# Whole-cell redox biocatalysis driven by photosynthesis – an integrated bioprocess design for phototrophic biocatalysts

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## Summary

Oxygenic photosynthesis constitutes a milestone of natural evolution and manifested in phototrophic organisms, such as cyanobacteria, algae, and plants. In nature, photosynthetic water oxidation served as new source for activated reduction equivalents while  $O_2$ , initially a by-product, accumulated in the environment. Redox enzymes utilizing  $O_2$  as electron acceptor and/ or oxygen donor developed and increased the evolutionary fitness of microorganisms harnessing these enzymes by providing them access to previously inaccessible carbon sources. Today, biocatalysis profits from these enzymes for the selective and specific conversion of substrates to fuels and value-added chemicals under mild reaction conditions. Thus far, redox biotransformations mainly rely on the application of isolated enzymes or chemoheterotrophic whole-cell biocatalysts such as *E. coli* or *Pseudomonas*. In these organisms, energy and reduction equivalents are accessed by the catabolism of carbohydrates such as glucose.

This thesis builds on a new research field that takes advantage of photosynthesis as the milestone of natural evolution. By the use of photoautotrophic organisms as biocatalytic host systems, redox reactions such as the reduction of protons to hydrogen or the oxyfunctionalization of hydrocarbons are fueled with  $O_2$  and/ or reduction equivalents deriving from photosynthetic water oxidation. Photobiocatalysis therefore allows atomefficient biotransformations and enables catalyst (re)generation based on an inorganic and abundant carbon source via  $CO_2$  fixation. In the present work, recombinant cyanobacterial strains harboring different oxygenases acting as redox enzymes were generated and investigated for photosynthesis-driven biocatalysis. Subsequently, biocatalyst, reaction, and process engineering strategies were approached for the bioprocess intensification of hydrocarbon oxyfunctionalizations.

A recombinant photobiocatalyst was constructed by the genetic introduction of the threecomponent alkane monooxygenase AlkBGT into the cyanobacterium *Synechocystis* sp. PCC 6803 (= Syn6803\_BGT). The strain catalyzed the hydroxylation of nonanoic acid methyl ester (NAME) to 9-hydroxynonanoic acid methyl ester (H-NAME) at a rate of 1.5 U g<sub>CDW</sub><sup>-1</sup>. Under exclusion of external O<sub>2</sub> supply, Syn6803\_BGT channeled 25% of the photosynthetically generated O<sub>2</sub> *in situ* into the hydroxylation of NAME. Thus far, oxygen gas-liquid mass transfer constituted a key limitation in O<sub>2</sub> dependent bioprocesses. The developed concept of *in situ* O<sub>2</sub> generation in the liquid phase overcomes this technical limitation and thus enables the implementation of fast hydrocarbon oxyfunctionalization processes that otherwise suffer from limited O<sub>2</sub> mass transfer.

After the first proof of catalytic oxyfunctionalization activity, an integrated bioprocess engineering strategy comprising reaction and process engineering was pursued. Optimization of expression and reaction conditions, e.g., by the supplementation of the

reaction medium with NaHCO<sub>3</sub>, enhanced the initial NAME oxyfunctionalization activity of Syn6803\_BGT to 3.0 U  $g_{CDW}$ <sup>-1</sup>. In addition, specific activities were shown to be independent of the light-intensity applied during biotransformation. Thus, AlkB was assumed to indirectly couple with the photosynthetic water oxidation, potentially via the catabolism of storage compounds. Productive biotransformations with a recombinant strain lacking the electron transferring enzyme rubredoxin reductase AlkT pointed to an electron transfer from the photosynthetic metabolism to AlkBG via endogenous proteins.

Continuously decreasing oxyfunctionalization activities and low biotransformation stabilities with a product yield on biomass of 0.5 mmol<sub>H-NAME</sub>  $g_{CDW}$ <sup>-1</sup> were observed during long-term biotransformation with Syn6803\_BGT. Growth experiments using non-recombinant *Synechocystis* sp. PCC 6803 cells supplied with pure NAME revealed high rates of substrate hydrolysis to nonanoic acid (NA) and severe cell toxification by both reactants NAME and NA. Diisononyl phthalate (DINP) was identified as a suitable organic carrier solvent for an *in situ* substrate supply approach, because it did not, in contrast to ethyl oleate, influence the cyanobacterial cell growth negatively. Subsequent, two-liquid phase biotransformations reduced cell toxification and simultaneously enhanced substrate mass transfer and reduced NAME hydrolysis. This resulted in enhanced initial NAME hydroxylation activities of 5.6 U g<sub>CDW</sub><sup>-1</sup> and prolonged biotransformation stabilities with specific yields on biomass of 3.8 mmol<sub>H-NAME</sub> g<sub>CDW</sub><sup>-1</sup>. Finally, scaling of the biocatalyst cultivation and two-liquid phase biotransformation from mL scale to a multi-liter photobioreactor demonstrated the technical applicability of Syn6803\_BGT for photobiocatalytic oxyfunctionalizations of unactivated hydrocarbons.

The scope of photosynthesis-driven hydrocarbon oxyfunctionalization was broadened by the construction of another recombinant cyanobacterial strain. A cytochrome P450 cyclohexane monooxygenase originating from *Acidovorax* sp. CHX100 was genetically introduced into *Synechocystis* sp. PCC 6803, resulting in Syn6803\_CYP. The strain converted cyclohexane to cyclohexanol at high rates of 24 U  $g_{CDW}^{-1}$ , which was as fast as the recombinant heterotrophic biocatalyst *Pseudomonas* sp. VLB120 harboring the very same enzyme system. In contrast to the oxyfunctionalization activity of Syn6803\_BGT, the oxyfunctionalization rate of Syn6803\_CYP was shown to be dependent on the light-intensity, indicating a direct electron transfer from the photosynthetic light reaction to the CYP enzyme, potentially via ferredoxins or ferredoxin reductases. Also here, two-liquid phase biotransformations enhanced substrate mass transfer rates and reduced substrate toxicity. This resulted in substantially higher initial oxyfunctionalization rates of nearly 40 U  $g_{CDW}^{-1}$ . Furthermore, the biotransformation stability was prolonged from 5 to 24 h, yielding 4.5 g  $g_{CDW}^{-1}$  of the oxyfunctionalized products cyclohexanol and cyclohexanone. During scaling of the reaction system from mL scale to a multi-liter stirred tank photobioreactor,

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substrate evaporation was overcome by a process operation without aeration. This process operation was enabled by the *in situ* O<sub>2</sub> generation from photosynthetic water oxidation. Finally, Syn6803\_CYP produced 2.6 g cyclohexanol from cyclohexane, water, and light and thus for the first time demonstrated the gram-scale production of oxyfunctionalized hydrocarbons with a photobiocatalytic host.

The implementation of bioprocesses on industrial scales requires high productivities and titers and thus the generation and utilization of high biomass concentrations. The technical requirements for efficient growth and use of photobiocatalysts basically rely on sufficient light input and distribution. However, scaling of established standard bioreactors, such as the applied stirred tank bioreactor, results in decreased surface to volume ratios which, in turn, lead to a diminished light availability within the reactor. Capillary reactors constitute a promising alternative reactor technology, providing high surface to volume ratios and thus efficient light input. Applying the microbial catalyst in a biofilm format further intensifies this technology, featuring self-immobilization, biocatalyst regeneration and high biomass retention. However, cultivation of Synechocystis sp. PCC 6803 in a biofilm-based capillary reactor was shown to result in low surface coverage and oxidative stress response due to elevated O<sub>2</sub> concentrations within the aqueous medium. In analogy to microbial mats occurring in nature, a new cultivation concept via the co-cultivation of Synechocystis sp. PCC 6803 with the biofilm supporting, heterotrophic strain Pseudomonas sp. VLB120 was established. This technology enabled stable and continuous cultivation at high cyanobacterial biomass concentrations. Furthermore, respiration of citrate by the heterotrophic strain reduced the oxidative stress resulting from supersaturated O<sub>2</sub> concentrations. Finally, cultivation of the mixed-species biofilm in a capillary reactor system enabled the retention of high biomass concentrations at 48  $g_{BDW}$  L<sup>-1</sup> composed of 85% (v/v) cyanobacterial cells. Such high biomass concentrations have not been reached before using standard reactor technologies like the stirred tank photobioreactor.

The results of this thesis show that photosynthesis-driven whole-cell oxyfunctionalization holds a huge potential to reach high, industrially relevant oxyfunctionalization productivities. To quantify the extent of photosynthetic water oxidation contributing to oxyfunctionalization bioprocesses, theoretical maximum productivities in the context of *in situ* O<sub>2</sub> supply in the liquid phase are discussed. For standard large-scale bioreactors a gas-liquid mass transfer constant  $k_La$  of 200 h<sup>-1</sup> is considered feasible, allowing maximum possible productivities of 9 g L<sup>-1</sup> h<sup>-1</sup>. Heterotrophic biocatalysts respire O<sub>2</sub> and thus inherently reduce this productivity to 5.6 g L<sup>-1</sup> h<sup>-1</sup>. In contrast, photoautotrophic biocatalysts alleviate the technical process limitation theoretically enabling productivities of up to 30 g L<sup>-1</sup> h<sup>-1</sup>. Thus, O<sub>2</sub> evolving biocatalysts bear a fundamental advantage over established, O<sub>2</sub>-respiring heterotrophic biocatalysts.

In conclusion, *Synechocystis* sp. PCC 6803 was shown to be a well suited phototrophic biocatalytic host, supplying activated reduction equivalents and  $O_2$  for hydrocarbon oxyfunctionalizations. For the first time, a reaction engineering strategy demonstrated the technical applicability of cyanobacteria for the conversion of toxic and volatile compounds. The mixed-species biofilm-based capillary reactor system demonstrated a promising process technology for the application of photobiocatalysts at high biomass concentrations. Future applications may comprise the coupling of other redox reactions with the photosynthetic water oxidation. For instance, the reduction of protons using e.g., hydrogenases, constitutes a valuable strategy for the eco-efficient production of hydrogen as zero-emission fuel gas using the energy of light. By the integration of biocatalyst, reaction, and process engineering strategies, this study paves the way for the implementation of photobiocatalysts for photosynthesis-driven and eco-efficient redox reactions.

## Zusammenfassung

Die oxygene Photosynthese stellt einen Meilenstein in der natürlichen Evolution dar und manifestierte sich in phototrophen Organismen wie zum Beispiel Cyanobakterien, Algen oder Pflanzen. Die photosynthetische Wasseroxidation diente der Natur als neue Quelle für aktivierte Reduktionsäquivalente. Sauerstoff, zunächst ein Nebenprodukt, reicherte sich auf der Erde an und bildete somit die Grundlage für die Entwicklung von Redoxenzymen, welche O<sub>2</sub> als Elektronenakzeptor und/ oder Sauerstoffdonor verwerteten. Die Nutzung dieser Enzyme ermöglichte Mikroorganismen zum Beispiel Zugang zu bisher unzugänglichen Kohlenstoffquellen, was zu einer Erhöhung ihrer evolutionären Fitness führte. Heute profitiert die Biokatalyse von solchen Redoxenzymen für die selektive und spezifische Umsetzung diverser Substrate unter milden Reaktionsbedingungen zu Kraftstoffen und hochwertigen Chemikalien. Bisher basieren Redoxbiotransformationen hauptsächlich auf dem Einsatz isolierter Enzyme sowie chemoheterotropher Ganzzellbiokatalysatoren wie *E. coli* oder *Pseudomonas.* Diese Organsimen gewinnen Energie und Reduktionsäquivalente aus dem Abbau von Kohlenhydraten wie Glukose.

Die vorliegende Dissertation baut auf einem neuen Forschungsbereich auf, der sich die Vorteile der Photosynthese als Meilenstein der natürlichen Evolution zu Nutze macht. Durch den Einsatz von photoautotrophen Organismen als Biokatalysoren werden Redoxreaktionen, wie die Reduktion von Protonen zu Wasserstoff oder die Oxyfunktionalisierung von Kohlenwasserstoffen, mit O<sub>2</sub> und/ oder Reduktionsäguivalenten aus der photosynthetischen Wasseroxidation angetrieben. Somit ermöglicht die Photobiokatalyse atom-effiziente Biotransformationen und Katalysator(re-)generation basierend auf der anorganischen und abundant verfügbaren Kohlenstoffguelle CO<sub>2</sub>. In dieser Arbeit wurden rekombinante cyanobakterielle Stämme zur Synthese verschiedener Oxygenase-Enzymsysteme erzeugt und anschließend für die Photosynthese-getriebene Biokatalyse eingesetzt. Integrierte Biokatalysator-, Reaktions- und Prozessentwicklungsstrategien erzielten anschließend eine Intensivierung der Photosynthese-getriebenen Oxyfunktionalisierung von Kohlenwasserstoffen.

Durch die heterologe Expression der Alkanmonooxygenase AlkBGT aus *Pseudomonas putida* GpO1 in das Cyanobakterium *Synechocystis* sp. PCC 6803 wurde ein rekombinanter Photobiokatalysator erzeugt (= Syn6803\_BGT). Der Stamm katalysierte die Hydroxylierung von Pelargonsäuremethylester (PSME) zu 9-Hydroxypelargonsäuremethylester (H-PSME) mit einer Rate von 1.5 U  $g_{ZTG}$ <sup>-1</sup>. Unter Ausschluss externer O<sub>2</sub> Zufuhr konnten 25% des photosynthetisch erzeugten O<sub>2</sub> *in situ* für die Hydroxylierung von PSME genutzt werden. Bisher stellte der Gas-flüssig Massentransfer von O<sub>2</sub> eine entscheidende Limitation der Skalierung von O<sub>2</sub>-abhängigen Bioprozessen dar. Das entwickelte Konzept der photosynthetischen *in situ* O<sub>2</sub> Erzeugung in der Flüssigphase umgeht diese technische

Limitation und ermöglicht somit die Implementierung von bisher O<sub>2</sub>-Massentransfer limitierten Prozessen zur schnellen Oxyfunktionalisierung von Kohlenwasserstoffen.

Unter Betrachtung eines integrierten Konzeptes zur Bioprozessentwicklung wurden im Anschluss die Expressions- und Reaktionsbedingungen, wie zum Beispiel die Komplementierung des Reaktionsmediums mit NaHCO<sub>3</sub>, optimiert. Dies erhöhte die initiale Rate der PSME Hydroxylierung auf 3 U g<sub>ZTG</sub><sup>-1</sup>. Syn6803\_BGT zeigte unter den eingesetzten Reaktionsbedingungen eine von der Lichtintensität unabhängige spezifische Reaktionsrate. Demnach wurde eine indirekte Kopplung der photosynthetischen Wasseroxidation mit AlkB vermutet, welches möglicherweise über den Abbau von Speicherstoffen wie Glykogen erfolgt. Die Hydroxylierung von PSME mit einem AlkB-enthaltenden cyanobakteriellen Stamm, welcher das elektronenübertragende Enzym Rubredoxin Reduktase AlkT nicht synthetisiert, belegte schließlich, dass endogene Proteine den Elektronentransfer von dem photosynthetischen Stoffwechsel zu AlkBG ermöglichen.

Die PSME Biotransformation mit Syn6803 BGT über einen längeren Zeitraum von 30 min bis über 24 h zeigte eine kontinuierlich sinkende spezifische Aktivität und somit Reaktionsstabilität mit einem spezifischen Ausbeute von  $0.5 \text{ mmol}_{\text{H-PSMF}} q_{\text{ZTG}}^{-1}$ . Wachstumsversuche mit nicht-rekombinanten Svnechocvstis sp. PCC 6803 Zellen zeigte signifikante Substrathydrolyse zu Pelargonsäure (PS), sowie eine starke eine Zelltoxifizierung durch die beiden Reaktanden PSME und PS. Zur Umgehung der Substrattoxizität sowie der Substratlimitierung wurde eine Strategie zur in situ Substratzufuhr über eine organische Trägerphase entwickelt. Diisononylphthalat (DINP) erwies sich dabei als geeignete organische Trägerphase da es, im Gegensatz zu Ethyloleat, keinen negativen Einfluss auf das Zellwachstum von Synechocystis sp. PCC 6803 zeigte. Anschließende Biotransformation mit organischer Trägerphase reduzierte die Zelltoxifizierung bei aleichzeitiger Erhöhung des PSME Massentransfers und reduzierter PSME Hydrolyse. Dies führte zu einer hohen initialen, spezifischen Rate der PSME Hydroxylierung von 5.6 U g<sub>ZTG</sub><sup>-1</sup> und einer verlängerten Biokatalysatorstabilität mit einer spezifischen Ausbeute von 3.8 mmol<sub>H-PSME</sub> q<sub>ZTG</sub><sup>-1</sup>. Letztlich demonstrierte die Skalierung der Biokatalysatorkultivierung sowie der Biotransformation mit organischer Trägerphase vom mL-Maßstab in den multiliter Rührkessel-Photobioreaktor die technische Anwendbarkeit von Syn6803 BGT für die photobiokatalytische Oxyfunktionalisierung von nicht-aktivierten Kohlenwasserstoffen.

Der Umfang der Photosynthese-getriebenen Oxyfunktionalisierung von Kohlenwasserstoffen wurde durch die Entwicklung eines weiteren Photobiokatalysators erweitert. Hierzu wurde eine Cytochrom P450 Cyclohexan-Monooxygenase aus *Acidovorax* sp. CHX100 genetisch in *Synechocystis* sp. PCC 6803 eingebracht (= Syn6803\_CYP). Der Stamm katalysierte die Hydroxylierung von Cyclohexan zu Cyclohexanol mit einer spezifischen Rate von 24 U g<sub>ZTG</sub><sup>-1</sup>. Dies entspricht der Hydroxylierungsrate des rekombinanten heterotrophen Biokatalysators

Pseudomonas sp. VLB120, welcher das gleiche Enzymsystem trägt. Im Gegensatz zu Syn6803 BGT zeigte Syn6803 CYP eine Lichtintensität-abhängige spezifische Aktivität. Dies wies somit auf einen direkten Elektronentransfer von der photosynthetischen Lichtreaktion zu der Monooxygenase hin. Auch hier konnte durch die Nutzung einer organischen Trägerphase der Substratmassentransfer erhöht und die Substrattoxizität reduziert werden. Dies erhöhte die initiale, spezifische Hydroxylierungsrate auf etwa 40 U g<sub>ZTG</sub><sup>-1</sup> und verlängerte die Biokatalysatorstabilität von 5 auf 24 h, was in einer spezifischen Ausbeute von 4.5 g q<sub>7TG</sub><sup>-1</sup> Cyclohexanol und Cyclohexanon resultierte. Während der anschließenden Skalierung der Biotransformation in den Rührkessel-Photobioreaktor konnte die Evaporation des leicht flüchtigen Substrates Cyclohexan durch eine Prozesskontrolle ohne Begasung, ermöglicht durch die in situ O2-Bildung, verhindert werden. Schließlich produzierte Syn6803 CYP 2.6 g Cyclohexanol aus Cyclohexan, Wasser und Licht und demonstrierte somit erstmals die Produktion von oxyfunktionalisierten Kohlenwasserstoffen im Gramm-Maßstab mithilfe eines photobiokatalytischen Hostsystems. Die Realisierung von Bioprozessen im industriellen Maßstab benötigt hohe Produktivitäten und Titer, und somit die Erzeugung und den Einsatz von hohen Biomassekonzentrationen. Die technischen Anforderungen für effizientes Wachstum und Nutzuna von Photobiokatalysatoren basiert unter Anderem auf einem ausreichenden Lichteintrag. Die Skalierung von etablierten Bioreaktoren, wie dem hier eingesetzten Rührkessel Bioreaktor, führt jedoch zu einem verringerten Oberflächen zu Volumen Verhältniss, welches im Weiteren zu einem verminderten Lichteintrag in den Reaktor führt. Kapillarreaktoren stellen eine vielversprechende alternative Reaktortechnologie dar, indem sie ein hohes Oberflächen zu Volumen Verhältnis und somit maximalen Lichteintrag ermöglichen. Der Einsatz von mikrobiellen Katalysatoren im Biofilmformat erlaubt eine kontinuierliche Prozessführung, die durch die selbständige Biokatalvsator Immobilisierung und Regenerierung sowie die Aufrechterhaltung hoher Biomassekonzentrationen bestärkt wird. Die Kultivierung von Synechocystis sp. PCC 6803 im Biofilm-basierten Kapillarreaktor wurde bereits etabliert, zeigte jedoch eine niedrige Besiedlung der Kapillaroberfläche und Reaktionen auf oxidativen Stress durch die Entwicklung von erhöhten O<sub>2</sub> Konzentrationen in der Flüssigphase. In Anlehnung an die in der Natur vorkommenden mikrobiellen Matten ("microbial mats") wurde ein neues Kultivierungskonzept über die Co-Kultivierung von Synechocystis sp. PCC 6803 mit dem Biofilm-bildendend, heterotrophen Stamm Pseudomonas sp. VLB120 etabliert. Die Veratmung von Citrat durch Pseudomonas SD. VLB120 reduzierte die Sauerstoffkonzentration und verhinderte somit den oxidativen Stress auf den phototrophen Organismus. Die neue Technologie ermöglichte schließlich die stabile und kontinuierliche Kultivierung von Synechocystis sp. PCC 6803 mit einer hohen Biomasse von 48 gzrg L<sup>-1</sup> bestehend aus etwa 85% (v/v) cyanobakteriellen Zellen. Biomassekonzentrationen in dieser Höhe konnten bisher nicht mit Standard-Reaktortechnologien wie dem Rührkessel-Photobioreaktor erreicht werden.

Die Ergebnisse dieser Dissertation zeigen, dass die Photosynthese-getriebene Ganzzell-Oxyfunktionalisierung von Kohlenwasserstoffen ein großes Potential für das Erreichen von industriell relevanten Produktivitäten aufweist. In einem übergeordneten Diskussionskapitel wurde das Potential der photosynthetischen Wasseroxidation für O2-abhängige Bioprozesse im Zusammenhang der in situ O2 Erzeugung in der Flüssigphase diskutiert und über theoretisch mögliche maximale Produktivitäten veranschaulicht. Heterotrophe Biokatalysatoren veratmen O<sub>2</sub> und reduzieren somit die maximal mögliche Produktivität auf 5.6 q<sub>Produkt</sub> L<sup>-1</sup> h<sup>-1</sup> bei einer vorausgesetzten Gas-flüssig Massentransferkonstanten k<sub>L</sub>a von 200 h<sup>-1</sup> für großtechnische Rührkesselreaktoren. Im Gegensatz dazu erhöhen photoautotrophe Biokatalysatoren die maximale Produktivität auf 30 g<sub>Produkt</sub> L<sup>-1</sup>h<sup>-1</sup> durch die in situ Erzeugung von O2. Damit erhalten O2-generierende Photobiokatalysatoren einen fundamentalen Vorteil gegenüber etablierten O<sub>2</sub>-verbrauchenden heterotrophen Biokatalysatoren.

Zusammenfassend wurde gezeigt, dass *Synechocystis* sp. PCC 6803 ein geeigneter phototropher Biokatalysator für den Zugang zu aktivierten Reduktionsäquivalenten und O<sub>2</sub> für die Oxyfunktionalisierung von Kohlenwasserstoffen darstellt. Erstmals demonstrierte eine Strategie zur Reaktionsentwicklung die technische Anwendbarkeit von Cyanobakterien zur Umsetzung von toxischen und leicht-flüchtigen Verbindungen. Der Co-Einsatz zweier Spezies aus zwei unterschiedlichen Trophien (heterotroph und phototroph) im System des biofilmbasierten Kapillarreaktors schaffte den Zugang zu hohen Biomassekonzentrationen des phototrophen Mikroorganismus *Synechocystis* sp. PCC 6803.

Zukünftige Anwendungen von Photobiokatalysatoren umfasst die Kopplung der photosynthetischen Wasseroxidation mit weiteren Redoxreaktionen. Zum Beispiel stellt die Reduktion von Protonen mithilfe von Hydrogenasen und Licht eine wertvolle Strategie zur Produktion von Wasserstoff als emissionsfreier Energieträger dar. Durch die Integration von Stamm-, Reaktions-, und Prozessentwicklungsstrategien ebnet diese Arbeit den Weg zur Implementierung von Photobiokatalysatoren für Photosynthese-getriebene und ökoeffiziente Redoxreaktionen.

## List of abbreviations

3-HP	3-hydroxypropionic acid
3-PG	3-Phosphoglycerate
а	Area
AlkB	Alkane Monooxygenase
AlkG	Rubredoxin
AlkJ	Alcohol dehydrogenase
AlkT	Rubredoxin Reductase
ad.	aqueous phase
ATP	Adenosine triphosphate
BDW	Biofilm dry weight
BEHP	Bis(2-ethylhexyl)phthalate
BVMO	Baever-Villiger monooxygenase
C3H	p-Coumarate-3-hydroxylase
CDH	Cyclohexanol dehydrogenase
CDW	Cell dry weight
CHYON	Cyclohexanone monooxygenase
CYP	Cytochrome P450 monooxygenase
CVPchy	
Cut hef	Cyclonexane monocxygeanse
	2.5 Dibromo 3 motbul 6 isopropylhopzogujpopo
	2,5-Dibioino-5-metryi-o-isopropyibenzoquinone
	Disvelopropul kotopo
DINP	Disononyi phinalale
DINISO	Dimethyl sulfoxide
D3P F	
E	Einstein (µmoi <sub>photons</sub> )
EDIA	Etnylenediamintetraacetic acid
FAD	Flavin adenine dinucleotide
FAME	Fatty acid methyl ester
Fd	Ferredoxin
Far	Ferredoxin reductase
FID	Flame ionization detector
FMN	Flavin mononucleotide
GAP	Glyceraldehyde 3-phosphate
GC	Gas chromatography
H <sub>cc</sub>	Henry volatility
HEPES	4-(2-Hydroxyethyl)-1-piperazinethanesulfonic acid
H-NAME	9-Hydroxynonanoic acid methyl ester
HPLC	High performance liquid chromatography
H-PSME	9-Hydroxypelargonsäuremethylester
IAM	lodoacetamide
IPTG	Isopropyl β-D-1-thiogalactopyranoside
ISPR	In situ product removal
ISSS	In situ substrate supply
K <sub>cat</sub>	Catalytic constant (s <sup>-1</sup> )
k <sub>L</sub>	Mass transfer coefficient
k∟a	Mass transfer constant
K <sub>m</sub>	Michaelis constant
Km	Kanamycin
KPi	Potassium phosphate buffer
lacl	Lac repressor
LED	Light-emitting diode
logP	Logarithmic octanol-water coefficient
MMO	Methane monooxygenase

	Nonanoic acid (reduced) Nicotinemide edening disuculactide (pheephete)
	(Teudeed) Nicolinamide adennie dinuculeolide (priospitale)
	Ontical density at 450 pm
OD450	Optical density at 750 nm
OEP	Oxygen evolution rate
OM	Oxygen evolution rate
org	
	Oxygen respiration rate
OTR	Oxygen transfer rate
P.,	Alk promoter
	Photosynthetically active radiation ( $\mu E m^2 s^{-1}$ )
PC.	Plastocyanin
Pdx	Putidaredoxin
PHA	Polyhydroxyalkanoate
PM	Plasma membrane
PMSE	Phenylmethylsulfonyl fluorid
PnrsB	NrsB promoter
PO	Plastoquinone
	Plastoguniol
PmpB	RnpB promoter
PS	Photosystem
Ps.	Pseudomonas sp. VLB120
PSME	Pelargonsäuremethylester
P <sub>tac</sub>	Tac promoter
Ptrc	Trc promoter
PTV	Programmed temperature vaporizer
R-1,5-BP	Ribulose 1,5-bisphosphate
RBS	Ribosomal binding site
RBS*	Optimized ribosomal binding site
RT	Room temperature
RubisCO	Ribulose bisphosphate carboxylase
SDS PAGE	Sodium dodecyl sulphate-polyacrylamide gel electrophoresis
sp.	Species
STR	Stirred tank bioreactor
StyAB	Styrene Monooxygenase
Syn6803	Synechocystis sp. PCC 6803
Т	Temperature
T <sub>An</sub>	Annealing temperature
TBS	Tris buffered saline
t <sub>Elong</sub>	Elongation time
Term	Terminator
TM	Thylakoid membrane
TN	Turnover number
I ÍN	l otal turnover number
U	Unit (µmol min <sup>-1</sup> )
XyIMO	Xylene monooxygenase
ZTG	Zelltrockengewicht

Chapter 1 General introduction

#### 1.1 Photosynthesis as a driver for eco-efficient oxygenase-based biotransformations

Oxygenic photosynthesis triggered a milestone in natural evolution, occurring 2-3 billion vears ago (Madigan and Martinko, 2006). The photosynthetic water oxidation provided a new source for reduction equivalents accessed by the energy of light. Oxygen, initially a byproduct, accumulated in the atmosphere after oxidizing abundant reduced substances such as FeS and drove the establishment of aerobic organisms. Various enzymes catalyzing a multitude of chemical reactions developed as a result of evolutionary adaptation to the oxic atmosphere. Oxygenases make use of  $O_2$  as oxygen donor and catalyze the oxyfunctionalization of diverse substrates. These enzymes increased the evolutionary fitness of microorganisms by enabling them to utilize previously inaccessible molecules as an organic carbon source. Today, organic chemistry profits from oxygenases which selectively and specifically catalyze, inter alia, hydrocarbon oxyfunctionalization reactions under mild conditions, generating value-added chemicals (Bühler and Schmid, 2004). Thus far, bioprocesses mainly rely on isolated enzymes or chemoheterotrophic whole-cell biocatalysts such as E. coli or Pseudomonads (Wachtmeister and Rother, 2016). In these organisms, energy and reduction equivalents are accessed by the catabolism of carbohydrates such as glucose. Although high reaction efficiencies, as well as the use of renewable organic carbons, contribute to the development of eco-efficient production processes, the implementation of such bioprocesses on industrial scales is rare.

The present study builds on a new research field that takes advantage of photosynthesis as the milestone of natural evolution. Photosynthetic water oxidation is coupled with oxygenases fueling oxyfunctionalization reactions with reduction equivalents and O<sub>2</sub> derived from water. The use of photoautotrophic host systems, therefore, enables atom-efficient bioprocesses and catalyst (re)generation based on the inorganic and abundant carbon source CO2. The following introduction briefly reviews the state of the art of oxyfunctionalization bioprocess development and outlines the new concept of photosynthesis-driven redox biotransformations. First, types and reaction mechanisms of oxygenase enzymes are explained. The following sections specify aspects relevant for industrial implementations and introduce the concept of integrated bioprocess design. The boundaries of current redox bioprocesses are then defined and followed by sections focusing on the new concept of photosynthesis-driven redox biotransformations. Oxygenic photosynthesis in general and the photosynthetic light reaction in detail are described, and trapping positions for heterologous redox enzymes are specified. Subsequently, the state of the art of photo-biotechnology is comprised. In the scope of the thesis, the current lack in developing photosynthesis-driven redox bioprocesses leads to the main research question and the key strategies used in the present dissertation.

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#### 1.2. Scope and mechanism of oxygenase enzymes

In nature, oxygenases ubiquitously occur in microorganisms, plants, fungi, and animals, and play a key role in numerous physiological mechanisms. As a subclass of oxidoreductases, they catalyze the transfer of electrons and oxygen, resulting in reduction and oxidation of atoms within respective substrates (**Figure 1.1**).



Figure 1.1: Scope of oxyfunctionalization reactions catalyzed by oxygenases. In nature, these enzymes harbor ubiquitous roles, e.g., in the synthesis of hormones and secondary metabolites, in the degradation/ catabolism of organic compounds, or in the detoxification of otherwise toxifying chemicals.

Organic carbon sources, such as camphor (Jones *et al.*, 1993), octane (van Beilen *et al.*, 1994), styrene (Mooney *et al.*, 2006), or xylene (Harayama and Rekik, 1990), are accessed by the enzymatic activation of hydrocarbon bonds. Plant toxicants, such as the furanocoumarin xanthotoxin (Schuler, 2011), or synthetic drugs, such as the neuroleptic levomepromazine (Wójcikowski *et al.*, 2014), are deactivated by initiating their catabolism. Steroid hormones are synthesized from cholesterol participated by various oxygenase enzymes (Payne and Hales, 2004), whereas cholesterol biosynthesis itself comprises an oxygenase enzyme (Laden *et al.*, 2000; Michal, 1999). In addition, various secondary metabolites, such as rosmarinic acid, are synthesized by this enzyme class (Petersen *et al.*, 2009).

#### 1.2.1 What is the molecular mechanism of oxygenases?

The first experimental step towards revealing the mechanism of oxygenases took place in 1955 and was conducted independently by the two scientists Howard S. Mason (Monooxygenase Phenolase) (Mason *et al.*, 1955) and Osamu Hayaishi (Dioxygenase Pyrocatechase) (Hayaishi *et al.*, 1955). Both proved the introduction of one (monooxygenase) or two (dioxygenase) oxygen atoms from  $O_2$  into an organic substrate yielding oxyfunctionalized hydrocarbon bonds. This was in contrast to the earlier assumption that  $H_2O$  is an exclusive oxygen donor in enzymatic catalysis. The main function of oxygenase enzymes lays in the activation of oxygen driven by the donation of electrons. These enzymes act as single or as multi-component systems, rely on redox partners, and receive electrons from cofactors such as NAD(P)H. Recognition, distance, electrostatic interactions between the partners, as well as redox potentials, are essentials for successful electron transfer. Nature developed different oxyfunctionalization mechanisms that are assigned to different enzyme subclasses by the architecture of their active site (**Figure 1.2**).



**Figure 1.2**: Core active sites of heme-dependent, non-heme, and flavin-dependent oxygenases. Next to the shown diiron(II, III)-superoxo complex in the non-heme diiron oxygenase active site, also diiron(III, IV)-oxo and diiron(IV)-oxo species are possible. Flavin-dependent oxygenases: Riboflavin R=H, Flavin mononucleotide FMN R=PO<sub>3</sub><sup>2-</sup>, Flavin adenine dinucleotide FAD R=ADP.

**Heme-dependent oxygenases.** Iron-coordinated active sites characterize one of the main subclasses of oxygenases, although also copper, manganese, cobalt, and nickel-dependent oxygenases are known (Fiedler and Fischer, 2017; Liang *et al.*, 2018b; Pazmino *et al.*, 2010). Heme-dependent monooxygenases are ubiquitous enzymes and occur in eukaryotes, archaea, and bacteria. Cytochrome P450 monooxygenases (CYPs) build the major fraction in this subclass. They were named by their specific light absorption ability at 450 nm resulting from the reduced CO-bound heme-complex which is used for enzyme quantification. In the

core of the active site, an iron atom is bound to protoporphyrin IX, while a cysteine acts as the fifth ligand. Upon reduction, the iron atom binds and activates  $O_2$  and substrate oxyfunctionalization can occur. Three-component monooxygenases composed of the heme-containing hydroxylase, a ferredoxin moiety that transfers electrons via  $Fe_2S_2$  clusters and a FAD-containing ferredoxin reductase that receives electrons from NADH are referred to class I CYPs. In contrast, class II type CYPs consist of a membrane-bound hydroxylase and a Flavin-containing ferredoxin reductase. Class III CYPs assemble the heme-containing hydroxylase as well as the Flavin-containing ferredoxin reductase. Necetarily, also a class IV CYP category was discovered that assembles the three components of heme-hydroxylase,  $Fe_2S_2$ -ferredoxin and Flavin-ferredoxin reductase in one protein.

Peroxygenases constitute another heme-dependent oxygenase subclass that is structurally related to CYPs and make use of  $H_2O_2$  as oxygen donor (Bormann et al., 2015; Wang et al., 2017). The reaction mechanism is independent of nicotinamide cofactors and other electron supplying proteins and resembles the peroxide shunt of CYPs.

**Non-heme iron oxygenases**. Non-heme iron oxygenases have evolved in parallel with cytochrome P450s (Jasniewski and Que Jr, 2018; Pazmino *et al.*, 2010). Both, mono- and dinuclear iron centers coordinated within the enzyme active site are known. Mono-nuclear active sites often occur in dioxygenases and lipoxygenases (Salomon *et al.*, 2013). Di-iron catalytic centers are bridged, e.g., by a glutamate residue, while glutamate or histidine residues arrange the octahedral coordination of the iron atoms and are complemented by solvent-derived water and hydroxide ions. Well studied non-heme diiron monooxygenases are the three-component soluble methane monooxygenase MMO (Dalton, 1980; Merkx *et al.*, 2001), the membrane-bound three-component alkane monooxygenase AlkBGT (Austin and Groves, 2011; Peterson *et al.*, 1966a), as well as the membrane-bound two-component xylene monooxygenases XylMO (Suzuki *et al.*, 1991).

**Flavin-based oxygenases.** The active site of oxygenases can also be built on carbon-based catalytic centers such as Flavin-containing (covalent = prosthetic) or Flavin-dependent (external Flavin = coenzyme) oxygenases (Liang *et al.*, 2018b; Pazmino *et al.*, 2010). Flavin-based enzymes are abundant in prokaryotic organisms and make use of Flavin Mononucleotide (FMN) or Flavin adenine dinucleotide (FAD) as cofactors. Examples are the FAD-containing squalene monooxygenase (Laden *et al.*, 2000), the external flavoprotein styrene monooxygenase StyAB (Hartmans *et al.*, 1990), and the Baeyer-Villiger diketocamphane monooxygenase (Jones *et al.*, 1993).

#### 1.2.2 Why are oxygenases interesting for the chemical industry?

As already highlighted by the physiological mechanisms in nature, both the reaction as well as the substrate variety covered by the oxygenase subclass is huge. Non-activated **hydrocarbons**, such as the alkanes octane (Peterson *et al.*, 1966a) and xylene (Suzuki *et al.*, 1991) are **hydroxylated**, while unsaturated hydrocarbons, such as styrene (Hartmans *et al.*, 1990) or squalene (Laden *et al.*, 2000) are **epoxidized**. Aldehydes and ketones are converted to the respective esters by **Baeyer-Villiger** Monooxygenases, as for example known for the oxidation of the cyclic ketone diketocamphane (Jones *et al.*, 1993) to the corresponding lactone. Next to hydrocarbons, also compounds containing heteroatoms such as sulfides or amines can be oxyfunctionalized to **sulfoxides** (Wójcikowski *et al.*, 2014) or **oximes** (Zhu *et al.*, 2013).

In addition to the huge chemical variety concerning the substrate scope, oxygenase enzymes act incomparably regio-, chemo-, and enantioselective by embedding their substrate in a well-aligned binding pocket (Liang *et al.*, 2018b). This, together with the fact that enzymes operate under mild conditions (neutral pH, low temperature, low pressure, aqueous solvents), turns oxygenases into a highly promising catalyst for the chemical industry. Oxyfunctionalized compounds are ubiquitous in all product classes of pharma, fine and bulk chemicals. Structural complex molecules are found in pharmaceutical compounds, such as the cholesterol-derived anti-inflammatory drug cortisone, and can be accessed by the application of oxygenases (Hudlicky and Reed, 2009). Chiral building blocks, such as chiral alcohols, complement the fine chemical industry. Oxyfunctionalized hydrocarbons function as building blocks for the polymer industry (Evonik Industries AG, 2013; Karande *et al.*, 2017; Ladkau *et al.*, 2016).

#### 1.3 Development of oxyfunctionalization bioprocesses

#### 1.3.1 Targets for industrial implementation

Referring to the Darwinian evolutionary theory, the driver for natural evolution is `survival of the fittest'. Oxygenase-catalyzed oxyfunctionalization reactions evolved within the framework of physiological mechanisms with the target of maximizing the efficiency of maintenance, growth, and reproduction. In contrast, chemical synthesis aims at maximum (oxyfunctionalized) product formation, irrespective of being driven by chemical, enzymatic or whole-cell (bio-) catalysis. Thus, bioprocess development tasks the change of the microbial objective from exclusive survival to the maximized production of target compounds.

The ambition of developing new processes relies on both, economic as well as ecologic aspects summarized by the descriptor `eco-efficiency' as done, e.g., by the World Business Council for Sustainable Development (WBCSD, 2000). On the one hand, economic feasibility refers to the margin between production cost and product value and is explicitly determined

by the capital investment costs (CapEx, e.g., equipment), the operational costs (OpEx, e.g., raw materials, utilities, waste, maintenance) and the manufacturability (Tufvesson *et al.*, 2010). On the other hand, ecologic aspects refer to a sustainable design of a chemical production process, being manifested in the twelve principles of Green Chemistry: Prevention, Atom Economy, Less Hazardous Chemical Synthesis, Designing Safer Chemicals, Safer Solvents and Auxiliaries, Design for Energy Efficiency, Use of Renewable Feedstocks, Reduce Derivatives, Catalysis, Design for Degradation, Real-Time Analysis for Pollution Prevention, Inherently Safer Chemistry for Accident Prevention (Anastas and Eghbali, 2010). Importantly, although often associated with the term "green", biocatalysis per se does not account for green chemistry, and careful quantification of the environmental impacts is essential (Ni *et al.*, 2014). In general, process efficiency directly affects the production costs and the raw material input, therefore being a crucial parameter in tuning the eco-efficiency during process development. Three key metrics determine the process efficiency (Straathof *et al.*, 2002):

- Productivity, space-time yield (g L<sup>-1</sup> h<sup>-1</sup>)
- product titer (g L<sup>-1</sup>), and
- product yield (g g<sub>substrate</sub><sup>-1</sup> or g g<sub>catalyst</sub><sup>-1</sup>)

The very consideration of economic viability requires productivities and titer of at least 0.001 g L<sup>-1</sup> h<sup>-1</sup> and 0.1 g L<sup>-1</sup>, respectively, for high-priced compounds mainly found in the pharmaceutical industries (Julsing *et al.*, 2008). For mid-priced chemicals, seen in the fine and the bulk chemical industry, the demand for efficiency further increases. Productivities and titers should be as high as 0.1 g L<sup>-1</sup> h<sup>-1</sup> and 1 g L<sup>-1</sup>, respectively. Concerning whole-cell biocatalytic applications, product yields on biocatalysts should range from 10 g g<sub>CDW</sub><sup>-1</sup> (pharmaceutical compounds) to 2000 g g<sub>CDW</sub><sup>-1</sup> (bulk chemicals) (Tufvesson *et al.*, 2010). Thus, biocatalytic activity, as well as stability, are two main parameters determining the successful implementation of a bioprocess.

#### 1.3.2 Concept of integrated bioprocess design

The eco-efficient use of oxygenases, irrespective of applied as isolated enzymes or in wholecells, meeting requirements of economy, ecology, and manufacturability is possible with a process design taking numerous different aspects into account. In a rational approach, the development of a bioprocess can pass four levels of engineering addressing enzyme, host, reaction, and process (**Figure 1.3**) (Karande *et al.*, 2016b; Schmid *et al.*, 2001; Willrodt *et al.*, 2015b). Within each level, the optimization of distinct targets is addressed by numerous strategies/ parameters. Thereby, the selection and technological implementation of these strategies is governed by the mutual interconnection of the four engineering levels.

The transfer of a microbial cell from its natural status to a well-functioning biocatalyst in a

technical setting changes the objective from survival to maximizing product formation (Volmer *et al.*, 2015). Deciphering these differences and similarities allows the optimization and particularly exploitation of technologies that were designed by natures evolution for chemical synthesis.



**Figure 1.3**: Concept of integrated bioprocess design. The development of bioprocesses meeting requirements of economy, ecology, and manufacturability necessitates the integrated consideration of the four levels of enzyme, host, reaction, and process engineering. Within each level, the optimization of distinct targets is addressed by numerous strategies/ parameters. Thereby, the selection and technological implementation of these strategies is governed by the mutual interconnection of the four engineering levels. Figure adapted from Schmid et al. 2001 (Schmid *et al.*, 2001).

Holistic biocatalysis cycles were developed guiding towards individual objectives such as aligning bioprocess development with physicochemical properties of the reactants or hydrocarbon oxyfunctionalization (Bühler and Schmid, 2004; Willrodt et al., 2015b). Although each development step requires in-depth knowledge of particular engineering technologies, the early integration of analysis as well as optimization strategies on all levels of engineering strengthens and accelerates bioprocess design. During (isolated enzyme or whole-cell) biocatalyst development, the optimization towards the final reaction and process setting is of high importance as, for instance, the microenvironment changes from mL-scale shake flask to m<sup>3</sup>-scale bioreactors which may result in fundamental changes concerning the process performance. Today, the process setup is designed to match the biocatalyst requirements. However, the reverse handling, e.g., by directed evolution of the biocatalysts under real process conditions, allows for selecting and engineering the biocatalyst to match the existing process design (Burton et al., 2002; Hibbert et al., 2005; Woodley, 2018). Particular technologies such as single-cell analysis support the evaluation of the performance of individual cells under reaction and process conditions and enable the identification and optimization of bottlenecks in the process efficiency induced for instance by heterogeneity and population dynamics (Rosenthal et al., 2017). Systems biology, which is the quantitative

description of cellular functions, e.g., using omics tools, becomes an integrating engineering tool by implementing the knowledge on reaction and process requirements of a targeted bioprocess with the rational engineering of the biocatalyst (Kuhn *et al.*, 2010a). A systematic understanding and the ability to address problems on all levels of bioprocess development enables prolonged and thus more efficient bioprocesses with enhanced yields and titers (Kadisch *et al.*, 2017b).

The following section introduces engineering strategies applied for improving the oxygenase bioprocess efficiency and is clustered according to the four levels of bioprocess design just introduced.

#### 1.3.3 Enzyme selection and engineering

Selectivity, activity, and stability are the key targets for enzyme selection and engineering and are quantified by the product composition, turnover number, and total turnover number. When starting bioprocess development, the choice of the right enzymatic catalyst is crucial. Screening and isolation of enzymes from natural sources with a microenvironment fitting to the intended bioprocess is very promising (Watts et al., 2005). One example is the catalyst CYP450chx used for cyclohexane oxyfunctionalization, which was identified from a bacterial strain isolated from a biotrickling filter applied for cleaning air containing cyclohexane as contaminant (Salamanca and Engesser, 2014; Salamanca et al., 2015). In case, the portfolio of the naturally available enzyme does not fit the required reaction requirements concerning selectivity, activity, or stability, enzyme engineering can be pursued to optimize the performance (Bloom et al., 2005: Bornscheuer et al., 2012: Kuchner and Arnold, 1997). The prospects of enzyme engineering technologies are studied extensively at one of the bestknown oxygenases, P450 BM3 (= CYP102A1) (Whitehouse et al., 2012). This class III CYP is the third isolated oxygenase from Bacillus megaterium. The non-engineered enzyme hydroxylates medium- to long-chain fatty acids  $(C_{12}-C_{20})$  at the sub-terminal positions using NADPH as a cofactor. P450 BM3 shows the highest known oxygenase activity ( $k_{cat}$  = 285 s<sup>-1</sup> determined via arachidonate-induced NADPH oxidation) (Noble et al., 1999). Protein engineering efforts can facilitate broader substrate diversity, higher activities towards nonnatural substrates, and increased catalyst lifetimes (Whitehouse et al., 2012). Rational design by molecular modeling and site-directed evolution of P450 BM3, for instance, enabled hydroxylation of the aromatic isoflavone daidzein at distinct positions (Ko et al., 2015). Random mutagenesis resulted in an enzyme capable of the hydroxylation of alkanes (Glieder et al., 2002). Site-directed mutagenesis enhanced the oxidation rate of polycyclic aromatic hydrocarbons 200-fold. Increasing product formation rates often goes along with increased unproductive NAD(P)H oxidation rates (uncoupling), mainly derived from the un-proper fitting of the substrate within the active site (Carmichael and Wong, 2001). Protein engineering can enhance the coupling efficiency and therefore the protein stability regarding the total turnover

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number (Fasan *et al.*, 2007). Another simple but efficient method of protein engineering is the design of synthetic fusion proteins (Yu *et al.*, 2015b). Electron transferring components, such as the reductase domain of P450 BM3, can be fused to oxygenase enzymes, enhancing the electron transfer efficiency (Scheps *et al.*, 2013). Multi-step reactions can profit from enzymes brought in spatial proximity resulting in the conversion of otherwise accumulating intermediates (Willrodt *et al.*, 2015a). In addition to the protein efficiency-determining metrics, the cofactor dependency of oxygenases influences the subsequent bioprocess design. This is especially important for whole-cell applications, where the scope of available cofactors varies among the microbial species. Using protein engineering, the NADPH – NADH cofactor dependency can be modulated as likewise shown for the P450 BM3 (Girvan *et al.*, 2011; Neeli *et al.*, 2005).

#### 1.3.4 Host selection and engineering

Once an appropriate (oxygenase) enzyme is chosen and, if necessary and successfully engineered, subsequent catalysis requires a suitable host system. Thereby, protein production, physiological suitability, metabolic efficiency, and cellular chassis, as well as cell integrity, are key targets that require special consideration and, if needed, optimization. Whether the microbial cell functions as protein production host only or as a whole-cell biocatalyst for the catalytic reaction is one of the first choices made during the bioprocess development. In the case of oxygenase-based catalysis, numerous advantageous for in vivo or in vitro applications, respectively, exist (de Carvalho, 2011). Whole-cells provide an endogenous cofactor as well as protein regeneration system. The microbial cell presents a natural environment, protecting the proteins from destabilizing conditions such as organic solvents. Inherently, in vivo application avoids the purification of, potentially membranebound, (multi-component) oxygenases. In contrast, the use of isolated enzymes provides high flexibility, e.g., for combining specific catalytic reactions for multi-step catalysis. Substrate and product mass transfer remain unlimited, and no side-reactions occur from microbial host intrinsic enzymes. Protein engineering enabled the stable use of oxygenases in organic media or ionic liquids. In-situ cofactor regeneration is possible, e.g., by enzymatic, chemical or electrochemical approaches.

**Host selection**. Natural sources already provide optimized microbial systems as a result of elaborate evolution. The native organism synthesizes the enzyme of choice in a correctly folded and therefore active conformation. Posttranslational modifications, such as glycosylation, and support of protein folding, e.g., by chaperones, are well-established in these organisms. In contrast to the natural host systems, the technical use of proteins demands high concentrations accompanied by simple cultivation technology (reducing production costs) and ease of manipulation (Carvalho, 2017). Typical organisms for biocatalytic enzyme production and application are prokaryotic microorganisms such as

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E. coli, Pseudomonads, Bacillus sp., and eukaryotic yeasts such as Saccharomyces cerevisiae or Pichia pastoris. Yeasts possess organelles providing compartmentalization and much space for the incorporation of membrane proteins as frequently the case of oxygenases. Some extremophile bacteria, often Pseudomonas species, show an increased tolerance towards solvents such as cyclohexane or styrene (Sardessai and Bhosle, 2004). This is beneficial for the application of such organic solvents as carrier phase for hydrophobic and therefore low water-soluble compounds, e.g., testosterone, as they predominantly occur as substrates for oxyfunctionalization catalysis (Kuhn et al., 2012a; Ruijssenaars et al., 2007). Given heme-containing oxygenases, host systems that endogenously synthesize aminolevulinic acid for porphyrin biosynthesis are preferred (Julsing et al., 2008; van Beilen et al., 2005). Different organisms can provide altered yields of product based on the same carbon source. During styrene epoxidation catalyzed by StyAB, for instance, 1.5 times higher vields of styrene oxide on glucose was observed using E. coli JM101 as host system in comparison to Pseudomonas sp. VLB120 (0.87 vs. 0.55 g<sub>oroduct</sub> g<sub>alucose<sup>-1</sup></sub>) (Kuhn et al., 2012a). Host intrinsic side reactions often occur and can be both adverse as well as beneficial for the desired reaction. Limonene hydroxylation using the CYP153A6, for instance, resulted in perillyl aldehyde and perillyl acid overoxidation catalyzed by a pseudomonas intrinsic dehydrogenase. A change of the biocatalytic chassis to E. coli W3110 supported the production of mainly perillyl alcohol by host intrinsic reduction of perillyl aldehyde back to perillyl alcohol (Cornelissen et al., 2013).

**Protein production.** Genetic manipulation and engineering of the selected microbial host system is the basis for successful overexpression of genes for heterologous protein production. Knowledge and use of methodologies on all levels of protein biosynthesis, including replication, transcription, translation, and posttranslational modification strengthen the control over protein production. While the use of plasmids as vectors for foreign genes is simple and fast, genome integration enables more stable genetic incorporation. A broad range of promoters, comprising constitutive as well as inducible expression systems, allow for the defined transcription of the genetic material at desired time-scales. In addition, the applied codon usage and ribosomal binding sites control the strength of translation. Modularization of genes in different operons tunes the ratio of multi-component protein systems. Introduction of specific helper proteins, such as chaperones or the maltose binding protein, support the proper and soluble protein folding. Overexpression of the glutamyl-tRNA reductase, a key enzyme catalyzing the rate-limiting reaction in heme biosynthesis, allows for proper cofactor incorporation also in *E. coli* (Harnastai *et al.*, 2006).

**Physiological suitability and metabolic efficiency.** Biocatalytic applications sometimes rely on more than one enzyme and connect to the microbial metabolism in different complexity (Schrewe *et al.*, 2013). Whereas the use of isolated enzymes is inherently

independent of the microbial host system, whole-cell biotransformations make use of the endogenous cofactor- or even co-substrate regeneration. Therefore, the physiological background has to suitable to accommodate the desired enzyme performance. When applying oxygenases in whole-cells, host-intrinsic side-reactions often interfere with the target reaction. In such cases, pathway engineering on endogenous enzymes is required. Identification and subsequent knock-out of the esterase BioH in *E. coli*, for instance, reduced the fatty acid methyl ester (FAME) hydrolysis by a factor of 22, enhancing the product yield for FAME hydroxylation (Kadisch *et al.*, 2017a).

The use of oxygenases implies the supply with electrons from respective cofactors. When applying whole-cell reaction systems, the supply with cofactors is highly dependent on the endogenous consumption of such. Metabolic engineering is a highly useful tool for optimizing the catalytic performance of a cell (Lin and Tao, 2017). Systems biology, comprising in silico modeling and multi-omics data analysis, allows for the identification of rate-limiting steps and following definition of targets for maximizing and balancing the (electron) flux towards the desired product. The genetic introduction of additional enzymes can increase fluxes. The coexpression of the alcohol dehydrogenase AlkJ, for instance, with the alkane monooxygenase enzyme system AlkBGT supported the irreversible oxidation of the hydroxylated fatty acid methyl ester to the targeted aldehyde compounds (Schrewe et al., 2014). Also, cofactor regeneration can be accelerated, e.g., by introducing an orthogonal cofactor re-regeneration system. The incorporation of a glucose uptake and NADP\*-dependent glucose dehydrogenase system in *E. coli*, for instance, 9-times increased the  $\alpha$ -pinene to  $\alpha$ -pinene oxide oxyfunctionalization rate catalyzed by P450 BM-3 (Schewe et al., 2008). The knock-out of non-efficient cofactor generating pathways, such as the glycolytic pathway, increases the flux through the pentose phosphate pathway and thus improves the cofactor generation yield on glucose (Fasan et al., 2011). The same effect could be achieved by the partial inactivation of competing pathways, such as endogenous respiration and fermentative pathways (Fasan et al., 2011).

Microorganisms often provide either NADH or NADPH as the main cofactor. A simple but effective metabolic engineering tool, if the applied oxygenase does not match the cellular cofactor supply, is the genetic introduction of a transhydrogenase that catalyzes the hydride transfer between the two nicotinamide dinucleotides (Blank *et al.*, 2010). Co-expression of an L-lactate dehydrogenase and a soluble transhydrogenase, for instance, increased the lactate production rate and yield in the cyanobacterium *Synechocystis* sp. PCC 6803 (Angermayr *et al.*, 2012).

**Cellular chassis & cell integrity.** The application of oxygenases in whole-cell biocatalysts relies on a biocatalytic host functioning as reaction chassis. Although the microbial metabolism can be optimized by metabolic engineering regarding balanced fluxes directing

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towards the chemical product, the whole-cell embodiment itself affects the reaction performance, inter alia, by the presence of cell membranes (and cell walls). Cellular engineering re-structures the microbial chassis, e.g., for the improved substrate uptake, product secretion, or toxic reactant export. The outer membrane of microbial cells functions as a barrier for hydrophobic compounds. Outer membrane pore proteins such as AlkL (Julsing et al., 2012b), OprG (Touw et al., 2010), OmpW (Hong et al., 2006), or FadL (van Den Berg et al., 2004) facilitate the uptake of oxyfunctionalization substrates by providing hydrophobic channels. Co-expression of AlkL in recombinant Pseudomonas putida KT2440 harboring CYP153A6, for instance, increases the hydroxylation activity of (S)-limonene to (S)-perillyl alcohol by a factor of five (Cornelissen et al., 2013). In addition, hydrophobic substrate uptake can be enhanced by engineering the lipopolysaccharide acylation state (Vorachek-Warren et al., 2002). Thus, lipopolysaccharide mutant strains of E, coli W3110 harboring P450 BM3 enabled the whole-cell oxyfunctionalization of the hydrophobic substrate linoleic acid (Lee et al., 2011). The secretion of oxyfunctionalized products is not inherently hampered as the oxyfunctionalization process itself increases the hydrophilicity of the respective substrates. In contrast, too much uptake of reactants, e.g. of organic solvents, is detrimental to the cells resulting in decreased bioprocess stability by microbial inactivation. Solvent extrusion, supported by efflux pumps such as TtgABC, TtgGHI, or SrpABC identified in various Pseudomonads, keeps the intracellular toxicant concentration low and therefore enables the survival or even growth of microorganisms under exposure of solvent compounds. Constitutive synthesis of the efflux pump TtgGHI in Pseudomonas sp. VLB120AC reduced the adaptation time to respective reaction conditions and, also, doubled the specific styrene epoxidation activity (Volmer et al., 2014).

The application of (oxygenase) enzymes in isolated form overcomes the need for reactant mass transfer. A sophisticated way of facilitating the direct contact between the catalyst and the substrate by the simultaneous preservation of enzyme stability and regeneration is the display of enzymes on the microbial surface (Schüürmann *et al.*, 2014). Also, the well-studied cytochrome P450BM3 was displayed on the cell surface of *E. coli* and enabled the hydroxylation of lauric acid, palmitic acid and arachidonic acid independent from membrane mass-transfer (Yim *et al.*, 2010). Easy separation from the reaction mixture and re-usability strengthened this method (Ströhle *et al.*, 2016). Exclusion of the enzyme from the microbial metabolism challenges the cofactor supply, although external supply with NAD(P)H via electrochemical, chemical and enzymatic regeneration systems were already developed successfully.

#### 1.3.5 Reaction engineering

Key optimization targets within the level of reaction engineering are biocatalyst production, reaction efficiency, and biocatalyst stability. Nature adapted its mechanisms according to the

present microenvironment. In contrast, biocatalyst generation and chemical conversion necessitate altered/ optimized growth and reaction conditions. Temperature, pH, and media composition (including, inter alia, ionic strength) are of high importance for both, the catalyst production and the chemical reaction. In the case of whole-cell biotransformations, the reaction medium does not only affect the oxyfunctionalization reaction itself, but also the state of the cellular metabolism. The depletion of nutrients, for instance, induces a non-growing state of the cell. Such resting cells can provide increased cofactor supply on the given energy source, as shown for the epoxidation of styrene to (*S*)-styrene oxide catalyzed by recombinant *E. coli* harboring a styrene monooxygenase (Julsing *et al.*, 2012a).

Throughout the whole reaction time, reactant concentrations have to match the enzyme or whole-cell kinetics, respectively. Michaelis-Menten kinetics, including product inhibition and reactant toxicity, are key aspects to be considered (Ringborg and Woodley, 2016). Oxyfunctionalization substrates often are hydrophobic and therefore lowly water soluble. Intercalation of such chemical compounds in the membranes of whole-cell biocatalysts results in cell disintegration, and therefore destabilization of the bioprocess (Sikkema et al., 1994). Solvents with a logarithmic octanol-water coefficient logP between 1 and 4 are considered to be highly toxic to cells (de Bont, 1998). On the one hand, a continuous substrate feed can prevent from supplying the toxic substrate in excess. Importantly, the feed rate has to match the oxyfunctionalization rate to keep the substrate concentration constantly low. In the example of fluorobenzene oxyfunctionalization to fluorocatechol catalyzed by Pseudomonas putida whole-cells, reactant inhibition was successfully overcome by such a substrate feeding strategy (Lynch et al., 1997). On the other hand, organic carrier solvents can be used to continuously provide the substrate to the aqueous phase, regulated by the organic: aqueous phase partitioning coefficient. The oxyfunctionalization of  $\alpha$ -pinene to  $\alpha$ pinene-oxide catalyzed by recombinant E. coli harboring a cytochrome P450 BM3 variant. for instance, revealed an optimal substrate concentration of 30% (v/v)  $\alpha$ -pinene dissolved in the organic carrier solvent disononyl phthalate (DINP) resulting in high initial specific activities and prolonged biotransformation stability (Schewe et al., 2009).

Oxyfunctionalization intermediates and products accumulating at concentrations toxic to the biocatalysts constitute another source of reduced biotransformation stability. The accumulation of hydrophobic compounds in the microbial membranes was estimated to induce cell breakdown at concentrations of 300 - 400 mM (Kratzer *et al.*, 2015). *In situ* product removal (ISPR) is a useful technique to retain low reactant concentrations (Lye and Woodley, 1999). Examples for ISPR comprise, amongst many others, liquid-liquid extraction, and solid-phase adsorption. Solid-phase *in situ* product extraction by adsorption to the hydrophobic Optipore L-493 resin, for instance, enhanced the rate and yield of the Baeyer-Villiger oxidation of bicyclo[3.2.0]hept-2-en-6-one to the corresponding lactones catalyzed by

recombinant *E. coli* harboring a cyclohexanone monooxygenase (Simpson *et al.*, 2001). The use of bis(2-ethylhexyl)phthalate (BEHP) as liquid extraction solvent during *E. coli* Xylene monooxygenase (XylMO) biotransformation, for instance, allowed for stable oxyfunctionalization of pseudocumene to the respective aldehydes and acids at high concentrations (Bühler *et al.*, 2002).

In addition to the prevention of catalyst inactivation and retention of highly volatile reactants in the reaction system, *in situ* substrate supply and product extraction also allow for the kinetic control of multi-step oxyfunctionalizations. Thus, the defined use of 2-liquid phase biotransformation directed the product formation pattern of the *E. coli* XyIMO reaction system to the accumulation of 3,4-dimethylbenzaldehyde (Bühler *et al.*, 2003b). Organic-carrier solvents are not only applicable for whole-cell applications, but also for the use of isolated oxygenase enzyme systems. Cytochrome P450 BM3 variants, for instance, could successfully be applied with cyclohexane as an organic carrier solvent for the hydroxylation of octane or myristic acid (Maurer *et al.*, 2005).

Next to the substrate supply and product extraction, the co-substrate  $O_2$  is one of the most critical parameters during oxyfunctionalization catalysis. The dissolved oxygen concentration influences the oxyfunctionalization rate and can affect the regioselectivity of the reaction. For instance, the impact of oxygen on the oxyfunctionalization of pentadecanoic acid catalyzed by cytochrome P450 BM-3 was investigated in both, isolated enzyme and whole-cell applications (Schneider *et al.*, 1999). Excess of oxygen resulted in the formation of hydroxypentadecanoic acids as well as ketohydroxy- and dihydroxypentadecanoic acids with an oxyfunctionalization rate of 2.1 U  $g_{CDW}^{-1}$  (*in vivo*) and 100 U  $g_{protein}^{-1}$  (*in vitro*), respectively. In contrast, oxygen-limited conditions resulted in decreased oxyfunctionalization rates of 1.25 U  $g_{CDW}^{-1}$  (*in vivo*) and 60 U  $g_{protein}^{-1}$  (*in vitro*), respectively, with hydroxypentadecanoic acids as the main hydroxy products.

#### 1.3.6 Process design & engineering

Process engineering focuses on the transfer of a developed bioprocess into a technical setting with special consideration of scaling, process duration, and product recovery. The technical setting is highly dependent on whether the process runs continuously or in batch mode. Scalability and the scale-up progress maintaining the reaction efficiency are prerequisites for the successful process development and, eventually, implementation.

**Scaling & process duration.** Optimal growth of the host system and efficient protein biosynthesis determine the catalyst production performance. On fermenter-scale, defined cultivation conditions of the recombinant expression systems are crucial for generating high catalyst concentrations. Development and optimization of a fed-batch strategy, for instance, allowed for the synthesis of the cytochrome P450 BM3 to a concentration of ~ 11% per g<sub>CDW</sub> of recombinant *E. coli* (Pflug *et al.*, 2007). Both, enzymes and whole cells can be applied for

catalysis in suspended or immobilized format (Es et al., 2015). Suspended biocatalysts avoid labor and cost-intensive development and preparation techniques. Existing production settings can be used for the industrial application. Mixing and therefore mass transfer is not limited by supporting materials, and the catalyst preserves its conformational freedom. Immobilization often possesses high stability, good storage possibilities, simplified catalyst recovery, and recyclability and thus mediates an increased yield on biocatalyst. Various immobilization techniques exist and are extensively applied in industry. Immobilization materials comprise, e.g., the nature-derived polymers collagen and alginate, or the synthetic polymer polyacrylamide. In view of whole-cell biocatalysts, certain bacteria, such as Pseudomonas sp. VLB120 (Gross et al., 2007), feature self-immobilization into a biofilm format (Halan et al., 2012). High catalyst density and enhanced resistance towards destabilizing environmental conditions allow for efficient bioprocessing (Gross et al., 2010). During the actual reaction process, the bioreactor facilitates efficient interaction of the biocatalyst with the (co-)substrate and, if required during the biotransformation process, adequate product extraction. In general, a bioreactor can be operated in batch or continuous mode and raises particular demands on the reactor design. Examples of bioreactor types comprise, inter alia, stirred tank reactors, fixed-bed reactors, or membrane reactors, mainly differing in the biocatalyst application format and the mixing type. Scaling under retention of the reaction parameters is crucial. The following paragraphs describe two examples of different bioreactor types and operation modes.

The stirred-tank bioreactor (STR) constitutes an industrial standard for fermentation and biocatalytic processes. The core of the STR represents a reaction vessel equipped with a stirring device for sufficient mixing of the reaction mixture (agitation). Often, the biocatalyst is applied in suspended format. The exchange between the gas and liquid phase mainly occurs via aeration. In batch mode, the reaction medium containing all necessary nutrients and, if required, the carbon source is provided to the biocatalyst right from the start of the reaction process. In a fed-batch mode, the substrate (e.g., an organic carbon source or the reaction substrate) is provided during the biotransformation process to avoid inhibition effects. During the discontinuous operation, the reactant concentrations continuously change over time. Laboratory scaling of a developed two-liquid phase bioprocess to a 30 L stirred-tank bioreactor, for instance, enabled the production 3,4-dimethylbenzaldehyde from pseudocumene with a productivity of 31 L<sup>-1</sup> d<sup>-1</sup> and a final product titer of 37 g L<sup>-1</sup> catalyzed by recombinant *E. coli* harboring a XyIMO (Bühler *et al.*, 2003a).

Capillary reactors comprise miniaturized reaction chambers combined with microfluidic devices. Continuous operation favors the use of biocatalysts immobilized on the inner surface of the capillary reactor, e.g., as a self-immobilized biofilm. The reaction medium and the substrate are continuously supplied, while the reaction product is continuously obtained

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at the reactor outlet. The application of air segments (plug flow) facilitates the exchange with the gas phase (Karande *et al.*, 2016b). On a laboratory scale, the application of *Pseudomonas* sp. VLB120 $\Delta$ C in a biofilm-based capillary reactor, for instance, allowed for the stable oxyfunctionalization of styrene to styrene-oxide for at least 50 days with an average volumetric productivity of 24 g L<sup>-1</sup> day<sup>-1</sup> (Gross *et al.*, 2010). Scaling takes place by numbering-up and comprises a, not yet industrially applied, promising alternative to stirredtank reactor processes enabling high product yields on biomass (Gross *et al.*, 2013).

**Product recovery.** Downstream processing (DSP) includes the separation of the product from the catalyst (cell harvest and disruption for whole-cell applications if the product accumulates intracellularly), product recovery, product concentration, product purification, and packing (Chmiel, 1991). Next to centrifugation and filtration this comprises, inter alia, precipitation, adsorption, solvent extraction, electrophoretic, and chromatographic methodologies. Often, *in situ* product removal (ISPR) strategies such as adsorption or solvent extraction are used for a continuous and stabilized bioprocess control. Although the DSP is a highly cost intensive (usually more than half of the total costs) part of a bioprocess, academic research on the systematic optimization of appropriate oxyfunctionalized product purification methodologies is rare.

#### 1.4 Towards photosynthesis-driven redox biotransformations

## 1.4.1 Boundaries of current oxyfunctionalization bioprocesses and the potential of photosynthesis

The introduced integration of strategies addressing the key targets for the development of efficient bioprocess leads to a complex interconnection of process parameters. In principle, constraints of the process efficiency within each process development level go back to catalyst activity, product inhibition/ toxicity, catalyst stability, and product recovery. The graphical visualization in a window of operation helps to classify the actual state of bioprocess development and to define the future engineering targets for achieving an eco-efficient production process (**Figure 1.4**) (Woodley and Titchener-Hooker, 1996).

In general, the left-hand site process boundary arises from the catalyst activity (determined by, e.g., the turnover number). The enzyme or whole-cell kinetics for product inhibition and product toxicity limit the maximum product titer and form an upper process boundary. The biocatalyst stability (determined by, e.g., the total turnover number) restricts the duration of a bioprocess. The lower process boundary is defined by the downstream processing methodology which becomes viable at a specific minimum product titer and the minimum amount of product per volume which is targeted in the process.

In a detailed view of the left-hand site process boundary of oxygenase biocatalysis,

especially the co-substrate supply restricts the maximum catalyst activity. Thus, the limited availability of  $O_2$  via gas-liquid mass transfer and the regeneration of NAD(P)H cofactors challenge the development of viable bioprocesses. Chemoheterotrophic whole-cell reaction systems provide reduction equivalents by the catabolism of organic carbon-based sources, such as glucose. However, high energy demand for growth and maintenance reduces the level of reduction equivalents that are accessible for the catalytic reaction (Blank *et al.*, 2008; Bühler *et al.*, 2008). In addition, microbial respiration reduces the amount of  $O_2$  available in the reaction system and technically challenges the reaction setup (Hilker *et al.*, 2006; Law *et al.*, 2006).



Reaction time / h

**Figure 1.4**: Window of operation with process boundaries for biocatalytic processes. In oxyfunctionalization processes, the catalyst specific activity is confined by the O<sub>2</sub> availability and NAD(P)H regeneration rate. While heterotrophic whole-cell biocatalysts are prone to limit both, photosynthetic water oxidation provides an extensive source of electrons and O<sub>2</sub>. Figure adapted from Schrewe et al. 2013 (Schrewe *et al.*, 2013).

Oxygenic photosynthesis provides an extensive source of both,  $O_2$  and reduction equivalents. Thus, by changing the biocatalytic host system from chemoheterotrophic to photoautotrophic organisms, in theory, allows for the unlimited exploitation of the oxygenase activity. Water serves as a carbon-independent source of both co-substrates accessed by the energy of light. The uncoupled fixation of inorganic carbon (CO<sub>2</sub>) enables cheap and sustainable catalyst (re)generation. Coupling of oxygenases to the photosynthetic water oxidation is highly promising for the development of eco-efficient production processes that are currently  $O_2$  and electron-limited but require high productivities. Especially when the production costs are essential, e.g., for low-cost products, the replacement of organic carbon sources such as glucose by  $CO_2$  is favorable.

#### 1.4.2 The mechanism of oxygenic photosynthesis

The application and development of photobiocatalytic host systems require an understanding of the underlying photosynthetic metabolism. Therefore, the following sections introduce the
mechanism of oxygenic photosynthesis, with focus on the photosynthetic water oxidation reaction and possible trapping positions for oxygenase enzymes.



**Figure 1.5**: Schematic representation of the photosynthetic light reaction. With the energy of light water is oxidized and electrons are transferred through the electron transport chain towards the cofactor NADPH, resulting in a proton motive force and the subsequent generation of ATP. Both, NADPH and ATP are used for the fixation of  $CO_2$  via the Calvin-cycle. PSII = photosystem II, PQ = plastoquinone (PQ), PQH<sub>2</sub> = plastoquinol, Cyt b6f = cytochrome b6f complex, PC = plastocyanin, PSI = photosystem I, Fd = ferredoxin, FdR = ferredoxin reductase.

Photoautotrophic organisms such as plants, algae, and cyanobacteria, convert light energy into chemical energy by the oxidation of water and fix  $CO_2$  for the generation of carbohydrates. In the primary, light-driven reaction the energy and electron carrier ATP and NADPH are generated via an electron transport chain (**Figure 1.5**). In the secondary reaction, ATP and NADPH are used for the fixation of  $CO_2$  and the generation of carbohydrates (**Figure 1.6**).





The uptake of light quanta (a physical unit for light energy) occurs by photopigments located within the thylakoid membranes. Various photopigments with different characteristics and

absorption spectra exist, allowing for the efficient usage of the whole range of light energy (Madigan and Martinko, 2006). Chlorophyll constitutes one of the main photopigments. It assembles a porphyrin scaffold with a coordinated magnesium ion in its centrum. Absorption of red and blue light results in a green color. In proteins, chlorophyll forms complexes of 50 to 300 molecules functioning as energy funnel directed towards the reaction center. The electron transport chain of the photosynthetic light reaction comprises two of such protein complexes:

- photosystem PSII containing chlorophyll P680 (absorption of far-red light)
- photosystem PSI containing chlorophyll P700 (absorption of near red light)

Phycobilins form another group of light-harvesting and light-energy transferring antenna pigments. The aggregates of open-chain tetrapyrroles, such as phycoerythrin (red), phycocyanin (blue), or allophycocyanin (blue), are closely linked to chlorophyll reaction centers. With decreasing light intensity, the phycobilin content increases. Carotenoids conduct a photoprotective role by quenching reactive oxygen species and absorption of harmful light. The long chain hydrocarbons with a conjugated double-bond system absorb blue light and thus appear yellow, red, brown, or green.

The photosynthetic light reaction is initiated at the photosystem PSII by the oxidation of water into  $O_2$ , protons and electrons. Subsequent absorption of light facilitates the electron excitation and thus transport through the electron transport chain. Second light absorption and electron excitation takes place at the photosystem PSI before the electron transfer proteins ferredoxin and ferredoxin reductase and finally the cofactor NADP+ are reduced. Location of the electron transport chain within the thylakoid membranes results in the formation of a proton gradient with high proton concentrations within the thylakoid lumen. Finally, this proton motive force drives the ATP synthase.

Generated ATP and NADPH then are used for the fixation of  $CO_2$  by the Calvin-cycle. In the first step,  $CO_2$  is fixed in ribulose 1,5-bisphosphate (R-1,5-BP) catalyzed by the ribulose bisphosphate carboxylase (RubisCO) resulting in two molecules of 3-phosphoglycerate (3-PG). Subsequently, the C<sub>3</sub>-molecule 3-PG is reduced to glyceraldehyde 3-phosphate (GAP) under consumption of ATP and NADPH. Finally, GAP molecules are either regenerated to R-1,5-BP by the consumption of ATP or taken up by reversed glycolysis for the generation of carbohydrates. Fixed carbon is either directly taken up by the metabolism for growth and maintenance or stored in storage compounds such as glycogen. In the absence of light (e.g., in the night), these polysaccharides then are catabolized again.

### 1.4.3 Trapping electrons from the photosynthetic light reaction for redox biocatalysis

Redox biocatalysis, such as catalyzed by oxygenase enzymes, requires the efficient coupling of the photosynthetic light reaction with the heterologous redox enzyme that makes use of

the activated reduction equivalents. The mainly reduced cofactor of photosynthesis is NADPH. However, the photosynthetic light reaction offers a multitude of positions for trapping the light-excited electrons by redox enzymes (Mellor *et al.*, 2017). Importantly, the transfer of electrons necessitates the interaction with electron transferring enzymes that match respective redox potentials. The Z-scheme of photosynthesis explains the redox pathway of, the by light, excited electrons and discloses the trapping positions for heterologous oxygenases (**Figure 1.7**).

Due to the spatial accessibility, PSI, ferredoxins, flavodoxins, and ferredoxin reductases are the most suitable trapping positions. In contrast, the localization of the copper-containing plastocyanin/ heme-containing cytochrome c6 in the thylakoid lumen places these proteins to hardly accessible trapping positions for heterologous redox enzymes. The fast exchange between electron transferring enzymes occurs if the distance between the central redox cofactors is below 14 Å. The relatively weak interactions rely on hydrophobic and electrostatic interactions, resulting in an unspecific binding pattern, allow the transfer of electrons to various downstream acceptor proteins. Ferredoxins, flavodoxins, plastocyanin, and cytochrome  $c_6$  are negatively charged and thus interact with the positively charged sites of the cytochrome b6f complex and the photosystem PSI.



**Figure 1.7**: Z-scheme representing the electron transfers within the photosynthetic light reaction. Electrons are transferred from proteins with a high redox potential to those with a low redox potential. Electrons are excited by the energy of light which takes place in the photosystems PSII and PSI. PSII = photosystem II, PQ = plastoquinone, Cyt b6f = cytochrome b6f complex, PC = plastocyanin, PSI = photosystem I, Fd = ferredoxin, FdR = ferredoxin reductase.

Downstream of the photosystem PSI, ferredoxins are the primary electron transferring enzymes. They distribute the reducing power within the metabolism of the photosynthetic organism. Electron transfer occurs via iron-sulfur clusters (Fe<sub>2</sub>S<sub>2</sub>, Fe<sub>3</sub>S<sub>4</sub>, Fe<sub>4</sub>S<sub>4</sub>). Rubredoxins have the same function but contain a single iron center. Both are one electron carriers. Thus the reduction of NADPH requires two electron transfer steps. Absent in plants, flavodoxins comprise functional homologs to ferredoxins. The FMN-based, one-electron carrier proteins

share a comparable redox potential but interact with even lower specificity than ferredoxins. Redox enzymes, such as oxygenases, often rely on functionally related electron transferring enzyme systems. Thus the exchange of these systems with those derived from the photosynthetic machinery is reasonable and facilitated by their promiscuity (Goñi *et al.*, 2009; Lacour and Ohkawa, 1999).

Numerous studies already conceptually investigated the exploitation of the photosynthetic water oxidation for redox reactions (**Table 1.1**). The different possibilities for trapping photosynthesis-derived electrons are explained best on the example of hydrogen production, which is the take-up of electrons for the reduction of protons to hydrogen. Hydrogenases can be coupled to the PSI by localizing both enzymes in spatial proximity (Ihara *et al.*, 2006b). Connection of both central Fe<sub>4</sub>S<sub>4</sub> clusters via a thiolated molecular wire enables a direct electron transfer (Lubner *et al.*, 2011). Alternatively, mediation of the electrons deriving from PSI to the hydrogenase, for instance, results from the fusion of PSI with a cytochrome c<sub>3</sub> (Ihara *et al.*, 2006a). In addition, hydrogen production is facilitated by the fusion of hydrogenases with photosynthesis deriving ferredoxins (Yacoby *et al.*, 2011). In general, the abstraction of electrons competes with the endogenous metabolism, such as CO<sub>2</sub> fixation (main part), nitrogen, and sulfur assimilation. Down-regulation of competing pathways and orthogonal re-direction of electrons, therefore, might be crucial.

### 1.4.4 Current state of photobiotechnology

Thus far, substantial effort was dedicated to the proof-of-concept studies coupling the photosynthetic light reaction with redox enzymes, and great success was achieved. The implementation of eco-efficient photosynthesis-driven redox biotransformations into suitable process settings, however, requires the identification of key limitations and engineering targets. Therefore, the following section briefly reviews the current state-of-the-art in photobiotechnology in analogy to the approach of addressing the levels of process development described above.

Selection of phototrophic host systems. The group of phototrophic organisms covers plants, algae, and cyanobacteria. Referring to the theory of endosymbiosis, ancestors of cyanobacteria stably incorporated into primitive eukaryotic cells, resulting in the development of chloroplasts present in plants and algae. Due to enhanced cell growth and genetic accessibility in comparison to plants and algae, cyanobacteria comprise promising host systems for photosynthesis driven biotechnological applications. *Synechocystis* sp. PCC 6803 presents a cyanobacterial model organism for which few engineering methodologies were already established (Ruffing, 2011). *Synechococcus elongatus* PCC 7942 constitutes another unicellular model organism, while various filamentous strains such as *Anabaena* sp. or *Nostoc* sp. are mostly studied in the context of hydrogen production.

Table 1.1: Photosynthesis-driven electron demanding reactions. DCMU = 3-(3,4-dichlorophenyl)-1,1-dimethylurea, specific inhibitor of photosystem II (PSII)
electron transport; IAM = Iodoacetamide; DBMIB = 2,5-dibromo-3-methyl-6-isopropylbenzoquinone; C3H = p-coumarate-3-hydroxylase.

Reaction	Host system	Information on mechanism	Rate	Ref
2-methylmaleimide	<i>Synechocystis</i> sp. PCC 6803 recombinant	DCMU reduces activity Light-dependent activity Low activity with DCMU in the absence of light	123 U g <sub>cow</sub> -1	(Köninger <i>et al.</i> , 2016)
2 H <sup>+</sup> + 2e <sup>-</sup> Hydrogenase H <sub>2</sub>	<i>Tetraspora</i> sp. CU2551 wildtype	-	20 U g <sub>CDW</sub> <sup>-1</sup>	(Maswanna <i>et al.</i> , 2018)
OH ADH Cyclohexanol Cyclohexanol Cyclohexanol Cyclohexanol	<i>Synechocystis</i> sp. PCC 6803 recombinant	DCMU reduces activity Light-dependent activity Low activity with DCMU in the absence of light	6 U g <sub>cdw</sub> -1	(Böhmer <i>et al.</i> , 2017)
$\begin{array}{c} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 $	Synechococcus sp. PCC 7002 recombinant	Active without native reductase DCMU reduces activity Light-dependent activity Almost no activity in the absence of light	31 mU g <sub>CDW</sub> -1	(Berepiki <i>et al.,</i> 2016)
$\begin{array}{c} & & & \\$	Synechococcus sp. PCC 7002 recombinant	Fused to photosystem I subunit PsaM → localization in the thylakoid membrane	27 U mg <sub>chlorophyll</sub> -1	(Lassen <i>et al.</i> , 2014a)
2 H* + 2e <sup>-</sup> Nitrogenase H <sub>2</sub>	Nostoc sp. PCC 7120 ΔhupW knock-out of uptake hydrogenase	-	14 U mg <sub>chlorophyll</sub> <sup>-1</sup>	(Nyberg <i>et al.</i> , 2015)
$\begin{array}{c} & & & \\$	<i>In vitro</i> CYP124 + PSI + Ferredoxin	Light-driven activity Catalase was added to prevent ROS deriving from CYP	7 U mg <sub>chlorophyli</sub> 1	(Jensen <i>et al.</i> , 2012)
7-ethoxycoumarin 7-hydroxycoumarin	In vitro	isolated cactus chloroplasts + yeast microsomes containing CYP1A1 fused with ferredoxin reductase	2.3 U mg <sub>chlorophyll</sub> <sup>-1</sup>	(Hara <i>et al</i> ., 1997)
$\underset{\substack{\mu \in \mathcal{O}} \\ \mu \in \mathcal{O}} \underset{\substack{\mu \in \mathcal{O}} \\ \mu \in \mathcal{O}} \underset{\substack{\mu \in \mathcal{O}} \\ \mu \in \mathcal{O}} \underset{\mu \in \mathcal{O}$	Synechocystis sp. PCC 6803 recombinant	Localization of CYP to thylakoid membranes	10 mU mg <sub>chlorophyli</sub> -1	(Wlodarczyk <i>et al.</i> , 2015)

Position	Host system	Information on mechanism	Pato	Pof
Hydrogenase	In vitro		Kale 1	Kei
2 H <sup>+</sup> + 2e <sup>-</sup>	Hydrogenase fused to PSI	Light-driven activity	9.7 mU mg <sub>chlorophyll</sub>	(Ihara <i>et al.</i> , 2006b)
	Nicofiana tabacum transgenic	Active only when targeted to chloroplasts	0.012 mU g <sub>leaf</sub> 1	(Okeefe <i>et al.</i> , 1994)
HO p-coumaric acid C3H HO HO Caffeic acid	<i>Synechocystis</i> sp. PCC 6803 recombinant	-	9.4 mU L <sup>-1</sup>	(Xue <i>et al.</i> , 2013)
$\begin{array}{c} & \\ & \\ & \\ & \\ & \\ & \\ & \\ & \\ & \\ & $	Synechococcus elongatus PCC 7942 wildtype	DCMU inhibits activity	active	(Nakamura and Yamanaka, 2002)
0 OH		Activity inhibited by DCMU (PSII), enhanced by IAM		
	Synechococcus elongatus PCC 7942	(Calvin-cycle) and DBMIB (Cytb6f)	active	(Yamanaka <i>et al.</i> , 2011)
TFA Trifluoro-phenylethanol	wiidtype	Low activity in the absence of light		
	In vitro			
	Isolated chloroplasts containing	active without soluble Ferredoxin	active	(Mellor et al., 2016)
	CYP79A1 fused to Ferredoxin			
Acetophenone S-phenylethanol	<i>Synechocystis</i> sp. PCC6803 wildtype	Enhanced yield via overexpression of FdR	active	(Luo <i>et al.</i> , 2018)

Engineering of photobiocatalytic hosts. Yet, genetic modification of cyanobacteria lacks a powerful genetic engineering toolbox. Genetic modifications either rely on a broad host range replicative plasmid (RSF origin of replication) or chromosomal integration into several neutral sites. Introduction of genetic materials is possible via natural transformation, electroporation or conjugation (Ruffing, 2011). Synechocystis sp. PCC 6803 and many other cyanobacteria contain multiple genome copies, necessitating full segregation of genetic insertions/ knockouts for stable genetic manipulation. In consequence of varying copy numbers and folding structures, the different insertion positions result in altered expression strengths. For Synechocystis sp. PCC 6803, the highest expression of a fluorescent reporter protein was achieved by integration into its endogenous plasmid (Ng et al., 2015). In general, the codon usage of Synechocystis sp. PCC 6803 is similar to other bacteria such as E. coli. The overexpression of genes can be performed via native promoter systems, such as the lightinducible P<sub>sbA2</sub> promoter (Heidorn *et al.*, 2011). The promoter natively controls the synthesis of a photosystem PSII subunit and results in a strong and, under standards cultivation conditions, constitutive expression. In addition, metal ion inducible promoter systems are used. The P<sub>nrsB</sub> promoter, for instance, natively controls nickel, cobalt, and zinc efflux pumps, and constitutes a highly tunable system with a relatively silent expression under non-induced conditions (Englund et al., 2016). Metal ions such as Ni<sup>2+</sup> are highly toxic to the bacterial cells and necessitate a well-balanced addition to the culture medium. Orthogonal expression systems, such as Ptrc (Huang et al., 2010) or Ptac (Albers et al., 2015), mainly rely on the IPTG-inducible lac expression system. However, its functionality is not comparable to established heterotrophic host systems such as E. coli, resulting in expression even in the absence of the inducing agent.

Analysis of all native *Synechocystis* sp. PCC 6803 ribosomal binding site (RBS) sequences resulted in an optimized RBS\* with 9 base pairs between the Shine-Dalgarno core sequence and start codon (Heidorn *et al.*, 2011). Evaluation of RBS\* with fluorescent reporter proteins showed high translation efficiency. Synthetic biology is required for the development of controllable and strong genetic engineering tools.

In contrast to the use of phototrophic organisms for biotransformation reactions, much research was already conducted on the development of fermentative production systems for hydrocarbon-based chemicals. Numerous photosynthesis-driven catalysts were generated and engineered to produce various compounds, such as ethanol (Liang *et al.*, 2018a), lactate (Angermayr *et al.*, 2012), isobutanol (Varman *et al.*, 2013), fatty acids (Ruffing, 2014), isoprene (Pade *et al.*, 2016), ethylene (Veetil *et al.*, 2017), itaconic acids (Chin *et al.*, 2015), carbohydrates (glucose, fructose) (Niederholtmeyer *et al.*, 2010), glycerol (Savakis *et al.*, 2015), erythritol (van der Woude *et al.*, 2016), or propandediol (David *et al.*, 2018; Li and Liao, 2013), from CO<sub>2</sub>. In addition, the feature of naturally synthesizing terpenoids and

isoprenoids renders them well suited as biocatalysts for pharmaceuticals, cosmetics, colorants, disinfectants, fragrances, flavorings, and agro-chemicals (Pattanaik and Lindberg, 2015). The production of 3-hydroxypropionic acid (3-HP) represents an example for extensive metabolic engineering of a phototrophic metabolism (Wang *et al.*, 2016b). First, the heterologous introduction of the malonyl-CoA reductase from *Chloroflexus aurantiacus* into *Synechocystis* sp. PCC 6803 and optimization of culture conditions enabled the CO<sub>2</sub>-based production of 32 mg L<sup>-1</sup> 3-HP. Subsequent change of the expression system, including inter alia the promoter strength, significantly enhanced the product titer to 692 mg L<sup>-1</sup>. Overexpression of the endogenous acetyl-CoA carboxylase and biotinilase, as well as the NAD(P) transhydrogenase, increased the supply of the precursor malonyl-CoA as well as the cofactor NADPH, respectively, achieving the production of 745 and 752 mg L<sup>-1</sup> 3-HP. The same product titers were observed after the inactivation of the competing pathways for PHA and acetate biosynthesis, respectively. Finally, the combination of these metabolic engineering approaches in one strain resulted in the production of ca. 837 mg L<sup>-1</sup> 3-HP from CO<sub>2</sub>.

Cultivation and process technologies. Numerous photobiotechnological processes were already developed for the generation of algal biomass for animal and human nutrition products, cosmetics, or for the extraction of high-value molecules such as fatty acids or pigments (Chaumont, 1993; Grobbelaar, 2009; Pulz, 2001; Singh and Sharma, 2012; Spolaore et al., 2006; Weissman et al., 1988). Traditional algal cultivation systems comprise open pond reactor systems (Figure 1.8 A). The production of lipids as biodiesel using the microalgae Graesiella sp. WBG-1, for instance, was carried out in a 40000 L raceway open pond bioreactor, comprising a surface area of 200 m<sup>2</sup> (20 x 10 x 0.2 m) (Wen et al., 2016). After 15 days of cultivation, the final biomass concentration was 138 g m<sup>-2</sup> corresponding to ca. 0.7 g<sub>CDW</sub> L<sup>-1</sup> and contained ca. 33% of the target lipids. In contrast to open systems, closed tubular photobioreactors reduce the risk of contaminations and thus, in theory, support the cultivation of genetically modified organisms (Wijffels et al., 2013). In addition, tubular photobioreactors, such as built at the AlgaePARC in Wageningen, Netherlands, increase the light input by increased surface to volume ratios (Figure 1.8 B) (Wijffels et al., 2013). A 500 km long tubular photobioreactor (700 m<sup>3</sup>) in Klötze, Germany, for instance, enables the production of  $130 - 150 t_{CDW}$  of the algae *Chlorella* per year (average productivity of 6.2 q<sub>CDW</sub> m<sup>-2</sup> day<sup>-1</sup>) (Spolaore et al., 2006).

By further increasing the surface area to volume ratio, an open thin-layer photobioreactor was developed recently (**Figure 1.8 C**) (Apel *et al.*, 2017). With this system, cultivation of the saline microalgae *Nannochloropsis salina* on a technical scale of 8 m<sup>2</sup> resulted in high final biomass concentrations of 50  $g_{CDW}$  L<sup>-1</sup> within 25 days (313  $g_{CDW}$  m<sup>-2</sup>). In addition to biomass production, photosynthetically active algae are applied during waste-water treatment as well.

Here, algal biofilms are grown on open surfaces such as polystyrene foam (Johnson and Wen, 2010) or concrete (Ozkan *et al.*, 2012) (**Figure 1.8 D**). Evaluation of the biofilm formation of the green alga *Botryococcus braunii* on concrete with a cultivation area of 0.275 m<sup>2</sup>, for instance, showed a biomass formation of ca. 25 g m<sup>-2</sup>, corresponding to a biomass concentration of ca. 96 g L<sup>-1</sup> (Ozkan *et al.*, 2012). Recently, the principle of miniaturization was intensified further and allowed for the cultivation of the model cyanobacterium *Synechocystis* sp. PCC 6803 as biofilm in a capillary reactor (**Figure 1.8 E**) (David *et al.*, 2015). This reaction system now awaits further evaluation of biomass concentrations and applicability for biocatalytic purposes.



**Figure 1.8**: Photobioreactor concepts with increasing surface-to-volume area. **A**) Open raceway pond, figure from (Wen *et al.*, 2016), **B**) Closed tubular photobioreactor, figure from (Wijffels *et al.*, 2013), **C**) Open thin-layer photobioreactor, figure from (Apel *et al.*, 2017), **D**) Biofilm-based cultivation on concrete, figure from (Ozkan *et al.*, 2012), **E**) Biofilm-based cultivation in a capillary reactor, figure from (David *et al.*, 2015).

### 1.5 Scope of the thesis

Much success was already achieved for the development of efficient oxyfunctionalization bioprocesses by the application of oxygenases in heterotrophic whole-cell host systems. However, several restrictions such as the technically limited O<sub>2</sub> supply and carbohydrate-based electron supply still limit their implementation on an industrial scale concerning production rates and costs. The use of phototrophic organisms as whole-cell biocatalysts for oxygenase-based biotransformations provides an alternative and promising technology for the eco-efficient production of oxyfunctionalized value-added chemicals. While numerous cyanobacterial or microalgal bioprocesses were already developed for CO<sub>2</sub>-derived fermentations, biotransformation processes relying on the generation of activated reduction equivalents as well as O<sub>2</sub> derived from photosynthetic water oxidation are rare. In this context, research mainly focuses on the demonstration of engineered catalysts with emphasis on the production of hydrogen (Das and Veziroğlu, 2001). Yet, an integrated bioprocess design for the application of phototrophic organisms in redox biotransformations beyond the proof-of-concept catalyst development is lacking (Fresewinkel *et al.*, 2014).

This thesis aims at the integrated application of biotechnological methods and strategies for the development of eco-efficient photosynthesis-driven oxyfunctionalization processes. The main research question combines the conceptual evaluation of photosynthetic electron and  $O_2$  supply with the technical applicability of cyanobacteria as phototrophic host organisms in a hydrocarbon oxyfunctionalization bioprocess. Using the guide of integrated bioprocess design depicted in **Figure 1.3**, biocatalyst, reaction, and process engineering tools are applied for the establishment of new, photosynthesis-driven bioprocesses.

**Chapter 3** comprises the development of a *Synechocystis* sp. PCC 6803 strain, heterologously synthesizing the alkane monooxygenase AlkBGT originating from *Pseudomonas putida* GPo1 (Syn6803\_BGT). This chapter presents the novel concept of *in situ* supply of O<sub>2</sub> from photosynthetic water oxidation for the hydroxylation of nonanoic acid methylester (NAME) to 9-hydroxynonanoic acid methylester (H-NAME). **Chapter 4** further details the Syn6803\_BGT photobiocatalyst in long-term biotransformations, exercises substrate mass transfer and reactant toxicity in a reaction engineering approach via two-liquid phase biotransformation and describes the applicability of the photobiocatalyst in a labscale stirred tank photobioreactor. **Chapter 5** shows the development and application of a *Synechocystis* sp. PCC 6803 strain, heterologously synthesizing the cytochrome P450 enzyme system originating from *Acidovorax* sp. CHX100 (Syn6803\_CYP) for the hydroxylation of the volatile and toxic substrate cyclohexane to cyclohexanol. **Chapter 6** addresses the key limitation of cultivation systems to achieve high cyanobacterial biomass concentrations and focuses on the application of *Synechocystis* sp. PCC 6803 in a high-cell density format. This is realized via a mixed-trophies biofilm-based capillary reactor setting

using *Synechocystis* sp. PCC 6803 in combination with *Pseudomonas* sp. VLB120. **Chapter 7** generally discusses the potential of phototrophic bacteria as host organisms for  $O_2$ -dependent reactions with a particular focus on *in situ*  $O_2$  supply via photosynthetic water oxidation in relation to other concepts facilitating the *in situ*  $O_2$  generation in the liquid phase. **Chapter 8** summarizes the outcome of this thesis and provides prospects for the development of eco-efficient whole-cell redox processes. In addition, the chapter gives further insights into how the results of this thesis may be implemented into a conceptual framework addressing  $O_2$ -sensitive reactions such as the production of hydrogen functioning as zero-emission fuel gas.

# Chapter 2 Materials & Methods

## 2.1 Chemicals

**Chemicals**. Nonanoic acid methyl ester (NAME.  $\geq$  97%). cvclohexanone (Cone. 99.5%), and diisononyl phthalate (DINP, technical grade) were purchased from Sigma-Aldrich (Steinheim, Germany), 9-hydroxynonanoic acid methyl ester (H-NAME, > 95%) was purchased from TCI Europe N.V. (Zwijndrecht, Belgium). Cyclohexane (Chx,  $\geq$  99.8%) and cyclohexanol (Col,  $\geq$ 99%) were purchased from Merck (Darmstadt, Germany). Nonanoic acid (NA,  $\geq$  97%) was obtained from Fluka Chemie GmbH (Buchs, Switzerland). All other chemicals were purchased from Carl-Roth GmbH (Karlsruhe, Germany), Merck (Darmstadt, Germany) or Sigma-Aldrich (Steinheim, Germany) in the highest purity available.

### 2.2 Bacterial strains and cultivation conditions

Bacterial strains. All cyanobacterial and E. coli strains and plasmids used in this thesis are listed in Table 2.1. Kanamycin was used as selection at a final concentration of 50 µg mL<sup>-1</sup>.

Strain/ Plasmid	Description	Reference
<i>Ε. coli</i> DH5α	F <sup>–</sup> Φ80lacZΔM15 Δ(lacZYA-argF) U169 recA1 endA1 hsdR17 (rK⁻, mK⁺) phoA supE44 λB⁻ thi-1 gyrA96 relA1	(Hanahan, 1983)
Synechocystis sp. PCC 6803	Geographical origin: California, USA; Received from Pasteur Culture Collection of Cyanobacteria (PCC, Paris, France)	(Stanier <i>et</i> <i>al.</i> , 1971)
<i>E. coli</i> W3110	F⁻, λ⁻, rph-1, IN( <i>rrnD-rrnE</i> )1	(Bachmann, 1996)
Pseudomonas sp. VLB120	Wild-type Pseudomonas; styrene prototroph	(Panke <i>et</i> <i>al.</i> , 1998)
pSB1AC3_Ptrc1O:GFPmut3B	pMB1, Ptrc10 promoter, <i>GFPmut3B</i> (BBa_E0040)	(Huang <i>et</i> <i>al.</i> , 2010)
pSB1AC3_PrnpB:lacl	pMB1, $P_{mpB}$ (constitutive promoter), lac repressor (lacl)	(Huang <i>et</i> <i>al.</i> , 2010)
pPMQAK1	Broad host range plasmid (RSF), mob genes, empty cloning vector	(Huang <i>et</i> <i>al.</i> , 2010)
pRSF_PrnpB:lacl_Ptrc1O (= pAH032)	RSF, lacl under control of PrmpB promoter, Ptrcto promoter, empty expression vector	Chapter 3
pBT10	CoIE1, pRO1600, alkane monooxygenase enzyme system <i>alkBFG</i> , <i>alkST</i> (originating from <i>Pseudomons</i> <i>putida</i> GPo1) under control of P <sub>alk</sub> promoter	(Schrewe <i>et</i> <i>al.</i> , 2011)
pRSF_Ptrc10:BGTII (= pAH042)	RSF, lacl under control of PrmpB, <i>alkBGT</i> genes under control of Ptre10 promoter (genes in a row, optimized RBS, C-terminal Strep-tag II), with central terminator (biobrick #BBa_B0015)	Chapter 3

Table 2.1: Strains/ plasmids used in this thesis.

pSEVA251	Broad host range plasmid (RSF), empty cloning vector	(Martínez- García <i>et</i> <i>al</i> ., 2014)
pRSF_nAlk (=pAH010)	RSF, alkane monooxygenase enzyme system alkBFG, alkST under control of Palk promoter	Chapter 4
pRSF_PAlk (=pAH008)	RSF, Palk regulatory system	Chapter 4
pRSF_PAlk:BGT (=pAH039)	RSF, <i>alkBGT</i> genes under control of P <sub>alk</sub> promoter (genes in a row, optimized RBS, C-terminal Strep-tag II)	Chapter 4
pRSF_Ptrc10:BGT (= pAH038)	RSF, lacl under control of $P_{rmpB}$ promoter, <i>alkBGT</i> genes under control of $P_{tre10}$ promoter (genes in a row, optimized RBS, w/o C-terminal Strep-tag II), with central terminator (biobrick #BBa_B0015)	Chapter 4
pRSF_Ptrc10:BGTII_2x (= pAH048)	RSF, lacl under control of $P_{rmpB}$ promoter, two copies of the operon containing the <i>alkBGT</i> under control of $P_{trc1O}$ promoter	Chapter 4
pRSF_Ptrc10:BII (= pAH044)	RSF, lacl under control of PrmpB promoter, <i>alkB</i> gene under control of Ptre10 promoter (optimized RBS, C- terminal Strep-tag II), with central terminator (biobrick #BBa_B0015)	Chapter 4
pRSF_Ptrc10:BGII (= pAH047)	RSF, lacl under control of P <sub>mpB</sub> promoter, <i>alkBG</i> genes under control of P <sub>tre10</sub> promoter (genes in a row, optimized RBS, C-terminal Strep-tag II), with central terminator (biobrick #BBa_B0015)	Chapter 4
pCom10_capro	CoIE1, pRO1600, CypP450 monooxygenase (CYPchx), ferredoxin reductase (FdR), ferredoxin (Fd), cyclohexanone monooxygenase (CHXON) and cyclohexanol dehydrogenase (CDH) (originating from <i>Acidovorax</i> sp. CHX100) under control of P <sub>alk</sub> promoter	(Karande <i>et</i> <i>al.</i> , 2017)
pRSF_Ptrc1O:CYP (= pAH050)	Based on pAH032; CYPchx, FdR, and Fd genes under control of Ptrc10 promoter (genes in a row, optimized RBS in front of CYP)	Chapter 5
pRSF_Ptrc10:BVMO (= pAH049)	Based on pAH032; BVMO (CHXON originating from <i>Acidovorax</i> sp. CHX100) under control of $P_{trc10}$ promoter (optimized RBS, C-terminal Strep-tag II)	Chapter 6

**Cultivation of** *E. coli* **strains**. Overnight cultures were inoculated from cryo-stocks and grown in LB medium at 37 °C and 180 rpm (2.5 cm amplitude) (Sambrook and Russell, 2001). Pre-cultures were inoculated with 500  $\mu$ L from this overnight culture and grown in 50 mL M9\* medium (US<sup>+Fe</sup> trace elements) in a 250 mL baffled shake flask at 30 °C and 180 rpm (2.5 cm amplitude) (Bühler *et al.*, 2003b; Panke *et al.*, 1999). M9\* main-cultures were grown as described before by inoculating with the M9\* pre-cultures to an OD<sub>450</sub> of 0.2. Gene expression was induced 4 h after inoculation using 0.025% (v/v) DCPK (P<sub>alk</sub> promoter system) or 1 mM IPTG (P<sub>trc10</sub> promoter system) for another 4 h. The correlation factor

0.166  $g_{CDW}$  L<sup>-1</sup> OD<sub>450</sub><sup>-1</sup> was used for the calculations of cell dry weight concentrations (Blank *et al.*, 2008).

Standard cultivation of *Synechocystis* sp. PCC 6803 strains. *Synechocystis* sp. PCC 6803 was grown in YBG11 medium based on Shcolnick et al. 2007 containing 50 mM HEPES (Shcolnick *et al.*, 2007). Standard cultivation was performed using 20 mL YBG11 medium in 100 mL baffled Erlenmeyer shaking flasks in an orbital shaker (Multitron Pro shaker, Infors, Bottmingen, Switzerland) at 30 °C, 150 rpm (2.5 cm amplitude), 50  $\mu$ E m<sup>-2</sup> s<sup>-1</sup> light intensity (LED), ambient CO<sub>2</sub> (0.04%) and 75% humidity. Growth was monitored by measuring the optical density at a wavelength of 750 nm using a spectrophotometer (Libra S11, Biochrom Ltd, Cambridge, UK). Pre-cultures were inoculated using 200  $\mu$ L of a cryostock and grown under standard conditions for 4 - 6 days. Main cultures were inoculated from this pre-culture, starting with an OD<sub>750</sub> of 0.08 and, if not stated otherwise, grown for 3 days under standard conditions before gene expression was induced using 2 mM IPTG.

**YBG11 medium composition**. 1.49 g L<sup>-1</sup> NaNO<sub>3</sub>, 0.074 g L<sup>-1</sup> MgSO<sub>4</sub> · 7 H<sub>2</sub>O, 0.031 g L<sup>-1</sup> K<sub>2</sub>HPO<sup>4</sup>, 10 mL L<sup>-1</sup> YBG11 trace elements (100x) , 0.019 g L<sup>-1</sup> Na<sub>2</sub>CO<sub>3</sub>, 50 mM HEPES (pH 7.2); YBG11 trace elements (100x): 3.6 g L<sup>-1</sup> CaCl<sub>2</sub> · 2 H<sub>2</sub>O, 0.63 g L<sup>-1</sup> citric acid, 0.28 g L<sup>-1</sup> boric acid, 0.11 g L<sup>-1</sup> MnCl<sub>2</sub> · 4 H<sub>2</sub>O, 0.02 g L<sup>-1</sup> ZnSO<sub>4</sub> · 7 H<sub>2</sub>O, 0.039 g L<sup>-1</sup> Na<sub>2</sub>MoO<sub>4</sub> · 2 H<sub>2</sub>O, 0.007 g L<sup>-1</sup> CuSO<sub>4</sub> · 5 H<sub>2</sub>O, 0.005 g L<sup>-1</sup> Co(NO<sub>3</sub>)<sub>2</sub> · 6 H<sub>2</sub>O, 0.16 g L<sup>-1</sup> FeCl<sub>3</sub> · 6 H<sub>2</sub>O, 0.6 g L<sup>-1</sup> Na<sub>2</sub>EDTA · 2 H<sub>2</sub>O

Light intensity and light spectra. The light intensity was measured by means of photosynthetically active radiation (PAR) in µE m<sup>-2</sup> s<sup>-1</sup>, determined using a universal light meter (ULM-500, Heinz Walz GmbH, Effeltrich, Germany) equipped with a MQS-B mini quantum sensor. Light spectra were measured using a light spectrometer (Tristan, m-u-t GmbH, Wedel, Germany) in the orbital shaker used for cultivation of *Synechocystis sp.* PCC 6803 (LED, Multitron Pro shaker, Infors, Bottmingen, Switzerland), for oxyfunctionalization activity measurements (fluorescence light tubes, Multitron, Infors HT, Bottmingen, Switzerland) and in the growth chamber used for cultivation on agar plates (fluorescence light tubes, poly klima GmbH, Freising, Germany) (Figure 2.1).

**Correlation factor OD**<sub>750</sub> - **cell dry weight (CDW).** The correlation of the optical density OD<sub>750</sub> to the cell dry weight (CDW) was determined for the recombinant strain *Synechocystis sp.* PCC 6803 pAH042 (= Syn6803\_BGT) grown under standard conditions. At respective time-points 30 mL of grown culture was harvested by centrifugation (15 min, 3180 g, 4 °C), washed once in 15 mL H<sub>2</sub>O, resuspended in 1.5 mL H<sub>2</sub>O, and dried in predried and pre-weighted glass tubes at 70 °C for 10 days. The cell dry weight was determined and correlated to the optical density with a resulting correlation factor of 0.2246 g<sub>CDW</sub> L<sup>-1</sup> OD<sub>750</sub><sup>-1</sup> (**Figure 2.2**).



Figure 2.1. Light spectra measured in incubators equipped with LED panels or fluorescent light tubes, respectively.



**Figure 2.2**: Determination of the correlation factor regarding biomass concentrations (g<sub>CDW</sub> L<sup>-1</sup>) at various optical densities OD<sub>750</sub>. (**A**) Growth curve of *Synechocystis* sp. PCC 6803 pRSF\_Ptrc10:BGTII, (**B**) Biomass concentrations measured as g<sub>CDW</sub> L<sup>-1</sup> at various optical densities.

#### 2.3 Plasmid constructions

Plasmid constructions were performed via *E. coli* DH5 $\alpha$  using the primer given in **Table 2.2** and the following protocols and cloning steps.

**Restriction** endonucleases used in this study were obtained from Thermo Scientific – Germany GmbH (Schwerte, Germany) and used according to the manufactures' user guide. **Amplification** of DNA fragments was performed by PCR applying the Phusion High Fidelity (HF) DNA polymerase from Thermo Scientific – Germany GmbH (Schwerte, Germany) according to the 3-step protocol described in the manufactures' user guide using primers purchased from Eurofins MWG (Ebersberg, Germany) listed in **Table 2.2**. Respective annealing temperatures ( $T_{An}$ ) and elongation times ( $t_{Elong}$ ) are given below. **Overlap-Extension PCR** (OE-PCR) was performed by applying 50 ng of each DNA Fragment to be fused in 100 µL of the standard PCR mix, initially missing the respective primer as these were added after 5 PCR cycles. **Dephosphorylation** of plasmid DNA was performed using the FastAP Thermosensitive Alkaline Phosphatase from Thermo Scientific – Germany GmbH (Schwerte, Germany) according to the manufactures' user guide. **Purification** of plasmid DNA and amplified DNA fragments was performed using the PCR clean-up gel extraction kit from MACHERY-NAGEL GmbH & Co. KG (MACHEREY-NAGEL GmbH & Co. KG, Düren, Germany). **Gibson cloning** was performed by an one-step isothermal in vitro recombinant cloning method described by Gibson *et al.*, 2009 (Gibson *et al.*, 2009). **Ligation** was performed using the T4 DNA Ligase from Thermo Scientific – Germany GmbH (Schwerte, Germany) according to the manufactures' user guide. **Verification** of cloning results was performed by sequencing by Eurofins MWG (Ebersberg, Germany).

Primer#	Function	Sequence $5' \rightarrow 3'$
PAH006	AlkT rev	GCATCATTGCTAATCAGG
PAH029	AlkG rev	TCACTTTTCCTCGTAGAGC
PAH030	nAlk rev	TGCAGGTCGACTCTAGAGGATCCCCGGGTCACTTTCCTCG
		TAGAGC
PAH037	nAlk fwd	CCGCGCGAATTCGAGCTCGGTACCCGCATCATTGCTAATCA
		GG
PAH043	P <sub>alk</sub> fwd	ATAACAATTTCACACAGGAGGCCGCTTAGATAATTCCTTGAC
FAD044	Falk IEV	
PAH055	Ptre10 <sup>.</sup> Term Part I fwd	
		TCACACATACTAGTACCAGGCATCAAATAAAACG
PAH056	Ptrc10:Term Partl rev	TATAAACGCAGAAAGGCCC
PAH057	Ptrc10:Term Part II	TGATTTCTGGAATTCGCGGCCGCTTTCTAGATTGACAATTAAT
	fwd	CATCCGGCTCGTATAATGTG
PAH058	Ptrc10:Term PartII rev	ACACCTTGCCCGTTTTTTTGCCGGACTGCAGTATAAACGCAG
		AAAGGCCC
PAH059	oAlkBII fwd	TGAGCGGATAACAATTTCACACATACTAGAGTAGTGGAGGTT
		ACTAGATGCTTGAGAAACACAGAG
PAH060	AlkB rev	CIACGAIGCIACCGCAG
PAH061	AlkG fwd	GAGTACCTCTGCGGTAGCATCGTAGTACTAGAGTAGTGGAG
		GTTACTAGATGGCTAGCTATAAATGCCC
PAH062	Alk I fwd	
	Euclop oPCTII fud	
FAR1003		
PAH064	AIKBGT fusion rev	
I AI IOO7	UAIRDITTEV	CGCAGAGG
PAH068	oAlkGII fwd	GAGCCACCCGCAGTTCGAAAAATAGTACTAGAGTAGTGGAG
,		GTTACTAGATGGCTAGCTATAAATGCCC
PAH069	oAlkGII rev	CTTTTCCTCGTAGAGCAC

**Table 2.2:** Primer used during cloning procedure for plasmids constructions. binding region, fusion, overlap to vector, restriction site, appendix( $P_{trc10}$ ), scar, **RBS**<sup>\*</sup>, Strep-taq II, stop

PAH070	oAlkTII fwd	GAGCCACCCGCAGTTCGAAAAATAGTACTAGAGTAGTGGAG
		GTTACTAGATGGCAATCGTTGTTGTTG
PAH071	oAlkTII rev	ATCAGGTAATTTTATACTCCC
PAH072	Fusion oBGII rev	<b>CTA</b> TTTTTCGAACTGCGGGTGGCTCCAAGCGCTCTTTTCCTC
		GTAGAGCAC
PAH073	Fusion oBGTII rev	CTTTCGTTTTATTTGATGCCTGGTACTATTTTTCGAACTGCGG
		GTGGCTCCAAGCGCTATCAGGTAATTTTATACTCCC
PAH074	AlkB fwd	ATGCTTGAGAAACACAGAG
PAH075	AlkBGT fusion fwd	GCGACTAATTTAATAAAAATTGGAGCTAGAG <b>TAGTGGAGGT</b> T
		ACTAGATGCTTGAGAAACACAGAG
PAH076	AlkBGT fusion rev	TGCAGGTCGACTCTCAAGCATATGGCTCTAGTAGCATCATTG
		CTAATCAGG
PAH077	Terminator fwd	<u>GGGAGGTATTGGACCGCATTGAACT</u> CTAGTATAAACGCAG
		AAAGGCCC
PAH078	Terminator rev	<u>ACGAGCCGGATGATTAATTGTCAAT</u> CTAGAGCCAGGCATCAA
		ATAAAACG
PAH079	AlkB rev	CTTTCGTTTTATTTGATGCCTGGTACTATTTTTCGAACTGCGG
		GTGGCTCCAAGCGCTCGATGCTACCGCAGAGG
PAH087	Ptrc10:BGT fwd	ATCAGCTCACTCAAAGGCGGTAATCTTGACAATTAATCATCC
		GGC
PAH090	Ptrc10:BGT rev	ATTTCGGCTGAGGGTAAAAGAACTCAATTGCGAGGAAGCCT
		GCATAAC
PAH091	BVMO fwd	TGAGCGGATAACAATTTCACACATACTAGAGTAGTGGAGGT
		ACTAGATGAAAAAAACCCCAACATCTGG
PAH092	BVMO rev	
		GGTGGCTCCAAGCGCTCTGGAATACGAAACCCTCG
PAH093	CYP fwd	
		ACTAGATGACTCAGACTGCTGCGGC
PAH094	CYP rev	<u>CITICGITTATTGATGCCTGGTA</u> TCAGTGCTGCCCTTGCG
SPAH017	Verification fwd	CCATCAAACAGGATTTTCG
SPAH023	Verification rev	TGCCACCTGACGTCTAAGAA

# Construction of pRSF\_Ptrc10:BGTII (=pAH042)

a) Construction of empty expression vector pAH032

Restriction:	pSB1AC3_Ptrc1O:GFPmut3B (Xbal + Pstl) → pSB1AC3 (Xbal, Pstl)
Amplification:	Ptrc10:Term part I from pSB1AC3_Ptrc10:GFP
	(PAH055 + PAH056 → 186 BP, T <sub>An</sub> : 60 °C, t <sub>Elong</sub> : 10 sec)
	Ptrc1O:Term part II from part I
	(PAH057 + PAH058 $\rightarrow$ 262 BP, T <sub>An</sub> : 72°C, t <sub>Elong</sub> : 10 sec)
Gibson cloning:	pSB1AC3 (Xbal, Pstl) + <i>Ptrc1O:Term</i> part II
	→ pSB1AC3_Ptrc1O:Term
Restriction:	pSB1AC3_Ptrc1O:Term (Xbal)
Dephosphorylation:	pSB1AC3_Ptrc1O:Term (Xbal) (FastAP, Thermo)
Restriction:	pSB1AC_PrnpB:lacl with (Xbal + Spel)
Ligation:	pSB1AC3_Ptrc1O:Term (Xbal) + PrnpB:lacl (Xbal_Spel) (1:2)
	→ pSB1AC3_PrnpB:lacl_Ptrc1O:Term

Verification by PCR:	Clones with the PrnpB:lacl fragment incorporated in the intended
	direction were determined by PCR
	(SPAH017 + SPAH023 $\rightarrow$ 500 BP, T <sub>An</sub> : 61°C, t <sub>Elong</sub> : 15 sec)
Restriction:	pPMQAK1 (EcoRI + PstI)
Restriction:	pSB1AC3_PrnpB:lacl_Ptrc1O:Term (EcoRI + PstI)
Ligation:	pPMQAK1 (EcoRI, PstI) + PrnpB:lacl_Ptrc10:Term (EcoRI, PstI) ( 1:5)
	→ pPMQAK1_PrnpB:lacl_Ptrc10:Term = pAH032
b) Construction of pR	SF_Ptrc1O:BGTII (pAH042)
Restriction:	pPMQAK1_PrnpB:lacl_Ptrc1O:Term (Spel)
Amplification:	oAlkBII from pBT10
	(PAH059 + PAH067 → 1283 BP, T <sub>An</sub> : 65°C, t <sub>Elong</sub> : 25 sec)
	oAlkGII from pBT10
	(PAH068 + PAH069 $\rightarrow$ 568 BP, T <sub>An</sub> : 60 °C, t <sub>Elong</sub> : 25 sec)
	oAlkTII from pBT10
	(PAH070 + PAH071 $\rightarrow$ 1204 BP, T <sub>An</sub> : 65°C, t <sub>Elong</sub> : 25 sec)
OE-PCR:	oAlkBII+ oAlkGII → oAlkBGII
	(PAH063 + PAH072 → 1859 BP, T <sub>An</sub> : 65°C, t <sub>Elong</sub> : 60 sec)
	oAlkBGII + oAlkTII → oAlkBGTII
	(PAH063 + PAH073 → 3096 BP, $T_{An}$ : 57°C, $t_{Elong}$ : 90 sec)
Gibson cloning:	pPMQAK1_PrnpB:lacl_Ptrc1O:Term (Spel) + <i>oAlkBGTII</i>
	→pPMQAK1_PrnpB:lacl_Ptrc10:BGTII_pre (w/o T <sub>central</sub> )
Restriction:	pPMQAK1_PrnpB:lacl_Ptrc10:BGTII_pre (Xbal)
Amplification:	Term from pSB1AC3_Ptrc1O:GFP
	(PAH077 + PAH078 → 191 BP, T <sub>An</sub> : 60 °C, t <sub>Elong</sub> : 5 sec)
Gibson cloning	pPMQAK1_PrnpB:lacl_Ptrc10:BGTII_pre (Xbal) + Term
	→ pRSF_Ptrc10:BGTII = pAH042
Construction of pRS	SF_nAlk (= pAH010)
Restriction:	pSEVA251 with Smal
Amplification:	native <i>alk</i> expression system from pBT10 (= <i>nAlk</i> )
	(PAH037+ PAH030 $\rightarrow$ 6747 BP, T <sub>An</sub> : 58°C, t <sub>Elong</sub> : 210 sec)
Gibson cloning:	pSEVA251 (Smal) + <i>nAlk</i> → pRSF_nAlk = pAH010
Construction of pRS	SF_Palk:BGT (= pAH039)
a) Construction empty	y expression vector pAH008
Restriction:	pSEVA251 with Xmal + XbaJI
Amplification:	Promoter system <i>P<sub>alkS</sub>alkS_P<sub>alkB</sub></i> from pBT10 (= <i>Palk</i> )
	(PAH043+ PAH044 $\rightarrow$ 3157 BP, T <sub>An</sub> : 65°C, t <sub>Elong</sub> : 60 sec)
Gibson cloning:	pSEVA251 (Xmal, XbaJI) + <i>Palk</i> → pRSF_Palk = pAH008

b) Construction of pRSF\_Palk:BGT (= pAH039)

Restriction:	pRSF_Palk with EcoRI
Amplification:	A/kB from pBT10
	(PAH074 + PAH060 $\rightarrow$ 1206 BP, T <sub>An</sub> : 60 °C, t <sub>Elong</sub> : 60 sec)
	AlkG from pBT10
	(PAH061 + PAH029 → 571 BP, T <sub>An</sub> : 65°C, t <sub>Elong</sub> : 25 sec)
	AlkT from pBT10
	(PAH062 + PAH006 $\rightarrow$ 1216 BP, T <sub>An</sub> : 65°C, t <sub>Elong</sub> : 25 sec)
OE-PCR:	$AlkB + AlkG \rightarrow AlkBG$
	(PAH074 + PAH029 $\rightarrow$ 1752 BP, T <sub>An</sub> : 60 °C, t <sub>Elong</sub> : 35 sec)
	$AlkBG + AlkT \rightarrow AlkBGT$
	(PAH075 + PAH076 $\rightarrow$ 3023 BP, T <sub>An</sub> : 60 °C, t <sub>Elong</sub> : 80 sec)
Gibson cloning:	pSEVA251_Palk (EcoRI) + <i>AlkBGT</i> → pRSF_Palk:BGT = pAH039

# Construction of pRSF\_Ptrc10:BGT (= pAH038)

Restriction:	pAH032 with Spel
Amplification:	AlkB from pBT10
	(PAH059 + PAH060 → 1253 BP, T <sub>An</sub> : 65°C, t <sub>Elong</sub> : 25 sec)
	AlkG from pBT10
	(PAH061 + PAH029 $\rightarrow$ 571 BP, T <sub>An</sub> : 65°C, t <sub>Elong</sub> : 25 sec)
	AlkT from pBT10
	(PAH062 + PAH006 → 1216 BP, T <sub>An</sub> : 65°C, t <sub>Elong</sub> : 25 sec)
OE-PCR:	$AlkB + AlkG \rightarrow AlkBG$
	(PAH063 + PAH029 $\rightarrow$ 1799 BP, T <sub>An</sub> : 65°C, t <sub>Elong</sub> : 60 sec)
	$AlkBG + AlkT \rightarrow AlkBGT$
	(PAH063 + PAH064 $\rightarrow$ 3023 BP, T <sub>An</sub> : 57°C, t <sub>Elong</sub> : 90 sec)
Gibson cloning:	pAH032 (SpeI) + AlkBGT $\rightarrow$ pRSF_Ptrc10:BGT_pre (w/o T <sub>central</sub> )
Restriction:	pRSF_Ptrc10:BGT_pre with Xbal
Amplification:	Term from pSB1AC3_Ptrc1O:GFPmut3B
	(PAH077 + PAH078 $\rightarrow$ 191 BP, T <sub>An</sub> : 60 °C, t <sub>Elong</sub> : 5 sec)
Gibson cloning:	pRSF_Ptrc1O:BGT_pre (Xbal) + <i>Term</i>
	→ pRSF_Ptrc10:BGT = pAH038
Construction of p	RSF_Ptrc1O:BGTII_2x (= pAH048)
Restriction:	pRSF_Ptrc1O:BGTII with MunI
Amplification:	Ptrc10:BGTII from pRSF_Ptrc10:BGTII
	(PAH087+ PAH090 → 3387 BP, $T_{An}$ : 72°C - 0.3°C cycle <sup>-1</sup> , $t_{Elong}$ : 60 sec
Gibson cloning:	pRSF_Ptrc10:BGTII (MunI) + <i>Ptrc10:BGTII</i>
	→ pRSF_Ptrc10:BGTII_2x = pAH048

# Construction of pRSF\_Ptrc10:BII (= pAH044)

Restriction:	pAH032 with Spel
Amplification:	alkB from pBT10
	(PAH059+ PAH079 $\rightarrow$ 1308 BP, T <sub>An</sub> : 64 °C, t <sub>Elong</sub> : 40 sec)
Gibson cloning:	pAH032 (SpeI) + $AlkB \rightarrow pRSF_Ptrc1O:BII_pre$ (w/o T <sub>central</sub> )
Restriction:	pRSF_Ptrc1O:BII_pre with Xbal
Amplification:	Term from pSB1AC3_Ptrc10:GFPmut3B
	(PAH077 + PAH078 → 191 BP, $T_{An}$ : 60 °C, $t_{Elong}$ : 5 sec)
Gibson assembly:	pRSF_Ptrc1O:BII_pre (Xbal) + <i>Term</i> → pRSF_Ptrc1O:BII = pAH044
Construction of pRS	F_P <sub>trc10</sub> :BGII (=pAH047)
Restriction:	pAH032 with Spel
Amplification:	alkB from pBT10
	(PAH074+ PAH067 $\rightarrow$ 1236 BP, T <sub>An</sub> : 67°C, t <sub>Elong</sub> : 25 sec)
	alkG from pBT10
	(PAH068+ PAH069 $\rightarrow$ 568 BP, T <sub>An</sub> : 61°C, t <sub>Elong</sub> : 25 sec)
OE-PCR:	$alkB + alkG \rightarrow alkBG$
	(PAH059+ PAH072 → 1884 BP, T <sub>An</sub> : 56°C, t <sub>Elong</sub> : 45 sec)
Gibson cloning:	pAH032 (SpeI) + $alkBG \rightarrow pRSF_Ptrc10:BGII_pre(w/o T_{central})$
Restriction:	pRSF_Ptrc10:BGII_pre with Xbal
Amplification:	Term from pSB1AC3_Ptrc10:GFPmut3B
	(PAH077 + PAH078 $\rightarrow$ 191 BP, T <sub>An</sub> : 60 °C, t <sub>Elong</sub> : 5 sec)
Gibson cloning:	pRSF_Ptrc1O:BGII_pre (Xbal) + Term
	→ pRSF_Ptrc10:BGII = pAH047

# Construction of pRSF\_Ptrc1O:CYP (= pAH050)

Restriction:	pAH032 with Spel	
Amplification:	CYP-FdR-Fd from pCom10_capro	
	(PAH093 + PAH094 $\rightarrow$ 2970 BP, T <sub>An</sub> : 72 °C, t <sub>Elong</sub> : 60 sec)	
Gibson cloning:	pAH032 (Spel) + <i>CYP-FdR-Fd</i>	
	→ pRSF_Ptrc10:CYP_pre (w/o T <sub>central</sub> )	
Restriction:	pRSF_Ptrc10:CYP_pre with Xbal	
Amplification:	Term from pSB1AC3_Ptrc1O:GFPmut3B	
	(PAH077 + PAH087 $\rightarrow$ 191 BP, T <sub>An</sub> : 60 °C, t <sub>Elong</sub> : 5 sec)	
Gibson cloning:	pRSF_Ptrc1O:CYP_pre (Xbal) + Term	
	→ pRSF_Ptrc10:CYP = pAH050	

### Construction of pRSF\_Ptrc10:BVMO (= pAH049)

Restriction:	pAH032 with Spel	
Amplification:	BVMO from pCom10_capro	
	(PAH091 + PAH092 $\rightarrow$ 1689 BP, T <sub>An</sub> : 72 °C, t <sub>Elong</sub> : 45 sec)	
Gibson cloning:	pAH032 (SpeI) + BVMO $\rightarrow$ pRSF_Ptrc10:BVMO_pre (w/o T <sub>central</sub> )	
Restriction:	pRSF_Ptrc10:BVMO_pre with Xbal	
Amplification:	Term from pSB1AC3_Ptrc1O:GFPmut3B	
	(PAH077 + PAH087 $\rightarrow$ 191 BP, T <sub>An</sub> : 60 °C, t <sub>Elong</sub> : 5 sec)	
Gibson cloning:	pRSF_Ptrc1O:BVMO_pre (Xbal) + Term	
	→ pRSF_Ptrc10:BVMO = pAH049	

Transformation, Transformation of Synechocystis sp. PCC 6803 was performed by electroporation based on a method described by Ferreira, 2014 (Ferreira, 2014). Electrocompetent cells were produced by growing a 50 mL YBG11 main culture (in 100 mL baffled shaking flask) to an OD<sub>750</sub> of 0.5 - 1. Cells were harvested by centrifugation (10 min, 3180 g, 4 °C), washed three times in 10 mL ice-cold HEPES buffer (1 mM, pH 7.5) and resuspended in 1 mL HEPES buffer (1 mM, pH 7.5). Electro-competent cells were stored at -80 °C in 5% (v/v) DMSO. For electroporation 0.2 - 1.0 ug of plasmid DNA were added to 60 µL of cells in an electroporation cuvette (2 mm electrode gap), pulsed with 2500 V for 5 ms (12.5 kV cm<sup>-1</sup>) (Eppendorf Eporator, Eppendorf Vertrieb Deutschland GmbH, Wesseling-Berzdorf, Germany) and subsequently transferred to 50 mL YBG11 medium (100 mL baffled shanking flask). After cultivation at standard conditions for 24 h, cells were harvested by centrifugation (10 min, 3180g, RT), resuspended in 100 µL YBG11 medium and plated on BG11 agar supplemented with 0.3% of sodium thiosulfate and 50 µg mL<sup>-1</sup> kanamycin. Plates were cultivated in a growth chamber for 4-6 days at 30 °C. 20-50 uE m<sup>-2</sup> s<sup>-1</sup> light intensity (fluorescence light tubes), ambient CO<sub>2</sub> (0.04%) and 80% humidity (poly klima GmbH, Freising, Germany). Single colonies were picked, plated on fresh BG11 agar and incubated as described before. The grown biomass was used to inoculate a 20 mL YBG11 pre-culture until cryo stocks were prepared from this pre-culture and stored in 5% (v/v) DMSO at -80 °C.

**BG11 agar plates**: 1.5 g L<sup>-1</sup> NaNO<sub>3</sub>, 0.075 g L<sup>-1</sup> MgSO<sub>4</sub>  $\cdot$  7 H<sub>2</sub>O, 0.036 g L<sup>-1</sup> CaCl<sub>2</sub>  $\cdot$  2 H<sub>2</sub>O, 0.006 g L<sup>-1</sup> citric acid, 0.04 g L<sup>-1</sup> K<sub>2</sub>HPO<sub>4</sub>, 0.006 g L<sup>-1</sup> ferric ammonium citrate, 0.001 g L<sup>-1</sup> Na<sub>2</sub>EDTA, 0.02 g L<sup>-1</sup> Na<sub>2</sub>CO<sub>3</sub>, 1 mL L<sup>-1</sup> BG11 trace elements (1000x), 0.3% Na<sub>2</sub>S<sub>2</sub>O<sub>3</sub>, 10 mM HEPES (pH 8), 1.5% agar; BG11 trace elements (1000x): 2.86 g L<sup>-1</sup> boric acid, 1.8 g L<sup>-1</sup> MnCl<sub>2</sub>  $\cdot$  4 H<sub>2</sub>O, 0.22 g L<sup>-1</sup> ZnSO<sub>4</sub>  $\cdot$  7 H<sub>2</sub>O, 0.39 g L<sup>-1</sup> Na<sub>2</sub>MoO<sub>4</sub>  $\cdot$  2 H<sub>2</sub>O, 0.08 g L<sup>-1</sup> CuSO<sub>4</sub>  $\cdot$  5 H<sub>2</sub>O, 0.05 g L<sup>-1</sup> Co(NO<sub>3</sub>)<sub>2</sub>  $\cdot$  6 H<sub>2</sub>O

### 2.4 Biochemical analysis of recombinant strains

Membrane fractionation of Syn6803 BGT using sucrose density gradient centrifugation. Membrane fractionation of Syn6803 BGT was performed using a protocol adapted from Omata and Murata et al. (Murata and Omata, 1988; Omata and Murata, 1983; Omata and Murata, 1984). If not stated otherwise, all steps were performed on ice. 50 mL of cyanobacterial cell culture (OD<sub>750</sub> > 40) were washed twice in 50 mL of buffer A (5 mM HEPES, pH 7 - sterile filtered, 1 mM phenylmethylsulfonyl fluorid (PMSF) - added just before use), resuspended in 100 mL lysis buffer (10 mM HEPES, pH 7, 600 mM sucrose, 5 mM EDTA. 50 mM NaCl. 2.5 g L<sup>-1</sup> lysozyme – added just before use) and incubated in a 250 mL baffled shake flask for 2 h at 50 µE m<sup>-2</sup> s<sup>-1</sup>, 30 °C, and 200 rom (2.5 cm amplitude). After centrifugation (10 min. 5000 g. 4 °C), the pellet was washed twice in 50 mL buffer B (20 mM HEPES, pH 7, 600 mM sucrose, 1 mM PMFS – added just before use), resuspended in 50 mL buffer B and supplemented with 50 µL DNAse I (final 5 U mL<sup>-1</sup>, stock: 5000 U mL<sup>-1</sup>, 1.3 mg mL<sup>-1</sup> DNAse I à 3755 U mg<sup>-1</sup> in 20 mM Tris pH 7.5, 1 mM MgCl<sub>2</sub> · 6 H<sub>2</sub>O, 50% glycerol). Cell disruption was conducted using FrenchPress (3 x 1900 Psi). After centrifugation (5 min, 5000 g, 4 °C), the supernatant was collected as total protein fraction and supplemented with 0.74 volumes of 90% sucrose dissolved in buffer B (= 50% total sucrose concentration). Sucrose density centrifugation was performed in thin wall polypropylene tubes (total volume 38.5 mL, Beckmann Coulter GmbH, Krefeld, Germany) using the following gradient: 15 mL of sample (50% sucrose), 10 mL 10% sucrose (in buffer B), 3 mL 30% sucrose (in buffer B), and 10 mL 10% sucrose (in buffer B). Ultracentrifugation was conducted at 130,000 g and 4 °C for 18 h. Fractions for plasma membrane (PM), thylakoid membrane (TM), and the red fraction were collected as depicted in Figure 2.3.



Figure 2.3: Picture (left) and schematic view (right) of membrane fractions containing respective proteins obtained after sucrose density centrifugation.

The outer membrane (OM) proteins in the pellet were resuspended in 250  $\mu$ L buffer C (20 mM HEPES, pH 7). PM and TM fractions were diluted 3-fold in buffer C, centrifuged again at 120,000g, 4 °C for 1 h and resuspended in 250  $\mu$ L buffer C. The red fraction was further separated by centrifugation (30 min, 10,000g, 4 °C). Protein concentrations were

measured using Bradford analysis (Bradford, 1976). All samples were stored at -20 °C for Western blot analysis.

Strep-tag purification of recombinant Synechocystis sp. PCC 6803 strains, Ca. 200 mL of cvanobacterial cell culture (OD<sub>750</sub> ca, 2) were harvested by centrifugation (5000g,  $4 \, ^{\circ}$ C, 10 min), washed in 25 mL TBS buffer (100 mM Tris-HCl pH 7.5, 150 mM NaCl, 1 mM phenylmethylsulfonyl fluorid (PMSF) - added just before use), and resuspended in 3 mL TBS buffer containing 100 µL of DNAse I (final 167 U. stock: 5000 U mL<sup>-1</sup>. 1.3 mg mL<sup>-1</sup> DNAse I à 3755 U mg<sup>-1</sup> in 20 mM Tris pH 7.5, 1 mM MgCl<sub>2</sub> · 6 H<sub>2</sub>O, 50% glycerol). Cell disruption was conducted using FrenchPress (2 x 1200 Psi). The total protein fraction in the supernatant was collected by centrifugation (5.000g, 4 °C, 10 min). Protein concentrations were quantified by the method of Bradford (Bradford, 1976). AlkB, AlkG, and AlkT were separated from the total protein fraction using Strep-Tactin Superflow chromatography according to the manufactory manual (IBA GmbH, Göttingen, Germany). 1.5 mL of the total protein sample were loaded to a pre-conditioned Strep-Tactin purification column (2 mL of 50% Strep-Tactin Superflow suspension, equilibrated with 2 mL buffer W (100 mM Tris-HCl pH 8.0, 150 mM NaCl, 1 mM EDTA)). Proteins were washed using 3 x 1 mL TBS buffer before Strep-tag proteins were eluted using 2 x 0.75 mL elution buffer (2.5 mM Desthiobiotin in TBS buffer). If required, proteins were 5x concentrated by acetone precipitation by adding 800 µL acetone to 200 µL of proteins, and incubation at -20 °C for ca. 16 h. Proteins were collected by centrifugation (17,000g, 4 °C, 10 min) and resuspended in 20 µL of SDS buffer.

**Cell disruption of** *Synechocystis* **sp. PCC 6803 using glass beads.** *Synechocystis* **sp.** PCC 6803 cells were cultivated as described before, harvested by centrifugation (10 min, 4 °C, 5000g) and stored at -20 °C. Cell disruption was performed with a homogenizer (Precellys Evolution Super Homogenizer, BERTIN TECHNOLOGIES, Saint Quentin en Yvelines Cedex, France) using glass beads in TBS-buffer (0.1 M Tris, 0.15 M NaCl, pH 7.5) containing 1 mM PMSF at an OD<sub>750</sub> of 20 (4 x 30 s at 17,000g, cooling with liquid nitrogen). Proteins in the supernatant were treated with 2x SDS-buffer at 99 °C for 10 min before 20 µL of each sample was loaded on SDS-gels.

SDS PAGE analysis and Western blot analysis. Protein separation was performed as described by Laemmli with a 3.6% acrylamide stacking and a 12% acrylamide separating gel (Laemmli, 1970). For Western blot analysis, proteins were transferred from acrylamide gels to a nitrocellulose membrane (0.45  $\mu$ m) using semi-dry blotting for 30 min at 0.8 mA cm<sup>-2</sup>. Detection of Strep-tagII-tagged proteins was performed using a Strep-Tactin-HRP antibody (IBA Lifesciences, Göttingen, Germany). Analysis of the purity of the plasma membrane protein fraction after membrane fractionation was performed using anti NrtA antibody. Visualization was followed using chemiluminescence (SuperSignal West Pico PLUS Chemiluminescent Substrate, ThermoFisher Scientific, Waltham, USA) and X-ray development.

Chapter 3 Overcoming the gas-liquid mass transfer of oxygen by coupling photosynthetic water oxidation with biocatalytic oxyfunctionalization

Bruno Bühler and Andreas Schmid coordinated the project and corrected the manuscript.

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### 3.1 Abstract

Gas-liquid mass transfer of gaseous reactants is a major limitation for high space-time yields, especially for  $O_2$ -dependent (bio)catalytic reactions in aqueous solutions. Herein, oxygenic photosynthesis was used for homogeneous  $O_2$  supply via *in situ* generation in the liquid phase to overcome this limitation. The phototrophic cyanobacterium *Synechocystis* sp. PCC 6803 was engineered to synthesize the alkane monooxygenase AlkBGT from *Pseudomonas putida* GPo1. With light, but without external addition of  $O_2$ , the chemo- and regioselective hydroxylation of nonanoic acid methyl ester to 9-hydroxynonanoic acid methyl ester was driven by  $O_2$  generated through photosynthetic water oxidation. Photosynthesis also delivered the necessary reduction equivalents to regenerate the Fe<sup>2+</sup> center in AlkB for oxygen transfer to the terminal methyl group. The *in situ* coupling of oxygenic photosynthesis to  $O_2$ -transferring enzymes now enables the design of fast hydrocarbon oxyfunctionalization reactions.

### 3.2 Introduction

Gas-liquid mass transfer defines the performance and efficiency of reactions in liquids with gaseous reactants. This is especially true for (bio)catalysts operating in agueous solutions (Chaudhari et al., 1995: Cornils and Herrmann, 2004: Law et al., 2006: Park, 2007: Wachsen et al., 1998).  $O_2$  is one of the most prominent gaseous reactants. As an oxidant for oxidative catalysis, O<sub>2</sub> is of great importance for the production of value-added chemicals and pharmaceuticals (Bühler et al., 2003a; Gavriilidis et al., 2016; Piera and Bäckvall, 2008; Shi et al., 2012). For the efficient use of  $O_2$  as a reactant, harsh reaction conditions with high temperatures and/or pressures are typically necessary. Such conditions may lead to severe safety and selectivity issues, often resulting in low reaction yields. They typically also necessitate highly regulated, elaborate, and thus expensive process control regimes (Gavriilidis et al., 2016; Osterberg et al., 2014; Schuchardt et al., 2001). Mild reaction conditions, high selectivities, and high yields are generally desirable for oxidative production processes and achieved most efficiently by enzyme catalysis (Bordeaux et al., 2012; Schmid et al., 2001). However, low gas-liquid mass transfer rates unfortunately constitute major limitations under such mild conditions (Law et al., 2006). Furthermore, the application of enzymes in whole cells, which is advantageous for oxygenases, suffers from a competition for O<sub>2</sub> between the target reaction and respiration (Duetz et al., 2001; Schrewe et al., 2013). A technical solution for increasing the O<sub>2</sub> gas-liquid mass transfer rate under ambient conditions is the utilization of O<sub>2</sub>-enriched air (Hilker et al., 2006). Yet, O<sub>2</sub> mass transfer is basically limiting the space-time yields of processes with high oxidation rates, especially in the production of bulk chemicals (Duetz et al., 2001; Garcia-Ochoa and Gomez, 2009; Gemoets et al., 2016; Law et al., 2006). To improve O2 mass transfer, various reactor concepts with different modes of gaseous reactant supply have been proposed (Gavriilidis et al., 2016). Examples include the utilization of bubble columns, gas-permeable membranes, segmented flow microreactors, or falling film microreactors (Bolivar et al., 2016; Gemoets et al., 2016; Greene et al., 2015; Kantarci et al., 2005; Karande et al., 2011; Tomaszewski et al., 2014).

Herein, we report a novel concept based on oxygenic photosynthesis for the homogeneous supply of  $O_2$  to an oxidation reaction. To date, several studies have investigated the coupling of light-driven electron activation to (enzymatic) reactions, both chemically and biotechnologically (Balcerzak *et al.*, 2014; Hisatomi *et al.*, 2014; Hollmann *et al.*, 2007; Köninger *et al.*, 2016; Lassen *et al.*, 2014b; Mifsud *et al.*, 2014; Okeefe *et al.*, 1994; Yu *et al.*, 2013). However, light-driven water oxidation has not been considered for the homogeneous supply of  $O_2$ . Photosynthesis generates  $O_2$  *in situ* within an aqueous liquid phase from water. This has the potential to basically overcome gas-liquid mass transfer limitations. Light-driven photosynthetic water oxidation is the core of our concept, delivering  $O_2$  homogeneously

within cells to the catalytically active oxygenase enzyme, thus driving the oxyfunctionalization reaction (**Figure 3.1**). The well-studied phototrophic cyanobacterium *Synechocystis* sp. PCC 6803 was chosen as the source for delivering O<sub>2</sub>. It was engineered for the synthesis of alkane monooxygenase AlkBGT originating from *Pseudomonas putida* GPo1 (hereinafter referred to as Syn6803\_BGT) (Peterson *et al.*, 1966b). The highly regioselective terminal oxyfunctionalization of nonanoic acid methyl ester served as the model oxidation reaction. It constitutes an industrially relevant example for the production of polymer building blocks from renewables (**Figure 3.1**) (Evonik Industries AG, 2013; Ladkau *et al.*, 2016; Schaffer and Haas, 2014; Schrewe *et al.*, 2014).



**Figure 3.1**: Homogenous  $O_2$  evolution coupled to an oxygenase-catalyzed oxyfunctionalization reaction. Water is oxidized by the photosynthetic cyanobacterium *Synechocystis* sp. PCC 6803, yielding  $O_2$  and activated reduction equivalents. The heterologously introduced alkane monooxygenase system AlkBGT captures both  $O_2$  and the reduction equivalents, and catalyzes the regiospecific oxyfunctionalization of nonanoic acid methyl ester (NAME) to 9-hydroxynonanoic acid methyl ester (H-NAME).

### 3.3 Materials and methods

**Chemicals and cultivation procedures**. Chemicals and cultivation procedures used in this study are described in **Chapter 2**.

**Bacterial strain**. The genetic introduction of the *alkBGT* genes encoding the alkane monooxygenase AlkB, the rubredoxin AlkG and the rubredoxin reductase AlkT into *Synechocystis sp.* PCC 6803 was achieved via an expression system located on the broad host range plasmid pPMQAK1 (Huang *et al.*, 2010). The cloning procedure for the resulting plasmid pAH042 is given in **Chapter 2**. Gene expression was based on the IPTG inducible  $P_{trc10}$  promoter system (Huang *et al.*, 2010) and translation was initiated via optimized ribosomal binding sites in front of each gene (Heidorn *et al.*, 2011); each gene sequence encoded a C-terminal Strep-tag II (Schmidt *et al.*, 1996) (**Figure 3.2**). *Synechocystis sp.* PCC 6803 harboring the plasmid pAH042 is hereinafter referred to as Syn6803\_BGT.



**Figure 3.2**: Schematic representation of the constructed expression system of the plasmid pAH042. RBS\* = ribosomal binding site optimized for *Synechocystis* sp. PCC 6803 (Heidorn *et al.*, 2011), STII = Strep-tag II (Schmidt *et al.*, 1996), T<sub>double</sub> = double terminator (biobrick #BBa\_B0015).

Whole-cell oxyfunctionalization using Syn6803 BGT. Oxyfunctionalization activity measurements were performed 24 hours after induction of gene expression. Cells were harvested by centrifugation (15 min. 2000 g. 4 °C) and resuspended in YBG11 medium (50 mM HEPES) to a final cell concentration of ca. 2 g<sub>CDW</sub> L<sup>-1</sup>. To 1 mL cell suspension in 11 mL screw cap glass tubes, the substrate NAME was added to a final concentration of 10 mM from a 2 M stock in ethanol. The biotransformation reaction was performed at 30 °C. 220 rpm (2.5 cm amplitude) in an orbital shaker equipped with fluorescence light tubes set to a light intensity of 30  $\mu$ E m<sup>-2</sup> s<sup>-1</sup> (Multitron, Infors HT, Bottmingen, Switzerland). The biotransformation reaction was guenched after respective time-points by addition of 1 mL of ice-cold diethylether containing 0.2 mM hexadecane as internal standard. After thorough mixing for 1 min (vortex) and phase separation performed by centrifugation (5 min, 3180 g, 4 °C), the organic phase was dried over anhydrous Na<sub>2</sub>SO<sub>4</sub> and analyzed via gas chromatography. Activity assays under anaerobic conditions were performed by degassing the cell suspension from oxygen by bubbling with nitrogen gas at 70 mL min<sup>-1</sup> for 10 minutes, followed by substrate addition in an anaerobic chamber in  $N_2$  atmosphere (100 ppm  $O_2$ , 1.6 ppm H<sub>2</sub>, 25 °C, 65% humidity). Afterwards the gas tight screwed glass tubes were treated as light described above, except for а changed intensity from 30 to 50 µE m<sup>-2</sup> s<sup>-1</sup>. The light spectrum applied for the determination of oxyfunctionalization activities under anaerobic conditions might vary as light tubes with the same specifications were used covered by a plastic hood (L18W/840, Lumilux Cool White, Osram, München, Germany).

Whole-cell oxyfunctionalization using *E. coli* W3110 (pAH042). Cells were grown as described before, harvested by centrifugation (5000g, 4 °C, 10 min) and resuspended in KPi buffer containing 1% glucose (pH 7.4) to respective biomass concentrations. Aliquots of 0.8 mL culture were provided in 2 mL reaction tubes and pre-warmed for 5 min at 30 °C and 1500 rpm (ThermoMixerC, Eppendorf, Wesseling-Berzdorf). The biotransformation reaction was started by adding 5 mM NAME (5  $\mu$ L of 0.8 M stock in ethanol). After 15 minutes of incubation time, the reaction was quenched using 0.8 mL ice-cold diethyl ether containing 200  $\mu$ M of hexadecane as internal standard and vortexing for 1 min before centrifugation (17000g, 4 °C, 5 min). The supernatant was dried over anhydrous Na<sub>2</sub>SO<sub>4</sub> and applied for GC analysis.

**Quantification of product formation**. The oxyfunctionalized product H-NAME was quantified using gas chromatoraphy (GC Trace 1310, Thermo Fisher Scientific, Waltham, USA) equipped with a TG-5MS capillary column (5% diphenyl / 95% dimethyl polysiloxane, 30 m, I.D.: 0.25 mm, film thickness: 0.25 µm, ThermoFisher Scientific, Waltham, USA) and a flame ionization detector (FID) operating at 320 °C, 350 mL min<sup>-1</sup> air flow, 30 mL min<sup>-1</sup> makeup gas flow and 35 mL min<sup>-1</sup> hydrogen gas flow. Nitrogen gas was applied as carrier gas with a constant flow of 1.5 mL min<sup>-1</sup>. The injection volume was set to 1 µL using a PTV injector, programmed with a temperature gradient of 10 °C s<sup>-1</sup> from 90-300 °C. Split transfer was applied after 0.5 min with a split ratio of 7. The oven temperature profile was: 1) 80 °C for 1 min, 2) 80-160 °C with 50 °C min<sup>-1</sup>, 3) 160-220 °C with 15 °C min<sup>-1</sup>, 4) 220-300 °C with 50 °C min<sup>-1</sup> and 5) 300 °C for 3.8 min.

**Oxygen evolution measurement**. Oxygen evolution measurements were performed using a Clark-type sensor, measuring the oxygen partial pressure (OX-MR microsensor, 400  $\mu$ m tip diameter, Unisense, Aarhus, Denmark) equipped with the respective microsensor amplifier (Microsensor multimeter, Unisense, Aarhus, Denmark) applied in gas tight glass chambers (MicroRespiration System, Unisense, Aarhus, Denmark). Oxygen evolution rates were calculated within 5 minutes of illumination at a light intensity of 50  $\mu$ E m<sup>-2</sup> s<sup>-1</sup> (fluorescence light tube).

### 3.4 Results

Syn6803\_BGT produced ca. 65  $\mu$ M 9-hydroxynonanoic acid methyl ester (H-NAME) from 10 mM nonanoic acid methyl ester (NAME) within 20 min under constant illumination. This translates into a specific oxidation rate of 1.5 ± 0.2 U g<sub>CDW</sub><sup>-1</sup> (**Table 3.1**) and demonstrates the functionality of the biocatalyst. However, a specific oxidation rate of 1.3 ± 0.1 U g<sub>CDW</sub><sup>-1</sup> was still measured in the dark, showing that reduction equivalents were supplied at almost the same rate with and without light (**Table 3.1**). Obviously, the catabolism of storage compounds enabled substantial NAD(P)H regeneration in the dark.

Upon successful construction of the functional phototrophic whole-cell biocatalyst, we evaluated the oxidation reaction for exclusive utilization of photosynthetically generated O<sub>2</sub>. The terminal hydroxylation of NAME by Syn6803\_BGT was studied under anaerobic, but otherwise identical conditions. H-NAME formation depended directly upon illumination and thus water oxidation. Product formation was not observed in the absence of light (**Figure 3.3**). The specific oxidation rate obtained under anaerobic conditions and illumination was  $0.9 \pm 0.1 \text{ U g}_{\text{CDW}^{-1}}$  (**Table 3.1**) de facto driven by O<sub>2</sub> generated in the photosynthetic light reaction.

The specific O<sub>2</sub> evolution rate of Syn6803\_BGT was determined separately in the absence of the substrate NAME, for assessing the fraction of photosynthetically generated O<sub>2</sub> captured by the monooxygenase (**Table 3.1**). With an O<sub>2</sub> evolution rate of  $3.7 \pm 0.5 \text{ U g}_{\text{CDW}^{-1}}$ ,

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corresponding to 100% of  $O_2$  available in the system (assuming no photorespiration), nearly 25% of the photosynthetically generated  $O_2$  was captured for terminal hydroxylation of NAME.

Table 3.1: Specific rates for the hydroxylation of nonanoic acid methyl ester to 9-hydroxynonanoic acid methyl ester and  $O_2$  evolution of Syn6803\_BGT.

Conditions	Specific production reaction rate / U g <sub>CDW</sub> <sup>-1</sup>
Aerobic, irradiated <sup>[a]</sup>	1.5 ± 0.2
Aerobic, in the dark <sup>[a]</sup>	1.3 ± 0.1
Anaerobic, irradiated <sup>[b]</sup>	0.9 ± 0.1
Anaerobic, in the dark <sup>[b]</sup>	0.0
Anaerobic, irradiated, OER [c]	$3.7 \pm 0.5$

Specific product formation rates are given with respect to the product formed after [a] 20 or [b] 30 min. [c] The specific  $O_2$  evolution rate (OER) was determined within the aqueous phase in a sealed, gasfree glass chamber in the absence of substrate. U = µmol min<sup>-1</sup>. Average values and standard deviations of at least two independent biological replicates are given.



**Figure 3.3**. *In situ* supply of photosynthetically generated  $O_2$  to the oxidizing enzyme AlkBGT in Syn6803\_BGT. The biotransformation experiment was performed under anaerobic conditions under irradiation (- $\blacktriangle$ -) or in the dark (-o-). Average values and standard deviations of two independent biological replicates are given. CDW = cell dry weight.

#### 3.5 Discussion

Diffusion of photosynthetically generated  $O_2$  may affect the reaction efficiency of the terminal hydroxylation and theoretically results in gas-liquid mass transfer processes within the assay system. The specific  $O_2$  accumulation rate in the aqueous phase was calculated to be 0.01 µmol min<sup>-1</sup> g<sub>CDW</sub><sup>-1</sup> assuming immediate  $O_2$  diffusion from the aqueous to the gaseous phase (aqueous/gaseous ratio 1:10, Henry volatility for  $O_2$  in water:  $H_{cc}=c_{aq}/c_{gas}=0.0297$  at 25 °C) (Sander, 2015). Thus the effective  $O_2$  concentration does not exceed 0.6 µM within

30 min of reaction time (applied biomass concentration: 2  $g_{CDW}$  L<sup>-1</sup>). In contrast, Michaelis constants ( $K_M$ ) of oxygenases with respect to  $O_2$  are typically in the range of 10-60  $\mu$ M (Duetz *et al.*, 2001). This, together with the high fraction of  $O_2$  captured by the monooxygenase (25%), suggests that the photosynthetically generated  $O_2$  is concentrated within the microbial cell and captured *in situ* by the monooxygenase before diffusing out of the cell. Although  $O_2$  can in principle diffuse across cellular membranes, the lipid bilayer system seems to pose a physical barrier that is beneficial for the intracellular oxidation process. These results are proof of concept for the *in situ* coupling of photosynthetic  $O_2$  evolution to  $O_2$ -dependent oxidation reactions. The photosynthetic light reaction was used for the intracellular supply of both activated reduction equivalents and  $O_2$ .

#### 3.6 Conclusions & Outlook

These results might be the starting point for the development of various efficient photosynthesis-driven oxyfunctionalization reactions. In the present case, future optimizations include an increase in the AlkBGT level in the cvanobacterial whole-cell biocatalyst (Oliver and Atsumi, 2014; Ruffing, 2011). This is obvious from comparing the transformation rates of NAME into H-NAME catalyzed by E. coli W3110 carrying the very plasmid pAH042 (10.0 ± 0.1 U q<sub>CDW</sub><sup>-1</sup>; Figure 10.1) with those of E. coli that strongly express alkBGT (104 - 128 U g<sub>CDW</sub><sup>-1</sup>) (Julsing et al., 2012b; Schrewe et al., 2011). Other targets are electron channeling and improved cultivation and bioreactor concepts. The cyanobacterial photosynthetic metabolism supports the supply of activated reduction equivalents at high rates (123 U  $q_{CDW}^{-1}$ ) (Köninger et al., 2016). Yet, the O<sub>2</sub> evolution rate determined in this study implies a photosynthetic activity of only 3.7 U g<sub>CDW</sub><sup>-1</sup>. This corresponds to a specific NAD(P)H regeneration rate of 7.4 U g<sub>CDW</sub><sup>-1</sup>. The theoretical maximum of this rate was estimated to be 850 U  $q_{CDW}^{-1}$  (assumptions for PSII:  $k_{cat}$ =1000 s<sup>-1</sup>, 10 mg  $q_{CDW}^{-1}$ ,  $M_W$  = 350 kDa) (Dismukes et al., 2009; Köninger et al., 2016; Shen, 2015). With high biomass concentrations (40 g<sub>CDW</sub> L<sup>-1</sup>), a theoretical maximum of 2040 mmol L<sup>-1</sup> h<sup>-1</sup> would be possible for the oxygen supply rate. This translates into a volumetric mass transfer coefficient  $k_{L}a$  of 4533 h<sup>-1</sup> for a bioreactor operated at 2.5 atm, 30 °C, and a residual O<sub>2</sub> concentration of 100 µM (typical conditions for large-scale bioreactor operation) (Duetz et al., 2001). In contrast, the  $k_1 a$  values of large-scale bioreactors are on the order of 200 h<sup>-1</sup> (Duetz et al., 2001). In addition, the use of photoautotrophic instead of chemoheterotrophic organisms largely relieves the competition for O<sub>2</sub> between oxygenation and respiration.

The development of photobioreactors enabling the generation of high biomass concentrations with high oxygen evolution activity is key for the future applicability of the presented concept (Kumar *et al.*, 2011). Biofilm cultivation in capillary microreactors constitutes one possible solution to increase the cyanobacterial biomass concentration (David *et al.*, 2015). Stable cyanobacterial biofilm cultivation has recently been achieved over

several weeks with retention of the photosynthetic activity throughout the biofilm. Reaction optimization addressing the key issue of photobioreactor development has the potential to facilitate currently oxygen-transfer-limited selective hydroxylation processes for the biocatalytic functionalization of hydrocarbons (Duetz *et al.*, 2001; Schrewe *et al.*, 2013). In summary, the *in situ* coupling of oxygenic photosynthesis to oxidizing enzymes provides a novel and safe access to  $O_2$  as a reactant for designing new reactions for oxidation catalysis.

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Chapter 4 Stabilization of photosynthesis-driven wholecell hydroxylation of nonanoic acid methyl ester by twoliquid phase biotransformation

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## 4.1 Abstract

Photoautotrophic organisms are promising hosts for biocatalytic oxyfunctionalizations because they supply reduction equivalents as well as O<sub>2</sub> via photosynthetic water oxidation. Thus far, research on photosynthesis-driven bioprocesses mainly focuses on strain development and the proof of principle in small-scale biocatalytic reaction setups. This study investigates the long-term applicability of the previously developed cyanobacterial strain Synechocystis sp. PCC 6803 BGT harboring the alkane monooxygenase system AlkBGT catalyzing terminal alkyl group oxyfunctionalization. For nonanoic acid methyl ester (NAME) hydroxylation, the biocatalyst showed light intensity-independent hydroxylation activity and substantial hydrolysis of NAME to nonanoic acid. Substrate mass transfer limitation. substrate hydrolysis, as well as substrate toxicity were overcome via in situ substrate supply by means of a two-liquid phase system. Usage of diisononyl phthalate as organic carrier solvent enabled 1.7-fold increased initial specific activities (5.6  $\pm$  0.1 U  $q_{CDW}^{-1}$ ) and 7.6-fold increased specific yields on biomass  $(3.8 \pm 0.1 \text{ mmol}_{H-NAME} \text{ } \text{g}_{CDW}^{-1})$  as compared to single aqueous phase biotransformation. Finally, the whole-cell biotransformation system was successfully scaled from 1 mL glass tube to 3 L stirred tank photo-bioreactor scale. This is the first study reporting on the application of the two-liquid phase concept for efficient phototrophic whole-cell biocatalysis.

## 4.2 Introduction

Oxygenases are powerful enzymes for regio-, chemo-, and stereoselective C-H oxyfunctionalization. Whole-cell biocatalysis systems based on chemoheterotrophic host organisms like *E. coli* or Pseudomonads have successfully been developed reaching titers and rates feasible for the chemical industries (Evonik Industries AG, 2013; Ladkau *et al.*, 2016; Panke *et al.*, 2002). Recently, photoautotrophic organisms such as cyanobacteria have been tested as alternative biocatalytic host systems for such biotransformations (Böhmer *et al.*, 2017; Lassen *et al.*, 2014b; Wlodarczyk *et al.*, 2015; Yamanaka *et al.*, 2015). Photosynthesis-driven NAD(P)H regeneration relies on electrons derived from water oxidation empowered by light energy. In contrast to chemoheterotrophic biocatalysts, which depend on organic carbon-based electron and energy sources like glucose, cofactor, biocatalyst, and enzyme (re)generation in photoautotrophic biocatalysts only requires water, inorganic CO<sub>2</sub>, and light. Furthermore, *in situ* O<sub>2</sub> generation upon photosynthetic water oxidation advances the applicability of whole-cell biocatalysts for oxyfunctionalization reactions by overcoming gas-liquid O<sub>2</sub> mass transfer limitations (**Chapter 3, Chapter 7**).

The oxyfunctionalization of fatty acid methyl esters (FAMEs) to respective alcohols, aldehydes, and acids, catalyzed by the alkane monooxygenase system AlkBGT, is a well-developed example for the use of chemoheterotorphic cells as host system for oxygenases. This three-component enzyme system originates from *Pseudomonas putida* GPo1 and consists of a rubredoxin reductase (AlkT), a rubredoxin (AlkG), and the monooxygenase component AlkB (McKenna and Coon, 1970; Peterson *et al.*, 1966b). In 2011, Schrewe *et al.* developed a recombinant *E. coli* strain, catalyzing the terminal hydroxylation of nonanoic acid methyl ester (NAME) to 9-hydroxynonanic acid methyl ester (H-NAME) at high specific rates (100 U g<sub>CDW</sub><sup>-1</sup>) (Schrewe *et al.*, 2011). Subsequent reaction engineering involving *in situ* product removal via a two-liquid phase approach enabled efficient terminal oxy- and aminofunctionalization of FAMEs at bioprocess relevant scales (Evonik Industries AG, 2013; Ladkau *et al.*, 2016; Schrewe *et al.*, 2014). Recently, we transferred the AlkBGT system via the plasmid pAH042 into the photoautotrophic host *Synechocystis* sp. PCC 6803 (henceforth referred to as Syn6803\_BGT) and experimentally proved the concept of photosynthesis-driven FAME oxyfunctionalization (**Chapter 3**).

In this study, the hydroxylation performance of Syn6803\_BGT was investigated in more detail, focusing on CO<sub>2</sub> and light availabilities as influencing factors during biocatalyst growth and biotransformation. Further, the long-term operational stability of photosynthesis-driven NAME biotransformation was evaluated. *In situ* substrate supply via a two-liquid phase system was tested to enhance and stabilize biocatalyst performance by overcoming reactant toxicity as well as mass transfer limitations. Finally, the reaction system is scaled from a glass tube to a stirred tank photo-bioreactor setting.

#### 4.3 Materials and Methods

Chemicals, bacterial strains, and plasmids. Chemicals used in this study are given in Chapter 2. Syn6803\_BGT, i.e., *Synechocystis* sp. PCC 6803 harboring the alkane monooxygenase system AlkBGT on plasmid pAH042, has been constructed in Chapter 3. Cloning procedures of this and further plasmids and strains used in this study are given in Chapter 2 (Table 2.1).

Cultivation of *Synechocystis* sp. PCC 6803. If not stated otherwise, shake flask cultivation of *Synechocystis* sp. PCC 6803 was performed as described in **Chapter 2** (YBG11 medium, 50 mM HEPES, 20 mL in 100 mL baffled Erlenmeyer flasks, 30 °C, 150 rpm, 2.5 cm amplitude, 50  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>, LED, ambient CO<sub>2</sub> (0.04%), 75% humidity). Kanamycin was used at a final concentration of 50  $\mu$ g mL<sup>-1</sup>. Gene expression was induced using 2 mM IPTG or 0.025% (v/v) DCPK. If required, 50 mM NaHCO<sub>3</sub> were supplied to the medium before sterile filtration (0.2  $\mu$ m). Nitrogen source-free YBG11 medium was supplemented with 0.17  $\mu$ M CoCl<sub>2</sub> · 6 H<sub>2</sub>O instead of Co(NO<sub>3</sub>)<sub>2</sub> · 6 H<sub>2</sub>O. The correlation factor 0.2246 was used for the conversion of OD<sub>750</sub> values to cell dry weight (CDW) concentrations in g<sub>CDW</sub> L<sup>-1</sup> (**Chapter 2**, **Figure 2.2**).

Cultivation of Syn6803\_BGT cells in the stirred tank photo-bioreactor Labfors 5 Lux (Infors AG, Bottmingen, Switzerland) was performed using 3 L YBG11 medium inoculated to an OD<sub>750</sub> of 0.08 using pre-cultures obtained via the standard cultivation protocol described above. Cultivation in photo-bioreactors was performed at a light intensity of 50  $\mu$ E m<sup>-2</sup> s<sup>-1</sup> from 0 to 30 h, 75  $\mu$ E m<sup>-2</sup> s<sup>-1</sup> from 30 to 48 h and 100  $\mu$ E m<sup>-2</sup> s<sup>-1</sup> from 48 to 96 h. The agitation speed was set to 300 rpm. The aeration rate was set to 3 L min<sup>-1</sup> (1 vvm) from 0 to 48 h and 5 L min<sup>-1</sup> (1.7 vvm) from 48 to 96 h using compressed air. The applied light spectrum is shown in **Figure 10.2**.

**Biotransformation procedures**. Whole-cell oxyfunctionalization activity assays were performed with cells cultivated as described above. Gene expression was induced two days after inoculation. At defined time-points, cells were harvested by centrifugation (5000g, 4 °C, 10 min) and resuspended in YBG11 medium (facultatively amended with nitrate, ammonium, and NaHCO<sub>3</sub>) to a final biomass concentration of ca.  $2 g_{CDW} L^{-1}$ . Exact biomass concentrations were determined via OD<sub>750</sub> measurement. Long-term oxyfunctionalization assays (> 30 min) were performed in YBG11 medium supplemented with 50 µg mL<sup>-1</sup> kanamycin and 2 mM IPTG. Aliquots of 1 mL were transferred to 11 mL screw cap glass tubes and pre-adapted for 10 min at 30 °C, 220 rpm (2.5 cm amplitude), and the chosen light intensity (typically 30 µE m<sup>-2</sup> s<sup>-1</sup>). The biotransformation reaction was started by adding 10 mM NAME (5 µL of 2 M stock in ethanol) or DINP containing different NAME concentrations. The reaction was quenched at defined time-points either by adding 1 mL ice-cold diethyl ether containing 200 µM hexadecane as internal standard (followed by extraction

for GC analysis) or, in case of two-liquid phase biotransformations, by cold centrifugation (4640g, 4 °C, 5 min).

Whole-cell oxyfunctionalization in the stirred tank photo-bioreactor Labfors 5 Lux (Infors AG, Bottmingen, Switzerland) was performed with cells derived from a 3 L photo-bioreactor culture three days after inoculation. Cells were harvested via centrifugation (4640g, 4 °C, 20 min) and resuspended in 0.6 L YBG11 medium containing 50 mM NaHCO<sub>3</sub>, 50  $\mu$ g mL<sup>-1</sup> kanamycin, and 2 mM IPTG, resulting in a final biomass concentration of 1.6 g<sub>CDW</sub> L<sup>-1</sup>. This cell suspension was returned into the photo-bioreactor followed by pre-conditioning at 30 °C, 300 rpm (impeller) and 100  $\mu$ E m<sup>-2</sup> s<sup>-1</sup> irradiation for 30 min. An aeration rate of 1.8 L min<sup>-1</sup> (2.2 vvm) with compressed air was chosen to ensure proper mixing of the two phases applied. The biotransformation was started by adding 0.21 L of DINP containing different NAME concentrations (10, 25, or 50% (v/v)). Samples were withdrawn at regular time intervals and immediately centrifuged (17000g, 4 °C, 10 min) to quench the reaction, separate the phases, and remove the cells.

**Analytical procedures**. Reactants (H-NAME, NAME, and NA) from aqueous phase samples were extracted using equal amounts of ice-cold diethyl ether containing 200  $\mu$ M hexadecane as internal standard. The ether phase was separated by centrifugation (17000g, 4 °C, 10 min) and dried over anhydrous Na<sub>2</sub>SO<sub>4</sub>, and subjected to GC analysis as described in **Chapter 3**. Reactants (H-NAME, NAME and NA) dissolved in DINP were diluted 10-fold in ice-cold diethyl ether containing 200  $\mu$ M hexadecane as internal standard. The ether phase was dried over anhydrous Na<sub>2</sub>SO<sub>4</sub> and used for GC analysis. Separation via GC was performed as described in **Chapter 3** with the modification that a pre-column (deactivated silica guard column, 2 m x 0.53 mm, Thermo Fisher Scientific, Milan, Italy), an integrated backflush system and a split ratio of 3 was applied. 1.5 min after injection, a backflush through the pre-column was applied.

#### 4.4 Results

### 4.4.1 Enhanced biocatalyst growth results in decreased biotransformation activities

As reported in **Chapter 3**, the recombinant strain Syn6803\_BGT is capable of hydroxylating NAME to H-NAME driven by photosynthetically derived  $O_2$ . To investigate factors influencing whole-cell biocatalyst performance in more detail, the impact of growth/ expression conditions on the specific hydroxylation activity was analyzed. Standard growth conditions comprised an ambient  $CO_2$  concentration of 0.04% and a light intensity of 50  $\mu$ E m<sup>-2</sup> s<sup>-1</sup> and resulted in a maximal specific activity of 2.1 ± 0.1 U g<sub>CDW</sub><sup>-1</sup> (**Table 4.1**, **Figure 10.3**). CO<sub>2</sub> availability and light intensity are the primary factors defining the cyanobacterial growth rate (Beardall and Raven, 2013). In the following experiment, CO<sub>2</sub> concentrations and light intensity were increased during cell growth to 2% and 100  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>, respectively. Only the

combined increase in CO<sub>2</sub> and light intensity significantly enhanced the growth rate in the exponential phase from 0.054 to 0.077 h<sup>-1</sup> (**Table 4.1**, **Figure 10.3**). In all cases, linear growth was observed after 48 h (time-point of induction of *alkBGT* expression), which increased from 0.065 to 0.086 and 0.130 OD<sub>750</sub> h<sup>-1</sup> upon elevation of the CO<sub>2</sub> level (2%) and both CO<sub>2</sub> level (2%) and light intensity (100  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>), respectively. However, the maximum hydroxylation activity decreased by a factor of two from 2.1 to 1.1 U g<sub>CDW</sub><sup>-1</sup> (**Table 4.1**, **Figure 10.3**). Next to an altered AlkBGT biosynthesis efficiency, changes in cell physiology may have caused this activity decrease.

 Table 4.1: Cell growth rates and maximum oxyfunctionalization activities of Syn6803\_BGT cultivated under different conditions.

Growth conditions	Exp. growth rate (until 48 h) / h <sup>-1</sup>	Linear growth rate (after 48 h) / OD <sub>750</sub> h <sup>-1</sup>	Expression time / h	Maximum specific activity / U gcow <sup>-1</sup>
50 µE, amb. CO <sub>2</sub>	0.054	0.065	24	2.1 ± 0.1
50 µE, 2% CO <sub>2</sub>	0.059	0.086	24	1.4 ± 0.1
100 µE, amb. CO <sub>2</sub>	0.059	0.063	7	2.2 ± 0.1
100 µE, 2% CO <sub>2</sub>	0.077	0.130	6	1.1 ± 0.1

Two days after inoculation, gene expression was induced using 2 mM IPTG. Standard oxyfunctionalization assays were performed at different time-points after induction of gene expression (YBG11, 2 g<sub>CDW</sub> L<sup>-1</sup>, 30  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>). Expression time for maximum specific activities is given. Average values and standard deviations of two independent biological replicates are given. Amb. = ambient, U = unit =  $\mu$ mol min<sup>-1</sup>, CDW = cell dry weight.

# 4.4.2 NaHCO<sub>3</sub> supply but not light intensity influence NAME hydroxylation during single phase biotransformation

To investigate the impact of reaction conditions on the NAME hydroxylation activity, different growth media as well as light intensities were tested during whole-cell biotransformations. First, the medium composition was changed with respect to carbon and nitrogen content from i) standard YBG11 medium to ii) YBG11 + NaHCO<sub>3</sub>, iii) YBG11 + NaHCO<sub>3</sub> w/o nitrate, and iv) YBG11 + NaHCO<sub>3</sub> + ammonium w/o nitrate. The supplementation of YBG11 with NaHCO<sub>3</sub> resulted in a 26% increase of the specific activity (**Figure 4.1 A**). The omission of nitrate as well as its replacement by ammonium, while maintaining NaHCO<sub>3</sub> supplementation, resulted in a slight activity decrease. Therefore, YBG11 + NaHCO<sub>3</sub> was used as reaction medium for NAME hydroxylation in the following experiments with variable light intensities. In the absence of light, cells showed a relatively high specific activity of 2.4 ± 0.1 U g<sub>CDW</sub><sup>-1</sup>, as it has been observed before under non-optimized conditions (**Figure 4.1 B**) (**Chapter 3**). An increase in light intensity up to 250  $\mu$ E m<sup>-2</sup> s<sup>-1</sup> resulted in strongly increasing O<sub>2</sub> evolution rates, but only a slight increase in specific hydroxylation activities with a maximum of 3.0 ± 0.1 U g<sub>CDW</sub><sup>-1</sup> reached at 30  $\mu$ E m<sup>-2</sup> s<sup>-1</sup> (**Figure 4.1 B**, **Figure 10.4**).



**Figure 4.1**: Impact of medium composition (**A**) and light intensity (**B**) on the specific oxyfunctionalization activity of Syn6803\_BGT. Cells were cultivated under standard conditions (YBG11, ambient CO<sub>2</sub>, 50  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>). Two days after inoculation, *alkBGT* expression was induced and cultivation was continued for 24 h. Oxyfunctionalization assays were performed using a biomass concentration of 2 g<sub>CDW</sub> L<sup>-1</sup>. (**A**) Assays were performed using given medium composition at 30  $\mu$ E m<sup>-2</sup> s<sup>-1</sup> using light tubes at light source. (**B**) Oxyfunctionalization assays were performed in YBG11 medium supplemented with NaHCO<sub>3</sub> at given light intensities using LEDs as light source. Oxygen evolution rates were determined in gas tight glass chambers as described in **Chapter 3** (2 g<sub>CDW</sub> L<sup>-1</sup>, YBG11). Average values and standard deviations of two independent biological replicates are given. U = unit = µmol min<sup>-1</sup>, CDW = cell dry weight.

As expected from the native localization of AlkB (Benson *et al.*, 1979), membrane fractionation and Western blot analysis revealed that the monooxygenase AlkB is localized in the cytoplasmic membrane of the cyanobacterial cells (**Figure 10.5**), which may not be optimal for efficient electron transfer. Interestingly, experiments with AlkB containing *Synechocystis* sp. PCC 6803 strains lacking AlkT or AlkGT revealed that electron transfer to AlkB strictly depends on AlkG but not on NADH-dependent AlkT (**Figure 4.2**). Obviously, AlkT can be replaced by endogenous AlkG reduction, with even slightly higher rates in the absence of AlkT. Thus, electron transfer via NADH, which does not constitute a primary electron shuttle in phototrophic metabolism (Mellor *et al.*, 2017), can be circumvented. Overall, these results indicate that, under the applied reaction conditions, the electron supply capacity of photosynthetic water oxidation does not limit the oxyfunctionalization performance of Syn6803\_BGT and that electron supply via carbohydrate catabolism, which may involve storage compounds such as glycogen, can substantially contribute to this electron supply.



**Figure 4.2**: Whole-cell NAME biotransformation activity of *Synechocystis* sp. PCC 6803 cells harboring AlkB (pAH044), AlkBG (pAH047), or AlkBGT (pA042). Cells were cultivated at standard conditions (YBG11, ambient CO<sub>2</sub>, 50  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>). Gene expression was induced two days after inoculation for 24 h. Oxyfunctionalization assays were performed at the given light conditions (2 g<sub>CDW</sub> L<sup>-1</sup>, YBG11 + NaHCO<sub>3</sub>). Average values and standard deviations of two independent biological replicates are given. U = unit = µmol min<sup>-1</sup>, CDW = cell dry weight.

## 4.4.3 Diisononyl phtalate (DINP) as carrier solvent overcomes substrate toxicity for *Synechocystis* sp. PCC 6803

So far, the biocatalytic performance of Syn6803\_BGT has been investigated in short-term assays, hiding potential biocatalyst stability issues. Long-term NAME hydroxylation experiments revealed a fast decrease in specific activity, resulting in a final specific product yield on biomass of 0.5 mmol g<sub>CDW</sub><sup>-1</sup> (Figure 4.3, Table 4.2).



**Figure 4.3:** Long-term NAME biotransformation with Syn6803\_BGT. Cells were cultivated under standard conditions (YBG11, ambient CO<sub>2</sub>, 50  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>). Gene expression was induced two days after inoculation for 4 h before cells were harvested and applied for the biotransformation (2 g<sub>CDW</sub> L<sup>-1</sup>, YBG11 + NaHCO<sub>3</sub>, 30  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>). The biotransformation reaction was initiated by the addition of 10 mM NAME. Each data-point represents the average value of two independent biological samples. U = unit =  $\mu$ mol min<sup>-1</sup>, CDW = cell dry weight.

Beside its hydroxylation, NAME was hydrolyzed to nonanoic acid (NA) at a constant rate of  $2.3 \pm 0.1 \text{ U} \text{ }_{\text{CDW}^{-1}}$ , resulting in substrate depletion after 26 h of reaction. The biotransformation yield thus was restricted by limited substrate availability, which, however, cannot explain the fast activity decrease. The latter may be due to reactant toxicity. Thus, the impact of NAME and NA on growth of wildtype *Synechocystis* sp. PCC 6803 was investigated. The addition of 1 mM NAME or NA largely restricted cell growth (**Figure 4.4**). Obviously, low concentrations of NAME and NA lead to cell toxification which may have caused biocatalyst instability. In conclusion, both reactant toxicity and substrate hydrolysis constitute critical factors affecting the hydroxylation performance of Syn6803\_BGT.



**Figure 4.4**: Cell growth of *Synechocystis* sp. PCC 6803 (pAH032) (empty expression plasmid) at different NAME (**A**), NA (**B**), or ethanol (**C**) concentrations. Cells were cultivated under standard conditions (YBG11, ambient CO<sub>2</sub>, 50  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>). Addition of reactants is indicated by an arrow. NAME concentrations are calculated based on the volume of the aqueous phase, while the solubility limit of NAME is 133  $\mu$ M. Error bars represent the standard deviation of two independent biological replicates.

To realize efficient substrate supply while maintaning substrate concentrations low but constant, *in situ* substrate supply (ISSS) strategies can be followed (Hilker *et al.*, 2008; Schmölzer *et al.*, 2012). Beside substate feeding, two-phase approaches such as organic/ aqueous two-liquid phase systems are promising, simultaneously allowing *in situ* product extraction (Leon *et al.*, 1998; Lye and Woodley, 1999). Thereby, a second organic liquid

phase serves as substrate reservoir continuously providing the substrate at desired concentrations. So far, organic carrier phases were not applied for cyanobacterial processes. As information on the compatibility of organic carrier solvents with cvanobacterial growth is largely missing, such compatibility was tested for the two solvents ethyl oleate (EO) and diisononyl phthalate (DINP), which, together with similar phthalates, have proven highly suitable in bioprocesses based on heterotrophic bacteria (Bühler et al., 2003b; Kuhn et al., 2012b; Schrewe et al., 2014; Willrodt et al., 2014). With YBG11 medium as aqueous phase, these solvents were found to provide a similar partitioning behavior, with a partition coefficient  $P_{organ}$  of (24.5 ± 3.5) x 10<sup>3</sup> for NAME. To test the compatibility of DINP and EQ with wildtype Synechocystis sp. PCC 6803, the carrier solvents were added to cultures at a 1:3 organic/aqueous phase ratio two days after inoculation. EO was found to substantially impair cell growth, which was not the case for DINP (Figure 4.5 A). Thus, cell growth with DINP containing 0, 5, 10, 25, 50, or 75% (v/v) NAME was evaluated. Concentrations up to 25% (v/v) NAME dissolved in DINP were found not to affect the cyanobacterial cell growth rate and can thus be considered suitable for two-liquid phase setups (Figure 4.5 B, Figure 10.6).



**Figure 4.5**: Compatibility of the organic carrier solvents ethyloleate (EO) and diisononyl phtalate (DINP) (**panel A**) and NAME dissolved in DINP at different concentrations (**panel B**) with *Synechocystis* sp. PCC 6803 cells lacking *alkBGT*. Cells were cultivated in YBG11 medium supplemented with (**panel A**) or without (**panel B**) NaHCO<sub>3</sub> under standard conditions (ambient CO<sub>2</sub>,  $50 \ \mu E \ m^2 s^{-1}$ ). Two days after inoculation, 7.5 or 15 mL aliquots were transferred into 100 or 250 mL shake flasks and supplemented with 2.5 or 5 mL organic phase, as indicated by the arrow in **panel A**. Cultivation was continued at a reduced shaking frequency of 100 rpm. **Panel B** shows growth rates after the addition of DINP containing different NAME concentrations, determined for day 2 to 4. Average values and standard deviations of two independent biological replicates are given.

# 4.4.4 The two-liquid phase approach improves specific activity and product yield of Syn6803\_BGT

To investigated if and to what extent the two-liquid phase system improves whole-cell biocatalyst stability, DINP containing 25% (v/v) NAME was added to cyanobacterial cultures in different organic:aqueous phase ratios of 1:1, 1:3, and 1:10, and product formation was followed for 27 h. In all cases, initial specific activities as well as specific product yields were enhanced compared to the single aqueous phase system (**Figure 4.6, Table 4.2**). The best results were obtained using a phase ratio of 1:3, which enhanced the initial specific activity (from 3.3 to  $5.2 \text{ U }_{\text{CDW}^{-1}}$ ) as well as the biotransformation stability, resulting in 6-fold increased specific product yields (**Table 4.2**). With a phase ratio of 1:10, the system appeared to become substrate mass transfer limited, whereas a high phase ratio of 1:1 lead to a reduced biocatalyst stability pointing to toxicity effects possibly mediated by direct contact of the cells with organic phase droplets and thus NAME, as it has been reported before for similar two-liquid phase systems (Bühler *et al.*, 2006; Park *et al.*, 2006; Schrewe *et al.*, 2011).



**Figure 4.6**: Impact of organic carrier solvent DINP containing 25% (v/v) NAME applied at different phase ratios on the long-term biotransformation stability with Syn6803\_BGT. Cells were cultivated under standard conditions in YBG11 medium for 2 days, induced with 2 mM IPTG for 4 h, harvested, and resuspended in YBG11 + 50 mM NaHCO<sub>3</sub> to a biomass concentration of 2 g<sub>CDW</sub> L<sup>-1</sup>. Biotransformations were initiated via the addition of 1, 0.33, or 0.1 mL of organic phase to 1 mL of cyanobacterial cultures in glass tubes. Average values and standard deviations are given for two independent biological replicates.

Elevated substrate concentrations have been found to be toxic and are thus expected to impare metabolism dependent whole-cell oxyfunctionalization activity and stability. Thus, the substrate concentration available in the aqueous phase was fine-tuned by applying different substrate concentrations (5%, 10%, 25%, 50%, 75%, and 100% (v/v) NAME) in the organic carrier solvent DINP added at an organic/aqueous phase ratio of 1:3. The substrate concentration applied significantly influenced the initial specific NAME hydroxylation rate,

which was highest at around 5.5 U  $g_{CDW}^{-1}$  with 25, 50, and 75% (v/v) NAME in DINP (Figure 4.7). Reduced hydroxylation rates at 5 and 10% (v/v) NAME indicated a substrate limitation, whereas high concentrations of 75 and 100% (v/v) NAME led to reduced initial activities and/or stabilities again indicating toxification of the cells.



**Figure 4.7**: Impact of different NAME concentrations within the organic carrier solvent DINP on the biotransformation performance of Syn6803\_BGT. Cells were cultivated, processed, and applied for long-term biotransformations as described in the legend of **Figure 4.6**. During biotransformations, different concentrations of NAME dissolved in DINP were applied at an organic:aqueous phase ratio of 1:3. **Panels A** and **B** show the courses of biomass-specific H-NAME accumulation and activities, respectively. **Panel C** shows initial specific activities calculated for the first 30 min of reaction. The dotted lines show the application of Michaelis-Menten kinetics for the data obtained with 5-50% NAME (v/v) in DINP. **Panel D** shows biomass-specific product yields. Average values and standard deviations of two independent biological replicates are given. U = unit = µmol min<sup>-1</sup>, CDW = cell dry weight, V<sub>max</sub> = maximal reaction velocity, K<sub>s</sub> = apparent substrate uptake constant.

Up to 50% (v/v) NAME, initial activities exhibited a Michaelis-Menten type dependency on the substrate concentration with an apparent maximal reaction velocity  $V_{max}$  of  $8.1 \pm 0.5 \text{ U g}_{CDW}^{-1}$  and an apparent substrate uptake constant  $K_S$  of  $22.1 \pm 2.5\%$  (v/v) NAME in DINP (= 1  $M_{org} \triangleq 39 \ \mu M_{aq}$ ). The data obtained with higher substrate concentrations did not fit classical substrate inhibition kinetics (v = Vmax \* [S] / (Ks + [S] \* (1 + [S] / Ki)), pointing to toxification of the cells rather than enzyme inhibition as the cause for the reduced initial

specific activities at high NAME concentrations. In conclusion, the application of NAME in DINP at a concentration of up to 50% (v/v) significantly increased biocatalyst performance enabling not only a high specific product yield of  $3.8 \pm 0.1$  mmol g<sub>CDW</sub><sup>-1</sup>, but also an increase in specific activity.

#### 4.4.5 NAME hydroxylation in a 3 L stirred tank photo-bioreactor

After successful stabilization of the NAME hydroxylation system, we set out to evaluate its scalability by transferring it from 1 mL glass tube- to a 3 L lab-scale stirred tank photobioreactor system. In contrast to cultivation and biotransformation in shake flasks and glass tubes, respectively, the photo-bioreactor setting provides an altered light input distribution, an aeration system continuously supplying compressed air into the medium, and stirring via impeller agitation, potentially affecting biocatalyst growth and physiology. First, the scaling of biocatalyst production was evaluated by growing the cells in the photo-bioreactor setting, induction 2 days after inoculation, and following oxyfunctionalization activity via short-term assays. During cultivation, the light intensity was increased after 30 and 48 h from 50 to 75 and 100  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>, respectively, and the aeration rate from 3 to 5 L min<sup>-1</sup> after 48 h to ensure optimal light and CO<sub>2</sub> supply.

Initial growth rates (0.059 h<sup>-1</sup> from 0 to 32 h) in the photo-bioreactor were similar to those obtained in shake flasks (**Table 4.1**). The highest specific oxyfunctionalization activity  $(3.3 \pm 0.1 \text{ U } \text{g}_{\text{CDW}^{-1}})$  was achieved for a broad time range after induction, i.e., 4 up to 24 h (**Figure 4.8 A**), and was very similar to the maximal activity obtained with cells cultivated in shake flasks (**Figure 10.7**).

After the successful transfer of Syn6803 BGT cultivation and induction to the photobioreactor scale, this transfer also was tested for the two-liquid phase biotransformation of NAME with Syn6803 BGT. For two-liquid phase biotransformations in stirred tank photobioreactors, organic DINP phases containing 10, 25, or 50% (v/v) NAME were applied. The highest initial specific activity of  $4.5 \pm 0.3 \text{ U} \,\text{g}_{\text{CDW}^{-1}}$  was achieved with 25% (v/v) NAME in DINP, enabling a final biomass-specific product yield of  $2.6 \pm 0.1 \text{ mmol } g_{CDW}^{-1}$  after 45 h of biotransformation (Figure 4.8, Table 4.2). In comparison to the small scale experiments, biocatalyst performance with 10 and 25% (v/v) NAME in DINP was slightly reduced in terms of initial specific activity (by 10 - 20%) and final biomass-specific product yield (by 0 - 20%) (Table 4.2). With 50% (v/v) NAME in DINP, this performance was more significantly reduced (by 54 and 50% in terms of initial activity and specific yield, respectively) indicating that the bioreactor conditions promoted biocatalyst inactivation especially when high NAME concentrations were applied (Bühler et al., 2002). Besides this, the successful scaling of biocatalyst growth and two-liquid phase biotransformation of NAME demonstrates the technical applicability of Syn6803 BGT for two-liquid phase biotransformations in a stirred tank photo-bioreactor setting.



**Figure 4.8**: Syn6803\_BGT growth and NAME hydroxylation performance using different amounts of NAME dissolved in DINP in a stirred tank photo-bioreactor setting. Cells were cultivated in 3 L YBG11 medium at 50 (0 - 30 h), 75 (30 - 48 h), and 100  $\mu$ E m<sup>-2</sup> s<sup>-1</sup> (48 - 96 h), 300 rpm, and aeration with compressed air at 3 (0 - 48 h) and 5 L min<sup>-1</sup> (48 - 96 h). Gene expression was induced two days after inoculation. **Panel A** shows the growth curve and the course of specific activities determined in short-term activity assays (2 g<sub>CDW</sub> L<sup>-1</sup>, YBG11 + NaHCO<sub>3</sub>, 30  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>) for cells harvested at different time points. Specific activities are given as average values with standard deviations of two replicates. Photo-bioreactor-based biotransformations (**panels B-D**) were performed with cells harvested 24 h after induction and resuspended to 1.6 g<sub>CDW</sub> L<sup>-1</sup> in 0.6 L of YBG11 medium containing 50 mM NaHCO<sub>3</sub>. The biotransformation reaction was started by the addition of 0.21 L DINP containing 10, 25, and 50% (v/v) NAME (**panels B, C**, and **D**, respectively). Average values and standard deviations refer to two analytical replicates. org = measured in the organic phase, aq = measured in the aqueous phase, U = unit = µmol min<sup>-1</sup>, CDW = cell dry weight.

## 4.5 Discussion

### 4.5.1 Substrate mass transfer, substrate hydrolysis, and reactant toxicity

Application of the two-liquid phase concept in principle may hamper biocatalysis with phototrophs due to shading. However, with phototrophic Syn6803\_BGT, two-liquid phase

NAME in DINP	org:aq phase ratio	NAME in aq phase¹ / μΜ	NA in aq phase² / μΜ	H-NAME / mmol <sub>total</sub> L <sub>aq phase<sup>-1</sup></sub>	Initial specific activity <sup>3</sup> / U g <sub>CDW</sub> -1	Initial hydrolysis rate <sup>3</sup> / U g <sub>CDW</sub> -1	Specific yield <sup>4</sup> / mmol <sub>total</sub> g <sub>CDW</sub> <sup>-1</sup>
Tube							
10 mM	w/o DINP	≤ 133⁵	1797 <sup>6</sup>	0.9 ± 0.1	3.3 ± 0.1	$2.3 \pm 0.1^{10}$	0.5 ± 0.1
25% (v/v)	1:1	58 ± 4	31	$3.7 \pm 0.3$	$4.8 \pm 0.4$	0.10 ± 0.01	$2.1 \pm 0.2$
25% (v/v)	1:3	54 ± 5	29	5.7 ± 0.3	$5.2 \pm 0.4$	0.47 ± 0.01	$3.2 \pm 0.2$
25% (v/v)	1:10	53 ± 3	53	4.7 ± 0.1	4.4 ± 1.5	1.74 ± 0.12	2.7 ± 0.1
5% (v/v)	1:3	10 ± 1	2	2.1 ± 0.1	1.5 ± 0.1	0.06 ± 0.01	1.1 ± 0.01
10% (v/v)	1:3	22 ± 1	7	$3.3 \pm 0.3$	3.1 ± 0.2	0.15 ± 0.01	1.8 ± 0.2
25% (v/v)	1:3	44 ± 4	25	5.7 ± 0.2	$5.2 \pm 0.4$	0.36 ± 0.01	3.0 ± 0.1
50% (v/v)	1:3	81 ± 5	78	7.3 ± 0.1	5.6 ± 0.1	0.92 ± 0.01	3.8 ± 0.1
75% (v/v)	1:3	120 ± 11	1797 <sup>6</sup>	5.9 ± 0.5	5.5 ± 0.1	2.00 ± 0.1	3.0 ± 0.2
100% (v/v)	1:3	≤ 133⁵	1797 <sup>6</sup>	2.8 ± 0.3	2.6 ± 0.1	5.23 ± 0.01	1.5 ± 0.2
STR <sup>7</sup>							
10% (v/v) <sup>8</sup>	1:3	29 to 91	5	2.6 ± 0.1	$2.3 \pm 0.2$	0.13 ± 0.02	1.7 ± 0.1
25% (v/v) <sup>9</sup>	1:3	64 to 133 <sup>5</sup>	35 ± 2 / 210 ± 3	$3.6 \pm 0.2 / 4.0 \pm 0.1$	$4.5 \pm 0.3$	$0.49 \pm 0.02$	2.3 ± 0.1 / 2.6 ± 0.1
50% (v/v)	1:3	83 to 133 <sup>5</sup>	332 ± 3	3.0 ± 0.1	2.6 ± 0.1	2.16 ± 0.06	1.9 ± 0.1

Table 4.1: Overview on NAME biotransformation experiments with Syn6803\_BGT applying different NAME concentrations in the organic carrier solvent DINP in small-scale or photo-bioreactor settings.

Average values with standard deviations are given for independent biological or analytical replicates. org = organic, aq = aqueous,  $U = unit = \mu mol min^{-1}$ , CDW = cell dry weight. <sup>1</sup> Average value or, in case of experiments in photo-bioreactors, concentration ranges referring to the total biotransformation time, <sup>2</sup> highest value during biotransformation, <sup>3</sup> for the first 30 min of reaction, <sup>4</sup> calculated based on the total amount of product in aqeous and organic phases divided by the initially applied biomass assuming no growth, <sup>5</sup> solubility of NAME in water (Chemspider database structure 14846), <sup>6</sup> solubility of NA in water (Chemspider database structure 7866), <sup>7</sup> technical replicates, <sup>8</sup> 31.5 h of reaction time, <sup>9</sup> 26.2/45 h of reaction time, <sup>10</sup> rate calculated for 24 h

biotransformation resulted in up to 1.7-fold increased initial specific hydroxylation activities (Table 4.2). This can be ascribed to reduced cell toxification/ substrate inhibition by decreased aqueous phase NAME concentrations or to an enhanced substrate mass transfer to the cells, possibly involving direct substrate transfer from organic solvent droplets to the cells as it has been observed before (Bühler et al., 2006; Park et al., 2006; Schrewe et al., 2011). Further, the presence of the organic phase significantly reduced substrate hydrolysis leading to only low final NA titers and thus, enabled higher product yields on substrate (Table 4.2, Figure 10.8). In whole-cell biocatalysis, cell toxification by hydrophobic reactants often affects biocatalyst and thus biotransformation performance. Hydrophobic compounds with logP<sub>(octanol/water)</sub> values between 2 and 4 typically impair cell viability via intercalation into microbial membranes (Laane et al., 1987; Sikkema et al., 1994). Using the empirical equation for predicting the concentration leading to membrane dissociation as reported by Sikkema et al. (1994) and Kratzer et al. (2015) for heterotrophic microorganisms, NAME (log P = 3.9) and NA (log P = 3.4) are expected to become toxic at agueous concentrations of 216 and 617 µM, respectively (Kratzer et al., 2015; Sikkema et al., 1994). Our results show an impaired growth at concentrations of 1 mM NAME (solubility in water is 133 µM) and 100 µM NA (Figure 4.4), indicating a higher sensitivity of Synechocystis sp. PCC 6803 compared to heterotrophic microorganisms. In addition to plasma membranes, phototrophic cells harbor thylakoid membranes containing the photosynthetic machinery of the light reaction. The disintegration of respective membranes may directly affect photosynthetic water oxidation and electron transport, and thus the energy metabolism and viability of phototrophic organisms. Consequently, in situ reactant supply and removal becomes highly important for the application of photoautotrophic whole-cell biocatalysts.

Overall, this study shows that the two-liquid phase concept can successfully be applied in light-dependent reaction setups based on phototrophic microorganisms, with benefits ranging from mass transfer over the handling of toxic compounds to the avoidance of side reactions.

#### 4.5.2 Specific oxyfunctionalization activity

Factors possibly limiting the oxyfunctionalization activity of Syn6803\_BGT include  $O_2$  supply, substrate mass transfer to the cells, substrate transfer over the cellular membranes, cell integrity, the intracellularly available AlkB activity, and electron supply. Considering the enhanced  $O_2$  evolution rates measured with increasing light intensities (**Figure 4.1 B**) and the high NAME hydroxylation activities (100 U g<sub>CDW</sub><sup>-1</sup>) achieved by recombinant *E. coli* containing AlkBGT (Schrewe *et al.*, 2011), limitations by  $O_2$  supply and substrate transfer over cellular membranes are improbable. The increase in specific activity in the presence of a second liquid organic phase indicated that substrate mass transfer to the cells and/ or substrate toxicity were critical factors. Besides and in parallel to NAME availability, the intracellular AlkBG(T) amount may constitute a limiting factor. Thus, excluding  $O_2$  as limiting

factor and knowing about the importance of controlled NAME supply as achieved via the twoliquid phase approach, intracellular AlkBGT synthesis and electron supply will be discussed in the following.

AlkBGT synthesis. In E. coli W3110 (pBT10), high specific oxyfunctionalization activities (100 U  $q_{CDW}^{-1}$ ) involved alkBGT overexpression based on a high copy number plasmid (pCOM10) and the strong promoter system (Paik) of the alk operon of P. putida GPo1 (Schrewe et al., 2011). The expression system applied in this study relies on a plasmid with a medium copy number in Synechocystis sp. PCC 6803 (RSF orign of replication, 10 - 30 copies per cell (Huang et al., 2010)) and a promoter system ( $P_{tre10}$ ) showing low specific activities in E. coli W3110 in comparison to the Palk promoter system (Figure 10.9). For Syn6803 BGT, SDS-PAGE (Figure 10.10) revealed only low specific AlkB concentrations in comparison to the total protein amount and to the AlkB amount present in recombinant E. coli exhibiting high oxyfunctionalization activities (100 U g<sub>CDW</sub><sup>-1</sup>) (Schrewe et al., 2011). Duplication of the operon within the expression plasmid as a first strategy to increase the AlkBGT expression level did not result in increased AlkB concentrations and thus hydroxylation rates (Figure 10.11). Controlled and high level expression of recombinant genes in cvanobacteria still remains challenging (Camsund and Lindblad, 2014; Englund et al., 2016). Thus, the development and application of more efficient expression systems for Synechocystis sp. PCC 6803 would be useful to facilitate a/kBG(T) overexpression and thus possibly enhance oxyfunctionalization activities.

The photosynthetic electron supply to AlkB. In general, the efficiency of electron supply to AlkB is determined by 1) the electron activation rate in the course of the photosynthetic light reaction, 2) the competition for reduction equivalents with the primary cellular electron demand, and 3) the transport of electrons from the photosynthetic electron transport chain to AlkB (Figure 4.9). As discussed before, the presence of a second liquid organic phase enhanced specific oxyfunctionalization activities of Syn6803 BGT, indicating a limitation in substrate availability in the single aqueous phase system. This and possibly the low AlkB amount within the cells obviously constituted the main limiting factors, which explains why increased photosynthetic water oxidation induced by increased light intensities (Figure 4.9 i) did not result in enhanced NAME oxyfunctionalization rates in single aqueous phase biotransformations (Figure 4.1 B). However, specific activities of Syn6803 BGT slightly increased upon NaHCO<sub>3</sub> supply (Figure 4.1 A). The primary cellular electron demand for. e.g., CO<sub>2</sub> fixation and nitrate assimilation, constitutes a major electron sink, which may compete with oxygenase catalysis, given a high capacity for the latter is present in the cell (Figure 4.9 ii). On the other hand, the presence of NaHCO<sub>3</sub> may promote enhanced rates of photosynthetic water oxidation via different regulatory mechanisms and thus increase electron flux towards electron transfer shuttles such as ferredoxin, NADPH, or NADH. The increased electron flux in turn may have caused the slight increase in NAME hydroxylation activity upon NaHCO<sub>3</sub> supply. The observed oxyfunctionalization activity in the absence of light and thus water oxidation (**Figure 4.1 B**) suggests that electrons for oxygenase catalysis were derived from the catabolism of storage compounds under these conditions (**Figure 4.9**).



**Figure 4.9**: Possible electron transfer pathways from the photosynthetic electron transport chain to AlkB. The circles indicate the three factors determining the electron transfer efficiency: i) rate of water oxidation, ii) competition of oxygenase catalysis with cellular metabolism, and iii) transport of electrons from the photosynthetic electron transport chain to AlkB. *In vitro* studies showed that the rubredoxin reductase AlkT receives electrons primarily from NADH and not from NADPH (indicated by crossed arrow [a]) (Peterson *et al.*, 1967), whereas the replacement of AlkT with a NADPH-dependent spinach ferredoxin reductase (indicated by bold line [b]) was functional (McKenna and Coon, 1970). In addition, AlkB containing *Synechocystis* sp. PCC 6803 is shown to require the rubredoxin AlkG (indicated by crossed arrows [c]), but not AlkT for NAME oxyfunctionalization. This indicates that electron transfer to AlkG and finally AlkB either occurs directly from the photosynthetic electron transport chain (bold line [d]) or via endogenous ferredoxin reductases (bold line [b]).

Further, the native "NADH-AlkT-AlkG-AlkB" electron transfer pathway was bypassed quite efficiently in *Synechocystis* sp. PCC 6803 containing AlkBG but lacking AlkT (**Figure 4.2**) (Benson *et al.*, 1977; McKenna and Coon, 1970; Peterson *et al.*, 1966a). Thereby, AlkG, which was required for productive electron transfer to AlkB, may have received electrons either directly from the photosynthetic electron transport chain or via the action of endogenous ferredoxin reductases (**Figure 4.9**). Functional replacement of the NADH-dependent rubredoxin reductase AlkT by an NADPH-dependent spinach ferredoxin reductase has been shown in *in vitro* studies (McKenna and Coon, 1970). The same was reported for recombinant CYP450 enzymes actively coupling with ferredoxins/ ferredoxin reductases originating from phototrophic species *in vitro* and *in vivo* (Hara *et al.*, 1997; Jensen *et al.*, 2012; Mellor *et al.*, 2016). Identification and overexpression of enzymes involved in this electron transfer might be a powerful strategy to improve the coupling of oxyfunctionalization and photosynthetic metabolism. In addition to the availability of proteins involved in electron transfer and oxyfunctionalization, their localization also may determine

oxyfunctionalization efficiency. AlkB was found to be localized in the cytoplasmic membrane of the cyanobacterial cells, as could be expected from its native localization in *Pseudomonas putida* GpO1 (**Figure 10.5**) (Benson *et al.*, 1979). In contrast, the water oxidation and photosynthetic electron transfer are located in the thylakoid membranes (Vermaas, 2001). The spatial separation of AlkB and photosynthetic electron transfer chain might impair electron transfer to AlkB. Recent studies investigated the anchoring of a recombinant cytochrome P450 monooxygenase in cyanobacterial thylakoid membranes, allowing for photosynthesis coupled oxyfunctionalization of tyrosine to p-hydroxyphenyl-acetaldoxime (Lassen *et al.*, 2014a). Relocalization of AlkB to the thylakoid membrane might be another promising strategy to enhance electron supply to AlkB.

#### 4.5.3 Scaling

Yet, process concepts specific for photosynthesis-driven biotransformations do not exist and are rare for H<sub>2</sub> production and product formation from CO<sub>2</sub> (Dasgupta et al., 2010; Fresewinkel et al., 2014). Light distribution, CO<sub>2</sub> supply, as well as substrate supply are critical process parameters to establish efficient reactor concepts. As a first step to evaluate scaling, the Syn6803 BGT-catalyzed NAME hydroxylation in a two-liquid phase system was transferred from 1 mL glass tube to a 3 L stirred-tank photo-bioreactor, which proofed to be successful. A similar biocatalyst performance as in the test tube system was achieved. However, specific yields were somewhat lower in comparison to the small-scale experiments. especially at high NAME concentrations in the organic phase (Table 4.2). The main difference to the small-scale setting was the mixing intensity, which was significantly higher in the stirred tank photo-bioreactor (2.2 vvm aeration, 300 rpm agitation). Direct contact of the cells with organic phase droplets, as discussed above as a possible reason for improved specific activities in the two-liquid phase system, may, on the other hand, promote biocatalyst toxification as also indicated by the adverse effect of high organic:aqueous phase ratios in small scale experiments (**Table 4.2**). The more intense mixing in the bioreactor leads to more frequent collision of cells with solvent droplets and thus can be expected to promote direct NAME transfer from the organic phase to the cells (Bühler et al., 2006; Bühler et al., 2002; Park et al., 2006). Thus, mixing and the NAME concentration constitute critical parameters in stirred tank bioreactors. In addition to such toxification, a pH shift due to intense aeration, which promoted degassing of  $CO_2$  derived from the NaHCO<sub>3</sub> in the medium (**Figure 10.12**). may have affected cell physiology and thus whole-cell biocatalyst performance. Beside pH control, strategies to overcome CO<sub>2</sub> degassing may become mandatory and include reduced agitation and the omission of aeration. Such oxyfunctionalization without aeration is enabled by the *in situ*  $O_2$  generation via photosynthetic water oxidation (**Chapter 3**, **Chapter 7**).

## 4.6 Conclusions

Photoautotrophic organisms are promising biocatalysts for oxyfunctionalization catalysis as they are capable of supplying reduction equivalents as well as O<sub>2</sub> via photosynthetic water oxidation. The previously developed whole-cell biocatalyst Syn6803\_BGT was found to involve endogenous pathways and enzymes in the supply of electrons supporting oxygenase catalysis. This included AlkT-independent electron transfer to AlkG and electron supply via the catabolism of storage compounds. The whole-cell reaction system was stabilized via a two-liquid phase approach enabling bioprocess relevant time scales of >24 h. The application of DINP as organic carrier solvent not only stabilized NAME hydroxylation via the attenuation of NAME toxicity, but also increased the specific biocatalyst activity most likely via an improved substrate mass transfer and reduced by-product formation. Thereby, this study demonstrated feasibility of the two-liquid phase approach for photobiotechnology. This and the successful transfer of the light-driven two-liquid phase biotransformation to a 3 L stirred tank photobioreactor scale paves the way for the technical application of cyanobacteria as phototrophic host organisms for efficient oxyfunctionalization biocatalysis.

## 4.7 Acknowledgments

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Chapter 5 Light-dependent and aeration-independent gram-scale hydroxylation of cyclohexane to cyclohexanol by CYP450 harboring *Synechocystis* sp. PCC 6803

Adrian Hochkeppel contributed to the biochemical analysis of the recombinant strain and the assessment of the biotransformation performance of the recombinant strain in the stirred tank photobioreactor under exclusion of aeration, coordinated and supervised by Anna Hoschek and Jörg Toepel. Rohan Karande, Jörg Toepel, Bruno Bühler, and Andreas Schmid coordinated the project and corrected the manuscript.

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## 5.1 Abstract

Oxvgenase-based whole-cell biocatalysis enables selective oxvfunctionalizations under mild conditions. Phototrophic organisms such as cyanobacteria are promising host systems for oxygenase catalysis as the photosynthetic water oxidation gives highly sustainable access to the required co-substrates that are activated reduction equivalents and O<sub>2</sub>. First studies have validated the functional coupling of oxygenase-enzyme systems to photosynthetic water oxidation. In this study, we developed a recombinant Synechocystis sp. PCC 6803 strain showing unprecedentedly high oxyfunctionalization activities for a photoautotrophic strain and evaluated its technical applicability. The strain functionally synthesizes a cytochrome P450 monooxygenase system originating from Acidovorax sp. CHX100 and enables the hydroxylation of cycloalkanes. For cyclohexane, the biocatalyst-specific reaction rate was found to be light-dependent reaching 24.0  $\pm$  0.6 U g<sub>CDW</sub><sup>-1</sup> at a light intensity of 150  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>. In situ substrate supply via a two-liquid phase system increased the initial specific activity to  $39.2 \pm 0.7 \text{ U} \,\text{g}_{\text{CDW}^{-1}}$  and stabilized the biotransformation by preventing cell toxification. This resulted in a 10 times increased specific product yield compared to the single aqueous phase system up to 4.5 g<sub>cyclohexanol</sub> g<sub>CDW</sub><sup>-1</sup>. Subsequently, the developed biotransformation system was successfully scaled from shake flask- to a 3 L stirred-tank photo-bioreactor setup. Thereby, the in situ generation of O2 via photosynthetic water oxidation allowed non-aerated process operation, thus circumventing substrate evaporation as the most critical factor limiting process performance and stability. In summary, 2.6 g cyclohexanol were generated from water, light, and cyclohexane. This paper exemplifies the technical applicability of cvanobacteria for light-driven oxyfunctionalization reactions involving highly toxic and volatile substrates. The design of scalable biotransformation technologies for photoautotrophs may well develop into promising photosynthesis-driven bioprocesses.

### 5.2 Introduction

Since a few years, cyanobacteria have gained attention as valuable biocatalysts for biotransformation reactions such as the oxyfunctionalization of hydrocarbons to the respective value-added compounds (Böhmer et al., 2017: Lassen et al., 2014b: Mellor et al., 2017). These whole-cell reaction systems utilize photosynthetic water oxidation as a source of activated reduction equivalents as well as O<sub>2</sub>, both co-substrates for oxygenase-catalyzed oxyfunctionalizations. Under high light conditions, the light reaction including water oxidation is considered not to limit growth, but rather has to be suppressed by phototrophic organisms in order to avoid damage by excessive buildup of reduction power. O<sub>2</sub>, and reactive oxygen species (Bailey and Grossman, 2008; Wilhelm and Selmar, 2011). The coupling of oxygenase catalysis to photosynthetic water oxidation provides a sink for reduction equivalents as well as  $O_2$ , potentially enabling high oxyfunctionalization rates. Recently, several studies demonstrated the functional introduction of oxygenases into diverse photosynthetic organisms and their coupling to photosynthetic water oxidation (Chapter 3) (Berepiki et al., 2016; Böhmer et al., 2017; Lassen et al., 2014a; Wlodarczyk et al., 2015), thus verifying the concept of photosynthesis-driven whole-cell oxyfunctionalization on laboratory scale. The applicability of cyanobacteria on technical scale, especially for the oxyfunctionalization of highly volatile and toxic substrates, however, has not been demonstrated, yet. Although the cultivation and reaction conditions of standard bioprocesses have to be modified by lighting systems to enable sufficient water oxidation, our recent study showed that established reaction engineering options such as two-liquid phase bioreactor setups are in principle applicable for photosynthetic biocatalysts (Chapter 4). The evaluation and intensification of such photosynthesis-driven bioprocessing for gram-scale hydroxylations, however, remains an open task.

Cyclohexanol constitutes an example for a high volume chemical produced via oxyfunctionalization, in this case from cyclohexane, and is of high commercial interest as a precursor for the synthesis of Nylon-6 and Nylon-6,6 building blocks (Schuchardt *et al.*, 1993). The current industrial production of cyclohexanol and cyclohexanone from cyclohexane involves the use of homogenous cobalt catalysts and high temperatures above 423 K and suffers from low selectivities (Schuchardt *et al.* 2001). Thus, numerous new heterogeneous chemocatalysts are under development. The enzymatic oxyfunctionalization of cyclohexane to cyclohexanol is a promising alternative route to the traditional chemical approaches as high selectivity can be achieved under mild conditions (Karande *et al.*, 2016a; Salamanca *et al.*, 2015). Cyclohexane reveals generic challenges for biocatalysis due to its low water solubility (650 µM), high volatility (0.15 atm m<sup>3</sup> mol<sup>-1</sup>), and high toxicity to microorganisms.

The focus of this work was to evaluate the potential of cyanobacteria as biocatalysts to meet these challenges and to develop a process setup suitable for cyclohexane oxidation. A recombinant *Synechocystis* sp. PCC 6803 strain harboring a cyclohexane monooxygenase, i.e., the cytochrome P450 monooxygenase from *Acidovorax* sp. CHX100 (Salamanca *et al.*, 2015), capable of hydroxylating cyclohexane at high rates was developed and evaluated regarding its oxyfunctionalization activity as well as stability under process conditions. An *in situ* substrate supply strategy involving a second liquid organic phase was followed, on the one hand, to attenuate cell toxification and thus improve process stability and, on the other hand, to improve substrate mass transfer and thus enhance productivity. Finally, the benefit of *in situ*  $O_2$  generation via photosynthetic water oxidation for the conversion of volatile cyclohexane under non-aerated process conditions was evaluated in a 3L stirred tank photobioreactor setup.

#### 5.3 Materials and Methods

**Chemicals, bacterial strains and plasmids**. Chemicals used in this study are given in **Chapter 2**. *Synechocystis* sp. PCC 6803 was transformed with the plasmid pAH050 harboring the cytochrome P450 enzyme system originating from *Acidovorax* sp. CHX100 resulting in the recombinant strain *Synechocystis* sp. PCC 6803 (pAH050) (hereinafter referred to as Syn6803\_CYP). Respective cloning was based on the broad-host-range vector pPMQAK1 (RSF origin of replication) involving transcriptional control by the P<sub>trc10</sub> promoter system (Huang et al., 2010) (for cloning procedure see **Chapter 2**).

**Cultivation of** *Synechocystis* **sp. PCC 6803**. If not stated otherwise, shake flask cultivation of *Synechocystis* **sp.** PCC 6803 was performed as described in **Chapter 2** (YBG11 medium, 50 mM HEPES, 20 mL in 100 mL baffled Erlenmeyer flasks, 30 °C, 150 rpm, 2.5 cm amplitude, 50  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>, LED, ambient CO<sub>2</sub> (0.04%), 75% humidity, start OD<sub>750</sub> ca. 0.08). Kanamycin was used at a final concentration of 50  $\mu$ g mL<sup>-1</sup>. Gene expression was induced 2 days after inoculation using 2 mM IPTG for 24 h. If required, 50 mM NaHCO<sub>3</sub> were supplied to the medium before sterile filtration (0.2  $\mu$ m). The correlation factor 0.2246 g<sub>CDW</sub> L<sup>-1</sup> OD<sub>750</sub><sup>-1</sup> was used for the conversion of OD<sub>750</sub> values to cell dry weight (CDW) concentrations in g<sub>CDW</sub> L<sup>-1</sup> (**Chapter 2, Figure 2.2**).

Cultivation of Syn6803\_CYP cells in the stirred tank photo-bioreactor Labfors 5 Lux (Infors AG, Bottmingen, Switzerland) was performed using 3 L YBG11 medium inoculated to an OD<sub>750</sub> of 0.08 using pre-cultures obtained via the standard cultivation protocol described above. Cultivation in photo-bioreactors was performed at a light intensity of 50  $\mu$ E m<sup>-2</sup> s<sup>-1</sup> from 0 - 30 h, 75  $\mu$ E m<sup>-2</sup> s<sup>-1</sup> from 30 - 48 h and 100  $\mu$ E m<sup>-2</sup> s<sup>-1</sup> from 48 to 96 h. The agitation speed was set to 300 rpm. The aeration rate was set to 3 L min<sup>-1</sup> (1 vvm) for 0 - 48 h and 5 L min<sup>-1</sup> (1.7 vvm) from 48 - 96 h using compressed air. The applied light spectrum is shown in **Figure 10.2**.

**Biotransformation procedures in shake flasks**. Standard oxyfunctionalization activity assays were performed by cultivating the cells as described above, harvesting by centrifugation (10 min, 5000g, rt) and resuspension in YBG11 medium (50 mM NaHCO<sub>3</sub>, 50  $\mu$ g mL<sup>-1</sup> kanamycin, 2 mM IPTG) to a final biomass concentration of ca. 1 g<sub>CDW</sub> L<sup>-1</sup>. Aliquots of 10 mL culture were provided in 100 mL baffled screw cap shake flasks and prewarmed for 10 min at 30 °C, 200 rpm (2.5 cm amplitude) and respective light intensity. The biotransformation reaction was started by adding 5 mM cyclohexane (5.17  $\mu$ L of pure substrate). If cyclohexane was supplied via the gas phase, 25 mL culture was provided in 250 mL baffled screw cap shake flasks equipped with an open glass inlet containing 1 mL cyclohexane (**Figure 5.2 A**). The reaction was quenched at respective time-points by adding 600  $\mu$ L reaction mixture to 600  $\mu$ L ice-cold diethyl ether containing 200  $\mu$ M of decane as internal standard before applied for GC analysis (see GC **analysis method 1**).

Two-liquid phase oxyfunctionalization was performed as described before, but with culture aliquots of 15 mL applied in 250 mL baffled screw cap shake flasks at 150 rpm (2.5 cm amplitude). The biotransformation reaction was started by adding 5 mL of the organic phase (5 - 20% cyclohexane in DINP). Samples from the organic phase were taken at respective time-points, quenched by centrifugation, and 10 times diluted in ice-cold diethyl ether containing 200  $\mu$ M of decane as internal standards before applied for GC analysis (see **GC analysis method 2**).

Biotransformation procedures in stirred tank photobioreactor. Whole-cell oxyfunctionalization in the stirred tank photo-bioreactor Labfors 5 Lux (Infors AG, Bottmingen, Switzerland) was performed with cells derived from a 3 L photo-bioreactor culture three days after inoculation. Three days after inoculation, cells were harvested by centrifugation (4640, 4 °C, 20 min) and resuspended in 1.2 L YBG11 medium containing 50 mM NaHCO<sub>3</sub>, 50 µg mL<sup>-1</sup> kanamycin and 2 mM IPTG, to a biomass concentration of 0.5 -0.8 q<sub>CDW</sub> L<sup>-1</sup>. Pre-conditioning in the photobioreactor was performed at 30 °C, 300 rpm (impeller), 150  $\mu$ mol m<sup>-2</sup> s<sup>-1</sup>, and, if not stated otherwise, at 0.15 L min<sup>-1</sup> aeration with compressed air for ca. 30 min. The biotransformation reaction was started by adding 400 mL of DINP containing 5% (v/v) cyclohexane. Samples were taken at regular time intervals and quenched by immediate centrifugation (17000g, 4 °C, 10 min). Organic phase portions were diluted 10 times in ice-cold diethyl ether containing 200 µM decane, dried over anhydrous Na<sub>2</sub>SO<sub>4</sub>, and subjected to GC analysis (see **GC analysis method 2**). Reactants in the aqueous phase were extracted using equal amounts of ice-cold diethyl ether, followed by drying over anhydrous Na<sub>2</sub>SO<sub>4</sub> and GC analysis (see **GC analysis method 1**).

**Determination of org:aq partition coefficients under abiotic conditions in 1.5 mL reaction tubes.** Partitioning of cyclohexane, cyclohexanol, cyclohexanone between YBG11 medium and DINP was determined using defined stock solutions in DINP (0.5 and 1 M for cyclohexane, 1 and 5 mM for cyclohexanol and cyclohexanone). 600  $\mu$ L of this stock solution was mixed vigorously with 600  $\mu$ L of YBG11 medium for 5 min and incubated for 2 h at 30 °C and 2000 rpm (ThermoMixerC, Eppendorf, Wesseling-Berzdorf, Germany). Phases were separated by centrifugation (10 min, 17,000g, room temperature). The aqueous phase then was extracted using an equal volume of diethyl ether (containing 0.2 mM decane as an internal standard). The organic phase was diluted in diethyl ether (0.2 mM decane). Quantification was performed by GC-FID analysis (see **GC analysis methods 1 and 2**, respectively).

**GC** analysis method 1 (Extracted aqueous phase sample). Cyclohexane, cyclohexanol, and cyclohexanone extracted from aqueous phase samples using dieethyl ether were quantified using a Trace 1310 gas chromatograph (Thermo Fisher Scientific, Waltham, USA) equipped with a TG-5MS capillary column (5% diphenyl / 95% dimethyl polysiloxane, 30 m, I.D.: 0.25 mm, film thickness: 0.25  $\mu$ m, ThermoFisher Scientific) and a flame ionization detector (FID) operated at 320 °C, 350 mL min<sup>-1</sup> air flow, 30 mL min<sup>-1</sup> makeup gas flow, and 35 mL min<sup>-1</sup> hydrogen gas flow. Nitrogen gas was applied as carrier gas at a constant flow rate of 1.5 mL min<sup>-1</sup>. The injection volume was set to 1  $\mu$ L injected by means of a PTV injector, programmed for a temperature gradient of 2°C s<sup>-1</sup> from 40-250 °C. A split ratio of 7 was applied. The oven temperature profile was: 1) 40 °C for 1 min, 2) 40-80 °C at 10 °C min<sup>-1</sup>, 3) 80-250 °C at 100 °C min<sup>-1</sup>, and 4) 250 °C for 2 min.

GC analysis method 2 (Samples containing organic carrier solvent DINP). Cyclohexane, cyclohexanol, and cyclohexanone dissolved in DINP were quantified using a Trace 1310 gas chromatograph (Thermo Fisher Scientific) equipped with the same column as used in method 1, a pre-column (deactivated silica guard column, 2 m x 0.53 mm, Thermo Fisher Scientific, Milan, Italy), an integrated backflush system, and a flame ionization detector (FID) operated as described for method 1. Nitrogen gas was applied as carrier gas at a constant flow of 1.5 mL min<sup>-1</sup>. The injection volume was set to 1  $\mu$ L injected by means of a PTV injector operating at the following temperature gradient: 1) 2 min at 250 °C, 2) 14.5 °C s<sup>-1</sup> from 250 to 400 °C, and 3) 400 °C for 5 min. A split ratio of 3 was applied. 2 min after injection, a backflush through the pre-column was applied. The oven temperature profile was: 1) 40 °C for 2 min, 2) 40-70 °C with 25 °C min<sup>-1</sup>, 3) 70-90 °C with 3 °C min<sup>-1</sup>, 4) 90-310 °C with 100 °C min<sup>-1</sup> and 5) 310 °C for 5 min.

## 5.4 Results

## 5.4.1 Syn6803\_CYP is active and shows light-dependent activity

Karande et al. 2016 reported the functional expression of the CYP450 monooxygenase genes from *Acidovorax* sp. CHX100 in recombinant *Pseudomonas taiwanensis* VLB120, enabling efficient cyclohexane hydroxylation driven by reduction equivalents derived from

chemoheterotrophic citrate catabolism. With the aim to drive this reaction by reduction equivalents (and  $O_2$ ) derived from photosynthetic water oxidation, the genes encoding this three-component monooxygenase system (composed of CYP = CYP450 monooxygenase component, FnR = FAD-ferredoxin reductase, and Fn = ferredoxin) were introduced into the cyanobacterium *Synechocystis* sp. PCC 6803 by means of the expression plasmid pAH050 (for cloning procedure see supplemental information). CYP450 synthesis in the resulting strain Syn6893\_CYP was verified by SDS-PAGE analysis, whereas protein bands for Fn and FnR could not be identified (**Figure 10.13**). At a light intensity of 50  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>, Syn6803\_CYP catalyzed cyclohexane hydroxylation at a rate of 17.9 ± 0.2 U g<sub>CDW</sub><sup>-1</sup>, proving the successful construction of a biocatalytically active strain.



**Figure 5.1**: Cyclohexane hydroxylation activity of Syn6803\_CYP in dependence of the light intensity applied. Cyclohexane oxidation to cyclohexanol (grey bars) and overoxidation of cyclohexanol to cyclohexanoe (dashed grey bars) is presented. For whole-cell oxyfunctionalization assays, cells were cultivated in YBG11 medium and resuspended in YBG11 supplemented with NaHCO<sub>3</sub> to a biomass concentration of ca. 1 g<sub>CDW</sub> L<sup>-1</sup>. Assays were performed with 10 mL of cell suspension in 100 mL screw capped and baffled shake flasks at 30 °C, 200 rpm (2.5 cm amplitude), and the indicated light-intensities. Reactions were started by adding cyclohexane to a concentration of 5 mM with respect to the aqueous phase volume and stopped after 10 min by quenching with diethylether. Each column represents average values and standard deviations of two independent biological replicates.

Increased light intensities resulted in enhanced oxyfunctionalization activities, with a maximum specific activity of  $26.3 \pm 0.6 \text{ U g}_{\text{CDW}^{-1}}$  at  $150 \,\mu\text{E} \,\text{m}^{-2} \,\text{s}^{-1}$  (**Figure 5.1**). Overoxidation of cyclohexanol to cyclohexanone was observed at a portion of ca. 10%. An increase of the light-intensity above  $150 \,\mu\text{E} \,\text{m}^{-2} \,\text{s}^{-1}$  did not result in higher, but in slightly decreased specific oxyfunctionalization activities, most likely due to photo-inhibition effects (Aro *et al.*, 1993; Nagy *et al.*, 1995). In the absence of light, cells showed a basal oxyfunctionalization activity of  $6.2 \pm 0.6 \,\text{U} \,\text{g}_{\text{CDW}^{-1}}$  and indicated the supply of reduction equivalents via the catabolism of storage compounds such as glycogen as it has been observed previously (**Chapter 4**). These results clearly show that Syn6803 CYP-catalyzed cyclohexane hydroxylation was

light-dependent and profited from increasing rates of water oxidation up to a light intensity of 150  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>.

## 5.4.2 Syn6803\_CYP activity is stable for 2 h before decreasing rapidly

For the development of efficient whole-cell oxyfunctionalization processes, beside high biocatalyst activities, biocatalyst and thus process stability constitutes a crucial aspect. In order to assess the long-term performance of Syn6803\_CYP, the reaction system was amended with a glass container containing 1 mL of pure cyclohexane for continuous substrate supply via the gas phase (**Figure 5.2 A**).



**Figure 5.2**: Long-term oxyfunctionalization by Syn6803\_CYP with cyclohexane supplied via the gas phase. The experiment was performed using freshly cultivated cells resuspended in 25 mL YBG11 (+NaHCO<sub>3</sub>, Km, IPTG) to a biomass concentration of ca 1 g<sub>CDW</sub> L<sup>-1</sup> in 250 mL screw capped baffled shake flasks equipped with an open glass inlet (**A**). The reaction was started by adding 1 mL of pure cyclohexane into the glass inlet, followed by cultivation at 30 °C, 150 rpm (2.5 cm amplitude), and 150  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>. **A**) Figure adapted from Karande et al. (2016). **B**) Each data point represents average values of two biological replicates with standard deviations.

At a light intensity of 150  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>, the cells showed similar cyclohexanol formation and thus initial specific activity (24.0 ± 0.6 U g<sub>CDW</sub><sup>-1</sup> for cyclohexanol production) as obtained upon 5 mM cyclohexane addition (**Figure 5.2 B**, **Table 5.1**). In the setting applied, cyclohexanol formation was accompanied by overoxidation to cyclohexanone at a comparatively low rate (0.2 ± 0.1 U g<sub>CDW</sub><sup>-1</sup>). The hydroxylation activity remained constant for 2 h, then rapidly decreased, and was virtually lost after 5 h of reaction. This activity loss might have been caused by toxification or inhibition by the substrate cyclohexane and/or the product cyclohexanol. The final specific yield on biomass accounted for 4.1 ± 0.4 mmol g<sub>CDW</sub><sup>-1</sup>.

# 5.4.3 Cyclohexane provided via gas phase leads to toxification of *Synechocystis* sp. PCC 6803, which can be attenuated applying a two-liquid phase system

To evaluate the impact of cyclohexane and cyclohexanol on cyanobacterial viability, we investigated the growth behavior of *Synechocystis* sp. PCC 6803 carrying the empty vector pAH032 upon reactant exposure.



**Figure 5.3**: Impact of cyclohexane and cyclohexanol on *Synechocystis* sp. PCC 6803 (pAH032) (empty plasmid) growth. Cells were cultivated under standard cultivation conditions as described in the material and methods section. A + B) Cyclohexane toxicity: After 2 days (indicated by arrow), the cultures were harvested and resuspended in YBG11 medium (+ 50 mM NaHCO<sub>3</sub>). Aliquots of 25 mL were applied in 250 mL screw cap baffled shake flasks equipped with an open glass inlet containing 1 mL cyclohexane. **B**) Cultures after 7 days of incubation. Left flask: control without cyclohexane, right flask: with cyclohexane. **C** + **D**) Cyclohexanol toxicity: After 2 days (indicated by arrow), 1 - 100 mM cyclohexanol was added to the aqueous phase. **D**) Cell growth rates determined in the linear growth phase (days 2-7). Average values and standard deviations of two independent biological replicates are given.

The application of cyclohexane in saturating concentrations (via glass inlet, solubility in water:  $650 \ \mu$ M) completely inhibited cell growth and led to a culture color change from green to blue indicating the lysis of cyanobacterial cells (**Figure 5.3 A**, **B**) (Harada *et al.*, 2009). The product cyclohexanol inhibited cell growth at concentrations above 10 mM (**Figure 5.3 C**, **D**).

The maximum product concentration achieved with cyclohexane provided in the gas phase did not exceed 4 mM (**Figure 5.2 B**). These results point out that cyclohexane toxicity constitutes a critical factor limiting Syn6803\_CYP whole-cell biocatalyst stability.

Substrate toxicity-related biocatalyst instability can be overcome via continuous substrate supply applying a feeding regime or a second liquid or solid phase. Respective concepts are widely established for heterotrophic strains to overcome mass transfer and toxicity issues (Hilker et al., 2008; Schmölzer et al., 2012). The compatibility of the second liquid phase DINP with Synechocystis sp. PCC 6803 has successfully been demonstrated in our previous study enabling cell growth and stabilization of the whole-cell biotransformation of toxic nonanoic acid methyl ester (Chapter 4). The organic-aqueous partition coefficient Porgan for cyclohexane in a DINP/YBG11 two-liquid phase system was determined to be 1775 ± 214 and can be considered appropriate for a 2-liquid phase biotransformation approach. Thus, the impact of cyclohexane dissolved in DINP on growth of Synechocystis sp. PCC 6803 containing the empty vector pAH032 was tested. Applying 2.5, 5, and 10% (v/v) of cyclohexane in DINP led to cell applomeration (hindering  $OD_{750}$  determination) and to a visually observable increase in applomerated biomass concentration (Figure 5.4). In contrast. 20% (v/v) of cvclohexane in DINP did not lead to such accompany and growth. but resulted in a culture color change from green to blue as observed before upon addition of cyclohexane via the gas phase. Overall, 2.5 - 10% (v/v) of cyclohexane in DINP appeared to constitute a feasible organic phase for two-liquid phase biotransformations.



**Figure 5.4**: Effect of cyclohexane dissolved in the organic carrier solvent DINP on cultures of *Synechocystis* sp. PCC 6803 (pAH032) (empty vector). Cells were cultivated under standard conditions for 2 days, before cultures were harvested and resuspended in YBG11 (+ 50 mM NaHCO<sub>3</sub>). Aliquots of 7.5 mL were applied in 100 mL screw capped baffled shake flasks. To each shake flask, 2.5 mL of DINP containing 0, 2.5, 5, 10, or 20% (v/v) cyclohexane were added, and cultivation was continued for another 5 days.

# 5.4.4 Two-liquid phase approach enhances biotransformation stability and the specific activity of Syn6803\_CYP

Next, the biocatalytic performance of Syn6803\_CYP in two-liquid phase systems was evaluated applying DINP phases containing 2.5, 5, 10, or 20% (v/v) cyclohexane at an organic:aqueous phase ratio of 1:3. The product formation performance was found to depend on the substrate concentration applied (**Figure 5.5 A**, **B**). The initial specific activity was constant for 2 h in all cases and increased with increasing substrate concentration (**Figure 5.5 C**).



**Figure 5.5**: Two-liquid phase biotransformation of cyclohexane using Syn6803\_CYP in shaking flasks. After 2 days of cultivation under standard conditions, oxygenase gene expression was induced by adding 2 mM IPTG, and cultivation was continued for 1 day. Then, cells were harvested, resuspended in YBG11 (NaHCO<sub>3</sub>, Km, IPTG) to a biomass concentration of ca. 1 g<sub>CDW</sub> L<sup>-1</sup>, and applied in aliquots of 18.75 mL in 250 mL screwed capped baffled shake flasks. Biotransformations were performed at 30 °C, 150 rpm (2.5 cm amplitude), and 150  $\mu$ E m<sup>-2</sup> s<sup>-1</sup> and were started by adding 6.25 mL DINP containing 2.5, 5, 10, or 20% (v/v) cyclohexane. After phase separation, cyclohexanol and cyclohexanone concentrations were determined in the organic phase. Aqueous concentrations were calculated based on the separately determined partitioning coefficients P<sub>org:aq</sub> for cyclohexanol (2.1 ± 0.1) and cyclohexanone (4.4 ± 0.7). Average values and standard deviations of two biological replicates are given.

The highest specific activity of  $39.2 \pm 0.7 \text{ U } \text{g}_{\text{CDW}^{-1}}$  was observed with 20% (v/v) cyclohexane in DINP, being 1.5 times higher than the activity obtained without organic carrier solvent (**Table 5.1**). This indicated an enhanced substrate mass transfer possibly via a direct contact of the cells with organic phase droplets (Bühler *et al.*, 2006; Park *et al.*, 2006) or substrate toxicity/inhibition in the absence of an organic phase. High cyclohexane levels led to impaired biocatalyst stability resulting in a comparatively low specific product (cyclohexanol + cyclohexanone) yield on biomass (**Figure 5.5 D**). The highest specific yield on biomass (45.4 ± 0.5 mmol  $g_{\text{CDW}^{-1}}$ ) was obtained using 10% (v/v) cyclohexane in DINP, constituting a 10 times increase compared to the single phase biotransformation (**Table 5.1**).

With increasing cyclohexane concentrations, cyclohexanol over-oxidation decreased indicating a competition of cyclohexane and cyclohexanol for the active site of the oxygenase (**Figure 5.5 B**). The initial specific whole-cell activity exhibited a Michaelis-Menten-type dependency on the cyclohexane concentration applied, with an apparent  $V_{max}$  of  $43.2 \pm 2.2 \text{ U g}_{CDW}^{-1}$  and an apparent  $K_S$  of  $2.9 \pm 0.5\%$  (v/v) cyclohexane in DINP. These kinetic characteristics of the whole-cell photobiocatalyst can be considered highly promising for technical scale biotransformations in photobioreactors.

## 5.4.5 Non-aerated bioprocessing facilitates gram-scale hydroxylation of cyclohexane in a stirred tank photo-bioreactor

After successful stabilization of the cvclohexane oxyfunctionalization reaction, scaling from shake flasks to a stirred tank photo-bioreactor was conducted. For this purpose, cells were cultivated and induced in photobioreactors containing 3 L YBG11 medium, followed by harvesting and resuspension in 1.2 L YBG11 (+ NaHCO<sub>3</sub>). The reaction was started by adding 0.4 L DINP containing 5% (v/v) cyclohexane to the photo-bioreactor setup aerated with compressed air. Within the first 5 h of reaction time, the specific cyclohexane oxvfunctionalization rate of 24.6 ± 0.4 U g<sub>CDW</sub><sup>-1</sup> was similar to that obtained in shake flasks, proving scalability to stirred tank photo-bioreactor setups (Figure 5.6 A). However, after 5 h of biotransformation, the biocatalyst activity started to decrease, resulting in a specific yield on biomass of 18 mmol  $q_{CDW}^{-1}$  after 24 h of reaction, half of the value achieved in shake flask experiments (Table 5.1). The partition coefficients for all reactants were similar to those determined in shake flasks and small reaction tubes (Figure 10.14, Table 10.1). Although the aeration rate of 0.15 L min<sup>-1</sup> was low, the substrate steadily evaporated over time, resulting in continuously decreasing substrate concentrations in both organic and aqueous phases. According to the cyclohexane hydroxylation kinetics estimated for the two-liquid phase system (Figure 5.5 C), this decreasing substrate concentration can be considered the cause for the decrease in specific activities. In addition, degassing of CO<sub>2</sub> originating from the dissolved NaHCO<sub>3</sub> leads to a pH increase (Figure 10.15 A), which may have contributed to the activity decrease.

Table 5.1: Process data obtained from biotransformation experiments using Syn6803\_CYP in shake flasks and stirred tank photo-bioreactors.

Distronoformation condition	Chx in	Chx in	Initial specific activity	Specific yield	Overoxidation
Biotransformation condition	org phase <sup>a</sup> / M	aq phaseª / µM	(2h) <sup>b</sup> / U g <sub>CDW</sub> <sup>-1</sup>	$/ \text{ mmol}_{Col+Cone} \text{ g}_{CDW}^{-1}$	/% <sub>Cone</sub> in product
Shake flask					
5 mM Chx	-	88 <sup>c</sup>	23.7 ± 0.5 <sup>e</sup>	-	~ 10
Chx via gas phase	-	654 <sup>d</sup>	$24.0 \pm 0.6$	4.1 ± 0.4	0.7 ± 0.1
2.5% (v/v) Chx in DINP	0.23	131	21.9 ± 0.6	$20.2 \pm 4.0$	12.1 ± 0.1
5% (v/v) Chx in DINP	0.46	261	27.2 ± 0.3	36.7 ± 6.3	$6.0 \pm 0.3$
10% (v/v) Chx in DINP	0.93	522	33.3 ± 0.3	$45.4 \pm 0.5$	$3.5 \pm 0.3$
20% (v/v) Chx in DINP	1.85	654 <sup>d</sup>	39.2 ± 0.7	19.7 ± 0.4	1.4 ± 0.1
Photo-bioreactor					
5% (v/v) Chx in DINP, with aeration	0.38 → 0.06	273 → 32	26.3 ± 0.6	$20.0 \pm 0.5$	9.3 ± 0.1
5% (v/v) Chx in DINP, w/o aeration	0.42 → 0.34	150 → 244	$34.9 \pm 0.3$	$49.4 \pm 0.3$	$4.6 \pm 0.1$

Chx = cyclohexane, Col = cyclohexanol, Cone = cyclohexanone.

<sup>a</sup> For shake flask experiments, theoretical numbers based on the molarity of 9.27 M for pure cyclohexane and its partition coefficient of P<sub>org:aq</sub> = 1775 in the DINP-YBG11 system are given.

<sup>b</sup> The specific activity given is based on the cyclohexanol and cyclohexanone concentrations determined in both phases.

<sup>c</sup> Concentrations calculated based on Henry coefficient for cyclohexane (0.15 atm m<sup>3</sup> mol<sup>1</sup>) and the gas:aq phase ratio of 9:1.

<sup>d</sup> The value for the solubility of cyclohexane in water is given (McAuliffe, 1966).

<sup>e</sup> The specific activity in the first 10 min of reaction is given.

To stabilize the substrate availability throughout the biotransformation, a bioreactor experiment without aeration was performed. Surrendering aeration indeed stabilized pH and cyclohexane concentrations in both phases, while the oxygen partial pressure stayed well above 100% of saturation during the entire process (**Figure 10.15 B**). The productive biotransformation time was significantly prolonged with a slow activity decrease up to 52 h, resulting in a specific yield of nearly 50 mmol  $g_{CDW}^{-1}$  (**Figure 5.6 B**, **Table 5.1**). The final product titer of  $31.5 \pm 0.3$  and  $11.5 \pm 0.1$  mM in the organic and aqueous phases, respectively, resulted in a total product amount of 2.6 g cyclohexanol. These results clearly emphasize the scalability of the process, whereby the handling of the volatile substrate cyclohexane is simplified by *in situ* O<sub>2</sub> supply via photosynthetic water oxidation.



**Figure 5.6**: Two-liquid phase biotransformation of cyclohexane using Syn6803\_CYP in a stirred-tank photo-bioreactor with (**A**) and without (**B**) aeration. Cells were applied at a concentration of 0.8 (**A**) and 0.5 g<sub>CDW</sub> L<sup>-1</sup> (**B**) in YBG11 (+ NaHCO<sub>3</sub>, Km, IPTG) as described in the materials in methods section. Biotransformations were performed at 30 °C, 150  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>, 300 rpm agitation, and 0.15 L min<sup>-1</sup> aeration with compressed air (only for **A**), using 1.2 L aqueous cell suspension and 0.4 L organic phase consisting of 5% (v/v) cyclohexane in DINP. Col = cyclohexanol, Cone = cyclohexanone.

#### 5.5 Discussion

Cyclohexanol is a key synthon mostly used in the production of polymer building blocks such as ε-caprolactone, ε-caprolactam, and adipic acid with an annual production in the million tons range (Schuchardt *et al.*, 1993; Weissermel and Arpe, 2008). However, the chemical synthesis of cyclohexanol is still challenging because of low selectivities (Schuchardt *et al.*, 2001). Biocatalysis provides an interesting alternative for the oxidation of cyclohexane providing high selectivities under mild conditions. In 2014, Salamanca et al. isolated the strain *Acidovorax* sp. CHX100, capable of growing on cyclohexane as sole carbon source, from a wastewater plant (Salamanca and Engesser, 2014). Characterization of this strain and subsequent recombinant gene overexpression in *Pseudomonas taiwanensis* VLB120 led to the identification of a novel cytochrome P450 monooxygenase system, which efficiently catalyzes the oxidation of cyclohexane to cyclohexanol (Karande *et al.*, 2016a; Salamanca *et al.*, 2015).

## 5.5.1 Light dependency

In this study, we present the cyanobacterium Synechocystis sp. PCC 6803 as an efficient alternative host system enabling light-driven cytochrome P450 catalysis, i.e., cyclohexane oxyfunctionalization, with water as cheap and readily available source for reduction equivalents and O<sub>2</sub>. Thereby, such light-driven oxyfunctionalization profits from the efficient electron supply via the photosynthetic electron transport chain to ferredoxin and NADP+ (Wilhelm and Selmar, 2011; Wilhelm and Wild, 1984). This is in contrast to photosynthesisdriven production of chemicals such as ethanol or lactate from CO<sub>2</sub>, which suffers from the low rate of CO<sub>2</sub> fixation by RuBisCO (Bathellier et al., 2018; Knoot et al., 2018). Overall, efficient coupling of redox enzymes with the photosynthetic light reaction enables high oxyfunctionalization rates that compete with or even outperform established heterotrophic biocatalysts (Chapter 7). With its electron transfer components ferredoxin and ferredoxin reductases, the CYP450 enzyme system applied in this study in principle depends on NADH as electron donor. However, not NADH but NADPH is the primary carrier of activated electrons produced in the photosynthetic light reaction. This discrepancy together with the high oxyfunctionalization rate obtained and its strong light-dependency indicates trapping of activated electrons directly from the photosynthetic electron transport chain via native or Acidovorax ferredoxin or from NADPH via native ferredoxin reductase. This electron transfer appears to be quite efficient given the comparatively high specific oxygenation activities achieved rivaling those reached with heterotrophic host strains (Schrewe et al., 2013). Efficient integration of heterologous enzyme systems into photosynthetic redox metabolism by adjusting the electron transferring pathways represents an important research field for the development of efficient photobiocatalytic processes (Khanna and Lindblad, 2015; Lassen et *al.*, 2014b),

## 5.5.2 Reactant toxicity

Next to biocatalyst design, the physicochemical properties of reactants often constrain the biocatalytic process performance and necessitate an adequate bioprocess design (Kim *et al.*, 2007; Willrodt *et al.*, 2015b). In this study, the applied substrate cyclohexane and the product cyclohexanol feature logPow values (logarithm of the partition coefficient in an octanol/water mixture) of 3.4 and 1.2, respectively. It has been shown that chemical compounds with logPow values between 2 and 4 typically are toxic to microorganisms (Laane *et al.*, 1987; Sikkema *et al.*, 1994). These compounds damage bacterial membrane integrity, resulting in the impairment of microbial activity. Membrane permeabilization-induced loss of biocatalytic activity upon cyclohexane exposure has been reported, e.g., for the typically solvent-tolerant

strain *Pseudomonas taiwanensis* VLB120 (Karande *et al.*, 2016a) and thus constitutes a key aspect for the photobiocatalytic reaction system investigated in this study. Via *in situ* substrate supply by means of a two-liquid phase system, the substrate concentration was kept below 654  $\mu$ M, which can be considered critical according to the empirical considerations reported by Sikkema et al. 1994 and Kratzer et al. 2015 for microbial cell toxification by hydrophobic substances (Kratzer *et al.*, 2015; Sikkema *et al.*, 1994). Thus, growth as well as the cyclohexane hydroxylation activity of Syn6803\_CYP were stabilized by overcoming cell toxification.

#### 5.5.3 Substrate volatility

During scale-up from shake flask to the stirred tank photo-bioreactor, a second physicochemical property of the substrate, namely its high volatility, constrained process durability. At a low aeration rate of 0.1 vvm, cyclohexane continuously evaporated from the reaction system and thus became the factor limiting the bioconversion rate and the final product yield. By omitting aeration, cyclohexane loss was largely avoided, enabling an increase of the biomass-specific product yield by a factor of 2.5 (**Figure 5.6**, **Table 5.1**). Such process management was possible, as O<sub>2</sub> together with activated electrons, both key substrates for the oxyfunctionalization reaction, was continuously provided via photosynthetic water oxidation (**Chapter 3**). In conclusion, the use of a cyanobacterial host strain enables oxygenase catalysis without aeration and thus the efficient conversion of a volatile substrate.

#### 5.5.4 Productivity

The production of fine-chemicals at industrially relevant scales necessitates productivities of at least 1 - 10 g L<sup>-1</sup> h<sup>-1</sup> (Straathof et al., 2002). With an average productivity of 0.04 g L<sup>-1</sup> h<sup>-1</sup>. the reaction system developed in this study requires further improvement by a factor of at least 25. Comparison of process parameters of the Syn6803 CYP-based whole-cell biotransformation of cyclohexane with an established E. coli driven process for the epoxidation of styrene reveals that the biotransformation durability of 52 h and the product vield on biomass with 4.9 g q<sub>CDW</sub><sup>-1</sup> are already valuable (**Table 5.2**) (Kuhn et al., 2010b). In addition, hydroxylation coupled to the metabolism of the heterotrophic host strains depends on an organic compound such as glucose as source of reduction equivalents, representing a significant environmental and cost factor (Kuhn et al., 2012b; Kuhn et al., 2010b). Photosynthesis-driven processes make use of inexpensive carbon ( $CO_2$ ) and electron ( $H_2O$ ) sources for biocatalyst and product synthesis and thus augur well for the development of economically viable processes involving redox chemistry for the production of chemicals and fuels. The specific cyclohexane oxyfunctionalization rates obtained here were equal or even higher than those reported for *Pseudomonas* sp. VLB120 harboring the very same CYP enzyme system (24.0 and 39 U g<sub>CDW</sub><sup>-1</sup> in aqueous and 2-liquid phase systems, respectively,
**Table 5.2**: Comparison of process performance parameters of photosynthesis- or heterotrophically driven biocatalytic oxyfunctionalizations and possible improvement strategies for the biotransformation catalyzed by Syn6803\_CYP.

Parameter	Syn6803_CYP <sup>a</sup>	E. coli JM101 (pSPZ10) <sup>b</sup>	Possible improvement strategies for Syn6803_CYP
Volume aq phase / L	1.2	1	Scaling
Volume org phase / L	0.4	1	Scaling
Substrate in org phase	5% Chx in DINP	8% styrene in BEHP	-
Maximum specific activity / U $g_{\text{CDW}}\text{-}^1$	34.9 ± 0.3	60	Increase of oxygenase expression levels, improved coupling to electron transport chain
Applied biomass concentration / $g_{\text{CDW}}\ L^{\text{-1}}$	0.5	5.4 – 39.3	Prolonged growth phase, improvement of growth conditions (CO <sub>2</sub> , light)
Durability / h	52	8	-
Glucose consumed / g	-	113.7	-
Average productivity / g $L_{aq}^{-1} h^{-1}$	0.04	11.08	Increase of biomass concentration, increase of specific activity
Specific yield / g g <sub>CDW</sub> -1	4.9	1.85	Continuous bioprocessing
Titer / g L <sub>aq</sub> -1	2.2	72.6	Increase of biomass concentration
Total product / g	2.6	72.6	Scaling

aq = aqueous, org = organic, U = µmol min<sup>-1</sup>, CDW = cell dry weight, Chx = cyclohexane, BEHP = bis(2-ethylhexyl)phthalate.

<sup>a</sup> this study; <sup>b</sup> E. coli JM101 catalyzing the oxyfunctionalization of styrene to styrene oxide (Kuhn et al., 2010b)

vs. 20-25 U  $g_{CDW}^{-1}$  in *P. taiwanensis* VLB120, Karande et al. 2016). However, the specific biocatalyst activity and especially the cell concentration in bioreactor settings still require engineering efforts (see possible improvement strategies in **Table 5.2**). The cultivation of cyanobacteria at cell densities of up to 50  $g_{CDW}$  L<sup>-1</sup> is possible using systems with enhanced CO<sub>2</sub> and light supply (Apel *et al.*, 2017; Bähr *et al.*, 2016; Dasgupta *et al.*, 2010). With the reaction system developed in this study (39 U  $g_{CDW}^{-1}$ ), such a cell concentration would already enable a cyclohexanol productivity of ~ 12 g L<sup>-1</sup> h<sup>-1</sup>. Further increase in productivity may be achieved by enhancing the specific oxyfunctionalization activities. An enoate reductase has been shown to trap electrons derived from the photosynthetic light reaction provides activated reduction equivalents at high rates of up to 850 U  $g_{CDW}^{-1}$  (assumptions:  $k_{cat}$  of PSII: 1000 s<sup>-1</sup>, 1% PSII  $g_{CDW}^{-1}$ , 350 kDa) (Dismukes *et al.*, 2009; Shen, 2015). With this high specific activity and a biomass concentration of 50  $g_{CDW}$  L<sup>-1</sup>, productivities of ~ 255 g L<sup>-1</sup> h<sup>-1</sup> are in theory possible and illustrate the potential of photorophic organisms as hosts for hosts for oxyfunctionalization biocatalysis.

#### 5.5.5 Scalability

For the development of eco-efficient bioprocesses, high productivities have to be accomplished at scale. In this study, a scale-up evaluation was performed based on the established stirred-tank bioreactor concept. Especially the generation of excess  $O_2$  during biotransformation without aeration, effecting a  $pO_2$  between 100 and 150% of air saturation throughout the entire process time, demonstrates the high capacity and suitability of photosynthetic biocatalysts for oxyfunctionalization bioprocesses, especially for those involving volatile substrates. However, efficient light supply constitutes a big challenge and a possible limitation for the further scaling of the stirred-tank bioreactor setup. To achieve high cell concentrations and thus high productivities, light intensities have to be increased, and/or additional light sources have to be installed within the reactor system. Alternatively, other reactor concepts such as biofilm-based capillary reactors can be applied (David *et al.*, 2015). Capillary reactors enable the establishment of a high irradiation surface area to volume ratio, facilitate continuous bioprocesses.

#### 5.6 Conclusions

Photosynthetic water oxidation catalyzed by photoautotrophic microorganisms encompasses a high potential for efficient biocatalytic oxyfunctionalization, providing activated reduction equivalents as well as O<sub>2</sub> at high rates. The present study reports on the establishment of a recombinant CYP450 harboring cyanobacterium enabling an unprecedentedly high lightdriven oxyfunctionalization activity. The specific cyclohexane hydroxylation rates achieved compare well to those of established heterotrophic strains. Further, the two-liquid phase concept enabled stable bioprocessing for 52 h, and *in situ*  $O_2$  generation allowed for a non-aerated process operation mode and thus gram-scale production of cyclohexanol from the volatile substrate cyclohexane. The reported concepts for biocatalyst and process engineering augur well for the future application of cyanobacteria for the ecologically as well as economically remunerative production of fine and even bulk chemicals via biotransformation reactions.

#### 5.7 Acknowledgments

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Chapter 6 Super-high cell density cultivation of *Synechocystis* sp. PCC 6803 in a mixed-trophies biofilm-based capillary reactor

Ingeborg Heuschkel performed biofilm experiments for the assessment of Syn6803\_CYP catalytic activities. Katja Bühler, Rohan Karande, Bruno Bühler and Andreas Schmid coordinated the project and corrected the manuscript.

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#### 6.1 Abstract

Cultivation of photoautotrophic organisms at high cell densities for photobiocatalytic applications still challenges the reactor and photobioprocess design. Reactor technologies providing high surface to volume ratios, such as biofilm-coated capillary reactors, are considered highly promising as they facilitate efficient light input and thus cell growth. However, in enclosed reactor systems  $O_2$  accumulates to high concentrations in the course of oxygenic photosynthesis, leading to oxidative stress and cell growth inhibition. In this study, we present an improved cultivation concept based on the co-cultivation of the photoautotrophic strain *Synechocystis* sp. PCC 6803 with the chemoheterotrophic  $O_2$ -respiring organism *Pseudomonas* sp. VLB120 in a biofilm-based capillary reactor. The chemoheterotrophic organism faciliated enhanced cyanobacterial surface coverage and reduced oxidative stress by the respiration of  $O_2$ . Eventually, the mixed-trophies cultivation technology enabled growth of cyanobacterial biofilms to super-high cell densities of up to 48 g<sub>BDW</sub> L<sup>-1</sup> and was demonstrated to be accessible for the biocatalytic oxyfunctionalization of hydrocarbons.

#### 6.2 Introduction

The application of photoautotrophic organisms for biocatalytic purposes constitutes a promising technology for the eco-efficient production of fuels and value-added chemicals. In contrast to chemoheterotrophic organisms, phototrophic microorganisms such as algae and cyanobacteria rely on water, light, and CO<sub>2</sub> as abundant sources for electrons, energy, and carbon, respectively. Yet, the cultivation of photobiocatalysts at high cell densities (HCD) still challenges the reactor and bioprocess design (Lima-Ramos et al., 2014). Reactor technologies providing high surface to volume ratios, such as capillary reactors (Karande et al., 2014; Wohlgemuth et al., 2015), are highly promising for the cultivation of HCD phototrophic organisms, as they facilitate efficient light input and distribution. Applying the microbial catalyst in a biofilm format further exploits this technology, featuring selfimmobilization, regeneration and high biomass retention and allowing a continuous process operation (Halan et al., 2012; Rosche et al., 2009). The capillary biofilm-based reactor concept was already successfully applied to heterotrophic microorganisms and was recently adapted to the cultivation of the cyanobacterium Synechocystis sp. PCC 6803 (David et al., 2015). However, as a consequence of photosynthetic water oxidation, cultivation of photoautotrophic organisms in enclosed reactor setups quickly becomes hampered by the local supersaturation of oxygen in the system (Huang et al., 2017; Weissman et al., 1988). Such growth inhibiting effects were also observed for the biofilm-based cultivation of Synechocystis sp. PCC 6803 by David et al. 2015. Thus, the stable cultivation of HCD photoautotrophic organisms in the capillary biofilm reactor necessitates solutions to extract excess oxygen from the liquid phase. Technical approaches aim at the elimination of supersaturated O<sub>2</sub> concentrations by facilitating gas exchange from the aqueous medium to the gaseous environment (Weissman et al., 1988). In that line, the insertion of air segments into the constant medium flow of the cyanobacterial-coated capillary reactor (Figure 6.1 top) most likely also stabilized the biofilm development of Synechocystis sp. PCC 6803 in David et al. 2015.

In this communication, we present an alternative and biologically-inspired concept to reduce aqueous phase oxygen concentrations by the co-cultivation of a chemoheterotrophic  $O_2$ -respiring organism (*Pseudomonas* sp. VLB120). The use of two microbial species with complementary metabolic activities results in an  $O_2$ -optimized microenvironment and thus reduced oxidative stress to the cells (**Figure 6.1 bottom**). Eventually, the mixed-trophies biofilm-based capillary reactor setting enables the retention of super-high biomass. Furthermore, the HCD cultivation system allows the biotechnological application of recombinant photobiocatalysts for the light-driven oxyfunctionalization of cyclohexane.



**Figure 6.1**: *Top:* Scheme of a segmented-flow capillary reactor. *Bottom:* Basic principle of protocooperation between two microbial species with complementary metabolic activities (chemoheterotrophic and photoautotrophic). Cells of both species are embedded in extracellular polymeric substances and form a three-dimensional biofilm on the inner surface of the capillary. O<sub>2</sub> respiration rates (chemoheterotrophic strain) and O<sub>2</sub> evolution rates (photoautotrophic strain) could balance the O<sub>2</sub> environment.

#### 6.3 Materials and methods

**Chemicals and bacterial strains**. Chemicals, construction and cloning of plasmids and strains used in this study are described in **Chapter 2**. *Synechocystis* sp. PCC 6803 and *Pseudomonas* sp. VLB120 harboring the empty expression plasmid pAH032 contain a kanamycin resistance cassette and are hereinafter referred to as Syn6803\_Km and Ps\_Km. *Synechocystis* sp. PCC 6803 and *Pseudomonas* sp. VLB120 harboring pAH050 contain a cyclohexane monooxygenase CYP enzyme system and are hereinafter referred to as Syn6803\_CYP and Ps\_CYP. *Synechocystis* sp. PCC 6803 harboring pAH042 contain the alkane monooxygenase system AlkBGT and is hereinafter referred to as Syn6803\_BGT. *Pseudomonas* sp. VLB120 harboring pAH049 contains a cyclohexanone Baeyer-Villiger monooxygenase and is hereinafter referred to as Ps\_BVMO.

**Pre-cultivation of** *Synechocystis* **sp. PCC 6803 strains.** Cells were grown in YBG11 medium supplemented with 50 mM NaHCO<sub>3</sub> (see medium composition below). Pre-cultures were inoculated in 20 mL medium in a 100 mL baffled shake flask using 200 µL of cryo-stock and cultivation was carried out at 30 °C, 50 µE m<sup>-2</sup> s<sup>-1</sup> (LED), ambient CO<sub>2</sub> (0.04%), 150 rpm (2.5 cm amplitude), and 75% humidity in an orbital shaker (Multitron Pro shaker, Infors, Bottmingen, Switzerland) for 4 days. From this pre-culture, main-cultures were inoculated starting with an OD<sub>750</sub> of 0.08 and cultivation was continued for another 4 days.

 YBG11 medium composition (50 mM NaHCO<sub>3</sub>, w/o citrate): 1.49 g L<sup>-1</sup> NaNO<sub>3</sub>, 0.074 g L<sup>-1</sup>

 MgSO<sub>4</sub> · 7 H<sub>2</sub>O, 0.031 g L<sup>-1</sup> K<sub>2</sub>HPO<sup>4</sup>, 10 mL L<sup>-1</sup> YBG11 trace elements (100x) , 0.019 g L<sup>-1</sup>

 Na<sub>2</sub>CO<sub>3</sub>, 50 mM HEPES (pH 7.2); YBG11 trace elements (100x): 3.6 g L<sup>-1</sup> CaCl<sub>2</sub> · 2 H<sub>2</sub>O,

 0.28 g L<sup>-1</sup> boric acid, 0.11 g L<sup>-1</sup> MnCl<sub>2</sub> · 4 H<sub>2</sub>O, 0.02 g L<sup>-1</sup> ZnSO<sub>4</sub> · 7 H<sub>2</sub>O, 0.039 g L<sup>-1</sup>

 $Na_2MoO_4 \cdot 2 \quad H_2O, \quad 0.007 \text{ g } \text{L}^{-1} \quad CuSO_4 \cdot 5 \quad H_2O, \quad 0.005 \text{ g } \text{L}^{-1} \quad Co(NO_3)_2 \cdot 6 \quad H_2O, \quad 0.16 \text{ g } \text{L}^{-1}$ FeCl<sub>3</sub> · 6  $H_2O, \quad 0.6 \text{ g } \text{L}^{-1} \quad Na_2EDTA \cdot 2 \quad H_2O, \quad 4.2 \text{ g } \text{L}^{-1} \quad NaHCO_3 \text{ (Shcolnick et al., 2007)}.$ 

**Pre-cultivation of** *Pseudomonas* **sp.** VLB120 strains. Overnight cultures were inoculated from a cryo-stock using 5 mL LB medium and grown at 30 °C and 200 rpm (2.5 cm amplitude) in an orbital shaker (Multitron Pro shaker, Infors, Bottmingen, Switzerland) (Sambrook and Russell, 2001). Pre-cultures were inoculated by adding 200  $\mu$ L of this overnight-culture to 20 mL M9 medium (5 g L<sup>-1</sup> citrate, US\* trace elements) and growth was continued for 24 h (Emmerling *et al.*, 2002). Main-cultures were cultivated for 8 h in 50 mL M9 medium (5 g L<sup>-1</sup> citrate, US\* trace elements) in 250 mL baffled shake flasks starting with an OD<sub>450</sub> of 0.2.

**Pre-mixing of bacterial strains.** 20 mL of each main culture (*Synechocystis* sp. PCC 6803, *Pseudomonas* sp.VLB120) were centrifuged (5000g, rt, 7 min), washed with 20 mL YBG11 and resuspended in 40 mL YBG11 medium. Optical densities after resuspension were  $OD_{750} = 2.2$  and  $OD_{450} = 2.4$ , respectively. 10 mL of *Synechocystis* sp. PCC 6803 were mixed with 10 mL of *Pseudomonas* sp. VLB120 in a 100 mL baffled shake flask and cultivation was continued at 30 °C, 50  $\mu$ E m<sup>-2</sup> s<sup>-1</sup> (LED), ambient CO<sub>2</sub> (0.04%), 150 rpm (2.5 cm amplitude), and 75% humidity in an orbital shaker (Multitron Pro shaker, Infors, Bottmingen, Switzerland) for 24 h. Single species control cultures were mixed with 10 mL of YBG11 medium.

**Technical setting of the capillary reactor system.** For biofilm cultivation, a capillary reactor system adapted from David et al. 2015 was applied (**Figure 6.2**) (David *et al.*, 2015). Serological pipettes functioned as capillaries for biofilm growth (1 mL, trimmed to a capillary volume of 1.2 mL by cutting the tip and the intake area; inner diameter of 3 mm, 16.6 cm length, Labsolute, Th. Geyer GmbH & Co. KG, Renningen, Germany). YBG11 medium (supplemented with 50 mM NaHCO<sub>3</sub>, with or without 0.4 g L<sup>-1</sup> citrate) was supplied via Tygon tubing (LMT-55, 2.06 mm inner diameter, 0.88 mm wall thickness; Ismatec, Wertheim, Germany) using a peristaltic pump (ISM939D; Ismatec, Wertheim, Germany). Air segments were supplied via Tygon tubing connected by a T-connector to the capillary reactor system. Injection ports were introduced in front of the capillaries for inoculation using a syringe. Fluorescence-light tubes were used as light source (50  $\mu$ E m<sup>-2</sup> s<sup>-1</sup> measured at the center of capillaries) with a light spectrum shown in **Chapter 2**. Gas exchange at medium inlet, for air segments, and at medium outlet was enabled through sterile filters (0.2  $\mu$ m). Cultivation was performed at rt (~26 °C).

**Inoculation of the capillary reactor system.** The capillaries of the reactor system were inoculated with single- and mixed-species cultures, respectively, by purging ca. 5 mL of each culture through the injection port. Medium flow was started 15 – 24 h after inoculation at a

rate of ~55  $\mu$ L min<sup>-1</sup>. If indicated, air segments were introduced 9 days after inoculation at a rate of ~55  $\mu$ L min<sup>-1</sup>, resulting in an increased overall flow rate of ~110  $\mu$ L min<sup>-1</sup> in these capillaries.



Figure 6.2: Technical setup of the capillary reactor system.

**O**<sub>2</sub> quantification in gas and in liquid phase. For O<sub>2</sub> gas analysis of air segments, bubble traps (sealed with a septum) were introduced downstream of capillaries one day before measurement to enable gas equilibrium. 100  $\mu$ L of gas phase were sampled from the bubble trap using a gas-tight syringe (Hamilton Company, Reno, Nevada, USA) and O<sub>2</sub> was quantified using gas chromatography (GC Trace 1310, Thermo Fisher Scientific, Waltham, USA) equipped with a TG-BOND Msieve 5A capillary column (30 m, I.D.: 0.32 mm, film thickness: 30  $\mu$ m, ThermoFisher Scientific, Waltham, USA) and a thermal conductivity detector (TCD) operating at 100 °C with a filament temperature of 300 °C, and a reference gas flow of 4 mL min<sup>-1</sup>. Argon gas was applied as carrier gas with a constant flow of 5 mL min<sup>-1</sup>. The injection temperature was set to 50 °C and a split ratio of 2 was applied. The oven temperature was kept constant at 35 °C for 3 min. O<sub>2</sub> concentrations in the liquid medium were quantified using a Clark-type flow-through sensor (OX-500 Oxygen Microsensor, Unisense, Aarhus, Denmark).

**Quantification of citrate concentration in the liquid phase using HPLC.** Samples were collected from the capillary outlet, centrifuged (17000g, 5 min, rt), and the supernatant was applied for high pressure liquid chromatography (Dionex Ultimate 300, Thermo Fisher Scientific, Waltham, USA) equipped with a ligand exchange column (HyperREZ XP Carbohydrate H+, 30 cm length, 7.7 mm diameter, 8  $\mu$ m particle size, ThermoFisher Scientific, Waltham, USA) and a variable wavelength detector operating at 210 nm. The column oven temperature was kept constant at 40 °C. 16 mM H<sub>2</sub>SO<sub>4</sub> was applied as carrier solvent at a flow rate of 0.75 mL min<sup>-1</sup>.

Syn6803\_CYP activity measurement in the Syn6803\_CYP + Ps\_CYP mixed-species biofilm setup. *CYP* gene expression was induced 36 days after inoculation by the addition of 2 mM IPTG to the supplied YBG11 medium. At day 37, cyclohexane was delivered in saturating concentrations via air and medium phase. For this purpose the air and medium flow was passed through a silicone tube, dipped into liquid cyclohexane allowing the cyclohexane to diffuse through the silicone tube into the medium and air stream.

**Ps\_BVMO activity measurement in the Ps\_BVMO + Syn6803\_BGT mixed-species biofilm setup**. *BVMO* gene expression was induced 15 days after inoculation using 2 mM of IPTG supplied with the YBG11 medium. At day 16, BVMO activity was measured by adding 5 mM of cyclohexanone to the YBG11 medium flow.

Quantification of cyclohexanol and caprolactone using gas chromatography (GC). Samples were collected from the reactor outflow and guenched with equal volumes of icecold diethyl ether, vortexed for 2 min, and centrifuged (17,000g, 2 min, rt). The ether phase was removed and dried over anhydrous Na<sub>2</sub>SO<sub>4</sub>. Quantification of caprolactone and cyclohexanol was performed using gas chromatography (GC Trace 1310, Thermo Fisher Scientific, Waltham, USA) equipped with a TG-5MS capillary column (5% diphenyl / 95% dimethyl polysiloxane, 30 m, I.D.: 0.25 mm, film thickness: 0.25 µm, Thermo Fisher Scientific, Waltham, USA) and a flame ionization detector (FID) operating at 320 °C, 350 mL min<sup>-1</sup> air flow. 30 mL min<sup>-1</sup> makeup gas flow and 35 mL min<sup>-1</sup> hydrogen gas flow. Nitrogen gas was applied as carrier gas with a constant flow of 1.5 mL min<sup>-1</sup>. The injection volume was set to 1 µL using a PTV injector, programmed with a temperature gradient of 10 °C s<sup>-1</sup> from 90 -300 °C. A split ratio of 11 was applied. For cyclohexanol quantification, the temperature profile of the oven was: 1) 40 °C for 1 min, 2) 40 – 80 °C with 10 °C min<sup>-1</sup>, 3) 80 – 250 °C with 100 °C min<sup>-1</sup>, and 4) 250 °C for 2 min. The oven temperature profile for caprolactone guantification was: 1) 40 °C for 3 min, 2) 40 - 170 °C with 15 °C min<sup>-1</sup>, 3) 170 - 300 °C with 100 °C min<sup>-1</sup>, and 4) 300 °C for 1 min.

**Quantification of cell number, cell volume, and biofilm dry weight.** For biomass harvest purposes, the reactor experiment was actively stopped by terminating the medium supply. The biofilm coated capillaries were disassembled and the biomass was removed from the capillaries by scratching and resuspension into a defined volume of water. The resulting culture was mixed vigorously for 1 minute before cell number and cell volume quantification using coulter counter measurement (Multisizer 3, 20 µm aperture,Beckman Coulter, Brea, CA). *Synechocystis* sp. PCC 6803 and *Pseudomonas* sp. VLB120 cells were differentiated by particles size of 0.4 - 1.6 µm and 1.6 - 6 µm, respectively. For biofilm dry weight determination, the remaining biomass was concentrated by centrifugation (5000g, 20 °C, 7 min), transferred to pre-dried and pre-weighted glass tubes, centrifuged again (10000g, 4 °C, 7 min), and the remaining pellet dried at 60 °C for 1 week.

#### 6.4 Results

To proof the technique of stably cultivating phototrophic microorganisms at high cell densities via a mixed-trophies biofilm-based capillary reactor, the two model strains *Synechocystis* sp. PCC 6803 and *Pseudomonas* sp. VLB120 were applied. *Synechocystis* sp. PCC 6803 is a well-known cyanobacterial model strain and widely used for studying photosynthesis-driven production of chemicals and fuels. *Pseudomonas* sp. VLB120 constitutes a chemoheterotrophic strain frequently applied for biocatalytic purposes with strong biofilm formation ability. First, single- and mixed-species of Syn6803\_Km and Ps\_Km were applied in the capillary reactor system. Six experimental setups using YBG11 medium (supplemented with 0.4 g L<sup>-1</sup> citrate if stated) for cell growth and without or with additional air segments were conducted. After five weeks of biofilm maturation, O<sub>2</sub> concentration in the liquid and gas phase as well as citrate consumption was measured. Afterwards, the cultivation system was actively terminated and characterized regarding photo-pigment formation (macroscopic), bio-volume of each species (cell number and cell volume), and total biofilm dry weight.

## 6.4.1 Cultivation of single species *Synechocystis* results in low surface coverage and impaired biofilm development.

First, biofilm and  $O_2$  formation in the capillary reactor were analyzed during cultivation of single species Syn6803\_Km. Cells cultivated without air segments resulted in weak biofilm formation with a low final biomass concentration of 2 g<sub>BDW</sub> L<sup>-1</sup> mainly located in the first part of the capillary tube (**Figure 6.3i**, **Table 6.1**, **Figure 6.4i**). In addition, photo-pigment formation seemed to be impaired indicated by a yellow/ light green outer appearance of the biofilm. O<sub>2</sub> concentrations measured in the aqueous phase were 3 fold above the saturation limit at ambient conditions (746 µM, **Table 6.1**, **Figure 6.4i**). The application of air segments promoted cyanobacterial growth resulting in a lush green colored biofilm and increased final biomass concentrations of 14 g<sub>BDW</sub> L<sup>-1</sup> (**Figure 6.3i**). In contrast to single phase cultivation, the use of air segments facilitated O<sub>2</sub> extraction from the liquid phase into the gas segments, reflected by an increased O<sub>2</sub> concentration of 24% measured in the gas phase in comparison to ambient O<sub>2</sub> concentration (21%) (**Table 6.1**). In general, surface coverage of single species Syn6803\_Km grown biofilm was inhomogeneous.

# 6.4.2 Co-cultivation of *Synechocystis* with *Pseudomonas* sp. VLB120 enhances cyanobacterial surface coverage and promotes biofilm formation to high cell densities.

In a next setting, Ps\_Km was co-cultivated with Syn6803\_Km. After five weeks of cultivation without air segments visible surface coverage was slightly enhanced in comparison to single species cultivation (**Figure 6.3ii** vs. **Figure 6.3i**). This resulted in three-times higher final

biofilm dry weight of 6  $g_{BDW}$  L<sup>-1</sup>, mainly consisting of cyanobacterial cells (98.3%) (**Table 6.1**). O<sub>2</sub> concentrations measured in the aqueous phase were, as expected, above the solubility limit at ambient conditions (**Table 6.1**, **Figure 6.4iii**). As observed before, the use of air segments resulted in extraction of O<sub>2</sub> into the air phase and promoted lush green cyanobacterial biofilm formation throughout the length of the capillary (**Figure 6.3iv**, **Table 6.1**). Overall, the co-cultivation of Syn6803\_Km with Ps\_Km promoted biofilm formation to a high final biofilm concentration of 32 g<sub>BDW</sub> L<sup>-1</sup> mainly consisting of cyanobacterial cells (99.3%) (**Table 6.1**, **Figure 6.4iv**).



Figure 6.3: Pictures of capillary reactors taken five weeks after inoculation. Syn6803\_Km = Synechocystis sp. PCC 6803 pAH032, Ps\_Km = Pseudomonas VLB120 pAH032, Mixed = Syn6803\_Km + Ps\_Km, BDW = biofilm dry weight.

#### 6.4.3 Citrate respiration relieves oxidative stress and supports the formation of superhigh density cyanobacterial biofilm.

In the following experiments, mixed-trophies cultivation was conducted as described above, but using YBG11 medium supplemented with citrate to promote  $O_2$  respiration by Ps\_Km. After five weeks of cultivation, the capillaries were entirely coated with rich green biofilm (**Figure 6.3v + vi**). Without air segments, respiration of citrate by Ps\_Km decreased the  $O_2$  concentration in the aqueous phase to anoxic conditions (**Table 6.1**, **Figure 6.4v**). As already observed before, the relief of supersaturating  $O_2$  concentrations, in this case via Ps\_Km respiration, had a positive impact on the cyanobacterial biofilm development. The cyanobacterial surface coverage was high and resulted in a final biofilm concentration of 48 g<sub>BDW</sub> L<sup>-1</sup> consisting of 85% cyanobacterial cells (**Table 6.1**). Upon the addition of air

segments, O<sub>2</sub> was again stripped into the gas phase (**Figure 6.4vi**). Surprisingly, the final biofilm dry weight was reduced to 19  $g_{BDW}$  L<sup>-1</sup> (92% cyanobacterial cells) (**Figure 6.3vi**, **Table 6.1**).

**Table 6.1**: Quantitative data obtained from single- and mixed-species biofilm cultivation in a tubular microreactor. Mixed-species = Co-culture of Syn6803\_Km and Ps \_Km, - Citrate = without organic carbon source, + Citrate = with 0.39 g L<sup>-1</sup> citrate as carbon source, - Air = without air segments, + Air = with air segments.

Experimental setup		O <sub>2</sub> in gas phase	O2 in aq. phase [1]	Citrate consumption	Biofilm dry weight [2] / g L <sup>-1</sup>			
		/% /μM /gL <sup>-</sup>		Ps.	Syn.	total		
Single Syn6803_Km								
i)	- Air	- Citrate	-	746	-	-	1.5	1.5
ii)	+ Air	- Citrate	23.9	284	-	-	13.7	13.7
Mixed-species								
iii)	- Air	- Citrate	-	923	-	0.1	5.8	5.9
iv)	+ Air	- Citrate	24.1	287	-	0.2	31.4	31.6
Mixed-species								
V)	- Air	+ Citrate	-	0	0.27	7.2	40.6	47.8
vi)	+ Air	+ Citrate	16.3	194	0.39	1.5	17.3	18.8

[1] Solubility of O<sub>2</sub> (at 26 °C, salinity of 3.5 g kg<sup>-1</sup>, 21% O<sub>2</sub> in gas phase): ~250  $\mu$ M; aqueous phase O<sub>2</sub> concentrations of experiments performed with air segments are theoretical numbers relvina on the partitioning between aas and aqueous phase. [2] The biofilm dry weight is calculated based on 1.2 mL tube volume. Ps. and Syn. specific biofilm dry weights are calculated based on cell numbers and cell volumes and the respective total biofilm dry weight, assuming that both strains constitute equal biovolume to biofilm dry weight ratio.



**Figure 6.4**: Oxygen concentrations and final biofilm dry weight of single- and mixed-species cultivation of Syn6803\_Km and Ps\_Km grown in biofilm-based capillary reactor. Cultivation was performed using YBG11 medium without or with citrate supplementation and without or with air segments.

## 6.4.4 The mixed-species biofilm-based capillary reactor setup enables biocatalytic reactions.

Mixed-species cultivation significantly enhanced cyanobacterial biofilm development and retention of HCD cyanobacterial biofilm. In order to test the new developed cultivation method for biocatalytic purposes, an exemplary whole-cell reaction was performed using recombinant strains harboring a cyclohexane CYP monooxygenase enzyme system. Syn6803\_CYP was co-cultivated with Ps\_CYP using air segments for O<sub>2</sub> extraction and YBG11 medium without organic carbon source to focus on photobiocatalytic hydroxylation activitiy. After 5 weeks of cultivation, *CYP* gene expression was induced using IPTG and cyclohexane was delivered to the biofilm via substrate saturated air- and medium flow. Cyclohexanol quantification of samples from the reactor outlet showed titers of 1.1 mM corresponding to a productivity of 7.5 g  $L_{tube}$ <sup>-1</sup> day<sup>-1</sup> (**Table 6.2**). The reaction was most likely catalyzed by the cyanobacterial strain, as no organic carbon source for the Ps\_CYP cell growth and cofactor regeneration was present and cultivation under light exclusion resulted in reduced product formation (data not shown). Thus, we could proof the accessibility of the cyanobacterial cells in the grown biofilm for biocatalytic purposes.

**Table 6.2:** Exemplary biocatalytic reactions conducted with recombinant strains applied in the mixedspecies biofilm based capillary reactor system. Syn\_CYP = *Synechocystis* sp. PCC 6803 pAH050, Ps\_CYP = *Pseudomonas* sp. VLB120 pAH050, Ps\_BVMO = *Pseudomonas* sp. VLB120 pAH049, Syn6803\_BGT = *Synechocystis* sp. PCC 6803 pAH042; + Citrate = with 0.46 g L<sup>-1</sup> citrate as carbon source, + Air = with air segments.

Recombinant biocatalytic strains	Reaction conditions	Reaction	Product concentration in reactor outlet	Productivity
Syn6803_CYP + Ps_CYP	- Citrate + Air	Cyclohexane → Cyclohexanol	1.1 mM	7.5 g L <sub>tube</sub> -1 day-1
Ps_BVMO + Syn6803_BGT	+ Citrate + Air	Cyclohexanone → Caprolactone	2.5 mM	19.4 g L <sub>tube</sub> -1 day-1

In a second reaction setup, two further recombinant strains, namely Syn6803\_BGT and Ps\_BVMO, were co-cultivated using air segments and YBG11 supplemented with citrate to promote chemoheterotrophic biocatalysis. After 15 days of cultivation, *AlkBGT* and *BVMO* gene expression was induced using IPTG and either pure NAME was supplied as additional organic phase or 5 mM of cyclohexanone were added to the cultivation medium. Analysis of the reactor outlet revealed no catalytic activity for Syn6803\_BGT. This might be explained by isufficient protein synthesis or unsufficient coupling of the photosynthetic metabolism with the heterologous enzyme system under the applied cultivation and reaction conditions, as already observed for biotransformations using suspended cultures (**Chapter 4**). In contrast, the chemoheterotrophic strain Ps\_BVMO catalyzed the Baeyer-Villiger oxidation of

cyclohexanone to caprolactone. The final titer of 2.5 mM caprolactone corresponds to a catalytic rate of ca. 19 g  $L_{tube}$ <sup>-1</sup> day<sup>-1</sup> (**Table 6.2**). Eventually, the mixed-species biofilm-based capillary reactor system enabled the biocatalytic functionality of both, the phototrophic biocatalysts and heterotrophic species.

#### 6.5 Discussion

In nature, oxygenic phototrophs and aerobic heterotrophs are embedded in a complex matrix of extracellular polymeric substances (EPS) to form stable microbial mats (Prieto-Barajas *et al.*, 2017). In such mats, the microbial consortium interacts in close cooperation, and thereby profits from complementary metabolic activities and taps new resources. In wastewater treatment plants microalgal/ cyanobacterial biofilms are applied in undefined consortia, e.g. for effluent oxygenation, heavy metal removal, and recycling of nitrogen and phosphorous (Barros *et al.*, 2018). The here presented technology exploits the concept of microbial mats in a defined and minimized biofilm system. The co-cultivation of the chemoheterotrophic, aerobic microorganism *Pseudomonas* sp. VLB120 strongly enhanced biofilm formation, maturation and surface coverage of the photoautotrophic cyanobacterium *Synechocystis* sp. PCC 6803. This phenomenon may be attributed to proto-cooperation, which is the beneficial but not essential interaction of organisms, and is described for the here applied cultivation system by the following sections.

Pseudomonas sp. VLB120 supports Svnechocvstis sp. PCC 6803 cell attachment. In principle, both strains produce EPS and thus facilitate biofilm formation. Using microscopy analysis of the harvested biofilm, the embedding of Syn6803 Km and Ps Km in a biofilm matrix was visible (Figure 6.5). However, also during cultivation without organic carbon source the presence of *Pseudomonas* had a positive impact on *Synechocystis* biofilm formation although the cultivation conditions did not support Pseudomonas growth (0.6% of total cell fraction) (Figure 6.3iii, Table 6.1). Most likely, the few observed Pseudomonas cells survived on EPS or cell debris of Svnechocvstis and in turn improved the cvanobacterial surface attachment e.g., via conditioning of the capillary surface. Unexpectedly, the application of air segments reduced growth of *Pseudomonas*. This might be explained by a hydrodynamic stress response of the cells induced by high fluidic and interfacial stresses in the capillary, which might require more energy for Pseudomonas cell maintenance and EPS formation. This was reflected by a higher specific citrate consumption of 0.26 g g<sub>PsBDW</sub><sup>-1</sup> in comparison to 0.04 g  $g_{PsBDW}^{-1}$  in single phase flow (**Table 6.1**). Thus, future optimization of the cultivation setting may involve the reduction of hydrodynamic stress e.g., via a reduced rate of air flow.



**Figure 6.5**: Microscopic image of a mixed-species biofilm containing *Synechocystis* sp. PCC 6803\_Km (Syn\_Km) and *Pseudomonas* VLB120\_Km (Ps\_Km), harvested from a capillary reactor. Scale bar equal to 10 µm.

Oxidative stress impairs cyanobacterial biofilm growth and can be relieved by O<sub>2</sub> respiration. During single phase cultivation supersaturating O<sub>2</sub> concentrations were measured which went along with impaired biofilm formation (Figure 6.4). High  $O_2$ concentrations can enhance the formation of radical oxygen species, which are side products generated during electron transport in oxygenic photosynthesis. Most likely these extreme O<sub>2</sub> concentrations led to oxidative stress and thus growth inhibition of Syn6803 km, resulting in visible photo-pigment reduction (yellowish/ light green outer appearance of the strain) observed towards the end of the capillary tube (Latifi et al., 2009; Narainsamy et al., 2016; Weissman et al., 1988). In contrast, the introduction of air segments as well the respiration of O<sub>2</sub> by *Pseudomonas* decreased the aqueous phase O<sub>2</sub> concentration to ambient or even anoxic levels, thus relieved oxidative stress and resulted in rich green, HCD biofilm (Figure 6.4). Overall, the dual trophies approach enabled the cultivation of photobiocatalysts in a stable and super-high cell density format which is currently a key-bottleneck in photobiotechnology. Furthermore, the applied biotransformation of cyclohexane to cyclohexanol demonstrated the applicability of the developd cultivation technology for biotechnological purposes.

The mixed-trophies capillary reactor system supports application the of chemoheterotrophic biocatalysts. Continuous production of chemicals using Pseudomonas sp. VLB120 in biofilm-based capillary reactors was already investigated in several studies (Gross et al., 2010; Karande et al., 2016b). As for many O2-dependent bioprocesses, oxygen mass transfer constitutes a main process limitation also during cultivation in such reactor systems. The introduction of air segments into the medium flow increases oxygen availability, but again becomes limited after a specific length of the capillary tube (Karande et al., 2014). In contrast, coupling photosynthetic O<sub>2</sub> generation with bacterial respiration relieves the process limitation of O2-dependent bioprocesses in theory independent of the tube length as long as light is available (**Chapter 7**). Already some decades ago the phenomenon of *in situ*  $O_2$  supply was transferred from nature to productive biotechnology utilizing defined co-cultures of algae and bacteria (Adlercreutz *et al.*, 1982; Adlercreutz and Mattiasson, 1982; Cheirsilp *et al.*, 2011; Papone *et al.*, 2012). Yet, this research either focused on immobilized cells embedded in artificial polymers such as alginate, or cell suspensions. In this study, growth of *Pseudomonas* sp. VLB120 in the capillary reactor was 6.5 times and citrate respiration 9 times higher than without the use of air segments, but solely due to the *in situ* supply of  $O_2$  originating from the co-cultured cyanobacterium (data for single species Ps\_Km not shown). Furthermore, Ps\_BVMO applied in the mixed-trophies reaction system was accessible for the hydroxylation of cyclohexanone to caprolactone and thus demonstrates the functionality of the developed technology also for chemoheterotrophic biocatalysis.

#### 6.6 Conclusion

In a mixed-trophies biofilm it was possible to co-cultivate the photoautotrophic *Synechocystis* sp. PCC 6803 with *Pseudomonas* sp. VLB120 over a time-period of five weeks to a high cell density of max. 48  $g_{BDW}$  L<sup>-1</sup>. This is the first cultivation technology allowing the defined, continuous cultivation of a phototrophic organism at super-high cell densities. Furthermore, the strains applied in the capillary reactor setup enabled the biocatalytic conversion of hydrocarbons to respective oxyfunctionalized value-added products. The concept now faces further implementation, evaluation and optimization of biocatalytic approaches and scale-up for the eco-efficient production of fuels and value-added chemicals.

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## Chapter 7 General discussion - *In situ* O<sub>2</sub> generation for biocatalytic oxyfunctionalization reactions

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#### 7.1 Abstract

O<sub>2</sub>-dependent whole-cell bioprocesses, such as C-H oxyfunctionalizations, are constrained by technically limited O<sub>2</sub> mass transfer and biocatalyst-inherent O<sub>2</sub> respiration. In large-scale bioprocesses, this restricts the maximum achievable productivity to 5.6 g<sub>product</sub> L<sup>-1</sup> h<sup>-1</sup> assuming a resting cell concentration of 9.4 g<sub>CDW</sub> L<sup>-1</sup>. This concept paper discusses strategies to enhance the O<sub>2</sub> availability for biocatalytic oxyfunctionalizations with a focus on the *in situ* generation of O<sub>2</sub> from water. This promising approach was addressed recently by the exploitation of microbial photosynthesis for light-driven C-H oxyfunctionalization. Via intracellular O<sub>2</sub> evolution, phototrophic biocatalysts increase the maximum achievable productivity well beyond technical boundaries. This fundamental advantage over O<sub>2</sub>-respiring biocatalysts now awaits scale-up evaluations, combining established cultivation technologies for phototrophic organisms with bioprocessing techniques for heterotrophic organisms.

#### 7.2 Introduction

Oxvaen-dependent reactions like reaioand enantiospecific hvdrocarbon oxyfunctionalizations are of outstanding interest for the chemical and pharmaceutical industries (Bühler et al., 2003a; Dong et al., 2018; Hollmann et al., 2011). For such reactions. efficient biocatalysis concepts have been developed that rely on oxygenases and electron supply via the metabolism of living microbial cells (Schmid et al., 2001; Schrewe et al., 2013; Wachtmeister and Rother, 2016). Commercial production of oxyfunctionalized fine and bulk chemicals necessitates a productivity of at least 1 - 10 g L<sup>-1</sup> h<sup>-1</sup> (Straathof et al., 2002; van Dien. 2013). To achieve this, biocatalysts are required that feature high specific activities of >100 U  $q_{CDW}^{-1}$  and/ or can be operated at high cell concentrations of >10  $q_{CDW}$  L<sup>-1</sup>. With a cellular oxygenase content of up to 12.5% of dry biomass (Tufvesson et al., 2010), the given whole-cell activity translates into an enzyme-specific activity of >0.8 U mg<sub>enzyme</sub>-1. In comparison to other industrially applied enzymes (e.g., lipases), the nature of oxygenases often limits the productivity due to a low k<sub>cat</sub> (typically in the range of 0.2 - 75 s<sup>-1</sup>) and limited enzyme stability (Duetz et al., 2001; Lundemo and Woodley, 2015). Thus, high biomass concentrations are essential for the production of large volume chemicals or energy carriers. The maximum applicable biomass concentration of O<sub>2</sub> respiring biocatalysts is constrained by the maximum net oxygen accumulation rate (=  $dO_2/dt$ ,  $\mu mol_{O2}$  min<sup>-1</sup> L<sup>-1</sup> = U L<sup>-1</sup>) of the bioprocess setup, constituting a critical process boundary for O<sub>2</sub>-dependent reactions (Duetz et al., 2001; Garcia-Ochoa and Gomez, 2009; Law et al., 2006; Margues et al., 2010). In classical biotransformation processes performed with heterotrophic microbes, this boundary depends on i) the bioreactor-intrinsic oxygen transfer rate (OTR) and ii) the biocatalyst specific oxygen respiration rate (ORR):

#### $dO_2/dt = OTR - ORR.$

The OTR is a physical parameter defined by the gas-liquid mass transfer constant  $k_{L}$  (m min<sup>-1</sup>), the interfacial area a (m<sup>2</sup>m<sup>-3</sup>), and the difference between the O<sub>2</sub> solubility C\* (µmol L<sup>-1</sup>) and the dissolved O<sub>2</sub> concentration in the liquid phase C (µmol L<sup>-1</sup>):

#### OTR = $k_La$ (C\*-C).

As the  $O_2$  solubility in aqueous media is relatively low under atmospheric conditions (~250 µM at 25 °C, 1 atm, and a salinity of 6 g kg<sup>-1</sup>) (Garcia and Gordon, 1992; Garcia and Gordon, 1993), the mass transfer term k<sub>L</sub>a is one of the most critical process parameters to be addressed during the scale-up of microbial bioprocesses (Marques *et al.*, 2010). It depends on the composition and physical properties of the gas and liquid phases (which also influence C\*) and on the mixing applied. Technical solutions to enhance the net oxygen accumulation rate aim at an OTR increase via the optimization of the hydrodynamics in

bioreactor setups, that is, the bioreactor geometry or the operational conditions (**Figure 7.1**) (Garcia-Ochoa and Gomez, 2009). Examples concern either  $k_La$  or C<sup>\*</sup>:

- k<sub>L</sub>a: increased aeration rate (Law *et al.*, 2006), improved mixing (stirrer speed, design), application of organic solvents (Kumar *et al.*, 2017; Shet *et al.*, 1997) or (nano)particles (Beenackers and van Swaaij, 1993; Olle *et al.*, 2006)
- C\*: application of O2-enriched air, increased pressure



**Figure 7.1**: Examples for technical solutions physically enhancing the O<sub>2</sub> transfer rate in bioreactors. (**top left**) Standard stirred tank bioreactor (STR), (**top right**) falling film microreactor (FFMR), and (**bottom**) aqueous-air segmented microreactor (adapted with permission from Karande et al. 2014 Copyright 2018 John Wiley and Sons.) (Karande *et al.*, 2014).

Further, the application of microreactors can significantly increase gas-liquid mass transfer by increasing the turbulence and thus  $k_{L}a$  compared to reactors with a lower surface to volume ratio. This was shown for oxidations catalyzed by glucose oxidase or D-amino acid oxidase in falling film microreactors (Bolivar *et al.*, 2016; Illner *et al.*, 2014) and styrene epoxidation by recombinant *Pseudomonas* sp. VLB120 using air segments in multiphasic biofilm-coated microreactors (Karande *et al.*, 2014) (**Figure 7.1**).

Besides physical solutions to increase the net oxygen accumulation rate, approaches using oxygen donors other than  $O_2$  (namely  $H_2O$  and  $H_2O_2$ ) have been reported. After reviewing  $O_2$ -related technical constraints critical for the implementation of large-scale whole-cell oxygenation bioprocesses, new concepts for *in situ*  $O_2$  generation in the liquid phase will be discussed.

#### 7.3 Constraints for standard large-scale whole-cell oxygenation bioprocesses

Successful scale-up of a bioprocess in a typically used stirred tank bioreactor (STR) depends on the power input available for  $O_2$  transfer. The maximum achievable  $k_La$  thus is scaledependent. Considering bioreactor-intrinsic constraints, a maximum  $k_La$  of 200 h<sup>-1</sup> can be considered feasible for large-scale STRs (> 1 m<sup>3</sup>) at 30 °C and an assumed average pressure of 2.5 atm, enabling a maximum OTR of 1500 U L<sup>-1</sup> (Duetz *et al.*, 2001). This OTR translates into a maximum productivity of  $9 \text{ g } \text{L}^{-1} \text{ h}^{-1}$  for a product with a molar mass of 100 g mol<sup>-1</sup> (**Figure 7.2**).



**Figure 7.2**: Maximum achievable productivity of  $O_2$ -dependent biocatalytic reactions as a function of the applied concentration of chemoheterotrophic whole-cell biocatalysts. The maximum applicable biomass concentration results from the bioreactor-intrinsic oxygen transfer rate (OTR) divided by the biocatalyst specific oxygen respiration rate and represents the biomass concentration, at which all  $O_2$  transferred into the aqueous medium is respired by the cells. The dashed line represents the productivity that can be achieved for a product with a molar mass of 100 g mol<sup>-1</sup> at a reasonable biocatalyst-specific oxyfunctionalization rate of 100 U g<sub>CDW</sub><sup>-1</sup>. The OTR is defined by the bioreactor-specific gas-liquid mass transfer term k<sub>L</sub>a (estimated to be 200 h<sup>-1</sup> in large scale reactors), the soluble  $O_2$  concentration (550 µM at 30 °C and 2.5 atm) and the dissolved oxygen concentration (100 µM), forming an upper process boundary (red line). With increasing concentration of  $O_2$ -respiring biocatalysts, the net oxygen accumulation rate (d $O_2/dt$ ) is reduced by the oxygen respiration rate (100 U g<sub>CDW</sub><sup>-1</sup> for growing, 60 U g<sub>CDW</sub><sup>-1</sup> for non-growing resting cells), shifting the upper boundary towards lower productivities (blue lines).

The maximum net oxygen accumulation rate depends on the OTR and the ORR. Growing chemoheterotrophic microbes like *Escherichia coli* respire  $O_2$  at a specific rate of ~100 U g<sub>CDW</sub><sup>-1</sup> (Calhoun *et al.*, 1993; Duetz *et al.*, 2001; Park, 2007; Shet *et al.*, 1997). Thus, dO<sub>2</sub>/dt is inversely proportional to the applied biocatalyst concentration. The maximum applicable biomass concentration is restricted to 15 g<sub>CDW</sub> L<sup>-1</sup> at which all available O<sub>2</sub> is used for respiration and the productivity for an O<sub>2</sub> dependent reaction is thus reduced to zero (**Figure 7.2**) (Duetz *et al.*, 2001). Non-growing (resting) cells exhibit a lower energy demand (only for maintenance) and thus a lower respiration rate of ~60 U g<sub>CDW</sub><sup>-1</sup> (calculated based on a glucose uptake rate of 0.62 mmol g<sub>CDW</sub><sup>-1</sup> h<sup>-1</sup> for resting *E. coli* JM101 with 6 O<sub>2</sub> molecules consumed per glucose molecule oxidized to CO<sub>2</sub>) (Julsing *et al.*, 2012a; van Beilen *et al.*, 2003). Their application thus increases the maximally applicable biomass concentration to

 $25 \text{ g}_{\text{CDW}} \text{ L}^{-1}$ . However, under aerobic conditions, the endogenous respiration remains indispensable for the application of chemoheterotrophic biocatalysts, enabling biocatalyst maintenance including, inter alia, protein regeneration. Careful adjustment of the biomass concentration is of upmost importance to maximize the productivity and avoid a limitation by O<sub>2</sub> (Baldwin and Woodley, 2006; Hilker *et al.*, 2006). For the industrial scale scenario defined above (molar mass<sub>product</sub> = 100 g mol<sup>-1</sup>, ORR = 60 - 100 U g<sub>CDW</sub><sup>-1</sup>, k<sub>L</sub>a = 200 h<sup>-1</sup>, specific oxygenation activity = 100 U g<sub>CDW</sub><sup>-1</sup>), 7.5 and 9.4 g<sub>CDW</sub> L<sup>-1</sup> of growing and resting chemoheterotrophic biocatalysts allow a maximum achievable productivity of 4.5 and 5.6 g L<sup>-1</sup> h<sup>-1</sup>, respectively (**Figure 7.2**). *In situ* O<sub>2</sub> generation or the application of oxygen sources other than O<sub>2</sub> are promising strategies to overcome the restrictions by the traditional external O<sub>2</sub> supply and are discussed in the following.

#### 7.4 Use of alternative oxygen donors to overcome O<sub>2</sub> limitations

Enzymes that use oxygen sources other than  $O_2$  represent an alternative to the use of catalysts based on oxygenases (Figure 7.3).





Peroxygenases utilize  $H_2O_2$  as oxygen donor (Bormann *et al.*, 2015; Wang *et al.*, 2017). Cytochrome P450 CYP119, for instance, catalyzes the epoxidation of styrene to styrene oxide via a peroxide shunt pathway (**Figure 7.3 A**) (Koo *et al.*, 2000). Up to now, the variety of reactions catalyzed by peroxygenases is limited. Future exploration of novel peroxygenases with a more diverse reaction scope can be considered a promising approach for preparative oxyfunctionalization chemistry (Wang *et al.*, 2017). Importantly, the high reactivity of  $H_2O_2$  necessitates its well-controlled supply to the reaction system. *In situ* generation of  $H_2O_2$  by enzymatic, e.g., via glucose oxidase (van de Velde *et al.*, 2000), electrochemical, i.e., via a cathode (Lütz *et al.*, 2004). or photocatalytic, e.g., via Flavin/ EDTA/ ho (Perez *et al.*, 2009; Zhang *et al.*, 2018), water oxidation successfully prevents the inactivation of the applied oxidoreductases (Bormann *et al.*, 2015). However, these

processes go along with  $O_2$  reduction and thus do not overcome the requirement for  $O_2$  dissolved in the aqueous phase.

In contrast, dehydrogenase-type enzymes such as molybdopterin-dependent hydroxylases use water as oxygen donor for the oxyfunctionalization of, however, rather activated carbon atoms (Hille *et al.*, 1998). The few examples showing the application of these enzymes for oxyfunctionalizations include the formation of *p*-hydroxybenzyl alcohol from *p*-cresol by the *p*-cresol methylhydroxylase or the hydroxylation of quinaldine to 4-hydroxyquinaldine using quinaldine 4-oxidase (**Figure 7.3 B**) (Hopper, 1978; Ütkür *et al.*, 2011).

Next to these enzymes, photochemically active catalysts such as ruthenium porphyrins have been developed relying on water as source of oxygen for the chemical oxyfunctionalization of olefins and sulfides (Fukuzumi *et al.*, 2012; Funyu *et al.*, 2003; Inoue *et al.*, 2005; Inoue *et al.*, 1994; Li *et al.*, 2011; Pagliaro *et al.*, 2005).

#### 7.5 In situ generation of O2 in the liquid phase

Already in 1977, Hans Günter Schlegel developed the concept of "aeration without air" by investigating the controlled supply of  $H_2O_2$  to microbial cultures synthetizing catalases. Catalases enzymatically cleave  $H_2O_2$ , *in situ* releasing  $O_2$  that can be taken up by cells for respiration, and thus reduce the need for external aeration (Nies and Schlegel, 1984; Rosenberg *et al.*, 1992; Schlegel, 1977; Sonnleitner and Hahnemann, 1997; Sriram *et al.*, 1998).



**Figure 7.4**: Electrochemical *in situ* O<sub>2</sub> generation for the hydroxylation of camphor to 5-exo hydroxyl camphor using CYP101 (Reipa *et al.*, 1997). Reduction equivalents were supplied from an antimony-doped tin oxide working electrode to CYP101 via putidaredoxin (Pdx). O<sub>2</sub> was generated at the platinum counter electrode and the reactor was operated anaerobically using an argon purge. Figure adapted from Reipa *et al.*, 1997 Copyright (2018) National Academy of Sciences.

Using electrolysis, water can be used for the *in situ* generation of  $O_2$  (Wang *et al.*, 2016a). At an electric potential of at least 1.23 V, water is electrolyzed to  $O_2$  and  $H_2$ . Electrochemical *in situ*  $O_2$  generation in aqueous media has successfully been coupled to hydrocarbon oxyfunctionalization, e.g., the hydroxylation of camphor to 5-exo-hydroxycamphor or the epoxidation of styrene to styrene oxide using CYP101 (**Figure 7.4**) (Mayhew *et al.*, 2000; Reipa *et al.*, 1997). From an energy perspective, the use of light energy for photocatalytic, photo-electrochemical, or photovoltaic-electrochemical water oxidation constitutes an economically and ecologically promising approach for the *in situ* generation of  $O_2$  (Abe, 2010; Jiao *et al.*, 2015; Li, 2017). Whereas many photo-/electro-/chemical concepts focus on  $H_2$  generation, the coupling of this  $O_2$  generation principle with enzymatic oxyfunctionalizations has yet to be demonstrated on technical scale.

#### 7.6 Exploitation of microbial photosynthesis for O<sub>2</sub>-dependent reactions

Following the principle of lichens (symbiosis of fungi with microalgae or cyanobacteria), Adlercreutz et al. reported in 1982 the co-immobilization of the algae *Chlorella pyrenoidosa* as natural  $O_2$  producer with  $O_2$ -respiring *Gluconobacter oxydans* (Adlercreutz *et al.*, 1982; Adlercreutz and Mattiasson, 1982). The defined mixed-cultures revealed a 5.4 times increased production of dihydroxyacetone from glycerol in comparison to the single species system without  $O_2$ -evolving algae.

Recently, we successfully exploited the cyanobacterium *Synechocystis* sp. PCC 6803 for the intracellular coupling of the photosynthetic  $O_2$  generation with the  $O_2$ -dependent C-H oxyfunctionalization of a fatty acid methyl ester (**Figure 7.5**) (**Chapter 3**).



**Figure 7.5**: Microbial photosynthesis as source of  $O_2$  for biocatalytic oxygenation. Phototrophic organisms like cyanobacteria oxidize water resulting in the intracellular formation of  $O_2$  and reduction equivalents, both required for oxygenase catalysis. PSII = photosystem II, OER = oxygen evolution rate, OTR = oxygen transfer rate.

Photoautotrophic whole-cell biocatalysts rely on photosynthetic water oxidation rather than the oxidation of organic compounds and  $O_2$  respiration for the supply of (bio)energy in the form of ATP and activated electrons (e.g., NAD(P)H). Thus, they are not only independent from extracellular  $O_2$  supply for growth and maintenance, but even increase the overall  $O_2$  supply.

The equation for the net oxygen accumulation rate then is expanded by the biocatalystspecific oxygen evolution rate (OER), while the negative impact of the ORR becomes small as long as light is available and photosynthetic water oxidation takes place:

$$dO_2/dt = OTR - ORR + OER.$$

In this case, the net oxygen accumulation rate correlates directly with the applied photobiocatalyst concentration enabling high productivities (**Figure 7.6**).



**Figure 7.6**: Maximally achievable productivity of O<sub>2</sub>-dependent biocatalytic reactions as a function of the applied concentration of chemoheterotrophic as well as photoautotrophic whole-cell biocatalysts. The dashed black line represents the productivity that can be achieved for a product with a molar mass of 100 g mol<sup>-1</sup> at a biocatalyst-specific oxyfunctionalization rate of 100 U  $g_{CDW}$ <sup>-1</sup>. The oxygen transfer rate (OTR) is defined by the bioreactor specific gas-liquid mass transfer coefficient  $k_{La}$  (estimated to be 200 h<sup>-1</sup> in large-scale bioreactors) and the soluble O<sub>2</sub> concentration, in principle forming an upper process boundary (red line). With increasing concentration of O<sub>2</sub>-respiring biocatalysts, the effective net oxygen accumulation rate (dO<sub>2</sub>/dt) is reduced by the biocatalysts specific oxygen respiration rate (100 U  $g_{CDW}$ <sup>-1</sup> for growing, 60 U  $g_{CDW}$ <sup>-1</sup> for non-growing cells), shifting the upper boundary towards lower productivities (blue lines). By contrast, photosynthetically active whole-cell biocatalysts enhance dO<sub>2</sub>/dt (green line) by their intrinsic O<sub>2</sub> evolution rate (maximally 850 U  $g_{CDW}$ <sup>-1</sup>), thus theoretically supporting significantly higher productivities. The green area indicates the expanded operational space of phototrophic biocatalysts. The dashed green lines represent a limitation of dO<sub>2</sub>/dt by the availability of light, which can be expected to occur at high cell densities due to shading effects and will depend on the reactor design.

This gives the photosynthetically active biocatalysts a sweeping advantage over  $O_2$ -respiring ones. The upper productivity limit is determined by the biocatalyst-specific oxyfunctionalization rate as long as this rate does not exceed the net oxygen accumulation rate. The OER at photosystem II (PSII) can in theory reach a maximum of 850 U  $g_{CDW}^{-1}$  (assumptions:  $k_{cat}$  of PSII: 1000 s<sup>-1</sup>, 1% PSII  $g_{CDW}^{-1}$ , 350 kDa), (Dismukes *et al.*, 2009; Shen,

2015) being in line with maximally measured OERs ranging from 50 to 910 U  $g_{CDW}^{-1}$  (Porankiewicz and Clarke, 1997; Thomas *et al.*, 1993; Touloupakis *et al.*, 2015; Wang *et al.*, 2012; Yao *et al.*, 2012; Zavřel *et al.*, 2016). However, it has to be considered that the OER at PSII depends on the available light intensity. Respiration and photorespiration (ribulose-1,5-bisphophate oxygenation catalyzed by RuBisCO) may limit the maximum net O<sub>2</sub> accumulation rate, e.g., as a result of shading at high cell densities (indicated by dashed green lines in **Figure 7.6**) (Peterhansel *et al.*, 2010; Vermaas, 2001).

Altogether, O<sub>2</sub>-evolving microorganisms provide the basis to realize oxyfunctionalization productivities far in excess of those achievable in large-scale bioreactors with external O<sub>2</sub> supply (> 9 g  $L^{-1}$  h<sup>-1</sup>). This requires the achievement of high specific oxygenation activities (≥ 100 U g<sub>CDW</sub><sup>-1</sup>) and cultivation of phototrophic biocatalysts to high cell densities (> 10 g<sub>CDW<sup>-1</sup></sub>) to be targeted via biocatalyst, bioreactor, and bioprocess engineering (Fresewinkel et al., 2014). Such high productivities augur well for the production of large volume base chemicals or energy carriers. Classically, high amounts of photosyntheticallyderived (algae) biomass are produced in open pond systems and are used for animal and human nutrition products, cosmetics, as well as for the extraction of high value molecules such as special fatty acids or pigments (Chaumont, 1993; Grobbelaar, 2009; Pulz, 2001; Singh and Sharma, 2012; Spolaore et al., 2006; Weissman et al., 1988). Meanwhile, also closed systems such as the tubular photo-bioreactor in Klötze. Germany (500 km total length and 700 m<sup>3</sup> volume) are developed successfully, producing 130-150 t dry biomass per year (Spolaore et al., 2006). In contrast to biomass producing systems, production systems utilizing phototrophic microorganisms as biocatalyst hold altered requirements with respect to safety, process regulation/ control, biomass production, and product recovery. In order to develop technically and economically viable production processes with (recombinant) photoautotrophic biocatalysts, the well-established advances in microbial fermentation technologies have to be complemented by methodologies for the efficient cultivation of phototrophs with a main focus on light distribution and - at least during growth/ biocatalyst production - carbon dioxide mass transfer (Fresewinkel et al., 2014). Recently, a number of promising cultivation concepts such as tubular, flat panel, and thin-layer reactors have been developed, enabling the generation of biomass concentrations of up to 50  $q_{CDW}$  L<sup>-1</sup> (Apel et al., 2017; Bähr et al., 2016; Dasgupta et al., 2010). These technologies primarily focus on the generation of CO<sub>2</sub>-derived chemical products and now have to be transferred to biotransformation applications, such as the oxyfunctionalization of hydrocarbons (Lippi et al., 2018). Beside biocatalyst growth to high concentrations (> 10  $g_{CDW}$  L<sup>-1</sup>), the technical reaction setting must allow efficient substrate mass transfer and high product titers including in situ product removal technologies for efficient post-process product recovery. The application of cyanobacterial biofilm-coated capillaries constitutes another promising technology, allowing for continuous bioprocessing (David *et al.*, 2015; Strieth *et al.*, 2018). High surface to volume ratios enhance the light distribution and therefore allow increased phototrophic biocatalyst growth and consequently increased productivities. Algal biofilms (such as *Chlorella* sp.) were reported to grow to cell densities of ca. 25 g m<sup>-2</sup> on polystyrene foam (Johnson and Wen, 2010). Growing such dense biofilms in tubes with an inner diameter of 2 mm, as it was shown for *Synechocystis* sp. PCC 6803 (David *et al.*, 2015), in theory enable biomass concentrations of up to 100 g<sub>CDW</sub> L<sub>tube<sup>-1</sup></sub>. With such a high biomass concentration and a specific activity of 100 U g<sub>CDW</sub><sup>-1</sup>, the application of phototrophic biocatalysts overcoming O<sub>2</sub> limitation would theoretically allow an increase of productivities from 5.6 up to 30 g<sub>product</sub> L<sup>-1</sup> h<sup>-1</sup> (100 g mol<sup>-1</sup> molar mass of the product) for efficient light-dependent biocatalytic oxyfunctionalization at scale.

#### 7.7 Conclusion

The *in situ* generation of  $O_2$  in the liquid phase has a large potential to overcome limitations of the productivity by the  $O_2$  availability in  $O_2$ -dependent whole-cell bioprocesses. Photosynthetically active biocatalysts that evolve  $O_2$  *in situ* via the photosynthetic water splitting reaction, which simultaneously supplies oxygenases with activated electrons, can efficiently overcome limitations by  $O_2$  mass transfer. Now, photo-bioreactor systems have to be developed that combine the technologies available for photo-biocatalyst cultivation and biotransformations. Photosynthesis has a great potential to considerably raise the productivity process boundary of biocatalytic oxyfunctionalizations in a highly eco-efficient way.

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### Chapter 8 Conclusions & Outlook

#### 8.1 Conclusions & Outlook

Biocatalysis targets the synthesis of fuels and chemical compounds using a biological system that is applied in a technological reaction setup (**Figure 8.1**). Oxygenic photosynthesis is a highly valuable driver for industrially relevant redox biotransformations such as the oxyfunctionalization of hydrocarbons (**Chapter 1**).



Figure 8.1: Conceptual design of photosynthesis-driven biotransformations. Redox enzymes (oxygenases) catalyze the conversion of substrates to the targeted oxyfunctionalized chemical products and are fueled with electrons and  $O_2$  derived from oxygenic photosynthesis. The applied technological system encloses the catalytic host and facilitates the supply with sufficient light, nutrients, and substrates as well as product extraction.

Via photosynthetic water oxidation, reduction equivalents as well as  $O_2$ , both co-substrates of oxygenases, are accessed by the energy of light. Isolated enzymes and chemoheterotrophic biocatalysts are frequently applied, while the photobiotechnological application of photoautotrophic organisms in redox biocatalysis is rare. This thesis aimed at the development and investigation of photosynthesis-driven oxyfunctionalization bioprocesses that go beyond the proof-of-concept catalyst development stage. An integrated bioprocess design concept (**Chapter 1**), comprising biocatalyst, reaction, and process engineering tools, was followed to conceptually evaluate the photosynthetic  $O_2$  and electron supply as well as the technical application of cyanobacteria as phototrophic biocatalysts. The following sections conclude the main outcomes of this work and provide prospects for the design of eco-efficient oxyfunctionalization bioprocesses.

**Synechocystis** sp. PCC 6803 is a suitable biocatalytic host for oxyfunctionalizations. Integrated bioprocess development relied on the construction of two recombinant cyanobacterial strains. The alkane monooxygenase enzyme system AlkBGT, originating from *Pseudomonas putida* GPo1, and a CYP enzyme system, originating from *Acidovorax* sp. CHX100, were genetically introduced into *Synechocystis* sp. PCC 6803 resulting in Syn6803\_BGT (**Chapter 3**) and Syn6803\_CYP (**Chapter 5**). Both strains functionally catalyzed the hydroxylation of nonanoic acid methyl ester (NAME) to 9-hydroxynonanoic acid methyl ester (H-NAME) and cyclohexane to cyclohexanol, respectively. Biochemical analysis revealed that, in comparison to the total endogenous protein amount, Syn6803\_BGT and

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Syn6803 CYP synthesized the heterologous proteins at rather low concentrations (Chapter 4, Chapter 5). Although Synechocystis sp. PCC 6803 constitutes the model organisms for photoautotrophic biocatalysts, controlled overexpression of genes and thus the synthesis of the target proteins at high specific concentrations is hindered by the limited availability of promoter and plasmid systems. Therefore, future developments have to address the elaboration on these genetic engineering tools for improving the expression system function. Next to low heterologous protein levels, Syn6803 BGT showed high catalytic activity towards the hydrolysis of the substrate NAME, resulting in the formation of the toxic reactant nonanoic acic (NA) (Chapter 4). Thus, the biocatalytic chassis may be engineered for the elimination of this side reaction. In a comparable study on several E. coli strains, the carboxylesterase BioH was identified as medium-chain length fatty acid methyl ester hydrolyzing enzyme and thus might be a potential target for a knock-out strategy in Syn6803 BGT (Kadisch et al., 2017a). The biocatalytic host system may also be changed to another cyanobacterial chassis potentially facilitating a reduced or even lacking side-reaction activity. Furthermore, phototrophic strains possessing accelerated growth rates for faster biocatalyst growth or enhanced solvent tolerance for improved reaction robustness would be relevant. A promising candidate for further evaluation is Synechococcus elongatus UTEX 2973 which was (re-) identified in 2015 and capable of growing at high rates with a doubling time of 2.1 h (in comparison 6.6 h for Synechocystis sp. PCC 6803) (Yu et al., 2015a). Eventually, the complementation of above described strain engineering strategies with the application of further oxygenases, e.g., the Baeyer-Villiger cyclohexanone monooxygenase, but also of other redox enzymes, such as hydrogenases, will broaden the reaction and thus the product scope of photosynthesis-driven biotransformations.

**Photosynthetic water oxidation is a valuable source of O**<sub>2</sub>. Biocatalyst characterization followed the biocatalyst development with a focus on evaluating the possibilities of linking photosynthetic O<sub>2</sub> and electron sources to productive biocatalysis. Under exclusion of external O<sub>2</sub>, Syn6803\_BGT captured nearly 25% of photosynthetically generated O<sub>2</sub> for the hydroxylation of NAME (**Chapter 3**). In addition, *in situ* O<sub>2</sub> supply allowed the operation of bioreactors without aeration during Syn6803\_CYP biotransformation, preventing substrate (cyclohexane) evaporation and thus enhancing process stability (**Chapter 5**). The *in situ* generation of photosynthetically generated O<sub>2</sub> is a highly promising concept for redox biocatalysis, overcoming the need for external gas-liquid mass transfer (**Chapter 7**). O<sub>2</sub>-respiring catalyst restrict the maximum achievable productivity to 5.6 g L<sup>-1</sup> h<sup>-1</sup>. In contrast, O<sub>2</sub>-evolving photobiocatalysts possess the ability to shift this O<sub>2</sub>-boundary far in excess of the reactor intrinsic oxygen transfer rate of 9 g L<sup>-1</sup> h<sup>-1</sup> (traditional large-scale stirred tank bioreactor). In conclusion, cyanobacteria inherently provide a promising technological solution for otherwise O<sub>2</sub> limited, large-scale redox bioprocesses.

*In situ* extraction of  $O_2$  potentially facilitates  $O_2$ -sensitive bioprocesses. The concept of *in situ* capturing photosynthetically generated  $O_2$  overcomes gas-liquid mass transfer limitations. In addition, it also features a promising solution for photosynthesis-driven, but  $O_2$ -sensitive bioprocesses. An example is the photosynthesis-driven production of hydrogen. Hydrogen with its high energy density is regarded as a favorable future zero-emission fuel gas. Production of hydrogen via coupling the photosynthetic water oxidation with hydrogenases constitutes a highly promising alternative technology to the power-demanding electrolysis of water. However, due to the inherent  $O_2$  generation during photosynthetic water oxidation, photobiotechnological production of hydrogen suffers from  $O_2$ -sensitive hydrogenases as well as the formation of explosive oxyhydrogen gas (Knallgas). Current approaches aim at the technical separation of the two gases or the identification and development of  $O_2$ -resistant hydrogenases with oxygenases as  $O_2$ -consuming enzyme (**Chapter 10.4**). Accumulating  $O_2$  is *in situ* captured at its place of generation, potentially preventing hydrogenase inactivation and furthermore reducing the risk of oxy hydrogen gas formation.

Photosynthetic water oxidation is a valuable source of activated reduction equivalents. So far, cofactor regeneration constitutes a key parameter in standard enzymatic as well as whole-cell redox biocatalysis. The photosynthetic light reaction provides a rich source of electrons originating from water, accessed by the energy of light. By increasing the light intensity, and thus the photosynthetic water oxidation rate, cyclohexane oxyfunctionalization activities of Syn6803 CYP were increased from 6 to 26 U g<sub>CDW</sub><sup>-1</sup> (Chapter 5). The rate of oxyfunctionalization equals the rate of heterotrophic biocatalysts harboring the very same enzyme system (Karande et al., 2016a) and thus demonstrates the successful change of the cofactor regeneration system from a carbohydrate-based to a photosynthesis driven metabolism. The characterization of the electron flux (electron balance) from water oxidation at the photosystems PSII to the heterologous redox enzyme will provide an understanding of, and potential engineering targets for the interplay of the introduced electron sink within the photosynthetic metabolism. On the one hand, the electron flux towards the oxygenase may be enhanced, e.g., by the knock-out of competing, electron demanding reactions as described in the general introduction (Chapter 1). On the other hand, the pathway of electron supply may be optimized, e.g., by engineering the cofactor specificity from NADH to NADPH-dependent oxygenases, the overexpression of endogenous reductases coupling with the introduced redox enzyme, or fusion of the heterologous enzyme in spatial proximity to the photosynthetic machinery (e.g., PSII). Importantly, determination of redox potentials of the heterologous redox enzyme and the endogenous electron transferring enzymes is a powerful strategy to disclose potential electron-accessing points allowing for maximum efficient electron abstraction.

Reaction engineering via two-liquid phase biotransformation stabilizes photosynthesis-driven C-H oxyfunctionalization. Biotransformation of pure substrates with Syn6803 BGT or Syn6803 CYP revealed a substantial reactant toxicity and mass transfer challenges. These issues tremendously affected the specific oxyfunctionalization rate (productivity) and biotransformation stability (yield and titer). In situ substrate supply via the application of a 2-liquid phase cultivation setup successfully enhanced the reaction performance with respect to productivities, yields on biomass, and titers for both reaction systems (Chapter 4, Chapter 5). In the case of Syn6803 BGT, the use of DINP as organic carrier phase additionally reduced the side-reaction of substrate hydrolysis, potentially enabling higher yields on the substrate. Eventually, for Syn6803 CYP, the reaction engineering approach resulted in 1.5 times enhanced initial specific activities of ca. 40 U  $g_{CDW}^{-1}$  and a pro-longed biotransformation stability of > 24 h resulting in 10 times increased final yields of 4.5 g<sub>product</sub> g<sub>CDW</sub><sup>-1</sup>. Further reaction engineering may even improve these productivities and yields e.g., by improvement of growth and reaction conditions including medium optimization, CO<sub>2</sub> and light supply. Furthermore, the consumption of materials as well as metabolic resources may be reduced by decoupling the biotransformation phase from growth. Bioprocesses based on heterotrophic whole-cells can benefit from the omission of growth-essential nutrients such as nitrogen or magnesium, thus preventing cell growth (Julsing et al., 2012a; McIver et al., 2008; Willrodt et al., 2016). The physiological state of these resting cells possesses decreased metabolic competition for reduced cofactors and thus enables higher reaction rates for product formation. The concept of production decoupled from growth might be beneficial for photosynthesis driven oxyfunctionalization as well, although the exclusion of nutrients such as nitrogen might be detrimental to the photosynthetic functionality of cyanobacteria as degradation of phycobilisomes (chlorosis) was observed (Richaud et al., 2001).

**Successful application of** *Synechocystis* **sp. PCC 6803 in a technical process setting.** The application of Syn6803\_BGT and Syn6803\_CYP in a technical process setting promoted the integrated development of a photobiocatalytic biotransformation process. Biocatalyst growth and gene expression were successfully transferred from a mL shake-flask to the multi-liter scale in a stirred-tank photobioreactor (Chapter 4, Chapter 5). Two-liquid phase biotransformations under process conditions without aeration enabled for the first time the photosynthesis-driven production of 2.6 g cyclohexanol from cyclohexane, water, and light. A further increase in total product amount will necessitate higher biomass concentrations, increased volumes and prolonged biotransformation times. Scaling of standard stirred tank bioreactors would result in decreased surface to volume ratios, resulting in impaired light distribution and thus photosynthetic activity. A highly promising technology for the cultivation of phototrophic organisms relies in the miniaturization of reaction systems. At the scale of a

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capillary reactor, the surface to volume ratio and thus the light distribution to the phototrophic organisms is maximized, allowing for high photosynthetic and thus biocatalytic activities. The operation of a mixed-species biofilm in a capillary reactor setting enabled the continuous cultivation of *Synechocystis* sp. PCC 6803 at exceptionally high biomass concentrations of 48  $g_{CDW}$  L<sup>-1</sup> (**Chapter 6**). The biofilm supporting, co-applied strain *Pseudomonas* sp. VLB120 enhanced the surface coverage and reduced oxidative stress by the respiration of O<sub>2</sub>. The capillary reactor setting now faces the integration of recombinant protein activity and, subsequently, reaction engineering strategies for appropriate substrate supply and product removal, including downstream processing. Finally, numbering up is a promising strategy for scaling the reaction system, retaining the advantage of the miniaturized setting, i.e., high surface to volume ratio.

#### 8.2 Concluding remarks

Combining the achievements of this thesis, comprising a specific initial activity of ca. 40 U  $g_{CDW}$ <sup>-1</sup>, a cyanobacterial biomass concentration of 41  $g_{CDW}$  L<sup>-1</sup>, and a biotransformation stability of 52 h in one bioprocess setting, would already facilitate industrially relevant productivities, titers and yields of ca. 10 g L<sup>-1</sup> h<sup>-1</sup>, 500 g L<sup>-1</sup> and 12.5 g  $g_{CDW}$ <sup>-1</sup>, respectively, for a 100 g mol<sup>-1</sup> molecular weight product. This requires the retention of the high specific activities throughout the entire biotransformation time. Using a standard stirred tank photobioreactor, high biocatalyst concentrations need to be realized. In turn, the application of a biofilm-capillary reactor system necessitates the implementation of high specific oxyfunctionalization activities. In conclusion, oxygenic photosynthesis constitutes a highly promising driver for redox biocatalysis. Continuing the integration of biocatalyst-, reaction-, and process engineering will facilitate the successful development of photosynthesis-driven redox biotransformations. Eventually, photosynthesis as the billion years old milestone of natural evolution may develop into a milestone for the eco-efficient production of fuels and value-added chemicals.
Chapter 9 References

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# Chapter 10 Appendix

## 10.1 Supporting information to Chapter 3



**Figure 10.1**: Product formation of recombinant *E. coli* W3110 (pAH042). The specific activity was  $10.0 \pm 0.1 \text{ U } \text{g}_{\text{CDW}^{-1}}$ , calculated for a reaction time of 30 min. Average values and standard deviations of two independent biological replicates are given.

### 10.2 Supporting information to Chapter 4



**Figure 10.2**: Normalized light spectrum of the stirred tank photo-bioreactor (Labfors 5 Lux, Infors AG, Bottmingen, Switzerland) used for the cultivation of *Synechocystis* sp. PCC 6803.



**Figure 10.3**: Influence of cell growth conditions on specific NAME oxyfunctionalization activity of Syn6803\_BGT. Cells were cultivated at indicated growth conditions, harvested at given time-points and standard oxygenation activity assays (2 g<sub>CDW</sub> L<sup>-1</sup>, YBG11, 30 µE m<sup>-2</sup> s<sup>-1</sup>) were performed.



**Figure 10.4**: Impact of light intensity on NAME biotransformation activity of Syn6803\_BGT. Cells were cultivated under standard conditions (YBG11, 50  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>, ambient CO<sub>2</sub>). Two days after inoculation, gene expression was induced for 24 h. Oxyfunctionalization assays were performed at given light intensities (2 g<sub>CDW</sub> L<sup>-1</sup>, YBG11 + NaHCO<sub>3</sub>).



**Figure 10.5**: Membrane fractionation analysis of Syn6803\_BGT. Cells were cultivated and induced in a stirred tank photo-bioreactor as described in the materials and methods section of **Chapter 4**, disrupted by French press and applied for sucrose density gradient centrifugation as described in **Chapter 2**. Subsequently, Western blot analysis was performed for Strep-tag identification. 10 µg of each protein fraction was loaded on SDS gel. Strep-tag protein ladder (IBA GmbH, Göttingen, Germany) or a pre-stained protein ladder (PageRuler Prestained Protein Ladder 26616, Thermo Fisher Scientific, Waltham, USA) were used. NrtA = Nitrate transport protein (localized in plasma membranes of *Synechocystis* sp. PCC 6803).



**Figure 10.6**: Cell growth of *Synechocystis* sp. PCC 6803 (pAH032) (empty expression plasmid) upon addition of DINP containing different NAME concentrations. Cells were cultivated under standard conditions for two days before aliquots of 7.5 mL were applied to fresh 100 mL shake flasks. Then, 2.5 mL of organic carrier solvent containing different NAME concentrations were added to the cultures (indicated by the arrow, organic:aqueous phase ratio of 1:3), and cultivation was continued under standard conditions with a reduced shaking frequency of 100 rpm (2.5 cm amplitude). Average values and standard deviations of two independent biological replicates are given.



**Figure 10.7**: Dependency of the oxyfunctionalization activity of Syn6803\_BGT on gene expression time. Cells were cultivated under standard conditions (YBG11, 50  $\mu$ E, ambient CO<sub>2</sub>), induced after 2, 3, 4, or 5 days (panels **A**, **B**, **C**, and **D**, respectively), and harvested at defined time points to determine oxyfunctionalization activities in short-term assays (2 g<sub>CDW</sub> L<sup>-1</sup>, YBG11 + NaHCO<sub>3</sub>, 30  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>). Non-induced cells (dashed bars) served as a control. Error bars represent the standard deviation of two independent biological replicates.



**Figure 10.8**: Impact of different NAME concentrations within the organic carrier solvent DINP on the NAME hydrolysis activity of Syn6803\_BGT. Cells were cultivated under standard conditions (YBG11, ambient CO<sub>2</sub>, 50  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>) and applied for long-term NAME biotransformations (YBG11 + NaHCO<sub>3</sub>, 2 g<sub>CDW</sub> L<sup>-1</sup>, 30  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>) using different concentrations of NAME dissolved in DINP added at an organic:aqueous phase ratio of 1:3. Initial specific activities were calculated for the first 30 min of reaction. Average values and standard deviations of two independent biological replicates are given. \* Only one biological replicate available; standard deviation of 10% was assumed. U = unit =  $\mu$ mol min<sup>-1</sup>, CDW = cell dry weight.



Figure 10.9: Analysis of expression system components used for the heterologous expression of alkBGT in E. coli W3110 and Synechocystis sp. PCC 6803 (Syn6803). Specific oxyfunctionalization activities of E. coli W3110 strains are based on 15 min resting-cell assays (performed as described in Chapter 3). Specific oxyfunctionalization activities of Syn6803 strains are based on 30 min standard reaction assays in YBG11 medium either without NaHCO3 or with 50 mM NaHCO3, as indicated. pRSF nAlk (=pAH010) constitutes a broad host range vector (RSF origin of replication) encoding the alkBFG and alkST operons in their native configuration under control of the Palk regulatory system of Pseudomonas putida GPo1. pRSF PAlk:BGT (= pAH039) constitutes a broad host range vector (RSF origin of replication) with the alkBGT genes in a single operon under control of the Palk regulatory system. pRSF Ptrc10:BGT (= pAH038) constitutes a broad host range vector (RSF origin of replication) containing the alkBGT genes in a single operon under control of the Ptrc10 promoter system. pRSF Ptrc10:BGTII (= pAH042) equals pAH038 with a Strep-tagII sequence added to the Cterminus of alkB, alkG, and alkT. pRSF Ptrc10:BGTII 2x (= pAH048) equals pAH042 with a second Ptrc1O:BGTII operon present in the same plasmid. "No growth" indicates that no colonies were formed upon transformation of Synechocystis sp. PCC 6803 with the respective plasmid. Growth rates are given for E. coli W3110 strains. The growth rates of recombinant Synechocystis sp. PCC 6803 did not vary between the strains. Average values and standard deviations of two independent biological replicates are given. U = unit = µmol min<sup>-1</sup>, CDW = cell dry weight.



**Figure 10.10**: SDS PAGE analysis of *E. coli* W3110 (**A** - **C**) and *Synechocystis* sp. PCC 6803 (= Syn6803) (**D**) harboring indicated plasmids. Cells were either disrupted by heat (*E. coli* W3110, 99 °C, 5 min) or using glass beads (Syn6803) as described in **Chapter 2**. Whole-cell protein fractions of 45  $\mu$ g<sub>CDW</sub> (**A** - **C**) or protein fractions of 10 or 20  $\mu$ g (**D**) were applied. **A**) pRSF\_nAlk =pAH010, pRSF\_Palk:empty = pAH008, pRSF\_Palk:BGT = pAH039, **B**) pRSF\_Ptrc10:Term = pAH032, pRSF\_Ptrc10:BGT = pAH042, **C**) pRSF\_Ptrc10:BGTII = pAH048, **D**) B = pAH044, BG = pAH047, BGT = pA042, BGT2x = pAH048. The expression systems located on respective plasmids are described in **Chapter 2**. M = unstained protein ladder (PageRuler Unstained Protein Ladder 26614, Thermo Fisher Scientific, Waltham, USA), STM = Strep-tag protein ladder (IBA GmbH, Göttingen, Germany).



**Figure 10.11**: Western blot analysis and NAME oxyfunctionalization activities of recombinant *Synechocystis* sp. PCC 6803 harboring one (pAH042) or two (pAH048) *Ptrc10:BGT* operons on the expression plasmid. Cells were cultivated under standard conditions (YBG11, ambient CO<sub>2</sub>,  $50 \ \mu \text{Em}^2 \text{ s}^{-1}$ ). Gene expression was induced two days after inoculation. Cells were harvested 24 h after induction of gene expression and subjected to cell disruption, Strep-tag purification, and Western blot analysis as described in **Chapter 2** (panel **A**) or to oxyfunctionalization assays (as described in the materials and methods section of **Chapter 4**), of which the results are shown in panel **B** for the strain containing two operon copies (pAH048). \* 10  $\mu$ g of total protein from supernatant after cell disruption, \*\* 20  $\mu$ L of elution fraction after Strep-tag purification (Elution was performed in the same volume as loaden on Strep-tag purification column), \*\*\* 20  $\mu$ L of 5x concentrated (via acetone precipitation) elution fraction.



Figure 10.12: pH values measured in a stirred tank photo-bioreactor with standard YBG11 medium under abiotic conditions (30 °C, 300 rpm) with and without aeration, respectively.



## 10.3 Supporting information to Chapter 5

**Figure 10.13**: SDS-PAGE analysis of *Synechocystis* sp. PCC 6803 harboring the empty plasmid pAH032 or the expression vector pAH050 (Syn6803\_CYP). Samples were taken from cultures cultivated in YBG11 medium for 3 days, while gene expression was induced after 2 days using 2 mM IPTG when indicated (= ind.). Cell disruption was performed using glass beads as described in **Chapter 2**. The band corresponding to the CYP enzyme (47.3 kDa) is indicated by an arrow. Protein bands for ferredoxin (12.4 kDa) and ferredoxin reductase (42.7 kDa) could not be identified. Ind. = induced. Marker: PageRuler Prestained Protein Ladder 26616 (Thermo Fisher Scientific, Waltham, USA).



Figure 10.14: Partition coefficients for cyclohexane, cyclohexanol, and cyclohexanone during twoliquid phase biotransformation of cyclohexane using Syn6803\_CYP in aerated (A) and non-aerated (B) stirred tank photo-bioreactors.

**Table 10.1**: Partition coefficients obtained during biotransformation in stirred tank photo-bioreactors in comparison to those obtained from abiotic measurement (Eppendorf-tube).

	Porg:aq (Chx)	Porg:aq (C-ol)	Porg:aq (C-one)
Abiotic (Eppendorf-tube)	1775 ± 214	2.1 ± 0.1	4.4 ± 0.7
STR with aeration	1502 ± 321	$2.0 \pm 0.2$	4.0 ± 1.4
STR without aeration	$2255 \pm 496$	$2.6 \pm 0.3$	$4.6 \pm 0.7$



**Figure 10.15**: pH and pO<sub>2</sub> courses during cyclohexane biotransformation using Syn6803\_CYP in aerated (**A**) and non-aerated (**B**) two-liquid phase stirred-tank photo-bioreactor setups. Biotransformation conditions were: 30 °C, 300 rpm, 150  $\mu$ E m<sup>-2</sup> s<sup>-1</sup>, and, only for **A**, 0.15 L min<sup>-1</sup> aeration with compressed air.

## 10.4 Patent application WO2018/162465 A



## WO 2018/162465 A1

#### Veröffentlicht:

- mit internationalem Recherchenbericht (Artikel 21 Absatz \_ 3)
- 3) vor Ablauf der für Änderungen der Ansprüche geltenden Frist; Veröffentlichung wird wiederholt, falls Änderungen eingehen (Regel 48 Absatz 2 Buchstabe h) mit dem Sequenzprotokollieti der Beschreibung (Regel 5 Absatz 2 Buchstabe a)

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Verfahren zur bioreaktiven Extraktion erzeugten Sauerstoffs aus einem Reaktionsraum, sowie Verwendung von phototrophen Mikroorganismen bei der Gewinnung von Wasserstoff

Die Erfindung betrifft ein Verfahren zur bioreaktiven Extraktion erzeugten Sauerstoffs aus einem Reaktionsraum.

Stand der Technik

Wasserstoff gilt als Energieträger der Zukunft, da er einerseits eine hohe Energiedichte aufweist und andererseits eine umweltverträgliche Energiequelle darstellt. Er steht in unbegrenzten Mengen zu Verfügung und lässt sich durch verschiedene Verfahren aus Wasser gewinnen. Wasserstoff kann in einer Brennstoffzelle wieder in Strom und Wärme zurück gewandelt werden, als Endprodukt entsteht wiederum lediglich Wasser. Mittels Wasserstoff lassen sich zumindest theoretisch riesige Energiemengen auch langfristig zwischenspeichern.

Zur Herstellung von Wasserstoff sind insbesondere die Elektrolyse und die photokatalytische Wasserspaltung zu nennen.

Die Elektrolyse ist eine altbekannte und bewährte Methode zur Erzeugung von Wasserstoff. Mit Hilfe elektrischen Stroms wird Wasser in Wasserstoff und Sauerstoff zerlegt. Diese Methode ist zurzeit nur dann wirtschaftlich, wenn genügend günstiger Strom zur Verfügung steht.

Die photokatalytische Wasserspaltung - die Spaltung von Wasser in Wasserstoff und Sauerstoff mittels Sonnenlicht - stellt eine technologisch wichtige Alternative zur energieaufwendigen elektrolytischen Wasserspaltung dar. In diesem Fall werden in der Regel Algen oder Cyanobakterien eingesetzt, welche unter bestimmten Bedingungen während des Stoffwechselprozesses Wasserstoff an die Umgebung abgegeben können. So kann man in Algenreaktoren mittels Photosynthese Sonnenlicht und Wasser direkt in Wasserstoff umwandeln. Der enzymatische Prozess besteht aus zwei Schritten. Durch die photosynthetische Lichtreaktion erfolgt im ersten Schritt eine Aufteilung des Wassers in Protonen, Elektronen und molekularen Sauerstoff. Durch zum Beispiel Hydrogenasen werden die Protonen im zweiten Schritt zu molekularem Wasserstoff reduziert. Bei dieser oxygenen, das heißt Sauerstoff-freisetzenden Photosynthese, arbeiten zwei große, Cofaktorhaltige Proteinkomplexe, das Photosystem I (PSI) und das Photosystem II (PSII) zusammen. Das PSII spaltet mit Hilfe von Lichtenergie Wasser in Protonen, Sauerstoff und Elektronen und transferiert letztere über eine Elektronentransportkette auf das PSI.

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Die Kopplung der Hydrogenase mit dem Photosystem I, sowie dem Wasser-spaltenden Photosystem II der Mikroorganismen ermöglicht demzufolge die Herstellung von Wasserstoff aus Licht und Wasser, bei der lediglich Sauerstoff als "Abfallprodukt" anfällt. Bei dem Aufeinandertreffen von Sauerstoff und Wasserstoff besteht durch die Bildung von Knallgas eine Explosionsgefahr. Zudem sind bekannte Hydrogenasen sauerstoffempfindlich. Es ist deshalb zunächst erforderlich, die Gase nach der Bildung schnell zu trennen, um die Explosionsgefahr (Entstehung von Knallgas) und die Degeneration der Hydrogenasen zu verringern. Das erfolgt zum Beispiel unter Verwendung Sauerstoff-resistenter Hydrogenasen (US 20090263846 A1), poröser Membranen (DE 102007002009 A1) oder zeitlicher Trennung von Sauerstoffbildung und Wasserstoffproduktion (US 4532210 A).

Diese Techniken besitzen wesentliche Nachteile, so unterdrücken die Sauerstoff-resistenten Hydrogenasen nicht die Bildung von Knallgas, die Membrantechnologie verhindert nicht die Inaktivierung eines Sauerstoff-sensitiven Enzymsystems und durch zeitliche Trennung von Sauerstoffbildung und Wasserstoffproduktion wird das Verfahren in eine produktive und nichtproduktive Phase geteilt. Demnach ist die photokatalytische Wasserstoffproduktion in großtechnischem Ausmaß an spezifische Bedingungen gebunden, die produktionstechnisch nicht oder nur unter hohem Kostenaufwand realisierbar sind.

Die Aufgabe der Erfindung besteht deshalb darin, ein Verfahren zur Wasserstoffproduktion bereitzustellen, das unerwünscht entstehenden molekularen Sauerstoff von der chemischen Produktion eines Zielprodukts trennt und die Nachteile des Standes der Technik, wie Explosionsgefahr durch Knallgasbildung, zwei Prozessphasen und Inaktivierung von Sauerstoff-sensitiven Enzymen, vermeidet. Insbesondere besteht die Aufgabe darin, umweltfreundliche, preiswerte und stabile Photokatalysatoren zu finden, die in der Lage sind, photosynthetisch entstehenden Sauerstoff während einer Wasserstoffproduktion zu binden.

Die Aufgabe wird durch ein Verfahren zur bioreaktiven Extraktion photokatalytisch erzeugten Sauerstoffs in einem Reaktionsraum erfüllt, das die folgenden Schritte umfasst:

 Bestrahlen zumindest eines phototrophen Mikroorganismus mit Licht unter anaeroben Bedingungen in einem Reaktionsraum, und

- in situ Binden von entstehendem Sauerstoff durch den Mikroorganismus.

Das erfindungsgemäße Verfahren überwindet technische Herausforderungen, die aufgrund von sauerstoffsensiblen Prozessen bzw. Edukten, Produkten und Enzymen entstehen. So können auch in sauerstoffproduzierenden enzymatischen Verfahren sauerstoffsensible Mikroorganismen und Enzyme eingesetzt werden, ohne dass die Leistungsfähigkeit beeinträchtigt wird. Prozesse, in denen sowohl Wasserstoff als auch Sauerstoff anfallen und

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die somit potenziell Knallgas produzieren, werden entschärft, da beide Reaktionspartner in situ getrennt werden.

Dies ist möglich, indem der Sauerstoff direkt am Ort seiner Entstehung eingefangen und enzymatisch gebunden wird. Damit ist der entstehende Sauerstoff direkt am Ort seiner Entstehung deaktiviert. Die Deaktivierung erfolgt beispielsweise durch die Oxidation eines ebenfalls im Reaktionsraum vorhandenen Substrats in Form einer chemischen Bindung des Sauerstoffs an das Substrat, aufgrund derer der Sauerstoff nicht wieder in den Reaktionsraum entlassen wird. Der Vorteil besteht daher insbesondere darin, dass der Sauerstoff nicht nur separiert oder maskiert ist, sondern chemisch deaktiviert ist. Somit weist der Reaktionsraum und insbesondere der Mikroorganismus bevorzugt ferner ein Sauerstoff verwertendes Substrat auf.

Darüber hinaus ermöglicht die Erfindung, die Sauerstoffdeaktivierung quantitativ zu regeln indem die sauerstoffverbrauchende Reaktion gesteuert wird. Somit kann ein zuvor definierter Betrag an Sauerstoff dem Reaktionsraum zur Verfügung gestellt werden, der im Bereich von 0 (entstehender Sauerstoff vollständig gebunden) bis 1 (kein Sauerstoff gebunden) liegt.

Durch geeignete Wahl des Substrats kann ferner ein oxidiertes Zielprodukt hergestellt werden, so dass die Bindung des im eigentlichen Zielprozess entstehenden störenden Sauerstoffs zu einem weiteren Wertschöpfungsschritt führt.

Vorliegend handelt es sich bei dem entstehenden Sauerstoff um molekular vorliegenden Sauerstoff.

Bevorzugt weist der Mikroorganismus ein sauerstoffumsetzendes Enzym auf oder produziert ein solches.

In weiter bevorzugter Ausführungsform ist das bevorzugte Zielprodukt Wasserstoff beziehungsweise Protonen, welche anschließend mit Elektronen zu Wasserstoffmolekülen reduziert werden. Alternativ ist das Zielprodukt Methanol, welches durch Reduktion von CO<sub>2</sub> mit den aus der Wasserspaltung stammenden Elektronen erzeugt wird. In beiden Fällen handelt es sich um einen Brennstoff, der beispielsweise als Ausgangsprodukt für eine Brennstoffzellenreaktion eingesetzt wird. Diese Reaktionen werden beispielsweise durch drei Dehydrogenasen, welche zu der Klasse der Oxidoreduktasen gehören, katalysiert.

$CO_2 + 2e^- \rightarrow Formiat$	(I)
Formiat+ $2e^- \rightarrow$ Formaldehyde	(11)
Formaledhyde + 2e <sup>-</sup> → Methanol	(III)

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Insbesondere weist der zumindest eine phototrophe Mikroorganismus daher ein Enzym ausgewählt aus der Gruppe Hydrogenase, Nitrogenase und/oder Oxidoreduktase auf.

Das Verfahren wird vorzugsweise in einem flüssigen, insbesondere wässrigen Medium durchgeführt. In bevorzugter Ausführungsform ist vorgesehen, in einem Prozess störenden Sauerstoff (O<sub>2</sub>) aus dem Reaktionsraum zu entfernen, der bei der photosynthetischen Lichtreaktion aus Wasser oder wässrigen Flüssigkeiten oder Lösungen unter Verwendung phototropher Mikroorganismen im Reaktionsraum entsteht. Dabei weist der phototrophe Mikroorganismus, mindestens ein sauerstoffumsetzendes Enzym auf oder produziert dieses. Gleichzeitig werden sauerstoffverwertende Substrate eingesetzt.

Vorteilhafterweise weist der Mikroorganismus neben der Hydrogenase, Nitrogenase und/oder Oxidoreduktase zumindest ein weiteres, sauerstoffumsetzendes Enzym auf. Insbesondere bei einer Kombination von Hydrogenase und einer Oxidoreduktase findet der Wasserstofferzeugende und der Sauerstoffumsetzende Prozessschritt im gleichen Mikroorganismus und damit ohne räumliche Trennung statt. Der Sauerstoff wird direkt nach dessen Produktion umgesetzt und erfindungsgemäß deaktiviert. In bevorzugter Ausführungsform ist vorgesehen, dass das weitere Enzym eine Oxidoreduktase, insbesondere Oxidase und Oxygenase, ist.

Alternativ liegt im Reaktionsraum ein weiterer Mikroorganismus vor, der das weitere Enzym aufweist. Mit anderen Worten, weist bevorzugt ein Mikroorganismus Hydrogenase, Nitrogenase und/oder Oxidoreduktase als Wasserstoff-produzierendes Enzym und zusätzlich Oxidoreduktase als Sauerstoff-umsetzendes Enzym auf, oder zwei verschiede im Reaktionsraum vorhandene Mikroorganismen weisen je eines dieser Enzyme auf. Vorliegend wird nur eine Kombination aus den genannten Enzymen explizit erwähnt, wobei auch sämtliche andere Kombinationen ausdrücklich vorgesehen sind. In der Ausführungsform verschiedener Mikroorganismen finden der sauerstofferzeugende und der sauerstoffumsetzende Prozess nicht im selben Mikroorganismus, aber dennoch im selben Reaktionsraum statt. Der Vorteil besteht insbesondere darin, dass der sauerstoff durch ein quantitatives Verhältnis der Mikroorganismen zueinander gesteuert werden kann.

Ferner ist bevorzugt, dass der Mikroorganismus selbst das Zielprodukt, also beispielsweise Wasserstoff oder Methanol, erzeugt. Mit anderen Worten, es wird in einer bevorzugten Ausführungsform des erfindungsgemäßen Verfahrens bei der Bestrahlung des zumindest einen phototrophen Mikroorganismus neben Sauerstoff auch Wasserstoff oder Methanol frei.

Somit sieht das erfindungsgemäße Verfahren in einer bevorzugten Ausführungsform vor, dass mindestens ein phototropher Mikroorganismus unter Lichteinwirkung mit Wasser oder
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einer wässrigen Flüssigkeit oder Lösung in Kontakt gebracht wird, wobei ein Mikroorganismus gewählt wird, der neben den Hydrogenasen weiterhin Oxidoreduktasen als Sauerstoff-umsetzende Enzyme aufweist oder produziert oder ein weiterer Mikroorganismus im gleichen Reaktionsraum gewählt wird, der Oxidoreduktasen als Sauerstoff-umsetzende Enzyme aufweist oder produziert.

Die Oxidoreduktase ist vorzugsweise ausgewählt aus der Gruppe der Oxidasen oder Oxygenasen, vorzugsweise Monooxygenasen, Dioxygenasen oder coenzym-unabhängige Oxygenasen. Eine Monooxygenase als Sauerstoff verbrauchendes Enzym sollte das Enzym der Wahl sein, wenn das stöchiometrische Gleichgewicht im Reaktionsraum von Interesse ist. Es ergibt sich folgendes Reaktionssystem:

Die photosynthetische Lichti	reaktion: 2 H <sub>2</sub> O		$\rightarrow$ 4 H <sup>+</sup> + O <sub>2</sub> +4e <sup>-</sup>	(IV)
Reaktion der Monooxygena	se: S + O <sub>2</sub> +2e <sup>-</sup> +	+ 2 H⁺	$\rightarrow$ S <sub>oxidiert</sub> + H <sub>2</sub> O	(V)
Reaktion der Hydrogenase	: 2 H <sup>+</sup> + 2 e <sup>-</sup>	$\rightarrow$ H <sub>2</sub>		(VI)

Besonders bevorzugt sind Oxidoreduktasen vom AlkB-Typ, die in der Literatur als Katalysatoren zur Herstellung überwiegend von weniger stark oxidierten Produkten bekannt sind. Diese eignen sich besonders um aus Alkanen und deren Carbonsäuren bzw. Carbonsäureestern, überwiegend Produkte höherer Oxidationsstufen herzustellen. -Derartige Oxidoreduktasen sind ferner zur selektiven Oxidation von Alkanen und deren Carbonsäuren bzw. -estern befähigt, wobei zu erwartende Nebenprodukte, insbesondere an anderen als endständigen Kohlenstoffatomen oxidierte Alkane, nur in unerwartet geringem Ausmaß oder überhaupt nicht in nachweisbaren Mengen herzustellen.

Vorliegend werden die Substrate vorzugsweise unter Verwendung einer Oxidoreduktase vom AlkB-Typ in Anwesenheit von Sauerstoff oxidiert. AlkB stellt eine zunächst aus dem AlkBGT-System aus *Pseudomonas putida Gpo1* bekannt gewordene Oxidoreduktase dar, die von zwei weiteren Polypeptiden, AlkG und AlkT, abhängig ist. AlkT wird als FAD abhängige Rubredoxin-Reduktase charakterisiert, die Elektronen aus NADH an AlkG weitergibt. Bei AlkG handelt es sich um ein Rubredoxin, ein eisenhaltiges Redoxprotein, das als direkter Elektronendonor für AlkB fungiert. In einer bevorzugten Ausführungsform wird unter demselben Begriff "Oxidoreduktase des alkB-Typs" ein Polypeptid mit einer Sequenzhomologie von zunehmend bevorzugt wenigstens 75, 80, 85, 90, 92, 94, 96, 98 oder 99 % zur Sequenz des AlkB von *Pseudomonas putida Gpo1* (Datenbankcode: CAB54050.1; dieser Datenbankcode stammt aus dem Stand der Technik, nämlich aus der NCBI Datenbank, genauer dem am 15. November 2011 online verfügbaren Release) mit der Fähigkeit, die erfindungsgemäßen Substrate, wie Alkane und deren Carbonsäuren zu

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oxidieren. In einer besonders bevorzugten Ausführungsform handelt es sich bei der Oxidoreduktase vom AlkB-Typ um eine mit den AlkG (CAB54052.1)- und AlkT (CAB54063.1)-Polypeptiden aus *Pseudomonas putida Gpo1* funktionell zusammenwirkende, Alkane oxidierende Oxidoreduktase. In einer bevorzugtesten Ausführungsform handelt es sich bei der Oxidoreduktase vom AlkB-Typ um AlkB aus dem AlkBGT-System aus *Pseudomonas putida Gpo1* oder eine Variante davon.

Mit besonderem Vorteil werden Substrate eingesetzt, die nach der Oxidation als Edukte weiterverwendet werden und sogenannte *value added products* für das erfindungsgemäße Verfahren bilden oder aber solche, die im Reaktionsraum unerwünscht sind und durch die Oxidation deaktiviert werden. Somit ist neben der Produktion des Zielprodukts, wie Wasserstoff oder Methanol, auch die Sauerstoffumsetzung ein Zielprozess des Verfahrens. Es handelt sich dann nicht mehr nur um die Bindung von unerwünschtem Sauerstoff, der die Produktion des ersten Zielprodukts stört, sondern um die Bindung von entstehendem Sauerstoff zu einem zweiten Zielprodukt. Ein Einsatzbeispiel, in dem ein unerwünschtes Edukt durch das erfindungsgemäße Verfahren durch Oxidation deaktiviert wird ist die Schmutzwasseraufbereitung. Hier liegen verschiedene Substrate als unerwünschte Stoffe im Schmutzwasser vor. Das Schmutzwasser wird durch Oxidation dieser Substrate aufgereinigt. Je nach eingesetztem Mikroorganismus wird dabei als erwünschtes Nebenprodukt beispielsweise Wasserstoff als Brennstoff produziert.

In bevorzugter Ausführungsform fungieren im erfindungsgemäßen Verfahren Kohlenstoffverbindungen als Substrate, die zugesetzt werden oder die sich in der wässrigen Ausgangslösung befinden. Dabei handelt es sich vorzugsweise um Carbonsäuren oder Carbonsäureester mittelkettiger Alkane mit einer C<sub>3</sub>-C<sub>20</sub>, insbesondere C<sub>5</sub>-C<sub>15</sub>, vorzugsweise C<sub>7</sub>-C<sub>10</sub> -Kette. Ein besonders bevorzugtes Beispiel ist Methylnonanoat (C<sub>8</sub>H<sub>17</sub>-COOH-CH<sub>3</sub>).

Das erfindungsgemäße Verfahren sieht bevorzugt vor, dass als phototropher Mikroorganismus Algen, Purpurbakterien oder Cyanobakterien eingesetzt werden, wobei Cyanobakterien bevorzugt sind. Diese betreiben Photosynthese und weisen sauerstoffumsetzende Enzyme auf, produzieren diese oder sind in geeignetem Maße zur genetischen Modifizierung geeignet, um derartige Enzyme aufzuweisen oder zu produzieren.

Mit besonderem Vorteil wird als Mikroorganismus ein, insbesondere genetisch modifizierter, Cyanobakterienstamm eingesetzt, der das Alkan-Monooxygenase-Enzymsystem AlkBGT aufweist.

In besonders bevorzugter Ausgestaltung des erfindungsgemäßen Verfahrens wird der genetisch modifizierte Cyanobakterienstamm Synechocystis sp. PCC6803 als

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Mikroorganismus eingesetzt. Dieser weist das Alkan-Monooxygenase-Enzymsystem AlkBGT auf.

Somit betrifft ein weiterer Aspekt der Erfindung eine Cyanobakterienzelle umfassend eine Hydrogenase und die von *alkBGT* kodierte Alkanmonooxygenase der SEQ ID NO: 1 (*aus Pseudomonas putida GPo1*) oder einer Variante davon, insbesondere einem Enzym, das zu mindestens 80% mit der SEQ ID NO: 1 identisch ist.

Die Lehre der vorliegenden Erfindung kann nicht nur unter Verwendung der exakten Aminosäure- oder Nukleinsäuresequenzen der hierin beschriebenen biologischen Makromoleküle ausgeführt werden, sondern auch unter Verwendung von Varianten derartiger Makromoleküle, die durch Deletion, Addition oder Substitution einer oder mehr als einer Aminosäure oder Nukleinsäure erhalten werden können.

In einer bevorzugten Ausführungsform bedeutet der Begriff "Variante" einer Nukleinsäureseguenz oder Aminosäureseguenz, im Folgenden gleichbedeutend und austauschbar mit dem Begriff "Homologen" gebraucht, wie hierin verwendet, eine andere Nukleinsäure- oder Aminosäureseguenz, die mit Hinblick auf die entsprechende ursprüngliche Wildtyp-Nukleinsäure- oder -aminosäureseguenz eine Homologie, hier gleichbedeutend mit Identität verwendet, von 70, 75, 80, 85, 90, 92, 94, 96, 98, 99 % oder mehr Prozent aufweist, wobei bevorzugt andere als die das katalytisch aktive Zentrum ausbildende Aminosäuren oder für die Struktur oder Faltung essentielle Aminosäuren deletiert oder substituiert sind oder letztere ledialich konservativ substituiert sind. beispielsweise ein Glutamat statt einem Aspartat oder ein Leucin statt einem Valin. Es besteht keine Notwendigkeit, dass die Sequenz über ihre gesamte Länge eine entsprechend hohe Homologie aufweist, erfindungsgemäß können auch Fusionsproteine oder für solche kodierende Nukleinsäuren verwendet werden, die einen Teil mit entsprechender Homologie und/oder Aktivität aufweist. Der Stand der Technik beschreibt Algorithmen, die verwendet werden können, um das Ausmaß von Homologie von zwei Seguenzen zu berechnen, z. B. Arthur Lesk (2008), Introduction to bioinformatics, 3rd edition.

In einer weiteren bevorzugteren Ausführungsform der vorliegenden Erfindung weist die Variante einer Aminosäure- oder Nukleinsäuresequenz, bevorzugt zusätzlich zur oben genannten Sequenzhomologie, im Wesentlichen die gleiche enzymatisch Aktivität des Wildtypmoleküls bzw. des ursprünglichen Moleküls auf. Zum Beispiel weist eine Variante eines als Protease enzymatisch aktiven Polypeptids die gleiche oder im Wesentlichen die gleiche proteolytische Aktivität wie das Polypeptidenzym auf, d.h. die Fähigkeit, die Hydrolyse einer Peptidbindung zu katalysieren. In einer besonderen Ausführungsform bedeutet der Begriff "im Wesentlichen die gleiche enzymatische Aktivität" eine Aktivität mit

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Hinblick auf die Substrate des Wildtyp-Polypeptids, die deutlich über der Hintergrundaktivität liegt oder/und sich um weniger als 3, bevorzugter 2, noch bevorzugter eine Größenordnung von den KM- und/oder kcat-Werten unterscheidet, die das Wildtyppolypeptid mit Hinblick auf die gleichen Substrate aufweist. In einer weiteren bevorzugten Ausführungsform umfasst der Begriff "Variante" einer Nukleinsäure- oder Aminosäuresequenz wenigstens einen aktiven Teil/oder Fragment der Nukleinsäure- bzw. Aminosäuresequenz.

Insbesondere in vorgenannter Ausführungsform wird als Substrat Methylnonanoat verwendet.

Ein weiterer Aspekt der Erfindung betrifft die Verwendung von phototrophen Mikroorganismen, die neben Hydrogenasen Oxidoreduktasen als Sauerstoff-umsetzende Enzyme aufweisen oder produzieren, bei der Gewinnung von Wasserstoff (H<sub>2</sub>) und Sauerstoff (O<sub>2</sub>) aus Wasser oder wässrigen Flüssigkeiten und Lösungen und zur simultanen in-situ Entfernung des Sauerstoffs (O<sub>2</sub>) unter Verwendung entsprechender Substrate, die mit dem Sauerstoff Produkte bilden. Bevorzugt betrifft die Erfindung die Verwendung von phototrophen Mikroorganismen, die neben Hydrogenasen Oxidoreduktasen als Sauerstoffumsetzende Enzyme aufweisen oder produzieren in dem erfindungsgemäßen Verfahren.

Insbesondere bevorzugt ist die Verwendung des erfindungsgemäßen Verfahrens bei der Schmutzwasseraufbereitung. Hierbei wird ein Gemisch undefinierter organischer Substanzen, die im Sinne der Erfindung als Substrate wirken, für die sauerstoffverwertende Reaktion des Mikroorganismus zur Verfügung gestellt. Die Wahl einer nicht spezifischen, nichtselektiven Oxygenierungsreaktion ermöglicht die Oxidation und damit die Inaktivierung der im Abwasser auftretenden Schadstoffe. Dabei findet vorteilhafterweise gleichzeitig eine Erzeugung von Wasserstoffgas als Quelle für Energieerzeugung und eine Oxidation von gelöstem organischen Kohlenstoff im Abwasser statt.

Als Mikroorganismus wird vorzugsweise ein Algenstamm, ein Purpurbakterienstamm oder ein Cyanobakterienstamm verwendet. Besonders bevorzugt wird ein Stamm, der das Alkan-Monooxygenase-Enzymsystem AlkBGT aufweist, wie beispielsweise Synechocystis sp. PCC6803, eingesetzt.

Das erfindungsgemäße Verfahren wird bevorzugt im Photobioreaktor durchgeführt. Somit betrifft ein weiterer Aspekt der Erfindung einen Photobioreaktor zur Ausführung des erfindungsgemäßen Verfahrens, insbesondere umfassend den genetisch modifizierten Cyanobakterienstamm *Synechocystis sp.* PCC6803, der das Alkan-Monooxygenase-Enzymsystem AlkBGT aufweist oder produziert. Hierbei liegt der Mikroorganismus, insbesondere der Bakterienstamm als Biofilm vor.

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Photobioreaktoren sind Fermenter, in denen die phototrophen Mikroorganismen zum Beispiel Algen, Cyanobakterien und Purpurbakterien kultiviert werden, in denen also entweder das Wachstum und die Vermehrung dieser Zellen ermöglicht wird oder die Produktion unterschiedlicher Substanzen mittels phototropher Zellen gefördert wird. Im Unterschied zu konventionellen biotechnischen Fermentationsprozessen sind phototrophe Vorgänge lichtabhängig. Um den Zellen einen aktiven Stoffwechsel zu ermöglichen, werden sie möglichst optimal sowohl mit Licht als auch mit verschiedenen Nährlösungen bzw. gelösten Substraten versorgt.

Die Photobioreaktoren variieren erheblich in Material und Konstruktionsweise. Ihnen allen gemein ist, dass sie auf Basis ihrer Konstruktion eine optimale Lichtversorgung der Mikroorganismen gewährleisten sollen. Auf dem Markt befinden sich zum Beispiel Reaktoren, die mit Kunststoff-Beuteln oder Schläuchen arbeiten oder Systeme die mit flachen Behältern oder Röhren die Biomasse in dünnen Schichten der Sonne exponieren.

Jeder Reaktor hat neben dem lichtdurchlässigen Photosyntheseteil auch einen Zulauf für CO<sub>2</sub> und Substrate und eine Einrichtung die Mikroorganismen zu ernten. Meist wird der Zustand und die Dichte der Kultur noch über eine sensible Mess-Elektronik detektiert, um regelnd eingreifen zu können.

Der Röhrenreaktor ist ein ausgereifter und bereits in Großanlagen verbauter Photobioreaktor. Die Mikroorganismensuspension wird in durchsichtigen Röhren aus Glas oder Plastik geführt und mittels einer Pumpe in Bewegung gehalten.

Der Helix- oder Coil-Reaktor ist im Grunde ein Röhrenreaktor, der allerdings keine Glasröhren einsetzt, sondern einen flexiblen Schlauch. Dieser wird dann kreisförmig angeordnet, die Prozessführung ähnelt dem Röhrenreaktor.

Der Beutel- oder Schlauch-Reaktor ist ein Photobioreaktor auf Basis von einzelnen Kompartimenten aus Kunststofffolie, oft hängend angeordnet. Es gibt hier auch Ansätze funktionale Kunststoffe einzusetzen und Ideen, die Beutel auf dem Wasser zu positionieren. Die Durchmischung erfolgt meist durch den CO<sub>2</sub>- Eintrag und ist damit relativ energieeffizient. Die Folie ist dabei nicht auf einen langfristigen Einsatz ausgerichtet, sondern wird von Zeit zu Zeit erneuert.

Beim Kessel-Reaktor wird ein üblicherweise säulenförmiger Flüssigkeitsbehälter eingesetzt, in dem die Algenbiomasse gezüchtet wird. Je nach Design des Behälters, wird über verschiedene Systeme Licht in den Behälter eingebracht. Dies kann Sonnenlicht sein, oder artifizielle Lichtquellen. Manche Ansätze nutzen dazu Linsensysteme und Lichtleiter. Eine

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Durchmischung kann über verschiedene Mechanismen erfolgen, wie zum Beispiel Gaseintrag oder Umwälzung durch Pumpen.

Im Flachplatten-Reaktor werden die Mikroorganismen dabei im Kulturmedium in flachen Schichten dem Licht ausgesetzt. Begrenzt wird der Reaktor durch Glas- oder Plastik-Platten, die Durchmischung erfolgt durch den Gaseintrag.

Im Dünnschicht-Reaktor, wird das Prinzip der Minimierung der Mikroorganismenschicht zur optimalen Lichtausbeute konsequent weiter verfolgt. Damit soll die Selbst-Überschattung dichterer Suspensionen gemindert werden. Immobilisierte Mikroorganismen werden dabei auf einem Trägermaterial dem Licht exponiert.

Erfindungsgemäß werden bevorzugt Röhrenreaktoren eingesetzt.

Zusammenfassend ermöglicht die Erfindung eine Kombinierung zweier bislang unabhängiger Techniken, die photokatalytische Wasserstoffgasproduktion und die photokatalytische Sauerstoffreaktion. Simultan zur Herstellung von Wasserstoff als Biotreibstoff wird dabei ein Substrat oxidiert und dabei deaktiviert oder ein Mehrwertprodukt hergestellt.

Die vorliegende Erfindung wird weiterhin durch die folgenden Figuren und nicht beschränkenden Beispiele veranschaulicht, denen weitere Merkmale, Ausführungsformen, Aspekte und Vorteile der vorliegenden Erfindung entnommen werden können.

 Figur 1: graphische Darstellung einer Extraktion von photosynthetisch erzeugtem Sauerstoff durch das Alkan-Monooxygenase Enzymsystem AlkBGT, welches genetisch in den Cyanobakterien-Stamm Synechocystis sp. PCC6803 eingeführt wurde, in erfindungsgemäßer Durchführung.

Zur Durchführung des erfindungsgemäßen Verfahrens kommen verschiedene Bedingungen in Frage. Essentiell ist dabei lediglich die Anwesenheit von molekularem Sauerstoff als Oxidationsmittel.

#### Beispiel 1:

Herstellung eines genetisch modifizierten Stamms - Synechocystis sp. PCC6803, enthaltend das Alkan-Monooxygenase Enzymsystem AlkBGT

Die Einführung der Gene kodierend für das Alkan-Monooxygenase Enzymsystem AlkBGT erfolgte über einen Plasmid-basierten Ansatz (pRSF\_Ptrc10:BGTII). Die folgenden Protokolle und Klonierungsschritte beschreiben die Konstruktion des Plasmides. In Tabelle 1

	aufgeführt, welche während des Klonierur	ngs-Verfahrens
verwendet und erzeugt wurden.		.90
Tabelle 1: Stämme/ Plasmid-Kons verwendet und erzeugt wurden.	struktionen die während des Klonierungs-Ver	fahrens
Stamm/ Plasmid	Beschreibung	Referenz
E. coli DH5α	F <sup>-</sup> Φ80 <i>lacZ</i> ΔM15 Δ( <i>lacZ</i> YA-argF) U169 recA1 endA1 hsdR17 (rK <sup>-</sup> , mK <sup>+</sup> ) phoA supE44 λB <sup>-</sup> thi <sup>1</sup> gyrA96 relA1	(Hanahan 198
	Geographische Ursprung: Kalifornien, USA	
Synechocystis sp. PCC6803	Erhalten von der Pasteur Culture Collection of Cyanobacteria (PCC, Paris, Frankreich)	(Stanier et 1971)
pBT10	Alkane-Monooxygenase Expressionssystem (alkBFG, alkST) in pCOM10	(Schrewe et 2011)
pSB1AC3_Ptrc1O:GFPmut3B	P <sub>trc10</sub> Promoter, GFPmut3B Gen (BBa_E0040) in pSB1AC3	(Huang et 2010)
pSB1AC3_Ptrc1O:Term	pSB1AC3 mit dem P <sub>trc10</sub> Promoter aus pSB1AC3_Ptrc10:GFPmut3B via Xbal, Pstl (Gibson Klonierung)	diese Arbeit
pSB1AC3_PmpB:lacl	PrnpB (konstitutiver Promoter des rnaseP Gens) kontrollierend eine Variante des lac Repressors lacl in pSB1AC3	(Huang et : 2010)
pSB1AC3_PrnpB:lacl_Ptrc1O:Te rm	pSB1AC3_Ptrc1O:Term mit PrnpB:lacl aus pSB1AC3_PrnpB:lacl via Xbal (Restriktion, Ligation)	diese Arbeit
pPMQAK1	Broad host range Plasmid, RSF ori, mob	(Huang et

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	Gene	2010)	
nPMOAK1 PropRilaci Ptro10.T	pPMQAK1 mit PrnpB:lacl_Ptrc1O:Term		
	aus pSB1AC3_PrnpB:lacl_Ptrc1O:Term	diese Arbeit	
em	via EcoRI, Pstl (Restriktion, Ligation)		
	pPMQAK1_PrnpB:lacl_Ptrc1O:Term mit		
pPMOAK1 PropBilact Ptro10-B	alkBGT Genen aus pBT10 (Gene		
GTI	aufeinander folgend , optimierte RBS, C-	diese Arbeit	
0111	terminaler Strep-tag II) via Spel (Gibson		
	Klonierung)		
	pPMQAK1_PrnpB:lacl_Ptrc1O:BGTII mit		
nRSE Ptrc10.BGTI	zusätzlichem Terminator (biobrick	diasa Arbait	
pror_racro.bom	#BBa_B0015 via Xbal (Gibson	GIGSC AIDER	
	Klonierung)		

Als Teil des Klonierungsverfahrens wurden die folgenden Verfahrensschritte wie Restriktion, Amplifizierung u.s.w. wie im Folgenden angegeben durchgeführt.

Die Restriktions-Endonukleasen wurden von Thermo Scientific - Germany GmbH (Schwerte, Deutschland) bezogen und entsprechend der Empfehlung eingesetzt.

Eine Amplifizierung von DNA Fragmenten wurde durch polymere Kettenreaktion (PCR) bei Anwendung der Phusion High Fidelity (HF) DNA Polymerase von Thermo Scientific – Germany GmbH (Schwerte, Deutschland) über das empfohlene 3-Schritt Protokoll mit entsprechenden Primern (aufgeführt in Tabelle 2) durchgeführt. Entsprechende Anlagerungs- Temperaturen (T<sub>An</sub>) und Elongations-Zeiten (t<sub>Ei</sub>) sind im jeweiligen Verfahrensschritt unten beschrieben.

Eine gewünschte Overlap-Extension\_PCR (OE-PCR) wurde durch Einsatz von je 50 ng der DNA Fragmente in einem 100 µL Standard PCR-Ansatz durchgeführt. Entsprechende Primer wurden nach 5 PCR Zyklen zugegeben.

Plasmid-DNA wurde mittels FastAP Thermosensitive Alkaline Phosphatase von Thermo Scientific – Germany GmbH (Schwerte, Deutschland) entsprechend der Empfehlung dephosphoryliert.

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Anschließe Fragmente KG (MACH	nd erfolgte über das EREY-NA	e eine Aufreinigung von Plasmid-DNA und amplifizierter DNA- PCR Clean-up Gel Extraktions-Kit von MACHERY-NAGEL GmbH & Co AGEL GmbH & Co. KG, Düren, Deutschland).
Gibson Klo	nierung er	rfolgte über eine einschrittige, isothermale, in vitro rekombinante
Klonierungs	smethode	beschrieben durch Gibson et al. 2009 (Gibson et al. 2009).
Ligation erf	olgte über Deutschla	r die T4 DNA Ligase von Thermo Scientific – Germany GmbH and) entsprechend der Empfehlung.
Schließlich Sequenzier	erfolgte e rung über	ine Verifizierung von PCR-amplifizierten DNA Sequenzen durch die Firma Eurofins MWG (Ebersberg, Deutschland).
Auf die in ⊺ mit der in T	Tabelle 1 abelle 1 v	genannten bekannten Verfahren wird in der vorliegenden Arbeit Bezu rermerkten Referenz Bezug genommen.
Tabelle 2: F	Primer die SEQ	während des Klonierungs-Verfahrens eingesetzt wurden.
	No.	Coquinz
PAH055	No. 1	TCCGGCTCGTATAATGTGTGGAATTGTGAGCGGATAACA ATTTCACACATACTAGTACCAGGCATCAAATAAAACG
PAH055 PAH056	No. 1 2	TCCGGCTCGTATAATGTGTGGAATTGTGAGCGGATAACA ATTTCACACATACTAGTACCAGGCATCAAATAAAACG TATAAACGCAGAAAGGCCC
PAH055 PAH056 PAH057	No. 1 2 3	TCCGGCTCGTATAATGTGTGGAATTGTGAGCGGATAACA ATTTCACACATACTAGTACCAGGCATCAAATAAAACG TATAAACGCAGAAAGGCCC TGATTTCTGGAATTCGCGGCCGCTTTCTAGATTGACAATT AATCATCCGGCTCGTATAATGTG
PAH055 PAH056 PAH057 PAH058	No. 1 2 3 4	TCCGGCTCGTATAATGTGTGGAATTGTGAGCGGATAACA ATTTCACACATACTAGTACCAGGCATCAAATAAAACG TATAAACGCAGAAAGGCCC TGATTTCTGGAATTCGCGGCCGCTTTCTAGATTGACAATT AATCATCCGGCTCGTATAATGTG ACACCTTGCCCGTTTTTTTGCCGGACTGCAGTATAAACG
PAH055 PAH056 PAH057 PAH058 PAH058 PAH069	No. 1 2 3 4	TCCGGCTCGTATAATGTGTGGAATTGTGAGCGGATAACA ATTTCACACATACTAGTACCAGGCATCAAATAAAACG TATAAACGCAGAAAGGCCC TGATTTCTGGAATTCGCGGCCGCTTTCTAGATTGACAATT AATCATCCGGCTCGTATAATGTG ACACCTTGCCCGTTTTTTTGCCGGACTGCAGTATAAACG CAGAAAGGCCC CTTTTCCTCGTAGAGCAC
PAH055 PAH056 PAH057 PAH058 PAH069 PAH070	No. 1 2 3 4 5 6	TCCGGCTCGTATAATGTGTGGAATTGTGAGCGGATAACA ATTTCACACATACTAGTACCAGGCATCAAATAAAACG TATAAACGCAGAAAGGCCC TGATTTCTGGAATTCGCGGGCCGCTTTCTAGATTGACAATT AATCATCCGGCTCGTATAATGTG ACACCTTGCCCGTTTTTTTGCCGGACTGCAGTATAAACG CAGAAAGGCCC CTTTTCCTCGTAGAGCAC GAGCCACCCGCAGTTCGAAAAATAGTACTAGAGTAGTGG
PAH055 PAH056 PAH057 PAH058 PAH069 PAH070 PAH071	No. 1 2 3 4 5 6 7	TCCGGCTCGTATAATGTGTGGAATTGTGAGCGGATAACA         ATTTCACACATACTAGTACCAGGCATCAAATAAAACG         TATAAACGCAGAAAGGCCC         TGATTTCTGGAATTCGCGGGCCGCTTTCTAGATTGACAATT         AATCATCCGGCTCGTATAATGTG         ACACCTTGCCCGTTTTTTTGCCCGGACTGCAGTATAAACG         CAGAAAGGCCC         CTTTTCCTCGTAGAGCAC         GAGCCACCCGCAGTTCGAAAAATAGTACTAGAGTAGTGG         AGGCTACCGCAGTTCGAAAAATAGTACTAGAGTAGTGG         AGGTTACTAGATGGCAATCGTTGTTGTTG         ATCAGGTAATTTTATACTCCC
PAH055 PAH056 PAH057 PAH058 PAH069 PAH070 PAH071 PAH072	No. 1 2 3 4 5 6 7 8	TCCGGCTCGTATAATGTGTGGAATTGTGAGCGGATAACA ATTTCACACATACTAGTACCAGGCATCAAATAAAACG TATAAACGCAGAAAAGGCCC TGATTTCTGGAATTCGCGGGCCGCTTTCTAGATTGACAATT AATCATCCGGCTCGTATAATGTG ACACCTTGCCCGTTTTTTTGCCGGACTGCAGTATAAACG CAGAAAGGCCC CTTTTCCTCGTAGAGCAC GAGCCACCCGCCAGTTCGAAAAATAGTACTAGAGTAGTGG AGGTTACTAGATGGCAATCGTTGTTG ATCAGGTAATTTTATACTCCC CTATTTTTCGAACTGCGGGTGGCTCCAAGCGCTCTTTTC CTCGTAGAGCAC
PAH055 PAH056 PAH057 PAH058 PAH058 PAH069 PAH070 PAH071 PAH072 PAH073	No. 1 2 3 4 5 6 7 8 9	TCCGGCTCGTATAATGTGTGGGAATTGTGAGCGGATAACA ATTTCACACATACTAGTACCAGGCATCAAATAAAACG TATAAACGCAGAAAGGCCC TGATTTCTGGAATTCGCGGGCCGCTTTCTAGATTGACAATT AATCATCCGGCTCGTATAATGTG ACACCTTGCCCGTTTTTTTGCCGGACTGCAGTATAAACG CAGAAAGGCCC CTTTTCCTCGTAGAGCAC GAGCCACCCGCAGTTCGAAAAATAGTACTAGAGTAGTGG AGGTTACTAGATGGCAATCGTTGTTGTTG ATCAGGTAATTTTATACTCCC CTATTTTTCGAACTGCGGGTGGCTCCAAGCGCTCTTTTC CTCGTAGAGCAC

$ \begin{array}{c} \mbox{CGGG1GGC1CCAAGCGC1TGAACTCTAGG1AATTTATACTCCCC} \\ \end{tabular} \\ \mbox{GGGAGGTATTGGACCGCATTGAACTCTAGGATATAAAACG} \\ \end{tabular} \\ \mbox{CGAGCCGGATGATTAATTGTCAATCTAGAGCCAGGCAT} \\ \mbox{CAGAAAGGCCC} \\ \mbox{ACGAGCCGGATGATTAATTGTCAATCTAGAGCCAGGCAT} \\ \mbox{CAAATAAAACG} \\ \mbox{CAAATAAAACG} \\ \end{tabular} \\ \mbox{SPAH017} 12 & \mbox{CCATCAACAGGATTTTCG} \\ \mbox{SPAH023} 13 & \mbox{TGCCACCTGACGTCTAAGAA} \\ \mbox{Konierungs-Verfahren} \\ \mbox{Konstruktion von pSB1AC3 Ptrc10:Term} \\ \mbox{Restriktion: } pSB1AC3 Ptrc10:GFP (Xbal + Pstl) \rightarrow pSB1AC3 (Xbal, Pstl) \\ \mbox{Amplifizierung: } Ptrc10:Term part I von pSB1AC3_Ptrc10:GFP (PAH055 + PAH056 \rightarrow 186 BP, T_Ari: 60°C, t_{Elong}: 10 sec) \\ \mbox{Ptrc10:Term part I } von part I \\ (PAH057 + PAH058 \rightarrow 262 BP, T_Ari: 72°C, t_{Elong}: 10 sec) \\ \mbox{Ptrc10:Term part I } von part I \\ (PAH057 + PAH058 \rightarrow 262 BP, T_Ari: 72°C, t_{Elong}: 10 sec) \\ \mbox{Ptrc10:Term part I } von part I \\ (PAH057 + PAH058 \rightarrow 262 BP, T_Ari: 72°C, t_{Elong}: 10 sec) \\ \mbox{Ptrc10:Term part I } von part I \\ (PAH057 + PAH058 \rightarrow 262 BP, T_Ari: 72°C, t_{Elong}: 10 sec) \\ \mbox{Ptrc10:Term part I } von part I \\ (PAH057 + PAH058 \rightarrow 262 BP, T_Ari: 72°C, t_{Elong}: 10 sec) \\ \mbox{Ptrc10:Term part I } \gamma pSB1AC3_Ptrc10:Term \\ \mbox{Konstruktion von pSB1AC3_Ptrc10:Term (Xbal) } Parto10:Term (Xbal) \\ \mbox{Dephosphorylierung: pSB1AC3_Ptrc10:Term (Xbal) } Parto10:Term (Xbal) \\ \mbox{Dephosphorylierung: pSB1AC3_Ptrc10:Term (Xbal) + PrnpB:lacl (Xbal + Spel) \\ \mbox{Ligation: } pSB1AC3_Ptrc10:Term (Xbal) + PrnpB:lacl (Xbal + Spel) \\ \mbox{Ligation: } pSB1AC3_Ptrc10:Term (Xbal) + PrnpB:lacl (Xbal + Spel) \\ \mbox{Ligation: } pSB1AC3_Ptrc10:Term (Xbal) + PrnpB:lacl (Xbal + Spel) \\ \mbox{Ligation: } pPMQAK1 PrnpB:lacl Ptrc10:Term \\ \mbox{Restriktion von pPMQAK1 PrnpB:lacl Ptrc10:Term (EcoRl + Pstl) \\ \mbox{Ligation: } pSB1AC3_PrnpB:lacl Ptrc10:Term (EcoRl + Pstl) \\ \mbox{Ligation: } pPMQAK1 (EcoRl, Pstl) + PrnpB:lacl_Ptrc10:Term \\ \mbox{Ligation: } pPMQAK1 PtrnpB:lacl_Ptrc10:Term \\ Ligation:$			
PAH077GGGAGGTATTGGACCGCATTGAACTCTAGTATATAAACG CAGAAAGGCCCPAH07810CAGAAAGGCCCPAH07811CAAATAAAACGSPAH01712CCATCAAACAGGATTTTCGSPAH02313TGCCACCTGACGTCTAAGAAKionierungs-VerfahrenKonstruktion von pSB1AC3 Ptrc10:TermRestriktion:pSB1AC3_Ptrc10:GFP (Xbal + Pstl) $\rightarrow$ pSB1AC3 (Xbal, Pstl)Amplifizierung:Ptrc10:Term part I von pSB1AC3_Ptrc10:GFP (PAH055 + PAH056 $\rightarrow$ 186 BP, T <sub>An</sub> : 60°C, t <sub>Elong</sub> : 10 sec)Ptrc10:Term part II von part I (PAH057 + PAH058 $\rightarrow$ 262 BP, T <sub>An</sub> : 72°C, t <sub>Elong</sub> : 10 sec)Gibson Klonierung:pSB1AC3 (Xbal, Pstl) + Ptrc10:Term part II $\rightarrow$ pSB1AC3 Ptrc10:TermKonstruktion von pSB1AC3_Ptrc10:TermKonstruktion von pSB1AC3_Ptrc10:Term (Xbal)Dephosphorylierung:pSB1AC3_Ptrc10:Term (Xbal)Dephosphorylierung:pSB1AC3_Ptrc10:Term (Xbal) (FastAP, Thermo)Restriktion:pSB1AC3_Ptrc10:Term (Xbal) (FastAP, Thermo)Restriktion:pSB1AC3_Ptrc10:Term (Xbal) (FastAP, Thermo)Restriktion:pSB1AC3_PtrpB:lacl Ptrc10:TermVerifizierung by PCR:Klone mit dem PrnpB:lacl Ftrc10:TermVerifizierung by PCR:Klone mit dem PrnpB:lacl Ftrc10:TermVerifizierung by PCR:Klone mit dem PrnpB:lacl Ptrc10:TermRestriktion:pPMQAK1_PrnpB:lacl_Ptrc10:TermRestriktion:pPMQAK1_PrnpB:lacl_Ptrc10:TermRestriktion:pPMQAK1_PrnpB:lacl_Ptrc10:TermRestriktion:pSB1AC3_PrnpB:lacl_Ptrc10:TermRestriktion:pPMQAK1 (EcoRI + Pstl)Ligation:pPMQAK1_PrnpB:lacl_Ptrc10:Term			CGGGTGGCTCCAAGCGCTATCAGGTAATTTTATACTCCC
$\begin{array}{cccc} PAH077 & 10 & CAGAAAGGCCC \\ ACGAGCCGGATGATTAATTGTCAATCTAGAGCCAGGCAT \\ PAH078 & 11 & CAAATAAAACG \\ \\ SPAH017 & 12 & CCATCAAACAGGATTTTCG \\ \\ SPAH023 & 13 & TGCCACCTGACGTCTAAGAA \\ \\ \hline \\ Klonierungs-Verfahren \\ \hline \\ Konstruktion von pSB1AC3 _ Ptrc10:Term \\ \\ Restriktion: & pSB1AC3 _ Ptrc10:GFP (Xbal + Pstl) \rightarrow pSB1AC3 (Xbal, Pstl) \\ Amplifizierung: & Ptrc10:Term part I von pSB1AC3 _ Ptrc10:GFP \\ & (PAH055 + PAH056 \rightarrow 186 BP, TAR; 60°C, tElang; 10 sec) \\ & Ptrc10:Term part I von part I \\ & (PAH057 + PAH058 \rightarrow 262 BP, TAR; 72°C, tElang; 10 sec) \\ \\ Gibson Klonierung: & pSB1AC3 _ Ptrc10:Term \\ \hline \\ Konstruktion von pSB1AC3 _ PtrpB:lacl _ Ptrc10:Term part II \\ & \rightarrow pSB1AC3 _ Ptrc10:Term (Xbal) \\ \\ Dephosphorylierung: & pSB1AC3 _ Ptrc10:Term (Xbal) \\ \\ Dephosphorylierung: & pSB1AC3 _ Ptrc10:Term (Xbal) (FastAP, Thermo) \\ \\ Restriktion: & pSB1AC3 _ Ptrc10:Term (Xbal) + PrnpB:lacl (Xbal_Spel) (1:2) \\ & \rightarrow pSB1AC3 _ Ptrc10:Term (Xbal) + Ptrc10:Term \\ \hline \\ Verifizierung by PCR:Klone mit dem PrnpB:lacl _ Ptrc10:Term \\ \\ Werifizierung by PCR:Klone mit dem PrnpB:lacl Fragment in gewünschter Richtung wurdendurch PCR bestimmt (SPAH017 + SPAH023 \rightarrow 500 BP, TAR: 61°C, tElang; 15 sec). \\ \hline \\ \hline \\ Konstruktion von pPMQAK1 _ PrnpB:lacl _ Ptrc10:Term (EcoRI + Pstl) \\ \\ \\ Igation: & pSB1AC3 _ PrnpB:lacl _ Ptrc10:Term (EcoRI + Pstl) \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\$			GGGAGGTATTGGACCGCATTGAACTCTAGTATATAAACG
PAH078ACGAGCCGGATGATTAATTGTCAATCTAGAGCCAGGCAT CAAATAAAACGPAH07811CAAATAAAACGSPAH01712CCATCAAACAGGATTTTCGSPAH02313TGCCACCTGACGTCTAAGAAKonstruktion von pSB1AC3Ptrc10:TermRestriktion:pSB1AC3_Ptrc1O:GFP (Xbal + Pstl) $\rightarrow$ pSB1AC3 (Xbal, Pstl)Amplifizierung:Ptrc10:Term part I von pSB1AC3_Ptrc10:GFP (PAH055 + PAH056 $\rightarrow$ 186 BP, T <sub>An</sub> : 60°C, t <sub>Elong</sub> : 10 sec)Ptrc10:Term part II von part I (PAH057 + PAH058 $\rightarrow$ 262 BP, T <sub>An</sub> : 72°C, t <sub>Elong</sub> : 10 sec)Gibson Klonierung:pSB1AC3_Ptrc10:TermKonstruktion von pSB1AC3_Ptrc10:TermKonstruktion von pSB1AC3_Ptrc10:TermKonstruktion:pSB1AC3_Ptrc10:Term (Xbal)Dephosphorylierung:pSB1AC3_Ptrc10:Term (Xbal) (FastAP, Thermo)Restriktion:pSB1AC3_Ptrc10:Term (Xbal) + PrnpB:lacl (Xbal_Spel) (1:2) 	PARU//	10	CAGAAAGGCCC
PARION11CAAATAAAACGSPAH01712CCATCAAACAGGATTTTCGSPAH02313TGCCACCTGACGTCTAAGAAKlonierungs-VerfahrenKonstruktion von pSB1AC3 Ptrc10:TermRestriktion:pSB1AC3_Ptrc10:GFP (Xbal + Pstl) $\rightarrow$ pSB1AC3 (Xbal, Pstl)Amplifizierung:Ptrc10:Term part I von pSB1AC3_Ptrc10:GFP (PAH055 + PAH056 $\rightarrow$ 186 BP, T <sub>An</sub> : 60°C, t <sub>Elong</sub> : 10 sec) Ptrc10:Term part II von part I (PAH057 + PAH058 $\rightarrow$ 262 BP, T <sub>An</sub> : 72°C, t <sub>Elong</sub> : 10 sec)Gibson Klonierung:pSB1AC3 (Xbal, Pstl) + Ptrc10:Term part II $\rightarrow$ pSB1AC3_Ptrc10:TermKonstruktion von pSB1AC3_Ptrc10:TermKonstruktion von pSB1AC3_Ptrc10:TermKonstruktion:pSB1AC3_Ptrc10:Term (Xbal)Dephosphorylierung:pSB1AC3_Ptrc10:Term (Xbal)Dephosphorylierung:pSB1AC3_Ptrc10:Term (Xbal)Dephosphorylierung:pSB1AC3_Ptrc10:Term (Xbal)Verifizierung by PCR:Klone mit dem PrnpB:lacl Ptrc10:TermVerifizierung by PCR:Klone mit dem PrnpB:lacl Fragment in gewünschter Richtung wurden durch PCR bestimmt (SPAH017 + SPAH023 $\rightarrow$ 500 BP, T <sub>An</sub> : 61°C, t <sub>Elong</sub> : 15 sec).Konstruktion:pSB1AC3_PrnpB:lacl_Ptrc10:TermRestriktion:pPMQAK1 (EcoRI + Pstl)Restriktion:pSB1AC3_PrnpB:lacl_Ptrc10:Term (EcoRI + Pstl)Ligation:pPMQAK1 (EcoRI, Pstl) + PrnpB:lacl_Ptrc10:Term			ACGAGCCGGATGATTAATTGTCAATCTAGAGCCAGGCAT
SPAH017       12       CCATCAAACAGGATTITCG         SPAH023       13       TGCCACCTGACGTCTAAGAA         Klonierungs-Verfahren       Konstruktion von pSB1AC3_Ptrc10:GFP (Xbal + Pstl) → pSB1AC3 (Xbal, Pstl)         Amplifizierung:       pSB1AC3_Ptrc10:GFP (Xbal + Pstl) → pSB1AC3 (Xbal, Pstl)         Amplifizierung:       Ptrc10:Term part I von pSB1AC3_Ptrc10:GFP (PAH055 + PAH056 → 186 BP, T <sub>An</sub> : 60°C, t <sub>Elong</sub> : 10 sec)         Ptrc10:Term part II von part I       (PAH057 + PAH058 → 262 BP, T <sub>An</sub> : 72°C, t <sub>Elong</sub> : 10 sec)         Gibson Klonierung:       pSB1AC3_Ptrc10:Term         Konstruktion von pSB1AC3_Ptrc10:Term       pSB1AC3_Ptrc10:Term         Konstruktion von pSB1AC3_Ptrc10:Term (Xbal)       psB1AC3_Ptrc10:Term (Xbal)         Dephosphorylierung:       pSB1AC3_Ptrc10:Term (Xbal)         Dephosphorylierung:       pSB1AC3_Ptrc10:Term (Xbal)         Dephosphorylierung:       pSB1AC3_Ptrc10:Term (Xbal)         Verifizierung by PCR:Klone mit dem PrnpB:lacl Ptrc10:Term         Verifizierung by PCR:Klone mit dem PrnpB:lacl Fragment in gewünschter Richtung wurden durch PCR bestimmt (SPAH017 + SPAH023 → 500 BP, T <sub>An</sub> : 61°C, t <sub>Elong</sub> : 15 sec).         Konstruktion von pPMQAK1 PrnpB:lacl Ptrc10:Term         Restriktion:       pPMQAK1 (EcoRI + Pstl)         Restriktion:       pSB1AC3_PrnpB:lacl Ptrc10:Term (EcoRI + Pstl)         Ligation:       pPMQAK1 (EcoRI, Pstl) + PrnpB:lacl_Ptrc10:Term (EcoRI, Pstl)	FAIl070	11	CAAATAAAACG
SPAH023       13       TGCCACCTGACGTCTAAGAA         Klonierungs-Verfahren       Konstruktion von pSB1AC3_Ptrc10:Term         Restriktion:       pSB1AC3_Ptrc10:GFP (Xbal + Pstl) → pSB1AC3 (Xbal, Pstl)         Amplifizierung:       Ptrc10:Term part I von pSB1AC3_Ptrc10:GFP (PAH055 + PAH056 → 186 BP, T <sub>An</sub> : 60°C, t <sub>Elong</sub> : 10 sec)         Ptrc10:Term part II von part I (PAH057 + PAH058 → 262 BP, T <sub>An</sub> : 72°C, t <sub>Elong</sub> : 10 sec)       Ptrc10:Term part II von part I (PAH057 + PAH058 → 262 BP, T <sub>An</sub> : 72°C, t <sub>Elong</sub> : 10 sec)         Gibson Klonierung:       pSB1AC3 (Xbal, Pstl) + Ptrc10:Term part II → pSB1AC3 (Xbal, Pstl) + Ptrc10:Term         Konstruktion von pSB1AC3 Ptrc10:Term       Konstruktion von pSB1AC3_Ptrc10:Term (Xbal)         Dephosphorylierung:       pSB1AC3_Ptrc10:Term (Xbal)         Dephosphorylierung:       pSB1AC3_Ptrc10:Term (Xbal)         Ligation:       pSB1AC3_Ptrc10:Term (Xbal)         y pSB1AC3_Ptrc10:Term (Xbal)       PsB1AC3_Ptrc10:Term         Verifizierung by PCR:Klone mit dem PrnpB:lacI Ptrc10:Term       Verifizierung by PCR:Klone mit dem PrnpB:lacI Ptrc10:Term         Verifizierung by PCR:Klone mit dem PrnpB:lacI Ptrc10:Term       Konstruktion von pPMQAK1 PrnpB:lacI Ptrc10:Term         Restriktion:       pPMQAK1 (EcoRI + Pstl)       Restriktion:         Restriktion:       pSB1AC3_PrnpB:lacI_Ptrc10:Term (EcoRI + Pstl)       Ligation:         pPMQAK1 PrnpB:lacI Ptrc10:Term       PMQAK1 PrnpB:lacI Ptrc10:Term <td>SPAH017</td> <td>12</td> <td>CCATCAAACAGGATTTTCG</td>	SPAH017	12	CCATCAAACAGGATTTTCG
Klonierungs-Verfahren         Konstruktion von pSB1AC3_Ptrc10:Term         Restriktion:       pSB1AC3_Ptrc10:GFP (Xbal + Pstl) $\rightarrow$ pSB1AC3 (Xbal, Pstl)         Amplifizierung:       Ptrc10:Term part I von pSB1AC3_Ptrc10:GFP (PAH055 + PAH056 $\rightarrow$ 186 BP, T <sub>An</sub> : 60°C, t <sub>Elong</sub> : 10 sec)         Ptrc10:Term part II von part I (PAH057 + PAH058 $\rightarrow$ 262 BP, T <sub>An</sub> : 72°C, t <sub>Elong</sub> : 10 sec)         Gibson Klonierung:       pSB1AC3 (Xbal, Pstl) + Ptrc10:Term part II $\rightarrow$ pSB1AC3 (Xbal, Pstl) + Ptrc10:Term part II $\rightarrow$ pSB1AC3_Ptrc10:Term         Konstruktion von pSB1AC3_PtrpB:lacl_Ptrc10:Term       Konstruktion von pSB1AC3_Ptrc10:Term (Xbal)         Dephosphorylierung:       pSB1AC3_Ptrc10:Term (Xbal)         Bestriktion:       pSB1AC3_Ptrc10:Term (Xbal) + PrnpB:lacl (Xbal + Spel)         Ligation:       pSB1AC3_PtrpB:lacl Ptrc10:Term         Verifizierung by PCR:Klone mit dem PrnpB:lacl Ftrc10:Term         Verifizierung by PCR:Klone mit dem PrnpB:lacl Fragment in gewünschter Richtung wurden durch PCR bestimmt (SPAH017 + SPAH023 $\rightarrow$ 500 BP, T <sub>An</sub> : 61°C, t <sub>Elong</sub> : 15 sec).         Konstruktion von pPMQAK1_PrnpB:lacl_Ptrc10:Term         Restriktion:       pSB1AC3_PrnpB:lacl_Ptrc10:Term         Restriktion:       pPMQAK1 (EcoRI + Pstl)         Restriktion:       pSB1AC3_PrnpB:lacl_Ptrc10:Term	SPAH023	13	TGCCACCTGACGTCTAAGAA
Konstruktion von pSB1AC3_Ptrc10:Term         Restriktion:       pSB1AC3_Ptrc10:GFP (Xbal + Pstl) $\rightarrow$ pSB1AC3 (Xbal, Pstl)         Amplifizierung:       Ptrc10:Term part I von pSB1AC3_Ptrc10:GFP (PAH055 + PAH056 $\rightarrow$ 186 BP, T <sub>An</sub> : 60°C, t <sub>Elong</sub> : 10 sec)         Ptrc10:Term part II von part I (PAH057 + PAH058 $\rightarrow$ 262 BP, T <sub>An</sub> : 72°C, t <sub>Elong</sub> : 10 sec)         Gibson Klonierung:       pSB1AC3 (Xbal, Pstl) + Ptrc10:Term part II $\rightarrow$ pSB1AC3_Ptrc10:Term         Konstruktion von pSB1AC3_PtrpB:lacl_Ptrc10:Term         Restriktion:       pSB1AC3_Ptrc10:Term (Xbal)         Dephosphorylierung:       pSB1AC3_Ptrc10:Term (Xbal) (FastAP, Thermo)         Restriktion:       pSB1AC3_Ptrc10:Term (Xbal) + PrnpB:lacl (Xbal + Spel)         Ligation:       pSB1AC3_Ptrc10:Term (Xbal) + PrnpB:lacl (Xbal Spel) (1:2) $\rightarrow$ pSB1AC3_PtrpB:lacl Ptrc10:Term         Verifizierung by PCR:Klone mit dem PrnpB:lacl Ptrc10:Term         Verifizierung by PCR:Klone mit dem PrnpB:lacl Fragment in gewünschter Richtung wurden durch PCR bestimmt (SPAH017 + SPAH023 $\rightarrow$ 500 BP, T <sub>An</sub> : 61°C, t <sub>Elong</sub> : 15 sec).         Konstruktion von pPMQAK1 PrnpB:lacl Ptrc10:Term         Restriktion:       pSB1AC3_PrnpB:lacl_Ptrc10:Term (EcoRI + Pstl)         Ligation:       pPMQAK1 (EcoRI, Pstl) + PrnpB:lacl_Ptrc10:Term (EcoRI, Pstl) (1:5) $\rightarrow$ pPMQAK1 PrnpB:lacl Ptrc10:Term	Klonierungs-	/erfahr	en
Restriktion: $pSB1AC3_Ptrc10:GFP$ (Xbal + Pstl) $\rightarrow pSB1AC3$ (Xbal, Pstl)Amplifizierung:Ptrc10:Term part I von $pSB1AC3_Ptrc10:GFP$ (PAH055 + PAH056 $\rightarrow$ 186 BP, T <sub>AR</sub> : 60°C, t <sub>Elong</sub> : 10 sec)Ptrc10:Term part II von part I (PAH057 + PAH058 $\rightarrow$ 262 BP, T <sub>AR</sub> : 72°C, t <sub>Elong</sub> : 10 sec)Gibson Klonierung: $pSB1AC3$ (Xbal, Pstl) + Ptrc10:Term part II $\rightarrow pSB1AC3_Ptrc10:Term$ Konstruktion von $pSB1AC3_Ptrc10:Term$ Restriktion: $pSB1AC3_Ptrc10:Term$ (Xbal)Dephosphorylierung: $pSB1AC3_Ptrc10:Term$ (Xbal)Pastriktion: $pSB1AC3_Ptrc10:Term$ (Xbal)Ligation: $pSB1AC3_Ptrc10:Term$ (Xbal) + PrnpB:lacl (Xbal + Spel)Ligation: $pSB1AC3_Ptrc10:Term$ (Xbal) + PrnpB:lacl (Xbal_Spel) (1:2) $\rightarrow pSB1AC3_Ptrc10:Term$ (Xbal) + PrnpB:lacl (Xbal_Spel) (1:2) $\rightarrow pSB1AC3_PtrnpB:lacl Ptrc10:TermVerifizierung by PCR:Klone mit dem PrnpB:lacl Fragment in gewünschter Richtung wurdendurch PCR bestimmt (SPAH017 + SPAH023 \rightarrow 500 BP, TAn: 61°C, tElong: 15 sec).Konstruktion von pPMQAK1 (EcoRI + Pstl)Restriktion:pSB1AC3_PrnpB:lacl_Ptrc10:TermRestriktion:pPMQAK1 (EcoRI, Pstl) + PrnpB:lacl_Ptrc10:Term (EcoRI + Pstl)Ligation:pPMQAK1 (EcoRI, Pstl) + PrnpB:lacl_Ptrc10:Term$	Konstruktion	von pS	B1AC3 Ptrc10:Term
Amplifizierung:       Ptrc10:Term part I von pSB1AC3_Ptrc10:GFP         (PAH055 + PAH056 $\rightarrow$ 186 BP, T <sub>An</sub> : 60°C, t <sub>Elong</sub> : 10 sec)         Ptrc10:Term part II von part I         (PAH057 + PAH058 $\rightarrow$ 262 BP, T <sub>An</sub> : 72°C, t <sub>Elong</sub> : 10 sec)         Gibson Klonierung:       pSB1AC3 (Xbal, PstI) + Ptrc10:Term part II $\rightarrow$ pSB1AC3_Ptrc10:Term         Konstruktion von pSB1AC3_Ptrc10:Term         Restriktion:       pSB1AC3_Ptrc10:Term (Xbal)         Dephosphorylierung:       pSB1AC3_Ptrc10:Term (Xbal) (FastAP, Thermo)         Restriktion:       pSB1AC3_Ptrc10:Term (Xbal) + PrnpB:lacl (Xbal + Spel)         Ligation:       pSB1AC3_PtrpB:lacl Ptrc10:Term         Verifizierung by PCR:Klone mit dem PrnpB:lacl Ptrc10:Term         Verifizierung by PCR:Klone mit dem PrnpB:lacl Ptrc10:Term         Konstruktion von pPMQAK1 PrnpB:lacl Ptrc10:Term         Restriktion:       pPMQAK1 (EcoRI + PstI)         Restriktion:       pSB1AC3_PrnpB:lacl_Ptrc10:Term (EcoRI + PstI)         Ligation:       pPMQAK1 (EcoRI, PstI) + PrnpB:lacl_Ptrc10:Term (EcoRI, PstI) (1:5)	Restriktion:		pSB1AC3_Ptrc1O:GFP (Xbal + PstI) → pSB1AC3 (Xbal, PstI)
$\begin{array}{llllllllllllllllllllllllllllllllllll$	Amplifizierung	g:	Ptrc10:Term part I von pSB1AC3_Ptrc10:GFP
Ptrc10:Term part II von part I (PAH057 + PAH058 $\rightarrow$ 262 BP, T <sub>An</sub> : 72°C, t <sub>Elong</sub> : 10 sec)Gibson Klonierung:pSB1AC3 (Xbal, PstI) + Ptrc10:Term part II $\rightarrow$ pSB1AC3 Ptrc10:TermKonstruktion von pSB1AC3 PrnpB:lacl Ptrc10:TermRestriktion:pSB1AC3_Ptrc10:Term (Xbal)Dephosphorylierung:pSB1AC3_Ptrc10:Term (Xbal) (FastAP, Thermo)Restriktion:pSB1AC3_Ptrc10:Term (Xbal) (FastAP, Thermo)Restriktion:pSB1AC3_Ptrc10:Term (Xbal) + PrnpB:lacl (Xbal + Spel)Ligation:pSB1AC3_Ptrc10:Term (Xbal) + PrnpB:lacl (Xbal_Spel) (1:2) $\rightarrow$ pSB1AC3_PtrpB:lacl Ptrc10:TermVerifizierung by PCR:Klone mit dem PrnpB:lacl Fragment in gewünschter Richtung wurden durch PCR bestimmt (SPAH017 + SPAH023 $\rightarrow$ 500 BP, T <sub>An</sub> : 61°C, t <sub>Elong</sub> : 15 sec).Konstruktion von pPMQAK1 (EcoRI + PstI)Restriktion:pSB1AC3_PrnpB:lacl_Ptrc10:TermRestriktion:pSB1AC3_PrnpB:lacl_Ptrc10:Term (EcoRI + PstI)Ligation:pPMQAK1 (EcoRI, PstI) + PrnpB:lacl_Ptrc10:Term (EcoRI, PstI) (1:5) $\rightarrow$ pPMQAK1 PrnpB:lacl_Ptrc10:Term			(PAH055 + PAH056 → 186 BP, T <sub>An</sub> : 60°C, t <sub>Elong</sub> : 10 sec)
$\begin{array}{llllllllllllllllllllllllllllllllllll$			Ptrc1O:Term part II von part I
Gibson Klonierung: $pSB1AC3$ (Xbal, PstI) + Ptrc10:Term part II $\rightarrow$ <u>pSB1AC3</u> <u>Ptrc10:Term</u> Konstruktion von <u>pSB1AC3</u> <u>Ptrc10:Term</u> Restriktion: $pSB1AC3$ _Ptrc10:Term (Xbal)         Dephosphorylierung: $pSB1AC3$ _Ptrc10:Term (Xbal)         Restriktion: $pSB1AC3$ _Ptrc10:Term (Xbal) (FastAP, Thermo)         Restriktion: $pSB1AC3$ _Ptrc10:Term (Xbal) + Spel)         Ligation: $pSB1AC3$ _Ptrc10:Term (Xbal) + PrnpB:lacl (Xbal_Spel) (1:2) $\rightarrow$ <u>pSB1AC3</u> <u>PtrnpB:lacl Ptrc10:Term</u> Verifizierung by PCR:Klone mit dem PrnpB:lacl Fragment in gewünschter Richtung wurden durch PCR bestimmt (SPAH017 + SPAH023 $\rightarrow$ 500 BP, T <sub>An</sub> : 61°C, t <sub>Elong</sub> : 15 sec).         Konstruktion von <u>pPMQAK1</u> PrnpB:lacl <u>Ptrc10:Term</u> Restriktion: <u>pPMQAK1 (EcoRl + Pstl)</u> Restriktion: <u>pSB1AC3_PrnpB:lacl_Ptrc10:Term</u> (EcoRl + Pstl)         Ligation: <u>pPMQAK1 (EcoRl, Pstl) + PrnpB:lacl_Ptrc10:Term</u> (EcoRl, Pstl) (1:5) $\rightarrow$ <u>pPMQAK1 PrnpB:lacl_Ptrc10:Term</u>			(PAH057 + PAH058 → 262 BP, T <sub>An</sub> : 72°C, t <sub>Elong</sub> : 10 sec)
	Gibson Klonie	erung:	pSB1AC3 (Xbal, Pstl) + Ptrc1O:Term part II
Konstruktion von pSB1AC3_PmpB:lacl_Ptrc1O:Term         Restriktion:       pSB1AC3_Ptrc1O:Term (Xbal)         Dephosphorylierung:       pSB1AC3_Ptrc1O:Term (Xbal) (FastAP, Thermo)         Restriktion:       pSB1AC3_Ptrc1O:Term (Xbal) + Spel)         Ligation:       pSB1AC3_Ptrc1O:Term (Xbal) + PrnpB:lacl (Xbal_Spel) (1:2)         → pSB1AC3_PrnpB:lacl_Ptrc1O:Term         Verifizierung by PCR: Klone mit dem PrnpB:lacl Fragment in gewünschter Richtung wurden durch PCR bestimmt (SPAH017 + SPAH023 → 500 BP, T <sub>An</sub> : 61°C, t <sub>Elong</sub> : 15 sec).         Konstruktion von pPMQAK1_PrnpB:lacl_Ptrc1O:Term         Restriktion:       pPMQAK1 (EcoRI + Pstl)         Restriktion:       pSB1AC3_PrnpB:lacl_Ptrc1O:Term (EcoRI + Pstl)         Ligation:       pPMQAK1 (EcoRI, Pstl) + PrnpB:lacl_Ptrc1O:Term (EcoRI, Pstl) ( 1:5)         → pPMQAK1_PrnpB:lacl_Ptrc1O:Term			→ pSB1AC3_Ptrc10:Term
Restriktion:       pSB1AC3_Ptrc10:Term (Xbal)         Dephosphorylierung:       pSB1AC3_Ptrc10:Term (Xbal) (FastAP, Thermo)         Restriktion:       pSB1AC3_Ptrc10:Term (Xbal) + Spel)         Ligation:       pSB1AC3_Ptrc10:Term (Xbal) + PrnpB:lacl (Xbal_Spel) (1:2)         → pSB1AC3_PtrpB:lacl Ptrc10:Term         Verifizierung by PCR:Klone mit dem PrnpB:lacl Fragment in gewünschter Richtung wurden durch PCR bestimmt (SPAH017 + SPAH023 → 500 BP, T <sub>An</sub> : 61°C, t <sub>Elong</sub> : 15 sec).         Konstruktion von pPMQAK1 PrnpB:lacl Ptrc10:Term         Restriktion:       pPMQAK1 (EcoRI + PstI)         Restriktion:       pSB1AC3_PrnpB:lacl_Ptrc10:Term (EcoRI + PstI)         Ligation:       pPMQAK1 (EcoRI, PstI) + PrnpB:lacl_Ptrc10:Term (EcoRI, PstI) (1:5)         → pPMQAK1_PrnpB:lacl_Ptrc10:Term	Konstruktion	von pS	B1AC3 PrnpB:lacl_Ptrc1O:Term
Dephosphorylierung: pSB1AC3_Ptrc10:Term (Xbal) (FastAP, Thermo)         Restriktion:       pSB1AC_PrnpB:lacl (Xbal + Spel)         Ligation:       pSB1AC3_Ptrc10:Term (Xbal) + PrnpB:lacl (Xbal_Spel) (1:2)         → pSB1AC3_PtrpB:lacl_Ptrc10:Term         Verifizierung by PCR:Klone mit dem PrnpB:lacl Fragment in gewünschter Richtung wurden         durch PCR bestimmt (SPAH017 + SPAH023 → 500 BP, T <sub>An</sub> : 61°C, t <sub>Elong</sub> : 15 sec).         Konstruktion von pPMQAK1_PrnpB:lacl_Ptrc10:Term         Restriktion:       pPMQAK1 (EcoRI + Pstl)         Restriktion:       pSB1AC3_PrnpB:lacl_Ptrc10:Term (EcoRI + Pstl)         Ligation:       pPMQAK1 (EcoRI, Pstl) + PrnpB:lacl_Ptrc10:Term (EcoRI, Pstl) ( 1:5)         → pPMQAK1_PrnpB:lacl_Ptrc10:Term	Restriktion:		pSB1AC3_Ptrc10:Term (Xbal)
Restriktion:       pSB1AC_PrnpB:lacl (Xbal + Spel)         Ligation:       pSB1AC3_Ptrc10:Term (Xbal) + PrnpB:lacl (Xbal_Spel) (1:2)         → pSB1AC3_PrnpB:lacl Ptrc10:Term         Verifizierung by PCR:Klone mit dem PrnpB:lacl Fragment in gewünschter Richtung wurden         durch PCR bestimmt (SPAH017 + SPAH023 → 500 BP, T <sub>An</sub> : 61°C, t <sub>Elong</sub> : 15 sec).         Konstruktion von pPMQAK1_PrnpB:lacl Ptrc10:Term         Restriktion:       pPMQAK1 (EcoRI + Pstl)         Restriktion:       pSB1AC3_PrnpB:lacl_Ptrc10:Term (EcoRI + Pstl)         Ligation:       pPMQAK1 (EcoRI, Pstl) + PrnpB:lacl_Ptrc10:Term (EcoRI, Pstl) ( 1:5)         → pPMQAK1_PrnpB:lacl_Ptrc10:Term	Dephosphory	lierung	: pSB1AC3_Ptrc1O:Term (Xbal) (FastAP, Thermo)
Ligation:       pSB1AC3_Ptrc10:Term (Xbal) + PrnpB:lacl (Xbal_Spel) (1:2)         → pSB1AC3_PrnpB:lacl_Ptrc10:Term         Verifizierung by PCR:Klone mit dem PrnpB:lacl Fragment in gewünschter Richtung wurden durch PCR bestimmt (SPAH017 + SPAH023 → 500 BP, T <sub>An</sub> : 61°C, t <sub>Elong</sub> : 15 sec).         Konstruktion von pPMQAK1_PrnpB:lacl_Ptrc10:Term         Restriktion:       pPMQAK1 (EcoRI + Pstl)         Restriktion:       pSB1AC3_PrnpB:lacl_Ptrc10:Term (EcoRI + Pstl)         Ligation:       pPMQAK1 (EcoRI, Pstl) + PrnpB:lacl_Ptrc10:Term (EcoRI, Pstl) ( 1:5)         → pPMQAK1_PrnpB:lacl_Ptrc10:Term	Restriktion:		pSB1AC_PrnpB:lacl (Xbal + Spel)
$ → \underline{pSB1AC3 PrnpB:lacl Ptrc10:Term} $ Verifizierung by PCR:Klone mit dem PrnpB:lacl Fragment in gewünschter Richtung wurden durch PCR bestimmt (SPAH017 + SPAH023 → 500 BP, T <sub>An</sub> : 61°C, t <sub>Elong</sub> : 15 sec). Konstruktion von <u>pPMQAK1 PrnpB:lacl Ptrc10:Term</u> Restriktion: pPMQAK1 (EcoRI + Pstl) Restriktion: pSB1AC3_PrnpB:lacl_Ptrc10:Term (EcoRI + Pstl) Ligation: pPMQAK1 (EcoRI, Pstl) + PrnpB:lacl_Ptrc10:Term (EcoRI, Pstl) ( 1:5)	Ligation:		pSB1AC3_Ptrc1O:Term (Xbal) + PrnpB:lacl (Xbal_Spel) (1:2)
Verifizierung by PCR:Klone mit dem PrnpB:lacl Fragment in gewünschter Richtung wurden durch PCR bestimmt (SPAH017 + SPAH023 → 500 BP, T <sub>An</sub> : 61°C, t <sub>Elong</sub> : 15 sec).         Konstruktion von pPMQAK1_PrnpB:lacl_Ptrc1O:Term         Restriktion:       pPMQAK1 (EcoRI + Pstl)         Restriktion:       pSB1AC3_PrnpB:lacl_Ptrc1O:Term (EcoRI + Pstl)         Ligation:       pPMQAK1 (EcoRI, Pstl) + PrnpB:lacl_Ptrc1O:Term (EcoRI, Pstl) ( 1:5)         → pPMQAK1_PrnpB:lacl_Ptrc1O:Term			→ pSB1AC3_PrnpB:lacl_Ptrc1O:Term
durch PCR bestimmt (SPAH017 + SPAH023 → 500 BP, T <sub>An</sub> : 61°C, t <sub>Elong</sub> : 15 sec).         Konstruktion von pPMQAK1_PmpB:lacl_Ptrc10:Term         Restriktion:       pPMQAK1 (EcoRI + Pstl)         Restriktion:       pSB1AC3_PrnpB:lacl_Ptrc10:Term (EcoRI + Pstl)         Ligation:       pPMQAK1 (EcoRI, Pstl) + PrnpB:lacl_Ptrc10:Term (EcoRI, Pstl) (1:5);         → pPMQAK1_PrnpB:lacl_Ptrc10:Term	Verifizierung	by PCF	R:Klone mit dem PrnpB:lacl Fragment in gewünschter Richtung wurden
Konstruktion von pPMQAK1_PrnpB:lacl_Ptrc10:Term         Restriktion:       pPMQAK1 (EcoRl + Pstl)         Restriktion:       pSB1AC3_PrnpB:lacl_Ptrc10:Term (EcoRl + Pstl)         Ligation:       pPMQAK1 (EcoRl, Pstl) + PrnpB:lacl_Ptrc10:Term (EcoRl, Pstl) ( 1:5)         → pPMQAK1_PrnpB:lacl_Ptrc10:Term	durch PCR be	estimm	t (SPAH017 + SPAH023 → 500 BP, $T_{An}$ : 61°C, $t_{Elong}$ : 15 sec).
Restriktion:       pPMQAK1 (EcoRI + Pstl)         Restriktion:       pSB1AC3_PrnpB:lacl_Ptrc10:Term (EcoRI + Pstl)         Ligation:       pPMQAK1 (EcoRI, Pstl) + PrnpB:lacl_Ptrc10:Term (EcoRI, Pstl) ( 1:5)         → pPMQAK1_PrnpB:lacl_Ptrc10:Term	Konstruktion	von pP	MQAK1 PrnpB:lacl Ptrc1O:Term
Restriktion:         pSB1AC3_PrnpB:lacl_Ptrc10:Term (EcoRI + Pstl)           Ligation:         pPMQAK1 (EcoRI, Pstl) + PrnpB:lacl_Ptrc10:Term (EcoRI, Pstl) ( 1:5)           → pPMQAK1_PrnpB:lacl_Ptrc10:Term	Restriktion:		pPMQAK1 (EcoRI + Pstl)
Ligation: pPMQAK1 (EcoRI, Pstl) + PrnpB:lacl_Ptrc10:Term (EcoRI, Pstl) ( 1:5) → pPMQAK1 PrnpB:lacl_Ptrc10:Term	Restriktion:		pSB1AC3_PrnpB:lacl_Ptrc1O:Term (EcoRI + Pstl)
→ pPMQAK1_PrnpB:lacl_Ptrc10:Term	Ligation:		pPMQAK1 (EcoRI, Pstl) + PrnpB:lacl_Ptrc1O:Term (EcoRI, Pstl) ( 1:5)
			→ pPMQAK1_PrnpB:lacl_Ptrc10:Term

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Konstruktion von pl	PMQAK1 PmpB:lacl_Ptrc1O:BGTII
Restriktion:	pPMQAK1_PmpB:lacl_Ptrc10:Term (Spel)
Amplifizierung:	oAlkBII (PAH059 + PAH067 → 1283 BP, $T_{An}$ : 65°C, $t_{Elong}$ : 25 sec)
	oAlkGII (PAH068 + PAH069 → 568 BP, $T_{An}$ : 60°C, $t_{Elong}$ : 25 sec)
	oAlkTII (PAH070 + PAH071 → 1204 BP, $T_{An}$ : 65°C, $t_{Elong}$ : 25 sec)
OE-PCR:	oAlkBII+ oAlkGII (PAH063 + PAH072 → 1859 BP, $T_{An}$ : 65°C,
t <sub>Elong</sub> : 60 sec)	
	→ oBGII
	oBGII + oAlkTII (PAH063 + PAH073 → 3096 BP,T <sub>An</sub> : 57°C, t <sub>Elong</sub> : 90
sec)	
	→oBGTII
Gibson:	pPMQAK1_PrnpB:lacl_Ptrc1O:Term (Spel) + oBGT
	→ pPMQAK1_PrnpB:lacl_Ptrc10:BGTII
Konstruktion von pl	RSF_Ptrc10:BGTII
Restriktion:	pPMQAK1_PrnpB:lacl_Ptrc1O:BGTII (Xbal)
Amplifizierung:	Term von pSB1AC3_Ptrc1O:GFP
	(PAH077 + PAH078 $\rightarrow$ 191 BP, T <sub>An</sub> : 60°C, t <sub>Elong</sub> : 5 sec)
Gibson:	pPMQAK1_PrnpB:lacl_Ptrc1O:oBGTII (Xbal) + Term
	→ pRSF_Ptrc10:BGTII
Wachstumsbeding	ingen für S <i>ynechocystis sp.</i> PCC6803
Synechocystis sp.	2006803 wurde in YBG11 medium, basierend auf Shoolnick et al. 2007
bei Zugabe von 50	mM HEPES Puffer kultiviert (Shcolnick et al. 2007). Als Selektionsdruck
wurden 50 µg ml <sup>-1</sup>	Kanamycin zugesetzt. Standard Kultivierungsbedingungen umfassen ein
Kulturvolumen von	20 mL YBG11 medium in 100 mL Erlenmever Schüttelflaschen mit
Schikane, welche in	einem Orbitalschüttler (Multitron Pro shaker, Infors, Bottmingen,
Schweiz) bei 150 m	om (2.5 cm Amplitude) eingesetzt wurden. Die Kultivierungstemperatur
betrug 30°C, bei ein	ner Lichtintensität von 50 µmol m <sup>-2</sup> s <sup>-1</sup> (LED), 0.04 % CO <sub>2</sub> und einer
Luftfeuchtigkeit von	75 %. Das Wachstum wurde über die optische Dichte bei einer
5	50 nm über ein Spektrophotometer (Libra S11, Biochrom Ltd. Cambridge,
Wellenlänge von 75	
Wellenlänge von 75 UK) verfolgt. Vorku	turen wurden über 200 µL einer Cryostock-Lösung innokuliert und unter
Wellenlänge von 75 UK) verfolgt. Vorku Standard-Bedingun	turen wurden über 200 µL einer Cryostock-Lösung innokuliert und unter gen für 4 - 6 Tage kultiviert. Hauptkulturen wurden ausgehend von dieser

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Vorkultur mit einer Start-OD<sub>750</sub> von 0.08 innokuliert und für 3 Tage unter Standard-Bedingungen kultiviert bis die Genexpression für einen weiteren Tag durch Zugabe von 2 mM IPTG induziert wurde.

$$\begin{split} & \mathsf{YBG11:}\ 1.49\ g\ \mathsf{L}^1\ \mathsf{NaNO_3},\ 0.074\ g\ \mathsf{L}^1\ \mathsf{MgSO_4} \cdot 7\ \mathsf{H_2O},\ 0.305\ g\ \mathsf{L}^1\ \mathsf{K_2}\mathsf{HPO_4},\ 10\ \mathsf{mL}\ \mathsf{L}^1\ \mathsf{YBG11}\\ & \mathsf{Spurenelemente}\ (100x)\ ,\ 0.019\ g\ \mathsf{L}^{-1}\ \mathsf{Na_2CO_3},\ 50\ \mathsf{mM}\ \mathsf{HEPES}\ (\mathsf{pH}\ 7.2),\ \mathsf{YBG11}\\ & \mathsf{Spurenelemente}\ (100x)\ ,\ 0.36\ g\ \mathsf{L}^{-1}\ \mathsf{CaCl_2} \cdot 2\ \mathsf{H_2O},\ 0.63\ g\ \mathsf{L}^{-1}\ \mathsf{Zitronensäure},\ 0.28\ g\ \mathsf{L}^{-1}\\ & \mathsf{Borsäure}\ ,\ 0.11\ g\ \mathsf{L}^{-1}\ \mathsf{MnCl_2} \cdot 4\ \mathsf{H_2O},\ 0.02\ g\ \mathsf{L}^{-1}\ \mathsf{ZnSO_4} \cdot 7\ \mathsf{H_2O},\ 0.039\ g\ \mathsf{L}^{-1}\ \mathsf{Na_2MoO_4} \cdot 2\ \mathsf{H_2O},\\ & 0.007\ g\ \mathsf{L}^{-1}\ \mathsf{CuSO_4} \cdot 5\ \mathsf{H_2O},\ 0.003\ g\ \mathsf{L}^{-1}\ \mathsf{FeCl_3} \cdot 6\ \mathsf{H_2O},\ 0.6\ g\ \mathsf{L}^{-1}\\ & \mathsf{Na_2EDTA} \cdot 2\ \mathsf{H_2O} \end{split}$$

Transformation von Synechocystis sp. PCC6803 durch Elektroporation

Transformation von Synechocystis sp. PCC6803 mit dem Plasmid pRSF\_Ptrc10:BGTII wurde über Elektroporation, basierend auf einer Methode nach Ferreira et al. 2014, durchgeführt (Universidade do Porto Ferreira 2014). Elektrokompetente Zellen wurden ausgehend von einer 50 mL YBG11 Hauptkultur (in 100 mL Erlenmeyer Schüttelkolben mit Schikane) mit einer OD<sub>750</sub> von 0.5 - 1 hergestellt. Die Zellen wurden durch Zentrifugation geerntet (10 min, 3180 g, 4°C), dreimal mit je 10 mL HEPES Puffer (1 mM, pH 7.5) gewaschen und in 1 mL HEPES Puffer resuspendiert. Die elektrokompetenten Zellen wurde nach Zugabe von 5 % (v/v) DMSO bei - 80°C gelagert. Zur Elektroporation wurden 0.2 - 1.0 ug Plasmid-DNA zu 60 uL elektrokompetenten Zellen in eine Elektroporationsküvette (2 mm Elektrodenabstand) gegeben, bei 2500 V für 5 ms gepulst (12.5 kV cm<sup>-1</sup>) (Eppendorf Eporator, Eppendorf Vertrieb Deutschland GmbH, Wesseling-Berzdorf, Deutschland) und anschließend in 50 mL YBG11 Medium (in 100 mL Erlenmeyer Schüttelkolben mit Schikane) transferiert. Nach Kultivierung unter Standard-Bedingungen für 24 h wurden die Zellen durch Zentrifugation geerntet (10 min, 3180 g, RT), in 100 µL YBG11 Medium resuspendiert und auf BG11 Agarplatten mit 50 µg mL<sup>-1</sup> Kanamycin ausgestrichen ((Stanier et al. 1971). Einzelne Kolonien wurden nach 4 – 6 Tagen bei 30°C, 20-50 µmol m<sup>-2</sup> s<sup>-1</sup> Lichtintensität (Leuchtstoffröhren), 0.04 % CO2 und 80 % Luftfeuchtigkeit (poly klima GmbH, Freising, Deutschland) auf frische BG11 Agarplatten transferiert und erneut inkubiert. Die Zellmasse einer Agarplatte wurde schließlich zur Innokulation einer 20 mL YBG11 Vorkultur genutzt.

 $\begin{array}{l} \mathsf{BG11} \ \mathsf{Agarplatten:} \ 1.5 \ \mathsf{g} \ \mathsf{L}^{-1} \ \mathsf{NaNO_3}, \ 0.075 \ \mathsf{g} \ \mathsf{L}^{-1} \ \mathsf{MgSO_4} \ \cdot \ 7 \ \mathsf{H_2O}, \ 0.036 \ \mathsf{g} \ \mathsf{L}^{-1} \ \mathsf{CaCl_2} \ \cdot \ 2 \ \mathsf{H_2O}, \\ \mathsf{0.006} \ \mathsf{g} \ \mathsf{L}^{-1} \ \mathsf{citric} \ \mathsf{acid}, \ 0.04 \ \mathsf{g} \ \mathsf{L}^{-1} \ \mathsf{K_2HPO_4}, \ 0.006 \ \mathsf{g} \ \mathsf{L}^{-1} \ \mathsf{Eisen-Ammonium-Citrat}, \ 0.001 \ \mathsf{g} \ \mathsf{L}^{-1} \\ \mathsf{Na_2EDTA}, \ 0.02 \ \mathsf{g} \ \mathsf{L}^{-1} \ \mathsf{Na_2CO_3}, \ 1 \ \mathsf{mL} \ \mathsf{L}^{-1} \ \mathsf{BG11} \ \mathsf{Spurenelemente} \ (1000x), \ 0.3 \ \ \mathsf{Na_2S_2O_3}, \ 10 \\ \mathsf{mM} \ \mathsf{HEPES} \ (\mathsf{pH \ 8}), \ 1.5 \ \ \mathsf{Magring} \ \mathsf{Agar;} \ \mathsf{BG11} \ \mathsf{Spurenelemente} \ (1000x) \ : \ 2.86 \ \mathsf{g} \ \mathsf{L}^{-1} \ \mathsf{Borsäure}, \ 1.8 \ \mathsf{g} \\ \end{array}$ 

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 $\begin{array}{l} L^{-1} \mbox{ MnCl}_2 \cdot 4 \mbox{ H}_2 O, \mbox{ 0.22 g } L^{-1} \mbox{ ZnSO}_4 \cdot 7 \mbox{ H}_2 O, \mbox{ 0.39 g } L^{-1} \mbox{ Na}_2 MoO_4 \cdot 2 \mbox{ H}_2 O, \mbox{ 0.08 g } L^{-1} \mbox{ CuSO}_4 \cdot 5 \mbox{ H}_2 O, \mbox{ 0.05 g } L^{-1} \mbox{ Co}(NO_3)_2 \cdot 6 \mbox{ H}_2 O, \mbox{ 0.39 g } L^{-1} \mbox{ Na}_2 MoO_4 \cdot 2 \mbox{ H}_2 O, \mbox{ 0.08 g } L^{-1} \mbox{ CuSO}_4 \cdot 2 \mbox{ H}_2 O, \mbox{ 0.08 g } L^{-1} \mbox{ 0.$ 

Figur 1 zeigt eine Bio-reaktive Extraktion von photosynthetisch erzeugtem Sauerstoff durch das Alkan-Monooxygenase Enzymsystem AlkBGT, welches genetisch in den Cyanobakterien-Stamm *Synechocystis sp.* PCC6803 eingeführt wurde. Die photosynthetische Lichtreaktion wurde durch Beleuchtung (Lichtintensität von 50 µmol m<sup>-2</sup>s<sup>-1</sup>) induziert, während die Kontroll-Reaktion ohne Beleuchtung stattfand. Als oxygeniertes Produkt wurde terminal hydroxyliertes Methyl-Nonanoat detektiert. CDW = Zelltrockengewicht.

Hierzu wurde das Alkan-Monooxygenase Enzymsystem AlkBGT in den Cyanobakterien-Stamm *Synechocystis sp.* PCC6803 eingesetzt (über das Plasmid pRSF\_Ptrc10:BGTII, siehe Herstellung des modifizierten Stamms oben), welcher ein potentieller Biokatalysator zur photosynthetischen Wasserstoff Produktion ist. Nach Umsetzung des Reaktionssystems von aeroben zu anaeroben Bedingungen und nach Zugabe von Methyl-Nonanoat als Substrat, konnte die Bildung von oxygeniertem Produkt bei Beleuchtung detektiert werden (Figur 1).

Da bei Reaktionsbedingungen in Dunkelheit keine Produktbildung beobachtet wurde, weisen die Ergebnisse nach, dass der für die Reaktion gebrauchte Sauerstoff aus der photosynthetischen Lichtreaktion stammte. Die spezifische Aktivität betrug 0,9 ± 0,1 µmol<sub>oxygeniertes Substrat</sub> min<sup>-1</sup> g<sub>CDW</sub><sup>-1</sup> für die ersten 30 Minuten. Die Sauerstoff-Bildungsrate bei gleicher Belichtungs-Intensität von 50 µmol m<sup>-2</sup> s<sup>-1</sup> betrug 3,7 ± 0,5 µmol<sub>o2</sub> min<sup>-1</sup> g<sub>CDW</sub><sup>-1</sup> (ohne Substrat-Zugabe). Somit konnten mit dem nicht-optimierten Biokatalysator bereits nahezu 25 % des entstandenen Sauerstoffes enzymatisch abgefangen werden. Bei Betrachtung der möglichen Verdünnung des Sauerstoffes aus der wässrigen Phase in die Gasphase (wässrig:Gas Phasen-Verhältnis 1:10, dimensionslose Henry Volatilität Hcc = caq/cgas für O2 in Wasser: 0.0297 bei 25°C (Sander 2015)) wird deutlich, dass der molekulare Sauerstoffe bereits an der Stelle seiner Erzeugung abgefangen und in das Substrat eingebunden wurde, bevor es in die Gasphase entwichen ist. Eine Optimierung des Oxygenierungs-Systems (zum Beispiel durch Erhöhung des Enzymgehaltes in der Zelle), ist möglich und würde den Anteil an extrahiertem Sauerstoff erhöhen.

#### Beispiel 2:

Technische Anwendung - Rohrbündelreaktor Konzept

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Die technische Umsetzung der beschriebenen Erfindung erfolgt bevorzugt über ein Konzept, in dem ein beleuchteter Rohrbündelreaktor zur Anwendung kommt, welcher suspendierte oder immobilisierte phototrophe Zellen beinhaltet. Ein Scale-Up des Rohrbündelreaktors in einen technischen Maßstab erfolgt durch einfache Erhöhung der Anzahl an eingesetzter Mikrokapillare. Als spezielle Form immobilisierter Zellen wird ein Biofilm-basierter Aufbau gewählt, welcher sich bereits für die Cyanobakterien-Spezies Synechocystis sp. PCC6803 als realisierbar erwies (David, C., K. Buhler and A. Schmid (2015). "Stabilization of single species Synechocystis biofilms by cultivation under segmented flow." J Ind Microbiol Biotechnol 42(7): 1083-1089). Diese technische Umsetzung bietet ein kontinuierliches Produktionssystem, welches die photosynthetische Wasserspaltung, die Wasserstoff-Produktion, die Sauerstoff Extraktion, sowie die Substrat Oxidation beinhaltet. Die nachgelagerte Aufbereitung wird dann durch das Abfangen des molekularen Wasserstoffes über die Gasphase und, bei Einsatz von Abwasser als Substrat, durch Rückführung des behandelten Abwassers zum weiterführenden Aufbereitungsprozess ermöglicht. Wird hingegen ein kombinierter biokatalvtischer Produktionsprozess beabsichtigt, ist eine Abtrennung des Produktes mit erhöhter Wertschöpfung zum Beispiel durch den Einsatz einer organischen Trägerphase durchzuführen. Die folgenden Beispiele enthalten Annahmen und Werte welche entsprechend der spezifischen Anwendung und der gewählten Rahmenbedingungen angepasst werden und zeigen das Potential der Erfindung.

#### Spezifische Aktivität bezüglich der Wasserspaltung durch das PSII

Die verwendeten Mikroorganismen weisen einen Gehalt von ca. 1% des Photosystems II auf, wobei das Photosystem II eine molare Masse von 350 kDa besitzt (g<sub>CDW</sub><sup>-1</sup>, Molekulargewicht PSII (Shen, J. R. (2015). "*The structure of photosystem II and the mechanism of water oxidation in photosynthesis*." <u>Annu Rev Plant Biol</u> 66: 23-48). Der höchste in vitro gemessene Wert wird von Dismukes et al. (Dismukes, G. C., R. Brimblecombe, G. A. Felton, R. S. Pryadun, J. E. Sheats, L. Spiccia and G. F. Swiegers (2009). "*Development of bioinspired Mn<sub>4</sub>O<sub>4</sub>-cubane water oxidation catalysts: lessons from photosynthesis.*" <u>Acc Chem Res</u> 42(12): 1935-1943.) mit 1000 s<sup>-1</sup> angegeben. Dies führt zu einer spezifischen Aktivität des PSII von 1700 µmol<sub>H2OSpaltung</sub> pro Minute je g<sub>CDW</sub><sup>-1</sup>. Daraus ergibt sich bezüglich einer Wasserstoffproduktion, einem Sauerstoffverbrauch und einer Substartoxidierung durch den Organismus von 850µmol<sub>H2OSpaltung</sub> pro Minute je g<sub>CDW</sub><sup>-1</sup>.

#### Produkt Ertrag durch einen Rohrbündelreaktor Prozess

Auf 20 000 Mikrokapillaren mit je 2 m Länge und 5 mm Durchmesser werden 10 g<sub>CDW</sub> L<sup>-1</sup> Biomasse mit einer volumetrischen Produktivität von 0.51 mol<sub>H2IO2Substrat</sub> L<sup>-1</sup> h<sup>-1</sup> eingesetzt.

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Es ergibt sich ein Gesamtvolumen von 785 L (39.3 mL Kapillare<sup>-1</sup>). Bei 2920 Sonnenstunden im Jahr (Licht Verfügbarkeit 8 h pro Tag, 365 Tage) produziert das System 1169 kmol Wasserstoff, sowie oxidiertes Substrat pro Jahr.

#### Energieertrag

Es gilt die Voraussetzung, dass der Prozess nicht durch die Hydrogenase limitiert ist. Auf Basis eines Molekulargewichts von 2 g/mol weist Wasserstoff eine volumetrische Produktaktivität von 1.02 g<sub>H2</sub> L<sup>-1</sup> h<sup>-1</sup>. Daraus ergibt sich ein Produktertrag von 2338 kg Wasserstoff pro Jahr von denen 60 % also 1402 kg rückgewonnen werden. Bei einem zugrunde gelegten Energiegehalt von 33.3 kWh je Kilogramm Wasserstoff (Wikipedia) kann mit dem erfindungsgemäßen Prozess eine Energie von 46 686 kWh pro Jahr generiert werden.

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Pater	ntansprüche
1.	Verfahren zur bioreaktiven Extraktion erzeugten Sauerstoffs aus einem Reaktionsraum, umfassend die folgenden Schritte:
	- bestamen zummeest eines proteitoprich min obiganismus und anzeroben Bedingungen in einem Reaktionsraum, und
	Oxidation eines Sauerstoff-verwertenden Substrats.
2.	Verfahren nach Anspruch 1, wobei der zumindest eine phototrophe Mikroorganismus, zumindest ein Sauerstoff-umsetzendes Enzym aufweist oder produziert.
3.	Verfahren nach Anspruch 2, wobei das zumindest eine Enzym ausgewählt ist aus der Gruppe Hydrogenase, Nitrogenase und/oder Oxidoreduktase.
4.	Verfahren nach einem der Ansprüche 1 bis 3, wobei bei der Bestrahlung des zumindest einen phototrophen Mikroorganismus neben Sauerstoff auch Wasserstoff oder Methanol frei wird.
5.	Verfahren nach einem der vorhergehenden Ansprüche, dadurch gekennzeichnet, dass die Oxidoreduktasen ausgewählt sind aus der Gruppe der Oxidasen oder Oxygenasen, vorzugsweise Monooxygenasen, Dioxygenasen oder coenzym- unabhängige Oxygenasen.
6.	Verfahren nach einem der vorhergehenden Ansprüche, wobei als phototropher Mikroorganismus Algen oder Cyanobakterien eingesetzt werden, vorzugsweise Cyanobakterien.
7.	Verfahren nach einem der vorhergehenden Ansprüche, dadurch gekennzeichnet, dass als Mikroorganismus ein, insbesondere genetisch modifizierter, Cyanobakterienstamm eingesetzt wird, der das Alkan-Monooxygenase-Enzymsystem AlkBGT aufweist.
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### WO 2018/162465 PCT/EP2018/055449 8. Verfahren nach einem der vorhergehenden Ansprüche, dadurch gekennzeichnet, dass der genetisch modifizierte Cyanobakterienstamm Synechocystis sp. PCC6803 eingesetzt wird, der das Alkan-Monooxygenase-Enzymsystem AlkBGT aufweist oder produziert. 9. Verfahren nach Anspruch 8, dadurch gekennzeichnet, dass als Substrat Methylnonanoat verwendet wird. 10. Verwendung von phototrophen Mikroorganismen, die neben Hydrogenasen, Nitrogenasen oder Oxidoreduktasen als Wasserstoff-produzierendes Enzym zusätzlich Oxidoreduktasen als Sauerstoff-umsetzende Enzyme aufweisen oder produzieren, bei der Gewinnung von Wasserstoff (H2) oder Methanol und Sauerstoff (O2) aus Wasser oder wässrigen Flüssigkeiten und Lösungen und zur simultanen insitu Entfernung des Sauerstoffs (O2) unter Verwendung entsprechender Substrate, die mit dem Sauerstoff Produkte bilden. 11. Photobioreaktor umfassend den genetisch modifizierten Cyanobacterienstamm Synechocystis sp. PCC6803, der das Alkan-Monooxygenase-Enzymsystem AlkBGT aufweist oder produziert.



			International app PCT/EP201	lication No 18/055449
A. CLASS INV. ADD.	IFICATION OF SUBJECT MATTER C12M1/00 C12M1/107 C12P5/03	2 C12P3	/00	
According	o International Patent Classification (IPC) or to both national classifica	tion and IPC		
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Documenta	tion searched other than minimum documentation to the extent that s	uch documents are incl	uded in the fields se	arched
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EPO-Ir	iternal, BIOSIS, Sequence Search, EM	BASE, WPI Da	ta	
C. DOCUN	IENTS CONSIDERED TO BE RELEVANT			
Category*	Citation of document, with indication, where appropriate, of the rele	evant passages		Relevant to claim No.
х	DE 10 2010 015807 A1 (EVONIK DEG [DE]) 20 October 2011 (2011-10-20 claims 12-15; examples	USSA GMBH Ə)		11
A	RAINER GROSS ET AL: "Engineered biofilms for continuous large sc production of n -octanol and ( S oxide", BIOTECHNOLOGY AND BIOENGINEERING vol. 110, no. 2, 1 February 2013 (2013-02-01), par 424-436, XP55490337, US ISSN: 0006-3592, DOI: 10.1002/bi	catalytic ale )-styrene , ges t.24629		1-11
A	DE 10 2007 002009 A1 (SALVETZKI 26 June 2008 (2008-06-26) cited in the application 	RALF [DE]) -/		1-11
X Fur	ther documents are listed in the continuation of Box C.	X See patent fa	mily annex.	
* Special *A* docum to be *E* earlier filing *L* docum cited speci *O* docum mean *P* docum the p	sategories of oited documents : ent defining the general state of the art which is not considered of particular relevance application or patent but published on or after the international date ent which may throw doubts on priority claim(s) or which is co establish the publication date of another of lation or other al reason (as specified) ent referring to an oral disclosure, use, exhibition or other a ent published prior to the international filing date but later than only date outained.	*T* later document pudate and not in o the principle or the second second second second second second second second second second *X* document of parti- considered to im combined with o being obvious to *&* document member *&* document member	blished after the inte onflict with the applic teory underlying the i or cannot be consid cournent is taken alor sular relevance; the c olve an inventive ste or more other suc a person skilled in th r of the same patent	mational filing date or priority ation but olted to understand invention laimed invention cannot be ered to involve an inventive se laimed invention cannot be p when the document is n documents, such combinatic family
Date of the	actual completion of the international search	Date of mailing of	the international sea	rch report
2	24 July 2018	01/08/	2018	
Name and	mailing address of the ISA/ European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk	Authorized officer		

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# Curriculum vitae

# Personal data

Name: Date of birth: Nationality: Family status:	Anna Hoschek 12.11.1989 in Marl, Germany German Single
Education	
11/ 2014 – 01/ 2019	<b>Ph. D. Student</b> at the Department of Solar Materials, Helmholtz- Centre for Environmental Research - UFZ, Leipzig, Germany, under supervision of Prof. Dr. Andreas Schmid and Prof. Dr. Bruno Bühler
10/ 2012 – 07/ 2014	<b>Studies in Chemical Biology</b> , Faculty of Chemistry and Chemical Biology, TU Dortmund University, Dortmund, Germany Degree: <b>Master of Science</b>
10/ 2009 – 09/ 2012	<b>Studies in Chemical Biology</b> , Faculty of Chemistry and Chemical Biology, TU Dortmund University, Dortmund, Germany Degree: <b>Bachelor of Science</b>
08/ 2006 – 10/ 2009	Hans-Böckler-vocational school, Marl, Germany Degree: State-certified <b>technical assistant in biology</b> (BTA)
08/ 2006 – 06/ 2009	Hans-Böckler-vocational school, Marl, Germany Degree: University entrance diploma ( <b>Abitur</b> )
08/ 2000 – 06/ 2006	Maristen Realschule (Secondary school), Recklinghausen, Germany Degree: Secondary school certificate ( <b>Fachoberschulreife</b> )

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