1. Interface Residue

```
> logit <- glm(Infection ~
Interface_Residues,data=data,family="binomial")
> summary(logit)

Call:
glm(formula = Infection ~ Interface_Residues, family = "binomial",
    data = data)

Deviance Residuals:
    Min      1Q   Median      3Q      Max
-1.9904  -0.3064   0.5155   0.5449   1.6819

Coefficients:
                   Estimate Std. Error z value Pr(>|z|)
(Intercept)         9.43109    4.27345   2.207   0.0273 *
Interface_Residues -0.11873    0.05901  -2.012   0.0442 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 20.597  on 16  degrees of freedom
Residual deviance: 14.490  on 15  degrees of freedom
AIC: 18.49

Number of Fisher Scoring iterations: 4
```

2. Van_der_Waals

```
logit <- glm(Infection ~ Van_der_Waals,data=data,family="binomial")
> summary(logit)

Call:
glm(formula = Infection ~ Van_der_Waals, family = "binomial",
    data = data)

Deviance Residuals:
    Min      1Q   Median      3Q      Max
-2.0717  -0.5572   0.5199   0.5871   1.5431

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    11.2770     5.0152   2.249   0.0245 *
Van_der_Waals   0.4294     0.2051   2.094   0.0363 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)
```

```
    Null deviance: 20.597  on 16  degrees of freedom
Residual deviance: 14.697  on 15  degrees of freedom
AIC: 18.697

Number of Fisher Scoring iterations: 4
```

3. Solvation polar

```
 logit <- glm(Infection ~ Solvation_Polar,data=data,family="binomial")
> summary(logit)

Call:
glm(formula = Infection ~ Solvation_Polar, family = "binomial",
    data = data)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.9850  -0.6936   0.5269   0.5807   1.6541

Coefficients:
                Estimate Std. Error z value Pr(>|z|)
(Intercept)      7.48307    3.43071   2.181   0.0292 *
Solvation_Polar -0.16464    0.08321  -1.979   0.0479 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 20.597  on 16  degrees of freedom
Residual deviance: 15.825  on 15  degrees of freedom
AIC: 19.825

Number of Fisher Scoring iterations: 4
```

4. Solvation Hydrophobic

```
> logit <- glm(Infection ~
Solvation_Hydrophobic,data=data,family="binomial")
> summary(logit)

Call:
glm(formula = Infection ~ Solvation_Hydrophobic, family = "binomial",
    data = data)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.9205  -0.3092   0.4363   0.4680   1.6999
```

```
Coefficients:
                    Estimate Std. Error z value Pr(>|z|)
(Intercept)          14.6096     6.2208   2.349   0.0188 *
Solvation_Hydrophobic 0.4715     0.2139   2.204   0.0275 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 20.597  on 16  degrees of freedom
Residual deviance: 11.700  on 15  degrees of freedom
AIC: 15.7

Number of Fisher Scoring iterations: 5
```

5.Entropy sidechain
```
> logit <- glm(Infection ~
Entropy_sidechain,data=data,family="binomial")
> summary(logit)

Call:
glm(formula = Infection ~ Entropy_sidechain, family = "binomial",
    data = data)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.7086  -0.3302   0.3950   0.4588   1.8552

Coefficients:
                  Estimate Std. Error z value Pr(>|z|)
(Intercept)         6.5753     2.6721   2.461   0.0139 *
Entropy_sidechain  -0.5896     0.2664  -2.214   0.0269 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 20.597  on 16  degrees of freedom
Residual deviance: 12.444  on 15  degrees of freedom
AIC: 16.444

Number of Fisher Scoring iterations: 5
```