

Supporting Information

Functional dissection and module swapping of fungal cyclooligomer depsipeptide synthetases

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1. Strains, plasmids, and culture conditions

Escherichia coli XL1-Blue (Agilent) was used for routine cloning and pJET1.2 (Fermentas) was used as the cloning vector. *E. coli* cells were grown in Luria-Bertani (LB) medium at 250 rpm and 37°C. When necessary, 50 µg mL⁻¹ ampicillin was added. *S. cerevisiae* BJ5464-NpgA (*MATα ura3-52 his3-Δ200 leu2- Δ1 trp1 pep4::HIS3 prb1 Δ1.6R can1 GAL*) was obtained from Dr. Nancy Da Silva at the University of California, Irvine. The strain was maintained on YPD (yeast extract/peptone/dextrose) agar plates at 30°C. The *E. coli*/*S. cerevisiae* shuttle vectors pXW55 and pXW06 were gifts from Dr. Yi Tang at the University of California, Los Angeles. pXW55 carries the ampicillin-resistance gene and *URA3* as the selection markers, and was used to express M1-M2 linker-containing or -lacking M23 of BbBEAS and BbBSLS. pXW06 carries the ampicillin-resistance gene and *TRP1* as the selection markers, and was used to express M1-M2 linker-containing or -lacking M1 of BbBEAS and BbBSLS.

Beauveria bassiana ATCC 7159 was obtained from the American Type Culture Collection and was grown in potato dextrose broth at 250 rpm and 28°C. The genomic DNA was extracted from the mycelia of the fungus and used as the template to amplify the *bbBeas* and *bbBsIs* gene fragments.

2. DNA manipulations

Isolation of plasmid DNA from *E. coli* was conducted with a GeneJET™ Plasmid Miniprep Kit (Fermentas) by following the manufacturer's instructions. Gene ligations were performed with T4 DNA ligase (New England Biolabs).

3. Gene amplification and plasmid construction

The gene fragments *bbBeasM1 with M1-M2 linker*, *bbBeas-M23 with M1-M2 linker*, *bbBeas-M1 without M1-M2 linker*, *bbBeasM23 without M1-M2 linker*, *bbBeasM1 with partial M1-M2 linker*, and *bbBeasM23a with partial M1-M2 linker* were amplified by PCR from the genomic DNA of *B. bassiana* ATCC 7159 with Phusion® High-Fidelity DNA Polymerase (New England Biolabs) with specific primers (Table S1). Similarly, *bbBsIsM1 with M1-M2 linker*, *bbBsIsM23 with M1-M2 linker*, *bbBsIsM1 without M1-M2 linker*, *bbBsIsM23 without M1-M2 linker*, *bbBsIsM1 with partial M1-M2 linker* and *bbBsIsM23a with partial M1-M2 linker* were amplified from the template. These gene fragments were ligated into the cloning vector pJET1.2 (Fermentas) to yield twelve plasmids including pDY38, pDY39, pDY60, pDY61, pDY62, pDY66, pDY69, pDY72, pDY90, pDY91, pDY94 and pDY95. These plasmids were confirmed by digestion checks and gene sequencing.

The *bbBeasM1 with M1-M2 linker* and *bbBeasM1 without M1-M2 linker* inserts were excised from pDY39 and pDY94 with *NdeI* and *PmeI* and ligated into pXW06 between the same sites to generate pDY45 and pDY99, respectively. The *bbBeasM23 with M1-M2 linker* and *bbBeas-M23 without M1-M2 linker* inserts were excised from pDY38 and pDY91 with *SpeI* and *PmlI* and ligated into pXW55 between the same sites to yield pDY58 and pDY98. The *bbBsIsM1 with M1-M2 linker* and *bbBsIsM1 without M1-M2 linker* inserts were excised from pDY69 and pDY95 with *NdeI* and *PmeI* and ligated into pXW06 between the same sites to generate pDY73 and pDY102. The *bbBsIsM23 with M1-M2 linker* and *bbBsIsM23 without M1-M2 linker* inserts were excised from pDY72 and pDY90 with *SpeI* and *PmlI* and ligated into pXW55 between the same sites to generate pDY78 and pDY97.

The *bbBsIsM23a with partial M1-M2 linker* insert was excised from pDY62 with *SpeI* and ligated into pDY60 at the same site to generate pDY68. Then the *bbBeasM1-bbBsIsM23a* insert

was excised from pDY68 with *Nde*I and ligated into the pDY42 (harboring the entire *bbBsls* gene) vector treated with *Nde*I to replace a fragment to afford pDY70. The *bbBeasM23a* with partial M1-M2 linker insert was excised from pDY66 with *Spe*I and ligated into pDY61 at the *Nhe*I site to generate pDY67. The *bbBslsM1-bbBeasM23a* insert was then excised from pDY67 with *Nde*I and ligated into the pDY37 (harboring the entire *bbBeas* gene) vector treated with *Nde*I to replace a fragment to generate pDY71.

The plasmids constructed in this work are shown in Table S2.

4. Transformation of *S. cerevisiae* BJ5464-NpgA and fermentation of the engineered strains

Plasmids were introduced into *S. cerevisiae* BJ5464-NpgA using the lithium acetate method. Correct transformants were selected by appropriate autotrophy. The engineered *S. cerevisiae* strain carrying pDY37, pDY42, pDY70 or pDY71 was fermented in a SC-Ura dropout medium (6.7 g L⁻¹ yeast nitrogen base; 20 g L⁻¹ glucose; 0.77 g L⁻¹ -Ura DO supplement) at 30°C with shaking at 250 rpm. When the OD₆₀₀ reached 0.6, equal volume of YP medium (10 g L⁻¹ yeast extract; 20 g L⁻¹ peptone) was added. The cultures were maintained under the same conditions for an additional 72 h to produce the cyclooligomer depsipeptides (CODs). Strains carrying a pXW55 derived plasmid and a pXW06 derived plasmid were fermented in a SC-Ura-Trp dropout medium (6.7 g L⁻¹ yeast nitrogen base; 20 g L⁻¹ glucose; 0.72 g L⁻¹ -Trp/-Ura DO supplement) at 30°C with shaking at 250 rpm until the OD₆₀₀ reached 0.6, and then equal volume of YP medium was added. The fermentation broths were cultured under the same conditions for an additional 72 h to produce the corresponding CODs.

5. Extraction and analysis of the products in the engineered *S. cerevisiae* strains

A typical procedure used to analyze the products in the engineered *S. cerevisiae* BJ5464-NpgA strains is given below. 100 mL of fermentation broth was centrifuged at $2,737 \times g$ for 5 min to separate the supernatant and the cells. The supernatant was extracted three times with 100 mL of ethyl acetate, and the cells were extracted twice with 50 mL of methanol. The extracts were then combined and evaporated *in vacuo* to dryness. The residue was re-dissolved in 500 μL of methanol and analyzed on an Agilent 6130 Single Quad LC-MS (C18, 5 μm , 4.6 mm $\times$ 250 mm column). A linear gradient of acetonitrile-water (containing 0.1% formic acid) was programmed from 80% to 100% over 20 min at a flow rate of 1 mL min⁻¹ and the metabolites were monitored at 210 nm. Standard curves based on the linear relationship between the amounts and the peak areas were established for beauvericin, beauvericin A, beauvericin B, beauvericin C and bassianolide for quantitative measurement of their production in different engineered strains.

Table S1 Primers used in this work. The restriction sites are in bold.

Primer	Sequence	Restriction sites
BEAS-M1-5	aa CATatg gagccgctcaaaaatgt	NdeI
BEAS-M1-short-3	aa GTTTAAAC tcacatcacggcctgaagacgag	PmeI
BEAS-M23-short-5	aa ACTAGT tcttactctcaaggctcgatt	SpeI
BEAS-M23-3	aa CACGTG tcacaaagccgagtttagac	PmlI
BSLS-M1-5	aa CATatg gagccaccaacaacgc	NdeI
BSLS-M1-short-3	aa GTTTAAAC tcaaatagctgcctggaggctgg	PmeI
BSLS-M23-short-5	aa ACTAGT tcatactcgcaaggctgact	SpeI
BSLS-M23-3	aa CACGTG tcataaagacgcattcaaagcc	PmlI
BSLS-M1-long-3	aa GTTTAAAC tcactgttcacaggaccatccaa	PmeI
BSLS-M23-long-5	aa ACTAGT gggtggcagctcaatgaccgt	SpeI
BEAS-M1-long-3	aa GTTTAAAC tcactgctcaacgggtccgtcca	PmeI
BEAS-M23-long-5	aa ACTAGT agcggcgattctacgccctc	SpeI
20120725BEAS-M1-3	aa ACTAGT gatggtcgagggcgtagaat	SpeI
20120725BSLS-M23a-5	aa ACTAGT atcccggcgctagctttgga	SpeI
20120725BSLS-M23a-3	aa ACTAGT gtg catatg ggatgcttgaaagt	NdeI, SpeI
20120725BSLS-M1-3	atccaaag ctagc gccgggat	NheI
20120725BEAS-M23a-5	aa ACTAGT ttgggacggaccggttgagca	SpeI
20120725BEAS-M23a-3	aa ACTAGT ttg catatg cgtggctggata	NdeI, SpeI

Table S2 Plasmids constructed in this work.

Plasmid	Description
pDY38	<i>bbBeasM23 with M1-M2 linker</i> in pJET1.2
pDY39	<i>bbBeasM1 with M1-M2 linker</i> in pJET1.2
pDY45	<i>bbBeasM1 with M1-M2 linker</i> in pXW06
pDY58	<i>bbBeasM23 with M1-M2 linker</i> in pXW55
pDY60	<i>bbBeasM1 with partial M1-M2 linker</i> in pJET1.2
pDY61	<i>bbBsIsM1 with partial M1-M2 linker</i> in pJET1.2
pDY62	<i>bbBsIsM23a with partial M1-M2 linker</i> in pJET1.2
pDY66	<i>bbBeasM23a with partial M1-M2 linker</i> in pJET1.2
pDY67	<i>bbBsIsM1-bbBeasM23a</i> in pJET1.2
pDY68	<i>bbBeasM1-bbBsIsM23a</i> in pJET1.2
pDY69	<i>bbBsIsM1 with M1-M2 linker</i> in pJET1.2
pDY70	<i>bbBeasM1-bbBsIsM23</i> in pXW55
pDY71	<i>bbBsIsM1-bbBeasM23</i> in pXW55
pDY72	<i>bbBsIsM23 with M1-M2 linker</i> in pJET1.2
pDY73	<i>bbBsIsM1 with M1-M2 linker</i> in pXW06
pDY78	<i>bbBsIsM23 with M1-M2 linker</i> in pXW55
pDY90	<i>bbBsIsM23 without M1-M2 linker</i> in pJET1.2
pDY91	<i>bbBeasM23 without M1-M2 linker</i> in pJET1.2
pDY94	<i>bbBeasM1 without M1-M2 linker</i> in pJET1.2
pDY95	<i>bbBsIsM1 without M1-M2 linker</i> in pJET1.2
pDY97	<i>bbBsIsM23 without M1-M2 linker</i> in pXW55
pDY98	<i>bbBeasM23 without M1-M2 linker</i> in pXW55
pDY99	<i>bbBeasM1 without M1-M2 linker</i> in pXW06
pDY102	<i>bbBsIsM1 without M1-M2 linker</i> in pXW06

BbBEAS	1	MEPLK-NVNTGQPCSTVFPF-VSDETVHEHLNGLYEEINRRFGLDRDAIETILPCTPFQYDVLDG	62
BbBSLS	1	MEPPN-NANTGQLGPTLP-----NGTVDLPTDLSREITRHFGLQEDEIEEILPCTPFQRDVIEG	58
XsBSLS	1	MASLNGMVGIGQHDPAITASSVPDDAGRHHNLRQVARRFGLDKAKIENILPCTPFQSDVMDC	64
FeESYN	1	MSLHTPSDGGQD--PALAS-----KTLCEQISRALGLGQDKIENIFPGTPFQRDVIDC	51
FvBEAS	1	MEYLTAVDGRQDLPTTEASF--CSHGDSPLNSSYEQIFHLYGLDSSRIEAIKPCTPFQDLMIDC	62
BbBEAS	63	AANDARHAVGHAMYEISQHVHVQRFIAAWRETVRRTPALRACTFTSTTGESFQLVLIRESEFVLSR	126
BbBSLS	59	ASDDKRRAVGHVVYEIPEDVDTERLAAAWKATVRYTPALRTCIFTSETGNAFQVVLRDYFFIFAR	122
XsBSLS	65	AVDDGRRAIIGHVVYEIPRNIDTQRLATAWKEVVVRQTPALRTCIFTSEAGDCFQVVLITESFFVWM	128
FeESYN	52	AADDKQRAVGHAVFEIPKDIIDAARLAAAWKETVLHTPALRTCTFTSKSGDVLQVVLIRDSFVFSW	115
FvBEAS	63	NALDKQSAIGHAVYDVPTDIDISRFALAWKEIVNQTPALRAFAFTSDSGKTSQVILKDSFVFSW	126
BbBEAS	127	IYWSSSSSLQAAVLKDETTAAIAGPRCNRILVLEDPDTRKQLLIWVHHLALVDSTVQEPILRRV	190
BbBSLS	123	MYCP-SAHLKSAIVKDEATAAAGPRCNRIVLTGEPNSKRRVLVWTFSHSFVDSAFQGRILQQV	185
XsBSLS	129	QITS---FDLKEAVQDEAGAAAGPRCNRIVLEDSSTKQRILLIWTFSHALVDNVLQERILRRV	189
FeESYN	116	MSGP-SVDLKKEAVQDEAAAAAGPRCNRIVLEDPDTKERQLIWTFSHALVDSTFQERILRRV	178
FvBEAS	127	MCWS-SSSSPDEVVRDEAAAAAGPRCNRIVLEDMQTKKCOLVWTFSHALVDVTQQRVLSRV	189
BbBEAS	191	IAAYKSEDDQL---DSLPLTPDSSGGSDSD-SFS-TIKMPRAFDQEKATQFWQRQISGLDASVF	249
BbBSLS	186	IAAYKDGHGRV---FSLQPTTDLTSENGD-HLS-TASERTVVIERATQFWQEKIHGLDASVF	244
XsBSLS	190	IAAYDGGN-----VQYAN-GLI-IANPQARDTEGAARFWRQHFDGLNASVF	234
FeESYN	179	IAAYKNDANDEHPRQFETPDSSQATPEEDLQPNESKMKIPQAADMDRAVEFWKDHLSGLKCFCL	242
FvBEAS	190	IAAYKHEKDTHT--RPETPESSDAT-DTDSQ-SFS-VSMSCEDNAVSATHEFWQTHLNDLNASVF	248
BbBEAS	250	PIPISSHLTTKIDAKIPIHYISWPASAAQHRWSSTTVCAALAVLLSRYSHSSEALFGVVTQVC	313
BbBSLS	245	PIPIPSHRKVEAIDARADHYLPCPP-FIQHEWSSTTVCRTALAILLARYTHSSEALFGVVTQS-	306
XsBSLS	235	PIPIPSHTVVEDTQSEHRISYPR-LAQKQWSNTAVCRAALAVLLARFTHAPEALFGVVTTERPH	297
FeESYN	243	PIPIVLSVVYAHDAKAEHRISYSS-SAQQKMSATICRTALAILLSRYTHSPEALFGIVTEQTP	305
FvBEAS	249	PIPISDHLMVENITTTAETHRITFPL-SQKALSNSAICRTALSLLSRYTHSDEALFGAVTEQSL	310
BbBEAS	314	MFEGQRLLINGPIIRSVVPFRVHCQPEQSVTDLLKSIASDNHDMRQFAHVGLCNISRIQDDQSAA	377
BbBSLS	307	-HEEHPLLLDGPPISTVVPFRVLCALNQSVMKMEATTHYDHDNRQFAHAGLCNISIRIGDDASAA	369
XsBSLS	298	AFKEQEHLMNSPIRTVVPPIRVLCASDQSVSDILRAITTHDDAMHEFEQAGLRNIRNAGDDASAA	361
FeESYN	306	LLEEQ-LMLDGPPIRTVVPPIRVSCASEQSVSDIMSTIDSYDQTYRQFAHAGLRNIASAGDDESAA	368
FvBEAS	311	PFDKH-YLADGTVQTVAPLRVHCQSNLRASDVMDAISSYDDRILGHAFPEGLRDIRNTGDNQSAA	373
BbBEAS	378	CRFQTVLISVSNRRSSEDAASGEVLQILQESEGFAPCADRALLRCETSRQGALLVARYDQGVIE	441
BbBSLS	370	CGFQTVLIMVTDISRT---AGDDETHQVLEESEKFIPTCTDRALLSCQMTDEGVLLVARYDQSILE	430
XsBSLS	362	CGFQTVLILVTDSDTP-QTPGSALHRIVEESDRFVPCNTRALLNCQMADDSALLVARYDQSVID	424
FeESYN	369	CGFQTVLIVSDGDAQP-ASTWEILKKTEPEGFIPCTNRALLSCQMTSSGAHLTARYDQSILID	431
FvBEAS	374	CGFQTVLILVTDGSHVN-NGINGELQQITESSHFMPCNNRALLLHCQMESSGALLVAYYDHNVID	436
BbBEAS	442	PPQMARFILRLQGLWLMELQSAADDALSVKQLDIVTREIDRAETISWNSDALEVQESLIHSAFVVR	505
BbBSLS	431	PLQMARFILRLQGLFLINKLQS-TDGSPCVGQLDVLAPEDRTEIRGWNSEPLQTDCLHSEVVVN	493
XsBSLS	425	SRDVARFILRLQGLGLIKQLQS-HAIDLPLGQLDVITQEDRAETISWNSDRLQTSDDVTIHDVIAKR	487
FeESYN	432	AEQMARILRLQGLHLIQNLQTSIDLQ--VEKVDMMTQEDWLEIRWNSDSIDAQDTLHSEMLKW	493
FvBEAS	437	SLQTTIRLLQGLQGLIKCLOSPDLSS-MAEINLMTEYIDRAETISWNSQPLEVQDTLHHEMLKA	499
BbBEAS	506	AAESPSDPAVLWSWDGAWTYSELDNVSSRLAAHIRSLDSHEQLIVPVYFEKSKWVASILAVLK	569
BbBSLS	494	AGDTPNKPAVCAWDGENTYSELNNVSSRLASYISSLDLG-QQLIVPIYLEKSKWVMAAILAVLK	556
XsBSLS	488	AADAPRKIAVSAWDGENTYNEINNVSSRLAGHIQSLDLGQGQAVIPLCFEKSQWVWAGMLAVLK	551
FeESYN	494	TSQSPNKAAVWDGENTYAELDNVSSRLAHINSIDLKGEHAIVPIYFEKSKWVWASMLAVLK	557
FvBEAS	500	VSHSPKTKATIQAWDGDWTYSELDNVSSRLAVHIKSLGLRAQQAIVPVYFEKSKWVWASMLAVLK	563
BbBEAS	570	AGHAFTLIDPKDFPARTTRIVQTSAKVALTSKLHQDTVQAIIIGRCITVVDDETVQSISGSASQCQ	633
BbBSLS	557	AGHAFTLIDPNDFPARTAQIILQASASTALTSALHQSKMQAVIGRCITVVDDELVTITTFEGSQ	620
XsBSLS	552	TGRAFTLIDPNSFARMSQVCROTSAKVALTSQLHYDTMRVVQGCITVVDENLLQSLPCDEDRL	615
FeESYN	558	AGHAFTLIDPSDFPARTAQVVQQTSAIVALTSKLHRETVQSTVIGRCITVVDDEFVKSIIPQ-SSEL	620
FvBEAS	564	SGNAFTLIDPNDFPARTAQVVQQTSAIVALTSKLHRETVQKLVIGRCITVVDDELLQSVISA-SDDF	626
BbBEAS	634	EKSELTVKPHNLAYAIFTSGSTGDPKGIMIEHQAFASCVAKFGPAL-IPHNARALQFASHGFGA	696
BbBSLS	621	VAS--AAKPGDLAYVIFTSGSTGDPKGIMIEHRAFYSSVVKFGKALGIRSSSTRALQFATHGFGA	682
XsBSLS	616	NPA--VK-PQDLAYVIFTSGSTGEPKGSIMIEHRGFTSCALKFGPALGINSSTRALQFASYAFGA	676
FeESYN	621	SAS--VK-AHDLAYVIFTSGSTGIPKGIMIEHRSFSSCAIKFGPALGITSSTRALQFGSHAFGA	681
FvBEAS	627	SSL--TK-SQDLAYVIFTSGSTGDPKGIMIEHRAFSSCALKFGASLGINSSTRALQFGTHAFGA	687
BbBEAS	697	CILEIIPTLIRGGCVCIPSDLDRMHNHIFDIRRYNVNWMMATPSYMTTFKPEDVPGLQTLILVG	760
BbBSLS	683	FLLEVLITTLIHGGCICVPSDDHRMHNHIFGFIROQNINWMMATPSYMTTMKPEDVPGLIETLVLVG	746
XsBSLS	677	CILEIIVTLLMHGGCVCIPSDDDRMNNVDFIKRSGVNWALLTPSFTGTIQPESVPGLQTLVLVG	740
FeESYN	682	CILEIMTTLIHGGCVCIPSDDDRMNNVLEFINRTNVQLGHATPSYMGTFQPEVVPGLKTLVLVG	745
FvBEAS	688	CILEIMTTLINGGCVCIPSDDDRMNHSIFINRYNVNWMMATPSYMGTFSPEDVPGLATLVLVG	751

BbBEAS	761	EQMSASVNATWASRLGLFDGYGQSESSICFVGKISPVSEANNIGRAVGANSWIVHFDDEPDR	823
BbBSLS	747	EQMSSSINDVWASELQLLDGYGQSESSICFVGKIDSSRDPNNLGWATIGANSWIINFDNPDQL	810
XsBSLS	741	EPMSATMRDWTAPRVRLINGYQSESATICSVTKINPFSSEPNSIGRAVGANFWITTFNEPNHL	804
FeESYN	746	EQMSASVNEVWAPRVQLINGYQSESSICCVAKISPGSSEPNNIGHAVGANSWIVDEDEPNRL	809
FvBEAS	752	EQMSSSVNAIWAPKQLQLINGYQSESSICFASNMS---TEPNNMGRAVGANSWVIDENDINRL	812
BbBEAS	824	APVGAVGELLIESPGIARGYLAPATVRNPFLETAPAWYAPRQPPTGVKFFYRTGDLARYAADGT	887
BbBSLS	811	VPIGATGELLIESPGIARGYLSQSTET-PFLERAPAWYASKQPPYGVKFFYRTGDLARYAPDGT	873
XsBSLS	805	VPIGCTGELVIESPGIARGYIVSPPRNSPFLAKAPAWYPTKQLPDGVKFFYRTGDLVCYRSDGT	868
FeESYN	810	APIGAVGELVIESAGIARDYIVAPTQKSPFKTAPTWYBAKQLPDGFKIYRTGDLACYASDGS	873
FvBEAS	813	VPIGAVGELVIESPGIARDYIVPPPPKSPFTTDIPSWEANTFPDGAFLYRTGDLARYASDGS	876
BbBEAS	888	IVCLGRIDSQVKIRGQRVEMGAVETRLRQOVPSDITVVAEAVKRSRSSGSTVITAFLLDSSDKN	951
BbBSLS	874	VICLGRMDSQVKIRGQRVELDAIENLLRQFPSDVTVVAEAVKRSDLPSSVITGFLISS--EY	935
XsBSLS	869	VYVLGRRDSQVKIRGQRVETSEVEAGLRQSSSHIMPVVEAVKRLDSSNSTVLVAFLLGLS---	929
FeESYN	874	IVCLGRMDSQVKIRGQRVELGAVETHLRQMPDDMTIVVEAVKFSDSSTTVITAFLLIGA----	933
FvBEAS	877	IVCLGRIDSQVKIRGQRVELGAEETHLRQMPDDLTVVEATKRSQSANSTSLIAFLLGSS--Y	938
BbBEAS	952	NSSAASAKDARILDQTTQEMNAKLCOVLPPHSVSPSCYICMHALPRTATGKVDRKTLRSIGSKL	1015
BbBSLS	936	VVGAPSTEDTYILDQVVTQETNAKMROILPAHSIPSFYICMKSLPRTATGKVDRRKLRISIGSSL	999
XsBSLS	930	-KGGEEAADAYILETSAGGINAKLQOVLPQHSIPSFYIRMKDLPCATGKTDRRRLRSIAISKL	992
FeESYN	934	---GEKNS--HILDQRTRETNAKMEQVLPRHISIPAFYISMNNLPQTATGKVDRRKLRIMGSKI	992
FvBEAS	939	--FGNRPDSAHILDHDTKAINIKLEQVLPRHISIPSFYICMLELPRATGKIDRRRLRIMGKDI	1000
BbBEAS	1016	LEQQAYKKSPETMQKSKSAETLETGPEAKLKEVWLQSENLEEAPKPCGASFFELGGDSITAIKM	1079
BbBSLS	1000	LALQAQSTAP---RSSQAPDASAG-VTKLEEVMMDIFNLTENSHNIGNFFAALGGDSITAIKM	1058
XsBSLS	993	LSBLFQNVAS---QPSAKHGSSATSTEDKLRIFWFRGNLDLKSNSGRASFFELGGDSITAIKM	1053
FeESYN	993	LSQKTHSTPS---QSQAAISSGTDYTKLESTWITSLDLEPGSANMSATFFEMGGNSITAIKM	1053
FvBEAS	1001	LDKQTQGAIV---QQAPALIPVFADTAAKLHSVWVQSLGIDEATVNVGATFFELGGNSITAIKM	1061
BbBEAS	1080	VNMARAAGTELKVSDFIQNPTTLARLQAVNSGSDSTPSTIITPFATIPASTWDGPV-EQSYSQGR	1142
BbBSLS	1059	VNMARAAGTQLKVSDFIQNPTTLASLQAATGGSS--MTVTS---IPALALDGPV-EQSYSQGR	1115
XsBSLS	1054	VNMARSAGIVLKVSDFIFHNPTLAGLIDVIGQGS--APYSP---IPTTTYSGPV-EQSYAQGR	1110
FeESYN	1054	VNMARSNGTELKVSDFIYNPTTLAGLKAIVIGTS--LPYSL---IPKVTRQGPVSEQSYAQNR	1111
FvBEAS	1062	VNMARSVGNDLKVSNIYQHPTLAGLSAVVKGDP--LSYTL---IPKSTHEGPV-EQSYSQGR	1118
BbBEAS	1143	WFLDQLDITGAVWYLIPYAVRMRGALNIDALRAALLALEQRHETLRTTTFENQNGVGVOIVHQLA	1206
BbBSLS	1116	WFLDQLEIGANWYTIPYAVRLRGPLDVALNRRALLALEKRHETLRTTTFEDQDGVGVQIITHETLL	1179
XsBSLS	1111	WFLDQLKLGSWYLIPYGVRRMGPLRVDLTIALLALEQRHETLRTTTFEERDGVGVQIVVHASI	1174
FeESYN	1112	WFLDQLSEGASWYLIPFAVRMRGPVDVDALTRALLALEQRHETLRTTTFENQDGVGVQIITHDRLS	1175
FvBEAS	1119	WFLDQLDVGSLWYLIPYAVRMRGPVNVDALRRALLALEQRHETLRTTTFEDQDGVGVQIVHEKLS	1182
BbBEAS	1207	KEKRLIDASS-HGDDGYLOPLEQEQTTPFDITSEAGWRASLTCVGEDHHVLSIVMHHIISDGWS	1269
BbBSLS	1180	DQRLRTINAD--HAD--YQLLKQEQTAPFNLAASESGWRVSLIRLDDDDNLSIVMHHIISDGWS	1239
XsBSLS	1175	KEKRLIDITDQKGD--YQSLQEQQAAPFDVITSEAGWRVSLIRLGEDDHILSIVMHHIISDGWS	1236
FeESYN	1176	KEKQVIDALD--GDEGGKTLYKVETTTFDITSEAGWSLTLIRLKGDDHILSIVMHHIISDGWS	1237
FvBEAS	1183	EEKVIDLACG--SLDLPFEVLNQEQTTFNLSSEAGWRATLLRAGEDDHILTIVMHHIISDGWS	1244
BbBEAS	1270	IDVLRQELIQLYAAVLHGDEDFLSAVSPLPIQYRDFSMQRR-QQVAEHDRQLQYWKQLADCS	1332
BbBSLS	1240	IDVLRRELQLYAAALHGADLFGSALSPLPIQYRDFSVWQKQDAQVAEHERQLQYWKQLADCS	1303
XsBSLS	1237	IDILRQELSKFYAAALRG-HDELSGISPLPIHYRDEFAVWQKQEEQVAEHQRLQLEYWTHQLADST	1299
FeESYN	1238	IDVLRRELQLYAAALQ-GKDFSSALTPLPPIQYSDFAVWQKQEAQAAEHERQLQYWKQLADSS	1300
FvBEAS	1245	IDVLRRLNLQLYSAAALKDSKDELSTALTPLPPIQYSDFAKQKQD--QFLEQEKQLNYWKKQLKDSS	1306
BbBEAS	1333	PAKLPTDFRPPPLSGDAGSVPEVETISGELFQKLHRCFNVSTSTPFVALLAAFRAAHYRLTGVD	1396
BbBSLS	1304	PAKLPTDFHRPALLSGKATTVPVTITISELYYRLQEFCTFNNTSEFVLLATFRAAHYRLTGVD	1367
XsBSLS	1300	PAEFLTDIPRPTILSGQAGFVPVTIDGELYKKLREFCKAQQMTSFAVLLAAFRAAHYRLTGAED	1363
FeESYN	1301	PAKIPTDFRPPDLSGDAGVVPVAIDGELYQKLGRFCNKHNSAFSTILLAAFRAAHYRLTAVDD	1364
FvBEAS	1307	PAKIPTDFARPALLSGDAGCVHVTIDGELYQSLRAFONEHNTTSFVLLAAFRAAHYRLTAVED	1370
BbBEAS	1397	AVIGTPIANRRNRPFLERLIGFFVNTQCMRITVDD-DTFEGLVRQVRRTTTEAFENEDVPFERV	1459
BbBSLS	1368	AVIGTPIANRRNRELENLIGFFVNTQCMRITINEDDTFESLVRQVRSTTTAAFEHEDVPFERV	1431
XsBSLS	1364	ATIGTPIANRRNRELENMIGFFVNTQCMRITIDGE-DTFESLVRQVRSTATAAFEHQDVPFERV	1426
FeESYN	1365	AVIGIPIANRRNRELENMIGFFVNTQCMRIADVDET-DTFESLVRQVRSTTTAAFAHEDVPFERV	1427
FvBEAS	1371	AVIGTPIANRRNRPFLDILIGCFVNTQCMRINIDHH-DTFGTLNQVKATTTAAFEHEDVPFERV	1433
BbBEAS	1460	VSANLPAGGGSRDLSQTPLAQLIFAVHVSQENLGRFEELEGESEPVANKKAYTRFDAEFHIFQTRD	1523
BbBSLS	1432	VSANLP---GSRDLSQNPLAQLVFATHSHKDLGKFELEALESEPLQNEVYTRFDAEFHIFQAPD	1492
XsBSLS	1427	VSALLP---GSRDTSRNPLVQLIFAVHVSQDDLGRFEELEGESEPVSNANVTRFDVEFHIFQEV	1487
FeESYN	1428	VSALQP---GHRDLSRTPLAQIMEFVHVSQKDLGRFEELEGESEPTASKKAYTRFDVEFHIFQAD	1488

FvBEAS	1434	VSAIQP---GSRDLSSSTPLAQILFAVHSQKDLGFEKFGLESVPVPSKMYTRFDMEFHLCQETD	1494
BbBEAS	1524	GLNGYLNFAAELFKLETMQNVVSVFLQILRHGLEQPKSLTSVLPLTDGKELDSMGLLKHFGHL	1587
BbBSLS	1493	GLTCYINFATELFKVFETIQNVVSVFLQILRHGLEHPQLISVVPLTDGLAELRSMGLLEIKK-V	1555
XsBSLS	1488	KLSGNFVFAADLFKLENIQNVVNVFYEILRQGDQPQPTAVLPLTDGLAELRSMGLLEIEK-A	1550
FeESYN	1489	GLKGSCNFATDLFKPETIQNVVSVFFQILRHGLDQPEICISVLPLTDGVEELRRDLLEIKR-T	1551
FvBEAS	1495	SLKGSVNFADLFKMETVENVVRVFEFELRNGIQSSRPVPSILPLTDGIVTLEKLDVLNVKH-V	1557
BbBEAS	1588	EYQRDSSSLVDIFRSQVATCPDTTDAVIDSSARLTYAQLDHQSNLLEAWIRRKGLPAESLVGVLSF	1651
BbBSLS	1556	EYPRDSSVVDVFRTQVASYPDTLAVVDSSSRSLTYAELDHQSDLLATWLRQQNLPTEALVVVLAP	1619
XsBSLS	1551	EYPRDSSVVDVFRDQVAHSDALAVTDSSSRSLTYAELDRKSDQLATWLRQQNMAAETVVGVLAP	1614
FeESYN	1552	NYPRDSSVVDVFREQAAANPEVLAVTDSSSRSLTYAELDNKSELLSRWLRFRNTPETLVSVLAP	1615
FvBEAS	1558	DYPRDSSLADVFQTVQVSAYPDSLAVVDSSCRLTYTELRQSDILAGWLRRRSPAETLVAVEAP	1621
BbBEAS	1652	RSCETITIAFLGILKANLAYLPDLDFKSPVSRMRDVLSDLPCHTITILLGSDVAAPDLELPCLELVR	1715
BbBSLS	1620	RSCETITITFLGILKANLAYLPDLDRSPITRMRDVLSTLPGRITALLCSDEVAPDFQLPSIELVR	1683
XsBSLS	1615	RSCQTITIAFLGILKASLAYLPFDVNIPAAQLQAVLSELSGHKLVLGSDTTAPKVQLSDVEFVR	1678
FeESYN	1616	RSCETIVAYVIGILKANLAYLPDLVRSPTVRMKDILSSVSGNTIVLMGSGVEDPGFDLPQLELVR	1679
FvBEAS	1622	RSCETIVAFEGVLKANLAYLPDLVRSPTVSRVQDILSGLSGPTLVLI GHDTAPDEEVTNVEFVR	1685
BbBEAS	1716	ISDALKS--GASAVNGSETTD--LSAPSANSLAYVLYTSGSTGFPKGVMVEHRAIVRLVQRGV	1775
BbBSLS	1684	IADALEEAAGMTSLNGHEHVP--VPSPSSTSLAYVLYTSGSTGFPKGVMTEHRAIVRLARSDI	1745
XsBSLS	1679	IKDITLH-----RDLNGHADVV--AASPSAKSLAYVIFTSGSTGFPKGVMVEHRSIIRLAKESNL	1736
FeESYN	1680	ITDTTDE----T----IEDVQ-DSPQPSATSLAYVLYTSGSTGFPKGVMTEHRAIVRLVKSNDL	1734
FvBEAS	1686	IRDALND----SNADGFEVIEHDSTKPSATSLAYVLYTSGSTGFPKGVMTEHRVILRTVTSGL	1745
BbBEAS	1776	ENFPPLRGAIMAHIFNTVFDGATVEIFLMLLNGGTLVCI DYLTTLISPKALETVFLREGINCAIM	1839
BbBSLS	1746	EDYRPACGDTMAHMFNTAFDGAIVETIYTMLLNGGTLVLCVDYMDTLSPKSLAEAVEKKEQVNATIM	1809
XsBSLS	1737	ISKLPT-AVTVGHISSIAFDAIIEVYITALLNGGTLVCI DYMTILDSKALEATFAREQVQAVLI	1799
FeESYN	1735	EGFPSP--ARMSNVFNPAFDGAIWEINWMLLNGGTLVCI DYLTTLIDGKELAAVEAKERVNAAFF	1796
FvBEAS	1746	ENYPSE--TRMAHMAIIAFDGASVEIYSALLFGRTLVCVDYMTTLDAHALKDVTFREHVNAAASH	1807
BbBEAS	1840	TPALLK-LYLANARDGLKGLDMLMVAGDRDFDQDAVEAQTLVRG-DCYNAYGPTENGVMSTLYK	1901
BbBSLS	1810	APALLK-LYLADARDALKGLDVLISGGDRDFDQDAVDAQSIVRG-SCYNGYGPTENGVFSTVYK	1871
XsBSLS	1800	TPALIK-QCLADAPAILAALDVLVSGGDRDFDQDAIAAQALVRG-GVYNAYGPTENGVMSTIYK	1861
FeESYN	1797	APAMLK-LYLVDAREALKNLDLFLVGGFERDFTKEAVEAMPLVRG-KIANIYGPTAAGIISTCYN	1858
FvBEAS	1808	VTSSSQDVPLRVFRRRLSRTLMMFFELVVTDTSTAPDALDAQGLYQVQCYNGYGPTENGVMSTIIP	1871
BbBEAS	1902	IDTDSFINGVPIGRAIDNSGAYITDPNQQLVGFGVLGELIVTGDGLARGYTDPALDRDRFVQV	1965
BbBSLS	1872	VDRNDPFVNGVPLGRAVNNSGAYVVDNRNQQLVGFGIIGELVVTDGGLARGYTERAFDQNRFTQL	1935
XsBSLS	1862	VTGNSFINGVPIGRAISNSGAYIMDPNQQLVPAGVMGELVVTDGGLARGYTDSTLDIDRFRVQV	1925
FeESYN	1859	IPKDBAYTNGVPIGGSIYNSGAYVMDPNQQLVGLGVMGELVVTDGQVGRGYTNPELNKNRFIDF	1922
FvBEAS	1872	IDTDSFINGVPIGRAINNNSGAYVVDPEQQLVGIGVMGELVVTDGGLARGYSKDALDENRFVHI	1935
BbBEAS	1966	VINGESVRARYRTGDRMRYRAGQDCLIEFFGRMDTQFKIRSNRIESAEEVAAILSHPLVRDAATV	2029
BbBSLS	1936	KVEGQSVRQYRTGDRVRYRVGEG-LIEFFGRMDTQFKIRSNRIEAGEVEAAILSHPAVRNAAVI	1998
XsBSLS	1926	NIDGQLVTARYRTGDRVRYRAGDG-QIEFFGRMDQQVKIRGHRIELAEVERAILSQNSVRDAVV	1988
FeESYN	1923	TIEGKTEKARYRTGDRMRARVGDG-LIEFFGRMDNQFKIRGNRIEAGEVESAMLSLKNVLNAAIV	1985
FvBEAS	1936	TVNDQTVKARYRTGDRVRYRIGDG-LIEFFGRMDTQFKIRGNRIESAEEVAAILRDSSVRDAVV	1998
BbBEAS	2030	VVGVEEQEPE-EMVGFVVAA--DDAVEQEATDNQVEGWQELFESSMYNGID-ALSPSALGKDT	2089
BbBSLS	1999	LR-VEEKLEP-EIVGFVVAEH-DDTAEQEEAGDQVEGWQAFESTTYTELD-TVSSSEALGKDFK	2058
XsBSLS	1989	IQ-NQEGGPE-EMVGFIVTQD-DHSTEQEEAGNHVEGWQDLEFESSTYADIN-TIDQSAL-HDFT	2047
FeESYN	1986	VRGGGEDEGELEMVGFIVADDKNDTTEEETGNQVEGWQDHFESGMYSDISTANDQSALGNDFK	2049
FvBEAS	1999	LQQN-EDQAP-EILGFVVADHDHSENDKQGSANQVEGWQDHFESGMYSDIG-EIDPSTLGSDFK	2059
BbBEAS	2090	GWTSMYDGSEIDKSEMQEWLDDTIHTLRDGHVFGHVLEIGTGGMILFNLGS-VESYVGLEPTK	2152
BbBSLS	2059	GWTSMYDGNEIDKAEMQEWLDDTIHTLTDGQALGHVLEIGTGSGMVLFNLGSGIQSFVGLEPSK	2122
XsBSLS	2048	GWTSMYDGSLINKAEMQEWLDDTIHTLTDGQALGHVLEIGTGSGMVMFNLGTGLQSYVGLEPSR	2111
FeESYN	2050	GWTSMYDGKDIDKGMQEWLDDAIHTLHNGQIERDVLEIGTGSGMILFNLNPGINSYVGLDPSK	2113
FvBEAS	2060	GWTSMYDGSQIDFDEMHEWLGETTRTTLHDNRSIGNVLEIGTGSGMILFNLDSRLVESYVGLEPSR	2123
BbBEAS	2153	SAAEFVNKAIKTLNLNLAGRAEVHTGTATDIDQLSGLRPDLVITNSVVOYFPPTVEYLTRVVDALV	2216
BbBSLS	2123	SAAAFVNNAIKSTPALAGRAQVFGVTATDTNKLDDLHPDLVIFNSVLQYFPPTRDYLERVVDALV	2186
XsBSLS	2112	SAAAFVNSTIKSTPALAGRAEVHGTATDISRLSGLCPDLVIVNSVVOYFPPTPHYLVEVVDTLA	2175
FeESYN	2114	SAAEFVNRAVESPKFAGAKVHVGMATDVNKLGEVHPDLVVFNNSVVOYFPPTPHYLAEVIDGLI	2177
FvBEAS	2124	SAAAFVNKATESIPSLAGAKVQVGTATDIDQVDDLHPDLVLVINSVIQYFPSPHYLAETADTLI	2187
BbBEAS	2217	RIRGVKRIEFFGDVRSQALHRQFLAACAHALG--KTATRDVRYMAEEREEREELLVEPAFFT	2278
BbBSLS	2187	HLRSAKRIEFFGDVRSYATNRHFLAARATYTLG--NHTTKDEVKKKMAEMEEREEREFLVEPAFFT	2248
XsBSLS	2176	RIRGVKRIEFFGDVRTATNRHFLAARAHALG--DKSTKESLRQKIAELEEREEREELLVEPAFFT	2237

FeESYN	2178	ALPSVKRIEFLGDIRSYATNGHFLLAARAHTLTGTNNNATKDRVRQKIQLERDEEEFLVEPAFFT	2241
FvBEAS	2188	HLPNVQRIFFGDVRSQATNEHFLLAARAHTLTG--KNAFKDDVRQKMAELEDMEEELLVEPAFFT	2249
BbBEAS	2279	ALMNRHPNLIQHVEILPKNIRATNELSAYRYAAVVHLRDPESAARFVYPIAADDWVDFQASQMR	2342
BbBSLS	2249	TLVNRLPD--VRHVEIIPKNMQATNELSAYRYAAVVHLRGSDELTRFVHPFKMDDWVDFQASHMH	2311
XsBSLS	2238	TLATRLPDQHEHVEILPKKMRATNELSAYRYAAVVHMRGSEERVQPVYPIINDNDWVDFQASQMD	2301
FeESYN	2242	TLKERRPDVVKHVEIIPKNNKATNELSAYRYTAVVHLRDET--DEPVYHTEKDSWVDFEAKQMD	2303
FvBEAS	2250	SLKDRFPGLEHVEILPKNMEAVNELSAYRYAAVVHVRGSLG-DELVLPEKDDWIDFQANQIN	2312
BbBEAS	2343	SDVIREYLRLSAGADTVAVCNIPYEKTIIFERLIVESLDDNTGSDAPQSR LHGRSLDGAPW-ISA	2405
BbBSLS	2312	KDALREYLRLAENTKTVAISNIPYKGTIFERQVVESLDE-TSEDAPHA-----SLDGAAW-ISA	2368
XsBSLS	2302	RDALLYLQRSADASTVAISNIPYSKTI LERHVESLDD--NGDNARS-----SLDGAAW-FSA	2357
FeESYN	2304	KTALLDHLRLSKDAMSVAVSNITYAHTAFERRIVESLDEDSKDDTKGT-----LDGAAW-LSA	2360
FvBEAS	2313	QKSLGDLIK-SSDAAIMAVSKIPFEITAFERQVVASINSN-----ID--EWQLST	2359
BbBEAS	2406	VRSDAESRASLSVPDLVQLAAESGFQVQVSAARQWSQSGALDAVFHRRHASSSQPTMRTLQFPF	2469
BbBSLS	2369	VRSDAKARSSLSVPDLVLLAKETGFRVEVSAARQWSQSGALDAVFHRYPA---EPGVRTLQFPF	2429
XsBSLS	2358	VRSDAERCASLSVTDLVQLGEEAGFRVEVSCARQWSQSGALDAVFHHYSP--AYKGARVLTIRFP	2419
FeESYN	2361	FRSEAENRASLTVPDILEIAKEAGFRVEVSAARQWSQSGALDAVFHHFFPP--SSTDRTLQFPF	2421
FvBEAS	2360	IRSEAEGDSSLSVPDIFRIAGEAGFRVEVSSARQWSQSGALDAVFHHC-----CSQGRTLVNFP	2418
BbBEAS	2470	DDNALRASATLITNRPLQLQRRRVAAQIRERLQTLVPSYMIPIAKIVVLQOMPLNANGKVDRKEL	2533
BbBSLS	2430	TDNDVRMSAPLTNQFLQLQKRRVAVQVREWLQDRIPSYMIPSHIVALQOMPLNTSGKVDRKEL	2493
XsBSLS	2420	TDQARRPATLITNRPLQLQSRREVSQVREELQVLLPSYMIPIARIVVVDQOMPLNASKVDRKEL	2483
FeESYN	2422	TDNELRSSLTLANRPLQLQRRRAALQVREKLQTLVPSYMVPPNIVVLDTMPLNTNGKIDRKEL	2485
FvBEAS	2419	TDHHLRGSDLLITNRPLQLQNRRIAIEVRERLRSLLP SYMIPSNIVVLQKMP LNANGKVDRKEL	2482
BbBEAS	2534	ARRARTTTMTKKKKFQRLASEPACFISDIEVALCEEATATFGMOVGISDHHFFKLGGHSLLATKL	2597
BbBSLS	2494	SRQAKAIKKVQKSAPP---TAPAFPLSEVEVMLCEEELTKTFEMDVNITDDFFQLGGHSLLATRL	2554
XsBSLS	2484	ARRAQVVPKSEAAPAQ-----VVPFLNEIEVMLCEEAFADVFGIDVVVTDNFFKLGGHSLMATKL	2541
FeESYN	2486	TRRARTLPKQQTAAFPV-----PDFPLSDIEITLCEEATEVFGMKVEISDHHFFQLGGHSLLATKL	2544
FvBEAS	2483	SRRAKVVPKQQTAAFL-----PTFPLISEVEVILCEEATEVFGMKVDITDHHFFNLGGHSLLATKL	2541
BbBEAS	2598	ISRVGDRILKARLTVKDVFDHPHISELAIVIREGLQN---VVPFVALNGGG-QAKQGSAGVVAERN	2657
BbBSLS	2555	VARTSHRIGARLTVKDVFDYPVHSELADIIRQQLASKNTLLPTASAGGGGQDKKESAG-VAPPT	2617
XsBSLS	2542	AARISRRIDARVSVKVEFDQPIVADLAASIRRGILASRN-LTPTTTFSGH--LGQVVSARVAERN	2602
FeESYN	2545	ISRIQHRLHVRVTVKDVFDSPVFADLAVIIRQGLAMQN---PVAEGQDK---QGWSRVVAPRT	2601
FvBEAS	2542	ISRIDQRILKVRITVKDVFDHPVFADLASVIRQGLGLQQ---FVSDGQG-----QDRSAHVAERN	2597
BbBEAS	2658	EMETMLCEEFANVLGMDVGVTDN--FFDLGGHSLMATKLAARIGRRLNNTTISVKVEFTEHPIVFQL	2720
BbBSLS	2618	OMEAMLC EE FANVLGMDVGITDN--FFDLGGHSLMATRLAARIGHRLNNTTISVKDIFSHFPVIFQL	2680
XsBSLS	2603	DIEAVLCKEFADVLGVLTLVSLTAFFDLGGHSLMATKLAARLSRLDAPISVKDIFDYFVPSKL	2666
FeESYN	2602	EVEKMLCEEFAAGLGVPVGITDN--FFDLGGHSLMATKLAVRIGRRLIRHHS-QGHLRLPCA FQL	2663
FvBEAS	2598	ETEAALLCDEFAKVLGFQVGITDN--FFDLGGHSLMATKLAVRIGRLDTTVSVKDVFDHEVLFQL	2660
BbBEAS	2721	ANSIEL-GQLES DR--VKHTMLADYTA FQLLSVEDLQGF LQNEISPOL ECAHGGTQDVYFATHM	2781
BbBSLS	2681	SAKIEV-SQLESSSG-GTDIKMPDYTA FQLIPADA EKFMQDHIYPQINFSQDMQDVYLATHM	2742
XsBSLS	2667	ANHIIH-TQFESYDL-TNGIPAADGASQLLAPEDFLAFIEREISPOLQYSSDTHLDVYRATQM	2728
FeESYN	2664	AKKIES-SHKSSEESGDDIQMADYTA FQLLDLEDPPQDFVQSQIRPOLDS CYGTIQDVYPSTQM	2726
FvBEAS	2661	AIAIDNLVQSKTNEIVGG-REMAEYSPQLLFTEDBEEFMASELKPOL E-LQETIQDIYPTQM	2722
BbBEAS	2782	QKAFLLCDASTGHFKPLVPFYIDFFPDS--DCSTIVEACSSLVKHFDMFRTVVVEAAGELYQVVL	2843
BbBSLS	2743	QQCFLRDV-FGRPKPLVPFYVEFFPDS--NPHTLATACTSLVDNYDIFRTIFVEAEGNLYQVVL	2803
XsBSLS	2729	QRLFLRNPRTGHPWTITPFCIDFFVDS--DCAKLAKACTSLVQHFDMFRTVFVLAAGQLHQVVL	2790
FeESYN	2727	QKAFLLFDPPTTGEPRGLVPFYIDFP SN--ADAETLTKAIGALVDKLDMFRTVFLEAAGDLYQVVV	2788
FvBEAS	2723	QKAFLLFDHTTARPRFPVPFYIDFFSTSEPDAAGLIKACESLVNLDIFRTVF AEASGELYQVVL	2786
BbBEAS	2844	EHDLDLQIDVVEIENVHAAINDFVDRIVEVPVHLGQPLQFTILKQASS--VRVLLCLSHALYDG	2906
BbBSLS	2804	KHINLDIDVVEIDANVHKTSSDLVDAIKEPVR LGQPMQVKVILKOTSS--VRVLLWL SHALYDG	2866
XsBSLS	2791	KQWDVPIETVEIETENINSATRAFLDLDLEKPVRLGEPVIRIAILKTKASPLRIILRMSHALYDG	2854
FeESYN	2789	EHNLPITETIETEKVNNTATGDYLDVHGKDPVRLGHPCIQFAILKTASS--VRVLLRMSHALYDG	2851
FvBEAS	2787	SCIDLP IQVLETEDNINTATNEFLDEFKPEPVR LGHPLIRFTILKOTKS--MRVIMRISHALYDG	2849
BbBEAS	2907	LSLEHVVRDLHMLKGRSLLPANQFSRYMQYMDHTRKACDFWRDVIQDTPTITVLGHVDAGGRE	2970
BbBSLS	2867	LSWEHIVRDLHILSKERSLLPATQFSRYMQYVDHTRGP CDFWRDVLQNAPIITNLSDAGSGGRP	2930
XsBSLS	2855	IELEQIVRS LHVLSGGSLFTPPKFARYMEHMANSRKDCYEFWRSVLQNSSMTSIESASSNARQ	2918
FeESYN	2852	LSFEYIVRGLHVLVSGRNLPPTQFARYMQYAAHSREEGYFPWFREVLQNA PMTVLHDTNNGMSE	2915
FvBEAS	2850	LSLEHVVRKLHMLVNGRSLLPFHQFSRYMQYTADGRESCHGFWRDVIQNTPTITISDDT--VVD	2911
BbBEAS	2971	LEVEAARTLHATKTIISIFLQAVRSSI--ITQATVFNAACALVLSRETGA KDVVFGRIVSGRQGI	3032
BbBSLS	2931	TKAGDPRVWHAGKVISGFSQAIRSS---ITQATVFNAACAIVLSKETGTDNVVFGRIVSGRQGI	2991

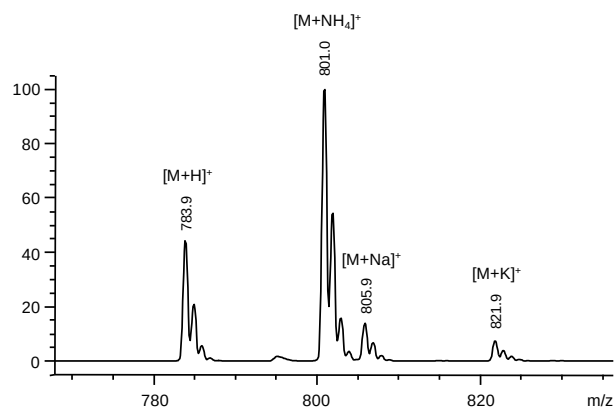
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FeESYN	2916	QEMPASKAVHLSEVNVVPAQAIRNSTN--TQATVENTACALVLAKESGSDVVFGRIVSGRQGL	2977
FvBEAS	2912	GNDATCKALHLISKIVNIPSOVLRGSSNIITQATVFENAACALVLSRESDSKDVVFGRIVSGRQGL	2975
BbBEAS	3033	PVSWQNIIVGPCTNAPVVRARIIDDDDDNHRQMLFDMQDYLLSLPFETIDFDEVRRSCTNWPAT	3096
BbBSLS	2992	PVRMQNIIGPCTNAPVRA-VVDAHG-NHQQMLFRLQEQYLLSLPYETIGFDEIKRSCTDWPD	3053
XsBSLS	2981	PIITQHVVGPCNTNIPVRL-CMDENP-NLRELLKMQDYLDLSPFETIGFDDLKKNCTEWSDE	3042
FeESYN	2978	PVVVQDIIGPCTNAPVHARVDDGNP---QRIIRDLRQYLRTLPFESIGFEEIKRNCTDWPEE	3038
FvBEAS	2976	PVEVQDIVGPCTNAPVRAHIESSDY---NQLLHDIQDYLLSLPHETIGFSDLKRNCTDWPEA	3036
BbBEAS	3097	ANNYACCTTYHDFSYHPSESEMQQORVEMGVLAARKDALLKEEPYDLAGIAGEVEFDGVHLQVTVV	3160
BbBSLS	3054	ARNYGCCVTYQNFYHPSEVDQORVEMGILAKKAELIKEEPLYNVAIAGEVEFDGVHLQVTVV	3117
XsBSLS	3043	TTYGCCIVYQNFNFHPESQVEEQRIQIGVLSREDQLANEASLHDLVLAGSPEFDGQHLHVTVV	3106
FeESYN	3039	LTFNSVCTYHNFYHPSEVDNQKVEMGVLAAYVELSENEPLYDLAIAGEVEADGVNLKVTVV	3102
FvBEAS	3037	ITNFSCCTYHNFYHPESQFEQORVEMGVLTAFVNTIEMDEPLYDLAIAGEVEFDGAGLKVTVI	3100
BbBEAS	3161	AKTRIFSEERAAAYLMEEVQRLTESLNSAL	3189
BbBSLS	3118	VDSQLFSQEGATHLMEQVCNTFQAINASL	3146
XsBSLS	3107	ANRQLCDDSRVKHMLEELCEMIETLSKALRDPYISDTNPANPESSLVAPVEIPRTPTNGFAPDI	3170
FeESYN	3103	AKARLYNEARIRHVLEEVCKTFNGLNEAL	3131
FvBEAS	3101	AKTQLFGRKRVEHLLLEVSKTEGLNSSL	3129
BbBEAS	3190		3189
BbBSLS	3147		3146
XsBSLS	3171	SSESRIHILGVGNLGKFVAHALRKRHPQLPITLLFHRADLVSEWDAAVKAITCVTSGVSDKSTG	3234
FeESYN	3132		3131
FvBEAS	3130		3129
BbBEAS	3190		3189
BbBSLS	3147		3146
XsBSLS	3235	FDVEFLSNSTGHKTLIKHLIVATRITYMTVSAVDLVKRRLESTSSILFLQNGMGKNRHRAMNDVK	3298
ESYN	3132		3131
FvBEAS	3130		3129
BbBEAS	3190		3189
BbBSLS	3147		3146
XsBSLS	3299	SRPSYWAGVCSCGVYPTSPFSIVHAGRGPIVLGRVLEEANDSPESTSAAASVAQDFMIQRLLP	3362
FeESYN	3132		3131
FvBEAS	3130		3129
BbBEAS	3190		3189
BbBSLS	3147		3146
XsBSLS	3363	DLEATLTTPNDIKEVQLQKLIVNSMINPLTVVFRCCNNGQLFGQPARLALMRTLDEAGEIVRAI	3426
FeESYN	3132		3131
FvBEAS	3130		3129
BbBEAS	3190		3189
BbBSLS	3147		3146
XsBSLS	3427	LPQESQKSGNSQLTNENLLAAVLRVAEMTGECCSSMLQDVQAGRRTIDHINGYLALQKRLGL	3490
FeESYN	3132		3131
FvBEAS	3130		3129
BbBEAS	3190		3189
BbBSLS	3147		3146
XsBSLS	3491	PYSNIETLVNMVQKGRAIVNGDIQSLFKMSGIKPMDLGKVLKAGSSNGAVAAYGKR	3546
FeESYN	3132		3131
FvBEAS	3130		3129

Fig. S1 Amino acid sequence alignment of five fungal CODs. BbBEAS: GenBank accession number ACI30655; BbBSLS: GenBank accession number ACR78148; XsBSLS: GenBank accession number ABR28366; FvESYN: GenBank accession number Q00869; FvBEAS: GenBank accession number AGC31490. The intermodular M1-M2 linker is boxed.

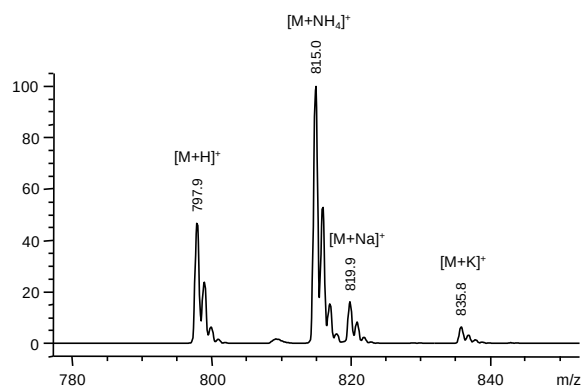
BbBEAS	1087	GLELKVSDIFQNPTLARLQAVMS	GDSTPSTITTPFATIPASTWDGPVE	QSYSQGRWFLDQLDI	1150
BbBSLS	1066	GIQLKVSDIFQNPTLASLQAAIG	SS--MTVTS----IPALALDGPVE	QSYSQGRWFLDQLEI	1123
VibH	1			MLLAQKPTWQRHLAYP	16
BbBEAS	1151	GAVWYLIPYAVRMRGAINIDALRA	ALLALEQRHETIRTTTFENQNGV	GVQIVHQRLAKELKIIDA	1214
BbBSLS	1124	GANWYTIFYAVRLRGFLDVDALNR	ALLALEKRHETIRTTTFEDQDGV	GVQIIHETILDQLRIINA	1187
VibH	17	HINLDTVAHSLRITGFLDITLLLR	ALHLTVSEIDLEFRARFSAQ---	GELYWHP--SPPIDYQDL	76
BbBEAS	1215	SSHGDGYLQPLEQEQTTPFDLTCE	AGWRAS--LICVGEDHHVLSIVM	HHIVSDGWSIDVLRQE	1276
BbBSLS	1188	D-HAD--YVQLLKQEQTAPFNLA	SESGWRVS--LIRIDDDDNILSIV	MHHIISDGWSIDVLRRE	1246
VibH	77	SIHLAEPLAWRQIEQDLQRSSTL	IDAPITSHQVYRLSHSEHLTYT	RAHHIVLDGYGMMLFEQR	140
BbBEAS	1277	LGQLYAAVLHGDEDFLSAVSPLP	IQYRDFSMWQRR-QQVAEHDRQ	LQYWRKQLADCSFAKLPTD	1339
BbBSLS	1247	LGQLYAAALHGADLFGSALSPLP	IQYRDFSVWQKQDAQVAEHER	QLOYWQKQLADCSFAKLPTD	1310
VibH	141	LSQHYQSLLSG-QTETAAFKPYQ	SLEEEAAYLTS----HRYWQDK	QFWQGYLR-EAPDLTLTS	198
BbBEAS	1340	FPRPILLSGDAGSVPEISGELFQ	KLHRECNVSTSTPFVALLAAFR	AHYRLTGVDDAVVGTPI	1403
BbBSLS	1311	FHRPALLSGKATTVPVTITSELY	YRLQEFCESTFNSTSFVLLAT	FRAAHYRLTGVDDAVIGTPI	1374
VibH	199	ATYDFQLS-HAVSLSYTLNSQLN	HLLKLAN-ANQIGWPDALVALC	ALYLESAEPDAPWLWLPF	260
BbBEAS	1404	ANRNRPLELERLIGFFVNTQCM	RITVDDD-DTFEGLVRQVRRTT	TEAFENEDVPERFVV	SAMPLPA 1466
BbBSLS	1375	ANRNRHLENLIGFFVNTQCMRI	TINEDEDTFESLVRQVRSTTT	AAFEHEDVPERFVV	SAMPLP- 1437
VibH	261	MNRWGSVLANVPGLMVNS-	-----	LPIILRLEAQQTS-	290
BbBEAS	1467	GGGSRDLISQTPLAQLIFAVHSQ	ENLCKFELEGLESEPVANKAY	TRFDAEFHLFQTRDGLNGY	LN 1530
BbBSLS	1438	--GSRDLSONPLAQLVFATIHSH	KDLCKFELEALESEPLQNEVY	TRFDAEFHFFQAPDGLTGY	IN 1499
VibH	291	--LGNYLKQS--GQAIRSLYLH--	GRYRIEQIE-----	Q--D--QG-LN	323
BbBEAS	1531	FAAELEFKLETMQNVSVFLQIL	RHGLEQPKSLISVLPLTDGL	KELDSMGLLKHHRGLEYQR	DSS 1594
BbBSLS	1500	FATELEFKVETIQNVSVFLQIL	RHGLEHPQTLISVVPLTDGL	AELRSMGLLEIKK-VEYPR	DSS 1562
VibH	324	AEQSYEMSP-----FINILP--	ESP-----	HEADCQTELKVLASGS	REG-----IN 363
BbBEAS	1595	LVDIFRSQVATCFDTIAVIDSS	ARLTYAQLDHQSNLLEAWIR	RKGLPAESLVGVLSPRSC	ETII 1658
BbBSLS	1563	VVDVFRTQVASYPDTLAVVDSS	SRLTYAELDHQSDLLATWLR	QQNLPTEALVVVLAPRSC	ETII 1626
VibH	364	FT--FR---GS-PQHELCLDIT	ADLASYPQSH-----	WQS-----	HCERFP 398
BbBEAS	1659	AFLGILKANLAYLPLDPKSPV	SRMRDVLSDLPGHTIILLGSD	VAPDLELPCELELVRI	SALKS 1722
BbBSLS	1627	TFLGILKANLAYLPLDIRSPIT	MRDVLSTLPGRTIALLCSDE	VAPDFQLPSIELVRI	ADALEE 1690
VibH	399	RFFEQLLARFQQVEQD----	VAR----LLAEPALAA	TTSTRATAS	436

Fig. S2 Amino acid sequence alignment of BbBEAS, BbBSLS and a stand-alone NRPS condensation domain VibH (GenBank accession number AAD48879). The intermodular M1-M2 linker is boxed.

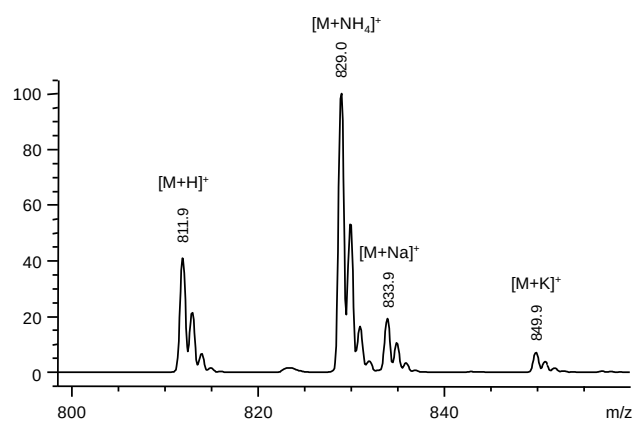
A



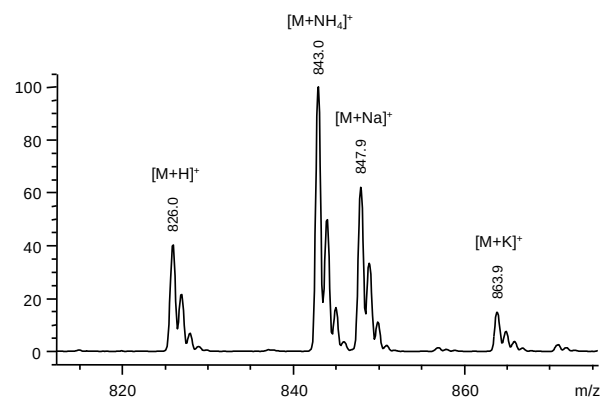
B



C



D



E

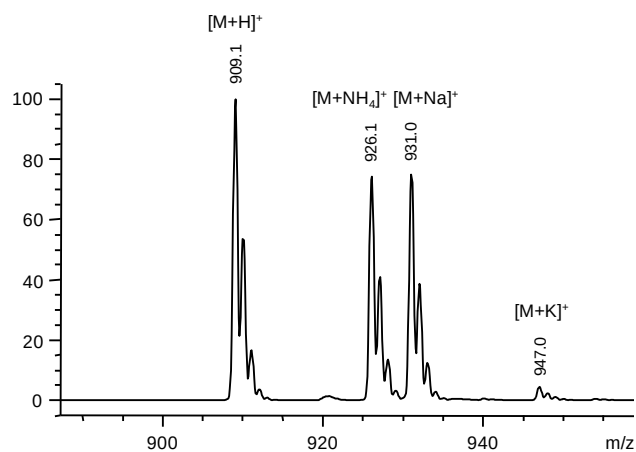


Fig. S3 ESI-MS spectra of beauvericin (A), beauvericin A (B), beauvericin B (C), beauvericin C (D) and bassianolide (E).