

for States to prepare teachers that are highly competent in the academic content areas in which they will be teaching.

(2) The percentage of program completers who are highly qualified teachers will increase in projects funded under the Teacher Quality Enhancement Partnership program.

There is no performance measure that focuses specifically on Teacher Quality Enhancement Grants for Recruitment.

VII. Agency Contact

FOR FURTHER INFORMATION CONTACT:

Luretha Kelley, U.S. Department of Education, 1990 K Street, NW., room 7096, Washington, DC 20006-8526. Telephone: (202) 502-7645 or e-mail: luretha.kelley@ed.gov.

If you use a telecommunications device for the deaf (TDD), you may call the Federal Relay Service (FRS) at 1-800-877-8339.

Individuals with disabilities may obtain this document in an alternative format (e.g., Braille, large print, audiotope, or computer diskette) on request to the program contact person listed in this section.

VIII. Other Information

Electronic Access to This Document: You may view this document, as well as all other documents of this Department published in the **Federal Register**, in text or Adobe Portable Document Format (PDF) on the Internet at the following site: <http://www.ed.gov/news/fedregister>.

To use PDF you must have Adobe Acrobat Reader, which is available free at this site. If you have questions about using PDF, call the U.S. Government Printing Office (GPO), toll free, at 1-888-293-6498; or the Washington, DC area at (202) 512-1530.

Note: The official version of this document is the document published in the **Federal Register**. Free Internet access to the official edition of the **Federal Register** and the Code of Federal Regulations is available on GPO Access at: <http://www.gpoaccess.gov/nara/index.html>.

Dated: March 16, 2005.

Sally L. Stroup,

Assistant Secretary for Postsecondary Education.

[FR Doc. 05-5544 Filed 3-18-05; 8:45 am]

BILLING CODE 4000-01-P

DEPARTMENT OF ENERGY

Recommendations for Sequencing Targets in Support of the Science Missions of the Office of Biological and Environmental Research (BER)

AGENCY: Office of Science; Office of Biological and Environmental Research; U.S. Department of Energy (DOE).

ACTION: Notice of recommendations for sequencing targets.

SUMMARY: This **Federal Register** Notice seeks the input and nominations of interested parties for candidate microbes, microbial consortia, and 250Mb-or-less-sized organisms for draft genomic sequencing in support of Office of Biological and Environmental Research (BER) programs, among them, the Genomics: GTL Program, the Climate Change Research Program, the Terrestrial Carbon Processes Program, the Natural and Accelerated Bioremediation Research (NABIR) Program, the Environmental Management Science Program (EMSP), the Ocean Science Program, and the Program for Ecosystem Research. Additional programs of relevance include the Energy Biosciences, and Nanoscale Science, Engineering and Technology Programs in the Office of Basic Energy Sciences. Nominated candidates should be relevant to DOE mission needs, e.g., organisms involved in environmental processes, including waste remediation, carbon management, and energy production. This announcement is not an offer of direct financial support for research on these organisms. Those nominations selected will result in the DNA sequence of selected organisms being determined at a draft level (6-8 X coverage) at the DOE Production Genomics Facility (PGF) at the Joint Genome Institute (JGI), (<http://www.jgi.doe.gov>). A subset of the selected organisms may be identified for sequence finishing. This announcement is designed to assist DOE in determining and prioritizing a list of microbes, microbial consortia, or modest-genome sized (not more than 250Mb) organisms (including eukaryotes) that address DOE mission needs. Following merit review, and a determination of satisfactory programmatic relevance, draft sequencing will be carried out at the PGF.

DATES: To assure consideration, nominations in response to this notice should be received by 4:30 p.m. (e.d.t.), July 14, 2005, to be accepted for merit review. It is anticipated that review will be completed early in the fall of 2005 with draft sequencing at the DOE PGF

to commence early in 2006, conditional upon the provision of high quality DNA.

ADDRESSES: Nominations responding to this notice should be sent to Dr. Daniel W. Drell, Office of Biological and Environmental Research, SC-72, Office of Science, U.S. Department of Energy, 1000 Independence Ave., SW., Washington, DC 20585-1290; e-mail is acceptable and encouraged for submitting nominations using the following addresses: kim.laing@science.doe.gov and daniel.drell@science.doe.gov.

FOR FURTHER INFORMATION CONTACT: Dr. Daniel W. Drell, SC-72, Office of Biological and Environmental Research, Office of Science, U.S. Department of Energy, 1000 Independence Ave. SW., Washington, DC 20585-1290, phone: (301) 903-4742, e-mail:

daniel.drell@science.doe.gov. The full text of this notice is available via the Internet using the following Web site address: <http://microbialgenome.org/>.

SUPPLEMENTARY INFORMATION: The DOE Office of Biological and Environmental Research supports fundamental research for a variety of missions (http://www.science.doe.gov/ober/ober_top.html). Relevant BER programs may include the the Genomics: GTL Program, the Climate Change Research Program, the Terrestrial Carbon Processes Program, the Natural and Accelerated Bioremediation Research (NABIR) Program, the Environmental Management Science Program (EMSP), the Ocean Science Program, and the Program for Ecosystem Science. Additional programs of relevance include the Energy Biosciences, and Nanoscale Science, Engineering and Technology Programs in the Office of Basic Energy Sciences. The Genomics:GTL Program, a partnership with the DOE Office of Advanced Scientific Computing Research, supports research into systems microbiology towards the comprehensive understanding of proteins and protein machines, gene regulatory networks, and microbial communities, and the development of computing and information infrastructure to enable a predictive understanding of biological systems. The Climate Change Research Program supports investigations of microbially-mediated fixation of atmospheric CO₂. The NABIR program supports research on microbial biotransformations and/or immobilization of metal and radionuclide wastes. The EMSP supports research into microbially-mediated biotransformations of DOE-relevant organic wastes such as chlorinated solvents. The Ocean

Sciences Program supports research to understand the ocean carbon cycle. The Program for Ecosystem Science supports research to understand and predict effects of environmental changes associated with energy production on the structure and functioning of important terrestrial ecosystems. In the Office of Basic Energy Sciences, the Energy Biosciences Program supports fundamental research in molecular-level studies on solar energy capture through natural photosynthesis; the mechanisms and regulation of carbon fixation and carbon energy storage; the synthesis, degradation, and molecular interconversions of complex hydrocarbons and carbohydrates. Aligned with this, the Nanoscale Science, Engineering and Technology Program supports studies of novel biosystems and their potential for materials synthesis, chemical catalysis, and materials synthesized at the nanoscale needed to develop future biotechnologies related to energy.

The purpose of this solicitation is to support these key DOE missions by generating and providing initial analyses of microbial DNA sequence information to further the understanding and application of microbiology relating to energy production, biochemical and biomaterials production, environmental carbon management, and environmental cleanup. Both terrestrial and ocean environments in which microbial flora contribute to the sequestration of carbon, particularly carbon dioxide, are of interest. Within the ocean environment, microbial flora that sequester or process carbon dioxide in both the eutrophic and "twilight" zones are of interest.

For more than ten years, sequencing of a variety of microorganisms that live in diverse environments has provided a considerable information base for scientific research related not only to DOE missions, but also to other federal agency missions and U.S. industry. (<http://www.tigr.org/tdb/mdb/mdbcomplete.html> <http://microbialgenome.org/organisms.shtml> and <http://genome.jgi-psf.org/microbial/>). Nonetheless, most of our current knowledge of microbiology still is derived from individual species that either cause disease or grow easily and readily as monocultures under laboratory conditions and are thus easy to study. The preponderance of species in the environment remains largely unknown to science. Many are thought to grow as part of interdependent consortia in which one species supplies a nutrient necessary for the growth of another. Little is known of the

organization, membership, or functioning of these consortia, especially those involved in environmental processes of DOE interest.

Genomic analyses of sequenced microbes have suggested that processes such as lateral gene transfers at various times in the evolutionary history of some microbial lineages may have blurred the understanding of their phylogenetic relationships. For this notice, groups of microbes that may have exchanged (or may be exchanging) genetic information via lateral gene exchange or plasmid mediated exchanges can be proposed if the processes of genetic exchange result in functions relevant to the DOE missions noted above.

Genomic analyses are badly needed of microbial consortia and species refractory to laboratory culture that play important roles in environments challenged with metals, radionuclides, or chlorinated solvents; can potentially generate energy compounds (*e.g.*, hydrogen or methane); or are involved in carbon sequestration. The candidate(s) being proposed must mediate or catalyze metabolic events that contribute to these processes. Priority will be given to studies on those microbes or microbial consortia that can bioremediate metals and radionuclides, degrade biomass and significant biopolymers such as celluloses and lignins, produce potentially useful energy-related materials (H_2 , CH_4 , ethanol, etc.), or fix or sequester CO_2 .

For this notice, candidate organisms (either individual organisms, consortia of organisms, or eukaryotes with small genomes) comprised of archaea, bacteria, fungi, algae, protists, and other eukaryotes with genome sizes not greater than 250 Mbp can be proposed for draft sequencing. For a current list of microbes that have been and are being sequenced by the DOE see <http://microbialgenome.org/organisms.shtml>. For a more comprehensive list of genomes (including microbes) being sequenced in the public sector, see <http://www.genomesonline.org>.

Aims: This request for nominations of candidate sequencing targets has two broad foci:

(1) Single organisms. These may be bacteria, archaea, fungi, microalgae or multicellular organisms with genomes not larger than 250Mb. The criteria that will be used to evaluate proposed candidates for draft sequencing will include:

(a) The candidate has significant relevance to the DOE missions noted above;

(b) To assess suitability for whole genome shotgun sequencing, preliminary data on genome size, repeat content, genome structure, GC content, polymorphism, and other characteristics are provided, especially for larger genomes;

(c) The source of genomic DNA (*i.e.*, strain or isolate, and researcher) is identified, and a clonal sample (or samples with low and characterized polymorphism) is available;

(d) A brief description of post sequencing follow-up work (*e.g.*, a data use plan and how will data be annotated to enable rapid and open use) is included, although funding will not be provided for these activities;

(e) The availability of a DNA/gene transfer system supporting genetic analyses is known;

(f) Biological novelty or uniqueness (*i.e.*, unusual genetically determined characteristics pertinent to DOE missions) is described;

(g) Place in the currently understood, 16s RNA based, "Tree of Life" is identified, *e.g.*, is the proposed candidate in a sparsely populated or more heavily populated section of the tree?

(h) A brief description of the scientific user community for the sequence information, and for the organism in general, is given;

(i) The potential impact on science is large;

(j) Explicit commitment to a data-release schedule, consistent with the guidelines given below is provided.

(k) Explicit commitment to the deposition of a culture of the proposed microbe to a publicly accessible repository is made.

(2) Currently unculturable or hard-to-culture organisms and environmental consortia. The review criteria that will be used to evaluate proposed candidates for draft sequencing will include most of the criteria listed above for single organisms (with less emphasis on genome size/structure, presence/absence of a genetic system, or position in the "Tree of Life" since it is recognized that few data on these attributes will be available), but in addition, the following considerations will be included:

(a) Some measure of the "complexity" of the target consortium being proposed, *e.g.*, approximate number of species, size(s) of genomes, and proportions of different members (it is understood that in most cases, only estimates of these parameters may be available) is discussed. When the environmental consortia are complex, approaches should be described to normalize the DNA libraries in order to reduce the

amount of sequencing required and assure adequate sampling of the complexity of the consortia. Additionally, the proposer(s) should be prepared to work together with JGI scientists to optimize the yield from the sequencing effort required;

(b) Past attempts to cultivate consortium members are described, *e.g.*, have any members of this consortium been successfully cultured;

(c) Some spatial/temporal/hydrochemical/geochemical or other characterization of the environment is given, *e.g.*, the physicochemical parameters of the site from which the selected community is derived; a description of the site contaminants; the accessibility of the site for future sampling; the adequacy of site documentation;

(d) If proposed, technical approaches and technology development specific for defining and isolating members of a given consortium are described;

(e) Some indication of the biological function of the relationships, within consortium members where available, along with a discussion of the scientific and programmatic importance of understanding these relationships is given;

(f) Information where available is given about the phylogenetic position(s) of the members of the consortium and what is known about closely related organisms.

(g) Available informatics tools and annotation plan (*e.g.*, for annotating genes from a consortium analysis or grouping identified genes into a putative "consortium phenotype" within the chosen environment) are described;

(h) Explicit commitment to a data-release schedule, consistent with the guidelines given below is provided.

Scientific community standards regarding access to sequencing data are evolving. BER conforms to the general guidance contained within the Draft Rapid Data Release Policy <http://www.genome.gov/page.cfm?pageID=10506537> for

"community resource projects." The usual and customary practice for the JGI is to put all sequencing data up on its Web site (<http://www.jgi.doe.gov>) at frequent and periodic intervals.

However, for the purposes of this notice, BER does not regard individual genome sequencing efforts involving less than 250Mb, or microbial community sequencing efforts, as requested herein, as "community resource projects" within the definition of the Draft Rapid Data Release policy. BER's position, which is provisional and subject to evolution, is that no more than 3 months from the completion of a "first

assembly" of the sequence for a single-genome project, the data will be released on the JGI web site or to a publicly accessible database with no use restrictions. For microbial community projects, the JGI will conduct normal QA/QC assessments on the sequence output (at approximately 2 X coverage), then discuss with the proposer(s) and with BER staff the extent to which sequencing will be continued to achieve a satisfactory genomic "view" of the selected microbial community. From the time of initiation of this discussion, not more than 3 months will be permitted to elapse before unconditional release of these data. Proposers should clearly understand that the priority in the sequencing queue that a selected project is given may be linked to the willingness of the proposer(s) to shorten this "embargo" period. BER is fully aware that some ambiguity remains in the precise initiation of this embargo period but stresses its intention and commitment to the rapid release, without any use restrictions, of this data into publicly accessible databases.

Upon selection of a nominated microbial sequencing target, BER expects that Principal Investigators will collaborate with the JGI by providing high quality, high MW genomic DNA for library construction as well as assisting in annotating the draft sequence data until a sufficiently complete annotation is achieved, understanding that this will be sensitive to hypothetical gene predictions and the usual uncertainties of annotation. Notification of successful proposals will take place sometime in November 2005 at which time the successful proposer is expected to work out a detailed and mutually satisfactory User Agreement with the JGI. This User Agreement will specify the expectations of the proposer and the commitment of JGI resources to the project, including the amount of sequencing capacity or megabases to be sequenced. *Sequencing will NOT begin prior to the finalization of this User Agreement.* Thus proposers are strongly encouraged to begin preparation of DNA BEFORE notification of successful proposals because from the date of the conclusion of the User Agreement, the proposer is expected to furnish the JGI with usable, high quality DNA within 6 months or risk losing her/his place in the sequencing. A separate communication with the detailed requirements for DNA will be sent to proposers whose nominations are accepted for sequencing. Following data acquisition and annotation, DOE expects that Principal Investigators whose nominations have been sequenced will

make good faith efforts to publish the results of their subsequent work in the open scientific literature, including both the genome sequences of the organisms sequenced under this notice as well as the annotation. BER also expects the Principal Investigator of a selected effort to either deposit a culture of the microbe or consortium into a publicly accessible collection or repository, or make it available directly so others can have access. These parties are encouraged to create process- and cost-effective partnerships that will maximize data production and analysis, data dissemination, and progress towards understanding basic biological mechanisms that can further the aims of this effort. Additionally, it must be explicitly understood that DOE will provide an assembled and computationally annotated draft (roughly 6 X; carried out in a paired-end sequencing approach) sequence of the microbe(s) selected, but that research using that sequence data should be funded from separate sources and/or separate solicitations. Finally, there is no commitment to finish a given drafted sequence, although this option may be considered at a later time for a selected subset of proposed candidates.

Submission Information: Interested parties should submit a brief white paper to either of the foci given above, consisting of not more than 5 pages of narrative exclusive of attachments (which should be kept to a minimum) responding to each of the specific criteria set forth. Electronic submission to (kim.laing@science.doe.gov and daniel.drell@science.doe.gov) is strongly encouraged. It is expected that the Principal Investigator will serve as the main point of contact for additional information on the nominated microbe. Nominations must contain a very short abstract or project summary and a cover page with the name of the applicant, mailing address, phone, fax, and e-mail. The nomination should include 2-page curriculum vitae of the key investigators; letters of intent (or e-mails) from collaborators (suggesting the size of the interested community) are permitted.

Nominations will be reviewed relative to the scope and research needs of the BER programs cited above. A brief response to each nomination will be provided electronically following merit and programmatic reviews.

Other useful Web sites include:

DOE JGI Microbial Sequencing Priorities for FY2005: <http://microbialgenome.org/>.

DOE Joint Genome Institute Microbial Web Page—<http://genome.jgi-psf.org/microbial/index.html>.

GenBank Home Page—<http://www.ncbi.nlm.nih.gov>.

DOE Genomics: GTL—<http://DOEGenomestolive.org>.

DOE Natural and Accelerated Bioremediation Research (NABIR) Program—<http://www.lbl.gov/nabir>.

Climate Change Research Program: http://www.science.doe.gov/ober/CCRD_top.html.

Terrestrial Carbon Processes Program: <http://www.science.doe.gov/ober/CCRD/tcp.html>.

Environmental Management Science Program (EMSP): http://www.science.doe.gov/ober/ERSD/ersd_ems.html.

Ocean Science Program: <http://www.science.doe.gov/ober/CCRD/oceans.html>.

Program for Ecosystem Research: <http://www.science.doe.gov/ober/CCRD/per.html>.

Ari Patrinos,

Associate Director of Science for Biological and Environmental Research.

[FR Doc. 05-5492 Filed 3-18-05; 8:45 am]

BILLING CODE 6450-01-P

DEPARTMENT OF ENERGY

Federal Energy Regulatory Commission

[Docket Nos. ER05-20-000 and ER05-20-001]

New Dominion Energy Cooperative; Notice of Issuance of Order

March 14, 2005.

New Dominion Energy Cooperative (New Dominion) as amended, filed an application for market-based rate authority, with an accompanying rate schedule. The proposed rate tariff provides for wholesale sales of energy and capacity at market-based rates. New Dominion also requested waiver of various Commission regulations. In particular, New Dominion requested that the Commission grant blanket approval under 18 CFR part 34 of all future issuances of securities and assumptions of liability by New Dominion.

On March 8, 2005, the Commission granted the request for blanket approval under part 34, subject to the following:

Any person desiring to be heard or to protest the blanket approval of issuances of securities or assumptions of liability by New Dominion should file a motion to intervene or protest with the Federal Energy Regulatory Commission, 888 First Street, NE., Washington, DC 20426, in accordance with Rules 211 and 214 of the Commission's Rules of

Practice and Procedure. 18 CFR 385.211, 385.214 (2004).

Notice is hereby given that the deadline for filing motions to intervene or protest is April 7, 2005.

Absent a request to be heard in opposition by the deadline above, New Dominion is authorized to issue securities and assume obligations or liabilities as a guarantor, indorser, surety, or otherwise in respect of any security of another person; provided that such issuance or assumption is for some lawful object within the corporate purposes of New Dominion, compatible with the public interest, and is reasonably necessary or appropriate for such purposes.

The Commission reserves the right to require a further showing that neither public nor private interests will be adversely affected by continued approval of New Dominion's issuances of securities or assumptions of liability.

Copies of the full text of the Commission's Order are available from the Commission's Public Reference Room, 888 First Street, NE., Washington, DC 20426. The Order may also be viewed on the Commission's Web site at <http://www.ferc.gov>, using the eLibrary link. Enter the docket number excluding the last three digits in the docket number filed to access the document. Comments, protests, and interventions may be filed electronically via the Internet in lieu of paper. See, 18 CFR 385.2001(a)(1)(iii) and the instructions on the Commission's Web site under the "e-Filing" link. The Commission strongly encourages electronic filings.

Magalie R. Salas,
Secretary.

[FR Doc. E5-1200 Filed 3-18-05; 8:45 am]

BILLING CODE 6717-01-P

DEPARTMENT OF ENERGY

Federal Energy Regulatory Commission

[Docket Nos. TX05-1-000 and TX05-1-002]

East Kentucky Power Cooperative, Inc.; Notice of Filing

March 11, 2005.

Take notice that on March 4, 2005, East Kentucky Power Cooperative, Inc. (East Kentucky) submitted for filing additional information in response to the Commission's order issued January 6, 2005, requesting the submission of additional information regarding the application filed October 1, 2004, by East Kentucky in the above-docketed proceeding.

Any person desiring to intervene or to protest this filing must file in accordance with Rules 211 and 214 of the Commission's Rules of Practice and Procedure (18 CFR 385.211, 385.214). Protests will be considered by the Commission in determining the appropriate action to be taken, but will not serve to make protestants parties to the proceeding. Any person wishing to become a party must file a notice of intervention or motion to intervene, as appropriate. Such notices, motions, or protests must be filed on or before the comment date. Anyone filing a motion to intervene or protest must serve a copy of that document on the Applicant and all parties to this proceeding.

The Commission encourages electronic submission of protests and interventions in lieu of paper using the "eFiling" link at <http://www.ferc.gov>. Persons unable to file electronically should submit an original and 14 copies of the protest or intervention to the Federal Energy Regulatory Commission, 888 First Street, NE., Washington, DC 20426.

This filing is accessible on-line at <http://www.ferc.gov>, using the "eLibrary" link and is available for review in the Commission's Public Reference Room in Washington, DC. There is an "eSubscription" link on the Web site that enables subscribers to receive e-mail notification when a document is added to a subscribed docket(s). For assistance with any FERC Online service, please e-mail FERCOnlineSupport@ferc.gov, or call (866) 208-3676 (toll free). For TTY, call (202) 502-8659.

Comment Date: 5 p.m. eastern time on March 21, 2005.

Magalie R. Salas,
Secretary.

[FR Doc. E5-1199 Filed 3-18-05; 8:45 am]

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DEPARTMENT OF ENERGY

Federal Energy Regulatory Commission

[Docket Nos. ER05-570-000 and ER05-570-001]

Hot Spring Power Company, LP; Notice of Issuance of Order

March 14, 2005.

Hot Spring Power Company, LP (Hot Spring), as amended, filed an application for market-based rate authority, with an accompanying rate tariff. The proposed rate tariff provides for wholesale sales of energy, capacity and ancillary services at market-based