a) D124V (3H2P)

b) D125H (1P1V)
Fig. S1 Representing the D124V, D125H and S134N mutated E-loops in whole protein structure. The individual E-loop for the respective mutations is shown in left side labelled with residue names and numbers a) D124V (PDB CODE: 3H2P) b) D125H (PDB CODE: 1P1V) and c) S134N (PDB CODE: 1OZU)

a) 5-Fluorouridine

b) Isoproteranol
c) \((4-(4\text{-methyl-1, 4-diazepan-1-yl})-2-(\text{trifluoromethyl}) \text{ quinazoline})\)

d) Uridine-5’-Monophosphate

Fig. S2 Representing the structure of various chemical compounds a) 5-Fluorouridine, b) Isoproteranol, c) \((4-(4\text{-methyl-1, 4-diazepan-1-yl})-2-(\text{trifluoromethyl}) \text{ quinazoline})\), d) Uridine-5’-Monophosphate.
Fig. S3 Representing the best docked structure of three mutated E-loops subjected to docking with 5-Fluorouridine [5UD], Isoproteranol [5FW] and 4-(4-methyl-1, 4-diazepan-1-yl)-2-(trifluromethyl) quinazoline [MDTQ]. a) D124V + 5UD, b) D124V +5FW, c) D124V + MDTQ, d) D125H + 5UD, e) D125H + 5FW, f) D125H + MDTQ, g) S134N + 5UD, h) S134N + 5FW, i) S134N + MDTQ.
a) RMSD for E-Loop in Native, Mutated forms along with mutated form interacted with Chemical Compounds

b) RMSD for E-Loop in Native, and Mutated forms along with mutated forms interacted with chemical compounds
Fig. S4 Representing the RMSD for different mutated E-loops interacting with 5-Fluorouridine [5UD] and Isoproteranol [5FW] along with native state E-loop. a) D124V mutated E-loop interacting with 5UD and 5FW, b) D125H mutated E-loop interacting with 5UD and 5FW, c) S134N mutated E-loop interacting with 5UD and 5FW.
Fig. S5 Representing the spatial distribution of Electrostatic potential across the box. a) D124V mutated E-loop interacting with different chemical compounds, b) D125H mutated E-loop interacting with different chemical compounds, c) S134N mutated E-loop interacting with different chemical compounds.
g) Interaction between Protein atom and 5-Flourouridine

h) Interaction between Protein atoms and MDTQ

- Electrostatic
- Van der Waals
- Total

TIME (ps)
Interaction between Protein atoms and Isoproterenol

Interaction ENERGY $kJ \cdot mol^{-1}$

TIME (ps)

- Electrostatic
- Van der Waals
- Total
Fig. S6 Representing Interaction energy for mutated E-loops with 5-Fluorouridine [5UD], 4-(4-methyl-1, 4-diazepan-1-yl)-2-(trifluromethyl) quinazoline [MDTQ] and Isoproteranol [5FW]. a) D124V+5UD, b) D124V+MDTQ, c) D124V+5FW, d) D125H+5UD, e) D125H+MDTQ, f) D125H+5FW, g) S134N+5UD, h) S134N+MDTQ, i) S134N+5FW.
Fig. S7 Representing the Free energy landscape of three mutated E-loops interacting with 5-Fluorouridine [5UD], Isoproteranol [5FW], 4-(4-methyl-1, 4-diazepan-1-yl)-2-(trifluromethyl) quinazoline [MDTQ] and Uridine-5'-Monophosphate [U5P] involving RMSD and Rg for the trajectory of 50ns for. a) D124V+5UD, b) D124V+5FW, c) D124V+U5P, d) D124V+MDTQ, e) D125H+5UD, f) D125H+5FW, g) D125H+U5P, h) D125H+MDTQ, i) S134N+5UD, j) S134N+5FW, k) S134N+U5P, l) S134N+MDTQ.