WHAT IS CLAIMED IS:

1. A cell comprising:

a first exogenous nucleic acid construct comprising a nucleotide sequence encoding an aminolevulinate synthase (ALAS) protein operably linked to a first promoter element, wherein the ALAS protein comprises an amino acid sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO: 29, wherein the ALAS protein comprises at least a first heme responsive motif (HRM), wherein the first HRM comprises the amino acid sequence of SEQ ID NO:32 except for a mutation relative to the amino acid sequence of SEQ ID NO:32, wherein the mutation relative to the amino acid sequence of SEQ ID NO:32 in the first HRM corresponds to a mutation of residue 12 or residue 39 of SEQ ID NO: 29, and wherein the ALAS protein catalyzes the transformation of glycine and succinyl-CoA to aminolevulinic acid; and

a second exogenous nucleic acid construct comprising a nucleotide sequence encoding a heme-binding protein

operably linked to the first promoter element or to a second promoter element.

2. The cell of claim 1, wherein the cell is a fungal cell, a yeast cell, a bacterial cell, an algal cell, a plant cell, an insect cell, or a mammalian cell.

3. The cell of claim 1, wherein the cell is a *Pichia pastoris* cell.

4. The cell of any one of claims 1-3, wherein the mutation of residue 12 or residue 39 of SEQ ID NO:29 is to arginine, histidine, lysine, serine, threonine, asparagine, glutamine, selenocysteine, glycine, proline, alanine, isoleucine, leucine, methionine, glutamic acid, aspartic acid, phenylalanine, tryptophan, tyrosine, or valine.

5. The cell of any one of claims 1-3, wherein the mutation of residue 12 or residue 39 of SEQ ID NO:29 is to a nonpolar aliphatic amino acid, an aromatic amino acid, a polar uncharged amino acid, or a positively charged amino acid.

6. The cell of any one of claims 1-3, wherein the mutation of residue 12 or residue 39 of SEQ ID NO:29 is to serine.

7. The cell of any one of claims 1-3, wherein the mutation of residue 12 or residue 39 of SEQ ID NO:29 is to alanine.

8. The cell of any one of claims 1-3, wherein the mutation of residue 12 or residue 39 of SEQ ID NO:29 is to phenylalanine.

9. The cell of any one of claims 1-3, wherein the mutation of residue 12 or residue 39 of SEQ ID NO:29 is to histidine.

10. The cell of any one of claims 1-9, wherein the mutation relative to the amino acid sequence of SEQ ID NO:32 in the first HRM corresponds to a mutation of residue 12 of SEQ ID NO: 29.

11. The cell of any one of claims 1-9, wherein the mutation relative to the amino acid sequence of SEQ ID NO:32 in the first HRM corresponds to a mutation of residue 39 of SEQ ID NO: 29.

12. The cell of claim 10, wherein the ALAS protein comprises a second HRM, wherein the second HRM comprises the amino acid sequence of SEQ ID NO:32 except for a mutation relative to the amino acid sequence of SEQ ID NO:32, wherein the mutation relative to the amino acid sequence of SEQ ID NO:32 in the second HRM corresponds to a mutation of residue 39 of SEQ ID NO: 29.

13. The cell of claim 12, wherein the mutation relative to the amino acid sequence of SEQ ID NO:32 in the first HRM and the mutation relative to the amino acid sequence of SEQ ID NO:32 in the second HRM are the same mutation.

14. The cell of claim 12, wherein the mutation relative to the amino acid sequence of SEQ ID NO:32 in the first HRM and the mutation relative to the amino acid sequence of SEQ ID NO:32 in the second HRM are not the same mutation.

15. The cell of claim 12, wherein:

(a) the mutation relative to the amino acid sequence of SEQ ID NO:32 in the first HRM corresponds to a mutation of residue 12 of SEQ ID NO: 29 to serine, and the mutation relative to the amino acid sequence of SEQ ID NO:32 in the second HRM corresponds to a mutation of residue 39 of SEQ ID NO: 29 to serine;

(b) the mutation relative to the amino acid sequence of SEQ ID NO:32 in the first HRM corresponds to a mutation of residue 12 of SEQ ID NO: 29 to alanine, and the mutation relative to the amino acid sequence of SEQ ID NO:32 in the second HRM corresponds to a mutation of residue 39 of SEQ ID NO: 29 to alanine;

(c) the mutation relative to the amino acid sequence of SEQ ID NO:32 in the first HRM corresponds to a mutation of residue 12 of SEQ ID NO: 29 to phenylalanine, and the mutation relative to the amino acid sequence of SEQ ID NO:32 in the second HRM corresponds to a mutation of residue 39 of SEQ ID NO: 29 to phenylalanine; or

(d) the mutation relative to the amino acid sequence of SEQ ID NO:32 in the first HRM corresponds to a mutation of residue 12 of SEQ ID NO: 29 to histidine, and the mutation relative to the amino acid sequence of SEQ ID NO:32 in the second HRM corresponds to a mutation of residue 39 of SEQ ID NO: 29 to histidine.

16. The cell of any one of claims 1-11, wherein the first HRM has the amino acid sequence of any one of SEQ ID NOs: 33-36 except for a mutation at residue 2 of any one of SEQ ID NOs:33-36, respectively.

17. The cell of claim 16, wherein the ALAS protein comprises a second HRM, wherein the second HRM has the amino acid sequence of any one of SEQ ID NOs: 33-36 except for a mutation at residue 2 of any one of SEQ ID NOs:33-36, respectively.

18. The cell of claim 12, wherein the first HRM has the amino acid sequence of any one of SEQ ID NOs: 33-36 except for a mutation at residue 2 of any one of SEQ ID NOs:33-36, respectively.

19. The cell of claim 18, wherein the second HRM has the amino acid sequence of any one of SEQ ID NOs: 33-36 except for a mutation at residue 2 of any one of SEQ ID NOs:33-36, respectively.

20. The cell of any one of claims 1-19, wherein the first exogenous nucleic acid construct comprises a nucleotide sequence having at least 90% sequence identity to the nucleotide sequence of SEQ ID NO: 28.

21. The cell of any one of claims 1-20, wherein the ALAS protein comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 29.

22. The cell of any one of claims 1-21, wherein the heme-binding protein is selected from the group consisting of a globin, a cytochrome, a cytochrome c oxidase, a ligninase, a catalase, and a peroxidase.

23. The cell of any one of claims 1-21, wherein the heme-binding protein is a leghemoglobin.

24. The cell of any one of claims 1-21, wherein the heme-binding protein comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 1-27.

25. A method of producing a heme-binding protein, the method comprising culturing the cell of any one of claims 1-24.

26. The method of 25, wherein the method produces the heme-binding protein at a titer that is at least 5% greater than a corresponding method comprising culturing a

cell comprising the second exogenous nucleic acid construct and lacking the first exogenous nucleic acid construct.

27. The method of claim 25 or claim 26, wherein the method produces the heme-binding protein at a titer that is at least 10% greater than a corresponding method comprising culturing a cell comprising the second exogenous nucleic acid construct and lacking the first exogenous nucleic acid construct.

28. The method of any one of claims 25-27, wherein the method is carried out in the absence of methanol.