# DISEASES FOUND IN MANURE: A SOLUTION PROPOSAL FOR REDUCTION

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## Background

- Efficient use of animal manure can significantly reduce greenhouse gas emissions [1].
- Animal manure contains a lot of harmful pathogens, including Providencia spp. [2], E. Coli [3], and Salmonella spp.
- We aim to reduce some of these pathogens by genetically modifying [4] animals for increased pathogenic resistance.

## Results

| Genes | sgRNA (highest CRISPRscan score) | Locus (location) |
|---|---|---|
| SCA2 | GTGAGCCGTGGCGTCCGGCGGGG | 5:37431924-37431947 (+) |
| IRG1 | TGGACGGCGGCGATCCAGGGGGG | 5:490869-490892 (+) |
| CD79B | GAAAGGAGTGATGTCCTCGTAGG | 27:1274554-1274577 (+) |
| PTPN3 | CGTCGTGGCGGTGGCCGCAACGG | 2:84350067-84350090 (-) |
| SMOC0 | GAAGGCAGGAGCCGACCCAAAGG | 5:27234138-27234161 (-) |
| **Genes** | **sgRNA** | **Locus (location)** |
| CCL19 | GCAGCAGTCTTCAGCGTCGTTGG | 8:76054763-76054786 (+) |
| CXCL12 | GTGAGTGCGCCCAGCGACCGGGG | 28:45022553-45022576 (+) |
| IL16 | AGCTTTGGGACCGCCGCCGGTGG | 21:27086808-27086831 (-) |
| IL2RA | GGCCGTCATGCGCTGCGTGGGGG | 13:17485934-17485957 (+) |
| IL1A | GTCATTATTTGGACCGGTATAGG | 11:46493661-46493684 (-) |

## Conclusion

- SgRNA sequences can be edited using CRISPR-Cas9 technology (or in a lab) to genetically modify an organism
- More genes with immunological properties (such as cytokines) should be sequenced
- CRISPR scan is not 100% accurate [9]
- No lab, limited time and technology
- These edits need to be tested to ensure accuracy of the genetic modification and to confirm there aren't any side effects

## Wrap-Up

The components of animal manure: nutrients, organic matter, solids, energy, and fiber can be utilized for products such as fertilizer and biofuels [1]. Harmful pathogens get in the way of this, but those harmful pathogens may be mitigated with genetic modification.

## Methods

We identified 5 genes in the chicken genome [5] and cow genome [6] with potential immunological properties. We used CRISPR scan [7]---a program designed by Yale University---to identify sgRNA sequences [8], which can be used for gene editing. We used the sequence with the highest CRISPRscan score which determines the sgRNA sequence with the highest efficiency.

| ▲1 CRISPRscan score ▼2 | Locus | Target sequence |
|---|---|---|
| 59 | 11:46493661-46493684 (-) | GTCATTATTTGGACCGGTATAGG |
| 30 | 11:46488009-46488032 (+) | CGTCGTTCAGGATGCATTCCTGG |
| 29 | 11:46487975-46487998 (-) | AGTATAATTCGAGATATGTCAGG |
| 26 | 11:46486086-46486109 (-) | AGACGAACCCGTCTTGCTAAAGG |
| 20 | 11:46488048-46488071 (+) | AGTTGTATTTCACGTTACTCTGG |
| 82 | 11:46482972-46482995 (-) | TGGGGTGCCATTGCCTTCTCCGG |
| 80 | 11:46489679-46489702 (-) | GTGGTGATGGTGGCAGCCAGTGG |
| 79 | 11:46482972-46482994 (-) | GGGGTGCCATTGCCTTCTCCGG |
| 66 | 11:46483176-46483199 (+) | GCCTGGTGGGCTGCCGTCTATGG |
| 61 | 11:46489678-46489701 (-) | TGGTGATGGTGGCAGCCAGTGGG |

## Acknowledgements


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# SOURCES


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