Im 21. Jahrhundert sind computergestutzte Methoden zu einem etablierten Werkzeug in der Pharmaindustrie geworden. Da viele Proteinstrukturen nur mit gro?em Aufwand experimentell aufgeklart werden konnen, wurden diverse in silico Methoden entwickelt, um ihre dreidimensionale Struktur aus der dazugehorigen Sequenz zu modellieren. Leider muss der Modellierungsprozess haufig an das Zielprotein angepasst oder die automatisch generierten Modelle von den Anwendern auf Basis ihres Fachwissens verfeinert werden, um letztendlich vernunftige Resultate zu erhalten.Das Ziel dieser Arbeit ist die Untersuchung der Anwendbarkeit automatischer in silico Modellierungsstrategien am Beispiel der G-Protein gekoppelten Rezeptoren (GPCRs). Zunachst analysieren wir bis zu welchem Grad verfugbare Proteinstruktur-Vorhersagemethoden fur die automatische Modellierung von GPCRs angepasst werden konnen. Anschlie?end entwickeln wir unser eigenes Verfahren und zeigen, dass dieses im Vergleich zu anderen modernen Methoden verbesserte Ergebnisse erzielt. Hervorzuheben ist dabei, dass unser Ansatz keinerlei Interaktion vom Anwender benotigt und somit auf alle GPCRs angewendet werden kann. Des Weiteren stellen wir eine neue sequenzbasierte Methode zur Vorhersage von so genannten Kinks in ?-Helices vor. Auch diese Methode ubertrifft die Vorhersagegenauigkeit vergleichbarer Ansatze.

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