Critical Roles of Iron and Other Metals in Algal Productivity

Metal requirements of the photosynthetic apparatus

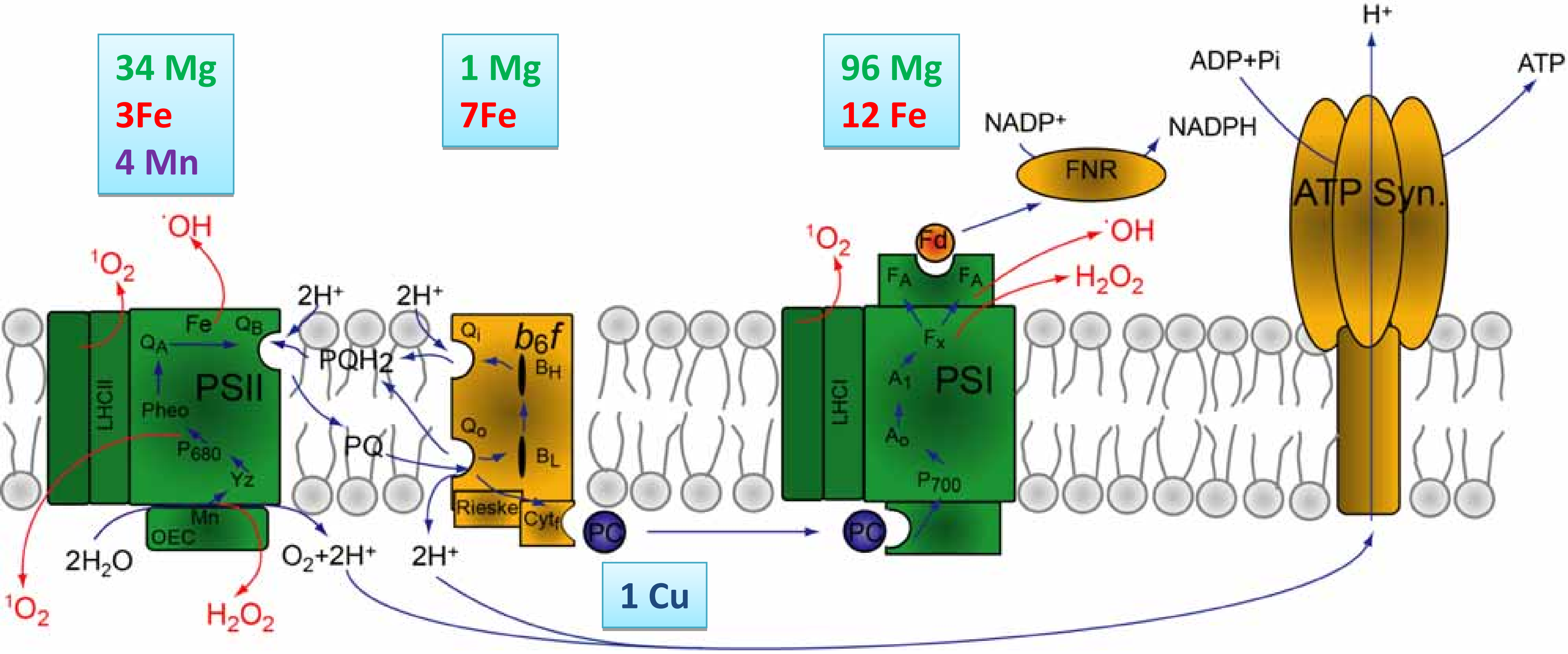
Reactive oxygen species: production hot sports in the photosynthetic apparatus

Mn: *Synechocystis* 6803 1x10^6, *Rhodobacter capsulatus* 1x10^4 , *E. coli* 1x10^4 atoms/cell

(Keren et al. 2002, Finney and O'Halloran 2003, Shcolnick et al. 2007)

Fe: *Synechocystis* 6803 5x10^6, *E. coli* 1x10^5 atoms/cell

(Keren et al. 2004, Finney and O'Halloran 2003)



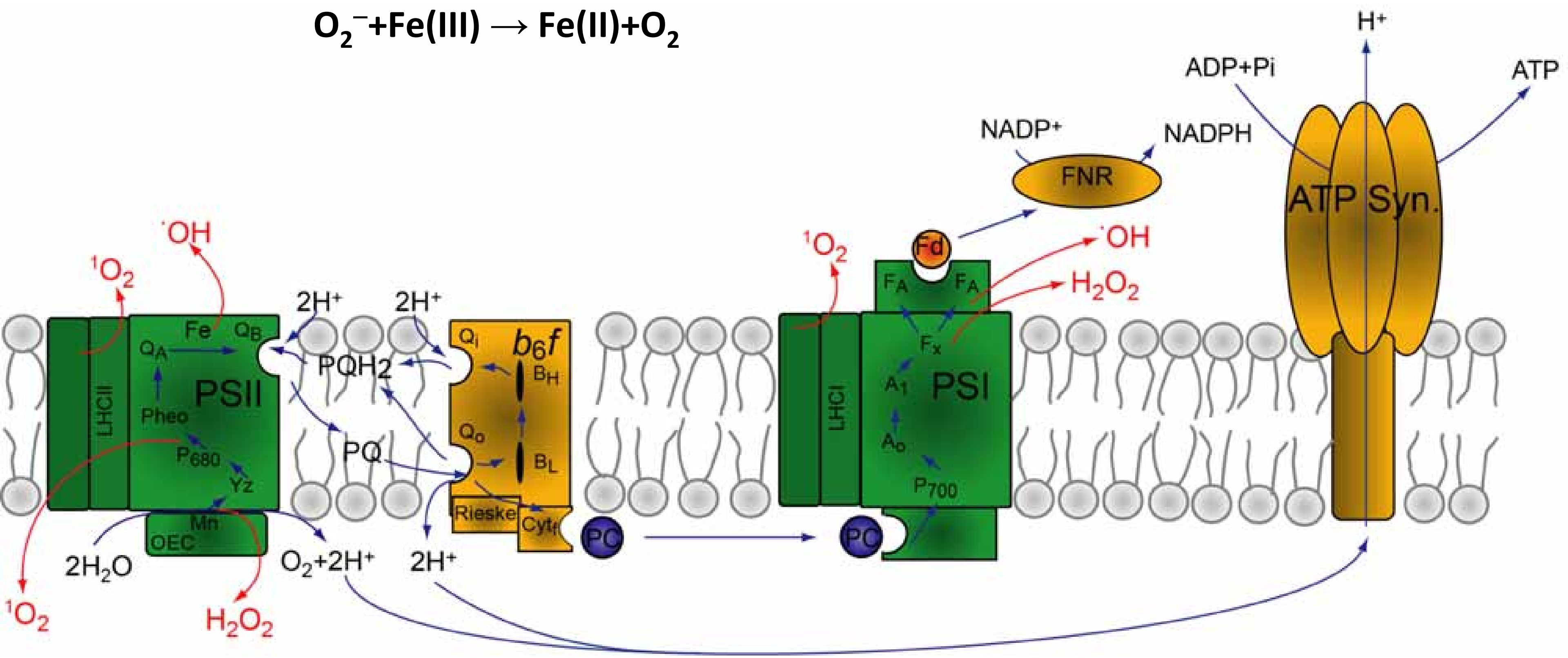
Iron is the forth most abundant element in the Earth's crust.

Fe(III) is virtually insoluble at neutral pH in the presence of oxygen.

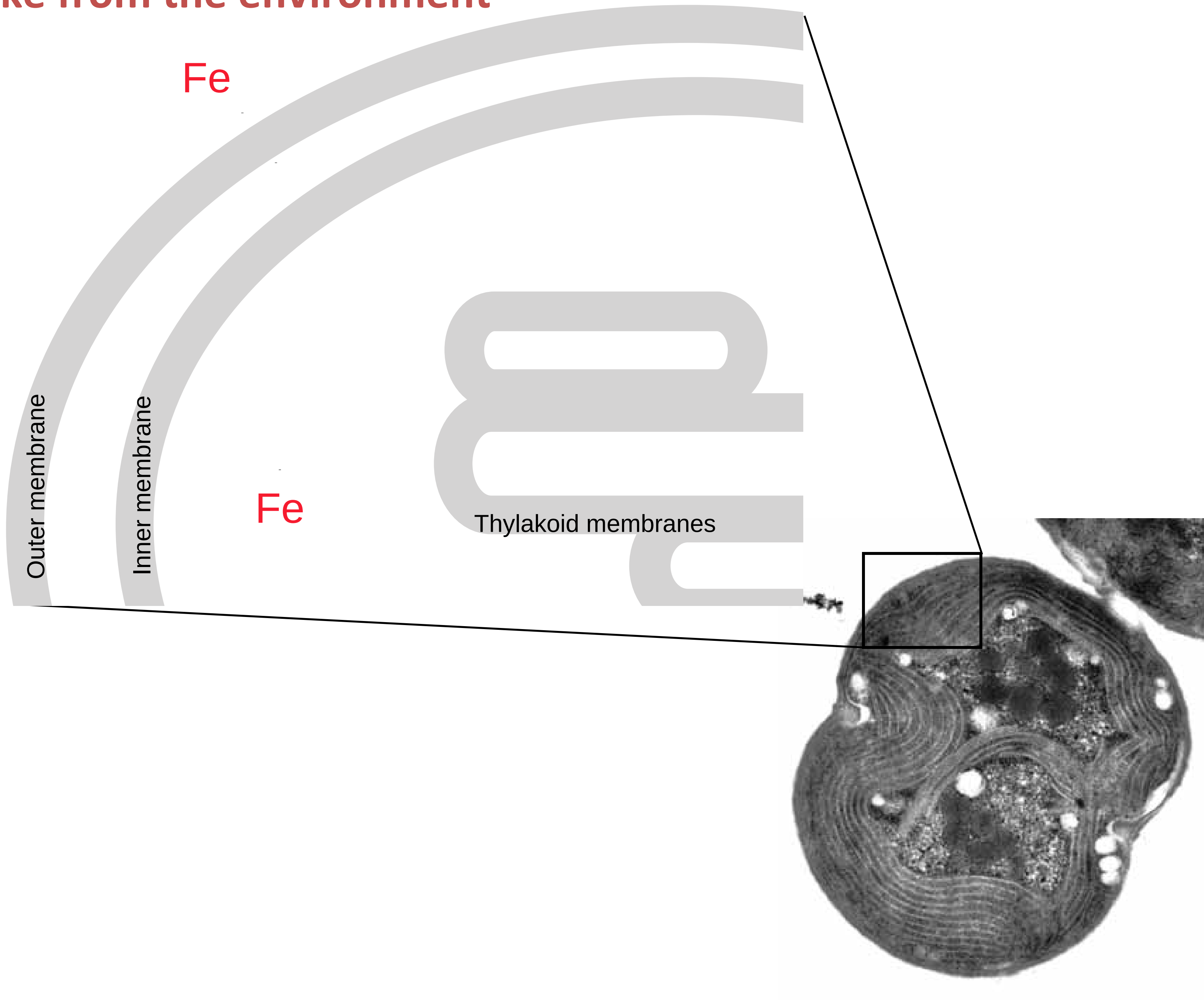
Fe(II) is soluble but prone to react with reactive oxygen species.

$H_2O_2 + Fe(II) \rightarrow Fe(III) + OH^- + OH^\cdot$ (Fenton reaction)

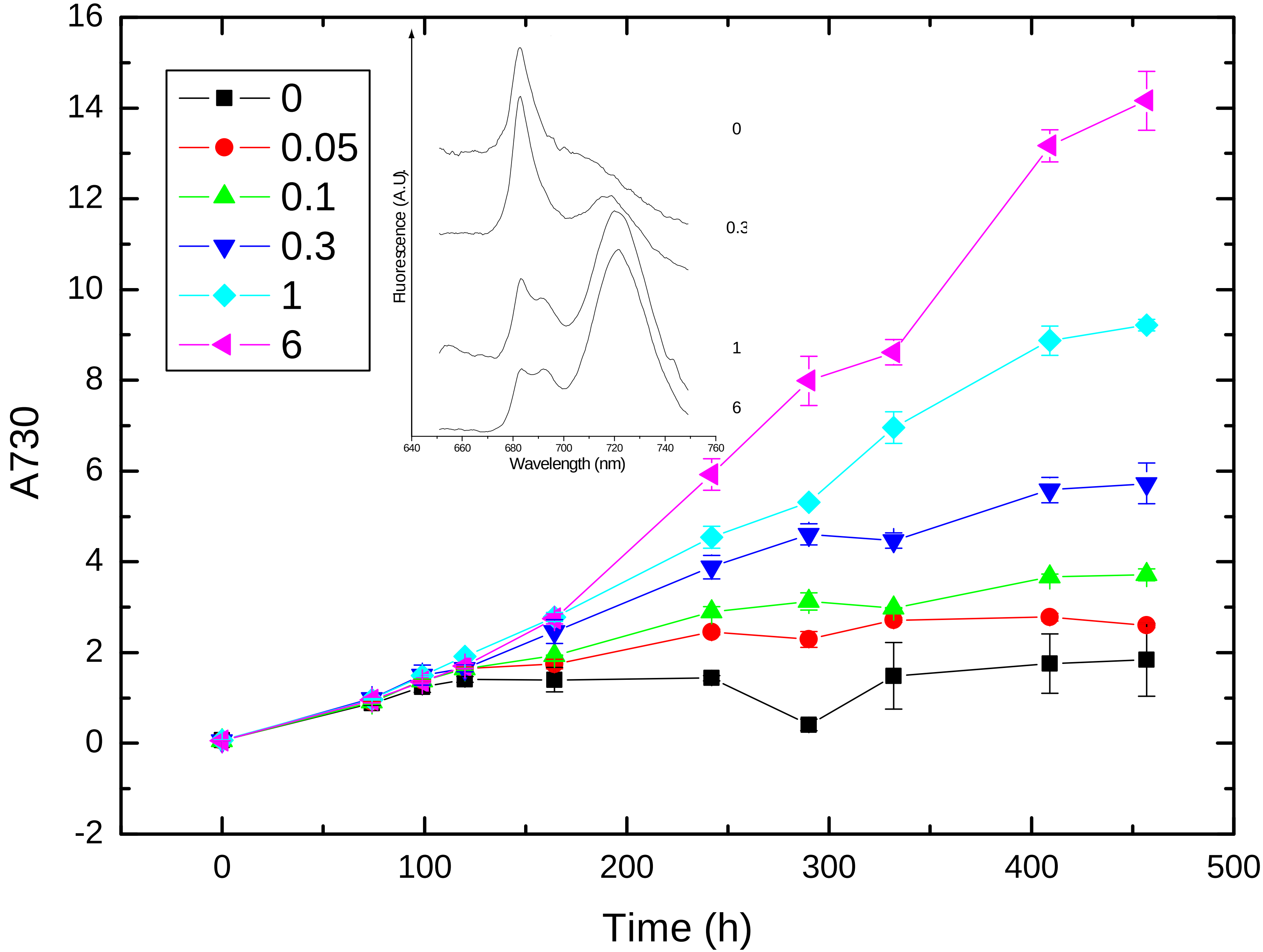
$O_2^- + Fe(III) \rightarrow Fe(II) + O_2$



Iron uptake from the environment

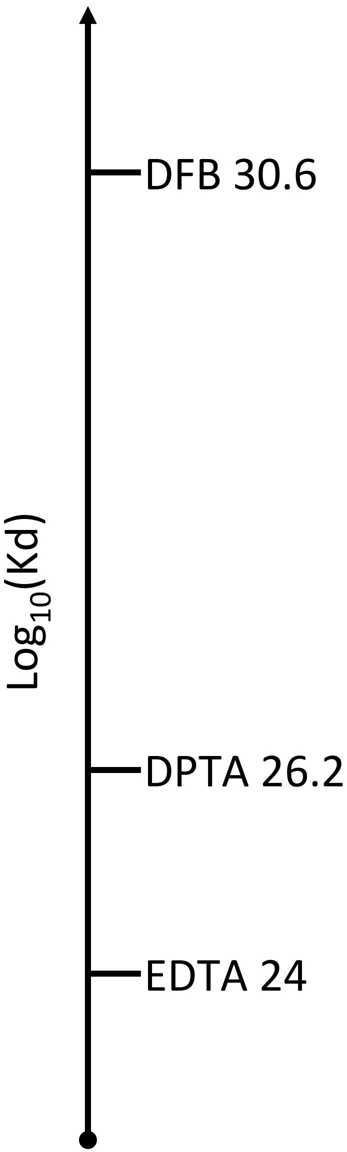


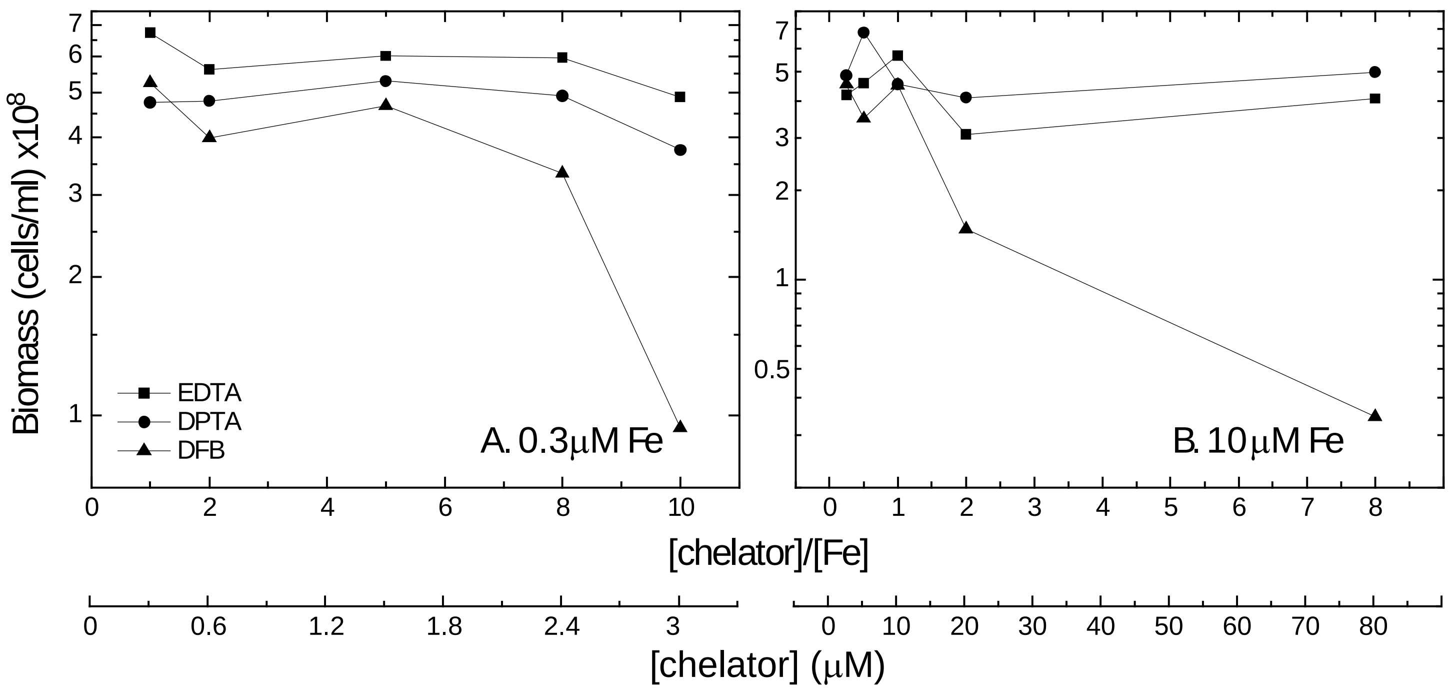
Iron uptake from the environment



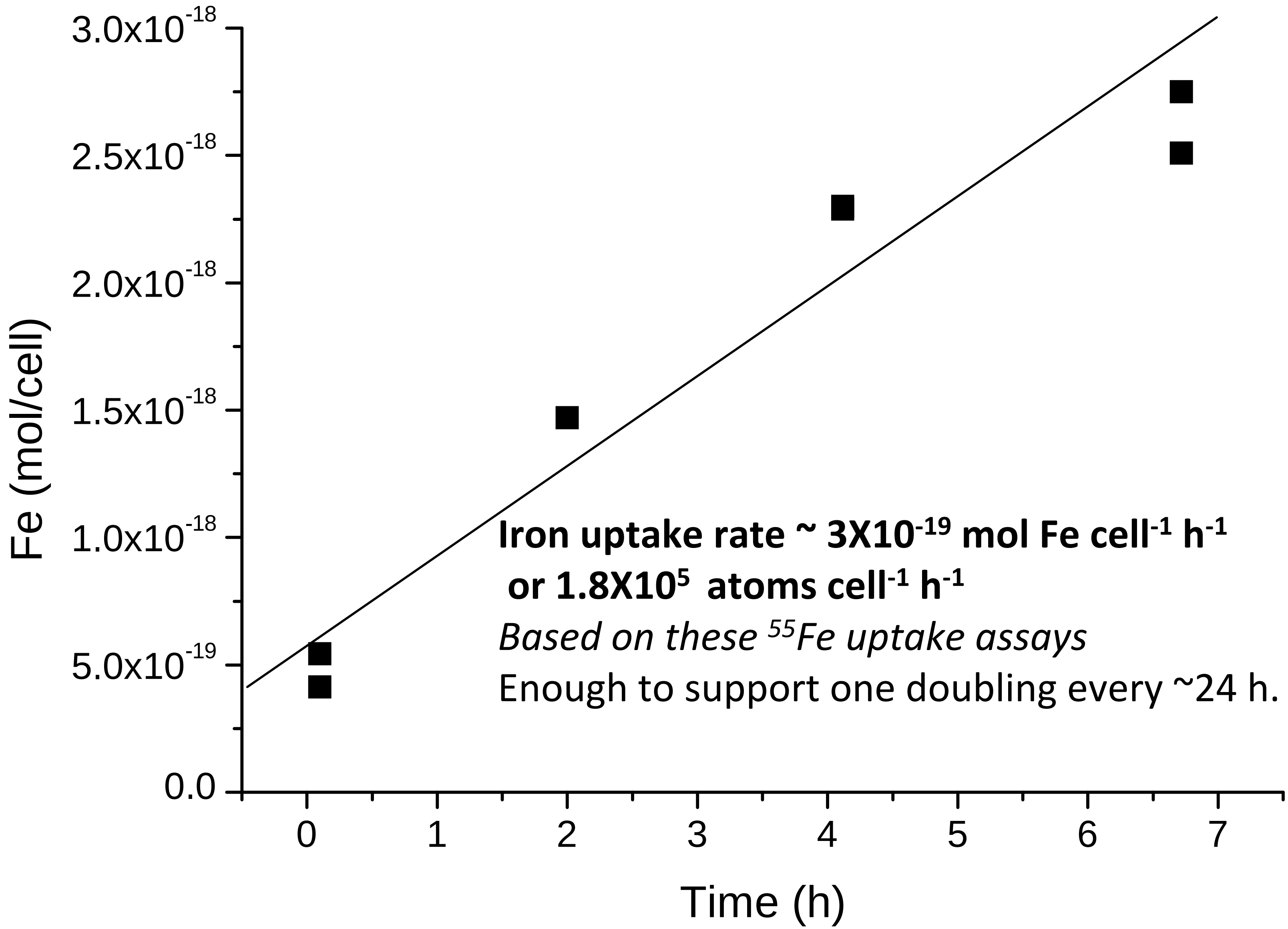
Uptake from the environment

Iron limitation by chelators

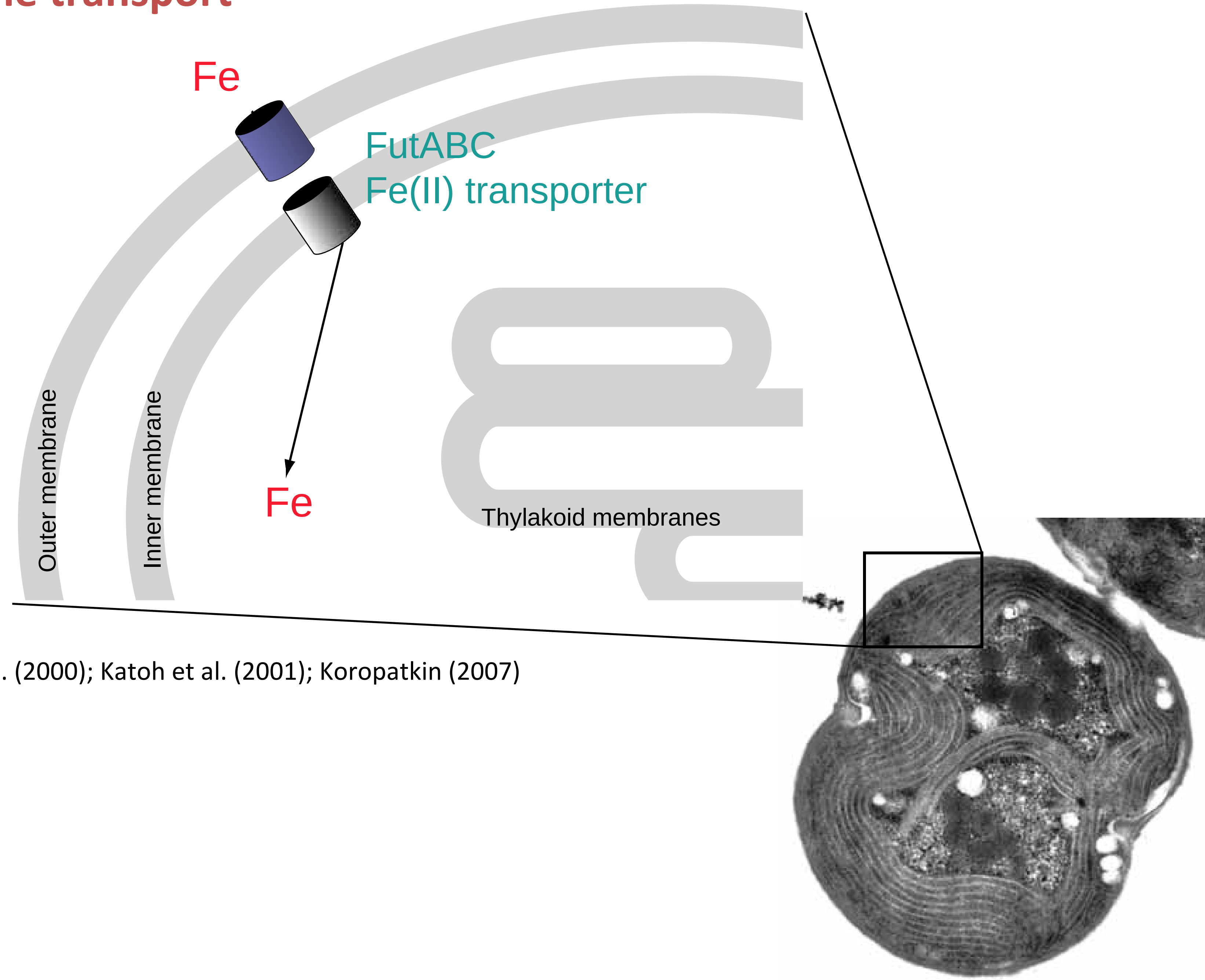




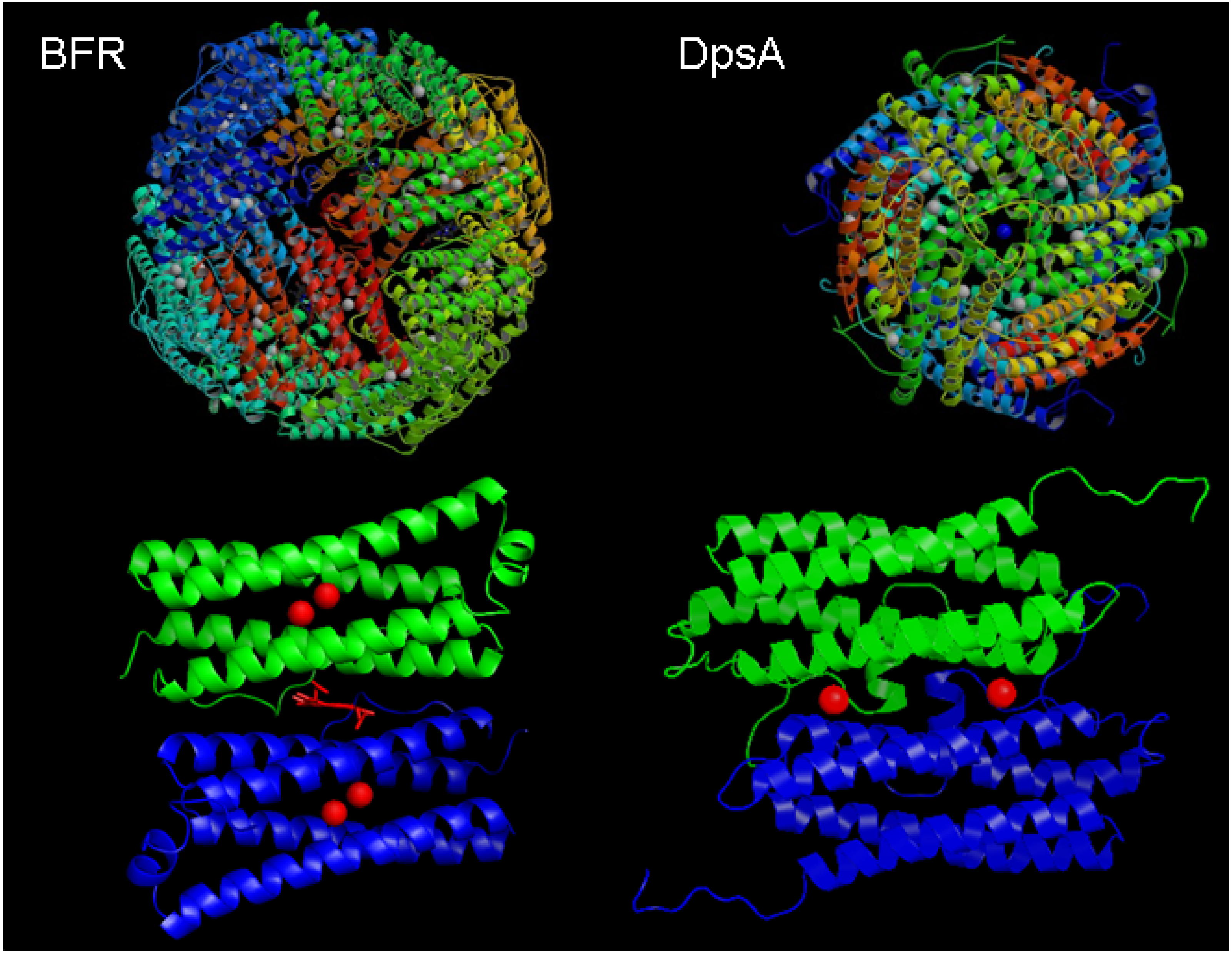
Uptake from the environment
Iron transport rates



Membrane transport



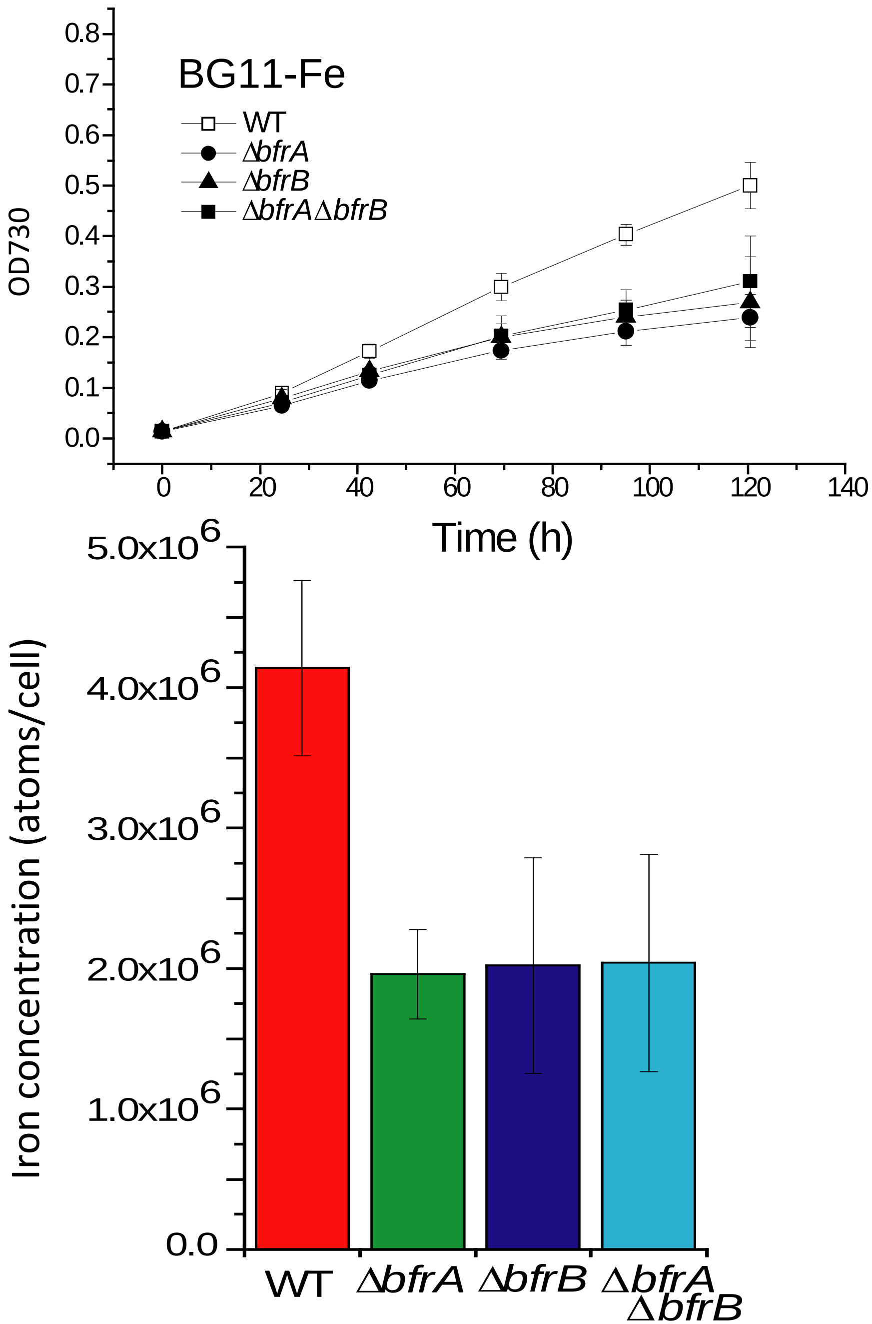
Katoh et al. (2000); Katoh et al. (2001); Koropatkin (2007)



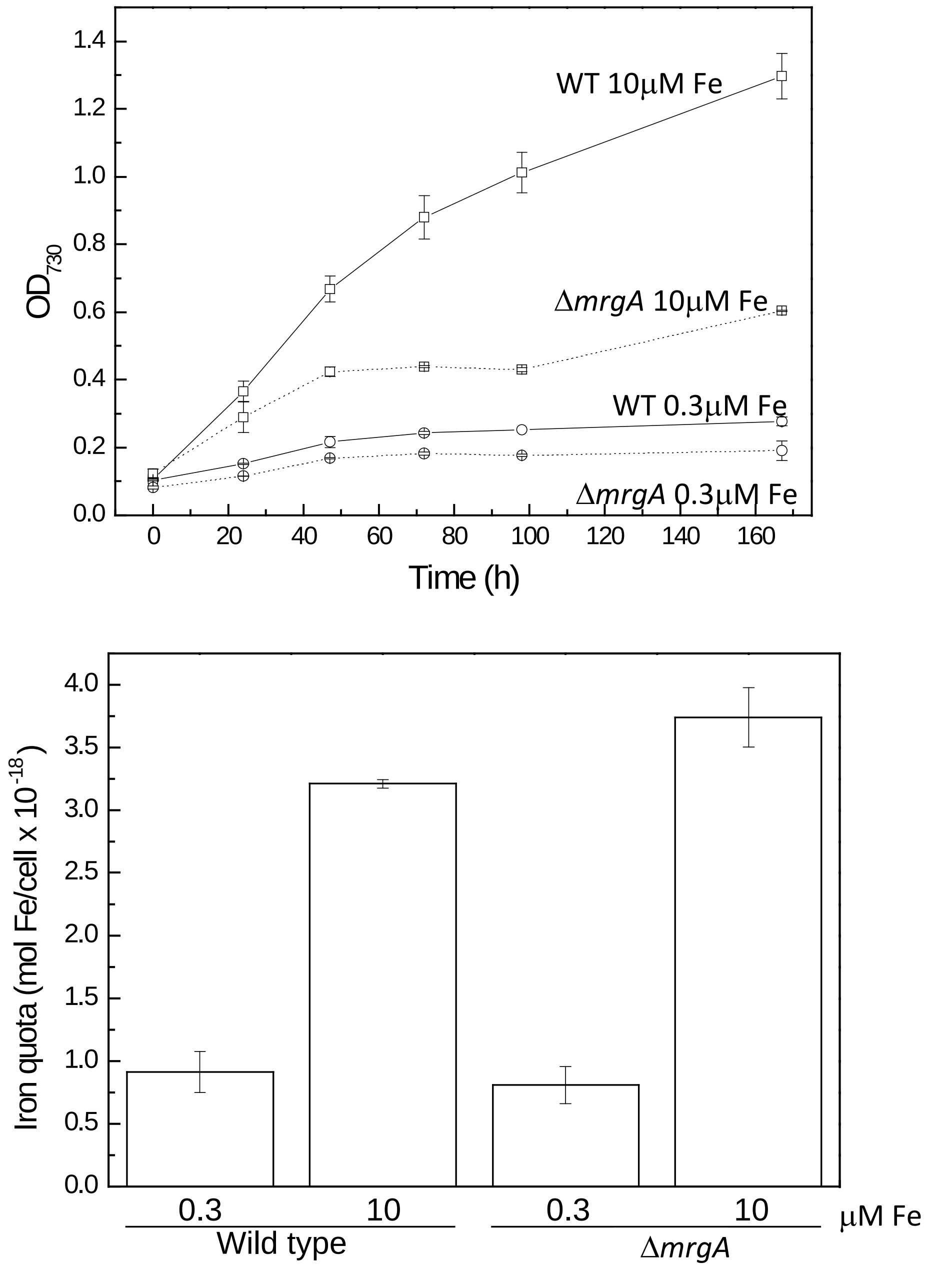
1BFR (Frolow et al., 1994) and 1MOJ (Zeth et al., 2004)

$2Fe(II) + O_2 + 4H_2O \rightarrow 2Fe(O)OH(s) + H_2O_2 + 4H^+$

$2Fe(II) + H_2O_2 + 2\,H_2O \rightarrow 2Fe(O)OH(s) + 4H^+$



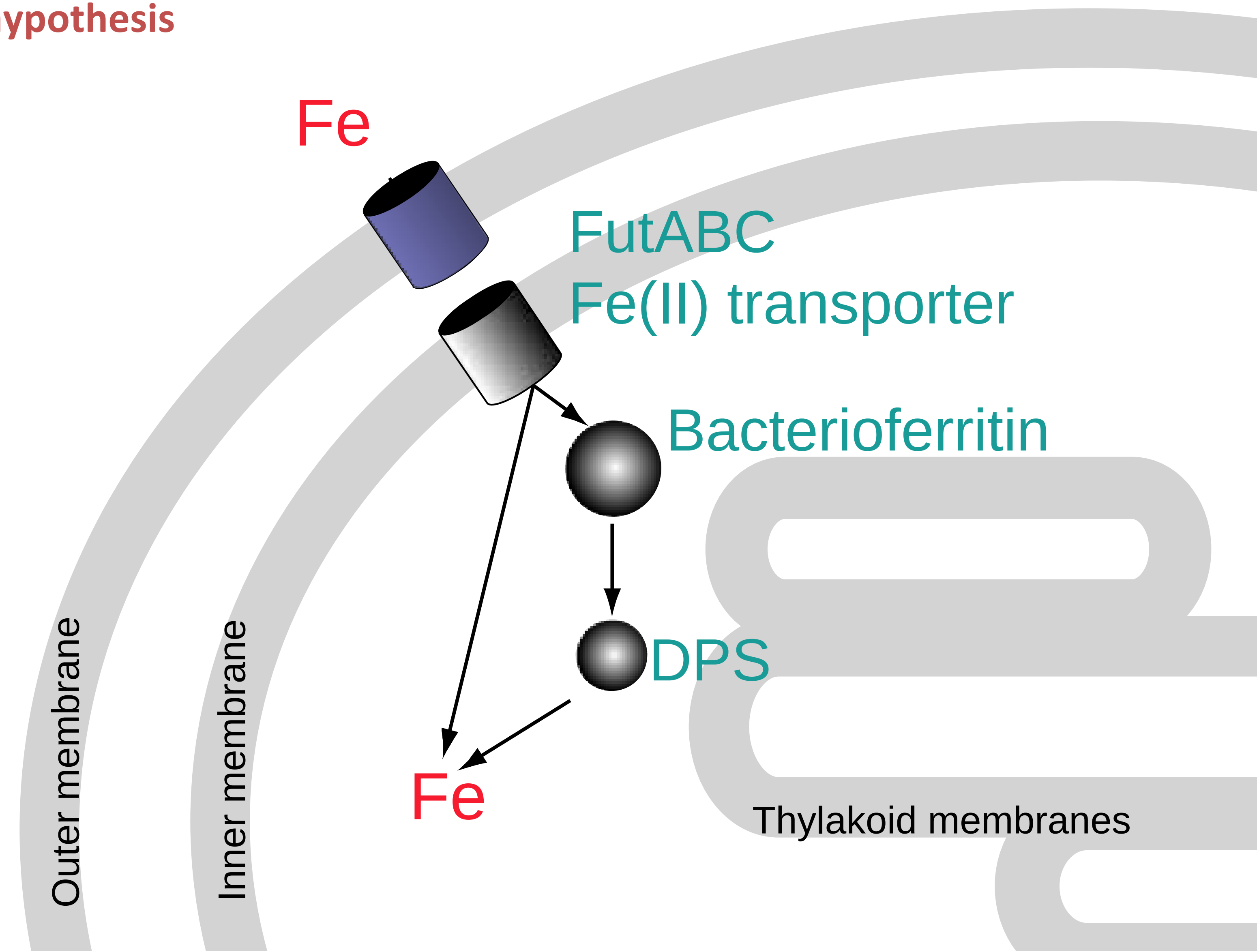
BG11-Fe
WT
ΔbfrA
ΔbfrB
ΔbfrAΔbfrB
OD730
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0
20
40
60
80
100
120
140
Time (h)
Iron concentration (atoms/cell)
0.0
1.0x10^6
2.0x10^6
3.0x10^6
4.0x10^6
5.0x10^6
WT
ΔbfrA
ΔbfrB
ΔbfrA ΔbfrB



WT 10μM Fe
ΔmrgA 10μM Fe
WT 0.3μM Fe
ΔmrgA 0.3μM Fe
OD730
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
0
20
40
60
80
100
120
140
160
Time (h)
Iron quota (mol Fe/cell x 10^-18)
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0
0.3
10
0.3
10
μM Fe
Wild type
ΔmrgA

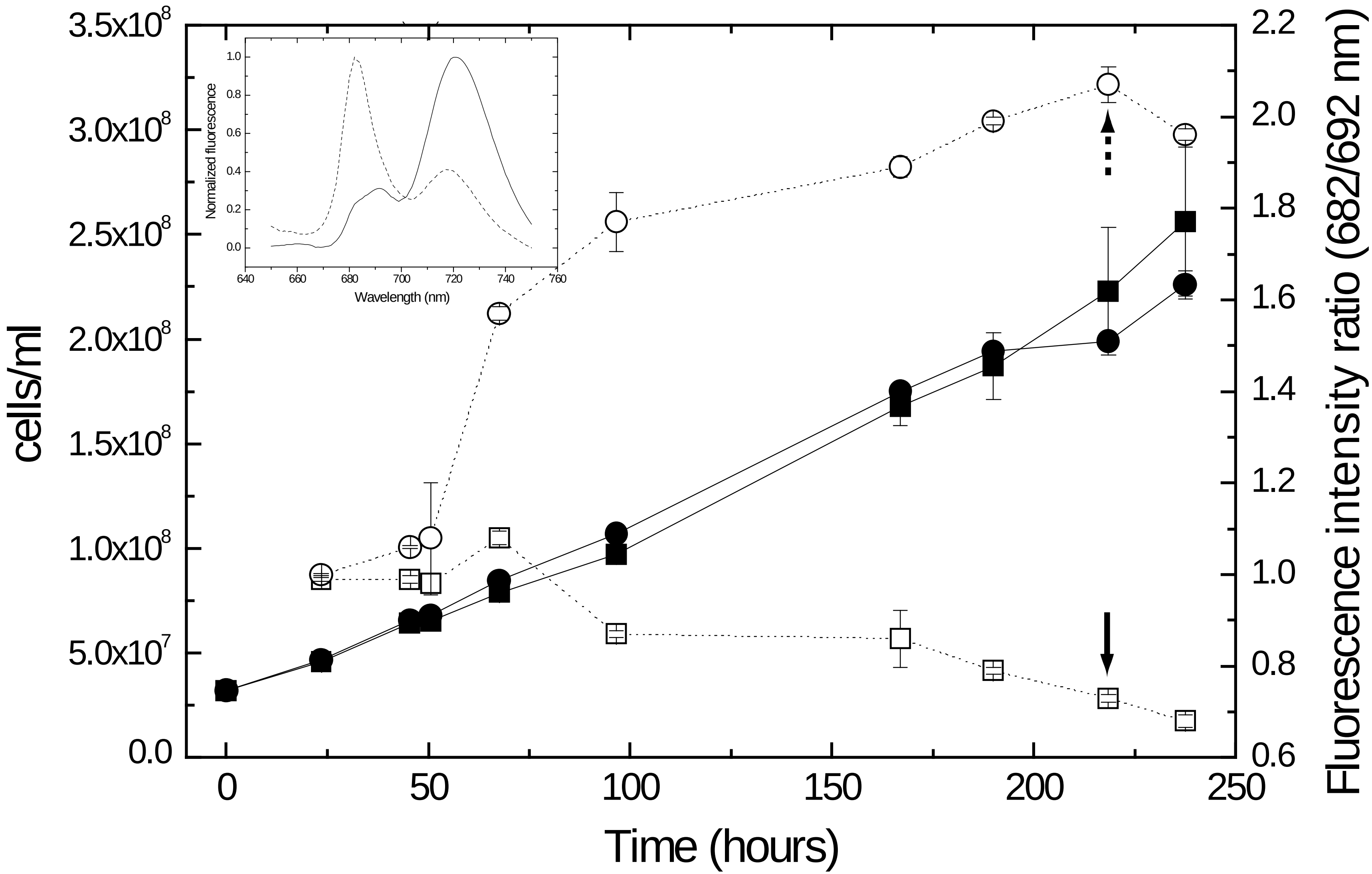
Intracellular iron trafficking

A working hypothesis



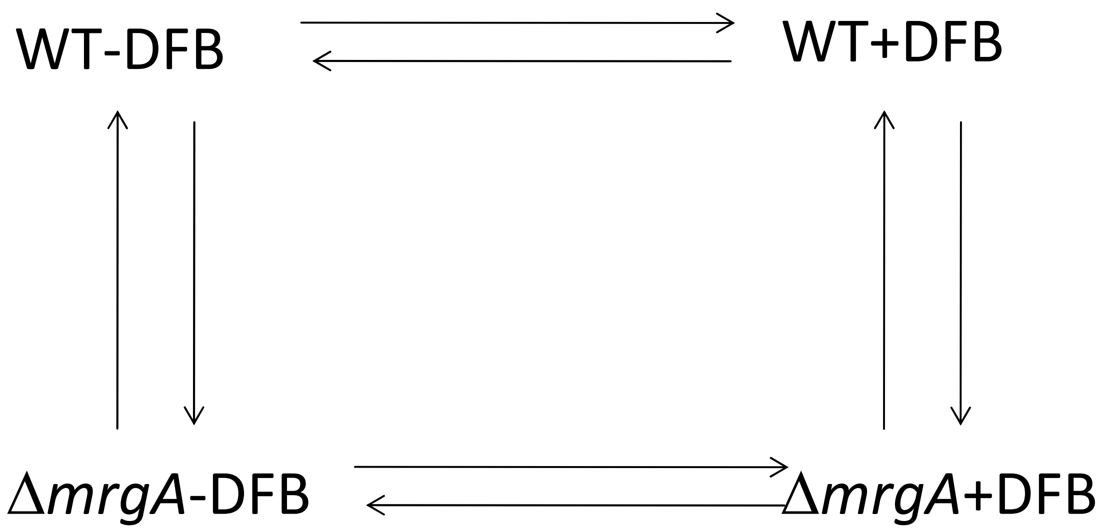
Experimental design

Iron limitation by chelators



Microarray experiments

4 way comparison design



Microarray experiments

Results summary

General pathway	*No. of genes*	*Differentially regulated genes* Δ*mrgA/WT*	*WT DFB/WT*	Δ*mrgA DFB/* Δ*mrgA*	Δ*mrgA DFB/ WT DFB*
Amino acid biosynthesis	83	1↓ 2↑	4↓ 1↑	16↓ 14↑	16↓ 6↑
Biosynthesis of cofactors, prosthetic groups, and carriers	116	3↓ 5↑	5↓ 8↑	10↓ 25↑	23↓ 18↑
Cell envelope	63	**0↓ 8↑**	3↓ 1↑	12↓ 5↑	9↓ 4↑
Cellular processes	61	3↓ 3↑	4↓ 1↑	8↓ 19↑	3↓ 13↑
Central intermediary metabolism	31	2↓ 1↑	0↓ 2↑	3↓ 3↑	4↓ 1↑
DNA replication, restriction, modification, recombination, and repair	51	3↓ 1↑	2↓ 0↑	5↓ 10↑	8↓ 6↑
Energy metabolism	86	1↓ 3↑	[illegible]	[illegible]	[illegible]
Fatty acid, phospholipid and sterol metabolism	34	2↓ 1↑	[illegible]	[illegible]	[illegible]
Hypothetical	449	41↓ 45↑	[illegible]	[illegible]	[illegible] ↑
Other categories	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
Photosynthesis and respiration	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
Purines, pyrimidines, nucleosides, and nucleotides	[illegible]	[illegible]	[illegible] 0↑	1↓ 2↑	3↓ 2↑
Regulatory functions	[illegible]	[illegible]	[illegible] 6↑	**22↓ 29↑**	**25↓ 16↑**
Transcription	[illegible]	[illegible]	[illegible] 2↑	3↓ 5↑	8↓ 3↑
Translation	146	17↓ 4↑	8↓ 3↑	33↓ 15↑	56↓ 11↑
Transport and binding proteins	169	9↓ 6↑	7↓ 17↑	18↓ 38↑	34↓ 14↑
Unknown	1267	19↓ 25↑	10↓ 11↑	38↓ 86↑	45↓ 64↑
Total	3165	127↓ 128↑	97↓ 92↑	342↓ 572↑	458↓ 321↑

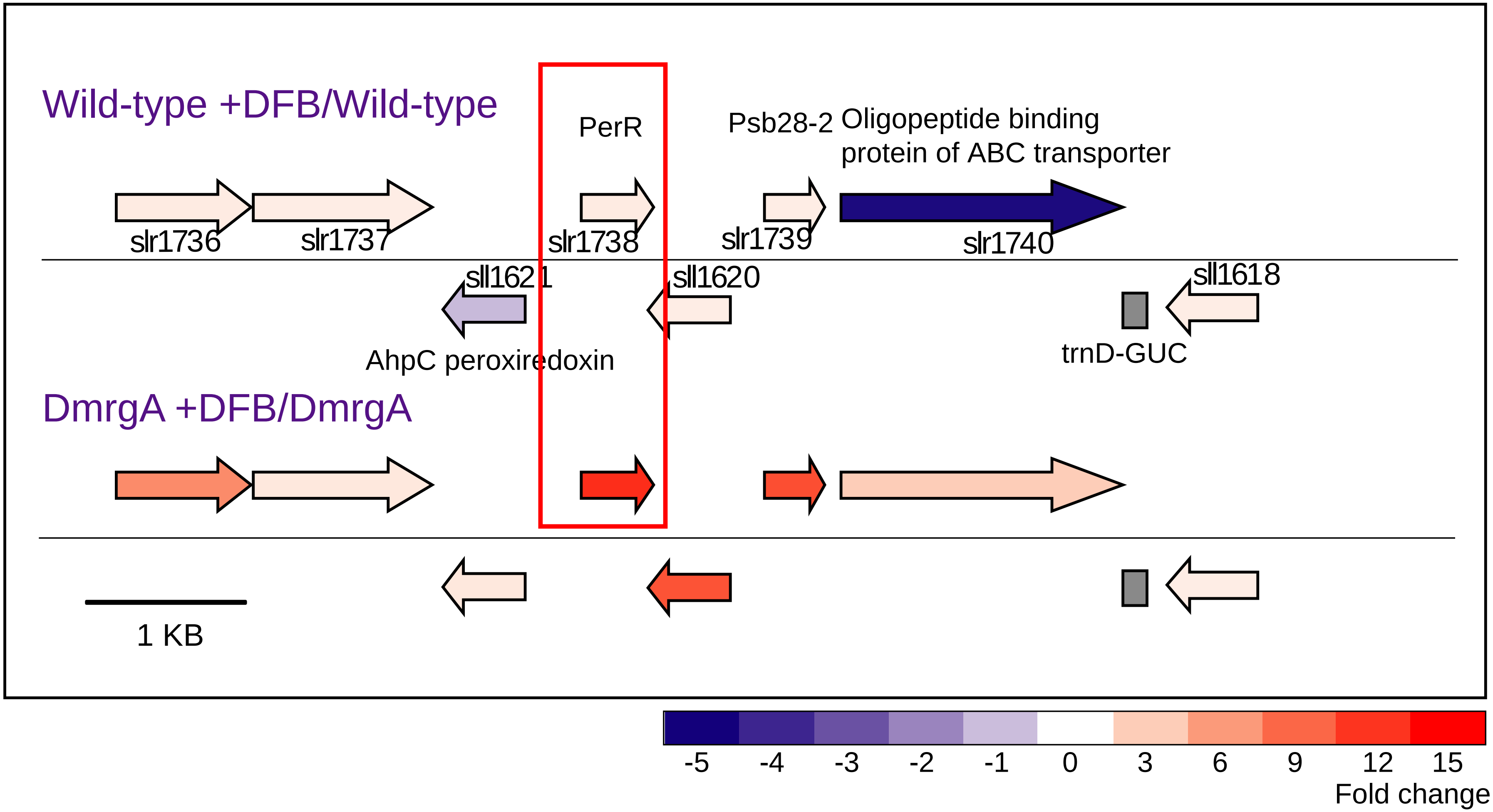
NADH dehydrogenase genes ↓
Phycobiliprotein genes ↓
Nitrogen assimilation ↓
Detoxification genes ↑

futC ↑
feoB ↑
slr1406 ↑
slr1316 –slr1319 ↑

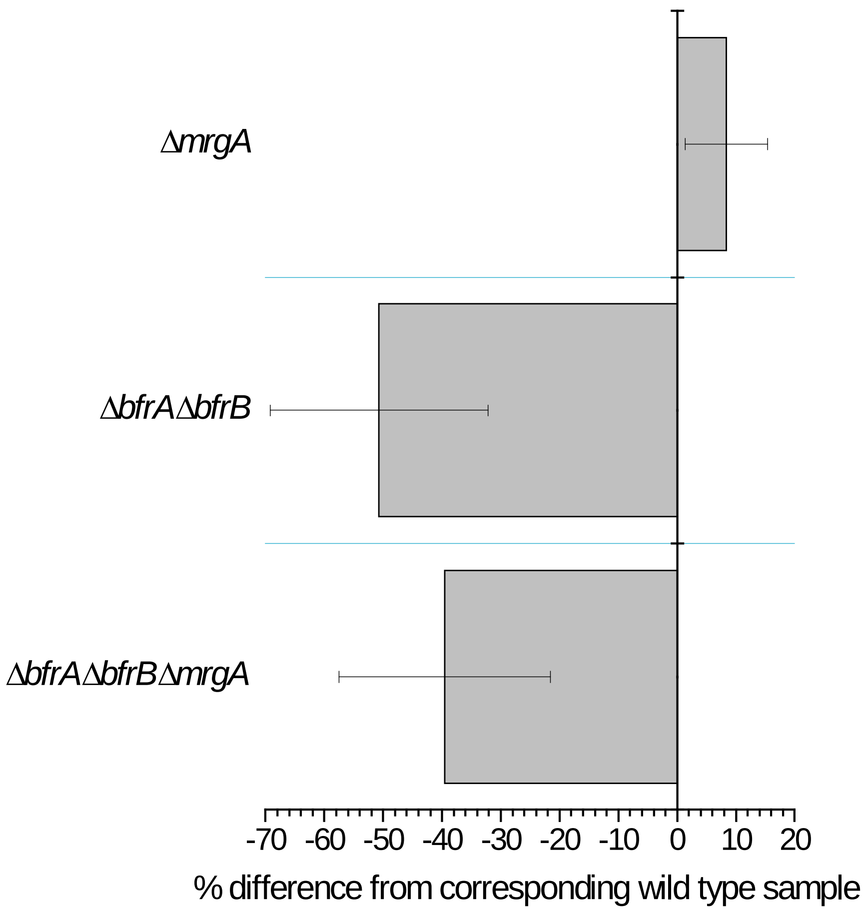
Table 1: differentially regulated genes in response to the DFB treatment or to deletion of *mrgA*, according to their functional category: Genes were considered deferentially regulated if |fold change|>1.4 and p<0.05. The number of transcripts that were down regulated by the treatment (DFB, Δ*mrgA* or both) is marked by ↓, the number of unregulated genes by ↑. Categories which are discussed in the manuscript appear in bold typeface.

Microarray experiments

Results summary

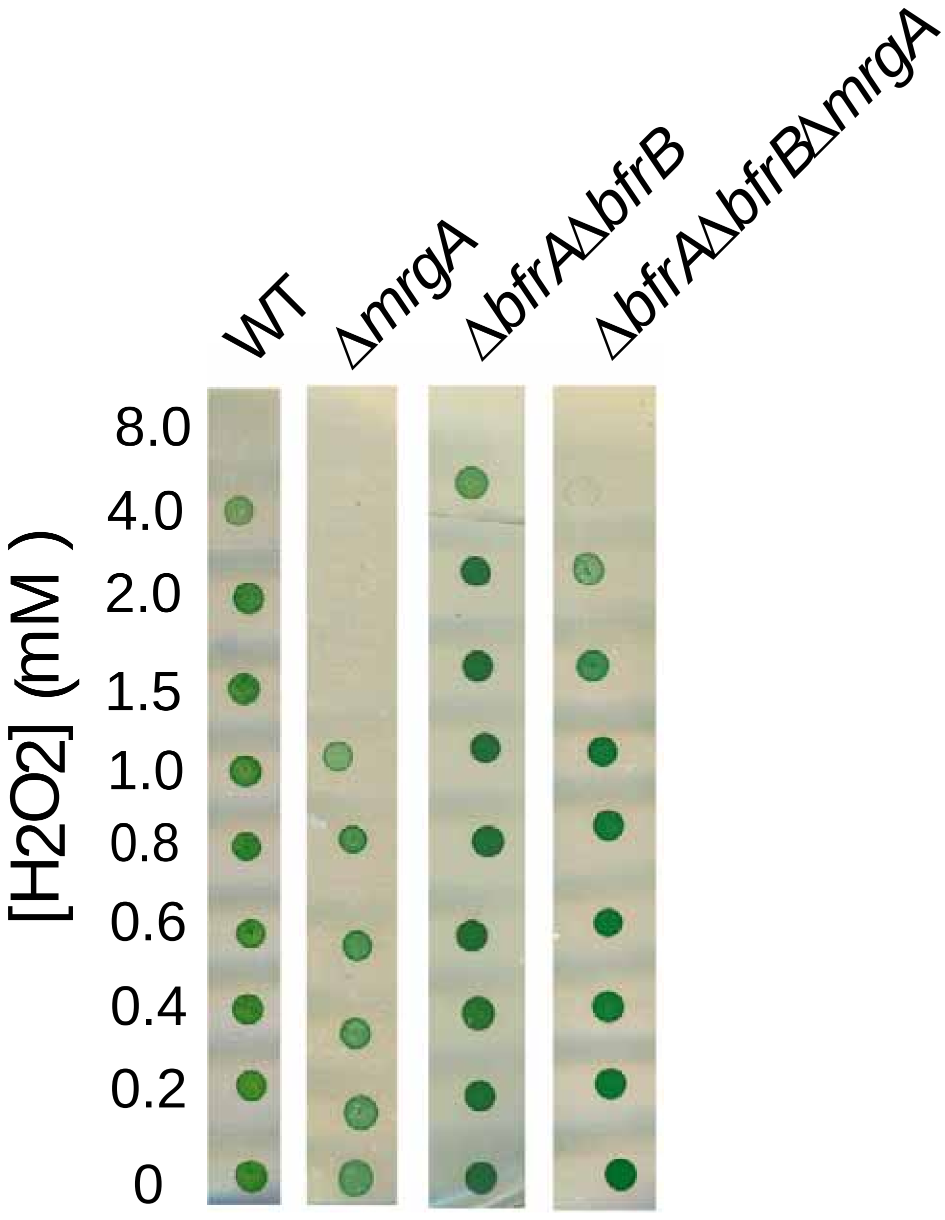


Integration of iron homeostasis and ROS chemistry

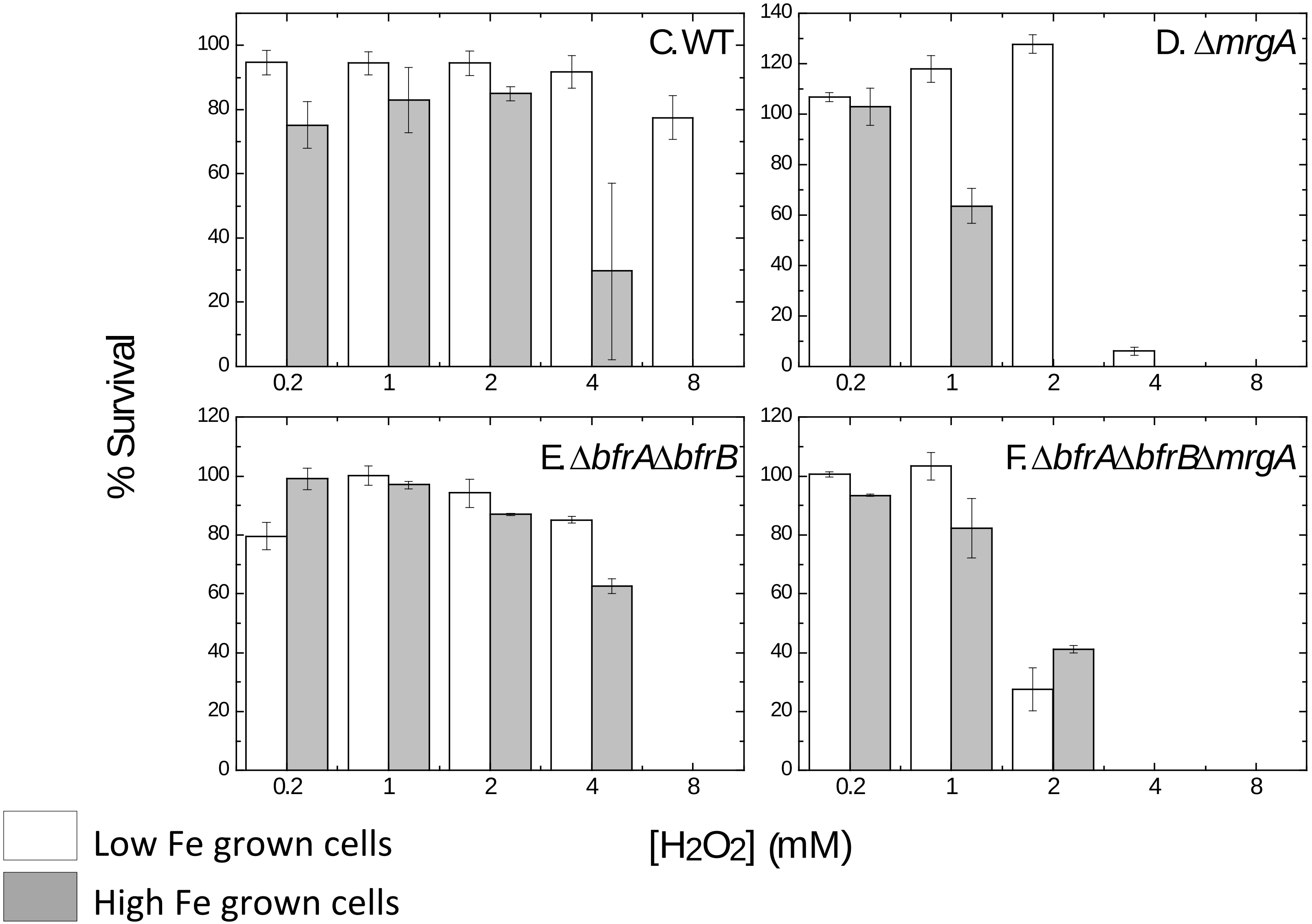


Integration of iron homeostasis and ROS chemistry

Cells grown in 10 μM Fe and exposed to H_2O_2 for 24 h in a 0 μM Fe medium

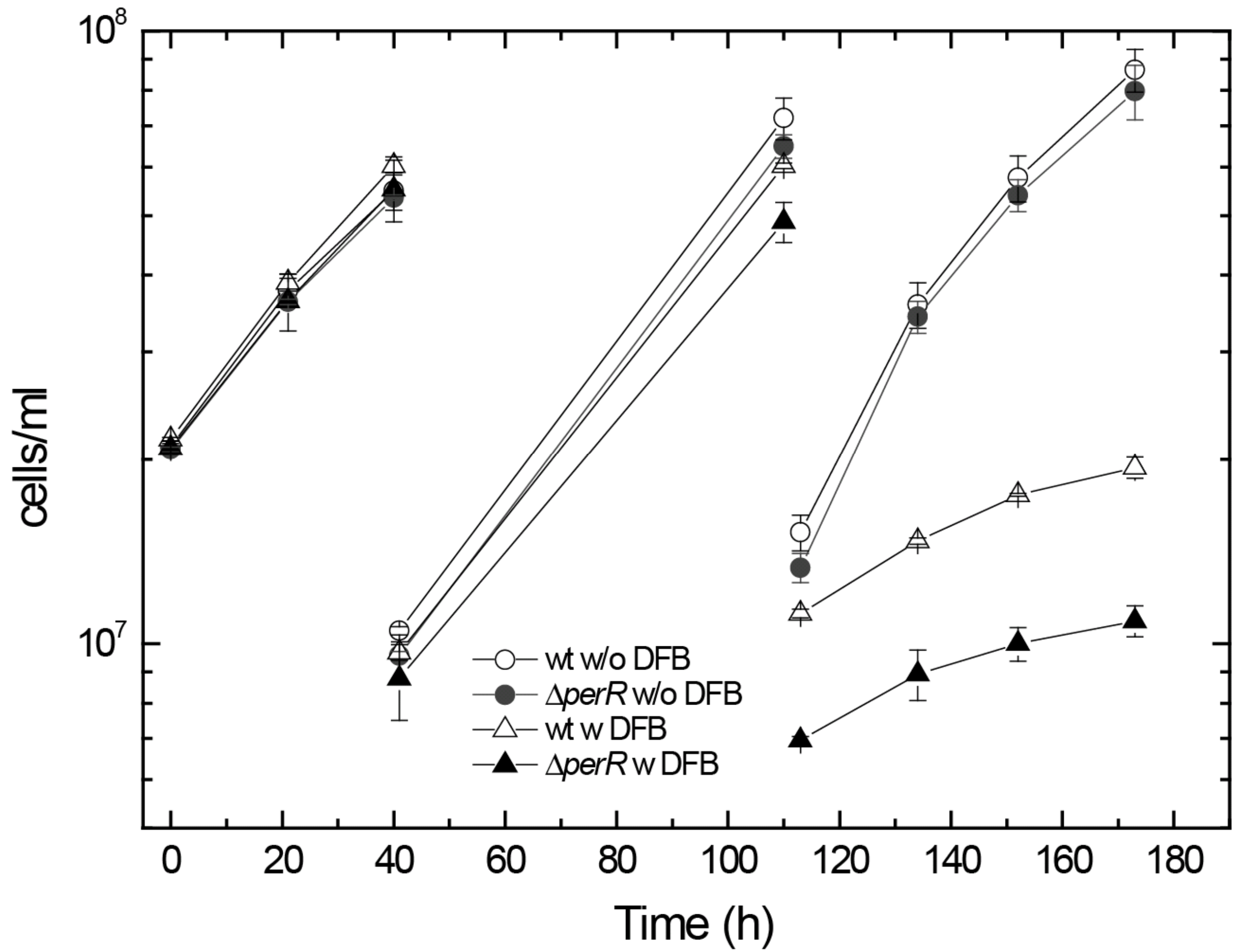


Integration of iron homeostasis and ROS chemistry



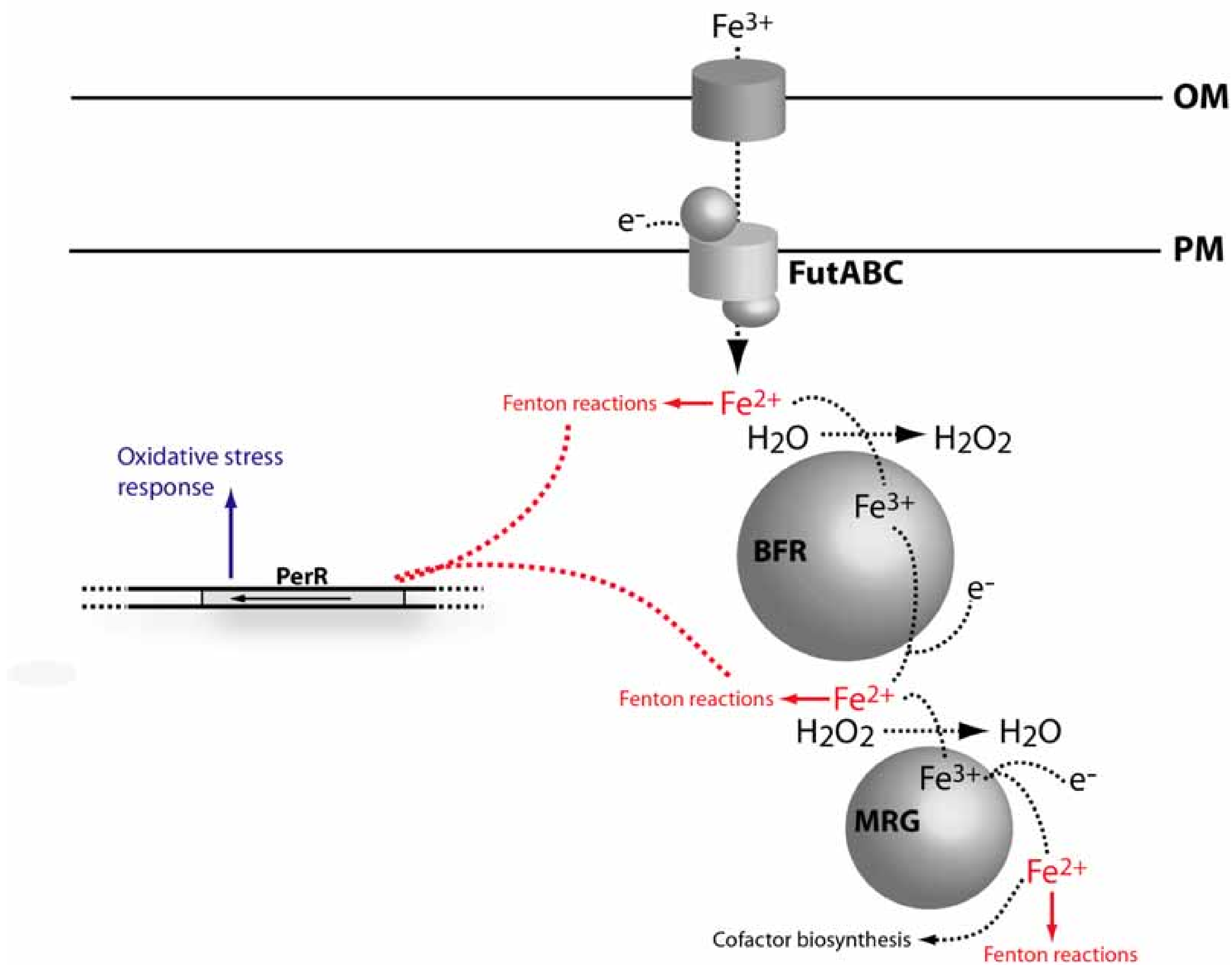
Integration of iron homeostasis and ROS chemistry

Role of PerR



Integration of iron homeostasis and ROS chemistry

Updated working hypothesis



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