Table S1. Conotoxins identified in *C. flavidus* cDNA library by BLAST searching against the NCBI nonredundant database using a cutoff of e-value of $<10^{-6}$. Underlined: predicted signaling sequence; bold underlined: predicted mature peptide region by ConoPrec on Conoserver. Mature peptides marked with "*" were predicted empirically.

Super-family	Name	Accession number	Prepropeptide Sequences	Predicted Mature Peptide Region	Clones	Cysteine Frame-work	Best Matching GI Number	e-value
A	Fla1.1	JX499074	MGMRMIFTVFLLVALATTVASFTLDRASNGRNAAADNKPSDWIALAIK**QCCRNPKCSQQGCP**	**QCCRNPKCSQQGCP**	1	I/II	74793917	7.00E-23
A	Fla1.2	JX499075	MGMRMMFTMFVLVVLATTVVSFPLDHASNGRDAAAYDKATPLIAR**DMEECCSHPACQGINPDYCD**	**DMEECCSHPACQGINPDYCD**	3	I/II	292630608	1.00E-17
A	Fla1.3	JX499076	MGMRMMFTMLLLVVLATTVVSFTLDHAFDGRNIAANNKATDLMALPVR**GCCSDPPCRHKHQDLC**G	**GCCSDPPCRHKHQDLC**	1	I/II	229485322	3.00E-21
A	Fla1.4	JX499077	MGMRMMFTMLLLVVLATTVVSFTLDHAFDGRNTAANNKATDLMALPVR**GCCSDPPCRHKHQDLC**G		6	I/II	229485322	3.00E-21
A	Fla1.5	JX499099	MLLLVVLATTVVSFTLDHAFDGRNTAANNKATDLMALPVR**GCCSDPPCRHKHQDLC**G		1	I/II	229485322	1.00E-16
A	Fla1.6	JX499078	MGMRMMFTVFLLVALATTVASFTLDHASNGRNAAADDNMSDWIAQALKR**CCGNPPCAHVNCR**GRR	**CCGNPPCAHVNCR**	1	I/II	74793917	1.00E-23
A	Fla1.7	JX499079 JX499080	MGMRMMFTVFLLVVLSTTVVSLPVDHASNGRDAAADSNAADQIAQTAR**DPCCSNPSCAQTHPEIC**RRMLQNPLNHDMSPSA	**DPCCSNPSCAQTHPEIC**	4	I/II	46405121	6.00E-15

A	Fla1.8	JX499081	MGMRMMLTVFLLVVLATTVVSDHASDGR**NTAAKVKYSKTQEECCPNPPCFAVNSALCGA**RR	**NTAAKVKYSKTQEECCPNPPCFAVNSALCGA**	1	I/II	229553924	1.00E-13
A	Fla6.1	JX499073	MGKRMVLTMFLLVVLATTVVSFTLDHASDSRGTAANDKATDQMALAVR**LDWCDDADFLVDHPELCGWDVCCAYPPCRHKHQDCNQ**GR	**LDWCDDADFLVDHPELCGWDVCCAYPPCRHKHQDCNQ**	2	VI/VII	229485321	4.00E-14
A	Fla6.2	JX499135	MVLTMFLLVVLATTVVSFTLDHASDSRGTAANDKATDQMALAVR**LDWCDDADFLVDHPELCGWDVCCAYPPCRHKHQDCNQ**GR		1	VI/VII	229485321	3.00E-12
B	Fla-1	JX499093	MLAHGDALTERRSADATALKPEPVLLQKSAARSTDDNDRDRLTQRKRILKKRGNTAR**GYEDHREIAETIRELQVP** *	**GYEDHREIAETIRELQVP** *	1	C0	212288186	1.00E-23
B	Fla-2	JX499106	MQLYTHLYLLVPLVAFHLILGTGMLAHGDALTERRSADATALKPEPVLLQKSAARSTDDNDRDRLTQRKRILKKRGNTAR**GYEDHREIAETIRELQVP** *		1	C0	326416228	4.00E-36
B	Fla-3	JX499094	MLAHGDALTERRSADATALKPEPVLLQKSAARSTDDNDRDRLTQRKRILKKRGNTAR**GYEEDWEIWENIRKLIEAGK** *	**GYEEDWEIWENIRKLIEAGK** *	1	C0	212288186	6.00E-22
B	Fla-4	JX499105	MQLYTHLYLLVPLVAFHLILGTGMLAHGDALTERRSADATALKPEPVLLQKSAARSTDDNDRDRLTQRKRILKKRGNTAR**GNEDHRETAETIRELQVP** *	**GNEDHRETAETIRELQVP** *	1	C0	326416228	1.00E-36
B	Fla-5	JX499108 JX499109	MQLYTHLYLLVPLVAFHLILGTGTLAHGDALTERRSADATALKPEPVLLQKSAARSTDDNDRDRLTQRKRILKKQGNMAR**GYEEDREIAETIRELNEAGK** *	**GYEEDREIAETIRELNEAGK** *	7	C0	326416228	2.00E-36
B	Fla-6	JX499107	MQLYTHLYLLVPLVAFHLILGTGMLAHGDALTERRSADATALKPEPVLLQKSAARSTDDNDRDRLTQRKRILKKRGNTAR**GYEEDWEYWETIRKLTEAGK** *	**GYEEDWEYWETIRKLTEAGK** *	1	C0	212288190	2.00E-35

B	Fla-7	JX499110	MQSFT**C**M**C**LLVPLLFFHLTQRSDTAGHGGAATDVRSADHVLKRFYHDFRRAPKRRSNDRYNRRQSTSVSLPLEILAEQTRER**SREASVEHLREIGR** *	**SREASVEHLREIGR** *	2	C0	326422284	3.00E-29
B	Fla-8	JX499111	MQSFT**C**M**C**LLVPLLFLHLTQRSDTAGHGGAATDVRSADHTLKRFHHDFRRAPKRRSNDRYNRRRSSTWTARLEIVFEDIR**REKAEDSREASV** *	**REKAEDSREASV** *	1	C0	326422284	4.00E-25
I2	Fla11.1	JX499100	MMFRLASVG**C**FLLVIGFLDLVRL**NVVLTYDCTEEGDYCAYDFECCFLNCCYGMCMGVCS**GRKRAHLHELLRHR	**NVVLTYDCTEEGDYCAYDFECCFLNCCYGMCMGVCS**	2	XI	290463144	4.00E-10
J	Fla-9	JX499131	MTSVQSVT**C**G**C**LLWLLLSVQLVTPGSPATAQLSRHRTSR**WTTEEFMEKVCFPHCAPGRPAHTGRDVAPSWI**RRRKRAMAV	**WTTEEFMEKVCFPHCAPGRPAHTGRDVAPSWI**	1	C2	117940164	1.00E-09
J	Fla-10	JX499132	MTSVQSVT**C**G**C**LLWLLLSVQLVTPGSPATAQLSRHRTSR**WTTEEFMEKVCFPYCAPGRPAHTGRDVAPSWI**RRRKRAMAV	**WTTEEFMEKVCFPYCAPGRPAHTGRDVAPSWI**	3	C2	326454636	1.00E-09
J	Fla-11	JX499133	MTSVQSVT**C**G**C**LLWLLLSVQLVTPGSPATAQLSRHRTYR**WTTEEFMEKVCFPYCAPGRPAHTGRDVAPSWI**RRRKRAMAV		1	C2	326454636	2.00E-09
J	Fla-12	JX499134	MTSVQSVT**C**G**C**LLWLLLSVQLVTPGSPATVQLSRHRTSR**WTTEEFMEKVCFPYCAPGRPAHTGRDVAPSWI**RRRKRAMAV		1	C2	326454636	3.00E-09
L	Fla14.1	JX499085	MKLSVTFIVVLMLTTSLTFGFSLSSNNGERAYGPRHSNVADQLVPREQASR**TCYPPCIGYTYCKSGTCEYRLGRASTVFL**KRQ	**TCYPPCIGYTYCKSGTCEYRLGRASTVFL**	1	XIV	326422276	2.00E-18
L	Fla14.2	JX499086	MKLSVTFIVVLMLTTSLTFGFSLSSNNGERAYGPRHSNVADQLVPREQASR**TCYPPCIGYTYCKSGTCEYRQGRASTVFL**KRQ	**TCYPPCIGYTYCKSGTCEYRQGRASTVFL**	2	XIV	326422276	2.00E-18

L	Fla14.3	JX499087	MKLSVTFIVVLMLTTSLTFGFSLSSNNGERAYGSHHSYVADQLVRRER**ASRACNPPCSDILTCLHGTCKHLGI**G	**ASRACNPPCSDILTCLHGTCKHLGI**	4	XIV	326422276	1.00E-17
M	Fla3.1	JX499096	MLKMGVVLFTFLVLFPLATLQLNADQHVARYAENKQNFNPNERMKMMLSALRQR**RCCISPACHKDCYCCL**	**RCCISPACHKDCYCCL**	1	III	74836928	6.00E-28
M	Fla3.2	JX499097	MLKMRVVLFTFLVLFPLATLQLDADQPRARYAENKQDFNRNERTKMILSAVSASMGRQRR**CCLWPECGGCVCCY**	**CCLWPECGGCVCCY**	2	III	74836928	1.00E-19
M	Fla3.3	JX499098	MLKMRVVLFTFRVLFPLATLQLDADQPRARYAENKQDFNRNERTKMILSAVSASMGRQRR**CCLWPECGGCVCCY**		1	III	74836928	5.00E-19
M	Fla3.4	JX499103	MMSKLGVLLTISLLLFPLTAVQLDGEQPVDLLALRTQDFAPEQSPWFDPVKR**CCSKYCWECTPCCPYSS**G	**CCSKYCWECTPCCPYSS**	3	III	326635518	2.00E-24
M	Fla3.5	JX499104	MMSKLGVLLTV**C**LLLFPLTALRLVRDQPAERPAKRTQDDIPNGQDPLIDR**QINCCPWPCPDSCHYQCCH**	**QINCCPWPCPDSCHYQCCH**	1	III	110278928	1.00E-13
M	Fla-13	JX499101	MMSKLGVLLTI**C**LLLFPLTAVPLDGDQPVDLPALRTQDFASEHSPGFDPVKR**QFICVQDIFCAVRGTV**	**QFICVQDIFCAVRGTV**	1	C2	74848622	7.00E-18
M	Fla-14	JX499102	MMSKLGVLLTI**C**LLLFPLTAVQLDGEQPVDLLALRTQDFAPEQSPWFDPVKR**GCSMYCWKCFPCCPN**G	**GCSMYCWKCFPCCPN**	1	C5	326635518	1.00E-24
M	Fla-15	JX499095	MLKMGVMLFTFLVLFHLAAPQLDADQPVARYAGNKPDFNPNKRMKMMSALRKR**GCCPPSLCDPGCDEGCCPVVTPAC**	**GCCPPSLCDPGCDEGCCPVVTPAC**	1	C7	74836925	2.00E-20
O1	Fla6.3	JX499083	MKLM**C**VLIIAVLFLTASQLITADYSRDKQEYRAERLRDAMGKFKGSR**SCGHSGAGCYSRPCCPGLHCSGTHAGGMCV**	**SCGHSGAGCYSRPCCPGLHCSGTHAGGMCV**	1	VI/VII	122011896	1.00E-34

O1	Fla6.4	JX499084	MKLM**C**VLIIAVLFLTASQLITADYSRDKQEYRAERLRDAMGKFKGSR**SCGHSGAGCYTRPCCPGLHCSGGQAGGLCV**	**SCGHSGAGCYTRPCCPGLHCSGGQAGGLCV**	1	VI/VII	122011896	4.00E-35
O1	Fla6.5	JX499088	MKLT**C**ALIVAMLFLTA**C**QLTTTDDSRGRQKYPTERLRVK**MRNPKLSKLTKTCDPPGDSCSRWYNHCCSKLCTSRNSGPTCSRP**	**MRNPKLSKLTKTCDPPGDSCSRWYNHCCSKLCTSRNSGPTCSRP**	2	VI/VII	122011877	7.00E-41
O1	Fla-16	JX499089	MKLT**C**ILIVAVLFSTAWTFVTVDDSINHLKYR**EWTDFKPWGKRIP**EARDKMKNLKFSKLDNKKRRL †	**EWTDFKPWGKRIP** †	1	C0	85717919	1.00E-09
O1	Fla-17	JX499090	MKLT**C**ILIVAVLFSTAWTFVTVDDSINHLKYR**EWTDFRPWGKRIP**EARDKMKNLKFSKLDNKKRRL †	**EWTDFRPWGKRIP †**	1	C0	85717919	2.00E-09
O1	Fla-18	JX499091	MKLT**C**VMIVAALFLTAWTFVTADNSKYELENR**GGLGHAGGWVKAGALGKDPGWGKRFL**MARDEMKNPKASKLVP †	**GGLGHAGGWVKAGALGKDPGWGKRFL** †	3	C0	85717919	3.00E-10
O1	Fla6.6	JX499092	MKLT**C**VMIVALLFLTAWAFVTADDLINKLENRGGWAQARGWGKPFAMARDEASKLDNEKR**CYDVGDFCGIPFIKNGNCCSQFCVFVCTPEW**	**CYDVGDFCGIPFIKNGNCCSQFCVFVCTPEW**	1	VI/VII	74848541	8.00E-18
O2	Fla6.7	JX499071	MEKLTSLLLVAALLMLTQTLIQGGGEDRPNKKFLQKIKSTAKR**DCTPPSSYCDYPEECCEVECGRHYCDWW**	**DCTPPSSYCDYPEECCEVECGRHYCDWW**	1	VI/VII	122011888	1.00E-24
O2	Fla6.8	JX499072	MEKLTSLLLVAALLMLTQTLIQGGREGRPKKFLQKIKSTAKR**ECTAPSGYCDYPEECCEVECGRHYCDWWY**	**ECTAPSGYCDYPEECCEVECGRHYCDWWY**	1	VI/VII	122011888	6.00E-23
P	Fla9.1	JX499082	MHLSLAGSAVLMLLLLFALGNFVGVQTGQIARDVDNGLLTDKHRDLQSLRKPMDFFKSLYKR**SSCGEDCWGDADCPNDCPYCVSNLSKCM**	**SSCGEDCWGDADCPNDCPYCVSNLSKCM**	1	IX	22001566	9.00E-12

T	Fla2.1	JX499114	MR**C**VPVFIILLLLSPSAPSVDAYPKTKDDVPLASFHDDAKRTLQRLWIK**GFCCNGYACWCSNF**R	**GFCCNGYACWCSNF**	1	I/II	122011898	6.00E-24
T	Fla5.1	JX499112	MR**C**VPVFIILLLLSPSAPSVDAHPKTKDDVPLASFHDDAKQTLQRLWIK**GSCCYESKPYCCHF**R	**GSCCYESKPYCCHF**	3	V	122011898	3.00E-22
T	Fla5.2	JX499113	MR**C**VPVFIILLLLSPSAPSVDAHPKTKDDVPLASFHDDAKRTLQRLWIK**ALCCYGYAFCCRL**GR	**ALCCYGYAFCCRL**	1	V	122011903	2.00E-26
V	Fla15.1	JX499116	MSTPKMTPFILLLLFSLMIR**C**GDGKAIQEDRDPSTRLLTGDKNRDLSVNRR**CFTCNGEKCCGDCLCSWDKDDCFCVLN**GK	**CFTCNGEKCCGDCLCSWDKDDCFCVLN**	1	XV	290463196	2.00E-14
V	Fla15.2	JX499120	MSTPKMTPFILLLLFSLTIR**C**GDGKAIQEDRDPSTRLLTGDKNRDLSVNRR**CFTCNGEKCCGDCLCSWDKDDCFCVLN**GK		1	XV	290463196	2.00E-14
V	Fla15.3	JX499117	MSTPKMTPFILLLLFSLTIR**C**GDGKAIQEDRDPSMRLLTGDKNRDLSVNRR**CFNCNGEICCGDCFCTSDKQYCFCRQF**RK	**CFNCNGEICCGDCFCTSDKQYCFCRQF**	1	XV	290463196	2.00E-11
V	Fla15.4	JX499118	MSTPKMTPFILLLLFSLTIR**C**GDGKAIQEDRDPSTRLLTGDKNRDLSVNRR**CFNCNGEICCGDCFCTSDKQYCFCRQF**RK		1	XV	290463196	2.00E-11
V	Fla15.5	JX499119	MSTPKMTPFILLLLFSLTIR**C**GDGKAIQEDRDPSTRLLTGDKNRDLSVNRR**CFNCNGEICCGDCFCTSDRQYCFCRQF**RK	**CFNCNGEICCGDCFCTSDRQYCFCRQF**	1	XV	290463196	2.00E-11
V	Fla15.6	JX499121	MSTPKMTPFILLLLFSLTIR**C**GDGKAIQEDRDPSTRLLTGDKNRDLSVNRR**CFTCNGEKCCGDCLCSWYKDDCFCVLN**GK	**CFTCNGEKCCGDCLCSWYKDDCFCVLN**	1	XV	290463196	1.00E-14
V	Fla15.7	JX499122	MSTPKMTPFILLLLFSLTIR**C**GDGKAIQEDRDPSTRLLTGDKNRDLSVNRR**CSSCNGEICCGSCFCFPHGKNCFCRQL**GK	**CSSCNGEICCGSCFCFPHGKNCFCRQL**	1	XV	290463196	1.00E-14

V	Fla15.8	JX499127	MSTPRMTPFILLLLFSLTIR**C**GDGKAIQEDRDPSARLLTGDKNHDLSVK**DDCNICGGEECCGRCTCAFGNCSCIAW**GK	**DDCNICGGEECCGRCTCAFGNCSCIAW**	1	XV	290463196	8.00E-20
V	Fla15.9	JX499128	MSTPRMTPFILLLLFSLTIR**C**GDGKAIQGDR**DPSASLLTGDKNHDLSVQIDCGTCDGEECCGVCICSFGNCSCTPW**GK	**DPSASLLTGDKNHDLSVQIDCGTCDGEECCGVCICSFGNCSCTPW**	1	XV	290463196	9.00E-19
V	Fla15.10	JX499129	MSTPRMTPFILLLLFSLTIR**C**GDGKVIQEDRDPSPRLLMGDKK**PCRPCAGIQCCGRCICFFYECGCEPW**GK	**PCRPCAGIQCCGRCICFFYECGCEPW**	1	XV	290463196	5.00E-08
V	Fla15.11	JX499130	MSTPRMTPFILLLLFSLTIR**C**GDGKVIQEDRDPSTRLLMGDKK**PCRPCDGIQCCGRCICFFYECGCEPW**GK	**PCRPCDGIQCCGRCICFFYECGCEPW**	1	XV	290463196	3.00E-07
V	Fla6.9	JX499123	MSTPRMMPFILLLLFSLTIR**C**GDGKAIQGDRDPSASLLKGDKSRDLLVKR**GCSICNGGQCCGLCLYSRIISRYMCLPVA**K	**GCSICNGGQCCGLCLYSRIISRYMCLPVA**	1	VI/VII	290463196	2.00E-12
V	Fla6.10	JX499125	MSTPRMMPFILLLLFSLTIR**C**GDGKAIQGDRDPSASLLTGDKSRDLLVKR**GCSICNGGQCCGLCLYSRIISRYMCLPVA**K		1	VI/VII	290463196	4.00E-13
V	Fla6.11	JX499124	MSTPRMMPFILLLLFSLTIR**C**GDGKAIQGDRDPSASLLTGDKSRDLLVKR**GCSICNGGQCCGLCLFSRIISRYMCLPVA**K	**GCSICNGGQCCGLCLFSRIISRYMCLPVA**	1	VI/VII	290463196	4.00E-13
V	Fla6.12	JX499126	MSTPRMTPFILLLLFSLIFR**C**GDGKAIQGDRDPSASLLTGDKSRDLLVK**TDCYNCDGEECCGRCLYSWPLQMFTCVTVE**K	**TDCYNCDGEECCGRCLYSWPLQMFTCVTVE**	1	VI/VII	290463196	3.00E-14
V	Fla6.13	JX499115	MSTARMTPFILLLLFSLTIR**C**GDGKAIQGDRDPSASLLTGHKSRDLSVK**TDCFYCNGVYCCHWCIYSAAEERLNCVNPW**K	**TDCFYCNGVYCCHWCIYSAAEERLNCVNPW**	1	VI/VII	290463196	3.00E-10

Q	Fla16.1		MHTLEMLLLLLLLLPLALGEGDGQAVAGDRNPSEARSTHEHFLQRLIR**LIHGSDCQPCGQYVCCPPWKYAEY**RRFT	**LIHGSDCQPCGQYVCCPPWKYAEY**	1	XVI	-	-
Q	Fla16.2		MHTLEMLLLLLLLLPLAPGEGDGQAVAGDRNPSEARSTHEHFLQRLIR**LIHGSDCQPCGQYVCCPPWKYAEY**RRFT		1	XVI	-	-
Q	Fla16.3		MHTLEMLLLLLLLLPLAPGEGDGQAVARDRNPSEARSTHEHFLQRLIRLIDGR**DCKLCGHDVCCDWA**	**DCKLCGHDVCCDWA**	1	XVI	-	-
Q	Fla16.5		MLLLLLLLLPLAPGEGDGQAVAGDRNPSEARSTHEHFLQRLIRLIDGR**DCKLCGHDVCCDWA**		1	XVI	-	-
Q	Fla16.4		MHTLEMLLLLLLLSPLALGEGDGQAVAGDRNPSEARSTHEHFLQRLLGRIDGR**DCQPCGHDVCCPP**	**DCQPCGHDVCCPP**	3	XVI	-	-
Q	Fla6.14		MHTLEMLLLLLLLLPLAPGEGDGQAVAGDRNPGEARSTHKRFLQRPARRIHRHR**CTPCGPDLCCEPGTTCDRVLHHTHFGEPSCSY**	**CTPCGPDLCCEPGTTCDRVLHHTHFGEPSCSY**	1	VI/VII	-	-