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Chapter 1 : BEC Foundations of Recombinant Microorganisms for Biomanufacturing - BTEC

Books by S. John Pirt, The Penicillin Fermentation, Stoichiometry & Kinetics of Microbial Growth (Greenwich Readers), Principles of microbe and cell cultivation, Control of Foam Formation & Antifoam Action in Aerated Systems, Product Formation in Cultures of Microbes & the Microbial Growth Process (Greenwich Readers), Total Biocombustion of Sewage Sludge by the Bicycle Process, Stoichiometry.

This is particularly important for research in microbial physiology, as the composition and behavior of microbes is strongly dependent on their growth environment. It has been pointed out repeatedly by eminent microbiologists that we should give more attention to the media and culturing conditions. However, this is obviously not adhered to with sufficient rigor as mistakes in basic cultivation principles are frequently found in the published research literature. The most frequent mistakes are the use of inappropriate growth media and little or no control of the specific growth rate, and some examples will be discussed here in detail. Therefore, this is a call for better microbiological craftsmanship when cultivating microbial cultures for physiological experiments. This call is not only addressed to researchers but it is probably even more important for the teaching of our discipline. Pirt stands for a quantitative approach to microbiology. During the first year of my Ph. Here, together with editorial comments pointing out the significance of individual articles, I found research papers, reviews and personal comments on basic, and often simple, questions concerning stoichiometry, kinetics, cultivation techniques, and physiology, written in unmatched clarity. Much later, when giving lecture and practical courses on microbial growth physiology and stress response to masters and Ph. D students, it became obvious to me that, for far too long, the teaching of the basic knowledge of essential techniques for cultivating microbial cells, of the advantages and disadvantages of different methods, and of the consequences on the experimental results obtained, had been neglected. This is mirrored by the fact that the commonly used microbiology text books cover this area in a superficial, inadequate way. Only in this way one gets an impression of the quality of the data and how to rate and interpret a piece of work. Moreover, the basic mostly stoichiometric points addressed below are valid also for microbial growth in nature and, therefore, they are relevant to biogeochemical issues, too. It is with this background in mind that I write these comments which for some may be considered to be rather a personal view on the current state of experimentation in research on microbial physiology. When preparing this contribution I went back to some of the early literature and â€" somewhat to my surprise â€" found that many of the points addressed here had actually been critically referred to much earlier. Unfortunately, it appears that during the last 50â€"60 years since the time of Monod and Pirt their messages have not reached the fertile ground they deserve. This started after the introduction of the technique for cultivating submerged batch cultures in shake flasks, which allowed the basic principles of stoichiometry of nutrition and cellular composition to be confirmed and established experimentally. The invention of the continuous chemostat culture technique the principle was already being used since the s in chemical synthesis and engineering and fermentations, Haddon, see also Panikov, then allowed microbial populations at physiological states set by the investigator to be maintained over an extended period of time. This again permitted reproducible examination of fundamental physiological questions during growth under defined environmental conditions as a function of specific growth rate. Another milestone with respect to understanding how microbial cells respond to their environment through regulating their physiological activities was the discovery of coordinate gene expression of lactose-utilizing enzymes in E. This led to the identification of operons and regulons and their master regulatory compounds. During this period microbial physiologists were driven by the desire to understand how a cell integrates the many reactions at the molecular and biochemical levels into a coordinated behavior that allows survival, successful competition for nutrients and hence proliferation. Outstanding accounts of the concepts and achievements of this time can be found in a fascinating collection of excellently written original articles, which also includes comments from the editor; this book should be basic reading for every microbiologist Dawson, In addition, several text books were

published at the end of this period e. The Shift to Novel Molecular Methods: This started in the mids with a method for sequencing proteins, followed some 20 years later by a technique that allowed the sequencing of DNA. Since the s, various methods have been developed for manipulating and synthesizing DNA and RNA, and for separating, visualizing and quantifying other cellular constituents, notably proteins and metabolites. Many of these methods allow the totality of certain molecular species and events to be monitored. In addition, the latter allows unanticipated aspects to be detected and for the system to be approached without pre-conceived ideas. The text book by Neidhardt et al. In combination with the ability to handle and analyze large data sets with computational informatics, this allows access to genomes, transcriptomes, proteomes, or metabolomes, not only of microbial populations in laboratory cultures, but also of natural consortia, and probably in the near future even routinely at the single cell level. Often, similar questions are addressed today as were posed earlier in the heydays of classic microbial physiology e. However, in many of the papers being published at present that are addressing physiological questions, I recognize a considerable imbalance in the attention given to molecular issues compared with that given to the media and cultivation conditions. The phenomenon is not new, though. For example, in his preface, Dawson had already commented: Perhaps it is because very few textbooks give growth more than a cursory mention that its basic significance is not generally recognized: The omission often leads to superficial experimentation and much wasted effort, thus cluttering the literature with a lot of meaningless data. This holds true not only for all cellular constituents and metabolic pools but also for the elemental composition of the microbial biomass; the latter is particularly relevant when considering quantitative nutritional aspects. Herbert phrased this rather explicitly more than 50 years ago: So much is this the case that it is virtually meaningless to speak of the chemical composition of a micro-organism without at the same time specifying the environmental conditions that produced it. Whereas the cellular fraction of C, O, and H remains within a narrow range, the portion with the major nutrients N, P, S, K, and Mg may actually vary 3- to fold. The fraction of trace elements can easily vary by two or more orders of magnitude Egli, Its absence from catalytic centers of, e. Needless to say, a growth medium should contain all these components in sufficient amounts in order to ensure good healthy and reproducible growth of a microbial culture during all phases of cultivation. Average elemental composition A and content of major cellular polymeric constituents of microbial biomass B , and range of variation with the corresponding environmental conditions condensed from Egli, The first point concerns the use of in appropriate media, and includes simple stoichiometric issues of nutrition; this point is independent of the method employed for culturing cells, i. The second point is a certain lack of control of specific growth rate over a sufficiently long time to perform experiments under balanced growth conditions; this point applies in particular to experiments performed in batch culture. This contribution will focus on these two points only, although a number of other points might also need more attention. They provide a stoichiometric link between the amount of a nutrient supplied in a medium and the biomass formed from it. The first growth yield factors were actually reported by Raulin, a student and collaborator of Pasteur cited in Pirt, , and these factors have a long tradition and have been confirmed for many different organisms. They can be applied for the design, analysis and optimization of media used for cultivation of bacterial cultures, including molds, yeasts, algae, and protozoa Pirt, ; Egli, Approximate yield factors for the quantitatively most relevant elements are listed in Table 1. Growth yield factors can be defined not only for nutrients that are built into the biomass, but also for electron donors and acceptors that serve as energy sources and terminal electron acceptors Egli, Yields vary according to cultivation conditions and those listed in Table 1 are average values relevant for carbon-limited growth. For example, when growing C-limited, microbes usually produce 8 g of dry biomass from 1 g of nitrogen; however, if the nitrogen source is limiting growth and carbon plus all other nutrients are in excess, many organisms are able to store excess available carbon in the form of intracellular reduced carbonaceous reserve materials, such as glycogen or PHB. This nutrient determines the requirement for all other sources of nutrients that have to be supplied in the medium. In a good medium an excess of all non-limiting nutrients is supplied and typical excess factors are also listed in Table 1. The growth yield factors given in Table 1 can be used to

design and to analyze mineral media. For simplicity, we concentrate here on defined mineral media to illustrate some of the quantitatively most critical points the case of complex media will be treated later. An example is given in Table 2 for a medium that has been widely used for cultivating E. Phosphorus, potassium and sulfur are supplied in large excess due to the buffering system used, whereas magnesium is most probably not present in sufficient excess. Availability of all trace elements, in particular of iron, is theoretically severely restricted in this medium. Thus, trace elements in particular were supplied as impurities rather than in defined amounts. In practice, however, there are a number of additional factors that influence the quality and performance of a medium pH, procedure of sterilization or temperature of storage, and occasionally also other unknown factors. Therefore, it is useful to confirm the growth-limiting factor for a given experimental setup with hard data. The nature of a growth-limiting nutrient in a particular medium and the growth yield factor can be confirmed experimentally in a straightforward way, namely by determining the concentration of biomass formed as a function of the concentration of a particular nutrient keeping all other medium components unchanged. This can be done either in batch experiments measuring the final concentration of dry biomass formed or in continuous culture at a constant dilution rate monitoring the steady-state dry biomass concentration. Examples are shown in Figure 1 for a bacterial and a yeast strain. The concentration of the produced biomass must be strictly proportional to the concentration of the limiting nutrient and the straight line should pass through the origin; if this is not the case, biomass formation is influenced by one or more unknown additional factors [discussed in Egli and Egli]. Also, in most of the examples given in Figure 1 the data suggest a clear-cut transition from nutrient-limited to non-limited conditions. The graph for the sulfur source, where the transition between the horizontal and the proportional growth region appears to occur gradually rather than abruptly, may indicate a more complex interaction of two or maybe even more factors simultaneously see e. Unfortunately, such basic tests are rarely carried out or reported, and many examples of the use of media that do not satisfy the basic requirements discussed above can be found in the literature. Experimental confirmation of stoichiometric limitation of growth of different nutrients for a bacterial Cometta et al. Both microbial strains were cultivated in a chemostat culture at a fixed dilution rate. A distinct transition from limitation to excess is observed for carbon-, nitrogen, and phosphorus-limited growth, whereas the transition between limitation and excess is not as distinct in the case of magnesium and sulfur. A,B Rearranged from Cometta et al. C Rearranged from Egli An extended review of how stoichiometric limitation of different types of nutrients affects gross composition and physiology of microbial cells during batch cultivation was published some time ago Wanner and Egli, The patterns of batch growth curves, dynamics of cellular composition, substrate utilization and product formation are shown in Figure 2 for a culture of Klebsiella pneumoniae cultivated in the same defined mineral medium but limited by either the source of carbon glucose , nitrogen ammonia , phosphorus phosphate , sulfur sulfate , or potassium K. In this example, the initial concentration of the limiting nutrient in the medium was chosen such that it should support the formation of 2 g L-1 of dry biomass indicated by the gray band. The data give an impression of the importance for ensuring cultivation under explicitly known nutritional conditions and support the elemental yield factors listed in Table 1. They also point to the effects of restricted nutrient availability, and visualize the effect of shifts in the nature of the limiting nutrient during batch cultivation on the growth behavior of microbial cultures. For example, judged from the pattern of the biomass concentration, the transition from C-excess to C-limitation occurs abruptly, whereas the transition from K-excess to K-limitation is not obvious and can be assessed only from the experimentally determined K-concentrations in the medium. In all cases, consumption of excess glucose continued at a similar rate after the different nutrients became limiting. In the S-limited data set, the pattern recorded for the concentrations of remaining sulfate and produced dry biomass suggests the transition from a low-affinity to a high-affinity transport system. Patterns of growth, nutrient consumption, product formation and gross cellular composition during batch growth of Klebsiella pneumoniae in a defined mineral medium limited by different nutrients. Top panels show concentrations of dry biomass and limiting nutrient; middle panels show concentrations of residual glucose and acetate formed in the medium; the bottom

panels show composition of biomass with respect to total protein and carbohydrates. Rearranged from Wanner and Egli Although the two concepts of cultivation are different, both allow environmental conditions for the culture to be maintained to ensure balanced growth conditions long enough to perform physiological experiments â€" if used properly. Some Remarks on Chemostat Cultivation The technique of continuous cultivation allows single-celled organisms to be cultured under balanced growth conditions over virtually the whole range of specific growth rates without changing the medium composition, by simply setting the dilution rate, D. An important advantage of chemostat cultivation is that cell density has â€" in theory â€" no effect on the physiological state as long as the limitation regime remains the same Herbert et al. This was experimentally demonstrated for E. However, recently it was found that there are exceptions to the rule, because cell density was shown to influence the speed of selection for mutants with improved transport affinity for the growth-limiting nutrient Wick et al. Nevertheless, in general, biomass concentrations in a chemostat culture can be adjusted according to analytical needs with no effect on the cellular physiology. Usually, very low cell densities are favorable for investigating growth kinetics Senn et al. Inappropriate use of continuous culture, however, may result from the use of unbalanced media that are not distinctly limited, or in which the growth-limiting factor shifts along with changes in the dilution rate. How this may happen and what the consequences are is visualized in the conceptual scheme in Figure 3A , which is linked with actual experimental data extracted from several reports on growth of Klebsiella pneumonia in chemostat culture with glycerol and ammonia as C- and N-source, respectively Figure 3B. In this example, a strain is cultivated in a chemostat at a fixed D and biomass production is studied as a function of the C:

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Chapter 2 : - Stoichiometry and Kinetics of Microbial Growth (Pirtferm Papers) by S.J Pirt

Description: Microbial Growth Kinetics opens with a critical review of the history of microbial kinetics from the 19th century to the present day. The results of original investigations into the growth of soil microbes in both laboratory and natural environments are summarised.

The use, distribution or reproduction in other forums is permitted, provided the original author s or licensor are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms. This article has been cited by other articles in PMC. Abstract Virtually every microbiological experiment starts with the cultivation of microbes. This is particularly important for research in microbial physiology, as the composition and behavior of microbes is strongly dependent on their growth environment. It has been pointed out repeatedly by eminent microbiologists that we should give more attention to the media and culturing conditions. However, this is obviously not adhered to with sufficient rigor as mistakes in basic cultivation principles are frequently found in the published research literature. The most frequent mistakes are the use of inappropriate growth media and little or no control of the specific growth rate, and some examples will be discussed here in detail. Therefore, this is a call for better microbiological craftsmanship when cultivating microbial cultures for physiological experiments. This call is not only addressed to researchers but it is probably even more important for the teaching of our discipline. Pirt stands for a quantitative approach to microbiology. During the first year of my Ph. Here, together with editorial comments pointing out the significance of individual articles, I found research papers, reviews and personal comments on basic, and often simple, questions concerning stoichiometry, kinetics, cultivation techniques, and physiology, written in unmatched clarity. Much later, when giving lecture and practical courses on microbial growth physiology and stress response to masters and Ph. D students, it became obvious to me that, for far too long, the teaching of the basic knowledge of essential techniques for cultivating microbial cells, of the advantages and disadvantages of different methods, and of the consequences on the experimental results obtained, had been neglected. This is mirrored by the fact that the commonly used microbiology text books cover this area in a superficial, inadequate way. Only in this way one gets an impression of the quality of the data and how to rate and interpret a piece of work. Moreover, the basic mostly stoichiometric points addressed below are valid also for microbial growth in nature and, therefore, they are relevant to biogeochemical issues, too. It is with this background in mind that I write these comments which for some may be considered to be rather a personal view on the current state of experimentation in research on microbial physiology. When preparing this contribution I went back to some of the early literature and â€” somewhat to my surprise â€” found that many of the points addressed here had actually been critically referred to much earlier. Unfortunately, it appears that during the last 50â€”60 years since the time of Monod and Pirt their messages have not reached the fertile ground they deserve. This started after the introduction of the technique for cultivating submerged batch cultures in shake flasks, which allowed the basic principles of stoichiometry of nutrition and cellular composition to be confirmed and established experimentally. The invention of the continuous chemostat culture technique the principle was already being used since the s in chemical synthesis and engineering and fermentations, Haddon, see also Panikov, then allowed microbial populations at physiological states set by the investigator to be maintained over an extended period of time. This again permitted reproducible examination of fundamental physiological questions during growth under defined environmental conditions as a function of specific growth rate. Another milestone with respect to understanding how microbial cells respond to their environment through regulating their physiological activities was the discovery of coordinate gene expression of lactose-utilizing enzymes in E. This led to the identification of operons and regulons and their master regulatory compounds. During this period microbial physiologists were driven by the desire to understand how a cell integrates the many reactions at the molecular and biochemical levels into a coordinated behavior

that allows survival, successful competition for nutrients and hence proliferation. Outstanding accounts of the concepts and achievements of this time can be found in a fascinating collection of excellently written original articles, which also includes comments from the editor; this book should be basic reading for every microbiologist Dawson, In addition, several text books were published at the end of this period e. The Shift to Novel Molecular Methods: This started in the mids with a method for sequencing proteins, followed some 20 years later by a technique that allowed the sequencing of DNA. Since the s, various methods have been developed for manipulating and synthesizing DNA and RNA, and for separating, visualizing and quantifying other cellular constituents, notably proteins and metabolites. Many of these methods allow the totality of certain molecular species and events to be monitored. In addition, the latter allows unanticipated aspects to be detected and for the system to be approached without pre-conceived ideas. The text book by Neidhardt et al. In combination with the ability to handle and analyze large data sets with computational informatics, this allows access to genomes, transcriptomes, proteomes, or metabolomes, not only of microbial populations in laboratory cultures, but also of natural consortia, and probably in the near future even routinely at the single cell level. Often, similar questions are addressed today as were posed earlier in the heydays of classic microbial physiology e. However, in many of the papers being published at present that are addressing physiological questions, I recognize a considerable imbalance in the attention given to molecular issues compared with that given to the media and cultivation conditions. The phenomenon is not new, though. For example, in his preface, Dawson had already commented: Perhaps it is because very few textbooks give growth more than a cursory mention that its basic significance is not generally recognized: The omission often leads to superficial experimentation and much wasted effort, thus cluttering the literature with a lot of meaningless data. This holds true not only for all cellular constituents and metabolic pools but also for the elemental composition of the microbial biomass; the latter is particularly relevant when considering quantitative nutritional aspects. Herbert phrased this rather explicitly more than 50 years ago: So much is this the case that it is virtually meaningless to speak of the chemical composition of a micro-organism without at the same time specifying the environmental conditions that produced it. Whereas the cellular fraction of C, O, and H remains within a narrow range, the portion with the major nutrients N, P, S, K, and Mg may actually vary 3- to fold. The fraction of trace elements can easily vary by two or more orders of magnitude Egli, Its absence from catalytic centers of, e. Needless to say, a growth medium should contain all these components in sufficient amounts in order to ensure good healthy and reproducible growth of a microbial culture during all phases of cultivation. Table 1 Average elemental composition A and content of major cellular polymeric constituents of microbial biomass B , and range of variation with the corresponding environmental conditions condensed from Egli,

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Chapter 4 : Methods for General and Molecular Microbiology : C. A. Reddy :

Get this from a library! Stoichiometry and kinetics of microbial growth Bioenergetics of microbial growth and product formation. [S John Pirt].

Conceived and designed the computational analysis: Performed the computational analysis: Performed the in-vivo experiments: Received Jun 8; Accepted May 8. Copyright Adadi et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are properly credited. This article has been cited by other articles in PMC. Abstract Identifying the factors that determine microbial growth rate under various environmental and genetic conditions is a major challenge of systems biology. While current genome-scale metabolic modeling approaches enable us to successfully predict a variety of metabolic phenotypes, including maximal biomass yield, the prediction of actual growth rate is a long standing goal. This gap stems from strictly relying on data regarding reaction stoichiometry and directionality, without accounting for enzyme kinetic considerations. Here we present a novel metabolic network-based approach, MetabOlic Modeling with ENzyme kineTics MOMENT , which predicts metabolic flux rate and growth rate by utilizing prior data on enzyme turnover rates and enzyme molecular weights, without requiring measurements of nutrient uptake rates. The method is based on an identified design principle of metabolism in which enzymes catalyzing high flux reactions across different media tend to be more efficient in terms of having higher turnover numbers. Extending upon previous attempts to utilize kinetic data in genome-scale metabolic modeling, our approach takes into account the requirement for specific enzyme concentrations for catalyzing predicted metabolic flux rates, considering isozymes, protein complexes, and multi-functional enzymes. These results support the view that a physiological bound on cellular enzyme concentrations is a key factor that determines microbial growth rate. Author Summary While current genome-scale metabolic modeling approaches enable us to successfully predict a variety of metabolic phenotypes, identifying the factors that determine microbial growth rate and the prediction of growth rates under various conditions is still an open challenge. The method is based on a finding that enzymes catalyzing high flux reactions tend to be more efficient in terms of having higher turnover numbers. These results suggest that a bound on cellular enzyme concentrations is a key factor that determines microbial growth rate. Introduction Traditional metabolic modeling techniques involve the reconstruction of kinetic models based on detailed knowledge on enzyme kinetic parameters for all enzymes in a certain system [1]. These models are limited to small-scale systems due to lack of sufficient data on kinetic constants and the highly complex nature of these models. An alternative approach called Constraint-Based Modeling CBM predicts certain steady-state cellular metabolic phenotypes in microorganisms on a genome-scale by relying solely on simple physical-chemical constraints, without requiring enzyme kinetic data [2] , [3] , [4]. CBM is now commonly used for metabolic engineering in microorganisms, predicting the effect of gene knockouts on organism viability [2]. The maximal biomass production rate predicted by FBA reflects optimal yield metabolism and is equal to the assumed uptake rate multiplied by maximal biomass yield. The prediction of actual growth rate by FBA is theoretically possible when experimental measurement of nutrient uptake rates is available and is used to constrain the uptake flux in the model or alternatively, by multiplying FBA-predicted biomass yield with the measured uptake rates. However, experimental studies have shown that microorganisms exhibit non optimal-yield metabolism under various conditions, for example, in the case of over-flow metabolism where excess nutrient uptake is metabolized inefficiently [5] , [6]. In fact, growth rate was found to be inversely correlated with biomass yield in some microorganisms under different growth environments see Section 4 in Supp. Hence, growth rate prediction obtained by FBA reflecting optimal yield metabolism are likely to be unrealistically high in many cases. Predicting the correct growth rate even when nutrient uptake rates are known is a challenging task. A more ambitious conceptual challenge is the prediction of growth rate without measurements of nutrient uptake

rates under a variety of environmental and genetic conditions. This was achieved by accounting for the enzyme concentrations required for catalyzed metabolic flux utilizing data on enzyme kinetic constants , considering a physiological upper bound on the total cellular volume used by metabolic enzymes. Other recent modeling approaches aim to predict cellular metabolism by integrating molecular crowding constraint with kinetic parameters: Another method recently shown to utilize enzyme turnover numbers to improve metabolic flux prediction is Integrative Omics Metabolic Analysis IOMA , requiring further quantitative proteomic and metabolomics data as input [13]. Another method that aims to predict cellular metabolism without requiring nutrient uptake rates is E-flux [14] , which relies on high-throughput gene expression data shown to predict growth rates in a qualitative manner. Still, none of these approaches were shown to successfully predict in a quantitative manner the growth rate of microbes across conditions, without utilizing a-priori data on nutrient uptake rates. In this paper, we present a method, MetabOlic Modeling with ENzyme kineTics MOMENT , for predicting metabolic fluxes and growth rates by accounting for the maximal cellular capacity for metabolic enzymes without the requirement of experimentally determined uptake rates. Extending upon FBAwMC, MOMENT accurately quantifies the enzyme concentrations required for catalyzing each metabolic reaction based on known kinetic constants, accounting for isozymes, protein complexes and multi-functional enzymes. Furthermore, MOMENT is shown to markedly improve the prediction performance of various metabolic phenotypes, including metabolic fluxes and expression level of metabolic genes. We begin our analysis by exploring the relation between enzyme kinetic parameters and measured metabolic flux, showing a design principle in which enzymes catalyzing high flux reactions across different media tend to be more efficient in terms of having higher turnover numbers hence requiring lower concentration to achieve a certain flux rate. This suggests that a a physiological constraint on total cellular enzyme concentration, which underlies MOMENT, significantly affects cellular metabolism and the evolution of enzyme kinetic parameters. Results The evolution of enzyme kinetic parameters optimizes metabolic flux An enzyme turnover number is defined as the maximal number of molecules of substrate that the enzyme can convert to product per catalytic site per unit of time. To infer genome-scale metabolic flux rates, we utilized several dozen metabolic fluxes under various growth rates in glucose minimal media obtained from Ishii et al. Specifically, this was done based on standard quadratic programming optimization by minimizing the Euclidian distance between the predicted and the measured fluxes to fit the predicted fluxes to measured ones [20]. Notably, this analysis does not make usage of kinetic data as input. As an alternative approach for inferring global flux distributions, we employed Flux Balance Analysis, followed by Flux Variability Analysis [21] , to identify metabolic reactions whose flux can be uniquely determined based on stoichiometric mass-balance constraints and maximal biomass yield assumption obtaining overall similar results in the analysis described below for the flux distributions obtained by the two approaches; Table S1 ; Figure S1. When comparing the enzyme kinetic parameters in E. These correlations suggest that higher selection pressure for enzymatic efficiency i. Notably, our results extend upon a recent finding that central metabolic enzymes have higher turnover rates than secondary metabolic enzymes [22] , by considering actual flux rates instead of relying on rough categorization of enzymes to primary and secondary metabolism.

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Chapter 5 : stoichiometry and kinetics of microbial growth | Download eBook pdf, epub, tuebl, mobi

Ecoenzymatic stoichiometry connects the elemental stoichiometry of microbial biomass and detrital organic matter to microbial nutrient assimilation and growth. We present a model that combines the kinetics of enzyme activity and community growth under conditions of multiple resource limitation with elements of metabolic and ecological.

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Growth kinetics are therefore an indispensable tool not only in the applied fields of industrial and environmental biotechnology, but also in fundamental areas such as microbial genetics.

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combines the kinetics of enzyme activity and community growth under conditions of multiple resource limitation with elements of metabolic and ecological stoichiometry theory.

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Stoichiometry of microbial growth. Types of growth media (defined, semi-defined, complex) and media optimization. Quantification of cell growth, growth yields and batch growth kinetics.