

Supplementary material to: Shah et al., Phytochromes from *P. syringae*

Figure S1: Sequence alignment of selected phytochromes

CLUSTAL 2.0.10 multiple sequence alignment

PstBphP1: Phytochrome1 of PSPTO DC3000 (locus_tag is PSPTO_1902)

PstBphP2: Phytochrome2 of PSPTO DC3000 (locus_tag is PSPTO_2652)

DrBphP: Phytochrome of *Deinococcus radiodurans*

PaBphP: Phytochrome of *Pseudomonas aeruginosa*

SyCph1: Phytochrome of *Synechocystis*

AtPhyA: Phytochrome of *Arabidopsis thaliana*

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1. PstBphP1      -----MSQLDKDAFEVLLANCADEP  20
2. PstBphP2      -----MIEHTLDANPDAALEAALAECAREP  25
3. DrBphP        -----MSRDPLPFPPLYLGGPEITTENCEREP  28
4. PaBphP        -----MTSITPVTLANCEDEP  16
5. SyCph1        -----MATTVQLSDQSLRQLETLA  19
6. AtPhyA        MSGSRPTQSSGSRRSRHSARI IAQTVDAKLHADFEESGSSFDYSTSVRVTVGPVVENQP  60

1. PstBphP1      -----IQFPGAIQPHGLLFTLKEPELTILQVSANVQSVLQKVPDQL-----  61
2. PstBphP2      -----IRIPGAIQPHGVLLSVAGDPLCIEQVSANCAKSLGLESAEL-----  66
3. DrBphP        -----IHIPGSIQPHGALLTADGHSGEVLQMSLNAATFLGQEP TVL-----  69
4. PaBphP        -----IHVPGAIQPHGALVTLR-ADGMVLAASENIQALLGFVASPG-----  56
5. SyCph1        -----IHTAHLIQPHGLVVVLQEPDLTISQISANCTGILGRSPEDL-----  60
6. AtPhyA        PRSDKVTTTYLHHIQKGLIQPFGCLLALDEKTFKVIAYSENASELLTMASHAVPSVGEH  120
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1. PstBphP1      ----AGQTLDCVLGAGWAEVIRSTSANDSLVDVPRLLMSVEGV-----EFEALLHRSQEA  112
2. PstBphP2      ----LGQPLSILLSAHSMLINQAYSQPAMPNSDPIRLTVRAV-----DYNASLSRAGDV  117
3. DrBphP        ----RGQTLAALLPEQWPALQALPPGCPDALQYRATLDWPAAG----HLSLTVHRVVGEL  121
4. PaBphP        ----SYLTQEQVGPVLRMLEEGLTGNGPWSN--SVETRIGEH----LFDVIGHYSYKEV  105
5. SyCph1        ----LGRTLGQVDFDSFQIDPIQSLTAGQISSLNPSKLRWVMGDDFVIFDGVFHRNSDG  116
6. AtPhyA        PVLGIGTDIRSLFTAPSASALQKALGFQDVSLNLPILVHCR TSAK---PFYAIHVRTGS  177
                :

1. PstBphP1      LVLELEIQDKAAQAISYS---ERTGNMGRMLRQLHAAAD--LQTLYEVSVREIQRM TG YD  167
2. PstBphP2      LIIELEPFVEAAHEQSR-----IITRVLRLNQAATT--LETLFDIGVHEIQAL TG YD  167
3. DrBphP        LILEFEPTAWDSTGPH-----ALRNAMFALESAPN--LRALAEVATQTVREL TG FV  171
4. PaBphP        FYLEFEIR TADTLSITS-----FTLNAQR IIAQVQLHND--TASLLSNVTDELRRM TG YD  158
5. SyCph1        LLVCELEPAYTSDNLPFL---GFYHMANAALNRLRQQAN--LRDFYDVIVVEVRRM TG FV  171
6. AtPhyA        I I I D F E P V K P Y E V P M T A A G A L Q S Y K L A A K A I T R L Q S L P S G S M E R L C D T M V Q E V F E L T G Y D  237
                : :      .      : :.      : . . : : **:*

1. PstBphP1      RVLIYRFEEEEGHGQVIAEASAPAMEL F N G L F F P A S D I P E Q A R E L Y R R N W L R I I P D A N Y T P  227
2. PstBphP2      RVMIYRFEP EGHGKVVAQAL T G P L P S Y S G L N F P G S D I P A Q A R E L Y R L N W I R L I P D A T Y V P  227
3. DrBphP        RVMLYKFAPDATGEVIAEARREGLHAF L G H R F P A S D I P A Q A R A L Y T R H L L R L T A D T R A A A  231
4. PaBphP        RVMAYRFRHDSGEVVAESRREDLESYLGQRYPASDIPAQARRLYIQNP I R L I A D V A Y T P  218
5. SyCph1        RVMLYRFDENNHGDVIAEDKRDDMEPYLGLHY P E S D I P Q P A R R L F I H N P I R V I P D V Y G V A  231
6. AtPhyA        RVMAYKFHEDDHGEVVSEVTKPGLEPYLGLHYPATDIPQAARFLFMKNKVRMIVDCNAKH  297
                **:  ** :  * . * : : : : : : : * : : * : : * : : * : : * : : *

1. PstBphP1      VPLVPQLRPDTQQQLDLSFSTLRSVSP I H C Q Y M K N M G V L S S M S V S L I Q G G K -----  278
2. PstBphP2      VALIPTLRPATGQPLDLSLSTLRSVSPVHCEYLK N M G V R S S M S I S L L D G G E -----  278
3. DrBphP        VPLDPVLNPTNAPTPLGGAVLRATSPMHMQYLRNMVGSSLSVSVVVG G Q -----  282
4. PaBphP        MRVFPALNPE T N E S F D L S Y S V L R S V S P I H C E Y L T N M G V R A S M S I S I V V G G K -----  269
5. SyCph1        VPLTPAVN P S T N R A V D L T E S I L R S A Y H C H L T Y L K N M G V G A S L T I S L I K D G H -----  282
6. AtPhyA        ARVLQDE--KLSFDLTLCGSTLRAPHSCHLQYMANMDSIASLVM AV V V N E E D G E G D A P D A  355
                :      * : ** : * * : ** . : * : : : : .

1. PstBphP1      -----LWGLISCGHRTPLYVSHELRSACQAIGQVLSLQISAMEALEVSRQRET K I Q  329
2. PstBphP2      -----LWGLITCSHPELLVSR EL R D A C A M I G Q L L S V K I S A I V A T H I Q R E R E E K V V  329
3. DrBphP        -----LWGLIACHHQTPYVLPDLRRTLE Y L G R L L S L Q V Q V K E A A D V A A F R Q S L R E  333
4. PaBphP        -----LWGLFSCHHMSPKLIYPVVRMSFQIFSQVCSAIVERLEQGRIAE L L R V S T E  320
5. SyCph1        -----LWGLIACHHQTPKVIPELRLKACEFFGRVVFNSISAQEDTETFDYRVQLAE  333
6. AtPhyA        TTQPQKRKRLWGLVVCNHTT PR F V P F P L R Y A C E F L A Q V F A I H V N K E V E L D N Q M V E K N I L R  415
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1. PstBphP1	TLQQLHQMMATSDTDFVDFGLAQPPQLLMDLVGATGVAIIEDRQTHCYGNCPEPSDIRALH	389
2. PstBphP2	LLGQLADAMNRADEHILHGLVSRPQLLQALTDQADGAVALIDDQVHLFGQCPTSEVVRALY	389
3. DrBphP	HHARVALAAASLSL-SPHDTLSDPALDLLGLMRAGGLILRFEGRWQTLGVEVPPAPAVDALL	392
4. PaBphP	RRALALARRARDAD-DLFGALAHPPDDGIAALIPCDGALVMLGGRTLSIRGDFEFQAGNVLQ	379
5. SyCph1	HEAVLLDKMTTAA-DFVEGLTNHPDRLLGLTGSQGAACIFGKLLILVGETPDEKAVQYLL	392
6. AtPhyA	TQTLLCDMLMRDA---PLGIVSQSPNIMDLVKCDGAALLYKDKIWKLGTTPEFHLQEI	472
	: : : * . * : :	
1. PstBphP1	TWMMAGGEP-----VYASHHLLSSVYPPGEAYQTLASGVVLMSLPKPVNDG	434
2. PstBphP2	QWIRDTGLTRQRSKERATGLQGLGVFHTDSMQRERPESAAAYRETASGVIAFTLPKPVDNA	449
3. DrBphP	AWLETQPGA-----LVQTDALGQLWPAGADLAPSAAGLLAI SVGEGWSEC	437
4. PaBphP	RLQRDPERD-----IYHTDNWPQP-SEDSPDGGDCCGVLAIRFHRQESGW	423
5. SyCph1	QWLENREVQD-----VFFTSSLSQIYPDAVNFKSVASGLLAIPIAR--HNF	436
6. AtPhyA	SWLCEYHMDSTG-----LSTDSLHDAGFPRALSLGDSVCGMAAVRISS--KDM	518
	: . . . * : *	
1. PstBphP1	VIWFRPEVKQSVQWSGDPNKPLNLDASDNTLR-LQPRTSFEIWKVEMTGIATKWSHGDFV	493
2. PstBphP2	VMWFRSRLASTMNSGNPAHHVSTRAAGSASHGLRPRQSFVVKQEVGTIARPWSRADLY	509
3. DrBphP	LVWLRPELRLVAVWGG-----ATPDQAKDDLGRHSFDTYLEEKRGYAEPPHWGPEIE	489
4. PaBphP	IFWFRHEEVHRIRWGGKPEKLLTIGPSG---PRLTPRGSFEAWEEVVRGHSTPWSSETDLA	480
5. SyCph1	LLWFRPEVLQTVNWGGDPNHAYEATQEDGK-TELHPRQSFDLWKEIVRLQSLPWQSVIEIQ	495
6. AtPhyA	IFWFRSHTAGEVVRWGGAKHD---PDDRDDARRMHRSSFKAFLEVVKTRSLPWKDYEMD	574
	: . * : * . * : * : *	
1. PstBphP1	AANDLRRSALENDLARQVSKQQAVRAR-----DELVAVVSHDLRNPMTVISMLCGMMQ	547
2. PstBphP2	GAEDIRRSALSDLERQVQREQAVRLR-----DELVAVVSHDLRNPMSIIIMQCGMMQ	563
3. DrBphP	EAQDLRDTLTGALGERLSVIRDLNRALTQSNAEWRQYGFVISHMQEPVRLISQFAELLT	549
4. PaBphP	IAEKLRLDLMELCLN---HAAEVDMMR-----QRLIAVLGHDLRNPLOSISMAAALLS	530
5. SyCph1	SALALKKAIIVNLILRQAEEAQLARNLERSNADLKKFAYIASHDLQEPNQSIVNYVQLLE	555
6. AtPhyA	AIHSLQLILRNAPKDSSETTDVNTKVIYSKLN--DLKIDGIQELEAVTSEMVRLETATVP	632
	: : . : . :	
1. PstBphP1	KS-FSSDGPHTSRRISTAITDMQQAASRMNVLLEDLLDTSKIEAGR-YTITPQPLEVSI	605
2. PstBphP2	RW-AVDDTNFENRNIRRALGTIEKATTRMNSLLEDLLDTAQIEAGR-YQLSRLALSVTSL	621
3. DrBphP	RQPRAQDGSPPSPQTERITGFLLETSRLRSITQDLHTYTALLSAP--PPVRRPTPLGRV	607
4. PaBphP	SS-DTRTTELR-----QHISASSSRMERLVSQLDMSRLQSGIGLTVNVPVTDVSQL	581
5. SyCph1	MR-YSEALDEDAKD---FIDFAVTGVSMLQTLIDDILTAKVDYQY---AQLTFTDVQEV	608
6. AtPhyA	LLAVDSDGLVNGWNTKIAELTGLSVDEAIGKHFLLTVEDSSVEIVKRMLENALEGTTEEQN	692
	: : : :	
1. PstBphP1	FEEAYTLLAPLAMDKSIEISFNAEPDIKVNADPERLFQVLSNLIIGNAIKFTP-----	657
2. PstBphP2	LEEACSLVMLTTEKNIENLCTSAQGLVIDADPERIFQVLSNLVGNAIKFTP-----	673
3. DrBphP	VDDVLQDLEPRIADTGASIEVAPELP-VIAADAGLLRDLLLHLIGNALTFGG-----	658
4. PaBphP	VRQIVCETDVAYPGLVIEIAIDPQVRAVDPD--RYAQVAANLLSNARHHGL-----	631
5. SyCph1	VDKALANLQRIEESGAEIEVGSMP--AVMADQIQLMQVFQNLIANGIKIFAGD-----	659
6. AtPhyA	VQFEIKTHLSRADAGPISLVVNACASRDLENVVGVCFAHDLTGQKTVMDFTRIEGDY	752
	. : . : : : . * . :	
1. PstBphP1	-----KLGRIGVAAMNGDEVVFTVRDSGEGIPPEQLPHIFERYWTVKEG	702
2. PstBphP2	-----KGGRINIDAVADGDDVLFVSDDGIGIPAQHLPIYIFQRYWSVKEG	718
3. DrBphP	-----PEPRIAVRTERQGAGWSIAVSDQGAGIAPYQERIFLLFQRLGSL	703
4. PaBphP	-----PGRPVLVTLTRQGDEVCLSVLNETSGLSEAQLANLFEPPKRESAD	676
5. SyCph1	-----KSPKIKIWGDRQEDAWVFAVDNGIGIDPQFFERI FVIFQRLHTR	704
6. AtPhyA	KAI IQNPNPLIPPIFGTDFGWCTEWNPAMSKLTGLKREEVIDKMLLGEVFGTQKSCCRL	812
	. : : : : *	
1. PstBphP1	NPT---GTGLGLYISQGIKAHGGELAAQSQVGHGSEFRFTVPIAH-----	745
2. PstBphP2	NPR---GNGLGLYICQGIITAHGGRLWADSSLDGVSFVFTLPMHQGQDTIGESTFLKQS	775
3. DrBphP	DEAL--GNLGLPLCRKIAELHGGTTLTVESAPGEGSTFRCWLPDAGPLPGAADA-----	755
4. PaBphP	NQRNRNGLGIGLYISQAIQAQHQGRIDVDCRDD-VITFCLRLPVRQAETGSSS-----	728
5. SyCph1	DEYK--GTGMGLAICKKIIIEGHQGIWLESNPGEGSTFFYFSIPIGN-----	748
6. AtPhyA	KNQE-AFVNLGIVLNNAVTSQDPEKVSFAFFTRGGKYVECLLCVSKKLDREGVVTVGFCF	871
	. : * : : . : :	
1. PstBphP1	-----	
2. PstBphP2	GTTHRLAQSISSKLERQQLEDRLTRAGLLNELNHVKNTLATVQAIASLTVNSSTS----	831
3. DrBphP	-----	
4. PaBphP	-----	
5. SyCph1	-----	

6. AtPhyA LQLASHELQQALHVQRLAERTAVKRLKALAYIKRQIRNPLSGIMFTRKMIEGTELGPEQR 931

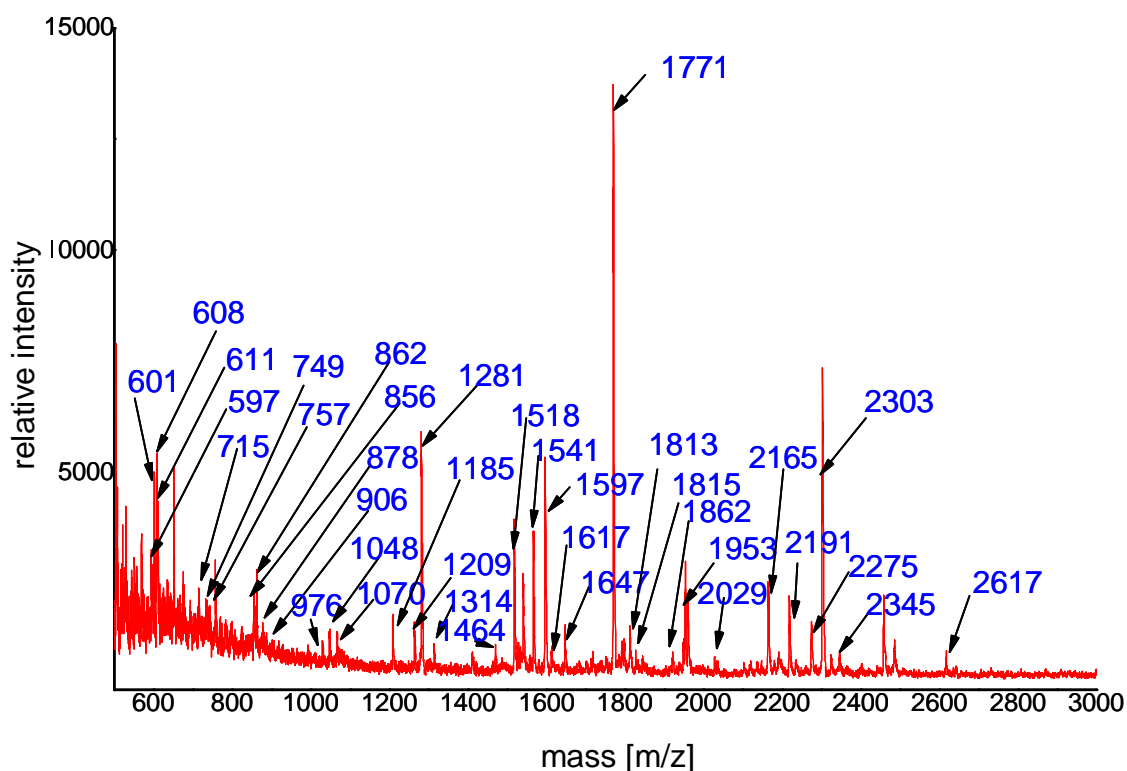
1. PstBphP1 -----
2. PstBphP2 -----LDSFRKSF DARLFALSQARA EWMSTELADLLAQLQDVNGGQHR 874
3. DrBphP -----
4. PaBphP -----
5. SyCph1 -----
6. AtPhyA RILQTSALCQKQLSKILDDSDLESII EGCLDLEMKEFTLNEVLTASTSQVMMKSNGKSVR 991

1. PstBphP1 -----
2. PstBphP2 ITFTGDPVRL EPRISLTL SMLV LHKLMANALQH GALSSPAGQVTVASTLNSHHNPPTLSID 934
3. DrBphP -----
4. PaBphP -----
5. SyCph1 -----
6. AtPhyA ITNETGEEVMSDTLYGDSIRLQQVLAD FMLMAVNFTPSGGQLTVSASLRKDQLGRSVHLA 1051

1. PstBphP1 -----
2. PstBphP2 WLETGPPVVASNVKGFGLRLIRRSIERELKGV DIKFASTGVSW SMLIPWPEKPESSL- 993
3. DrBphP -----
4. PaBphP -----
5. SyCph1 -----
6. AtPhyA NLEIRLTHTGAGIPEFLLNQMF GTEEDVSEEGLSLMVSRKLVKLMNGDVQYLRQAGKSSF 1111

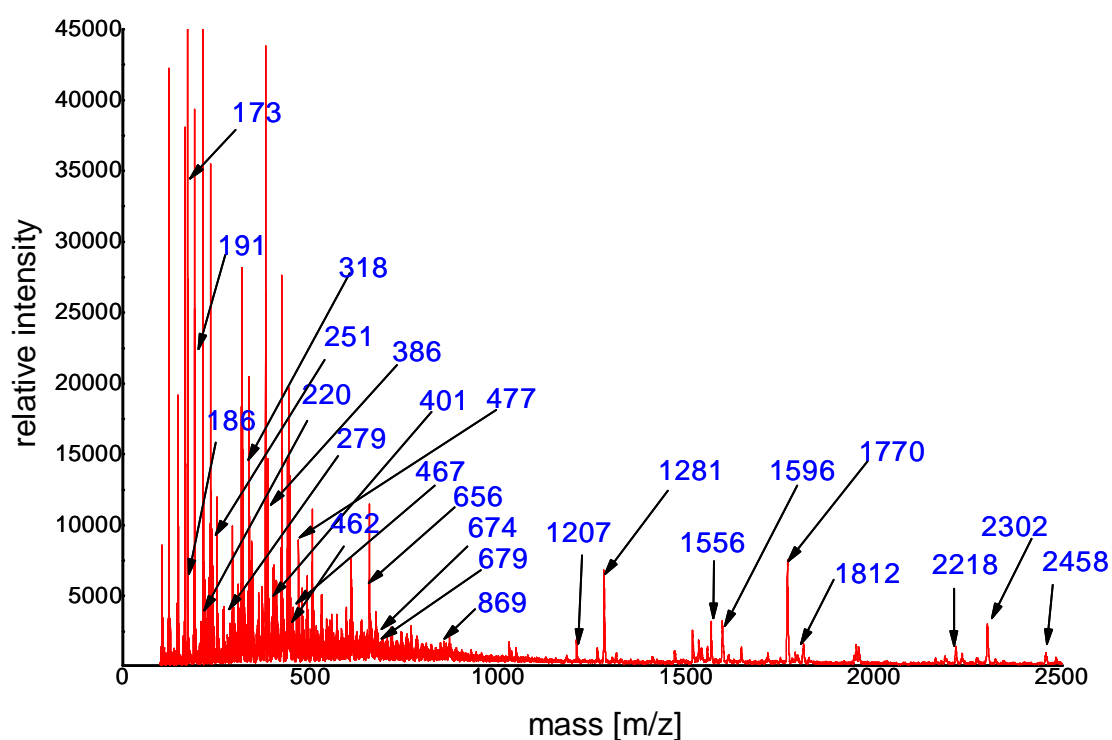
1. PstBphP1 -----
2. PstBphP2 -----
3. DrBphP -----
4. PaBphP -----
5. SyCph1 -----
6. AtPhyA IITAE LAAANK 1122

Figure S2: (Top) MALDI-TOF detected peptide pattern of Pstbph1, obtained from trypsin digestion; (bottom): coverage of the protein sequence with identified peptides shown in yellow. The first amino acid following a trypsin cleavage is indicated in bold and in red.



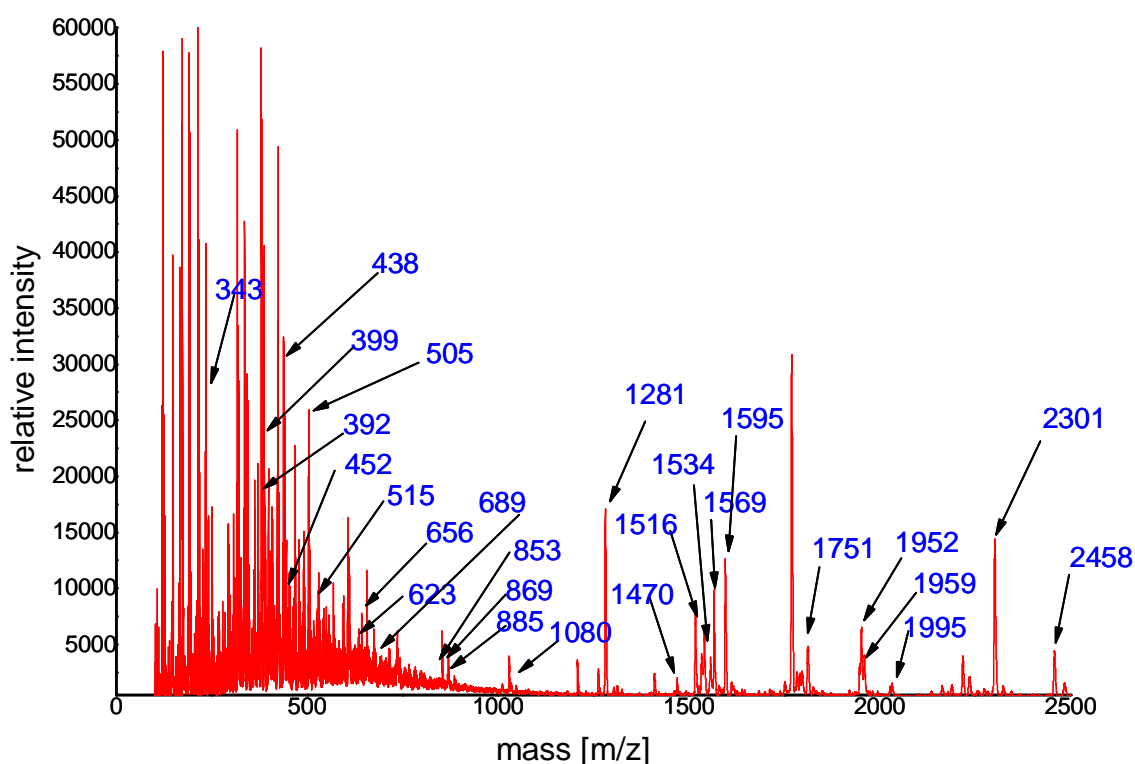
MSQLDK D AFE	VLLANCADEP	IQFPGAIQPH	GLLFTLKEPE	LTILQVSANV	QSVLGKVPDQ
LAGQTLDCVL	GAGWAEVIR S	TSANDSLVDV	PRLMSVEGV	EFEALLHRSQ	EALVLELEIQ
DK AA QAISYS	ERTGNMGR M L	RQLHAAADLQ	TLYEVSUREI	QRMTGYDRVL	IYR F EEEGHG
QVIAEASAPA	MELFNGLFFP	ASDIPEQARE	LYRRN W LRII	PDANYTPVPL	VPQLRPDTQQ
QLDLSFSTLR	S VSPIHCQYM	KNMGVLSMS	VSLIQGGK L W	GLISCGHR T P	LYVSHELRSA
CQAIGQVLSL	QISAMEALEV	SR Q RETK I QT	LQQLHQMMAT	SDTDVFDGLA	QQPQLLMDLV
GATGVAIIED	R Q THCYGNCP	EPSDIR A LHT	WMMAGGEPVY	ASHHLSSVYP	PGEAYQTLAS
GVLAMSLPKP	VDNGVIWFRP	EVK Q SVQWSG	DPNKPLNLDA	SDNTLRLQPR	TSFEIWK V EM
TGIATK W SHG	DVFAANDLRR	S ALENDLAR Q	VSKEQQAVRA	R DELVAVVSH	DLR N PMTVIS
MLCGMMQK S F	SSDGPHTSRR	ISTAIDTMQQ	AASRMNVLLE	DLLDTSK I EA	GRYTITPQPL
EVSQIFEEAY	TLLAPLAMDK	SIEISFNAEP	DIKVNADPER	LFQVLSNLIG	NAIK F TPK L G
RIGVAAMSNG	DEVVFTVRDS	GEGIPPEQLP	HIFERYWTVK	E GNPTGTGLG	LYISQGIKA

Figure S3: (Top) MALDI-TOF detected peptide pattern of Pstbph2, obtained from trypsin digestion; (bottom): coverage of the protein sequence with identified peptides shown in yellow. The first amino acid following a trypsin cleavage is indicated in bold and in red.



MIEHTLDANP	DAALEAALAE	CAREPIR	I PG	AIQPHGVLLS	VAGDPLCIEQ	VSANCAKSLG
L ESAELLGQP	LSILLSAAHS	MLINQAYSQP	AMPNSDPIRL	TVRAVDYNAS	LSRA	GDVLI
ELEPFVEAAH	EQSR	I ITRVL	RNLQAATTLE	TLFDIGVHEI	QALTGYDRVM	IYRFEPEGHG
KVVAQALTGP	LPSYSGLNFP	GSDIPAQARE	LYRLNWIRLI	PDATYVPVAL	IPTLRPATGQ	
PLDLSLSTLR	S VSPVHCEYL	KNMGVRSMS	ISLLDGGELW	GLITCSHPEP	LLVSREL	R DA
C AMIGQLLSV	K ISAIVATHI	QREREKVV	LGQLADAMNR	ADHEILHGLV	SRPQLLQALT	
QADGAAVLID	DQVHLFGQCP	TSEEVRALYQ	WIRDTGLTR	Q RSKE	RATGLQ	GLGVFHTDSM
QR	E RPESAAY	RETASGVIAF	TLPKPVDNAV	MWFRS	QLAST	MNWSGNPAHH
VSTRAAGSAS	GLRPR	Q SFAD	VWKQEVGTIA	RPWSRADLYG	AEDIRRS	SALE
SDLERQVQRE	QEAVRLR	D EL	VAVVSHDLRN	PMSI	IIMQCG	MMQR
WAVDDT	NFENR	N IRRA	LGTI	EKA	TTR	MNSLLEDLLD
TAQIEAGR	Y Q	LSRL	LALSVTS	LLEEACSLLV	MLTTEKNIEL	NCTSAQGLVI
DADPERI	FQV	LSNLVGNAIK	FTPKGGRI	NI	DAVADGDDVL	FRVSDDGIGI
PAQHLPIYIFQ	RYWSVK	E GNP	RG	NGLGLYIC	QGIITAHGGR	LWADSSLD
SG	SVFSFTLPMH	QGQDTIGEST	FLK	Q SGTTHR	LAQS	ISSKLE
RQ	LEDRLTR	A GLLNELNHR	VKN	TLATVQA	IASLTVNSST	SLDSFRK
SFD	ARLFALSQAR	AEW	MSTELAD	LLAQLQDVNG	GQHR	I TFTGD
PVRLEPRISL	TL	S	MVLHKL	M	ANALQHGALS	SPAGQVTVAS
PPVVASNVKG	FGLR	L IRRSI	ER	E LK	GKVDI	KFASTGVSWS
MLIPWPEKPE	SSL					

Figure S4: (Top) MALDI-TOF detected peptide pattern of the heme oxygenase PstbphO; (bottom): coverage of the protein sequence with identified peptides shown in yellow. The first amino acid following a trypsin cleavage is indicated in bold and in red.



M PASFSPTP	PK L IGALRAE	TNQLHVQLEK	R MPFFSSVLD	HALYLR L LQA	YGFYAPLEA
ALR D STFMPR	A LTPDDR I KT	CVLVK D LAL	GMSEHDIR Q L	PQCTQLPITN	SPGACLGVMY
VLEGATLGGQ	VLRRE V LK R L	GLDEYSGAAF	LDVYGAETGP	R WK V FLNHLD	AVPRGVEFTE
AAHAAHSTF	ACFEHWLDGQ	EVLL			