CLAIMS

1. An affinity column for isolating nucleic acid from a sample, the column comprising: a first solid support in fluid communication with a second solid support, said first solid support comprising one or more of a cell binding moiety, a cell disrupting reagent, and an enzyme, and said second solid support comprising at least one nucleic acid binding moiety wherein the nucleic acid binding moiety is an antibiotic; and a third solid support, wherein said third solid support is in removable fluid communication with said second solid support.

2. The affinity column of claim 1, wherein the cell disrupting reagent is a detergent or a chaotropic salt.

3. The affinity column of claim 1, wherein the cell disrupting reagent is a virus disrupting reagent.

4. The affinity column of any one of claims 1-3, wherein the first solid support comprises a cell binding moiety, a cell disrupting reagent, and an enzyme.

5. The affinity column of any of claims 1-4, wherein the antibiotic is selected from the group consisting of amikacin, gentamycin, kanamycin, neomycin, streptomycin, tobramycin, WP631, WP762, Daunorubicin, Echinomycin, tetracycline, and paraomycin.

6. The affinity column of any one of claims 1-3, wherein the third solid support comprises one or more of a nucleic acid stabilizing molecule, an elution buffer, and a molecule that forms an elution buffer when mixed with an aqueous solution.

7. An affinity matrix for the non-sequence specific isolation of nucleic acid from a sample, said affinity matrix comprising at least one nucleic acid binding moiety bound to a solid support, wherein the at least one nucleic acid binding moiety is an antibiotic.

8. A method for isolating nucleic acid from a sample comprising at least one nucleic acid, the method comprising:

(i) providing an affinity matrix comprising at least one nucleic acid binding moiety covalently bound to a solid support, wherein the at least one nucleic acid binding moiety is selected from streptomycin and tetracycline, wherein prior to contacting the sample, the affinity matrix is free of nucleic acid;

(ii) contacting the affinity matrix with a sample for a sufficient time to allow the affinity matrix to non-specifically bind said at least one nucleic acid from the sample, thereby creating a nucleic acid bound-affinity matrix; and

(iii) eluting the at least one nucleic acid from the nucleic acid-bound affinity matrix with an elution buffer thereby isolating nucleic acid.

9. The affinity column of claim 6, wherein said elution buffer comprises a chaotrope.

10. The affinity matrix of claim 7, wherein the antibiotic is selected from the group consisting of amikacin, gentamycin, kanamycin, neomycin, streptomycin, tobramycin, WP631, WP762, Daunorubicin, Echinomycin, tetracycline, and paraomycin.

11. The method of claim 8, wherein the sample is a biological sample.

12. The method of claim 11, wherein the biological sample is selected from the group consisting of blood, mucous, serum, saliva, urine, lymph, cerebrospinal fluid, and semen.

13. The method of claim 12, wherein the biological sample is blood.

14. The method of claim 8, wherein the at least one nucleic acid binding moiety is streptomycin.

15. The method of claim 8, wherein the at least one nucleic acid binding moiety is tetracyclin.

16. The method of claim 8, wherein the elution buffer comprises an aqueous solution containing 0.001 M to 0.1 M salt.