# Purification and characterisation of a DyP-type peroxidase produced by the native strain, *Streptomyces albidoflavus* BSII#1, and its application in coupling of phenolic monomers

## Supplementary material

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### Keywords:

actinobacteria, biocatalysis, DyP-type peroxidase, purification, Streptomyces

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**Figure S1:** SDS-PAGE gel with samples from each purification step for the peroxidase from *Streptomyces albidoflavus* BSII#1. Lane 1, protein size marker (10 to 250 kDa). Lanes 2 and 3, crude enzyme boiled in DTT-containing and  $\beta$ -mercaptoethanol-containing loading buffer, respectively. Lanes 4 and 5, acid fraction boiled in DTT-containing loading buffer and  $\beta$ -mercaptoethanol-containing loading buffer, respectively. Lanes 6 and 7, the acetone fraction boiled in DTT-containing and  $\beta$ -mercaptoethanol-containing loading buffer, respectively. Lanes 6 and 7, the acetone fraction boiled in DTT-containing and  $\beta$ -mercaptoethanol-containing loading buffer, respectively. The arrows point to the most prominent protein bands with sizes estimated at (a) 26.6 kDa and (b) 24.4 kDa.

Table S1: Comparison of the kinetic constants of the peroxidase from *Streptomyces albidoflavus* BSII#1 with other peroxidases for the oxidation of 2,4-dichlorophenol.

Microorganism	K <sub>m</sub>	V <sub>max</sub>	Reference
Streptomyces albidoflavus BSII#1	0.95 mM	0.12 mmol min <sup>-1</sup>	This study
Streptomyces avermitilis UAH30	1.45 mM	Not determined	[1]
Streptomyces sp. F6616	1.52 mM	Not determined	[2]
ALiP-P3 (Streptomyces viridosporus T7A)	0.37 mM	465.8 nmol mg protein <sup>-1</sup> min <sup>-1</sup>	[3]
Streptomyces sp. AD 001	1.70 mM	529.7 nmol mg protein <sup>-1</sup> min <sup>-1</sup>	[4]
HRP	0.84 mM	Not determined	[5]
P. chrysosporium	0.79 μM	Not determined	[6]
S. albidoflavus TN644	0.23 mM	Not determined	[7]



**Figure S2:** UV/Vis scan of the peroxidase. A peak corresponding to the Soret band characteristic of haem peroxidases is visible at approximately 400 nm.



**Figure S3:** LC-MS analysis of the purified peroxidase from *Streptomyces albidoflavus* BSII#1. (a) HPLC chromatogram with major peak at 48 min (presumed to be the peroxidase of interest). (b) MS spectra of the peak at 48 min.



а



**Figure S4**: Results obtained for the AAI (a) and ANI (b) analysis between *Streptomyces albidoflavus* BSII#1 and *Streptomyces albidoflavus* NRRL B-1271<sup>T</sup>.

#### Former class \*New class



0.2

**Figure S5**: Neighbor-joining tree of DyP-type peroxidase sequences representative of the different DyP-type classes. The peroxidase from *Streptomyces albidoflavus* BSII#1 clusters with peroxidases within class I.

#### Consensus

- Streptomyces\_albidoflavus\_BSII\_1\_
  Escherichia\_coli\_K12\_Peroxidase\_YcdB\_P31545
  Thermobifida\_fusca\_YX\_Dye\_decolorizing\_peroxidase\_TfuDyP\_Q47KB1
- Rhodococcus jostii RHA1\_Peroxidase\_DyPA\_Q0S4I5
  Thermobifida\_cellulosilytica\_DyP\_type\_peroxidase\_4GS1\_U3KRF5
- 6. Streptomyces\_coelicolor\_M145\_Peroxidase\_4GT2\_Q9ZBW9
- 7. Streptomyces\_coelicolor\_M145\_Peroxidase\_4GRC\_Q9RKQ2 8. Bacillus\_subtilis\_168\_Peroxidase\_BsDyP\_P39597
- 9. Bacillus subtilis subsp natto BEST195 Peroxidase YwbN D4G313

		M×	DXDXX		XXX	- × × S R	R×LI	LXXX	G A	XXLA	XG XX G	GXXXG	xx-xx	×	XXXAX	PXXXX	
1	1	MA	<mark>D</mark> TPL-		QR	- PVT R	RRLI	GTA	G A	TGLA		AAAG	ΥΤΑΑΑ	P	SETVT	PLTEV	50
1	2	MQ	<mark>YK</mark> DEN		GVN	I-EP <mark>S</mark> R	RRLI	LKVI	G A	LALA	GS0	сруан	AQ-KT	Q SA -	PGTLS	PDA	49
	3	MT	EP <mark>D</mark> T-		ERK	(-GS <mark>SR</mark>	RGFI	LAGL	G A	AA <mark>l</mark> t	GAGI	<b>MAA</b> G	EV-LR	PLLPDS	SDP A <mark>a</mark> s i	PEAEQRLRM	59
4	4	MI	. – – – – – МТ <mark>D</mark> РТ	G	-TTDTTTSVDERK	(-GM <mark>SR</mark>	RRLI	FGAV	' <mark>G A</mark>	– G A A		G A L V G	RA	TA-	<mark>A</mark> E <mark>f</mark>	PPLS-	55
1	5	GSHEAV	/RPLLP <mark>D</mark> S <mark>D</mark> SE		Q-PDF	VDAQR	L D M/	A									29
(	6	MP	<mark>D</mark> QSIP	QTRSPEATRGTPGP	LDSDNPGAATAPQ	– G V <mark>S R</mark>	RRLI	LGTA	G A	TGLV	LGAA	<b>AAA</b> G	YA-AA	P	SSAAT	PLTSL	75
1	7	MT	<mark>D</mark> T <mark>D</mark> SP		APAF	- SP <mark>SR</mark>	RSL	IGWG	G A	- G L A	LGAAA	AAGG	AV-AM	D RA -	GADAD	P A G A D	53
1	8	MS	. – – – – – <mark>D</mark> EQK –		KPE	-QIH <mark>R</mark>	RDI	LKWG	AMAG	AAVA	IGAS	G L - G G	LA-PL	v	Ο ΤΑ <mark>Α</mark> ΚΙ	PSKKDEKE	54
-	9	MS	<mark>D</mark> EQK-		KPE	-QIH <mark>R</mark>	RDI	LKWG	AMAG	AAVA	IGAS	<mark>G</mark> L – G <mark>G</mark>	LA-PL	v	QTAAK	PSKKDEKE	54

XXXXXXFXGXHQAGIXTPXQAXXH	XXAFDVXXX-XR	XXXXALLRXWT)	(XAXRLTAGXXXX-X)	×××××××PP×DTG×	X-XXLXPSXLTVTXG
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1	GSRREM <mark>F</mark> HVK <mark>HQPGITTP</mark> LH <mark>A</mark> RG <mark>H</mark> LI <mark>AFD</mark> LAPGAG <mark>R</mark> KEAA <mark>ALLR</mark> RWSQT <mark>ADRLMAG</mark> EPAP-AGGH <mark>DTG</mark> IA-LDAG <mark>PS</mark> ALTV	TFG 133
2	RNEKQP <mark>FYG</mark> EHQAGILTPQQAAMMLV <mark>AFDV</mark> LAS-DKADLER <mark>LFR</mark> LLTQRFAFLTQGGAAP-ETPNPRL <mark>PPLD</mark> SGILGGYIAPDNLTI	TLS 13
3	AAQRADATAAPQPGISGPAPAFVHVIALDLAEE-ARKNPDTARDSAAAALRSWTELAARLHEESPHDIAEGAAS-AGLLPASLMV	TVG 14
4	HADVVA <mark>FRGEHQAGIVTPAQDRM</mark> HFV <mark>AFDV</mark> TTK-S <mark>R</mark> EELE <mark>ALL</mark> KK <mark>WT</mark> EM <mark>AARMTAG</mark> EEATPDGAIGDGAYVPPS <mark>DTG</mark> EA-LG <mark>L</mark> PASQLTL	TIG 140
5	-RRRADANAAPQPGISGRAPAFVHVIAFDLAEP-ARAEPAAAREGAATALRTWAEHAARLHADGPEGAAS-AGLLPASLMV	TIG 110
6	GSERAM <mark>FHG</mark> KHQP <mark>GITTPMQA</mark> RG <mark>HLVAFD</mark> LAAGAG <mark>R</mark> KEAA <mark>ALLR</mark> RWSDT <mark>ARRLMAG</mark> EPAGSR <mark>DT</mark> DVA-RDAG <mark>PS</mark> SLTV	TFG 15
7	AGSAVP <mark>FHG</mark> AHQAGIATPVQDRL <mark>H</mark> FA <mark>AFDV</mark> TTE-D <mark>R</mark> AAFV <mark>ALL</mark> KE <mark>WT</mark> AA <mark>ARRLTAG</mark> HAVG-EGAYGGLPEAPPDDTGEA-LG <mark>LKPSRLT</mark> L	TIG 143
8	EEQIVP <mark>FYG</mark> KHQAGITTAHQTYVYFA <mark>ALDV</mark> TAK-DKSDIIT <mark>LFRNWT</mark> SLTQMLTSGKKMSAEQRNQYL <mark>PPQDTG</mark> ES-AD <mark>LSPS</mark> NLTV	TFG 142
9	EEQIVP <mark>FYG</mark> K <mark>HQAGITT</mark> AHQTYVYFA <mark>A</mark> LDVTAK-DKSDIIT <mark>LFRNWT</mark> SLTQMLTS <mark>G</mark> KKMSSEQRNQYL <mark>PPQDTG</mark> ES-AD <mark>LSPS</mark> NLTV	TFG 143

		FG%SLF%RFGL%%%RP%ALA%LP%F%%D%LD%%%%GGD%%%Q%CADD%%VA%HALR%L%%%A%%%%VRW%%%GF%R%%%A%%%-%%TPRNL%GF	
	1	FGHSFFARTGLEKQRPAALDPLPEFSSDRLDPRRSNGDLWVQIGADDALVAFHALRAVQKDAGQAARVRWQMDGFNRSPGATEK-PMTTRNLMGQ	226
	2	VGHSLFDERFGLAPOMPKKLOKMTRFPNDSLDAALCHGDVLLOICANTODTVIHALRDIIKHTPDLLSVRWKREGFISDHAARSKGKETPINLLGF	233
	3	IGGSLLSAIDAEDRRPDALADLPEFSTDDLHPRWCGGDFMLOVGAEDPMVLTAAVEELVAAAADATAVRWSLRGFRRTAAAARDPDATPRNLMGO	240
	4	FGPSLEDDREGEASKKPAALVDLPHERADNLDPARSGGDIAIOACANDPOVAVHAIRNLARVAEGTASVRWSOLGEGRTSSTSTT-ODTPRNLEGE	241
	5	TGGSLLEAMDAADRRPDALADLPEFATDDLRPRWCGGDLMLOVGAEDPMVLAAAVDELVAATAPTTTVRWSLRGERRTAAAAODPDATPRNLMGO	205
	6	FGHSFFGRTGLEEORPVALDPLPDFSSDHLDKNRSNGDLWVOIGADDALVAFHALRAIORDAGAAARVRWOMNGFNRSPGATAH-PMTARNLMGO	249
	7	FGPSLETREGLADLRPEALADLPKEPGDNLDRARSGGDLCVQACADDPQVAVHAIRNLARIGEGKVVVRWSOLGEGKTSSTTPD-EQTPRNLUGE	237
	8	FGPGFFEKDGKDRFGLKSKKPKHLAALPAMPNDNLDEKOGGGDICIOVCADDEOVAFHALRNLLNOAVGTCEVREVNKGFLSGGKN-GETPRNLFGF	238
	9	FOR FEEKDOK DREGLKSKKPKHLAAL PAMPNDNLDEK OG GODICTOVCADDEOVAFHALRNLLNOAVGTCEVREVNKGELSGGKN-GETPRNLEGE	238
	-		
		KDGTXNPXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	
	1	IDGINNPVPSDED-FAIRVRVPADGDPAWMAGGSVVVFRRIRMLLDDWERLSVAGQEAVMGRRRADGAPLIGGTETTEPDLERVGEDGDLVI	317
	2	KDGTANPDSQNDKLMQKVVWVTADQQEPAWTIGGSYQAVRLTQFRVEFWDRTPLKEQQTTFGRDKQTGAPLGMQHEHDVPDYAS-DPEG-KVT	324
	3	IDGIANPAQDHPL-FDRTITARPADNPAHAWMDGGSYLVVRRIRMLLTEWRKLDVAARERVIGRRLDIGAPLGSRNETDPVVLSARDEEGEPLI	333
1	4	KDGTNNIKAEEPSILDQHVWVASGDDQAWMGGGAYLVARRIRMLIEQWDRTVLGEQERVIGRSKGTGAPLSGKAEFDELDLDSKKGH-DPVI	332
	5	IDGTANPAQDHPL-FTRTVTAPPADDPAHAWMDGGSYLVVRIRMLLDEWRRLDVPDRERVIGRHLDTGAPLGGEKETDPVVLTARDADGRLVI	298
	6	VDGIRNPRPGEAD-FDRRIFVPEEPEAGRGGPAWMANGSYVVVRRIRMLLDDWEELSLKAQEDVIGRRKSDGAPLSGGSGATESTEMDLERTDGSGELVV	348
	7	KDGTRNIAGTEKDRLDRFVWAAEKDGTPWMTGGSYLVARRIRMHIETWDRASLQEQEDVFGRDKGEGAPVGKAKERDEPFLKAM	321
	8	KDGTGNQSTKDDTLMNSIVWIQSGEPDWMTGGTYMAFRKIKMFLEVWDRSSLKDQEDTFGRRKSSGAPFGQKKETDPVKLNQI	321
	9	<mark>KDGF</mark> GNQSTEDDSLMNSI <mark>VWV</mark> QSGEPD <mark>WMTGGTYMAFRKIKMFLEIWDR</mark> SSLKDQEDTF <mark>GRRK</mark> SSGAPFGQKK <mark>ETD</mark> PVKLNQ <mark>I</mark>	321
		P×NAHVRLA×P××N×GA×MLRRGYSY×XG×D×-×G××DAGLLF×××Q×DP××GFVPVQR×L×-×GDALNEYI×H×GSAL-FAVPGG×××G-×Y×GQ×L	
	1	PLNAHARITRPDQNGGAAMLRRPFSYHDGIDE-EGVPDAGLLFLCWQADPLRGFVPVQRKLD-RGDALSAFIRHEASGL-YAVPGGARKG-GYVGQEL	411
	2	ALDSHI <mark>RLANP</mark> RTAESESSL <mark>MLRRGYSY</mark> SL <mark>G</mark> VTN-S <mark>G</mark> QL <mark>DMGLLF</mark> VCY <mark>QHDLEKGFLTVQKRLNGEALEEY</mark> VKPIGGGYF <b>FALPG</b> VKDAN-D <mark>YFG</mark> SAL	420
	3	PENAHVRLASPENNLGARMFRRGYSYDQGWRD-DGVRDAGLLFMAWQGDPATGFIPVQRSLADQGDALNRYIRHEGSAL-FAVPAA-REG-RYLGQDL	427
	4	DVDAHVRLASAQELGGIQILRRGYNFTDGSDG-FGHLDAGLFFIAYCRNPQEQFVPMQLNLS-RNDAMNEYIQHVGSAL-FACPPGLAEG-QYWGQGL	426
	5	PEDAHVRLANPEN NLGARMVRRGYNYDEGWRD-DGVRDAGLLFMAWQGNPATGFVPVQRSLVEQGDALNRYTRHEGSAL-FAVPAA-TAD-RYPGQDL	392
	6	PINAHARITRPDQNGGAAMVRRPFSYHDGFDA-DGVPDAGLLFVCWQADPLRGFVPVQRKLD-RGDALSQFIRHEASGL-FAVPGGAAEG-EYVGQRL	442
	7	KPDAHVRLAHPDSNGGATLLRRGYSFTDGTDG-LGRLDAGLFFLAYQRDIRTGFVPVQRNLATDALNEYIQHVGSAV-FAVPPGVRDADDWWGSTL	415
	8	PSNSHVSLAKSTGKQILRRAFSYTEGLDPKTGYMDAGLLFISFQKNPDNQFIPMLKALS-AKDALNEYTQTIGSAL-YACPGGCKKG-EYIAQRL	413
	9	PSNSHVSLAKSTGKQILRRAFSYTEGLDPKTGYMDAGLLFISFQKNPDNQFIPMLKALS-AKDALNEYTQTIGSAL-YACPGGCKKG-EYIAQRL	413



**Figure S6:** Amino acid sequence alignment of representative DyP-type peroxidases within class I of this protein family. The blue inverted triangles indicate the residues around the haem moiety (H = haem ligand; other four amino acids forms the hydrogen peroxide binding pocket). The black box shows the highly conserved GXXDG motif found in all DyP-type peroxidases.

Table S2: Combinations of phenolic monomers that were coupled using the peroxidase from *Streptomyces albidoflavus* BSII#1.

Substrate 1	Substrate 2	Observed [M-1]	Expected [M]
guaiacol	chlorogenic acid	475.1257	476.1257
guaiacol	syringaldazine	481.1594	482.1594
guaiacol	caffeic acid	301.0733	302.0733
catechol	<i>p</i> -coumaric acid	271.0613	272.0613
catechol	ferulic acid	301.0721	302.0721
catechin	syringaldazine	647.1469	648.1469
catechin	<i>p</i> -coumaric acid	451.1377	452.1377
catechin	guaiacol	411.1087	412.1087
catechin	cinnamyl alcohol	421.1289	422.1289
catechin	caffeic acid	467.0988	468.0988
catechin	catechol	397.0902	398.0902

## Nucleotide and amino acid sequences, DyP-type peroxidase, Streptomyces albidoflavus BSII#1

> Predicted dye-decolorizing peroxidase (DyP), YfeX-like subgroup, *Streptomyces albidoflavus* BSII#1

> Predicted dye-decolorizing peroxidase (DyP), YfeX-like subgroup, *Streptomyces albidoflavus* BSII#1

MADTPLQRPVTRRRLLGTAGATGLALGVTGAAAGYTAAAPSETVTPLTEVGSRREMFHVKHQPGITTPLHARGHLIAFDLAPGAGRKEAAALLRRWSQTADRLMAG EPAPAGGHDTGIALDAGPSALTVTFGFGHSFFARTGLEKQRPAALDPLPEFSSDRLDPRRSNGDLWVQIGADDALVAFHALRAVQKDAGQAARVRWQMDGFNRSP GATEKPMTTRNLMGQIDGTNNPVPSDEDFATRVRVPADGDPAWMAGGSYVVFRRIRMLLDDWEKLSVAGQEAVMGRRKADGAPLTGGTETTEPDLERVGEDG DLVIPLNAHARITRPDQNGGAAMLRRPFSYHDGIDEEGVPDAGLLFLCWQADPLRGFVPVQRKLDRGDALSAFIRHEASGLYAVPGGARKGGYVGQELLEG

### **Supplementary Methods and Materials**

#### Storage of Purified Peroxidases

Aliquots of the ultrafiltrate fraction were mixed with glycerol to achieve final glycerol concentrations of between 2.5% and 25% (v/v) in 1 ml volumes in Eppendorf tubes. The tubes were divided into three sets which were incubated at ambient temperature (25±2°C), 4°C and at -20°C. Residual peroxidase activity for each glycerol concentration at each storage temperature was determined on a weekly basis for a period of six weeks.

#### Functional expression of an extracellular peroxidase

*Streptomyces albidoflavus* BSII#1 was cultivated under the optimal conditions for the production of extracellular peroxidase [8]. Total RNA was extracted using the ISOLATE II RNA mini kit (Bioline, London, United Kingdom) as per the manufacturer's instruction. RNA was converted to cDNA using the Maxima H minus first strand cDNA synthesis kit (Thermo Fischer Scientific, Bellfonte, USA) according to the manufacturer's instruction. cDNA was used as a template in PCR reactions with primers specific to the gene encoding for the dye decolourising peroxidase (s16.1\_F 5'-GATCGACGGCACCAACAATC-3' and s16.1\_R 5'-GTCGTGGTATGAGAAGGGGC-3'). PCR conditions were as follows: an initial denaturation (96°C for 2 min), 30 cycles of denaturation (96°C for 45 s), annealing (56°C for 30 s) and extension (72°C for 1 min), and a final extension (72°C for 5 min). The 358 bp amplicon was purified using the Stratec Molecular MSB® Spin PCRapace kit and sequenced. The sequence was submitted for BLASTn analysis and compared to the genome information. To ensure that the RNA was not contaminated with genomic DNA, a 16S rRNA gene PCR reaction was setup as previously described [9].

#### **Supplementary Results**

#### Stability of the Partially Purified Peroxidase in Storage

The stability of the partially purified peroxidase stored in different glycerol concentrations (up to 25% v/v glycerol) at three different storage temperatures (ambient, 4°C and -20°C) was assessed over a period of 6 weeks. Maximum activity retained in samples containing no glycerol and stored at ambient temperature and 4°C was 22.3±0.9% and 63.8±1.2%, respectively. Optimum storage conditions included the addition of 7.5-10% glycerol and storage at - 20°C (85.8±1.7% activity retained after 6 weeks).

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