

(~25)-GNHD/E) is found in a wide variety of phosphoesterases (Koonin, 1994; Zhuo *et al*, 1994), ranging from eubacteria to vertebrates, including 5'-nucleotidase (Table 1-1).

SOURCE	MOTIF I	MOTIF II	MOTIF III
Bacteriophage λ PPase	16 WVV L CYT	17 LISV LV	17 AV QMM
ApaH	4 YLI V CYD	17 LWLT LVA	19 LVL LHL
RdgC	154 TVC L KLD	17 YVFN FV	23 LN DSV
PPZ	415 KIV V QYG	16 YLFL YV	23 LL CAN
PP1	57 KIC V QYS	16 YLFL YV	23 LL CAS
<i>E. coli</i> exonuclease SBCD	4 LHTS W LGQN	28 IIVA VFT	25 VLA SVA
ORF3	4 LHTA W LGKT	28 IVMA AFT	26 VIA NPD
GP47	4 LNL W LGVK	29 WIQY IFV	26 TIV LHY
SHP	6 AQIT L LLVD	28 LLS LS D	21 AIA QPE
<i>C. burnetii</i> unknown ORF	9 AQVS L LTSE	27 IFIT IS D	21 VIP DVN
CpdB	27 METT L SNMM	33 LVDN LIQG	31 GTL FNY
VNTD	41 LHTN H RFW	31 LLSG INTG	23 MAL FDN
<i>H. sapiens</i> 5'-nucleotidase	32 LHTN V SRLE	37 LLDA QYQG	23 MAL FDN
ACL	45 LAFN F NLE	43 VVSA LISAS	24 DAV FDR
<i>E. coli</i> 5'-nucleotidase	37 LHTN H HFW	31 LLSG INTG	23 MAI FDN
ASM	202 LFLT L WDHD	60 VYWT IPAHA	31 PAV SIP
DBR1	7 AVQGCC QLN	17 LILL FQSI	36 FIG SMR

Table 1-1: Sequence alignment of conserved phosphoesterase domains

Sequence alignment by Zhuo *et al*, 1994. Conserved residues are shaded, and numbers between domains indicate the number of separating amino acids. Source abbreviations are as follows: ApaH: *E. coli* diadenosine tetraphosphatase; RdgC: *D. melanogaster* retinal degeneration protein; *S. cerevisiae* phosphoprotein phosphatase PP-Z1; PP1: *Zea mays* phosphoprotein phosphatase PP1; ORF3: *B. subtilis* hypothetical protein; GP47: Bacteriophage T4 exonuclease protein GP47; SHP: *Synechococcus sp.* hypothetical protein; CpdB: *E. coli* 2',3'-cyclic nucleotide 2'-phosphodiesterase; VNTD: *Vibrio parahaemolyticus* 5'-nucleotidase; ACL: *Acinetobacter calcoaceticus* unknown ORF L; ASM: *Homo sapiens* sphingomyelin phosphodiesterase; DBR1: *S. cerevisiae* RNA debranching enzyme.

Identification of this phosphoesterase signature motif suggests that this diverse group of enzymes uses elements of a common catalytic strategy for phosphate ester hydrolysis (Zhuo *et al*, 1994). Mutagenesis studies undertaken on the bacteriophage λ PPase have confirmed the critical roles of a number of residues, highly conserved throughout the PPase family, in metal ion binding and catalysis for this enzyme (Zhuo *et al*, 1994). It should be noted that bacteriophage λ PPase does not have a permanently associated metal ion, and is not a metallo-enzyme in that sense. Mn^{2+} or Ni^{2+} activates phosphatase activity, however, and other transition metal ions such as Zn^{2+} , Cu^{2+} and