```
         α1                    β1              β2         α2            α3
2W0N  GHMGLEPYEISTLFEQR---QAMLQSIKEGVVAVDD-RGEVTLINDAAQELLNY---RKS
2GJ3  -------------ELLPEIFRQTVEHAPIAISITDL-KANILYANRAFRTITG-Y-GSEE
3B33  -SNAMDTSLPSAILNNMV----------TATLILDDG-LAIRYANPAAELLFS-QS-AKR


         α4           α5          β3            β4
2W0N  QDDEKLSTLSHS--WSQVV-DVSEVLRD----GTPRRDEEITIK---D---RLLLINTVP
2GJ3  VLGKNESIL-SN--GTTPRLVYQALWGRLAQKKPWSGVLVNRR--KDK-TLYLAELTVAP
3B33  IVEQSLSQLI--QHASLDLALLTQPLQSGQSI----TDSDVTFVVD--GRPLMLEVTVSP


         β5
2W0N  VRSN-GVIIGAISTFRDKT---
2GJ3  VLNEAGETIYYLGMHRDTSELH
3B33  ITWQRQ--LMLLVEMRKID---
```

Figure S2: An example multiple sequence alignment of PAS domains. Sequences are labeled with their PDB identifiers. The alignment was generated using PRALINE. α-helix and β-strand assignments obtained from each PDB entry are marked in red and blue shades, respectively, and they are labeled above the alignment. Sequences used are: 2W0N (DcuS, *Escherichia coli*), 2GJ3 (NifL, *Azotobacter vinelandii*), and 3B33 (NR(II), *Vibrio parahaemolyticus*). The entire alignment including all identified PAS domain sequences with their secondary structures is available from: http://bioinfolab.unl.edu/emlab/PAS_PDC

```
              α1              α2            α3
3BY8  GSSQISDMTRDGLANKALAVARTLADSPEIRQGLQKKPQESGIQAIAEAVRKRNDLLFIV
1P0Z  -----EERLHYQVGQRALIQAMQISAMPELVEAVQKRD-LARIKALIDPMRSFSDATYIT
3B42  ------RSSLDLQLKNARNLAGLII--HDIDGYMMKGD-SSEVDRFISAVKSKNFIMDLR


       β1    β2     α4        α5          β3            β4
3BY8  VTDMQSLRYSHPEAQRIGQPFKGDDILKALN-GEENVAINRGFLAQALRVFTPIYDENH-
1P0Z  VGDASGQRLYHVNPDEIGKSMEGGDSDEALINAKSYVSVRKGSLGSSLRGKSPIQDATG-
3B42  VFDEQAKEVSPTPSQTPNAKI----QQAIAAGRTLEFKET-LDGKRTLSLVLPFPNEQRC


            β5        α6
3BY8  --------KQIGVVAIGLELSRVTQQINDSRW
1P0Z  --------KVIGIVSVGYTIEQLEHH------
3B42  QSCHDAGAAYLGGLLVTTSIEEGYEGARH---
```

Figure S3: An example multiple sequence alignment of PDC domains. Sequences are labeled with their PDB identifiers. The alignment was generated using PRALINE. α-helix and β-strand assignments obtained from each PDB entry are marked in red and blue shades, respectively, and they are labeled above the alignment. Sequences used are: 3BY8 (DcuS, *Escherichia coli*), 1P0Z (CitA, *Klebsiella pneumoniae*), and 3B42 (Mcp40H-20, *Geobacter sulfurreducens*). The entire alignment including all identified PDC domain sequences with their secondary structures is available from: http://bioinfolab.unl.edu/emlab/PAS_PDC