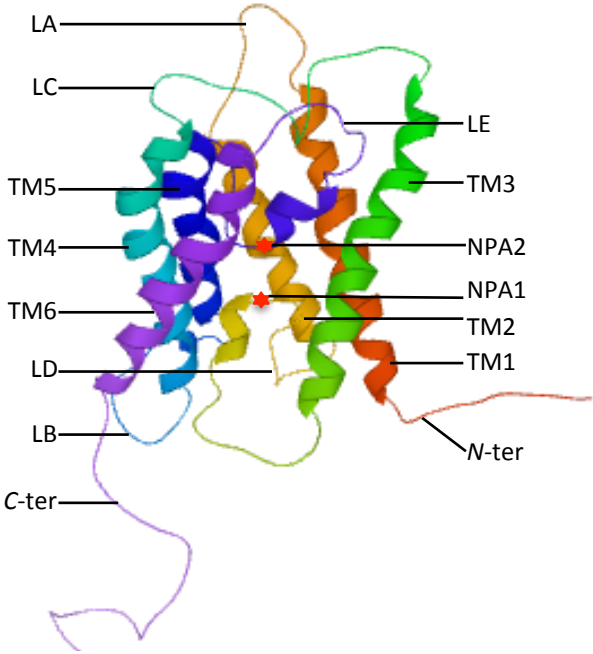


Figure S5

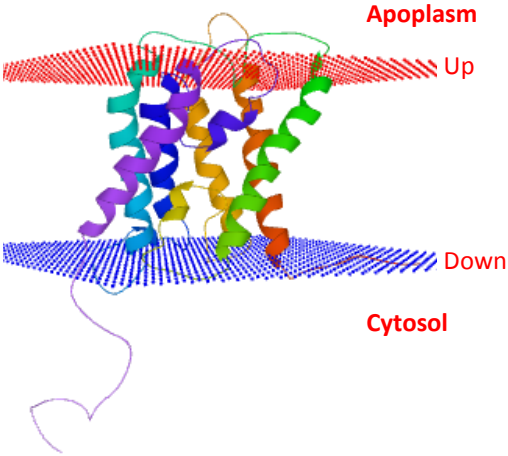
Figure S5. Predicted 3D models of the *Bpe*AQP monomers (*Bpe*PIP1s; *Bpe*PIP2s; *Bpe*TIPs; *Bpe*XIPs; *Bpe*NIPs; *Bpe*SIPs). Structures were generated by using the PHYRE2.0 Protein Fold Recognition server, using the Normal mode modeling based on alignment to experimentally solved protein structures, and built with the Mole2.5 software. Each structure is supported by the hydropathy and charge, indexes of the channel (right of the 3D modelisation), obtained by MOLE2.5 software. Each member is represented in lateral view. Models were visualized by rainbow color from *N*- to *C*-terminus, where the intracellular (B,D) and extracellular (A,C,E) loops, and transmembrane helices are shown, as firstly illustrated with the control structure (*So*PIP2,1 from *Spinacia oleracea*) with its lateral and top views, plus a representation of the structure embedded in the membrane.

Control structure, *SoPIP2;1*

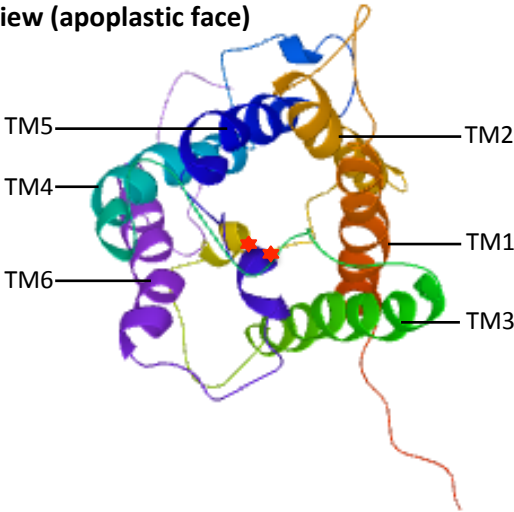
Lateral view



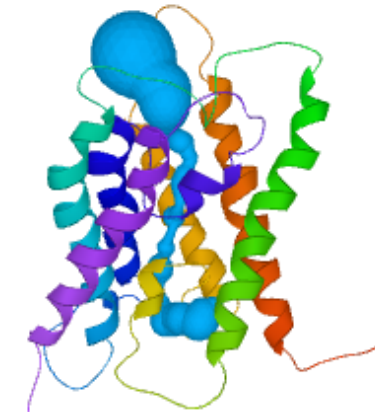
SoPIP2;1 structure embedded in the membrane



Top view (apoplastic face)

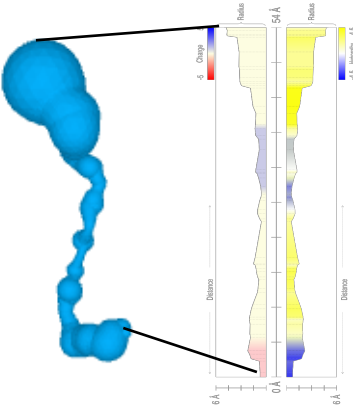


Physicochemical properties of *SoPIP2;1*pore structure



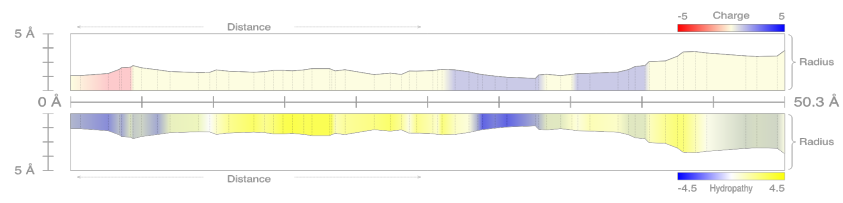
Model dimensions (Å) of *SoPIP2;1*

X:76.562 Y:49.788 Z:51.612

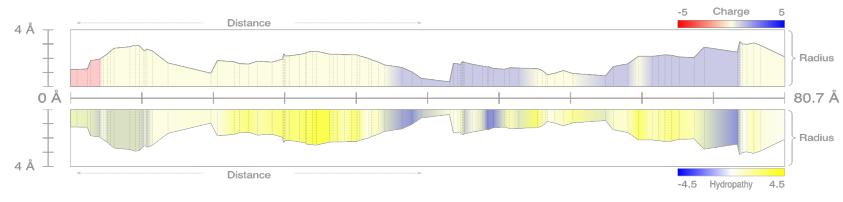


Length of the channel : 54 Å
Radius of the channel bottleneck : 0.6 Å
Average of hydrophobicity : 1.27
Charge : 0
Polarity (Average of lining amino acid polarities) : 8.47
Mutability, Average of relative mutability : 86
Lipophilicity, logP-scale : 1.04
Lipophilicity, logD-scale : 0.85
Ionizable residues : 2

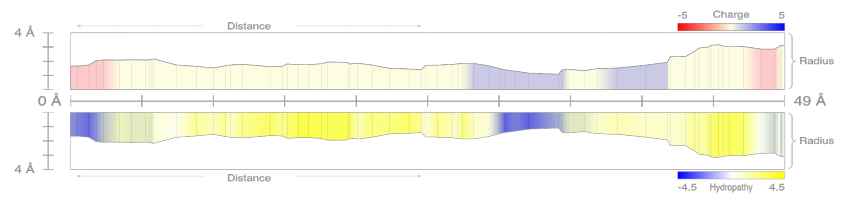
BpePIP1;1



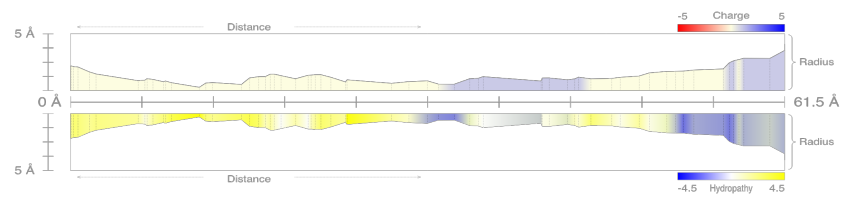
BpePIP1;2



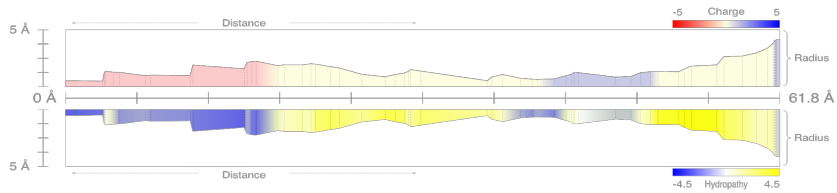
BpePIP1;3



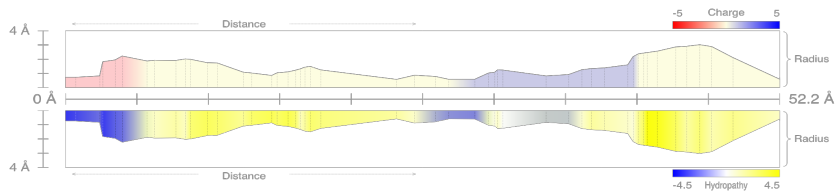
BpePIP1;4



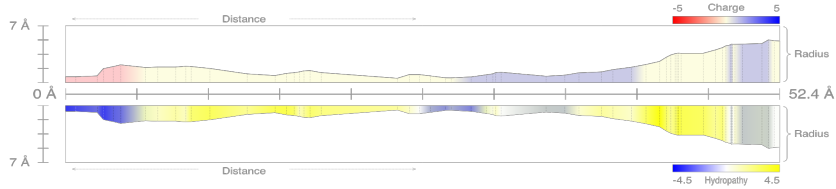
BpePIP2;1



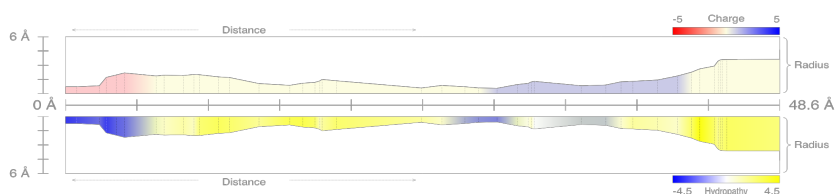
BpePIP2;2



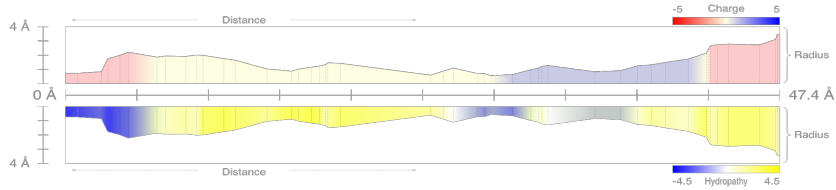
BpePIP2;3



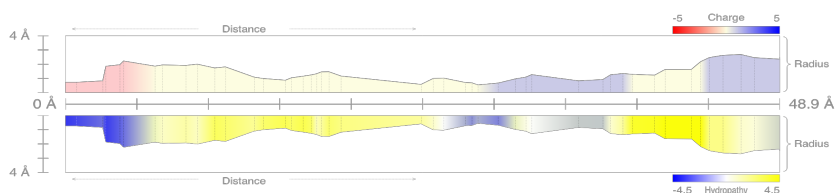
BpePIP2;4

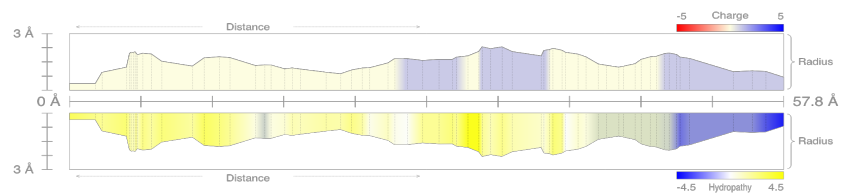
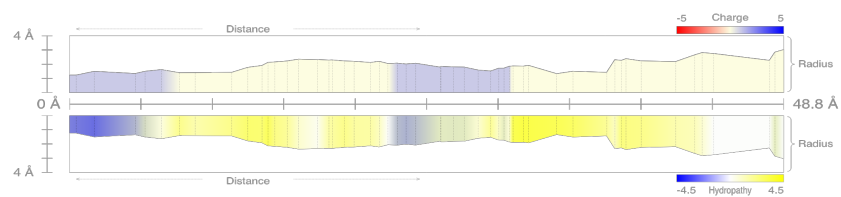
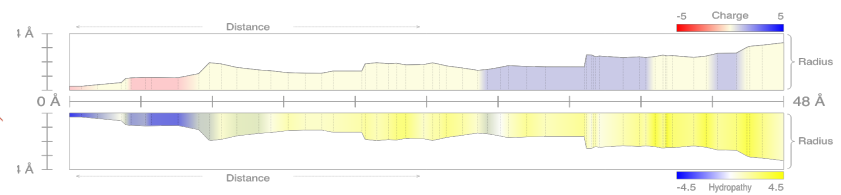
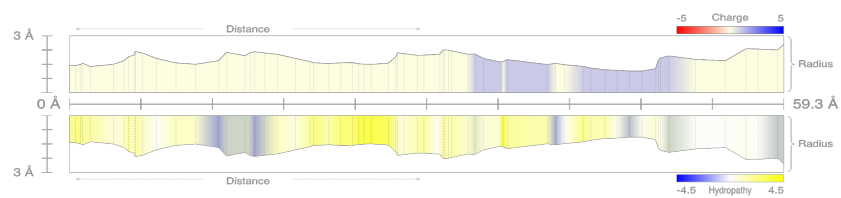


BpePIP2;5

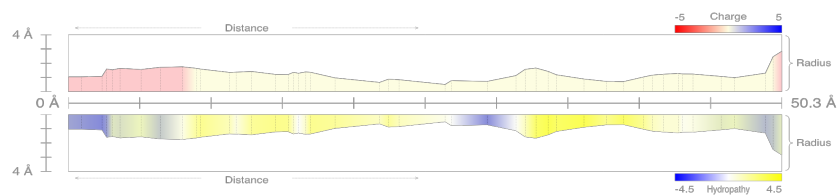


BpePIP2;6

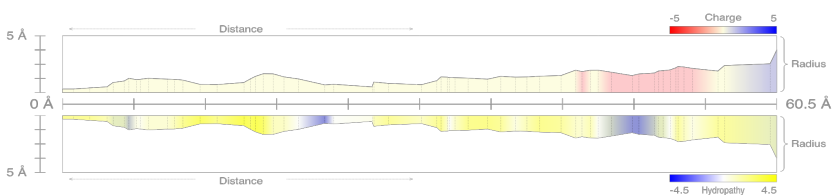


BpeXIP1;1***BpeXIP1;2******BpeXIP1;3******BpeXIP2;1***

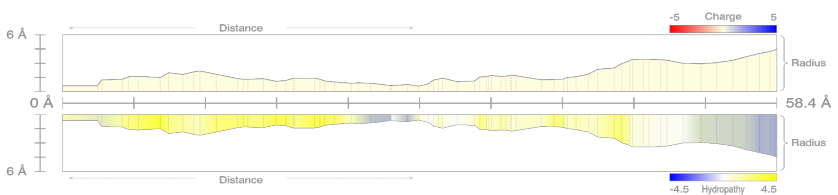
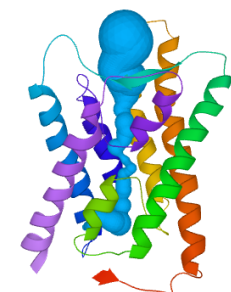
BpeTIP1;1



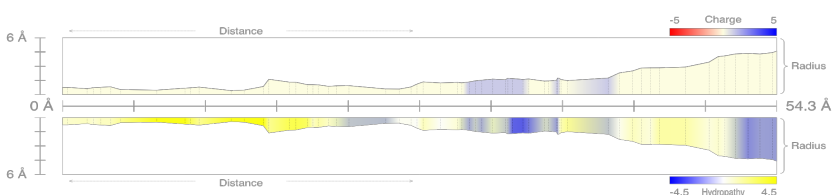
BpeTIP1;2



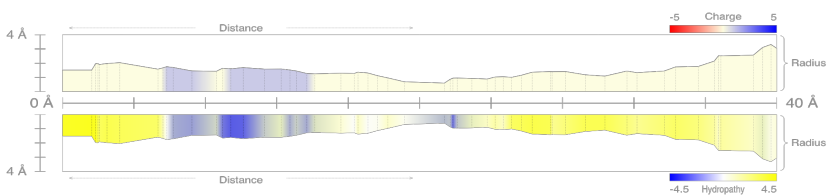
BpeTIP1;3



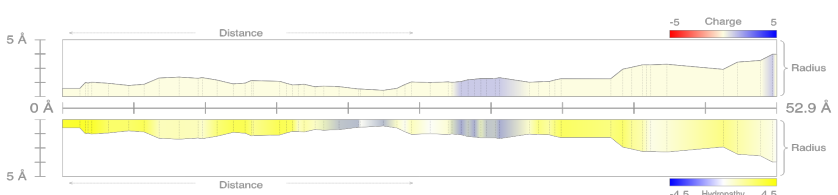
BpeTIP2;1



BpeTIP2;2

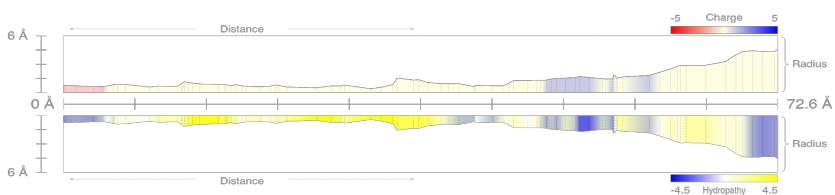


BpeTIP3;1

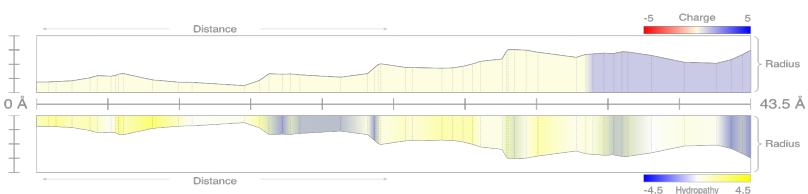


BpeTIPs

BpeTIP4;1

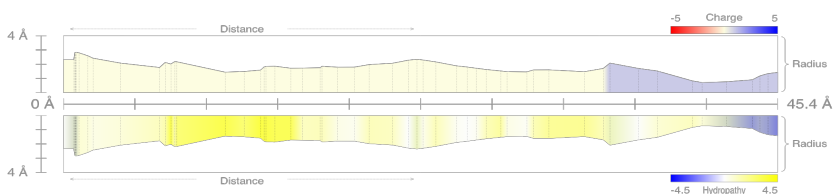
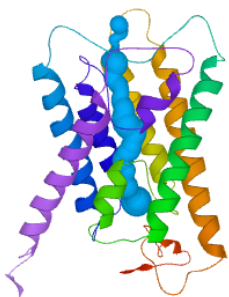


BpeTIP5;1

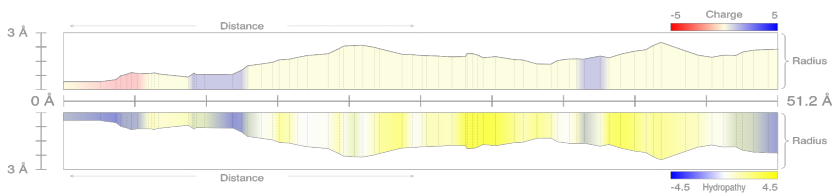


BpeNIPs

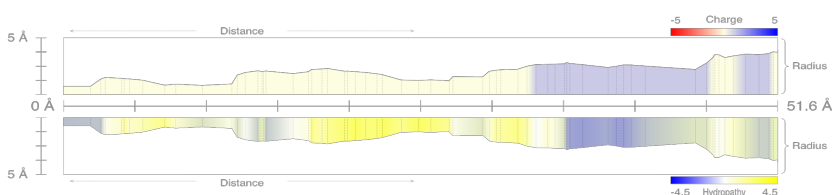
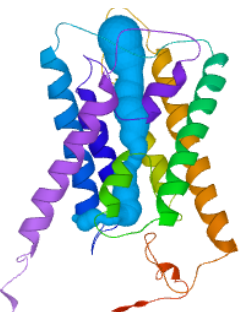
BpeNIP1;1



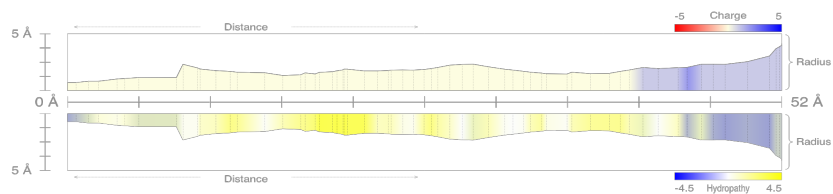
BpeNIP1;2



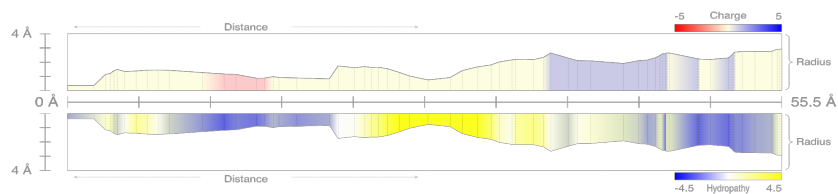
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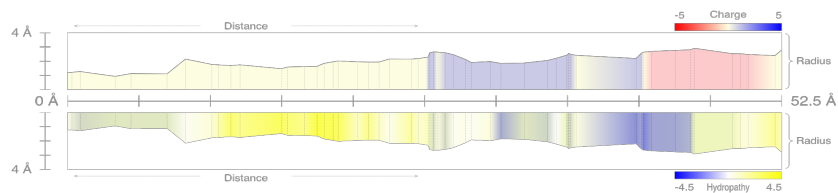
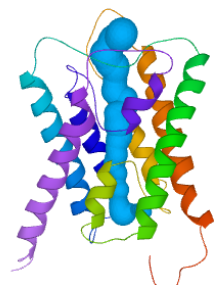
BpeNIP4;1



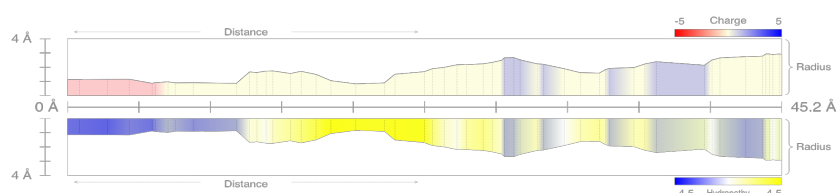
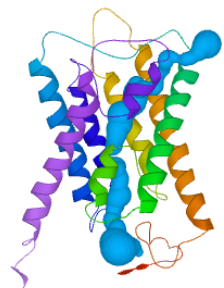
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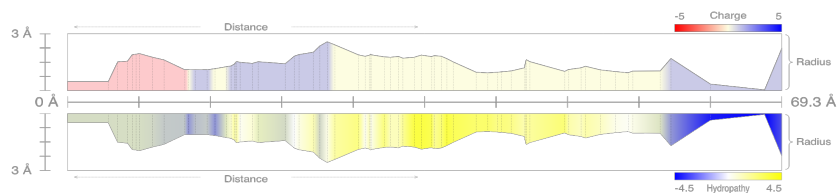
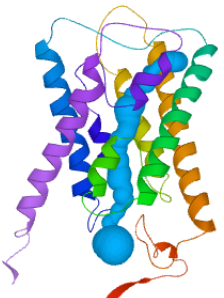
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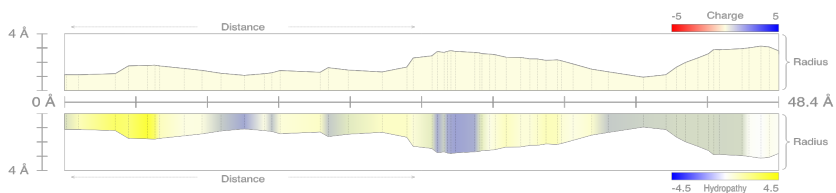
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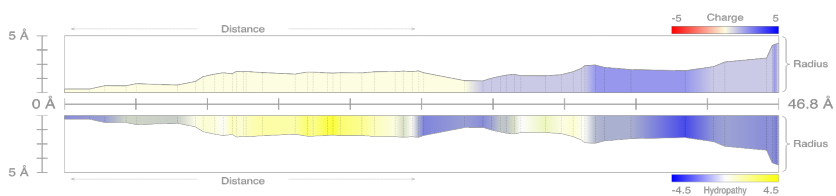
BpeNP7;1



BpeSIP1;1



BpeSIP1;2



BpeSIP2;1

