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Supplementary Materials for

Characterization of imine reductases in reductive amination for the exploration of structure-activity relationships

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Supplementary Materials and Methods

1 Supplementary figures and tables

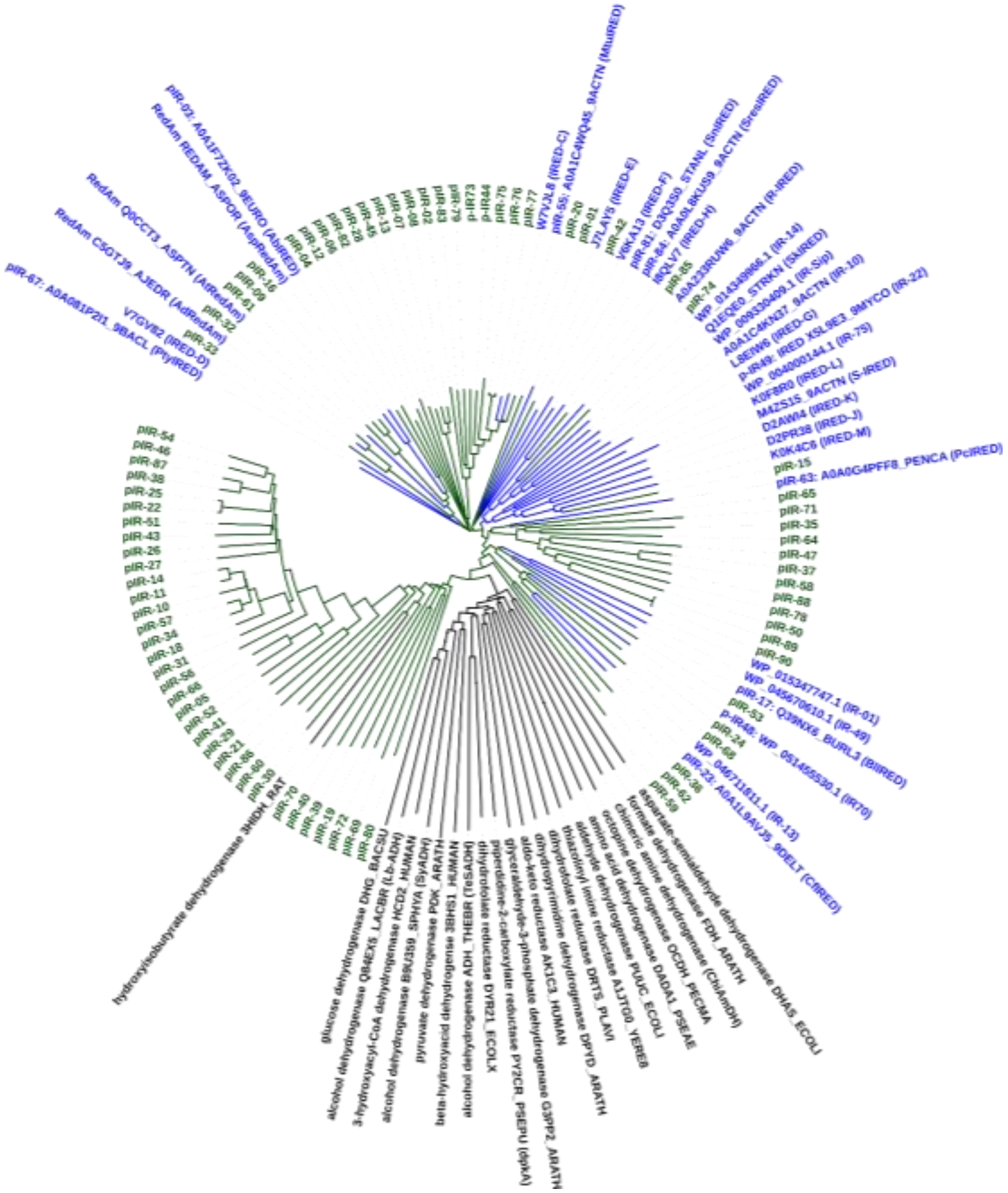
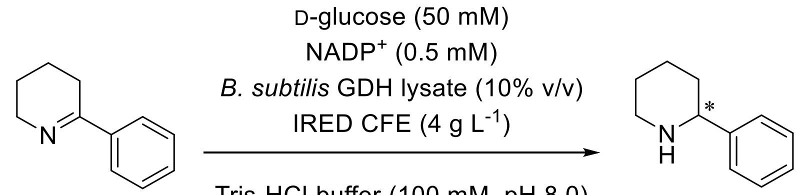


Figure S1. Putative IREDs in phylogenetic context with other families of dehydrogenases. The putative IREDs (green) are displayed alongside a number of previously described IREDs (blue) and characterised dehydrogenase enzymes (black).



D-glucose (50 mM)
NADP$^+$ (0.5 mM)
B. subtilis GDH lysate (10% v/v)
IRED CFE (4 g L^{-1})

Tris-HCl buffer (100 mM, pH 8.0)
30°C, 18 hours

1
10 mM

2

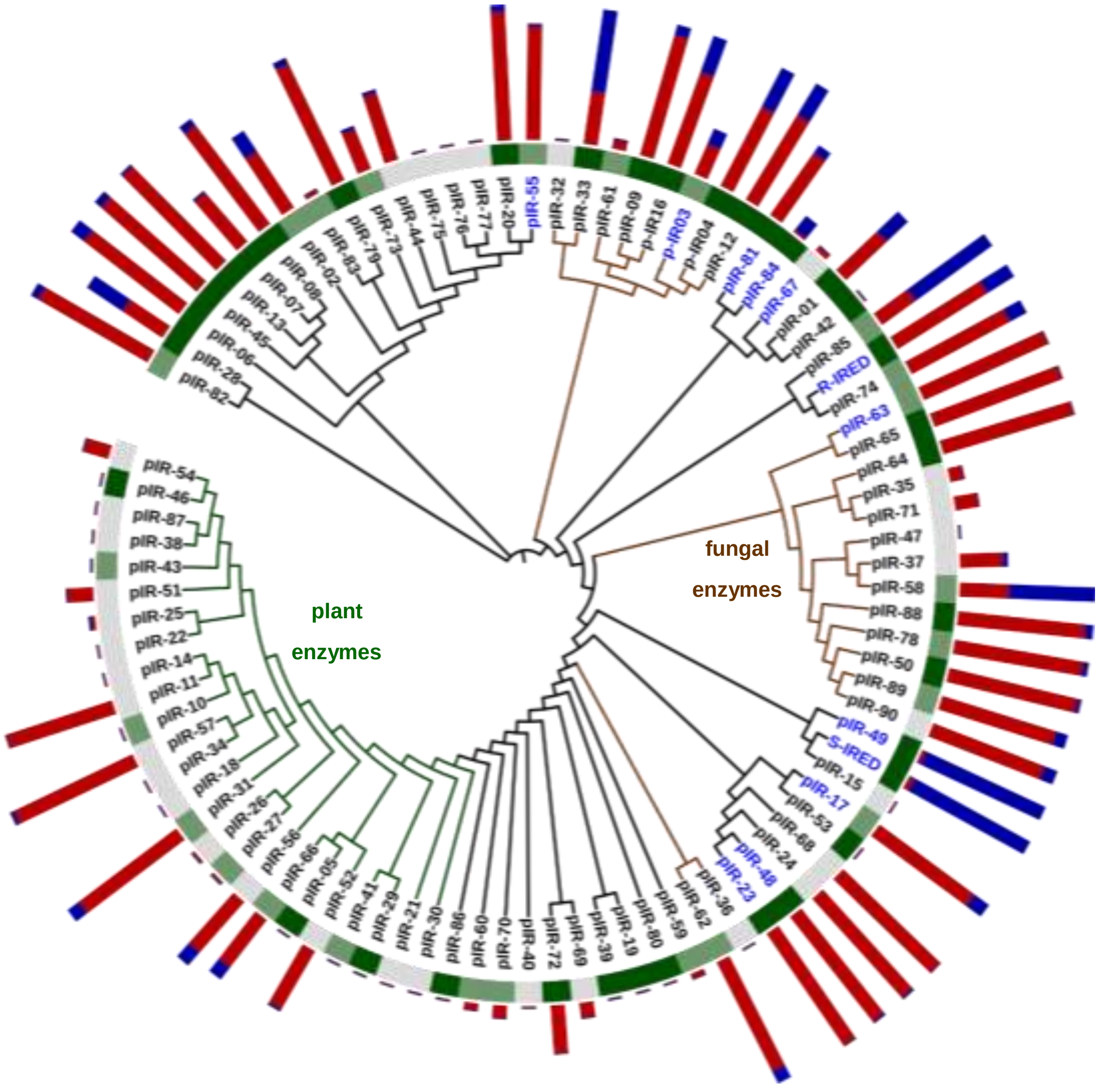


Figure S2. Initial characterisation of putative IREDs. Soluble expression in *E.coli* (green) and conversions to (*R*)-**2** (blue) and (*S*)-**2** (red, up to >99%) are shown, with stronger colours and larger bars corresponding to higher expression or conversion. Previously described IREDs are labelled in blue. Conversions were determined by GC-FID with comparison to chemically-synthesized standards.

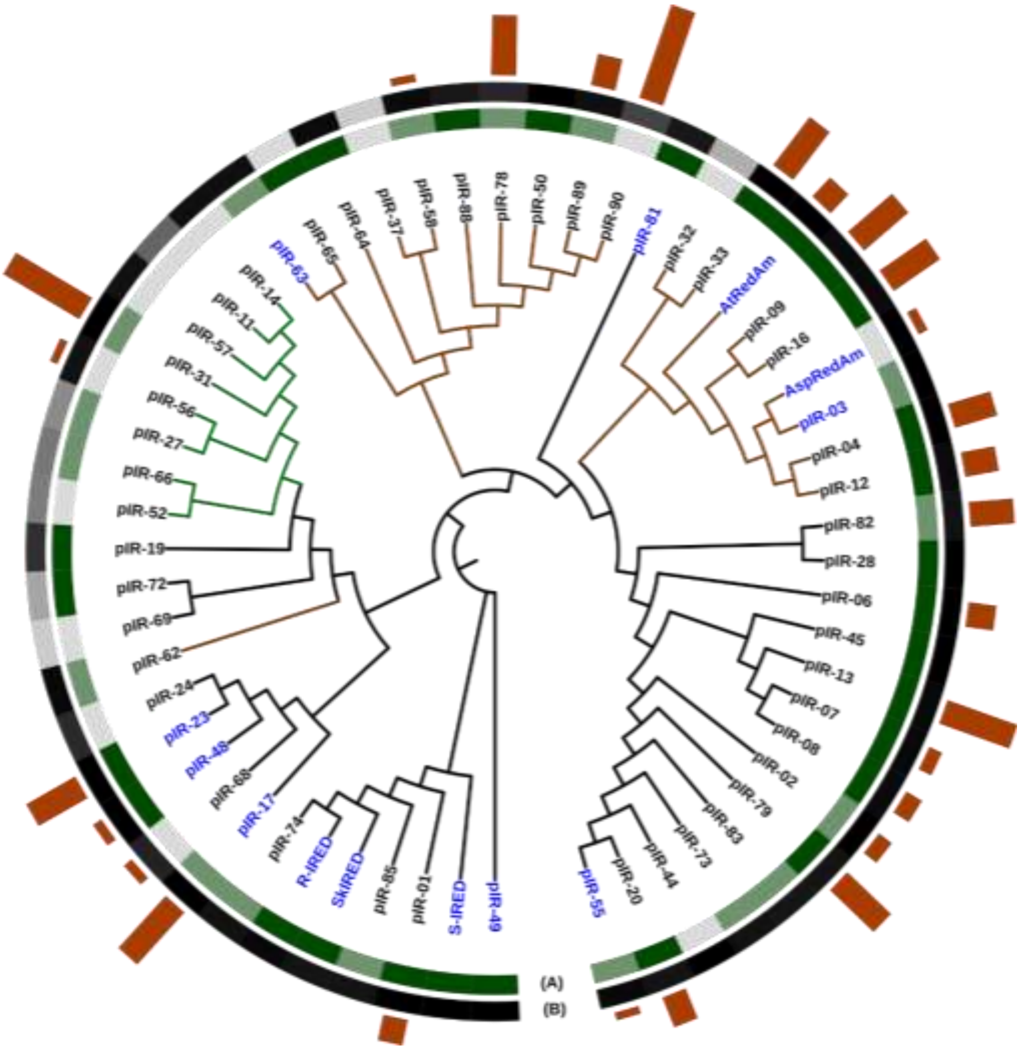


Figure S3. Isopropylamine as a nucleophile. Soluble expression in *E. coli* (**A**) and conversion to **3** (up to >99%) with 10 mM cyclohexanone and 100 mM cyclopropylamine at 30°C (**B**) are shown, with brown bars showing conversion to **8** (up to 49%) with 10 mM cyclohexanone and 100 mM isopropylamine at 37°C. Previously described IREDs are labelled in blue. Conversions were determined by GC-FID with comparison to chemically-synthesized standards, with darker colors and larger bars corresponding to higher conversions.

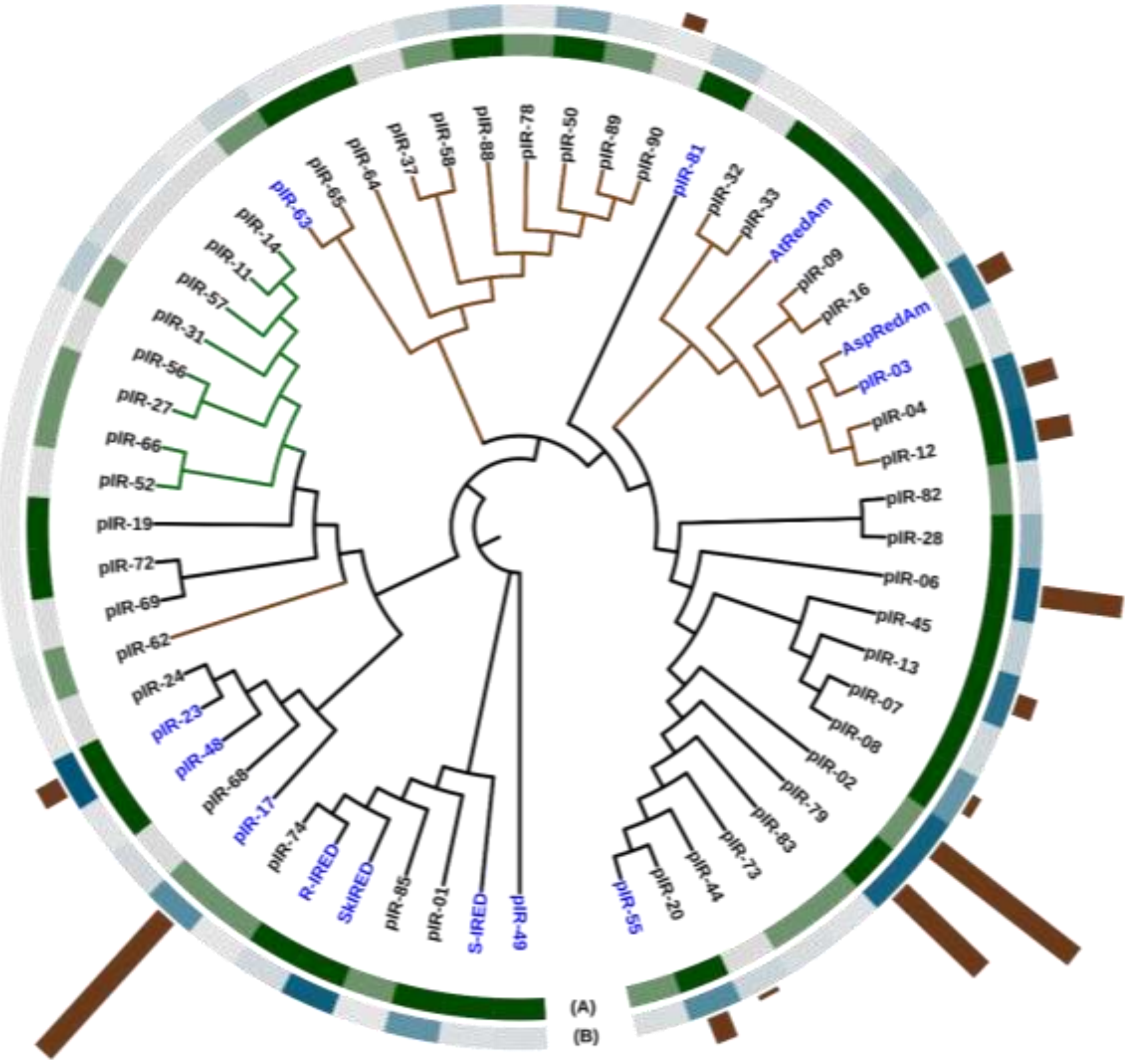
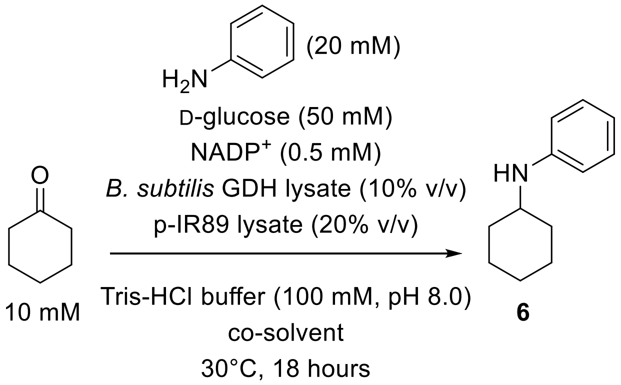


Figure S4. Reductive aminations with benzylamine. Soluble expression in *E. coli* (**A**) and conversion to **8** (up to 96%) with 10 mM cyclohexanone and 100 mM benzylamine at 30°C (**B**) are shown, with brown bars illustrating conversion to **14** (up to 74%) with methoxyacetone and benzylamine at 30°C.

Table S1. Conversions to 6 with a range of co-solvents. The total volumes of the biotransformations were 500 µL including any co-solvent, and cyclohexanone was added from a 250 mM aqueous stock solution to avoid any addition of DMSO to the transformations. [a]Conversions were determined by GC-FID with comparison to a chemically-synthesized standard.



Entry	Co-solvent	Conversion to Product (%)[a]
1	10% v/v EtOH	9
2	20% v/v EtOH	<1
3	50% v/v EtOH	<1
4	10% v/v cyclohexane	41
5	20% v/v cyclohexane	39
6	50% v/v cyclohexane	18
7	10% v/v DMSO	26
8	20% v/v DMSO	31
9	50% v/v DMSO	2
10	10% v/v MTBE	1
11	20% v/v MTBE	3
12	50% v/v MTBE	<1
13	none	7

Table S2. Comparison of proposed catalytic residues between IREDs. A sequence alignment allows comparison of residues in the AspRedAm active site to analogous residues in SkIRED, p-IR23, p-IR48 and a number of novel IREDs. All gave >90% conversion to **3** in the rective amination of cyclohexanone with cyclopropylamine.

	93	169	177	210	239	240
AspRedAm	N	D	Y	W	M	Q
SkIRED	S	D	W	G	T	H
p-IR08	N	D	Y	W	M	Q
p-IR09	N	D	Y	W	M	Q
p-IR13	N	D	Y	M	M	Q
p-IR14	T	K	A	A	H	F
p-IR16	N	D	Y	W	M	Q
p-IR19	T	K	A	V	L	G
p-IR23	S	D	W	T	A	H
p-IR28	T	D	D	W	M	Q
p-IR48	S	D	W	F	A	H
p-IR83	T	D	Y	W	M	Q

Table S3. Extended active sites of enzymes with varying conversions to 11. (A) Comparison of theoretical extended active site residues in AspRedAm to the analogous residues in the novel IREDs p-IR07, p-IR08, p-IR13 and p-IR28. **(B)** Comparison of theoretical extended active site residues which vary across the novel IREDs p-IR07, p-IR08, p-IR13 and p-IR28**.**

(A)	**13**	**17**	**65**	**91**	**93**	**118**	**119**	**121**	**122**	**124**	**125**	**131**	**132**	**169**
AspRedAm	M	L	C	L	N	I	M	V	P	M	I	V	L	D
p-IR07	M	L	C	L	N	I	M	V	P	M	I	F	I	D
p-IR08	M	L	C	L	N	I	M	V	P	M	I	F	I	D
p-IR13	M	L	C	L	N	I	M	V	P	M	I	F	I	D
p-IR28	M	L	C	L	T	I	M	V	P	M	I	F	I	D

	170	**172**	**173**	**176**	**177**	**179**	**180**	**183**	**210**	**214**	**217**	**218**	**221**	**232**
AspRedAm	L	L	L	M	Y	L	F	F	W	M	Y	L	I	T
p-IR07	I	L	L	M	Y	Y	F	V	W	M	F	L	S	T
p-IR08	I	L	L	M	Y	Y	F	V	W	M	F	L	S	T
p-IR13	I	L	L	M	Y	N	F	V	W	M	F	L	T	R
p-IR28	I	L	L	L	D	I	L	Y	W	M	L	F	L	A

	235	**236**	**237**	**239**	**240**	**244**	**246**	**247**	**261**	**264**	**268**	**280**	**281**
AspRedAm	S	N	L	M	Q	V	N	I	I	I	I	D	L
p-IR07	S	N	I	M	Q	Y	N	L	L	L	M	D	L
p-IR08	S	N	I	M	Q	F	N	L	L	L	M	D	L
p-IR13	S	N	I	M	Q	F	N	L	L	L	M	D	L
p-IR28	S	N	L	M	Q	M	Q	M	I	M	I	D	S

(B)	**93**	**176**	**177**	**179**	**180**	**183**	**217**	**218**	**221**
p-IR07	N	M	Y	Y	F	V	F	L	S
p-IR08	N	M	Y	Y	F	V	F	L	S
p-IR13	N	M	Y	N	F	V	F	L	T
p-IR28	T	L	D	I	L	Y	L	F	L

	232	**237**	**244**	**246**	**247**	**261**	**264**	**268**	**281**
p-IR07	T	I	Y	N	L	L	L	M	L
p-IR08	T	I	F	N	L	L	L	M	L
p-IR13	R	I	F	N	L	L	L	M	L
p-IR28	A	L	M	Q	M	I	M	I	S

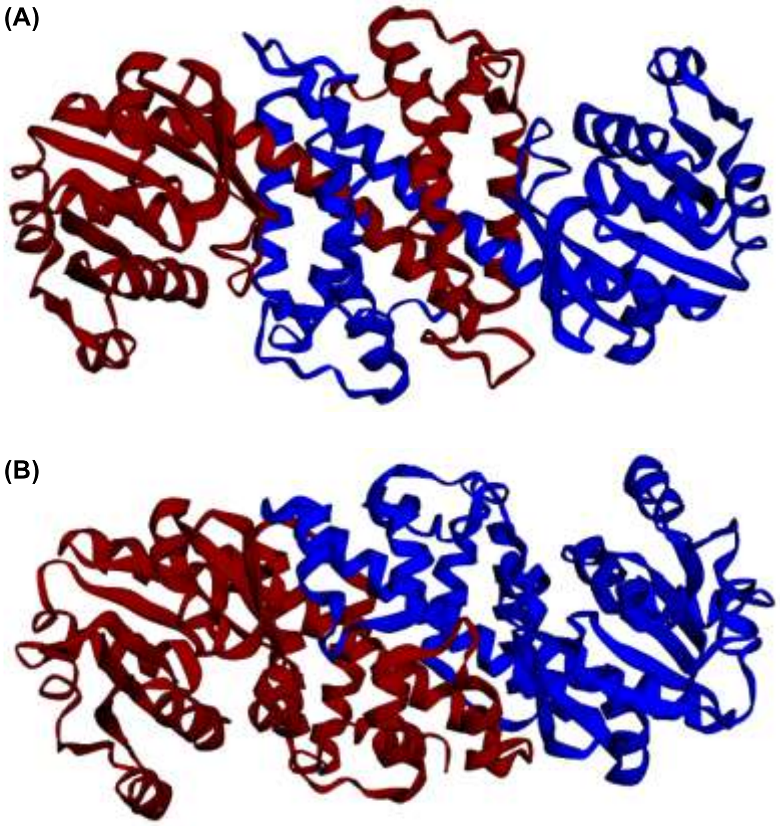


Figure S5. IRED quaternary structures. (A) Crystal structure of AspRedAm with NADP$^+$ bound (PDB code: 5G6R) and **(B)** homology model of p-IR14 from *A. thaliana*, based on β-HAD*At*, PDB code: 3DOJ.

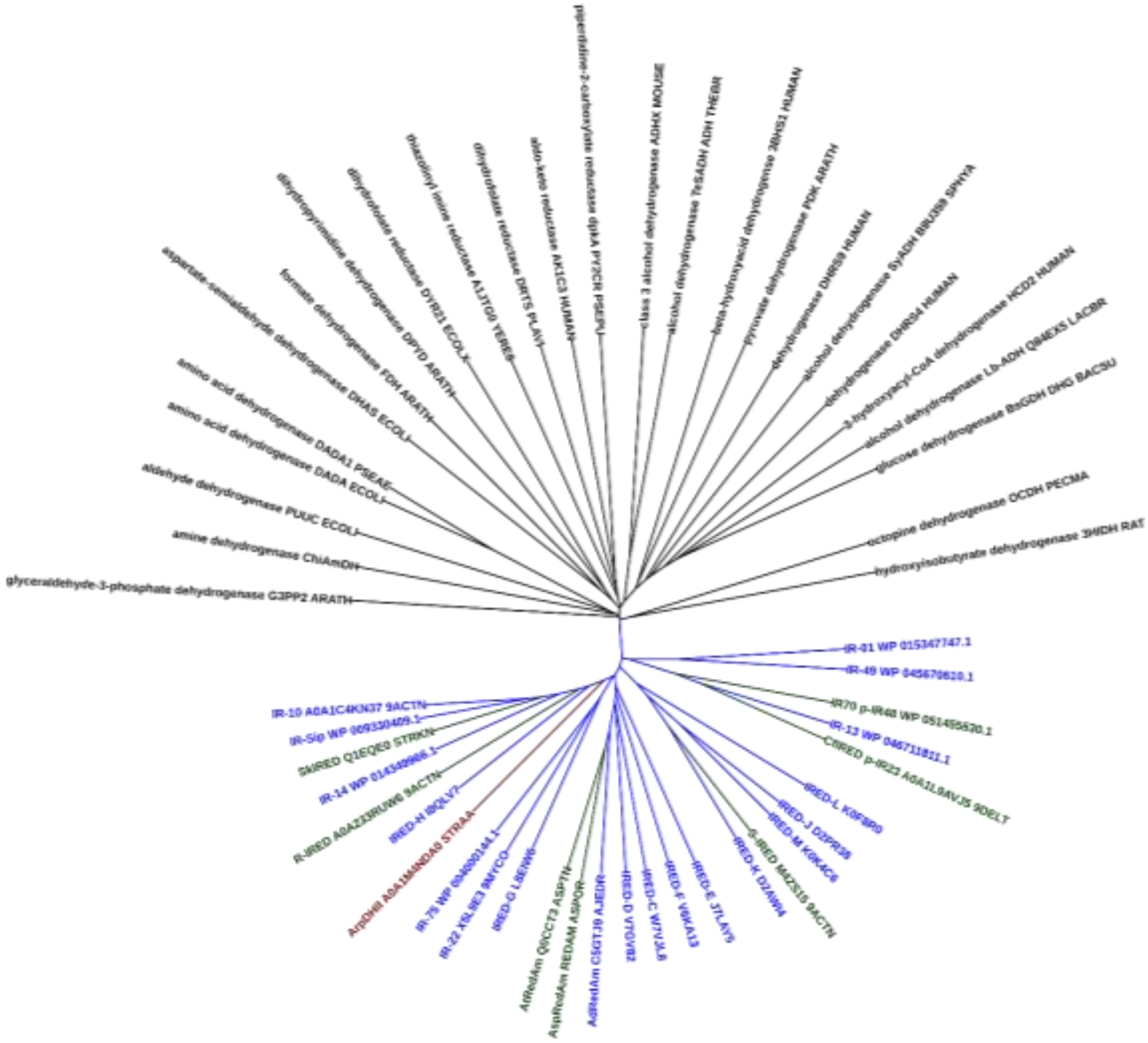
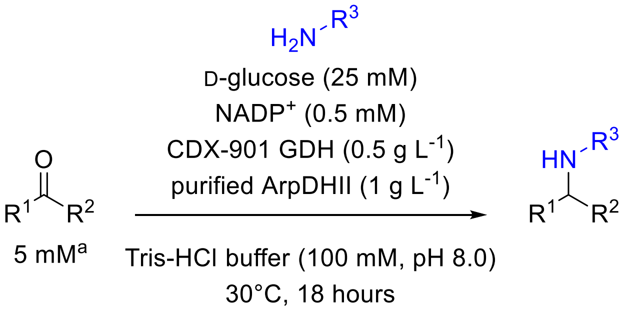


Figure S6. ArpDHII in phylogenetic context. Relationship of the ArpDHII enzyme (red) to previously described IREDs (blue), including several of those described in this work (green). Other dehydrogenase enzymes are shown in black.

Table S4. Reaction conditions and conversions obtained with ArpDHII. Conversions were determined by GC-FID with comparison to chemically-synthesized standards, and are compared to conversions obtained with purified AspRedAm (*2*). ^{a}Aldehyde and ketone substrates were diluted from 1 M stock solutions in DMSO.



Entry	**Carbonyl Substrate**	**Amine Nucleophile**	**[Amine Nucleophile] / mM**	**Enzyme**	**Product (%)**
1	cyclohexanone	propargylamine	5	AspRedAm	94
2				ArpDHII	18
3		cyclopropylamine	5	AspRedAm	90
4				ArpDHII	93
5		allylamine	5	AspRedAm	73
6				ArpDHII	9
7		methylamine	10	AspRedAm	95
8				ArpDHII	15
9		benzylamine	5	AspRedAm	84
10				ArpDHII	2
11		isopropylamine	100	AspRedAm	94
12				ArpDHII	<1
13	hydrocinnamaldehyde	propargylamine	20	AspRedAm	97
14				ArpDHII	97
15		cyclopropylamine	20	AspRedAm	>97
16				ArpDHII	>97
17		allylamine	20	AspRedAm	>97
18				ArpDHII	89
19	1-indanone	propargylamine	250	AspRedAm	64
20				ArpDHII	<1

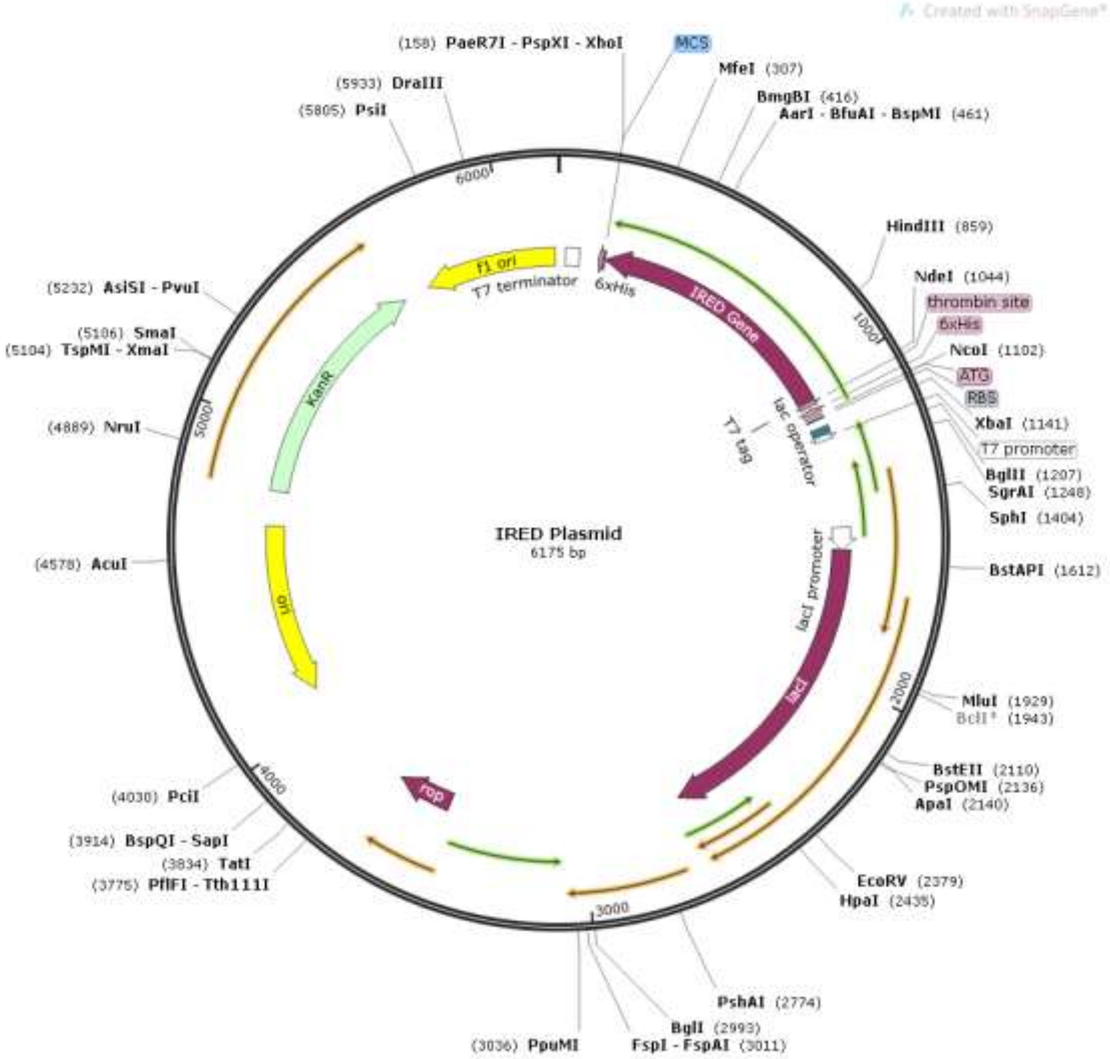
2 Supplementary materials and methods

2.1 General

Solvents used were of HPLC grade, and when necessary were further dried over molecular sieves. Analytical thin-layer chromatography (TLC) was performed using commercially available pre-coated plates (Macherey-Nagel Polygram SIL G/UV254) with visualisation by UV light (at 254 nm) and ninhydrin dip. Column chromatography was performed on silica gel (Fluka, Buchs, Switzerland, 220 - 440 mesh). In cases where a large number of biotransformations were run in parallel, workup was performed with the aid of a Hamilton Microlab STAR liquid handling system (Hamilton, Bonaduz, Switzerland), and where necessary, samples were derivatized using acetic anhydride with an excess of triethylamine at 25°C prior to analysis.

Spectra from ^1H and ^{13}C NMR runs were recorded on a Bruker Avance 400 instrument (400 MHz for ^1H and 100 MHz for ^{13}C) in $CDCl_3$ or CD_3OD using residual protic solvent as an internal standard. Reported chemical shifts (δ) in parts per million (ppm) are relative to the residual protic solvent signal ($CHCl_3$ in $CDCl_3$: $^1H = 7.26$; $CDCl_3$, $^{13}C = 77.0$; CH_3OH in CD_3OD: $^1H = 3.31$, $^{13}C = 49.0$). Coupling constants (*J*) are quoted in Hz and are rounded to the nearest 0.1 Hz. ^1H multiplicities are reported as follows: singlet (s), doublet (d), triplet (t), quartet (q), multiplet (m), or broad resonance (br), or a combination of these. High-resolution mass spectrometry (HRMS) was recorded using a Waters LCT time-of-flight mass spectrometer, connected to a Waters Alliance LC (Waters, Milford, MA, USA). Data were processed with Waters Masslynx software. GC analysis was performed on either an Agilent 7890B gas chromatograph with a flame ionization detector (FID) and autosampler equipped with a 30 m Phenomenex ZB WAXplus column with 0.25 mm inner diameter and 0.25 µm film thickness or an Agilent 6850 gas chromatograph with a flame ionization detector (FID) and autosampler equipped with a 25 m CP-Chirasil-DEX CB column with 0.25 mm inner diameter and 0.25 µm film thickness (Agilent, Santa Clara, CA, USA). GC-MS analyses were performed on an Agilent 7890B gas chromatograph coupled to an Agilent 5977B mass spectrometer with an electron ionization source (EI) operating at 70 eV and equipped with a 30 m HP-1 ms fused silica capillary column with 0.25 mm inner diameter and 0.25 µm film thickness.

2.2 IRED cloning



Plasmid map for cloned IREDs. The IRED gene cloned is into a pET-28b (+) vector between *Nde*I and *Xho*I restriction sites.

IREDs of fungal origin. [a]p-IR03 and p-IR63 were previously characterized by Zawodny *et al.* (*24*).

Enzyme	**Organism**	**UniProt ID**	**Identity with AspRedAm**
AspRedAm	*Aspergillus oryzae*	REDAM_ASPOR	100.0%
p-IR03[a]	*Aspergillus bombycis*	A0A1F7ZK02_9EURO	84.4%
p-IR04	*Aspergillus calidoustus*	A0A0U5GEY4_9EURO	62.4%
p-IR09	*Aspergillus lentulus*	A0A0S7DXU4_9EURO	57.3%
p-IR12	*Aspergillus nidulans*	Q5AUX5_EMENI	57.5%
p-IR16	*Aspergillus udagawae*	A0A0K8L8S9_9EURO	58.3%
p-IR32	*Emmonsia parva*	A0A0H1B7G6_9EURO	43.3%
p-IR33	*Emmonsia pasteuriana*	A0A1J9QMV6_9EURO	50.0%
p-IR35	*Exophiala aquamarina*	A0A072NZT1_9EURO	30.7%
p-IR36	*Fonsecaea multimorphosa*	A0A178C791_9EURO	26.8%
p-IR37	*Fusarium oxysporum*	W9Z6K1_FUSOX	35.4%
p-IR47	*Microdochium bolleyi*	A0A136IJF0_9PEZI	27.6%
p-IR50	*Madurella mycetomatis*	A0A175WBH2_9PEZI	29.7%
p-IR58	*Nectria haematococca*	C7Z324_NECH7	32.8%
p-IR61	*Penicillium arizonense*	A0A1F5L0A3_9EURO	54.6%
p-IR62	*Pochonia chlamydosporia*	A0A179G8F8_METCM	31.7%
p-IR63[a]	*Penicillium camemberti*	A0A0G4PFF8_PENCA	34.3%
p-IR64	*Pseudogymnoascus* sp. VKM F-4516	A0A094D824_9PEZI	35.5%
p-IR65	*Purpureocillium lilacinum*	A0A179GW01_9HYPO	39.2%
p-IR71	*Rhinocladiella mackenziei*	A0A0D2H0B2_9EURO	26.5%
p-IR78	*Stachybotrys chartarum*	A0A084RCS9_STACH	36.3%
p-IR88	*Torrubiella hemipterigena*	A0A0A1TF30_9HYPO	31.4%
p-IR89	*Myceliophthora thermophila*	G2QG78_MYCTT	31.3%
p-IR90	*Myceliophthora thermophila*	N/A	31.3%

IREDs of plant and mammalian origin.

Enzyme	Organism	UniProt ID	Identity with AspRedAm
p-IR-5	*Araucaria cunninghamii*	A0A0D6R2X8_ARACU	20.8%
p-IR10	*Arabis alpina*	A0A087GHW2_ARAAL	19.8%
p-IR11	*Arabidopsis lyrata*	D7MD48_ARALL	20.0%
p-IR14	*Arabidopsis thaliana*	3HID1_ARATH	18.3%
p-IR18	*Brassica rapa* subsp. *pekinensis*	M4DQA1_BRARP	19.1%
p-IR21	*Corchorus capsularis*	A0A1R3HV54_COCAP	20.0%
p-IR22	*Citrus clementina*	V4UJW6_9ROSI	19.0%
p-IR25	*Citrus sinensis*	A0A067FGQ9_CITSI	19.5%
p-IR26	*Cucumis sativus*	A0A0A0LIQ8_CUCSA	20.3%
p-IR27	*Daucus carota subsp. sativus*	A0A161WTE2_DAUCA	20.3%
p-IR31	*Eucalyptus grandis*	A0A059CN57_EUCGR	19.1%
p-IR34	*Eutrema salsugineu*	V4KLI0_EUTSA	20.6%
p-IR38	*Gossypium hisutum*	A0A1U8PU55_GOSHI	17.7%
p-IR40	*Homo sapiens*	GLYR1_HUMAN	10.8%
p-IR43	*Jatropha curcas*	A0A067KFP5_JATCU	18.7%
p-IR46	*Lupinus angustifolius*	A0A1J7FZG6_LUPAN	20.0%
p-IR51	*Morus notabilis*	W9T391_9ROSA	19.4%
p-IR52	*Marchantia polymorpha* subsp. *polymorpha*	A0A176VNX2_MARPO	17.4%
p-IR54	*Medicago truncatula*	G7L7F1_MEDTR	21.1%
p-IR56	*Nicotiana attenuata*	A0A1J6KVX5_NICAT	17.1%
p-IR57	*Noccaea caerulescens*	A0A1J3E499_NOCCA	20.9%
p-IR66	*Picea sitchensis*	A9NZ37_PICSI	18.9%
p-IR87	*Theobroma cacao*	A0A061GU76_THECC	20.4%

IREDs of bacterial origin. [a]p-IR17, p-IR23, p-IR55, p-IR67, p-IR 81 and p-IR84 were previously characterized by Zawodny *et al.* (*24*). [b]p-IR48 was previously characterized by France *et al.* (*8*). [c]p-IR49 was previously characterized by Roiban *et al.* (*9*).

Enzyme	**Organism**	**UniProt ID**	**Identity with AspRedAm**
p-IR01	*Allokutzneria albata*	A0A1G9V2F1_9PSEU	37.2%
p-IR02	*Allokutzneria albata*	A0A1G9SYK8_9PSEU	38.9%
p-IR06	*Actinoalloteichus hymeniacidonis*	A0A1D8BXU6_9PSEU	40.3%
p-IR07	*Amycolatopsis japonica*	A0A075UU84_9PSEU	43.3%
p-IR08	*Amycolatopsis keratiniphila*	A0A1H2GBD9_9PSEU	41.4%
p-IR13	*Amycolatopsis regifaucium*	A0A154MR77_9PSEU	42.0%
p-IR15	*Amycolatopsis thermoflava*	WP_027931120.1	30.2%
p-IR17[a]	*Burkholderia lata*	Q39NX6_BURL3	27.6%
p-IR19	*Burkholderia vietnamiensis*	A4JAJ9_BURVG	20.1%
p-IR20	*Couchioplanes caeruleus*	A0A1K0GAQ1_9ACTN	38.9%
p-IR23[a]	*Cystobacter ferrugineus*	A0A1L9AVJ5_9DELT	29.0%
p-IR24	*Chelatococcus sambhunathii*	A0A0K6H4A1_9RHIZ	24.8%
p-IR28	*Devosia geojensis*	A0A0F5FDU7_9RHIZ	42.1%
p-IR29	*Draconibacterium orientale*	X5E3Y1_9BACT	17.2%
p-IR30	*Desulfosporosinus orientis*	G7W7U0_DESOD	21.9%
p-IR39	*Granulicella mallensis*	G8P071_GRAMM	21.2%
p-IR41	*Isosphaera pallida*	E8QYX7_ISOPI	19.0%
p-IR42	*Jiangella alkaliphila*	A0A1H2IPN0_9ACTN	37.6%
p-IR44	*Kitasatospora cheerisanensis* KCTC 2395	A0A066Z502_9ACTN	27.7%
p-IR45	*Kibdelosporangium phytohabitans*	A0A0N9HVM7_9PSEU	42.7%
p-IR48[b]	*Microvirga lupini*	WP_051455530.1	31.9%
p-IR49[c]	*Mycobacterium magaritense*	X5L9E3_9MYCO	30.5%
p-IR53	*Minicystis rosea*	A0A1L6L1L9_9DELT	27.9%
p-IR55[a]	*Micromonospora tulbaghiae*	A0A1C4WQ45_9ACTN	37.5%
p-IR59	*Pseudomonas aeruginosa*	Q9I1R8_PSEAE	19.9%
p-IR60	*Pseudomonas aeruginosa*	A0A1F0IHK4_9PSED	19.3%
p-IR67[a]	*Paenibacillus tyrfis*	A0A081P2I1_9BACL	40.7%
p-IR68	*Rhizobium gallicum*	A0A0B4XDG7_9RHIZ	25.6%
p-IR69	*Rivularia* sp. *PCC 7116*	K9RL01_9CYAN	17.2%
p-IR70	*Rhodococcus jostii*	Q0S7N9_RHOJR	19.5%
p-IR72	*Rhodobacter sphaeroides*	Q3IXE7_RHOS4	21.5%
p-IR73	*Streptomyces albus*	A0A0B5EJP8_STRA4	39.1%
p-IR74	*Streptomyces albus*	A0A0B5EWU4_STRA4	30.9%
p-IR75	*Streptomyces avermitilis*	N/A	38.1%
p-IR76	*Streptomyces canus*	N/A	41.6%
p-IR77	*Streptomyces canus*	N/A	41.6%
p-IR79	*Streptomyces chattanoogensis*	A0A0N0XYF8_9ACTN	40.8%
p-IR80	*Synechococcus elongatus*	A0A0H3K567_SYNP6	20.7%
p-IR81[a]	*Stackebrandtia nassauensis*	D3Q3S0_STANL	39.5%
p-IR82	*Streptomyces noursei* ATCC 11455	A0A1B2GW12_STRNR	38.6%
p-IR83	*Streptomyces purpeofuscus*	WP_030392279.1	38.5%
p-IR84[a]	*Streptomyces resistomycificus*	A0A0L8KUS9_9ACTN	38.9%
p-IR85	*Streptomyces rimosus*	N/A	38.3%
p-IR86	*Thermobifida fusca*	Q47QG6_THEFY	21.8%

2.3 Protein sequences

2.3.1 Glucose dehydrogenase sequence

> *B. subtilis* GDH (*Bacillus subtilis*, DHG_BACSU) (*9*)
MGSSHHHHHHSSGLVPRGSHMYPDLKGKVVAITGAASGLGKAMAIRFGKEQAKVVINYYS
NKQDPNEVKEEVIKAGGEAVVVQGDVTKEEDVKNIVQTAIKEFGTLDIMINNAGLENPVP
SHEMPLKDWDKVIGTNLTGAFLGSREAIKYFVENDIKGNVINMSSVHEVIPWPLFVHYAA
SKGGIKLMTETLALEYAPKGIRVNNIGPGAINTPINAEKFADPKQKADVESMIPMGYIGE
PEEIAAVAAWLASKEASYVTGITLFADGGMTQYPSFQAGRG*

2.3.2 Characterized and putative imine reductase sequences

>AspRedAm (*Aspergillus oryzae*, REDAM_ASPOR) (*2*)
MGSSHHHHHHSSGLVPRGSHMSKHIGIFGLGAMGTALAAKYLEHGYKTSVWNRTTAKAIP
LVEQGAKLASTISEGVNANDLIIICLLNNQVVEDALRDALQTLPSKTIVNLTNGTPNQAR
KLADFVTSHGARYIHGGIMAVPTMIGSPHAVLLYSGESLELFQSIESHLSLLGMSKYLGT
DAGSASLHDLALLSGMYGLFSGFLHAVALIKSGQDTSTTATGLLPLLTPWLSAMTGYLSS
IAKQIDDGDYATQGSNLGMQLAGVENIIRAGEEQRVSSQMILPIKALIEQAVGEGHGGED
LSALIEYFKVGKNVD*

>AtRedAm (*Aspergillus terreus*, Q0CCT3_ASPTN) (*2*)
MGSSHHHHHHSSGLVPRGSHMATTTTTTKLTIFGLGAMGTAMATQFLKQGHTPTVWNRTA
AKANPLVEQGAHLAATIPAAIAASPLLIFCLLDNAAVEQTLAAGPPSLAGKTILNLTNGT
PSQARRLATLASARGARYFHGGIMATPDMIGAPHAVILYSGGGSAETYASVEGVLAVLGS
GKYLGDDAGSASLHDLALLSGMYGLFAGFLHATALVRSEGEGVSATEFLGLLAPWLQAMT
GYLGLLARQIDDGVYTAQTSNLEMQLVALENACAASREQGVSAEVMLPLKGLVERAVREG
RGGHDISSLIDYFRNASV*

>SkIRED (*Streptomyces kanamyceticus*, Q1EQE0_STRKN) (*30*)
MGSSHHHHHHSSGLVPRGSHMPDNPSTKGRMMRNQQAEHTPVTVIGLGLMGQALAGAFLG
AGHPTTVWNRTAAKAEPLVARGAKSAGSVAEAVAASPLVVVCVSDYDAVHALLDPLDGTA
LQGRTLVNLTSGTSAQARERAAWADGRGADYLDGAILAGPAAIGTADAVVLLSGPRSAFD
PHASALGGLGAGTTYLGADHGLASLYDAAGLVMMWSILNGFLQGAALLGTAGVDATTFAP
FITQGIGTVADWLPGYARQIDDGAYPADDAAIDTHLATMEHLIHESEFLGVNAELPRFIK
ALADRAVADGHGGSGYPALIEQFRTHSGK*

>R-IRED (*Streptomyces* sp. 3587, M4ZRJ3_9ACTN) (*12*)
MGSSHHHHHHSSGLVPRGSHMGDNRTPVTVIGLGLMGQALAAAFLEAGHTTTVWNRSAGK
AEQLVSQGAVQAATPADAVAASELVVVCLSTYDNMHDVIGSLGESLRGKVIVNLTSGSSD
QGRETAAWAEKQGVEYLDGAIMITPPGIGTETAVLFYAGTQSVFEKYEPALKLLGGGTTY
LGTDHGMPALYDVSLLGLMWGTLNSFLHGVAVVETAGVGAQQFLPWAHMWLEAIKMFTAD
YAAQIDAGDGKFPANDATLETHLAALKHLVHESEALGIDAELPKYSEALMERVISQGHAK
NSYAAVLKAFRKPSE*

>S-IRED (*Streptomyces* sp. 3546, M4ZS15_9ACTN) (*13*)
MGSSHHHHHHSSGLVPRGSHMSKQSVTVIGLGPMGQAMVNTFLDNGHEVTVWNRTASKAE
ALVARGAVLAPTVEDALSANELIVLSLTDYDAVYAILEPVTGSLSGKVIANLSSDTPDKA
REAAKWAAKHGAKHLTGGVQVPPPLIGKPESSTYYSGPKDVFDAHEDTLKVLTNADYRGE
DAGLAAMYYQAQMTIFWTTMLSYYQTLALGQANGVSAKELLPYATMMTSMMPHFLELYAQ
HVDSADYPGDVDRLAMGAASVDHVLHTHQDAGVSTVLPAAVAEIFKAGMEKGFAENSFSS
LIEVLKKPAV*

>ArpDHII (*Streptomyces argillaceus*, A0A1M4NDA0_STRAA) (*26*)

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MGSSHHHHHHSSGLVPRGSHMSNTNQGPVTVLGLGMMGAALATAFVKNGNPTTVWNRSAD
KADALVEQGAVFAADIKQAIEASPVVVACVSTYEVLNDLFAGAADELKGKVVINLTSGTP
EDARALAVWAEQNGVRYLDGAIMAVPQMIGLPQALIFYAGAQEVYAEHEELLKPLAGTNV
YLGADTGVAMIYDLGLLSLLWSSLAGYFHAVALVNSAGVSAEAFTPFALTWIEHVITPSI
PQSAKEIDSASFDTEISSLGVNKAAIEHLVATSKQLGINSDFSAAIQALIERRVEQGHAG
HSLASLVEAFKQG*
```

>p-IR01 (*Allokutzneria albata*, A0A1G9V2F1_9PSEU)

```
MGSSHHHHHHSSGLVPRGSHMSTKKVTVIGLGSLGSALAAALLRTGHDVTVWNRTPEKAE
ALVAQGATRADTVAEAAAASPVVIVCVFDTEAARELLAPIQAGKAVVNLTSGSPDEAREL
AAWAASRGVDYLDGAVMAVPAAIGTPDAFVMYSGSREVFDAHRAALDSFGASHFLGEDAG
VAEFHDLGLLYAGYATLVGFLNSVAIVGTAGVTARELLPLVTTWLTGMVAYLADVAREVD
ERDYTDGASSVAINQVALDKIIAASRAAGVSPDLLLPFKELLDRRAADGHARDSASSVIE
LLRPGIHPE*
```

>p-IR02 (*Allokutzneria albata*, A0A1G9SYK8_9PSEU)

```
MGSSHHHHHHSSGLVPRGSHMTDTSAKLTLLGLGAMGSALATAWLAADYDITVWNRTASR
AEPLRTLGAQVADTAADAVAANDLVVACLLDDASVRSTLDGVDLTGKDLINLTTGTPGSG
RELAACATARGARYVDGGIMAVPPMIGVPDSGAYVFYSGSAAAFEAHRDALAVGAGTKFV
GEDPGFAALYDVALLSAMTGMFAGVSHAFALVRKENIDPREFAGLVSGWITAMSGYAHGI
AEHLASGDYTTGVTSNLAMMVEGNATMLRTAHEQGVSPELLEPFMRLMRQRVDDGHGDED
TTGVIDLLLSRR*
```

>p-IR03, AbIRED (*Aspergillus bombycis*, A0A1F7ZK02_9EURO) (*24*)

```
MGSSHHHHHHSSGLVPRGSHMSKHISIFGLGAMGAALAARYLEHGYKTTVWNRTTAKATP
LVEQGAKLASTISEGINASDLIIICLLNNEAAEDILRDVFHSLSSKTIVNLTNGTPYQAR
NLADFVTSNGARYIHGGIMAVPAMIGSPHAVLLYSGGSFELFQSIESHLSLLGMSKFLGT
DAGSASLHDLALLSGMYGLFSGFLHAVALIKSEQSKTATGLLPLLTPWLSAMMGYLSSIA
SQIDEGDYATQGSNLEMQLVGVENILKAGKEQGISSQMILPMKALIEKAVGEGHGGEDLS
VLIDYFKGEKSLE*
```

>p-IR04 (*Aspergillus calidoustus*, A0A0U5GEY4_9EURO)

```
MGSSHHHHHHSSGLVPRGSHMSTITLFGLGAMGKALAAKYIEKGYTTTIWNRTPSKAAPL
VEKGAKLANTVGEGLASADLIILCLLDNASVRQTLDQATAALNGKTVINLTNGTPSQARE
TSEWVISHGAQYIHGGIMAVPDMIGSPHAVLLYSGESAETFSRVEAHLSHLGTSKFLGTD
PGSASLHDLALLSGMYGLFSGFFHATALVKSQPGTTATGFVQLLTPWLSAMTHYLGALAK
QIDEGDYATQGSNMAMQVTGVQNIVRASEEAGVTADLIMPILGRMTRAAEAGYADVDVSA
VIEFMKE*
```

>p-IR05 (*Araucaria cunninghamii*, A0A0D6R2X8_ARACU)

```
MGSSHHHHHHSSGLVPRGSHMADKPRVGWIGTGVMGQAMCGHILKDGYPVRVFNRTPSKA
QTLIENGALMAENPKSVAEGSDVVFTIVGYPHDVSEVILGDKGVLQGLKPGGVIVDMTTS
EPSLAQKIYKFAKERGCESVDAPVSGGDKGAKGGTLAIFAGGDEKVVETLKPLFDCMGKV
TYMGGPGLGQCTKLGNQITIASTMVGLVEGMVFAHKAGLDVETYIRAISSGAAGSKSLEL
YANRILKGDFEPGFFVNHFVKDLGISLRECQQMGLSLPGLALAQQLYVSLKAHGEGNLGT
QALVLALERLNNVQLPRMQ*
```

>p-IR06 (*Actinoalloteichus hymeniacidonis*, A0A1D8BXU6_9PSEU)

```
MGSSHHHHHHSSGLVPRGSHMPESTTPSTATPVTIIGLGAMGTALANAFLDAGHSTTVWN
RTAARATALAARGAHHAETVTEAIAASPLVIACVLDYDAFHETLAPATDALAGRALVNLT
NGTPKQARETASWAADHRIDYLDGGIMAIPPGIATPDSFILYSGPLGTFEAHRSTLEVLG
AANHVGTDHGLASLHDLALLTGMYGMFAGILQAFALIDSEGIPAGDLAPMLTNWLTGMAH
SVAHYAQQIDTGDYETGVVSNLAMQSAGFANLVQAGEDQGVDVGLLRPLFELMRHQVAAG
YGNGDVASVIELIRREERRQPAKSPGADKITRARRP*
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>p-IR07 (*Amycolatopsis japonica*, A0A075UU84_9PSEU)

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MGSSHHHHHHSSGLVPRGSHMSEHGKTPVTVLGLGAMGTALVEALLAAGHPVTAWNRTAS
```

WAEAVAAQGASVASTISEALAANTIVIACLLDYDSVHEVLDPVAAELEGRQLINLTNGTP
GQAREMSAWAEGLGAAYLDGGIMAVPPMIGTPAAFIFYSGSGTVFGHARTALDTFGGVNY
LGADPGLAPLHDIALLSGMYGYFVGVIQAYALVGSAGVKAREFAPLLRGWLDAMGGFLER
SAEQIDDGDYVTDVVSNIGMQAAAYPNLAQAAEDQGISAELLTPLQSLMDKRVARGHGAE
DLIGVIELLKK*

>p-IR08 (*Amycolatopsis keratiniphila*, A0A1H2GBD9_9PSEU)
MGSSHHHHHHSSGLVPRGSHMSEHGKTPVTVLGLGAMGTALVEALLTAGHPVTVWNRTAS
RTEAVAAKGASVASTVSEALAADTNAIVLACLLDYDSVHEVLDPVAAELAGRQLINLTNG
TPGQAREMNAWAEELGAAYLDGGIMAVPPMIGTPAAFIFYSGSGTVFGRARTALETFGGV
NYLGADPGLAPLHDIALLSGMYGYFVGVIQAYALVGSAGVKAREFAPLLRGWLDAMGGFL
ERSAEQIDDGDYMTDVVSNIGMQAAAFPNLAKAAADQGISAELLTPLQPLMDKRVADGHG
AEDLIGVIELLKK*

>p-IR09 (*Aspergillus lentulus*, A0A0S7DXU4_9EURO)
MGSSHHHHHHSSGLVPRGSHMSSVSIFGLGAMGTALASRFLEEKYKVAVWNRSPEKASPL
LEKGATLSHTALDGINASDLIVICLLDNAAVQATLNSALEHLRGKTIINLTNGTPDQARK
LSDLIVSHGAQYVHGGIMATPSMIGSPHALVLYSGSPDAFKTAEADLSVLAKCIFLGEDA
GSASLHDLALLSGMYGLFSGFLHATALVRSSTPAVKFVDLLVPWLGAMTEYTKGMAKQID
EGNYASEGSNLGMQLVAIQNIIDASAAQQVSADFIRPMKEFMEKAVVAGHGGDDISSLID
FVKST*

>p-IR10 (*Arabis alpina*, A0A087GHW2_ARAAL)
MGSSHHHHHHSSGLVPRGSHMPLLLRRYLSPSVVSSSFLRRSMAYSSISTDPINPSYSSI
STDPINPSNTKIGWIGTGVMGRSMCGHLIRAGYSVTVFNRTISKAQTLLDMGAKLADSPS
SVASQSDVVFSIVGYPSDVRNVLLDPNSGALSGLRKGGVLVDMTTSEPSLAEEIAKSASS
VHCFSIDAPVSGGDLGAKNGKLSIFTGGDETTVKRLDPLFSLMGKVNFMGTSGKGQFAKL
GNQITIASTMLGLVEGIIYAHKSGLDVKKFLEAISTGAAGSKSIDLYGDRIMKRDFDPGF
YVNHFVKDLGICLNECQRMGLALPGLALAQQLYLSLKAHGQGDLGTQALILALERLNNVK
IDFY*

>p-IR11 (*Arabidopsis lyrata*, D7MD48_ARALL)
MGSSHHHHHHSSGLVPRGSHMPLLLRRFLSPSVVSSFFLRRSMASSSISSDPITPSNTKI
GWIGTGVMGRSMCGHLIKAGYTVTVFNRTISKAQTLIDMGANLADSPNSVASQSDVVFTI
VGYPSDVRHVLLDPKSGALSGLQQGGVLVDMTTSEPSLAEEIAKAASFENCFSIDAPVSG
GDLGAKNGKLSIFAGGDETTVKRLDPLFSLMGKVNFMGTSGKGQFAKLANQITIASTMLG
LVEGLTYAHKAGLDVKKFLEAISTGAARSKSIDLYGDRILKRDFDPGFYVNHFVKDLGIC
LNECQRMGLALPGLALAQQLYLSLKAHGEGGLGTQALILALERLNNVSVQPSVS*

>p-IR12 (*Aspergillus nidulans*, Q5AUX5_EMENI)
MGSSHHHHHHSSGLVPRGSHMSKISLFGLGSMGQALAHRYIDTGYTTTVWNRTPEKAQSS
GLIQKGAHQALTVAEGLEAADMVILCLLDNASVRETLSKAVTSLSGKTIVNLTNGTPTQA
RDLSEWAGAHGAEYIHGGIMAVPDMISSGSPHSILLYSGKSNEVFTRIEPDLAHLGAAKF
LGTDPGSASLHDLALLSGMYGLFSGFFHATALVRSQSDTTSEGFLELLIPWLGAMTHYLG
GLAKQIDSGDYTTQGSNIAMQVAGLENIIAASEEVGVTPAFILPIQRLMKRAADEGHGNT
DISSLIQYLRTRE*

>p-IR13 (*Amycolatopsis regifaucium*, A0A154MR77_9PSEU)
MGSSHHHHHHSSGLVPRGSHMTEHGKTPVTVLGLGAMGTALVEALLAAGHPVTAWNRTAS
RAEGVAAKGASVASTVSEALAANKTVIACLLDYDSVHEVLDPVASGLEGRQLINLTNGTP
GQAREMSAWAEELGAEYLDGGIMAVPPMIGTPGAFIFYSGSGTVFGQARTALDTFGGVNY
LGADPGLAPLHDIALLSGMYGNFIGVIQAFALVGSAGVKAREFAPLLRGWMDAMSGFLER
TAELIDDGDYERGVVSNIGMQAAAFPNLAKAAEEQGISAELLAPLQPLMDKRVAAGHGAE
DLVGVIELLKK*

>p-IR14 (*Arabidopsis thaliana*, 3HID1_ARATH)
MGSSHHHHHHSSGLVPRGSHMPLLLRRFPSPSVVSSFFLRRSMASSTISSDIITPSNTKI
GWIGTGVMGRSMCGHLIKAGYTVTVFNRTISKAQTLIDMGANVADSPNSVAEQSDVVFTI

VGYPSDVRHVLLDPKSGALSGLRQGGVLVDMTTSEPSLAEEIAKAASFKNCFSIDAPVSG
GDLGAKNGKLSIFAGGDETTVKRLDPLFSLMGKVNFMGTSGKGQFAKLANQITIASTMLG
LVEGLIYAHKAGLDVKKFLEAISTGAAGSKSIDLYGDRILKRDFDPGFYVNHFVKDLGIC
LNECQRMGLALPGLALAQQLYLSLKAHGEGDLGTQALLLALERLNNVSVQSSDS*

>p-IR15 (*Amycolatopsis thermoflava*, WP_027931120.1)
MGSSHHHHHHSSGLVPRGSHMTSATVIGLGPMGQAMVRVLLEHGTAVTVWNRTKSRADDV
VARGAVLAGTPAEALKAAGLVILSLTDYQAMYDVLGDAGEALAGRVVVNLSSDTPQRTRE
AAAWLAKRGATLVAGGIMVPAPLVGAEASYVFYSGPRDVFAEHEPVLRHIGRPEYLGEDH
GLAQLFYQAELTVFLTSLSAYLQAFALLAAEGADPARLVPFAREVSGLAASYLDETVSQT
RARAYPGDLSTATMMGATAEHILQACRDAGVDLALPEAVKSQYDRAIAAGHGGDNWTSLW
EVVAKR*

>p-IR16 (*Aspergillus udagawae*, A0A0K8L8S9_9EURO)
MGSSHHHHHHSSGLVPRGSHMSSVSIFGLGAMGKALASRFLAEKYKVAVWNRSPEKASPL
LEKGATLSHTAVDGINASDLIIICLLDNAAVQATLDSALDRLHGKTIVNLTNGTPDQARK
LSDLIVSHGAQYVHGGIMATPSMIGSPHALVLYSGSPDAFNAAEADLSVLANCVFLGEDA
GSASLHDLALLSGMYGLFSGFLHATALVKSSTPAVKFLDLLVPWLGAMTEYTKGMAKQID
EGQYASEGSNLAMQLVAVENIIDASAAQQVSADFIRPMKEFMEKAVAAGHGGDDISSLID
FVKST*

>p-IR17, BlIRED (*Burkholderia lata*, Q39NX6_BURL3) (*24*)
MGSSHHHHHHSSGLVPRGSHMANTVTAQAISVIGLGAMGAALAEALLAADHRVTVWNRTA
SKSAALGEVGAQVAHSAAEAIDASQVVVVCVLDYGASDSLLRTPDVAARLKGKTIIQLTT
GTPEDAREASEWAREHDVAYLDGTIGCYPKDIGTSDGSILYAGSRSTFEALRPTLANLSG
HALFVGERFGNAAILDGAVVGSFSLGAALGFLYGAAVCDAEGISLDTYLSLALARRPFVE
DTLQTCVQMIKKGNYSGSQATLDSWAAGIGQLVAYSQESGTDSSYPQEVLARLQQAVAKG
HGQHELAAVFECFRKPLANRG*

>p-IR18 (*Brassica rapa*, M4DQA1_BRARP)
MGSSHHHHHHSSGLVPRGSHMPLLLRRPLSPSVVSSFFLRRRSMSSKSDPISPSNTRIGW
IGTGVMGRSMCGHLIKAGYSVTVFNRTISKAQPLLAMGANLAASPNSLASQSDVVFSIVG
YPSDVRRVLLDPTSGALSGLSPGGVLVDMTTSEPSLAEEISKSASSAGCFSVDAPVSGGD
LGAKNGKLSIFAGGDEATVKRLDPLFRLMGKVNFMGASGKGQFAKLANQITIASTMVGLV
EGIVYAHKAGLDVRKFLEAISTGAAGSKSIDLYGERILKRDFDPGFYVDHFVKDLGICLN
ECQRMGLALPGLALAQQLYLSLKAHGEGGLGTQALILALERLNNVSVQPSVS*

>p-IR19 (*Burkholderia vietnamiensis*, A4JAJ9_BURVG)
MGSSHHHHHHSSGLVPRGSHMDLGFIGLGEMGQAIATNLLKAGHTVRVWNRSRERAEPLA
ALGAQIVATPADAFRGDAVFSMLADDAAARDVFDDALLAQAPRGLIHVNMATVSVALAES
LAHAHASRGLDYVAAPVMGRPDVAAAARLTIMAGGPAEAIDRVQPLFDAIGQKTWRFGSL
PQHANIAKIAANFTLASAIETLGEASALLGAHGVAMRDFLDVITSSVFPGPVYAGYGGMI
AERSYEPARFKARLGLKDVRLALQAGDAASVPLPVASVVRDSLLDALAHGGGDQDFAVLG
EVALRRAGR*

>p-IR20 (*Couchioplanes caeruleus*, A0A1K0GAQ1_9ACTN)
MGSSHHHHHHSSGLVPRGSHMAQNSVEKAPVTLLGLGAMGTALARTWLAGGHPLTVWNRT
PARAAALSPEGARVADSAAAAVAANTLVVVCLLDDASVEEVLAGTDLADKDLVNLTTSTP
AQARARAEWARERGARYLDGGIMAVPPMIGVPEIGGYVFYSGSRELFERHQQTLGVPAGT
TYVGQDAGFAALHDVALLSAMYGMFAGAAHAFALIRKEDIDPASLAPLLADWLVAMAPTV
HQTADQLRSGDYTKGVVSSLAMQVAGTPTFLDTAAQQGVSPELLSPYFTLMRRRLAEGSA
EEDLTGVIDLLVRK*

>p-IR21 (*Corchorus capsularis*, A0A1R3HV54_COCAP)
MGSSHHHHHHSSGLVPRGSHMETPYPTPISPTQTRIGWIGIGVMGAAMASHLLSAGYSVT
IYARNPSKAASLQSQGAHLANSPQQLARQCDVVFTMVGNPQDVRQTVLESDGILSGLKPG
AVIVDHTSSSPSLAREIYASARKKGCWSVDAPVSGGDIGAREGKLAIFAAGVCAVVEWLK

PLFDLMGRVTYMGEAGCGQSCKIGNQIMVGANLMGLSEGLVFAEKAGLDLKKYMEAIRGG
SAGSMAMELWGRRIIERDFKPGGFAEYMVKDMGMGVDVVKEEDDGKVMVLPGAALGKQMF
SAMVANGDGKLGTQGLITVVERINGK*

>p-IR22 (*Citrus clementina*, V4UJW6_9ROSI)
MGSSHHHHHHSSGLVPRGSHMPPLLPLLLVLRSRTAHSYSLSVSSLVTLLLRRRSMATVA
STDPVCPTNTRVGWIGTGVMGRSMCAHLLNAGYTVTVFNRTLSKAQPLLDIGAHLADSPH
SLASQSDVVFSIVGYPSDVRHVLLHPSSGALSGLRPGGIIVDMTTSEPSLASELSAAASS
KNCSAIDAPVSGGDRGAKTGTLAIFAGGDESVVQKLNPLFALMGKVNYMGGSGKGQFAKL
ANQITIASTMVGLVEGMVYAHKAGLNVELFLNAISTGAAGSKSLDLYGSRILKRDFEPGF
YVNHFVKDLGICLKECQNMGLALPGVALAQQLYLSLKAHGEGNLGTQALILALERLNNVR
LDNAVASKPSA*

>p-IR23, CfIRED (*Cystobacter ferrugineus*, A0A1L9AVJ5_9DELT) (*24*)
MGSSHHHHHHSSGLVPRGSHMKPGISVLGTGRMGSALVGAFLKQGYNVAVWNRTKSKCAP
LAALGARVATTVRDAVADAEVVVVNVNDYVTSEALLRQDDVTKGLRGKLIVQLTSGSPRQ
AREMAAWARQHELQYLDGAIMGTPNFIGEPGGTILYSGPGALFEKYKPVLLVLGGNSLHV
GSDVGHASALDSALLSFLWGSMFGVLQAVSVCEAEGLPLGAYMEYVQATKPMVDGAVTDF
VKRIQTGRFAGDEKTLATVEAHHGALRHLIELCEEHGIHHAVPAAFGQLFQAALQAGHAQ
DDFAVLNKFMK*

>p-IR24 (*Chelatococcus sambhunathii*, A0A0K6H4A1_9RHIZ)
MGSSHHHHHHSSGLVPRGSHMTKTCVVGAGRMGSAFARALLAEGIETRVWNRSPEKVAPL
VAAGAHAPESLAEAVAASDVVIVNVIDYAAADALLRMLAVERALAGKVVVQLTSGSPRQA
REAGRWAAERDIAYLDGAIMATPNFIGGAETTILYSGMRQAFERHRDVLRVFGGNGVFVG
EDAGHASALDTGLLTQMWGKLFGTLQALAVVRAEGFGLEAYARYMRDFQLVVDAATDDLI
ARVGEGRWRGDAATLATIEAHYSAFHHLLAIGDEHGLDRALPAALDGLFKAALAAGHAAD
DFAALMRFIERGGVRHAA*

>p-IR25 (*Citrus sinensis*, A0A067FGQ9_CITSI)
MGSSHHHHHHSSGLVPRGSHMPPLLPLLLVLRSRTAHSYSLSVSSLVTLLLRRRSMATVA
STDPVCPTNTRIGWIGTGVMGRSMCAHLLNAGYTVTVFNRTLSKAQPLLDIGAHLADSPH
SLASQSDVVFSIVGYPSDVRHVLLHPSSGALSGLRPGGIIVDMTTSEPSLASELSAAASS
KNCSAIDAPVSGGDRGAKTGTLAIFAGGDESVVQKLNPLFALMGKVNYMGGSGKGQFAKL
ANQITIATTMVGLVEGMVYAHKAGLNVELFLNAISTGAAGSKSLDLHGSRILKRDFEPGF
FVNHFVKDLGICLKECQNMGLALPGLALAQQLYLSLKAHGEGNLGTQALILALERLNNVR
LDNAVASKPSA*

>p-IR26 (*Cucumis sativus*, A0A0A0LIQ8_CUCSA)
MGSSHHHHHHSSGLVPRGSHMPIQFSLRSLYTQSHKLTPTLSLPFLSFLRRTMSTSGDIV
SPSTTRVGWIGTGVMGCSMCSHIIKAGYKLTVFNRTISKAQPLLDLGANLATSPLAVAAQ
SDVVFSIVGYPSDVRSVLLDPSSGALAGLRPGGVLIDMTTSEPSLASEIAASATAKGCGA
IDAPVSGGDRGAKNATLAIFAGGDEDEVQRLSPLFSLLGKVNYMGESGKGQFAKLANQIT
IASTMVGLVEGMIYAKKAGLDVGLFLNAISTGAAGSKSLDLYGSRILKRDFEPGFFVNHF
VKDLGICLKECQNMGLALPGLALAQQLYVSLKAYGEGNLGTQALILSLERLNNVSLEGSG
SS*

>p-IR27 (*Daucus carota*, A0A161WTE2_DAUCA)
MGSSHHHHHHSSGLVPRGSHMSSITTAEPRSPSNTRLGWIGTGVMGLSMCSHLLKAGYTL
TVFTRTQSKAQPLLDLGAKWAASPSSVASQSDVVFSIVGYPSDVRHVTLHPNSGALSGLN
PGGILVDMTTSDPSLAVEIADAAAAKGCFSVDAPVSGGDRGARNGSLSIFAGGDKKVIDT
LSPLFNLLGKVNYMGVSGKGQFAKLGNQITIASTMVGLIEGMMFAHKAGLDLSLFINAIS
TGAAGSKSLELYGYRILKRDFEAGFFVNHFVKDLGICLRECQNMGIALPGLALAQQLYVS
LQAHGEGDLGTQALVLALERLNNVSLQSVASSTEMA*
>p-IR28 (*Devosia geojensis*, A0A0F5FDU7_9RHIZ)
MGSSHHHHHHSSGLVPRGSHMTTISILGLGAMGTALANALLDAGHAVTVWNRTPGKDEAL
VSRGARRAQTPAEAIAASELVVICLVDYAGVETMLASAEKELSGRVVANLTTGTPKQARA
LAAWVEAQGAAYVDGGIMAVPPMIGTPASFIFYSGNQPAFERHKAALEAFGDAVYVGPDA
GAAPLNDIALLGILDGILSGYLHAAALIRASGGTAEGFTPLARRWAESMISLFPDLAKQI

DSGDYRAEGGSNLAMQAAAMDQMVEAARDEGVDPVLIEPMRALIHQRVADGFGTDDSAGV
IELLFLNGRGKR*

>p-IR29 (*Draconibacterium orientale*, X5E3Y1_9BACT)
MGSSHHHHHHSSGLVPRGSHMKKDITIGWIGTGVMGTSMLGHLNKAGYECITYTRTKSKA
ESLLANGVKWADSPAEVAAVSDVIFTIVGFPKDVREVYFGEKGILAKAKPGAVLVDMTTT
EPSLAVEIYEAAKVKGIQSVDAPVSGGDVGAKNGTLSIMAGGEKEAFDKVYPLFESMGKQ
IVYQGAAGSGQHTKMCNQITIAGTMIGVCEALLYGHKAGLDLPTMLSSISGGAAGCWTLD
NLAPRIVNRNFDPGFFVEHFIKDMGIALKEAEAMGLSLPGLALVKQLYLAVQAQGHGKLG
THALTLALEKLSGL*

>p-IR30 (*Desulfosporosinus orientis*, G7W7U0_DESOD)
MGSSHHHHHHSSGLVPRGSHMKVGFIGIGAMGKPMAQNILRAGYSLYVNDVNEAALQELV
AEGAKKAENPRELAREVDVVITMLPNGAVVEQVLLGEQGIFAGAKPGFTVIDMSSVGPTF
TQKMAKLASDRQVGYMDAPVSGGVKGAEAGTLTIMVGGEKELVQRYHSLLEVMGKKIYHV
GKTGAGDAVKIVNNLLLGINMAAAAEAFVLGTKLGLDPQVLLEIISVSSGSSYALTAKMP
NFIFKGQFEAGFAIDLQYKDLELAVQTAKEAKIPMLLTNVAQQVFEQARAAGLGRDDISA
VIKPLEDLMKIKVRA*

>p-IR31 (*Eucalyptus grandis*, A0A059CN57_EUCGR)
MGSSHHHHHHSSGLVPRGSHMPMPSSLPLTGLLRSASPPSSSALYLLLRRAMSSAAAASD
PIAPSNTRVGWIGTGVMGRSMCGHLIGAGFAVTVFNRTVSKAQPLLDMGARLADSPRSLA
ALSDVVFSIVGYPSDVRSVLLDPSSGALASLRPGGVLVDMTTSDPSLAEEISAAASAKGC
HAVDAPVSGGDRGARNAALAIFAGGDPATVRRLEPLFSVMGKVNYMGGPGKGQFAKLGNQ
ITIASTMVGLVEGMVYAYKAGLDVGMFVSAISTGAAGSKSLDLYGNRILQRDFEAGFYVN
HFVKDLGICLKECERMGLALPGLALAQQLYLSLKAHGEGNLGTQALILALERLNNVKLEN
AGSSNV*

>p-IR32 (*Emmonsia parva*, A0A0H1B7G6_9EURO)
MGSSHHHHHHSSGLVPRGSHMANSPVTVFGLGAMGTALATQFLQKGHKTTVRNRTAAKAQP
LIAIGASHAPTIASAAAASSILIICQLDKTSVMQTLQQAPTAWATKTIVDLTNGTPAHARE
TADWALAHGAQYIHGGIMAVPSMIGQPHAMILYSGPAEVGMYGLFSGFTHAVALVQSANVP
AAGFVATQLIPWLTAMTQHLNLLATQVDEKDYGDGGSSLDMQAKAAPNILEASAAQGVSVE
LIQPIFKLIERRVEEGGGSEGLAALVGMIMKAGTKDSV*

>p-IR33 (*Emmonsia pasteuriana*, A0A1J9QMV6_9EURO)
MGSSHHHHHHSSGLVPRGSHMENSPVTVFGLGAMGTALATQFLRKHHRTTVWNRTAAKAKS
LIASGASHAPTISSAASASSLLIICQSNKDSVLQTLQQEPAAWAGKTIVDLTNGTPAHARE
TAEWALAHGAQYIHGGIMAVPSMIGQPHAVILYSGPGKVFEEVKETLDAVGSSTYVGEDVG
LASLHDLALLSGMYGLFSGFTHAVAMVRSARVPAAGFVATQLIPWLTAMTQHLNMLAKQVD
DEDFGDGGSSLEMQAHAVPNVLEASEAQGVSVELIRPIFMLIEKRVGEGGGKEGLSALVHM
IMKGA*

>p-IR34 (*Eutrema salsugineu*, V4KLI0_EUTSA)
MGSSHHHHHHSSGLVPRGSHMASKSISSVPINPSNTRIGWIGTGVMGRSMCGHLIRAGYSV
TVFNRTVSKAQTLIDMGAKLADSPNSLAAQSDVVFSIVGYPSDVRHVLLDPISGALSGLNP
GGVLVDMTTSEPSLAEEISKAASSANCFSIDAPVSGGDLGAKNGKLAIFAGGDETTVKRLD
PLFSLMGKVNFMGTSGKGQFAKLANQITIASTMLGLVEGMIYAHKSGLDVKKFLKAISTGA
AGSKSIDLYGDRILKRDFDPGFYVNHFVKDLGICLKECQRMGLALPGLAIAQQLYLSLKAH
GEGDLGTQALILSLERLNNVSVQPIM*

>p-IR35 (*Exophiala aquamarina*, A0A072NZT1_9EURO)
MGSSHHHHHHSSGLVPRGSHMTSATSGITLVGLGNMGAALAHAFLKSGCLLTVWNRTSTR
PTVVEAIKAGASFEPDLAKAISANSTIVFCVLEYKNIYQGLEPLVTSGVLKGKTMVNLTN
GTPRDARDADKWFKDHGVASYFDGGIMVTPQNVGTPVSVVLISGEDESLLESRGVKDLIG
AIGAPDYKGEDPGVAAGYDLALLAGMIGMFIGSLTALAMIQKQLDRAKSTAGANGAKETA
TTGGLTEVVTTYFNPLLTALIPHNELLATAIDNNDQDNNHGNPMEMMRVAMHNIIRGCEE

EGVDAENLRHFAGLADQVVHLHGPDSGLAWVHSLLLK*

>p-IR36 (*Fonsecaea multimorphosa*, A0A178C791_9EURO)
MGSSHHHHHHSSGLVPRGSHMAISSASQQAAEREVERSVSVLGLGQMGFAVAQAFTKKGY
KTTVWNRTAAKARPLVAAGAIVATSVGDCIASNQLVLSCFIETQVLIEVLKTVDPQLCRG
RVLVDFASGTLRETRQFQTIARELSFAYIRGSIASTPPYVGSSQIHAWYCGNETIFRSIQ
PDLAALAQPGYIDNDPGTIALHECAGGNIFYAFAAGFVQAMAVVKASGKCHPGGAEDFVN
KFMIPFLHTFPDTFRDWAHQIDNQNYDAHGKGARLGQSAKSINLMRRFNTELGLTSVILD
PVLSLIKHRIAQGGSNEELSSLVETIADSKAGI*

>p-IR37 (*Fusarium oxysporum*, W9Z6K1_FUSOX)
MGSSHHHHHHSSGLVPRGSHMTTSQSLTFLGLGNMGSALVQALLKASHKVTIWNRTTARP
QVRAAVEAGAILEADVQTVISRNNIIVICLLDYSSINNVLDDIPTPAFKGKTIVNLTNGT
PKQAREMANWATSHSAKQYFDGAVMVTPQMIGGPQSFFVVSGETPEAFKPIASFLEPLGR
PEYLGTAIDAAARYDLAALSSMYGMFSGMFVAMALLKKGHAIADEKLEPVVSGSLNPFLG
ALISYNGLIARSWDDKAWDDNLGNPIGMQAQALGNILEACRDDGMDDGFLKNLTTAMERV
VKDRGENGGIAVIGEYLLNGRLSNE*

>p-IR38 (*Gossypium hisutum*, A0A1U8PU55_GOSHI)
MGSSHHHHHHSSGLVPRGSHMRSLSYLLGSLSRYFPHSQSSSTPHLTFLLRSMATSAAAG
PINPSNTRLGWIGTGVMGRSMCAHLINAGYSLTVFNRTLSKAQPLVDMGARLAQTPHDLA
AQSDVVFSIVGYPSDVLQVLLDPVNGALSGLRPGGILVDMTTSEPSLAVEISTAASSKNC
SSIDAPVSGGDRGAKNGTLAIFAGGDEAIVNRLNPIFTLMGKVNYMGPSGKGQFAKLANQ
ITIASTMVGLVEGIIYAHKAGLNVASFLDAISTGAAGSKSLDLYGSRILKRDFDPGFFVN
HFVKDLGICLKECQNMGLALPGLALAQQLYLSLKAHGEGNLGTQALILALERLNNATLGS
*

>p-IR39 (*Granulicella mallensis*, G8P071_GRAMM)
MGSSHHHHHHSSGLVPRGSHMRVAFLGLGKMGSALVPHLLNAGCEVTVWNRSSPAAKELA
SKGATVALSAAEAVNSCEVVFSLLLNDAALEEVLFDGGVLDAMPKDAVHVSVGTISVALA
KRLTLEHAKRGHRYVGAPVFGRPNVAAEGKLWTVVGGAKEAVQSVRSLLESYTRGMTVVS
EEPWSAHAMKLAGNFSVAAMVATLSEAMMVAESMGVSPELFVEMANSATFRSPLYEVYGK
TLTNPPKEVGASMELGEKDVRLFREAAAANGVKTPLAELMGKNFDAAIEAGMKDHDWATG
YYELVRKRQVEEPVAL*

>p-IR40 (*Homo sapiens*, GLYR1_HUMAN)
MGSSHHHHHHSSGLVPRGSHMAAVSLRLGDLVWGKLGRYPPWPGKIVNPPKDLKKPRGKK
CFFVKFFGTEDHAWIKVEQLKPYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTS
SHNSSDDKNRRNSSEERSRPNSGDEKRKLSLSEGKVKKNMGEGKKRVSSGSSERGSKSPL
KRAQEQSPRKRGRPPKDEKDLTIPESSTVKGMMAGPMAAFKWQPTASEPVKDADPHFHHF
LLSQTEKPAVCYQAITKKLKICEEETGSTSIQAADSTAVNGSITPTDKKIGFLGLGLMGS
GIVSNLLKMGHTVTVWNRTAEKCDLFIQEGARLGRTPAEVVSTCDITFACVSDPKAAKDL
VLGPSGVLQGIRPGKCYVDMSTVDADTVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLV
ILAAGDRGLYEDCSSCFQAMGKTSFFLGEVGNAAKMMLIVNMVQGSFMATIAEGLTLAQV
TGQSQQTLLDILNQGQLASIFLDQKCQNILQGNFKPDFYLKYIQKDLRLAIALGDAVNHP
TPMAAAANEVYKRAKALDQSDNDMSAVYRAYIH*

>p-IR41 (*Isosphaera pallida*, E8QYX7_ISOPI)
MGSSHHHHHHSSGLVPRGSHMTSSPSLPTVAPGRTRVGWIGTGVMGRWMCGHLMNAGYAA
TVYNRTQSKARELIDRGATLATNPREVAEASDVIFTIVGFPSDVRQVILGSDGVLAGAKP
GAIVVDMTTSEPELAREIHRVAAARGVHAIDAPVSGGDLGAREARLSIMVGGDPEPVAAV
QPLFQIMGKTIVHQGPPGAGQHTKMVNQILIAGNMVGVCEALLYGYKAGLDLTTVLQSVS
GGAAGSWSLSNLAPRILKGDMTPGFYVEHFIKDMGIALAEARRMKLALPGLALVEQLYQA
LAAQGHARDGTQALTHALARLSGFEWKAVVTTTQGQS*

>p-IR42 (*Jiangella alkaliphila*, A0A1H2IPN0_9ACTN)
MGSSHHHHHHSSGLVPRGSHMTDHHPVTVIGLGAMGREIARVLLEAGHPTTVWNRNLERA
VDLVSQGATRADTVVAAVGASPLVLVCVLDYAATRELLEPIAADLAGRTVVQLTTGTPKQ
ARELAEWAAGHGIDYVDSGMMATPPMIGRPGSTFLYSGDEAAFERYRPALDLLGTSRWFG
ADAGLASLYDLALLSGMYTMFAGFLHGAAMVGTAGVSAADFAESAGDWLRAMTVSLPYAA
TFVDSGDYTTDVQDVEFNKSALDVIVQASIDQGVAPDLVAPIHELLARQLAEGHGKEAFD
RIIESIRPAVTRPA*

>p-IR43 (*Jatropha curcas*, A0A067KFP5_JATCU)
MGSSHHHHHHSSGLVPRGSHMILSLLRSRSHDFNTSRIHFTLPLSLFFRRSMATTTESAS
PSNTRVGWIGTGVMGRSMCAHLIKAGYSLTVFTRTLSKAQPLVDMGANLAQSPLAVASQS
DVVFSIVGFPSDVRQVLLDSTTGALQGLRPGGILVDMTTSDPSLASEISAAASAKNCHSI
DAPVSGGDRGAKNGTLAIFAGGDEAVIDRLNPLFALMGKLNYMGAPGKGQFAKLANQITI
ACTMVGLVEGIIYAYKAGLNVEHYLNAISTGAAGSKSLESYGARILKRDFEAGFYVNHFV
KDLGICLKECQNMGLALPGLALAQQLYLSLKAHGEGNLGTQALILALERLNNVSLENLAS
LQPAA*

>p-IR44 (*Kitasatospora cheerisanensis* KCTC 2395, A0A066Z502_9ACTN)
MGSSHHHHHHSSGLVPRGSHMSRLPSAVSEYSTRGGTSSYETRCTMPSDSNSRRCEASTF
SVTPGSSRRSSPNRRHGCSCSAHRISTFHLPPITSIAASIPQTCPSGVPGLFSVAMPPPL
RPAGSPRGKHPPESAYLITTGPWTSLIGMAHTTVDPTAKTPVTLLGLGAMGTALARTWLA
AGHPVTVWNRTPSRATALAADGASVAATAAEAVAANTLVVVCLLDDASIDQALAGTDLTG
RDLVNLTTSTPEQARARAAWAHERGARYLDGGIMAVPPMIGVPQAGGYVFYSGSRELFDR
HRPTLAVPVDTRWVGEDPGHAALHDVALLSAMYGMFAGAAHAFALIRKEDIDPTALAPLL
ADWLTAMAPAVHQTADQLRTGDYTTNVVSNLAMQVAGTPTFLATAEQQGVSPELLTPYFD
LMRRRLAEGNGNEDLTGVVDLLLR*

>p-IR45 (*Kibdelosporangium phytohabitans*, A0A0N9HVM7_9PSEU)
MGSSHHHHHHSSGLVPRGSHMPDLSKPAVTVLGLGDMGSALARALLKAGYPTTVWNRTPE
KAKPLVEAGATHAPTVADAVTASRLVIVCLLDYKSVTDVLDTARDALTGKVLVNLTNGTP
GQARELATRYDVDYLDGGIMAIPPMIGAPPAFVFYSGSRSAFDTNKQVFEAFGGTNYVST
DAGFAALYDIGLLSGMYGMFVGALHALSLVTSAGVPAQEFAPLLKQYVSAMLGSIDGMAE
QIDKQDYAIDVVSNIGMQSEAYVNLTLSAEELGMSPELLAPLGPLMARRVADGHGHEDIA
GVVEILKKGKK*

>p-IR46 (*Lupinus angustifolius*, A0A1J7FZG6_LUPAN)
MGSSHHHHHHSSGLVPRGSHMASSTAAEPISPSNTRLGWIGTGVMGQSMCAHLIRAGYTL
TVFNRTPSKAQPLLDLGAHQAHSPQALASQSDVVFSIVGYPSDVRSVLLDPTSGVLSGLL
PGGILVDMTTSEPSLAVEIAAAAAEKNCHSVDAPVSGGDRGAKNGTLAIFAGGDKDTVHR
LEPLFSLLGKVNYMGGSGKGQFAKLANQITIASTMVGLVEGMVYAHKAGLDVGLWLDAIS
TGAAGSKSLDLYGQRILKRDLDPGFYVNHFVKDLGICLKECQNMGIALPGLALAQQLYVS
LKAHGEGNLGTQALILVLERLNNVSLAPAASSS*

>p-IR47 (*Microdochium bolleyi*, A0A136IJF0_9PEZI)
MGSSHHHHHHSSGLVPRGSHMRPCVGNMGTAAIQALRKASHSVTIWNRTKSRPQVQAAID
AGATFEPDLAQALSRSGVIVLCLLDYATITKIFSSIGEPGAVLKGKSVINLTNGTPKEAR
EMETYFTSLGTIVYLDGAIMVTPQMVGGPHAFLFLSGGQGSTETPDGATSRLVELVSPIG
KPDYLGADVGAASRYDLASLAPMYGMFAGGFLGMALLKRGKPNAKLVPVVQEKIVPMIAA
LVPYMTGIARAWDAEDWVENDGNPVGMMAVGVQNILAAAADEGVDGTVLEEFGGLMEKVE
RDHGYDAGIAAVGTYLMK*
>p-IR48, IR70 (*Microvirga lupini*, WP_051455530.1) (*8*)
MGSSHHHHHHSSGLVPRGSHMKSKVCVLGAGRMGSSIARCLVSHGYQTWVWNRTAAKCEP
LAALGATVALSVEDGIRAADVVIINVLDYAASSASLRQDSVISGLAGKTVVQLTSGSPRL
AREEALWVESHGASYLDGAIMATPDFLGRPEATLLYSGPREVFEVHKGLLSTLGGGTSYV
GENPGQASALDTALLTQMWGGLFGALQGMAVVEGENLNLETFRHQLTAFKPVVDAALFDL
IDRTIARRFAGDETTLASLGAHYSAFQHLLEACEEQGLDASLPNAMDRFFRQALSLGGPE
SDFASLAPLFRANHTVAPFAELANA*

>p-IR49, IR-22 (*Mycobacterium mageritense*, X5L9E3_9MYCO) (*9*)

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MGSSHHHHHHSSGLVPRGSHMKSKVCVLGAGRMGSSIARCLVSHGYQTWVWNRTAAKCEP
LAALGATVALSVEDGIRAADVVIINVLDYAASSASLRQDSVISGLAGKTVVQLTSGSPRL
AREEALWVESHGASYLDGAIMATPDFLGRPEATLLYSGPREVFEVHKGLLSTLGGGTSYV
GENPGQASALDTALLTQMWGGLFGALQGMAVVEGENLNLETFRHQLTAFKPVVDAALFDL
IDRTIARRFAGDETTLASLGAHYSAFQHLLEACEEQGLDASLPNAMDRFFRQALSLGGPE
SDFASLAPLFRANHTVAPFAELANA*
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>p-IR50 (*Madurella mycetomatis*, A0A175WBH2_9PEZI)

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MGSSHHHHHHSSGLVPRGSHMATITSIGIGNMGAALATALLKSSSPPMNVTIWNRTASRP
QVQSLISAGAIFEPSLAAALASSEVILLCLLDYPAISSVFSQVDASAKPLAGKTILNLTN
GTPKQARDMEAFFKSLGAAVYFDGGVMVTPQLVGTPAAFVVLSGETEQAYNERLANAGLL
SPVGAVLYIAPDPGAASLVDCAALAAMYGMFIGAFTGIGLLKRQKHERDGEAAGAKAMVD
KVMVPVLTALVPYVGLLAEQVDKEAWMDDLGNPLAMQAEGVRNIMQSCEDEGVDGTGLKF
LSKLMEKGVKEGFGPGGVAVVAKYLMK*
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>p-IR51 (*Morus notabilis*, W9T391_9ROSA)

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MGSSHHHHHHSSGLVPRGSHMPLSLPLRSLSSHHSSFNISSLSLRLLTHLHRSMATAAAA
EPTICPSNTRVGWIGTGVMGRSMCAHLINAGYTLTVFNRTLSKAQPLLDMGAHLAHSPLA
VASQSDVVFSIVGFPSDVRSVLLDPSSGTLAGLRPGGVLVDMTTSEPSLAAEISSAAASK
GCSSIDAPVSGGDRGAKNGTLAIFAGGEESVIHRLNPLFSLLGKVNYMGGPGRGQFAKLA
NQITIASTMVGLVEGMIYAHKAGLDVAMFLDAISTGAAGSKSLDLYGARILKRDFEPGFF
VNHFVKDLGICLKECQNLGLGLPGLALAQQLYLSLKAHGEGNLGTQALILALERLNNVSL
ESGGCSSSPAPAN*
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>p-IR52 (*Marchantia polymorpha*, A0A176VNX2_MARPO)

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MGSSHHHHHHSSGLVPRGSHMMGGTPACPTAQLVLRVFNHGRDNGHLSQSSLITLYQVAQ
SPTAPLLACTPIPAIVDSRCVGLNFCTVSMAQSEAVKEIVSDQTRVGWIGTGVMGQAMCG
HILAAGFQVSVYNRTASKAQDLCSKGATMADSPLSVAQQSDVVFTIVGYPSDVREVMLGE
KGILKGLRPGGIVVDMTTSQPSLARELSLAAKERSCESIDAPVSGGDKGAKSGTLAIMVG
GEKNTFELLAPLFKCMGNATYMGPAGSGQSCKLANQVTIASTMIGLVEGMIYAQKAGLNV
DTFLQAISGGAAGSKSLELYSGRIRNRDFDPGFYVNHFVKDLGIALEECRNMDLALPGLA
LAQQLYVSLKAHGEGALGTQALILALERLNNIKQ*
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>p-IR53 (*Minicystis rosea*, A0A1L6L1L9_9DELT)

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MGSSHHHHHHSSGLVPRGSHMGAALARAYINAGHRVTVWNRSPSKAEPFQGQAKVAETAA
QACSESDLTIVSVSNYQASDEVLRTPLAEQAAKGRTIVQLTSGTPGDARSGAAWAQEHGI
EYLDGCILAYPSYIGGEQTTIFYSGPKALYDRHEATLRVIGGGTSHVGEPIGAAATLDCA
LLESYYGATLAFLHGAAICRSEKFPLDAYFAGVQAIMPLISITADMCKRMLATGDFKGTD
CTLDIHAGAIQHIVRLSRENNVDRRIPELILSYFDRALKLGHGSDEMAAVINAIQEPPRG
*
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>p-IR54 (*Medicago truncatula*, G7L7F1_MEDTR)

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MGSSHHHHHHSSGLVPRGSHMPLPFLRFRSLYRHSHTHLLTRHFMATSEPITPSNTRLGW
IGTGVMGQSMCAHLIRSGYTLTVFNRTPSKAQPLLDIGATLATSPHAVASQSDVVFSIVG
YPSDVRSVLLDPNTGALAGLKSGGILVDMTTSDPSLAVEIADAASVKSCHSIDAPVSGGD
RGAKNGTLAIFAGGDESIVKKLSPLFSSLGKVNYMGTSGKGQFVKLANQITIASTMVGLV
EGMVYAHKAGLDVGLYLDAISTGAAGSKSLELYGKRILKRDFEAGFYVNHFVKDLGICLK
ECEKMGIALPGLALAQQLYVSLKAHGEGNLGTQALILVLERLNNVSLPPSVI*
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>p-IR55, MtuIRED (*Micromonospora tulbaghiae*, A0A1C4WQ45_9ACTN) (*24*)

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MGSSHHHHHHSSGLVPRGSHMAPNTVDKTPVTLLGLGAMGTALARTWIAAGHPLTVWNRT
PARAAAISDEGAGLADSAAAAVAANTLVVVCLLDDDSVGEVLAGTDLTGKDLVNLTTGTP
AEARSRAEWARERGARYLDGGIMAVPPMIGLPEAGGYVFYSGSRELFERHRETLGVPAGT
TYVGRDAGFAALHDVALLSAMYGMFAGAAHAFALIRKEDIDPASLAPLLADWLVTMAPAV
HQTADQLRGGDYTKGVVSSLAMQVAGTPTFLSTAEQQGVSPELLSPYFELMRRRLAQGGG
EEDLTGVIDLLVRGPDHVRTSARTARTSWR*
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>p-IR56 (*Nicotiana attenuata*, A0A1J6KVX5_NICAT)

MGSSHHHHHHSSGLVPRGSHMRFMRLLRLLPNHQFHCYVPQAIFTTSAGTTTHLHHTMET
ATTEAINPSNTRLGWIGTGVMGRSMCAHLINAGYTLTVFTRTPSKAQELISMGAHWVDSP
KAVASQSDVVFSIVGYPSDVRHVILDSNSGALSGLRPGGVIIDMTTSEPSLAVEIYSAAS
AAGCSAVDAPVSGGDLGARNAALSIFAGGDESIILRLNPLFNLLGRVYYMGAPGKGQFTK
LGNQVVIASTMVGLCEGLIYAHKAGLDLNMFLNAISTGAAGSKSLDLYGSRILSRDFEPG
FYVNHFVKDLGICLRECQNMGLALPGLALAQQLYLSLKAHGEGNFGTQALILALERINNL
SLASSSSVGKP*

>p-IR57 (*Noccaea caerulescens*, A0A1J3E499_NOCCA)
MGSSHHHHHHSSGLVPRGSHMPLLLRRSFSPSVVSSFFRRFSMASKSISSDPINPSNTRI
GWIGTGVMGRSMCGHLIRAGYSVTVFNRTISKAQTLVDMGAKLAESPSSLAAQSDVVFSI
VGYPSDVRHVLLDPNSGALSGLNPGGVLVDMTTSEPSLAEEISEAASSGNCFSIDAPVSG
GDLGAKNGKLAIFAGGDETTVKRLDPLFSLMGKVNFMGTSGKGQFAKLANQITIASTMLG
LVEGIIYAHKAGLDVRKFLEAISTGAAGSKSIDLYGDRILKRDFDPGFYVNHFVKDLGIC
LKECERMGLALPGLALAQQLYLSLKAHGEGDLGTQALILALERLNNVSVS*

>p-IR58 (*Nectria haematococca*, C7Z324_NECH7)
MGSSHHHHHHSSGLVPRGSHMATPQALTFLGLGNMGSALVQTLLKASHRVTIWNRTVDRP
QVKAAVEAGAILEVDVQTAISRNNIIVICLLDYSSIKTALAGISASALDGKTIVNLTNGT
PKQAREMAAWTASHSAKHYFDGAVMVTPQMIGGPQSFFVVSGQTSEAFKPIASLLEPIGR
PEYLGTAIDAAARYDLAALSSMFGMFSGMFVAMALLKKGHTKTDEKLEPVVSGSLNPFLG
ALIPYNGLLARSWDDKAWDDNLGNPIGMQVQALRNILEACRDDGMDDGFLKNLTTVMEGV
VKDRGENGGIAVIGEYLLNGRLTKE*

>p-IR59 (*Pseudomonas aeruginosa*, Q9I1R8_PSEAE)
MGSSHHHHHHSSGLVPRGSHMREHNDESFEFEVSVIGLGAMGTIMAQALLGQGRRVAIWN
RSPGKAAALVAAGAHLCESAEAALAASPATIFVLLDNQATHEVLGMPGVMQALANRTIVD
YTTNARDEGLALQSLVNRAGGHYVKGMIVAYPRNVGRRESHSIHTGDPEAFERHRALLEG
LAGHTTFLPWDEALAFATVLHAHAFAAMVAFFEAVGAGVHFGLPPSKTARLMLDTSRFFV
ADALEEAVRRLEAQDFAGDQARLDVHAQAFAHIAGALHAQGAWTPVFDALCQAVQRAAAM
GYGDQDIVAVTRLFARECDTASAAGQ*

>p-IR60 (*Pseudomonas aeruginosa*, A0A1F0IHK4_9PSED)
MGSSHHHHHHSSGLVPRGSHMSASLPSLAFAGLGLMGVPMCRRLLAAGYPLAVWNRSPGK
RELLAAEGAKAVEVPAELAADAEILMLCLADTAAVREVVFGAGGIVENARPGQLLVDFSS
AEPAATREMAAELEARCGVRWVDAPVSGGTPGAESGSLAIMAGGRAADIERLRPVLSRLG
QRLTRMGEVGAGQVTKVCNQMIVACNALVIAEVVALAERAGVDASLVAPALAGGFADSKP
LQILAPQMAESRYEPVKWHVRTLLKDLDTAVKLSREQGAATPMSGLAAQLMRLHGSQGYL
ERDPATLVEQYRTAVE*

>p-IR61 (*Penicillium arizonense*, A0A1F5L0A3_9EURO)
MGSSHHHHHHSSGLVPRGSHMSSVSILGLGAMGTALAARFLEKKYKVAVWNRSPEKASPL
LDKGANIAQTAVDGINASDLIIICLLDNAAVQTTLAGALDQLQGKTIVNLTNGTPDQARK
MSDLIVGHGARYVHGGIMATPSMIGSPHALVLYSGSQQAFKASEPDMLMLAKCVFVSEDA
GAASLHDLALLSGMYGLFSGFLHATALVRSSTPAVKFMDLLVPWLGAMTEYTKRMAKQID
EGNYASEGSNIAMQLVAIQNIIDTSAAQKVSADFIRPMKQFMEKAVAAGHSGDDISALIY
FAKPS*

>p-IR62 (*Pochonia chlamydosporia*, A0A179G8F8_METCM)
MGSSHHHHHHSSGLVPRGSHMSSEQTVSVLGLGLMGSALAKALVQNGWKTTVWNRSPEKA
QPLVELGASASTTAADCVRASRVIITCVMDPAALQGILKTLTQEDCKGRILVDYTSGVPS
EMRKCEDQALALSLKYFHGAILTMPSLIGMSTSTLLHSGADEITFESINPVLKAFGQSIY
LGQDASWATLQEGILGCCFYGFAGGFVQAMALLKSSSFYVPGGAQTLMSQGILPLLTEQF
PHIFADLARQIDEQAYDSEGNGIRLDTLKSSLEQLIRVNSEQGLVSNAFDPMLSLLKARI
AQGGAAEEMSGLVEAISNPPKQT*

>p-IR63, PcIRED (*Penicillium camemberti*, A0A0G4PFF8_PENCA) (*24*)
MGSSHHHHHHSSGLVPRGSHMSTSEPKSISILGLGQMGHAIASNFVSQGFKTFVWNRTPS

KAADLVEQGAIQSPSSTECIRSSPLSILCVNTDDIVMDILAAAGDIPGHTIVNIVNGSPQ
QVRKTAEKSISQYMAAGYLHGSVMASPGLVRSGGAMTIFAGSSETFKKWELTLQPLGVTL
WLLDDVGAAPLYDCSLLSILSGIFSGFMQALAMIGAAGHSETEFARGFVVPLLGQMEEWL
VRTAEEVQNKDYVAEKNGSPIAVQLDSTKHIFETAKELGVSSRLLQGFLDVVKEGVQRGQ
GREEISGLVRLLREPK*

>p-IR64 (*Pseudogymnoascus* sp. VKM F-4516, A0A094D824_9PEZI)
MGSSHHHHHHSSGLVPRGSHMTTTTEISIIGLGNMGTALAHTFLKANKTLTIWNRTPTAP
SITALISAGATFVPSLPTALSASPLIILCILDYPAIDSLFATLPPGILKDKIIINLTNGT
PRQARHLATWMQDNGVANYLDGGIMATPDMIGTPASSLFISGADEPAFASVKEEIAILGA
PRYMGTDPGAAALYDLALLAGMYGMFAGSLTAMALMRRLGGEETLEARVEGLLNPWMAAL
IPYQAAMAGSVDRGSFEALGNPVGMQREALKNILRACEEEGVDGGCLGYFEGLVGRVVED
KGGDGGLAGVEGLLGSKE*

>p-IR65 (*Purpureocillium lilacinum*, A0A179GW01_9HYPO)
MGSSHHHHHHSSGLVPRGSHMTTNTSLSGQDVSVIGLGNMGVAIANCLLRAGATVTVWNR
TASKAEQLIAQGALLALSPSACISASPITIICLLSNATAEQALSDVQDLSRRTIINLTNG
SPGQARQMATLLQSQKGARYIHGAIMVPPLLLGQPTSVTLCSGPSDVFHACTSVLSALGT
PRHVGEDISQASLLDNALLSLMGGIFEGWVQALAIVQRGGVDEVEFATGLAGPFVKAMAD
WLPRIAESVRDEQYVGGSPLRMQLEALDNIAVTGEELGVGVLLGELRGVMERAVTLGKGE
EGIAGLVPLLTGKK*

>p-IR66 (*Picea sitchensis*, A9NZ37_PICSI)
MGSSHHHHHHSSGLVPRGSHMAAEKPRVGWIGTGVMGQAMCGHILSAGYSVTVFNRTLSK
AQTLCDRGAIMVDSPKSVAAESDIVFTIVGYPQDVREVIIGENGVLQGLKPGGTVVDMTT
SEPSLAREIIDYAKQRGCESVDAPVSGGDKGAKAGALAIFAGGEETVVEGLKPLFDCMGK
VTYMGGPGLGQCTKLGNQITIASTMVGLVEGMVYAHKAGLDVEMYIKAISAGAAGSRSLD
LYADRILRRDFDPGFFVNHFVKDLGISLRECQQMGLSLPGLALAQQLYVSLKAHGEGNLG
TQALVLALERLNNVQLPKIG*

>p-IR67, PtyIRED (*Paenibacillus tyrfis*, A0A081P2I1_9BACL) (*24*)
MGSSHHHHHHSSGLVPRGSHMNSSPNEKENHENAGADSRTPVTVIGLGMMGTALAEAFLK
AGHRTTVWNRSADKADALVAKGAIRAATAAEAVSASPLIVVCVLDYEAAHEILGSVGGLL
TGRTLVNLTNGKPEQARKAAKWAAEQGADYLDGGIMAIPQMIAGPGALLLYSGSPGAFET
YRGELDVLGASQYLGEDAGLAALYDLALLSAMYGMFGGFYHAVALVGTEKVEASAFTALV
IPWLQAMMASLPLQAQAMDANVHATDVSSLYINKIGFVNLIKASQEQGISTELVAPLQAL
VDRAVAEGYGADGLSRLAGLLKKPQ*

>p-IR68 (*Rhizobium gallicum*, A0A0B4XDG7_9RHIZ)
MGSSHHHHHHSSGLVPRGSHMTSQILEFNSMTTIGFFGAGRMGASLVRTLAKSGHEVHVW
NRTAAKAEALAPFGVQPRPTPEAAAAEAEIVFVNLLDYAASDAQLRKPEVTQALKGKLLV
QLTSGSPKAARDTGAWATGHGIAYLDGAIMATPNVIGEPDTLILFAGSKSLYQKHERVFV
ALGGKSAFLSEDFGAASALDSALLGQMWGTLFGTLQALAINRAENIDADAYSTYLKLVQP
VIDGAERDLMQRVHDGRDRGDDETFATIAAHNVALQHLRHINAERGLNPVLADAFDSLFT
TAIQNGHVGDDFAILARFMRAP*

>p-IR69 (*Rivularia* sp. PCC 7116, K9RL01_9CYAN)
MGSSHHHHHHSSGLVPRGSHMQQIYCIHRQIKLSNMNKQKVTVLGLGAMGSRMGVNLLKA
GYSVTVWNRSPKPTEALAAKGAVVATTPKLAVKEADVVISMVTDSDASRAVWLDSETGAL
SAMRQSAIAIESSTLTVSWVKELATEFKHSGIAFLDAPVVGTRPQADSGNLIYLIGGEIE
TLKQAENIFLSAGGGKINHAGEIGKGMAMKLAVNAMFGIQVAAISEIIGMLIKNGFGLEK
AVQYLAELPVTSPAAKNAANLILKGNHAAMFPIDLVEKDFRYVMQTAKDVEAASPISEAI
HRVYLDAVDKGYGGDNITGVAKLFV*

>p-IR70 (*Rhodococcus jostii*, Q0S7N9_RHOJR)
MGSSHHHHHHSSGLVPRGSHMTTTEQVSVGYIGLGNMGAPMAKRLLDRPGGLIVCDTRPEA
LEPFGKAGARVTSSPREVAENADVISVTVLNDEQVRAVVTQILDTARPGTVVAVHSTISDV

TAVELADRCRAHGVDLIDAPVSGGAPGALEGKLAVMVGASDDAFEKVREPFGHWAELVVHA
GDVGAGTRMKLARNLLHFISFTAAAEAQRLAEAAGLDITELGKVVRHTDAITGGAGAIMLR
DTTDALDETDNWYPIMTHVRDLGEKDLSLAIGLGERLDVALPLARLALTGLGPGLGVDSTV
DKKEQP*

>p-IR71 (*Rhinocladiella mackenziei*, A0A0D2H0B2_9EURO)
MGSSHHHHHHSSGLVPRGSHMSSTTSHITLVGLGNMGTALAHALVKAGRRVTIWNRAGTRP
SVSELVQVGAGYGPELPRAIAGSSTIIFCVLDYNSIHQVMDPVVTSQGTDAREMDRWMHKH
GAARYFDGGIMVTPQLISTSTSFILCSGENEALFNDSDVIDLIIILGRPHYVASDPGAAAL
YDLSLLAGMFGMFAGSMTAMALMQKQIHRDGNRPHSPSGAVKFTLEDRVSTLLNPLLNALV
PYTLNIAQSITSGRMDENFGNPMAMVSMAMQNVLRACEEEGVDGGSLKYFADLMKAVVDER
GGEVGIGWVSTLLTK*

>p-IR72 (*Rhodobacter sphaeroides*, Q3IXE7_RHOS4)
MGSSHHHHHHSSGLVPRGSHMSDTVVGIAGTGRMGTAFARRLRETGTPVRVWNRSSDRTG
AAVDAGAEAVALEALAEADLVLLSLTDAAAAEAVLAGMGAALAGRIVVEMSTLLPDQAEA
LEAQATALGAQFLHCPVGGTVAPALKGQLLGFAGGPAETLEQARPVLERLCRRVEHLGSV
GAAARMKLAVNLPLALYWQTLGESLLLLRGAGIPAEQAIGLMAESSGGPAVLKNRAQVVV
ETLEGADQRGTFDIAGLAKDLHLALALAEREGAALPLSAAAEERYRAALEAGLGRFDGAS
LARRTAEG*

>p-IR73 (*Streptomyces albus*, A0A0B5EJP8_STRA4)
MGSSHHHHHHSSGLVPRGSHMAQNAVEKTPLTLLGLGAMGTALARAWLAAGHQVTVWNRT
PGRAAPLVAEGAVLAESAAAAVAANSLVVLCLLDEASVEEVLAGTEPAGKDLVNLTTGTP
AEARARAAWASARDARCLDGGIMAVPPMIGVPASGAYVFYSGSHELFTRHRETLAVPAGT
TWTGTDPGHAALHDVALLSAMYGMFAGTAHAFALIRGEDIDPVAFAPLLADWLTAMAPAV
HRTAERLKSGDLTGDVVSDLAMQTAGVPTFLGTAEQQGVSPELLSPYFALMRRRLAEGGG
GEDLAGLIDLLRRAPGTAA*

>p-IR74 (*Streptomyces albus*, A0A0B5EWU4_STRA4)
MGSSHHHHHHSSGLVPRGSHMAGTDRTPVTVIGLGLMGQALASAFVAAGHPTTVWNRSAD
KAAAVVEQGTVLADTPAEAVAASELLVVCLLDNDAVHAVLDPVAGSLAGRVVANLTSGSS
DQARENAAWAEEVGFRYLDAAIMTVPAAVGAPESVVFYSGPREAYDRHSDTLRLLGGGTT
HLGEDHALSALYDVSLLGVMWGTLNSFLQGAALLSTAEVKAADFLPLALKWIDTVKLFAT
DYAAQIDQKDGAFPANDATMEVHLGAVRHLLHESEAQGVNAELPRFVHALMERTVAKGFG
QNSYASMSELFRTPEK*

>p-IR75 (*Streptomyces avermitilis*)
MGSSHHHHHHSSGLVPRGSHMLITPEPVTSLIGMTQNAVEKTPVTMLGLGAMGTALARTW
LAAGHRLTVWNRTPARAAALATEGARVADSAAEAVAANTLVIVCLLDDSSVDEVLAGIDL
ADTDLVNLTTSTPAQARARAEWANERGARYLDGGIMAVPPMIGVPEAGSYVFCSGSRELF
ERHQETLGIPAGTTYVGMDAGFAALHDMALLSAMYGMFAGVAHAFALIHKEDIDPTSLAP
MLADWLVAMAPAVHQTADHLRSGDYTKGVVSTLAMQVAGTPTFLSTAEQQGVSPELLSPY
FELMRRRLAEGSGEEDLTGVINLLVH**

>p-IR76 (*Streptomyces canus*)
MGSSHHHHHHSSGLVPRGSHMTQNAVEKESVTLLGLGAMGTALARTWLAAGHPLTVWNRT
PARAASLAADGAKVADSAAAAVAANALVVVCLLDDASVEDALTGTDLAGKDLVNLTTSTP
AQARARAEWARERGARYLDGGIMAVPPMIGVPESGGYIFYSGSPELFQRHRETLVVPAGT
VYVGHDAGFAALYDMALLSAMYGMFAGAAHAFALIRKEDIDPASLAPLLADWLVAMAPAV
HRTADQLRSGDYTQGVVSNLAMQVAGTPAFVSAAEQQGVSPELLSPYFALMRRRLAEGSG
EEDLTGVIDLLVR*

>p-IR77 (*Streptomyces canus*)
MGSSHHHHHHSSGLVPRGSHMTQNAVEKESVTLLGLGAMGTALARTWLAAGHPLTVWNRT
PARAASLAADGAKVADSAAAAVAANALVVVCLLDDASVEDALAGTDLAGKDLVNLTTSTP
AQARARAEWARERGARYLDGGIMAVPPMIGVPESGDYIFYSGSPELFQRHRETLVVPAGT

VYVGHDAGFAALYDMALLSAMYGMFAGAAHAFALIRKEDIDPASLAPLLADWLVAMAPAV
HRTADQLRSGDYTQGVVSNLAMQVAGTPAFVSAAEQQGVSPELLSPYFALVRRRLAEGSG
EEDLTGVIDLLVR*

>p-IR78 (*Stachybotrys chartarum*, A0A084RCS9_STACH)
MGSSHHHHHHSSGLVPRGSHMSSQITCIGIGNMGAALAQALLKAETPVTIWNRTVDRPQV
KAVIEAGGILEPNIELAIQKSDIIVICVLNYETIFHALAPLKSSTSPLANKKIINLTNGT
PRQAREAEEWMNARGASQYFDGAVMVTPSLVDSPHSFLVYSGESEDDFSSVATALKPLGQ
ALYVAPDASAASAFDLAALAAMYGMFSGAFIGMSLLKRQFGKTVPGVDKVVLPVLTALVP
YVGLIAKSVDEKSWMEDNLGNPLAMQLAGVGNILQACKDEGVHGAGLEFLAAMMERAVGE
GAGDGGVAAVGDYYLVD*

>p-IR79 (*Streptomyces chattanoogensis*, A0A0N0XYF8_9ACTN)
MGSSHHHHHHSSGLVPRGSHMTDNKVGSSHDTAGTRPLTLLGLGAMGAALGHAWLAAGYP
LTVWNRTPGRAEPLAAQGAQVAGTAAEAVAANRLVVVCLLNDDTLGETLDGVDLAGKDLV
NLTTSTPGQARVRAEWARERGARFLDGGIMAVPPMIGAPGSGASVFYSGSRALFDAHAEA
LAVPAGTAYVGEDPGFAALHDVALLSAMYGMFAGVAHAFALIRKEEIPPKDFAPLLSGWL
TAMTSSVHQAAAQLESGDYTKNVVSNLAMQVAGSETLLGTAEEQGVSAELLTPYLALMER
RLAEGHGDEDTTGLIDLLVRRTGR*

>p-IR80 (*Synechococcus elongatus*, A0A0H3K567_SYNP6)
MGSSHHHHHHSSGLVPRGSHMVGEQETRMRCGLIGTGLLGTAIAERLLTVGQLLTVWNRT
AERSQPLVALGATIAPTPAALLADCEVCLLLLSDAEAIAATLLTEESRSQLVGKTIIQMG
TISPAESRAIADQIAAAGGQYLEAPVLGSLPEARNGTLIVMVGAEPAVFEQWRSLLCHLS
PEPEWIGPIGTAATLKLALNQLIGSLTSAFGGSLALLQRSGLAVEPFMAILRQSALYAPT
FDKKLSRLLSHQYDNPNFPTTHLAKDLRLFRETAADLGITTDAVEGVESIVQKAIAQGWG
DQDYSALYEAINPDSN*

>p-IR81, SnIRED (*Stackebrandtia nassauensis*, D3Q3S0_STANL) (*24*)
MGSSHHHHHHSSGLVPRGSHMTKTPVSVIGLGRMGATIAEIYLREGHPTTVWNRTPAKAE
PLLAKGARPAATVAEAVAASPVSVIMLADDTVVRASLESATSELDGRTIVNLTTGRPDEA
RELGDWLAGHGAEYLDGGVLGVPQTLATPESVIIYSGSTAANQRHGEIVAALGTARYLGA
DHGLASLNDMAILSGMYGLFSGYFHSVAMVDSEGFKAAEFTKDLLIPWLRSIVDVLPTLA
DEIDSGDYPVNFSNLDVNVAGIENIMRTSRSQGVTDAPLVPLRDALAAQQEKGHGEASFS
RAVEELKSSE*

>p-IR82 (*Streptomyces noursei* ATCC 11455, A0A1B2GW12_STRNR)
MGSSHHHHHHSSGLVPRGSHMSVDDSVGNAAGNAVGQVEGNSAVNAAGNAAGAAARRNVA
VLGLGDMGTALAAALLAAGHRVTVWNRTARKADGLVEQGARRAASPAEAIGASDVVIVCI
LDYADVAPLLSDDGADAALKGKVVVNVTNGSPAEARELAERVAGLGADYLDGGIMAVPEI
IGAPQAVVLYSGAKDAFEAHREVLDAFAGSVYLGADPGLAPLNDLALLSGMYGMFGGFLH
AAGLVRSAGGNVTAFTTELLIPWLRAMADSQLPAMAAQVDSGDYGATGSNLAMQVSHDAI
GDVSRAQGVSTELFAPLWELMKRRVADGHGAESVGGVVELVHPREARA*

>p-IR83 (*Streptomyces purpeofuscus*, WP_030392279.1)
MGSSHHHHHHSSGLVPRGSHMTTNDTATRPGSTPSATTAPAPLTLLGLGAMGAALADAWL
SAGHPLTVWNRTAARAEPFAAKGAITAATPAAAVAANRLVVVCLLDDESVGEALAGVDLT
GKDIVDLVTGTPGTARARAAWAADRGARYLDGGIMAVPPMIGVPQAGPYVFYSGSRELFE
EHREVLAVPAGTRYVGEDAGFAALHDVALLSAMYGMFAGVAHAFALVREESVDPVAFAPL
LSSWLTAMTGSVATTARQLAAGDYTEGVVSDLAMQVAGVPTFLRTAEEQGVSAELLTPYF
DLMKRRLVADARHGAEDLTGVVDLLRG*

>p-IR84, SresIRED (*Streptomyces resistomycificus*, A0A0L8KUS9_9ACTN) (*24*)
MGSSHHHHHHSSGLVPRGSHMSNTSPVTVLGLGDMGRALAAAFLAEERATTVWNRTAAKA
DELISLGAVRADSVAEAVTGSPLVVVCLLDYGVVRETLEPVAGQLRGRTVVNLTNGTPSQ
AAEMAAWVTGHGGDYLDGGIMAVPTTVATPEAFILYSGEQRIFDTYRGVLGELGSARYLG
DDIGLASLYDLALLSGMHLMFDGFHHAVAMATSQEGGSAFGFTELLVPWLTNMARLLPAF

AAEVDADLTTAAEPRLTQGLDVQVSGLANIMDAARDAGVSTTPLESSMAALEALLAHGHK
VWSAPASVRQLRTAP*

>p-IR85 (*Streptomyces rimosus*)
MGSSHHHHHHSSGLVPRGSHMRSEPAAVTVLGLGSMGTALAGALLKGGHATTVWNRSPHK
AKPLAERGATVAATPEEAVAASPLLIACVLDYAALHTVLDPVADSLAGKTLVNLTSGSPE
QAAEAAAWARAHGAHYLDGAIMTTPPGVGSPEMMFLYSGERTVFDTHRPVLASLGDPLHL
GTDPGLASLYDAALLGLMWAAMTGWLHGTALVGAEGTPATAFTPVAIRWLSAVTGFLTTY
APQVDAGHYPGDDATVDVQIAAIDHLIHAAAARGVDNALPELLKATMERTRAAGHGSSSY
ASVIETLRKAAGTR*

>p-IR86 (*Thermobifida fusca*, Q47QG6_THEFY)
MGSSHHHHHHSSGLVPRGSHMARIAFIGLGIMGSPMAVHFHNAGHQVVGYNRTPAKTKAL
VEAGGTAAASVSEAVADADVVALMVTDTPDVVEVLTGAGGVFETAKPGTLIIDFSTIRPD
VTADLAAQARSRGLRMVDAPVSGGEVGAQNATLSIMVGGTEEDFAAARPFLEVVGKTIVH
VGPSGSGQTVKAANQLIVAGHLAVLAEAIVFLEAYGVDVSAALDVLGGGLARSAIMEHKA
ELMRRRSFTPGFRLDLHHKDLGIVTTAAREAGVVIPVAAAAAQLIAAARANGDGDLDHSA
LFRTIARLSGRD*

>p-IR87 (*Theobroma cacao*, A0A061GU76_THECC)
MGSSHHHHHHSSGLVPRGSHMRSLPFLLRTLSRHYLHSQTPSPPHLTFLHRSMATSATAE
PISPSNTRLGWIGTGVMGRSMCAHLINAGYTLTVFNRTLSKAQPLVDMGARLAQTPHDLA
AQSDVVFSIVGYPTDVRQVLLDPTNGALSGLSPGGVLVDMTTSEPSLAVEISAAASSKNC
SSIDAPVSGGDRGAKNGTLAIFAGGDEAIVRRLNPLFTLMGKVNYMGPSGKGQFAKLANQ
ITIASTMVGLVEGIVYAHKAGLNVASFLDAISTGAAGSKSLDLYGSRILKRDFEPGFFVN
HFVKDLGICLKECQNMGLALPGLALAQQLYLSLKAHGEGNLGTQALILALERLNNVTLDS
*

>p-IR88 (*Torrubiella hemipterigena*, A0A0A1TF30_9HYPO)
MGSSHHHHHHSSGLVPRGSHMNMTTSRNVTAFGVGNMGAALAHALLKADTKVTIWNRTVD
RPQVQSVLKAGATLEADVKAAISGSSDILLFCLIDYDAMYKTLEPIKGTSDGLAGKTIVN
VTNGTPQQALEMRDWIKARGAARYFDGAVLVTPQMVATPQSLLVYSGESQETFDNIKTIL
QPLGTPLYYGPQVDAAAAQDLAMLATMYGMFYGAFVGFGILKRSGQGQDVKVAPGTKQIT
IPVMAALTEYLGLLADVIDSEDWASNGGNPLLMQVAGVANIIQAAKDANVNASGLEVLAE
AMGKAVEDGWADGNVAAAAKFI*

>p-IR89 (*Myceliophthora thermophila*, G2QG78_MYCTT)
MGSSHHHHHHSSGLVPRGSHMATITSIGIGNMGAALASALLKSVGLRQLTIWNRTADRPQ
VKSLVEQGAHFEPSVAAAVARSDTILICLLDYQTVTAVFEAISPGGLAGKTVINVTNGTP
RQAREAEARFKGLGAAAAYFDGGIMVTPQQIGTPEAFVILSGEDESAFRAAGGPAELLEP
IGAIQYVASDAGAAALYDLAALAAMFGMFAGAFTGIALLKKQKRQRQDGGKEEGDRDNKA
LAKPATDSVIVPVLNALVPYVGMIADEVDRENWMNDMGNPLKMQAIALHNILRACEEEGV
DGEGLKFISRRMDRAVADGFGPGGVSAIARYMFK*

>p-IR90 (*Myceliophthora thermophila*)
MGSSHHHHHHSSGLVPRGSHMATITSIGIGNMGAALASALLKSVGLRQLTIWNRTADRPQ
VKSLVEQGAHFEPSVAAAVARSDTILICLLDYQTVIAVFEAISPGGLAGKTVINVTNGTP
RQAREAEARFKGLGAAAAYFDGGIMVTPQQIGTPEAFVILSGEDESAFRAAGGPAELLEP
IGAIQYVASDAGAAALYDLAALAAMFGMFAGAFTGIALLKKQKRQRQDGGKEEGDRDNKA
LAKPATDSVIVPVLNALVPYVGMIADEVDRENWMNDMGNPLKMQAIALHNILRACEEEGV
DGEGLKFISRRMDRAVADGFGPGGVSAIARYMFK*

2.4 Sequence alignments of imine reductase variants

2.4.1 Putative imine reductases Q82Q44_STRAW and p-IR75 from *S. avermitilis*

```
Q82Q44_STRAW       1 -MITPEPVTSLIGMTQNAVEKTPVTMLGLGAMGTALARTWLAAGHRLTVW     49
                      :||||||||||||||||||||||||||||||||||||||||||||||||
p-IR75             1 MLITPEPVTSLIGMTQNAVEKTPVTMLGLGAMGTALARTWLAAGHRLTVW     50

Q82Q44_STRAW      50 NRTPARAAALAAEGARVADSAAEAVAANTLVIVCLLDDSSVDEVLAGIDL     99
                     |||||||||||.||||||||||||||||||||||||||||||||||||||
p-IR75            51 NRTPARAAALATEGARVADSAAEAVAANTLVIVCLLDDSSVDEVLAGIDL    100

Q82Q44_STRAW     100 ADTDLVNLTTSTPAQARARAEWANERGARYLDGGIMAVPPMIGVPEAGSY    149
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
p-IR75           101 ADTDLVNLTTSTPAQARARAEWANERGARYLDGGIMAVPPMIGVPEAGSY    150

Q82Q44_STRAW     150 VFCSGSRELFERHQETLGIPAGTTYVGMDAGFAALHDMALLSAMYGMFAG    199
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
p-IR75           151 VFCSGSRELFERHQETLGIPAGTTYVGMDAGFAALHDMALLSAMYGMFAG    200

Q82Q44_STRAW     200 VAHAFALIHKEDIDPTSLAPMLADWLVAMAPAVHQTADHLRSGDYTKGVV    249
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
p-IR75           201 VAHAFALIHKEDIDPTSLAPMLADWLVAMAPAVHQTADHLRSGDYTKGVV    250

Q82Q44_STRAW     250 STLAMQVAGTPTFLSTAEQQGVSPELLSPYFELMRRRLAEGSGEEDLTGV    299
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
p-IR75           251 STLAMQVAGTPTFLSTAEQQGVSPELLSPYFELMRRRLAEGSGEEDLTGV    300

Q82Q44_STRAW     300 INLLVH    305
                     ||||||
p-IR75           301 INLLVH    306
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2.4.2 Putative imine reductases A0A117QYA8_9A and p-IR76

```
A0A117QYA8_9A      1 MTQNAVEKESVTLLGLGAMGTALARTWLAAGHPLTVWNRTPARAASLAAD     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
p-IR76             1 MTQNAVEKESVTLLGLGAMGTALARTWLAAGHPLTVWNRTPARAASLAAD     50

A0A117QYA8_9A     51 GAKVADSAAAAVAANALVVVCLLDDASVEDALAGTDLAGKDLVNLTTSTP    100
                     ||||||||||||||||||||||||||||||||.|||||||||||||||||
p-IR76            51 GAKVADSAAAAVAANALVVVCLLDDASVEDALTGTDLAGKDLVNLTTSTP    100

A0A117QYA8_9A    101 AQARARAEWARERGARYLDGGIMAVPPMIGVPESGGYIFYSGSPELFQRH    150
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
p-IR76           101 AQARARAEWARERGARYLDGGIMAVPPMIGVPESGGYIFYSGSPELFQRH    150

A0A117QYA8_9A    151 RETLVVPAGTVYVGHDAGFAALYDMALLSAMYGMFAGAAHAFALIRKEDI    200
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
p-IR76           151 RETLVVPAGTVYVGHDAGFAALYDMALLSAMYGMFAGAAHAFALIRKEDI    200

A0A117QYA8_9A    201 DPASLAPLLADWLVAMAPAVHRTADQLRSGDYTQGVVSNLAMQVAGTPAF    250
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
p-IR76           201 DPASLAPLLADWLVAMAPAVHRTADQLRSGDYTQGVVSNLAMQVAGTPAF    250

A0A117QYA8_9A    251 VSAAEQQGVSPELLSPYFALMRRRLAEGSGEEDLTGVIDLLVR    293
                     |||||||||||||||||||||||||||||||||||||||||||
p-IR76           251 VSAAEQQGVSPELLSPYFALMRRRLAEGSGEEDLTGVIDLLVR    293
```

2.4.3 Putative imine reductases A0A117QYA8_9A and p-IR77

```
A0A117QYA8_9A      1 MTQNAVEKESVTLLGLGAMGTALARTWLAAGHPLTVWNRTPARAASLAAD     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
p-IR77             1 MTQNAVEKESVTLLGLGAMGTALARTWLAAGHPLTVWNRTPARAASLAAD     50

A0A117QYA8_9A     51 GAKVADSAAAAVAANALVVVCLLDDASVEDALAGTDLAGKDLVNLTTSTP    100
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
p-IR77            51 GAKVADSAAAAVAANALVVVCLLDDASVEDALAGTDLAGKDLVNLTTSTP    100

A0A117QYA8_9A    101 AQARARAEWARERGARYLDGGIMAVPPMIGVPESGGYIFYSGSPELFQRH    150
                     |||||||||||||||||||||||||||||||||||.||||||||||||||
p-IR77           101 AQARARAEWARERGARYLDGGIMAVPPMIGVPESGDYIFYSGSPELFQRH    150

A0A117QYA8_9A    151 RETLVVPAGTVYVGHDAGFAALYDMALLSAMYGMFAGAAHAFALIRKEDI    200
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
p-IR77           151 RETLVVPAGTVYVGHDAGFAALYDMALLSAMYGMFAGAAHAFALIRKEDI    200

A0A117QYA8_9A    201 DPASLAPLLADWLVAMAPAVHRTADQLRSGDYTQGVVSNLAMQVAGTPAF    250
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
p-IR77           201 DPASLAPLLADWLVAMAPAVHRTADQLRSGDYTQGVVSNLAMQVAGTPAF    250

A0A117QYA8_9A    251 VSAAEQQGVSPELLSPYFALMRRRLAEGSGEEDLTGVIDLLVR    293
                     ||||||||||||||||||||:||||||||||||||||||||||
p-IR77           251 VSAAEQQGVSPELLSPYFALVRRRLAEGSGEEDLTGVIDLLVR    293
```

2.4.4 Putative imine reductases A0A0M9XDJ7_ST and p-IR85

```
A0A0M9XDJ7_ST      1 MRSEPAAVTVLGLGSMGTALAGALLKGGHATTVWNRSPHKAKLLAERGAT     50
                     ||||||||||||||||||||||||||||||||||||||||||.|||||||
p-IR85             1 MRSEPAAVTVLGLGSMGTALAGALLKGGHATTVWNRSPHKAKPLAERGAT     50

A0A0M9XDJ7_ST     51 VAATPEEAVAASPLVIACVLDYAALYTVLDPVADSLAGKTLVNLTSGSPE    100
                     ||||||||||||||:||||||||||:||||||||||||||||||||||||
p-IR85            51 VAATPEEAVAASPLLIACVLDYAALHTVLDPVADSLAGKTLVNLTSGSPE    100

A0A0M9XDJ7_ST    101 QAAEAAAWARSHGAHYLDGAIMTTPPGVGSPEMMFLYSGERTVFDTHRPA    150
                     ||||||||||:||||||||||||||||||||||||||||||||||||||.
p-IR85           101 QAAEAAAWARAHGAHYLDGAIMTTPPGVGSPEMMFLYSGERTVFDTHRPV    150

A0A0M9XDJ7_ST    151 LASLGDPLYLGTDPGLASLYDAALLGLMWAAMTGWLHGTALVGAEGTPAT    200
                     ||||||||:|||||||||||||||||||||||||||||||||||||||||
p-IR85           151 LASLGDPLHLGTDPGLASLYDAALLGLMWAAMTGWLHGTALVGAEGTPAT    200

A0A0M9XDJ7_ST    201 AFTPVAIRWLSAMTGFLTTYAPQVDAGHYPGDDATVDVQIAAIDHLIHAA    250
                     ||||||||||||:|||||||||||||||||||||||||||||||||||||
p-IR85           201 AFTPVAIRWLSAVTGFLTTYAPQVDAGHYPGDDATVDVQIAAIDHLIHAA    25

A0A0M9XDJ7_ST    251 AARGVDNALPELLKATMERTRAAGHGSSSYASVIETLR-AAGTR    293
                     |||||||||||||||||||||||||||||||||||||| |||||
p-IR85           251 AARGVDNALPELLKATMERTRAAGHGSSSYASVIETLRKAAGTR    294
```

2.4.5 Putative imine reductases p-IR89 (G2QG78_MYCTT) and p-IR90

```
G2QG78_MYCTT       1 MATITSIGIGNMGAALASALLKSVGLRQLTIWNRTADRPQVKSLVEQGAH     50
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
p-IR90             1 MATITSIGIGNMGAALASALLKSVGLRQLTIWNRTADRPQVKSLVEQGAH     5

G2QG78_MYCTT      51 FEPSVAAAVARSDTILICLLDYQTVTAVFEAISPGGLAGKTVINVTNGTP    100
                     |||||||||||||||||||||||||.||||||||||||||||||||||||
p-IR90            51 FEPSVAAAVARSDTILICLLDYQTVIAVFEAISPGGLAGKTVINVTNGTP    100

G2QG78_MYCTT     101 RQAREAEARFKGLGAAAAYFDGGIMVTPQQIGTPEAFVILSGEDESAFRA    150
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
p-IR90           101 RQAREAEARFKGLGAAAAYFDGGIMVTPQQIGTPEAFVILSGEDESAFRA    150

G2QG78_MYCTT     151 AGGPAELLEPIGAIQYVASDAGAAALYDLAALAAMFGMFAGAFTGIALLK    200
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
p-IR90           151 AGGPAELLEPIGAIQYVASDAGAAALYDLAALAAMFGMFAGAFTGIALLK    200

G2QG78_MYCTT     201 KQKRQRQDGGKEEGDRDNKALAKPATDSVIVPVLNALVPYVGMIADEVDR    250
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
p-IR90           201 KQKRQRQDGGKEEGDRDNKALAKPATDSVIVPVLNALVPYVGMIADEVDR    250

G2QG78_MYCTT     251 ENWMNDMGNPLKMQAIALHNILRACEEEGVDGEGLKFISRRMDRAVADGF    300
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
p-IR90           251 ENWMNDMGNPLKMQAIALHNILRACEEEGVDGEGLKFISRRMDRAVADGF    300

G2QG78_MYCTT     301 GPGGVSAIARYMFK    314
                     ||||||||||||||
p-IR90           301 GPGGVSAIARYMFK    314
```

2.5 Production of *B. subtilis* glucose dehydrogenase

The gene for the glucose dehydrogenases from *Bacillus subtilis* was subcloned into a pET-15b vector. For the transformation of plasmid DNA into *E. coli*, chemically competent *E. coli* cells were thawed on ice for ten minutes. The *B. subtili*s GDH/pET-15b plasmid DNA solution (1 µL) was added to the cell suspension and gently mixed. The cells were incubated on ice for 30 min, after which the cells were heat shocked. DH5α cells, for DNA isolation and sequencing, were heat shocked at 42°C for thirty seconds, while BL21 (DE3) cells for protein expression were heat shocked at 42°C for ten seconds. Following this, the cells were returned to ice for ten minutes. SOC media (300 µL) was added and the cells incubated at 37°C with shaking at 250 rpm for one hour prior to plating onto LB agar supplemented with ampicillin (100 mg L^{-1}).

Production of the *B. subtilis* GDH biocatalyst was achieved in *E. coli* BL21 (DE3) cells which had been transformed with the BsGDH/pET-15b plasmid. A single colony picked from an agar plate grown overnight was inoculated into 5 mL LB medium supplemented with ampicillin (100 mg L^{-1}) and incubated overnight at 37°C in an orbital shaker at 250 rpm. This starter culture was used as the inoculum for a 500 mL culture in LB medium supplemented with ampicillin (100 mg L^{-1}). The culture was then incubated at 30°C in an orbital shaker at 250 rpm until it reached an OD_{600nm} of between 0.6 and 0.8. IPTG (0.5 mM) was added to induce protein expression, after which cell cultivation was continued at 20°C and 250 rpm for 16 hours.

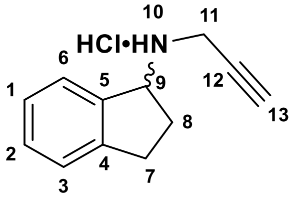
Cells from a 500 mL culture were harvested by centrifugation (2,831 rcf, 20 min) and the pellet resuspended in 100 mL postassium phosphate buffer (100 mM, pH 7.0). Following cell disruption by sonication (4°C, 20 min, 30 sec pulse, 30 sec off, repeat x 20), the suspension was centrifuged at 39,191 rcf for 20 min. The resulting clarified lysate was either divided into aliquots, snap-frozen in liquid nitrogen and stored at -80°C until use, or snap-frozen in liquid nitrogen, lyophilized and then stored at -20°C until use.

2.6 Synthetic procedures and characterisation data for chemical standards

2.6.1 Reductive amination procedure A

To a stirred solution of 1-indanone (264 mg, 2.0 mmol) in dry THF (10 mL, 200 mM) under N_2 were added the amine nucleophile (2.2 mmol – 4.0 mmol), $Na(OAc)_3BH$ (0.636 g, 3.0 mmol) and glacial AcOH (154 µL, 2.0 mmol). The reaction was stirred for 16 hours at 20°C under N_2 then quenched by addition of 5 M NaOH (10 mL) and extracted with EtOAc (3 x 20 mL). The combined organic phases were then extracted with 1 M HCl (3 x 20 mL) and the aqueous phase basified (pH 12) by addition of 5 M NaOH. The product was extracted with EtOAc (3 x 20 mL). The combined organic phases were washed with brine (20 mL), dried over $MgSO_4$ and the solvent removed under reduced pressure to afford the corresponding secondary amine.

***N*-propargyl-1-aminoindan 10**

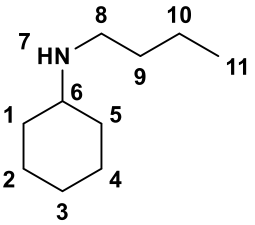


Grey solid isolated, 49% yield. **^{1}H NMR** δ_H (400 MHz, $CDCl_3$): 7.80 – 7.71 (m, 1 H, C3-*H*), 7.39 – 7.21 (m, 3 H, C1-*H*, C2-*H*, C6-*H*), 4.95 – 4.88 (m, 1 H, C9-*H*), 3.67 – 3.61 (br s, 2 H, C11-*H*), 3.44 (dt, *J* = 8.2, 8.1 Hz, 1 H, C7-H_a), 2.97 – 2.87 (m, 1 H, C7-H_b), 2.59 (t, *J* = 2.6 Hz, 1 H, C13-*H*), 2.50 – 2.39 (m, 2 H, C8-*H*). **^{13}C NMR** δ_C (100 MHz, $CDCl_3$): 145.4 (*C*5), 135.6 (*C*4), 130.1 (*C*6), 127.0 (*C*3), 126.4 (*C*1/*C*2), 125.6 (*C*1/*C*2), 78.2 (*C*12), 73.3 (*C*13), 60.7 (*C*9), 33.5 (*C*11), 30.5 (*C*7), 28.8 (*C*8). **HRMS** calcd. for $C_{12}H_{14}N^+$ 172.1126 $[M]^+$, found 172.1120.

2.6.2 Reductive amination procedure B

To a stirred solution of the ketone (2.0 mmol) in dry MeOH (5 mL) over 4 Å molecular seives under N_2 was added the amine nucleophile (2.2 - 4.0 mmol). The reaction was stirred at 20°C overnight, after which the solution was cooled to 0°C and $NaBH_4$ (0.151 g, 4.0 mmol) added over 10 minutes. The mixture was stirred for a further 2 hours, then the solvent removed under reduced pressure. The resulting slurry was resuspended in EtOAc (10 mL), filtered, and the solid washed with EtOAc (2 x 5 mL). The combined organic phases were extracted with 1 M HCl (3 x 10 mL). The combined aqueous phases were then basified (pH 12) with 5 M NaOH and extracted with EtOAc (3 x 10 mL). The combined organic phases were washed with brine (10 mL), dried over $MgSO_4$ and the solvent removed under reduced pressure to afford the corresponding secondary amine.

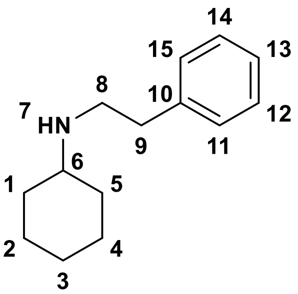
***N*-butylcyclohexylamine 4**



Yellow oil isolated, 88% yield. **^{1}H NMR** δ_H (400 MHz, $CDCl_3$): 2.59 (t, *J* = 7.3 Hz, 2 H, C8-*H*), 3.44 – 3.33 (m, 1 H, C6-*H*), 1.90 – 1.80 (m, 2 H, C1-*H*, C5-*H*), 1.76 – 1.65 (m, 2 H, C2-*H*, C4-*H*), 1.64 – 1.52 (m, 1 H, C3-*H*), 1.50 – 1.38 (m, 2 H, C9-*H*), 1.37 – 0.97 (m, 7 H, C1-*H*, C2-*H*, C3-*H*, C4-*H*, C5-*H*, C10-*H*), 0.89 (t, *J* = 7.2 Hz, 3 H, C11-*H*). **^{13}C NMR** δ_C (100 MHz, $CDCl_3$): 56.6 (*C*6), 46.4 (*C*8), 33.2

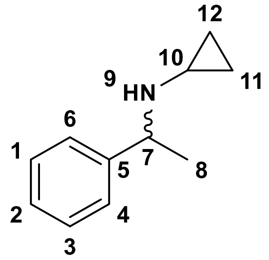
(*C*1, *C*5), 32.2 (*C*9), 25.9 (*C*2, *C*4), 24.8 (*C*3), 20.3 (*C*10), 13.7 (*C*11). **HRMS** calcd. for $C_{10}H_{22}N^+$ 156.1752 $[M+H]^+$, found 156.1754.

***N*-cyclohexylphenethylamine 5**



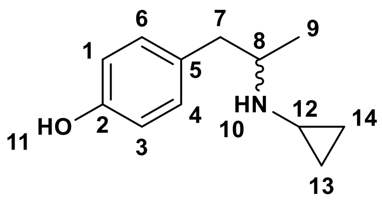
Orange oil isolated, 80% yield. **^{1}H NMR** δ_H (400 MHz, $CDCl_3$): 7.41 – 7.20 (m, 5 H, C11-*H*, C12-*H*, C13-*H*, C14-*H*, C15-*H*), 3.06 – 2.91 (m, 2 H, C8-*H*), 2.90 – 2.77 (m, 2 H, C9-*H*), 2.57 – 2.46 (m, 1 H, C6-*H*), 2.36 (br s, 1 H, N7-*H*), 1.99 – 1.87 (m, 2 H, C1-*H*, C5-*H*), 1.83 – 1.71 (m, 2 H, C2-*H*, C4-*H*), 1.70 – 1.61 (m, 1 H, C3-*H*), 1.37 – 1.07 (m, 5 H, C1-*H*, C2-*H*, C3-*H*, C4-*H*, C5-*H*). **^{13}C NMR** δ_C (100 MHz, $CDCl_3$): 139.5 (*C*10), 128.3 (*C*11, *C*15/*C*12, *C*14), 128.1 (*C*11, *C*15/*C*12, *C*14), 125.8 (*C*13), 56.3 (*C*6), 47.5 (*C*8), 35.7 (*C*9), 32.6 (*C*1, *C*5), 25.7 (*C*2, *C*4), 24.7 (*C*3). **HRMS** calcd. for $C_{14}H_{22}N^+$ 204.1752 $[M+H]^+$, found 204.1749.

***N*-(1-phenylethyl)cyclopropylamine 11**



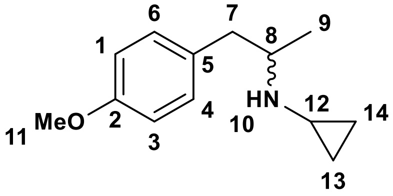
Yellow oil isolated, 31% yield. **^{1}H NMR** δ_H (400 MHz, $CDCl_3$): 7.34 – 7.14 (m, 5 H, C1-*H*, C2-*H*, C3-*H*, C4-*H*, C6-*H*), 3.83 (q, *J* = 6.7 Hz, 1 H, C7-*H*), 3.01 (br s, 1 H, N9-*H*), 1.95 – 1.86 (m, 1 H, C10-*H*), 1.34 (d, *J* = 6.7 Hz, 3 H, C8-*H*), 0.39 – 0.25 (m, 4 H, C11-*H*, C12-*H*). **^{13}C NMR** δ_C (100 MHz, $CDCl_3$): 144.8 (*C*5), 128.4 (*C*1, *C*3), 126.7 (*C*2, *C*4, *C*6), 58.4 (*C*7), 28.7 (*C*10), 23.0 (*C*8), 6.04 (*C*11, *C*12). **HRMS** calcd. for $C_{11}H_{16}N^+$ 162.1283 $[M+H]^+$, found 162.1283.

4-(2-(cyclopropylamino)propyl)phenol 12



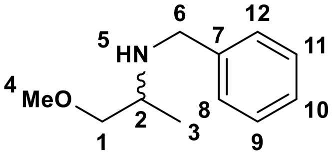
Orange oil isolated, 87% yield. **^{1}H NMR** δ_H (400 MHz, $CDCl_3$): 7.01 (d, *J* = 8.1 Hz, 2 H, C4-*H*, C6-*H*), 6.74 (d, *J* = 8.1 Hz, C1-*H*, C3-*H*), 3.12 – 3.02 (m, 1 H, C8-*H*), 2.79 – 2.68 (m, 1 H, C7-H_a), 2.65 – 2.56 (m, 1 H, C7-H_b), 2.16 – 2.09 (m, 1 H, C12-*H*), 1.17 (d, *J* = 6.2 Hz, 2 H, C9-*H*), 0.61 – 0.37 (m, 4 H, C13-*H*, C14-*H*). **^{13}C NMR** δ_C (100 MHz, $CDCl_3$): 155.4 (*C*2), 130.2 (*C*4, *C*6), 129.24 (*C*5), 115.7 (*C*1, *C*3), 55.8 (*C*8), 41.6 (*C*7), 28.5 (*C*12), 19.2 (*C*9), 6.3 (*C*13, *C*14). **HRMS** calcd. for $C_{12}H_{18}NO^+$ 192.1388 $[M+H]^+$, found 192.1378.

N-(1-(4-methoxyphenyl)propan-2-yl)cyclopropylamine 13



Yellow oil isolated, 81% yield. **^{1}H NMR** δ_{H} (400 MHz, CDCl$_3$): 7.12 (d, *J* = 8.6 Hz, 2 H, C4-*H*, C6-*H*), 6.85 (d, *J* = 8.6 Hz, 2 H, C1-*H*, C3-*H*), 3.80 (s, 3 H, C11-*H*), 3.06 – 2.95 (m, 1 H, C8-*H*), 2.71 (dd, *J* = 6.7, 6.5 Hz, 1 H, C7-*H$_a$*), 2.56 (dd, *J* = 13.5, 6.5 Hz, 1 H, C7-*H$_b$*), 2.06 (tt, *J* = 6.8, 7.2 Hz, 1 H, C12-*H*), 1.11 (d, *J* = 6.4 Hz, 3 H, C9-*H*), 0.54 – 0.26 (m, 4 H, C13-*H*, C14-*H*). **^{13}C NMR** δ_{C} (100 MHz, CDCl$_3$): 157.8 (*C*2), 131.3 (*C*5), 130.0 (*C*4, *C*6), 113.6 (*C*1, *C*3), 55.4 (*C*11), 55.0 (*C*8), 42.4 (*C*7), 28.5 (*C*12), 20.2 (*C*9), 6.9 (*C*13, *C*14). **HRMS** calcd. for $C_{13}H_{20}NO^{+}$ 206.1545 [M+H]$^{+}$, found 206.1547.

N-benzyl-1-methoxy-2-propylamine 14



Colourless oil isolated, 80% yield. **^{1}H NMR** δ_{H} (400 MHz, CDCl$_3$): 7.34 – 7.03 (m, 5 H, C8-*H*, C9-*H*, C10-*H*, C11-*H*, C12-*H*), 3.81 (s, 2 H, C6-*H*), 3.67 (d, *J* = 6.6 Hz, 1 H, C1-*H$_a$*), 3.50 (d, *J* = 6.6 Hz, 1 H, C1-*H$_b$*), 3.27 (s, 3 H, C4-*H*), 2.93 – 2.84 (m, 1 H, C2-*H*), 2.73 (br s, 1 H, N5-*H*), 1.01 (d, *J* = 6.5 Hz, 3 H, C3-*H*). **^{13}C NMR** δ_{C} (100 MHz, CDCl$_3$): 140.3 (*C*7), 128.3 (*C*8, *C*12/*C*9, *C*10), 128.1 (*C*8, *C*12/*C*9, *C*10), 127.4 (*C*10), 58.7 (*C*2), 51.7 (*C*4), 51.2 (*C*6), 45.5 (*C*1), 16.8 (*C*3). **HRMS** calcd. for $C_{11}H_{18}NO^{+}$ 180.1388 [M+H]$^{+}$, found 180.1376.

2.7 Chromatographic analysis

2.7.1 Conditions and retention times

2.7.1.1 Analysis with Agilent 7890B gas chromatograph

Retention times for GC-FID analysis with an achiral stationary phase. Phenomenex ZB WAXplus column, inlet temperature: 250°C, detector temperature: 225°C, flow rate: 5.0 mL min^{-1}, temperature program: 50°C (0.5 min), 50°C min^{-1} (250°C), 250°C (0.5 min).

Compound	Retention Time / min
cyclohexanol	1.8
2-methylcyclohexanol	1.8
1-indanol	3.3
1-phenylethanol	2.7
1-(4-hydroxyphenyl)-2-propanol	3.8
1-(4-methoxyphenyl)-2-propanol	3.9
1-methoxy-2-propanol	1.3
cyclohexanone	1.4
2-methylcyclohexanone	1.5
1-indanone	3.2
acetophenone	2.4
1-(4-hydroxyphenyl)-2-propanone	3.4
1-(4-methoxyphenyl)-2-propanone	3.4
methoxyacetone	0.9
butylamine	0.8
phenethylamine	2.4
aniline	2.6
benzylamine	2.3
N-cyclopropylcyclohexylamine **3**	1.6
N-butylcyclohexylamine **4**	2.0
N-phenethylcyclohexylamine **5**	3.7
N-cyclohexylaniline **6**	3.5
N-benzylcyclohexylamine **7**	3.3
N-isopropylcyclohexylamine **8**	1.7
N-(2-methylcyclohexyl)acetamide	3.2 (A), 3.3 (B)
N-(1-phenylethyl)cyclopropylamine **10**	2.4
N-propargyl-1-aminoindan **11**	3.5
N-(4-hydroxy)cyclopropylamphetamine **12**	3.5
N-(4-methoxy)cyclopropylamphetamine **13**	3.6
N-benzyl-1-methoxypropan-2-amine **14**	2.8

2.7.1.2 Analysis with Agilent 6850 gas chromatograph

Retention times for GC-FID analysis under general conditions with a chiral stationary phase. CP-Chirasil-Dex CB column, inlet temperature: 200°C; detector temperature: 250°C; flow rate: 1.2 mL min^{-1}; temperature program: 50°C (0 min), 5°C min^{-1} (200°C), 200°C (2 min).

Compound	**Retention Time / min**
cyclohexanol	12.9
1-indanol	19.3 (A), 19.4 (B)
cyclohexanone	10.3
2-methylcyclohexanone	9.7 (A), 9.8 (B)
1-indanone	18.0
acetophenone	11.9
1-(4-hydroxyphenyl)-2-propanone	26.2
1-(4-methoxyphenyl)-2-propanone	20.1
methoxyacetone	3.1
phenethylamine	13.6
aniline	13.1
benzylamine	13.0
N-cyclopropylcyclohexylamine **3**	14.2
N-butylcyclohexylamine **4**	14.3
N-phenethylcyclohexylamine **5**	25.0
N-cyclohexylaniline **6**	18.9
N-benzylcyclohexylamine **7**	24.2
N-isopropylcyclohexylamine **8**	11.2
2-methylcyclohexylamine **9**	9.5 (A), 10.6 (B)
rac-*N*-propargyl-1-aminoindan **10**	21.6 (*S*), 21.8 (*R*)
rac-*N*-(1-phenylethyl)cyclopropylamine **11**	15.8 (A), 15.9 (B)
rac-*N*-(4-hydroxy)cyclopropylamphetamine **12**	25.5
rac-*N*-(4-methoxy)cyclopropylamphetamine **13**	27.3
rac-*N*-benzyl-1-methoxypropan-2-amine **14**	18.4

Retention times for GC-FID analysis of substrates and products under conditions optimized for faster analysis of higher-boiling compounds with a chiral stationary phase. CP-Chirasil-Dex CB column, inlet temperature: 200°C; detector temperature: 250°C; flow rate: 1.2 mL min^{-1}; temperature program: 50°C (0 min), 10°C min^{-1} (110°C), 5°C min^{-1} (200°C), 200°C (2 min).

Compound	**Retention Time / min**
2-phenylpiperidine **1**	14.9
2-phenylpiperideine **2**	16.7

Retention times for GC-FID analysis of substrates and products under conditions optimized for separation of high-boiling enantiomers with a chiral stationary phase. CP-Chirasil-Dex CB column, inlet temperature: 200°C; detector temperature: 250°C; flow rate: 1.2 mL min^{-1}; temperature program: 50°C (0 min), 10°C min^{-1} (150°C), 3°C min^{-1} (200°C), 200°C (2 min).

Compound	**Retention Time / min**
2-phenylpiperideine **1**	16.7
N-acetyl-2-phenylpiperidine	20.7 (*S*), 21.0 (*R*)

Retention times for GC-FID analysis of substrates and products under conditions optimized for faster separation of low- and high-boiling compounds with a chiral stationary phase. CP-Chirasil-Dex CB column, inlet temperature: 200°C; detector temperature: 250°C; flow rate: 1.2 mL min^{-1}; temperature program: 50°C (0 min), 10°C min^{-1} (120°C), 5°C min^{-1} (160°C), 10°C min^{-1} (200°C), 200°C (2 min).

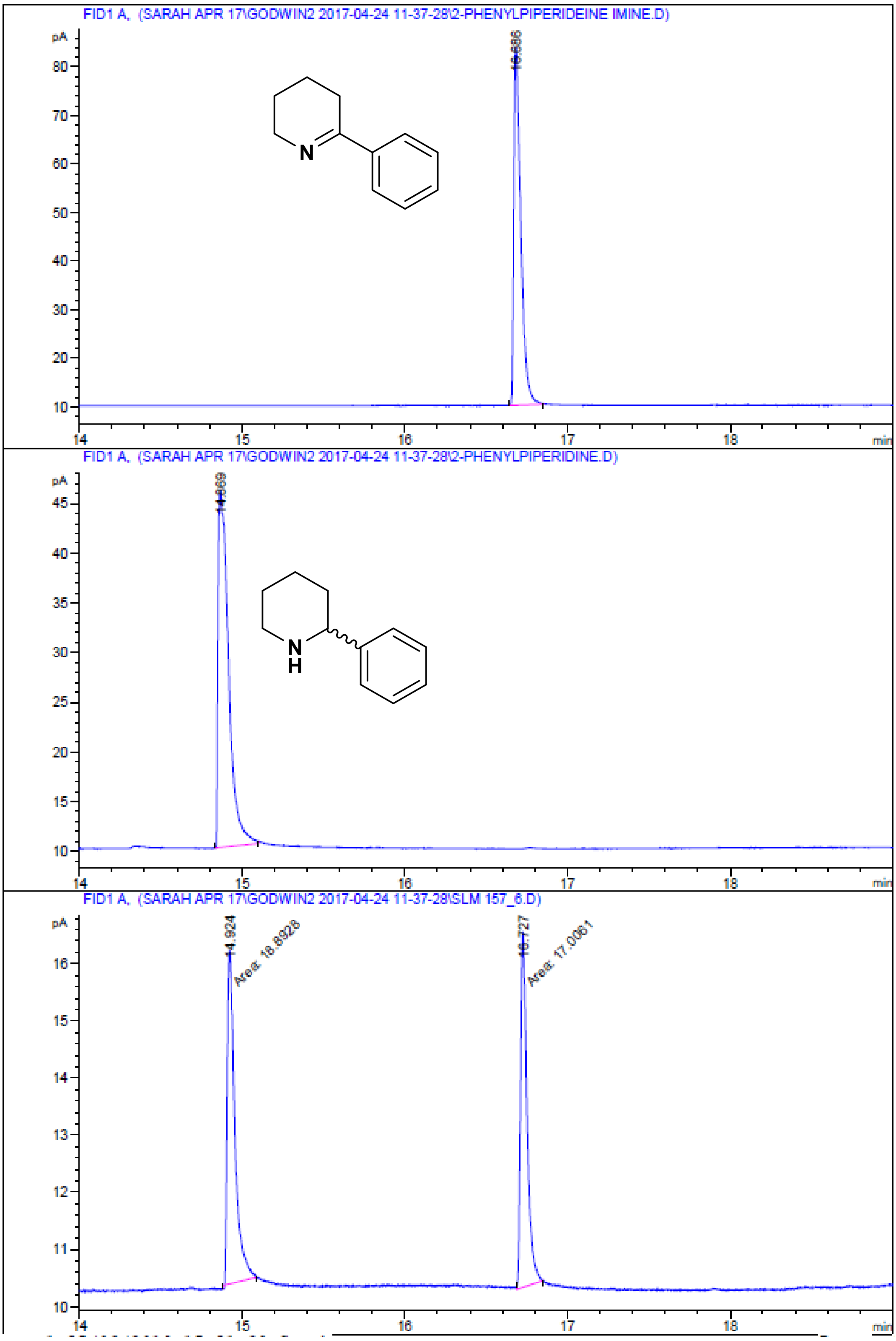
Compound	**Retention Time / min**
cyclohexanone	6.0
aniline	7.7
N-cyclohexylaniline **6**	17.9

Retention times for GC-FID analysis of substrates and products under conditions optimized for faster separation of low-boiling compounds with a chiral stationary phase. CP-Chirasil-Dex CB column, inlet temperature: 200°C; detector temperature: 250°C; flow rate: 1.2 mL min^{-1}; temperature program: 50°C (0 min), 10°C min^{-1} (100°C), 5°C min^{-1} (130°C), 10°C min^{-1} (200°C), 200°C (2 min)

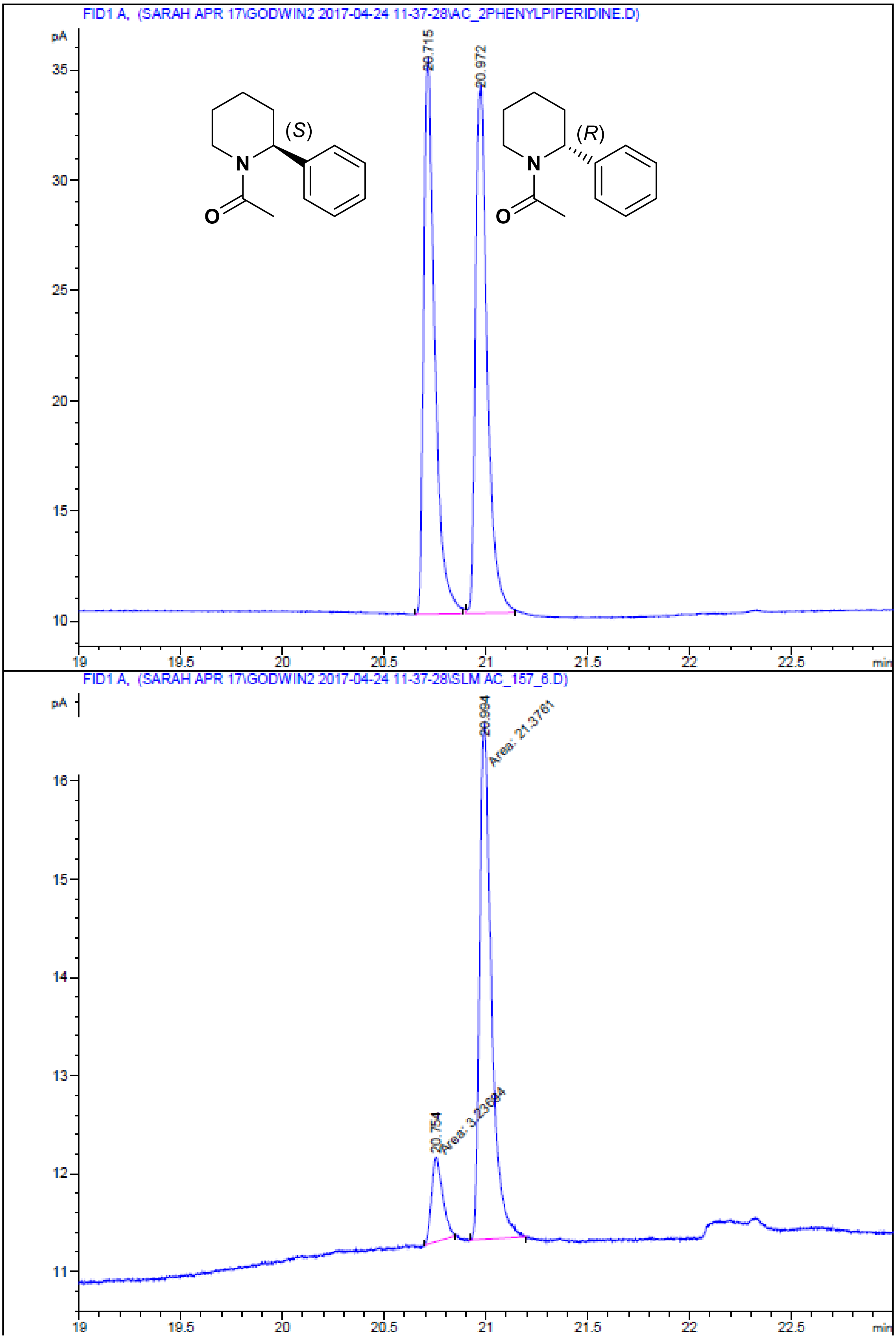
Compound	**Retention Time / min**
cyclohexanone	6.5
N-cyclopropylcyclohexylamine	9.5

2.7.2 Chromatograms

2.7.2.1 Example chromatograms for biocatalytic imine reduction

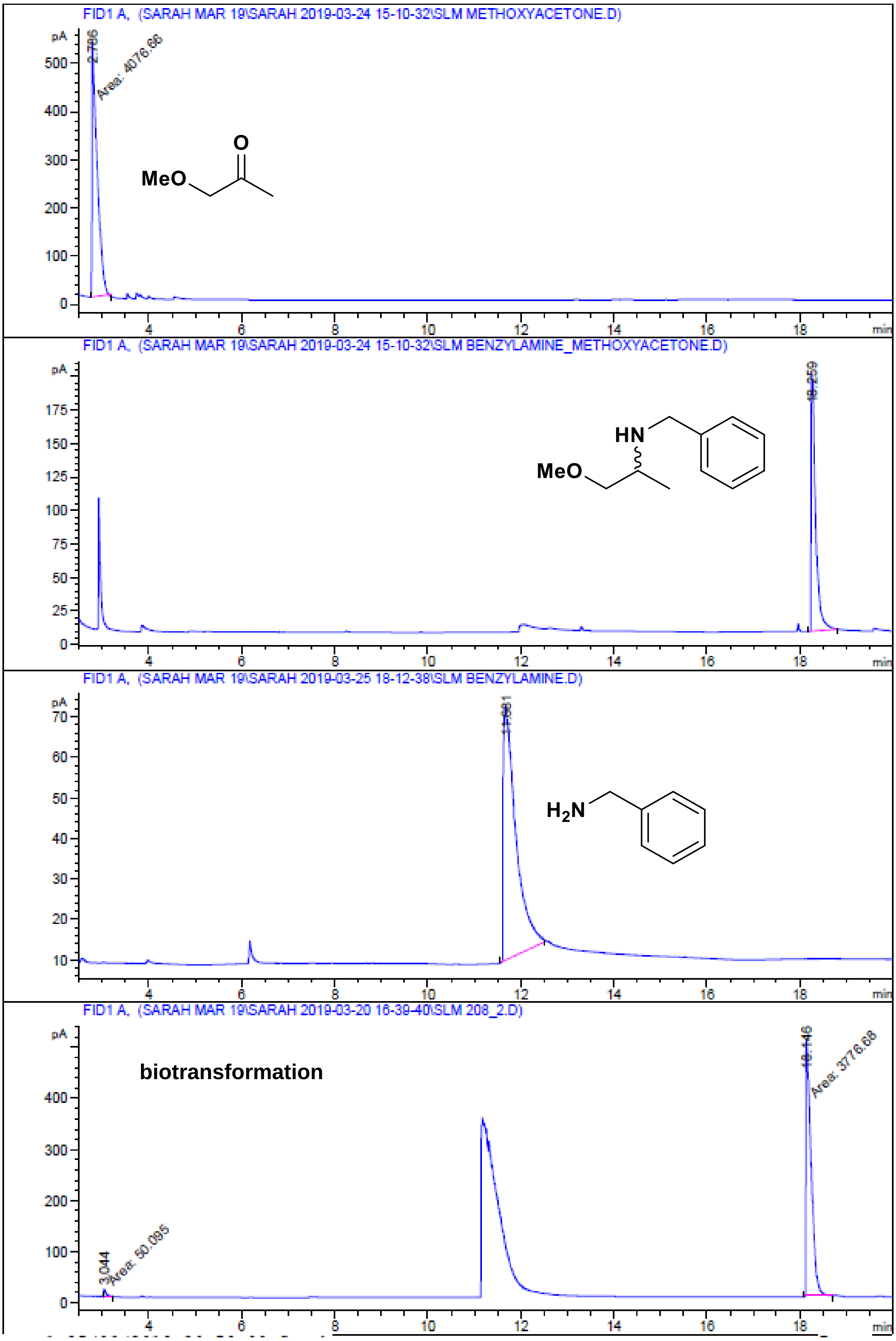


Typical GC-FID chromatogram for the biocatalytic reduction of imines. Reduction of **1** using p-IR84 and *B. subtilis* GDH.



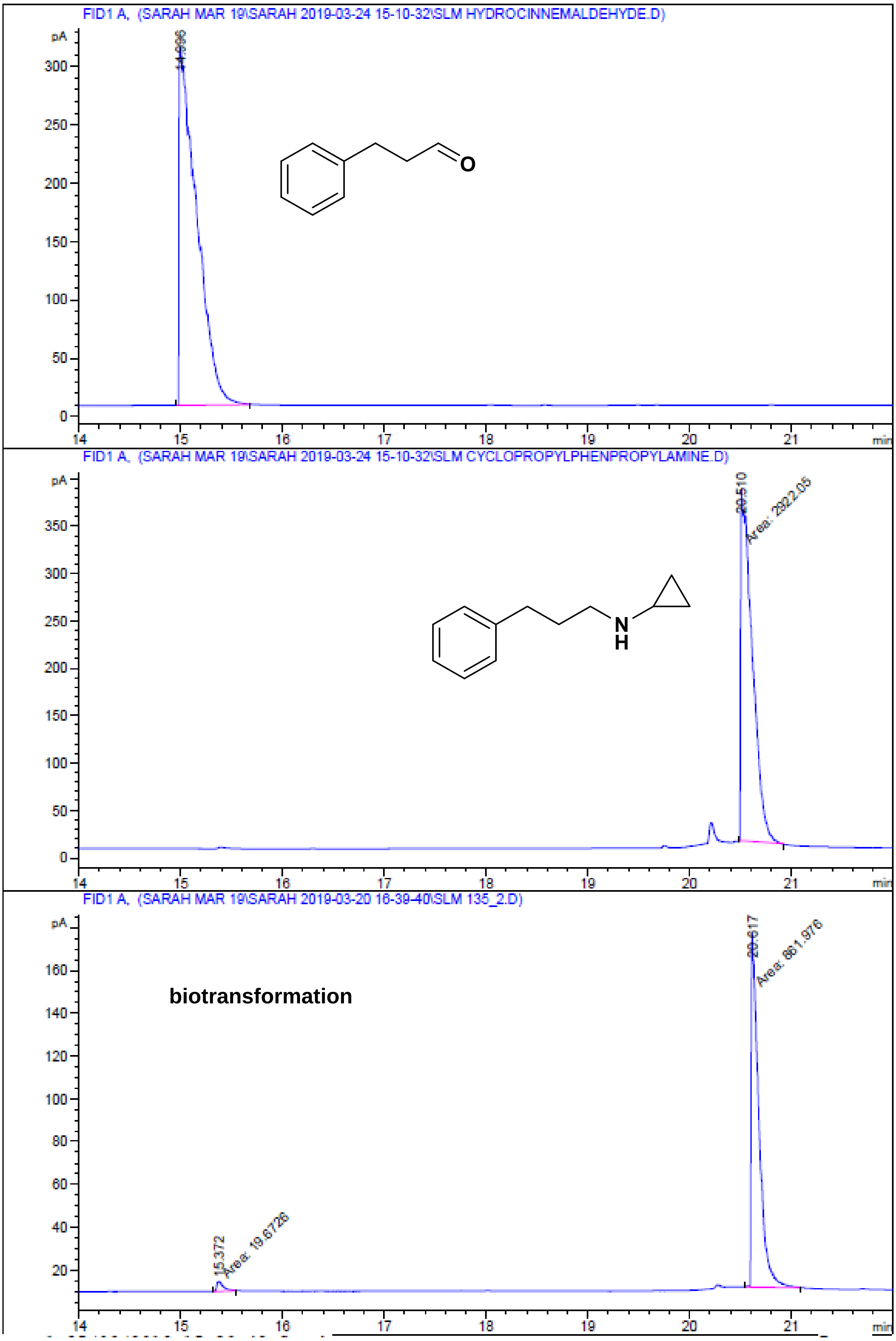
Typical GC-FID chromatogram for determination of enantiomeric excess. Reduction of **1** using IRED p-IR84 and *B. subtilis* GDH.

2.7.2.2 Example chromatograms for reductive aminations with cell-free extract



Typical GC-FID chromatogram for biocatalytic reductive amination with IRED CFE. Reductive amination of methoxyacetone with benzylamine using IRED p-IR79 and *B. subtilis* GDH.

2.7.2.3 Example chromatograms for reductive aminations with purified enzyme



Typical GC-FID chromatogram for biocatalytic reductive amination with purified IRED. Reductive amination of hydrocinnamaldehyde with cyclopropylamine using ArpDHII and *B. subtilis* GDH.