CLAIMS:

1. An isolated genetically engineered bacterium, wherein the bacterium has been transformed by at least one polynucleotide molecule; the at least one polynucleotide molecule comprising a heterologous mercury(II) reductase (*MerA*) gene, operably linked to at least one promoter, and comprising at least one mutation which renders the gene product capable of reducing ionic metal to elemental metal as metal nanoparticles.

2. The isolated bacterium of claim 1, wherein the *MerA* gene comprises one or more mutations which encode amino acid substitutions, wherein the amino acid substitutions are at positions selected from the group comprising V317, Y441, C464, A323D, A323D (delΔ324-365), A414E, G415I, E416C, L417I, I418D and A422N of the MerA coding sequence, and/or

wherein said ionic metal is ionic gold (Au^{3+}) which is reduced to elemental gold as gold nanoparticles, or ionic silver (Ag^{+}) which is reduced to elemental silver as silver nanoparticles and/or wherein said at least one isolated bacterium has reduced reductive capacity for mercury substrate when compared to a bacterium comprising a non-mutated *MerA* gene.

3. An isolated genetically engineered bacterium, wherein the bacterium has been transformed by at least one polynucleotide molecule; the at least one polynucleotide molecule comprising a heterologous hydrogen cyanide synthase gene and a heterologous 3-phosphoglycerate dehydrogenase mutant gene operably linked to at least one promoter.

4. The isolated bacterium of claim 3, wherein the hydrogen cyanide synthase gene is *hcnABC* and/or the 3-phosphoglycerate dehydrogenase mutant gene is *serA* and/or wherein the isolated genetically engineered bacterium further comprises at least one polynucleotide molecule comprising, in order from N-terminus to C-terminus of the recombinant DNA molecule;

(i) a *golS* transcriptional activator gene operably linked to a constitutive promoter, and a *ph1F* repressor gene operably linked to a P_{golTS} or P_{golB} promoter;

(ii) a promoter activated by CviR and an operator of PhlF, and

(iii) one or more of said heterologous hydrogen cyanide synthase gene and said heterologous 3-phosphoglycerate dehydrogenase mutant gene operably linked to the CviR-activated promoter.

5. The isolated bacterium of claim 4, wherein the *golS* gene is codon optimized for *C. violaceum* and/or wherein the *golS* gene is a mutant selected from GolSmt1_A38I, GolSmt2_A38Q&N97D, GolSmt3_A38K&V60L and GolSmt4_D33P.

6. The isolated bacterium of any one of the previous claims, wherein the bacterium is selected from the group comprising *Chromobacterium violaceum*, *Pseudomonas fluorescens*, *P. aeruginosa* and *Eschericia coli* and/or wherein the bacterium is stable at pH 10.

7. A process for recovering elemental gold or silver, as gold nanoparticles from ionic gold (Au3+) or as silver nanoparticles from ionic silver (Ag+), respectively, said process comprising the steps of:

a) contacting the isolated genetically engineered bacterium according to any one of claims 1 to 6 with a leachate comprising ionic gold (Au3+) and/or ionic silver (Ag+); and

b) recovering the elemental gold and/or silver nanoparticles from the leachate.

8. The process according to claim 7, wherein the said contact is performed in alkaline conditions.

9. A method for producing an isolated genetically engineered bacterium, wherein the bacterium has been transformed by at least one polynucleotide molecule; the at least one polynucleotide molecule comprising a heterologous mercury(II) reductase (*MerA*) gene, operably linked to at least one promoter, and comprising one or more mutations which renders the gene product capable of reducing ionic gold (Au^{3+}) to elemental gold as gold nanoparticles, or ionic silver (Ag^{+}) which is reduced to elemental silver as silver nanoparticles, said method comprising the steps:

a) performing error-prone PCR on a gene encoding mercury(II) reductase (MerA);

i) transforming at least one bacterium with the products of said PCR;

ii) selecting transformants that grow on a media comprising Au^{3+} and/or Ag+; or

b) performing multiple site-saturated mutagenesis by overlap-extension PCR on a gene encoding mercury(II) reductase (MerA);

i) transforming at least one bacterium with the products of said PCR;

ii) selecting transformants that grow on a media comprising Au^{3+} and/or Ag^{+}.

10. The method of claim 9, wherein in part a) the PCR is performed with forward and reverse primers, wherein the forward primer comprises the nucleotide sequence set forth in SEQ ID NO: 1 and the reverse primer comprises the sequence set forth in SEQ ID NO: 2 and/or wherein in part b) the PCR is performed with primers containing NNK and/or MNN at the target sites V317, Y441 and C464, and/or

wherein said selection involves at least 2 forms of selection, wherein one form comprises selection on agar plates comprising Au^{3+} and/or Ag^{+} and another form comprises selection in liquid culture comprising Au^{3+} and/or Ag^{+}.

11. An isolated genetically engineered bacterium, wherein the bacterium has been transformed by at least one polynucleotide molecule; the at least one polynucleotide molecule comprising a heterologous nitrilase gene, the product of which causes cyanolysis of hydrogen cyanide, operably linked to at least one promoter.

12. The isolated genetically engineered bacterium of claim 11, wherein the heterologous nitrilase gene encodes an enzyme selected from the group comprising cyanide dehydratase and cyanide hydratase, and/or wherein the at least one polynucleotide molecule further comprises a heterologous formate dehydrogenase gene, a heterologous glutamate dehydrogenase gene and a heterologous phosphoenolpyruvate carboxylase gene operably linked to at least one promoter, and/or

wherein the bacterium is selected from the group comprising *Chromobacterium violaceum*, *Pseudomonas fluorescens*, *P. aeruginosa* and *Eschericia coli*.

13. A process of synthetic cyanide lixiviant production, said process comprising:

contacting at least one recombinant cyanogenic bacterium with glycine,

wherein the bacterium comprises a heterologous hydrogen cyanide synthase gene and a heterologous 3-phosphoglycerate dehydrogenase mutant gene operably linked to at least one promoter.

14. The process of claim 13, wherein the hydrogen cyanide synthase gene is hcnABC and/or the 3-phosphoglycerate dehydrogenase mutant gene is serA, and/or wherein the recombinant cyanogenic bacterium further comprises at least one polynucleotide molecule comprising, in order from N-terminus to C-terminus of the recombinant DNA molecule;

(i) a *golS* transcriptional activator gene operably linked to a constitutive promoter, and a *ph1F* repressor gene operably linked to a P_{golTS} or P_{golB} promoter;

(ii) a promoter activated by CviR and an operator of PhlF, and

(iii) one or more of said heterologous hydrogen cyanide synthase gene and said heterologous 3-phosphoglycerate dehydrogenase mutant gene operably linked to the CviR-activated promoter.

15. The process of claim 14, wherein the *golS* gene is codon optimized for *C. violaceum,* and/or wherein the *golS* gene is a mutant selected from GolSmt1_A38I, GolSmt2_A38Q&N97D, GolSmt3_A38K&V60L and GolSmt4_D33P, and/or

wherein the at least one recombinant cyanogenic bacterium is tolerant at about pH 10, and/or

wherein the synthetic cyanide lixiviant production is performed in a single reactor together with metal for bioleaching.

16. At least one isolated recombinant cyanogenic bacterium, capable of synthetic cyanide lixiviant production, as defined in any one of claims 13 to 15.

17. The at least one recombinant cyanogenic bacterium of statement 16, selected from the group comprising *Chromobacterium violaceum*, *Pseudomonas fluorescens*, *P. aeruginosa* and *Eschericia coli.*

18. A process of synthetic cyanolysis, said process comprising contacting at least one recombinant cyanolytic bacterium with nitriles including cyanide present after bioleaching of electronic waste, wherein the at least one bacterium is engineered to express at least one nitrilase enzyme.

19. The process of claim 18, wherein the at least one nitrilase enzyme is selected from the group comprising cyanide dehydratase and cyanide hydratase, and/or wherein the at least one recombinant cyanolytic bacterium is further engineered to express formate dehydrogenase, glutamate dehydrogenase and phosphoenolpyruvate carboxylase, and/or

wherein the at least one nitrilase enzyme is derived from at least one bacterial species selected from the group comprising *Pseudomonas pseudoalcaligenes* (nit), *Synechocystis* sp. PCC 6803 chromosome (SC-nit), cyanide dihydratase from *Bacillus pumilus* (BP-cynD) and *Pseudomonas stutzeri* (PS-cynD).

20. An isolated recombinant DNA molecule comprising, in order from N-terminus to C-terminus of the recombinant DNA molecule;

(i) a *golS* transcriptional activator gene operably linked to a constitutive promoter, and a *ph1F* repressor gene operably linked to a P_{golTS} or P_{golB} promoter;

(ii) a promoter activated by CviR and an operator of PhlF, and

(iii) one or more cyanogenic genes operably linked to the CviR-activated promoter.

21. The isolated recombinant DNA molecule of claim 20, wherein the *golS* transcriptional activator gene is a mutant selected from the group comprising or consisting of GolSmt1_A38I, GolSmt2_A38Q&N97D, GolSmt3_A38K&V60L and GolSmt4_D33P.

22. Use of a deactivated Cas9 comprising mutations H840A and D10A in the HNH endonuclease domain and the RuvC endonuclease domain, respectively, and an sgRNA to inhibit transcription of one or more genes in the *Chromobacterium violaceum* genome by targeting the promoter region of said one or more genes.

23. The use of claim 22, wherein the deactivated Cas9-encoding gene is operably linked to a P_{araBAD} promoter and the RNA guide (sgRNA)-encoding gene is operably linked to a strong constitutive promoter such as J23119.

24. An isolated recombinant DNA molecule comprising a golTSB operon, wherein the operon comprises in order from N-terminus to C-terminus of the recombinant DNA molecule; *golT* operably linked to j23119 promoter, *golS*, *golB* operably linked to golB promoter, and a reporter gene, such as *GFP*.