

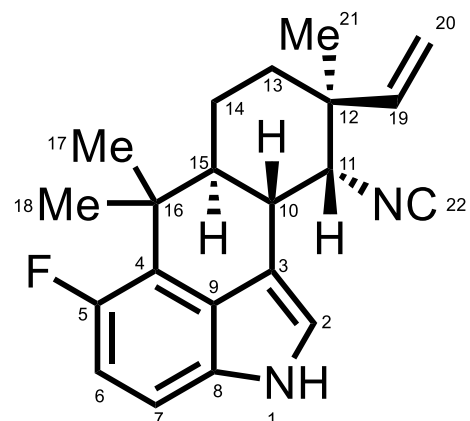
Supplemental Table

Table S1: Assigned numeral representation for the synthetic substrates, prenyltransferase and the Stig cyclases involved in the biosynthesis of natural and unnatural hapalindole/fischerindole are shown.

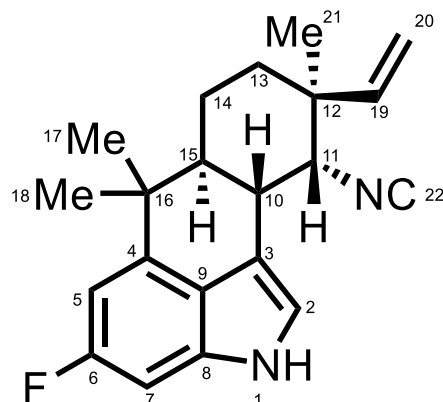
Synthesis/ Designated Protein	Substrate	Product	Assigned Number
Natural hapalindole/fischerindole system			
Synthesized	geranyl pyrophosphate (GPP)		1
Synthesized	<i>cis</i> -indole isonitrile		2
Enzymes			
Prenyltransferase (FamD2)	1 and 2	<i>cis</i> -indole isonitrile-GPP (3GC)	3
Sig cyclases			
FamC1	3	12- <i>epi</i> -hapalindole U	4
FamC1 and FamC4	3	Hapalindole U	5
FamC3 and FamC4	3	Hapalindole H	6
FisC	3	12- <i>epi</i> -fischerindole U	7
Unnatural hapalindole/fischerindole system			
Synthesized	5-fluoro- <i>cis</i> -indole isonitrile		9
Synthesized	6-fluoro- <i>cis</i> -indole isonitrile		10
Enzymes			
FamC1	1 and 9	5-fluoro-12- <i>epi</i> -hapalindole U	15
FamC1	1 and 10	6-fluoro-12- <i>epi</i> -hapalindole U	16
FisC	1 and 9	5-fluoro-12- <i>epi</i> -fischerindole U	17
FisC	1 and 10	6-fluoro-12- <i>epi</i> -fischerindole U	18

Table S2: Proteomics analysis of FamD2 expression in the TT-assay containing exogenous plasmids FamD2, and the substrates 1 and 2 during *cis*-indole isonitrile-GPP intermediate 3 synthesis. The sequence highlighted in yellow showed the coverage of the synthesized protein. Note: Please see attached Excel Sheet 1

FamD2		
Total peptide	25	
Unique peptide	25	
Total PSM	906	
Coverage (%)	72.49	
Annotated Peptide Sequence	Sequence Positions	PSM FamD2
[-].MNDVNR.[I]	FamD2[1-6]	1
[R].IRTDIINVAK.[T]	FamD2 [7-16]	30
[R].TDIINVAK.[T]	FamD2 [9-16]	11
[K].TFGAEYSEK.[V]	FamD2 [17-25]	14
[K].VLDEVFQVFGEQFADNSFMIR.[T]	FamD2 [26-46]	155
[R].TSNKQPK.[L]	FamD2 [47-54]	10
[R].TSNKQPKLGCYFR.[Y]	FamD2 [47-60]	2
[K].QPKLGCYFR.[Y]	FamD2 [51-60]	7
[K].LGCYFR.[Y]	FamD2 [55-60]	16
[R].YHEEDESQGLAWDIAR.[K]	FamD2 [61-77]	335
[R].KSGLLSDQGRPVVDQLIPEICETFPIMADGVDFDVK.[H]	FamD2 [78-112]	45
[K].SGLLSQGRPVVDQLIPEICETFPIMADGVDFDVK.[H]	FamD2 [79-112]	28
[K].IWQSIK.[G]	FamD2 [118-123]	12
[K].GVVPVQDAFK.[L]	FamD2 [124-133]	22
[K].LSLPASVTTHSDFLK.[N]	FamD2 [134-148]	42
[K].HHTSEYYK.[N]	FamD2 [178-185]	1
[R].LCFYLPFLNR.[E]	FamD2 [224-233]	5
[R].EAVPQNLLNPLLK.[K]	FamD2 [234-246]	42
[R].EAVPQNLLNPLLKK.[Y]	FamD2 [234-247]	14
[K].KYINEAPALVDNPGFILGWSFGPQGK.[G]	FamD2 [247-273]	10
[K].YINEAPALVDNPGFILGWSFGPQGGK.[G]	FamD2 [248-273]	16
[K].VDVDYHGR.[T]	FamD2 [279-286]	3
[R].TVPLFMK.[V]	FamD2 [287-293]	64
[R].TVPLFMKVHSQPLPK.[A]	FamD2 [287-301]	1
[K].VHSQPLPK.[A]	FamD2 [294-301]	6
<p>FamD2 MNDVNRIRTDIINVAKTFGAEYSEKVLDEVFQVFGEQFADNSFMIRTSN KQPKLGCYFRYHEEDESQGLAWDIARKSGLLSQGRPVVDQLIPEICE TFPIMADGVDFDVKHGLAKIWQSIKGVVPVQDAFKLSLPASVTTHSDF LKNHHLDALYAFGIDYHHSSVNLDFDYHPKHHTSEYYKNLLQDLQF QPPSDELLELLTNGEIALTFNFASPRIERLCFYLPFLNREAVPQNLLNPL LKKYINEAPALVDNPGFILGWSFGPQGGKGTYYTKVDVDYHGRTVPLF MKVHSQPLPKAADFALAQ, 309 residues</p>		

Table S3: NMR characterization of 5-fluoro-12-*epi*-hapalindole U (15)[α]_D²⁵=+7.7 (c=0.07, CH₂Cl₂)

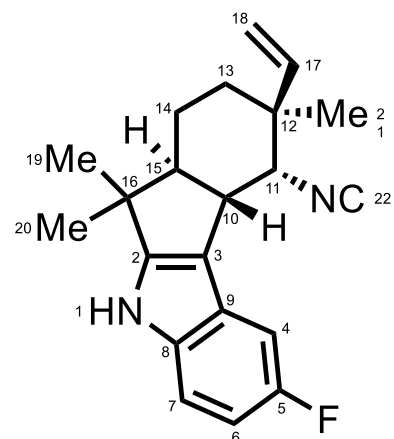
Position	¹³ C shift (ppm) (Fluorine coupling) C ₆ D ₆	¹ H shift (ppm), multi (J) C ₆ D ₆	COSY	HMBC
1		6.55, bs	2	
2	118.03	6.35, s	1	3, 4, 8, 9
3	113.75			
4	124.13, d, (13.1)			
5	154.29, d, (236.7)			
6	112.75, d, (29.2)	7.01, dd, (12.9, 4.4)	6	4,5,8
7	109.71, d, (10.1)	6.69, dd, (3.0, 8.7)	7	4,5,9
8	130.96			
9	127.08, d, (8.6)			
10	34.58	2.90, d, (11.5)	15	
11	63.35	3.90, s	10	10,12,13,15
12	39.73			
13	31.27	1.66, d, (3.7) & 1.44, m	14	12,14,15,21
14	21.17	1.48, d, (3.7) & 1.27, m	13,15	13, 15,21
15	43.98	1.98, td, (12.0, 3.4)	10,14	10,11,13,14,16,17,18
16	37.27			
17	23.07	1.11, s	18	9, 15, 16, 18
18	25.05	1.63, s	17	9, 15, 16, 17
19	142.17	5.39, dd, (17.7, 11.0)	20	11,12,13,21
20	114.47	(cis) 4.91, d, (11.0) (trans), 4.84, d, (17.7)	19	12, 19,21
21	28.35	1.18, s		11, 12, 13, 19
22	160.84			

Table S4: NMR characterization of 6-fluoro-12-*epi*-hapalindole U (16)[α]_D²⁵=+12.9 (c=0.04, CH₂Cl₂)

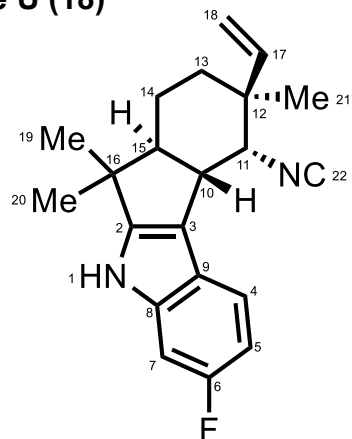
Position	¹³ C shift (ppm) (Fluorine coupling) C ₆ D ₆	¹ H shift (ppm), multi (J) C ₆ D ₆	COSY	HMBC
1		6.51, bs		
2	116.62, d, (3.2)	6.29, s		3, 8, 9
3	113.12			
4	142.37, d, (8.7)			
5	102.96, d, (25.9)	6.93, dd, (11.0, 1.8)		6,7,9
6	162.10, d, (236.5)			
7	95.36, d, (27.4)	6.69, d, (9.8)		5,6,9
8	134.02			
9	122.36			
10	34.88	2.95, d, (11.5)	15	3,15
11	63.45	3.88, s	10	10,12,13,15
12	39.81			
13	31.08	1.66, m & 1.43, m	14	11,15
14	21.66	1.41, d, (3.7) & 1.26, m	13,15	19
15	43.57	1.93, td, (11.9, 3.5)	10,14	
16	37.44			
17	24.26	1.14, s	18	4, 15, 16, 18
18	24.96	0.89, s	17	4, 15, 16, 17, 19
19	142.55	5.40, dd, (17.7, 11.0)	20	11, 12, 13
20	114.49	(cis) 4.92, d, (11.0) (trans), 4.85, d, (17.7)	19	12,19
21	28.27	1.17, s		11, 12, 13, 19
22	160.88			

Table S5: NMR characterization of 5-fluoro-12-*epi*-fischerindole U (17)

$[\alpha]_{D}^{25} = +12.0$ (c=0.15, CH₂Cl₂)



Position	¹³ C shift (ppm) (Fluorine coupling) C ₆ D ₆	¹ H shift (ppm), multi (J) C ₆ D ₆	COSY	HMBC
1		6.43, bs		2,3,8,9
2	153.90			
3	115.16			
4	103.93, d, (23.1)	7.27, dd (9.4,2.5)	6	3,5,6,8
5	159.42, d, (233.5)			
6	109.07, d, (26.3)	6.99, td, (9.0, 2.6)	7	4,5,8
7	112.55, d, (10.1)	6.81, dd, (8.8, 4.4)	6	4,5,9
8	136.53			
9	124.63, d, (10.1)			
10	42.37	2.88, m	11,15	3,9,14,15
11	62.21	3.95, d (3.0)	11	3,12,13,15,17,22
12	41.04			
13	31.82	1.55, m	14	11,12,14,15,17
14	20.81	1.34, ddd (13.1, 6.8, 4.0) & 1.23, m	13,15	12,13,15
15	55.21	2.36, ddd (13.3, 10.6, 3.3)	10, 14	10,14,16,19
16	40.18			
17	143.02	5.31, dd (17.6, 11.0)	18	11,13,12,21
18	114.16	(cis) 4.87, d (11.1) (trans) 4.84, d (17.7)	17	12,17,21
19	24.93	1.01, s		2,15,16,20
20	20.78	0.74, s		2,15,16,19
21	28.15	1.13, s		11,12,13,17
22	161.39			

Table S6: NMR characterization 6-Fluoro-12-*epi*-Fischerindole U (18) $[\alpha]_D^{25} = +10.8$ (c=0.16, CH₂Cl₂)

Position	¹³ C shift (ppm), (Fluorine coupling) C ₆ D ₆	¹ H shift (ppm), multi (J) C ₆ D ₆	COSY	HMBC
1		6.38, bs		
2	152.16, d, (3.5)			
3	114.88			
4	119.18, d, (10.1)	7.20, dd, (8.6, 5.3)	5	3,8,9
5	108.67, d, (24.2)	6.99, td, (9.1, 2.4)	4	6,7,9
6	159.78, d, (235.6)			
7	98.80, d, (25.9)	6.85, dd, (9.8, 2.3)		5,6,8,9
8	139.95, d, (12.0)			
9	121.08			
10	42.51	2.89, m	11, 15	15
11	62.44	4.03, s	10	10,12,13,15,22
12	41.03			
13	31.87	1.56, m	14	11,12,14,15,21
14	20.82	1.35, m & 1.24, m	13	10,13,15
15	55.21	2.36, ddd, (13.4, 10.6, 3.2)	10, 14	14,19
16	40.25			
17	143.08	5.34, dd, (17.5, 11.0)	18	11,12,13
18	114.16	Cis 4.89, d, (11.0) Trans 4.87, d, (17.5)	17	12,17
19	25.07	1.02, s	20	2,15,16,20
20	20.70	0.74, s	19	2,15,16,19
21	28.17	1.15, s		11,12,13,17
22	161.26			

**Table S7: Amino acid sequences of cyclases
Protein Sequences**

FamC1

MKRKLVAVVFLIFICLGINTPAHATSAVSIPIINNAGFENPFMDVVDDYTIDTPPGWTTYDPNNLVPEKRTT
WTSNNGVGYVGPQTQFYNQLAPEGRNIGYIYLSQNP GSGVAGFEQILDATLEPDTKYTLTVDVGNLAGTF
KGLSFAGFPGYRVELLAGDTVLAADHNNLFIKEGEFKTSTVITYTSTAKDLHLGQKLGIRLVNLLQDKFSGL
DFDNVRLTTEPTET

FamC2

MKRNLVAAIVLLIYICSGINTPANA AVTTSIPIKNPGFEEPILKVEGDYDIDAPPGWTTYNPNGLIPEKRTKW
TSNNGVGHVGPNYGQLFYNQQLPEGKNIGFVYLAQKTGSGIAGFEQTLDAVLEPNTSYKLIVDIGNFGGMF
KGVSFAGFPGYRVELLAGDTVLAADHNNLYIKDGEFKTSTVITFTSAANNPYLGQKLGIRLINLLQDKFSGL
DFDNVRLITETVDT

FamC3

MKLKSVAVVFLIFICLGINTPANATGAVSIPIKNAGFEDPFLEVVDYTVNTPPGWSTYDPNGLIPEQPTVQ
TSYVGVNTNATPSSAFYDQKVPEGRNMGSVYLAHEPGSGIAGLEQTLDTVLESNKNYLLVDIGNSADGYK
DISLADFPGYRVELLAGDKVIAVDHNSVYIKEGEFKTSMIKFTAKPDSPYLGQKLGIRLINSLQTLSGNIDFD
NVRLSVESAVI

FisC

MKRNFIIAAIVLLVYICFGISISANAASAVSIPIKNAGFEEPSLTVEDYTYTIDTPPGWITYDPNGLVPAKRTRIT
SNNGVGYTGPN S AYYNHKAPEGRNVAVVYLAQEIGSGIAGLEQTLDAVLKPNTKYTLTVDIGNSGGSFQG
FPLDGFPGYRVELLAGDTVLAADQN NLYIKEKDFKTTT VTFIATPESPYLGQHLGIRLINPLQKFGSGVDFD
NVRLTAEP AET

FimC5

MKRNFIIAAIVLLVYIFSGINVFANAASAVCIPIKNAGFEEPILQIEDDYTIDTPPGWITYDPGGLVPAKRTRIT
SNNGVGYTGSNSEFYNHKAPEGRNVAVVYLAQEIGSGIAGLEQTLDAVLKPNTKYTLTVDIGNSGGSFQK
TLDGFPGYRIELLAGDTVLAADHNTLYIKEKDFKSTTVTFTATPESPYLGQHLGIRLINPLQKFGSGVDFD
VRLTAEP AET