***Protein structure to identify potential allosteric hotspots in the context of deep sequencing***

***Identifying potential allosteric hotspots using protein dynamics: interpreting conservation in deep sequencing***

***Identifying potential allosteric hotspots using protein dynamics: application to conservation in deep sequencing***

***Identifying allosteric hotspots with dynamics: application to conservation in deep sequencing***

***Leveraging protein conformational change to identify potential allosteric hotspots in the context of deep sequencing***

**Leveraging protein conformational change to identify potential allosteric hotspots: applications to deep sequencing**

**Leveraging conformational heterogeneity to identify potential allosteric hotspots: applications to deep sequencing**

**Leveraging conformational change to identify potential allosteric hotspots: applications to deep sequencing**

**Leveraging protein conformational change to identify potential allosteric hotspots for interpreting deep sequencing data**

**Combining structure and dynamics to elucidate allosteric regulation: applications in deep sequencing**

**Structure and dynamics as a means of elucidating allosteric regulation in the context of sequence conservation**

**Conformational change as a means of identifying potential allosteric hotspots: applications to deep sequencing**

**Predicting critical regulatory elements in structure for elucidating conserved coding elements in genomes**

**Predicting critical regulatory elements in structure for understanding conservation signatures in genomes**

**Allosteric elements in structure & conservation signatures in genomes**

**Allosteric elements in structure for understanding conservation signatures in genomes**

**Large-scale predictions of allosteric hotspots for evaluating conservation in large-scale sequence data**

**Protein conformational change to predict allosteric residues and elucidate conserved sequences**

**Highly efficient predictions of allosteric hotspots enable analyses in the context of deep sequencing**

**Efficient predictions of allosteric residues with analysis in the context of deep sequencing**

**Rapid prediction of allosteric residues for elucidating signatures of conservation in deep sequence reads**

**Structurally-informed predictions of allosteric hotspots with applications in deep sequencing**

**Database-scale predictions of allosteric hotspots with applications to deep sequencing**

**Identification of potential allosteric hotspots and applications to deep sequencing**

***Structure, conformational change, and variation: a large-scale framework for combining allostery and deep sequencing***

**Structure, conformational change, and sequence reads: a large-scale framework for unifying allostery and conservation**

**Allosteric regulation as a unifying framework for investigating conformational heterogeneity and sequence conservation**

**~~~~~~~~~~~~~~~~~~~~~~~~**

**Titles below titles were considered in P2 Struct Mtg**

**Predicting allosteric residues on a large-scale using conformational change: applications in deep sequencing**

**Leveraging database-scale predictions of allosteric residues in the context of conformational change, inter-species conservation, and deep sequencing**

**Leveraging large-scale predictions of allosteric residues in the context of conformational change, inter-species conservation, and deep sequencing**

**Large-scale predictions of allosteric residues using models of conformational change, inter-species conservation, and deep sequencing**

**Characterizing evolutionary constraints on residues critical for allosteric motions**

**Characterizing evolutionary constraints on critical residues for allosteric motions**

**Characterizing evolutionary constraints on residues critical for allosteric motions**

**A method to identify allosteric residues in proteins: relation to cryptic conservation**

**Using models of conformational change to infer allosteric residues**

**Identifying residues critical for allostery**

**Using models of conformational changes to identify allosteric residues**

**Identifying residues critical for allostery: relation to sequence conservation**