

Supporting Information

Substrate Specificity of Protein Tyrosine Phosphatases 1B, RPTP α , SHP-1, and SHP-2[†]

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Table S1. *S. antibioticus* Tyrosinase Substrates Selected from MX¹X²X³X⁴X⁵LNBBRM-PEGA Library (randomly picked from ~20% colored beads)

Intensely Colored (42)				Medium Colored (18)		Lightly Colored (20)	
Y ASSA	CD Y SE	Y EEQP	A Y EQT	FEP Y A	Y DV Y M	H Y NYA	E Y ASN
GG Y YA	Y QTTE	P Y NSP	PV Y YT	M Y SFF	Y FDDP	F Y CGC	Y AFLM
PQ Y GC	Y DNAG	I Y CTP	LDE Y A	Y NLNF	Y SH Y T	V Y YPD	DT Y PS
DQ Y YC	LA Y EG	AE Y SQ	ACH Y A	D Y TVF	Y CSEV	L Y IAF	LI Y AD
HE Y AD	HLS Y G	CGH Y Q	CGTC Y	CGQ Y F	HELE Y	FC Y EF	HPPE Y
Y VDGD	A Y SQH	Y NNAS	DAQ Y	GL Y FG	LLNG Y	ID Y HH	ING Y
DD Y ND	DGE Y I	Y SEHS	QSG Y	Y H Y NG	Y IHI Y	FI Y SI	LVFG Y
APG Y D	Y ENPL	Y HHSS	EHQ Y	QC Y IH	PTFM Y	Y HD Y I	GNPH Y
Y HQHE	I Y SGN	P Y DTS	VHAS Y	LL Y MH		IPP Y L	MIAQ Y
D Y DIE	Y LNPP	QDT Y S		ML Y YN		FT Y CN	DC Y TY
Y THQE	Y CSPP	L Y GNT					

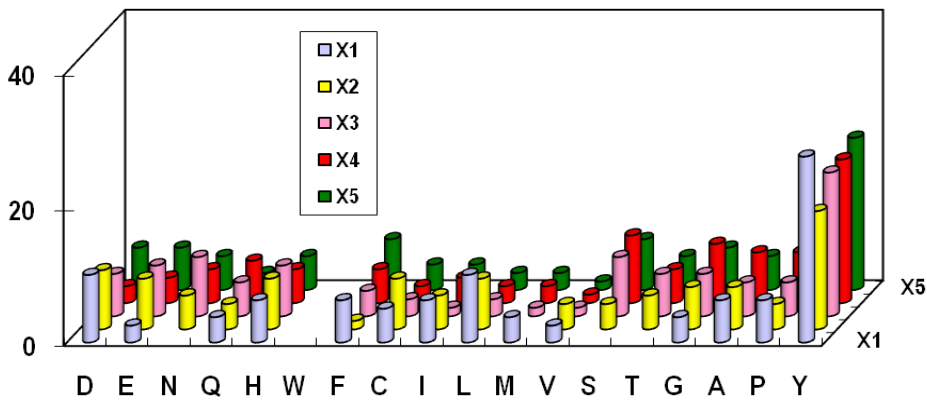


Figure S1. Sequence independence of *S. antibioticus* tyrosinase. The y axis represents the percentage of selected peptides that contained a particular amino acid (x axis) at a given position within the peptide (X¹ to X⁵, on the z axis). C, Abu; M, Nle.

Table S2. Most Preferred PTP1B Substrates Selected from Library I (SAXXXXXpYAABBRM-resin; total of 322 sequences from 15 independent screening experiments)^a

Class I					Class II			
ADHDW	DSQDT	FRQNV	LEGNV	VTDSM	AQWRF	RQRYT	TRWNR	RKWHF
ADHFW	DTADV*	FSDFD	LEHDG	SEWIN	EWRRV	RRFHP	WARRS	RLRXX
AKREW	DTEQD	FSDSD	LFEWD	SLNFE	FFHRR	QPKKK	WKFNR	RNRIH
ASENL	DTGDM	FSFNN	LQYDN	SPEGP	FKFRT	PRARM	WKKDR	RMRHR
ASHNQ	DTLGN	FSGNM	LWEKD	SRHEW	FRIRR	RRRSD	WKQRT	RPRRH
ASLTD	DTNAV	FSHFE	MFTDD	SSENA	FRKRV	RRHGF	WKRKA	RRGHM
ASMTN	DTQTM	FSISP	MHMMA	SSFDV	FRRFA	RRHNL	WKRKH	RRGRS
ASQDN	DTSWE	FSSDD	MSLGD	STENQ	FRRHV	RRIIN	WKRSR	RRHFA
ASSDD*	DTWDV	FSTSM	NDHDL	STGNN	FRYIK	RRIRQ	WMRKQ	RRHQK
ATDDL	DVWDA	FSWDE	NDLYE	TDLWL	HQYRR	RRIST*	WRRNT	RRISS
ATENL	DVWDF	FTDAE	NDWNP	TGTGH	HRRRV	RRKAM	XKHRI	RRKAI
ATGLL	DWDIS	FTDQA	NETSE	TIPVY	IRRHF	RRNRP	YRRRM	RRKAW
ATGQD	DWDTA	FTDQD	NHLES	TQENM	KRHRF	RRPTS	ARKRI*	RRNFA
ATGSS	DWEHM	FTEFI	NSSLD	TWFDT	KRKLK	RRQFS	RRRHI	RRNQK
ATHFE	EDAFW	FTHDQ	NWDDA	VEQDV	KRSRM	RRQHI	RWKQS	RRQTA
ATMID	EDWEA	FTISD	PDHEM	VITDY	LRRRM	RRQRF	TRRGI	ARKRM
ATNMA	EDWGP	FTKDE	PFDEP	VSANQ	PKRRF	RRQSL	QRRRS	FKNRS
ATRPP	EESHL	FTMAA	PFXED	VSFDM	QMRRF	RRRFQ	RAHRH	FRNRQ
ATQND	EFDIS	FTNRQ	PSWDM	VSNGV	RFFRN	RRRGF	RARRF	GRRQI
ATVSQ	EGDVD	FTPEI	PTFGA	VTKDD	RFRGK	RRRXX	RHRPG	GRRFR
AVWEM	EIWND	FTSGA	PTKDA	VTNDA	RGHKL	RRSNI	RIHKA	KFNHR
AWFEW	EMPDM	FTSGL	PTVGL	VTQDQ	RGMRH	RRSRQ	RIKXX	KKRFA
AWMTW	EMPXX	FYRAE	QDVDA	WDTDI	RGRHF	RRSWA	RKFRR	KNRKE
DASQD	EMPYI	GSANQ	QEGMW	WEDIA	RHRFG	RRWGA	RKHTF	KRKVF
DDAWS	EQNAW	HFTNE	QGTGS	WEDQF	RHRKM	RRYPT	RKKGI	KRRXX
DDWDV	ESFDA	HIDDV	QIPDW	WEHSD	RIRFR	RVNRT	RKRNY	LKRRV
DDWNW	ESFDQ	HSESN	QENENQ	WGGLD	RKFAR	RVRRH	RKRPI	NKKRW
DEWFS	ETDFA	HTNRQ	QTDDT	WGTDS	RKGRH	RWKTR	RKRLK	MRRNR
DEYQM	ETFGQ	HWESM	QTDGD	WHFDA	RKNHS	RWRAI	RKSNP	VRRSA
DFPAQ	ETGFD	IRDEP	QTKDA	WNTTD	RKRNI	TRHRS	RKTKW	WKNKS
DFWDT	ETGMV	ISDNS	RFAIY	WQNNK				
DGINI	ETPIA	ETNDF	RFQHA	WSKDA				
DGTNS	ETDSW	ISNSN	RHQWA	WTEDS				
DMFDV	ETSGS	ITEEA	RHVQT	WVEDI				
DMIDV	ETWDD	ITGDW	RQTNA	WVWGH				
DSDAW	ETWTS	ITMDQ	RRANI	WWDAD				
DSEQI	EWSEM	ITNND	RRFQE	YHYDA				
ATIND	EYDWE	IWINA	RRLNV	TDESD				
DSFDW	FDYQM	KFQED	RTDSI					
DSMDI	FGSDS	KQTTQ	RTHDM					
DSMNI	FPAXX	KTIWD	RWQTT					

^aM, Nle; X, amino acid whose identity could not be unambiguously determined; Y, F₂Y.

* Sequences selected for kinetic analysis.

Table S3. Peptides that are resistant to PTP1B dephosphorylation (colorless beads selected from Library I, SAXXXXXpYAABBRM-resin). M, Nle; X, unidentified amino acid; Y, F₂Y.

MAGWI	IFKLW	IIFQQ	SLTFI	LMMMG	IVMWA
SAFFI	VFMGW	IIGMV	WLRVI	XMMII	LVFAW
TAFII	VFVAW	IITXX	WLTVV	ITIIR	LVMFA
VATVF	FGGIW	KIGFF	AMIMV	ITMQW	MVMWF
FFVEF	IGFFM	MIFWV	FMVMQ	LTIVV	VVFIF
FFVVG	EIFFV	LLTMM	HMVVI	FVMMV	SWWWW
NFINI	EIIIK	SLFII	LMFEW	FVFMF	

Table S4. Most Preferred PTP1B Substrates Selected from C-Terminal Libraries II (W[TS][DE][DE]VpYXXXX-LNBBRM-PEGA) and III (WAAAAPYXXXXNNBBRM-PEGA)^a

Library II	Library III				
	Class I		Class II		
WSDDVpYSFAF	<u>FEDED</u>	<u>DWDIW</u>	<u>DQEFI</u>	KRKFA	QRRNR
WSDDVpYWDWA	<u>WEDYE</u>	<u>EMDEW</u>	<u>DEDWT</u>	NIRRH	RRQPR
WXXXVpYWDDW	<u>YDEDF</u>	<u>EADDF</u>	<u>ENDTW</u>	RSYHI	HRARR
WXXXVpYXXEA	<u>WDEIG</u>	<u>QADWE</u>		RLRKI	RLPRR
WSDDVpYWSEF	<u>WEDQG</u>		GFEXX	KRHRI	TVRRR
WXXXVpYTREW	<u>FDDIN</u>	<u>DDFFF</u>	MDXXX	RFERRI	RKQWR
WXXXVpYXXEW	<u>FDDIP</u>	<u>DDYGP</u>	DXXXX	LTRRI	NRRFS
WXXXVpYXXEW	<u>WDDIW</u>	<u>DEFHY</u>	DXXXX	RIRIK	GKRRS
WXXXVpYXIEW	<u>WDKRR</u>	<u>EEFFI</u>	EXXXX	RRRIK	KRRRS
WSDDVpYDTFW	<u>FNSDF</u>	<u>EEYEF</u>		RRIRK	SRRRV
WSEDVpYSWQM	<u>YDGGF</u>	<u>EDFWD</u>		ITRRK	GKRXX
WTDDVpYAWSF	<u>SDELM</u>	<u>EEWSE</u>		TRWRK	RQRXX
WSDEVpYDMWD	<u>QDEMF</u>	<u>EEWDM</u>		XXRTK	RRRXX
WXXXVpYXQWD				RFRRN	XHRNV
WSEDVpYWEWE	<u>WIDEI</u>	<u>DWWEV</u>		RNKRP	RAQIR
WSDDVpYWDWS	<u>WWDEE</u>	<u>EWWDs</u>		HRNHR	RQRMR
WTEDVpYXXXXY	<u>YWHDE</u>	<u>DAMDF</u>		RNMKR	
	<u>TWDEK</u>	<u>VDYNY</u>		RNPKR	
	<u>TVDFE</u>	<u>SNMPE</u>			

^aM, Nle; X, unidentified amino acids; Y, F₂Y.

Table S5. Most Preferred PTP1B Substrates Selected from Library VI (ANNX⁶X⁵X⁴X³X²X¹AABRRM-PEGA; total of 129 sequences from 5 independent screening experiments)^a

Class I				Class II
pYpYpYIRpY	pYWTWpYpY	FpYEpYWpY	DApYEDpY	RREXXpY
pYpYpYNVpY	pYIWQpYpY	VpYTpYIpY	DApYIEpY	RRRPKpY
pYpYpYpYpYW	pYSWGpYpY	HpYFEpYpY	EApYWWpY	RRHRFpY
pYpYIpYWH	pYWGPpYpY	YpYSEpYpY	XXpYWEpY	RRQWHpY
pYpYFRpYpY	pYWTIpYpY	XpYWLpYpY	VWpYNDpY	RRSHQpY
pYpYHLpYpY	pYEWYEpY	XpYWLpYpY	FGpYAWpY	KMRRFpY
pYpYpVpYpY	pYEWGpY	QpYWPpYpY	AGpYSWpY	RFKRNpY
pYpYGDWpY	pYEVWMpY	DpYDWDpY	XXpYPWpY	RNKRVPY
pYpYATWpY*	pYEISMpY	VpYEIWPY	XXpYWGpY	RHIRWpY
pYpYHSWpY	pYFDDWpY	MpYDYWPY	WGpYNMpY	RQTRIPY
pYpYMMHpY	pYADWWpY	YpYDPWPY	NGWpYpYpY	RNIFRpY
pYpYQXXpY	pYFVDFpY	WpYFDEpY	XXWpYpYpY	RNXXXpY
pYpYEVWpY	pYWLENpY	WpYNDWpY	XXXpYpYpY	MKRRIPY
pYpYWNVpY	pYFPIWPY*	GpYMEWPY	WEFpYQpY	QRRRMpY
pYDpYGFpY	pYNSMWpY	XpYIDWPY	AMDpYMpY	XKRRQpY
pYFpYDFpY	pYVSGWpY	XpYVDWpY	YTEpYTpY*	XRRGApY
pYFpYMDpY	pYXXXXpY	WpYFDVpY	FWSpYRpY	ARWARpY
pYWpYTEpY	NpYpYpYpYpY	VpYADHpY*	FAPpYWpY	XARHRpY
pYGpYAFpY	XpYpYpYFpY	YpYNAWPY	XWVpYGpY	ANRWIPY
pYMpYGMpY	FpYpYFDpY	ApYAPWPY	XEAWpYpY	QARFVpY
pYWRpYpYpY	WpYpYMRpY	EIpYpYWpY	VWEFpYpY*	LAMRTpY
pYWEpYMpY	IpYpYPWpY	IGpYpYDpY	DAFWEpY*	LpYHRWR
pYGGpYFpY	WpYpYWNpY	QWpYpYpY	KFEDTpY	
pYTQpYWpY	WpYpYTapY	GIpYpYMpY	QXXXDpY	
pYWVpYTpY	XpYpYWDpY	WFpYGpYpY	XXXWApY	
pYMLpYHpY	XpYpYWLpY	XWpYpYpY	XXXFQpY	
pYIWDpYpY	FpYDpYFpY	DEpYFWpY		

^aM, Nle; X, amino acid whose identity could not be unambiguously determined; Y, F₂Y.

*Sequences selected for kinetic analysis.

Table S6. Most Preferred SHP-1 Substrates Selected from Library I (SAXXXXXpYAABBRM-PEGA; total of 230 sequences from six independent screening experiments)^a

W	D	E	D	D	M	W	E	W	E	W	D	E	E	W	S	E	I	D	W	T	D	E	W	F
M	E	D	D	D	W	M	E	F	D	F	D	D	E	W	W	D	Y	D	S	A	D	E	Y	F
W	F	D	E	E	F	W	E	N	E	A	E	D	D	W	W	E	W	E	P	W	D	D	S	F
S	W	D	D	E	W	W	D	G	D	V	E	E	D	W	I	E	W	D	S	W	E	D	V	F
P	W	D	D	E	F	Y	D	I	D	F	D	E	E	L	N	E	Y	D	M	Q	D	D	Q	W
W	T	D	D	D	W	S	E	Q	D	N	E	D	D	I	I	D	W	D	I	I	D	D	Q	W
W	L	E	D	D	W	M	D	N	E	Q	E	D	D	M	G	D	W	D	M	G	D	E	M	W
W	A	D	D	E	W	T	D	M	D	D	Q	D	E	W	I	D	Y	D	M	W	E	D	Y	S
W	A	D	E	D	W	V	E	A	D	D	L	D	D	W	A	E	W	E	A	Y	D	E	F	T
W	M	D	E	E	G	T	D	A	D	E	M	D	D	W	W	D	S	D	S	W	D	E	F	L
W	D	W	D	E	E	E	W	I	D	D	W	D	D	A	F	E	S	D	T	I	D	D	Y	S
W	E	Y	D	E	E	D	V	N	D	E	F	E	D	M	W	D	G	D	M	M	D	E	W	S
W	E	W	E	E	D	E	T	G	D	D	T	E	E	Q	F	D	I	D	I	T	E	D	F	I
I	D	Y	D	D	W	E	N	Y	E	D	P	D	D	M	E	H	W	D	F	P	E	D	W	I
D	L	W	D	E	F	E	S	Y	E	D	L	D	D	V	D	S	F	D	W	P	D	E	F	I
E	W	T	D	E	W	D	G	W	D	E	L	E	D	V	D	L	F	D	F	W	E	D	S	T
D	W	P	D	D	F	E	M	F	D	W	H	E	D	F	E	I	F	D	F	W	D	E	G	S
N	W	F	D	D	M	E	S	W	D	H	W	D	E	M	E	F	T	D	W	W	D	E	Q	V
P	F	F	D	D	I	D	A	W	E	N	F	E	D	F	E	F	T	D	Y	W	D	E	A	I
I	W	Y	E	D	F	E	Y	N	D	I	T	D	D	W	E	L	L	D	F	L	E	E	S	I
W	A	W	E	D	W	D	W	A	D	I	G	D	D	W	D	Y	W	D	I	E	S	D	F	W
A	V	W	D	D	W	E	F	I	D	I	A	D	D	Y	E	F	F	D	M	D	W	D	N	W
P	M	W	E	D	M	E	W	I	D	V	I	D	D	Y	E	P	W	E	N	D	W	D	F	S
F	W	L	D	E	F	E	T	T	D	G	G	E	D	W	E	G	Y	D	M	D	W	E	F	T
L	W	Q	D	E	W	D	G	T	D	A	W	D	D	S	D	F	N	D	T	D	Y	E	Y	L
I	W	N	E	D	W	D	S	V	D	T	W	E	D	M	E	W	V	D	T	D	W	E	V	Q
M	W	N	E	D	W	E	T	V	D	I	W	E	D	I	E	W	G	D	M	E	W	D	A	M
I	W	P	D	D	W	D	L	G	D	I	W	D	E	P	P	F	W	D	M	F	W	E	Q	T
W	M	N	D	E	E	N	W	Y	E	W	Q	D	D	T	G	N	W	D	M	W	F	D	N	L
W	A	G	D	D	D	T	F	Y	E	Y	L	E	D	S	W	F	P	D	Q	A	S	E	S	N
W	I	A	D	D	E	Y	Q	Y	D	F	S	E	D	V	F	M	N	D	I	E	E	S	W	W
S	T	N	D	E	D	W	A	F	D	W	N	D	E	I	A	S	N	D	N	D	D	V	F	W
M	G	S	D	D	D	F	P	W	D	I	T	D	D	Q	T	S	N	D	V	E	E	W	G	Y
D	D	D	T	D	E	F	G	W	E	V	S	D	D	L	P	T	S	D	I	D	D	V	V	W
D	E	D	I	E	E	W	W	T	D	E	E	H	D	W	D	E	E	H	W	D	D	L	F	L
E	D	E	M	D	D	Y	W	P	D	D	D	Y	D	Y	E	D	E	W	F	E	D	I	F	M
W	E	D	N	E	D	M	W	T	D	D	E	Q	D	W	D	D	E	T	W	E	E	W	G	M
W	E	E	Q	D	D	W	T	S	D	E	D	S	D	F	D	D	D	A	F	A	E	W	Q	W
W	D	D	I	E	E	W	I	N	D	D	D	Y	D	I	D	E	D	W	N	F	D	W	N	V
E	W	D	Q	E	D	W	Q	I	D	E	E	W	D	V	D	D	D	F	I	G	E	S	G	T
D	W	D	I	D	N	Y	F	P	E	G	D	W	D	W	D	E	D	Y	L	E	W	G	V	Q
D	Y	D	G	D	W	F	L	P	D	M	D	W	D	F	E	D	E	G	T	Q	W	F	S	H
D	W	D	L	E	F	Q	V	N	D	P	D	F	D	W	D	D	D	N	I	W	S	F	I	P
D	Q	D	G	D	E	E	D	E	F	V	E	W	D	Y	T	E	D	F	W	T	F	T	G	A
G	W	E	W	D	F	D	D	D	F	A	E	Y	D	F	Q	E	D	Y	F	Y	M	P	Q	Q
A	F	D	Y	E	W	E	E	D	F	I	D	T	E	W	N	D	D	F	Y	Q	G	T	S	P

^aM, Nle; Y, F₂Y. Bold-faced sequences were selected for kinetic analysis.

Table S7. Most Preferred SHP-2 Substrates Selected from Library I (SAXXXXXpYAABBRM-PEGA; total of 255 sequences from eight independent screening experiments)

E	E	D	E	D	S	W	E	S	D	F	K	D	D	I	F	E	A	D	W	D	E	E	N	S	
D	W	D	D	D	T	W	E	S	D	F	Y	E	D	F	P	D	L	D	W	E	D	E	S	M	
W	N	D	D	D	W	N	E	N	D	W	F	D	E	F	L	E	P	E	W	E	D	D	N	L	
F	Q	E	D	D	W	M	E	T	E	L	F	D	D	W	F	D	F	D	I	W	E	D	Q	W	
F	T	E	D	E	W	I	D	I	D	I	W	E	E	F	F	D	F	D	L	A	D	D	L	W	
W	I	D	E	D	D	E	F	W	D	V	W	E	E	F	F	E	W	E	V	W	E	E	F	N	
W	D	H	D	E	D	E	Y	Y	D	F	Q	D	D	W	I	E	Y	D	T	I	D	D	W	S	
N	D	Y	E	D	E	D	Y	Y	E	F	N	D	E	F	I	D	Y	D	M	S	E	E	W	I	
I	D	W	D	E	E	E	V	W	D	W	V	E	D	F	M	E	F	D	I	I	D	D	Y	L	
P	D	Y	D	E	D	E	M	W	E	W	A	E	E	Y	A	E	W	E	M	W	D	D	S	S	
W	D	S	D	D	E	D	W	G	D	M	L	E	E	W	F	D	N	E	T	W	D	D	Q	T	
W	E	Q	D	D	E	E	W	I	D	F	W	E	E	S	F	E	I	D	T	W	E	D	T	T	
W	D	S	E	D	F	E	F	W	E	W	F	D	D	I	F	E	N	D	I	W	E	E	Q	S	
F	D	L	D	E	F	D	Y	F	D	F	W	E	D	I	F	W	D	A	D	V	F	E	D	S	T
F	E	M	E	E	W	D	N	W	D	F	W	D	E	A	W	E	P	E	V	W	D	D	S	A	
F	D	I	E	D	I	E	W	T	D	T	W	D	D	T	D	T	W	D	Y	W	D	E	T	L	
E	W	H	D	D	I	E	W	T	D	I	F	D	D	S	V	Y	M	D	F	I	D	D	I	N	
E	Q	F	D	E	W	D	N	T	D	V	W	D	D	M	D	Y	M	D	F	D	Y	M	D	F	
D	A	F	D	D	W	E	P	N	D	G	W	E	D	I	D	Y	M	D	F	E	Q	Q	D	W	
D	G	F	D	E	W	E	T	G	E	A	W	E	D	V	E	Q	Q	D	W	D	N	D	W	F	
D	W	I	E	E	D	F	Y	W	D	W	Q	E	D	T	D	L	V	D	W	E	W	D	S	W	
W	Y	H	D	D	D	N	Y	W	E	W	T	E	D	N	E	Y	F	D	I	D	I	D	S	W	
I	F	W	E	D	E	W	N	W	E	W	Q	D	D	L	D	L	W	E	T	D	M	D	N	W	
I	F	Y	E	D	D	W	V	W	D	F	S	E	D	A	D	L	F	D	M	D	M	D	N	W	
F	Q	F	D	D	E	W	G	W	D	F	Q	E	D	V	D	V	W	D	M	E	Y	E	W	S	
W	Q	W	E	D	D	A	W	S	D	D	A	W	S	D	F	S	E	D	V	E	M	W	D	I	
W	P	Y	E	D	E	N	F	G	D	F	T	E	D	P	E	G	F	D	I	E	W	E	W	I	
F	M	F	E	D	D	S	M	N	E	W	M	D	D	P	D	W	S	D	S	D	S	E	F	M	
F	W	Q	D	E	E	D	D	D	I	W	L	D	E	I	E	F	I	D	T	E	A	D	W	M	
W	W	V	D	D	F	E	E	D	F	W	G	D	E	I	D	W	S	E	A	E	I	E	W	M	
W	Y	P	D	E	W	E	D	E	F	W	I	E	E	V	D	W	M	D	I	D	W	D	S	L	
W	Q	V	D	D	M	D	E	D	W	Y	P	E	D	L	E	W	L	D	I	D	W	D	Q	V	
V	D	E	W	E	I	D	E	D	Y	S	M	D	D	T	D	F	G	D	V	E	W	D	Q	V	
W	E	E	S	D	A	E	E	D	Y	I	T	E	D	M	D	S	I	D	S	E	W	D	L	V	
W	D	D	Q	D	W	E	D	D	L	L	G	E	D	V	D	T	M	D	M	E	T	D	S	T	
W	E	E	T	D	W	D	E	E	I	D	D	M	D	W	V	W	N	D	F	F	H	E	S	F	
F	D	D	N	E	N	D	D	E	I	E	D	G	D	W	W	S	Q	D	F	Q	M	D	F	M	
W	E	D	M	E	P	D	D	E	M	E	E	L	D	F	F	M	Q	D	F	W	V	D	Q	S	
F	D	D	I	D	E	F	E	D	F	E	D	I	E	W	N	A	W	E	M	L	M	E	S	M	
E	F	D	W	D	E	W	E	E	W	D	E	W	D	V	W	Y	P	D	M	M	M	E	S	M	
D	T	E	W	E	D	Q	E	D	F	E	E	V	D	T	G	W	Q	D	V	D	D	I	N	W	
E	V	E	Y	D	D	A	E	D	W	D	D	P	D	I	W	N	N	D	M	E	E	Q	W	T	
D	W	D	S	E	D	F	E	D	S	D	E	M	D	A	W	A	Q	D	I	D	E	F	S	V	
E	W	D	V	D	D	W	E	E	T	E	E	L	D	M	W	P	V	D	V	E	E	N	S	I	
T	W	E	Y	E	D	W	D	D	V	E	D	P	E	V	D	E	E	W	W	W	E	A	T	W	
L	F	E	W	E	D	W	E	E	V	A	D	F	D	F	E	E	E	F	W	G	D	F	N	I	
W	N	E	F	E	E	W	D	E	M	I	D	W	D	Y	D	E	D	T	W	W	E	Q	G	I	
W	V	D	Y	E	E	W	E	E	A	W	E	S	E	Y	E	E	E	W	S	W	D	T	G	I	
F	M	D	W	E	D	D	T	E	V	W	D	L	D	F	D	E	D	F	M	D	P	H	V	V	
F	P	D	W	E	D	Q	E	E	M	W	D	P	D	Y	E	D	D	Y	L	D	F	T	N	M	
I	T	D	Y	D	E	G	D	D	I	F	D	G	D	F	D	D	D	T	T	D	F	P	S	V	

M, Nle; Y, F₂Y.

Table S8. Most Preferred Substrates Selected from Library II (W[TS][DE][DE]VpYXXXX-LNBBRM-PEGA; total of 71 complete and 9 partial sequences for SHP-1 and 51 complete and 5 partial sequences for SHP-2)

SHP1		SHP2	
Type I (29)	WSEdVpYNDFW	Type I (33)	Type II (11)
WSDDVpYWFAD	WSDDVpYNDWW	WTEDVpYWWDA	WTDDVpYADWW
WSDDVpYFWDA		WTDDVpYWWEW	WTEDVpYYDWS
WSDDVpYWFDY	Type III (23)	WTDDVpYWWFD	WTEDVpYWDSY
WTEDVpYFWDN	WSDDVpYEWAD	WSDDVpYWWID	WTDEVpYWDWL
WTDDVpYIWDW	WTDDVpYEWDI	WSDEVpYWWQW	WTDDVpYWELE
WTDDVpYWYED	WSEdVpYDWEp	WTDDVpYWFey	WSDDVpYWESW
WSDDVpYWVEE	WTDDVpYDFEW	WTDDVpYWFew	WTDEVpYWEWN
WTEDVpYFWEF	WTEDVpYDYEW	WTEDVpYWYDV	WSDEVpYWEWD
WTDDVpYWFEG	WSEdVpYEGEW	WTDEVpYWYEE	WSEdVpYFEEW
WSEdVpYWWEG	WTEDVpYDIFf	WTEDVpYWYDV	WTDEVpYFEWW
WTEDVpYWWEG	WSDDVpYEIFY	WTDEVpYWYEE	WSDDVpYWNFD
WTEDVpYWWEG	WTEDVpYEMFY	WTDDVpYWGDF	
WTDDVpYWFEL	WSEdVpYDFYy	WSDDVpYWIDY	Type III (8)
WTDDVpYWIEW	WTDDVpYEGYw	WTEDVpYWMEW	WTEDVpYDYyy
WTDDVpYYFFE	WSDDVpYEWGE	WSDEVpYWVDW	WTDDVpYDLWF
WSDDVpYWYFE	WTDDVpYDYHW	WSEdVpYWVWQ	WTDDVpYDMWW
WTDDVpYYWID	WTDDVpYDFIw	WSEdVpYFWDA	WTDDVpYDWFM
WSEdVpYWWID	WTDDVpYDWNy	WSDEVpYFWDW	WTDEVpYDWYD
WTDDVpYWMTD	WTDDVpYEYMy	WSDEVpYFWEV	WTEDVpYDWQW
WSEdVpYFFWD	WSDEVpYDVFW	WTDEVpYFWEV	WTDEVpYEWEF
WSDEVpYFWDE	WTDEVpYEVFW	WTDEVpYFWTE	WTDEVpYEWEF
WSDEVpYWVEF	WSDEVpYDMWD	WSDEVpYFWLE	
WSDEVpYYWEF	WXXXVpYNWEW	WTeeVpYYWYD	Type IV (1)
WSDEVpYWWEN	WSDDVpYTWFD	WTeeVpYYyDW	WTDDVpYDEMw
WTDEVpYWTWD	WTDEVpYTWYD	WTEDVpYFFDF	
WTEDVpYWFkw	WTEDVpYsFWE	WTDEVpYlWWD	WXXXVpYXEEW
WTDEVpYIFWM		WTDDVpYTWdW	WTDDVpYXXEi
WSEdVpYYSEW	Type IV (5)	WTeeVpYTWdW	WSDDVpYXXXX
WTEDVpYWSWE	WTDDVpYDDWA	WTDDVpYTWYe	WSDDVpYXXXXW
	WSDDVpYEDeY	WSDDVpYVWEF	WTDDVpYXXXX
Type II (14)	WTDDVpYEDYw	WSEdVpYAWeF	
WTEDVpYWDDF	WTEDVpYDEYw	WTEDVpYAWeF	
WSDDVpYWEED	WTDEVpYEQYy	WSDEVpYAWeF	
WSEdVpYYEEW			
WSDDVpYWDFG	WTXXVpYXEEW		
WTEDVpYWDYD	WXXXVpYXWEW		
WSEdVpYFDWD	WSDXVpYXWNW		
WTEDVpYWEWD	WXXXVpYXdWY		
WSDDVpYWDWG	WSEdVpYIXXy		
WTEDVpYWEWN	WTEDVpYXXXXM		
WSDDVpYFEWT	WSDDVpYEXXW		
WTDEVpYFDfE	WSDDVpYWXXX		
WTEDVpYGDfW	WSDDVpYXXXX		

M, Nle; Y, F₂Y; X, residues that could not be unambiguously determined.

Table S9. Most Preferred Substrates Selected from Library III (WAAAAPYXXXXXNNBBRM-PEGA; total of 33 complete sequences for SHP-1 and 41 complete sequences for SHP-2)

SHP1			SHP2			
GYDED	DEYEA	EDYWS	AEDYF	DNFFE	DDWLE	QXXXW
NLDLE	DDDFE	EDFDT	FANHV	DSEME	DEYYF	TDXXX
TEDNM	DEHEF	EDTQV	FEEEY	DWDWT	EEEMF	DXXXD
GRGRI	DEPIF	DDVAW	YDDET	DFMDF	EDDSF	XXXDW
	DDWNF	DDMEW	YDEEW	ESWDD	EDEDY	
ETDYD	EDADY	EDWEW	WTDED	EFFDI	DDEFD	
DLYDE	EDEEY		LDADY	EFMED	EEYQD	
DWWE	EDFGY	DDXXX	LEEDF	EFEEM	EEWPI	
DFEYE	DDWGY	EXXXE	GDDEI	EFDDY	EDDVN	
EFDSW	DDYEP	EXXRT	GEDWA	EWMED	EDQES	
ETDDF	EDWTQ	EXXXT	GEDYY	EWLDE	DDEEW	
EVDDG	EDEV		GEWME	ELVDE	EEYEW	
EMDEG			QEWDD	ENWEE	EDYSW	
DVWEL				EWEE		
EVEEM				ERYIE		
EVENQ						

M, Nle; Y, F₂Y; X, residues that could not be unambiguously determined.

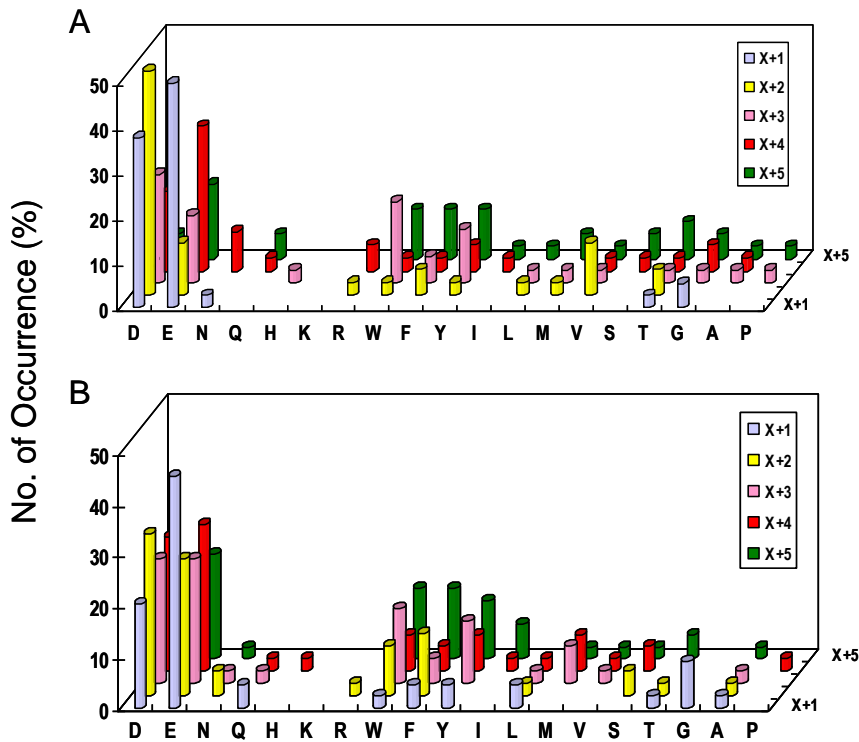


Figure S3. Amino acid composition of the most preferred substrates of SHP-1 (A) and SHP-2 (B) on the C-terminal side of pY (from screening against library III, WAAAAPYXXXXXNNBBRM-PEGA). The y axis represents the percentage of selected peptides that contained a particular amino acid (x axis) at a given position within the peptide (pY+1 to pY+5, on the z axis). M, Nle; Y, F₂Y.

Table S10. Most Preferred SHP-1 and SHP-2 Substrates Selected from Library IV (AXXXXXpYXXXXXXNNBRM-resin)*

SHP-1															SHP-2																		
Q	N	S	D	E	pY	E	W	E	T	F	E	F	N	F	pY	T	W	A	E	N	N	I	S	D	D	pY	W	S	D	M	V		
S	F	W	E	D	pY	T	D	V	A	G	V	D	W	Q	N	pY	D	D	V	P	W	E	E	V	D	pY	Q	E	G	F	L		
P	Q	W	E	D	pY	F	T	D	A	A	R	D	K	I	F	pY	D	I	D	E	E	I	S	E	F	D	pY	M	E	A	Q	I	
V	R	Q	D	D	pY	M	W	E	N	V	P	E	N	T	F	pY	E	F	D	W	N	P	A	E	T	D	pY	W	A	V	V	D	
D	N	E	A	E	pY	A	E	D	W	D	I	E	P	W	A	pY	W	A	E	T	Q	F	D	S	E	pY	L	D	M	D	Q		
W	G	D	V	D	pY	F	S	L	G	D	E	G	N	W	A	pY	W	A	E	D	G	Q	E	S	I	D	pY	N	A	W	E	T	
N	E	V	A	E	pY	E	L	D	W	E	D	T	I	N	W	pY	D	M	D	F	Q	D	F	W	D	pY	A	D	A	S	W		
D	T	Q	E	pY	V	E	W	P	V	G	S	I	Q	F	pY	D	E	W	D	A	D	F	F	F	E	pY	E	P	E	E	L		
T	N	I	W	D	pY	D	D	F	W	Q	P	T	T	W	pY	D	E	G	D	A	D	F	F	F	E	pY	E	P	E	E	L		
D	I	N	W	D	pY	A	T	F	F	D	V	W	N	N	L	pY	D	P	F	E	D	D	F	I	E	pY	Q	D	N	D	D		
F	I	E	D	V	pY	D	S	G	L	W	V	T	N	P	F	pY	W	D	E	A	E	E	E	P	N	G	D	pY	W	M	D	P	I
E	A	E	E	L	pY	A	I	P	I	F	I	S	W	Q	M	pY	T	D	D	E	A	E	E	N	F	I	D	pY	E	D	I	L	I
I	D	G	D	S	pY	S	F	Q	W	E	F	I	Q	S	N	T	pY	N	D	G	T	D	E	S	W	P	D	pY	Q	E	D	T	
D	W	I	D	P	pY	N	E	P	W	V	Q	I	F	X	X	pY	D	E	W	D	T	X	X	X	X	X	X	X	X	X	X	X	X
S	W	I	D	F	pY	E	D	Q	V	A	X	X	X	X	X	pY	E	D	E	W	I	X	X	X	X	X	X	X	X	X	X	X	X
G	V	G	E	A	pY	D	W	M	D	F	X	X	X	X	X	pY	E	D	W	E	R	X	X	X	X	X	X	X	X	X	X	X	X
F	W	A	D	G	pY	D	M	A	N	E	X	X	X	X	X	pY	E	D	T	W	A	X	X	X	X	X	X	X	X	X	X	X	X
G	W	T	D	M	pY	A	D	D	L	S	X	X	X	X	X	pY	D	D	S	Q	D	X	X	X	X	X	X	X	X	X	X	X	X
V	P	N	E	T	pY	W	D	D	L	Q	X	X	X	X	X	pY	E	L	E	P	H	X	X	X	X	X	X	X	X	X	X	X	X
I	F	Q	D	S	pY	Q	S	F	E	E	X	X	X	X	X	pY	E	N	D	A	W	D	N	X	X	X	X	X	X	X	X	X	X
G	P	L	E	M	pY	S	F	D	I	E	X	X	X	X	X	pY	D	V	W	E	V	X	X	X	X	X	X	X	X	X	X	X	X
D	D	E	W	L	pY	E	V	P	N	E	X	X	X	X	X	pY	D	I	A	Q	I	X	X	X	X	X	X	X	X	X	X	X	X
V	D	E	W	F	pY	A	A	D	E	Q	X	X	X	X	X	pY	E	E	T	W	D	X	X	X	X	X	X	X	X	X	X	X	X
A	I	D	Q	A	pY	E	E	G	W	F	X	X	X	X	X	pY	W	D	V	G	-	X	X	X	X	X	X	X	X	X	X	X	X
V	I	D	I	I	pY	E	D	N	M	W	X	X	X	X	X	pY	A	E	T	W	D	X	X	X	X	X	X	X	X	X	X	X	X
A	H	D	R	V	pY	D	W	D	D	F	X	X	X	X	X	pY	V	T	D	M	W	X	X	X	X	X	X	X	X	X	X	X	X
W	F	E	G	P	pY	D	M	D	D	T	X	X	X	X	X	pY	A	T	D	I	I	X	X	X	X	X	X	X	X	X	X	X	X
F	T	D	P	W	pY	E	M	E	N	D	X	X	X	X	X	pY	X	X	X	R	W	X	X	X	X	X	X	X	X	X	X	X	X
P	S	D	I	M	pY	S	I	D	T	E	I	G	S	X	X	pY	N	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
N	P	D	G	W	pY	M	Q	W	E	E	X	X	X	X	X	pY	S	H	F	X	X	X	X	X	X	X	X	X	X	X	X	X	X
T	I	D	V	W	pY	D	M	D	G	N	E	I	D	W	A	L	R	V	E	D	G	N	I	S	D	D	pY	W	S	D	M	V	
E	I	D	W	L	pY	R	V	E	D	G	A	D	I	A	V	L	R	V	E	D	G	N	I	S	D	D	pY	Q	E	G	F	L	
A	D	I	A	V	pY	E	G	E	W	D	F	E	Q	L	T	pY	E	S	F	E	I	A	S	E	F	D	pY	M	E	A	Q	I	
F	E	Q	L	T	pY	E	S	F	E	I	D	D	S	M	E	R	V	E	D	E	R	X	X	X	X	X	X	X	X	X	X	X	X
D	D	S	M	L	pY	E	F	D	R	V	E	E	M	V	S	pY	D	P	D	E	R	X	X	X	X	X	X	X	X	X	X	X	X
W	E	M	V	S	pY	M	E	Q	D	E	E	F	P	W	F	pY	E	V	D	E	E	H	E	X	X	X	X	X	X	X	X	X	X
H	E	F	P	W	F	pY	A	L	E	E	G	F	N	I	M	pY	D	I	D	D	K	I	F	N	I	M	pY	D	I	D	D	K	
I	F	N	I	M	pY	D	I	D	D	K	F	I	N	T	pY	E	D	W	S	E	E	F	I	N	T	pY	E	D	W	S	E	E	
A	F	W	N	A	pY	Q	D	W	Q	E	A	F	W	N	A	pY	Q	D	W	Q	E	E	A	F	W	N	A	pY	Q	D	W	Q	E
-	N	F	F	E	pY	Q	F	E	G	I	-	D	F	F	E	M	pY	D	S	F	L	I	-	D	F	F	E	M	pY	D	S	F	L
-	D	X	X	X	pY	D	L	D	L	L	D	X	X	X	X	pY	D	L	D	L	L	L	D	X	X	X	X	X	X	X	X	X	X
X	X	X	X	X	pY	D	L	V	I	A	X	X	X	X	X	pY	D	L	V	I	A	X	X	X	X	X	X	X	X	X	X	X	X
E	X	X	X	X	pY	D	E	X	X	A	X	X	X	X	X	pY	D	E	X	X	A	X	X	X	X	X	X	X	X	X	X	X	X
I	X	X	X	X	pY	D	M	W	D	E	X	X	X	X	X	pY	D	M	W	D	E	X	X	X	X	X	X	X	X	X	X	X	X
X	X	D	S	N	pY	W	D	E	R	X	X	X	X	X	X	pY	W	D	E	R	X	X	X	X	X	X	X	X	X	X	X	X	
X	X	H	X	X	pY	W	E	E	W	P	X	X	X	X	X	pY	W	E	E	W	P	X	X	X	X	X	X	X	X	X	X	X	
X	X	X	X	X	pY	W	D	V	V	X	X	X	X	X	X	pY	W	D	V	V	X	X	X	X	X	X	X	X	X	X	X	X	X
X	X	X	X	X	pY	M	E	D	A	V	X	X	X	X	X	pY	M	E	D	A	V	X	X	X	X	X	X	X	X	X	X	X	X
H	A	X	X	X	pY	I	D	F	E	D	X	X	X	X	X	pY	I	D	F	E	D	X	X	X	X	X	X	X	X	X	X	X	X
I	X	X	X	X	pY	M	E	M	D	D	X	X	X	X	X	pY	M	E	M	D	D	X	X	X	X	X	X	X	X	X	X	X	X
R	X	X	X	X	pY	L	D	F	S	F	X	X	X	X	X	pY	L	D	F	S	F	X	X	X	X	X	X	X	X	X	X	X	X
X	X	X	X	X	pY	S	D	N	A	I	X	X	X	X	X	pY	S	D	N	A	I	X	X	X	X	X	X	X	X	X	X	X	X
X	X	X	X	X	pY	W	K	D	E	E	X	X	X	X	X	pY	W	K	D	E	E	X	X	X	X	X	X	X	X	X	X	X	X
T	X	X	X	X	pY	W	K	D	E	E	X	X	X	X	X	pY	W	K	D	E	E	X	X	X	X	X	X	X	X	X	X	X	X
X	X	X	X	X	pY	S	A	E	E	H	X	X	X	X	X	pY	S	A	E	E	H	X	X	X	X	X	X	X	X	X	X	X	X
Q	X	X	X	X	pY	S	A	E	E	H	X	X	X	X	X	pY	S	A	E	E	H	X	X	X	X	X	X	X	X	X	X	X	X

*M, Nle; X, residues that could not be unambiguously determined. Acidic, basic, and aromatic residues are shaded in red, blue, and gray, respectively.

Table S11. Most Preferred SHP-1 Substrates Selected from Library VI (ANNX⁶X⁵X⁴X³X²X¹AABBRM-PEGA; total of 98 sequences from 3 independent screening experiments)^a

pYpYpYMGpY	pYVpYGWpY	pYSKAIpY	PpYpYEEpY	VEpYDFpY
pYpYpYHMPY	pYIAPpYpYpY	pYTGLMpY	SpYpYEVpY	QWpYDDpY
pYpYpYGRW	pYIIpYpYpY	pYIVDSpY	VpYpYMNpY	VWpYDGpY
pYpYpYNTpY	pYIEpYVpY	pYYAESpY*	VpYpYSVpY	DWpYDMpY
pYpYpYSWHpY	pYFNpYFpY	pYEHGSpY	XpYpYpYWM	VWpYDVpY
pYpYpYAFpY	pYNPpYWpY	pYIITSpY	VpYEpYMpY	DFpYFDpY
pYpYpYEVSpY*	pYASpYDpY	pYEVFTpY	PpYNpYApY	MWpYGDpY
pYpYpYpYpY	pYITpYWpY	pYDSSTpY	WpYApYDS	TEpYNWpY
pYSpYMpYpY	pYGWpYGpY	pYTSDVpY	FpYNTpYpY	WEpYNEpY
pYApYpYpY	pYETpYpY	pYGTpYpY	LpYEDWpY	GIpYQWpY
pYEpYpYpY	pYESpYpY	pYDQYpY	IpYIDSpY	MEpYSSpY
pYEpYpYpY	pYGSIpYpY	pYAIGWpY	SpYEFVpY	SVpYSApY
pYYpYpYpY	pYEWGApY	pYDVSWpY	DpYDMpYpY	IDpYVEpY
pYHpYpYpY	pYWVTDpY	pYSATWpY	TpYASFpY	PITApYpY
pYIpYpYpY	pYTRFEpY	pYSApYpYI	DpYTWepY	MEESDpY
pYIpYpYpY	pYEWGGpY	IpYpYpYpY	YpYXXXpY	FDFDWpY
pYIpYpYpY	pYXXXGpY	DpYpYGLpY	DGpYpYpY	WDSEApY
pYIpYpYpY	pYTFpYpY	DpYpYpYpY	FApYASpY	DMSESpY
pYTpYpYpY	pYGSFLpY	DpYpYQWpY	WSpYADpY*	pYHRHIN
pYTpYpYpY	pYVEINpY	GpYpYDNpY		

^aM, Nle; X, amino acid whose identity could not be unambiguously determined; Y, F₂Y.

*Sequences selected for kinetic analysis.

Table S12. Peptides that are resistant to SHP-1 or SHP-2 dephosphorylation (colorless beads selected from Library II, W[ST][DE][DE]VpYXXXX-LNBBRM-PEGA)

SHP1				SHP2		
WHFA	MMMI	DYDQ	RKMT	MRYF	WRII	WWNM
LFFF	MYRI	FSDQ	YMRV	SFMF	WQMI	WWKN
VYHF	FRFK	FTFR	IVRV	IMMF	WRVI	WNFQ
LLKF	WIYK	FWYR	LVRV	MAWF	FKWI	RRKS
FHLY	NGTK	VRKR	IMRV	FTWF	IIMK	WWKS
KMTY	FYHM	FSMR	MIVV	IYFY	LVMK	FRYT
IHWY	YYIM	FIRR	WVWV	VFTY	IFHL	VMHV
YVWY	FFMM	YIRR	IHKW	WFMG	VILL	
IWMG	FYRM	MYFT	WFQW	FRAI	IIMM	

M, Nle; Y, F₂Y.

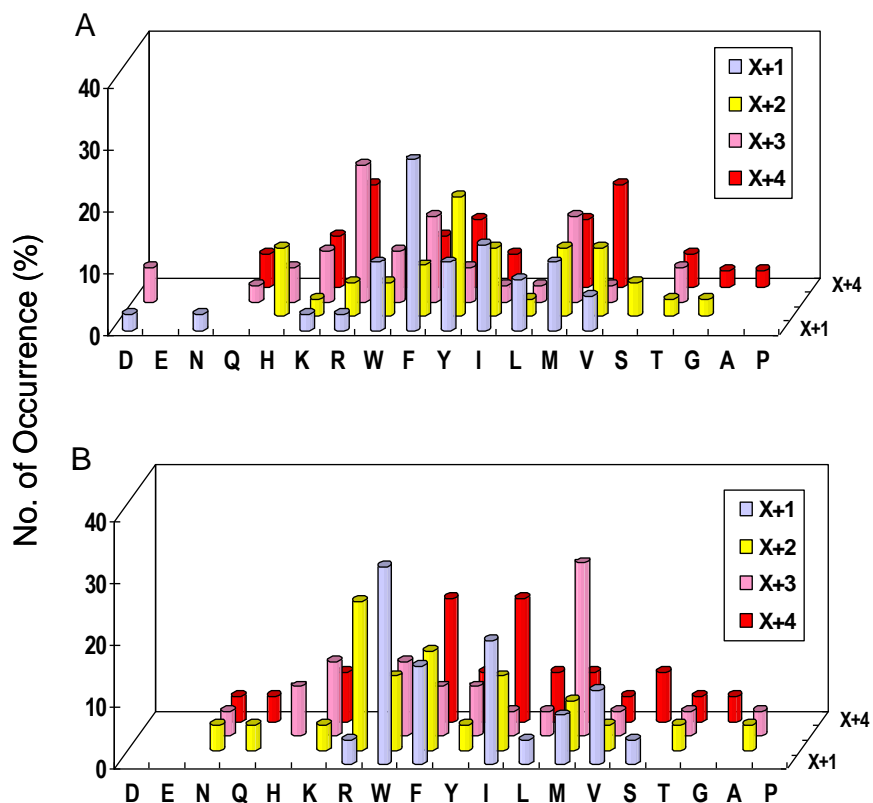


Figure S3. Amino acid composition of the peptide sequences that are resistant to SHP-1 (A) or SHP-2 action (B) (colorless beads selected from library II, W[ST][DE][DE]VpYXXXX-LNBBRM-PEGA). The y axis represents the percentage of selected peptides that contained a particular amino acid (x axis) at a given position within the peptide (pY+1 to pY+5, on the z axis). M, Nle; Y, F₂Y.

Table S13. Most Preferred RPTP α Substrates Selected from Library I (SAX₅pYAABBRM-resin)^a

RRKPF	KSRFF	KRXXX
VKQWR	NKRFF	IVRRW
RRAXX	FRPKF	RHXXX
FWKKN	FHRKF	MRWRN
KNWRR	RSRIF	RKQWR
KKFNW	WRAQR	RIKAW
RFRNI		

^aM, Nle; X, unidentified amino acids; Y, F₂Y.**Table S14.** Most Preferred RPTP α Substrates Selected from Library VII (Alloc-ASX₅pYAABBRM-resin, with reduced Arg and Lys contents)^a

ALSID	VSGEA	TVDHT	SGNSQ	IEWTG	TGDTM
TWDAG	IFIFP	TWGHE	STNSE	IEWTG	TNGTG
DWYDI	TWDFP	TWAHD	SWDSV	LEPTM	TNGTG
ETGDA	WMEFD	NWDIF	TEQSL	LHETI	TTITA
FNLDW	ITSGI	WEAID	TWTSA	LVNVA	VHPTD
LWEDI	MVTGP	IIEKY	WAFSD	MEITA	VMETE
MWSDF	NISGP	MLEKY	WIESG	MVSTA	VMETM
QEGDW	NQWGM	EMELF	AFETG	MVATA	VPHTA
TFHDI	TFGGH	LESLF	AVETA	MWETA	DDYWY
TGLDS	TNAGS	AEINW	DIHTA	NFITA	DFYWE
TSFDD	TYTGD	IWDNV	EIDTA	NHTTA	DWDWW
TSWDV	WLTGP	MYENI	EMETI	PFVTP	ESHWQ
WDFDF	YMYGD	TSYNN	ENDTA	QIATA	SDMWS
ARSEL	NTYHR	TAEQA	EVPTA	SDHTA	SFSWP
ESMEL	SAIHD	TLGQM	FEETM	SDGTS	
FDWEW	SDSHS	FESSM	FPETG	SEVTI	
SGTEP	TDAHM	FMSSA	HQVTA	SEWTL	
TGIEM	TDQHF	GELSF	HYITT	SHSTG	

^aM, Nle; X, unidentified amino acids; Y, F₂Y.

Table S15. Most Preferred RPTPa Substrates Selected from Library IV (AX₅pYX₅NNBBRM)^a

At 150 mM NaCl			
LTIAQpYRMRKR	QTKRNpYARRRQ	XXXXWpYQFKHK	AKIGHpYFARFR
NWMKKpYGRRMN	KREFWpYRSPNR	MHRHIpYHRTRM	VPWQNpYANRFR
MRNGApYFRRRK	XXXXXpYIKINN	XXXXXpYRNTXX	KRRHMpYLGRL
IMTNFpYKNNRR	QMPSFpYMRMRM	TKFAEpYRRRI P	NPKVApYKRFLR
IDDRMpYKRNR F	XXXXIpYRRKIR	PRHNWpYGAHRM	MRI RTpYRGPKA
WQGPSpYLRTRK	RSTFIpYRRKDR	ITDLLpYNQGGL	FHNWKpYGRLRK
RHRNWpYQKSIR	XXXXXpYMRRHR	KKQIWpYQSQKR	FRANA pYRRTXX
PFPGLpYRHRHR	XXXXXpYKRDKK	IQTIHpYRNRRM	KRFPLpYLNKRF
XXXXXpYMKKTR	XXXXIpYRRKRI	XXXXXpYRKTRR	KRRNWpYGGERF
RFNQWpYQKKGW	QLKPFpYAMKRF	KTANI pYRFSRV	
RIMGQpYRRPIR	RVSHMpYHFKRA	PNNIKpYRSRRR	
At 300 mM NaCl			
FQRQKpYRRRXX	XXXXNpYVPWRK		
GNVIWpYRNQGP	MPKPRpYMMVXX		
XXKKFpYRKGA K	RLRRFpYGIANR		
HPRLMpYKRNFV	XDKR VpYRHKNR		
NRKKWpYGIRQA	ARRPFpYKARKR		
TARFKpYAKRRH	GHNDVpYDKRVK		
ERRKFpYRWRGT	STHHKpYRRRFL		
At 500 mM NaCl			
PKRLMpYRISQK	NRISLpYRENRR		
RVKRFpYARTNK	PWNNMpYAPNWT		
XXRPLpYXXQHK	XXXXXpYSPKNR		
XXXXIpYKTKRR	NSMGIpYKDRWK		
DTRAFpYGWPRK	XXTTRpYGVNKR		
KRQQVpYESRRW	VPNRVpYXXXWQ		
RPNI R pYQSRRF	WGGQMpYRRQIS		

^aM, Nle; X, unidentified amino acids; Y, F₂Y.

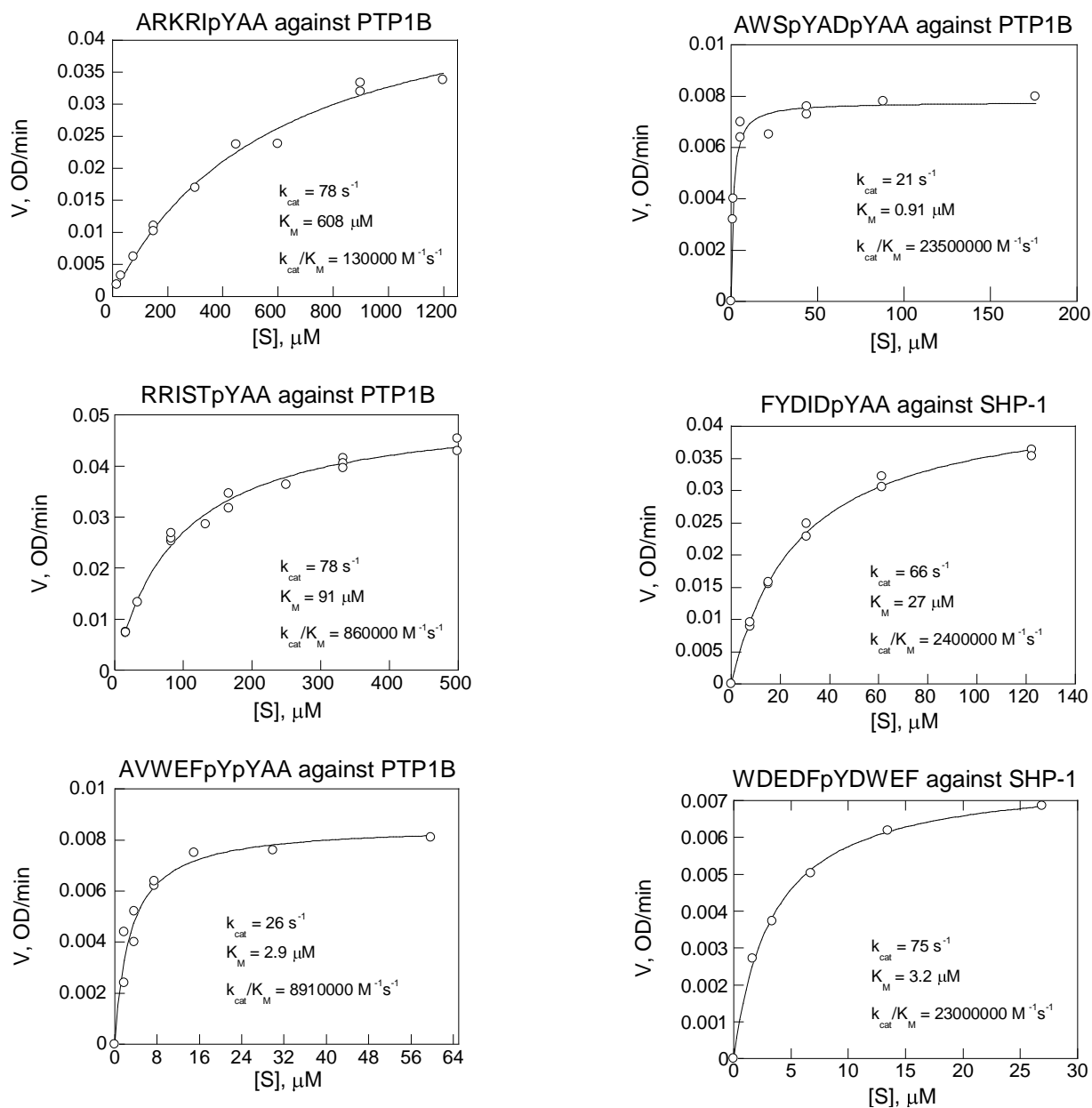


Figure S4. Representative V vs $[S]$ plots for PTP1B and SHP-1 against pY peptides.