

|               |                             |
|---------------|-----------------------------|
| Email         | l.a.kelley@imperial.ac.uk   |
| Description   | P0AD03                      |
| Date          | Thu Jan 5 11:19:33 GMT 2012 |
| Unique Job ID | 27829163bd5e48f3            |

|                     | 1                                                              | 10  | 20  | 30  | 40  | 50  | 60 |
|---------------------|----------------------------------------------------------------|-----|-----|-----|-----|-----|----|
| Sequence            | MALNTPQITPTKKITVRAIGEELPRGDYQRCPCQCDMLFSLPEINSHQSAYCPRCQAKIR   |     |     |     |     |     |    |
| Secondary structure |                                                                |     |     |     |     |     |    |
| SS confidence       |                                                                |     |     |     |     |     |    |
| Disorder            | ????????????????????? ? ? ? ? ?                                |     |     |     |     |     |    |
| Disorder confidence |                                                                |     |     |     |     |     |    |
|                     | 70                                                             | 80  | 90  | 100 | 110 | 120 |    |
| Sequence            | GRDWSLTRLAAMAF TMLLMPFAWGEPLLHIWLLGIRIDANVMQGIWQMTKQGDAITGSM   |     |     |     |     |     |    |
| Secondary structure |                                                                |     |     |     |     |     |    |
| SS confidence       |                                                                |     |     |     |     |     |    |
| Disorder            | ? ? ? ? ? ? ? ? ? ?                                            |     |     |     |     |     |    |
| Disorder confidence |                                                                |     |     |     |     |     |    |
|                     | 130                                                            | 140 | 150 | 160 | 170 | 180 |    |
| Sequence            | VFFCVIGAPLILVTSLAYLWFGNRLGMNLRPVLMLERLKEVWMLDIYLVGIGVASIKVQ    |     |     |     |     |     |    |
| Secondary structure |                                                                |     |     |     |     |     |    |
| SS confidence       |                                                                |     |     |     |     |     |    |
| Disorder            | ? ? ? ?                                                        |     |     |     |     |     |    |
| Disorder confidence |                                                                |     |     |     |     |     |    |
|                     | 190                                                            | 200 | 210 | 220 | 230 | 240 |    |
| Sequence            | DYAHIQAGVGLFSFVALVILTTVTLSHLNVEELWERFYPQRPATRRDEKLRVCLGCHFTG   |     |     |     |     |     |    |
| Secondary structure |                                                                |     |     |     |     |     |    |
| SS confidence       |                                                                |     |     |     |     |     |    |
| Disorder            | ? ? ? ? ? ? ? ? ? ?                                            |     |     |     |     |     |    |
| Disorder confidence |                                                                |     |     |     |     |     |    |
|                     | 250                                                            | 260 | 270 | 280 | 290 | 300 |    |
| Sequence            | YPDQGRGRCPRCHILRLRRRHSLQKCVAAALLASIVLLLPANLLPISIIYLVNNGRQEDTIL |     |     |     |     |     |    |
| Secondary structure |                                                                |     |     |     |     |     |    |
| SS confidence       |                                                                |     |     |     |     |     |    |
| Disorder            | ? ? ? ? ? ? ? ?                                                |     |     |     |     |     |    |
| Disorder confidence |                                                                |     |     |     |     |     |    |
|                     | 310                                                            | 320 | 330 | 340 | 350 | 360 |    |
| Sequence            | SGIMSLASSNIAVAGIVFIASILVFPFTKVI VMFTLLLSIHFKCQQGLRTRILLRMTVWI  |     |     |     |     |     |    |
| Secondary structure |                                                                |     |     |     |     |     |    |
| SS confidence       |                                                                |     |     |     |     |     |    |
| Disorder            | ? ? ? ? ? ?                                                    |     |     |     |     |     |    |
| Disorder confidence |                                                                |     |     |     |     |     |    |
|                     | 370                                                            | 380 | 390 | 400 | 410 | 420 |    |
| Sequence            | GRWSMLDLFVILSLTMSLINRDQILAF TMGPAAFYFGAAVILTILAVEWLDSRLLWDAHES |     |     |     |     |     |    |
| Secondary structure |                                                                |     |     |     |     |     |    |
| SS confidence       |                                                                |     |     |     |     |     |    |
| Disorder            | ? ? ? ? ? ?                                                    |     |     |     |     |     |    |
| Disorder confidence |                                                                |     |     |     |     |     |    |

