

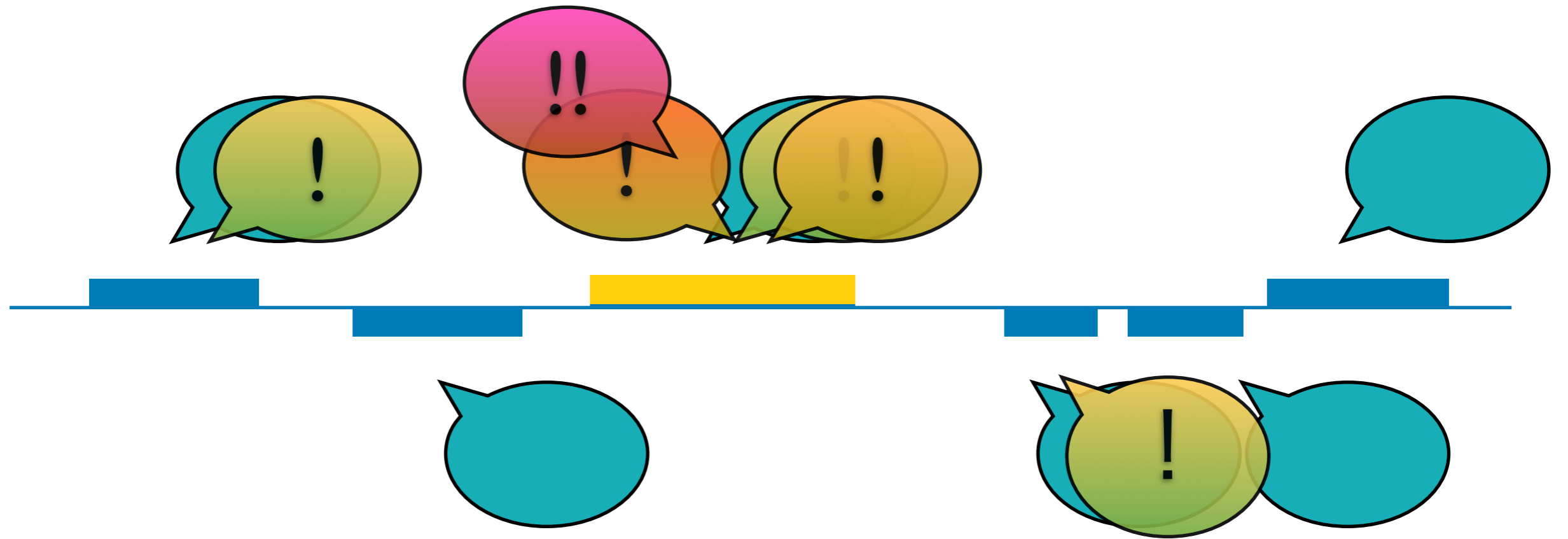
Plant and plant-related bacteria genome projects @ Kazusa

| species | Publication | gene No | Feature |
|--|-------------------------------|------------|--------------------------------|
| <i>Synechosystis</i> PCC 6803 | Kaneko <i>et al.</i> , 1996* | 3672 | cyanobacterium |
| <i>Arabidopsis thaliana</i> | Kaneko <i>et al.</i> , 2000 | 6124 | model plant |
| <i>Mesorhizobium loti</i> | Kaneko <i>et al.</i> , 2000 | 7283 | rhizobium |
| <i>Anabaena</i> PCC 7120 | Kaneko <i>et al.</i> , 2001 | 6132 | N-fixation cyanobacterium |
| <i>Thermosynechococcus elongatus</i> | Nakamura <i>et al.</i> , 2002 | 2477 | thermophilic cyanobacterium |
| <i>Bradyrhizobium japonicum</i> | Kaneko <i>et al.</i> , 2002 | 8317 | rhizobium |
| <i>Gloeobacter violaceus</i> | Nakamura <i>et al.</i> , 2003 | 4431 | cyanobacterium |
| <i>Microcystis aeruginosa</i> | Kaneko <i>et al.</i> , 2007 | 6312 | cyanobacterium |
| <i>Lotus japonicus</i> | Sato <i>et al.</i> , 2008 | 30799 | model legume plant |

*Re-annotated in 2002

ソーシャルブックマークによるゲノムアノテーション

ユーザからのフィードバックを容易に、簡便に、速攻で反映



<http://a.kazusa.or.jp>



Kazusa DNA Res. Inst.

現在までの成果

📍 高度情報集積データベースの開発・運用

📍 KazusaAnnotation: <http://a.kazusa.or.jp/>

📍 KazusaNavigation: <http://navi.kazusa.or.jp/>

📍 KazusaWiki: <http://wiki.kazusa.or.jp/>

📍 ゲノムアノテーション情報の蓄積・公開

📍 文献情報と実験情報をマニュアルで蓄積

📍 3,004報 95,152エントリの入力

📍 情報を閲覧するためのビューワの開発



Gene Indexing

Coordinated High-Light Response of Genes Encoding Subunits of Photosystem I Is Achieved by AT-Rich Upstream Sequences in the Cyanobacterium *Synechocystis* sp. Strain PCC 6803^V

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Received 16 December 2006/Accepted 23 January 2007

Genes encoding subunits of photosystem I (PSI genes) in the cyanobacterium *Synechocystis* sp. strain PCC 6803 are actively transcribed under low-light conditions, whereas their transcription is coordinately and rapidly down-regulated upon the shift to high-light conditions. In order to identify the molecular mechanism of the coordinated high-light response, we searched for common light-responsive elements in the promoter region of PSI genes. First, the precise architecture of the *psaD* promoter was determined and compared with the previously identified structure of the *psaAB* promoter. One of two promoters of the *psaAB* genes (P1) and of the *psaD* gene (P2) possessed an AT-rich light-responsive element located just upstream of the basal promoter region. These sequences enhanced the basal promoter activity under low-light conditions, and their activity was transiently suppressed upon the shift to high-light conditions. Subsequent analysis of *psaC*, *psaE*, *psaK1*, and *psaL1* promoters revealed that their light response was also achieved by AT-rich sequences located at the -70 to -46 region. These results clearly show that AT-rich upstream elements are responsible for the coordinated high-light response of PSI genes dispersed throughout *Synechocystis* genome.

Photosynthetic organisms have ability to cope with the changes in light environment by modulating both the structure and the function of the photosynthetic machinery (31, 59). A typical example is the flexible control of the amounts of photosystem (PS) and light-harvesting antenna complexes depending on the availability of light energy (4, 27, 38). Under light-limiting conditions, the amount of these complexes is maintained at high level, because maximal capture of light energy is required to fulfill the energy demand of cells. Under light-saturating conditions, on the other hand, they are largely down-regulated since absorption of excess light energy tends to cause the generation of harmful reactive oxygen species (6).

The dynamics of reaction center complexes during the process of high-light (HL) acclimation have been well characterized in cyanobacteria. Amount of PSI is more strictly down-regulated than that of PSII upon the exposure to HL (28, 40). The analysis of the *pmgA* mutant deficient in down-regulation of PSI content revealed that the selective repression of PSI is essential for growth under continuous HL conditions (28, 54). Although the primary determinant of PSI content under HL conditions has not been identified, transcriptional regulation is likely to be one of the important factors. The cyanobacterial PSI complex is comprised of about 11 subunits, with some exceptions (23), and genes encoding these subunits (PSI genes) are dispersed throughout the genome. In *Synechocystis* sp.

strain PCC 6803, PSI genes are actively transcribed under low-light (LL) conditions, whereas their transcription is coordinately and rapidly down-regulated upon the shift to HL conditions (26, 29, 30, 42, 57), except for the *psaK2* gene encoding an HL-inducible isoform of the PsaK subunit (19). PSI transcripts become barely detectable within 1 h of HL exposure and then gradually reaccumulate after 3 h. The change in promoter activities of PSI genes is well coincident with the change in transcript levels (42, 43), suggesting that the coordinated light response of PSI genes is achieved at the level of transcriptional regulation. In the course of HL acclimation, cells need to activate genes related to several processes such as CO₂ fixation, protection from photoinhibition, and general stress management (29). The down-regulation of high promoter activities of PSI genes upon the shift to HL conditions may be important not only for the repression of PSI content, but also for the recruitment of RNA polymerases to active transcription of such HL-inducible genes.

As the first step for the elucidation of the molecular mechanism of coordinated HL response of PSI genes in *Synechocystis* sp. strain PCC 6803, we recently dissected the promoter architecture of the *psaAB* genes encoding reaction center subunits (43). The *psaAB* genes have two promoters, P1 and P2, both of which are responsible for the photon flux density-dependent transcription. Deletion analysis of the upstream region of *psaAB* fused to bacterial luciferase reporter genes (*luxAB*) indicated that the light responses of P1 and P2 are achieved in different manners. The *cis* element required for the light response of P1, designated as PE1, was located just upstream of the -35 element of P1 and was comprised of AT-rich sequence. PE1 activated P1 under LL conditions, and the down-regulation of P1 was achieved by rapid inactivation of PE1 upon the shift to HL conditions. On the other hand, the *cis* element required for the light response of P2, designated as

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^V Published ahead of print on 2 February 2007.

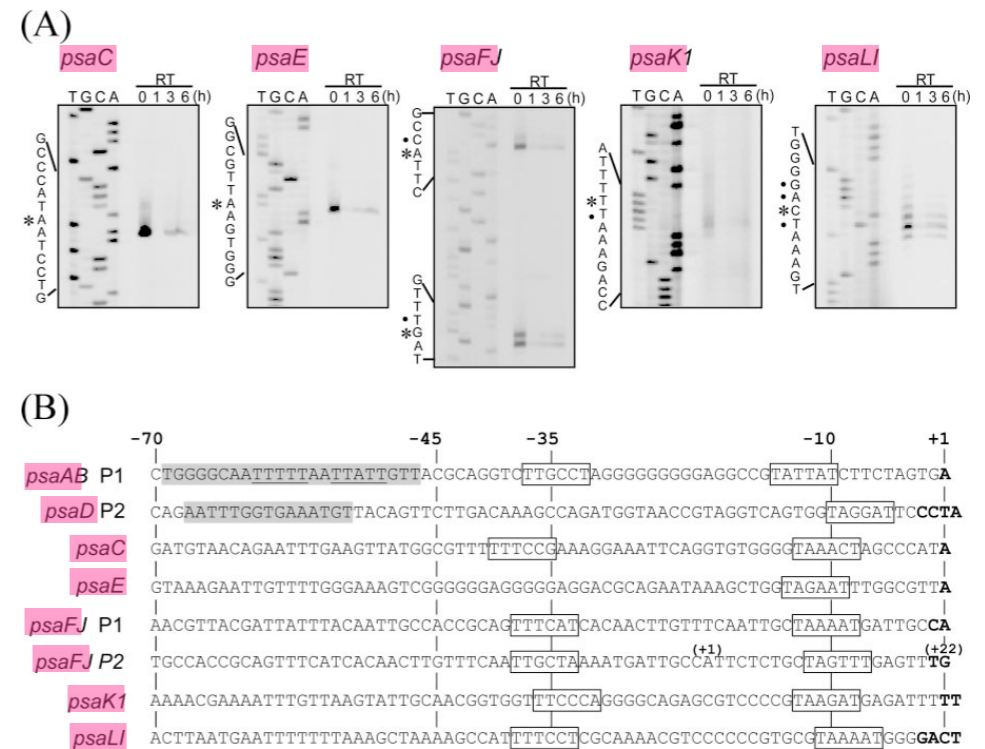


FIG. 3. Mapping of the 5' ends of PSI transcripts. (A) Total RNA was isolated from the wild-type cells incubated under HL conditions for 0, 1, 3, and 6 h and used for primer extension analysis of *psaC*, *psaE*, *psaFJ*, *psaK1*, and *psaL1*. Detected 5' ends of the major transcripts are indicated by asterisks, and those of minor ones are indicated by dots. (B) Nucleotide sequences of the core promoter and its upstream region of PSI promoters. The promoters are aligned according to the major transcriptional start point noted as +1. Putative -35 and -10 hexamers are boxed. Light-responsive positive elements identified in *psaAB* and *psaD* promoters are shaded in gray. The nucleotides shown to be critical for the light response of *psaAB* promoter (43) are underlined. The numbers in parentheses shown above the nucleotide sequence of the P2 promoter of *psaFJ* indicate the position according to the major transcriptional start point of the P1 promoter.

the analysis since the arrangement of regulatory elements for two overlapping promoter is difficult to predict without precise promoter analysis.

Effect of the -70 to -46 region on the promoter activity of PSI genes. Figure 4A shows the bioluminescence level of *Synechocystis* cells harboring PSI promoter-*luxAB* reporter genes with or without the upstream region under LL conditions. The reporter activities of the downstream promoter fragments alone were generally low, but there existed some differences among them. For example, the promoter activity of the downstream region was low in the case of *psaD* [(8.2 ± 0.2) × 10⁵ relative units/OD₇₃₀] and *psaK1* [(2.3 ± 0.4) × 10⁵ relative units/OD₇₃₀], whereas that of *psaL1* was significantly high [(1.1 ± 0.2) × 10⁷ relative units/OD₇₃₀]. It is possible that the high activity of the *psaL1* promoter is brought about by a positive regulatory element located within the downstream region. When the AT-rich upstream region was added, each promoter displayed much higher activity compared with the corresponding derivative containing only the downstream region. This demonstrates that the -70 to -46 region can work as a posi-

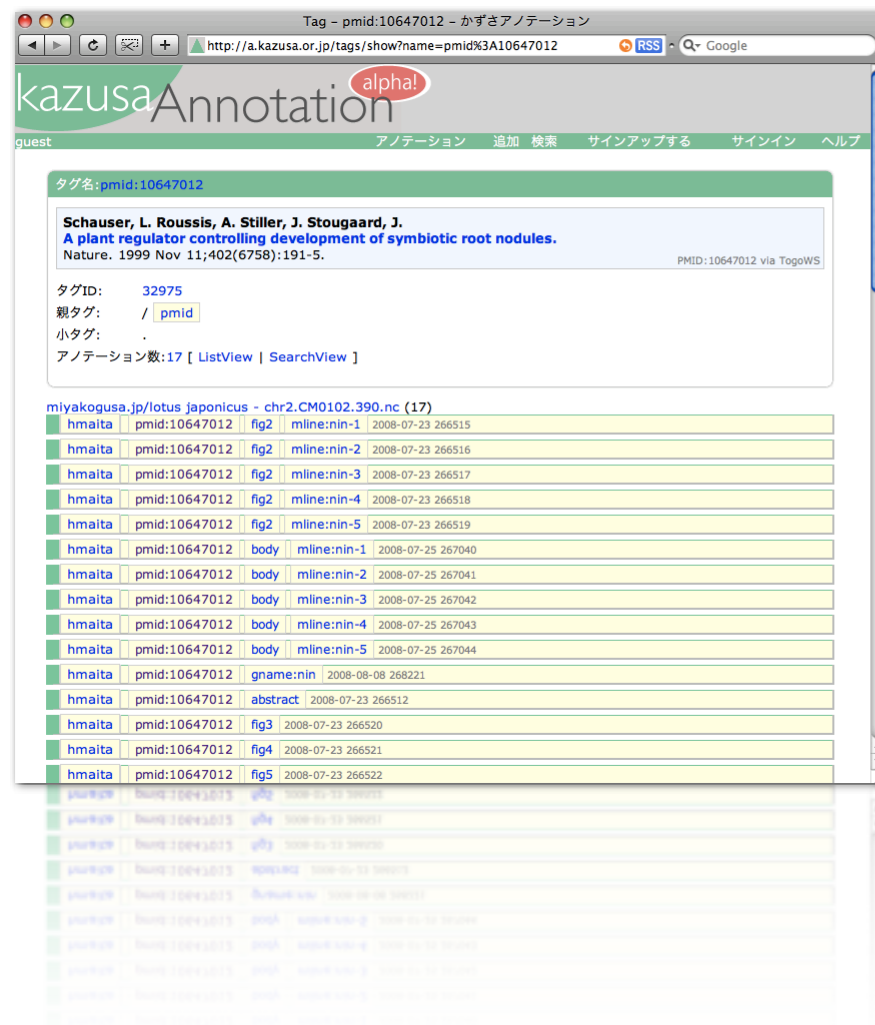
tive regulatory element for every PSI gene examined here. The low activity of *psaD* and *psaK1* promoters was largely up-regulated in the presence of the upstream region by 40.1- and 99.9-fold, respectively. On the other hand, strong promoter activity of *psaL1* was not enhanced as much by the upstream region (5.1-fold). As a result, similar promoter activity (around 5.0 × 10⁷ relative units/OD₇₃₀) was attained among PSI genes irrespective of the activity of the downstream promoter region.

Next, we transformed *E. coli* cells with the above mentioned reporter constructs and measured the level of bioluminescence to see whether the upstream region can work as a positive regulatory element in *E. coli* cells (Fig. 4B). In all strains harboring PSI promoter-*luxAB* constructs, the luminescence level was higher than that of the control cells having promoterless *luxAB* genes [(1.4 ± 0.5) × 10⁸ relative units/OD₆₀₀], showing that PSI promoters can be recognized by RNA polymerase of *E. coli*. The rank orders of promoter strength are similar in both *Synechocystis* and *E. coli* cells. Namely, the activities of the downstream promoter fragments of *psaD* and *psaK1* were low [(2.4 ± 1.0) × 10⁸ relative units/OD₆₀₀ and

ソーシャルブックマーク (SBM) による 遺伝子 = URL への文献情報蓄積

slr0473 Cph I, phytochrome

<http://bacteria.kazusa.or.jp/cyanobase/Synechocystis/cgi-bin/orfinfo.cgi?title=Chr&name=slr0473>



Tag - pmid:10647012 - かずさアノテーション

http://a.kazusa.or.jp/tags/show?name=pmid%3A10647012

kazusaAnnotation

guest アノテーション 追加 検索 サインアップする サインイン ヘルプ

タグ名: pmid:10647012

Schauser, L. Roussis, A. Stiller, J. Stougaard, J.
A plant regulator controlling development of symbiotic root nodules.
Nature. 1999 Nov 11;402(6758):191-5. PMID:10647012 via TogoWS

タグID: 32975
親タグ: / pmid
小タグ: .
アノテーション数: 17 [ListView | SearchView]

myakogusa.jp/lotus japonicus - chr2.CM0102.390.nc (17)

| | | | | |
|--------|---------------|-----------|-------------|-------------------|
| hmaita | pmid:10647012 | fig2 | mline:nin-1 | 2008-07-23 266515 |
| hmaita | pmid:10647012 | fig2 | mline:nin-2 | 2008-07-23 266516 |
| hmaita | pmid:10647012 | fig2 | mline:nin-3 | 2008-07-23 266517 |
| hmaita | pmid:10647012 | fig2 | mline:nin-4 | 2008-07-23 266518 |
| hmaita | pmid:10647012 | fig2 | mline:nin-5 | 2008-07-23 266519 |
| hmaita | pmid:10647012 | body | mline:nin-1 | 2008-07-25 267040 |
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| hmaita | pmid:10647012 | body | mline:nin-3 | 2008-07-25 267042 |
| hmaita | pmid:10647012 | body | mline:nin-4 | 2008-07-25 267043 |
| hmaita | pmid:10647012 | body | mline:nin-5 | 2008-07-25 267044 |
| hmaita | pmid:10647012 | gname:nin | | 2008-08-08 268221 |
| hmaita | pmid:10647012 | abstract | | 2008-07-23 266512 |
| hmaita | pmid:10647012 | fig3 | | 2008-07-23 266520 |
| hmaita | pmid:10647012 | fig4 | | 2008-07-23 266521 |
| hmaita | pmid:10647012 | fig5 | | 2008-07-23 266522 |

[pmid: 92785 | 3] [introduction]

[pmid: 92785 | 3] [results]

[pmid: 92785 | 3] [discussion]

[pmid: 92785 | 3] [table |]

[pmid: 92785 | 3] [fig3]

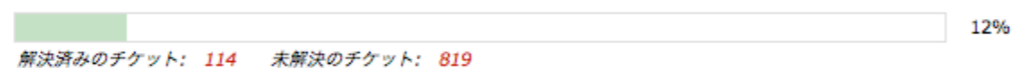


プロGRESS

2008-1-25

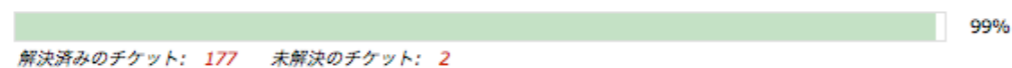
Rhizobia

マイルストーン: **[Rhizo] Bradyrhizobium japonicum USDA110**
完了期限が設定されていません



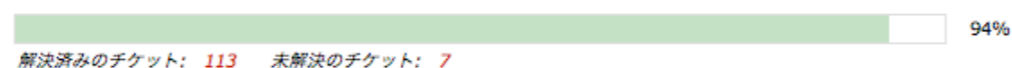
114 papers

マイルストーン: **[Rhizo] Mesorhizobium loti MAFF303099**
完了期限が設定されていません



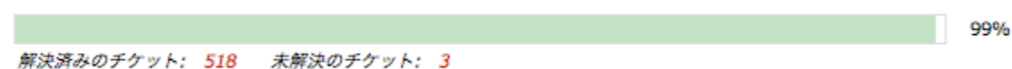
177 papers

マイルストーン: **[Rhizo] Sinorhizobium meliloti strain 1021**
完了期限が設定されていません



113 papers

マイルストーン: **[cyano] Anabaena sp. PCC7120**
完了期限が設定されていません

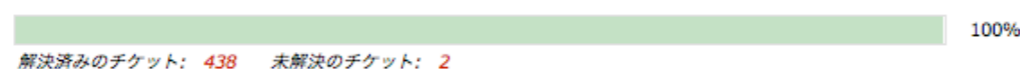


518 papers

- 2008-7-25 Anabaenaの名前の表記ゆれにより検索対象から落ちていた文献を追加しました

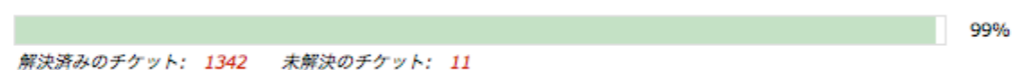
Cyano-
bacteria

マイルストーン: **[cyano] Synechococcus sp. PCC7942**
完了期限が設定されていません



438 papers

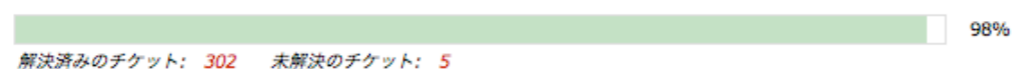
マイルストーン: **[cyano] Synechocystis sp. PCC6803**
完了期限が設定されていません



1342 papers

Legume

マイルストーン: **[plant] Lotus japonicus**
完了期限が設定されていません



302 papers

Total 95152 entries

KazusaAnnotation: <http://a.kazusa.or.jp/>

kazusaAnnotation alpha!

ようこそ ゲスト さん

アノテーション 検索... サインアップ... サインイン ヘルプ

syn:slr0473

編集

ページID: 2

タイトル: CyanoBase/Synechocystis - syn:slr0473

URL: <http://bacteria.kazusa.or.jp/cyanoBase/Synechocystis/cgi-bin/annotation.cgi>

Gene name (3): **cph1** hik35 phy

PubMed ID (47): 15641769 11806940 11560494 9342316 12047374 17199291 10613860 15774880 12010493 11277928 16751241 17034247 10949378 18000013 15938613 10978170 16539742 15757650 15291308 12913140 18571200 15350144 16868740 15653792 16096278 17720783 12446635 9097043 15944148 10716932 12480098 11555279 16887842 15699194 16533061 16452410 10420848 16853666 000076152 11289505 11532008 11299378 16228363 9278513 16585762 12240834 12039966

ユーザ (13): yoshimura_h Cyanogene yanakahira synobu hkane CYORF Kazusa takutsu makotokasai kashima mitsuyo

ブックマーク: 353エントリ

タグ (144): results discussion introduction abstract pmid:15641769 fig3 materials and methods pmid:11806940 CyanoGenes:1759 pmid:11560494 pmid:9342316 fig1 fig2 syn:slr0473 pmid:12047374 Table1 fig4 pmid:10613860 gname:cph1 pmid:17199291 pmid:15774880 pmid:16751241 CyanoGenes:297 pmid:12010493 CyanoGenes:403 CyanoGenes:125 pmid:11277928 CyanoGenes:298 CyanoGenes:638 pmid:18000013 pmid:10949378 fig5 CyanoGenes:558 pmid:17034247 table2 pmid:15938613 pmid:10978170 CyanoGenes:Contact CyanoGenes:Investigator CyanoGenes:GeneticBackground pmid:16539742 CyanoGenes:Date CyanoGenes:AdditionalInformation CyanoGenes:DrugMarker pmid:15757650 pmid:15291308 pmid:12913140 CyanoGenes:Segregation ppi:bait Category:C CyanoGenes:DNA:no pmid:18571200 fig7 CyanoGenes:Mutant:yes fig6 ppi:prey pmid:15653792 table3 pmid:16868740 CyanoGenes:GeneName fig8 pmid:15350144 CYORF:CYREF pmid:9097043 fig10 ppi:ssr1375 ppi:ssr1375:slr0473 pmid:17720783 table4 Category:A CyanoGenes:Mutant:no CyanoGenes:MutantName pmid:15944148 pmid:12446635 pmid:16096278 pmid:16533061 body title conclusion gene table5 pmid:11555279 pmid:12480098 pmid:15699194 gname:hik35 pmid:16887842 pmid:10716932 fig9 fig11 CyanoGenes:MutationType pmid:11532008 CYORF:kid pmid:000076152 pmid:11299378 pmid:16585762 pmid:10420848 CYORF:uniprot_def pmid:12039966 pmid:11289505 ppi:sl1244 ppi:slr0473:sl1920 pmid:16853666 Category:D evid:ide gname:phy CYORF:start_pos goid:0009883 ppi:slr0473:sl1244 UniProt:Q55168 ppi:sl1920 histidinekinase evid:ipi CYORF:pos Experimental Section CyanoGenes:DNA:yes scheme1 CYORF:orf_id CYORF:definition ppi:ssr2422 CYORF:uniprot_acc pmid:16228363 ppi:sl0507:slr0473 CyanoGenes:Phenotype:no pmid:16452410 CYORF:length figure goid:0005515 ppi:slr0473:slr0806 ppi:slr0473:ssr2422 CyanoGenes:DrugDirection ppi:sl0507 pmid:12240834 pmid:9278513 ppi:slr1529 result CYORF:genename fig12 CYORF:cyanobase_def CyanoGenes:ProductName phytochrome ppi:slr0473:slr1529 ppi:slr0806 CyanoGenes:MedlineID CyanoGenes:Function

編集: このエントリのアノテーションを編集

Gene ID

Gene name

Literatures

Curator

Tag cloud

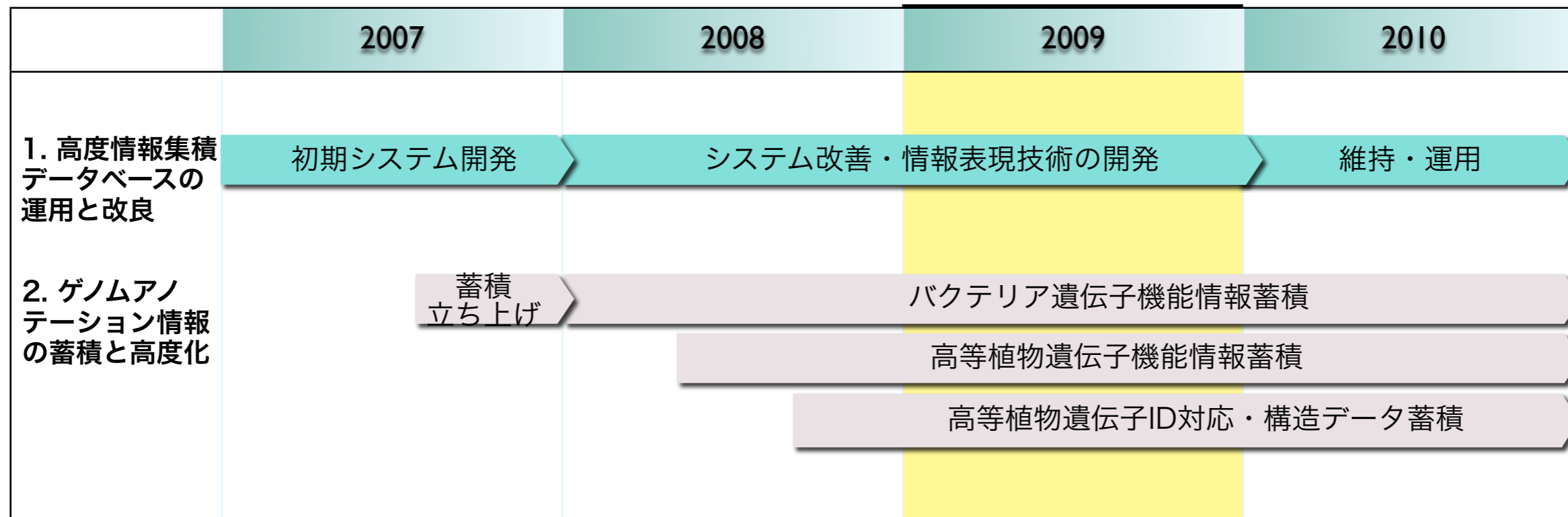


植物および植物関連微生物のゲノム情報データベース統合と高度化@かずさ H21実施計画案

| | |
|---------------------------------|---|
| <h2>1. 高度情報集積データベースの運用と改良</h2> | <p>分子データ上のポジションを統合のための基盤情報とし、<u>アノテーション・キュレーションの統合と高度化</u>を可能とするデータベース (KazusaAnnotation: http://a.kazusa.or.jp/) を植物および植物関連微生物のゲノム解析情報を対象として運用しつつ、ユーザの要望を汲みあげて改善を加え、さらなる利便性の向上を行う。</p> <p>同時に以下の項目も実施する</p> <ul style="list-style-type: none">・集積した情報から生物学的な意味を取り出すための情報表現技術・情報を閲覧するためのビューワ(genoDivePro, genoDiveEu)の改善と提供・データベース中の遺伝子名や遺伝子IDの食い違いを解決 |
| <h2>2. ゲノムアノテーション情報の蓄積と高度化</h2> | <p>かずさDNA研究所でゲノム塩基配列が決定されたモデル生物を中心に、より<u>広範な生物種の遺伝子情報について、引き続き論文記載情報および実験情報の蓄積業務を実施</u>し、ゲノムの位置情報と論文記載情報の統合を図る。</p> <ul style="list-style-type: none">・登録した情報は、KazusaAnnotationシステムなどから完全公開・効率的なアノテーションを行うための方法の開発・アノテーター・キュレーターの育成、技術向上のためにIT技術を利用したミーティング手法などを開発 |



4年間の中でのH2I (2009)年度



- 更に1,500 報以上の文献情報蓄積
 - ・ シアノバクテリア
 - ・ 根粒菌
 - ・ シロイヌナズナ (植物の統合)

- 集積した情報から生物学的な意味を取り出すための情報表現技術
- ビューワの改善と提供
- 食い違う遺伝子名やIDの統合
- アノテーション手法の改善

アノテーション 体制の整備

KDRI DB Resources

RhizoBase: The Genome Database for Rhizobia. Includes search fields for keyword and Gene ID, and a list of genomes with details like Mesorhizobium loti MAFF302099.

CyanoBase: The Genome Database for Cyanobacteria. Includes search fields and a list of genomes like Synechocystis sp. PCC 6803.

miyakogusa.jp: Lotus japonicus predicted gene keyword search interface. Includes a search box and a bar chart showing predicted genes.



KazusaAnnotation

Annotation作業を通じてのレビュー

Annotation情報の統合

Annotation Meeting
物理的・仮想的

機能・内容改善

遠隔地Curator

Annotation, Curation

問題発見, 問題共有



trac: Integrated SCM & Project Management. Shows a roadmap and milestones for RhizoBase and CyanoBase.

KazusaNavigation: Forum for discussion. Includes a table of discussion topics and a table of markers with accession numbers and primer information.

KazusaAnnotation website interface. Shows a list of recent annotations with details like 'CyanoBase/synpcc7942 - syn:Synpcc7942_0225' and '2 annotations'.



Kazusa DNA Res. Inst.

The bibliome of *Synechocystis* sp. PCC 6803

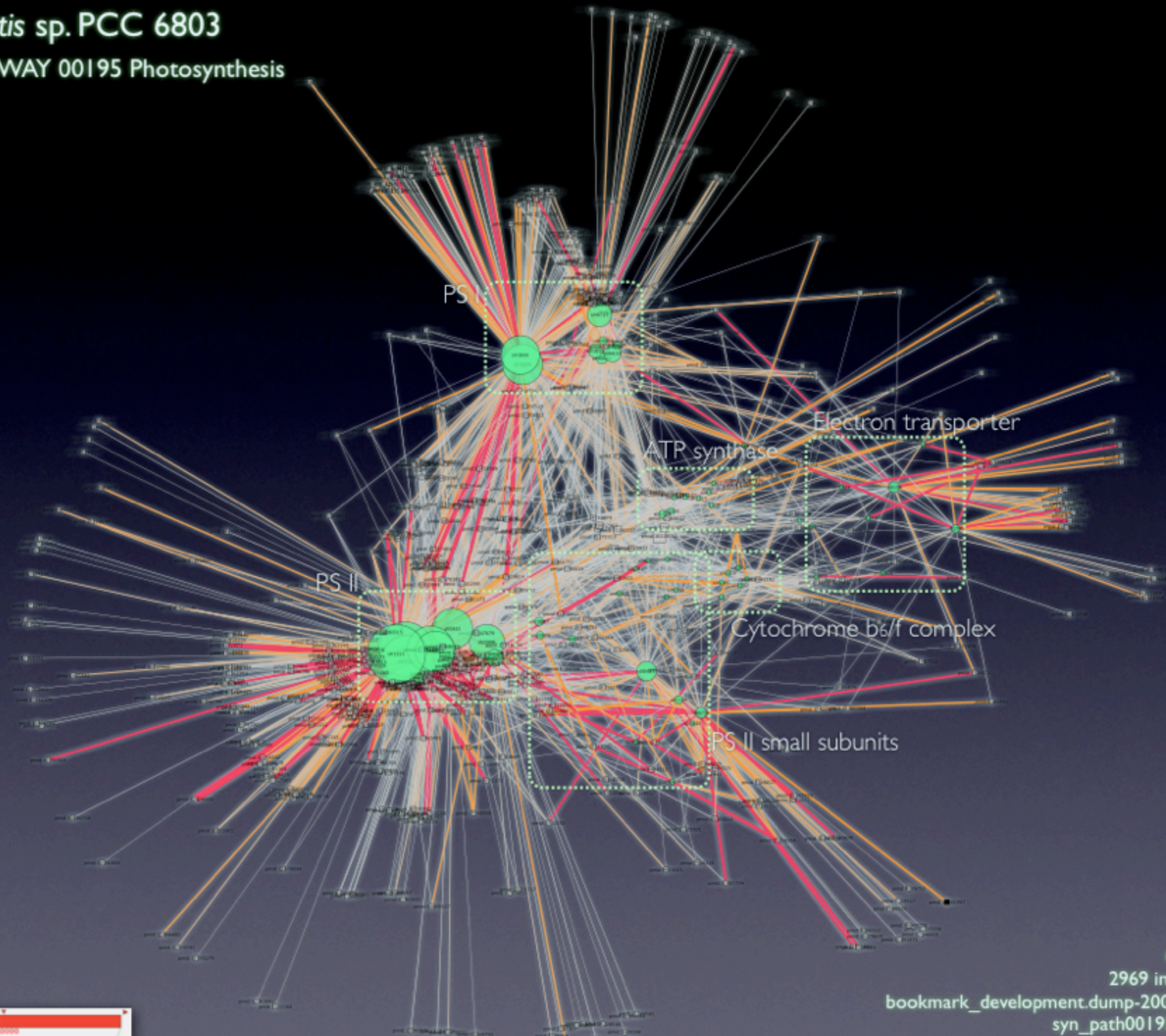
- 1,244 full-text papers
- 11,783 associations between papers and genes

Green circle: gene
Gray square: paper



Synechocystis sp. PCC 6803

KEGG PATHWAY 00195 Photosynthesis



636 nodes

2969 interactions

bookmark_development.dump-2008-4-14.sql

syn_path00195_cyt2.pdf

S. Okamoto and Kazusa SGA team

