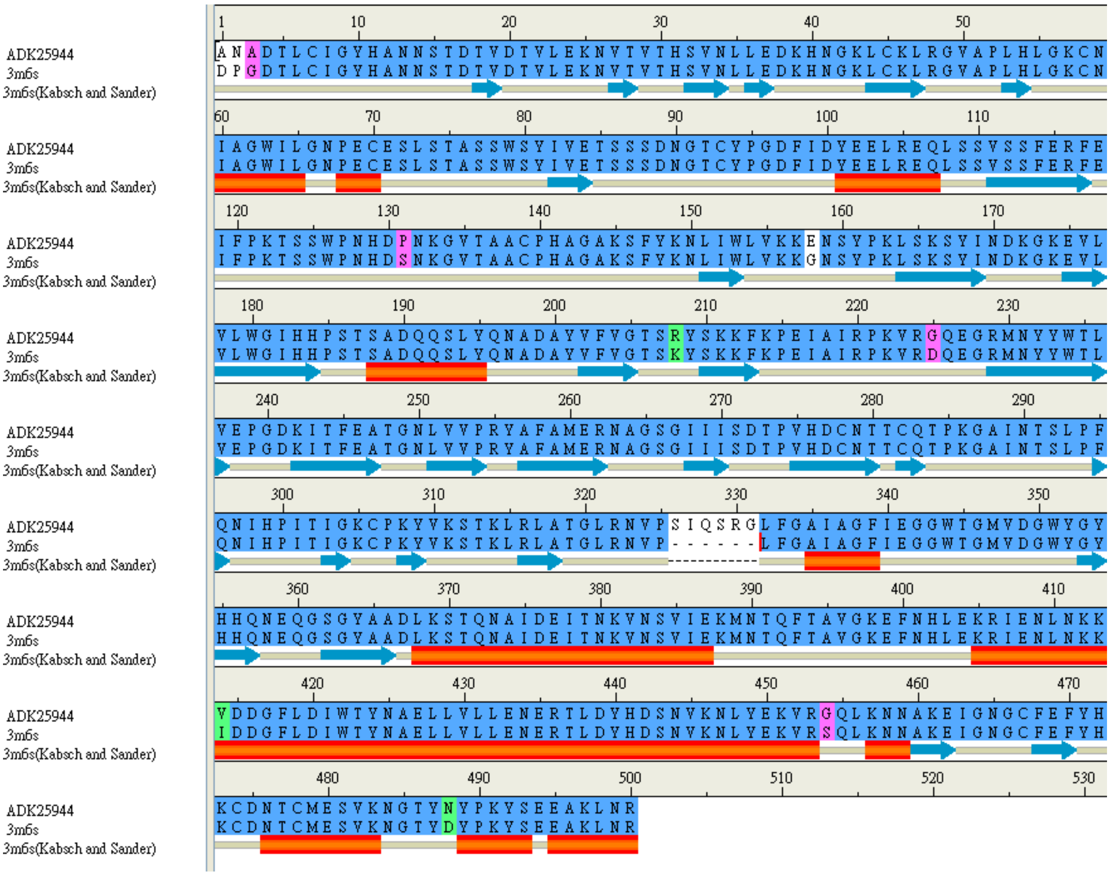

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ADK25944                    ANADTLCIGYHANNSTDTVDTVLEKNVTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCN
3m6s                        DPGDTLCIGYHANNSTDTVDTVLEKNVTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCN
3m6s(Kabsch and Sander)

ADK25944                    IAGWILGNPECESLSTASSWSYIVETSSSDNGTCYPGDFIDYEELREQLSSVSSFERFE
3m6s                        IAGWILGNPECESLSTASSWSYIVETSSSDNGTCYPGDFIDYEELREQLSSVSSFERFE
3m6s(Kabsch and Sander)

ADK25944                    IFPKTSSWPNHDPNKGVTAACPHAGAKSFYKNLIWLVKKENSYPKLSKSYINDKGKEVL
3m6s                        IFPKTSSWPNHDSNKGVTAACPHAGAKSFYKNLIWLVKKGNSYPKLSKSYINDKGKEVL
3m6s(Kabsch and Sander)

ADK25944                    VLWGIHHPSTSADQQSLYQNADAYVFVGTSRYSKKFKPEIAIRPKVRGQEGRMNYYWTL
3m6s                        VLWGIHHPSTSADQQSLYQNADAYVFVGTSKYSKKFKPEIAIRPKVRDQEGRMNYYWTL
3m6s(Kabsch and Sander)

ADK25944                    VEPGDKITFEATGNLVVPRYAFAMERNAGSGIIISDTPVHDCNTTCQTPKGAINTSLPF
3m6s                        VEPGDKITFEATGNLVVPRYAFAMERNAGSGIIISDTPVHDCNTTCQTPKGAINTSLPF
3m6s(Kabsch and Sander)

ADK25944                    QNIHPITIGKCPKYVKSTKLRLATGLRNVPSIQSRGLFGAIAGFIEGGWTGMVDGWYGY
3m6s                        QNIHPITIGKCPKYVKSTKLRLATGLRNVP------LFGAIAGFIEGGWTGMVDGWYGY
3m6s(Kabsch and Sander)

ADK25944                    HHQNEQGSGYAADLKSTQNAIDEITNKVNSVIEKMNTQFTAVGKEFNHLEKRIENLNKK
3m6s                        HHQNEQGSGYAADLKSTQNAIDEITNKVNSVIEKMNTQFTAVGKEFNHLEKRIENLNKK
3m6s(Kabsch and Sander)

ADK25944                    VDDGFLDIWTYNAELLVLLENERTLDYHDSNVKNLYEKVRGQLKNNAKEIGNGCFEFYH
3m6s                        IDDGFLDIWTYNAELLVLLENERTLDYHDSNVKNLYEKVRSQLKNNAKEIGNGCFEFYH
3m6s(Kabsch and Sander)

ADK25944                    KCDNTCMESVKNGTYNYPKYSEEAKLNR
3m6s                        KCDNTCMESVKNGTYDYPKYSEEAKLNR
3m6s(Kabsch and Sander)
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Figure S1. Sequence alignment between new H1 (ADK25944) and template H1 sequence (3M6S). The identity and similarity were 96.8 % and 97.4 % respectively.

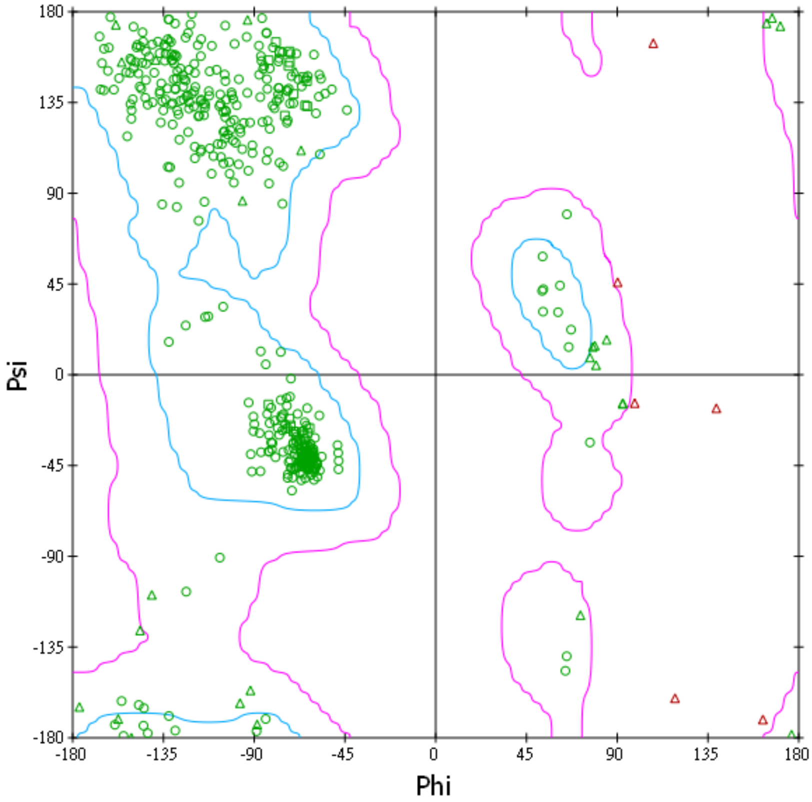

Figure S2. The Ramachandran plot of modeled H1 structure constructed through homology modeling. The generated plot indicates that 94.2 % of the residues were located in the favored region (cyan area), 4.6 % of residues were located in semi-favored region (magenta area), and 1.2 % of residues were located in disfavored region.

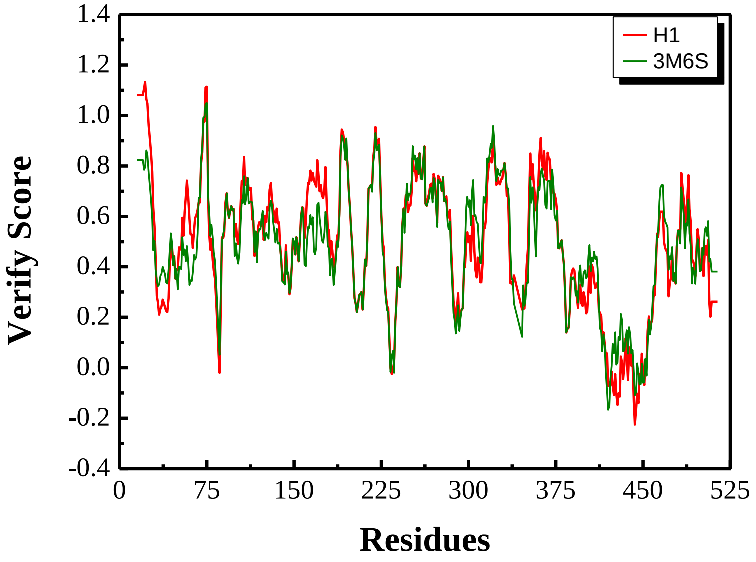

Figure S3. The profile-3D results of modeled and template H1 structures (3M6S). The binding site residues Lys71, Asp103, Asn104, and Arg238 have positive scores, indicating reasonable conformation.