

|               |                             |
|---------------|-----------------------------|
| Email         | l.a.kelley@imperial.ac.uk   |
| Description   | P30864                      |
| Date          | Thu Jan 5 11:46:41 GMT 2012 |
| Unique Job ID | 2644b262e3825524            |

|                     | 1          | 10         | 20                                       | 30 | 40 | 50 | 60 |
|---------------------|------------|------------|--|----|----|----|----|
| Sequence            | MKATSEELAI | FVSVVESGSF | SRAAEQLGQANSAVSRAVKKLEMKLGVSLLNRTTRQLSLT |    |    |    |    |
| Secondary structure |            |            |  |    |    |    |    |
| SS confidence       |            |            |  |    |    |    |    |
| Disorder            | ?          | ?          | ?  | ?  |    |    |    |
| Disorder confidence |            |            |  |    |    |    |    |

  

|                     | 70  | 80 | 90 | 100 | 110 | 120 |
|---------------------|---|----|----|-----|-----|-----|
| Sequence            | EGERYFRRVQSILQEMAAAESEIMETRNTPRGLLRIDAATPVVLHFLMPLIKPFRERYP |    |    |     |     |     |
| Secondary structure |   |    |    |     |     |     |
| SS confidence       |   |    |    |     |     |     |
| Disorder            |   |    | ?  | ?   | ?   | ?   |
| Disorder confidence |   |    |    |     |     |     |

  

|                     | 130   | 140 | 150 | 160 | 170 | 180 |
|---------------------|---|-----|-----|-----|-----|-----|
| Sequence            | EVTLSLVSSETIINLIERKVDVAIRAGTLTDSSLRARPLFNSYRKIIASPDYSRYGKPE |     |     |     |     |     |
| Secondary structure |   |     |     |     |     |     |
| SS confidence       |   |     |     |     |     |     |
| Disorder            |   |     | ?   | ?   |     |     |
| Disorder confidence |   |     |     |     |     |     |

  

|                     | 190   | 200 | 210 | 220 | 230 | 240 |
|---------------------|---|-----|-----|-----|-----|-----|
| Sequence            | TIDDLKQHICLGFTEPASLNTWPFIARSDGQLHEVKYGLSSNSGETLKQLCLSGNGIACLS |     |     |     |     |     |
| Secondary structure |   |     |     |     |     |     |
| SS confidence       |   |     |     |     |     |     |
| Disorder            | ?   |     | ?   | ?   | ?   | ?   |
| Disorder confidence |   |     |     |     |     |     |

  

|                     | 250   | 260 | 270 | 280 | 290 | 300 |
|---------------------|---|-----|-----|-----|-----|-----|
| Sequence            | DYMI DKEI ARGELVELMADKVLVPVEMPFSAVYYSDRAVSTRI RAFI DFLSEHVKTAPGGA |     |     |     |     |     |
| Secondary structure |   |     |     |     |     |     |
| SS confidence       |   |     |     |     |     |     |
| Disorder            |   |     | ?   |     |     | ?   |
| Disorder confidence |   |     |     |     |     |     |

  

|                     | V | R | E | A |
|---------------------|---|---|---|---|
| Sequence            | V | R | E | A |
| Secondary structure |   |   |   |   |
| SS confidence       |   |   |   |   |
| Disorder            | ? | ? | ? | ? |
| Disorder confidence |   |   |   |   |

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand