

Visual Gene Developer 1.0 Build 606 [Sample construct - GFP v3.vgd]

File Edit Function Data Analysis Tool Network computing Window Help

New Open Save Project Explorer Toolbox Workspace

Project Explorer

Project

- Codon usage & W-table
- Gene construct
- Configuration
- Gene optimization
- Layer view

Toolbox

Refresh

Pre-defined tool

- CAI and GC content
- Codon usage table
- Repeated sequence
- Sequence comparison
- mRNA structure (fast)
- mRNA structure (slow)

User-defined tool

- GC content profile v2
- mRNA profile v2
- CAI profile v2

Codon bias diagram (based on RSCU)

Copy image Copy raw data Clone

PropertyBag Library

Reload New PropertyBag file Add new PropertyBag Delete PropertyBag Edit PropertyBag

Module Library

Reload New Script file Add new Module Delete Module Edit Module

Essential Script.vgs

- Common coding region
- Non-coding region
- Multiple cloning site
- Restriction enzyme site
- Monte-Carlo Codon Optim
- Check excluded sequenc
- Check restriction enzyme
- Check repeated sequenc
- Check CAI
- Check stable mRNA struc
- CAI
- Nc
- Mismatched DNA
- GC content
- mRNA -> Gibbs energy
- mRNA -> Structure
- ...

Module Editor [Essential Script.vgs : Codon bias diagram]

Test run Zoom Syntax coloring Show PropertyBag Stop (developing)

Source code Registration Category Sub

```
066 **** Draw codon bias diagram ****
067 CustomUI.Set_Font 8
068 For q = Current_ConstructIndex to Construct_End
069     SourceSeq=GeneConstruct.ParameterValue(q,ComponentIndex,"Modified DNA")
070     GeneService.Calculate_CodonUsage SourceSeq
071
072     CurrentY=(q-Current_ConstructIndex+1)*LineHeight+23
073     If q=Int(q/5)*5 Then
074         CustomUI.DrawString 5,CurrentY-1,CStr(q),"Black"
075     End If
076
077     Output_Str=Output_Str + CStr(q) + VbTab
078
079     For Triplet_1st=1 to 4
080         For Triplet_2nd=1 to 4
081             For Triplet_3rd=1 to 4
082                 CurrentTriplet=IndexToCGAT(Triplet_1st)+IndexToCGAT(Triplet_2nd)
083                 CurrentTriplet=CurrentTriplet+IndexToCGAT(Triplet_3rd)
084                 CodonAddress64 =GeneService.Get_CodonAddress_Type64(CurrentTriplet)
085                 CodonRSCU=GeneService.Get_CodonUsage_RSCU(CodonAddress64 )
086                 CurrentX=((Triplet_1st-1)*16+(Triplet_2nd-1)*4+(Triplet_3rd-1))*LineWidth+30
087                 CustomUI.Set_FillColor_byRGB CodonRSCU/3*255,0.255,CodonRSCU/3*255
088                 CustomUI.FillRectangle CurrentX,CurrentY,LineWidth,LineHeight
089             Next Triplet_3rd
090         Next Triplet_2nd
091     Next Triplet_1st
092     Output_Str=Output_Str + CStr(CodonRSCU) + VbTab
093 End For
```

Property Bag Editor [Sample PropertyBag.vgd]

Add parameter Delete parameter

Property bag

Parameter	Value
Original AA (Length=0)	
Original DNA (Length=0)	
Modified DNA	

GC content analysis

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CAI profile diagram

Copy image Copy raw data

mRNA binding energy profile

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