

Results from stepwise-binomial logistic regression (method: backward) and Bootstrap resampling with replacement method.

The model with the best results in the analysis included amino acids tyrosine and phenylalanine.

```
> library(MASS)
> mod_step <- stepAIC(mod1, direction = "backward", trace = F)
> mod_step

Call:  glm(formula = Time_point ~ Tyr + Phe, family = "binomial", data =
data2)
```

```
Coefficients:
(Intercept)          Tyr          Phe
    -95.398         3.444        12.763
```

```
Degrees of Freedom: 85 Total (i.e. Null); 83 Residual
Null Deviance:      109.9
Residual Deviance: 44.06      AIC: 50.06
```

```
> library(bootStepAIC)
> mod_boot <- boot.stepAIC(mod1, data = data2, B=50)
There were 50 or more warnings (use warnings() to see the first 50)
> mod_boot
```

Summary of Bootstrapping the 'stepAIC()' procedure for

```
Call:
glm(formula = Time_point ~ ., family = "binomial", data = data2)
```

```
Bootstrap samples: 50
Direction: backward
Penalty: 2 * df
```

Covariates selected

```
(%)
Tyr 86
Phe 82
His 46
Lys 46
Trp 42
Met 34
Leu 26
Val 24
Asn 18
```

Coefficients Sign

```
+ (%) - (%)
Phe 100.00 0.00
Tyr 100.00 0.00
Lys 95.65 4.35
Asn 77.78 22.22
Trp 71.43 28.57
Leu 46.15 53.85
Val 41.67 58.33
Met 29.41 70.59
His 0.00 100.00
```

Stat Significance

(%)
Phe 68.29
Tyr 51.16
Trp 42.86
Met 41.18
Asn 33.33
Lys 30.43
Val 25.00
His 21.74
Leu 7.69

The stepAIC() for the original data-set gave

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(Intercept)	Tyr	Phe
-95.398	3.444	12.763

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Null Deviance: 109.9

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Stepwise Model Path

Analysis of Deviance Table

Initial Model:

Time_point ~ Asn + Val + Met + Leu + Tyr + Phe + Lys + His +
Trp

Final Model:

Time_point ~ Tyr + Phe

Step	Df	Deviance	Resid. Df	Resid. Dev	AIC
1			76	39.96552	59.96552
2 - Leu	1	0.02320367	77	39.98872	57.98872
3 - Met	1	0.02213946	78	40.01086	56.01086
4 - Asn	1	0.06069513	79	40.07156	54.07156
5 - Val	1	0.10460726	80	40.17617	52.17617
6 - Trp	1	0.91316813	81	41.08933	51.08933
7 - Lys	1	1.60707345	82	42.69641	50.69641
8 - His	1	1.36787326	83	44.06428	50.06428