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A Unified Nomenclature for Peroxisome Biogenesis Factors

Ben Distel,* Ralf Erdmann,‡ Stephen J. Gould,§ Günter Blobel,|| Denis I. Crane,¶ James M. Cregg,** Gabriele Dodt,‡ Yukio Fujiki,‡‡ Joel M. Goodman,§§ Wilhelm W. Just,||| Jan A.K.W. Kiel,¶¶ Wolf-Hubert Kunau,‡ Paul B. Lazarow,*** Guy P. Mannaerts,‡‡‡ Hugo W. Moser,§§§ Takashi Osumi,||| Richard A. Rachubinski,¶¶¶ Adelbert Roscher,**** Suresh Subramani,‡‡‡‡ Henk F. Tabak,* Toshiro Tsukamoto,||| David Valle,§§§§ Ida van der Klei,¶¶ Paul P. van Veldhoven,‡‡‡ and Marten Veenhuis¶¶

*Department of Biochemistry, Academical Medical Centre, University of Amsterdam, Meibergdreef 15, 1105 AZ Amsterdam, The Netherlands; †Institut für Physiologische Chemie, Ruhr-Universität Bochum, 44780 Bochum, Germany; ‡Departments of Biological Chemistry and Cell Biology and Anatomy, The Johns Hopkins University School of Medicine, Baltimore, Maryland 21205; ‡‡Laboratory of Cell Biology, Howard Hughes Medical Institute, The Rockefeller University, New York 10021; ¶The School of Biomolecular and Biomedical Science, Griffith University, Brisbane, QLD 4111, Australia; **The Department of Chemistry, Biochemistry, and Molecular Biology, Oregon Graduate Institute of Science and Technology, Portland, Oregon 97291; ‡‡‡Department of Biology, Faculty of Science, Kyushu University, Fukuoka, Japan; §§Department of Pharmacology, University of Texas Southwestern Medical Center, Dallas, Texas 75235; |||Institute für Biochemie I, D-69120 Heidelberg, Germany; ¶¶Department of Microbiology, Groningen Biomolecular Sciences and Biotechnology Institute, Biological Centre, University of Groningen, Kerklaan 30, 9751 NN Haren, The Netherlands; ***The Department of Cell Biology and Anatomy, Mount Sinai School of Medicine, New York 10029; ‡‡‡‡Afdeling Farmakologie, Faculeit Geneeskunde, Katholieke Universiteit Leuven, B-3000 Leuven, Belgium; §§§The Kennedy Krieger Institute and The Department of Neurology, The Johns Hopkins University School of Medicine, Baltimore, Maryland 21205; |||‡‡‡Department of Life Science, Himeji Institute of Technology, Hyogo, Japan; ¶¶¶Department of Anatomy and Cell Biology, University of Alberta, Edmonton, Canada; ****Department of Clinical Chemistry and Biochemistry, Children's Hospital, Munich, Germany; ‡‡‡‡The Department of Biology, The University of California, San Diego, La Jolla, California 92093-0322; §§§§The Howard Hughes Medical Institute and the Department of Pediatrics, The Johns Hopkins University School of Medicine, Baltimore, Maryland 21205

FOR the past 10 years, there has been substantial progress in the field of peroxisome biogenesis. One key to this progress has been the use of genetic approaches in a wide variety of experimental organisms (4, 8, 11, 15, 18, 21, 26, 35, 38, 47, 48). To date, these systems have been used to identify thirteen proteins required for peroxisome biogenesis, three of which have also been shown to be defective in the lethal peroxisome biogenesis disorders. However, the diversity of experimental systems has also led to a profusion of names for peroxisome assembly genes and proteins. These include the acronyms PAS, PAF, PER, PAY, PEB, and PMP and span an even greater array of numbering systems. At the request of the Editors of *The Journal of Cell Biology* and for the benefit of all concerned, we considered several options for gene and protein names, numbering systems, and possible definitions for the types of genes and protein to be included. We propose here a unified protein and gene nomenclature for peroxisome biogenesis factors.

Proteins involved in peroxisome (microbody) biogenesis (inclusive of peroxisomal matrix protein import, membrane biogenesis, peroxisome proliferation, and peroxi-

some inheritance) will be designated peroxins, with PEX representing the gene acronym. However, even though defects in peroxisomal metabolic enzymes or transcription factors may affect peroxisome proliferation and/or morphology, such proteins shall not be included in this group. The proteins and genes will be numbered by date of published characterization, both for known factors and for those identified in the future. When necessary, species of origin may be specified by one letter abbreviations for genus and species (e.g., *ScPEX1*¹ for the *Saccharomyces cerevisiae* PEX1 gene). To minimize ambiguities in naming additional proteins that may be identified in the future, we urge authors before publication to contact an ad hoc nomenclature committee (see below) who will be responsible for numbering new peroxins.

The new nomenclature for peroxisome assembly genes and proteins is outlined in Table I. Questions should be addressed to the first three authors of this letter, who organized the nomenclature revision and who will comprise the nomenclature committee for the next 12 months. We thank *The Journal of Cell Biology* for stimulating the unification of our nomenclature and for providing the opportunity to present our resolution. We hope that these

Please address all correspondence to Dr. Stephen J. Gould, Departments of Biological Chemistry and Cell Biology and Anatomy, The Johns Hopkins University School of Medicine, 725 North Wolfe Street, Baltimore, MD 21205. Tel: (410) 955-3085. Fax: (410) 955-0215. E-Mail: Stephen.Gould@gmail.bs.jhu.edu

1. Abbreviations used in this paper: Sc, *Saccharomyces cerevisiae*; Pp, *Pichia pastoris*; Rn, *Rattus norvegicus*; Hs, *Homo sapiens*; Pa, *Podospira anserina*; Hp, *Hansenula polymorpha*; Yl, *Yarrowia lipolytica*; Cb, *Candida boidinii*; PBD, peroxisome biogenesis disorder.

Table I. Description of Peroxins and PEX Genes

PEX gene	Peroxin characteristics	Former name
PEX 1	117–127 kD AAA ATPase; subcellular distribution is unknown.	<i>ScPAS1</i> (12) <i>PpPAS1</i> (16)
PEX 2	C ₃ HC ₄ zinc-binding integral peroxisomal membrane protein; 35–52 kD; mutations responsible for complementation group 10 of the PBD.	<i>RnPAF1</i> (33) <i>HsPAF1</i> (29) <i>PaCAR1</i> (2) <i>PpPER6</i> (40)
PEX 3	51–52-kD integral peroxisomal membrane protein lacking similarity to other proteins.	<i>ScPAS3</i> (17) <i>HpPER9</i> (1) <i>PpPAS2</i> (43)
PEX 4	21–24-kD peroxisome-associated ubiquitin-conjugating enzyme.	<i>ScPAS2</i> (42) <i>PpPAS4</i> (3)
PEX 5	PTS1 receptor; 64–69-kD protein containing 8–7 tetratricopeptide repeats; localized to the cytoplasm and peroxisome; mutations responsible for complementation group 2 of the PBD.	<i>PpPAS8</i> (24) <i>ScPAS10</i> (37) <i>HsPXR1</i> (5) <i>HsPTS1R</i> (13, 44) <i>HpPER3</i> (36) <i>HpPAH2</i> (27) <i>Y1PAY32</i> (31)
PEX 6	Belongs to the AAA family of ATPases; 112–127 kD; localized to cytoplasm and peroxisome; mutations responsible for complementation group 4 of the PBD.	<i>PpPAS5</i> (30) <i>ScPAS8</i> (39) <i>Y1PAY4</i> (25) <i>RnPAF2</i> (34) <i>HsPXAAA1</i> (45)
PEX 7	PTS2 receptor; 42-kD protein containing 6 WD40 repeats localized to the cytoplasm and peroxisome.	<i>ScPAS7</i> (23) <i>ScPEB1</i> (46)
PEX 8	71–81-kD peroxisome-associated protein containing a PTS1 signal.	<i>HpPER1</i> (41) <i>PpPER3</i> (20)
PEX 9	42-kD integral peroxisomal membrane protein lacking similarity to other proteins.	<i>Y1PAY2</i> (6)
PEX 10	C ₃ HC ₄ zinc-binding integral peroxisomal membrane protein; 34–48 kD.	<i>HpPER8</i> (32) <i>PpPAS7</i> (19)
PEX 11	27–32-kD peroxisome-associated protein involved in peroxisome proliferation.	<i>ScPMP27</i> (9, 22) <i>CbPMP30</i> (28)
PEX 12	48-kD C ₃ HC ₄ zinc-binding integral peroxisomal membrane protein.	<i>PpPAS10</i> (18)
PEX 13	SH3-containing, 40–43-kD integral peroxisomal membrane protein; binds the PTS1 receptor (7, 10, 14).	

changes will make it easier for the general scientific community, as well as ourselves, to follow the interesting and exciting research on peroxisome biogenesis.

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