WHAT IS CLAIMED IS:

1. A mutein of the pyrroline-5-carboxylate reductase 1 (PYCR1), wherein at least one of the amino acid residues at sequence positions 4 to 220 and 222 to 266 of the wild type amino acid sequence of PYCR1 as set forth in Swiss-Prot Accession No. P32322 is mutated.

2. A mutein of PYCR1, comprising a mutation of at least one of the amino acid residues at sequence positions 4 to 266 of the wild type amino acid sequence of PYCR1 as set forth in Swiss-Prot Accession No. P32322, wherein the mutation leads to a reduced function or loss of function of the mutein compared to the wild-type protein.

3. The mutein according to claim 1 or 2, wherein at least one of the amino acid residues at sequence positions 4, 119, 179, 189, 206, 251, 257 and 266 is mutated.

4. The mutein according to claim 3, wherein the mutation of the amino acid residue at sequence position 4 is a frameshift mutation leading to a translation stop codon occurring at the codon that encodes for sequence position 50 of the wild type amino acid sequence of PYCR1.

5. The mutein according to claim 3, wherein the amino acid residue at sequence position 119 is replaced by glycine or histidine.

6. The mutein according to claim 3, wherein the amino acid residue at sequence position 179 is replaced by a hydrophilic amino acid, wherein the hydrophilic amino acid is a hydroxyl-containing amino acid.

7. The mutein according to claim 6, wherein the hydroxyl-containing amino acid is serine or threonine.

8. The mutein according to claim 3, wherein the amino acid residue at sequence position 189 is replaced by a hydrophobic amino acid, wherein the hydrophobic amino acid is an aliphatic amino acid.

9. The mutein according to claim 8, wherein the aliphatic amino acid is selected from the group consisting of isoleucine, leucine and valine.

10. The mutein according to claim 3, wherein the amino acid residue at sequence position 206 is replaced by an aromatic amino acid or a positively charged amino acid.

11. The mutein according to claim 10, wherein the aromatic amino acid is selected from the group consisting of phenylalanine, tyrosine and tryptophan.

12. The mutein according to claim 10, wherein the positively charged amino acid is arginine or lysine.

13. The mutein according to claim 3, wherein the amino acid residue at sequence position 251 is replaced by histidine.

14. The mutein according to claim 3, wherein the amino acid residue at sequence position 257 is replaced by a hydrophilic amino acid, wherein the hydrophilic amino acid is a hydroxyl-containing amino acid.

15. The mutein according to claim 14, wherein the hydroxyl-containing amino acid is serine or threonine.

16. The mutein according to claim 3, wherein the amino acid residue at sequence position 266 is replaced by glutamine or asparagine.

17. The mutein according to any of claims 1 to 16, wherein the mutation of at least one of the amino acid residues of the wild type amino acid sequence of PYCR1 as set forth in Swiss-Prot Accession No. P32322 is a single nucleotide polymorphism (SNP) or is selected from the group consisting of substitution, deletion, insertion and combinations thereof.

18. A nucleic acid molecule comprising a nucleotide sequence encoding a mutein according to any of claims 1 to 17.

19. A method of determining in a subject a predisposition of having an age-related disorder associated with pyrroline-5-carboxylate reductase 1 (PYCR1), the method comprising analyzing a nucleic acid sample obtained from a subject for the presence of a nucleotide sequence encoding a mutein according to any of claims 1 to 17, wherein the presence of the nucleotide sequence indicates a predisposition of the subject having or being at risk for having the age-related disorder.

20. The method according to claim 19, wherein the age-related disorder is selected from the group consisting of cutis laxa (wrinkly skin syndrome), de Barsy syndrome and gerodermia osteodysplasia.

21. Use of a nucleic acid molecule comprising a nucleotide sequence encoding a mutein according to any of claims 1 to 17 for diagnosing or determining a predisposition of having an age-related disorder associated with PYCR1.

22. A method of identifying a compound capable of modifying the expression of a PYCR1 gene, the method comprising:

a. contacting a compound of interest with a nucleic acid molecule comprising a nucleotide sequence encoding pyrroline-5-carboxylate reductase 1 (PYCR1) or a functional fragment or mutant thereof,

b. measuring the expression of the nucleotide sequence encoding pyrroline-5-carboxylate reductase 1 (PYCR1) or a functional fragment or functional mutant thereof, and

c. comparing result of the measurement obtained from step (b) with that of a control measurement without addition of the compound of interest.

23. A method of modifying the expression of a PYCR1 gene in a cell, the method comprising introducing a nucleic acid molecule comprising a nucleotide sequence encoding pyrroline-5-carboxylate reductase 1 (PYCR1) or a functional fragment or functional mutant thereof into the cell.

24. The method according to claim 23, wherein the nucleic acid molecule is operably linked to a regulatory sequence to allow expression of the nucleic acid molecule, wherein the regulatory sequence comprises a promoter sequence.

25. Use of a nucleic acid molecule comprising a nucleotide sequence encoding pyrroline-5-carboxylate reductase 1 (PYCR1) or a functional fragment or functional mutant thereof in the manufacture of a medicament for treating a subject having an age-related disorder associated with PYCR1 or being at risk to develop an age-related disorder associated with PYCR1, wherein the age-related disorder is selected from the group consisting of cutis laxa (wrinkly skin syndrome), de Barsy syndrome and gerodermia osteodysplasia.

26. A genetically modified animal, wherein the genetically modified animal comprises a nucleic acid encoding pyrroline-5-carboxylate reductase 1 (PYCR1), wherein the nucleic acid is inactive, wherein the inactive nucleic acid leads to a loss of function of the PYCR1, and wherein the genetically modified animal is a xenopus, rodent or a fish.

27. A method of modifying the expression of the PYCR1 gene in an animal, the method comprising administering to the animal a compound capable of modifying the expression of the PYCR1 gene, wherein the compound comprises a nucleic acid molecule that is capable of modifying the expression of the PYCR1 gene.

28. The method according to claim 27, wherein the nucleic acid molecule is selected from the group consisting of antisense RNA, short interfering RNA (siRNA), micro RNA (miRNA), peptide nucleic acid (PNA) and combinations thereof.

29. A method of identifying a compound capable of modifying the expression of a PYCR1 gene, the method comprising:

a. administering the compound of interest to a genetically modified animal according to claim 26; and

b. determining whether the compound is capable of modifying the expression of the PYCR1 gene.

30. A method of identifying a compound capable of modifying the expression of a PYCR1 gene, the method comprising:

a. providing an isolated skin flap comprising at least one layer of living animal skin, said flap being attached to a test animal; and

b. applying the compound of interest to the living animal skin, wherein the skin flap includes cells that express the mutein as defined in any of claims 1 to 17.

31. The method according to claim 30, wherein the cells are fibroblasts.

32. The method according to claim 30 or 31, wherein the skin flap comprises living human skin on one surface and living animal skin on the other surface.

33. The method according to any of claims 30 to 32, wherein the skin flap is being served by an isolated vasculature, wherein the isolated vasculature is attached to the test animal.

34. The method according to any of claims 30 to 33, further comprising obtaining a sample of DNA from the skin flap to measure the expression of the PYCR1 gene or removing at least one sample of blood from the isolated vasculature, wherein the contents of the blood removed is being analysed.

35. The method according to any of claims 30 to 34, wherein the living animal skin is of the same or different species than the test animal.

36. The method according to claim 35, wherein the test animal is selected from the group consisting of mouse, rat, squirrel, chipmunk, gopher, porcupine, beaver, hamster, gerbil, guinea pig, chinchilla, prairie dog, and groundhog.

37. The method according to claim 36, wherein the test animal is athymic.