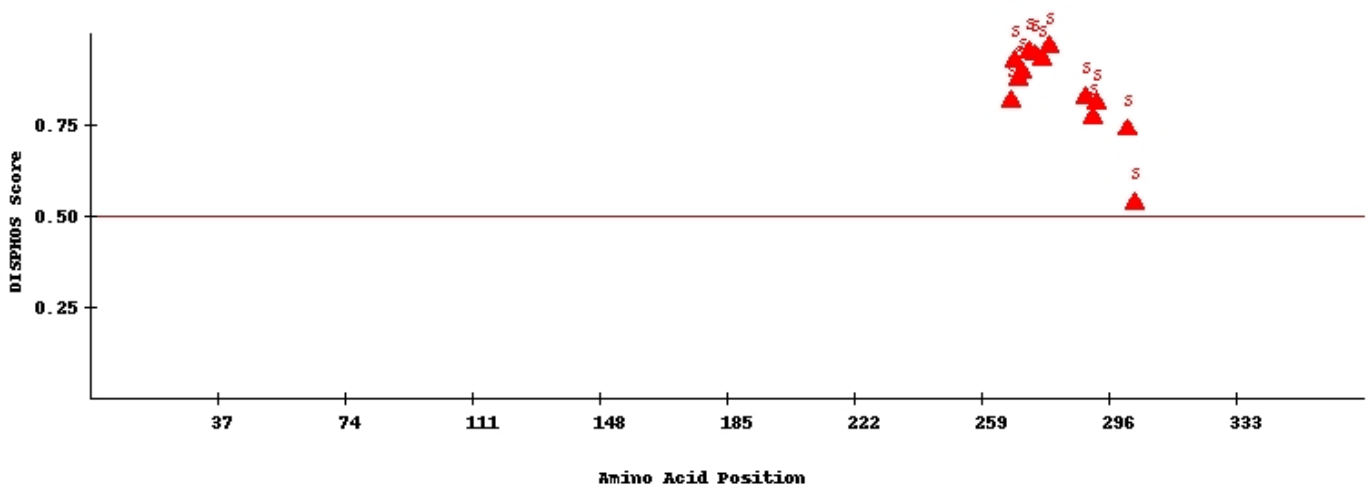


DISPHOS Results

> LiSIR2rp1

MTASPRAPHQEHVLGEP^TLEGLAH^YIREKNVRRILVLVGAGASVAAGIPDFR^SPD^TGI^YANLGK^YN
 LEDP^TDAF^SL^TLLREKPEIF^YS^IARELN^LWPGHFQ^PTAVHHFIRLLQDEGRLLRCCT^QNI^DGLEKA
 AGV^SPELLVEAHGSFAAAACIECH^TPF^SIEQ^NYLEAM^SG^TV^SRC^ST^CGGIVKPNVFFGENLPDAF
 FDALHHDAPIAELV^IIIG^TSMQVHPFALLPCVVPK^SVPRVVMNRERVGGLLFRFPDDPLN^TVHEDA
 VAKEGR^SS^SS^SQ^SR^SP^SA^SPRREEGG^TED^SP^SS^SPNEEVEEA^ST^SS^SS^SDG^YG^QY^GD^YHAHPDVCRDVL^F
 RGDCQENVV^TLAE^YLGL^SEALAKRMRL^SDAAPATAQRAPNET

results



Statistics

Number of phosphorylated serines: 13 out of 31 (41.935%)
 Number of phosphorylated threonines: 0 out of 17 (0.000%)
 Number of phosphorylated tyrosines: 0 out of 9 (0.000%)

| Position | Residue | Score | Sequence | Yes/No |
|----------|---------|-------|-------------------------------------|--------|
| 2 | T | 0.095 | ***MTASPR | |
| 4 | S | 0.180 | *MTASPRAP | |
| 18 | T | 0.036 | LGEPTLEGL | |
| 25 | Y | 0.041 | GLAHYIREK | |
| 43 | S | 0.051 | GAGASVAAG | |
| 53 | S | 0.091 | PDFRSPDTG | |
| 56 | T | 0.023 | RSPDTGIYA | |
| 59 | Y | 0.128 | DTGIYANLG | |
| 65 | Y | 0.044 | NLGKYNLED | |
| 71 | T | 0.017 | LEDP ^T DAFS | |
| 75 | S | 0.059 | TDAF ^S L ^T LL | |
| 77 | T | 0.005 | AFSL ^T LLRE | |

| | | | | |
|-----|---|-------|---------------------|-----|
| 87 | Y | 0.029 | PEIF Y SIAR | |
| 88 | S | 0.081 | EIFY S IARE | |
| 103 | T | 0.027 | HFQP T AVHH | |
| 123 | T | 0.005 | LRCC T QNIID | |
| 136 | S | 0.100 | AAGV S PELL | |
| 146 | S | 0.073 | EAHG S FAAA | |
| 157 | T | 0.014 | IECH T PFSI | |
| 160 | S | 0.026 | HTPF S IEQN | |
| 165 | Y | 0.024 | IEQN Y LEAM | |
| 170 | S | 0.052 | LEAM S GTVS | |
| 172 | T | 0.005 | AMSG T VSRC | |
| 174 | S | 0.034 | SGTV S RCST | |
| 177 | S | 0.030 | VSRC S TCGG | |
| 178 | T | 0.020 | SRC S TCGGI | |
| 217 | T | 0.003 | IIIG T SMQV | |
| 218 | S | 0.008 | IIGT S MQVH | |
| 234 | S | 0.102 | VVPK S VPRV | |
| 259 | T | 0.114 | DPLN T VHED | |
| 271 | S | 0.821 | KEGR S SSSQ | YES |
| 272 | S | 0.932 | EGR S SSSQS | YES |
| 273 | S | 0.878 | GR S SSQSR | YES |
| 274 | S | 0.899 | R S SSQSR | YES |
| 276 | S | 0.955 | SS S QSRSPS | YES |
| 278 | S | 0.947 | SQ S RSPSAS | YES |
| 280 | S | 0.934 | SR S PASPR | YES |
| 282 | S | 0.969 | SP S APRRE | YES |
| 290 | T | 0.294 | EEGG T EDSP | |
| 293 | S | 0.831 | GTED S PSSP | YES |
| 295 | S | 0.774 | ED S PS | YES |
| 296 | S | 0.814 | DS S PNEE | YES |
| 305 | S | 0.742 | VEEA S TSSS | YES |
| 306 | T | 0.065 | EEA S TSSSS | |
| 307 | S | 0.541 | EAS S TSSSD | YES |
| 308 | S | 0.480 | AST S SSDG | |
| 309 | S | 0.481 | ST S SSDGY | |
| 310 | S | 0.346 | TSS S SDGYG | |

| | | | |
|-----|---|-------|-----------|
| 313 | Y | 0.483 | SSDGYGQYG |
| 316 | Y | 0.216 | GYGQYGDYH |
| 319 | Y | 0.165 | QYGDYHAHP |
| 341 | T | 0.004 | ENVVTLAEY |
| 345 | Y | 0.031 | TLAEYLGLS |
| 349 | S | 0.109 | YLGLSEALA |
| 359 | S | 0.389 | RMRLSDAAP |
| 365 | T | 0.279 | AAPATAQRA |
| 373 | T | 0.051 | APNET**** |

*An asterisk indicates prediction by similarity to the training sequences