資料　6

「ライフサイエンス統合データベース開発運用」（統合データベース開発：植物及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）

実施機関：かずさディー・エヌ・エー研究所
担当責任者：中村保一

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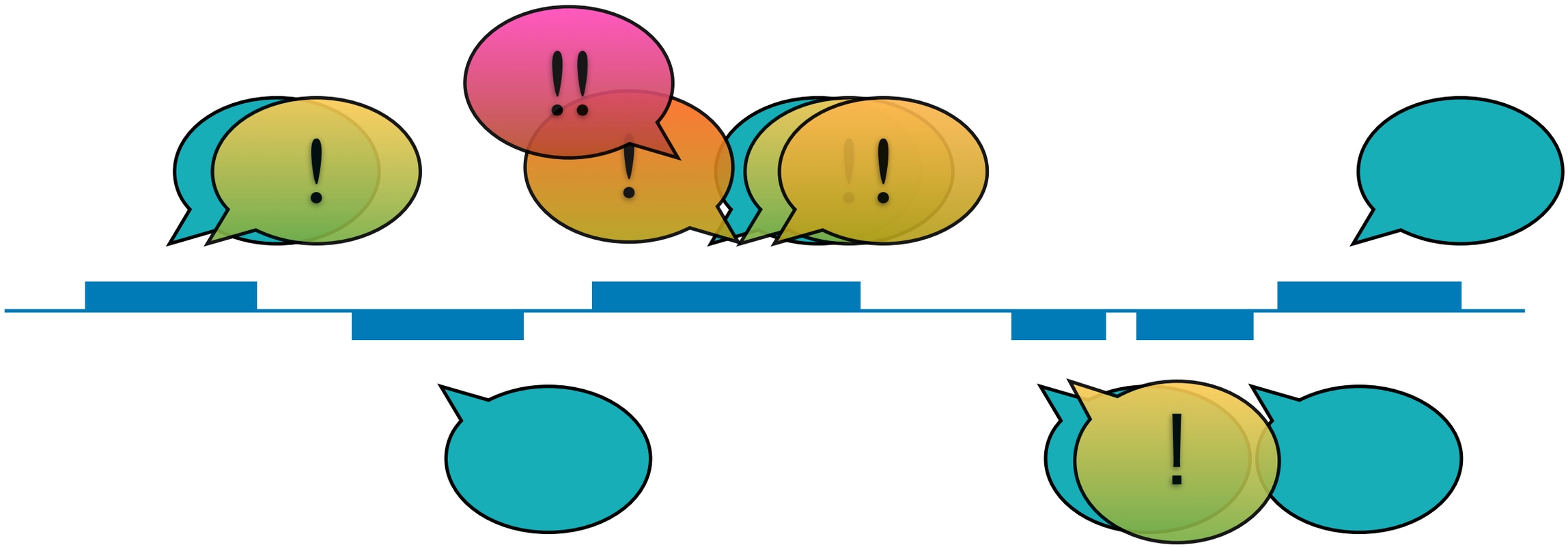
ゲノム上の「ポジション」へのアノテーションの蓄積

フィードバックや論文情報を容易に、簡便に、リアルタイムで追加反映



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成果報告

- **高度情報集積データベースの運用・改善**
  - 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人力で高速に蓄積、即時公開
  - (3,004→) 5,613報 (95,152→) 145,890エントリ入力
- **蓄積した情報を閲覧する方法の開発**

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論文からの “Gene Indexing”

JOURNAL OF BACTERIOLOGY, Apr. 2007, p. 2750–2758 Vol. 189, No. 7
0021-9193/07/$08.00+0 doi:10.1128/JB.01903-06

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▽

Masayuki Muramatsu† and Yukako Hihara*

Department of Biochemistry and Molecular Biology, Faculty of Science, Saitama University, 255 Shimo-okubo, Saitama 338-8570, Japan

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 *psaLI* 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 CO_2 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

* Corresponding author. Mailing address: Department of Biochemistry and Molecular Biology, Faculty of Science, Saitama University, 255 Shimo-okubo, Saitama 338-8570, Japan. Phone: 81-48-858-3396. Fax: 81-48-858-3384. E-mail: hihara@molbiol.saitama-u.ac.jp.
† Present address: Department of Integrated Biosciences, Graduate School of Frontier Sciences, University of Tokyo, Kashiwa, Chiba 277-8562, Japan.
▽ Published ahead of print on 2 February 2007.

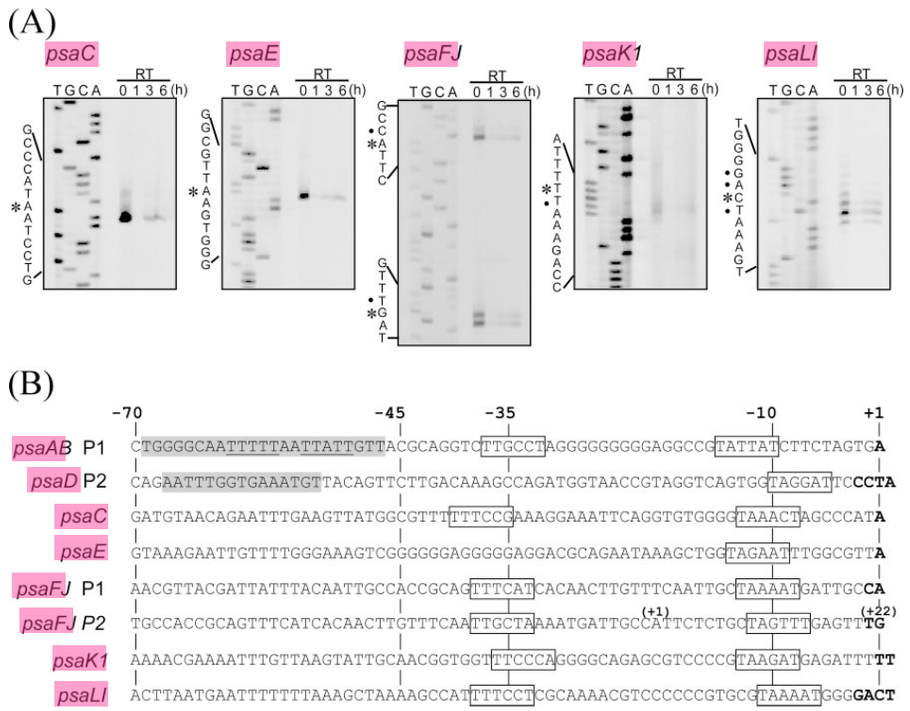


FIG. 3. Mapping of the 5′ ends of PSI transcripts. (A) Total RNA was isolated from the wild-type cells incubated under HL conditions for 0, 1, 3, and 6 h and used for primer extension analysis of *psaC*, *psaE*, *psaFJ*, *psaK1*, and *psaLI*. Detected 5′ ends of the major transcripts are indicated by asterisks, and those of minor ones are indicated by dots. (B) Nucleotide sequences of the core promoter and its upstream region of PSI promoters. Transcriptional start points are shown in boldface letters. 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.

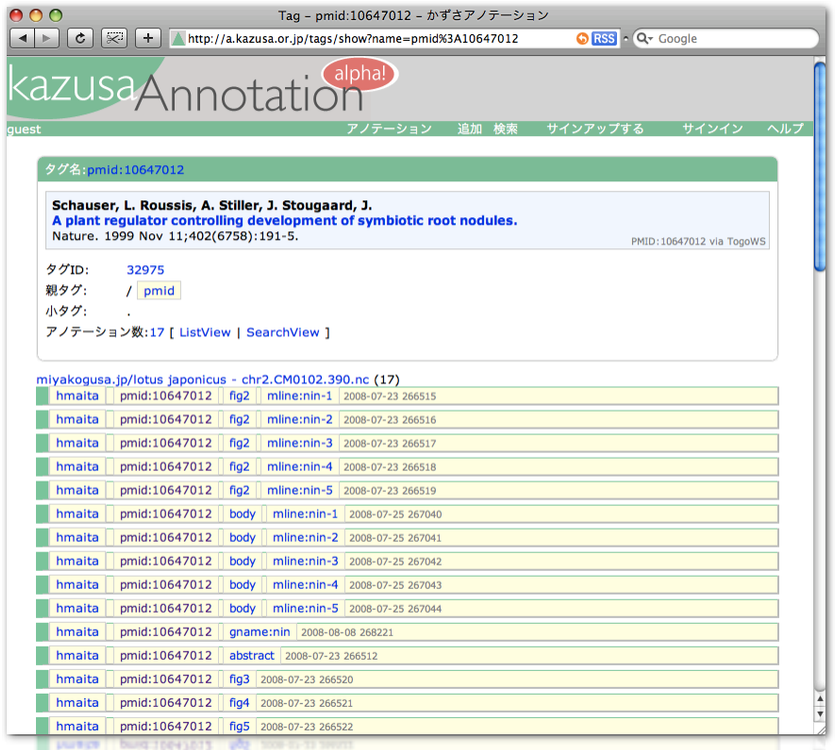
Effect of the −70 to −46 region on the promoter activity of PSI genes. Figure 4A shows the bioluminescence level of *Synechocystis* cells harboring PSI promoter-*luxAB* reporter genes with or without the upstream region under LL conditions. The reporter activities of the downstream promoter fragments 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* [$(8.2 \pm 0.2) \times 10^5$ relative units/OD_{730}] and *psaK1* [$(2.3 \pm 0.4) \times 10^5$ relative units/OD_{730}], whereas that of *psaLI* was significantly high [$(1.1 \pm 0.2) \times 10^7$ relative units/OD_{730}]. It is possible that the high activity of the *psaLI* 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 positive 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 *psaLI* was not enhanced as much by the upstream region (5.1-fold). As a result, similar promoter activity (around 5.0×10^7 relative units/OD_{730}) 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 [$(1.4 \pm 0.5) \times 10^8$ relative units/OD_{600}], 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 [$(2.4 \pm 1.0) \times 10^8$ relative units/OD_{600} 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 Cph1, phytochrome

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



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Gene Indexing 入力・公開状況

Organisms	Papers
Lotus japonicus	297
Mesorhizobium. loti MAFF303099	178
Sinorhizobium. meliloti st.1021	163
Bradyrhizobium japonicum USDA110	933
Rhizobium sp. NGR234	125
Rhizobium leguminosarum bv. viciae 3841	1,162
Anabaena sp. PCC 7120	588
Synechocuccus elongatus PCC 7942	449
Chlorobium tepidum TLS	174
Synechocystis sp. PCC 6803	1,490
Nostoc punctiforme ATCC 29133	54
Total	5,613

Data entries	145,890

9, Dec., 2009

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

OpenID認証

kazusa Annotation alpha!

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

かずさアノテーションはソーシャル・ゲノム・アノテーションツール。

検索　もっと検索する...

アノテーション	genes	タグ
249,082	26,764	36,968

トップ画面

最近のアノテーション

Genome:Synechocystis sp. PCC 6803/Photosystem II - KazusaWiki 97518 59 annotations
http://wiki.kazusa.or.jp/Genome:Synechocystis_sp._PCC_6803/Photosystem_II
hkane pmid:14670603 fig2
09:56:55

Genome:Synechococcus sp. PCC 7002/Photosystem II - KazusaWiki 97254 64 annotations
http://wiki.kazusa.or.jp/Genome:Synechococcus_sp._PCC_7002/Photosystem_II
hkane pmid:14670603 discussion
09:55:54

Genome:Synechocystis sp. PCC 6803/Photosystem II - KazusaWiki 97518 59 annotations
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Cyanobase/Synechocystis - syn:slr1604 493 91 annotations
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hkane pmid:14670603 gname:ftsH3
09:51:18

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Genome:Synechocystis sp. PCC 6803/Photosystem II - KazusaWiki wiki.kazusa.or.jp
59 annotations 新しいアノテーションを追加する
タグ pmid:15779895 1 conclusions 1 fig1 1 pmid:15491162 2 materials and methods 4 pmid:12427987 3 pmid:14761990 2 fig2 1 pmid:14670603 6 pmid:8425056 2 fig5 1 results 9 pmid:16349056 1 pmid:9274055 5 fig3 1 fig8 2 pmid:14728683 8 pmid:11557052 4 discussion 9 fig7 2 title 4 pmid:1421151 1 pmid:15653799 1 experimental procedures 1 pmid:8219045 8 pmid:19397890 2 pmid:16912048 8 table2 1 fig4 1 pmid:9414557 1 body 2 abstract 8 pmid:8425045 3 pmid:15697214 1 introduction 13

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yn　アノテーション　追加　検索　☆　遺伝子　論文　サインアウト　ヘルプ

Gene ID

6803:slr0473

bookmark先 URL

cyanobase/Synechocystis - s6803:slr0473 編集

タイトル:	cyanobase/Synechocystis - s6803:slr0473
URL	http://genome.kazusa.or.jp/cyanobase/Synechocystis/genes/slr0473
ページID:	69607
Gene names (3):	cph1 17 hik35 3 phy 1
PubMed IDs (52):	18799745 19 11806940 17 15641769 17 11560494 15 9342316 15 12047374 13 17199291 11 10613860 11 15774880 11 11277928 10 12010493 10 16751241 10 17034247 9 18000013 9 10949378 9 10978170 8 11029065 8 15938613 8 16539742 7 15757650 6 15291308 6 18621684 5 12913140 5 18571200 5 16868740 4 15350144 4 15653792 4 15944148 3 9097043 3 17720783 3 12446635 3 16096278 3 15699194 2 12480098 2 16887842 2 10716932 2 11555279 2 17211581 2 18419737 2 16533061 2 18606800 2 10420848 1 16452410 1 16853666 1 11289505 1 19351534 1 11299378 1 16228363 1 9278513 1 12240834 1 16585762 1 12039966 1

文献 PMID

PPI データ

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ユーザ（15）:	yoshimura_h 128 Cyanogene 73 yanakahira 59 synobu 45 sakudesu 23 hkane 17 CYORF 13 Kazusa 9 takutsu 8 makotokasai 6 mnaka 5 category 2 kashima 2 mitsuyo 1 yn 1
アノテーション:	392 エントリ [SearchView | TableView | GeneIndexingView | IndexedRefView | ReferenceView]
タグ（146）:	results 33 discussion 30 introduction 29 abstract 22 materials and methods 21 fig3 20 fig2 16 fig1 16 fig4 15 CyanoGenes:1759 15 syn:slr0473 13 table1 12 CyanoGenes:125 10 CyanoGenes:297 10 CyanoGenes:403 10 CyanoGenes:298 10 table2 10 CyanoGenes:558 9 CyanoGenes:638 9 fig5 9 CyanoGenes:Contact 7 CyanoGenes:Date 7 CyanoGenes:GeneticBackground 7 CyanoGenes:Investigator 7 CyanoGenes:AdditionalInformation 7 CyanoGenes:DrugMarker 6 table3 5 Category:C 5 CyanoGenes:DNA:no 5 fig7 5 CyanoGenes:Segregation 5 fig6 5 title 4 CyanoGenes:GeneName 4 fig8 4 CyanoGenes:Mutant:yes 4 table4 3 CyanoGenes:Mutant:no 3 body 3 CyanoGenes:MutantName 3 CYORF:CYREF 3 Category:A 3 fig10 3 fig9 2 acknowledgement 2 fig11 2 table5 2 gene 2 results and discussion 2 conclusion 2 CyanoGenes:MutationType 2 CYORF:uniprot_acc 1 Category:D 1 result and discussion 1 CYORF:kid 1 CYORF:start_pos 1 CYORF:pos 1 Experimental Section 1 CYORF:definition 1 scheme1 1 UniProt:Q55168 1 CYORF:uniprot_def 1 CyanoGenes:MedlineID 1 CYORF:length 1 CyanoGenes:Phenotype:no 1 figure 1 CYORF:orf_id 1 CYORF:cyanobase_def 1 CyanoGenes:DrugDirection 1 result 1 fig12 1 CYORF:genename 1 CyanoGenes:ProductName 1 CyanoGenes:DNA:yes 1 CyanoGenes:Function 1
編集	アノテーションを編集

キュレータ名

タグ一覧

ここをクリック→次スライド

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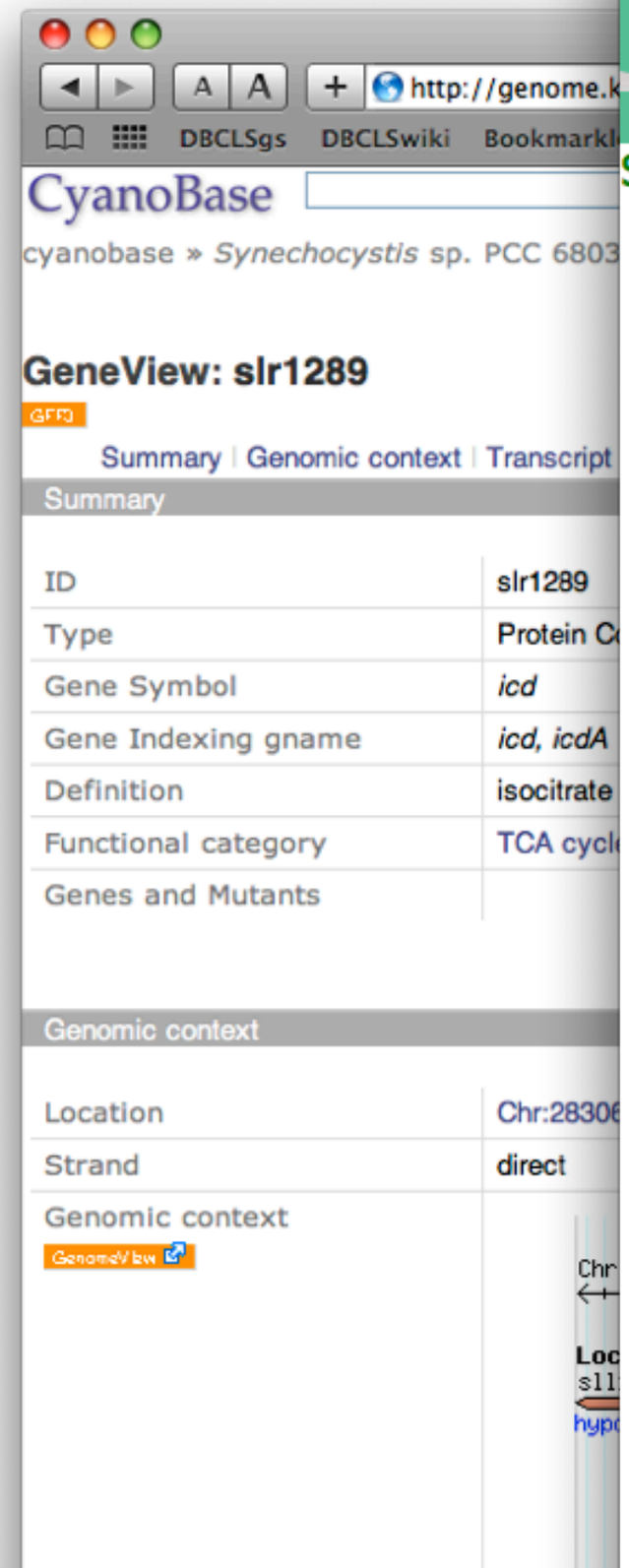
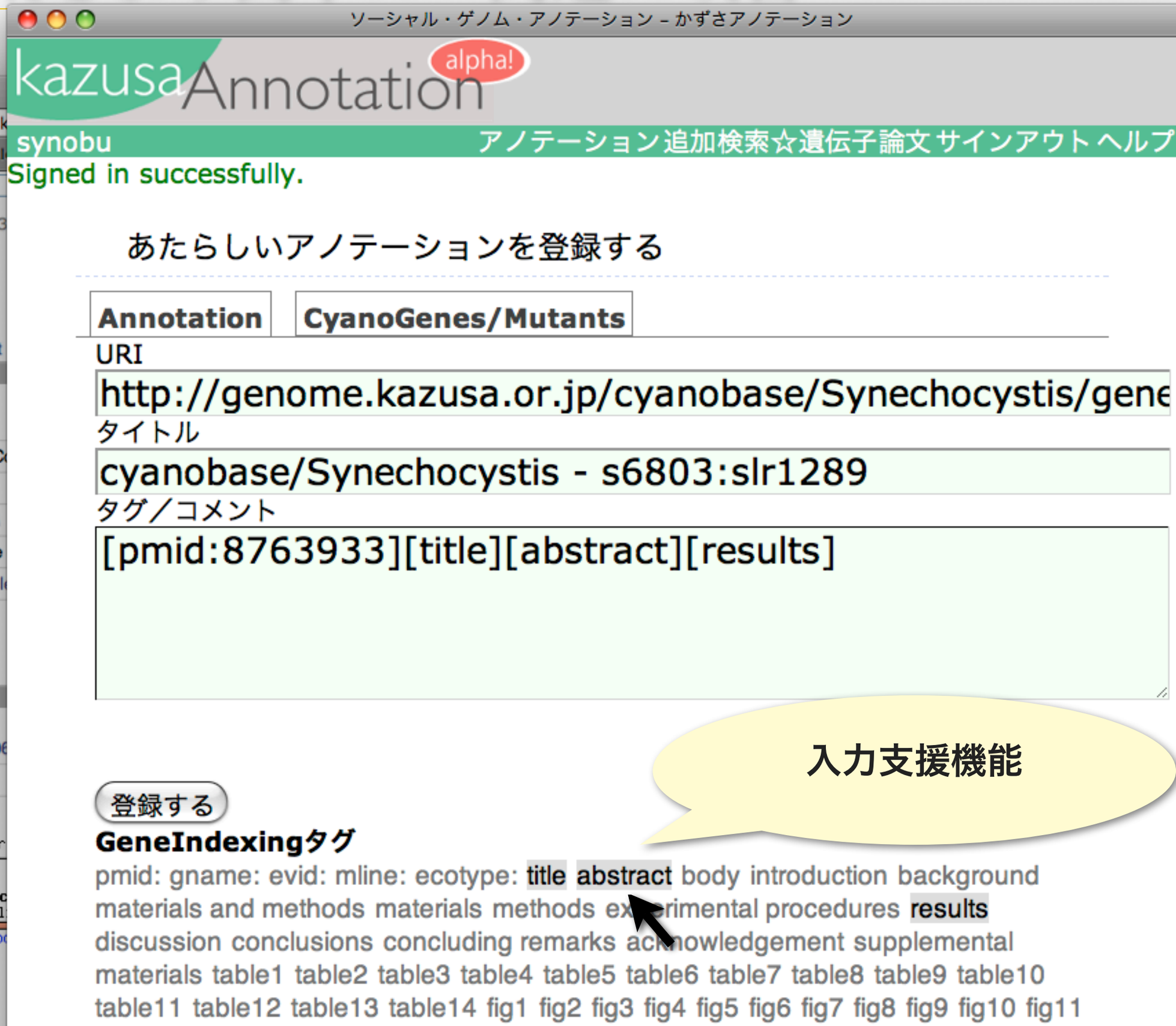
入力編集をより簡単に・高速に改善





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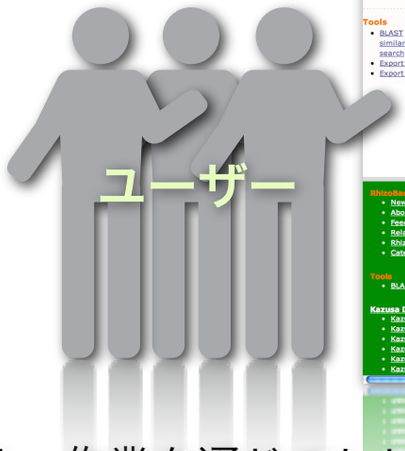
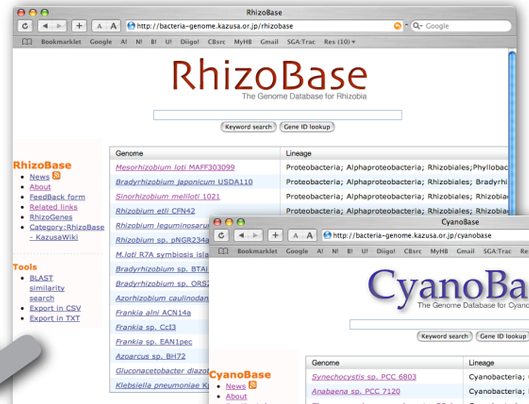
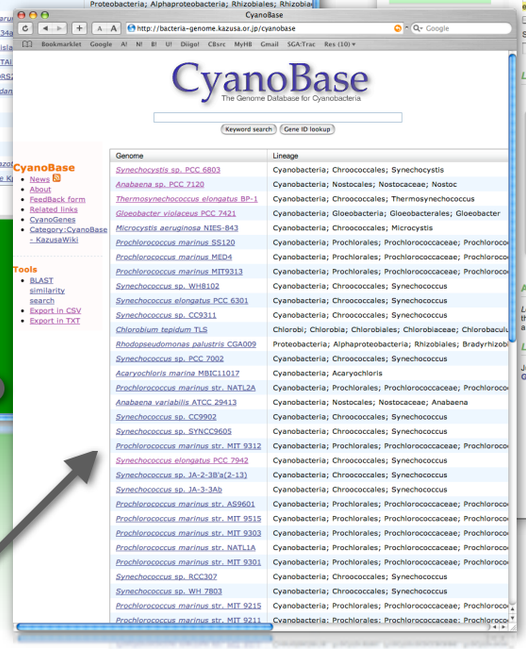


Annotation作業を通じてレビュー

KDRI DB Resources





システム開発者

KazusaAnnotation

Annotation情報の統合

Annotation Meeting

物理的・仮想的

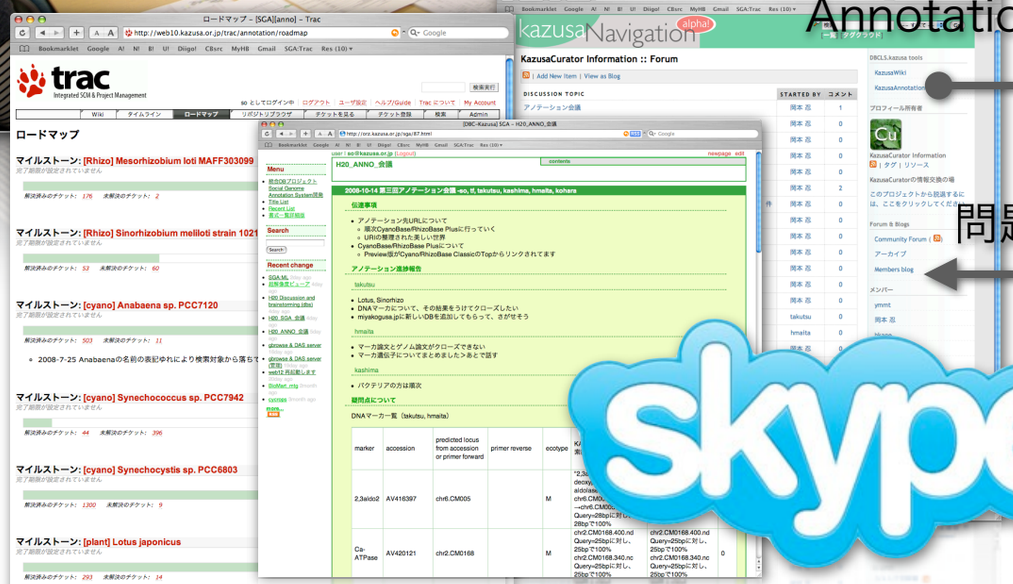
機能・内容改善要望

遠隔地キュレーター

USTREAM.TV

Annotation, Curationデータ保存

問題発見, 問題共有



蓄積した情報の利用・閲覧方法の開発

CyanoBase search in Gene symbols, Defi

cyanobase » *Synechocystis* sp. PCC 6803 » genes » slr0473

GeneView: slr0473

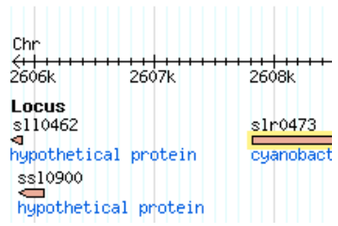
GFF3

Summary | Genomic context | Transcript | Peptide | Protein domains | Mu

Summary

ID	slr0473
Type	Protein Coding
Gene Symbol	*cph1, hik35*
Gene Indexing gname	*cph1, hik35, phy*
Definition	cyanobacterial phytochrome 1, two-compc
Functional category	Regulatory functions
Genes and Mutants	Gene: by Teruo Ogawa (1998-04-15) Gene: phy by Masahiko Ikeuchi (1999-09- Gene: phy by Masahiko Ikeuchi (1999-09- Gene: Hik35 by Iwane Suzuki (2000-05-25 Mutant: Δphytochrome by Teruo Ogawa (Mutant: SK35 by Teruo Ogawa (2003-05-(Mutant: Δhik35 by Iwane Suzuki (2007-11

Genomic context

Location	Chr:2607812..2610058
Strand	direct
Genomic context GenomeView	

ゲノムデータベースに
“Gene Indexing” した情報を
即時公開

References

? | +/- | Top

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Ultrafast dynamics of phytochrome from the cyanobacterium synechocystis, reconstituted with phycocyanobilin and phycoerythrobilin.
Biophys J. 2002 Feb;82(2):1004-16. PMID:11806940 | Abstract | MeSH | Related Articles | Sections | Gene Index |
Ti Ab In Mm Re Di Co Fi Ta | abstract introduction materials and methods results discussion table1 fig2 fig3 fig4 fig5 fig6 fig7 fig8 fig9 fig10 fig11 fig12

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Biochemistry. 2005 Jan 18;44(2):450-61. PMID:15641769 | Abstract | MeSH | Related Articles | Sections | Gene Index |
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Light-induced proton release and proton uptake reactions in the cyanobacterial phytochrome Cph1.
Biochemistry. 2001 Sep 25;40(38):11460-71. PMID:11560494 | Abstract | MeSH | Related Articles | Sections | Gene Index |
Ti Ab In Mm Re Di Co Fi Ta | abstract introduction materials and methods results discussion table1 table2 table3 fig1 fig2 fig3 fig4 fig5

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Light-dependent regulation of cyanobacterial phytochrome expression.
J Bacteriol. 2000 Jan;182(1):38-44. PMID:10613860 | Abstract | MeSH | Related Articles | Sections | Gene Index |
Ti Ab In Mm Re Di Co Fi Ta | abstract introduction materials and methods results discussion fig1 fig2 fig3 fig4 fig5 fig6

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Plant Mol Biol. 2000 May;43(1):113-20. PMID:10949378 | Abstract | MeSH | Related Articles | Sections | Gene Index |
Ti Ab In Mm Re Di Co Fi Ta | abstract introduction materials and methods results discussion table1 fig1 fig2 fig3 fig4

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Formation of the early photoproduct lumi-R of cyanobacterial phytochrome cph1 observed by ultrafast mid-infrared spectroscopy.
J Am Chem Soc. 2007 Jan 10;129(1):126-32. PMID:17199291 | Abstract | MeSH | Related Articles | Sections | Gene Index |
Ti Ab In Mm Re Di Co Fi Ta | Experimental Section scheme1 figure title abstract introduction results discussion table1 fig1 fig2 fig3 fig4

8. Wilde, A. Fiedler, B. Borner, T.
The cyanobacterial phytochrome Cph2 inhibits phototaxis towards blue light.
Mol Microbiol. 2002 May;44(4):981-8. PMID:12010493 | Abstract | MeSH | Related Articles | Sections | Gene Index |
Ti Ab In Mm Re Di Co Fi Ta | abstract introduction materials and methods results discussion fig1 fig3 fig4 fig5 fig6

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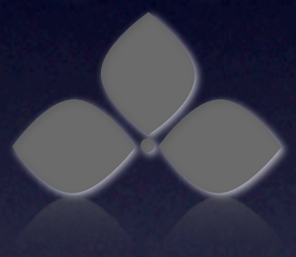
Pleiotropic effect of a histidine kinase on carbohydrate metabolism in Synechocystis sp. strain PCC 6803 and its requirement for heterotrophic growth.
J Bacteriol. 2005 Apr;187(7):2368-76. PMID:15774880 | Abstract | MeSH | Related Articles | Sections | Gene Index |
Ti Ab In Mm Re Di Co Fi Ta | gname:cph1 abstract introduction materials and methods results discussion table1 table2 fig2 fig3 fig5

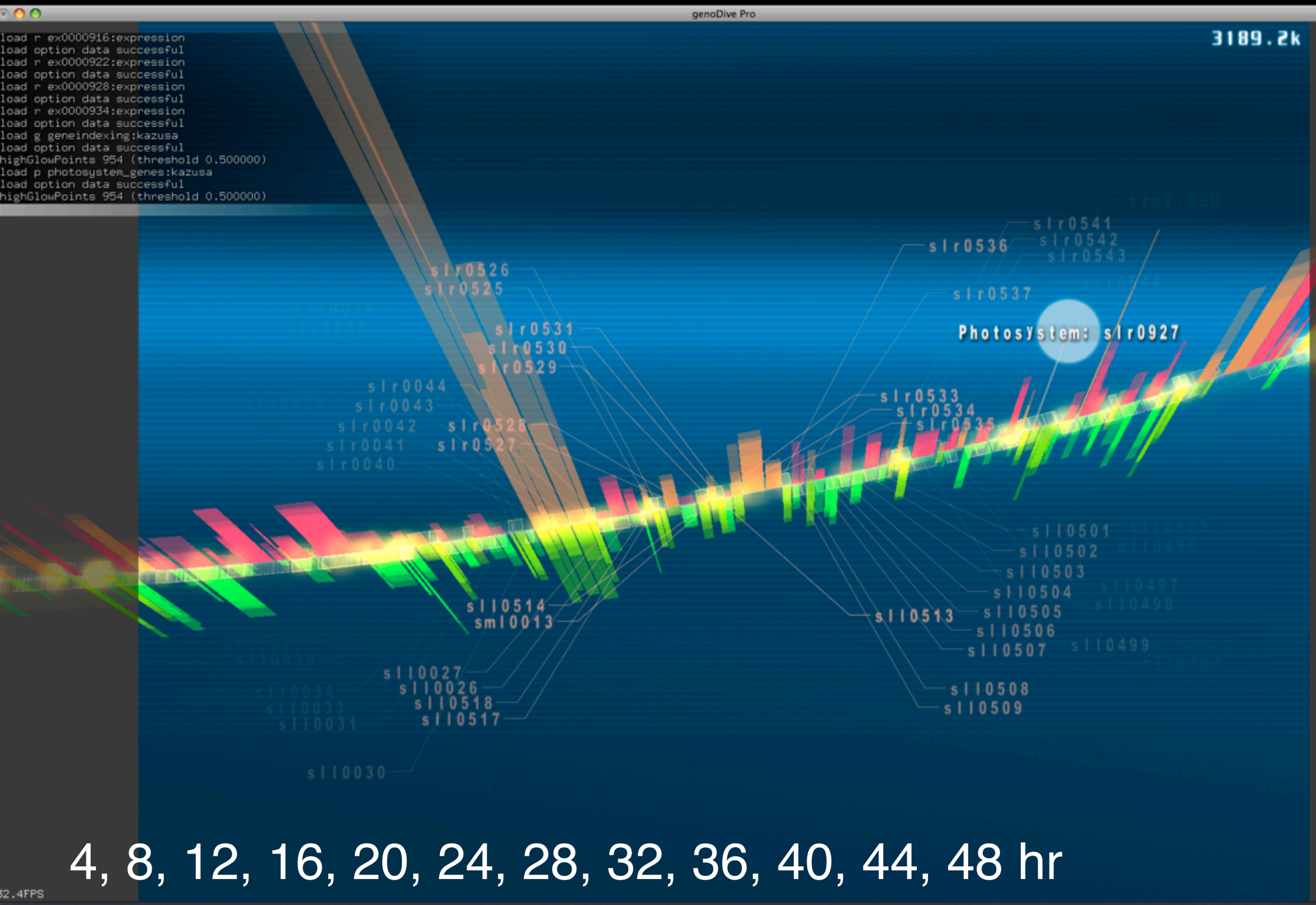
10. Essen, L. O. Mailliet, J. Hughes, J.
The structure of a complete phytochrome sensory module in the Pr ground state.
Proc Natl Acad Sci U S A. 2008 Sep 23;105(38):14709-14. Epub 2008 Sep 17. PMID:18799745 | Abstract | MeSH | Related Articles | Sections | Gene Index |
Ti Ab In Mm Re Di Co Fi Ta | gname:cph1 results and discussion result and discussion title abstract introduction materials and methods acknowledgement fig1 fig2 fig3 fig4

11. Hubschmann, T. Borner, T. Hartmann, E. Lamparter, T.

DAS Viewer



genoDive Pro / Eu

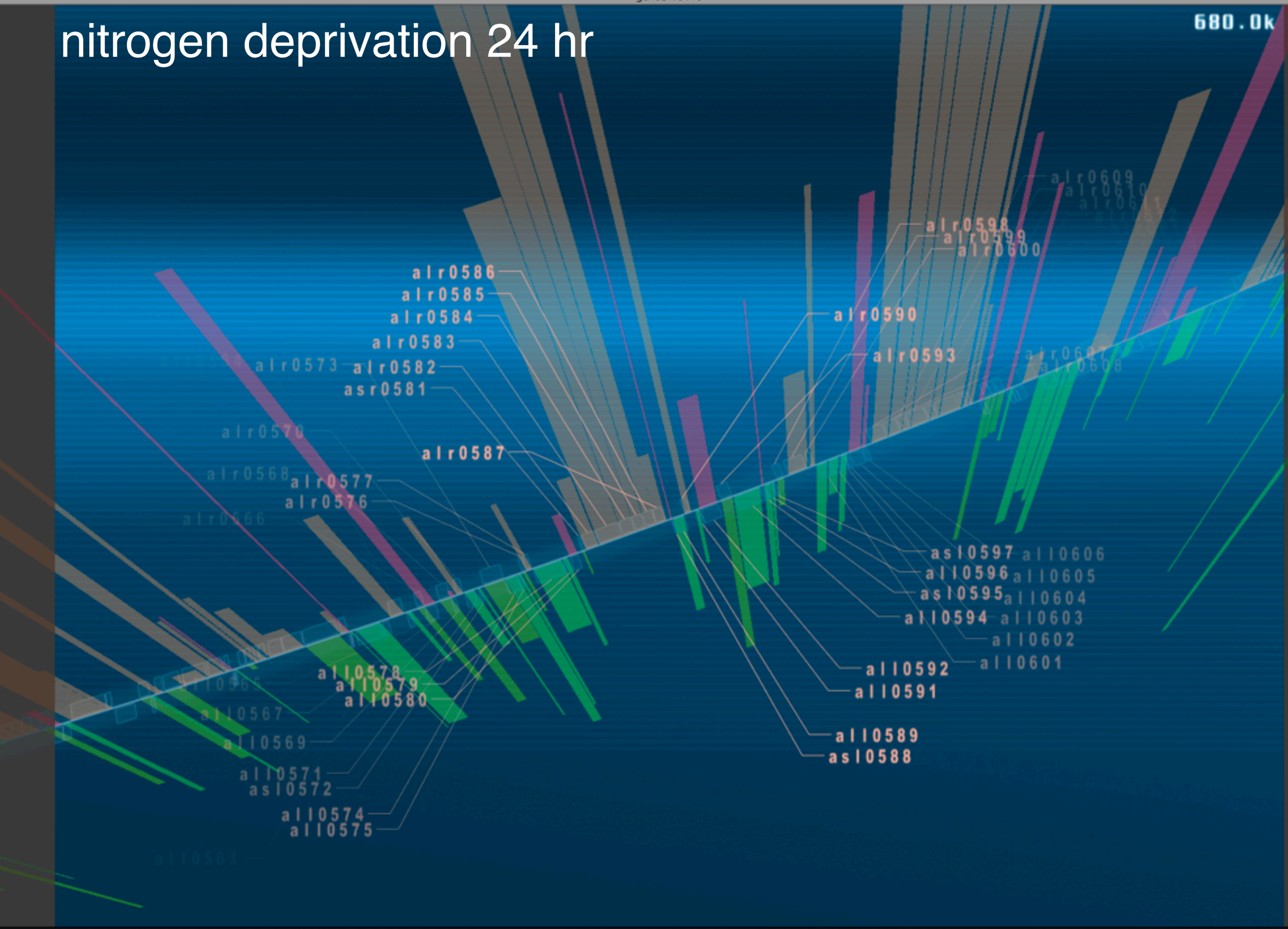


4, 8, 12, 16, 20, 24, 28, 32, 36, 40, 44, 48 hr

after transfer to continuous light condition_1

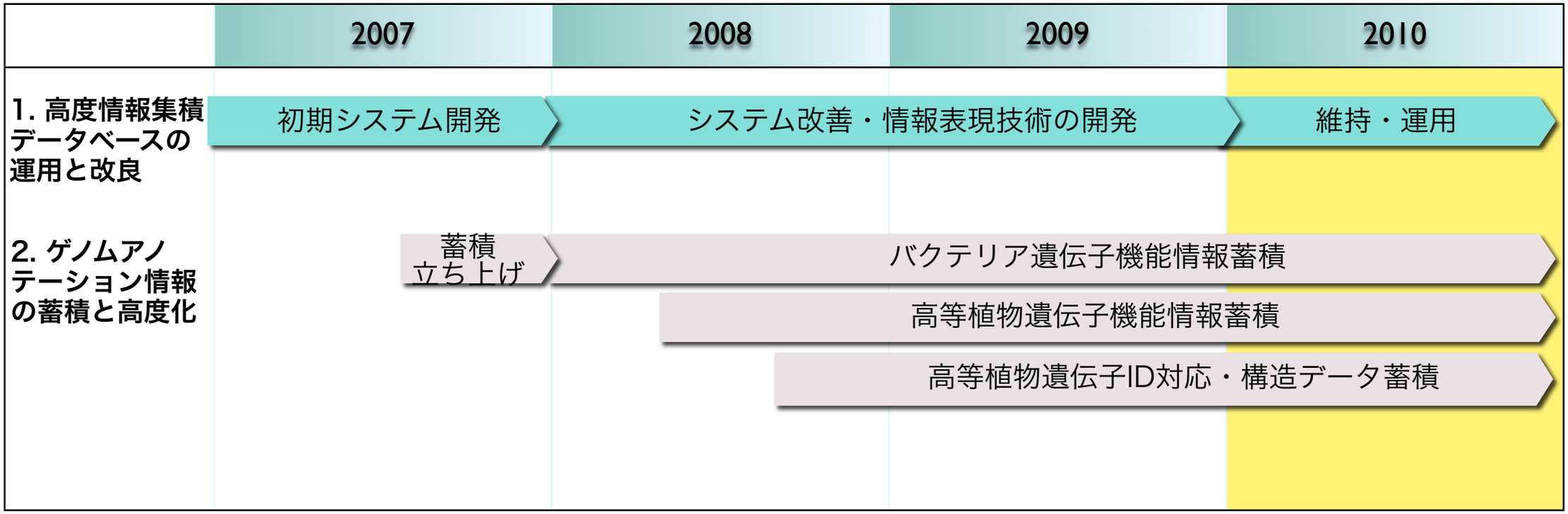
Kucho et. al J Bacteriol. 2005 Mar;187(6):2190-9.

nitrogen deprivation 24 hr



Ehira et al. Mol Microbiol. 2006 Mar;59(6):1692-703.

H22 (2010)年度の重点は新規開発から運用・改善のための開発と蓄積公開へ



- 維持を容易にするための開発
- 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の結合
- アノテーション手法の改善

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実施体制

- 中村保一 (遺伝研; かずさDNA研特別客員研究員)
- 岡本忍 (DBCLS)
- 藤沢貴智 (かずさDNA研・統合DBプロジェクト研究員)
- 中尾光輝 (DBCLS)

- 遠隔雇用キュレータ（下線はDNA研雇用・青字は男性）
  - 博士: 吉村（東京） 山本（京都） 矢野（川崎）
  - 修士: 谷中（つくば） 阿久津（木更津） 鐘ケ江（東京） 笠井（つくば）

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