Sixteen types of scientific contributions of high-to-moderate significance made by Guptasarma and/or the Guptasarma lab over the years

1. Novel mechanisms of bacterial gene regulation

- **Replication-induced transcription (RIT):** PG proposed that the transcription of genes that normally remain buried within the bacterial nucleoid is induced by replication.
  - Guptasarma P. (1995) Does replication-induced transcription regulate synthesis of the myriad low copy number proteins of Escherichia coli? *Bioessays* **17**, 987-97.

  This hypothesis has been tested and experimentally verified (see below).
  - Wang M, Zhang J, Xu H, Golding I. (2019) Measuring transcription at a single gene copy reveals hidden drivers of bacterial individuality. *Nat Microbiol.* **4**, 2118-2127.
  - Golding I. (2020) Revisiting Replication-Induced Transcription in Escherichia coli. *Bioessays* **42**, e1900193.
- **Transcription-assisted transcription (TAT):** PG proposed that transcriptional elongation by RNA polymerase on rotation-restricted DNA on nucleoid surfaces can only occur through cooperation amongst RNA polymerases.
  - Guptasarma P. (1996) Cooperative relaxation of supercoils and periodic transcriptional initiation within polymerase batteries. *Bioessays* **18**, 325-32.

  This hypothesis too has tested and experimentally verified (see below).
  - Kim S, Beltran B, Irnov I, Jacobs-Wagner C. (2019) Long-Distance Cooperative and Antagonistic RNA Polymerase Dynamics via DNA Supercoiling. *Cell* **179**, 106-119.
  - Kim S. (2020) Better Together: Co-operation and Antagonism between RNA Polymerases during Transcription In Vivo. *Bioessays* **42**, e1900215.

2. Novel functions discovered in nucleoid-associated (DNA-binding) proteins

- **Binding of HU to lipopolysaccharide (LPS)**: The PG group showed that HU, a histone-like, nucleoid-associated protein (NAP), uses its DNA-binding sites to bind to LPS (lipopolysaccharide) on bacterial outer membranes.
  - Thakur B, Arora K, Gupta A, Guptasarma P. (2021) The DNA-binding protein HU is a molecular glue that attaches bacteria to extracellular DNA in biofilms. *J. Biol. Chem*. **296**, 100532.
- **Spontaneous liquid-liquid phase separation (LLPS) of HU and Dps with DNA:** The PG group showed that NAPs compact and condense DNA through liquid-liquid phase separation (LLPS) facilitated by charge neutralization reducing DNA's rigidity, allowing it to occupy tiny physical volumes.
  - Gupta A, Joshi A, Arora K, Mukhopadhyay S, Guptasarma P. (2023) The bacterial nucleoid-associated proteins, HU and Dps, condense DNA into context-dependent biphasic or multiphasic complex coacervates. *J. Biol. Chem.* **299,** 104637.

3. Molecular evolution of oxidation in protein turnover-challenged cellular environments

- **Tryptophan presence facilitates cataracts:** PG and Balasubramanian showed that hydroxyl radicals that can be generated by tryptophan cause protein aggregation in cataract through crosslinking of damaged histidine side chains to glutamates/aspartates.
  - Guptasarma P, Balasubramanian D, Matsugo S, Saito I. (1992) Hydroxyl radical mediated damage to proteins, with special reference to the crystallins. *Biochemistry* **31**, 4296-4303.
- **Tryptophan absence prevents chromosomal oxidation:** The PG group showed that sunlight-induced chromosomal oxidation is prevented by the evolution of tryptophan avoidance in buried DNA-binding proteins.
  - Gupta A, Venkatesh AR, Arora K, Guptasarma P. (2023) Avoidance of the use of tryptophan in buried chromosomal proteins as a mechanism for reducing photo/oxidative damage to genomes. *J. Photochem. Photobiol.* **245**, 112733.

4. Improved plastic degradation by enzymes

- **Synergizing cutinases and carboxylesterares:** The PG group pioneered the application of enzyme synergy to polyethylene terephthalate (PET) degradation, resulting in the first lab-scale production of pure terephthalic acid (TPA) from PET.
  - Mrigwani A, Thakur B, Guptasarma P. (2022) Conversion of polyethylene terephthalate into pure terephthalic acid through synergy between a solid-degrading cutinase and a reaction intermediate-hydrolysing carboxylesterase. *Green Chem*. **24**, 6707-6719.
- **Improving PET-degrading cutinases through rational engineering:** The PG group competed in a friendly race to engineer two thermophile cutinases to produce three of the world's five best PET-degrading enzymes/approaches.
  - Mrigwani A, Pitaliya M, Kaur H, Kasilingam B, Thakur B, Guptasarma P. (2023) Rational mutagenesis of Thermobifida fusca cutinase to modulate the enzymatic degradation of polyethylene terephthalate. *Biotechnol Bioeng*. **120**, 674-686.

5. Novel molecular explanations for certain human diseases

- **Calcium-binding by β2m causes dialysis-related amyloidosis (DRA):** The PG group showed that beta-2-microglobulin (β2m) molecules form calcium binding-dependent micro-aggregates that fail to cross dialysis membranes, grow larger and then deposit in bone interstices to eventually form amyloids.
  - Kumar S, Sharma P, Arora K, Raje M, Guptasarma P. (2014) Calcium binding to beta-2-microglobulin at physiological pH drives the occurrence of conformational changes which cause the protein to precipitate into amorphous forms that subsequently transform into amyloid aggregates. PLoS One. **9**, e95725.
- **Estrogen-binding by arsenic disrupts estrogen signalling in wound healing:** The PG group showed that arsenic binds specifically and tightly to estradiol (estrogen) through pnictide bonds, leading to reduced estrogen signalling, and explaining why excess arsenic in ground-water affects nutritionally-challenged and nutritionally-privileged women differently.
  - Kumar S, Mukherjee TK, Guptasarma P. (2016) Arsenic and 17-β-estradiol bind to each other and neutralize each other's signaling effects. *Biochem Biophys Res Commun.* **477**, 575-580.

6. Novel discoveries in the area of protein fluorescence

- **A novel fluorescence in proteins:** The PG group discovered a novel fluorescence arising from the excitation of a lone pair of electrons on carbonyl oxygen atoms that quantum-tunnels to other peptide bonds, with implications for electrical conduction and electron transfer in proteins. The excitation peaks at ~387 nm. The emission displays secondary structure-dependence.
  - Shukla A, Mukherjee S, Sharma S, Agrawal V, Radha Kishan KV, Guptasarma P. (2004) A novel UV laser-induced visible blue radiation from protein crystals and aggregates: scattering artifacts or fluorescence transitions of peptide electrons delocalized through hydrogen bonding? *Arch Biochem Biophys*.**428**, 144-53.
  - Guptasarma P. (2008) Solution-state characteristics of the ultraviolet A-induced visible fluorescence from proteins. *Arch Biochem Biophys.* **478**, 127-9.

  The above discovery has been verified and exploited by tens of research groups during the last decade, and has kick-started applications in biomedical imaging, biomolecular electronics and crystallography.
- **Contamination of fluorescence resonance energy transfer (FRET) by radiative transfer:** PG and Bakthisaran Raman provided the first demonstration that steady-state measurements of fluorescence resonance energy transfer (FRET) are contaminated by radiative (trivial) energy transfer involving reabsorption of donor-emitted photons.
  - Guptasarma P, Raman B. (1995) Use of tandem cuvettes to determine whether radiative (trivial) energy transfer can contaminate steady-state measurements of fluorescence resonance energy transfer. *Anal Biochem*. **230**, 187-91.

  The above discovery is recommended as essential reading for FRET experiments by Lakowicz's canonical book on fluorescence spectroscopy.

7. Novel inventions in protein mass spectrometry

- **Fluorescamine reacts with N-termini at pH 6.0 to facilitate N-terminal sequencing:** The PG group discovered that fluorescamine reacts specifically only with alpha-amino groups when pH if lowered to 6.0. This led to the first amino-terminal mass-tagging technique for aiding identification/sequencing of N-terminal tryptic peptides in peptide mass fingerprints (PMF).
  - Dhaunta N, Fatima U, Guptasarma P. (2011) N-Terminal sequencing by mass spectrometry through specific fluorescamine labeling of α-amino groups before tryptic digestion. *Anal Biochem.* **408**, 263-8.
- **An aminopeptidase facilitates single-stage MS-based peptide sequencing:** The PG group developed the first viable method for use of an aminopeptidase to perform amino-acid sequencing of tryptic (and other) peptides using MALDI-TOF MS, without using fragmentation-based two-stage mass spectrometry.
  - Kishor N, Guptasarma P. Direct N-terminal sequencing of polypeptides using a thermostable bacterial aminopeptidase and MALDI-TOF mass spectrometry. Anal Biochem. 2015 Nov 1;488:6-8.

8. Novel discoveries/ inventions in DNA/Protein electrophoresis

- **Causes of anomalous electrophoretic mobility in proteins:** The PG group discovered two of several reasons that cause proteins to move anomalously mobility on denaturing gels such as SDS-PAGE, and showed how these offer insights into protein conformational stability, folding status, and effects of excessive negative charge on the binding of sodium dodecyl sulphate (SDS).
  - Mukherjee S, Sharma S, Kumar S, Guptasarma P. (2005) Slow irreversible unfolding of Pyrococcus furiosus triosephosphate isomerase: separation and quantitation of conformers through a novel electrophoretic approach. *Anal Biochem.* **347**, 49-59.
  - Tiwari P, Kaila P, Guptasarma P. (2019) Understanding anomalous mobility of proteins on SDS-PAGE with special reference to the highly acidic extracellular domains of human E- and N-cadherins. *Electrophoresis* **40**, 1273-1281.

- **Discovery of mRNA secondary structure through anomalous DNA sequencing:** The PG group discovered how secondary structures in DNA oligonucleotides (mimicking secondary structures in RNA) cause anomalous mobility in DNA sequencing, and how this can be used to identify mRNA secondary structures reducing protein expression.
  - Kapoor D, Chandrayan SK, Ahmed S, Guptasarma P. (2007) Using DNA sequencing electrophoresis compression artifacts as reporters of stable mRNA structures affecting gene expression. *Electrophoresis* **28**, 3862-3867.

9. Novel mechanisms in human immunobiology

- **Diet-induced chronic inflammation begets hyperinflammation upon viral infection:** PG and Manni Luthra-Guptasarma hypothesized that hyperinflammation is nothing but the ultra-fast arising and ultra-slow abatement of acute inflammation in a background of pre-existing chronic inflammation, caused through cytokine overlap.
  - Luthra-Guptasarma M, Guptasarma P. (2021) Does chronic inflammation cause acute inflammation to spiral into hyper-inflammation in a manner modulated by diet and the gut microbiome, in severe Covid-19? *Bioessays* **43**, e2000211.
- **Immunoglobulins act as prion plaster-casts (moulds) to catalyze protein misfolding:** PG proposed that prions also propagate through moulding by scrapie prion-cognate antibodies which arise through T-cell-independent B-cell-activation stimulated by aggregates formed by misfolded prions hosting non-native conformational epitopes, following encounters between prions and naïve B-cells in gut mucosal-associated lymphoid tissue (MALT).
  - Guptasarma, P. (1999) Proposing T-independent B-cell activation by prion rods: Could disease result from "chaperoning" of nascent prions by PrPsc-cognate immunoglobulins? *Curr. Sci.* **77**, 508–514.

10. Novel explorations of sequence-structure relationships in protein folding

- **Mirror-imaging of protein structure through amino acid 'retro' & 'inverso' modifications:** PG pioneered the concept of 'retro-proteins' (backbone-reversed proteins), and 'inverso proteins' (chirally-inverted proteins), arguing that the former must adopt topological mirror-images of the native protein, and the latter must adopt atom-for-atom mirror-images of the native protein.
  - Guptasarma P. (1992) Reversal of peptide backbone direction may result in the mirroring of protein structure. *FEBS Letters* **310**, 205-210.
  - Shukla A, Raje M, Guptasarma P. (2003) A backbone-reversed form of an all-beta alpha-crystallin domain from a small heat-shock protein (retro-HSP12.6) folds and assembles into structured multimers. *J. Biol. Chem.* **278,** 26505-26510.
- **Global conservative mutagenesis conserves early folding and challenges late folding stages:** The PG group pioneered the concept of 'global conservative site-directed mutagenesis' to replace most amino acids in the sequence of a protein by others possessing the same nature but different identity, to show that folding still occurs through conservation of early folding mechanisms.
  - Ahmed S, Kapoor D, Singh B, Guptasarma P. (2008) Conformational behavior of polypeptides derived through simultaneous global conservative site-directed mutagenesis of chymotrypsin inhibitor 2. *Biochim Biophys Acta* **1784,** 796-805.

11. Understanding (and exploiting) unusual functions in carbohydrate-active enzymes

- **A two-site activity-coupled amylase/glucanotransferase:** The PG group showed that hyperthemophile glucanotransferases display both amylase and glucanotransferase activities and operate through a complex 'split' active site involving hydrolytic and glucose-transferring functions that can operate individually as well as in a combined fashion, very likely driven by inter-domain and inter-subunit motions.
  - Kaila P, Mehta GS, Dhaunta N, Guptasarma P. (2019) Structure-guided mutational evidence and postulates explaining how a glycohydrolase from Pyrococcus furiosus functions simultaneously as an amylase and as a 4-α-glucanotransferase. *Biochem Biophys Res Commun.* **509**, 892-897.
  - Kaila P, Guptasarma P. (2019) An ultra-stable glucanotransferase-cum-exoamylase from the hyperthermophile archaeon Thermococcus onnurineus. *Arch Biochem Biophys.* **665**, 114-121.
- **A moon-lighting triosephosphate isomerase that also function as an endoglucanase:** The PG group showed that *Pyrococcus furiosus* triosephosphate isomerase also moonlights as an endoglucanase because this hyperthermophile archaeon's genome codes for no other intracellular endoglucanases.
  - Sharma P, Guptasarma P. (2017) Endoglucanase activity at a second site in Pyrococcus furiosus triosephosphate isomerase-Promiscuity or compensation for a metabolic handicap? *FEBS Open Bio.* **7**, 1126-1143.

12. Understanding and manipulating the aggregation and misfolding of proteins

- **Survival of native structure in misfolded/aggregated proteins:** Using low-resolution electronic and vibrational spectroscopic methods (and other biochemical/biophysical methods), the PG group pioneered the study of protein aggregates to address unconventional questions concerning (a) the relative extents of native-like structure in different types of amorphous and amyloid protein aggregates, and (b) the importance (or lack thereof) of molecular recognition in the formation of such aggregates.
  - Sharma S, Guptasarma P. (2008) Dimorphic aggregation behavior of a fusion polypeptide incorporating a stable protein domain (EGFP) with an amyloidogenic sequence (retroCspA). *FEBS Lett* **582**, 2203-11.
  - Sharma S, Guptasarma P. (2008) Evidence of native-like substructure(s) in polypeptide chains of carbonic anhydrase deposited into insoluble aggregates during thermal unfolding. *Protein J* **27**, 50-8.
  - Fatima U, Singh B, Subramanian K, Guptasarma P. (2012) Insufficient (sub-native) helix content in soluble/solid aggregates of recombinant and engineered forms of IL-2 throws light on how aggregated IL-2 is biologically active. *Protein J* **31**, 529-43.
  - Fatima U, Sharma S, Guptasarma P. (2010) Structures of differently aggregated and precipitated forms of gamma B crystallin: an FTIR spectroscopic and EM study. *Protein Pept Lett* **17**, 1155-62.
- **Blocking of protein aggregation:** The PG group pioneered the use of small-molecules and peptides as chaperones, to prevent the heat-dependent aggregation of proteins through intermolecular hydrophobic or hydrogen bonding interactions.
  - Kundu B, Guptasarma P. (1999) Hydrophobic dye inhibits aggregation of molten carbonic anhydrase during thermal unfolding and refolding. *Proteins* **37**, 321-4.
  - Kundu B, Shukla A, Guptasarma P. (2002) Manipulation of unfolding-induced protein aggregation by peptides selected for aggregate-binding ability through phage display library screening. *Biochem Biophys Res Commun* **291**, 903-7.
  - Kundu B, Shukla A, Guptasarma P. (2003) Peptide scanning-based identification of regions of gamma-II crystallin involved in thermal aggregation: evidence of the involvement of structurally analogous, helix-containing loops from the two double Greek key domains of the molecule. *Arch Biochem Biophys* **410**, 69-75.

13. Understanding and manipulating the kinetic thermal stability of proteins

- **Protein kinetic stability increases with reduced cooperativity of folding/unfolding:** The PG group showed that protein kinetic thermal stability rises in proportion with a slowing down of unfolding caused by increased autonomy of sub-structure formation, influenced greatly by protein surface electrostatics (primarily salt bridges) and aromatic clusters.
  - Chandrayan SK, Guptasarma P. (2008) Partial destabilization of native structure by a combination of heat and denaturant facilitates cold denaturation in a hyperthermophile protein. *Proteins* **72,** 539-46.
  - Chandrayan SK, Prakash S, Ahmed S, Guptasarma P. (2014) Hyperthermophile protein behavior: partially-structured conformations of Pyrococcus furiosus rubredoxin monomers generated through forced cold-denaturation and refolding. *PLoS One* **9**, e80014.
  - Prakash S, Sundd M, Guptasarma P. (2014) The key to the extraordinary thermal stability of P. furiosus holo-rubredoxin: iron binding-guided packing of a core aromatic cluster responsible for high kinetic stability of the native structure. *PLoS One* **9**, e89703.
  - Khan JM, Sharma P, Arora K, Kishor N, Kaila P, Guptasarma P. (2015) The Achilles' Heel of "Ultrastable" Hyperthermophile Proteins: Submillimolar Concentrations of SDS Stimulate Rapid Conformational Change, Aggregation, and Amyloid Formation in Proteins Carrying Overall Positive Charge. *Biochemistry* **55**, 3920-36.
- **Protein kinetic stability can be altered through electrostatic/aromatic reengineering**: The PG group showed that it is possible to increase, or decrease, a protein's kinetic thermal stability by causing it to have fewer, or more, surface salt bridges. Separately, the group also showed how altered residue configuration in an aromatic cluster can upgrade ordinary stability to extraordinary kinetic stability in a hyperthermophile rubredoxin.
  - Chandrayan SK, Guptasarma P. (2009) Attenuation of ionic interactions profoundly lowers the kinetic thermal stability of Pyrococcus furiosus triosephosphate isomerase. *Biochim Biophys Acta* **1794**, 905-12.
  - Dhaunta N, Arora K, Chandrayan SK, Guptasarma P. (2013) Introduction of a thermophile-sourced ion pair network in the fourth beta/alpha unit of a psychophile-derived triosephosphate isomerase from Methanococcoides burtonii significantly increases its kinetic thermal stability. *Biochim Biophys Acta* **1834**, 1023-33.

14. Understanding and manipulating the TIM barrel (or beta/alpha barrel) protein fold/motif

- **Playing with the TIM barrel architecture for fun:** PG argued that triosephosphate isomerase (TIM)-type barrels must fold during translation in order to be able to place slower-folding beta sheets at their cores and faster-folding alpha-helices at their peripheries. The PG group scrambled the order of occurrence of beta/alpha units in yeast TIM to produce folded non-native beta/alpha structures that demonstrated the plasticity of occurrence of hydrophobic and hydrogen-bonding interactions in the stabilization of beta/alpha barrel topology and architecture.
  - Maiti S, Luthra-Guptasarma M, Guptasarma P. (2002) Phenomenological perspectives on the folding of beta/alpha-barrel domains through the modular formation and assembly of smaller structural elements. *IUBMB Life* **54**, 213-21.
  - Shukla A, Guptasarma P. (2004) Folding of beta/alpha-unit scrambled forms of S. cerevisiae triosephosphate isomerase: Evidence for autonomy of substructure formation and plasticity of hydrophobic and hydrogen bonding interactions in core of (beta/alpha)8-barrel. *Proteins* **55**, 548-57.

- **Playing with the TIM barrel architecture to make new enzymes:** The PG group demonstrated the autonomy of half-barrel motifs in the formation of TIM (or beta/alpha) barrels by (a) producing chimeras of different TIM barrel cellulase/endoglucanase-derived half barrel motifs and (b) showing that such chimeras can display enzymatic cellulase/endoglucanase.
  - Sharma P, Kaila P, Guptasarma P. (2016) Creation of active TIM barrel enzymes through genetic fusion of half-barrel domain constructs derived from two distantly related glycosyl hydrolases. *FEBS J* **283**, 4340-4356.

15. Understanding and manipulating enzymes through protein engineering

- **A surface-transplantation technique for proteins:** The PG group developed a protein-engineering method for the re-surfacing of beta sheets and deployed it to create a meso-active thermo-stable cellulase through the transplantation of a mesophile cellulase-derived enzyme active surface onto the structural scaffold of a homologous thermophile-derived cellulase.
  - Kapoor D, Kumar V, Chandrayan SK, Ahmed S, Sharma S, Datt M, Singh B, Karthikeyan S, Guptasarma P. (2008) Replacement of the active surface of a thermophile protein by that of a homologous mesophile protein through structure-guided 'protein surface grafting'. *Biochim Biophys Acta* **1784**, 1771-6.

  This patented method (which holds product and process patents in the US and numerous other countries) has also been applied to performing whole-surface transplants, and enzyme active site transplants.
  - Kapoor D, Singh B, Subramanian K, Guptasarma P. (2009) Creation of a new eye lens crystallin (Gambeta) through structure-guided mutagenic grafting of the surface of betaB2 crystallin onto the hydrophobic core of gammaB crystallin. *FEBS J* **276,** 3341-53.
  - Kapoor, D., Singh, B., Karthikeyan, S., Guptasarma, P. (2010) A functional comparison of the TET aminopeptidases of P. furiosus and B. subtilis with a protein-engineered variant recombining the former's structure with the latter's active site. *Enzyme and Microbial Technology* **46**, 1-8.
  - US Patents US-9062296-B2 & US-9663773-B2

16. Understanding and manipulating non-enzyme proteins through protein engineering

- **Rational protein engineering to derive useful new enzymes and proteins:** The PG group has deployed recombinant wild-type and engineered enzymes and proteins in numerous studies of biomolecular phenomena other than the ones described above, and towards many applications. All of these papers present some work of significance, but mostly as stand-alone studies examining some esoteric question.
  - Kundu B, Guptasarma P. (2002) Use of a hydrophobic dye to indirectly probe the structural organization and conformational plasticity of molecules in amorphous aggregates of carbonic anhydrase. *Biochem Biophys Res Commun* **293**, 572-7.
  - Shukla A, Raje M, Guptasarma P. (2003) A backbone-reversed all-beta polypeptide (retro-CspA) folds and assembles into amyloid nanofibres. *Protein Eng* **16**, 875-9.
  - Mukherjee S, Shukla A, Guptasarma P. (2003) Single-step purification of a protein-folding catalyst, the SlyD peptidyl prolyl isomerase (PPI), from cytoplasmic extracts of Escherichia coli. *Biotechnol Appl Biochem* **37**, 183-6.
  - Kundu B, Shukla A, Chaba R, Guptasarma P. (2004) The excised heat-shock domain of alphaB crystallin is a folded, proteolytically susceptible trimer with significant surface hydrophobicity and a tendency to self-aggregate upon heating. *Protein Expr Purif* **36,** 263-71.
  - Mukherjee S, Guptasarma P. (2005) Direct proteolysis-based purification of an overexpressed hyperthermophile protein from Escherichia coli lysate: a novel exploitation of the link between structural stability and proteolytic resistance. *Protein Expr Purif* **40**, 71-6.
  - Shukla A, Sharma S, Guptasarma P. (2007) Confocal spectrofluorimetric evidence for the hetero-aggregation of sequence-scrambled forms of two model all-beta sheet proteins. *Int J Biol Macromol* **41**, 650-4.
  - Chandrayan SK, Dhaunta N, Guptasarma P. (2008) Expression, purification, refolding and characterization of a putative lysophospholipase from Pyrococcus furiosus: retention of structure and lipase/esterase activity in the presence of water-miscible organic solvents at high temperatures. *Protein Expr Purif* **59**, 327-33.
  - Ahmed S, Shukla A, Guptasarma P. (2008) Folding behavior of a backbone-reversed protein: reversible polyproline type II to beta-sheet thermal transitions in retro-GroES multimers with GroES-like features. *Biochim Biophys Acta* **1784**, 916-23.
  - Ahmed S, Guptasarma P. (2008) Design of a soluble mini-protein through tandem duplication of the minimally engineered beta hairpin 'tongue' motif of alpha-hemolysin. *Biochimie* **90**, 957-67.
  - Shukla A, Raje M, Guptasarma P. (2008) Coalescence of spherical beads of retro-HSP12.6 into linear and ring-shaped amyloid nanofibers. Biochemistry (Mosc). **73**, 681-5.
  - Verma A, Sharma S, Ganguly NK, Majumdar S, Guptasarma P, Luthra-Guptasarma M. (2008) Identification and characterization of a spontaneously aggregating amyloid-forming variant of human PrP((90-231)) through phage-display screening of variants randomized between residues 101 and 112. *Int J Biochem Cell Biol*, **40**, 663-76.
  - Sharma P, Guptasarma P. (2015) 'Super-perfect' enzymes: Structural stabilities and activities of recombinant triose phosphate isomerases from Pyrococcus furiosus and Thermococcus onnurineus produced in Escherichia coli. *Biochem Biophys Res Commun* **460**, 753-8.
  - Sebastian Samuel J, Kumar D, Chodisetti SB, Agrewala JN, Singh B, Guptasarma P, Sarkar D. (2015) Probing protease sensitivity of recombinant human erythropoietin reveals α3-α4 inter-helical loop as a stability determinant. *Proteins* **83**(10):1813-22.
  - Kumari A, Kaila P, Tiwari P, Singh V, Kaul S, Singhal N, Guptasarma P. (2018) Multiple thermostable enzyme hydrolases on magnetic nanoparticles: An immobilized enzyme-mediated approach to saccharification through simultaneous xylanase, cellulase and amylolytic glucanotransferase action. *Int J Biol Macromol* **120**, 1650-1658.
  - Kumari A, Kishor N, Guptasarma P. (2018) Characterization of a mildly alkalophilic and thermostable recombinant Thermus thermophilus laccase with applications in decolourization of dyes. *Biotechnol Lett* **40**, 285-295.
  - Thakur B, Gupta A, Guptasarma P. (2021) A novel protein-engineered dsDNA-binding protein (HU-Simulacrum) inspired by HU, a nucleoid-associated DNABII protein. *Biochem Biophys Res Commun* **534,** 47-52.

- Arora K, Thakur B, Gupta A, Guptasarma P. (2021) HU-AB simulacrum: Fusion of HU-B and HU-A into HU-B-A, a functional analog of the Escherichia coli HU-AB heterodimer. *Biochem Biophys Res Commun* **560**, 27-31.
- Arora K, Thakur B, Mrigwani A, Guptasarma P. (2021) N-Terminal Extensions Appear to Frustrate HU Heterodimer Formation by Strengthening Intersubunit Contacts and Blocking the Formation of a Heterotetrameric Intermediate. *Biochemistry* **60,** 1836-1852.