BIOGRAPHICAL SKETCH

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NAME: **Marta Filizola**

eRA COMMONS USER NAME (credential, e.g., agency login): **mfilizola**

POSITION TITLE: **Professor and Dean**

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University "Federico II", Naples, Italy	B.S.	10/1993	Chemistry
University "Federico II", Naples, Italy	M.S.	10/1993	Chemistry (Crystallography)
II University of Naples, Naples, Italy	Ph.D.	01/1999	Comput. Chemistry
Molecular Research Institute, Mt. View, CA	Post-Doc	06/2001	Comput. Biophysics

A. Personal Statement

I am a tenured Full Professor in the Departments of Pharmacological Sciences and Neuroscience at the Icahn School of Medicine at Mount Sinai (formerly known as Mount Sinai School of Medicine). I am also Dean of the Graduate School of Biomedical Sciences at Mount Sinai). The overall goal of my research program is to obtain rigorous mechanistic insight into the structure, dynamics, and function of important classes of membrane proteins and prominent drug targets, such as G protein-coupled receptors (GPCRs) and β3 integrins. Understanding the molecular mechanisms underlying the complex biological functions of these proteins has direct translational relevance because it informs the rational discovery of potentially improved therapeutic agents, as my collaborative patent applications demonstrate. To date, I have contributed > 100 peer-reviewed publications to the areas of computational chemistry/biophysics and drug discovery, and I have delivered > 50 invited talks. I have served on several scientific review committees, and I am also listed as an inventor on 10 issued patents and PCT patent applications. My laboratory's research has consistently been funded by the National Institutes of Health since 2005. My lab has used several computational structural biology tools, ranging from molecular modeling, bioinformatics, cheminformatics, molecular dynamics simulations, and rational drug design approaches. We have pioneered the use of enhanced sampling algorithms in the study of ligand binding, activation, allostery, and oligomerization of GPCRs in general, and opioid receptors in particular. Examples of recent publications from my lab are:

a. Shang, Y., Yeatman, H.R., Provasi, D., Alt, A., Christopoulos, A., Canals, M., and Filizola, M. "Proposed Mode of Binding and Action of Positive Allosteric Modulators at Opioid Receptors" (2016) *ACS Chemical Biology;* 11(5):1220-9
b. Schneider, S., Provasi, D., Filizola, M. "How Oliceridine (TRV-130) Binds and Stabilizes a μ-Opioid Receptor Conformational State that Selectively Triggers G Protein-Signaling Pathways." (2016) *Biochemistry* 55(46):6456-6466
c. Bisignano, P., Burford, N.T., Shang, Y., Marlow, B., Livingston, K.E., Fenton, A.M., Rockwell,K., Budenholzer, L., Traynor, J., Gerritz, S.W., Alt, A., and Filizola, M. "Ligand-Based Discovery of a New Scaffold for Allosteric Modulation of the mu-Opioid Receptor" (2015) *Journal of Chemical Information & Modeling* 55(9):1836-43.
d. Schneider, S., Provasi, D. & Filizola, M. "The Dynamic Process of Drug-GPCR Binding at Either Orthosteric or Allosteric Sites Evaluated by Metadynamics" (2015) *Methods in Molecular Biology*, 1335:277-294.

B. Positions and Honors

Positions and Employment

7/01-6/03 Instructor, Dept. of Physiology & Biophysics, Mt. Sinai School of Medicine (MSSM), NYC.

1/04-6/05	Instructor, Dept. of Physiology & Biophysics, Weill Medical College of Cornell University, NYC
7/05-6/07	Assist. Research Professor, Dept. of Physiology & Biophysics, WMC of Cornell University, NYC
7/07-6/10	Adjunct Assistant Professor, Dept. of Physiology & Biophysics, WMC of Cornell University, NYC.
7/07-6/10	Assistant Professor (Tenure-Track), Dept. of Structural and Chemical Biology, MSSM, NYC
7/10-6/14	Associate Professor (with Tenure since Jan 2013), Dept. of Structural and Chemical Biology, Icahn School of Medicine at Mount Sinai (ISMMS), NYC
9/12-3/15	Co-Director of the Graduate Program in *Structural/Chemical Biology and Molecular Design (SMD)* of the Graduate School of Biological Sciences at ISMMS.
7/14-2016	Full Professor with Tenure, Dept. of Structural and Chemical Biology, ISMMS, NYC.
3/15-1/16	Co-Director of the Graduate Program in *Biophysics and Systems Pharmacology (BSP)* of the Graduate School of Biological Sciences at ISMMS.
2015-2016	Full Professor with Tenure, Dept. of Pharmacol. and Syst. Therapeutics, ISMMS, New York, NY.
2015-present	Full Professor with Tenure, Dept. of Neuroscience, ISMMS, New York, NY.
7/16-present	Full Professor with Tenure, Dept. of Pharmacological Sciences, ISMMS, NYC.

Honors and Patents

Fellowship to perform studies abroad, University "Federico II" in Naples (Italy), 1994; Grant-in-aid, Centre de Supercomputació de Catalunya, Barcelona (Spain), 1995-1997; Nominated - *European Doctor in Biotechnology*, European Association for Higher Education in Biotechnology, 1999; National Research Service Award T32 DA07135, National Institute on Drug Abuse (NIDA), 2001; *The Doctor Harold and Golden Lamport Award* for Excellence in Basic Research, Mount Sinai School of Medicine in NYC, 2008; Independent Scientist Award (K02), NIH-NIDA, 2009-present; Teragrid/XSEDE award (MCB080077), 2008-present; Director Discretionary Award UT-NTNL0149, National Institute for Computational Sciences (NICS), 2011-2012; Distinguished Speaker at Torrey Pines Institute for Molecular Studies, Port St. Lucie, FL, 2013; Member of the Faculty of 1000 for Pharmacology and Drug Discovery, 2013; Tenure, Icahn School of Medicine at Mount Sinai, 2013; International Society of Quantum Biology and Pharmacology (ISQBP) Loew Lectureship 2016, ISQBP President's meeting, Bergen, Norway, June 19-22, 2016; Delta Omega Public Health Honorary Induction, Delta Omega Honor Society, May 10, 2017; Patent applications: "Organic Compounds (Anti-platelet agents)" PCT/US11/44267 (July 15, 2011), PCT/US2013/021749 (Jan. 16, 2013), US14/ 372488 (July 16, 2013); 61/768,205 "Kappa Opioid Receptor Selective Compounds, Compositions, and Uses Thereof", U.S. Patent and Trademark Office (Feb. 22, 2013); "Tetrahydronaphthyridinepentanamide integrin antagonists" (US 62/358,330, Aug. 12, 2016); "SOX11 Inhibitors for the Treatment of Mantle Cell Lymphoma" (US 62/376,056, Aug. 29, 2016).

Other Experience and Professional Memberships

Staff Scientist at Molecular Research Institute in Mountain View, CA, 2001; Editorial Board Member, *Open Access Bioinformatics* (2008-present), and *Advances and Applications in Bioinformatics and Chemistry* (2007-present), Dove Press; Grant Reviewer for: Cutting Edge Basic Research Award (CEBRA) from U.S. Army Research Office and NIH-NIDA, 2006; NIH-MNPS Study Sections 2/07, 6/07, 10/07, 2/08, 5/08, 2/15; NIH-NIDA ZRG1 MNPS-C(04)S 5/08; NIH-NIDA ZRG1 MDCN-C(02)M 6/ 08; NSF-MCB Biomolecular Systems 10/08, 9/09; NIH-ZRG1 BCMB-B (02) M 9/10; NIH-ZRG1 MDCN-P (91) S, 6/11; NIH-BPNS Study Section, 6/12; NIH-BST Study Section, 7/12; NIH-ZRG1 BCMB-D (40) P, 2/13; NIH- ZRG1 MDCN-R (40), 7/14; NIH-ZRG1 MDCN-C (94), 7/15; Guest Editor for *PLOS Computational Biology,* 2012, 2013; Edited a book entitled "G Protein-Coupled Receptor Modeling and Simulation" for Springer Science + Business Media, 2013; Member, NIH-BPNS Study Section, Center for Scientific Review, Appointed July 2013-June 2019; Scientific Advisory Board Member for the 2nd GPCR Targeted Screening Conference of the Global Technology Community (GTC) on May 7-8, 2015 in Berlin, Germany; Member of the GPCR Expert Target Panel for a knowledge management center for the NIH Program Illuminating the Druggable Genome, IDG Steering Committee Face-to-Face meeting, Apr 7-9, 2015 Albuquerque, NM; Edited a book entitled "G Protein-Coupled Receptors in Drug Discovery**"** in the *Methods in Molecular Biology* lab protocol series, Publisher: Springer, 2015.; Member of Committee for Professional Opportunities for Women of the Biophysical Society, 7/15-6/18; Member of peer review team evaluating Rockefeller University's institutional accreditation by NYS Board of Regents and Commissioner of Education.

C. Contributions to Science

1. Dynamic Models of Opioid Receptors

Opioid receptors are important drug targets for pain management, drug abuse/addiction, and mood disorders. We have a long history of work on these GPCR subtypes, having contributed over the past ~20 years to several structural and mechanistic insights into their pharmacology and signaling. Most recently, we have focused on

their dynamics, seeking answers to questions like: How does an opioid drug bind to his receptor? How can sodium ions modulate opioid receptor activity? What are the likely interfaces of opioid receptor homodimers? What are the molecular determinants responsible for opioid allosteric modulation and functional selectivity?

a) Provasi, D., Bortolato A., Filizola, M. "Exploring Molecular Mechanisms of Ligand Recognition by Opioid Receptors with Metadynamics." *Biochemistry* (2009) 48 (42): 10020-10029. *(Cited 48 times)*
b) Filizola M. & Devi, L.A. "How opioid drugs bind to receptors" *Nature* (2012) 485, 314-7. *(Cited 42 times)*
c) Johnston, J.M., Aburi, M., Provasi, D., Bortolato, A., Urizar, E., Lambert, N.A., Javitch, J.A., Filizola, M. "Making Structural Sense of Dimerization Interfaces of Delta Opioid Receptor Homodimers", *Biochemistry* (2011) 50(10):1682-1690 *(Cited 59 times).*
d) Shang, Y., LeRouzic, V., Schneider, S., Bisignano, P., Pasternak, G.W., Filizola, M. "Mechanistic Insights into the Allosteric Modulation of Opioid Receptors by Sodium Ions" *Biochemistry* (2014) 53(31):5140-9. *(Cited 33 times)*

2. *Structure-Guided Drug Discovery and Chemotype Optimization*

The recent high-resolution crystal structures of several GPCR or integrin types have offered tremendous opportunities for computer-aided drug discovery/optimization approaches to discover novel and selective binders as some of our recent publications demonstrate. By combining our virtual screening, cheminformatics, and MD simulations, with collaborative functional and structural studies, as well as chemical synthesis, we have recently contributed to the discovery of (i) the atypical scaffold mitragynine as a potent opioid receptor modulator (in collaboration with D. Sames at Columbia University and S. Majumdar at Memorial Sloan Kettering Cancer Center, (ii) a novel agonist of the kappa-opioid receptor (in collaboration with J.A. Javitch at Columbia U. and T. Prisinzano at Kansas U.); (iii) novel positive allosteric modulators of the delta-opioid and mu-opioid receptors (in collaboration with N. Burford, A. Alt, and S. Gerritz at BMS, M. Canals and A. Christopoulos at Monash U., and J. Traynor at U. of Michigan); (iv) a μOR-δOR heteromer-biased agonist with antinociceptive activity (in collaboration with L. Devi at Mount Sinai and P. Hodder at Scripps), (v) a small-molecule inhibitor for treating mantle cell lymphoma (in collaboration with A. Aggarwal, J. Jin, and S. Parekh, at Mount Sinai); and (vi) novel antagonists of the αIIbβ3 and αVβ3 receptors that limit conformational reorganization of the receptors, thus resulting in improved therapeutics (in collaboration with B.S. Coller at Rockefeller U., M. Foley at the Tri-institutional Drug Discovery Institute, and C. Thomas at the NIH).

a) Negri, A., Rives, M.L., Caspers, M.J., Prisinzano, T.E., Javitch, J.A., and Filizola, M. "Discovery of a Novel Selective Kappa-Opioid Receptor Agonist Using Crystal Structure-Based Virtual Screening" *Journal of Chemical Information and Modeling* (2013) 53: 521-526*. (Cited 37 times)*
b) Burford, N., Livingston, K., Canals, M., Ryan, M., Budenholzer, L., Han, Y., Shang, Y., Herbst, J.J., O'Connell, J., Banks, M., Zhang, L., Filizola, M., Bassoni, D., Wehrman, T., Christopoulos, A., Traynor, J., Gerritz, S., Alt, A. "Discovery, Synthesis and Molecular Pharmacology of Selective Positive Allosteric Modulators of the δ-Opioid Receptor" (2015) *Journal of Medicinal Chemistry* 8(10):4220-9 *(Cited 16 times)*.
c) Zhu, J., Choi, W.-S., McCoy, J.G., Negri, A., Zhu, J., Naini, S., Li, J., Shen, M., Huang, W., Bougie, D., Rasmussen, M., Aster, R., Thomas, C.J., Filizola, M., Springer, T.A., and Coller, B.S. "Structure-Guided Design of a High Affinity Platelet Integrin αIIbβ3 Receptor Antagonist That Disrupts Mg^{2+} Binding to the MIDAS" *Science Translational Medicine* (2012) 4(125):1-13. *(Cited 40 times)*
d) Gomes, I., Fujita, W., Gupta, A., Saldanha, A.S., Negri, A., Pinello, C.E., Roberts, E., Filizola, M., Hodder, P., and Devi, L.A. "Identification of a μOR-δOR heteromer-biased agonist with antinociceptive activity" *Proc. Natl. Acad. Sci. USA* (2013) 110(29):12072-7. *(Cited 59 times)*

3. Molecular Modeling and Enhanced Molecular Dynamics Simulations

Among the milestones that we were able to accomplish under the auspices of continued NIH funding over the past 12 years are the design, testing, and implementation of innovative computational strategies to build improved molecular models of GPCRs and to study, more efficiently, the conformational plasticity and dynamical nature of liganded or unliganded, single or interacting, receptors within their natural lipid environment. In particular, we pioneered the use of enhanced, molecular dynamics (MD)-based computational strategies in combination with either atomistic or coarse-grained (CG) system representations to improve dynamic molecular models of GPCR molecular recognition, activation, and oligomerization, with the ultimate goal of elucidating receptor allostery and functional selectivity for successful use in rational drug design. In particular, we were able: (i) to obtain reliable models of ligand-bound conformations of GPCRs that do not require very long and computationally inefficient standard MD simulations, (ii) to establish a possible molecular basis for the functional selectivity of GPCRs through the prediction of ligand-specific conformations, and (iii) to advance current

understanding of the role of oligomerization in receptor function through the generation of novel testable hypotheses of specific mutations that could eventually be used to modulate receptor function. While the specific computational methods we explored are not new from an algorithmic standpoint, we developed some distinctive combinations of such methods, and showed in recent publications that they are indeed able to generate ligand-specific conformations of both isolated and interacting, inactive and active, GPCRs that are consistent with experimental data. Notably, the methodologies we developed represent fundamental tools that can be generalized to other transmembrane receptors, as well as broadly to other proteins.

a) Mobarec, J.C., Sanchez, R., and Filizola, M. "Modern Homology Modeling of G-Protein Coupled Receptors: Which Structural Template to Use?" *J. Med. Chem.* (2009) 52 (16), 5207-16. *(Cited 132 times)*

b) Fribourg, M., Moreno, J.L., Holloway, T., Provasi, D., Baki, L., Mahajan, R., Park, G., Adney, S.K., Hatcher, C., Eltit, J.M., Ruta, J.D., Albizu, L., Li, Z., Umali, A., Shim, J., Fabiato, A., MacKerell, A.D. Jr., Brezina, V., Sealfon, S.C., Filizola, M., Gonzalez-Maeso, J., Logothetis, D.E. "Decoding the Signaling of a GPCR Heteromeric Complex Reveals a Unifying Mechanism of Action of Antipsychotic Drugs" *Cell* (2011) 147 (5):1011-1023; *(Cited 146 times)*

c) Provasi, D., Camacho-Artacho, M., Negri, A., Mobarec, J.C., Filizola, M. "Ligand-Induced Modulation of the Free-Energy Landscape of G Protein-Coupled Receptors Explored by Adaptive Biasing Techniques." *PLOS Comp. Biol.* (2011) 7(10):e1002193. *(Cited 47 times)*

d) Provasi, D. & Filizola, M. "Putative Active States of a Prototypic G-Protein Coupled Receptor from Biased Molecular Dynamics." *Biophysical J.* (2010) 19(10):2347-2355. *(Cited 37 times)*

4. <u>Mechanistic Insights into GPCR Dimerization/Oligomerization</u>

Compelling evidence that models of GPCR signaling must consider oligomeric assemblies rather than isolated monomers started to appear in the literature during my postdoctoral training. Many of the published studies described (i) effects resulting from activating one GPCR in the presence of another and (ii) modulation of the activity of one receptor using ligands targeting another one. Whether these effects resulted from downstream crosstalk or from differential signaling of a receptor complex has so far been difficult to ascertain for the largest subfamily A of GPCRs. My lab has been hard at work in the area of GPCR oligomerization, contributing to their recognition, nomenclature, storing, structural models, and estimates of relative stability. We are committed to providing a rigorous mechanistic insight into the spatio-temporal organization of GPCRs in living cells at a level of molecular detail that is unattainable using current experimental techniques alone, but is required for an ultimate understanding of the role of GPCR oligomerization in receptor function.

a) González-Maeso, J., Ang, R., Yuen, T, Chan, P., Weisstaub, N.V., López-Giménez, J., Zhou, M., Okawa, Y., Callado, L.F., Milligan, G., Gingrich, J.A., Filizola, M., Meana, J.J., Sealfon, S.C. "Identification of a Novel Serotonin/Glutamate Receptor Complex Implicated in Psychosis" *Nature* (2008) 452(7183):93-97; *(Cited 545 times)*

b) Guo, W., Urizar, E., Kralikova,M., Mobarec, J.C., Shi, L., Filizola, M., Javitch, J.A. "Dopamine D2 Receptors Form Higher Order Oligomers at Physiological Expression Levels" *The EMBO Journal*, (2008) Sep 3;27(17):2293-304; *(Cited 267 times)*

c) Khelashvili, G., Dorff, K., Shan, J., Camacho-Artacho, M., Skrabanek, L., Vroling, B., Bouvier, M., Devi, L., George, S.R., Javitch, J.A., Lohse, M.J., Milligan, G., Neubig, R., Palczewski, K., Parmentier, M., Pin, J.-P., Vriend, G., Campagne, F., Filizola, M. "GPCR-OKB: A database for G protein-coupled receptor oligomers." *Bioinformatics* (2010) 26(14):1804-1805. *(Cited 64 times)*

d) Johnston, J.M., Wang, H., Provasi, D., Filizola, M. "Assessing the Relative Stability of Dimer Interfaces in G Protein-Coupled Receptors." *PLOS Computational Biology* (2012) 8(8): e1002649. *(Cited 56 times)*

5. <u>Contributions to the Integrin Field</u>

A close and productive collaboration (a total of 13 publications so far) with the laboratory of Dr. Barry Coller at Rockefeller University has kept part of my research interests focused on the study of structure-function relationships of both αIIbβ3 and αVβ3 integrins. My lab's interest in these systems stems from the exciting computational challenges they pose, and the opportunity to develop and/or apply cutting-edge computational approaches that will render accurate representations of the dynamic allosteric mechanisms regulating integrin function. During the past 15 years we have been able to provide an innovative structure-guided approach to the functional studies carried out in the lab of our experimental collaborator. Specifically, we have contributed: i) Early three-dimensional molecular models of αIIbβ3 using αVβ3 as a template; ii) Important structural insights into the ligand-associated metal binding site (LIMBS, later re-termed SyMBS) of β3 integrins from MD simulations; iii) Specific molecular determinants for limiting extension at the αIIb genu or ligand binding to integrin

αIIbβ3; iv) Information about the overall common conformational changes occurring in β3 integrins upon hybrid domain swing-out using targeted MD simulations; v) Mechanistic information about αIIbβ3- and αVβ3-specific antagonists that stabilize the receptors in their resting states; vi) Structure-guided design of potent pure antagonist of β3 receptors; vii) Identification of novel antagonists by virtual screening; viii) Multimicrosecond, all-atom MD simulations of the talin-driven inside-out activation mechanism of αIIbβ3 integrin; and ix) Predictions of the functional effect of αIIbβ3 variants defined by next-generation sequencing.

a) Zhu, J., Zhu, J., Negri, A., Provasi, D., Filizola, M., Coller, B.S., Springer, T.A. "Closed headpiece of integrin αIIbβ3 and its complex with an αIIbβ3-specific antagonist that does not induce opening" *Blood* (2010) 116 (23):5050-5059. *(Cited 73 times)*

b) Zhu, J., Choi, W.-S., McCoy, J. G., Negri, A., Zhu, J., Naini, S., Li, J., Shen, M., Huang, W., Bougie, D., Rasmussen, M., Aster, R., Thomas, C. J., Filizola, M., Springer, T. A., Coller, B. S. "Structure-Guided Design of a High-Affinity Platelet Integrin $\alpha_{IIb}\beta_3$ Receptor Antagonist That Disrupts Mg^{2+} Binding to the MIDAS." *Science Translational Medicine* (2012) 4: 125ra32 *(Cited 40 times)*

c) Negri, A., Li, J., Naini, S., Coller, B.S., Filizola, M. "Structure-Based Virtual Screening of Small-Molecule Antagonists of Platelet Integrin $\alpha_{IIb}\beta_3$ that Do Not Prime the Receptor to Bind Ligand" *Journal of Computer-Aided Molecular Design* (2012) 26 (9): 1005-1015 *(Cited 12 times)*

d) Buitrago, L., Rendon, A., Liang, Y., Turro, E., Simeoni, I., Negri, A., ThromboGenomics Consortium, Filizola, M., Ouwehand, W.H., Coller, B.S. "αIIbβ3 Variants Defined by Next Generation Sequencing: Predicting Variants Likely to Cause Glanzmann Thrombasthenia" (2015) *Proc. Natl. Acad. Sci. USA*, 112(15):E1898-907. *(Cited 15 times)*

Complete List of Published Work in MyBibliography (from a total of more than 100 peer-reviewed publications): https://www.ncbi.nlm.nih.gov/myncbi/browse/collection/45838592/?sort=date&direction=descending

D. Research Support

Ongoing Research Support

- NIH/NIDA - R01 DA034049 (Filizola, PI) 06/15/12 - 05/31/18 (no cost extension)
  Dynamic Mechanisms of GPCRs Targeted by Drugs of Abuse. The overall goal of this project is to advance our current understanding of fundamental basic mechanisms of mu-opioid receptor function, and pave the way to novel therapeutic strategies against drug abuse and addiction.
- NIH/NIDA - K02 DA026434 (Filizola, PI) 04/01/14 - 03/31/19
  Structural Aspects of Oligomerization in the Function of GPCRs. This is an Independent Scientist Award (KO2) providing support for Dr. Filizola's continued career development as an independent investigator.
- NIH/NIDA - R01 DA038882 (Filizola, MPI with Lohse) 07/01/15 - 04/30/20
  Biophysical Approaches to Investigate the Biological Significance of GPCR Dimers. The overall goal of the studies proposed in this application is to lay the foundation for understanding the role of dimerization/oligomerization in the function of G Protein-Coupled Receptors.
- NIH/NIMH - R21 MH107053 (Filizola, PI) 03/01/16 - 02/28/18
  Enhanced Molecular Dynamics Methods to Investigate GPCR Ligand Binding. The overall goal of this application is to delineate an efficient computational strategy that is capable of predicting accurate kinetic quantities related to GPCR ligand binding.
- NIH/NHLBI - R01 HL019278 (Coller, PI; Filizola, PI of subcontract) 06/01/17 - 05/31/21
  Integrin alphaIIbbeta3 Structure, Activation, and Ligand Binding. This project is focused on achieving a better understanding of ligand binding to αIIbβ3 while searching for improved therapeutics based on rigorous criteria.
- Celgene / Research Agreement (Parekh, Jin, Filizola, Aggarwal PIs) 7/1/2017 – 6/30/2021
  Roadmap to IND: Developing a Small-molecule Inhibitor for Treating Mantle Cell Lymphoma. The objective of this project is to develop lead and backup drug candidates via extensive optimization and complete IND enabling studies.

Overlap

None. Please note that the K02 is a career development award focused on investigating GPCR oligomerization. As such, the ongoing grants that focus on GPCRs are included within the K02 protected time.