The novel influenza A virus (H1N1 swine flu) belonging to Orthomyxoviridae Family, causes respiratory diseases and is known to be pandemic at phase 6 with 30,000 cases reported in 74 countries of the world. Because of the development of resistance to drugs and antivirals i.e. amantadine, rimantadine, seltamivir, zanamivir, the only effective therapy emerging against the influenza subtypes is the epitope based vaccine to control the rapidly growing viral disease, that reduce the adverse effects. At present, 17 Asian countries have reported sequences of full genome of H virus. The protein sequences have been used in the immunoinformatics study and construction of phylogenetic trees. All the epitopes were predicted against selected alleles of 10 MHC I Supertypes (A2, A3, B7, B15, A24, 844, 857, ABX, 827 and BX) and 8 MHC II alleles of Supertype DRB1 that covers 99% Asian population. Promiscuous epitopes from conserved regions were selected as antigenic candidates for future epitope based vaccine design. The maximum number of MHCI epitopes was from H viral protein P81 followed by P82 and PA, and MHC II epitopes from PB2 followed by PB and PA. These epitopes have important implications for the rational design of. CTL epitope based Hi Ni vaccines and diagnostics that will be effective for all the Asian population. The phylogenetic analysis divides H1N1 whole genome sequences into different clades viz., M M2, PB1 and HA and PB2 and PA show closer resemblance to each other. This information would be important for prediction of structural and functional aspects of unknown proteins which is the prerequisite for docking analysis during drug and vaccine designing.