Acronyms and Abbreviations

A² authorities and accountabilities

API application programming interface

BRENDA BRaunschweig ENzyme DAtabase

CAMERA Community Cyberinfrastructure for Advanced Marine Microbial Ecology Research and Analysis

CARO Common Anatomy Reference Ontology

CAZy Carbohydrate-Active enZYmes database

CBoL Consortium for the Barcode of Life

CBP consolidated bioprocessing

CheBI Chemical Entities of Biological Interest

ChIP chromatin immunoprecipitation

CL cell type ontology

CMR Comprehensive Microbial Resource

CO₂ carbon dioxide

Co-IP co-immunoprecipitation

CPRO cardio pulmonary respiratory ontology

CRISPR clustered regularly interspaced short palindromic repeats

DBMS database management system

DNA deoxyribonucleic acid

DOE Department of Energy

EM electron microscopy

EMSA electrophoretic mobility shift assay

EML environmental markup language

EnvO environmental ontology

ESG Earth System Grid II

ExPASy Expert Protein Analysis System

ESTs expressed sequence tags

FIGfams protein families generated by the Fellowship for Interpretation of Genomes

FISH fluorescence in situ hybridization

FMA Foundational Model of Anatomy

FMP Foundational Model of Physiology

FTP file transfer protocol

GEBA Genomic Encyclopedia of Bacteria and Archaea

GEO Gene Expression Omnibus

GH glycoside hydrolase

GKB GTL Knowledgebase

GO Gene Ontology

ESTs expressed sequence tags

GOS Global Ocean Sampling

GSC Genomic Standards Consortium

GT glycosyl transferase

GTL DOE's Genomics:GTL program (formerly Genomes to Life)

HUPO Human Proteome Organization

ICAT isotope-coded affinity tag

ICoMM International Census of Marine Microbes

IMG/M DOE Joint Genome Institute's Integrated Microbial Genome/ Metagenome database

INCITE DOE's Innovative and Novel Computational Impact on Theory and Experiment program

ISCB International Society for Computational Biology

ITRAQ isobaric tag for relative and absolute quantitation

JGI DOE's Joint Genome Institute

KEGG Kyoto Encyclopedia of Genes and Genomes

LANL DOE's Los Alamos National Laboratory

LBNL DOE's Lawrence Berkeley National Laboratory

LIMS Laboratory Information Management System

LLNL DOE's Lawrence Livermore National Laboratory

MALDI-TOF matrix-assisted laser desorption/ ionization–time of flight

MeDICi Middleware for Data-Intensive Computing

MGED Microarray and Gene Expression Data

MIAME Minimum Information about a Microarray Experiment

MIAPE Minimum Information about a Proteomics Experiment

MIGS Minimum Information about a Genome Sequence

MIMIx Minimum Information Required for reporting a Molecular Interaction Experiment

MIMS Minimum Information about a Metagenome Sequence

mRNA messenger RNA

MS mass spectrometry

NAD nicotinamide adenine dinucleotide

NCBI National Center for Biotechnology Information

ncRNA noncoding RNA

NDB Nucleic Acid Database

NMR nuclear magnetic resonance

NPP net primary production

OBER Office of Biological and Environmental Research

OBO Open Biomedical Ontologies

ORNL DOE's Oak Ridge National Laboratory

OWL Web ontology language

PaTO phenotypic quality ontology (formerly phenotype and trait ontology)

PDB Protein Data Bank

PEDRo Proteome Experimental Data Repository

Pfam Protein Families Database

PI principal investigator

PMBMS pyrolysis molecular beam mass spectrometry

PNNL DOE's Pacific Northwest National Laboratory

PRISM PNNL's Proteomics Research Information Storage and Management system

PRO protein ontology

PSI Proteomics Standards Initiative

QA quality assurance

QC quality control

R² roles and responsibilities

RNA ribonucleic acid

RNAO RNA ontology

rRNA ribosomal RNA

RuBisCo ribulose-1,5-bisphosphate carboxylase/ oxygenase

SBML systems biology markup language

SciDAC DOE's Scientific Discovery through Advanced Computing program

SCOP Structural Classification of Proteins

SILAC stable isotope labeling with amino acids in cell culture

SNPs single nucleotide polymorphisms

SO sequence ontology

SOA service-oriented architecture

SOAP (formerly Simple Object Access Protocol)

SOPs standard operating procedures

SSU rRNA small subunit rRNA

TF transcription factor

TFBS transcription factor–binding site

TIGR The Institute for Genomic Research

TRN transcriptional regulatory networks

tRNA transfer RNA

TSSs transcription start sites

UDDI Universal Description, Discovery, and Integration

UniProt Universal Protein Resource

UPSIDE uniform principle for sharing integral data and materials expeditiously

VIMSS Virtual Institute for Microbial Stress and Survival

XML Extensible markup language

Y2H Yeast two-hybrid