

```

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

                α4                α5                β3                β4
2W0N    QDDEKLSLTSHS--WSQVV-DVSEVLRD----GTPRRDEEITIK---D---RLLLINTVP
2GJ3    VLGKNEISIL-SN--GTPRLVYQALWGRLAQKKPWSGVLVNRR--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    GSSQISDMTRDGLANKALAVARTLADSPETIROGLQKKPQESG IQAIAEAVRKRNDLLFIV
1P0Z    -----EERLHYQVGQRALIQAMQISAMPPELVEAVQKRDLARIKALIDPMRSFSDATYIT
3B42    -----RSSLDLQQLKNARNLAGLI I--HDIDGYMKGDSSEVDRFISAVKSKNFIMDLR

                β1    β2    α4    α5    β3    β4
3BY8    VTDMQSLRYSHPEAQRIGQPFKGGDDILKALN-GEENVAINRGFLAQLRVFTPIYDENH-
1P0Z    VGDASGQRLYHVNPEIGKSMEGGDSDEALINAKSYVSVRKGSLGSSLRGKSPIQDATG-
3B42    VFDEQAKEVSPTPSQTPNAKI----QQAIAAGRTLEFKET-LDGKRTLSTLVLPFPNEQRC

                β5    α6
3BY8    -----KQIGVVAIGLELSRVTQQINDSRW
1P0Z    -----KVIGIVSVGYTIEQLEHH-----
3B42    QSCHDAGAAYLGLLVTTSTIEEGYEGARH---

```

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