

BIOGRAPHICAL SKETCH

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NAME Chapman, Michael S.		POSITION TITLE Professor of Biochemistry & Molecular Biology & Richard T. Jones chair in Structural Biology	
eRA COMMONS USER NAME mschapman			
EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)			
INSTITUTION AND LOCATION	DEGREE (if applicable)	YEAR(s)	FIELD OF STUDY
University of London, Kings College, England	BSc. / AKC	1982	Cell & molecular Biology
University of London, Birkbeck College	MSc.	1983	Crystallography
University of California, Los Angeles	Ph.D.	1987	Biochemistry
Purdue University	(Post-Doc)	1988-93	Macromolecular Structure

A. Positions and Honors.**Employment**

- 1988-93 Post-doctoral Assoc., Dept. of Biological Science, Purdue Univ. (with Michael Rossmann)
 1993-98 Asst. Prof., Dept. of Chemistry (Courtesy appts. in Biology & Physics), Florida State Univ.
 1998-03 Assoc. Prof., Dept. of Chemistry, Florida State Univ. (Courtesy appt. in College of Med.)
 1998-01 Associate Director, Institute of Molecular Biophysics
 2000-06 Director, Center of Excellence in Biomolecular Computer Modeling & Simulation
 2003-06 Professor, Dept. of Chemistry & Biochemistry, Florida State University
 9/2006- Professor, Dept. of Biochemistry & Molecular Biology, Oregon Health & Science University

Professional Service

- 1999-06 Executive Board & various standing committees, SERCAT APS x-ray beam line.
 2001 Conference Chair: Computational Structural Biology—From Simulation to Exper. & Back
 2002 Chair, Gordon Research Conference – Diffraction Methods in Structural Biology

Federal Committees

- 1997 NIH Special Panel NLS3 & *Exp. Virol.* Temporary Member & Outside Consultant
 1999- Reviewer, NSF MCB, UK Gov.—Welcome Trust Joint Infrastructure Fund
 2000-07 NIH Special Panels – chair of 5 panels + member of 8 others
 2004 NIH Virology A study section, temporary member;
 2005-8 NIH Macromolecular Structure & Function C panel member

Recent Honors

- 2000 President's Developing Scholar Award, Florida State University
 2005- Fellow, American Association for the Advancement of Science

B. Selected Peer Reviewed Publications (selected from 79, in chronological order).

2. Chapman, M., Suh, S. W., Cascio, D., Smith, W. W. & Eisenberg, D. (1987). Sliding-layer conformational change limited by quaternary structure in plant RuBisCO. *Nature* **329**, 354-356.
 6. Chapman, M. S., Suh, S. W., Curmi, P. M. G., Cascio, D., Smith, W. W. & Eisenberg, D. S. (1988). Tertiary Structure of Plant RuBisCO: Domains and their Contacts. *Science* **241**, 71-74.
 13. Tsao, J., Chapman, M. S., Agbandje, M., Keller, W., Smith, K., Wu, H., Luo, M., Smith, T. J., Rossmann, M. G., Compans, R. W. & Parrish, C. (1991). The Three-Dimensional Structure of Canine Parvovirus and its Functional Implications. *Science* **251**, 1456-1464.
 14. Chapman, M. S., Tsao, J. & Rossmann, M. G. (1992). *Ab initio* Phase Determination for Spherical Viruses: Parameter Determination for Spherical Shell Models. *Acta Crystallogr.* **A48**, 301-312.
 20. Chapman, M. S. & Rossmann, M. G. (1993). Structure, Sequence and Function Correlations among Parvoviruses. *Virology* **194**, 491-508.
 21. Chapman, M. S. & Rossmann, M. G. (1993). Comparison of Surface Properties of Picornaviruses:

- Strategies for hiding the Receptor Site from Immune Surveillance. *Virology* **195**, 745-765.
23. Chapman, M. S. (1994). Sequence Similarity Scores and the Inference of Structure/Function Relationships. *Computer Applications in the Biosciences (CABIOS)* **10**, 111-119.
 24. Chapman, M. S. (1995). Restrained Real-Space Macromolecular Atomic Refinement using a New Resolution-Dependent Electron Density Function. *Acta Crystallogr.* **A51**, 69-80.
 25. Chapman, M. S. & Rossmann, M. G. (1995). Single-stranded DNA-protein interactions in Canine Parvovirus. *Structure* **3**, 151-62.
 29. Xie, Q. & Chapman, M. S. (1996). Canine parvovirus capsid structure, analyzed at 2.9 Å resolution. *J. Mol. Biol.* **264**, 497-520.
 30. Zhou, G., Parthasarathy, G., Somasundaram, T., Ables, A., Roy, L., Strong, S. J., Ellington, W. R. & Chapman, M. S. (1997). Expression, Purification from Inclusion Bodies, and Crystal Characterization of Transition State Analog Complex of Arginine Kinase: a Model for Studying Phosphagen Kinases. *Prot. Sci.* **6**, 444-9.
 37. Zhou, G., Wang, J., Blanc, E. & Chapman, M. S. (1998). Determination of the Relative Precision of Atoms in a Macromolecular Structure. *Acta Crystallographica* **D54**, 391-9.
 38. Zhou, G., Somasundaram, T., Blanc, E., Parthasarathy, G., Ellington, W. R. & Chapman, M. S. (1998). Transition state structure of arginine kinase: Implications for catalysis of bimolecular reactions. *Proc. Natl. Acad. Sci., USA* **95**, 8449-54.
 39. Chen, Z., Blanc, E. & Chapman, M. S. (1998). Real Space Molecular Dynamics Refinement. *Acta Crystallographica* **D55**: 464-8.
 40. Chen, Z., Blanc, E. & Chapman, M. S. (1999). Improved free R-factors for the cross-validation of structures. *Acta Crystallographica* **D55**: 219-224.
 42. Zhou, G., Ellington, W.R. & Chapman, M.S. (2000). Induced Fit in Arginine Kinase. *Biophys J* **78**: 1541-1550.
 43. Bertram, R., J. R. Quine, M. S. Chapman and T. A. Cross (2000). "Atomic Refinement Using Orientational Restraints from Solid-State NMR." *J. Magnetic Resonance*, **147**: 9-16.
 46. Chen, L.F., E. Blanc, M.S. Chapman, and K.A. Taylor. 2001. Real space refinement of acto-myosin structures from sectioned muscle. *J Struct Biol* **133**:221-32.
 47. Chen, Z., and M.S. Chapman. 2001. Conformational Disorder of Proteins Assessed by Real-Space Molecular Dynamics Refinement. *Biophys J* **80**:1466-1472.
 48. Korostelev, A., Bertram, R., and Chapman, M.S. 2002. Simulated Annealing Real-Space Refinement as a Tool in Model Building. *Acta Crystallogr.* **D58**: 761-767.
 50. Fabiola, F., Bertram, R., Korostelev, A., and Chapman, M.S. 2002. An improved hydrogen bond potential: impact on medium resolution protein structures. *Protein Sci* **11**: 1415-1423.
 51. Xie, Q., Bu, W., Bhatia, S., Hare, J., Somasundaram, T., Azzi, A., and Chapman, M.S. 2002. The atomic structure of adeno-associated virus (AAV-2), a vector for human gene therapy. *Proc Natl Acad Sci USA* **99**: 10405-10410.
 52. Yousef, M.S., Fabiola, F., Gattis, J., Somasundaram, T., and Chapman, M.S. 2002. Refinement of Arginine Kinase Transition State Analogue Complex at 1.2 Å resolution; mechanistic insights. *Acta Crystallogr. D. Biol. Crystallogr.* **58**: 2009-2017.
 53. Yousef, M.S., Clark, S., Pruet, P.S., Somasundaram, T., Ellington, W.R., and Chapman, M.S. 2003. Induced Fit in Guanidino Kinases - Comparison of Substrate-free and Transition State Analog Structures of Arginine Kinase. *Protein Sci.* **12**: 103-111.
 54. Xie, Q., T. Somasundaram, S. Bhatia, W. Bu, and M.S. Chapman, Structure determination of adeno-associated virus 2: three complete virus particles per asymmetric unit. *Acta Crystallogr D Biol Crystallogr*, 2003. **59**: 959-70.
 55. Gao, H., J. Sengupta, M. Valle, A. Korostelev, N. Eswar, S.M. Stag, P. VanRoey, R.K. Agrawal, S.C. Harvey, A. Sali, M. Chapman, and J. Frank, *Study of the Structural Dynamics of the E. coli 70S Ribosome Using Real Space Refinement.* *Cell*, 2003. **113**: 789-801.
 57. Pruet, P.S., A. Azzi, S.A. Clark, M. Yousef, J.L. Gattis, T. Somasundaram, W.R. Ellington, and M.S. Chapman, *The putative catalytic bases have, at most, an accessory role in the mechanism of arginine*

- kinase. **J Biol Chem**, 2003. 29: 26952-7.
58. Bertram, R., T. Asbury, F. Fabiola, J. R. Quine, T. A. Cross and M. S. Chapman (2003). "Atomic Refinement with Correlated Solid-State NMR Restraints." **J. Mag. Res.**, 2003. 163: 300-9.
59. Chen, J.Z., Furst, J., Chapman, M.S., and Grigorieff, N. 2003. Low-resolution structure refinement in electron microscopy. **J Struct Biol** 144: 144-151.
60. Azzi, A., Clark, S.A., Ellington, W.R., and Chapman, M.S. 2004. The Role of Phosphagen Specificity Loops in Arginine Kinase. **Protein Sci.** 13: 575-585.
61. Gattis, J. L., E. Ruben, Fenley, M.O., Ellington, W.R., and Chapman, M.S (2004). "The active site cysteine of arginine kinase - structural and functional analysis of partially active mutants." **Biochemistry**, 43: 8680-8689.
62. Xie, Q., Hare, J., Bu, W., Jackson, W., Turnigan, J., and Chapman, M. S. (2004) Large-scale Preparation, Purification and Crystallization of Wild-type Adeno-Associated Virus 2, **Journal of Virological Methods**, 122: 17-27
63. Korostelev, A., Fenley, M. O., and Chapman, M. S. (2004) Impact of a Poisson-Boltzmann Electrostatic Restraint on Protein Structures Refined at Medium Resolution, **Acta Crystallogr. D, Biol. Crystallogr.**, 60: 1786-1794.
64. Quine, J.R., Cross, T.A., Chapman, M.S. and Bertram, R., 2004. Mathematical Aspects of protein structure determination with NMR orientational restraints. **Bull. Math. Biol.** 66: 1705-1730.
65. Fabiola, F. and Chapman, M.S. (2005) Fitting of High Resolution Structures into Electron Microscopy Reconstruction Images, **Structure**, 13: 389-400.
66. Davulcu, O., S. A. Clark, M. S. Chapman and J. J. Skalicky (2005). "Main chain ¹H, ¹³C, and ¹⁵N resonance assignments of the 42 kDa enzyme arginine kinase." **Journal of Biological NMR**, 32: 178.
67. Ruben, E. A., Evanseck, J. D., and Chapman, M. S. (2005) A theoretical study of N-phosphoryl-guanidinium tautomers - influences of hyperconjugation on N-P bond strength, **Journal of the American Chemical Society**, 127: 17789-17798.
71. Fabiola, F., Korostelev, A. & Chapman, M. S. Cross-validation with Over-sampled Structure Factors. **Acta Crystallogr D Biol Crystallogr**, 62: 227-38 (2006).
72. Quine, J.R., Achuthan, S., Asbury, T., Bertram, R., Chapman, M.S., Hu, J. and Cross, T.A., 2006. Intensity and mosaic spread analysis from PISEMA tensors in solid state NMR. **J. Mag. Res.**, 179: 190-198.
73. Murray, S., Nilsson, C. L., Hare, J. T., Emmett, M. R., Korostelev, A., Ongley, H., Marshall, A. G. & Chapman, M. S. Characterization of the Capsid Protein Glycosylation of Adeno-associated Virus (AAV-2) by High Resolution Mass Spectrometry. **Journal of Virology**, 80: 6171-6 (2006).
74. Mitra, K., Schaffitzel, C., Fabiola, F., Chapman, M. S., Ban, N. & Frank, J. Elongation arrest by SecM via a cascade of ribosomal RNA rearrangements. **Molecular Cell**, 22: 533-43 (2006).
75. Mitchell, D. A. J., O'Donnell, J., Hare, J. T. & Chapman, M. S. Serotype-Specific Detection During Laboratory Preparation of Adeno-Associated Virus. **J. Virological Methods**, 136: 277-82 (2006).
76. Asbury, T., Bertram, R., Quine, J. R., Achuthan, S., Chapman, M. S. & Cross, T. A. PIPATH: and Algorithm for Assignment of PISEMA Data. **Journal of Magnetic Resonance**, 183: 87-95 (2006).
77. Chapman, M.S. Normalizing Normal Mode Analysis; **Structure**, 15: 135-6 (2007).
78. Ruben, E.A., Chapman, M.S. & Evanseck, J.D. Hydrogen Bonding Mediated by Key Orbital Interactions Determines Hydration Enthalpy Differences of Phosphate Water Clusters; **J Physical Chemistry A**, 111: 10804-14 (2007).
79. Ruben, E.A., M.S. Chapman, and J.D. Evanseck, Anomeric effect in "high energy" phosphate bonds – selective destabilization of the scissile bond and modulation of the exothermicity of hydrolysis. **J Am Chem Soc**, 130: 3349-58 (2008).
80. Xie, Q., Ongley, H. M., Hare, J., and Chapman, M. S. (2008). Crystallization and preliminary X-ray structural studies of adeno-associated virus serotype 6. **Acta Crystallogr Sect F Struct Biol Cryst Commun** 64: 1074-8.
81. O'Donnell, J., Taylor, K. A., and Chapman, M. S. (2008). Adeno-Associated Virus and its Primary Cellular Receptor - Cryo-EM structure of a Heparin Complex. **Virology** *accepted*.

C. Research Support

Ongoing Research

<u>1R01 GM66875-06 Chapman (PI)</u> NIH NIGMS Structure-Function of AAV - a Viral Gene Therapy Vector. The goal is structural characterization of viral-host interactions through crystallography, biophysical techniques & molecular virology to understand cell entry & antibody recognition. Role: PI	2/1/03– 7/31/11
<u>1R01 GM77643-01 Chapman (PI)</u> NIH NIGMS Functional Dynamics during Induced-fit Turnover. The goal is NMR and crystallographic characterization of protein dynamics during the turnover cycle of an induced-fit two-substrate enzyme. Role: PI	2/1/07 – 1/31/11
<u>1R01 GM078538-01 Chapman (PI)</u> NIH NIGMS Refinement of Macromolecular Assembly Structure using Electron Microscopy. The goal is development of optimal methods for fitting x-ray crystallographic component structures into complex structures visualized by cryo-electron microscopy. Role: PI	6/1/07 – 5/31/11
<u>S10-RR024561-01 Taylor, K.A. (PI); Chapman (Co-PI)</u> NIH NCRR CryoEM Equipment Enhancements for Florida State University. (FEI Vitrobot, Gatan Plasma Cleaner, Gatan cryotomography holder and a high tilt, dual axis tomography holder)	4/1/08– 3/31/09
<u>S10-RR025080-01 Taylor, K.A. (PI); Chapman (Co-PI)</u> NIH NCRR Purchase of a FEI Titan Krios for 3-D EM. Role: One of 5 primary users, will use the automated electron microscope remotely for studies of adeno-associated virus complexed with receptors and antibodies.	7/1/08– 6/30/09
<u>Oregon Nanoscience and Microtechnologies Institute: Nanometrology and Nanoelectronics Initiative: Minot, E. (PI); Chapman (Co-PI) (pending)</u> Electronic detection of single molecule dynamics Role: Assist in the attachment of enzymes (esp. arginine kinase) to nanotubes for detection of single-molecule dynamics	01/01/09 – 12/31/09

Completed Research (last 3 years)

<u>NIH NCRR S10 RR020919 Taylor, K.A. (PI); Chapman (Co-PI)</u> Purchase of a large format CCD camera for 3-D EM.	4/1/05– 3/31/07
<u>Center of Excellence: 5-1303-0633 Chapman (PI through 9/06)</u> FSU Research Foundation, Cornerstone Program Biomolecular Computer Modeling & Simulation The goal is to develop new center in computational structural biology. Role: PI – leading faculty recruitment, building research & training infrastructure.	4/22/00– 6/30/07
<u>NIH 1P01 GM64676 Cross (PI)</u> Membrane Protein Structural Genomics: <i>M. tuberculosis</i> . 13-investigator consortium to develop methods of membrane protein structure determination, and to apply them to samples of <i>M. tuberculosis</i> . Role: Co-Investigator leading sub-project to develop software for refinement of structures vs. combinations of x-ray crystallographic, solid-state NMR and electron microscope data.	9/28/01- 8/31/07