

## LYMPHOCYTE ACTIVATION: THE COMING OF THE PROTEIN TYROSINE PHOSPHATASES

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### 1. ABSTRACT

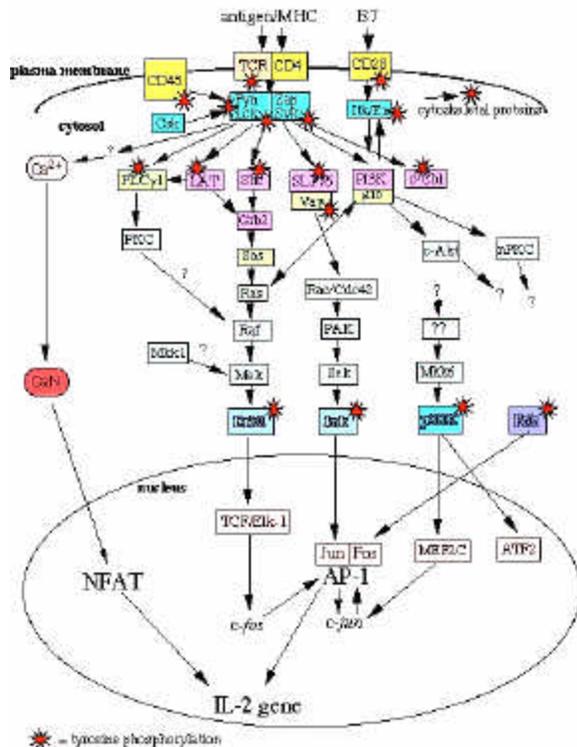
The molecular mechanisms of signal transduction have been at the focus of intense scientific research worldwide. As a result, our understanding of protein tyrosine kinase-mediated signaling has advanced at an unprecedented pace during the past decade. In contrast, the study of protein tyrosine phosphatases is in its infancy, but is currently gathering momentum and is predicted to become a "hot topic" in the field within the next few years. This review summarizes the current state-of-the art in our understanding of the structure, regulation and role of protein tyrosine phosphatases in lymphocyte activation.

### 2. INTRODUCTION

Phosphorylation of proteins on tyrosyl residues is an important mechanism for many signal transduction pathways controlling cell growth, differentiation and development (1-3). Although the phosphotyrosine (PTyr)

content of cellular proteins is the net result of the opposing effects of protein tyrosine kinases (PTKs) and protein tyrosine phosphatases (PTPases), most investigators have concentrated on the PTKs, many of which were cloned and sequenced nearly two decades ago. The first PTPase was not cloned until 1990 and most PTPases have been known for less than five to seven years. Although our progress has been remarkable, and clearly is accelerating, very little is still known about most of these enzymes. It is also likely that many more PTPases remain to be discovered. Presently some 50 mammalian PTPases have been described and a recent estimate puts the total number of PTPase genes in the human genome at 500 (4). This number should be compared to the predicted number of recognized genes for protein kinases: 1,000-3,000 (2), of which roughly half are thought to be specific for tyrosine. Despite this estimated ratio of PTKs to PTPases, the level of PTyr in normal cells is only 0.1-0.01% of acid-stable protein-bound phosphate,

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**Figure 1.** Schematic overview of main signaling pathways in T lymphocyte activation. The most important co-receptors are shown in yellow, the PTKs are dark blue, the secondary signaling molecules are adapters (pink) or enzymes (pale green), small GTPases are even paler green, the downstream Ser/Thr protein kinases are pale blue, and transcription factors are flesh colored, calcineurin (CaN) is red. Tyrosine phosphorylated proteins, which are substrates for PTPases, are indicated with a red star.

or 3-4 orders of magnitude lower than the level of phosphoserine (PSer) and phosphothreonine (PThr), suggesting that the cellular PTPases readily counteract the PTKs in normal cells. Whether this is due to a high number of expressed PTPases, high expression levels of some PTPases, or high specific activity, is not known. Importantly, even a small increase in steady-state tyrosine phosphorylation caused by deregulation or overexpression of some PTKs, notably members of the Src family (5), can induce acute malignant transformation and uncontrolled proliferation of cells. Also physiological processes mediated by tyrosine phosphorylation (e.g. signal transduction) are accompanied by relatively small and transient increases in cellular PTyr. Thus, it seems clear that PTPases play an important role in the maintenance of normal cell physiology by counteracting substrate phosphorylation by the PTKs. To complicate matters, we and others have found that some PTPases directly regulate the PTKs, either negatively or positively (5-10), by dephosphorylating specific regulatory tyrosine phosphorylation sites in these PTKs. At the same time, some PTPases are also phosphorylated by the PTKs (11-20), indicating that PTK - PTPase interactions can be rather complex. There are already examples of PTPases that are

regulated by phosphorylation on tyrosine, threonine or serine residues and therefore also must be dephosphorylated by themselves ('autodephosphorylation') or by other protein phosphatases, perhaps forming 'phosphatase cascades' analogous to the kinase cascades involved in many signal transduction processes.

Like most normal cells, resting lymphocytes contain very low levels of PTyr, presumably reflecting the finding that overall PTPase activity is several orders of magnitude higher than overall PTK activity (6). This conclusion is in agreement with the truly dramatic increase in intracellular tyrosine phosphorylation that follows a brief treatment of T cells with membrane-permeable PTPase inhibitors, such as phenylarsine oxide (21) or pervanadate (22,23). The increase in PTyr-content after addition of these pharmacological agents is detectable within seconds and quickly reaches levels that far exceed the response to any physiological stimuli. These experiments underscore the importance of PTPases in the maintenance of the resting levels of tyrosine phosphorylation. Since these inhibitors also cause many functional events of T cell activation (22,23) and prevent reversion of activated T blasts to a resting state (24), it seems that PTPases play a crucial part in maintenance of the resting phenotype of lymphocytes.

Lymphocyte activation is a convenient and popular model for studying signal transduction and mitogenesis. Consequently, the molecular mechanisms of antigen receptor-mediated signaling are relatively well understood (although many questions do remain unresolved). When lymphocytes are activated by ligation of their receptors or other mitogens together with appropriate co-receptors or accessory molecules, there is a very rapid, but transient, increase in PTyr in a number of cellular proteins (25-27, reviewed in 28,29). Our observation (30) that inhibition of this response by pharmacological means blocks lymphocyte activation completely gave rise to the current dogma that the first event triggered by receptor ligation is the activation of one or several PTKs (5,30,31). Several PTKs are currently known to participate in the initiation of lymphocyte activation. Using homologous recombination, transgenic mice, and mutant cell lines, it has been demonstrated that two members of the Src family of PTKs, Lck and Fyn, are important (31-39) in T cells, although their relative contribution and redundancy remains unclear. In B cells, the corresponding Src family PTKs are Lyn, Blk and Fyn, while natural killer (NK) cells also utilize c-Fgr (5). The two Syk family PTKs ZAP-70 and Syk are also activated within the first minute (28,40) and lack of a functional *zap* gene is known to cause a severe immunodeficiency in humans (41). TCR crosslinking also transiently activates the Csk kinase (42), which negatively regulates Lck and Fyn (43). Finally, the Tec family PTKs Btk and Itk/Emt (44,45) are activated in B cells and T cells, respectively. The importance of these PTKs is also demonstrated by the transforming capacity of some of them (5) and the observed changes in amount or function of them in malignancies, e.g. in T cell lymphomas (46-48), and in T cell anergy (5).

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The molecular mechanisms of signal transduction and lymphocyte activation have been intensely studied during past few years (5,49-51). The major signaling pathways are delineated schematically in figure 1. It has been firmly established which PTKs carry the main responsibility for initial signal transmission and these enzymes, their physiological importance, regulation, and substrates have been thoroughly studied. In contrast, it is far from clear which PTPases are involved in lymphocyte activation, how they are regulated or what substrates they act on. In fact, it is likely that the most important PTPases have not yet been found. Although the main focus of most researchers has been on the PTKs, it is generally acknowledged that PTPases are likely to be equally important in the propagation and coordination of the signaling cascades (52-56). We predict that there will be a sharply increasing interest in PTPases within the next few years, accompanied by many significant breakthroughs in our understanding of these enzymes and their roles in physiological processes. They will also become the focus of targeted drug discovery for the treatment of human diseases. This review will present all the PTPases that are known or suspected to be expressed in lymphocytes. We will summarize and discuss their known, suspected or potential roles in lymphocyte physiology.

### 2. 1. PTPases present in lymphocytes

The purification to homogeneity in 1988 of the first PTPase, PTP1B from human placenta (57,58), and the subsequent isolation of its cDNA in 1990 (59), provided the required basis for a search for related genes using a number of molecular biology techniques. The sequence of PTP1B also revealed that a well-known molecule, the leukocyte common antigen CD45, was a PTPase with two catalytic domains in tandem in its cytoplasmic tail (60). Thus it became clear from the very start that PTPases can be transmembrane molecules or entirely intracellular enzymes, and that they can have more than one PTPase domain. During the early part of the 90s, a number of PTPases related to PTP1B and CD45 were discovered in eukaryotic cells from yeast to man (52-56). All these enzymes share several regions of homology, including a well-conserved signature sequence motif (HCXXGXXR). PTP1B was recently crystallized and its three-dimensional structure solved (61). The structure showed that the cysteine residue of the signature sequence resides at the bottom of a deep hydrophobic catalytic pocket and is a crucial component of the catalytic machinery (62). Specificity for phosphotyrosine is, at least partly, determined by the depth of the pocket (63). During catalysis the phosphate moiety is transferred from the substrate to the cysteine to form an enzyme-phosphocysteine intermediate, which is regenerated through the formation of free phosphate with the help of a water molecule (64).

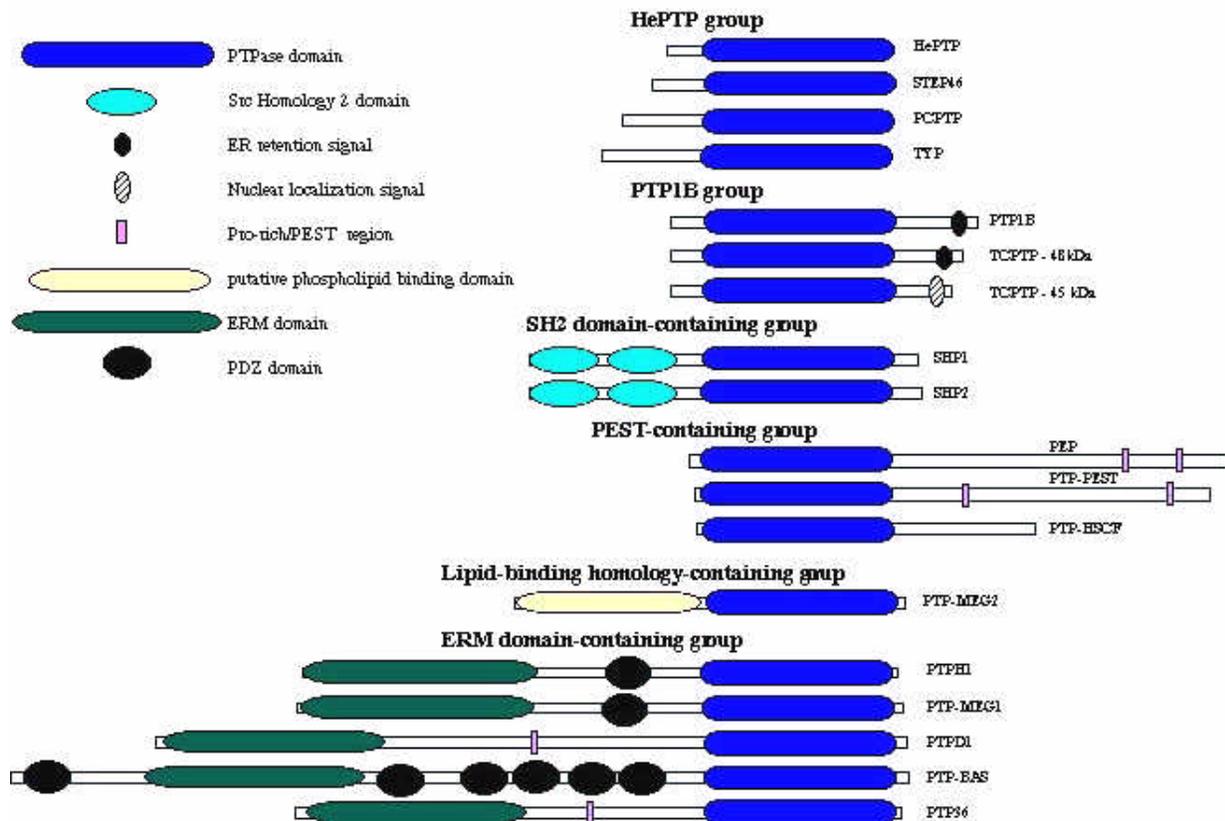
The "classical" PTPases comprises the largest family of PTPases and contains all currently known transmembrane enzymes, as well as PTP1B, and several related intracellular enzymes, all with a ~250 amino-acid catalytic domain with a relatively high degree of similarity. All intracellular members of this family have one copy of the catalytic domain, which can be located anywhere in the

molecules. In contrast, many transmembrane PTPases have two PTPase domains in tandem in their intracellular C-terminal part. In many cases, the second domain appears to be enzymatically inactive and its function remains speculative. The classical PTPases can be further subdivided in subfamilies or groups based on overall structure and the presence of other domains (figure 2). For example, the group consisting of SHP1 and SHP2 is characterized by two SH2 domains in the N-terminal half of the molecule and a PTPase domain in the C-terminal half. Another group, often referred to as the "cytoskeletal" PTPases, is characterized by an N-terminal region of homology to band 4.1 and other cytoskeletal proteins (termed the ERM domain), a central region often with at least one PDZ domain, and a C-terminal PTPase domain. The PEST group consists of enzymes with an N-terminal PTPase domain and C-terminal region rich in proline, glutamic acid, serine and threonine. These enzymes will all be discussed in detail below.

In addition to the "classical" family of PTPases with a high degree of similarity to PTP1B and CD45, another family of enzymes that not only dephosphorylate PTyr, but also Pser and PThr, was discovered by K. Guan and J. Dixon (65). The founding member of this family of dual-specific protein phosphatases was the VH1 protein from Vaccinia virus (65). A closely related enzyme was subsequently found in mammalian cells and termed VHR for VH1-related (66). The majority of the members of the dual-specificity phosphatase group specifically dephosphorylate PThr and PTyr in one or several kinases that belong to the MAP kinase family (reviewed in 67-69). Interestingly, there are currently 9 known dual-specificity phosphatases (often collectively termed MKPs), but only 7 known MAP kinases: Erk1, Erk2, Erk5, Jnk1, Jnk2, p38, and p38beta. One reason for this excess of phosphatases might be that some of them have restricted expression profiles, while the MAP kinases are expressed in all tissues and cell types. Thus, only a few MKPs might be present in any one cell. The structure of these enzymes is presented in figure 3.

Finally, a number of much more distantly related proteins have been identified, which may be specific for PTyr, but in some cases are dual-specific or have an unclear specificity in intact cells. These enzymes share the CXXXXXXR motif with the classical PTPases, and include the cell cycle regulators CDC25 (70) and KAP (71), and the low Mr PTPases LMPTP (72), PRL-1 (73), PRL-2 (74), PRL-3 (74). Finally, two enzymes that have the PTPase signature sequence, PTEN (75,76) and CEL-1 (77), were recently discovered to be specific for non-protein substrates: PTEN dephosphorylates inositol phospholipids (78) and the *C. elegans* protein CEL-1 dephosphorylates RNA as part of the mRNA capping process (77). Thus, the "PTPase signature sequence" is not unique to enzymes hydrolyzing phosphoesters in protein substrates. Rather it seems that the PTPases have evolved from several different ancestral cysteine-based hydrolases specific for many other types of substrates. These primordial enzymes apparently provided a starting point for the evolution of PTPases in parallel with the appearance of dual-specific protein

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**Figure 2.** Structure of the intracellular classical PTPases. The enzymes are aligned for their ~260-amino acid PTPase domain and the location of different domains (key in upper left had corner) indicated. All PTPases are shown in the same scale, except PTP-BAS, which is shown shorter than its actual relative size. CAAX, isoprenylation/farnesylation signal.

kinases (e.g. Mek) and PTKs during the transition from unicellular to multicellular organisms some 570-600 million years ago.

Lymphocytes express many, but not all, of the known PTPases (table 1). The leukocyte common antigen, CD45, seems to be the predominant transmembrane PTPase on most leukocytes, and it is expressed at very high levels in lymphocytes. Very little is known about other transmembrane PTPases in lymphocytes. Therefore, we have decided to ignore them in this review. Table 1 contains all currently known intracellular PTPases, including their numerous synonyms. For many, the information on their tissue distribution has not been published and it remains unclear if they are present in lymphocytes.

### 2. 2. The targets and specificity of PTPases in lymphocyte activation

Many molecules that regulate lymphocyte activation become transiently tyrosine phosphorylated following receptor ligation (figure 1). As a general rule, these molecules are phosphorylated on multiple sites with each site potentially having its own specific impact on the function of the molecule. Each site may be phosphorylated by a different PTK (43,131), even if target sites for individual PTKs often are clustered. Naturally, all these

proteins must also be substrates for cellular PTPases. It remains unknown, however, how many PTPases are required. Are PTPases very specific for their substrates? How many substrates does each PTPase have? The case of the MAP kinase-specific phosphatases suggests that the number of phosphatases may even exceed the number of their targets.

Recent findings indicate that many PTPases display a high degree of substrate specificity. As in the case of the PTKs, PTPases are often remarkably selective when tested *in vitro* towards phosphorylated peptides and proteins, and it is widely held that they are even more selective in intact cells. Some PTPases seem to prefer PTyr residues preceded and followed by specific amino acid residues (132,133). For example, PTP1B strongly prefers acidic residues N-terminal of the target phosphotyrosine and a methionine or glycine immediately C-terminal of it (132). In intact cells, this intrinsic substrate specificity is combined with a selective targeting of the enzyme to specific subcellular compartments or to multisubunit protein complexes by the presence of protein-protein interaction domains or "zip codes" (134). Examples include the binding of SHP1 and SHP2 via their SH2 domains to certain tyrosine phosphorylated sites on other proteins, the association of the non-catalytic C-termini of TCPTP with substrate proteins or regulators, the binding of proteins

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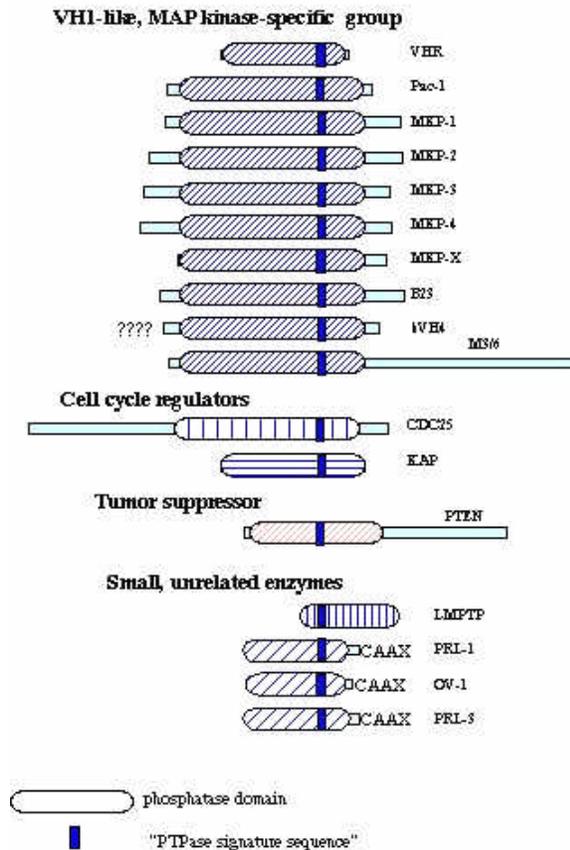
**Table 1.** Currently known mammalian cytoplasmic PTPases

<b>PHOSPHATASE (SYNONYMS)</b>	<b>CHR. LOC.</b>	<b>PROTEIN Mr</b>	<b>IN</b>	<b>T</b>	<b>REF<sup>a)</sup></b>
<b>I. CLASSICAL PTPases</b>					
<b>HePTP group</b>					
HePTP (LCPTP)	1q32.1	38-40 kDa	Yes		79,80
STEP	11p15.2-p15.1	20 <sup>b)</sup> , 38 <sup>b)</sup> , 46, 61	No		81
PCPTP (=PTPBR7, PC12-PTP1)		42, 65 kDa	No		82, 83, 84
TypPTP		40, 45 kDa	No		85
<b>PTP1B group</b>					
PTP1B	20q13.1-13.2	50 kDa	No		59
TCPTP (=MPTP, PTP-S)	18p11.2-11.3	45, 48 kDa	Yes		86
<b>SH2 domain-containing group</b>					
SHP1 (=PTP1C, SH-PTP1, HCP, PTPN6)	12p12-13	67 kDa	Yes		87-90
SHP2 (=SH-PTP2, Syp, PTP1D, PTP2C, SH-PTP3,	12q24.1	70 kDa	Yes		91-94
<b>PEST-containing group</b>					
PEP		110 kDa	Yes		87
PTP-PEST (=PTP-P19, PTPG1)	7q11.23	89/97 kDa	Yes		95-97
PTP-HSCF		50 kDa	No		98-102
<b>Lipid-binding homology-containing group</b>					
PTP-MEG2		68 kDa	Yes		103
<b>ERM domain-containing group</b>					
PTPH1		104 kDa	Yes		104
PTP-MEG1		106 kDa	Yes		105
PTPD1 (=PTP2E, PTP-RL10)		130 kDa	No		106-108
PTPD2		unknown	No		106
BA14		290 kDa	No		109
PTP-BAS (=FAP-1, PTP1E, RIP, PTPL1, PTP-BL,	4q21.3	275 kDa	Yes		110-113
PTP36 (=PEZ)	1q32.2-41	130 kDa	Yes		114,115
<b>II. DUAL-SPECIFIC PHOSPHATASES</b>					
<b>VH1-like, MAP kinase-specific group</b>					
VHR	17q21	21 kDa	Yes		66
Pac-1 (=DUSP2)	2q11.2-q11	32 kDa	Yes		116
MKP-1 (=CL100, 3CH134, erp,hVH1)	5q34-35	39 kDa	Yes		117-119
MKP-2 (=TYP1, hVH2, DUSP4)	8p11-p12	43 kDa	Yes		120,121
MKP-3 (=Pyst1, rVH6, DUSP6)	12q22-q23	42 kDa	No		122,123
MKP-4	Xq28	42 kDa	?		124
MKP-X (=Pyst2, B59, DUSP7)	3p21	39 kDa	Yes		122,125,126
B23 (=hVH3)	10q25	44 kDa	?		127
hVH4	10q11	?	?		128
M3/6 (=hVH5, HB5)	11p15.5	69 kDa	?		129,130
<b>Cell cycle regulators</b>					
CDC25A	3p21	52-72kDa	Yes		70
CDC25B	20p13	52-72kDa	Yes		70
CDC25C		52-72kDa	Yes		70
KAP		24 kDa	?		71
<b>Tumor suppressor</b>					
PTEN (=MMAC1, TEP1)	10q23.3	45 kDa	Yes		75,76
<b>III. SMALL, UNRELATED ENZYMES</b>					
LMPTP(low MrPTP,AcP,BHPTP)	2p25	18 kDa	Yes		72
PRL-1	6q12	20 kDa	Yes		73
OV-1 (PRL-2, PTP4A)	17q12-21	20 kDa	Yes		74
PRL-3		20 kDa	No		74

<sup>a)</sup> Original cloning papers

<sup>b)</sup> Isoforms devoid of PTPase domain

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**Figure 3.** Structure of dual-specificity phosphatases and low-molecular weight PTPases. The enzymes are aligned for their "PTPase signature sequence". The extent and exact placement of the phosphatase domain is uncertain in many. We have included the CH2 domain in the phosphatase domain. A low degree of amino acid similarity to other enzymes is indicated by a different shading of the domain. In PTEN, the phosphatase domain overlaps with a tensin homology region (in pink).

with SH3 domains to the proline-rich regions of PTP-PEST and PEP, and the potential association of some PTPases with transmembrane proteins or cytoskeletal elements via ERM and PDZ domains. These will all be discussed in detail below.

An important group of PTPase substrates are the PTKs involved in lymphocyte signal transduction. With the probable exception of Csk, these enzymes are all negatively and positively regulated by phosphorylation of multiple tyrosine residues (5-9,43,44,131,135-138). The CD45 PTPase is known to positively regulate the Src family PTKs by dephosphorylating their C-terminal negative regulatory site (discussed below). Other PTPases may also act on this site (139). Several other PTPases are very likely to participate in the regulation of the PTKs, particularly by dephosphorylating the sites that CD45 does not act on. We have observed that the autophosphorylation site of Lck, Tyr-394, and the site in the SH2 domain, Tyr-192, both become rapidly phosphorylated in cells treated with PTPase inhibitors (131,140), suggesting that they are

normally efficiently dephosphorylated by one or several PTPases. Likewise, both Syk (141) and Zap (142) become hyperphosphorylated within seconds after the addition of pervanadate. This response is also seen in CD45-negative cells (our unpublished observation). Taken together, these observations suggest that these PTKs are under very efficient control by PTPases, most likely several of them.

A large number of substrates for the PTKs have been identified, although it remains largely unknown which PTK phosphorylates these substrates under physiological conditions. It is even less clear which PTPases that dephosphorylate these proteins. These signaling molecules include components of many known pathways and in some instances their phosphorylation has been shown to switch on the pathway. For example, phosphorylation of phospholipase C $\gamma$ 1 at Tyr-783 leads to its activation (143-147) and subsequent hydrolysis of membrane inositol trisphosphate and activation of protein kinase C through diacylglycerol formation (148). Another mechanism by which tyrosine phosphorylation regulates signaling events is by inducing physical association of proteins. For example, phosphorylation of the LAT (149) and Shc (150) proteins, causes them to bind the Grb2 adapter molecule, which, in turn, associates with Sos, a guanine nucleotide exchange factor for the small membrane-associated G protein Ras (151,152). Activated GTP-bound Ras then recruits the cytosolic inactive form of the Ser/Thr protein kinase c-Raf, causing its membrane translocation and activation (153,154). Raf, in turn, activates a cascade of Ser/Thr kinases, including Mek (155,156), which activates the mitogen-activated protein (MAP) kinases Erk1 and, in T cells particularly, Erk2 (157,158). Erk1 and 2 then phosphorylate additional kinases and the cascade culminates in the phosphorylation of transcription factors and cell cycle regulators (159,160). An important downstream target of Erk is the Elk-1 transcription factor, which participates in the transcriptional control of the *c-fos* protooncogene. Erk is known to be important in many events of lymphocyte physiology, such as development (161), cytokine production (162), proliferation (163) and energy (164).

A parallel, but distinct, kinase cascade is initiated by tyrosine phosphorylation of Vav (165), an important (166,167), 95-kDa multidomain protein, which is a guanine nucleotide exchange factor for the small G protein Rac (168). GTP-bound Rac subsequently activates one or several protein kinases, which in turn activate Mkk4 (also called Sek), a dual-specificity protein kinase, which specifically activates the MAP kinases Jnk1 and Jnk2 (169,170). These two kinases are often referred to as stress-activated protein (SAP) kinases as this pathway is particularly efficiently switched on by stimuli such as heat shock, UV light, pro-inflammatory cytokines, etc. A main target for Jnk1 and 2 is the c-Jun protooncogene product (169), which together with the Fos proteins form the AP-1 dimer, an important transcription factor that cooperates with NFAT, NF-kappaB and Oct proteins in activation of cytokine genes in activated lymphocytes (171-174). A third kinase cascade includes Mkk3 and 6, which activate the

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p38 MAP kinase (175). There is at least one more, poorly understood, kinase cascade that leads to activation of the 80-kDa Erk5 MAP kinase.

Other cellular proteins that become tyrosine phosphorylated in triggered T cells include the protooncogene product c-Cbl (176), a 120-kDa protein with multiple potential tyrosine phosphorylation sites and proline-rich regions for binding of SH2 and SH3 domains, *e.g.* of phosphatidylinositol 3-kinase p85, Grb2 (177), and Zap-70 (178). The 76-kDa SLP-76 (179), which also has an SH2 domain, associates with the SH3 and SH2 domains of Vav and the SH3 domains of Grb2 (179). It was recently shown that SLP-76 is important in T cell development (180) and in TCR signaling for coupling the receptor to phospholipase C $\gamma$ 1 (181). The 36-38-kDa LAT protein (149) is also somehow involved in linking the TCR to phospholipase C $\gamma$ 1 (182), and it may serve as the main mechanism for tyrosine phosphorylation-dependent recruitment of phosphatidylinositol 3-kinase to the plasma membrane (183,184).

Finally, an interesting group of PTPase substrates is the PTPases themselves. Several PTPases have been reported to be phosphorylated on tyrosine residues (11-20). However, the significance of this modification is in many cases still unclear. Often the stoichiometry is very low and PTyr is only detected in the PTPase after treatment of the cells with potent PTPase inhibitors, such as phenylarsine oxide or pervanadate. On the other hand, in some cases a catalytically inactive mutant of the PTPase becomes much more phosphorylated than the active enzyme, suggesting that it normally is able to autodephosphorylate. This would explain why strong pharmacological inhibition is required to preserve the phosphorylation through the immunoprecipitation procedure. It could also be argued that even a very low stoichiometry phosphorylation could be highly significant in intact cells, for example if the phosphorylated form specifically interacts with other proteins. The relevance of tyrosine phosphorylation of PTPases can only be tested by mapping the site(s), changing these tyrosine residues to phenylalanines by site-directed mutagenesis, and using these mutants in functional experiments.

### 3. CLASSICAL PTPases

#### 3. 1. CD45 - a positive regulator of T cell activation

The first PTPase whose function in TCR-initiated T cell activation was elucidated is the transmembrane receptor-like CD45 PTPase, which is abundantly expressed on the surface of all nucleated hematopoietic cells (185,186). The enzyme has a long and slender extracellular domain, which is variable due to alternative splicing of exons 4, 5, and 6 during processing of the primary RNA transcript. As a result the mature mRNA encodes a protein that contains all, some, or none of the sequences encoded by these three exons. The smallest CD45 isoform, termed CD45-R0, lacks these sequences and has a relative molecular weight of 180 kDa, while the largest, CD45-RABC, contains them all and has a Mr of 220-240 kDa.

The extracellular domain of CD45 is also heavily glycosylated being rich in sialic acid and galactose amine (187). These carbohydrates make CD45 a good ligand for some lectins, including animal galectins (188). Different leukocyte populations and subtypes have different expression patterns of CD45 isoforms, each individual cell usually expressing several isoforms. It seems likely that the different isoforms have somewhat different physiological functions, perhaps through differences in interaction with other surface proteins resulting in enhanced or reduced juxtaposition with other signaling molecules (*e.g.* CD4-Lck). Our understanding of the alternative splicing of CD45 and its role in lymphocyte physiology is still rudimentary. Nevertheless, it seems that much of the initial enthusiasm sparked by the discovery that it is a PTPase (60), now has dissipated and that only a few laboratories still focus on this molecule and its role in leukocyte physiology. Consequently, our understanding of CD45 has progressed relatively little in the last few years. As recent reviews (*e.g.* 186) contain essentially all current knowledge, we will summarize the state-of-the-art quite briefly.

T lymphocytes lacking CD45 fail to respond to stimulation by antigen or mitogenic antibodies (189). Responsiveness is restored upon reexpression of wild-type CD45 (190), or by expression of chimeric molecules containing the intracellular domain of CD45 fused to transmembrane and extracellular parts from heterologous proteins (191,192) or by the intracellular domain of CD45 alone (193) targeted to the plasma membrane by addition of the myristoylation signal contained within the first N-terminal amino acids of c-Src, the "SH4 domain" (5). Under physiological conditions, however, it is likely that the alternatively spliced extracellular domain of CD45 also plays an important role (194), perhaps by regulating the interaction with other surface proteins. The requirement for CD45 in T cell activation seems to reside at a very early stage in the signal transduction cascade, since, in the absence of CD45, the rapid receptor-triggered tyrosine phosphorylation of cellular proteins is severely reduced (195), resulting in impaired activation of phospholipase C (196) and disturbed calcium homeostasis (197). Experiments with B lymphocytes and other leukocytes have largely confirmed the central role of CD45 in signaling through receptors that primarily use Src family PTKs for signal transmission. Other receptor systems, *e.g.* for cytokines or growth factors, are not perturbed by the lack of CD45. The role of CD45 in T cell signaling is also seen as a failure in thymic development in mice with CD45-negative thymocytes lacking exon 6 of the CD45 gene (198).

It seems that the main mechanism by which CD45 influences TCR-induced tyrosine phosphorylation is by positively regulating the Src-family PTKs Lck and Fyn (5-10, 199-202) in T cells, and other members of the Src family in other cell types. Dephosphorylation of these kinases occurs at their C-terminal negative regulatory site (reviewed in 5), and correlates with responsiveness of the T cells to TCR/CD3 stimulation (202). Consequently, we

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have hypothesized (9) that the main physiological role of CD45 is to counteract the suppressive effect of the Csk kinase, which rephosphorylates the C-terminal tail of Src family PTKs (reviewed in 5), and thereby to keep a sufficiently large fraction of the cellular pool of Src family PTKs active and able to participate in signal transmission. This function of CD45 seems to be constitutive and not significantly modified by receptor ligation. On the other hand, there is evidence that CD45 does not treat all Src family members equally. In T cells, for example, CD45 does not seem to have the same affinity for Fyn as for Lck. Although some skewing may arise from differences in expression levels or subcellular location, there is data to support the notion that the N-terminus of Lck allows the kinase to increase its interaction with CD45 compared to other Src-like kinases (203). This physical interaction of Lck with CD45 can be visualized by co-capping and is strong enough for co-immunoprecipitation .

The expression of CD45 has also been found to affect the phosphorylation state of Zap (142) and Syk (our unpublished observation) in one pair of CD45<sup>+</sup> and CD45<sup>-</sup> cells, the murine YAC-1 T lymphoma. A physical association of Zap with CD45 was seen by co-immunoprecipitation and by co-capping experiments and Zap was constitutively tyrosine phosphorylated in the CD45<sup>-</sup> YAC-1.N1 clone (142). Although a direct action of CD45 on Zap or Syk has not been excluded, it appears more likely that the effects of CD45 on Syk and Zap are indirect. Instead, there is evidence suggesting that TCR-zeta is a physiological substrate for CD45 (204). Since dephosphorylation of TCR-zeta would prevent the association of Zap and its subsequent activation by Lck, it seems that CD45 can have a negative influence on signaling, which is opposite to its positive effects of Lck and Fyn. This may explain the contradictory results obtained with anti-CD45 mAbs, which can be either stimulatory or inhibitory for T cell activation. It may also be important to note that results obtained in CD45<sup>-</sup> variants of several transformed T cell lines are partly contradictory. For example, while Lck is hyperphosphorylated only at Tyr-505 and has a low catalytic activity in most T cells lacking CD45, it also becomes hyperphosphorylated at the positive regulatory site, Tyr-394, and is catalytically activated in the YAC1.N1 (10). Although this effect is reversed by re-expression of CD45 (193), it is clear that CD45 is not the main PTPase responsible for Tyr-394 dephosphorylation as the authors propose. In other T cells lacking CD45, Tyr-394 of Lck is not phosphorylated, but phosphate does accumulate at this site if the cells are treated with a PTPase inhibitor (our unpublished observation). The YAC-1 cell line might be deficient in some other PTPase. PTPase inhibitors also induce hyperphosphorylation of Syk and Zap in T cells lacking CD45, suggesting that a PTPase distinct from CD45 dephosphorylates these PTKs as well.

The physical size of CD45 has puzzled scientists. The extracellular domain of CD45 forms a long rod, which exceeds the TCR and its co-receptors several fold in length, and thereby would prevent interaction of the TCR with MHC molecules on the surface of another cell. There is

recent insight into the mechanics of T cell contact with antigen-presenting cells that overcomes this dilemma. By immunofluorescence staining and computer-enhanced confocal microscopy, A. Kupfer's laboratory has found that CD45 leaves the small area that forms the contact with the antigen-presenting cell (205,206). At the same time, the TCR and its co-receptors accumulate in this area, as do Lck and other signaling molecules on the cytoplasmic face of the contact area. These results suggest that signaling from the TCR proceeds without being counteracted by the PTPase domains of CD45 as long as the contact with the antigen-presenting cell is maintained. As CD45 might be the PTPase that dephosphorylates the ITAMs of the TCR-zeta, the exclusion of CD45 would strongly promote the phosphorylation of these sites. On the other hand, the absence of CD45 in the contact area will also prevent dephosphorylation of the negative regulatory sites in Lck and Fyn, causing their inactivation. We have measured the turnover of phosphate at this site of these PTKs (140) and found it to be relatively slow. Thus, the activity of Lck and Fyn molecules that are out of CD45's reach in the contact area will remain active for sufficiently long periods of time. This new findings underscore the importance of studying PTPases not only on a biochemical level, but also as components in a highly organized, three-dimensional context within living cells.

### 3. 2. HePTP - a cytosolic leukocyte-specific PTPase

The hematopoietic protein tyrosine phosphatase (HePTP) was originally cloned from human T lymphocytes (79,80). The gene is expressed exclusively in thymus and at lower levels in spleen, and in most leukemic cell lines examined, including the Jurkat T leukemia cells (our observation), HL-60 (promyelocytic leukemia), NALM-6 (pre-B cell line), Tall-1 (T cell leukemia cell line), PEER (T cell leukemia line) and RPM18226 (myeloma cell line). HePTP is not detected in non-hematopoietic tissues (79,80,207) or cell lines. HePTP belongs to a group of PTPases with currently 3 other members, STEP (for striatum-enriched phosphatase; ref. 81), PCPTP1 (82-84), and Typ (85). Interestingly, at least the two former come in many different isoforms due to alternative mRNA splicing (208-210) or translational initiation (82). The four genes of this family are all expressed in different tissues; STEP mainly in brain, particularly, striatum (81) and PCPTP1 in lung, heart and brain, particularly in cerebellum, but not in striatum (82), and Typ only in spermatocytes (85). Thus, hematopoietic cells express only HePTP and none of the other family members.

The exon/intron structure of the HePTP gene has been determined (207). It is located on chromosome 1q32.1 (211) and is organized into 11 exons, including the 5'-noncoding first exon and the 3'-noncoding exon. The exon/intron structure is very similar to that of the phosphatase domains of human CD45 (212). Particularly the splicing sites for exons 4 to 10, which encode the conserved catalytic PTP domain, arise at the same position as in the CD45 gene. Interestingly, the CD45 gene is located on human chromosome 1 at q31-q32, quite close to HePTP at 1q32.1. Together with their common restriction to hematopoietic cells and the relatively high (53.8%)

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degree of amino acid identity between their catalytic domains, it seems likely that they arose by gene duplication of a primordial gene. In contrast to CD45, however, HePTP consists of only a single PTPase domain, which occupies the C-terminal 3/4 of the enzyme and is preceded by a ~80-amino acid non-catalytic N-terminus (figure 2).

There is some controversy regarding the first N-terminal amino acids of HePTP. Brent Zanke's group (79) cloned the cDNA for HePTP from human peripheral T lymphocytes and found the open reading frame to encode a protein of 339 amino acids (38 kDa). Simultaneously, Adachi's team (80) isolated a cDNA clone from a human T cell PEER cDNA library, which encoded a protein of 360 amino acids, which they termed LCPTP for Leukocyte PTP. Comparison of the two cDNAs indicates that they correspond to the same gene. However, they differ in the presence of a single nucleotide in LCPTP (missing in HePTP) that results in a frame-shift and 21 extra amino acid residues in the N-terminus of LCPTP. However, from Met-22 of LC-PTP, the two proteins are nearly identical. A few single base differences that result in amino acid changes are present at positions 235 (His in HePTP versus Gln in LCPTP), 236 (Val in HePTP versus Leu in LCPTP) and 337 (Ala in HePTP and Asp in LCPTP). These substitutions are probably insignificant and they could represent allelic variation or be due to mutations in the transformed PEER leukemia cells from which LCPTP was cloned. A third group (213) isolated the cDNA encoding the rat equivalent of the human HePTP from a rat basophilic leukemia mast cell cDNA library. The rat and human sequences share 77 and 91 % identity at the nucleotide and amino acid levels, respectively. The protein expressed in the mast cells was of a size (~40kDa) and PI (6.9) predicted from the deduced amino acid sequences, which agrees in the extreme N-terminus with LCPTP.

The lack of putative transmembrane sequences or recognizable signal motifs in HePTP for subcellular targeting suggests that the enzyme might be soluble in the cytosol. Indeed, immunofluorescence microscopy indicates that HePTP is localized only to discrete globular compartments within the cytoplasm of mast cells and not in the nucleus or associated with the cell surface membrane (213). In T cells, the immunofluorescence is quite evenly distributed throughout the cytosol (our unpublished observation).

Recent experiments have begun to shed some light on the biological function of HePTP. Ectopic expression of HePTP in NIH3T3 cells resulted in altered cell morphology, disorganized growth, anchorage independent colony formation and subtle differences in the pattern of tyrosine phosphoproteins compared to control cell lines (211). In hematopoietic cells, the first indication of a role of HePTP in cell proliferation or differentiation came from the finding that the HePTP gene is located on the long arm of chromosome 1, which is often found in extra copies (trisomy) in bone marrow cells from patients with myelodysplastic syndrome (214,215), which is characterized by reduced hematopoiesis and increased risk of acute leukemia. Indeed, amplification and

overexpression of HePTP has been reported in a case of myelogenous leukemia (211). Deletions of 1q32 have also been reported in non-Hodgkin lymphomas and chronic lymphoproliferative disorders (216). Together, these findings suggest that excess HePTP may correlate with reduced proliferation (in myelodysplasia) and loss of HePTP with increased cell proliferation and/or survival. A connection with proliferation is also supported by the finding that the HePTP gene is transcriptionally activated in T cells treated with interleukin-2 (180). Although mRNA levels also increased several fold upon stimulation of normal mouse lymphocytes with phytohemagglutinin, lipopolysaccharide, Concanavalin A or anti-CD3 (79), the HePTP protein was present in resting cells and its amount increased only moderately. HePTP has also been reported to become phosphorylated on tyrosine in RBL-2H3 mast cells stimulated through their Fc-epsilonRI (213).

We have found that transient expression of HePTP in T cells causes a clear reduction in antigen receptor-induced transcriptional activation of a reporter gene driven by a NFAT/AP-1 element taken from the interleukin-2 gene promoter (217). In contrast, a catalytically inactive C270S mutant of HePTP had no effect, suggesting that the PTPase activity of HePTP was required for inhibition (217). HePTP also reduced TCR-induced activation of the mitogen-activated protein (MAP) kinase Erk2, but not of the N-terminal c-Jun kinase (Jnk). HePTP also did not affect the activity or phosphorylation of MEK, the upstream activator of Erk, and all examined tyrosine phosphorylation events upstream of MEK appeared intact. Furthermore, we found that HePTP binds specifically to Erk2 and p38 kinase in intact T cells and dephosphorylates the critical PTyr in their activation loop (218,219). This reaction causes rapid inactivation of the bound Erk or p38. The region of HePTP responsible for the specific binding to Erk and p38 was mapped to the non-catalytic N-terminus of HePTP, which also is phosphorylated by Erk and p38 at Thr-45 and Ser-72. We propose that HePTP is a negative regulator of T cell activation, and acts by specifically reducing the activation of the Erk and p38 MAP kinase pathways. We speculate that this function of HePTP can be regulated through modulation of its expression levels and through post-translational modifications, such as phosphorylation on serine, threonine and tyrosine. The relation to dual-specific MAP kinase phosphatases is discussed below under these enzymes.

### 3. 3. TCPTP - a PTPase of the endoplasmic reticulum

The T cell PTPase, TCPTP, is an intracellular enzyme with a single catalytic domain, which is located in its N-terminus (figure 2). Its cDNA was originally isolated in 1989 by Deborah Cool and co-workers from a human peripheral T-cell cDNA library (86), and it encodes a 48-kDa protein (86,220) with 65% sequence identity to the first cloned PTPase, PTP1B (59). In 1992, Mosinger and co-workers (221) described a cDNA encoding the mouse homologue of TCPTP (termed MPTP), which predicted a protein of 383 amino acids with Mr~44,640. The similarity between MPTP and human TCPTP is 88.8% at the nucleic acid level and 93.2% at the amino acid. However, the

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human and murine open reading frames differed markedly at their 3' ends. This puzzle was solved by the realization that there is a splice donor site (AGGT) present in the human TCPTP cDNA at the position where the sequence diverges from the murine cDNA, suggesting the primary transcript undergoes an alternative splicing event that results in two isoforms differing in their C-termini. This has been confirmed. The larger protein is approximately 48 kDa and its C-terminus contains a hydrophobic and basic endoplasmic reticulum-retention signal, which is lacking in the smaller, 45-kDa isoform (221,222). Instead the smaller protein contains a nuclear localization signal, Arg-Lys-Arg-Lys-Arg, which immediately precedes the splice junction (223). Accordingly, the 45-kDa isoform is nuclear. The rat homologue of TCPTP (termed PTP-S for protein tyrosine phosphatase of spleen) has also been cloned (224) and it is 95% identical to the human protein within the catalytic domain. There is also evidence for alternative splicing in the rat, perhaps giving rise to more than two isoforms (225).

Although TCPTP was isolated from T cells (86) and from spleen (221,224), it is not restricted to lymphoid cells, but is found in a variety of cell types and tissues. The expression is low in embryonic stem cells and increases during later stages of mouse development (221). Highest expression of the major RNA transcript of 1.9kb was observed in the ovaries, testes, thymus and kidneys. A second RNA transcript of ~1.3kb, was detected exclusively in the testes. The TCPTP gene was found to be located on chromosome 18p11.2-11.3 (226).

Mice with a TCPTP<sup>null</sup> mutation were recently generated in M. Tremblay's laboratory (227). The three genotypes (+/+, +/-, and -/-) showed the normal Mendelian 1:2:1 segregation at birth demonstrating that the absence of TCPTP was not lethal in utero. However, all TCPTP<sup>-/-</sup> mice grew poorly and died by 3-5 weeks of age, having enlarged spleens and lymph nodes. These mice also exhibited specific defects in their bone marrow, in B cell lymphopoiesis, and in their erythropoiesis, as well as impaired T and B cell functions. However, myeloid and macrophage development in the bone marrow and T cell development in the thymus were not significantly affected. Furthermore, bone marrow transplantation experiment showed that the lymphoid problems in TCPTP<sup>-/-</sup> animals were not due to defects in the hematopoietic stem cells, but rather to a stromal cell deficiency. Although these findings do not exclude the possibility that TCPTP plays an important role in lymphocytes, they indicate that TCPTP is not an indispensable component of the lymphocyte development or activation machinery.

Despite the generation of knock-out mice, the physiological function and substrates of TCPTP remain poorly understood. The high degree of sequence similarity between TCPTP and PTP1B, with as high as 85% sequence similarity within the catalytic domain, predicted that they may have similar physiological functions and modes of regulation. This prediction has been partly fulfilled, but there are also important differences between the two proteins. Both enzymes are targeted to the endoplasmic

reticulum through their carboxy-terminal segments (220,228-232). The C-termini also suppress the catalytic activity of the native enzymes (228), suggesting the existence of an intramolecular regulatory mechanism. Accordingly, truncation of the C-terminus of TCPTP results in a constitutively active cytosolic protein (228). Expression of such a 37-kDa C-terminally deleted form of TCPTP caused BHK cells to become multinucleated and it suppressed *v-fms*-induced transformation of rat-2 cells (233,234). However, correct subcellular localization is likely to be crucial for targeting TCPTP to its physiological substrates, and overexpression of wild-type TCPTP has little effect on the morphology or growth of cells.

Recently, a number of associated proteins and putative substrates for TCPTP have been described. Tiganis and co-workers (235) isolated three proteins, p97, p116 and p120, that interacted with the alternative C-termini of TCPTP. p120 interacted with the longer C-terminus, while p116 and the nuclear import factor p97 bound to the basic residues of the TCPTP bipartite nuclear localization signal, which targets the 45-kDa TCPTP isoform to the nucleus. These findings are consistent with the notion that the alternative C-terminal segments of the TCPTP isoforms target the enzyme to defined intracellular locations through specific interactions with regulatory proteins.

Lammers and co-workers (236) reported that both PTP1B and the 48-kDa isoform of TCPTP preferentially dephosphorylated the precursor forms of several receptor tyrosine kinases during their synthesis in the endoplasmic reticulum. This feature was not shared by two other intracellular PTPases, PTPH1 and SHP-1. Substrates included the epidermal growth factor receptor and the adapter protein Shc (237). It seems therefore that PTP1B and TCPTP counteract the autophosphorylation of receptor tyrosine kinases during their synthesis and posttranslational processing. We have found that expression of TCPTP in T cells, even at 10-100 fold above endogenous levels, has no effects on TCR signaling as measured by many different parameters from early tyrosine phosphorylation events to the transcriptional activation of the interleukin-2 gene. However, TCPTP does reduce the basal tyrosine phosphorylation of several PTKs if they, too, are overexpressed at sufficiently high levels, presumably being abundant also in the endoplasmic reticulum. In agreement with the notion that the 48-kDa TCPTP has a localized housekeeping function, we have found that this enzyme is quite promiscuous *in vitro* compared to other PTPases.

The role of the smaller form of TCPTP is less clear. A substrate-trapping mutant (D182A) of the 45-kDa TCPTP isoform transiently overexpressed in COS cells underwent a change in localization, exiting the nucleus and accumulating in the cytoplasm in response to epidermal growth factor (235). It bound PTyr-containing proteins of approximately 50, 57, 64, and 180 kDa. Of these, the 57- and 180-kDa proteins were identified as Shc and the epidermal growth factor receptor, respectively. No effects were seen on epidermal growth factor-induced MAP kinase activation, but the association of Shc with Grb2 was reduced. Whether the endogenous 45-kDa TCPTP remains

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**Table 2.** ITIM containing receptors

RECEPTOR	LIGAND	EXPRESSION PATTERN	REFERENCE
<b>I. Type I transmembrane molecules with Ig-like domains</b>			
Fc-gamma-RIIB (human and mouse)	Fc of IgG	many lymphoid/myeloid cells	255
CD22 (human and mouse)		B cells	256,257
p58 (KIR, human)	MHC	NK cells, small subset of T cells	258,259
p70 (KIR, human)	MHC	NK cells, small subset of T cells	260,261
LAIR-1 (human)	?	NK cells, B cells, T cells, monocytes	262
LIR-1 (human)	?	B cells, monocytes	263
ILT-2 (human)	?	many leukocytes	264,265
ILT-3 (human)	?	myeloid cells, antigen presenting cells	266
ILT-4 (human)	?	myelomonocytic cells	265
ILT-5 (human)	?	myelomonocytic cells	265
gp49B1 (mouse)	?	mast cells, basophils, NK cells	267,268
p91/PIR-B (mouse)	?	B cells, myeloid lineage cells	269
MAFA	?	mast cells	270
<b>II. C-type lectin group</b>			
CD72 (human and mouse)	carbohydrate	B cells	271
NKG2A/B (human)	MHC	NK cells, small subset of T cells	272,273
Ly-49 (mouse)	MHC	NK cells, small subset of T cells	274,275

in the nucleus at all times or cycles to the cytoplasm, remains to be clarified. A number of nuclear proteins contain PTyr, including MAP kinases, transcription factors and the Abl kinase and its substrates. The 45-kDa form of TCPTP may act on any of these, and could thereby have an important regulatory role in cell growth, differentiation or apoptosis.

### 3. 4. SHP1 - a negative regulator of signaling

The approximately 100-amino acid residue Src Homology 2 (SH2) domain is a hemispherical protein-protein interaction domain that specifically binds to phosphotyrosine-containing peptide sequences in other cellular proteins. Two PTPases are currently known that have SH2 domains, namely SHP1 (previously PTP1C, SHP, HCP, or SH-PTP1) and SHP2 (also known as PTP1D, PTP2C, SH-PTP2, or Syp). These two PTPases are similar in overall structure; both have two SH2 domains in the N-termini and a catalytic PTPase domain in the C-termini followed by a short C-terminal tail with two tyrosine phosphorylation sites. SHP1 is expressed at highest levels in cells of hematopoietic origin, while SHP2 is ubiquitous. Lymphocytes contain easily detectable levels of both. An alternative splicing of a 39-amino acid fragment in the C-terminal SH2 domain of SHP1 (238-240) creates some heterogeneity in the apparent molecular size of SHP1. There are also two naturally occurring point-mutations in the *shp1* gene in the two mouse strains *motheaten* (*me*) and *viable motheaten* (*me<sup>v</sup>*) (241), in the former leading to premature termination of the protein, and in the latter strain causing the expression of functionally deficient SHP1 protein (238-241). These two mouse strains have been tremendously valuable in the search for the function and importance of SHP1. The majority of data indicate that SHP1 acts as an important negative regulator of many signaling systems in hematopoietic cells.

The posttranslational regulation of the catalytic activity of SHP1 and SHP2 proteins is at least partly clear. The role of the two SH2 domains seems to be twofold: regulation of the catalytic activity of the enzyme and physical localization of the protein to its physiological sites of action. The first task is accomplished by a physical association of the N-terminal SH2 domain with the catalytic domain resulting in a strong suppression of the phosphatase domain (242,243). This interaction, which occurs in a PTyr-independent manner, is disrupted by binding of a PTyr-containing peptide ligand to the SH2 domain. As a consequence of SH2 domain engagement, the catalytic domain is liberated and activated up to 100-fold (242,244). As predicted by this intramolecular suppression, investigators have found that removal of the SH2 domains increases the enzymatic activity (242,244-247, and own observations). The second SH2 domain does not seem to participate in regulation of catalytic activity and only serves as a recruiting domain (242,243). Its importance lies in its participation in the synergistic binding of SHP1 to doubly phosphorylated ligands (248,249). Thus, the ligand specificity of the SH2 domains of SHP1 are largely responsible for juxtaposing SHP1 to certain phosphorylated cellular proteins that are, or associate with, the physiological substrates for the PTPase. At the same time, SHP1 is activated at the site of binding. On the other hand, studies where the tandem SH2 domains were exchanged between SHP1 and SHP2 indicated that substantial specificity also resides in the catalytic domain (250,251).

The ligand specificity of the SH2 domains of SHP1 has been determined. The preferred sequence is now referred to as the immunoreceptor tyrosine-based inhibition motif (ITIM), Val/Ile-Xaa-PTyr-Xaa-Xaa-Leu/Val (where Xaa represents any amino acid) (252-254). This motif is found in many different proteins, many of which are transmembrane receptors for inhibitory ligands (table 2).

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Another potential mode of regulation is the phosphorylation of SHP1 at Tyr-538 (Tyr-536 in mouse SHP1) upon various extracellular stimuli (276-277), and also at Tyr-566 (Tyr-564 in mouse SHP1) in the Lck-overexpressing thymoma cell line LSTRA and in T cells (278). *In vitro*, Lck readily phosphorylates both these sites (our unpublished observation). Phosphorylation of these tyrosines does not seem to affect the enzymatic activity of SHP1, but both are in an optimal sequence for binding to the SH2 domain of the Grb2 adaptor protein (279). Indeed, association of SHP1 with Grb2 has been reported in P815 mastocytoma cells and in bone marrow derived macrophages but not in T cells (280,281).

### 3. 4. 1 Role of SHP1 in B cells

B lymphocyte activation is accomplished by binding of soluble multivalent antigen to the B cell antigen receptor (BCR) (282-284), which consists of a transmembrane immunoglobulin D or M molecule, having two heavy chains and two light chains, and at least two invariant glycoproteins MB-1 (Ig-alpha) and B29 (Ig-beta). Recognition of antigen is mediated by the variable portion of the Ig chains, and must lead to crosslinking or oligomerization of BCRs to cause signals to be transmitted into the cell. While the Ig heavy chains have very short cytoplasmic tails (the light chains are solely extracellular), the MB-1 and B29 polypeptides have long intracellular tails and are thought to be mainly responsible for signal transmission. A number of other transmembrane glycoproteins also participate as co-receptors, accessory molecules, or alternative routes of activation. These include CD19, TAPA-1, Leu13, the CR2 complement receptor (CD21) and CD40.

B cell activation is inhibited by co-ligation of the BCR with the type IIB receptor for the Fc portion of immunoglobulin G, Fc-gammaRIIB (252,253). Under physiological conditions, this co-ligation and juxtaposition of the two receptors occurs when there are circulating antigen-antibody complexes that bind and co-cluster the receptors. Under these circumstances, there is less need for more antibodies and, accordingly, B cell activation will be suppressed. The molecular mechanisms of this inhibition of BCR signaling by a juxtaposed Fc-gammaRIIB has been partly clarified. A key event is the phosphorylation of Fc-gammaRIIB on tyrosine within its cytoplasmic ITIM sequence (253), followed by recruitment of SHP1 and another SH2 domain-containing molecule, SHIP, which is a inositol polyphosphate 5-phosphatase (253). Inhibition of BCR signaling then occurs through dephosphorylation of protein substrates by SHP1 and inositol-containing phospholipids and soluble inositol polyphosphate second messengers by SHIP. The exact targets for SHP1 in this system are not entirely clear. It seems that dephosphorylation of CD19 (252,285) is important, and the finding that signaling by Fc-gammaRIIB was deficient in *me/me* mice, confirms that SHP1 plays an important role (252,286). In contrast, two reports suggest that SHIP, but not SHP1, is required for Fc-gammaRIIB-mediated inhibitory signaling in B cells (287,288).

SHP1 also associates with the ITIM-containing CD22 molecule in B cells (289). CD22 also functions as a inhibitory signaling molecule. Results obtained with mice deficient in the B cell-specific Src family PTK Lyn, indicate that this kinase is required for the tyrosine phosphorylation of CD22, its association with SHP1, and the suppressive function of CD22 on BCR signaling (290). Recently, the ITIM containing paired Ig-like receptor B (PIR-B) on murine B cells was shown to associate with SHP1, SHP2, and SHIP *in vitro*, but only with SHP1 at detectable levels *in vivo* (291). Furthermore, when a chimera between the extracellular domain of Fc-gammaRIIB and the cytoplasmic domain of PIR-B was transfected into a Fc-gammaRIIB-negative mouse B cell lymphoma and co-crosslinked to the BCR, the intracellular free calcium release and NFAT activation was inhibited compared to stimulation by BCR crosslinking alone (292). The tyrosine phosphorylated chimera was able to bind SHP1 and SHP2, but not SHIP, and mutational studies showed that Tyr-771 and to some extent also Tyr-801 in the cytoplasmic domain of PIR-B were essential for maintaining the inhibitory capabilities of the chimera (292). Finally, as shown with a SHP1/SHP2 deficient chicken B cell line (individually deficient and in combination), both SHP1 and SHP2 are required for the inhibitory function of PIR-B (292).

### 3. 4. 2. The function of SHP1 in Natural Killer Cells

Natural Killer (NK) cells are large granular lymphocytes that are devoid of T or B cell antigen receptors and that express unique lineage-specific receptors, including CD56, CD16 and a number of killer cell inhibitory receptors (KIRs). The role of NK cells is to recognize defective cells, e.g. tumor cells or virus-infected cells, and lyse them (293). Recognition is mediated by the KIRs (253,254,294), which bind to specific MHC class I molecules and suppress the killer instinct of the NK cell. Conversely, in the absence of normal (e.g. missing, altered or foreign) class I molecules, the suppression does not occur and the NK cell eliminates the target. NK cells also recognize antibody-coated target cells via their CD16 molecule, which is a transmembrane splice form of the type III Fc receptor for IgG (Fc-gammaRIIA) (295-297). This 50-70 kDa highly glycosylated protein has only 25 cytoplasmic residues, but associates with a homodimer of the zeta-chain (of the TCR) (298-300), or a heterodimer consisting of the TCR-zeta and the gamma chain of the high affinity Fc receptor for IgE (Fc-epsilonRI) (301). CD16 transmits a positive signal that induces killing of the target cells, termed antibody-dependent cytotoxicity, ADCC.

SHP1 is thought to be the key signaling molecule in the function of the KIRs (287,288,302) and of the functionally, but not structurally, related NKG2A and B receptors (303). The cytoplasmic domain of the KIRs contain one or two ITIM sequences. SHP1 was reported to associate with the human p58KIR in a NK cell line, and introduction of an inactive SHP1 mutant in the same cell line reduced the inhibitory function of p58 in target cell lysis (302). The involvement of SHP1, but not SHIP, in

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KIR-mediated inhibition of target cell lysis has been supported by other investigations (287,288).

Subsets of T and NK lymphocytes express the CD94-NKG2A/B heterodimer, which recognizes the MHC class I molecule. Anti-CD16 induced specific cell lysis by a interleukin-2 dependent NK cell line was inhibited when anti-NKG2A or anti-CD94 was crosslinked at the same time, and the same pattern was observed with anti-CD3-induced specific cell lysis by a melanoma specific cytotoxic T lymphocyte (CTL) clone (303). NKG2A contains two intracytoplasmic ITIM like sequences and when tyrosine phosphorylated, both of them can associate with the SH2 domains of SHP1 and 2 *in vitro* (but not with SHIP), suggesting that SHP1/2 are involved in the CD94/NKG2A mediated inhibition of both antigen induced T cell response and antibody induced NK cell cytotoxicity (303).

### 3. 4. 3. SHP1 in T cell signaling

In contrast to the well established role of SHP1 in B lymphocytes and NK cells, it is less clear how important SHP1 is for T cell development and function. This is partly due to the absence of well-studied ITIM-containing inhibitory receptors on T cells. The recent cloned LAIR-1 might be such a molecule as it is expressed in most T cells (263), but its function is only now beginning to be investigated.

Studies with *motheaten* mice suggest that SHP1 may play a negative role in the T cell receptor (TCR) signaling. Thymocytes from these mice show enhanced and prolonged tyrosine phosphorylation of TCR-zeta and CD3 as well as prolonged MAP kinase activation upon TCR stimulation (304). It was also reported (305) that thymocytes from *me/me* mice incorporated 3- to 5-fold more [<sup>3</sup>H]-thymidine in response to TCR-stimulation than thymocytes from normal mice. The response to interleukin-2 response was unchanged (305). This paper also showed increased tyrosyl phosphorylation of several cellular substrates, correlating with increased kinase activity of the Src-family kinases Lck and Fyn, suggesting that SHP1 is involved in the inactivation of Lck and Fyn (305). Interestingly, the catalytic activity of c-Src in thymocytes from *me/me* mice was substantially lower than in normal thymocytes, but could be enhanced by *in vitro* exposure to SHP1 (306). Furthermore, SHP1 preferentially dephosphorylated c-Src isolated from Jurkat T cells at its inhibitory site of tyrosine phosphorylation, Tyr-527, indicating that SHP1 is involved in the activation of this kinase (306). This is apparently not true for other related kinases (e.g. Lck and Fyn), and it seems not to have any significant effect on T cell activation. In Jurkat T cells, expression of a chimera between the extracellular and transmembrane domain of the HLA-A2 molecule and SHP1 was unable to rescue TCR-mediated signal transduction in the CD45-deficient J45.01 variant of Jurkat (307). However, expression of the chimera in normal Jurkat cells diminished the inositol phosphate production as well as NFAT/AP-1 promoter activity, confirming that SHP1 can regulate the TCR response. Finally, the direct regulation of ZAP-70 by SHP-1 in T cells has also been suggested (308). Other investigations based on *in vitro*

studies or transfection of heterologous cells also show that SHP1 has many potential substrates, e.g. co-expression of SHP1 with ZAP-70, Lck, and TCR-zeta chain in Sf21 insect cells show that SHP1 can dephosphorylate all of them *in vivo* (309).

Despite the finding that the response to interleukin-2 is unaltered in thymocytes from *motheaten* mice, Migone and coworkers (310) showed that interleukin-2 induced association of SHP1 to the interleukin-2 receptor complex of T cells, and that SHP1 was able to decrease the tyrosine phosphorylation level of the 75-kDa beta subunit of the interleukin-2 receptor and the associated tyrosine kinases JAK1 and JAK3 (310). Interestingly, SHP1 expression is decreased or undetectable in many interleukin-2 independent HTLV-I transformed T cell lines that exhibit constitutive JAK/STAT activation, indicating that SHP1 downregulates the interleukin-2 induced signaling response in T cells (310).

### 3. 4. 4. Role of SHP1 in other hematopoietic receptor systems

SHP1 also plays a negative regulatory role in signaling through the erythropoietin receptor (EpoR) (311,312), growth hormone receptor (313,314), the stem cell factor receptor, c-Kit (247,248,213), colony-stimulating factor-1 receptor, CSF-1R (281,318), the receptor for interleukin 3 (319,320), and the receptors for interferon alpha and beta (321,322). These receptors are either PTKs themselves (c-Kit and CSF-1R), or use Jak family PTKs for signaling. Generally, SHP1 binds directly to these receptors via its SH2 domains and subsequently dephosphorylates either the receptor, the associated PTKs, or their substrates. For example, in the case of the EpoR, receptor ligation induces recruitment of Jak2, which phosphorylates itself, the receptor, and other proteins, thereby initiating a signaling cascade that leads to growth and/or differentiation. Following phosphorylation of EpoR at Tyr-429, SHP1 binds to this site via its SH2 domains and subsequently dephosphorylates Jak2 leading to termination of the proliferative signals (311,312). SHP1 also binds to c-Kit via its SH2 domains, and observations made in *motheaten* mice suggest that SHP1 directly dephosphorylates and regulates c-Kit (320). The preferred binding site of SHP1 on c-Kit is Tyr-569, and Tyr-567 might contribute to this interaction (316). When Tyr-569 was mutated to phenylalanine and the construct transfected into Ba/F3 cells, the association was disrupted and the cells hyperproliferated in response to stem cell factor. Macrophages from *me/me* mice also proliferate more in response to CSF-1 than control cells and their CSF-1R is hyperphosphorylated, indicating that SHP1 also is a critical negative regulator of CSF-1R signaling (281). The negative feedback role of SHP1 in all these receptor systems probably explain the multiple and severe abnormalities in the development and function of the hematopoietic cells in the *motheaten* mice (238,239,241).

In conclusion, it is becoming clear that SHP1 is an important negative regulator of most hematopoietic-specific signaling systems. In contrast, expression of SHP1 in non-hematopoietic cells, does not affect, or even

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augments, signaling from receptors for epidermal growth factor, platelet-derived growth factor, insulin or interferon-gamma (323-326). Although the mechanisms for SHP1 recruitment have been elucidated in great detail, the exact substrates for SHP1 in most receptor systems remain unclear.

### 3. 5. SHP2 - a positive regulator of signaling?

Despite their structural similarity (figure 2), SHP1 and SHP2 differ substantially in their physiological functions. In many systems, SHP2 seems to behave mainly as a positive regulator of signals leading to activation of the MAP kinase pathway. The mechanism of this positive role remains unclear. Initial reports suggested that tyrosine phosphorylation of SHP2 in its C-terminal tail was responsible for enhanced recruitment of Grb2 to the membrane and thereby translocation of Sos and activation of Ras (327,328). Although this mechanism may operate under some circumstances, there is also evidence that the PTPase activity of SHP2 is important for the enhancement of MAP kinase activation (our unpublished observation).

#### 3. 5. 1. SHP2 in lymphocytes

In T lymphocytes, SHP2 has been reported to become phosphorylated on tyrosine upon TCR triggering (16) [although negative results have also been published (329)] as well as after addition of interleukin-2 (330). Studies of a murine hematopoietic cell BAF-B03 transfectant clone expressing interleukin-2 receptors showed that the tyrosine phosphorylation of SHP2 required both the serine-rich as well as the acidic region within the beta chain of the receptor (330). The acidic region interacts with Src-family protein tyrosine kinases and co-expression in COS cells showed that Lck is capable of tyrosine phosphorylating SHP2 (330). It was also recently shown that expression of SHP2 augments TCR-induced MAP kinase activation (331) albeit to a relatively small extent. An earlier report from the same group found a 110-120 kDa protein that was tyrosine phosphorylated upon TCR stimulation and co-immunoprecipitated with SHP2 from Jurkat cells (329). These authors conclude that the 110-kDa protein is a homologue of the Dos (Daughter-of-Sevenless) protein, and that its dephosphorylation by SHP2 is involved in regulation of the MAP kinase pathway (330). A negative function for SHP2 in T cells was suggested by the finding that SHP2 associates with the inhibitory CTLA-4 receptor in mice (332). This report has not yet been confirmed by others.

A function of SHP2 in adhesion was suggested by the finding that SHP2 associated through its SH2 domains with the tyrosine phosphorylated form of the adhesion molecule PECAM-1 (CD31), which is involved in migration of hematopoietic cells across the endothelium (333). In B cells, integrin activation leads to tyrosine phosphorylation of the 130-kDa docking molecule Cas, followed by recruitment of Fyn and SHP2, indicating a modulator role of Cas signaling complexes by SHP2 and Fyn (334).

SHP2 has been reported to bind to many of the receptors that also bind SHP1 and it is unclear if the

function of SHP2 in these cases overlaps that of SHP1. For example, a few investigators report that SHP2 binds to some of the KIR family members; however, whether SHP2 *in vivo* plays any role in KIR signaling is still uncertain (335,336).

#### 3. 5. 2. Function of SHP2 in other hematopoietic receptor systems

SHP2 also associates with a number of hematopoietic receptors for growth factors and cytokines. These include the stem cell factor receptor c-Kit, in which binding was mapped to Tyr-567 (337). When Tyr-567 was mutated to phenylalanine and the receptor transfected into Ba/F3 cells, binding to SHP2 was abrogated compared to c-Kit wild-type transfected Ba/F3 cells, and the cells hyperproliferated indicating that SHP2 plays a negative role in the c-Kit signaling pathway (337). Erythropoietin, a growth factor for stem cells committed to the erythroid line, induces association of SHP2 to Tyr-401 on the erythropoietin receptor, followed by tyrosine phosphorylation of SHP2 and association with Grb2 (338-340). Granulocyte-macrophage colony-stimulating factor (GM-CSF) and macrophage colony-stimulating factor (M-CSF) also caused tyrosine phosphorylation of SHP2 (341-344).

Interleukin-3, a potent growth factor for many progenitor and myeloid cells, induced tyrosine phosphorylation and activation of SHP2 (345), and an association between SHP2 and Grb2, PI3K, SHIP, the beta subunit of the interleukin-3 receptor, as well as the unknown tyrosyl-phosphorylated proteins p100, p97, and p135 (345-350). Interleukin-4 and insulin, on the other hand, caused an association of SHP2 through its SH2 domains with insulin receptor substrate-2 in a murine myeloid cell line (351).

Interleukin-5, a regulator of the growth and function of eosinophils, induced rapid tyrosine phosphorylation of SHP2 and association to Grb2 and interleukin-5 receptor beta (352). SHP2 antisense oligonucleotides inhibited tyrosine phosphorylation of microtubule-associated protein kinase and reverse the eosinophil survival advantage provided by interleukin-5, suggesting a positive role for SHP2 in interleukin-5 signaling (352).

Interleukin-6 stimulation induced association of SHP2 to the signal transducing beta-subunit of the receptor (gp130), which is shared with the receptors for leukemia inhibitory factor, ciliary neurotrophic factor, interleukin-11, oncostatin M, and cardiotrophin-1, followed by tyrosine phosphorylation of SHP2 (possibly by a JAK kinase) and association to Grb2 (353-356).

#### 3. 5. 3. SHP2 in nonhematopoietic receptor systems

Growth hormone (GH) receptor stimulation results in tyrosine phosphorylation of IRS-2 and the association of IRS-2 to SHP2 (357). Recent investigations indicate that SHP2 plays a positive role in the GH signaling, and that GH stimulation induced association of SHP2 with JAK2 and SIRPalph (358,359).

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Growth factor receptors that recruit SHP2 include the alpha and beta isoforms of the platelet-derived growth factor receptor (93,327,328,360,361), and the receptors for epidermal growth factor (93,362), insulin (363-365), insulin-like growth factor-1 (364), fibroblast growth factor (366) and nerve growth factor (367).

Cells expressing the chronic myelogenous leukemia-associated p210 Bcr-Abl or p190 Bcr-Abl oncogene show constitutive tyrosine phosphorylation of SHP2 and a complex formation between Bcr-Abl, SHP2, and Grb2 (368,369). In Bcr-Abl transfected BaF3 cells, SHP2 was shown to co-immunoprecipitate with SHIP, Bcr-Abl, Cbl, and also two novel tyrosyl-phosphorylated proteins p97 and p135 (349,350). SHP2 binds Bcr-Abl via its N-terminal SH2 domain, and deletion of the N-terminal tetramerization domain of Bcr-Abl abolished this association as well as the tyrosine phosphorylation of SHP2 (368-370).

A putative SHP2 binding protein and/or substrate called SHPS-1 (for SHP substrate 1) from rat and its human equivalent, SIRPalpha1, were recently described (371-373). Overexpression of this molecule in NIH3T3 cells resulted in decreased MAP kinase activation and proliferation upon stimulation of the cells with insulin, epidermal growth factor, or platelet-derived growth factor (372). Expression of dominant negative SHP2 constructs or a SIRP 1 construct with point-mutations in the four potential SHP2 binding sites indicated that the inhibitory effect correlated with association between SHP2 to SIRPalpha1. This effect could be mediated by sequestering SHP2 away from activated receptor tyrosine kinases (372). Studies with SHPS-1, however, concluded that overexpressed SHPS-1 had no major effect on the epidermal growth factor-induced MAP kinase activation (374).

Taken together, all the findings summarized above (as well as a large number of additional papers) indicate that SHP2 may carry out its function through dual physical association with activated transmembrane receptors together with a set of downstream signaling molecules. Some of these associations are mediated by the SH2 domains of SHP2, leading to the activation of the enzyme, while other interactions are mediated by Grb2 binding to the phosphorylated C-terminal tyrosines of SHP2. Although some of the substrates for SHP2 have been characterized, it is unclear which category of binding molecules are the principal substrates of SHP2 and whether any of the identified ones mediate the observed biological effects of SHP2. The binding of Grb2 to tyrosine phosphorylated SHP2 may result in enhanced activation of the Ras/MAP kinase signaling pathway if the bound Grb2 is complexed to the Sos guanine nucleotide exchange factor. This remains unclear. It is also plausible that the bound Grb2 binds any of a number of other recognized ligands for its SH3 domains, such as SLP-76 (179), Vav (16,375), c-Cbl (177), or phosphatidylinositol 3-kinase p85 (16,177). These molecules, or additional proteins bound to them, may serve as substrates for SHP2. This would provide a mechanism for a targeted dephosphorylation of

selected substrates in a SHP2 tyrosine phosphorylation-dependent manner.

### 3. 6. PTPases of the PEST-containing group

Three PTPases, PEP (87), PTP-PEST (95-97), and PTP-HSCF (for hematopoietic stem cell factor (98), also known as PTP-K1 (99), PTP20 (100), FLP1 (for fetal liver phosphatase 1, ref. 101), or PTP-BDP1 (for brain derived phosphatase, ref. 102), are currently members of the group of enzymes with sequences enriched in proline, glutamic acid, serine and threonine (PEST), which were earlier thought to be signature motifs for rapid degradation of cellular proteins by a non-lysosomal, ubiquitination- and ATP-dependent pathway (376). However, direct measurements indicate that the half-lives of PEST-containing PTPases are quite ordinary; suggesting that the PEST sequences do not target the proteins to accelerated proteolysis (377,378). Instead, these motifs seem to play other roles, such as association with Src Homology 3 (SH3) domains in other proteins.

PEP, PTP-PEST and PTP-HSCF share a common overall structure with an N-terminal catalytic domain and a non-catalytic C-terminal segment of about 500 amino acid residues, which contains the PEST-sequences (figure 2). The extreme C-termini contain a highly conserved 24-amino acid proline-rich region that was proposed to be involved in nuclear targeting at least in some members of the PEST-PTPases (377,101). However, it has been demonstrated that these enzymes are predominantly cytoplasmic (96,99,378,379).

The regulation of the catalytic activity of the PEST family PTPases is poorly understood. PTP-PEST has been shown to be phosphorylated in vitro by both cyclic AMP-dependent protein kinase and protein kinase C (380), which are known to have overlapping substrate specificity. The major sites were identified as Ser-39 and Ser-435. Phosphorylation of the former causes a reduction in catalytic activity of PTP-PEST (380).

The physiological substrates for PEST family PTPases remain unknown, but a few recent papers have begun to explore this issue. The ubiquitously expressed PTP-PEST has been demonstrated to interact, directly or indirectly, with several different proteins including the adapter proteins Shc (381,382), Grb2 (383), Cas (384), Csk (385) and the focal adhesion-associated protein paxillin (386). In contrast to PTP-PEST, PEP is expressed only in hematopoietic cells (87), where it is reported to associate with Csk (379). Recently, PTP-HSCF, which is preferentially expressed in hematopoietic progenitor cells in the bone marrow (98,99), was shown to interact with a novel SH3-containing member of the actin-associated protein family termed PSTPIP (for proline, serine, threonine phosphatase interacting protein; ref. 387). This cytoskeletal protein is tyrosine phosphorylated in *v-src* transformed cells and is probably dephosphorylated by PTP-HSCF (387). PSTPIP is homologous to the *Schizosaccharomyces pombe* protein CDC15p, a phosphoprotein involved in formation of the cleavage furrow during cytokinesis (388). The SH3 domain of

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PSTPIP is also most similar to that of a number of known cytoskeletal regulatory proteins including myosin, spectrin, fodrin, and hematopoietic specific protein (HSP) and cortactin (388). Interestingly, tyrosine phosphorylation of cortactin is enhanced in cells isolated from mice deficient in the Csk kinase (389). Thus, it seems that there might be a functional connection between this group of PTPases, Csk and the membrane cytoskeleton. This system may play a role in signal transduction or cell division.

Although the regulation of Csk function is still poorly understood, it is clear that it inactivates Src family kinases through phosphorylation of their inhibitory C-terminal tyrosine, Tyr-505 in Lck and Tyr-528 in Fyn (5,9,43,390). Csk has been shown to be mainly localized to the cytoplasm with a minor fraction in the plasma membrane (43), but also to focal adhesions in transfected HeLa cells (391,392). Both the SH2 and SH3 domains of Csk were responsible for the targeting to focal adhesions (391). Targeting of Csk to the plasma membrane by an added myristylation site increased the negative regulatory influence of Csk on Lck and Fyn in T cells and thereby reduced TCR-induced tyrosine phosphorylation and interleukin-2 production (393). PEP is mainly localized to cellular membranes and to some extent to the cytosol and nucleus (385). It is tempting to speculate that unbound PEP is a cytoplasmic protein, but becomes redistributed within the cell to close proximity to specific target molecules when associated with Csk. It is also tempting to speculate that the function of PEP (and PTP-PEST) is coupled to the function of Csk. In this case, PEP would be expected to dephosphorylate Src family kinases, e.g. at their positive regulatory site (Tyr-394 in Lck), or proteins in physical proximity of these kinases. This site is also the target for the SH2 domain of Csk (394), which may help juxtapose the PEP bound to the SH3 domain of Csk. We are currently addressing this hypothesis experimentally.

### 3. 7. PTP-MEG2 - a PTPase with a putative lipid-binding domain

PTP-MEG2 was cloned from a megakaryocytic cell line, MEG-01, and is expressed in many hematopoietic, epithelial, fibroblastic and other transformed cell lines (103). Currently, the 68 kDa PTP-MEG2 is the sole representative of a PTPase containing a 250 amino-acid N-terminus with 28% identity with cellular retinaldehyde-binding protein and 24% identity with SEC14p, a yeast protein with phosphatidylinositol transfer activity (figure 2). The presence of this region prompted P. Majerus and his group, who identified and cloned PTP-MEG2 (103), to suggest that the enzyme interacts with phospholipids, perhaps being regulated by them or being involved in the interaction between phospholipids and tyrosine phosphorylation.

### 3. 8. The band 4.1 homology (or ERM) domain-containing PTPases

This group of intracellular PTPases currently includes seven enzymes, PTPH1 (104), PTP-MEG1 (105), PTPD1 (106-108), the only partially known PTPD2 (106), BA14 (109), PTP36 (114; also known as PEZ (115) and a particularly large enzyme cloned by several groups and

named FAP-1 (110), PTP-BAS, PTP1E, PTPL1, RIP, PTP-BL, the 4 first being the human gene, the two latter murine (111-113). This group of PTPases is characterized by an N-terminal region with relatively high homology to the cytoskeletal protein band 4.1, followed by a variable central segment, and a C-terminal PTPase domain. In some members, the central segment contains one (PTPH1, PTP-MEG1) or several (PTP-BAS) of the newly recognized protein-protein interaction domain termed the PDZ domain (figure 2). Although the physiological function of these enzymes is poorly understood, the presence of the band 4.1 homology and the PDZ domains suggest that these proteins may accumulate at the interface between the cytoskeleton and the plasma membrane. Furthermore, the PDZ domain in some members is likely to facilitate the identification of binding proteins and putative substrates. Indeed, FAP-1 has already been shown to associate with the Fas (CD95) receptor through the third and fifth PDZ domains binding to the extreme C-terminus of Fas (110).

The band 4.1 homology domain is an approximately 300-amino acid region found in several cytoskeletal proteins, such as in band 4.1, ezrin, talin, radixin, moesin, merlin (395) and this group of PTPases. The domain has also been termed the ERM domain (in reference to ezrin, radixin and moesin) and is thought to be an independently folded protein-protein interaction module. In the case of the band 4.1 protein in erythrocytes, the ERM domain is involved in binding to basic amino acid motifs in two membrane proteins, glycophorin and p55 (396-398). Likewise, other proteins with ERM domains are thought to localize to cytoskeleton-plasma membrane interfaces where they may play regulatory or structural roles. Whether the ERM-containing PTPases are also associated with the cytoskeleton and the plasma membrane, remains to be clarified.

In addition to a possible function in targeting the enzyme to the cytoskeleton and plasma membrane, the ERM domain of at least PTPH1 also serves a regulatory role for the PTPase itself. Removal of this region by limited trypsin cleavage stimulated the dephosphorylation of some in vitro substrates (399). PTPH1 was also recently found to associate with the 14-3-3 protein (400). The binding was abolished by pretreating PTPH1 with potato acid phosphatase and was greatly enhanced by treating PTPH1 with Cdc25C-associated protein kinase. Two motifs RSLSVE (residues 356-361) and RVDSEP (residues 832-837) in PTPH1 were identified as the binding sites in a serine phosphorylation-dependent manner (400). Thus, the action of PTPH1 on tyrosine phosphorylated targets may be regulated through serine phosphorylation of PTPH1.

The central segment of PTPH1, PTP-MEG1, and perhaps PTPD1 contain a single copy of the PDZ domain, while PTP-BAS contains a total of six PDZ domains, one in the extreme N-terminus and five between the ERM domain and the PTPase domain. The PDZ domain derives its acronym from three proteins that contain repeats of this domain: the mammalian postsynaptic density protein PSD-95; the *discs-large* tumor suppressor protein Dlg from *Drosophila*; and the mammalian tight junction protein ZO1

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(401,402). Recently, the PDZ domain from PSD-95 was crystallized with a bound peptide ligand (403) and it is clear that the PDZ domain is a structural entity involved in protein-protein interactions. Different PDZ domains have distinct specificities, many binding specifically to the C-terminal tail of proteins with the sequence Thr/Ser-Xaa-Val-COOH (404). The PSD-95 PDZ domain, for example, binds to such sequences in the C-terminus of shaker-type potassium channels and of the NR2 modulatory subunit of the NMDA-type glutamate receptor (405,406). Another group of PDZ domains selected peptides with hydrophobic or aromatic side chains at the C-terminal three residues (404). It also seems that some PDZ domains can dimerize or bind internal (i.e. not C-terminal) peptide sequences in other proteins. Recently, the PDZ domain in PTP-BAS was found to bind to a protein termed RIL at an internal segment consisting of a LIM domain (for Lin-11, Isl-1, Mec-3 homology) (407). The structural basis and specificity of PDZ domains binding LIM motifs remains to be determined. Together all the new discoveries suggest that the PDZ domain(s) in the ERM-family PTPases are likely to serve in coordinating interactions with specific transmembrane membrane proteins, signaling molecules or substrates. In agreement with this notion, it has been found that PTP-BAS/FAP-1 interacts with the cytosolic domain of Fas/CD95. Fas is a cell surface receptor which is expressed on a variety of normal and neoplastic cells, while the ligand for Fas is expressed predominantly on cytolytic T cells (408). Ligation of Fas induces programmed cell death by apoptosis of cells, including of T cells in human immunodeficiency virus-infected individuals (409). The C-terminal 15 amino acids of Fas represent a negative regulatory domain, the deletion of which facilitates death signaling by the receptor (110,410). The extreme C-terminus is also the binding site for the third and fifth PDZ domain of PTP-BAS/FAP1, suggesting that this PTPase may play a negative regulatory role in FAS signaling (110,410). FAP-1 expression is highest in tissues and cell lines that are relatively resistant to Fas-mediated cytotoxicity.

Very few papers published to date deal with the expression and possible function of the ERM domain PTPases. The available information suggests that lymphocytes express at least PTP-MEG1, PTP36 and FAP-1, perhaps also some PTPH1, while PTPD1 and PTPD2 are not present in hematopoietic cells. Of these PTPases, FAP-1 may participate in Fas-mediated signaling as described above, while the 130-kDa PTP36 may play a role in thymic maturation of T cells as the gene is expressed predominantly in the immature CD4<sup>+</sup>8<sup>+</sup> cells in the thymus (114). PTP36 does not contain a recognizable PDZ domain, but has a proline-rich region possibly serving as a binding site for an SH3 domain.

### 4. DUAL-SPECIFICITY PROTEIN PHOSPHATASES

The founding member of the group of enzymes that dephosphorylate not only PTyr, but also Pser and PThr is the Vaccinia virus protein VH1 (65). Additional dual-specificity protein-tyrosine phosphatases (table 1 and figure 3) were subsequently identified based on their sequence

similarity to VH1 and their ability to hydrolyze PTyr, Pser, and PThr monoesters in protein substrates (67-70). This group of phosphatases have the PTPase signature sequence, including the catalytic cysteine residue. Outside this conserved active site, however, this group of enzymes share very limited amino acid sequence homology with other members of the PTPase family.

#### 4. 1. VHR, a dual specificity phosphatase of unknown function

The first mammalian dual-specific PTPase to be recognized was the human VHR (for VH1-related) discovered by S. Aaronson's laboratory by an expression cloning approach (66). The 21-kDa VHR protein was found to dephosphorylate both PTyr in a number of growth factor receptors and Pser in myelin basic protein (66). Recently, VHR was crystallized and its three-dimensional structure solved (411). The structure revealed that the catalytic center of VHR is composed of the same structural elements as the catalytic domains of other PTPases (70), including the cysteine (C124) in the bottom of the catalytic cleft. Mutagenesis experiments and kinetic analyses has identified C124 (412) as crucial and D92 as the general acid in the first step of the reaction and its conjugate carboxylate as a general base in the breakdown of the phosphoenzyme intermediate (413,414). For VHR, phosphoenzyme formation appears to be the rate-limiting step in hydrolysis under most conditions since no burst is seen in rapid-reaction kinetic experiments. Ser-131 has been proposed to donate a proton to stabilize the thiolate leaving group; mutation of this residue to alanine decreases the rate of phosphoenzyme intermediate breakdown and results in a burst pattern of hydrolysis (415,416).

The VHR mRNA is approximately 4.2 kb and is expressed in most tissues with highest levels in breast, ovary, heart, brain and skeletal muscle. Lymphocytes contain easily detectable amounts of the VHR protein. The human VHR gene was localized to human chromosome 17q21 in a region thought to contain BRCA1, a locus that confers susceptibility to breast and ovarian cancer, but VHR was recently found to not be identical with the BRCA1 gene (417).

Despite being the first recognized dual-specific PTPase, the physiological function of VHR have remained obscure. In vitro, VHR can dephosphorylate both PTyr and PThr in synthetic phosphopeptides based on the MAP kinases (418,419), but its substrate(s) in intact cells are unknown.

#### 4. 2. MAP kinase phosphatases

The majority of the VH1-related enzymes identified to date are specific for one or several members of the MAP kinase family and efficiently dephosphorylate the PTyr and PThr in their activation loops. These two residues (e.g. Thr-183 and Tyr-185 in Erk2) must both be phosphorylated for the kinase to be catalytically active. Thus, dephosphorylation of either or both is sufficient for a complete inactivation of the MAP kinase. Accordingly, the MAP kinase phosphatases (often called MKPs) play important roles in several cellular signaling processes in

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**Table 3.** Currently known MAP kinase-specific phosphatases

PROTEIN (SYNONYMS)	SIZE	SPECIFICITY
VHR	21 kDa	?
Pac-1	32 kDa	Erk, p38
MKP-1 (=CL100, 3CH134, erp, hVH1)	39 kDa	Erk, Jnk
MKP-2 (=TYP1, hVH2, DUSP4)	43 kDa	Erk2=Jnk=p38
MKP-3 (=Pyst1, rVH6, DUSP6)	42 kDa	Erk1,2 only
MKP-4	42 kDa	Erk1,2>p38=Jnk
MKP-X (=Pyst2, B59, DUSP7)	39 kDa	Erk1,2
B23 (=hVH3)	44 kDa	Erk
hVH4	?	?
M3/6 (=hVH5, HB5)	69 kDa	Jnk=p38>>>>>Erk

response to environmental signals, such as mitogenesis, programmed cell death, differentiation and secretion of cytokines (67-69). The two first enzymes found to have specificity for MAP kinases were Pac-1 (116) and MKP-1 (Mitogen-activated protein kinase phosphatase), the latter a gene cloned by several groups under various names (117-119). Subsequently, a number of related proteins have been discovered, many having a restricted tissue distribution. While most of these enzymes can dephosphorylate all MAP kinase family members, they usually show a preference for one or a few MAP kinases (table 3). Nevertheless, their exact specificities in intact cells remain unclear.

Lymphocytes express primarily the Pac-1 protein (116), which is encoded by an immediate early gene. Accordingly, the protein is not present in resting lymphocytes, but its mRNA is induced by mitogens even in the presence of protein synthesis inhibitors. The Pac-1 protein becomes detectable in 30-60 min after cell stimulation and resides in the nucleus, where the majority of the activated and phosphorylated MAP kinases also are. Thus, Pac-1 is ideally suited for dephosphorylation of the activated Erk kinases and thereby resetting the MAP kinase pathway. It is worth noting, however, that the activation of Erk2 in lymphocytes peaks at around 5 min after stimulation and then returns to near basal levels by 10 – 15 min, at which time Pac-1 or other inducibly expressed dual-specificity phosphatases are still undetectable. In fibroblasts lacking MKP-1 (420), also encoded by an immediate early gene (421), the activation of MAP kinase also proceeds normally. In contrast, when MKP-1 is expressed in cells under a non-inducible promoter, it strongly blocks MAP kinase activation by active Ras (422) or by extracellular stimuli (118,119,421). Disruption of the *mkp-1* gene does not affect the development of mice (420). The downregulation of MAP kinase activity that occurs before synthesis of Pac or MKP-1 protein in lymphocytes could be explained by the presence of other dual-specific phosphatases. For example, MKP-3, which is not expressed in lymphocytes (123), is not inducible, but present in resting cells. At present, however, no constitutively expressed dual-specific MAP kinase phosphatases are known in lymphocytes. Instead, we have found that the strictly phosphotyrosine-specific PTPase HePTP is involved in regulation of Erk and p38 MAP kinases in T

cells (217,218). HePTP is expressed in resting T cells and forms a physical complex with Erk and p38 (218), in which it can dephosphorylate the bound MAP kinase and inactivate it. Upon activation of the MAP kinases by Mek or Mkk6, a fraction of the activated MAP kinase molecules dissociate from HePTP through a phosphorylation-dependent mechanism, and translocate to the nucleus (218). HePTP is exclusively cytosolic, and apparently does not follow the activated MAP kinases to the nucleus, where they can phosphorylate their targets unopposed by phosphatases until the dual-specific phosphatases are induced and synthesized.

Of all the presently cloned MAP kinase phosphatases, only a few are active against the p38 and Jnk kinases. The human VH5 (mouse M3/6) has a high preference for these kinases over Erk (129), while MKP-2 dephosphorylates both Erk and Jnk with comparable efficiency (120). Both these enzymes are nuclear, but MKP-2 is induced with much slower kinetics than MKP-1 (120).

In conclusion, the MKPs are a diverse group of mainly inducible, nuclear enzymes, although their transcriptional regulation varies, and some also reside in the cytosol. Their specificity is, at least partly, governed by physical association with one or several members of the MAP kinase family. For most MKPs, however, their specificity in intact cells remains unclear. The physiological function of the MKPs is apparently not the fine-tuning of MAP kinases, a role reserved for HePTP (and perhaps other related PTPases), but the termination of signals through these kinases.

### 4. 3. PTEN

PTEN (phosphatase and tensin homologue deleted on chromosome ten), a candidate tumor-suppressor gene identified on chromosome 10, also known as MMAC1 (mutated in multiple advanced cancers), shares homology (figure 3) with the PTP family, as well as with the cytoskeletal protein tensin (75,76,423). PTEN was isolated from chromosome 10q22-23 that is frequently deleted or mutated in ~45% of endometrial cancers, ~30% of glioblastomas, and at lesser frequencies in a wide range of other human cancers, such as prostate, human brain, breast

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and kidney cancer (75,422). Abnormalities of 10q were found in lymphoproliferative diseases (424,425), and mutations of PTEN were found in leukemia cell lines (426,427). These findings suggested that disruption of PTEN is necessary for the development of specific forms of cancers. PTEN also functions during normal development. Germline mutations of PTEN are found in three related human autosomal dominant disorders, Cowden disease, Lhermitte-Duclos disease (428) and Bannayan-Zonana syndrome (429). All these disorders share similar pathological traits, such as the formation of multiple benign tumors (mostly hamartomas) and an increased incidence of malignant cancers (428,429).

PTEN encodes the catalytic “PTPase” signature motif in a context resembling the dual-specificity phosphatases (430). However, PTEN does not dephosphorylate P<sub>Ser</sub> or P<sub>Thr</sub>, and it prefers P<sub>Tyr</sub> in extremely acidic substrates, exhibiting almost 50 times more activity toward poly-acidic substrates than towards more traditional substrates (430). The extreme selectivity of PTEN toward acidic substrates *in vitro* suggests that the physiological substrates also will be acidic. It is possible that the acidic character may be manifested by proteins that are phosphorylated on multiple sites (430). Recently Maehama and co-workers (78) found that overexpression of PTEN reduced insulin-induced phosphatidylinositol (3,4,5)-triphosphate production in human 293 cells without effecting insulin-induced phosphoinositide 3-kinase activation. PTEN catalyzed dephosphorylation of phosphatidylinositol (3,4,5)-triphosphate, specifically at position 3 on the inositol ring. PTEN also exhibited 3-phosphatase activity toward inositol (1,3,4,5)-tetrakisphosphate. These data suggested that PTEN may act *in vivo* as a regulator of phosphatidylinositol (3,4,5)-triphosphate, which produces a substrate that can be recycled by PI3-kinase (78). Thus, it now seems that PTEN is the enzyme that directly counteracts phosphatidylinositol 3-kinase, which often plays an important role in growth signaling and modulation of the cytoskeleton (431,432). This may well explain the function of PTEN as a tumor suppressor and its role in cytoskeletal organization. It remains to be determined how PTEN is regulated and whether it does also dephosphorylate protein substrates *in vivo*.

A number of point mutations of PTEN which have been found from tumor samples, tumor cell lines, and germ-line mutations shown disrupt PTEN phosphatase activity (75,423,428,429,433-436). The point mutations have been found in three major clusters in PTEN. One cluster surrounds the catalytic motif, which is predicted to disrupt enzymatic activity, either by disrupting the catalytic cysteine directly or by altering the orientation of this cysteine in the catalytic cleft (437,438). The second cluster surrounds the conserved aspartic acid residue required for the release of the product. The third cluster, near the last conserved structural feature of the PTP fold, an alpha-helix, also disrupts PTEN activity (437,438). These data indicated that the enzymatic activity of PTEN is necessary for its ability to act as a tumor suppressor (439), and suggested that PTEN may suppress tumor cell growth by opposing the action of protein kinases.

PTEN also exhibits extensive sequence homology along much of its length to the cytoskeletal protein tensin. Tensin is a Src homology 2 (SH2) domain containing protein which binds to actin and localizes to focal adhesions, where it is thought to play a role in the assembly of signaling complexes (440). Tamura and colleagues (441) found that integrin mediated cell spreading and the formation of focal adhesions were down-regulated by wild type PTEN but not by PTEN with an inactive phosphatase domain. PTEN interacted with the focal adhesion kinase FAK and reduced its tyrosine phosphorylation. Overexpression of FAK partially antagonized the effects of PTEN. PTEN phosphatase may function as a tumor suppressor by negatively regulating cell interactions with the extracellular matrix (441). PTEN may also act as a docking protein in the assembly of multi-protein signaling complexes. Alternatively, all observed effects could be due to the dephosphorylation of 3-phosphorylated inositol phospholipids. Identification of the physiological substrates for PTEN, whether they are only lipids or also phosphoproteins, will be required to reveal the biological function of PTEN and eventually may lead to the characterization of a novel signaling pathway.

### 4. 4. CDC25 and KAP

The eukaryotic cell cycle is regulated by a family of protein kinases, termed CDKs (for cyclin-dependent kinases), which control the progression through the cell cycle at critical transition points. The 34-kDa CDC2 kinase bound to cyclin B is crucial for the G<sub>2</sub>-M transition. The CDC25 family of dual-specificity phosphatases (70,442) play an important role in the control of CDC2 kinase/cyclin B by dephosphorylating residues Thr-14 and Tyr-15 in CDC2, thereby activating it (443). This activation serves as a trigger for entry into mitosis (444).

CDC25 contain the “PTPase” signature sequence (figure 3) and share some limited amino acid-similarity with the other dual-specificity phosphatases, notably a small sequence termed the CH<sub>2</sub> domain. There are three genes for CDC25, termed A, B, and C (70), and the primary transcripts can undergo alternative splicing to produce additional variation in the proteins (445). CDC25 overexpression has been detected one third of primary breast cancers (446), adding this phosphatase to the list of oncogenes/anti-oncogenes within this class of enzymes. As CDC25 is not directly involved in lymphocyte activation, we refer to the many excellent reviews on this topic (70, 447).

The KAP phosphatase (71) is also very distantly related to other phosphatases (figure 3). It is a nuclear enzyme that binds CDC2 and CDK2, and probably participates in the control of the cell cycle (71).

## 5. LOW MOLECULAR WEIGHT PTPases

### 5. 1. LMPTP

The low molecular weight PTPase, LMPTP, was originally purified from liver by Heinrichson as an acid phosphatase (449) and was subsequently purified to homogeneity and its amino acid sequence determined (450, 451). Even before its cDNA was isolated (72,452), it was clear that several isoforms or related enzymes exist. It was

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subsequently found that the primary transcript undergoes an alternative splicing event in which either exon 3 or exon 4 is excised (453). This results in two different isoforms: LMPTP-A, which contains exon 3 and moves a bit slower on SDS gels, and the faster moving LMPTP-B, which contains exon 4-encoded amino acids. We have also detected a third splice form, which lacks both exon 3 and exon 4 (454). This isoform, which we term LMPTP-C, is only 15-16 kDa and lacks catalytic activity *in vitro*. The corresponding mRNA can be detected in all tissues and cell lines examined, and is at least as abundant as the other isoforms. The LMPTP-C protein can also be visualized by Western blotting (454). The LMPTP gene is highly conserved through evolution from yeast to man. The homologues from budding yeast (*Saccharomyces cerevisiae*), Ltp1 (455), and fission yeast (*Schizosaccharomyces pombe*), Stp1 (456), are 39% and 42% identical to the mammalian enzyme, respectively. Very recently (457), a homologous gene was found in the prokaryote *Acinetobacter johnsonii*. The protein was found to have PTPase activity *in vitro* and to dephosphorylate a novel bacterial PTK that autophosphorylated on tyrosine (457). This suggests that LMPTPs are likely to be involved in the regulation of an ancient and perhaps fundamental cellular function. On the other hand, disruption of the two yeast genes did not cause any observable loss of viability or phenotypic changes (455,456).

Already in 1989, G. Ramponi's group showed that LMPTP readily dephosphorylates PTyr in a protein substrate as well as free PTyr, while not hydrolyzing PThr or PSer (458). LMPTP also dephosphorylates other aromatic phosphates *in vitro* (459), and is not yet entirely clear if LMPTP acts only as a PTPase in intact cells. The amino acid sequence of LMPTP showed that the enzyme contains a minimal PTPase signature sequence, which is the only recognizable homology to other PTPases, and which is found in a unique location in the sequence: in the extreme N-terminus (figure 3). LMPTP is also remarkably small, only 18 kDa, which is much less than the mere PTPase domain of classical PTPases. The crystal structure of LMPTP-A (460) and LMPTP-B(461) reveal that the cysteine residue (C12) of the signature sequence is located in a catalytic pocket much like in other PTPases, while the rest of the enzyme has a unique folding. Cys-12 was already known from biochemical studies to be crucial for catalysis (459,462). The amino acids encoded by exons 3 or 4 (referred to as the 'variable loop') form one side of the catalytic pocket, indicating that the two isoforms are likely to select substrates with different amino-acid residues next to the target PTyr. The two isoforms also differ in catalytic properties and stimulation by nucleotides (462).

The biological function of LMPTP is still unclear. A number of reports by G. Ramponi's group suggest that LMPTP negatively regulates cell growth and transformation by oncogenes (463,464) and counteracts the platelet-derived growth factor (465,466) and insulin (467) receptors by dephosphorylating specific tyrosine residues on these receptors. Also in our hands (454), overexpression of LMPTP-A or -B in NIH3T3 cells causes some reduction in growth factor-induced gene activation. Interestingly, the

inactive LMPTP-C isoform had the opposite effect, suggesting that it might compete with endogenous LMPTP in a dominant negative fashion. We have also found that LMPTP-B is phosphorylated on tyrosines 131 and 132 in T cells and that such phosphorylation *in vitro* activates the enzyme (18). In co-transfected COS cells, the T cell Src-family kinase Lck was particularly efficient in phosphorylating LMPTP. A recent paper by Rigacci and co-workers reported that LMPTP-A is tyrosine phosphorylated in v-Src transformed NIH3T3 cells, and that Src was able to phosphorylate LMPTP *in vitro* (19). Interestingly, the C isoform was not phosphorylated by Lck in co-transfected COS cells or even *in vitro*, despite still having the two tyrosines. This indicates that the three-dimensional folding of LMPTP is important for the recognition of Tyr-131 and Tyr-132 by Lck. These two residues are next to the catalytic pocket and it is conceivable that their phosphorylation affects the interaction of LMPTP with substrates. The amino acid residues encoded by exons 3 or 4 form the other rim of the catalytic cleft, and are therefore likely to affect substrate binding.

In conclusion, LMPTP is a small phosphatase with strong preference for PTyr over PSer or PThr, but with somewhat unclear substrate specificity in intact cells. The specificity and activity of the enzyme are regulated by alternative splicing and tyrosine phosphorylation, but its physiological substrates and biological function remain unclear.

### 5. 2. PRL-1, 2 and 3 - isoprenylated nuclear enzymes

The first gene of this family, PRL-1, was identified as an immediate early gene in proliferating hepatocytes (73), giving the gene its name PRL-1 for phosphatase of regenerating liver-1. More recently, two additional members of the family, termed OV-1 (or PRL-2) and PRL-3 were described (74). PRL-1 and OV-1 were also found in a screen for proteins that are isoprenylated or farnesylated (468). This covalent modification with a hydrophobic group occurs on a C-terminal cysteine residue (468) and confers affinity for cellular membranes in the case of the Ras proteins. The PRL phosphatases, however, are located in the nucleus and their overexpression has a positive effect on cell growth and can induce tumor formation (73,468,469). The substrates and physiological function of these enzymes remain to be discovered.

## 6. CONCLUDING REMARKS

Our understanding of the role of tyrosine phosphorylation in the regulation of cell proliferation and transmembrane signaling has improved greatly during the past few years. Still, many important questions remain open, particularly with regard to the PTPases that both counteract the PTKs and regulate them. Given the central role of lymphoid cells in host defense, a deeper understanding of these molecular events would greatly aid the design of rational pharmacological approaches to modulate the immune system, augment defense against pathogens and interfere with the growth of lymphoid leukemias, a process that may be associated with aberrant signaling events. The known crystal structure and small

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size of many PTPases make them ideal targets for rational drug design. Before these enzymes can become sufficiently attractive as targets for the pharmaceutical industry, however, we must gain considerably more insight into their physiological functions and importance. We also need to clarify their substrate specificity and selectivity, their redundancy and their regulation.

Lymphocytes express many PTPases, only some of which have currently understood functions. These include CD45, SHP1 and HePTP. There is recent evidence (470), however, that T cell membranes contain a PTPase activity that efficiently keeps the TCR signal transduction machinery, including the Src and Syk family PTKs, in a resting phosphorylation state. Inhibition of this activity, which was not attributable to CD45, SHP1 or HePTP, induced the same ordered sequence of phosphorylation events as normally seen after TCR ligation (470). It remains to be seen if this membrane-bound PTPase is identical to one or several PTPases discussed in this review or yet another novel enzyme.

A very exciting new area of investigation is the involvement or loss of PTPases in human malignant diseases. The surface expression of CD45 has long been used as a marker for differentiation of leukemic cells (471,472). There is no evidence, however, that CD45 would be directly associated with the transforming event or progression of leukemias or lymphomas. The first examples of a potential role for a PTPase in neoplasia was the finding that HePTP might be overexpressed in myelodysplasia and deleted in leukemias (211). The recent discovery that both PTEN is deleted or mutated in multiple human cancers, including leukemias, and that and CDC25 is overexpressed in many cancers, add to the notion that PTPases are likely to be involved in clinically relevant carcinogenesis. Finally, loss of MKP-1 expression or activity was found to be associated with malignant transformation and clinical progression in a subset of epithelial tumors (473). As overexpression of many PTKs can cause malignant transformation, it is natural to assume that loss of the PTPases that counteract them would also cause neoplasia. Furthermore, genetic damage is perhaps more likely to cause deletion or loss of function rather than overexpression and gain of function. We predict that several PTPase genes will be found in the near future to be altered in human malignancies. This underscores the importance of studying these enzymes and the value of increased understanding of their regulation and substrates for a rational drug development to treat human diseases.

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