

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 (<i>Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.</i>)			
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
 2000-09 NIH Special Panels – chair of 5 panels + member of 9 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 82, 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., Pruetz, 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. Stagg, 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. Pruetz, 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. & Cross, T.A., 2006. Intensity & mosaic spread analysis from PISEMA tensors in solid state NMR. *J. Mag. Res.*, 179: 190-8.
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'Donnel, 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* 64: 1074-8.
81. O'Donnell, J., Taylor, K. A., and Chapman, M. S. (2009). Adeno-Associated Virus and its Primary Cellular Receptor - Cryo-EM structure of a Heparin Complex. *Virology in press*.

82. Lerch, T.F., Xie, Q., Ongley, H.M., Hare, J. and Chapman, M.S. (2009). Twinned Crystals of Adeno-associated Virus Serotype 3b Prove Suitable for Structural Studies. **Acta Crystallogr Sect F** *in press*.

C. Research Support

Ongoing Research

1R01 GM66875-06 Chapman (PI)

2/1/03–

NIH NIGMS

7/31/11

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

1R01 GM77643-01 Chapman (PI)

2/1/07 –

NIH NIGMS

1/31/11

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

1R01 GM078538-01 Chapman (PI)

6/1/07 –

NIH NIGMS

5/31/11

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

S10-RR024561-01 Taylor, K.A. (PI); Chapman (Co-PI)

4/1/08–

NIH NCRR

3/31/09

CryoEM Equipment Enhancements for Florida State University. (FEI Vitrobot, Gatan Plasma Cleaner, Gatan cryotomography holder and a high tilt, dual axis tomography holder)

S10-RR025080-01 Taylor, K.A. (PI); Chapman (Co-PI)

7/1/08–

NIH NCRR

6/30/09

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.

Oregon Nanoscience and Microtechnologies Institute: Nanometrology and Nanoelectronics Initiative: Minot, E. (PI); Chapman (Co-PI) (pending)

01/01/09

Electronic detection of single molecule dynamics

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12/31/09

Role: Assist in the attachment of enzymes (esp. arginine kinase) to nanotubes for detection of single-molecule dynamics

Completed Research (last 3 years)

NIH NCRR S10 RR020919 Taylor, K.A. (PI); Chapman (Co-PI)

4/1/05–

Purchase of a large format CCD camera for 3-D EM.

3/31/07

Center of Excellence: 5-1303-0633 Chapman (PI through 9/06)

4/22/00–

FSU Research Foundation, Cornerstone Program

6/30/07

Biomolecular Computer Modeling & Simulation

The goal is to develop new center in computational structural biology.

Role: PI – leading faculty recruitment, building research & training infrastructure.

Principal Investigator/Program Director (Last, First, Middle): CHAPMAN, Michael Stewart

NIH 1P01 GM64676 Cross (PI)

Membrane Protein Structural Genomics: *M. tuberculosis*.

13-investigator consortium to develop methods of membrane protein structure determination, and to apply them to samples of *M. tuberculosis*.

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