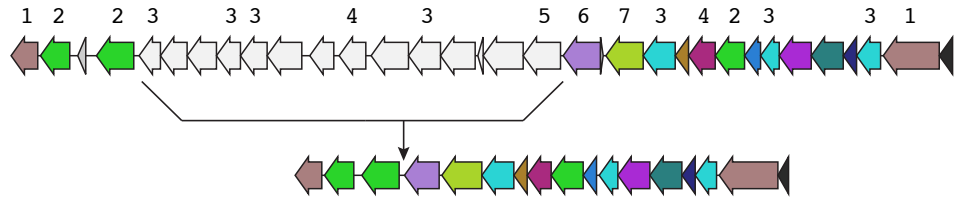
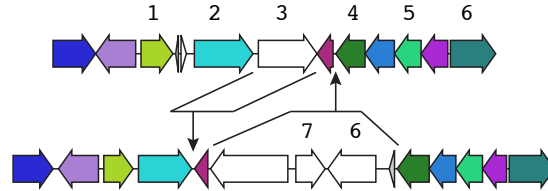


*Escherichia coli* MS 107-1  
HMPREF9345\_01709 - 017041  
35 kb



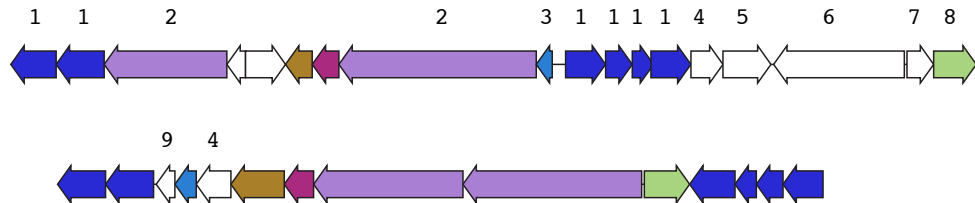
- |   |                                   |   |                    |
|---|-----------------------------------|---|--------------------|
| 1 | chain-length determinant protein  | 5 | phosphotransferase |
| 2 | sugar dehydrogenase / dehydratase | 6 | phosphoglucomutase |
| 3 | glycosyltransferase               | 7 | sugar isomerase    |
| 4 | sugar epimerase                   |   |                    |

*Streptomyces clavuligerus* ATCC 27064  
SCLAV\_0153-0165  
17 kb



- |   |                         |   |                               |
|---|-------------------------|---|-------------------------------|
| 1 | phosphotransferase      | 5 | enoyl-CoA hydratase/isomerase |
| 2 | amidase                 | 6 | AMP-dependent synthetase      |
| 3 | germacradienol synthase | 7 | pentalenene synthase          |
| 4 | acetyltransferase       |   |                               |

*Saccharopolyspora spinosa* NRRL 18395  
SspiN1\_010100010924-010100011009  
37 kb



*Streptomyces coelicolor* A3(2)  
SCO7690-7677 (coelibactin gene cluster)  
24 kb

- |   |                                 |   |                          |
|---|---------------------------------|---|--------------------------|
| 1 | transporter protein             | 6 | MSAS polyketide synthase |
| 2 | nonribosomal peptide synthetase | 7 | 3-oxoacyl-(ACP) synthase |
| 3 | thioesterase                    | 8 | AMP-dependent ligase     |
| 4 | cytochrome P450                 | 9 | methyltransferase        |
| 5 | carboxamide synthase            |   |                          |