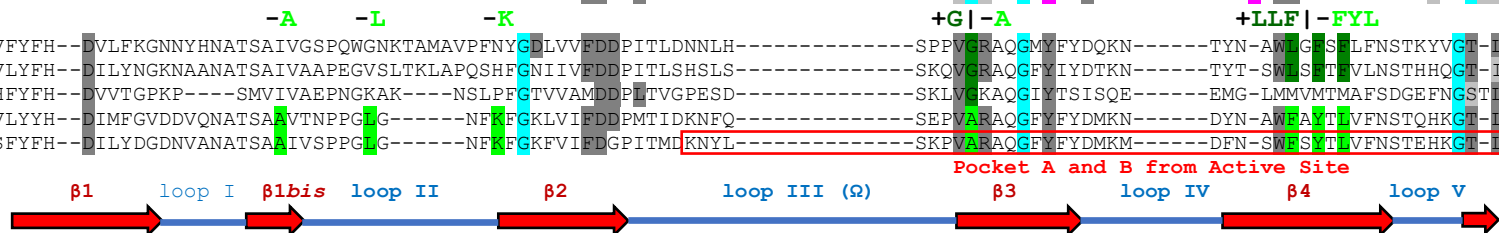


Figure S1: Alignment of the 48 sequences of DPLs from bacteria and five selected plant DP sequences in clustal0 on Uniprot server (Align tools)

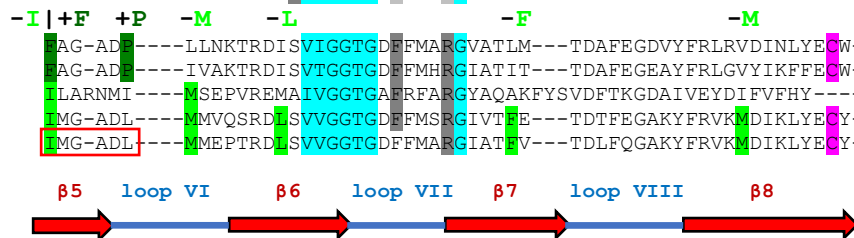
Streptomyces_sp._Root1304	-----MSRSFR---R---FAVLGV---TVAAAFG-----A-VVPVAADSGDGFE	36
Streptomyces_sp._PanSC19	-----MTRSSR---R---IGALCA---TVAAAFG-----AAPAPVSADDGDGFE	37
Streptomyces_sp._62	-----MTRSRF---R---IGALCAS---TVAAVSFA-----AAAAPAHAAAGDGFE	37
Sphaerobacter_thermophilus	-----MRVALMRMTGRWVA--L---VGAAVLAITSLLVVP-----RVAGQQGQTIV	43
Kutzneria_albida_DSM_43870	-----MA---TPAEL---SRRAAL---FAAPAVAAG---GLVLAGSS-----PAAASANETIK	41
Streptomyces_vietnamensis	-----MIRSLRTG---T---LGVITAA---AIAAVAFG-----AAPFSAFADDGEGFE	39
Streptomyces_viridochromogenes	-----MTRTIR---R---IGTLGA---TVAAVAFG-----A-VAPVQADNGDGFE	36
Cystobacter_fuscus	-----MRK---AMF---L---AVSVVSL---TTPMLGV---D-----NAHAEEESWT	32
Streptomyces_bottropensis	-----MTM---KKF---RLAAVLVATVCVL---AALGLSVA-----QAEFQSSSRHGRATT	42
Nocardioides_iriomotensis	-----MRS---KVV---VAGTVATV---VAGTVLT-----V-SAAQGERAAPR	33
Methylomicrobium_alcaliphilum	-----MFD---SLD---R---LI-LLVY---FLSMTACT-----H-CMPKT	27
Archangium_violaceum_Cb_v176	-----MLL---M---A---VLT---AAPMLSCV---N-----NAPAEAAWT	26
Chloroflexi_bacterium_GWC2_73_18	-----MLR---RLF---VVGAVVAL---VAVAVSA-----TALAAGDQAAGKT	34
Nocardia_mexicana	-----MQHEKAI---FKRISI---GVAAA---SLLVGVT-----SGCSEEQTSAASEPEVHE	43
Gammaproteobacteria_bacterium_HGW	-----MSD---SL---G---PI-LLVC---FLSMTACT-----HSMPT	26
Cystobacter_fuscus_DSM_2262	-----MLGCV---D-----NVPAAEESWT	15
Archangium_gephyra	-----MRK---TIL---M---A---VLT---AAPMLSCA---N-----NGPAEEAAWT	29
Cystobacter_ferrugineus	-----MLGCV---D-----NSQAEEESWT	15
Streptomyces_sp._SA15	-----MGFTRRPFP---FLAVAVLGGSAVL---ALI---LPASAEV---ASQQTAI PAATLPADGSSSEKST	55
Stigmatella_erecta	-----MNKPKKTGKLQ---AVQ---W---AGGTL---AAPGLCA---RAHADEPWT	40
Streptomyces_alboflavus	-----MGNNNRPL---FKRIAALS LATVAV---GVFAAGG---ANADA---SKKS RVEVIE	45
Streptomyces_sp._NWU339	-----MGFAGRPLI---FLAIAVLGG SAGL---ALI---GSASADV---IPLKTAETAATHPADGSSSVKST	55
Streptomyces_formicae	-----MENGKRRPL---LVKCAALS LVAAGV---GVLA VGS---AAADT---SGKDRAEVIE	45
Streptomyces_sp._CB02400	-----MGFAGRPFII---FFAVAVLGG SAGL---TLI---GPASADA---VPPETAPAAA PRPDGSSSAKSRA	55
Streptomyces_caelestis	-----MGFAGRPFII---FLTVAVLGG SAGL---AVI---TSASADV---APRKAAPTAAARPGDGSSSVKSRA	55
Pseudonocardiales_bacterium	-----M---RRS---RTIPLVLGGLAAA---LAVGTS AVSLATSAD---AATSAGSSNDRHWRTT	48
Methylomicrobium_kenyense	-----MHG---HCF---R---IA-YAGL---LLCAVGC A---RVVPQT	27
Streptomyces_griseoruber	-----MTM---RKP---RLAAVLAATTCAV---LVAGV SVA---QAGDRTAGHRGGPAV	42
Chloroflexi_bacterium	-----MLSQRKLI A---LLALLML---ALSACTPV---VPAATAGLTQTYAPGEAAHVLE	47
Thiogranum_longum	-----MH---IFR---Y---AA-TCA---ALLLGA---AEAPLQ	27
Streptomyces_fungicidicus	-----MNIAGRPFII---FLAVAVLGG SAGL---ALI---GPASADV---APRKAASTVAPHTDDGSPAKSRT	55
Streptomyces_toyocaensis	-----MGFTGRPFII---FLAVAVLGG SAGT---ILI---DPASAGV---VPSETAPAA PRPDGSSSAKSRT	55
Streptomyces_showdoensis	-----MTGSFR---R---MGALGA---TAAVLALG---T-AAPASADNGDGFE	36
Enterobacter_ludwigii	-----MNR---KIV---A---I---VAL---LVAGITQA---T---SSHNPETLRRNEIH	34
Stigmatella_aurantiaca	-----MRKLKETGKMQQ---AVL---W---AG---TLL---AAPGLG---SAHADEPWT	40
Modestobacter_sp._DSM_44400	-----	
Streptomyces_radiopugnans	-----MGFSARPLA---FLAAAVLGG SAGL---TLV---GPASAGA---DPQKATVNAATRPADASPAKSRT	55
Methylomicrobium_buryatense	-----MTACT-----H-CMPKT	11
Vitiosangium_sp._GDMCC_1.1324	-----M---AVFVVPF---AVQSGCS---EAKAEESWT	25
Archangium_sp._Cb_G35	-----M---A---VVT---AAPMLSCA---N---NAPAEAAWT	23
Cellulomonas_aerilata	-----M---RRS---LTAALLAG-LGVL---ALGSSSAA---D---SADADRSSSGRAATLR	42
Streptomyces_sp._NRRL_S-4	-----MGFAGRPFII---FLAVAVLGG SAGL---ATL---GSASADV---VPQKAAATAEAHPADGSSSEKST	55
Streptomyces_silvensis	-----MENSRRPL---LRKCAALS LVAAVV---GVLA VGS---AAADTSDTS AKDRTEVIE	48
Streptomyces_sp._CNZ306	MTNFLDGAAGLLVRLRSHIRSAALPSVNRPTRRRPGKAWVALTLFIPNTEATMRFARRHFT---FLAVAVFGGSAGL---TLN---GAASADA---IPQKTAATAATHPGDGSSSARGRT	108
Streptomyces_sp._RV15	-----MKIGKRRIR---HAAL---AT---VATLTS LAIIAGGPGSGDGQDTKDET PVPAPRGDRPQKEVSPGEGRT	63
Streptomyces_regalis	-----	
Streptomyces_sp._13-12-16	-----MGFAGRPFM---FFAVAVLGG SAGI---ALI---GPASADV---VPPETAPAAA PRPDGTS SAKSRA	55
Streptoalloteichus_hindustanus	-----MNRTLA IAGAVALT---GVLGAGLST-----LGGPAAAE TEAAGRAVTL D	43
Hyalangium_minutum	-----	
F.intermedia FiDIR1	-----MVSKTQIVALFLCFLT---S-----TSSATY-----G---RKPRPRRCKE	35
P. sativum DRR206	-----MGSKLPVL---FVFM---F-----ALSSAI-----P---NKRKPYKPK	33
G. echinata PTS1	-----MAKSTFFISLTLPFLLLSVTA-----TYQSM-----SPTVLGFQEEKFTH	43
A.Thaliana atDIR5	-----MVGQMK---FLFLFVLVLT---TVISAR-----K---PSKSQPKPK	37
A.Thaliana atDIR6	-----MAFLVEKQLFKALFSFLLVLLFSD-----TVLSF-----R---KTIDQKKPKH	42

	D	S	G	FD	L	IGS VGR	G	T C	CVV	C	T	M L	I G	L							
Streptomyces_sp._Root1304	FTLYAK--EVPAP-----	GGDQ----	SGPPSKVGE	TFTFAD	DLYKTK--GGE-----	KVGRD	GVCAVVRV--	SGTSVEAN	CVGTF----	ELDGG	PGPGOLA	113									
Streptomyces_sp._PanSC19	FTLYAK--QIPPP-----	ATSE-----	SNPPPKVGT	PTVFAD	DLFRTK--GGD-----	KVGRD	GVSCAVVRV--	SGDQVDMN	CVGTII----	VINGG	PGGQIT	114									
Streptomyces_sp._62	FTLYAK--QVPAA-----	GASA-----	SMPAPKVG	DLTTFAD	DLYKTK--GGD-----	KVGRD	GVTCVVRV--	SGDQADMN	CVGTII----	VINGG	PGGQIT	114									
Sphaerobacter_thermophilus	IDVAFD-QPNIHR-LAEAPA----	GAWP-----	ARGEVS	SGGGKIFD	GLDEATE-----	QIGEF	YFYGVTSA----	PEYFETA	ANHLFEVAR	FELWQ	GSID	126									
Kutzneria_albida_DSM_43870	LVA--A--RSKNS-----	-----	LSATPA	FGTFPFAMQ	LEFDANAA-----	AAGD	SGSAHGIVNVN	TPDTPPKVI	VQMSL----	VKLGF	NGELH	112									
Streptomyces_vietnamensis	FTLYAK--QVPPP-----	GTNE-----	SSPPPVG	DHPVHADD	DLYKTK--GGD-----	TVGRD	GVCAVVRV--	SGDQVDMN	CVGTII----	LINGG	PGGQIA	116									
Streptomyces_viridochromogenes	LTLYAK--EVPAP-----	GADE-----	SGPPEVGD	VFTVADD	DLYKTK--GGD-----	KVGRD	GVCAVVRV--	SGTQADVNC	CVGTF----	VINGG	PGGQIT	113									
Cystobacter_fuscus	LTTIADARSGIASPVDL-----	-----	APPGDSPG	DMFVFD	QPLLNEAK-----	ENIGS	NSGYCIRTL	P-----	GQFSE	CQWTL-----	TMADG	IT	108								
Streptomyces_bottropensis	FTVIEH--ADTDTVVDL-----	-----	GPRGDS	IGDTLAFGN	PIYDTAG-----	NRAGD	SQSGCVRTKV	-----	GTAWEC	SWTIT-----	TLNGG	SIV	112								
Nocardioides_iriomotensis	ITVVEH--AVSDALVDL-----	-----	APDGD	SNGLLT	FANPVYDRTN-----	S-----	RKVG	RDQSGCIR	TVV-----	GEAWC	CSFIT-----	WLKGS	IT	104							
Methylomicrobium_alcaliphilum	LITIADARTHQAQLVDI-----	-----	GELGDTEG	DILTDFD	QPLLDEQG-----	SRIGN	NSGMCIRTRV	-----	GHSFQ	CQWTL-----	TMTNG	SIQ	99								
Archangium_violaceum_Cb_v176	LNTIADARSGIATPVDL-----	-----	GPPGDSPG	DMFVFD	QPLLNEAK-----	ETIGS	NSGYCIRTL	P-----	GQFSE	CQWTL-----	TMAGT	IT	98								
Chloroflexi_bacterium_GWC2_73_18	LRVVEH--AVSDSVVDL-----	-----	APSGDSL	GDVLAGN	PIFDAAD-----	D-----	HEIGR	DQGYCVRTN	V-----	GEAWE	CNWTV-----	ILARG	SIT	105							
Nocardia_mexicana	LQV----TTDQYSALDL-----	-----	GSSGT	SVGMD	DVSGSAMKDS-----	-----	KVG	NAGSGCQ	ATHV--DGEK	VTTQCLIT	M-----	ELEA	GALA	113							
Gammaproteobacteria_bacterium_HGW	LITIADARTHQAQLVDI-----	-----	GELGDTEG	DILTDFD	QPLLDEQG-----	-----	SG	IGNNSGICIR	TRV-----	GHSFQ	CQWTL-----	TMKNG	SIQ	98							
Cystobacter_fuscus_DSM_2262	LNTIADARSGIATPVDL-----	-----	APPGDSPG	DMFVFD	QPLLNEAK-----	-----	ENIGS	NSGYCIRTL	P-----	GQFSE	CQWTL-----	TMADG	IT	87							
Archangium_gephyra	LNTIADARSGIATPVDL-----	-----	DPPGDSPG	DMFVFD	QPLLNEAK-----	-----	ETIGS	NSGYCIRTL	P-----	GQFSE	CQWTL-----	TMADG	IT	101							
Cystobacter_ferrugineus	MTTIADARSGIASSVDL-----	-----	GTPGDSPG	DMFVFD	QPLLNEAK-----	-----	ENIGS	NSGYCIRTL	P-----	GQFSE	CQWTL-----	TMADG	IT	87							
Streptomyces_sp._SA15	IRV--VAGLQVGEELD-----	-----	GAPGRSVG	DQFVFSG	NLSSTRGSEEE-----	-----	RVVGR	FGGFCVIT	DLE-----	RNAGQ	CSSTA-----	VLPEG	QIT	130							
Stigmatella_erecta	FTTIADARSGIATPVDL-----	-----	GAPGDSPG	DMFVFD	QPLLNEAK-----	-----	QNIGS	NSGYCIRTL	P-----	GQFNE	CQWTL-----	TLADG	IT	112							
Streptomyces_alboflavus	LQL-----KDLEYESFDL-----	-----	GKPGPSL	GDMTVYC	ATAVENGR-----	-----	NVGR	GAGTSQV	VSA--RGGK	VTSQAVIT	I-----	ELKRG	SIT	115							
Streptomyces_sp._NWU339	IRV--EARLQAGEELD-----	-----	GATGRSVG	DQFVFSG	NLVSTEGPE-E-----	-----	RFVGR	FGGFCVIT	DLE-----	CNAGQ	CSSTA-----	VLPEG	QIT	129							
Streptomyces_formicae	LQI-----KDLEYKAIDV-----	-----	GPTGPGL	GDMSVYF	CATAVENGR-----	-----	TVGR	GAGTSQV	VSV--DGER	HTSQAVIT	I-----	ELERG	SIT	115							
Streptomyces_sp._CB02400	IRV--EARLHVGEELD-----	-----	GAAGRSVG	DQFVFSG	NLVSTEGRE-E-----	-----	RVVGR	IGGFCVIT	DLE-----	RNAGQ	CSTA-----	VLPEG	QIT	129							
Streptomyces_caelestis	IRV--EARLRVGEELD-----	-----	GATGRSIG	DQFVFSG	NLSAEGAG-E-----	-----	RLVGR	IGGFCVIT	DLE-----	RNAGF	CTSTA-----	VLPEG	QIT	129							
Pseudonocardiales_bacterium	LKFVEH--ETGASQADL-----	-----	PPAGPSVG	DNFFGTN	PLFNESD-----	T-----	RQVGR	QVGFCTQ	ASKT--TPAV	LYCDLTY-----	QLANG	MIT	121								
Methylomicrobium_kenyense	LVTIADARADKARVTDL-----	-----	GDPGDSPG	DILTDFD	QPLLDTRQ-----	-----	KPIGS	NSGFCVIR	TRV-----	GHSFQ	CQWTL-----	TLQDG	SIQ	99							
Streptomyces_griseoruber	FTVIEH--ADTDTVVDL-----	-----	GPRGDS	IGDTLAFGN	PIYDTAG-----	-----	HQVGS	QSGCVRTKV	-----	GTAWEC	SWTIT-----	TLNGG	SIV	112							
Chloroflexi_bacterium	FDVAEDMNRFIFD-QDV-----	-----	VY-----	DDGMPAD	SSSFTIRG	YLYEPG	TLNGSNGVNP	PDGSPEF	PDKVI	GEW-----	ICQYMI	--	NDAGH	TGGVWFSTQ	FFQLG	TEP	CAQTV	146			
Thiogranum_longum	LVTIADARTDKAQVIDT-----	-----	GEPGD	SVGDI	LTFDQPLL	DEHK-----	-----	QPVGN	NSGACIR	TRV-----	AHSFQ	CQWTL-----	SLDGG	TIQ	99						
Streptomyces_fungicidicus	IRV--EAQLQVGEELD-----	-----	GATGRSVG	DQFVFSG	NLMSTEGTE-G-----	-----	HSVGR	IGGFCVIT	DLE-----	RNAGQ	CVSTA-----	VLAGG	QIT	129							
Streptomyces_toyocaensis	IHV--QARLHVGEELD-----	-----	GAAGRSVG	DQFVFSG	DLTSSGAE-E-----	-----	RVVGR	ISGFCVIT	DLE-----	RNAGQ	CSTA-----	VLPEG	QIT	129							
Streptomyces_showdoensis	FTLYAK--EVPGP-----	TASE-----	SAPAK	LGESFA	FADLYKTKDAGGD-----	-----	KVGRD	GGTCVAV	RT-----	GDPMD	LQCVITV-----	VLNGG	PGGOLA	114							
Enterobacter_ludwigii	IITIADGTRGEKRTVNT-----	-----	GQNGP	SPGDLFV	FDPQLMDQHR-----	-----	RDIGT	NSGYCVTKI	-----	GVHSQ	CQWTL-----	KTYG	STVV	106							
Stigmatella_aurantiaca	FTTIADARSGIANSVDL-----	-----	GAPGDSPG	DMFVFD	QPLLNEAK-----	-----	QNIGS	NSGYCIRTL	P-----	GQFNE	CQWTL-----	TLADG	IT	112							
Modestobacter_sp._DSM_44400	-----MDGE-----	-----	EDESAP	VGSRL	FISEALYETDDGT-T-----	-----	RGDEV	GRTHIECTA	QVY-----	DFTFA	CDIAFV	F-----	DSGSQL	HGS	69						
Streptomyces_radiopugnans	IRV--EARLQVGEELD-----	-----	GTTGRSVG	DQFVFSG	NLVSTEGPE-E-----	-----	RPVGR	FGGFCVIT	DLE-----	RNAGQ	CSSTA-----	VLPEG	QIT	129							
Methylomicrobium_buryatense	LITIADARTHQAQLLDI-----	-----	GELGDTEG	DILTDFD	QPLLDEQG-----	-----	SRIGN	NSGMCIRTRV	-----	GHSFQ	CQWTL-----	TMKNG	SIQ	83							
Vitiosangium_sp._GDMCC_1.1324	LTTIADARSGIASPVDL-----	-----	GAPGDSPG	DMFVFD	QPLLDEAK-----	-----	QTIGS	NSGYCIRTL	P-----	GQFSE	CQWTL-----	TMADG	IT	97							
Archangium_sp._Cb_G35	LNTIADARSGIATPVDL-----	-----	GPPGDSPG	DMFVFD	QPLLNEAK-----	-----	ETIGS	NSGYCIRTL	P-----	GQFSE	CQWTL-----	TMADG	IT	95							
Cellulomonas_aerilata	YD-VEF--TSGFLLDFGPHGVREVASFQ-----	-----	DPFSPSR	GDQVVFED	TLRRGE-----	-----	PVAS	GGGTCTVT	AVVPSDT	PLRLS	CVATY-----	ELPGG	QVA	127							
Streptomyces_sp._NRRL_S-4	IRV--EARLQAGEELD-----	-----	GATGRSVG	DQFVFSG	NLASTGGPA-E-----	-----	RSVGR	FGGFCVIT	DLE-----	RNAGQ	CSSTA-----	VLPEG	QIT	129							
Streptomyces_silvensis	LQM----RDLEQKALDL-----	-----	GPKGPSL	GDMSIFC	ATVVENGR-----	-----	TVGR	GAGTAQV	VYL--DGG	RRTS	QAVIT	I-----	ELERG	SIT	118						
Streptomyces_sp._CNZ306	ISL--EAQLQVGEELD-----	-----	GATGRTVG	DQFVFSG	NLVSTEGQG-E-----	-----	RPVGR	FGGFCVIT	DLE-----	RNAGQ	CSSTA-----	VLPEG	QIT	182							
Streptomyces_sp._RV15	IQV--EANVQVAEELD-----	-----	GAPGRSVG	DQFVFSG	NLSAEDP-D-----	-----	RVIGR	FSEFCVIT	DLE-----	RNAGQ	CMLTA-----	VLPGG	QIT	136							
Streptomyces_regalis	--M--EANVQTGEELD-----	-----	GAPGRSIG	DQFVFGR	SLSPADEP-D-----	-----	RVIGR	FSEFCVIS	DLE-----	RNAGF	CMLTA-----	VLEGG	QIT	71							
Streptomyces_sp._13-12-16	IHV--EARLRVGEELD-----	-----	GAAGRSVG	DQFVFSG	DLTSAEGGG-E-----	-----	SVIGR	IGGFCVIT	DLE-----	RNAGQ	CSTA-----	VLPEG	QIT	129							
Streptoalloteichus_hindustanus	LHV----ANDQFAA	HDI-----	GQPGKSL	GDMTVYS	DKMVRDGR-----	-----	EVGED	GGTCVVT	THV--DGR	PR	SINCVIT	I-----	RLAEG	QIT	113						
Hyalangium_minutum	-----MFVFD	QPLLNEAG-----	-----	QNIGS	NSGYCIRTL	P-----	GQFSE	CQWTL-----	-----	-----	-----	-----	TMSD	GSIT	46						
	-A	-L	-K				+G	-A		+LLE	-FYL										
F._intermedia_FiDIR1	LVFYFH--DVL	FKGN	NYHN	NATSAIV	SGSPQWGN	KTAMAV	FPNYSGLLV	FDDPIT	LDDNNLH-----	-----	SPPV	RAQGMFYD	QKN-----	TYN	AWG	SLF	NSTKY	VGT--LN	131		
P._sativum_DRR206	LVLYFH--DILY	NGKNA	ANATSAI	VAAPE	GVSLTK	LAPQSH	FGNIIV	FDDPIT	LSHSL-----	-----	SKQV	RAQGFYI	YDTKN-----	TYT	SW	SL	VLN	STHHQ	GT--IT	129	
G._echinata_PTS1	LHFFYH--DVVT	GPKP---SMV	IVAEP	NGKAK---NSL	PF	TVVAMD	DPITV	GPESD-----	-----	-----	SKLV	RAQGTYS	ISQE-----	EMG	LM	MVMT	MAFSD	GEFNG	STLS	132	
A._Thaliana_atDIR5	FVLYYH--DIM	FVDDVQ	NATSAIV	TNP	PGLG---NFK	F	GKLVI	FDDPMT	IDKNFQ-----	-----	SEP	VARAQGFY	FYDMKN-----	DYN	AW	FA	TV	VFN	STQHK	GT--LN	127
A._Thaliana_atDIR6	FSFYFH--DILY	DGDN	VANATSAI	VSP	PGLG---NFK	F	GKVI	FDGPIT	MTKNYL-----	-----	SKPV	ARAQGFY	FYDMKM-----	DFN	SW	SL	TV	VFN	STEHK	GT--LN	132



A Y S
P GGTG F RG

Streptomyces_sp._Root1304	GQTLATFTDTSAGAPAAFDVA	VTGGTGDEFK	NARGYIRSTPDG---	DYE---	RMEFHINVR-----	166		
Streptomyces_sp._PanSC19	AQALTTFTDTSNDSPSAFDLA	VTGGTGDEFK	DARGYIRSTPDG---	DYD---	RMEFHINTR-----	167		
Streptomyces_sp._62	AQALATVDITNEAPALDIA	VTGGTGDEFK	QARGYIRSTPDG---	DYD---	RMEFHITTR-----	167		
Sphaerobacter_thermophilus	VMGTVTTF---RG---TSLHS	ITGGTGAYAMARGE	CTEEMVA---SR---	RGRFTCYIER-----	173			
Kutzneria_albida_DSM_43870	LSTEHPPL---VLPSPVDNPLA	IVGGCGKYATARGE	GTISYPS---PD---	RINLTNLNVRTD-----	164			
Streptomyces_vietnamensis	AQALTTFTDTSNDTPSAFDLA	VTGGTGDEFK	SARGYIRVTPDG---	DYD---	RMDFHIPTKR-----	169		
Streptomyces_viridochromogenes	AQALVTFTDTSAAEAPAAFDVA	ITGGTGDEFK	DARGYVRTTPDG---	DYE---	RMEFHINVR-----	166		
Cystobacter_fuscus	VAGREAE---SG---TSLIE	IVGGTGAYVVGAS	GVLTTPTPNG---	DR---	TFTQVLTFLKPKQ-----	154		
Streptomyces_bottropensis	AQGPFFYD---TA---DSTLAI	ITGGTGKWRTARG	QMQLHARD---	AKG-SAYDFTFAVKR-----	161			
Nocardioides_iriomotensis	VEGPFYD---AH---PSVMAI	ITGGTGAYARARG	VMHLAARN---	SQG-TAFTFRFVIR-----	152			
Methylomicrobium_alcaliphilum	VAGREFD---KG---TSVIAI	IVGGTGGRYSGIS	GQMESVNNG---	DG---	TFTQILHYWVQ-----	147		
Archangium_violaceum_Cb_vi76	VAGREAE---TG---TSLIE	IIIGGTGTTEGAS	GVLTTPTPNG---	DR---	TFTQVLTLLKPKK-----	148		
Chloroflexi_bacterium_GWC2_73_18	VEGPFYD---DL---RDSPLA	ITGGTGAYLNARG	QMTLHARN---	AGG-TAFDFTIYHIVG-----	155			
Nocardia_mexicana	VQALWIK---GT---SPLDMA	ITGGTGAYRNARG	VVRFWDIA---	TP---	NERLRTEIFY-----	161		
Gammaproteobacteria_bacterium_HGW	LAGREFD---TG---TSVIAI	IVGGTGQYSAIS	GQMESVNNG---	DG---	TFTQILHYWVQ-----	146		
Cystobacter_fuscus_DSM_2262	VAGREAE---TG---PSSIE	IVGGTGAYVVGAS	GVLLTTPNG---	DR---	TFTQVLTFLKPKQ-----	137		
Archangium_gephyra	VAGREAE---TG---TSLIE	IIIGGTGTTEGAS	GVLTTPTPNG---	DR---	TFTQVLTLLKPKK-----	151		
Cystobacter_ferrugineus	VAGREAE---SG---PSSIE	IIIGGTGAYEGAS	GVLLTTPNG---	DR---	TFTQVLTFLKPKQ-----	137		
Streptomyces_sp._SA15	VQGEQIG---IPVPSFVNA	ITGGTGERKAR	QVVTQRVLT---	PA---	TWQLTTFEVLVDVQPSR	SRDGLNRSQQPTPTPPSFP	206	
Stigmatella_erecta	VAGRESD---TG---TSMIE	VAGGTGNYLGVK	QVLATTPNG---	DR---	TFTQVLSLIKAAP-----	162		
Streptomyces_alboflavus	MQSLRPE---EA---SSVMDA	ITGGTGAIFKDA	GSVRYWDIN---	TP---	QERLRAEILH-----	163		
Streptomyces_sp._NWU339	VQGEQAG---IPVPSFVDA	ITGGTGERKAR	QVVTQRVLT---	PA---	IWQLTTFEVDVQPHRT	GDGRSPTKVPMRMPPSFP	205	
Streptomyces_formicae	MQSLQAS---DA---RSLDMA	ITGGTGAIFKDA	RGTARYWDIA---	TP---	QERMRAEILH-----	163		
Streptomyces_sp._CB02400	VQGEQAG---IPVPFVVNA	ITGGTGERRAH	QVVTQRVLT---	PA---	TWQLTFELSDVVRPHRT	EDGRGPAAEAPTVPVRPSFP	205	
Streptomyces_caelestis	IQGEQAG---IPVPAFVNA	ITGGTGERKAR	QVVTQRVLT---	PA---	TWQLTTFEADVPPHRA	EDGRSPSAAPMPVSPSLG	205	
Pseudonocardiales_bacterium	VHGIYDV---AA---GKVVA	SVTGGTGAYVNAR	GEAISVFGP---	VKSTHSITLVF-----	168			
Methylomicrobium_kenyense	VAGREFD---EG---SSDIA	IVGGTGGEYA	IRGQVESVNNG---	DG---	TFTQTLHYWIDCR-----	149		
Streptomyces_griseoruber	VQGPFFHD---AA---DSTLAI	ITGGTGKWRTARG	QMHLHARD---	AKG-SAYDFTFAVER-----	161			
Chloroflexi_bacterium	VTQGYEL---ADTDVSIARA	ITGGTGEFKLARGE	STQTLTG---	LNATEGVNLRVQIAVEK-----	201			
Thiogranum_longum	VAGREFD---TG---ISTMS	IVGGTGIIYAGIR	GDMSINNN---	DG---	TFTQTLRYRLMP-----	148		
Streptomyces_fungicidicus	IQGEQAG---IPAPSPVNA	ITGGTGERKAR	QVVAQRVLT---	PA---	TWRLTTFEVSVDVQSHQ	AGDARDPFEVPMPMPSPSFP	205	
Streptomyces_toyocaensis	VQGEQAG---IPVPAPVNA	ITGGTGEFTA	HQQLRQVLT---	PA---	TWQLTYQLSDVVRPHRP	EDGRSPAKEPTAPPSPRP	205	
Streptomyces_showdoensis	LQTLAAVDPDDEAPPALDIA	ITGGTGDEFENAR	GWVRSTPDG---	DWS---	RMDFHIATR-----	167		
Enterobacter_ludwigii	VAGQEAEE---SG---ISILAV	IGTTGKESGFM	GEMTSEPNG---	DG---	TFTQKLTFLRP-----	154		
Stigmatella_aurantiaca	VAGRESD---TG---TSMIE	VVGGTGNYLGVK	GMLATTPNG---	DR---	TFTQVLSLIKATP-----	162		
Modestobacter_sp._DSM_44400	VDFSTQS---ETEALQFDIA	VTGGTGDIYSRAK	GVNLLDIS---	EDPEAE-TETLYE---AHRG-----	123			
Streptomyces_radiopugnans	VQGEQAG---IPAPGPVNA	ITGGTGERKAR	QVVTQRVLT---	PA---	TWRLTTFEISDVRPHR	AGGGHSLPEVSAPKPPSLT	205	
Methylomicrobium_buryatense	VAGREFD---TG---TSAIA	IVGGTGQYSGIS	GQMESVNNG---	DG---	TFTQILHYWVQ-----	131		
Vitiosangium_sp._GDMCC_1.1324	VAGREAE---NG---TSYIE	IVGGTGTYLGV	SVLATTTPNG---	DR---	TFTQVLTLLKAK-----	146		
Archangium_sp._Cb_G35	VAGREAE---TG---TSLIE	IIIGGTGTTEGAS	GVLTTPTPNG---	DR---	TFTQVLTLLKPKK-----	145		
Cellulomonas_aerilata	VQGRITN---AP---EKTAV	VGGTGGRYAGAA	GEFTLTFEG---	DG---	TGSAVFRLRR-----	174		
Streptomyces_sp._NRRL_S-4	VQGEQAG---IPVPKTVNA	ITGGTGERKAR	QVVTQRVLT---	PA---	TWQLTTFEVSMDQPHR	ARDGRIPSEAP--TPPSFP	203	
Streptomyces_silvensis	MQALQPS---DA---RSLDMA	ITGGTGAIFRDAR	TAHYWDIA---	TP---	KERMRAEILH-----	166		
Streptomyces_sp._CNZ306	VQGEQAG---IPVPSFVNA	ITGGTGERKAR	QVVTQRVLT---	PS---	TWKLTFEVLVDVQHRT	GDGPTPSEVPMPVPPTSP	258	
Streptomyces_sp._RV15	VQGEQEG---IPTPTSVTNA	ITGGTGERDA	QCGMTLKVLT---	AA---	TWAIITFQVTDH-----	187		
Streptomyces_regalis	VQGEQDG---IPTPTSATNA	ITGGTGERKAR	QAGMTLEVLS---	AA---	TWVITFQLADR-----	122		
Streptomyces_sp._13-12-16	VQGEQAG---IPVPFVVNA	ITGGTGERRAH	QVVTQRVLT---	PA---	TWQLTFELSGVRPHRT	EDGRGPAAEAPTVPHPSSP	205	
Streptoalloteichus_hindustanus	AQGLWDD---GT---SPMQMA	ITGGTGAYRNAR	GYLQAWDIIH---	TP---	KERYRIQVSL-----	161		
Hyalangium_minutum	VAGREAE---TG---PSQIE	IVGGTGAYLGV	SGVLVTTTPNG---	DR---	TFTQVLTLLIRPNS-----	96		
	-I +F	+P	-M	-L	-F	-M		
F._intermedia_FiDIR1	AG-ADL	---LLNKTRDIS	VIGGTGDEFMARG	GVATLM---	TDAFEG	GDVYFRLRV	DINLYECW-----	186
P._sativum_DRR206	AG-ADL	---IVAKTRDIS	VTGGTGDEFMHRG	GIATIT---	TDAFEG	EAYFRLGVYIK	FFECW-----	184
G._echinata_PTS1	ILARNMI	---SEPVRREMA	IVGGTGAERFARG	YAQAQKFYS	VDFTKGD	AIVEYDIFVFHY-----	188	
A._Thaliana_atDIR5	IMG-ADL	---MMVQSRDI	SVVGGTGDEFMSR	GIVTTE---	TDTFEG	AKYFRVKMDIKLYE	CY-----	182
A._Thaliana_atDIR6	IMG-ADL	---MMEPTRDI	SVVGGTGDEFMARG	GIATITV---	TDLFQ	GAKYFRVKMDIKLYE	CY-----	187



Legend:

-  -> Amino acids involved in the formation of (+)-pinoresinol in lignans forming DPs
-  -> Amino acids involved in the formation of (-)-pinoresinol in lignans forming DPs
-  -> Amino acids particularly preserved between plant DPs and DPLs (often Glycines)
-  -> Notorious conserved amino acids
-  -> Cysteines
-  -> Cysteines predicted in the formation of disulfide bonds
- XXXX -> Amino acids constituting the predicted signal peptide
-  : loop between β -sheet on AtDIR6 protein sequence
-  :beta strand localization on AtDIR6 protein sequence

Groupe I, Groupe II, Groupe III, Groupe IV and Groupe V on the phylogenetic tree. Selected **DPs from plants**