University of Birmingham

Dr Scott White BSc PhD

Reader in Structural Biology

School of Biosciences (/schools/biosciences/index.aspx)

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About

Dr Scott White is an experienced structural biologist speciallising in the application of x-ray crystallography to the structure and function of enzymes and their substrate, inhibitor or drug-bound complexes. He is also a Welfare Tutor and the Mitigations Officer for the School of Biosciences. He is the coordinator of the UK Midland's Block Allocation Group (BAG) for the European Synchrotron Radiation Facility in Grenoble and, a member of the Peer Review Panel at the Diamond Synchrotron, Oxon, UK.

Qualifications

BSc (University of Edinburgh)

PhD (University of Edinburgh)

Biography

Dr Scott White was born in Edinburgh and studied in the same city before moving to St. Louis, Missouri, USA as a post-doctoral fellow at Washington University School of Medicine. Starting out in Chemistry, he moved into the Life Sciences via Bio-Inorganic Chemistry during graduate studies before specialising in crystallographic methods to study protein structure and function. He moved to the University of Birmingham in 1995.

Teaching

Dr White teaches protein structure and function, biophysical methods, esp. crystallography, bioenergetics, viral structure & symmetry, and molecular graphics. He is a keen advocate of bringing experiments and demonstrations back into the lecture theatre, and using software to produce self-marking assessments, personalised/individual assessments and problem-based learning to enhance student learning and development.

Postgraduate supervision

For a list of possible PhD projects offered by Dr White:

www.findaphd.com/search/customlink.asp?inst=birm-Biol&supersurname=White (http://www.findaphd.com/search/customlink.asp?inst=birm-Biol&supersurname=White)

Research

Research Theme within School of Biosciences: **Molecular and Cell Biology (/research/activity/cellbiology/index.aspx)**

Structural Biology of Proteins, Enzymes and Macromolecular Complexes

The function of a protein is largely determined by its 3-D structure. Our group probes the relationship between protein structure and its function to determine the nature of protein-ligand and protein-protein interactions, features which are central to protein, enzyme and cell functions.

We are using protein x-ray crystallography to study a number of systems including: phosphatases, including exopoly and pyrophosphatases; aldoketoreductases and nitroreductases, enzymes targetted in anticancer therapies, and DNA-binding proteins. In each case we are determining structures of wild-type and engineered mutant enzymes, in the absence or presence of bound ligands, inhibitors or substrate analogues, in order to gain insight into protein function or further structure-based drug design.

Publications

The specificity of proton-translocating transhydrogenase for nicotinamide nucleotides. (http://www.ncbi.nlm.nih.gov/pubmed/20732298)

Huxley L, Quirk PG, Cotton NP, White SA, Jackson JB.

Biochim Biophys Acta. 2011 Jan;1807(1):85-94. Epub 2010 Aug 21.

The homodimeric GBS1074 from Streptococcus agalactiae. (http://www.ncbi.nlm.nih.gov/pubmed/21045286)

Shukla A, Pallen M, Anthony M, White SA.

Acta Crystallogr Sect F Struct Biol Cryst Commun. 2010 Nov 1;66(Pt 11):1421-5. Epub 2010 Oct 27.

Order and disorder in the domain organization of the plasmid partition protein KorB. (http://www.ncbi.nlm.nih.gov/pubmed/20200158)

Rajasekar K, Muntaha ST, Tame JR, Kommareddy S, Morris G, Wharton CW, Thomas CM, White SA, Hyde EI, Scott DJ.

J Biol Chem. 2010 May 14;285(20):15440-9.

Characterization of two novel aldo-keto reductases from Arabidopsis: expression patterns, broad substrate specificity, and an open active-site structure suggest a role in toxicant metabolism following stress. (http://www.ncbi.nlm.nih.gov/pubmed/19616008)

Simpson PJ, Tantitadapitak C, Reed AM, Mather OC, Bunce CM, White SA, Ride JP.

J Mol Biol. 2009 Sep 18;392(2):465-80.

Steady-state and stopped-flow kinetic studies of three Escherichia coli NfsB mutants with enhanced activity for the prodrug CB1954. (http://www.ncbi.nlm.nih.gov/pubmed/19580253)

Jarrom D, Jaberipour M, Guise CP, Daff S, White SA, Searle PF, Hyde EI.

Biochemistry. 2009 Aug 18;48(32):7665-72.

Mutations of key hydrophobic surface residues of 11 beta-hydroxysteroid dehydrogenase type 1 increase solubility and monodispersity in a bacterial expression system. (http://www.ncbi.nlm.nih.gov/pubmed/19507261)

Lawson AJ, Walker EA, White SA, Dafforn TR, Stewart PM, Ride JP.

Protein Sci. 2009 Jul;18(7):1552-63.

Structure of rat odorant-binding protein OBP1 at 1.6 A resolution. (http://www.ncbi.nlm.nih.gov/pubmed/19390145)

White SA, Briand L, Scott DJ, Borysik AJ.

Acta Crystallogr D Biol Crystallogr. 2009 May;65(Pt 5):403-10.

Differential specific radiation damage in the Cu II-bound and Pd II-bound forms of an alpha-helical foldamer: a case study of crystallographic phasing by RIP and SAD. (http://www.ncbi.nlm.nih.gov/pubmed/18323621)

Fütterer K, Ravelli RB, White SA, Nicoll AJ, Allemann RK.

Acta Crystallogr D Biol Crystallogr. 2008 Mar;64(Pt 3):264-72.

Ugochukwu, E., Lovering, A.L., Mather, O.C., Young, T.W. and White, S.A. (2007) "The crystal structure of the cytosolic exopolyphosphatase from Saccharomyces cerevisiae reveals the basis for substrate specificity." J. Mol. Biol. 371: 1007-1021.

Obiozo, U.M., Brondijk, T.H., White, A.J., van Boxel, G., Dafforn, T.R., White, S.A. and Jackson, J.B. (2007) "Substitution of tyrosine 146 in the dI component of proton-translocating transhydrogenase leads to reversible dissociation of the active dimer into inactive monomers." J Biol Chem. 282: 36434-36443.

Race, P.R., Lovering, A.L., White, S.A., Grove, J.I., Searle, P.F., Wrighton, C.W. and Hyde, EI. (2007) "Kinetic and structural characterisation of Escherichia coli nitroreductase mutants showing improved efficacy for the prodrug substrate CB1954." J Mol Biol. 368: 481 - 492.

Bhakta, T, Whitehead, S.J., Snaith, J.S., Dafforn, T.R., Wilkie, J, Rajesh, S, White, S.A. and Jackson, JB. (2007) "Structures of the dI2dIII1 complex of proton-translocating transhydrogenase with bound, inactive analogues of NADH and NADPH reveal active site geometries." Biochemistry. 46: 3304 - 3318.

Brondijk, T.H., van, Boxel, G.I., Mather, O.C., Quirk, P.G., White, S.A. and Jackson, JB. (2006) "The role of invariant amino acid residues at the hydride transfer site of proton-translocating transhydrogenase." J Biol Chem. 281: 13345 - 13354.

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Lovering, A.L., Ride, J.P., Bunce, C.M., Desmond, J.C., Cummings, S.M. and White, SA. (2004) "Crystal structures of prostaglandin D(2) 11-ketoreductase (AKR1C3) in complex with the nonsteroidal anti-inflammatory drugs flufenamic acid and indomethacin." Cancer Res. 64: 1802 - 1810.

Singh, A, Venning, J.D., Quirk, P.G., van, Boxel, G.I., Rodrigues, D.J., White, S.A. and Jackson, JB. (2003) "Interactions between transhydrogenase and thio-nicotinamide Analogues of NAD(H) and NADP(H) underline the importance of nucleotide conformational changes in coupling to proton translocation." J Biol Chem. 278: 33208 - 33216.

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Ahn, S, Milner, A.J., FÂ¸tterer, K, Konopka, M, Ilias, M, Young, T.W. and White, SA. (2001) "The 'open' and 'closed' structures of the type-C inorganic pyrophosphatases from Bacillus subtilis and Streptococcus gordonii." J Mol Biol. 313: 797 - 811.

Lovering, A.L., Hyde, E.I., Searle, P.F. and White, SA. (2001) "The structure of Escherichia coli nitroreductase complexed with nicotinic acid: three crystal forms at 1.7 A, 1.8 A and 2.4 A resolution." J Mol Biol. 2001 May 25;309(1):203-13.

Cotton, N.P., White, S.A., Peake, S.J., McSweeney, S and Jackson, JB. (2001) "The crystal structure of an asymmetric complex of the two nucleotide binding components of proton-translocating transhydrogenase." Structure. 9: 165 - 176.

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