

**Eukaryotic Algae***Chlorophyta (Green Algae)**Chlamydomonas reinhardtii* ... IYQVENGKGAM...*Monoraphidium braunii* ... VYQIENGKGAM...*Bryopsis maxima* ... TSQVRNGKGAM...*Euglenophyta**Euglena gracilis* ... EYQVRNGKGPM...*Euglena viridis* ... EYQVRNGKGPM...*Phaeophyta (Brown Algae)**Petalonia fascia* ... TYQVTNGKNAM...*Alaria esculenta* ... TYQVTNGKNAM...*Rhodophyta (Red Algae)**Porphyra tenera* ... TYQVQNGKNAM...*Porphyra purpurea* ... TYQVTNGKNAM...*Xanthophyta (Yellow Algae)**Bumilleriopsis filiformis* ... TYQVTNGKNAM...*Chrysophyta (Golden Algae)**Monochrysis lutheri* ... VYQVTNGKNAM...**Cyanobacteria***Spirulina maxima* ... AYQVTNGKNAM...*Synechococcus lividus* ... IYQVQHGKNAM...*Synechococcus sp.* ... MYQVQNGKNAM...*Synechococcus (Strain PCC 7942)* ... TTQVTNGKGAM...*Synechocystis (Strain PCC 6803)* ... VAQITNGNGAM...*Microcystis aeruginosa* ... VTQVTKGMGAM...*Anacystis nidulans* ... TTQVTNGKGAM...*Aphanizomenon flos-aquae* ... GAQVTNGKNAM...*Plectonema boryanum* ... IAQVTHGKGAM...*Anabaena variabilis* ... VAQVTNGKGAM...*Anabaena (Strain PCC 7120)* ... IAQVTNGKNAM...*Anabaena (Strain PCC 7937)* ... IAQVTNGKNAM...

**Figure S1.** Residues 50 through 60 in all known sequences of cytochrome  $c_6$ . The residue Tyr51, which is aligned with the dipole moment of the protein, is replaced by non-aromatic amino acids in cytochrome  $c_6$  of many species.

**Eukaryotic Algae**

<i>Chlorophyta (Green Algae)</i>	
<i>Chlamydomonas reinhardtii</i>	... MPAWADRLSEE...
<i>Monoraphidium braunii</i>	... MPAWDGRLDED...
<i>Bryopsis maxima</i>	... MPAWSDRLDDE...
<i>Euglenophyta</i>	
<i>Euglena gracilis</i>	... MPAWEGVLSED...
<i>Euglena viridis</i>	... MPAWEGVLDES...
<i>Phaeophyta (Brown Algae)</i>	
<i>Petalonia fascia</i>	... MPAFGGRLSET...
<i>Alaria esculenta</i>	... MPAFGSRLAET...
<i>Rhodophyta (Red Algae)</i>	
<i>Porphyra tenera</i>	... MPAFGGRLVDE...
<i>Porphyra purpurea</i>	... MPAFGGRLVDE...
<i>Xanthophyta (Yellow Algae)</i>	
<i>Bumilleriopsis filiformis</i>	... MPAFGGRLSDS...
<i>Chrysophyta (Golden Algae)</i>	
<i>Monochrysis lutheri</i>	... MPAFGGRLIEDD...
<b>Cyanobacteria</b>	
<i>Spirulina maxima</i>	... MPGFNGRLSPK...
<i>Synechococcus lividus</i>	... MPAFAGRLTDE...
<i>Synechococcus sp.</i>	... MPAFGGRLSEA...
<i>Synechococcus (Strain PCC 7942)</i>	... MPAFGSKLSAD...
<i>Synechocystis (Strain PCC 6803)</i>	... MPGFKGRISDS...
<i>Microcystis aeruginosa</i>	... MPAFGGRLSAE...
<i>Anacystis nidulans</i>	... MPAFGAKLSAD...
<i>Aphanizomenon flos-aquae</i>	... MPAFGIRLKAEE...
<i>Plectonema boryanum</i>	... MPAFKGRLSDD...
<i>Anabaena variabilis</i>	... MPAFKGRLKPE...
<i>Anabaena (Strain PCC 7120)</i>	... MPAFKGRLKPE...
<i>Anabaena (Strain PCC 7937)</i>	... MPAFKGRLKPD...

**Figure S2.** Residues 60 through 70 in all known sequences of cytochrome  $c_6$ . Only tryptophane (W) or phenylalanine (F) is found at position 63. The aromatic group may interact with cationic the side chain of arginine (R) or lysine (K) at position 66 to form a cation- $\pi$  complex. This cationic residue is missing in the two Euglenophyta.

**Higher Plants**

<i>Populus nigra</i> (poplar)	... YSFYCSPHQGA...
<i>Phaseolus vulgaris</i> (French bean)	... YSFYCSPHQGA...
<i>Vicia faba</i> (broad bean)	... YKFYCSPHQGA...
<i>Pisum sativum</i> (graden pea)	... YKFYCSPHQGA...
<i>Nicotiana tabacum</i> (tobacco)	... YTFYCAPHQGA...
<i>Solanum tuberosum</i> (potato)	... YTFYCAPHQGA...
<i>Solanum crispum</i> (potato tree)	... YSFYCSPHQGA...
<i>Lycopersicon esculentum</i> (tomato)	... YTFYCAPHQGA...
<i>Lactuca sativa</i> (lettuce)	... YSFYCAPHQGA...
<i>Capsella bursa-pastoris</i>	... YSFYCAPHQGA...
<i>Arabidopsis thaliana</i> (cress)	... YGFYCAPHQGA...
<i>Silene pratensis</i> (white campion)	... YKFYCAPHAGA...
<i>Spinacia oleracea</i> (spinach)	... YKFYCSPHQGA...
<i>Cucumis sativus</i> (cucumber)	... YSFYCSPHQGA...
<i>Cucurbita pepo</i> (squash)	... YSFYCSPHQGA...
<i>Petroselinum crispum</i> (parsley)	... YKFYCEPHAGA...
<i>Daucus carota</i> (carrot)	... YKFYCEPHAGA...
<i>Mercurialis perennis</i>	... YSFYCSPHQGA...
<i>Sambucus nigra</i> (european elder)	... YKFYCSPHQGA...
<i>Rumex obtusifolius</i> (bitter dock)	... YSFYCSPHQGA...
<i>Hordeum vulgare</i> (barley)	... YGFYCEPHAGA...
<i>Oryza sativa</i> (rice)	... YGFYCEPHAGA...

**Eukaryotic Algae**

<i>Chlorophyta</i> (Green Algae)	
<i>Chlamydomonas reinhardtii</i>	... YGYYCEPHQGA...
<i>Chlorella fusca</i>	... YGYFCEPHQGA...
<i>Scenedesmus obliquus</i>	... YGYFCEPHQGA...
<i>Ulva arasaki</i>	... YGVYCEPHAGA...
<i>Enteromorpha prolifera</i>	... YGVYCDPHSGA...

**Cyanobacteria**

<i>Prochlorothrix hollandica</i>	... YSFYCTPHRGA...
<i>Synechocystis</i> (Strain PCC 6803)	... YTYYCEPHRGA...
<i>Anabaena variabilis</i>	... YTFYCEPHRGA...
<i>Anabaena</i> (Strain PCC 7937)	... YSFYCEPHRGA...
<i>Anabaena</i> (Strain PCC 7120)	... YTFYCEPHRGA...
<i>Phormidium laminosum</i>	... YTYYCAPHRGA...

**Figure S3.** Residues 80 through 90 in all known sequences of plastocyanin. The tyrosine (Y) at position 83 is replaced by a phenylalanine (F) in two of the sequences. The aromatic group may interact with the cationic side chain of Arg88, which is conserved in cyanobacterial plastocyanin, to form a cation- $\pi$  complex.

**Higher Plants**

<i>Brassica rapa</i> (turnip)	... VLANGKKGALN...
<i>Oenothera hookeri</i> (primrose)	... VLANGKKGGLN...
<i>Nicotiana tabacum</i> (tobacco)	... VLANGKRGGLN...
<i>Spinacia oleracea</i> (spinach)	... VLANGKKGGLN...
<i>Glycine max</i> (soybean)	... VLANGKKGALN...
<i>Pisum sativum</i> (garden pea)	... VLANGKKGALN...
<i>Vicia faba</i> (broad bean)	... VLANGKKGALN...
<i>Triticum aestivum</i> (wheat)	... VLANGKKGGLN...
<i>Zea mays</i> (maize)	... VLANGKKGGLN...
<i>Oryza sativa</i> (rice)	... VLANGKKGGLN...
<i>Pinus thunbergii</i> (green pine)	... VLANGKKGALN...
<i>Marchantia polymorpha</i>	... VLANGKKGSLN...

**Eukaryotic Algae**

<i>Chlorophyta</i> (Green Algae)	
<i>Chlamydomonas reinhardtii</i>	... VLANGKKGDLN...
<i>Bacillariophyta</i> (Diatoms)	
<i>Odontella sinensis</i>	... VGANGKKADLN...
<i>Glaucophyta</i>	
<i>Cyanophora paradoxa</i>	... IQANGQKGPLN...
<i>Rhodophyta</i> (Red Algae)	
<i>Porphyra purpurea</i>	... ILGNGSKGGLN...
<b>Cyanobacteria</b>	
<i>Synechocystis</i> (Strain PCC 6803)	... VLDGSKGGLN...
<i>Synechococcus</i> (Strain PCC 7002)	... VLDGSKGGLN...
<i>Nostoc</i> (Strain PCC 7906)	... VGADGSKVGLN...
<i>Phormidium laminosum</i>	... VQADGSKGPLN...

**Figure S4.** Residues 60 through 70 in all known sequences of cytochrome *f*. The residue Lys65 is missing in the cytochromes *f* from cyanobacteria and some primitive eukaryotic algae.