

REPORT DOCUMENTATION PAGEForm Approved
OMB NO. 0704-0188

Public Reporting burden for this collection of information is estimated to average 1 hour per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing the collection of information. Send comment regarding this burden estimates or any other aspect of this collection of information, including suggestions for reducing this burden, to Washington Headquarters Services, Directorate for Information Operations and Reports, 1215 Jefferson Davis Highway, Suite 1204, Arlington, VA 22202-4302, and to the Office of Management and Budget, Paperwork Reduction Project (0704-0188), Washington, DC 20503.

1. AGENCY USE ONLY (Leave Blank)

2. REPORT DATE
21 Sep 20053. REPORT TYPE AND DATES COVERED
Final 17 Feb 2003 – 16 May 20054. TITLE AND SUBTITLE
NYS Center of Excellence in Bioinformatics5. FUNDING NUMBERS
G DAAD19-03-1-0021

6. AUTHOR(S)

Dr. Bruce Holm

7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES)
Research Foundation of SUNY
Suite 211, 520 Lee Entrance
Amherst, NY 142288. PERFORMING ORGANIZATION
REPORT NUMBER

9. SPONSORING / MONITORING AGENCY NAME(S) AND ADDRESS(ES)

U. S. Army Research Office
P.O. Box 12211
Research Triangle Park, NC 27709-221110. SPONSORING / MONITORING
AGENCY REPORT NUMBER

44871.1-LS

11. SUPPLEMENTARY NOTES

The views, opinions and/or findings contained in this report are those of the author(s) and should not be construed as an official Department of the Army position, policy or decision, unless so designated by other documentation.

12 a. DISTRIBUTION / AVAILABILITY STATEMENT

Approved for public release; distribution unlimited.

12 b. DISTRIBUTION CODE

13. ABSTRACT (Maximum 200 words)

This Center is made up of an integrated set of research projects in five areas. The overall mission of the center is to utilize state-of-the-art systems biology approaches to the generation of novel therapies and diagnostics for human diseases. Drug Discovery & Delivery: Biologically relevant compounds that can be linked to effects on specific gene expression patterns, creating new drug targets. Included in this program are two new start-up companies. Cancer: Identify targets to inhibit tumor growth and cell proliferation. Neurodegenerative Disease: Investigating the disease mechanisms of several neurological disorders, including Alzheimer's, MS, Krabbe's and Parkinson's disease. Major themes include demyelination, amyloid plaque formation, and loss of cellular function. Cardio-Vascular disease; Mechanisms by which inflammatory processes associated with clinical aspiration events progress to pneumonitis and ventilator-associated pneumonias; sudden cardiac failure due to arrhythmias. Pathogenesis & Biodefense: Investigation of virulence factors for bacteria and viruses important in human disease and in bio-warfare. Novel vaccines and anti-microbial agents will be developed based on structure-function understanding of these factors. Data Intensive Core; Analysis of genomic, proteomic, epidemiological and clinical data, imaging, and modeling.

14. SUBJECT TERMS

15. NUMBER OF PAGES

16. PRICE CODE

17. SECURITY CLASSIFICATION
OR REPORT
UNCLASSIFIED18. SECURITY CLASSIFICATION
ON THIS PAGE
UNCLASSIFIED19. SECURITY CLASSIFICATION
OF ABSTRACT
UNCLASSIFIED20. LIMITATION OF ABSTRACT
UL

NSN 7540-01-280-5500

Standard Form 298 (Rev.2-89)
Prescribed by ANSI Std. Z39-18
298-102

Enclosure 1

The **New York State Center of Excellence in Bioinformatics and Life Sciences** has been established in Buffalo, NY and is in the process of further developing its infrastructure and hiring faculty members in necessary areas. The **Center of Excellence** has designed several inter-related specialty laboratories that can function alone and in sequence to facilitate the process of disease mechanism, diagnosis, and therapy discovery. The high-throughput analysis begins with the gene, but those genes must be associated with a systematic process for the development and curation of clinically relevant databases. In the **Interventional Population Health Observatory**, Public Health specialists utilize techniques in molecular epidemiology, biostatistics, and telehealth to merge medical informatics with traditional bioinformatics to create a linkage between clinical samples, longitudinal medical information, and functional genomics. Public Health, with a high technology component, therefore becomes the “front end” of the Buffalo bioinformatics initiative, and thereby gives the Center a unique element with both short-term and long-term tangible benefits at local, state, national, and international levels. The **Health Observatory** also serves as the responsible unit within the Center of Excellence for the development of syndromic surveillance and emergency response programs that are related to biodefense and disaster management.

In the **Molecular Targeting Laboratory**, a large number of agents (combinatorially synthesized compounds, drugs, or toxicants) are screened efficiently in live cells for effects on specific gene expression pathways. This Laboratory is also developing a parallel approach for applications to microbial pathogens that should dramatically speed the process of target identification relative to biodefense applications. The strategy of the Molecular Targeting Lab is broadly extensible, and not limited to predetermined target pathways. The initial screen in the Molecular Targeting Laboratory does not seek the specific target; the pharmacophore and a family of responsive cell mutants are delivered to the **Gene Expression Laboratory** for high throughput microarray dissection of the target gene product and ancillary gene expression pathway. Subsequently, the **Proteomics and Structural Biology Laboratory** has been established to identify the gene product targets of the pharmacophore and determine tertiary structures.

The **Disease Modeling Laboratory** has been established to work out *in vivo* proof of concept studies. The **Clinical Pharmacology Laboratory** has been established for Phase I studies, frequently utilizing the Clinical Research Center (CRC) within the Buffalo VA hospital. All aspects of the discovery process utilize the data storage, data mining and analysis, and virtual reality visualization expertise and infrastructure of the **Biomedical Informatics Laboratory**. In addition, this latter group is also engaged in independent research in areas of computational infrastructure, data mining, data fusion, and data visualization research.

Each individual specialty laboratory within the Center is led by an internationally recognized leader in his or her field. Each of the specialty teams has already been highly successful at securing other additional extramural funding for scientific operations. All aspects of the discovery process utilize the data storage, data mining and analysis, and virtual reality visualization expertise and infrastructure of the **Biomedical Informatics Laboratory**. The Center for Computational Research (CCR), which is part of the New York State Center of Excellence in Bioinformatics and Life Sciences and recently named as one of the top 10 academic supercomputing facilities in the country, provides high performance supercomputing and data storage infrastructure. It is one of only three sites in the world selected to beta-test Intel's next generation chip-the 64-bit Itanium processor. A key test for much of the new IT

technology is how it performs with *SnB*, the protein-structure software developed by UB scientists Dr. Russ Miller and Dr. Herbert Hauptman, based on Dr. Hauptman's Nobel Prize winning algorithm. This bioinformatics program is currently the software of choice for more than 500 drug design and research labs.

The CCR's current computer systems are capable of carrying out more than 9.6 trillion operations per second (teraflops). One advantage of the UB CCR design strategy relative to other supercomputing sites is that it maintains computers designed around all three of today's most popular parallel computing architectures; *shared memory* (SGI Origin 2000), *distributed memory* (IBM SP, SUN cluster, SGI cluster, Dell cluster), and *distributed shared memory* (IBM SP, SGI cluster, Dell cluster). This diversity allows our researchers to design, test, and distribute software that is optimized for the various parallel computers available in the marketplace. The CCR also supports all major parallel programming languages. The current technology infrastructure includes:

- 128 processor SGI Origin 2000 supercomputer
- 78 processor IBM RS/6000 SP supercomputer
- Solaris/Linux cluster of 64 Sun Ultra5 workstations
- 150 processor SGI cluster of 1GHz Pentium III chips
- Pyramid Systems ImmersaDesk Visualization system
- SGI Onyx2 Infinite Reality2 graphics computer
- MechDyne 9'x10' Immersive Wall powered by an SGI Onyx2
- Infinite Reality2 graphics computer
- Fakespace RAVE passive stereo module powered by an SGI
- Onyx 3400 computer with Infinite Reality 3 graphics
- Cluster of SGI Octanes, SGI O2s, SUN Ultra 80s, & SUN Ultra 60s
- Web-based geographically distributed communication capabilities
- 2000 Dell dual processor systems consisting of:
 - 2 1.0GHz Pentium3 Processors with 1 GB RAM
 - 236GB local disks
 - 50 42U racks
 - 4 cisco 6513 switches, 11*48p 10/100, 1*16p 1000

Compaq Storage Area Network-10 terabytes of archived data with ≥ 23 dual-attached SAN I/O nodes (one per 64 compute hosts), using NFS server over gigabit connection.

Section a

Papers published in peer-reviewed journals:

Ionov, Y., **Nowak, N.**, Perucho, M., Markowitz, S., Cowell, J.K. Manipulation of nonsense mediated decay identifies gene mutations in colon cancer cells with microsatellite instability. *Oncogene*, 23:639-645, 2004.

Cowell, J.K., Wang, Y.D., Head, K., Conroy, J., McQuaid, D. **Nowak, N.J.** Identification and characterization of constitutional chromosome abnormalities using arrays of bacterial artificial chromosomes. *The British Journal of Cancer*, 90:4-860-865, 2004.

Cowell, J.K., Barnett, G., **Nowak, N.J.** Characterization of the 1p/19q Chromosomal Loss in Oligodendrogliomas Using CGHa. *J Neuropathol Experimental Neurology*, 63:2:151-158, 2004.

Cowell, J.K., Matsui, S.I., Wang Y.D., LaDuca, J., Conroy, J., McQuaid, D., **Nowak, N.J.** Application of bacterial artificial chromosome array-based comparative genomic hybridization and spectral karyotyping to the analysis of glioblastoma multiforme. *Cancer, Genetics and Cytogenetics*, 151:1:36-51, 2004.

Collins, Y., Tan, D.F., Pejovic, T., Mor, G., Qian, F., Rutherford, T., Varma, R., McQuaid D., Driscoll, D., Jiang, M., Deeb, G., Lele, S., **Nowak, N.**, Odunsi, K. Identification of differentially expressed genes in clinically distinct groups of serous ovarian carcinomas using cDNA microarray. *Int J Molecular Medicine*, 14:1:43-53, 2004.

M.L. Green and R. Miller, A client-server prototype for application grid-enabling template design, *Parallel Processing Letters*, Vol. 14, No. 2 (2004), pp. 241-253. [Paper.pdf](#) [Paper.ps](#)

M.L. Green and R. Miller, Molecular structure determination on a computational & data grid, *Parallel Computing Journal* 30 (2004), pp. 1001-1017. [Paper.pdf](#)

M.L. Green and R. Miller, Evolutionary molecular structure determination using grid-enabled data mining, *Parallel Computing Journal* 30 (2004), pp. 1057-1071. [Paper.pdf](#)

L. Boxer and R. Miller, Coarse Grained Gather and Scatter Operations with Applications, *Journal of Parallel and Distributed Computing* 64 (2004), pp. 1297-1310. [Paper.pdf](#)

Fischer D, Rychlewski L, Dunbrack RL, Ortiz, AR, Elofsson A. CAFASP3: The Third Critical Assessment of Fully Automated Structure Prediction Methods. *Proteins*;53:503-516, 2003.

Siew N, Azaria Y, **Fischer D**. The ORFanage: an ORFan database. *Nucl. Acid Research*; 32, D281-D283, 2004.

Shmueli H, Dinitz E, Dahan I, Eichler J, **Fischer D**, Shaanan B. Poorly-conserved ORFs in the genome of the archaeon *Halobacterium* sp. NRC-1 correspond to expressed proteins. *Bioinformatics*, 1248-1253, 2004

Bujnicki, J. and **Fischer, D**. 'Meta' Approaches to Protein Structure Prediction. Chapter in *Nucleic Acids and Molecular Biology*, Vol. 15. pp 23-34. Janusz M. Bujnicki (Ed.). Practical Bioinformatics. Springer-Verlag Berlin Heidelberg, 2004.

Fischer D, Pas J, Rychlewski L. The PDB-Preview Database: A Repository of In-Silico Models of “on-hold” PDB entries. Bioinformatics; in press, 2004

Siew, N., and **Fischer, D**. Structural Biology Sheds Light on the Puzzle of Genomic ORFans. J. Mol. Biol; 342:369-373, 2004

NOTTER RH, **HOLM BA**

Basic science research on clinical exogenous surfactants: composition, activity, viscosity, and utility in lung injury.

Neonatal Intensive Care, 17(2) 3-7 (2004)

JOHNSTON CJ, **HOLM BA**, and FINKELSTEIN JN.

"Differential responses of the Lung to Ozone and LPS Exposures During Postnatal Development."

Experimental Lung Research, 30(7):599-614 (2004)

DAVIDSON BA, KNIGHT PR WANG Z, CHESS PR, **HOLM BA**, RUSSO TA, HUTSON A, and NOTTER RH

“Surfactant Alterations in Acute Inflammatory Lung Injury From Aspiration of Acid and Gastric Particulates.”

Exp Lung Research, 30(7) 535-557 (2004)

José J.C. Teixeira-Dias, Thomas R. Furlani, Kevin S. Shores and James F. Garvey, “Transition states for H atom transfer reactions in the CH₂CH₂OH Radical: the effect of a water molecule”, Physical Chemistry Chemical Physics, **5**, 5063 – 5069 (2003).

J. Rappleye, M. Innus, C.M. Weeks, and R. Miller, *SnB v2.2: An Example of Crystallographic Multiprocessing*, *Journal of Applied Crystallography* **35**, 2002, pp. 374-376.

C.M. Weeks, R.H. Blessing, R. Miller, R. Mungee, S.A. Potter, J. Rappleye, G.D. Smith, H. Xu, and W. Furey, Towards automated protein structure determination: *BnP*, the *SnB*-PHASES interface, *A. Kristallogr.* **217**, 2002, pp. 1-8.

M.L. Green and R. Miller, Grid computing in Buffalo, *Annals of the European Academy of Sciences*, 2003, pp. 191-218.

Sait S, Qadir M, Conroy J, Matsui S, Nowak NJ, Baer M. Double minute chromosomes in acute myeloid leukemia and myelodysplastic syndrome: Identification of new amplification regions by fluorescence in situ hybridization and spectral karyotyping. *Genes, Chromosomes and Cancer*. 34:42-47, 2002.

Chandrasekharappa S, Holloway A, Iyer V, Monte D, Murphy M, Nowak NJ. DNA Microarrays. *Generation of Probes for Spotted Microarrays*. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York. Editors: David Howell and Joseph Sambrook.

Sossey-Alaoui K, Head K, **Nowak N**, Cowell JK. Genomic Organization and Expression Profile of the Human and Mouse WAVE Gene Family. *Mammalian Genome*, 14(5):314-322, 2003.

Bruce, C.K., Howard P., **Nowak, N.J.**, Hoban, P.R. Molecular analysis of region t(5;6) (q21;q21 in Wilms tumor. *Cancer Genet Cytogenet* 141(2):106-113, 2003.

Gong, S., Zheng, C. , Doughty, M.L., Losos, K., Didkovsky, N., Schambra, U., **Nowak, N.J.**, Joyner A, Leblanc, G., Hatten, , M., Heintz, N. A gene expression atlas of the central nervous system based on bacterial artificial chromosomes. *Nature* 425:917-925, 2003.

Hackett, C., Hodgson, G., Law, M., Fridlyand, J., Osoegawa, K., De Jong, P., **Nowak, N.J.**, Pinkel, D., Albertson, D., Jain, A., Jenkins, R, Gray, J., Weiss, W. Genome-wide array CGH analysis of murine neuroblastoma reveals distinct genomic aberrations which parallel those in human tumors. *Cancer Research* 63:5266-5273, 2003.

Ramos-Nino, M.E., Heintzm, N., Scapoli, L., Martinelli, M., Land, S., **Nowak, N.**, Haegens, A., Manning, B., Manning, N. Gene profiling and kinase screening in asbestos-exposed epithelial cells and lungs. *American Journal of Respiratory Cell and Molecular Biology* 29:3(2):S51-S58, 2003.

P. Pokarowski, A. Kolinski, J. Skolnick. A minimal physically realistic protein-like lattice model: Designing an energy landscape that ensures all-or-none folding to a unique native state. *Biophysical Journal*. 2003; **84**(3): 1518-26.

T. Haliloglu, A. Kolinski, J. Skolnick. Use of NMR Residual Dipolar Coupling (RDCs) as Restraints in *ab initio* Protein Structure Prediction. *Biopolymers* (in press).

Sikorski, A. Kolinski, J. Skolnick. Computer simulation of protein folding with a small number of distance restraints, *Acta Biochimica Polonica* 2002; **49**:683-692 (2002)

H. Lu, L. Lu, J. Skolnick. Development of Unified Statistical Potentials Describing Protein-Protein Interactions. *Biophysical Journal*. 2002; **84**(3): 1895-901.

D. Kihara, J. Skolnick. The PDB is a Covering Set of Small Protein Structures. *Journal of Molecular Biology* 2003;**333**:393-802.

J. Skolnick, Y. Zhang, A. Arakaki, M. Betancourt, A. Szilagyi, D. Kihara. Touchstone: A Unified Approach to Protein Structure Prediction. *Proteins CASP5 Special Issue* 2003;**53**:469-479.

L. Lu, A. Arakaki, H. Lu, J. Skolnick. Multimeric Threading Based Prediction of Protein Interactions on a Genomic Scale: Application to the *Saccharomyces Cerevisiae* Proteome. *Genome Research* 2003;**13**:1146-1154.

Y. Zhang, A. Kolinski, J. Skolnick. Touchstone II: A New Approach to *ab initio* Protein Structure Prediction. *Biophysical Journal* 2003;**85**: 1145-1164.

Kolinski, P. Klein, P. Romiszowski, J. Skolnick. Unfolding of Globular Proteins: Monte Carlo Dynamics of a Realistic Reduced Model. *Biophysical Journal*. 2003;85: 3271-3278.

W. Li, Y. Zhang, D. Kihara, Y. Huang, D. Zheng, G. Montelione, A. Kolinski, J. Skolnick. Touchstonex: Protein Structure Prediction Using Sparse NMR Data. *Proteins* 2003: 53(2):290-306.

W. Tian, J. Skolnick. How Well is Enzyme Function Conserved? *Journal of Molecular Biology* 2003;333:863-882.

Hay, J., Beutner, E. and Natelson, B. Immune parameters in Chronic Fatigue Syndrome. Recent Advances in Molecular Biology, Allergy and Immunology. 148-156, 2002.

Lynch, J., Kenyon, T., Grose, C., Hay, J and Ruyechan, W. Physical and functional interaction between the VZV IE63 and IE62 proteins. *Virology*, 302, 71-82, 2002

Arvin, A., Sharp, M., Moir, M., Kinchington, P., Sadeghi-Zadeh, M., Ruyechan, W. and Hay, J. Memory cytotoxic T-cell responses to viral tegument and regulatory proteins encoded by ORFs 4, 10, 29 and 62 of VZV. *Viral Immunol.* 15, 507-516, 2002.

Ruyechan, W., Peng, H., Yang, M. and Hay, J. Cellular factors and IE62 activation of VZV promoters. *J. Med. Virol.* 70, S90-94, 2003

Ito, H., Sommer, M., Zerboni, L., He, H., Boucaud, D., Hay, J., Ruyechan, W and Arvin, A. Promoter sequences of VZV gI targeted by cellular transcription factors Sp1 and USF determine virulence for human skin and T-cells in the SCIDhu mouse. *J. Virol.*, 77, 489-498, 2003

Peng, H., He, H., Hay, J. and Ruyechan, W.T. Interaction between the VZV IE62 major transactivator and the cellular transcription factor Sp1. *J. Biol. Chem.*, 278, 38068-38076, 2003.

DE, TAPAS K., RODMAN TJ, BERGEY EJ, **HOLM BA**, PRASAD PN
“Brimonidine Formulation in Polyacrylic Acid Nanoparticles for Ophthalmic Delivery”
J. Microencapsulation, 2003

King DM, Wang Z, Palmer HJ, Holm BA, Notter RH: Bulk shear viscosities of endogenous and exogenous lung surfactants. *Am J Physiol* 282:L277-L284, 2002.

HOLM BA, BERGEY EJ, TAPAS D, RODMAN DJ, KAPOOR R, LEVY L, FRIEND CS and PRASAD PN. “Nanotechnology in BioMedical Applications” *Molecular Crystals and Liquid Crystals* 374:589-598 (2003)

RussoTA, Bartholomew LA, Davidson BA, Helinski JD, Carlino UB, Knight PR, Beers MF, Atochina EN, Notter RH, Holm BA. Total extracellular surfactant is increased but abnormal in a rat model of Gram-negative bacterial pneumonia. *Am J Physiol* 283:L655-L663, 2003.

Baiker, A., Bagowski, C., Ito, H., Sommer, M., Zerboni, L., Fabel, K., Hay, J., Ruyechan, W.T and Arvin, A.M. The IE63 protein of VZV: analysis of functional domains required for replication in vitro and for T-cell and skin tropism in the SCIDhu model in vivo. J. Virol., 78, 1181-1194, 2003.

Section b

Papers published in non-peer-reviewed journals or in conference proceedings

NOTTER RH, FINKELSTEIN JN, **HOLM BA**, eds.
“Lung Injury: Mechanisms, Pathophysiology, and Therapy”
Lung Biology in Health and Disease Series-NHLBI
Marcel Dekker, 2004

NOTTER RH, FINKELSTEIN JN, **HOLM BA**,
“Introduction to Lung Injury”
In ,“Lung Injury: Mechanisms, Pathophysiology, and Therapy”
Notter, Finkelstein, and Holm, Eds.
Lung Biology in Health and Disease Series-NHLBI
Marcel Dekker, (2004)

WANG Z, **HOLM BA**, MATALON S, and NOTTER RH
“Surfactant Activity and Dysfunction in Lung Injury”
In ,“Lung Injury: Mechanisms, Pathophysiology, and Therapy”
Notter, Finkelstein, and Holm, Eds.
Lung Biology in Health and Disease Series-NHLBI
Marcel Dekker, (2004)

FINKELSTEIN JN, **HOLM BA**, O REILLY, and NOTTER RH
“Cellular and Animal Models of Lung Injury”
In ,“Lung Injury: Mechanisms, Pathophysiology, and Therapy”
Notter, Finkelstein, and Holm, Eds.
Lung Biology in Health and Disease Series-NHLBI
Marcel Dekker, (2004)

CHESS, FINKELSTEIN JN, **HOLM BA**, and NOTTER RH
“Surfactant Replacement Therapy in Lung Injury”
In ,“Lung Injury: Mechanisms, Pathophysiology, and Therapy”
Notter, Finkelstein, and Holm, Eds.
Lung Biology in Health and Disease Series-NHLBI
Marcel Dekker, (2004)

NOTTER RH, FINKELSTEIN JN, **HOLM BA**,
“Future Direction in Lung Injury Research”
In ,“Lung Injury: Mechanisms, Pathophysiology, and Therapy”

Notter, Finkelstein, and Holm, Eds.
Lung Biology in Health and Disease Series-NHLBI
Marcel Dekker, (2004)

R. Miller, Parallel Processing Architectures, *Concise Encyclopedia of Computer Science*, E.D. Reilly, ed., John Wiley & Sons, Ltd., New Jersey, 2004, pp. 598-601.

R. Miller, Parallel Processing Algorithms, *Concise Encyclopedia of Computer Science*, E.D. Reilly, ed., John Wiley & Sons, Ltd., New Jersey, 2004, pp. 601-602.

Nowak, N.J. : The BAC Resources. Current Protocols in Human Genetics, 2004.

Section d

Manuscripts submitted, but not published

Wang Z, Schwan AL, Lairson LL, O'Donnell JS, Byrne GF, Foye A, Holm BA, Notter RH: Surface activity of a synthetic lung surfactant containing a phospholipase-resistant phosphonolipid. *Am J Physiol (Lung Cell Molec Physiol)*, In Press, 2003.

Hay, J. and Ruyechan, W.T. Alphaherpesvirus DNA replication. In "Human herpesviruses: biology, therapy and immunoprophylaxis" Cambridge University Press. In press, 2003.

NOTTER RH, FINKELSTEIN JN, **HOLM BA**, eds.
"Lung Injury: Mechanisms, Pathophysiology, and Therapy"
In press (2003), Lung Biology in Health and Disease Series-NHLBI

NOTTER RH, FINKELSTEIN JN, **HOLM BA**,
"Introduction to Lung Injury" In "Lung Injury: Mechanisms, Pathophysiology, and Therapy"
Notter, Finkelstein, and Holm, Eds. Lung Biology in Health and Disease Series-NHLBI
In Press, (2003)

WANG Z, **HOLM BA**, MATALON S, and NOTTER RH
"Surfactant Activity and Dysfunction in Lung Injury" In "Lung Injury: Mechanisms, Pathophysiology, and Therapy" Notter, Finkelstein, and Holm, Eds. Lung Biology in Health and Disease Series-NHLBI, In Press, (2003)

FINKELSTEIN JN, **HOLM BA**, O REILLY, and NOTTER RH
Cellular and Animal Models of Lung Injury" In "Lung Injury: Mechanisms, Pathophysiology, and Therapy" Notter, Finkelstein, and Holm, Eds. Lung Biology in Health and Disease Series-NHLBI, In Press, (2003)

CHESS, FINKELSTEIN JN, **HOLM BA**, and NOTTER RH
"Surfactant Replacement Therapy in Lung Injury" In "Lung Injury: Mechanisms, Pathophysiology, and Therapy" Notter, Finkelstein, and Holm, Eds. Lung Biology in Health and Disease Series-NHLBI, In Press, (2003)

NOTTER RH, FINKELSTEIN JN, **HOLM BA**,

“Future Direction in Lung Injury Research” In ,“Lung Injury: Mechanisms, Pathophysiology, and Therapy” Notter, Finkelstein, and Holm, Eds. Lung Biology in Health and Disease Series- NHLBI, In Press, (2003)

Ionov, Y., **Nowak, N.**, Perucho, M., Markowitz, S., Cowell, J.K. Manipulation of nonsense mediated decay identifies gene mutations in colon cancer cells with microsatellite instability. In press, 2003.

Cowell, J.K., Wang, Y.D., Head, K., Conroy, J., McQuaid, D. **Nowak, N.J.** Identification and characterization of constitutional chromosome abnormalities using arrays of bacterial artificial chromosomes. In press, 2003.

Cowell, J.K., Barnett, G., **Nowak, N.J.** Characterization of the 1p/19q Chromosomal Loss in Oligodendrogliomas Using CGHa. In press, 2003.

Matsui, S.I., LaDuca, J., Rossi, M.R., **Nowak, N.J.**, Cowell, J.K. Molecular characterization of a consistent 4.5 megabase deletion in 4q28 in prostate cancer cells. Cancer, Genetics and Cytogenetics, In Press.

Snijders AM, **Nowak NJ**, Huey B, Fridlyand J, Law S, Conroy J, Tokyusu T, Demir K, Chiu R, Mao J-H, Jain AN, Jones SJM, Balmain A, Pinkel D, Albertson GH. Mapping segmental and sequence variations among laboratory mice using BAC array CGH. Genome Research, In Press. Kimura MT, Mori T, Conroy J, **Nowak NJ**, Satomi S, Tamai K, Nagase H. Two functional coding single nucleotide polymorphisms in STK15 (Aurora-A) co-ordinately increase esophageal cancer risk. Accepted; Pending Revision

Drazinic CM, Ercan-Sencicek AG, Gault LM, Hisama FM, Wumsiyeh MB, **Nowak NJ**, Cubells JF, State MW. Rapid array-based genomic characterization of a subtle structural abnormality: A patient with psychosis and der(19)t(5;18)(p14.1;p11.23) Am J Med Genetics, In Press.

Rychlewski, L., and **Fischer, D.** LiveBench-8: The large-scale, continuous assessment of Automated Protein Structure Prediction. Protein Science; in press, 2004.

Saini, H.K., and **Fischer, D.** Meta-DP: Domain Prediction Meta Server. Submitted, 2004.

RYAN RM, STERNBERG Z, D’ANGELIS CA, NIELSEN LC, WANG , BEVILACQUA WF, PIWKO JG, LOPEZ AR, WILLIAMS TC, **HOLM BA**, and SWARTZ DD.
“Hyperoxia Increases Neonatal Rabbit KGF but Exogenous KGF Treatment Does Not Decrease Mortality.”
Am J Physiol, submitted (2004)

HOLM BA, SHARMA A, IRISH MS, CHESS P, PATEL A, and GLICK PL.

"Ventilatory Stretch Induces Pulmonary Surfactant Synthesis and Secretion in Congenital Diaphragmatic Hernia Lamb Model."
Am J Physiol, submitted (2004)

PATEL A, SOKOLOWSKI J, and **HOLM BA**.
"Type II Cell Energetics and Surfactant Metabolism in Hyperoxic Lung Injury."
Am J Physiol, submitted (2004)

LEWIS NA, GLICK PL, TOSSMAN J, SWARTZ DA, D'ANGELIS CA, **HOLM BA**
"The Effects of Antenatal Vitamin A on Lung Function in the Fetal Lamb Model of Congenital Diaphragmatic Hernia"
J Pediatric Surgery, (2004) submitted