Supplementary Information

In Silico Studies of Interactions of Peptide Conjugated Cholesterol Metabolites and Betulinic acid with EGFR, LDR and N-terminal Fragment of CCKA Receptors

*Madeline M. Bashant, Saige M. Mitchell, Lucy R. Hart, Charlotta G. Lebedenko and Ipsita A. Banerjee**

Department of Chemistry, Fordham University 441 East Fordham Road, Bronx New York 10458, USA

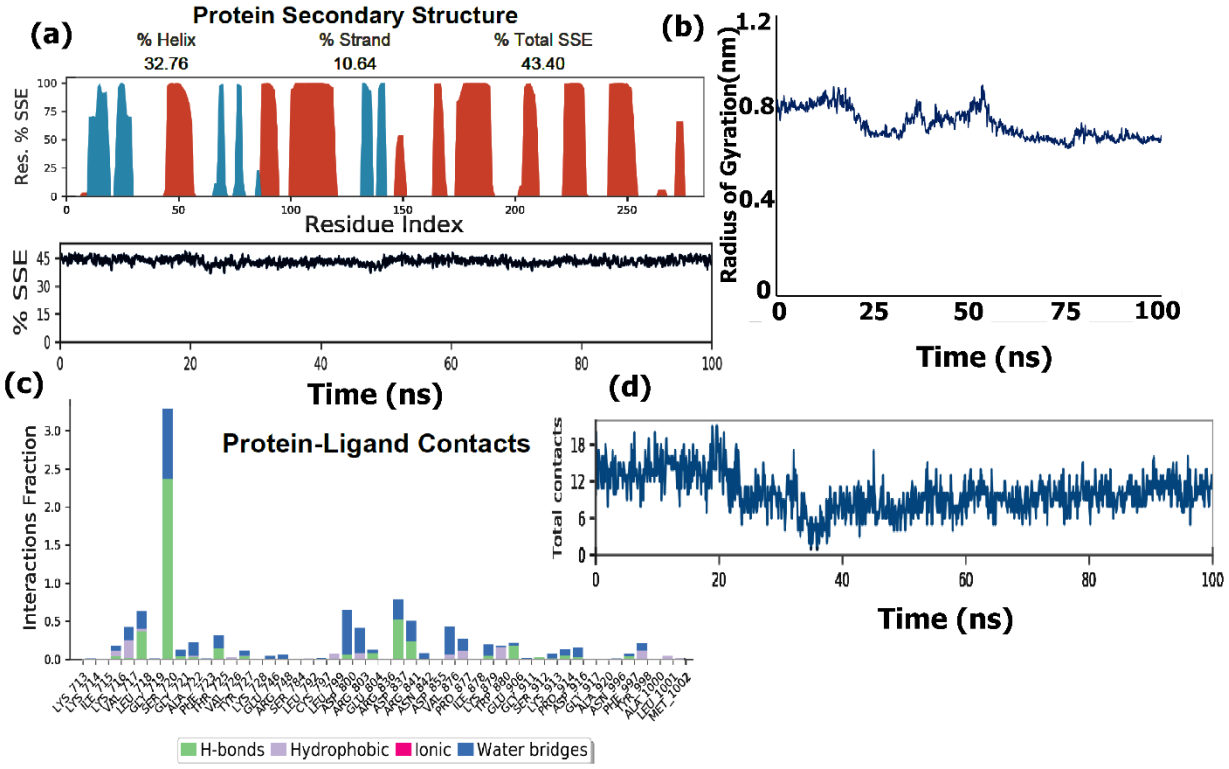

Figure S1. (a) Receptor secondary structure elements (SSE) distribution during the simulation of unconjugated tumor targeting peptide complexed with EGFR receptor (2RGP). (Orange = alpha helices; blue = beta strands and white = loops). The graphical plot shows the SSE composition for each trajectory frame over the course of the simulation. (b) Radius of gyration of neat tumor targeting peptide ligand during the simulation period; (c) Receptor contacts with the tumor targeting peptide monitored throughout the simulation showing hydrogen bonds, hydrophobic, ionic interactions and water bridges normalized over the course of the trajectory. A value of 0.7 suggests that interaction is maintained during 70% of the simulation time. Values over 1.0 indicate protein residues that may make multiple contacts of same subtype with the neat tumor targeting peptide ligand (d) Total number of specific contacts the receptor makes with the neat tumor targeting peptide over the course of the trajectory.

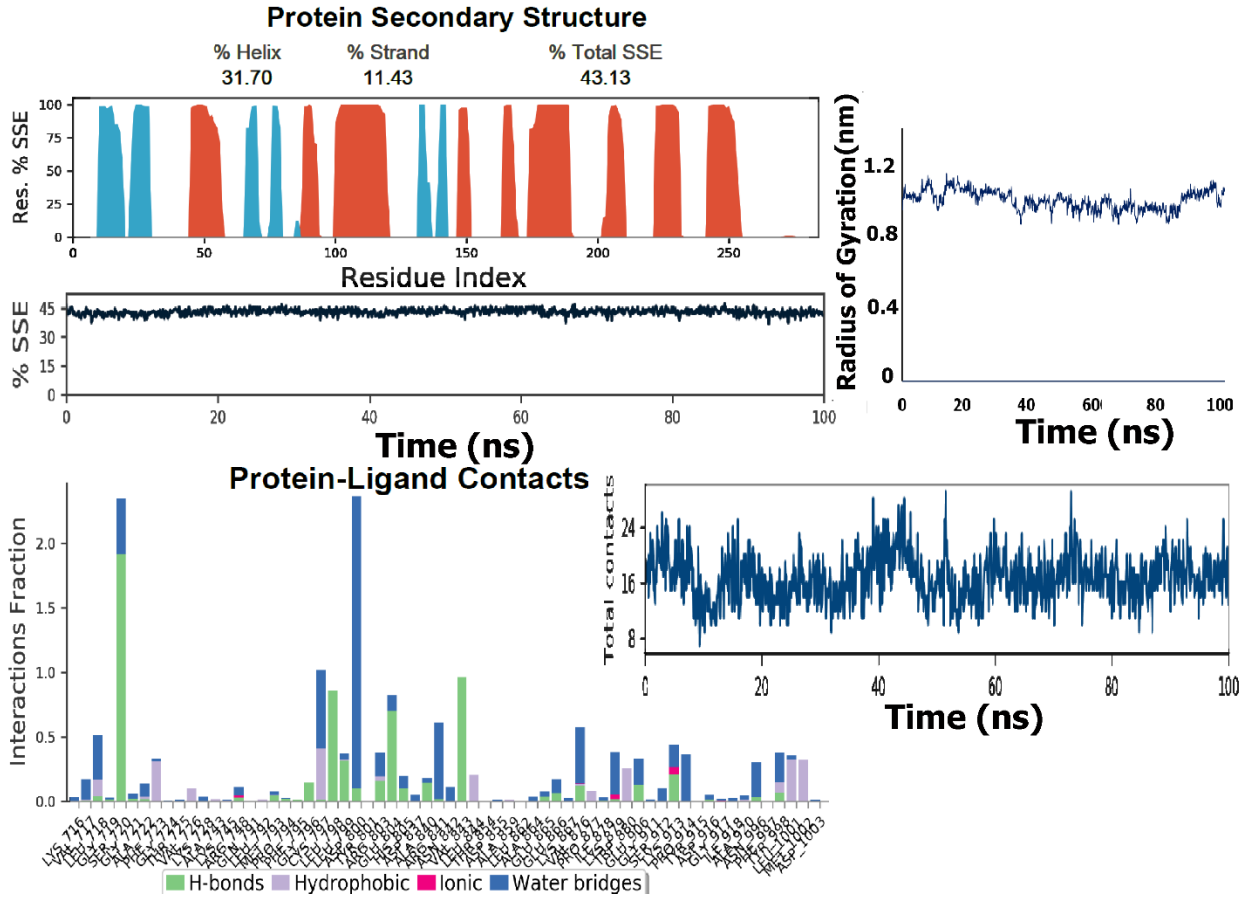

Figure S2. (a) Receptor secondary structure elements (SSE) distribution during the simulation of BT-peptide conjugate complexed with EGFR (2RGP) receptor. (Orange = alpha helices; blue = beta strands and white = loops). The graphical plot shows the SSE composition for each trajectory frame over the course of the simulation. (b) Radius of gyration of BT-peptide conjugate ligand during the simulation period; (c) Receptor contacts with the BT-peptide conjugate monitored throughout the simulation showing hydrogen bonds, hydrophobic, ionic interactions and water bridges normalized over the course of the trajectory. A value of 0.7 suggests that interaction is maintained during 70% of the simulation time. Values over 1.0 indicate protein residues that may make multiple contacts of same subtype with the neat tumor targeting peptide ligand (d) Total number of specific contacts the receptor makes with the BT-peptide conjugate over the course of the trajectory.

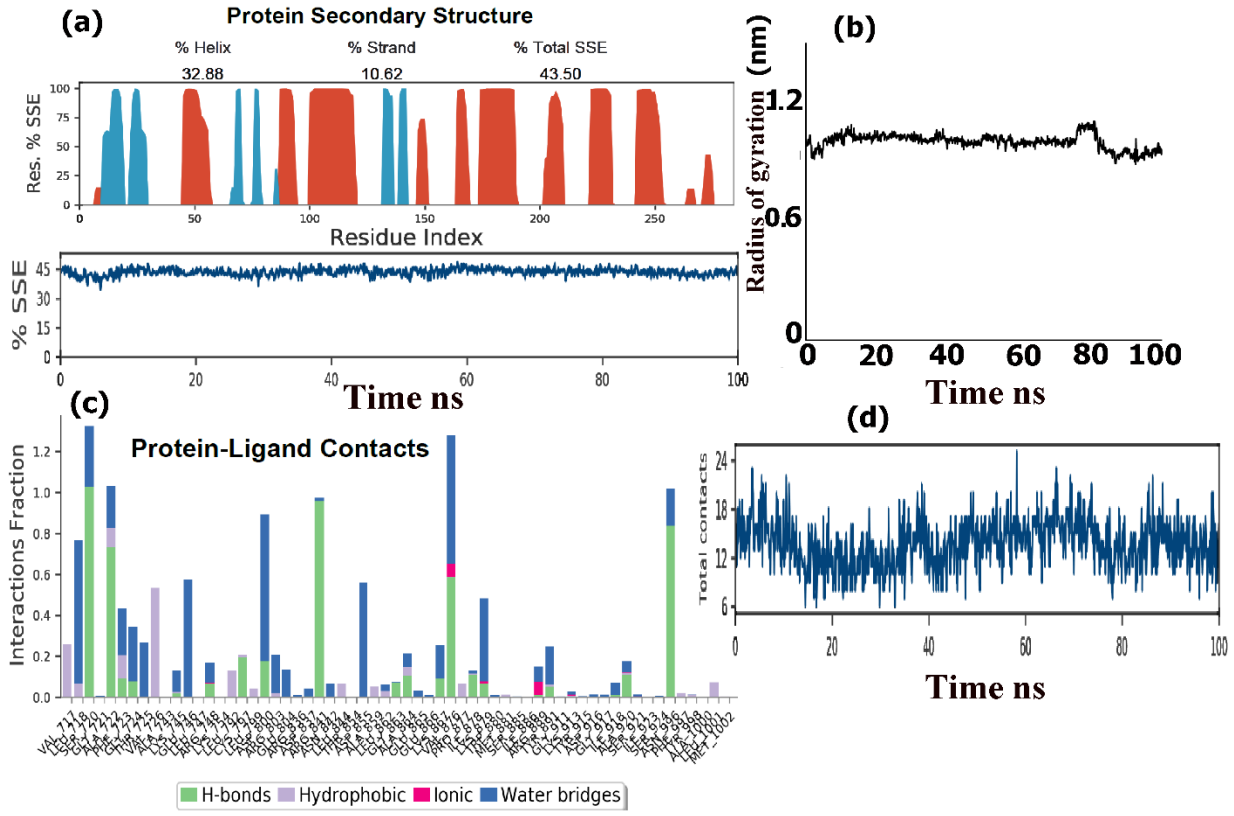

Figure S3. (a) Receptor secondary structure elements (SSE) distribution during the simulation of 3HC-peptide conjugate complexed with EGFR (2RGP) receptor. (Orange = alpha helices; blue = beta strands and white = loops). The graphical plot shows the SSE composition for each trajectory frame over the course of the simulation. (b) Radius of gyration of 3HC-peptide conjugate ligand during the simulation period; (c) Receptor contacts with the 3HC-peptide conjugate monitored throughout the simulation showing hydrogen bonds, hydrophobic, ionic interactions and water bridges normalized over the course of the trajectory. A value of 0.7 suggests that interaction is maintained during 70% of the simulation time. Values over 1.0 indicate protein residues that may make multiple contacts of same subtype with the neat tumor targeting peptide ligand (d) Total number of specific contacts the receptor makes with the 3HC-peptide conjugate over the course of the trajectory.

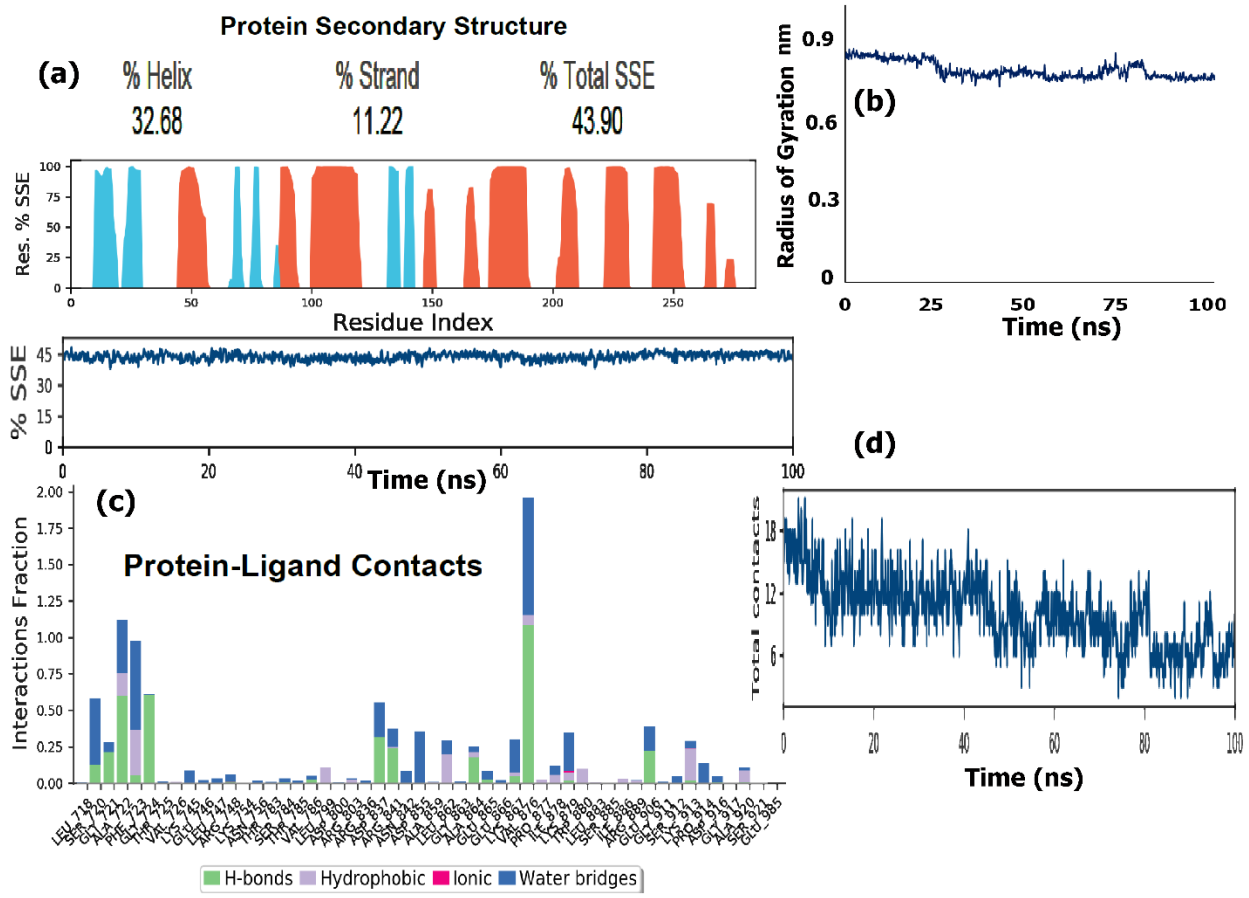

Figure S4. (a) Receptor secondary structure elements (SSE) distribution during the simulation of 3OC-peptide conjugate complexed with EGFR (2RGP) receptor. (Orange = alpha helices; blue = beta strands and white = loops). The graphical plot shows the SSE composition for each trajectory frame over the course of the simulation. (b) Radius of gyration of 3OC-peptide conjugate ligand during the simulation period; (c) Receptor contacts with the 3OC-peptide conjugate monitored throughout the simulation showing hydrogen bonds, hydrophobic, ionic interactions and water bridges normalized over the course of the trajectory. A value of 0.7 suggests that interaction is maintained during 70% of the simulation time. Values over 1.0 indicate protein residues that may make multiple contacts of same subtype with the neat tumor targeting peptide ligand (d) Total number of specific contacts the receptor makes with the 3OC-peptide conjugate over the course of the trajectory.

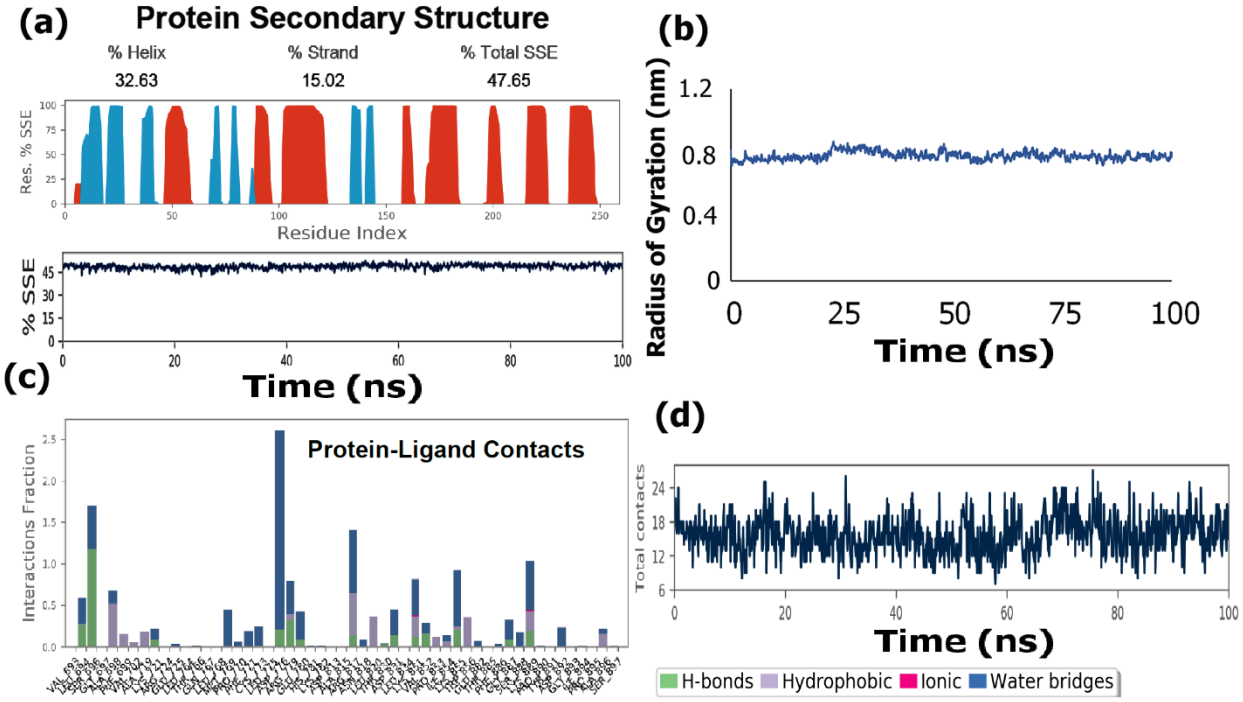

Figure S5. (a) Receptor secondary structure elements (SSE) distribution during the simulation of unconjugated tumor targeting peptide complexed with EGFR receptor (3LZB). (Orange = alpha helices; blue = beta strands and white = loops). The graphical plot shows the SSE composition for each trajectory frame over the course of the simulation. (b) Radius of gyration of neat tumor targeting peptide ligand during the simulation period; (c) Receptor contacts with the tumor targeting peptide monitored throughout the simulation showing hydrogen bonds, hydrophobic, ionic interactions and water bridges normalized over the course of the trajectory. A value of 0.7 suggests that interaction is maintained during 70% of the simulation time. Values over 1.0 indicate protein residues that may make multiple contacts of same subtype with the neat tumor targeting peptide ligand (d) Total number of specific contacts the receptor makes with the neat tumor targeting peptide over the course of the trajectory.

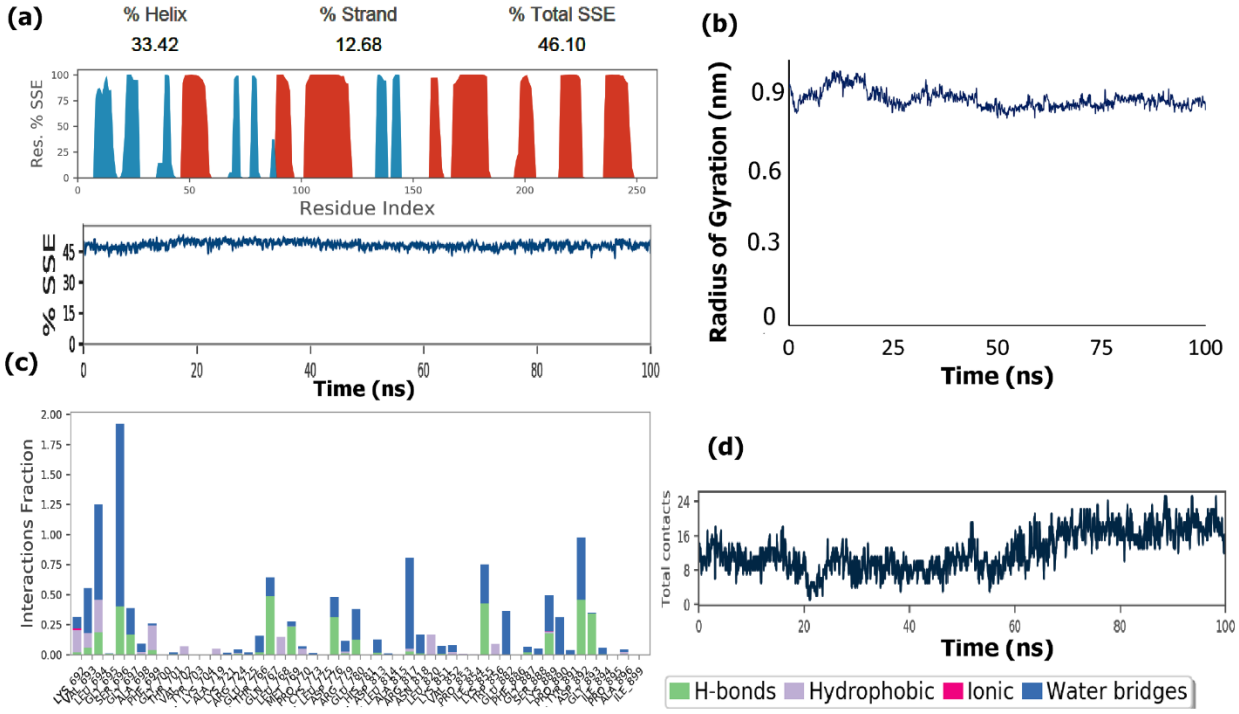

Figure S6. (a) Receptor secondary structure elements (SSE) distribution during the simulation of BT-peptide conjugate complexed with EGFR (3LZB) receptor. (Orange = alpha helices; blue = beta strands and white = loops). The graphical plot shows the SSE composition for each trajectory frame over the course of the simulation. (b) Radius of gyration of BT-peptide conjugate ligand during the simulation period; (c) Receptor contacts with the BT-peptide conjugate monitored throughout the simulation showing hydrogen bonds, hydrophobic, ionic interactions and water bridges normalized over the course of the trajectory. A value of 0.7 suggests that interaction is maintained during 70% of the simulation time. Values over 1.0 indicate protein residues that may make multiple contacts of same subtype with the neat tumor targeting peptide ligand (d) Total number of specific contacts the receptor makes with the BT-peptide conjugate over the course of the trajectory.

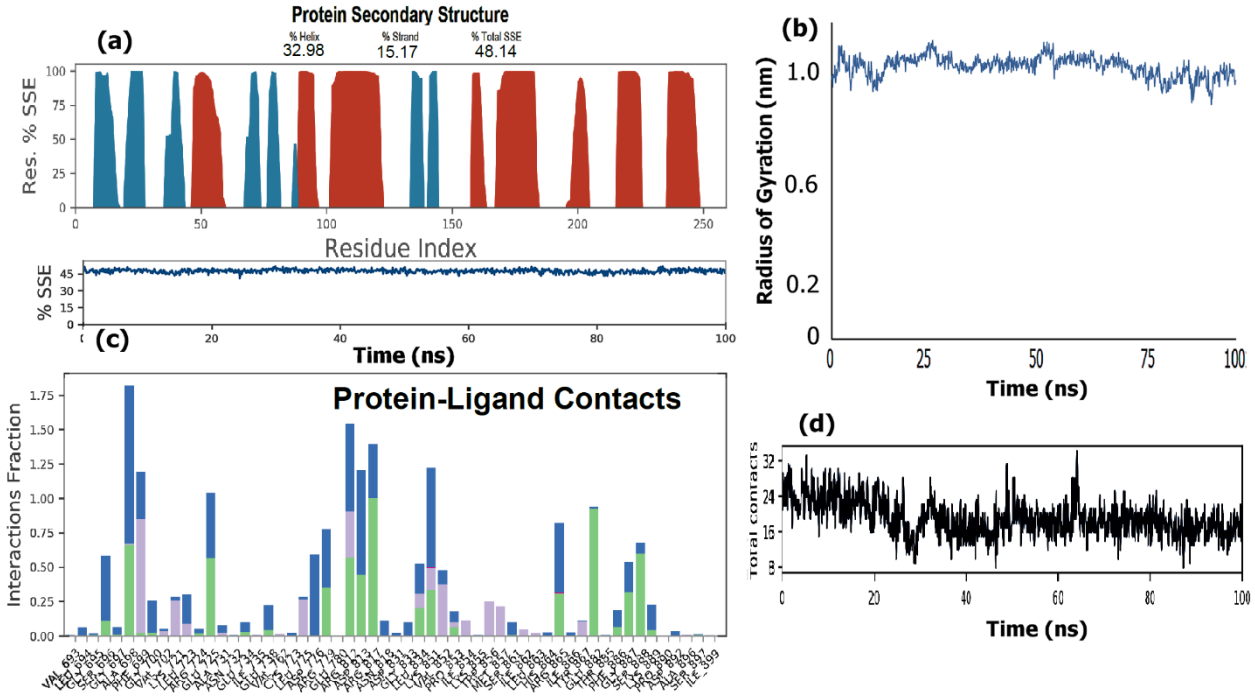

Figure S7. (a) Receptor secondary structure elements (SSE) distribution during the simulation of 3HC-peptide conjugate complexed with EGFR (3LZB) receptor. (Orange = alpha helices; blue = beta strands and white = loops). The graphical plot shows the SSE composition for each trajectory frame over the course of the simulation. (b) Radius of gyration of 3HC-peptide conjugate ligand during the simulation period; (c) Receptor contacts with the 3HC-peptide conjugate monitored throughout the simulation showing hydrogen bonds, hydrophobic, ionic interactions and water bridges normalized over the course of the trajectory. A value of 0.7 suggests that interaction is maintained during 70% of the simulation time. Values over 1.0 indicate protein residues that may make multiple contacts of same subtype with the neat tumor targeting peptide ligand (d) Total number of specific contacts the receptor makes with the 3HC-peptide conjugate over the course of the trajectory.

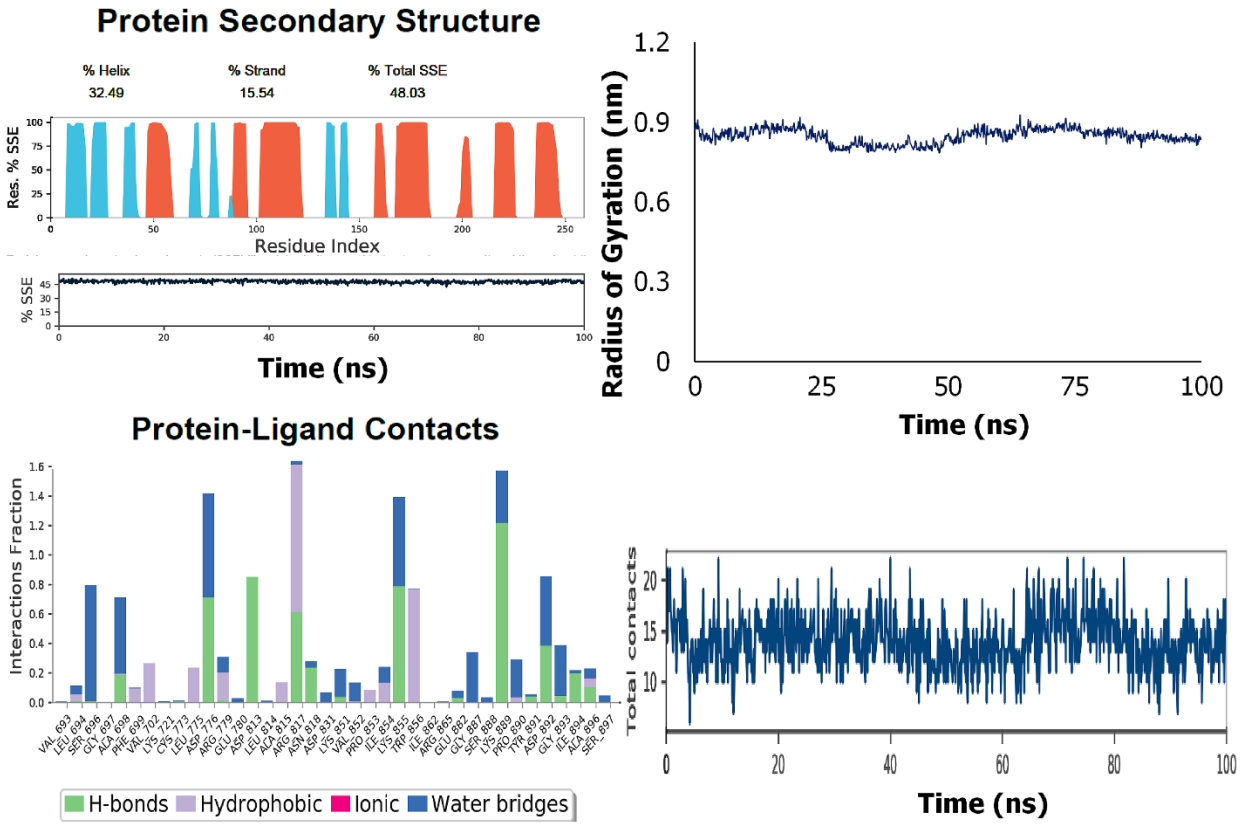

Figure S8. (a) Receptor secondary structure elements (SSE) distribution during the simulation of 3OC-peptide conjugate complexed with EGFR (3LZB) receptor. (Orange = alpha helices; blue = beta strands and white = loops). The graphical plot shows the SSE composition for each trajectory frame over the course of the simulation. (b) Radius of gyration of 3OC-peptide conjugate ligand during the simulation period; (c) Receptor contacts with the 3OC-peptide conjugate monitored throughout the simulation showing hydrogen bonds, hydrophobic, ionic interactions and water bridges normalized over the course of the trajectory. A value of 0.7 suggests that interaction is maintained during 70% of the simulation time. Values over 1.0 indicate protein residues that may make multiple contacts of same subtype with the neat tumor targeting peptide ligand (d) Total number of specific contacts the receptor makes with the 3OC-peptide conjugate over the course of the trajectory

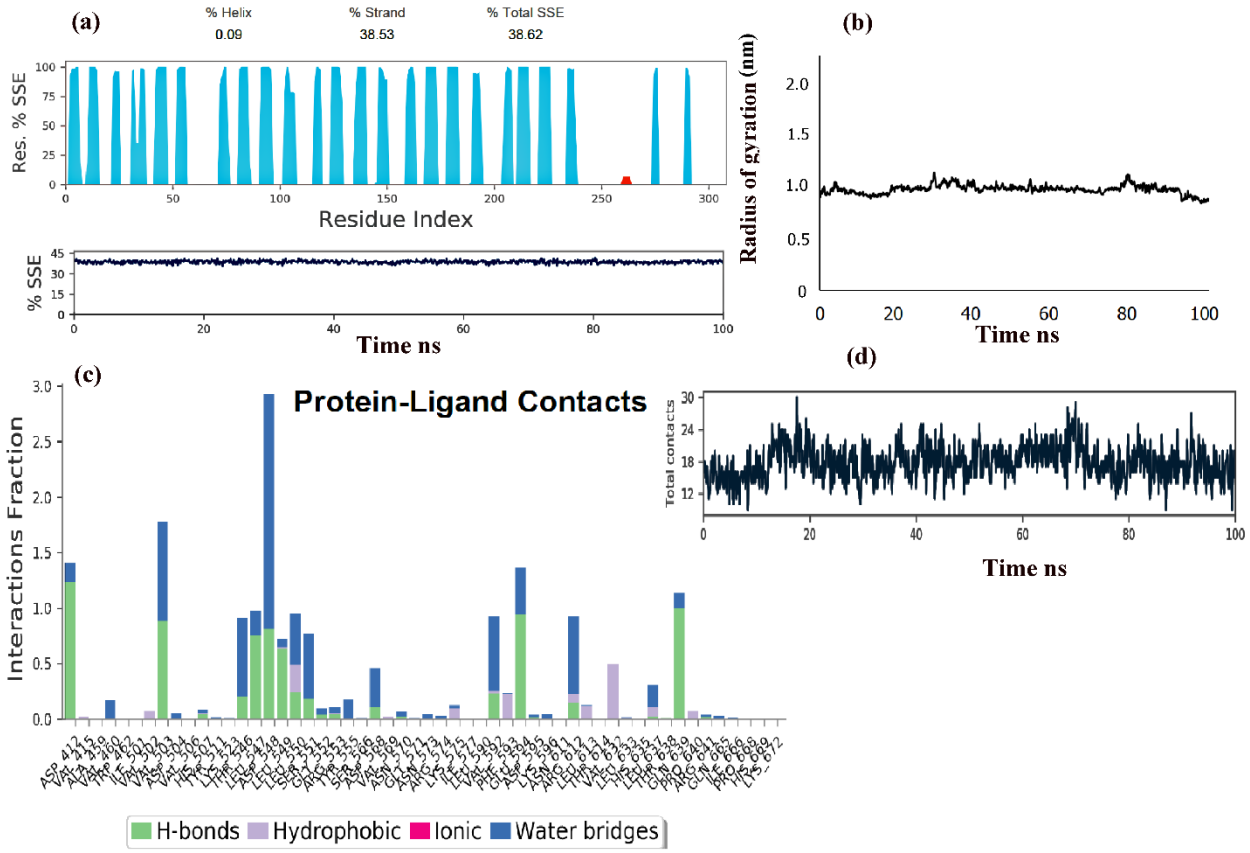

Figure S9. (a) Receptor secondary structure elements (SSE) distribution during the simulation of neat tumor targeting peptide complexed with LDLR receptor. (Orange = alpha helices; blue = beta strands and white = loops). The graphical plot shows the SSE composition for each trajectory frame over the course of the simulation. (b) Radius of gyration of neat tumor targeting peptide ligand during the simulation period; (c) Receptor contacts with the tumor targeting peptide monitored throughout the simulation showing hydrogen bonds, hydrophobic, ionic interactions and water bridges normalized over the course of the trajectory. A value of 0.7 suggests that interaction is maintained during 70% of the simulation time. Values over 1.0 indicate protein residues that may make multiple contacts of same subtype with the neat tumor targeting peptide ligand (d) Total number of specific contacts the receptor makes with the neat tumor targeting peptide over the course of the trajectory.

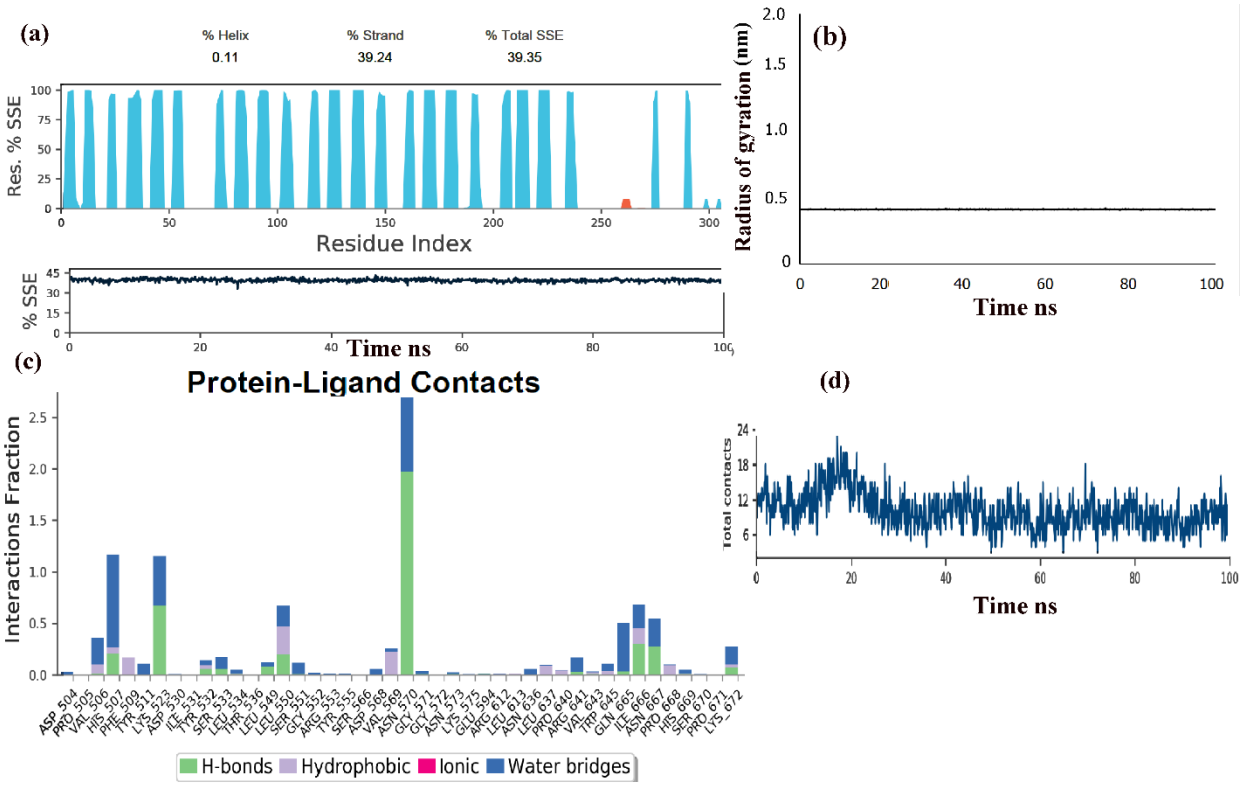

Figure S10. (a) Receptor secondary structure elements (SSE) distribution during the simulation of BT-peptide conjugate complexed with LDLR receptor. (Orange = alpha helices; blue = beta strands and white = loops). The graphical plot shows the SSE composition for each trajectory frame over the course of the simulation. (b) Radius of gyration of BT-peptide conjugate ligand during the simulation period; (c) Receptor contacts with the BT-peptide conjugate monitored throughout the simulation showing hydrogen bonds, hydrophobic, ionic interactions and water bridges normalized over the course of the trajectory. A value of 0.7 suggests that interaction is maintained during 70% of the simulation time. Values over 1.0 indicate protein residues that may make multiple contacts of same subtype with the neat tumor targeting peptide ligand (d) Total number of specific contacts the receptor makes with the BT-peptide conjugate over the course of the trajectory.

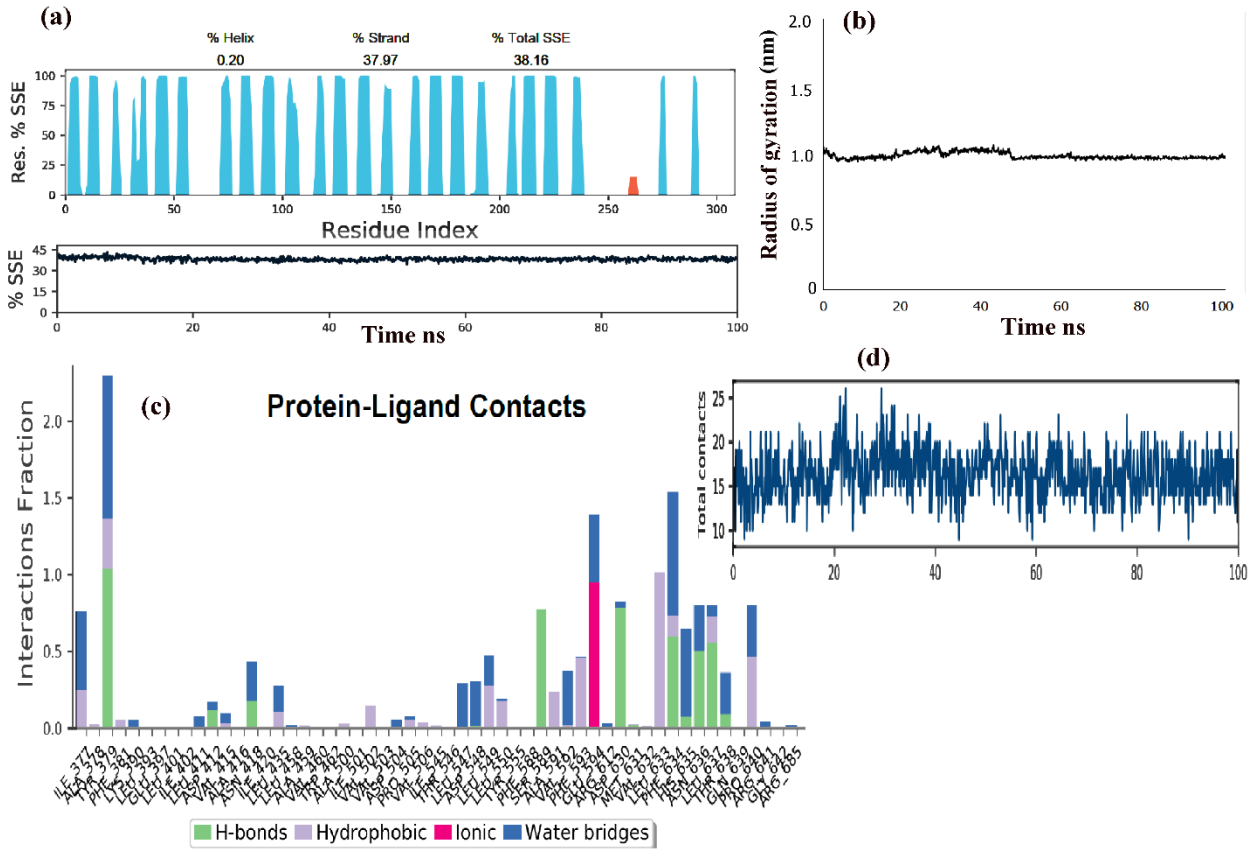

Figure S11. (a) Receptor secondary structure elements (SSE) distribution during the simulation of 3HC-peptide conjugate complexed with LDLR receptor. (Orange = alpha helices; blue = beta strands and white = loops). The graphical plot shows the SSE composition for each trajectory frame over the course of the simulation. (b) Radius of gyration of 3HC-peptide conjugate ligand during the simulation period; (c) Receptor contacts with the 3HC-peptide conjugate monitored throughout the simulation showing hydrogen bonds, hydrophobic, ionic interactions and water bridges normalized over the course of the trajectory. A value of 0.7 suggests that interaction is maintained during 70% of the simulation time. Values over 1.0 indicate protein residues that may make multiple contacts of same subtype with the neat tumor targeting peptide ligand (d) Total number of specific contacts the receptor makes with the 3HC-peptide conjugate over the course of the trajectory.

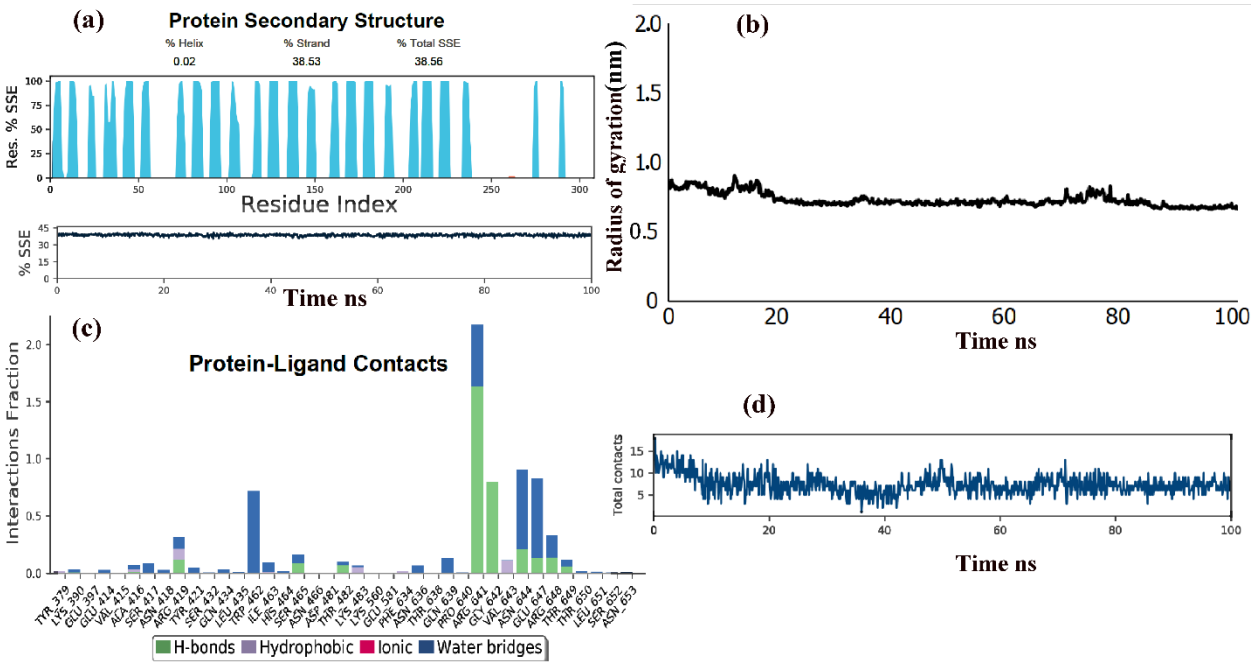

Figure S12. (a) Receptor secondary structure elements (SSE) distribution during the simulation of 3OC-peptide conjugate complexed with LDLR receptor. (Orange = alpha helices; blue = beta strands and white = loops). The graphical plot shows the SSE composition for each trajectory frame over the course of the simulation. (b) Radius of gyration of 3OC-peptide conjugate ligand during the simulation period; (c) Receptor contacts with the 3OC-peptide conjugate monitored throughout the simulation showing hydrogen bonds, hydrophobic, ionic interactions and water bridges normalized over the course of the trajectory. A value of 0.7 suggests that interaction is maintained during 70% of the simulation time. Values over 1.0 indicate protein residues that may make multiple contacts of same subtype with the neat tumor targeting peptide ligand (d) Total number of specific contacts the receptor makes with the 3OC-peptide conjugate over the course of the trajectory.

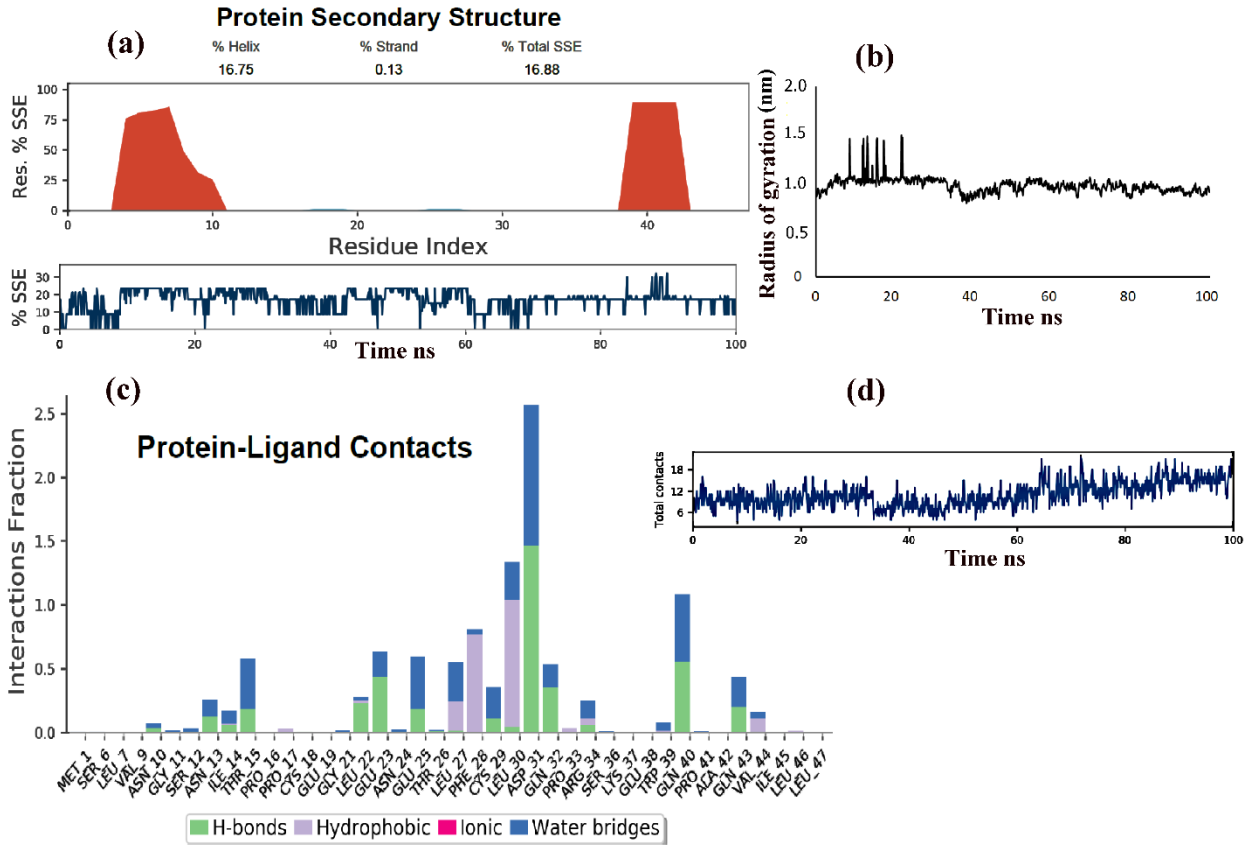

Figure S13. (a) Receptor secondary structure elements (SSE) distribution during the simulation of neat tumor targeting peptide complexed with N-terminal fragment (1-47) of CCKA-R. (Orange = alpha helices; blue = beta strands and white = loops). The graphical plot shows the SSE composition for each trajectory frame over the course of the simulation. (b) Radius of gyration of neat tumor targeting peptide ligand during the simulation period; (c) Receptor contacts with the tumor targeting peptide monitored throughout the simulation showing hydrogen bonds, hydrophobic, ionic interactions and water bridges normalized over the course of the trajectory. A value of 0.7 suggests that interaction is maintained during 70% of the simulation time. Values over 1.0 indicate protein residues that may make multiple contacts of same subtype with the neat tumor targeting peptide ligand (d) Total number of specific contacts the receptor makes with the neat tumor targeting peptide over the course of the trajectory.

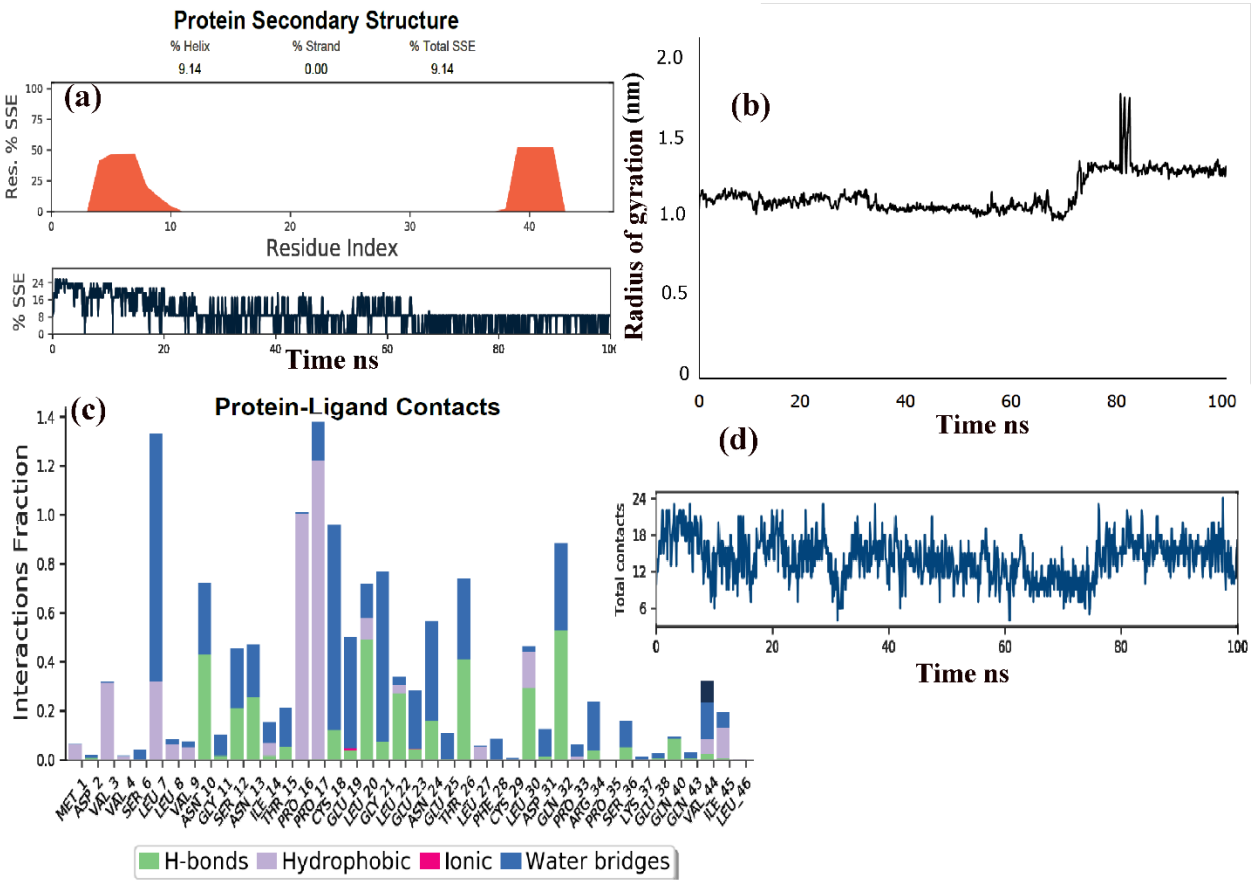

Figure S14. (a) Receptor secondary structure elements (SSE) distribution during the simulation of BT-peptide conjugate complexed with N-terminal fragment (1-47) of CCKA-R. (Orange = alpha helices; blue = beta strands and white = loops). The graphical plot shows the SSE composition for each trajectory frame over the course of the simulation. (b) Radius of gyration of BT-peptide conjugate ligand during the simulation period; (c) Receptor contacts with the BT-peptide conjugate monitored throughout the simulation showing hydrogen bonds, hydrophobic, ionic interactions and water bridges normalized over the course of the trajectory. A value of 0.7 suggests that interaction is maintained during 70% of the simulation time. Values over 1.0 indicate protein residues that may make multiple contacts of same subtype with the neat tumor targeting peptide ligand (d) Total number of specific contacts the receptor makes with the BT-peptide conjugate over the course of the trajectory.

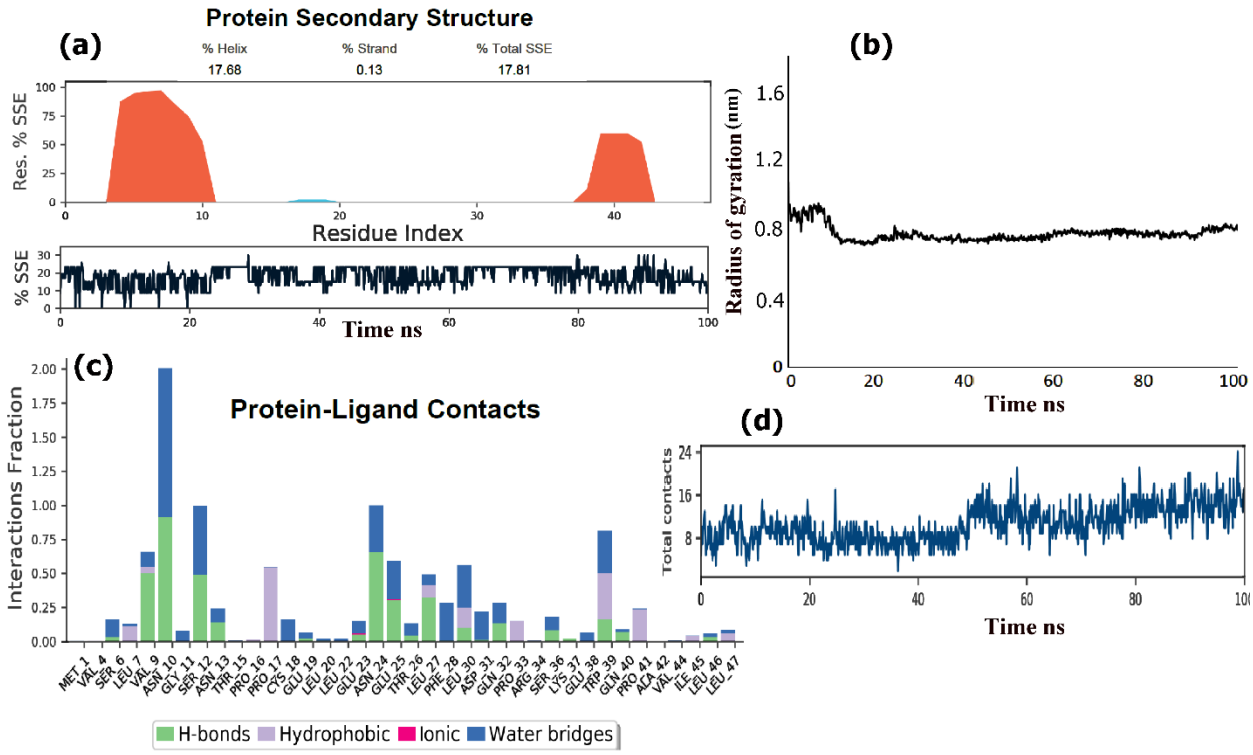

Figure S15. (a) Receptor secondary structure elements (SSE) distribution during the simulation of 3HC-peptide conjugate complexed with N-terminal fragment (1-47) of CCKA-R. (Orange = alpha helices; blue = beta strands and white = loops). The graphical plot shows the SSE composition for each trajectory frame over the course of the simulation. (b) Radius of gyration of 3HC-peptide conjugate ligand during the simulation period; (c) Receptor contacts with the 3HC-peptide conjugate monitored throughout the simulation showing hydrogen bonds, hydrophobic, ionic interactions and water bridges normalized over the course of the trajectory. A value of 0.7 suggests that interaction is maintained during 70% of the simulation time. Values over 1.0 indicate protein residues that may make multiple contacts of same subtype with the neat tumor targeting peptide ligand (d) Total number of specific contacts the receptor makes with the 3HC-peptide conjugate over the course of the trajectory.

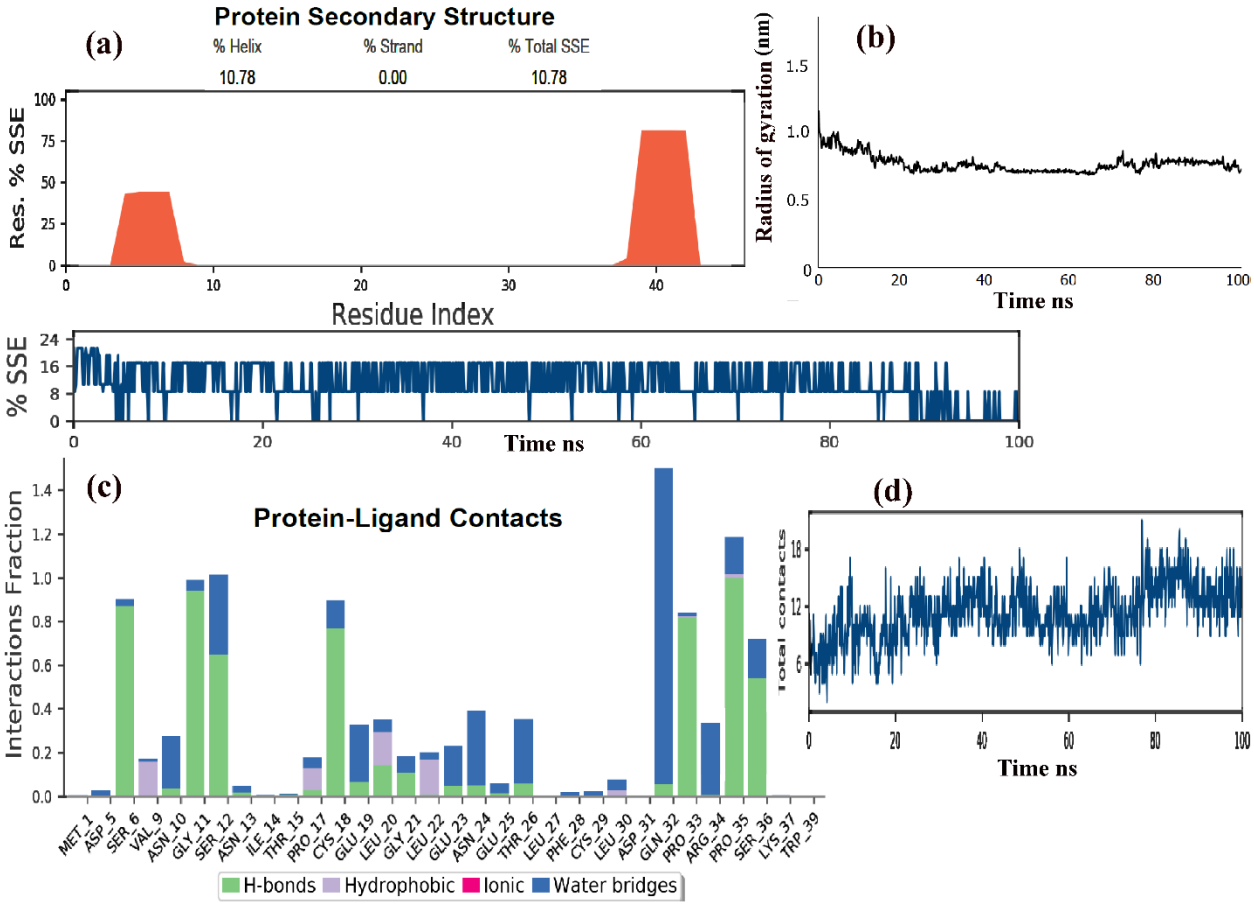

Figure S16. (a) Receptor secondary structure elements (SSE) distribution during the simulation of 3OC-peptide conjugate complexed with N-terminal fragment (1-47) of CCKA-R. (Orange = alpha helices; blue = beta strands and white = loops). The graphical plot shows the SSE composition for each trajectory frame over the course of the simulation. (b) Radius of gyration of 3OC-peptide conjugate ligand during the simulation period; (c) Receptor contacts with the 3OC-peptide conjugate monitored throughout the simulation showing hydrogen bonds, hydrophobic, ionic interactions and water bridges normalized over the course of the trajectory. A value of 0.7 suggests that interaction is maintained during 70% of the simulation time. Values over 1.0 indicate protein residues that may make multiple contacts of same subtype with the neat tumor targeting peptide ligand (d) Total number of specific contacts the receptor makes with the 3OC-peptide conjugate over the course of the trajectory.