

**The 17th West Coast Protein Crystallography Workshop 2005**

<b>FIRST AUTHOR</b>	<b>POSTER TITLE</b>
Aishima, Jun	Automated crystallographic building of ligands
Arndt, Joseph	Crystal structure of Botulinum neurotoxin serotype G catalytic domain
Axelrod, Herbert	The Structures of Two Homologs from <i>Agrobacterium tumefaciens</i> Show a Ferredoxin-Like Split beta-alpha-beta Fold
Barnali, Neel	A computational method for identification of the microbial selenoproteome
Barondeau, Dave	Nickel superoxide dismutase (NiSOD): assembly, structure, and function
Bauer, Cary	Recent Advances in Technology for Home Laboratory X-Ray Systems
Brooks, B.E.	The roles of glutamates 90 and 120 in drug binding by QacR, a multidrug-resistance regulator
Busam, Rob	Exonuclease 1 - structural basis of processivity
Cao, Xiaohang	Crystal structure of the human copper-zinc superoxide dismutase mutant C57S: structural consequences of the loss of the intrasubunit disulfide bond
Chai, Qing	Endocannabinoid Signaling - Crystal Structure of Fatty Acid Amide Hydrolase
Chartron, Justin	Crystallization of APS Reductase from <i>Pseudomonas aeruginosa</i>
Cohen, Aina	Improved Efficiency at Protein Crystallography Beamlines through Automation
Compaan, Deanne	The crystal structure of the OX40-OX40L complex reveals an extensive interface between a small divergent ligand and a more conventional receptor
Das, Debanu	Crystal structure of a hypothetical protein unique to mycoplasmas reveals a novel fold and structural similarity to invertase inhibitor and a cyclin homolog
diLuccio, Eric	X-ray structure at 2.3 Å of D-xylulose Kinase from <i>Escherichia coli</i>
Doukov, Tzanko	Recent improvements at the SSRL beam lines
Endrizzi, James	Structural basis for nucleotide regulation of <i>E. coli</i> CTP synthetase
Estebanez-Perpina, Eva	3D screening for Blockers of Androgen Receptor-Coregulators Assembly
Fan, Li	Crystal structure of <i>Archaeoglobus fulgidus</i> XPB: structural basis for damaged DNA unwinding
Feese, Michael	Topoisomerase I poisoning by camptothecins: homocamptothecin AG260 binds in the E-ring open carboxylate form
Franklin, Matthew	Engineering ML-IAP to produce an extraordinarily potent caspase-9 inhibitor: implications for Smac-dependent anti-apoptotic activity of ML-IAP
Galaleldeen, Ahmad	The crystal structure of the pathogenic SOD1 mutant A4V in its metal-free form
Ghate, M.	Search for a Stable p38 Cryoprotectant
Gonzalez, Ana	Two-wavelength MAD in the presence of radiation damage: A case study
Griffith, Mark	High Throughput Technologies in Structural Biology
Han, Gye Won	Application of Xpleo in the X-Ray Structure Determination of a Putative Lipote-Protein Ligase from <i>Streptococcus pneumoniae</i> Tigr4.
Harries, William	The Structure and Function of Bovine AQP0 as Revealed by X-ray Crystallography
Heffron, Susan	Processing a twinned and highly mosaic data set of elongation factor, EF-Tu
Hoffman, Katherine	Characterization of the multiple transferable resistance repressor (MtrR) from <i>Neisseria gonorrhoea</i> , a TetR family member
Huffman, Joy	Snapshots of an 8-oxoguanine DNA glycosylase reveal the mechanisms of recognition and repair
Hunsicker-Wang, Laura	Crystallographic and biochemical analysis of recombinant and mutant cytochrome ba3 oxidase from <i>Thermus thermophilus</i>
Johnson, Sean	Structural studies of Spt6
Joseph, Jeremiah	Functional and structural proteomics of SARS-CoV: defining a paradigm for a rational therapeutic and prophylactic response to emerging infectious disease
Jouravel, Natalia	Engineering an Ionic Dimer Interface into the Thyroid Hormone Receptor
Katz, Brad	Structure-Based Design of Potent, Selective, Short Hydrogen Bond-Mediated factor VIIa Inhibitors
Kelch, Brian	Sidechain Distortion: A Mechanism for Enhancing Kinetic Stability?
Kelch, Brian	Crystal Structures and Folding Landscapes of Kinetically Stable Extremophilic Proteases
Kuznetsov, Yuri	Structures of Ty3 Retrotransposon Particles and Chlorella Virus PBCV-1 revealed by Atomic Force Microscopy.
Larson, Steven	The structure of an anti-tumor CH2-domain deleted humanized antibody

Li, Huiying	Crystal structure of a novel RuBisCo-like protein from the green sulfur bacterium <i>Chlorobium tepidum</i>
Li, H.	Structural basis for the selective inhibition of neuronal nitric oxide synthase
Link, Todd	Structure of <i>T.gondii</i> adenosine kinase active site mutants
Little, John	Establishing a comprehensive structural analysis of spliceosome components
Liu, Jinyu	Crystal structure of PhoU protein: a new class of metalloprotein contained multinuclear iron clusters
Lohman, Jeremy	Development of a More Oxidizing Redox Sensitive Green Fluorescent Protein
Lougheed, J.	Crystal structures of the phosphorylated and unphosphorylated kinase domains of the cdc42-associated tyrosine kinase ACK1
Lovell, Scott	Crystal structures of nucleotide and non-nucleotide bound FtsZ from <i>Bacillus subtilis</i>
Lu, Heshu	Crystal structure of a human cyclin-dependent kinase 6 complex with a flavonol inhibitor, fisetin
Luz, John	Crystallographic and genetic insights into xol-like GHMP kinases, a novel family of developmental regulators
Macbeth, Mark	The crystal structure of the catalytic domain of hADAR2 at 1.7Å
Makino, Debora	Structure determination process of four different crystal forms of an immunoglobulin light-chain dimer
Makino, Debora	Panicum mosaic virus crystals: growth and analysis by X-ray diffraction and atomic force microscopy
Marchand, Marie-Claude	Ninety-six (96) crystallization optimization conditions in less than 10 minutes using a new pre-filled microplate
Maris, Ann	NtrC1 DNA binding domain is disordered in crystals and shows order by nuclear magnetic resonance
Mathews, Irimpan	Structure of an intein naturally lacking both an N-terminal nucleophile and the conserved intein penultimate histidine at 1.35Å resolution
Miercke, Larry	High-Performance Size Exclusion Chromatography as a Fundamental Tool for the Production of High-Quality Soluble and Membrane Protein Crystals
Misono, Kunio	Crystal structures of atrial natriuretic peptide (ANP) receptor extracellular domain with and without bound hormone: a novel hormone-induced rotation mechanism for transmembrane signaling
Mooers, Blaine	Extension of Direct Methods to 2268 Atoms in the Ab Initio Determination of the Unknown Structure of Bacteriophage P22 Lysozyme
Moriarty, Nigel	PHENIX: a tool for high-throughput crystallography of protein-ligand complexes
Newberry, Kate	Structure of a novel transcriptional regulator from <i>Bacillus subtilis</i> in complex with alpha CTD of RNA polymerase
Ng, Ho-Leung	Observation of alternative native protein conformations by X-ray crystallography
Nollert, Peter	Improved Crystal Detection by Bulk Crystal Contrast Enhancement
Ongaro, J	Comparative modeling and simulated docking studies of some bacterial ADP glucose pyrophosphorylases: insights on catalysis, regulation and drug discovery
Peters-Libeu, Clare	Working with Lipid-Rich Protein Crystals: Tips and Tricks Based on Our Experience
Qiu, Yue	Uncoupling and constitutive activation of the ANP receptor by mutations at dimer interface: Identification of the apo-dimer quaternary structure
Richard, Stephane	Biosynthetic diversification of natural products: structural basis for promiscuous aromatic prenyltransferase activity
Rouhani, Shahab	Crystallization Of Membrane Proteins From Connected-Bilayer Gels Formed with Phospholipids
Sambashivan, Shilpa	A ribonuclease A amyloid with a domain-swapped, native-like structure
Sarma, Ganapathy	In-house, low resolution, sulfur SAD phasing of Tox-A - a host-selective toxin
Savage, David	Structure and Selectivity of Aquaporin Z
Scheer, J.	A mechanism for allosteric inhibition of caspase-1 at the dimer-dimer interface
Schubert, Heidi	Structural and functional characterization of Gun4: elucidation of its role in formation of the plastid-to-nucleus signaling molecule, magnesium protoporphyrin IX
Schulze-Gahmen	Resistance Regulator QacR: Discrimination or Selection
Schuman, Jason	Role of Glu 57&58 in the Promiscuous Binding Behavior of the Multidrug
Seetharaman, Sai	Crystal structure of human SOD1 mutant D124V
Shia, Steven	Conformational Lability in the Active Site of Hepatocyte Growth Factor Activator
Shin, David	<i>Alvinella pompejana</i> : a eukaryotic thermophile for structural analysis of complex protein systems
Shu, Xiaokun	Structural basis for spectral variations in fluorescent mFruits: a novel third ring and an unusual hydrogen bond
Staker, Bart	Dual inhibitor complex of the human topoisomerase I covalent DNA complex with topotecan and the minor binding groove binding compound Hoecsht-33342
Stanfield, Robyn	Structural Studies of Shark New Antigen Receptors

Stroud, James	Fluorescence Studies of NFAT Support Crystallographic Observations
Sundaresen, Vidyasankar	Conformationally coupled hydride transfer and proton pumping in trypanthhydrogenase
Thomas, L.M.	Structural study of the biofilm dispersal agent Despersin B from Actinobacillus actinomycetemcomitans
Toppani, Dominique	Hardware-software solution for automated crystal recognition
Uysal, Serdar	Chaperone-Assisted Crystallography
van de Bedem, Henry	Real-space protein-model completion: an inverse-kinematics approach
VanDemark, Andrew	Structure of the tandem bromodomain from Rsc4
Verdino, Petra	Evolution of ligand recognition and specificity of the catalytic antibody 1E9
Villasenor, A.	The Optimum Size of Crystal Screens
Wang, Ying	The interaction of p53 with new drugs
Warfel, Jennifer	Crystal structure of lactate dehydrogenase from chicken breast muscle
Whitson, Lisa	The effect of zinc deficiency on the structure of human copper-zinc superoxide dismutase and implications for FALS
Wolf, Guenter	Automatic Data Processing for High Throughput X-ray Structure Determination
Wood, Timothy	Mechanism of GFP fluorophore synthesis: electrostatic role of arginine 96 in chromophore cyclization
Wu, Ping	Crystal Structures of VEGF in complex with two Fabs
Xu, Qian Steven	Crystal Structures of a Phosphotransacetylase from Bacillus subtilis and its Complex with Acetyl Phosphate
Xu, Qingping	Protein structures with unknown ligands
Yadav, Maneesh	Caged protons for macromolecular crystal growth