

Phylogenetic tree showing relationships between various sequences, likely related to the H1N1 influenza virus. The tree is rooted at the top and branches downwards. The sequences are labeled with accession numbers and identifiers, such as H1N1_2009, H1N1_2009, H1N1_2009, etc. The tree is color-coded by sequence type: blue for H1N1_2009, red for H1N1_2009, green for H1N1_2009, and yellow for H1N1_2009. The tree is divided into several major clades, including H1N1_2009, H1N1_2009, H1N1_2009, and H1N1_2009. The tree is rooted at the top and branches downwards. The sequences are labeled with accession numbers and identifiers, such as H1N1_2009, H1N1_2009, H1N1_2009, etc. The tree is color-coded by sequence type: blue for H1N1_2009, red for H1N1_2009, green for H1N1_2009, and yellow for H1N1_2009. The tree is divided into several major clades, including H1N1_2009, H1N1_2009, H1N1_2009, and H1N1_2009.