
VICENTE MENDOZA REYES, Ph.D.

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Scientific & Academic Profile: <http://ronininstitute.org/research-scholars/vicente-reyes/>
Scientific Research Activities: https://www.researchgate.net/profile/Vicente_Reyes/

FIELDS OF INTEREST:

- **Computational Biology & Bioinformatics (Proteomics)**
- **Structural Bioinformatics, Biological Data Mining**
- **Mathematical Biology (Biomathematics), Theoretical Biology, Biological Complexity**
- **Structural Biology (Macromolecular X-Ray Crystallography); Structure-Based Drug Design**
- **Pedagogy in Quantitative, Computational & Mathematical Life Sciences**

EDUCATION:**Degrees:**

Ph.D. Chemistry, California Institute of Technology, Pasadena, California, USA
(conc. in molecular biology & biochemistry)
B. S. Mathematics (*magna cum laude*) Univ. of the Philippines, Diliman, Philippines
(conc. in pure mathematics & operations research)
B. S. Chemistry (*magna cum laude*) Univ. of the Philippines, Diliman, Philippines
(conc. in organic chemistry & biochemistry)

Certificates / Diplomas:

Spec. Cert. in Data Mining, UCSD School of Extended Studies, **Winter 2007**
Prof. Cert. in Bioinformatics, UCSD School of Extended Studies, **Spring 2004**
Spec. Cert. In Bioinformatics, UCSD School of Extended Studies, **Spring 2002**

OTHER TRAINING:

- **MATLAB Intensive Training I:** MATLAB Fundamentals, Programming Techniques and Use in Building GUIs; Las Vegas, NV, Aug. 1-5, 2011
- **MATLAB Intensive Training II:** MATLAB Optimization Techniques, Data Processing and Visualization, and Statistical Methods; New York City, NY, Aug. 22-25, 2011
- **MATLAB Intensive Training III:** MATLAB Simulation Techniques: Simulink, Integrating Code with Simulink, etc.; Washington, D.C., Dec. 12-17, 2011

CAREER HISTORY:

Member Scientist, Institute for Globally Distributed Open Research & Education 02/2018 -- present
 Email: vicente.reyes@igdore.org
<https://igdore.org/researchers/>

Founder & Executive Director mid-2017 – present
 Rochester Center for Biocomputing and Biomathematics R&D, Inc.
 “Biomedical and Clinical Data Mining for Precision Medicine”
 (incorporated 08-24-17 | F# 6521460 DE | SR 20175877347)
(currently in incubation period)

Research Scholar, Ronin Institute 12/2016 -- present
 Email: Vicente.Reyes@ronininstitute.org
<http://ronininstitute.org/research-scholars/vicente-reyes/>

Member Scientist, Complex Biological Systems Alliance 12/2016 -- present
 Email: Vicente.M.Reyes@cbsaimt.com
<http://www.cbsaimt.com/l---z.html#Reyes>

Personal Independent Study Mid-Career Sabbatical: 08/2012 – 12/2016

a.) Mathematical / Theoretical Biology (*theory and applications*)

Graph/Network Theory, Dynamical Systems Theory, Fractal Theory, Statistical Mechanics/ Thermodynamics, Chaos Theory, Catastrophe Theory, Swarm Theory, Quaternion Theory; Octonion Theory; Percolation Theory; Mathematical Structures & Morphisms; Bifurcation Theory; Category Theory; Representation Theory; Tensor Theory; Ergodic Theory; Eigenvalue/ Eigenfunction Theory; Vector Calculus; Lebesgue Measure & Integration; Density Functional Theory; Countability & Denumerability Theory; Transfinite Number Theory; Inverse Problems, Calculus of Variations; Operator Theory; Integral Equations; Functional Analysis; Finite Differences; Difference Equations; Nonstandard Analysis; Type Theory; Topology; Naïve and Axiomatic Set Theory; Set Density Theory; String Theory, Fractional Calculus; Spectral Theory; Sigma Algebra; Numerical Analysis; Group Theory for Chemistry & Biology; Potential Theory; Harmonic Analysis; Fourier Theory; Game Theory; Mathematical Physics; Ordinary, Partial & Numerical Differential Equations; Differential Geometry; Axiomatic Probability Theory, etc.]

b.) Computer Science (*theory and applications*)

Automata Theory & Turing Machines; Computability Theory; Computational Complexity Theory; Computer Architecture; Theory & Analysis of Algorithms; Theory of Data Types and Structures; Boolean Algebra and Logic; Mathematical Logic; Complex Adaptive Systems; Machine Learning & Artificial Intelligence; Quantum Computing & Programming; Church Lambda Calculus; Proof Theory; Type Theory; Model Theory; Coding Theory; Mathematical Theory of Information; Information Entropy Theory; Computer Vision Theory; Relational Algebra; The Master Theorem (Algorithms); Finite State Machines; Context-Free Languages & Grammars; Curve (2D and 3D) and Surface Fitting; Decidability/ Undecidability Theory; Satisfiability and 3-Satisfiability; Deterministic & Nondeterministic FSA; Massive Data Sets (“Big Data”); Quantum Information Theory; Turing Machines: Generalized, Universal, Existential and Alternating; Recursion Theory; NP-Hard and NP-Complete Problems; L-Systems and Lattices; Graph Algorithms; Linear Programming; Non-Linear Programming; Quadratic Programming; Convex Programming; Dynamic Programming; Integer Programming; Stochastic Programming; Matroid Theory and Greedy Algorithms; Approximation Algorithms; DNA & Membrane Computing; Cellular Automata; Cryptography & Cyber-security; Computer Graphics; Computer Languages; Emerging Technologies (most fields); etc.]

c.) Biophysics / Biophysical chemistry

Macromolecular x-ray crystallography; protein (multidimensional) NMR; mass spectroscopy; atomic force microscopy; electron microscopy; cryoelectron microscopy; dynamic light scattering (DLS); fluorescence resonance energy transfer (FRET); electrophysiology; bioenergetics; radioisotope dating technologies; biomolecular hydrodynamics (biology at low Reynolds numbers); molecular resonance imaging (MRI); quantum biology; quantum-coherent electronic energy transfer (QCEET); organismal magnetoreception; orchestrated objective reduction (OrchOR); electron paramagnetic (spin) resonance (EPR/ESR); membrane biophysics; medical biophysics; astrobiology; fluorescence correlation spectroscopy (FCS); Fourier transform Infra-red (FTIR) spectroscopy & microscopy; Raman spectroscopy & microscopy; optical luminescence) dating technology; confocal fluorescence microscopy; high-resolution transmission electron microscopy (HRTEM); macromolecular simulation; magnetic proteins; optical & magnetic tweezers; biomechanics; microscale thermophoresis (MST); neutron spin echospectroscopy (NSES); cytological patch clamping; dual polarization interferometry; biophotonics; light-activated drugs; biomembrane electrostatics; biomolecular nonlinear optics (NLO); x-ray micro-tomography; fluorescence nanoscopy (STED, FPALM, etc.)]

d.) Biomaterials / Materials Science:

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biomaterials (BMs) for drug delivery, gene therapy, scaffolds in tissue engineering, regenerative medicine, autograft, allograft or xenograft as transplant materials, in spine surgery, cochlear implants, vascular grafts, nerve conduits, artificial ligaments and tendons; biologically inspired & biomimetic materials; host responses to biomaterials; biocompatibility; therapeutic and diagnostic colloids; biosensor materials & mechanisms; 3D-printable BMs; polymeric surfaces; hydrogels in medicine; nano-structured hydrogels; natural BMs; biofouling; biomineralization; self-assembly & self-organization of BMs; synthetic biodegradable polymers; virus-based methods of manufacturing; molecular design of BMs; interactions at the biointerface; surface-active BMs; smart BMs; antithrombogenic polymers; sol-gel materials for bioceramic applications; titanium in medicine; chitin- and chitosan-based BMs; foreign body reaction to BMs; biophotonics; label-free technologies; bioactive glasses; MXenes; nano-geno-toxicology; synthetic & self-assembling nanococoons; structural hierarchy of BMs; photopolymerizable hydrogels; Biomaterials Properties Database (Univ. of Michigan);

e.) Pharmacoinformatics / Pharmacology / Pharmaceutical Science:

<ongoing>

principles of drug discovery and development; L-ADME; pharmacokinetics & pharmacodynamics; pharmacogenetics & pharmacogenomics; pharmacology of anesthesia; pharmacology of pain; pharmacology of antidepressants; pharmacology of hypertension; pharmacology of myocarditis (cardiac inflammation); pharmacology of monoclonal antibodies; pharmacology of cannabis (marijuana); pharmacology of resveratrol and curcuminoids; pharmacology of migraine headache; pharmacology of statins; pharmacology of neurotransmission; pharmacology of Ca^{++} signaling; pharmacology of cAMP and cGMP signaling; drug databases and resources from the web: Cambridge (Small Molecule) Structural Database (CSD); Click2Drug: Directory of Computer-Aided Drug Design Tools; Controlled Substances Act (CSA) and Drug Enforcement Administration (DEA) Schedules I-V controlled substances; WHO Model List of Essential Medicines; Anatomical Therapeutic Chemical Classification System (ATCCS); Top 200 Drugs (2015); RxMed; RxList; Hopkins ABX (Antibiotics) Database; The Vaccines Database; Drugs in Clinical Trials Database (DCTDB); USP-NF (United States Pharmacopeia–National Formulary) Online; International Nonproprietary Names (INN); Nomenclature of Monoclonal Antibodies (NMAb); The NLM Drug Information Portal; Drugs@FDA; PubChem (NCBI); ChemIDplus (US DHHS); ToxNet (Toxicology Database); New edicines in Development Database (NMDDb); PharmWeb

f.) Medical Informatics / Fundamental Principles of Medicine:

<ongoing>

Human anatomy and physiology; fundamental principles of medicine: cardiovascular diseases; pulmonary diseases; hematologic diseases; oncologic diseases; gastrointestinal diseases; renal diseases, incl. fluid & electrolyte disorders and hypertension; allergic & immunologic disorders; infectious diseases; endocrine & metabolic diseases; rheumatic diseases; neurologic disorders; dermatologic disorders; Computational Medicine; Personalized medicine; Medical Informatics Tools and Resources from the Web: International

Statistical Classification of Diseases and Related Health Problems, 10th revision (ICD-10); International Classification of diseases, 10th Revision, Diagnosis Codes/Clinical Modification (ICD-10-CM); International Classification of Diseases, 10th Revision, Procedure Coding System (ICD-10-PCS); Automated Diagnosis; Systematized Nomenclature of Medicine (SNOMED); International Classification of Primary Care (ICPC); International Classification of Diseases for Oncology, Third Edition (ICD-O); International Classification of Diseases for Oncology, 3rd ed., Morphology Codes (ICD-O-3-MC); NCI SEER Program; Undiagnosed Diseases Program Database @ Office of Rare Diseases, NIH (ORDR, NIH); Medscape/WebMD; MedicineNet; EMedicine; MedSeq

Assistant Professor , Dept. of Biological Sciences, SBMS, COS, R.I.T. (<i>computational biology/bioinformatics</i>)	10/2008- 07/2012
IRACDA Postdoctoral Fellow & Assistant Project Scientist , UC San Diego School of Medicine, Dept. of Pharmacology, (<i>computational biology/structural bioinformatics</i>)	02/2004 – 08/2008
Structural Bioinformatics Researcher , San Diego Supercomputer Center, (<i>structural bioinformatics</i>)	10/2002- 01/2004
Bioinformatics studies , UCSD School of Extended Studies, La Jolla, CA, (<i>general bioinformatics</i>)	06/2000 – 09/2002
Senior Research Associate , The Scripps Research Institute, La Jolla, CA, (<i>protein x-ray crystallography; structure-based drug design</i>)	04/1995 – 05/2000
Postdoctoral Biochemist , Dept. of Chem. & Biochem., UCSD, La Jolla, CA, (<i>protein x-ray crystallography; structural enzymology</i>)	02/1992 - 03/1995
Postdoctoral Biologist , Dept's. of Biol. & Med., UCSD, La Jolla, CA (<i>HIV/AIDS molecular biology</i>)	01/1990 – 07/1991
Postdoctoral Research Fellow , Lab.Tum. Cell Biol., NCI/NIH, Bethesda, MD (<i>HIV/AIDS molecular biology</i>)	03/1988 – 12/1989
Graduate Student & Teaching Assistant , Dept. of Biol., CIT, Pasadena, CA (<i>gene expression molecular biology</i>)	10/1983 – 02/1988
Instructor in Mathematics , Dept. of Math., Univ. of the Philippines, Diliman, Quezon City, PHILIPPINES (<i>differential and integral calculus I, II, and III; statistics & probability</i>)	06/1980 - 08/1982

AWARDS:

- **Nominated:** Eisenhower Outstanding Teaching Award, SY 2011-12, R.I.T.
 - Outstanding Alumni "ATOM" Awards (1 of 50), M.S.H.S. 50th Anniversary Celebration, Oct. 2013
 - IRACDA Postdoctoral Scholars Program, NIGMS, NIH, 2004-'07
 - Bioinformatics Career Development WIA Award, State of California, 2002-'03
 - Postdoctoral Research Fellowship, NIGMS, NIH, 1992-'95
 - John E. Fogarty International Postdoctoral Research Fellowship, NCI, NIH, 1988-'89
 - Laszlo Zechmeister Graduate Fellowship in Chemistry, Caltech, 1983-'85
 - Nat'l. Undergrad. Science & Mathematics Scholarships, NSDB, Philippines, 1976-'80
-

INTERNATIONAL CAREER / WORK EXPERIENCE (outside U.S.):

- 2 ¼ years of college-level teaching at the University of the Philippines, Diliman, Quezon City, Philippines (Department of Mathematics; **see above**)

RECENT COLLABORATIONS (institute-wide, nationwide & worldwide):

- Prof. James Halavin, Dept. of Mathematics, COS, RIT (w/ grad. student J. DeFelice)
- Prof. Anthony Harkin, Dept. of Mathematics, COS, RIT
- Prof. Paul Craig, Dept. of Chemistry, COS, RIT (w/ grad. students A. Banerjee and S. Cheguri)
- Prof. Michael Osier, Dept. of Biology, COS, RIT (w/ grad. student J. DeFelice)
- Prof. Anne Haake, Dept. of Info. Sci & Techn., GCCIS, RIT (w/ grad. student M. McCreary)
- Prof. Stephen Welle, Dept. of Medicine, Univ. of Rochester Medical Center (w/ grad. students R. Rodrigues and M. Manivannan)
- Drs. Tom Mariani and Soumyroop Bhattacharya (w/ grad. student S. Shimpi)

FORMAL GRANTSMANSHIP TRAINING:

- NIGMS/UoK Internet Grant Writing Workshop (<http://www.uky.edu/Projects/GrantWriting>), University of Kentucky, Lexington KY, Prof. Donald Frazier, UoK Sch. of Med., Director, May, 2005
- NIGMS/UoK Internet Grant Writing Workshop (<http://www.uky.edu/Projects/GrantWriting>), University of Kentucky, Lexington KY, Prof. Donald Frazier, UoK Sch. of Med., Director, May, 2006
- NIGMS/UoK Internet Grant Writing Workshop (<http://www.uky.edu/Projects/GrantWriting>), University of Kentucky, Lexington KY, Prof. Donald Frazier, UoK Sch. of Med., Director, May, 2007
- Grant Writing Workshop-Seminar, Grant Writers' Seminars and Workshops, LLC (<http://www.grantcentral.com>), Drs. Stephen W. Russell & David C. Morrison, Lecturers, Pasadena Civic Auditorium, Pasadena, CA Sept., 2005
- Grant Writing Boot Camp, RIT SRS, sponsor, Rochester, NY, Nov. 22-23, 2010
- NIH New Investigators Conference (The Sloane Foundation, sponsor), Cold Spring Harbor Laboratories, Cold Spring Harbor, Long Island, NY, March 14, 2011

COPYRIGHTS & PATENTS (provisional):

- "Novel, Analytical Algorithm for High-Throughput Structure-Based Prediction of Ligand Binding Sites in Proteins" (under UCSD review; Docket # SD2007-164).
- "Novel, Analytical Algorithm for High-Throughput Structure-Based Prediction of Protein-Protein Interaction Partners" (under UCSD review; Docket # SD2007-165)
- "Representing Protein Structures in Spherical Coordinates: Two Applications" (under UCSD review; Docket # SD2008-087).
- "Two Algorithms For Quantifying Ligand Binding Site Burial in Proteins" (under UCSD review; Docket # SD2008-086).

SCIENTIFIC EDITORIAL REVIEW BOARD MEMBER FOR:

- Frontiers in Bioinformatics and Computational Biology
- Journal of Computational Biology and Bioinformatics Research
- Journal of Bioinformatics in Nutrition (Signpost Open Access)
- Journal of Computational Biology and Bioinformatics Research (guest, 2014)

PUBLICATIONS* (incl. e-PUBLICATIONS*):

**for abstracts, please see:*

URL #1: <http://www.pubfacts.com/author/Vicente+M+Reyes>

URL #2: <http://www.mathpubs.com/author/Vicente+M.+Reyes>

URL #3: <https://scholar.google.com/citations?user=OTPAflAAAAAJ&hl=en>

URL #4: https://www.researchgate.net/profile/Vicente_Reyes

37. **Reyes, V.M.** "Analytical (Deterministic) Methods of Computational Epitope Mapping and Other Novel Methods of Protein Surface Representation and Analysis," (invited editorial), *Frontiers in Comp. Biol. & Bioinform.* [e-pub ahead of publication: [arXiv.org/abs/.....](https://arxiv.org/abs/1602.08111) [Quantitative Biology: Biomolecules]] (in progress). Full article: <http://>

36. **Reyes, V.M.** "Further Application of Representing Protein 3D Structures in Spherical (ρ , ϕ , θ) Coordinates: Projection of the Protein Surface onto the 2D Plane Using Cartographic Methods." (2017) [e-pub ahead of publication: [arXiv.org/abs/.....](https://arxiv.org/abs/1602.08111) [Quantitative Biology: Biomolecules]] (in progress). Full article: <http://>

35. Priya P.* and **Reyes, V.M.** "A Cancer Biotherapy Resource" (2015) [e-pub of *M.S. thesis: arxiv.org/abs/1602.08111 ; Quantitative Biology: Biomolecules]. Full article: arxiv.org/ftp/arxiv/papers/1602/1602.08111.pdf

34. DeFelice, J.* and **Reyes, V.M.**, "Spherical Distance Metrics Applied to Protein Structure Classification" (2015) [e-pub of *M.S. thesis: arxiv.org/abs/1602.08079 ; Quantitative Biology: Biomolecules]. Full article: [arXiv.org/ftp/arXiv/papers/1602/1602.08079.pdf](https://arxiv.org/ftp/arXiv/papers/1602/1602.08079.pdf)

33. Cheguri, S.* and **Reyes, V.M.** "Size-Independent Quantification of Ligand Binding Site Depth in Receptor Proteins" (2015) [e-pub of *M.S. thesis, part 1: arxiv.org/abs/1602.08115 ; Quantitative Biology: Biomolecules]. Full article: arxiv.org/ftp/arxiv/papers/1602/1602.08115.pdf

32. Cheguri, S.* and **Reyes, V.M.** "Representing Rod-Shaped Protein 3D Structures in Cylindrical Coordinates" (2015) [e-pub of *M.S. thesis, part 2: arxiv.org/abs/1602.08113 ; Quantitative Biology: Biomolecules]. Full article: arxiv.org/ftp/arxiv/papers/1602/1602.08113.pdf

31. Banerjee A.* and **Reyes, V.M.** "Prediction of Flavin Mononucleotide (FMN) Binding Sites in Proteins Using the 3D Search Motif Method and Double-Centroid Reduced Representation of Protein 3D Structures" (2015) [e-pub of *M.S. thesis: arxiv.org/abs/1602.08119 ; Quantitative Biology: Biomolecules]. Full article: arxiv.org/ftp/arxiv/papers/1602/1602.08119.pdf

30. Sheth, V.N.* and **Reyes, V.M.** "Visualization of Protein 3D Structures in Reduced Representation with Simultaneous Display of Intra- and Inter-Molecular Interactions" (2015) [e-pub of *M.S. thesis: arxiv.org/abs/1602.08117 ; Quantitative Biology: Biomolecules]. Full article: arxiv.org/ftp/arxiv/papers/1602/1602.08117.pdf

29. **Reyes, V.M.** "Implementation of the Spherical Coordinate Representation of Protein 3D Structures and its Applications Using FORTRAN 77/90 Language." (2015) [e-pub ahead of publication: [arXiv.org/abs/1512.00424](https://arxiv.org/abs/1512.00424) [Quantitative Biology: Biomolecules]] (to be submitted to a peer- reviewed journal for publication in 2016/2017). Full article: [arXiv.org/ftp/arXiv/papers/1512/1512.00424.pdf](https://arxiv.org/ftp/arXiv/papers/1512/1512.00424.pdf)

28. **Reyes, V.M.** "Implementation of the Tangent Sphere and Cutting Plane Methods in the Quantitative Determination of Ligand Binding Site Burial Depths in Proteins Using FORTRAN 77/90 Language." (2015) [e-pub ahead of publication: [arXiv.org/abs/1512.00423](https://arxiv.org/abs/1512.00423) [Quantitative Biology: Biomolecules]] (to be submitted to a peer- reviewed journal for publication in 2016/2017). Full article: [arXiv.org/ftp/arXiv/papers/1512/1512.00423.pdf](https://arxiv.org/ftp/arXiv/papers/1512/1512.00423.pdf)

27. **Reyes, V.M.** "Implementation of The Double-Centroid Reduced Representation of Proteins and its Application to the Prediction of Ligand Binding Sites and Protein-Protein Interaction Partners Using FORTRAN 77/90 Language." (2015) [e-pub ahead of publication: [arXiv.org/abs/1512.00003](https://arxiv.org/abs/1512.00003) [Quantitative Biology: Biomolecules]] (to be submitted to a peer- reviewed journal for publication in 2016/2017). Full article: [arXiv.org/ftp/arXiv/papers/1512/1512.00003.pdf](https://arxiv.org/ftp/arXiv/papers/1512/1512.00003.pdf)
26. **Reyes, V.M.** "A Global and Local Structure-Based Method for Predicting Binary Protein-Protein Interaction Partners: Proof of Principle and Feasibility." (2015) [e-pub ahead of publication: [arXiv.org/abs/1505.01144](https://arxiv.org/abs/1505.01144) [Quantitative Biology: Biomolecules]] (to be submitted to a peer- reviewed journal for publication in 2016/2017). Full article: [arXiv.org/ftp/arXiv/papers/1505/1505.01144.pdf](https://arxiv.org/ftp/arXiv/papers/1505/1505.01144.pdf)
25. **Reyes, V.M.** "Structure-Based Function Prediction of Functionally Unannotated Structures in the PDB: Prediction of ATP, GTP, Sialic Acid, Retinoic Acid and Heme-bound and -Unbound (Free) Nitric Oxide Protein Binding Sites." (2015) [e-pub ahead of publication: [arXiv.org/abs/1505.01143](https://arxiv.org/abs/1505.01143) [Quantitative Biology: Biomolecules]] (to be submitted to a peer- reviewed journal for publication in 2016/2017). Full article: [arXiv.org/ftp/arXiv/papers/1505/1505.01143.pdf](https://arxiv.org/ftp/arXiv/papers/1505/1505.01143.pdf)
24. **Reyes, V.M.** "An Automatable Analytical Algorithm for Structure-Based Protein Functional Annotation via Detection of Specific Ligand 3D Binding Sites: Application to ATP (ser/thr Protein Kinases) and GTP (Small Ras-type G-Proteins) Binding Sites" (2015) [e-pub ahead of publication: [arXiv.org/abs/1505.01141](https://arxiv.org/abs/1505.01141) [Quantitative Biology: Biomolecules]] (to be submitted to a peer- reviewed journal for publication in 2016/2017). Full article: [arXiv.org/ftp/arXiv/papers/1505/1505.01141.pdf](https://arxiv.org/ftp/arXiv/papers/1505/1505.01141.pdf) (submitted Jan. 2017 for publication in "Math. for Applic's.")
23. **Reyes, V.M.** "Two Complementary Methods for Relative Quantification of Ligand Binding Site Burial Depth in Proteins: The 'Cutting Plane' and 'Tangent Sphere' Methods" (2015) [e-pub ahead of publication: [arXiv.org/abs/1505.01142](https://arxiv.org/abs/1505.01142) [Quantitative Biology: Biomolecules]] (to be submitted to a peer- reviewed journal for publication in 2016/2017). Full article: [arXiv.org/ftp/arxiv/papers/1505/1505.01142.pdf](https://arxiv.org/ftp/arxiv/papers/1505/1505.01142.pdf)
22. Cheguri, S. and **Reyes, V.M.**, "A Database/Webserver for Size-Independent Quantification of Ligand Binding Site Burial Depth in Receptor Proteins: Implications on Protein Dynamics", J. Biomol. Struct. & Dyn., Book of Abstracts, Albany 2011: The 17th Conversation, June 14-18, 2011, Vol. 28 (6) June 2011, p. 1013
21. Cheguri, S. and **Reyes, V.M.**, "Using Cylindrical Coordinates to Represent Rod-Shaped and Other Fibrous Protein 3D Structures: Potential Advantages and Applications", J. Biomol. Struct. & Dyn., Book of Abstracts, Albany 2011: The 17th Conversation, June 14-18, 2011, Vol. 28 (6) June 2011, p. 1014
20. DeFelice and **Reyes, V.M.**, "Towards a Spherical Coordinate System Metric for Quantitative Comparison of Protein 3D Structures", J. Biomol. Struct. & Dyn., Book of Abstracts, Albany 2011: The 17th Conversation, June 14-18, 2011, Vol. 28 (6) June 2011, p. 1015
19. Priya, P. and **Reyes, V.M.**, "Cancer Meets the "Omics": A Comprehensive Cancer Biotherapy Database with Links to Multiple Bioinformatics Websites/WebServers - Facilitating the Search for Anticancer Biological Agents", J. Biomol. Struct. & Dyn., Book of Abstracts, Albany 2011: The 17th Conversation, June 14-18, 2011, Vol. 28 (6) June 2011, p. 1016
18. **Reyes, V.M.**, "Using Cartographic Techniques to Project Protein 3D Surfaces onto the 2D Plane: Potential Applications and Implications", J. Biomol. Struct. & Dyn., Book of Abstracts, Albany 2011: The 17th Conversation, June 14-18, 2011, Vol. 28 (6) June 2011, p. 1017
17. **Reyes, V.M.**, "Representation of Protein 3D Structures in Spherical (ρ, ϕ, θ) Coordinates and Two of Its Potential Applications", Interdiscip. Sci.: Comp. Life Sci., Sept. 2011, Vol. 3, No. 3, pp. 161-174.
16. **Reyes, V.M.*** & Sheth, V.N., "Visualization of Protein 3D Structures in 'Double-Centroid' Reduced Representation: Application to Ligand Binding Site Modeling and Screening" (March 2013) Essential

Reference: Bioinformatics - Concepts, Methodologies, Tools, and Applications; Information Resources Management Association, ed.; Ch. 59, Vol. 2, Sect. 4: Cases and Applications, pp. 1158-1173.

15. **Reyes, V.M.*** & Sheth, V.N., "Visualization of Protein 3D Structures in 'Double-Centroid' Reduced Representation: Application to Ligand Binding Site Modeling and Screening" (March 2011), Handbook of Research in Computational and Systems Biology: Interdisciplinary Approaches, IGI-Global/Springer, Ch. 26, pp. 583-598;

14. **Reyes, V.M.**, "Modeling Protein-Protein Interface Interactions as a Means for Predicting Protein-Protein Interaction Partners." J. Biomol. Struct. & Dyn., Book of Abstracts, Albany 2009: The 16th Conversation, June 16-20, 2009, Vol. 26 (6), 06/2009, p. 873

13. **Reyes, V.M.**, "Pharmacophore Modeling Using a Reduced Protein Representation as a Tool for Structure-Based Protein Function Prediction", J. Biomol. Struct. & Dyn., Book of Abstracts, Albany 2009: The 16th Conversation, June 16-20, 2009, Vol. 26 (6), 06/2009, p. 873

12. **Reyes, V.M.**, "Pharmacophore Modeling Using a Reduced Protein Representation: Application to the Prediction of ATP, GTP, Sialic Acid, Retinoic Acid, and Heme-Bound and -Unbound Nitric Oxide Binding Proteins", J. Biomol. Struct. & Dyn., Book of Abstracts, Albany 2009: The 16th Conversation, June 16-20, 2009, Vol. 26 (6), 06/2009, p. 874

11. **Reyes, V.M.**, "Representing Protein 3D Structures in Spherical Coordinates – Two Applications: 1. Detection of Invaginations, Protrusions, and Potential Ligand Binding Sites; and 2. Separation of Protein Hydrophilic Outer Layer from the Hydrophobic Core ", J. Biomol. Struct. & Dyn., Book of Abstracts, Albany 2009: The 16th Conversation, June 16-20 2009, Vol. 26 (6), 06/2009, pp. 874-5

10. **Reyes, V.M.**, "Two Complementary Methods for Quantifying Ligand Binding Site Burial Depth in Proteins: The "Cutting Plane" and the "Tangent Sphere Methods", J. Biomol. Struct. & Dyn., Book of Abstracts, Albany 2009: The 16th Conversation, June 16-20 2009, Vol. 26 (6), 06/2009, p. 875

9: Li, W., Byrnes, R.W., Hayes, J., Birnbaum, A., **Reyes, V.M.**, Shahab, A., Mosley, C., Pekurovsky, D., Quinn, G.B., Shindyalov, I.N., Casanova, H., Ang, L., Berman, F., Arzberger, P.W., Miller, M., Bourne, P.E. "The Encyclopedia of Life Project: Grid Software and Deployment." New Gener. Comp. (June 2004) 22:127-136.

8: Bourne, P., Miller, M., Baldrige, K., Baru, C., Berman, F., Byrnes, R., Casanova, H., Cotofana, N., Fountwain, T., Greenberg, J., Li, W., Mosley, C., Pekurovsky, D., Quinn, G., **Reyes, V.**, Shin, P., Shindyalov, I., Veretnik, S. "Encyclopedia of Life: to Open New Chapter of Biological Discovery." SDSC & NPACI EnVision, (Jan.-Mar. 2003) Vol. 19, No. 1, pp. 3-5

7: **Reyes, V.M.**, Greasley, S.E., Stura, E.A., Beardsley, G.P., Wilson, I.A. "Crystallization and preliminary crystallographic investigations of avian 5-aminoimidazole-4-carboxamide ribonucleotide transformylase-inosine monophosphate cyclohydrolase expressed in Escherichia coli." Acta Crystallogr D Biol Crystallogr. (2000) Aug;56 (Pt 8):1051-4.

6: Lee, H., ***Reyes, V.M.**, Kraut, J. "Crystal structures of Escherichia coli dihydrofolate reductase complexed with 5-formyltetrahydrofolate (folinic acid) in two space groups: evidence for enolization of pteridine O4." Biochemistry. (1996) Jun 4;35(22):7012-20.
(*corresponding author)

5: **Reyes, V.M.**, Sawaya, M.R., Brown, K.A., Kraut, J. "Isomorphous crystal structures of Escherichia coli dihydrofolate reductase complexed with folate, 5-deazafolate, and 5,10-dideazatetrahydrofolate: mechanistic implications." Biochemistry. (1995) Feb 28;34(8):2710-23.

- 4: **Reyes, V.M.**, Abelson, J.N. "In vitro synthesis of end-mature, intron-containing transfer RNAs." *Methods Enzymol.* (Nov. 1989);180:63-9.
- 3: **Reyes, V.M.**, Abelson, J. "Substrate recognition and splice site determination in yeast tRNA splicing." *Cell.* (1988) Nov 18;55(4):719-30.
- 2: **Reyes, V.M.**, Abelson, J. "A synthetic substrate for tRNA splicing." *Anal Biochem.* 1987 Oct;166(1):90-106.
- 1: **Reyes, V.M.**, Newman, A., Abelson, J. "Mutational analysis of the coordinate expression of the yeast tRNA^{Arg}-tRNA^{Asp} gene tandem." *Mol Cell Biol.* (1986) Jul;6(7):2436-42.

GRADUATE & UNDERGRADUATE STUDENT ADVISEES:

- **Vrunda Sheth**, M.S., successfully defended thesis "Visualization of Protein 3D Structures in Reduced Representation with Simultaneous Display of Intra- and Inter-molecular Interactions", October 23, 2009
- **James DeFelice**, M.S., successfully defended thesis "Spherical Distance Metrics Applied to Protein Structure Classification", May 18, 2011
- **Srujana Cheguri**, M.S., successfully defended thesis "I. Two Complementary Methods for Quantifying Ligand Binding Site Depth in Proteins: The 'Secant Plane' and 'Tangent Sphere' Methods; II. Using Cylindrical (ρ, θ, z) Coordinates to Represent Rod-Shaped and Elongated Protein 3D Structures", November 15, 2011
- **Arkanjan Banerjee**, M.S., scheduled to defend thesis, "Binding Site Modeling and Screening for Flavin Moiety-Containing Ligands", December 2011
- **Preeti Priya**, M.S., scheduled to defend thesis "Cancer Meets the "Omics": A Comprehensive Cancer Biotherapy Database with Links to Multiple Bioinformatics Websites/WebServers - Facilitating the Search for Anticancer Biological Agents", Winter/Spring 2012
- **Umesh Puttegowda**, M.S., scheduled to defend thesis, "Structure-Based Design of Inhibitor Against Ebola Virus Infection", Spring 2012
- **Connor Fortin**, B.S., "Structural Bioinformatics Studies on Metal Binding Sites in Metalloproteins" (current)
- **Andrew Clark**, M.S. thesis, "Construction of Alpha Helix, Beta Sheet and Loop Libraries from Proteins in the PDB," defense TBA
- **Dong Jin Kim**, M.S. thesis, "Structural Bioinformatics Studies on Amino Acid Sidechain Orientations in Staphylococcal Nuclease," defense TBA

M.S. THESIS RESEARCH COMMITTEE MEMBER FOR:

- **Richard Rodrigues**, M.S., successfully defended thesis, "RNA Sequencing ('RNA-Seq') Analysis from the Triceps Muscle of Normal and Myostatin-Deficient Mice Using Various Tools," Nov. 14, 2011
- **Swati Shimpi**, M.S., thesis, "Discovering the role of SERPINE2 in COPD," defense scheduled for Spring 2012
- **Manimozhi Manivannan**, M.S., thesis, "Transcriptional Analysis of the Effect of Flu Vaccination on B and Peripheral Blood Mononuclear Cells using RNA Sequencing ('RNA-Seq')," defense scheduled for Spring 2012
- **Mark McCreary**, M.S. thesis, "Computational Epitope Mapping", defense TBA

RESEARCH GROUP ALUMNI and CAREER STATUSES:

- **Vrunda Sheth**, M.S., Scientist, Life Technologies, Inc., Beverly, MA (f.k.a. Applied Biosystems, Inc.)
- **Srujana Cheguri**, M.S., Technologist, Sloan-Kettering Memorial Cancer Center, New York City, NY
- **James DeFelice**, M.S. (career status TBA)

- **Wan Munirah Wan Mohamad**, B.S. “Library of Protein-Protein Interface Interactions Using the Double Tetrahedral Binding Site Motif Model, Part 1” (career status TBA)
- **Muhamad Hanafi Hazemi**, B.S., “Library of Protein-Protein Interface Interactions Using the Double Tetrahedral Binding Site Motif Model, Part 2” (career status TBA)

TEXTBOOKS IN PREPARATION: (with the R.I.T. Press)

- Bioinformatics: An “Omics” Approach
- Proteomics: From A Structural Perspective
- UNIX and Perl Scripting for Computational Biology (with “sed” and “awk”)

PRESENTATIONS and PARTICIPATIONS (since January 2009):

- Open Access/Open Science Mini-Workshop/Seminar: “Open Scholarship: What Does it Mean for Us?” October 27, 2017, Rush Rhees Library, University of Rochester, Rochester, NY
- Sixth Annual Joint Conference of the Upstate Chapters of the American Statistical Association (“UPSTAT-2017”), College, Buffalo, NY, April 21st-22nd, 2017
Oral Research Presentation: “The ‘Cutting Plane’ and ‘Tangent Sphere’ Methods: Two Complementary Methods for Relative Quantification of Ligand Binding Site Burial Depth in Proteins”
- Fifth Annual Joint Conference of the Upstate Chapters of the American Statistical Association (UP-STAT 2016), Canisius College, Buffalo, NY, April 22nd-23rd, 2016
Oral Research Presentation: “A Short Survey of Computational Structural Proteomics Research Using the Protein Data Bank (PDB) as Main Dataset”
- Fourth Annual Joint Conference of the Upstate Chapters of the American Statistical Association (UP-STAT 2015), SUNY Geneseo, NY, April 10th-11th, 2015
Poster Presentation: “A Combined Deterministic and Stochastic Procedure for Biological Data Mining: Prediction of Binary Protein-Protein Interaction Partners” with Vrunda N. Sheth (M.S. Bioinformatics graduate) & Wan Munirah Wan Mohamad (B.S. Biotechnology graduate)
- Jackson State University, Department of Biology, College of Science, Engineering and Technology, Jackson, MS 39217, June 19, 2014
Research Seminar title: “Computational Prediction of Ligand Binding Sites and Catalytic Sites in Proteins (Enzymes) Using a Novel Reduced Protein Representation ”
- New Jersey Center for Science, Technology & Mathematics, Kean University, Union, NJ 07083 March 6, 2014
Research Seminar title: “Prediction of Ligand Binding Sites in Proteins Using the Double Centroid Reduced Protein Representation ”
- New Jersey Center for Science, Technology & Mathematics, Kean University, Union, NJ 07083 March 6, 2014
Student Lecture: “Introduction to Macromolecular X-Ray Crystallography and its Important Role in Biology Research”
- University of Maryland - University Center, Bioinformatics Division, Department of Information Systems & Technology, Adelphi, MD, 20783, January 18, 2013
Seminar title: “Bioinformatics as a Scientific Discipline: Graduate Program and Curriculum”
- Kazakhstan Embassy, Washington D.C., U.S.A., for Dept. of Computational Sciences, School of Science and Technology, Nazarbayev University, Astana, Kazakhstan, November 15, 2012

Seminar title: "What is X-Ray Crystallography? (The Role of Macromolecular X-Ray Crystallography in Biological Research)"

- Ph.D. Colloquium Series, Golisano College of Computational & Information Sciences, RIT campus, March 16, 2012

Research seminar title: "Computational Proteomics Projects in the Reyes Research Group and their Potential Applications"

- Open Forum with the Upstate New York Translational Research Network, August 11, 2011, Idea Factory, Wallace Library, RIT campus

Research seminar title: "Computational Epitope Prediction"

- 17th Conversation on BSDIE (Biological Structure, Dynamics, Interaction and Expression), SUNY-Albany, Albany, NY, June 14-18, 2011

Poster #1: Cheguri, S. and **Reyes, V.M.**, "A Database/Webserver for Size-Independent Quantification of Ligand Binding Site Burial Depth in Receptor Proteins: Implications on Protein Dynamics"

Poster #2: Cheguri, S. and **Reyes, V.M.**, "Using Cylindrical Coordinates to Represent Rod-Shaped and Other Fibrous Protein 3D Structures: Potential Advantages and Applications"

Poster #3: DeFelice and **Reyes, V.M.**, "Towards a Spherical Coordinate System Metric for Quantitative Comparison of Protein 3D Structures"

Poster #4: Priya, P. and **Reyes, V.M.**, "Cancer Meets the "Omics": A Comprehensive Cancer Biotherapy Database with Links to Multiple Bioinformatics Websites/WebServers - Facilitating the Search for Anticancer Biological Agents"

Poster #5: **Reyes, V.M.**, "Using Cartographic Techniques to Project Protein 3D Surfaces onto the 2D Plane: Potential Applications and Implications"

- **Imagine RIT**, May 7, 2011:

Poster presented with Bioinformatics Classes of Winter 2010 and 2011: "Structure-Based Function Assignment of Novel Proteins in the Protein Data Bank (PDB) Deposited without Functional Annotation"

- **The Bioinformatics Cluster Seminar Series**, University of Rochester Medical Center, Rochester, NY, March 10, 2011

Research seminar title: "Representing Protein 3D Structures in Spherical and Cylindrical Coordinates: Potential Applications"

- Invited Plenary Speaker, **ICCSB** (Int'l. Conference on Computational and Systems Biology) **2010**, Hangzhou/Shanghai, China, Oct. 21-23, 2010: Research paper submitted 7/14/2010

Research seminar title: "Representation of Protein 3D Structures in Spherical (ρ, ϕ, θ) Coordinates and Two of Its Applications"

- Gordon Research Conference on IDRs (Intrinsically Disordered Regions) and Unfoldomics, Davidson, NC (Davidson College), 7/11-7/16/2010; presented one poster; actively participated in post-talk discussions

Poster: Characterizing the Interactions Between Protein & Lipid Moieties at Lipidation & Lipid Binding Sites in Proteolipids/Lipoproteins; and (II.) Determining the Loop Propensities of the 20 Amino Acids"

- Gordon Research Conference on Biopolymers, Newport, RI (Salve Regina University), 6/06-6/11/2010; presented two posters; actively participated in post-talk discussions

Poster #1: Visualization of Protein 3D Structures in 'Double-Centroid' Reduced Representation: Application to Ligand Binding Site Modeling and Screening

Poster #2: Separation of a Protein's Outer Layer from Its Inner Core Using Spherical Coordinate Representation: Potential Application to Computational Epitope Mapping and Detection of Deeply Buried Active Sites

- Gordon Research Conference on Proteins, Holderness, NH (Holderness School), 06/21-06/26/2009; presented two posters; actively participated in post-talk discussions

Poster #1: Two Novel Methods for Protein Structure Analysis: (1.) Spherical Coordinate Representation of Protein Structures; and (2.) Quantification of Ligand Binding Site Burial Using the 'Cutting Plane' and 'Tangent Sphere' Methods

Poster #2: Modeling of, and Screening for, Ligand Binding Sites and Protein-Protein Interface Interactions as Tetrahedral Motifs in Reduced Protein Representation: Applications to Protein Function Prediction

- 16th Conversation on BSDIE (Biological Structure, Dynamics, Interaction and Expression, SUNY-Albany, Albany, NY, June 16-20, 2009

Poster #1: Representing Protein 3D Structures in Spherical Coordinates: Two Applications: (1.) Detection of Invaginations and Protrusions on the Protein Surface; and (2.) Separating the Protein Hydrophobic Inner core from the Hydrophilic Outer layer

Poster #2: Two Complementary Methods for Quantifying Ligand Binding Site Burial Depth In Proteins: (1.) The "Cutting Plane" Method; and (2.) The "Tangent Sphere" Method

Poster #3: Pharmacophore Modeling Using a Reduced Protein Representation as a Tool for Structure-Based Protein Function Prediction

Poster #4: Pharmacophore Modeling Using a Reduced Protein Representation: Application to ATP, GTP, Sialic Acid, Retinoic Acid and Heme-Bound and -Unbound Nitric Oxide

Poster #5: Modeling Protein-Protein Interface Interactions as a Means for Predicting Protein-Protein Interaction Partners

- Pacific Symposium on Biocomputing, Jan. 5-9, 2009, Big Island, Hawaii

Poster #1: Representing Protein 3D Structures in Spherical Coordinates: Two Applications: (1.) Detection of Invaginations and Protrusions on the Protein Surface; and (2.) Separating the Protein Hydrophobic Inner core from the Hydrophilic Outer layer

Poster #2: Two Complementary Methods for Quantifying Ligand Binding Site Burial Depth In Proteins: (1.) The "Cutting Plane" Method; and (2.) The "Tangent Sphere" Method

Poster #3: Pharmacophore Modeling Using a Reduced Protein Representation as a Tool for Structure-Based Protein Function Prediction

Poster #4: Pharmacophore Modeling Using a Reduced Protein Representation: Application to ATP, GTP, Sialic Acid, Retinoic Acid and Heme-Bound and -Unbound Nitric Oxide

Poster #5: Modeling Protein-Protein Interface Interactions as a Means for Predicting Protein-Protein Interaction Partners

- ISBRA 2009 (5th International Symposium on Bioinformatics Research and Applications), May 13 -16, 2009, Nova Southeastern University, Ft. Lauderdale, FL (with bioinformatics graduate student, Vrunda Sheth)

Poster: "Visualization of Protein 3D Structures in Reduced Representation with Simultaneous Display of Intramolecular H-bond and van der Waals Interactions"

- **Imagine RIT**, May 2, 2009:

- Grad student, Vrunda Sheth (w/ V. Reyes) poster: "Visualization of Protein 3D Structures in Reduced Representation with Simultaneous Display of Intramolecular H-bond and van der Waals Interactions"

- Undergrad student, Wan Munirah Wan Mohamad (w/ V. Reyes) poster: "Building a Library of Protein-Protein Binary Complex (PPBC) Interfacial Interaction Models Using a Reduced Protein Representation"

- RIT's I.T. Collaboratory Access Grid Seminar Series, "Visualization of Protein 3D Structures in Double-Centroid Reduced Representation" Vicente Reyes, and Vrunda Sheth, Dept. of Biological Sciences, Bioinformatics Program, R.I.T. (broadcast over the Access Grid from RIT's I.T. Collaboratory), Jan. 22, 2009.

- R.I.T. Biology Dept. Seminar Series, "Two Structural Proteomics Algorithms and Their Applications", Dec. 15, 2008

- R.I.T. Mathematics Dept. Colloquium Series, "Two Structural Proteomics Algorithms and Their Applications", Feb. 4, 2009

- R.I.T. Undergraduate Research Program for the Hearing Impaired (PI's: Drs. Hyla Sweet & Dina Newman), Slide Slam, Oct. 24, 2008 and Sept. 9, 2009

Presentations Before Joining R.I.T. in Fall 2008:

- IRACDA Conference, June 2007, La Jolla, CA
- IRACDA Conference, June 2006, Kansas City, MO
- IRACDA Conference, June 2005, Tucson, AZ
- IRACDA Conference, June 2004, Atlanta, GA
- Sackler N.A.S. Symposium, "Frontiers in Bioinformatics: Unsolved Problems and Challenges", U.C. Irvine, 2005
- Protein Function Prediction Conference , UC San Diego, La Jolla, CA, 2007
- Li, W., Shindyalov, I.N., Quinn, G., Mosley, C., Pekurovsky, D., Baldrige, K., Rowley, J., Cotofana, N., Reyes, V.M., Byrnes, R., Amoreira, C., Potier, Y., Casanova, H., Hayes, J., Birnbaum, A., Miller, M., and Bourne, P.E., ".....," PRAGMA Proceedings, Fukuoka, Japan, 2003
- Miller, M.A., Shindyalov, I.N., Quinn, G., Li, W., Mosley, C., Pekurovsky, D., Baldrige, K., Rowley, J., Cotofana, N., Reyes, V.M., Byrnes, R., Amoreira, C., Potier, Y., Casanova, H., Hayes, J., Birnbaum, A., and Bourne, P., "High Throughput Proteomics and the Encyclopedia of Life", Global Grid Forum (GGF) 7, Proceedings, xxxxx-xxxxxx, 2003 [https://forge.gridforum.org/docman2/ViewProperties.php?group_id=39&document_content_id=592]
- Reyes, V.M., "De novo Purine Biosynthetic Enzyme, GAR Transformylase, as Target for Structure-Based Anti-Cancer Drug Design," Oral Presentation, Genomatika, La Jolla, California, September 10, 2001.
- Reyes, V.M., "Crystallographic Studies of Escherichia coli GAR Transformylase and Avian AICAR Transformylase: Implications on Drug Design," Oral Presentation, SBI (Structural Bioinformatics, Inc.), San Diego, California, April 28, 2000.
- Greasley, S., Reyes, V.M., Stura, A.E., Haynes, N., Boger, D., Wilson, I., Warren, M.A., & Benkovoic, S.J., "Towards Rational Drug Design: Crystal Structures of Glycinamide Ribonucleotide Transformylase", poster presentation, The XVII Congress and General Assembly of the International Union of Crystallography, Washington State Trade and Convention Center, Seattle, Washington, August 8-17, 1996
- Reyes, V.M., "X-ray Crystallographic Analysis of the Dihydrofolate Reductase Reaction Mechanism: Deducing the structure of the Transition State," Oral presentation, Chemistry Seminar Series, Spring 1995, Department of Chemistry, San Diego State University, San Diego, California, March 20, 1995
- Reyes, V.M., "Crystallographic Structural Analysis of Ten E. coli DHFR Ligand Complexes: Structural Rationalization of the Kinetic Properties of the Enzyme Mechanism and Clues to the Structure of Its Transition State," poster presentation, 21st Crystallographic School and Symposium, International School of Crystallography, Erice, Sicily, Italy, May 27-June 5, 1994
- Reyes, V.M., "5'-Capping of HIV-1 Messenger RNA in HeLa, H9, and HIV-1-infected H9 Cell Extracts," poster presentation, RNA Tumor Viruses Meeting, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, May 24-28, 1989
- Reyes, V.M., "Substrate Recognition and Splice Site Selection by the S. cerevisiae tRNA Splicing Endonuclease," Oral presentation, Southern California Yeast Genetics Meeting, University of California, Irvine, California, November 21, 1987
- Reyes, V.M., "Yeast tRNA Splicing in Vitro," Oral presentation, RNA Processing Meeting, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, May 13-17, 1987
- Reyes, V.M., "Effects of Specified Base Substitutions on in vitro Splicing of S. cerevisiae tRNA Precursor," poster presentation, RNA Processing Meeting, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, May 14-18, 1986

RESEARCH GRANT PROPOSALS SUBMITTED (since Summer 2010):

- **NSF ABI #1:** "Use of a Reduced Protein Representation for the Modeling and Screening of Ligand Binding Sites: A Structure-Based Protein Function Prediction Method" (Summer 2010)
- **NSF ABI #2:** "Use of Spherical and Cylindrical Coordinate Systems to Represent Protein 3D Structures: Applications to Epitope Mapping and Ligand Binding Site Prediction" (Summer 2010)

- **NIH RO1 #1:** “A Reduced Protein Representation for Modeling and Screening Ligand Binding Sites” (Summer 2010)
- **NIH RO1 #2:** “Using Spherical and Cylindrical Coordinates to Represent Protein 3D Structures” (Summer 2010)
- **RIT OVPR #1:** “Construction of A Comprehensive Cancer Biotherapy Database As a Resource For Patients and Researchers” (Summer 2010)
- **RIT OVPR #2:** “Construction of A Protein Alpha Helix, Beta Sheet And Loop Databases To Discover ‘Rules’ For Protein Folding” (Summer 2010)
- **RIT-RGH Alliance Seed Funding Program:** “Construction of a Comprehensive Cancer Biotherapy Database/Webserver as a Resource for Patients/Researchers” (Summer 2010)
- **RIT Grant Writers’ Boot Camp:** “Construction of a Comprehensive Cancer Biotherapy Database as a Resource for Patients and Researchers” (Fall 2010)
- **Beckman Research Scholars’ Program** (with Prof. Paul Craig, Dept. of Chemistry, RIT; Summer 2011)

COURSES TAUGHT at R.I.T. (since March 2009):

- Perl for Bioinformatics, Spring 2009, 2010 and 2011
- UNIX Under the Hood, Fall 2010
- Bioinformatics, Winter 2010, 2011 and 2012
- Bioinformatics Seminar:
 “Protein-Protein Interactions,” Fall 2009
 “Cancer Biotherapy from the Informatics Perspective,” Fall 2010
 “The Protein Folding Problem,” Fall 2011
- Proteomics & Molecular Modeling, Spring 2009, 2010, 2011 and 2012

COURSES TAUGHT before joining R.I.T. in Fall 2008:

- Calculus with Analytic Geometry I (Univ. of the Philippines, 1980’s)
- Calculus with Analytic Geometry II (Univ. of the Philippines, 1980’s)
- Calculus with Analytic Geometry III (Univ. of the Philippines, 1980’s)
- Fundamentals of Probability and Statistics (Univ. of the Philippines, 1980’s)
- Calculus for Pre-Medicine Students (Univ. of the Philippines, 1980’s)
- Macromolecular X-Ray Crystallography (a segment of) (Univ. of Calif., San Diego, 1990’s)
- Biochemistry (San Diego State Univ., 1990’s)
- Biology 101 (San Diego State Univ., 2000’s)

GRANT AWARDS (since March 2009):

- F.E.A.D. Summer Research Funding Award, College of Science, R.I.T., Summer 2009
- A.R.R.A. Summer Research Funding Award, R.I.T./R.G.H. Alliance, Summer 2009
- F.E.A.D. Summer Research Funding Award, College of Science, R.I.T., Summer 2010

MISCELLANEOUS ITEMS:

- Member, External Faculty, Ph.D. Program of the Golisano Institute of Computing and Information Sciences, R.I.T. (Prof. P.-C. Shi, director)
- Member, Center for Applied and Computational Mathematics, Dept. of Mathematics, R.I.T. (Prof. A. Harkin, director)

MEMBERSHIP IN PROFESSIONAL SOCIETIES:

- Member, IEEE Bioinformatics and Computational Biology
- Member, Protein Society
- Member, SIAM (Society for Industrial and Applied Mathematics)

RELEVANT SKILLS:

- Managerial / Management skills (large and small groups)
- Mentoring & Advising skills (on-on-one)
- Classroom teaching / lecturing skills
- Scientific Research Article and Review Writing
- Scientific Journalism / Editing skills
- Course / Curriculum development
- Program (undergraduate and graduate) initiation and development
- Grant-writing / Grant application and follow-up
- Business Plan Writing
- Business Entity Creation and Incorporation
- Research Program Management & Supervision (incl. Project Management)
- Symposium /Conference / Workshop organization and management
- Scientific Research Article Review, Analysis and Critique
- Workplace Conflict Mediation
- Programming Language Skills: Fortran 77/90; UNIX; C-Shell Programming; Sed & Awk; Perl; C; C++;
R; Weka Data Mining; Python; MatLab; Mathematica; Microsoft Office Suite;
etc., Biocomputing skills: (too many to enumerate here)

CITIZENSHIP:

U.S.A. (naturalized August 2000)

INTERESTS OUTSIDE OF CAREER:

Western classical music, international cuisine, good movies, world history & geopolitics, law & jurisprudence

<unabridged version>

<last updated January 2018>