1. **M. Michael Gromiha, Editor (2020) Protein Interactions: computational methods, analysis and applications, World Scientific, Singapore.**
2. A. Kulandaisamy, Jan Zaucha, Dmitrij Frishman and **M. Michael Gromiha** (2020) MPTherm-pred: Analysis and prediction of thermal stability changes upon mutations in transmembrane proteins. *J Mol Biol.* (in press).
3. U. Rangaswamy, S.A.P. Dharshini, D. Yesudhas and **M. Michael Gromiha** (2020) VEPAD-Predicting the effect of variants associated with Alzheimer's disease using machine learning. *Comp Biol Med.* 103933.
4. A. Shanmugam, N. Muralidharan, D. Velmurugan and **M. Michael Gromiha** (2020) Therapeutic targets and computational approaches on drug development for COVID-19. *Curr Top Med Chem.* (in press).
5. S. Sudhakara, C. Ramakrishnan, **M. Michael Gromiha** and A. Chadha (2020) New insights into the stereospecific reduction by an (S) specific carbonyl reductase from Candida parapsilosis ATCC 7330: Experimental and QM/MM studies. *Catal Sci Technol.* 10, 5925-34.
6. S. Jemimah and **M. Michael Gromiha** (2020) Insights into changes in binding affinity caused by disease mutations in protein-protein complexes. *Comp Biol Med.* 103829.
7. A. Kulandaisamy, R. Sakthivel and **M. Michael Gromiha** (2020) MPTherm: Database for Membrane Protein Thermodynamics for understanding folding and stability. *Brief Bioinf.* (in press).
8. N. Muralidharan, R. Sakthivel, D. Velmurugan and **M. Michael Gromiha** (2020) Computational studies of drug repurposing and synergism of lopinavir, oseltamivir and ritonavir binding with SARS-CoV-2 protease against COVID-19. *J Biomol Struct Dyn.* (in press).
9. S. Jemimah, K. Yugandhar and **M. Michael Gromiha** (2020) Binding affinity of protein-protein complexes: experimental techniques, databases and computational methods. In "Protein interactions: computational methods, analysis and applications", (Ed. M.M. Gromiha), World Scientific, Singapore, pp 87-108.
10. A. Srivastava, D. Yesudhas, A. Kulandaisamy, N. Muralidharan, C. Ramakrishnan, R. Nagarajan and **M. Michael Gromiha** (2020) Computational approaches for understanding the recognition mechanism of protein–nucleic acid complexes. In "Protein interactions: computational methods, analysis and applications", (Ed. M.M. Gromiha), World Scientific, Singapore, pp 169-216.
11. D. Yesudhas, A. Srivastava, N. Muralidharan, A. Kulandaisamy, R. Nagarajan and **M. Michael Gromiha** (2020) Prediction of nucleic acid binding proteins and their binding sites. In "Protein interactions: computational methods, analysis and applications", (Ed. M.M. Gromiha), World Scientific, Singapore, pp 217-242.
12. K. Veluraja, N. R. Siva Shanmugam, J. Jino Blessy, R. A. Jeyaram, B. Lalithamaheswari and **M. Michael Gromiha** (2020) Protein-carbohydrate complexes: binding site analysis, prediction, binding affinity and molecular dynamics simulations. In "Protein interactions: computational methods, analysis and applications", (Ed. M.M. Gromiha), World Scientific, Singapore, pp 299-332.
13. V. Kanakaveti, P. Anoosha, R. Sakthivel, S.K. Rayala and and **M. Michael Gromiha** (2020) Quantitative structure-activity relationship in ligand-based drug design: concepts and applications. In "Protein interactions: computational methods, analysis and applications", (Ed. M.M. Gromiha), World Scientific, Singapore, pp 333-349.
14. N.R.S. Shanmugam, J. Blessy, K. Veluraja and **M. Michael Gromiha** (2020). ProCaff: protein-carbohydrate complex binding affinity database. *Bioinformatics* 36(11), 3615-3617
15. V.R. Muddapu, S.A.P. Dharshini, V. Srinivasa Chakravarthy and **M. Michael Gromiha** (2020). Neurodegenerative diseases – Is metabolic deficiency the root cause? *Frontiers Neurosci.* 14, 213.
16. A. Shanmugam, C. Ramakrishnan, D. Velmurugan and **M. Michael Gromiha** (2020). Identification of potential inhibitors for targets involved in dengue fever. *Curr Topics Med Chem.* 20, 1738-1756.
17. A. Srivastava, D. Yesudhas, C. Ramakrishnan, S. Ahmad and **M. Michael Gromiha** (2020). Role of disordered regions in transferring tyrosine to its cognate tRNA. *Int J Biol Macromol.* 150:705-713
18. P. Rawat, R. Prabakaran, R.Sakthivel, A. Mary Thangakani, Sandeep Kumar and **M. Michael Gromiha** (2020). CPAD 2.0: A repository of curated experimental data on aggregating proteins and peptides. *Amyloid* 27, 128-133.
19. C. Ramakrishnan, R. Nagarajan, M. Sekijima and **M. Michael Gromiha** (2020). Molecular dynamics simulations of cognate and non-cognate AspRS-tRNA Asp complexes. *J Biomol Str Dyn.* (in press)
20. V. Kanakaveti, A. Shanmugam, C. Ramakrishnan, P. Anoosha, R. Sakthivel, S.K. Rayala and **M. Michael Gromiha** (2020). Computational approaches for identifying potential inhibitors on targeting protein interactions in drug discovery. *Adv Prot Chem Str Biol.* 121, 25-47.
21. S. Akila Parvathy Dharshini, Y-h. Taguchi and **M. Michael Gromiha** (2020). Identifying suitable tools for variant detection and differential gene expression using RNA-seq data. *Genomics.* 112(3):2166-2172..

22. A. Kulandaisamy, J. Zaucha, R. Sakthivel, D. Frishman and **M. Michael Gromiha** (2020) Pred-MutHTP: Prediction of disease-causing and neutral mutations in human transmembrane proteins. *Human Mutation.* 41, 581-590.

23. S. Jemimah, M. Sekijima and **M. Michael Gromiha** (2020) ProAffiMuSeq: Sequence-based method to predict the binding free energy change of protein-protein complexes upon mutation using functional classification. *Bioinformatics.* 36:1725-1730.

24. P. Rawat, R. Prabakaran, S. Kumar and **M. Michael Gromiha** (2020). AggreRATE-Pred: A mathematical model for the prediction of change in aggregation rate upon point mutation. *Bioinformatics.* 36:1439-1444.

25. R. A. Jeyaram, C. Anu Radha, **M. Michael Gromiha** and K. Veluraja (2020). Design of fluorinated sialic acid analog inhibitor to H5 Hemagglutinin of H5N1 Influenza virus through Molecular Dynamics simulation study. *J Biomol Str Dyn.* 38, 3504-3513.

26. R Nikam and **M. Michael Gromiha** (2019). Seq2Feature: a comprehensive web-based feature extraction tool. *Bioinformatics* 35:4797-4799.

27. S. Akila Parvathy Dharshini, Y-h. Taguchi and **M. Michael Gromiha** (2019) Investigating the energy crisis in Alzheimer disease using transcriptome study. Sci Rep 9, 18509.

28. S. Chiba, M. Ohue, A. Gryniukova, P. Borysko, S. Zozulya, N. Yasuo, R. Yoshino, K. Ikeda, W-H. Shin, D. Kihara, M. Iwadate, H. Umeyama, T. Ichikawa, R. Teramoto, K-Y. Hsin, V. Gupta, H. Kitano, M. Sakamoto, A. Higuchi, N. Miura, K. Yura, M. Mochizuki, C. Ramakrishnan, A. Mary Thangakani, D. Velmurugan, **M. Michael Gromiha**, I. Nakane, N. Uchida, H. Hakariya, M. Tan, H. Nakamura, S.D. Suzuki, M. Ito, M. Kawatani, K. Kudoh, S. Takashina, K. Yamamoto, Y. Moriwaki, K. Oda, D. Kobayashi, T. Okuno, S. Minami, G. Chikenji, P. Prathipati, C. Nagao, A. Mohsen, M. Ito, K. Mizuguchi, T. Honma, T. Ishida, T. Hirokawa, Y. Akiyama and M. Sekijima (2019) A prospective compound screening contest identified broader inhibitors for Sirtuin 1. Scientific Reports, 9(1), 19585.

29. A. Sharma, A. Biswas, L. Hongde, S. Sen, P. Anoosha, P. Katsonis, O. Lichtarge, T.C. Dakal, U. Maulik, **M. Michael Gromiha**, S. Bandyopadhyay, M. Ludwig, F.G. Holz, K.U Loeffler, M.C. Herwig-Carl (2019) Mutational landscape of the BAP1 locus reveals an intrinsic control to regulate the miRNA network and the binding of protein complexes in uveal melanoma. Cancers 11(10), E1600.

30. P. Parasuraman, J.F.A. Selvin, **M. Michael Gromiha** , K. Fukui and K. Veluraja (2019). Investigation on the binding specificity of Agrocybe cylindracea galectin towards α(2,6)-linked sialyllactose by molecular modelling and molecular dynamics simulations. *J Carb Chem.* 38, 566-585

31. Popov P, Bizin I, A. Kulandaisamy, **M. Michael Gromiha** and Frishman D(2019). BorodaTM: prediction of disease-associated mutations in membrane proteins with known 3D structure. *PLoS ONE*, 14(7):e0219452.

32. P Uma Rani, K VishnuPriya, M.K.N. Sai Varsha, M Nikunj, C Shivam, N Manoj, R Thiagarajan, R Manikandan, **M. Michael Gromiha** and D Madhulika (2019). Amarogentin, a secoiridoid glycoside, activates AMP-activated protein kinase (AMPK) to exert beneficial vasculo-metabolic effects. *BBA – General Subjects* 1863:1270-1282.

33. V. Kanakaveti, R. Sakthivel, S.K. Rayala and **M. Michael Gromiha** (2019). Forging new scaffolds from old: Combining Scaffold hopping and Hierarchical virtual screening for identifying novel Bcl-2 inhibitors. *Curr Top Med Chem.* 19(13):1162-1172.

34. T. Amemiya, **M. Michael Gromiha** K. Horimoto and K. Fukui (2019). Drug repositioning for dengue hemorrhagic fever by integrating multiple omics analyses. *Sci. Rep.* 9, 523.

35. R.A. Jeyaram , T.R.K Priyadarzini , C. Anu Radha , N.R. Siva Shanmugam , C. Ramakrishnan , **M. Michael Gromiha** and K. Veluraja (2019). Molecular dynamics simulation studies on influenza A virus H5N1 complexed with sialic acid and fluorinated sialic acid. *J Biomol Struct Dyn.* 37(18):4813-4824.

36. A. Kulandaisamy, S. Binny Priya, R. Sakthivel, Dmitrij Frishman and **M. Michael Gromiha**(2019). Statistical analysis of disease-causing and neutral mutations in human membrane proteins. *PROTEINS* 87, 452-466.

37. K. Ganesan, A. Kulandaisamy, S. Binny Priya, and **M. Michael Gromiha**(2019). HuVarBase: A human variant database with comprehensive information at gene and protein levels. *PLoS ONE* 14(1), e0210475.

38. **M. Michael Gromiha**, R. Nagarajan and S. Selvaraj (2019). Protein structural bioinformatics: an overview. *Encyc Bioinf Comp Biol.* 2, 445-459. INVITED REVIEW.

39. V. Kanakaveti, P. Anoosha, R. Sakthivel, S. K. Rayala and **M. Michael Gromiha** (2019). Influence of amino acid mutations and small molecules for targeted inhibition of proteins involved in cancer. *Curr Top Med Chem.* 19, 457-466.

40. S. Akila Parvathy Dharshini, Y-h. Taguchi and **M. Michael Gromiha**(2019). Exploring the selective vulnerability in Alzheimer disease using tissue specific variant analysis. *Genomics.* 111, 936-949

41. S. Binny Priya and **M. Michael Gromiha** (2019). Structural insights into the aggregation mechanism of huntingtin exon 1 protein fragment with different polyQ-lengths. *J Cell Biochem.* 120, 10519-10529.

42. S. Anusuya, **M. Michael Gromiha** (2019). Structural basis of flavonoids as dengue polymerase inhibitors: Insights from QSAR and docking studies. *J Biomol Struct Dyn.* 37:104-115.

43. P. Rawat, S. Kumar and **M. Michael Gromiha**(2018). An in-silico method for identifying aggregation rate enhancer and mitigator mutations in proteins. *Int J Biol Macromol.* 118, 1157-1167.

44. D-S. Huang, **M. Michael Gromiha**, K. Han A. Hussain (Editors) Lecture Notes in Artificial Intelligence(2018). Springer, Heidelberg, Vol. 10956.

45. A. Kumaraswamy, A. Mamidi, P. Desai, A. Sivagnanam, L.R. Perumalsamy, C. Ramakrishnan, **M. Michael Gromiha** K. Rajalingam and S. Mahalingam (2018). The non-enzymatic RAS effector RASSF7 inhibits oncogenic c-Myc function. *J Biol Chem.* 293(40),15691-15705.

46. D-S. Huang , V. Bevilacqua and **M. Michael Gromiha**(2018). Guest Editorial for Special Section on the 12th International Conference on Intelligent Computing (ICIC) *IEEE/ACM Trans Comput Biol Bioinform.* 15(5),1433-1435.

47. A. Srivastava, S. Ahmad and **M. Michael Gromiha**(2018). Deciphering RNA-Recognition Patterns of Intrinsically Disordered Proteins. *Int J Mol Sci.* 19(6), 1595.

48. N.R. Siva Shanmugam, J. Fermin Angelo Selvin, K. Veluraja and **M. Michael Gromiha**. Identification and analysis of key residues involved in folding and binding of protein-carbohydrate complexes. *Protein Pept Lett.* 25(4),379-389.

49. S. Jemimah, **M. Michael Gromiha** (2018). Exploring additivity effects of double mutations on the binding affinity of protein-protein complexes. *Proteins.* 86(5), 536-547.

50. A. Kulandaisamy, S. Binny Priya, R. Sakthivel, S. Tarnovskaya, I. Bizin, P. Hönigschmid, D. Frishman and **M. M. Gromiha** (2018). MutHTP: Mutations in Human Transmembrane Proteins. *Bioinformatics.* 34(13), 2325-2326.

51. C. Ramakrishnan, A. M. Thangakani, D. Velmurugan, D. A. Krishnan, M. Sekijima, Y. Akiyama and **M. Michael Gromiha** (2018). Identification of type I and type II inhibitors of c-Yes kinase using in silico and experimental techniques. *J Biomol Struct Dyn.*36(6), 1566-1576.

52. A. Kulandaisamy, A. Srivastava,R. Nagarajan and **M. Michael Gromiha** (2018). Dissecting and analyzing key residues in protein-DNA complexes. *J Mol Recog.* 31(4).

53. A. Kulandaisamy, A. Srivastava, P. Kumar, R. Nagarajan, S. Binny Priya and **M. Michael Gromiha** (2018).Identification and analysis of key residues in protein-RNA complexes. *IEEE/ACM Trans Comput Biol Bioinform.* 15(5), 1436-1444.

54. **M. Michael Gromiha**, K. Yugandhar, and S. Jemimah (2017) Protein-protein interactions: scoring schemes and binding affinity. *Curr Opin Struct Biol.*, 44, 31-38.

55. P. Anoosha, R. Sakthivel, **M. Michael Gromiha** (2017). Investigating mutation-specific biological activities of small molecules using quantitative structure-activity relationship for epidermal growth factor receptor in cancer. *Mutat Res.* , 806, 19-26.

56. S. Chiba, T. Ishida, K. Ikeda, M. Mochizuki, R. Teramoto, Y-h Taguchi, M. Iwadate, H. Umeyama, C. Ramakrishnan, A. M. Thangakani, D. Velmurugan, **M. Michael Gromiha**, T. Okuno, K. Kato, S. Minami, G. Chikenji, S.D. Suzuki, K. Yanagisawa, W.H. Shin, D. Kihara, K. Yamamoto, Y. Moriwaki, N. Yasuo, R. Yoshino, S. Zozulya, P. Borysko, R. Stavniichuk, T. Honma, T. Hirokawa, Y. Akiyama, M. Sekijima (2017). An iterative compound screening contest method for identifying target protein inhibitors using the tyrosine-protein kinase Yes. *Sci Rep.*,7(1):12038.

57. S. Jemimah, K. Yugandhar, **M. Michael Gromiha** (2017). PROXiMATE: a database of mutant protein–protein complex thermodynamics and kinetics. *Bioinformatics*, 33(17), 2787-2788.

58. S. D. Huang, A. Hussain,,K. Han,**M. Michael Gromiha** (Editors) Lecture Notes in Artificial Intelligence(2017), Springer, Heidelberg, Vol. 1036.

59. R. Prabakaran, D. Goel, S. Kumar and **M. Michael Gromiha** (2017) Aggregation prone regions in human proteome: Insights from large-scale data analyses. *Proteins*, 85(6):1099-1118.

60. **M. Michael Gromiha** and K. Yugandhar (2017) Integrating computational methods and experimental data for understanding the recognition mechanism and binding affinity of protein-protein complexes. *Prog Biophys Mol Biol.* **, 128,** 33-38.

61. V. Kanakaveti, R. Sakthivel, Suresh K. Rayala and **M. Michael Gromiha** (2017) Importance of functional groups in predicting the activity of small molecule inhibitors of Bcl-2 and Bcl-xL. *Chem Biol Drug Des.***, 90,** 308-316

62. A. Kulandaisamy, V. Lathi, K. ViswaPoorani, K. Yugandhar, and **M. Michael Gromiha** (2017) Important amino acid residues involved in folding and binding of protein-protein complexes. *Int J Biol Macromol.*, 94 (Pt A), 438-444.

63. K. Yugandhar and **M. Michael Gromiha** (2017) Computational Approaches for Predicting Binding Partners, Interface Residues, and Binding Affinity of Protein-Protein Complexes. *Methods Mol Biol.*, 1484, 237-253.

64. S. Anusuya and **M. Michael Gromiha** (2017) Quercetin derivatives as non-nucleoside inhibitors for dengue polymerase: molecular docking, molecular dynamics simulation and binding free energy calculation, *J Biomol Struct Dyn.*, **35,** 2895-2909 .

65. S. Anusuya, M. Kesherwani, K. Vishnupriya, A. Vimala, G. Shanmugam, D. Velmurugan and **M. Michael Gromiha** (2017) Drug-Target Interactions: Prediction Methods and Applications. *Curr Protein Pept Sci.*, **18,** 1-25.

66. M. Kesherwani, **M. Michael Gromiha**, K. Fukui and D. Velmurugan (2017) Identification of novel natural inhibitor for NorM -A Multidrug and Toxic compound extrusion Transporter-An in silico molecular modeling and simulation studies. *J Biomol Struct Dyn.*, **35,** 58-77.

67. P. Chaudhary, A. N. Naganathan, **M. Michael Gromiha** (2016) Prediction of change in protein unfolding rates upon point mutations in two state proteins. *Biochim Biophys Acta.* 1864(9), 1104-1109.

68. D-S. Huang, V. Bevilacqua, and **M. Michael Gromiha** (2016) Guest Editorial for Special Section on the 10th International Conference on Intelligent Computing (ICIC). *IEEE Trans. Comp. Biol. Bioinf.*, 13, 1-3.

69. S. Muthusamy, M. Prakash, C. Ramakrishnan, **M. Michael Gromiha** and V. Kesavan (2016) Organocatalytic Enantioselective Assembly of Spirooxindole-naphthopyrans through Tandem Friedel-Crafts Type/Hemiketalization. *ChemCatChem*, 8, 1708-1712.

70. R. Nagarajan and **M. Michael Gromiha** (2016) Computational Analysis of SimilarProtein-DNA Complexes from Different Organisms to Understand Organism Specific Recognition. *Lect. Notes Comp. Sci.*, 9772, 888-894.

71. E. L. Folador, P. V. S. D. de Carvalho, W. M. Silva, R. S. Ferreira, A. Silva, **M. Michael Gromiha**, P. Ghosh, D. Barh, V. Azevedo, and R. Rottger (2016) In silico identification of essential proteins in Corynebacterium pseudotuberculosis based on protein-protein interaction networks. *BMC Systems Biology*, 1, 103.

72. K. Yugandhar and **M. Michael Gromiha** (2016) Analysis of protein-protein interaction networks based on binding affinity. *Current Protein & Peptide Science*, 17(1): 72-81.

73. S. Anusuya, D. Velmurugan and **M. Michael Gromiha** (2016) Identification of Dengue Viral RNA Dependent RNA Polymerase Inhibitor using Computational Fragment Based Approaches and Molecular Dynamics Study. *Journal of Biomolecular Structure and Dynamics*, 34(7), 1512-32.

74. R. Nagarajan, A. Archana, A. Mary Thangakani, S. Jemimah, D. Velmurugan and **M. Michael Gromiha** (2016) PDBparam: Online Resource for Computing Structural Parameters of Proteins. *Bioinformatics and Biology Insights*, 10, 73-80.

75. C. Magyar, **M. Michael Gromiha,** Z. Savoly, and I. Simon (2016) The role of stabilization centers in protein thermal stability. *Biochemical and biophysical research communications*, 471(1), 57-62.

76. **M. Michael Gromiha,** P. Anoosha, and Liang-Tsung Huang (2016) Applications of Protein Thermodynamic Database for Understanding Protein Mutant Stability and Designing Stable Mutants. *Methods Mol Biol.*, 1415, 71-89.

77. A. Mary Thangakani, R. Nagarajan, S. Kumar, R. Sakthivel, D. Velmurugan and **M. Michael Gromiha*** (2016) CPAD, Curated Protein Aggregation Database: A Repository of Manually Curated Experimental Data on Protein and Peptide Aggregation. *PLoS One*, 11(4), e0152949.

78. S. Kumar, A. Mary Thangakani, R. Nagarajan, Satish K. Singh, D. Velmurugan and **M. Michael Gromiha*** (2016) Autoimmune Responses to Soluble Aggregates of Amyloidogenic Proteins Involved in Neurodegenerative Diseases: Overlapping Aggregation Prone and Autoimmunogenic regions. *Scientific Reports*, 6, 22258.

79. D. R. Tompa, **M. Michael Gromiha** and K. Saraboji* (2016) Contribution of main chain and side chain atoms and their locations to the stability of thermophilic proteins. *J. Mol. Graph. Model*, 64, 85-93.

80. P. Anoosha, R. Sakthivel, **M. Michael Gromiha***(2016) Exploring preferred amino acid mutations in cancer genes: Applications to identify potential drug targets. *Biochimica et Biophysica Acta (BBA) – Molecular Basis of Disease*, 1862(2), 155-165

81. N. Saranya, KM Saravanan, **M. Michael Gromiha**, S. Selvaraj* (2016) Analysis of secondary structural and physico-chemical changes in protein-protein complexes. *J Biomol Struct Dyn.*, 34(3):508-16.

82. P. Anoosha, Liang-Tsung Huang, R. Sakthivel, D. Karunagaran, **M. Michael Gromiha***(2015) Discrimination of driver and passenger mutations in epidermal growth factor receptor in cancer.Mutation Research/Fundamental and Molecular Mechanisms of Mutagenesis, 780, 24-34.

83. R. Nagarajan, Sonia P Chothani, C. Ramakrishnan, M. Sekijima, **M. Michael Gromiha*** (2015) Structure based approach for understanding organism specific recognition of protein-RNA complexes, Biology Direct, 10:8.

84. Priyashree Chaudhary, Athi N. Naganathan, **M. Michael Gromiha*** (2015) Folding RaCe: A Robust Method for Predicting Changes in Protein Folding Rates upon Point Mutations. Bioinformatics, 31(13), 2091-2097.

85. S. Kumar, R.H. Robins, P.M. Buck, T.P. Hickling, A. M. Thangakani, L. Li, S. K. Singh, **M Michael Gromiha** (2015) Biopharmaceutical Informatics: Applications of Computation in Biologic Drug Development. In "Developability of Biotherapeutics" (Eds) S. Kumar and S.K. Singh, CRC Press, New York, pp 3-34.

86. Veeramani Murugan, Ponnusamy Parasuraman, Jeyasigamani FA Selvin, Thanu RK Priyadarzini, **M Michael Gromiha**, Kazuhiko Fukui, Kasinadar Veluraja* (2015) Geometry Optimization of Carbohydrate Binding Sites of Influenza: A Quantum Mechanical Approach.Journal of Carbohydrate Chemistry, 34(7), 409-429.

87. Ponnusamy Parasuraman, Veeramani Murugan, Jeyasigamani FA Selvin, **M Michael Gromiha**, Kazuhiko Fukui, Kasinadar Veluraja* (2015) Theoretical investigation on the glycan-binding specificity of Agrocybe cylindracea galectin using molecular modeling and molecular dynamics simulation studies.Journal of Molecular Recognition, 28(9), 528–538

88. Huntaro Chiba, Kazuyoshi Ikeda, Takashi Ishida, **M. Michael Gromiha**, Y-h Taguchi, Mitsuo Iwadate, Hideaki Umeyama, Kun-Yi Hsin, Hiroaki Kitano, Kazuki Yamamoto, Nobuyoshi Sugaya, Koya Kato, Tatsuya Okuno, George Chikenji, Masahiro Mochizuki, Nobuaki Yasuo, Ryunosuke Yoshino, Keisuke Yanagisawa, Tomohiro Ban, Reiji Teramoto, C. Ramakrishnan, A. Mary Thangakani, D Velmurugan, Philip Prathipati, Junichi Ito, Yuko Tsuchiya, Kenji Mizuguchi, Teruki Honma, Takatsugu Hirokawa , Yutaka Akiyama* (2015) Identification of potential inhibitors based on compound proposal contest: Tyrosine-protein kinase Yes as a target. Scientific Reports, 5, 17209.

89. P. Anoosha, R. Sakthivel, **M. Michael Gromiha***(2015) Prediction of protein disorder upon amino acid substitutions, Analytical Biochemistry, 491, 18-22

90. S. Anandakumar, S. Vijayakumar, N. Arumugam, **M Michael Gromiha** (2015) Mammalian Mitochondrial ncRNA Database. Bioinformation 11, 512-513.

91. A. Vimala*, C. Ramakrishnan, **M. Michael Gromiha*** (2015) Identifying a potential receptor for the antibacterial peptide of sponge Axinella donnani endosymbiont. Gene, 566(2), 166-174.

92. M. Xavier Suresh, **M. Michael Gromiha**, Makiko Suwa (2015) Development of a Machine Learning Method to Predict Membrane Protein-Ligand Binding Residues Using Basic Sequence Information. Advances in Bioinformatics, 1-7

93. **M. Michael Gromiha***, P. Anoosha, D. Velmurugan, K. Fukui (2015) Mutational studies to understand the structure-function relationship in multidrug efflux transporters: application for distinguishing mutants with high specificity. International Journal of Biological Macromolecules,75, 218-224.