SUPPLEMENTARY MATERIAL

Analysis of Biological Diversity between the cyanobacteria Cylindrospermospsis and Sphaerospermopsis

Reno Nooblath

Federal University of Pará (UFPA), reno.bioinfo@gmail.com, +55 (91) 98208-1316, Augusto Corrêa Street, 01 – Bairro Guamá – CEP 66075-110 Belém–Pará – Amazônia, Brasil.

Daniel Gomes

Federal University of Pará (UFPA), daniel.h.gomes18@gmail.com, +55 (91) 98126-7143, Augusto Corrêa Street, 01 – Bairro Guamá – CEP 66075-110 Belém – Pará – Amazônia, Brasil.

Vinícius Abreu

Federal University of Pará (UFPA), vabreuufpa@gmail.com, +55 (91) 99810-7845, Augusto Corrêa Street, 01 – Bairro Guamá – CEP 66075-110 Belém –Pará – Amazônia, Brasil.

Sintia Silva de Almeida

Federal University of Pará (UFPA), sintiaalmeida@gmail.com, +55 (91) 98218-2015, Augusto Corrêa Street, 01 – Bairro Guamá – CEP 66075-110 Belém – Pará – Amazônia, Brasil.

Table S1 . Origin of the *Cylindrospermopsis* and *Sphaerospermopsis* strains used in this study and their taxonomic identification on NCBI, organized in ascending order based on the number of scaffolds..

Organism	Taxonomy ID	Scafolds	Origin of Sample	Size	GC%
C. raciborskii KLL07	683357	1	Israel	3.80818	40.2
C. raciborskii N8	1524929	1	China	3.85717	40.1
C. raciborskii Cr2010	2108055	1	Netherlands	3.75785	40.2
C. curvispora GIHE G1	2666332	2	South Korea	4.05721	40117
C. raciborskii DSH	3117726	2	China	4.0	40
C. raciborskii GIHE 2018	2588993	3	South Korea	3.62982	40.2
C. raciborskii CS-505	533240	6	Australia	3.9	40
R. brookii D9	533247	47	Brazil	3.2	40
C. raciborskii CENA 302	1170768	58	Brazil	3.5	40
C. raciborskii CENA 303	1170769	77	Brazil	3.4	40.5
C. raciborskii MVCC14	940191	99	Uruguay	3.6	40.1
C. raciborskii KL1	2787621	100	USA	3.7	40
C. raciborskii PAMP2012	2969974	134	Brazil	3.2	40
C. sp. CR12	1747196	136	Malaysia	3.7	40
C. raciborskii MVCC 19	940192	155	Uruguay	3.5	40
C. raciborskii CS508	533243	162	Australia	3.6	40
C. raciborskii CYRF	2021698	166	Brazil	4.2	40
C. raciborskii 1523720	77022	173	Índia	3.2	40
C. raciborskii CYLP	2021699	188	Brazil	4.2	40
C. raciborskii CHAB3438	1480071	189	China	3.5	40.5
C. raciborskii ITEPA-A1	1810942	195	Brazil	3.6	40

S. torques-reginae ITEP-024	984208	1	Brazil	5.3	37.5
S. kisseleviana NIES-73	1973480	2	Japan	5.4	37.5
S. sp. SIO1G1	2607814	38	Puerto Rico	5.2	36.5
S. sp. FACHB-1194	2692862	108	China	5.4	37.5
S. sp. LEGE 08334	1828651	119	Mexico	5.5	37
S. sp. LEGE 00249	1380707	177	Portugal	5.3	37.5

Table S2. 16S rRNA Sequences used in this study.

Organism	16S rRNA Sequences
>Cylindrospermopsis_raciborskii_KLL07_GEN_REF	

>Cylindrospermopsis_raciborskii_KLL07_GEN_REF
GAACGGGATGCTTAGGCATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTCCAGGTCGGGGATAACAGTTG
GAAACGACTGCTAATACCGGATGTGCCGAGAGGTGAAAGATTTATTGCCTGGAGATGAGCTCGCGTCTGATTAGCTAGTT
GGTGGTGTAAGGGACCACCAAGGCATCGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAAGAAAGTGACGGTACTTGAGGAATAAGCATCGGCTAACTC
CGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGCAGGTGGAACT
GAAAGTCTGCTGTTAAAGAGTTTGGCTTAACCAAATAAAAGCGGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAA
AGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGTAACT
GACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGG
CGTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAA
CTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAG
ACTTGACATCCTGCGAATCCTGGTGAAAGCTGGGAGTGCCTTAGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAG
CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCT
AGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACA
CGTACTACAATGCTGCGGACAGAGGGCAGCGAGCCAGGGATGGCAAGCGAATCCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA

GGTAGGACTGGTGACTGGGGTGAAGTCGT
>Cylindrospermopsis_curvispora_GIHE_G1_GEN
GAACGGGATGCTTAGGCATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTCCAGGTCGGGGATAACAGTTG
GAAACGACTGCTAATACCGGATGTGCCGAGAGGTGAAAGATTTATCGCCTGGAGATGAGCTCGCGTCTGATTAGCTAGTT
GGTGGTGTAAGGGACCACCAAGGCGTCGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAAGAAAGTGACGGTACTTGAGGAATAAGCATCGGCTAACTC
CGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGCAGGTGGAACT
GAAAGTCTGCTGTTAAAGAGTTTGGCTTAACCAAATAAAGCGGTGGAAACTACAGAACTAGAGTGTGGTAGGGGCAAA
AGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCATAACT
GACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGG
CGTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAA
CTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAG
ACTTGACATCCTGCGAATCCCAGTGAAAGCTGGGAGTGCCTTAGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAG
CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCT
AGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACA
CGTACTACAATGCTACGGACAGAGGGCAGCGAGCCAGGGATGGCAAGCGAATCCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCG
>Cylindrospermopsis_raciborskii_CENA302_GEN
GAACGGGATGCTTAGGCATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTCCAGGTCGGGGATAACAGTTG
GAAACGACTGCTAATACCGGATGTGCCGAGAGGTGAAAGATTTATCGCCTGGAGATGAGCTCGCGTCTGATTAGCTAGTT
GGCGGTGTAAGGGACCACCAAGGCATCGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAAGAAAGTGACGGTACTTGAGGAATAAGCATCGGCTAACTC
CGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGCAGGTGGAACT
GAAAGTCTGCTGTTAAAGAGTTTGGCTTAACCAAATAAAGCGGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAA
AGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGTAACT
GACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGG
CGTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAA
CTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAG

ACTTGACATCCTGCGAATCCCGGTGAAAGCTGGGAGTGCCTTAGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAG
CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCT
AGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACA
CGTACTACAATGCTACGGACAGAGGGCAGCGAGCCAGGGATGGCAAGCGAATCCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCG
>Cylindrospermopsis_raciborskii_CENA303_GEN
GAACGAGATGCTTAGGCATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTCCAGGTCGGGGACAACAGTTG
GAAACGACTGCTAATACCGGATGTGCCGAGAGGTGAAAGATTTATCGCCTGGAGATGAGCTCGCGTCTGATTAGCTAGTT
GGCGGTGTAAGGGACCACCAAGGCATCGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAAGAAAGTGACGGTACTTGAGGAATAAGCATCGGCTAACTC
CGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGCAGGTGGAACT
GAAAGTCTGCTGTTAAAGAGTTTGGCTTAACCAAATAAAAGCGGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAA
AGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGTAACT
GACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGG
CGTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAA
CTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAG
ACTTGACATCCTGCGAATCCCGGTGAAAGCTGGGAGTGCCTTAGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAG
CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCT
AGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACA
CGTACTACAATGCTACGGACAGAGGGCAGCGAGCCAGGGATGGCAAGCGAATCCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCGT
>Cylindrospermopsis_raciborskii_CHAB3438_GEN
GAACGGGATGCTTAGGCATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTCCAGGTCGGGGATAACAGTTG
GAAACGACTGCTAATACCGGATGTGCCGAGAGGTGAAAGATTTATTGCCTGGAGATGAGCTCGCGTCTGATTAGCTAGTT
GGTGGTGTAAGGGACCACCAAGGCGTCGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAAGAAAGTGACGGTACTTGAGGAATAAGCATCGGCTAACTC

CGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGCAGGTGGAACT
GAAAGTCTGCTGTTAAAGAGTTTGGCTTAACCAAATAAAAGCGGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAA
AGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGTAACT
GACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGG
CGTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAA
CTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAG
ACTTGACATCCTGCGAATCCGGTGAAAGCTGGGAGTGCCTTAGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAGC
TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCTA
GAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACAC
GTACTACAATGCTACGGACAGAGGGCAGCGAGCCAGGGATGGCAAGCGAATCCAGAAACCGTAGCTCAGTTCAGATCGA
AGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCCT
TGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCGT
>Cylindrospermopsis_raciborskii_Cr2010_GEN
GAACGGGATGCTTAGGCATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTCCAGGTCGGGGATAACAGTTG
GAAACGACTGCTAATACCGGATGTGCCGAGAGGTGAAAGATTTATTGCCTGGAGATGAGCTCGCGTCTGATTAGCTAGTT
GGTGGTGTAAGGGACCACCAAGGCGTCGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAAGAAAGTGACGGTACTTGAGGAATAAGCATCGGCTAACTC
CGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGCAGGTGGAACT
GAAAGTCTGCTGTTAAAGAGTTTGGCTTAACCAAATAAAAGCGGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAA
AGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGTAACT
GACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGG
CGTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAA
CTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAG
ACTTGACATCCTGCGAATCCTGGTGAAAGCTGGGAGTGCCTTAGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAG
CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCT
AGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACA
CGTACTACAATGCTACGGACAGAGGGCAGCGAGCCAGGGATGGCAAGCGAATCCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCGT

>Cylindrospermopsis_raciborskii_CS_505_GEN
GAACGGGATGCTTAGGCATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTCCAGGTCGGGGATAACAGTTG
GAAACGACTGCTAATACCGGATGTGCCGAGAGGTGAAAGATTTATTGCCTGGAGATGAGCTCGCGTCTGATTAGCTAGTT
GGTGGTGTAAGGGACCACCAAGGCGTCGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAAGAAAGTGACGGTACTTGAGGAATAAGCATCGGCTAACTC
CGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGCAGGTGGAACT
GAAAGTCTGCTGTTAAAGAGTTTGGCTTAACCAAATAAAGCGGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAA
AGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGTAACT
GACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGG
CGTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAA
CTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAG
ACTTGACATCCTGCGAATCCCGGTGAAAGCTGGGAGTGCCTTAGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAG
CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCT
AGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACA
CGTACTACAATGCTACGGACAGAGGGCAGCAAGCCAGGGATGGCAAGCGAATCCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCG
>Cylindrospermopsis_raciborskii_CS_508_GEN
GAACGGGATGCTTAGGCATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTCCAGGTCGGGGATAACAGTTG
GAAACGACTGCTAATACCGGATGTGCCGAGAGGTGAAAGATTTATTGCCTGGAGATGAGCTCGCGTCTGATTAGCTAGTT
GGTGGTGTAAGGGACCACCAAGGCGTCGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAAGAAAGTGACGGTACTTGAGGAATAAGCATCGGCTAACTC
CGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGCAGGTGGAACT
GAAAGTCTGCTGTTAAAGAGTTTGGCTTAACCAAATAAAGCGGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAA
AGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGTAACT
GACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGG
CGTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAA
CTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAG
ACTTGACATCCTGCGAATCCCGGTGAAAGCTGGGAGTGCCTTAGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAG

CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCT
AGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACA
CGTACTACAATGCTACGGACAGAGGGCAGCAAGCCAGGGATGGCAAGCGAATCCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCGT
>Cylindrospermopsis_raciborskii_CYLP_GEN
GAACGGGATGCTTAGGCATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTCCAGGTCGGGGATAACAGTTG
GAAACGACTGCTAATACCGGATGTGCCGAGAGGTGAAAGATTTATCGCCTGGAGATGAGCTCGCGTCTGATTAGCTAGTT
GGCGGTGTAAGGGACCACCAAGGCATCGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAAGAAAGTGACGGTACTTGAGGAATAAGCATCGGCTAACTC
CGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGCAGGTGGAACT
GAAAGTCTGCTGTTAAAGAGTTTGGCTTAACCAAATAAAGCGGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAA
AGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGTAACT
GACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGG
CGTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAA
CTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAG
ACTTGACATCCTGCGAATCCCGGTGAAAGCTGGGAGTGCCTTAGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAG
CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCT
AGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACA
CGTACTACAATGCTACGGACAGAGGGCAGCGAGCCAGGGATGGCAAGCGAATCCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCGT
>Cylindrospermopsis_raciborskii_CYRF_GEN
GAACGGGATGCTTAGGCATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTCCAGGTCGGGGATAACAGTTG
GAAACGACTGCTAATACCGGATGTGCCGAGAGGTGAAAGATTTATCGCCTGGAGATGAGCTCGCGTCTGATTAGCTAGTT
GGCGGTGTAAGGGACCACCAAGGCATCGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAAGAAAGTGACGGTACTTGAGGAATAAGCATCGGCTAACTC
CGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGCAGGTGGAACT

GAAAGTCTGCTGTTAAAGAGTTTGGCTTAACCAAATAAAAGCGGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAA
AGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGTAACT
GACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGG
CGTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAA
CTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAG
ACTTGACATCCTGCGAATCCCGGTGAAAGCTGGGAGTGCCTTAGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAG
CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCT
AGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACA
CGTACTACAATGCTACGGACAGAGGGCAGCGAGCCAGGGATGGCAAGCGAATCCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCGT
>Cylindrospermopsis_raciborskii_DSH_GEN
GAACGGGGTGCTTAGGCATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTCCAGGTCGGGGATAACAGTTG
GAAACGACTGCTAATACCGGATGTGCCGAGAGGTGAAAGATTTATTGCCTGGAGATGAGCTCGCGTCTGATTAGCTAGTT
GGTGGTGTAAGGGACCACCAAGGCGTCGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCGTAAGGAAGAAAGTGACGGTACTTGAGGAATAAGCATCAGCTAACTCC
ATTAACAACGGCAGCGATAATACGGAGGATTTGAAGCGTTATCCAAGATGATTGGGCGTAAAGGGTCTGCGGGTGGAAC
TGAAAGTCTGCTGTTAAAGAGTTTGGCTTAGCAAATAAAAGCGGTGGAAACTACAGAACTAGAGTGCGGTAGGAGCAAA
AGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGTAACT
GACACTGAGGGACGAAAGCTAGAGGCGAATGGGATTAGATACCCCAGTAGTCCTGTCCGTAAACGATGGATCACTGGGC
GTGGCTTGTATCGACTTGAGCCGTGCGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGAGTACGCACGCAAGTGTGAAC
TCAAAGGAATTGACGAAGCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAGACTT
GACATCCTGCGAATCCTGGTGAAAGCTGGGAGTGCCTTCGGGGCGCAGAGACGGGTGGTGCATGGCTGTCGTCAGCTCGT
GTCGTGAGATGTTGGGTTAAGTCCCGCAACTTGAGACGCAACCCTCGTTTTTAGTTGCCAGCATTAAATTGGAAACTCTAG
AGAGACTGCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCGGCATACCCCTTACGTCTTGAGCTACACACGT
ACTACAATGCTACGGACAGAGGGCAGCAAGCGGGATGGCAGCGAATCAAGAAACCGTAGCTCAGTTCAGATCGAAGGCT
GCAACTCGCCTTCGTGAAGGGAGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCAGGCTTATGTTA
CTGCCCGTCACACCATGGAGATTGGTCACCGCTTGAAGTCGTTACCCCAACCGAAAGGAGGATGCCTAAAATGGGACTGG
TGACTGGGGTGAAGTCGT

>Cylindrospermopsis_raciborskii_GIHE_2018_GEN
GAACGGGATGCTTAGGCATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTCCAGGTCGGGGATAACAGTTG
GAAACGACTGCTAATACCGGATGTGCCGAGAGGTGAAAGATTTATTGCCTGGAGATGAGCTCGCGTCTGATTAGCTAGTT
GGTGGTGTAAGGGACCACCAAGGCGTCGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAAGAAAGTGACGGTACTTGAGGAATAAGCATCGGCTAACTC
CGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGCAGGTGGAACT
GAAAGTCTGCTGTTAAAGAGTTTGGCTTAACCAAATAAAAGCGGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAA
AGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGTAACT
GACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGG
CGTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAA
CTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAG
ACTTGACATCCTGCGAATCCTGGTGAAAGCTGGGAGTGCCTTAGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAG
CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCT
AGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACA
CGTACTACAATGCTACGGACAGAGGGCAGCGAGCCAGGGATGGCAAGCGAATCCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCG
>Cylindrospermopsis_raciborskii_isolate_1523720_GEN
GAACGGGATGCTTAGGCATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTCCAGGTCGGGGATAACAGTTG
GAAACGACTGCTAATACCGGATGTGCCGAGAGGTGAAAGATTTATTGCCTGGAGATGAGCTCGCGTCTGATTAGCTAGTT
GGTGGTGTAAGGGACCACCAAGGCGTCGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGATACGG
CCCAGACTCCTACGGGAGGCAGCCGTGGGGAATATTGGACCATGGGCGAAAGCCTGATCCAGCGATGCCGCGTGTGTGA
AGAAGGCCTGCGGGTTGTAAAGCACTTTCGGCGGGGAGAATGAAGCCATCTCTAATATAGATGGTTGAAGATGTTACCCG
CAAAAGAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCGAGCGTTAATCGGAATTACTGGGCG
TAAAGGGTGTGTAGGCGGTTAGATAAGTTAGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCGCCTAATACTGTCTAG
CTAGAGTATTGTAGAGGAAAGTGGAATTTCCGGTGTAGCGGTGAAATGCGTAGATATCGGAAGGAACATCAGTGGCGAA
GGCGACTTTCTGGACAAATACTGACGCTGAGACACGAAAGCATGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCAT
GCTGTAAACGATGAAGACTGGCTGTTGGGAACCTACAAGGTTCTTAGTAGCGAAGCTAACGCGTTAAGTCTTCCGCCTGG
GGAGTACGGCCGCAAGGTTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGCGGTTTAATTCGAT
GCTACGCGAAAAACCTTACCAACCCTTGACATGGTGGTCGCGGATCACAGAGATGAGATCCTTCAGTTCGGCTGGACCAC

ACACAGGTGTTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCATTCTT
ATTTGCCAGCGAGTAATGTCGGGAACTATAAGAAAACTGCCGGCCCTAAGCCGGAGGAAGGTGAGGACGAGGTCAAGTC
ATCATGGCCCTTATGGGTTGGGCTACACGCGTGCTACAATGGTATCTACAGAGGGAAGCAATATGGCGACATGGAGCAAA
TCCTCAAAAGATATCTCAGTTCGGATTGGTCTCTGCAACTCGAGACCATGAAGTTGGAATCGATAGTAATCGCAGATCAG
CATGCTGCGGTGAATATCTTCCTGAGCCTTGT
>Cylindrospermopsis_raciborskii_ITEP_A1_GEN
GAACGGGATGCTTAGGCATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTCCAGGTCGGGGATAACAGTTG
GAAACGACTGCTAATACCGGATGTGCCGAGAGGTGAAAGATTTATCGCCTGGAGATGAGCTCGCGTCTGATTAGCTAGTT
GGCGGTGTAAGGGACCACCAAGGCATCGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAAGAAAGTGACGGTACTTGAGGAATAAGCATCGGCTAACTC
CGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGCAGGTGGAACT
GAAAGTCTGCTGTTAAAGAGTTTGGCTTAACCAAATAAAGCGGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAA
AGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGTAACT
GACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGG
CGTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAA
CTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAG
ACTTGACATCCTGCGAATCCCGGTGAAAGCTGGGAGTGCCTTAGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAG
CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCT
AGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACA
CGTACTACAATGCTACGGACAGAGGGCAGCGAGCCAGGGATGGCAAGCGAATCCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCGT
>Cylindrospermopsis_raciborskii_MVCC14_GEN
GAACGGGATGCTTAGGCATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTCCAGGTCGGGGATAACAGTTG
GAAACGACTGCTAATACCGGATGTGCCGAGAGGTGAAAGATTTATCGCCTGGAGATGAGCTCGCGTCTGATTAGCTAGTT
GGCGGTGTAAGGGACCACCAAGGCATCGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAAGAAAGTGACGGTACTTGAGGAATAAGCATCGGCTAACTC
CGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGCAGGTGGAACT
GAAAGTCTGCTGTTAAAGAGTTTGGCTTAACCAAATAAAGCGGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAA

AGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGTAACT
GACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGG
CGTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAA
CTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAG
ACTTGACATCCTGCGAATCCCGGTGAAAGCTGGGAGTGCCTTAGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAG
CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCT
AGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACA
CGTACTACAATGCTACGGACAGAGGGCAGCGAGCCAGGGATGGCAAGCGAATCCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCG
>Cylindrospermopsis_raciborskii_MVCC19_GEN
GAACGGGATGCTTAGGCATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTCCAGGTCGGGGATAACAGTTG
GAAACGACTGCTAATACCGGATGTGCCGAGAGGTGAAAGATTTATCGCCTGGAGATGAGCTCGCGTCTGATTAGCTAGTT
GGCGGTGTAAGGGACCACCAAGGCATCGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAAGAAAGTGACGGTACTTGAGGAATAAGCATCGGCTAACTC
CGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGCAGGTGGAACT
GAAAGTCTGCTGTTAAAGAGTTTGGCTTAACCAAATAAAGCGGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAA
AGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGTAACT
GACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGG
CGTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAA
CTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAG
ACTTGACATCCTGCGAATCCCGGTGAAAGCTGGGAGTGCCTTAGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAG
CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCT
AGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACA
CGTACTACAATGCTACGGACAGAGGGCAGCGAGCCAGGGATGGCAAGCGAATCCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCG

>Cylindrospermopsis_raciborskii_N8_GEN
GAACGGGATGCTTAGGCATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTCCAGGTCGGGGATAACAGTTG
GAAACGACTGCTAATACCGGATGTGCCGAGAGGTGAAAGATTTATTGCCTGGAGATGAGCTCGCGTCTGATTAGCTAGTT
GGTGGTGTAAGGGACCACCAAGGCGTCGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAAGAAAGTGACGGTACTTGAGGAATAAGCATCGGCTAACTC
CGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGCAGGTGGAACT
GAAAGTCTGCTGTTAAAGAGTTTGGCTTAACCAAATAAAGCGGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAA
AGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGTAACT
GACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGG
CGTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAA
CTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAG
ACTTGACATCCTGCGAATCCTGGTGAAAGCTGGGAGTGCCTTCGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAG
CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCT
AGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACA
CGTACTACAATGCTACGGACAGAGGGCAGCGAGCCAGGGATGGCAAGCGAATCCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCGT
>Raphidiopsis_brookii_D9_GEN
GAACGAGATGCTTAGGCATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTCCAGGTCGGGGACAACAGTTG
GAAACGACTGCTAATACCGGATGTGCCGAGAGGTGAAAGATTTATCGCCTGGAGATGAGCTCGCGTCTGATTAGCTAGTT
GGTGGTGTAAGGGACCACCAAGGCATCGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAAGAAAGTGACGGTACTTGAGGAATAAGCATCGGCTAACTC
CGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGCAGGTGGAACT
GAAAGTCTGCTGTTAAAGAGTTTGGCTTAACCAAATAAAGCGGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAA
AGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGTAACT
GACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGG
CGTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAA
CTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAG
ACTTGACATCCTGCGAATCCCAGTGAAAGCTGGGAGTGCCTTAGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAG

CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCT
AGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACA
CGTACTACAATGCTACGGACAGAGGGCAGCGAGCCAGGGATGGCAAGCGAATCCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCGT
>Sphaerospermopsis_torques_reginae_ITEP_024_GEN_REF
GAACGAAATCTTCGGATTTAGTGGCGGACGGGTGAGTAACGCGTGAGAATTTGGCTTCAGGTCGGGGACAACAGTTGGA
AACGACTGCTAATACCGGATGTGCCGGAAGGTGAAAGATTTATCGCCTGAAGATAAGCTCGCGTCTGATTAGCTAGTTGG
TGGTGTAAGGGACTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCC
CAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGG
AAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAAAAAATGACGGTACTTGAGGAATAAGCATCGGCTAACTCCG
TGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGTAGGTGGTACTGA
AAGTCTGCTGTTAAAGAGCAAGGCTCAACCTTGTAAAGCAGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAAAG
GAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGCAACTG
ACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGGC
GTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAAC
TCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAGA
CTTGACATCCTGCGAATCCCGGTGAAAGCTGGGAGTGCCTTAGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAGC
TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGATGGGCACTCTA
GAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACAC
GTACTACAATGCTACGGACAAAGGGCAGCTACACAGCGATGTGATGCAAATCCAAAAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGTTTGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCGT
>Sphaerospermopsis_kisseleviana_NIES_73_GEN
GAACGGACTCTTAGGAGTTAGTGGCGGACGGGTGAGTAACGCGTGAGAATTTGGCTTCAGGTCGGGGACAACAGTTGGA
AACGACTGCTAATACCGGATGTGCCGGAAGGTGAAAGATTTATCGCCTGAAGATAAGCTCGCGTCTGATTAGCTAGTTGG
TGGTGTAAGGGACTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCC
CAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGG
AAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAATGCAATGACGGTACTTGAGGAATAAGCATCGGCTAACTCCG
TGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGTAGGTGGTACTGA

AAGTCTGCTGTTAAAGAGCAAGGCTCAACCTTGTAAGAGCAGTGGAAACTACAGAACTGGAGTGCGGTAGGGGCAAAAG
GAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGCAACTG
ACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGGC
GTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAAC
TCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAGA
CTTGACATCCTGCGAATTTTCCTGAAAGGGAAAAGTGCCTTCGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAGC
TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGATGGGCACTCTA
GAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACAC
GTACTACAATGCTACGGACAAAGGGCGGCTACACAGCGATGTGATGCAAATCTCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCGT
>Sphaerospermopsis_aphanizomenoides_1LT27S09_SILVADB_EX
GAACGGGATCTTAGGATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATTTGGCTTCAGGTCGGGGACAACAGTTGGA
AACGACTGCTAATACCGGATGTGCCGGAAGGTGAAAGATTTATCGCCTGAAGATAAGCTCGCGTCTGATTAGCTAGTTGG
TGGTGTAAGGGACTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCC
CAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGG
AAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAAGAAAGTGACGGTACTTGAGGAATAAGCATCGGCTAACTCCG
TGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGTAGGTGGTACTGA
AAGTCTGCTGTTAAAGAGCAAGGCTCAACCTTGTAAGAGCAGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAAAG
GAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGCAACTG
ACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGGC
GTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAAC
TCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAGA
CTTGACATCCTGCGAATTTTCCTGAAAGGGAAAAGTGCCTTCGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAGC
TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGATGGGCACTCTA
GAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACAC
GTACTACAATGCTACGGACAAAGGGCGGCTACACAGCGATGTGATGCAAATCTCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCGT

>Sphaerospermopsis_aphanizomenoides_NRERC_603_NO_GEN_EX
GAACGGGATCTTAGGATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATTTGGCTTCAGGTCGGGGACAACAGTTGGA
AACGACTGCTAATACCGGATGTGCCGGAAGGTGAAAGATTTATCGCCTGAAGATAAGCTCGCGTCTGATTAGCTAGTTGG
TGGTGTAAGGGACTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCC
CAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGG
AAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAAGAAAGTGACGGTACTTGAGGAATAAGCATCGGCTAACTCCG
TGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGTAGGTGGTACTGA
AAGTCTGCTGTTAAAGAGCAAGGCTCAACCTTGTAAGAGCAGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAAAG
GAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGCAACTG
ACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGGC
GTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAAC
TCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAGA
CTTGACATCCTGCGAATCTCGGTGAAAGCTGAGAGTGCCTTCGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAGC
TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGATGGGCACTCTA
GAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACAC
GTACTACAATGCTACGGACAAAGGGCGGCTACACAGCGATGTGATGCAAATCTCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCGT
>Sphaerospermopsis_aphanizomenoides_NRERC_607_NO_GEN_EX
GAACGGGATCTTAGGATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATTTGGCTTCAGGTCGGGGACAACAGTTGGA
AACGACTGCTAATACCGGATGTGCCGGAAGGTGAAAGATTTATCGCCTGAAGATAAGCTCGCGTCTGATTAGCTAGTTGG
TGGTGTAAGGGACTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCC
CAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGG
AAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAAGAAAGTGACGGTACTTGAGGAATAAGCATCGGCTAACTCCG
TGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGTAGGTGGTACTGA
AAGTCTGCTGTTAAAGAGCAAGGCTCAACCTTGTAAAGAGCAGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAAA
GGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGCAACT
GACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGG
CGTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAA
CTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAG
ACTTGACATCCTGCGAATCTCGGTGAAAGCTGAGAGTGCCTTCGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAG

CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGATGGGCACTCT
AGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACA
CGTACTACAATGCTACGGACAAAGGGCGGCTACACAGCGATGTGATGCAAATCTCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCGT
>Sphaerospermopsis_oumiana_NIES_1679_NO_GEN_EX
GAACGGACTCTTAGGAGTTAGTGGCGGACGGGTGAGTAACGCGTGAGAATTTGGCTTCAGGTCGGGGACAACAGTTGGA
AACGACTGCTAATACCGGATGTGCCGGAAGGTGAAAGATTTATCGCCTGAAGATAAGCTCGCGTCTGATTAGCTAGTTGG
TGGTGTAAGGGACTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCC
CAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGG
AAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAATGCAATGACGGTACTTGAGGAATAAGCATCGGCTAACTCCG
TGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGTAGGTGGTACTGA
AAGTCTGCTGTTAAAGAGCAAGGCTCAACCTTGTAAGAGCAGTGGAAACTACAGAACTGGAGTGCGGTAGGGGCAAAAG
GAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGCAACTG
ACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGGC
GTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAAC
TCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAGA
CTTGACATCCTGCGAATTTTCCTGAAAGGGAAAAGTGCCTTCGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAGC
TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGATGGGCACTCTA
GAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACAC
GTACTACAATGCTACGGACAAAGGGCGGCTACACAGCGATGTGATGCAAATCTCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCGT
>Sphaerospermopsis_reniformis_NIES_1949_GEN_EX
GAACGGACTCTTAGGAGTTAGTGGCGGACGGGTGAGTAACGCGTGAGAATTTGGCTTCAGGTCGGGGACAACAGTTGGA
AACGACTGCTAATACCGGATGTGCCGGAAGGTGAAAGATTTATCGCCTGAAGATAAGCTCGCGTCTGATTAGCTAGTTGG
TGGTGTAAGGGACCACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCC
CAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGG
AAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAATGCAATGACGGTACTTGAGGAATAAGCATCGGCTAACTCCG
TGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGTAGGTGGTACTGA

AAGTCTGCTGTTAAAGAGCAAGGCTCAACCTTGTAAGAGCAGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAAAG
GAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGCAACTG
ACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGGC
GTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAAC
TCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAGA
CTTGACATCCTGCGAATTTTCCTGAAAGGGAAAAGTGCCTTCGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAGC
TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGATGGGCACTCTA
GAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACAC
GTACTACAATGCTACGGACAAAGGGCGGCTACACAGCGATGTGATGCAAATCTCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCGT
>Sphaerospermopsis_sp_FACHB_1094_GEN_EX
GAACGGACTCTTAGGAGTTAGTGGCGGACGGGTGAGTAACGCGTGAGAATTTGGCTTCAGGTCGGGGACAACAGTTGGA
AACGACTGCTAATACCGGATGTGCCGGAAGGTGAAAGATTTATCGCCTGAAGATAAGCTCGCGTCTGATTAGCTAGTTGG
TGGTGTAAGGGACTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCC
CAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGG
AAGGCTCTTGGGTCGTAAACCTCTTTTCTCAAGGAAGAATGCAATGACGGTACTTGAGGAATAAGCATCGGCTAACTCCG
TGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGTAGGTGGTACTGA
AAGTCTGCTGTTAAAGAGCAAGGCTCAACCTTGTAAGAGCAGTGGAAACTACAGAACTAGAGTGCGGTAGGGGCAAAAG
GAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTTTGCTAGACCGCAACTG
ACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGGC
GTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAAC
TCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAGA
CTTGACATCCTGCGAATTTTCCTGAAAGGGAAAAGTGCCTTCGGGAGCGCAGAGACAGGTGGTGCATGGCTGTCGTCAGC
TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGATGGGCACTCTA
GAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACAC
GTACTACAATGCTACGGACAAAGGGCGGCTACACAGCGATGTGATGCAAATCTCAGAAACCGTAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGGTGACTGGGGTGAAGTCGT

>Anabaena_cylindrica_FACHB_243_GEN
GAACGGAATCCTTAGGGATTTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTTCAGGTCGGGGACAACAGTTG
GAAACGACTGCTAATACCGGATATGCCGAGAGGTGAAAGATTAATTGCCTGGAGATGAGCTCGCGTCTGATTAGCTAGTT
GGTGGGGTAAGAGCCTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCAGGGAAGAAAAAATGACGGTACCTGAGGAATAAGCATCGGCTAACTC
CGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGCGTCCGCAGGTGGCCAT
GTAAGTCTGCTGTTAAAGAGTCATGCTTAACATGATAAAAGCAGTGGAAACTACAGAGCTAGAGTACGTTCGGGGCAGA
GGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGCTCTGCTAGGCCGTAAC
TGACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAG
GCGTGGCTTGTATCGACCCGAGCCGTGCCGTAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAA
ACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAA
GGCTTGACATGTCGCGAATCTTTCTGAAAGGAGAGAGTGCCTTCGGGAGCGCGAACACAGGTGGTGCATGGCTGTCGTCA
GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTC
TAGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACAC
ACGTACTACAATGCTACGGACAAAGGGCAGCTACACAGCGATGTGATGCTAATCTCATAAACCGTAGCTCAGTTCAGATC
GCAGGCTGCAACTCGCCTGCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGC
CTTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTA
AGGTAGGACTGGTGACTGGGGTGAAGTCGT
>Anabaena_cylindrica_PCC_7122_GEN
GAACGGAATCCTTAGGGATTTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTTCAGGTCGGGGACAACAGTTG
GAAACGACTGCTAATACCGGATATGCCGAGAGGTGAAAGATTAATTGCCTGGAGATGAGCTCGCGTCTGATTAGCTAGTT
GGTGGGGTAAGAGCCTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCAGGGAAGAAAAAATGACGGTACCTGAGGAATAAGCATCGGCTAACTC
CGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGCGTCCGCAGGTGGCCAT
GTAAGTCTGCTGTTAAAGAGTCATGCTTAACATGATAAAAGCAGTGGAAACTACAGAGCTAGAGTACGTTCGGGGCAGA
GGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGCTCTGCTAGGCCGTAAC
TGACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAG
GCGTGGCTTGTATCGACCCGAGCCGTGCCGTAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAA
ACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAA
GGCTTGACATGTCGCGAATCTTTCTGAAAGGAGAGAGTGCCTTCGGGAGCGCGAACACAGGTGGTGCATGGCTGTCGTCA

GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTC
TAGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACAC
ACGTACTACAATGCTACGGACAAAGGGCAGCTACACAGCGATGTGATGCTAATCTCATAAACCGTAGCTCAGTTCAGATC
GCAGGCTGCAACTCGCCTGCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGC
CTTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCGAAAGGAGGGGGATGCCTA
AGGTAGGACTGGTGACTGGGGTGAAGTCGT
>Anabaena_sp_90_GEN
GAACGGAATCTTTAGGGATTTAGTGGCGGACGGGTGAGTAACGCGTAAGAATCTACCTTCAGGTTGGGGACAACCACTGG
AAACGGTGGCTAATACCGAATGTGCCGAGAGGTGAAAGGCTTGCTGCCTGAAGAAGAGCTTGCGTCTGATTAGCTAGTTG
GTGGGGTAAGAGCCTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGC
CCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAG
GAAGGCTCTTGGGTTGTAAACCTCTTTTCTCAGGGAAGAAAAAAATGACGGTACCTGAGGAATAAGCATCGGCTAACTCC
GTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCCGCAGGTGGCATTG
TATGTCTGCTGTTAAAGAGTTTGGCTCAACCAAATCAAAGCAGTGGAAACTACAAAGCTAGAGTATGGTCGGGGCAGAG
GGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAGGCGCTCTGCTAGGCCAAAACT
GACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGG
TGTAGCTCGTATCGACCCGAGCTGTACCGTAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCAGGCAACTGTGAAA
CTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAG
GCTTGACATGTCACGAATCCCGGCGAAAATTGGGAGTGCCTTAGGGAGCGTGAACACAGGTGGTGCATGGCTGTCGTCAG
CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCT
AGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACA
CGTACTACAATGCTCCGGACAAAGGGCAGCTACACAGCGATGTGATGCGAATCTCATAAACCGGAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCGTTACCCCAACCTTTTGGAGGGGGATGCCTAA
GGTAGGACTGATGACTGGGGTGAAGTCGT
>Anabaena_sp_299_NO_GEN
GAACGGAATCTTTAGGGATTTAGTGGCGGACGGGTGAGTAACGCGTAAGAATCTACCTTCAGGTTGGGGACAACCACTGG
AAACGGTGGCTAATACCGAATGTGCCGAGAGGTGAAAGGCTTGCTGCCTGAAGAAGAGCTTGCGTCTGATTAGCTAGTTG
GTGGGGTAAGAGCCTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGC
CCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAG
GAAGGCTCTTGGGTTGTAAACCTCTTTTCTCAGGGAAGAAAAAAATGACGGTACCTGAGGAATAAGCATCGGCTAACTCC
GTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCCGCAGGTGGCATTG

TATGTCTGCTGTTAAAGAGTCTGGCTCAACCAGATCAAAGCAGTGGAAACTACAAAGCTAGAGTATGGTCGGGGCAGAG
GGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAGGCGCTCTGCTAGGCCAAAACT
GACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGG
TGTAGCTCGTATCGACCCGAGCTGTACCGTAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCAGGCAACTGTGAAA
CTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAG
GCTTGACATGTCACGAATCCCGGCGAAAGTTGGGAGTGCCTTAGGGAGCGTGAACACAGGTGGTGCATGGCTGTCGTCAG
CTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCT
AGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACA
CGTACTACAATGCTCCGGACAAAGGGCAGCTACACAGCGATGTGATGCGAATCTCATAAACCGGAGCTCAGTTCAGATCG
AAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCGTTACCCCAACCTTTTGGAGGGGGGATGCCTAA
GGTAGGACTGATGACTGGGGTGAAGTCGT
>Anabaena_sphaerica_FACHB_251_GEN
GAACGGAATGCTTAGGCATTTAGTGGCGGACGGGTGAGTAACGCGTGAGAATTTGGCTTCAGGTCGGGGACAACAGTTG
GAAACGACTGCTAATACCGGATATGCCGGAAGGTGAAAGATTTATTGCCTGGAGATAAGCTCGCGTCTGATTAGCTAGTT
GGTGGGGTAAGAGCCTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTCGTAAACCTCTTTTCTCAGGGAAGAAAAAAATGACGGTACCTGAGGAATAAGCATCGGCTAACTC
CGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCTGTAGGTGGTGCT
GTAAGTCTGCTGTTAAAGAGTCACGCTCAACGTGATAAAGCAGTGGAAACTACAGGACTAGAGTGCGTTCGGGGCAGA
AGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAAGCGTTCTGCTAGGCCGCAAC
TGACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAG
GCGTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAA
ACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAA
GACTTGACATGTCGCGAATCTCGGTGAAAGCTGAGAGTGCCTTCGGGAGCGCGAACACAGGTGGTGCATGGCTGTCGTCA
GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTC
TAGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGAGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACAC
ACGTACTACAATGCTACGGACAAAGGGCAGCAAGCTAGCGATAGCAAGCAAATCTCATAAACCGTAGCTCAGTTCAGAT
CGAAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGG
CCTTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCATTACCCCAACCTTTTGGAGGGGGGATGCCT
AAGGTAGGACTGGTGACTGGGGTGAAGTCGT

>Aphanizomenon_flos_aquae_DEX188_GEN
GAACGGTCTTTTAGGAGACAGTGGCGGACGGGTGAGTAACGCGTAAGAATCTACCTTCAGGTTGGGGACAACCACTGGA
AACGGTGGCTAATACCGAATGTGCCGAGAGGTGAAAGGCTTGCTGCCTGAAGAAGAGCTTGCGTCTGATTAGCTAGTTGG
TAGTGTAAGAGACTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCC
CAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGG
AAGGCTCTTGGGTTGTAAACCTCTTTTCTCAGGGAAGAACAGAATGACGGTACCTGAGGAATAAGCATCGGCTAACTCCG
TGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCCGCAGGTGGCATTGT
AAGTCTGCTGTTAAAGAGTTTGGCTCAACCAAATAAGAGCAGTGGAAACTACAAAGCTAGAGTGTGGTCGGGGCAGAGG
GAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCAGTGGCGAAGGCGCTCTGCTAGGCCGAGACTG
ACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGGC
GTAGCTCGTATCGACCCGAGCTGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCAGGCAACTGTGAAAC
TCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAGG
CTTGACATGTCACGAATCCTATTGAAAGATGGGAGTGCCTTCGGGAGCGTGAACACAGGTGGTGCATGGCTGTCGTCAGC
TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGATGGGCACTCTA
GAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACAC
GTACTACAATGCTCCGGACAAAGGGCAGCTACACAGCGATGTGATGCGAATCTCATAAACCGGAGCTCAGTTCAGATCGA
AGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCCT
TGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCGTTACCCCAACCTATTGGAGGGGGATGCCTAAG
GTAGGACTGATGACTGGGGTGAAGTCGT
>Aphanizomenon_flos_aquae_FACHB_1171_GEN
GAACGGTCTTTTAGGAGACAGTGGCGGACGGGTGAGTAACGCGTAAGAATCTACCTTCAGGTTGGGGACAACCACTGGA
AACGGTGGCTAATACCGAATGTGCCGAGAGGTGAAAGGCTTGCTGCCTGAAGAAGAGCTTGCGTCTGATTAGCTAGTTGG
TAGTGTAAGAGACTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCC
CAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGG
AAGGCTCTTGGGTTGTAAACCTCTTTTCTCAGGGAAGAACAGAATGACGGTACCTGAGGAATAAGCATCGGCTAACTCCG
TGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCCGCAGGTGGCATTGT
AAGTCTGCTGTTAAAGAGTTTGGCTCAACCAAATAAGAGCAGTGGAAACTACAAAGCTAGAGTGTGGTCGGGGCAGAGG
GAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCAGTGGCGAAGGCGCTCTGCTAGGCCGAGACTG
ACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGGC
GTAGCTCGTATCGACCCGAGCTGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCAGGCAACTGTGAAAC
TCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAGG
CTTGACATGTCACGAATCCTATTGAAAGATGGGAGTGCCTTCGGGAGCGTGAACACAGGTGGTGCATGGCTGTCGTCAGC

TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAGGTTGGGCACTCTA
GAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACAC
GTACTACAATGCTACGGACAAAGGGCAGCTACACAGCGATGTGATGCGAATCTCGTAAACCGTAGCTCAGTTCAGATCGA
AGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCCT
TGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCGTTACCCCAACCTATTGGAGGGGGATGCCTAAG
GTAGGACTGATGACTGGGGTGAAGTCGT
>Aphanizomenon_flos_aquae_KM1D3_PB_GEN
GAACGGTCTTTTCGGAGATAGTGGCGGACGGGTGAGTAACGCGTAAGAATCTACCTTCAGGTTGGGGACAACCAGTGGA
AACGGTGGCTAATACCCAATGTGCCGAGAGGTGAAAGGCTTGCTGCCTGAAGAAGAGCTTGCGTCTGATTAGCTAGTTGG
TGGGGTAAAAGCCTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCC
CAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGG
AAGGCTCTTGGGTTGTAAACCTCTTTTCTCAGGGAAGAACAAAATGACGGTACCTGAGGAATAAGCATCGGCTAACTCCG
TGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCCGCAGGTGGCATTGT
AAGTCTGCTGTTAAAGAGTTTGGCTCAACCAAATAAAAGCAGTGGAAACTACAAAGCTAGAGTGTGGTCGGGGCAGAGG
GAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAGGCGCTCTGCTAGGCCAAGACTG
ACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGGC
GTAGCTCGTATCGACCCGAGCTGTGCCGTAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCAGGCAACTGTGAAAC
TCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAGG
CTTGACATGTCACGAATTCCGTTGAAAGATGGAAGTGCCTTCGGGAGCGTGAACACAGGTGGTGCATGGCTGTCGTCAGC
TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCTA
GAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACAC
GTACTACAATGCTACGGACAAAGGGCAGCTACACAGCGATGTGATGCGAATCTCATAAACCGTAGCTCAGTTCAGATCGA
AGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCCT
TGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCGTTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGATGACTGGGGTGAAGTCGT
>Dolichospermum_circinale_AWQC310F_GEN_OBS
GAACGGTCTTTTAGGAGACAGTGGCGGACGGGTGAGTAACGCGTAAGAATCTACCCTCAGGTCGGGGACAACCACTGGA
AACGGTGGCTAATACCGGATGTGCCGAGAGGCGAAAGGCTTGCTGCCTGGGGAAGAGCTTGCGTCTGATTAGCTAGTTGG
TAGTGTAAGGGACTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCC
CAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGG
AAGGCTCTTGGGTTGTAAACCTCTTTTCTCAGGGAAGAACAGAATGACGGTACCTGAGGAATAAGCATCGGCTAACTCCG
TGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGAGTCCGTAGGTGGCATTGA

AAGTCTGCTGTTAAAGAGTCTAGCTCAACTAGATAAAAGCAGTGGAAACTACAAAGCTAGAGTTTGGTCGGGGCAGAAG
GAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAGGCGTTCTGCTAGGCCGAGACTG
ACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGGC
GTAGCTCGTATCGACCCGAGCTGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCAGGCAACTGTGAAAC
TCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAGG
CTTGACATGTCACGAATCCTGTAGAAACATAGGAGTGCCTTAGGGAGCGTGAACACAGGTGGTGCATGGCTGTCGTCAGC
TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGATGGGCACTCTA
GAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACAC
GTACTACAATGCTACGGACAAAGGGCAGCTACACAGCGATGTGATGCGAATCTCATAAACCGTAGCTCAGTTCAGATCGA
AGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCCT
TGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCGTTACCCCAACCTATTGGAGGGGGATGCCTAAG
GTAGGACTGATGACTGGGGTGAAGTCGT
>Dolichospermum_flos_aquae_LEGE_04289_GEN_OBS
GAACGGTCTTTTAGGAGACAGTGGCGGACGGGTGAGTAACGCGTAAGAATCTACCCTCAGGTCGGGGACAACCACTGGA
AACGGTGGCTAATACCGGATGTGCCGAGAGGTGAAAGGCTTGCTGCCTGGGGAAGAGCTTGCGTCTGATTAGCTAGTTGG
TAGTGTAAGGGACTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCC
CAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGG
AAGGCTCTTGGGTTGTAAACCTCTTTTCTCAGGGAAGAAAAAATGACGGTACCTGAGGAATAAGCATCGGCTAACTCCG
TGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCCGCAGGTGGCATTGT
AAGTCTGCTGTTAAAGAGTTTGGCTCAACCAAATAAAAGCAGTGGAAACTACAAAGCTAGAGTTTGGTCGGGGCAGAGG
GAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCAGTGGCGAAGGCGCTCTGCTAGGCCGAGACTG
ACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGGC
GTAGCTCGTATCGACCCGAGCTGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCAGGCAACTGTGAAAC
TCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAGG
CTTGACATGTCACGAATCCTGTGGAAACATAGGAGTGCCTTAGGGAGCGTGAACACAGGTGGTGCATGGCTGTCGTCAGC
TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCTA
GAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACAC
GTACTACAATGCTACGGACAAAGGGCAGCTACACAGCGATGTGATGCGAATCTCGTAAACCGTAGCTCAGTTCAGATCGA
AGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCCT
TGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCGTTACCCCAACCGAAAGGAGGGGGATGCCTAA
GGTAGGACTGATGACTGGGGTGAAGTCGT

>Dolichospermum_sp_UHCC_0260_GEN
GAACGGAATCTTTAGGGATTTAGTGGCGGACGGGTGAGTAACGCGTAAGAATCTACCTTCAGGTCGGGGACAACCACTG
GAAACGGTGGCTAATACCGGATGTGCCGAGAGGTGAAAGGCTTGCTGCCTGAAGAAGAGCTTGCGTCTGATTAGCTAGTT
GGTGGGGTAAGAGCCTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGG
CCCAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGA
GGAAGGCTCTTGGGTTGTAAACCTCTTTTCTCAGGGAAGAAAAAAATGACGGTACCTGAGGAATAAGCATCGGCTAACTC
CGTGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCCGCAGGTGGCATT
GTATGTCTGCTGTTAAAGAGTCTGGCTCAACCAGATCAAAGCAGTGGAAACTACAAAGCTAGAGTATGGTCGGGGCAGA
GGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAGGCGCTCTGCTAGGCCAAAAC
TGACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAG
GTGTAGCTCGTATCGACCCGAGCTGTACCGTAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCAGGCAACTGTGAA
ACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAA
GGCTTGACATGTCACGAATTCCGGCGAAAGTTGGGAGTGCCTTAGGGAGCGTGAACACAGGTGGTGCATGGCTGTCGTCA
GCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTC
TAGAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACAC
ACGTACTACAATGCTCCGGACAAAGGGCAGCTACACAGCGATGTGATGCGAATCTCATAAACCGGAGCTCAGTTCAGATC
GAAGGCTGCAACTCGCCTTCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGC
CTTGTACACACCGCCCGTCACACCATGGAAGTTGGTCACGCCCGAAGTCGTTACCCCAACCTTTTGGAGGGGGATGCCTA
AGGTAGGACTGATGACTGGGGTGAAGTCGT
>Nodularia_harveyana_Huebel_1983_300_NO_GEN
GAACGGAATCTTAGGATTTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTAGCTTCAGGTCGGGGACAACCACGGGA
AACTGTGGCTAATACCGGATATGCCGAGAGGTGAAAGGCTTGCTGCCTGAAGATGAGCTCGCGTCTGATTAGCTAGTTGG
TAGAGTAAAAGCCTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCC
CAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGG
AAGGCTCTTGGGTTGTAAACCTCTTTTCTCAAGGAAGAAAAAAATGACGGTACTTGAGGAATAAGCATCGGCTAACTCCG
TGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCCGCAGGTGGCAATGT
AAGTCTGCTGTTAAAGAATGAGGCTCAACCTCATCAAAGCGGTGGAAACTACACAGCTAGAGTGCGTTCGGGGTAGAGG
GAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCAGTGGCGAAGGCGCTCTACTAGGCCGCAACTG
ACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGGC
GTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAAC
TCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAGA
CTTGACATGTTGCGAATCTTTGTGAAAGCAGAGAGTGCCTTCGGGAGCGCAAACACAGGTGGTGCATGGCTGTCGTCAGC

TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGATGGGCACTCTA
GAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACAC
GTACTACAATGCTACGGACAAAGGGCAGCTACACAGCAATGTGATGCAAATCTCAGAAACCGTAGCTCAGTTCAGATCGC
AGGCTGCAACTCGCCTGCGTGAAGTAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCCT
TGTACACACCGCCCGTCACACCATGGAAGCTGGTCACGCCCGAAGTCGTTACCCCAACTTTTAGGAGAGGGGGATGCCGA
AGGTAGGACTGGTGACTGGGGTGAAGTCGT
>Nodularia_sp_LEGE_06071_GEN
GAACGGTCTCTTCGGAGATAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGGCTTCAGGTCGGGGACAACCACTGGA
AACGGTGGCTAATACCGGATATGCCGAGAGGTGAAAGGCTTGCCGCCTGAAGATGAGCTCGCGTCTGATTAGCTAGTAGG
TGTGGTAAAGGCGCACCTAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCC
CAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGG
AAGGCTCTTGGGTTGTAAACCTCTTTTCTCAGGGAAGAAAAAAATGACGGTACCTGAGGAATAAGCATCGGCTAACTCCG
TGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCCGCAGGTGGCTATGT
AAGTCTGCTGTTAAAGAACTTAGCTTAACTAGGTAAAGCAGTGGAAACTACAAGGCTAGAGTGCGTTCGGGGTAGAGG
GAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCAGTGGCGAAGGCGCTCTACTAGGCCGCAACTG
ACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGGC
GTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCAGGCAACTGTGAAAC
TCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAGA
CTTGACATGTCGCGAATCTCTCTGAAAGGAGAGAGTGCCTTCGGGAGCGCGAACACAGGTGGTGCATGGCTGTCGTCAGC
TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCTA
GAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACAC
GTACTACAATGCTACGGACAAAGGGTAGCTACACAGCAATGTGATGCCAATCTCAGAAACCGTAGCTCAGTTCAGATCGC
AGGCTGCAACTCGCCTGCGTGAAGGAGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCCT
TGTACACACCGCCCGTCACACCATGGAAGCTGGTCACGCCCGAAGTCGTTACCCCAACTTTTCGGAGAGGGGGATGCCGA
AGGCAGGACTGGTGACTGGGGTGAAGTCGT
>Nodularia_sp_NIES_3585_GEN
GAACGGGATCTTAGGATCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTAGCTTCAGGTCGGGGACAACCACGGGA
AACTGTGGCTAATACCGGATATGCCGAGAGGTGAAAGGCTTGCTGCCTGAAGATGAGCTCGCGTCTGATTAGCTAGTAGG
TGTGGTAAAAGCGCACCTAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCC
CAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGG
AAGGCTCTTGGGTTGTAAACCTCTTTTCTCAGGGAAGAAAAAAATGACGGTACCTGAGGAATAAGCATCGGCTAACTCCG
TGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCCGCAGGTGGCTATGT

AAGTCTGCTGTTAAAGAACTTAGCTTAACTAGGTAAAAGCAGTGGAAACTACAAGGCTAGAGTGCGTTCGGGGTAGAGG
GAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCAGTGGCGAAGGCGCTCTACTAGGCCGCAACTG
ACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGGC
GTGGCTTGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAAC
TCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAGA
CTTGACATGTCGCGAATCTGATTGAAAGGTCAGAGTGCCTTCGGGAGCGCGAACACAGGTGGTGCATGGCTGTCGTCAGC
TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCTA
GAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACAC
GTACTACAATGCTACGGACAAAGGGCAGCTACACAGCAATGTGATGCCAATCTCAGAAACCGTAGCTCAGTTCAGATCGC
AGGCTGCAACTCGCCTGCGTGAAGTCGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCCT
TGTACACACCGCCCGTCACACCATGGAAGCTGGTCACGCCCGAAGTCGTTACCCCAACTGTTCGCAGAGGGGGATGCCGA
AGGCAGGACTGGTGACTGGGGTGAAGTCGT
>Nodularia_sphaerocarpa_UHCC_0038_GEN
GAACGGTCTCTTCGGAGATAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTAGCTTCAGGTCGGGGACAACCACTGGA
AACGGTGGCTAATACCGGATATGCCGAGAGGTGAAAGGCTTGCTGCCTGAAGATGAGCTCGCGTCTGATTAGCTAGTAGG
TGTGGTAAAAGCGCACCTAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCC
CAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGG
AAGGCTCTTGGGTTGTAAACCTCTTTTCTCAGGGAAGAAAAAATGACGGTACCTGAGGAATAAGCATCGGCTAACTCCG
TGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCCGCAGGTGGCTATGT
AAGTCTGCTGTTAAAGAACCTAGCTTAACTAGGTAAAAGCAGTGGAAACTACAAGGCTAGAGTGCGTTCGGGGTAGAGG
GAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCAGTGGCGAAGGCGCTCTACTAGGCCGCAACTG
ACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGGC
GTGGCTTGTATCGACCCAAGCCGTGCCGTAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAAC
TCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAGA
CTTGACATGTCGCGAATCTTCTTGAAAGGGAAGAGTGCCTTCGGGAGCGCGAACACAGGTGGTGCATGGCTGTCGTCAGC
TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCTA
GAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACAC
GTACTACAATGCTACGGACAAAGGGTAGCTACACAGCAATGTGATGCCAATCTCAGAAACCGTAGCTCAGTTCAGATCGC
AGGCTGCAACTCGCCTGCGTGAAGTCGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCCT
TGTACACACCGCCCGTCACACCATGGAAGCTGGTCACGCCCGAAGTCGTTACCCCAACTTTTCGGAGAGGGGGATGCCGA
AGGCAGGTCTGGTGACTGGGGTGAAGTCGT

>Nodularia_spumigena_CCY9414_GEN
GAACGGTCTCTTCGGAGATAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTAGCTTCAGGTCGGGGACAACCACGGGA
AACTGTGGCTAATACCGGATATGCCGAGAGGTGAAAGGCTTGCTGCCTGAAGATGAGCTCGCGTCTGATTAGCTAGTAGG
TGTGGTAAAAGCGCACCTAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCC
CAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGAGG
AAGGCTCTTGGGTTGTAAACCTCTTTTCTCAGGGAAGAAAAAATGACGGTACCTGAGGAATAAGCATCGGCTAACTCCG
TGCCAGCAGCCGCGGTAATACGGAGGATGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTCCGCAGGTGGCTATGT
AAGTCTGCTGTTAAAGAACCTAGCTTAACTAGGTAAAAGCAGTGGAAACTACAAGGCTAGAGTGCGTTCGGGGTAGAGG
GAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCAGTGGCGAAGGCGCTCTACTAGGCCGCAACTG
ACACTGAGGGACGAAAGCTAGGGGAGCGAATGGGATTAGATACCCCAGTAGTCCTAGCCGTAAACGATGGATACTAGGC
GTGGCTCGTATCGACCCGAGCCGTGCCGGAGCTAACGCGTTAAGTATCCCGCCTGGGGAGTACGCACGCAAGTGTGAAAC
TCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAAGA
CTTGACATGTCGCGAATCTCTCTGAAAGGAGAGAGTGCCTTCGGGAGCGCGAACACAGGTGGTGCATGGCTGTCGTCAGC
TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTCGTTTTTAGTTGCCAGCATTAAGTTGGGCACTCTA
GAGAGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCAGCATGCCCCTTACGTCTTGGGCTACACAC
GTACTACAATGCTACGGACAAAGGGCAGCTACACAGCAATGTGATGCAAATCTCACAAAACCGTAGCTCAGTTCAGATCG
CAGGCTGCAACTCGCCTGCGTGAAGTCGGAATCGCTAGTAATTGCAGGTCAGCATACTGCAGTGAATTCGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGCTGGTCACGCCCGAAGTCGTTACCCCAACTGTTCGCAGAGGGGGATGCCG
AAGGCAGGACTGGTGACTGGGGTGAAGTCGT
>Synechococcus_elongatus_PCC_6301_GEN
GAACGGGCTCTTCGGAGCTAGTGGCGGACGGGTGAGTAACGCGTGAGAATCTGCCTACAGGACGGGGACAACAGTTGGA
AACGACTGCTAATACCCGATGTGCCGAGAGGTGAAACATTTATGGCCTGTAGATGAGCTCGCGTCTGATTAGCTAGTTGG
TGGGGTAAGGGCCTACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCC
CAGACTCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGCAAGCCTGACGGAGCAACGCCGCGTGGGGGAGG
AAGGTTTTTGGACTGTAAACCCCTTTTCTCAGGGAAGAAGAAAGTGACGGTACCTGAGGAATAAGCCTCGGCTAATTCCG
TGCCAGCAGCCGCGGTAATACGGGAGAGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGTCCGCAGGCGGTTAATC
AAGTCTGTTGTCAAAGCGTGGGGCTCAACCTCATACAGGCAATGGAAACTGATTGACTAGAGTATGGTAGGGGTAGCGG
GAATTCCAGGTGTAGCGGTGAAATGCGTAGATATCTGGAAGAACACCAGCGGCGAAAGCGCGCTACTGGGCCATAACTG
ACGCTCATGGACGAAAGCTAGGGGAGCGAAAGGGATTAGATACCCCTGTAGTCCTAGCCGTAAACGATGAACACTAGGT
GTTGCGTGAATCGACCCGCGCAGTGCCGTAGCCAACGCGTTAAGTGTTCCGCCTGGGGAGTACGCACGCAAGTGTGAAAC
TCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCAGGG
TTTGACATCCCCCGAATCTCTTGGAAACGAGAGAGTGCCTTCGGGAGCGGGGAGACAGGTGGTGCATGGCTGTCGTCAGC

TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCACGTTTTTAGTTGCCATCATTCAGTTGGGCACTCTA
GAGAAACTGCCGGTGACAAACCGGAGGAAGGTGTGGACGACGTCAAGTCATCATGCCCCTTACATCCTGGGCTACACAC
GTACTACAATGCTCCGGACAGCGAGACGCGAAGCCGCGAGGTGAAGCAAATCTCCCAAACCGGGGCTCAGTTCAGATTG
CAGGCTGCAACTCGCCTGCATGAAGGCGGAATCGCTAGTAATCGCAGGTCAGCATACTGCGGTGAATACGTTCCCGGGCC
TTGTACACACCGCCCGTCACACCATGGAAGTTGGCCATGCCCGAAGTCGTTACCCTAACCGTTCGCGGAGGGGGGCGCCG
AAGGTAGGGCTGATGACTGGGGTGAAGTCGT

Table S3. Sequences of 31 conserved proteins in cyanobacteria used in this study.

Organism	Sequence
>Cylindrospermopsis_curvispora_GIHE_G1	

MQIPRLHPDTVEEVKHRADIVDVISDYVVLRRRGKDFVGLCPFHEEKTPSFTVSPTKQIYYCFGCQASGNAIKFIMDLNKRQFAE
VVLDLAKRYQVPVKTLAPEQRQELQRQLSLREQLFEVLASTSQFYQHVLRQDIGQQALQYLQGKRFLKTETVEKFALGYAPPG
WETLYHYLVENKNYPAHLVEKAGLIKPRKEGGGYYDVFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFDKSKTLF
ALDLAKDAISKLDQAVVVEGYFDAIALHAKGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATERAIGEISNL
AYKGEVQLKILHIPDGKDADEYLKNHSVTDYGQLLVDAPLWLDWQIAQVIQGRDLKQPTDFQLVSREFVKLLQKILNSDTLNY
YISHCAEILSLGDSRLIPLRVENLITQVTPTAILRPTPNSTIWSKTSPISHPQPSLLEQAEGLLLRIFLHCPQERQVIIETLGSSNLEFSV
SHHRFLWEKSLQFPSQTLDLISQLQNLYLETQNDLGPVQHIFQLNEKNKQEILLRTNQLVQAAIACMEKVFRENRYRHFLELWQ
KTDPNTPDQYNLYAQTIYADKMRIQELSKQRQLSIADLIDMTLAEAESTMKKTVEATQKAFNSIRTGRANASLLDKVQVEYY
GNPAPLKSLANITTPDASTILIQPYDRTSLNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSERRKELVKLAAKYAEEGRVGIRNIRR
DALDSIRKQQKAADISEDESRDQQDKLQKITNIYTAKIDELLAEKEKDISTVMPVIEKKRTRDLPQINERIRFPKIRVIDSEGAQLG
IMAPLEALRLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVKQAERF
LKDGDKVKATVMFRGREIQHSDLAETLLNRMATDLEPFGEVQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIEKISLERNLP
RLAVQSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIDGEGFRVLSTKTIVEEVTNCDHQISLDEVQQVAPEAQSGD
SVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSFGQPEVEAELPKRE
QLPNDTYRSNATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAVDTL
DRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIGKEGQN
VRLAARLTGWKIDIKDQAKYDYGAEDAKFAAVRANYQDESNQPDSQFEVREEEYEDDPDEGEDEFNSMGEENMSKKSLASLS
AADISDKRALVRVDFNVPVDNQGNITDDTRIRAALPTIQDLISKGAKVILASHFGRPKGVDEKLRLTPVAKRLSELLGQEVIKTD
DCIGDDVTAQVAALEKGQVLLLENVRFYKEEENNDPEFARQLAANADFYVNDAFGTAHRAHASTEGVTKYLSPSVAGYLVEK

ELQYLQGAIEAPQRPLVAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEQDKLELASSLEKEAAKRGVT
LLLPTDIVAADKFAPDADAVTVSIDHIPDDRMGLDIGPESVKVFQAALADCKTVIWNGPMGVFEFDKFAVGTEAIAQTLAEIGK
TGATTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGKVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRD
YSVSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGGTVQVIP
HITNEIKERVIRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGKQNVLYMHVTLLPWIASAGEMKTKPTQHSVKELRSI
GIQPDILVCRCDRPIPVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQREPDLTHWETMVERMSHP
QSPVEIAIVGKYVRLGDAYLSVVESLRHAAIATYGDLRLRWVNSEILEVEPPDNYLLGVDGIIVPGGFGIRGVDGKISAIEYARN
QQIPFLGLCLGMQCSIIEWARNVEGLVGANSAEFDPQTDYPVINLLPEQQDVIDLGGTMRLGLYPCHVQPNTLAFDLYQEEVIY
ERHRHRYEFNNLYRNHLLNSGYVISGTSPDGRLVEIVEYPKHPFFIACQFHPEFQSRPSHPHPLFKGFMEAAISHTHQGSAPMVK
KVSRRLQALQAKVEERDYAPLEALALLKETATAKFPEAAEAHIRLGIDPKYTDQQLRTTVVLPKGTGQIVRVAVIARGEKVTEA
TNAGADIAGSEELIDEIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDIASAISEFKAGKLEFRADRTGIV
HVMFGKASFTPEDLLVNLKALQETIDRNRPSGAKGRYWRTFYISATMGPSIKIDINALRDLKTTDAAMGTRSYRPYTPSTRQVTI
SDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRDITATVIAVEYDPNRNARIALVEYEDGEKRYI
LHPNGLKVGAKITAGPQAPFEDGNALPLGNIPLGTNVHNVEMTPGKGGQIVRAAGATAQLMAKEGNYVTLKLPSGEVRMVRR
ECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPALGAKTRKRKKASS
KLIVRRRRKSSKRGRGGRQSMSVGILGTKLGMTQIFDEAGVSIPVTVIKAGPCTVTQVKTQPTDGYCAIQVGYGEVKPKALNKP
KLGHLAKSSAGPVRYLNEYRTDTAGDYALGQEIKADIFSVGQIVDVIGTSIGRGFAGNQKRNNFGRGPMSHGSKNHRAPGSIGA
GTTPGRVYPGKRMAGRLGGSRVTVRKLTVVKVDAERNLILIKGAIPGKPGGLVNVVPTTKVGNKMVESTVKNWQGEEVGQTS
FELRVAKEETASHIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFGPKPRDFNIKL
NRKERRLALRTAFVSRREDLIVVEEFTDQLQRPKSKELVAALARWGAEADQKTLLILSEIGQSTETISLSARNVENIKVIAADQL
NVFDLLHADKIVVTSSALTKIQEVYSAMATTRLKTLYSQTIVPKLTQQFQYTNVHQVPKVLKVTVNRGLGEAAQNAKALEASL
SEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSAKSFDGRGNYTLGVREQLIFPE
VEYDRIDQIRGLDISIITTAKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGTKVVVKGPKGELSRDLPAHVTVSQ
SGETLLVTRRDDTRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGANLVLNIGYSHQVQIEPPAGVQFAVEN
NTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRKAGKTGGKGKMAKKVVAVIKLALNAGKANPAPPVGP
ALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSDQPNKKKVGSITRTQLKEIAQT
KLPDLNANDIEAAMNIVEGTAKNMGVTVKDMSTATDQILEQLKSLTLLEAAELVKQIEEAFGVSAAAPVGGMAVIAAPGGAA
AAEVVEEQTEFDVILQEVPADKKIAVLKIVREITGLGLKEAKELVESTPKAVKEGVNKESADDISKKITEAGGKVTIKMSSKTYL
PPEEEIKRDWYVVDAADKRLGRLATEIAMVLRGKRKAEYTPHLDTGDFVVVINAEKVVVTGKKQSQKLYRRHSGRPGGMKT
ETFAKLQQRLPERIVEHAVKGMLPKNSLGRQLFTKLKVYSGSTHPHTAQKPKELIINTIPGENMIQPQTYLNVADNSGARKLMCI
RVLGAGNRRYGGVGDRIIAVVKDAQPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKEGNPKGTRVFGPVARE
LRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRRAMTRYIRRGGKIWIRI

FPDKPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQPQEQEMNAQEIIRSIEA
EQLKSDLPQIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSPRIDNIKIMRRGKVRR
AKLYYLRQLSGKATRIKQRFDRALMTRVKRGNVARNRRNKILKLAKGFRGSHSTLFRTANQQVMKALRSAYRDRKKKKRDF
RRLWITRINAASRQQGLSYSQLIGNLKKANVELNRKMLAQLAVLDPTTFAKVAELASSVKGNMAHKKGTGSTRNGRDSNAQR
LGVKRFGGQVVRAGNILVRQRGTKFHPGNNVGIGNDDTLFALIDGVVTFERKGKSRKKVSVYPRVTEEAVASMNNENYMEPS
FLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGHNYKLKEPKYSVEESKRRDSTYGVQMYVPTRLLNKETGDIK
EQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDLVWVRIDKTRKLSV
QVLLKALGLSDNEILDALRHPEYFQKTIEKEGQFSEEEALLELYRKLRPGEPPTVMGGQQLLESRFFDPKRYDLGRVGRYKLNK
KLRLSVPDTTRVLTPGDILSAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRERMTVSDAEVLTPASLV
NPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEGPNAGLIGSLATHA
RVNQYGFLETPFRPVENGRVCYEKPPVYMTADEEDDLRVAPGDIPVDDNGQILGIQVPVRYRQEFSTTTPEQVDYVAVSPVQIV
SVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSGMVIVSRTDGDVVYVDATEIRVRVKEKAALT
NRESESIPHKPQEIKYVLSKYQRSNQDTCLNQKPLVRIGEKVIAGQVLADGSSTEGGELALGQNVIVAYMPWEGYNYEDAILISE
RLVQEDVYTSIHIEKFEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRVGAWVESGDILVGKVTPKGESDQPPEEKLLRAIFG
EKARDVRDNSLRVPNGEKGRVVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKGIISRILPLEDMPYLP
DGTPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGEESSRRIVHGKLWEAREETSRDWVYNPENPGKI
MVYDGRTGEPFDRAVTVGIAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQGGGQRFGEMEVWALEAFGAAYTLQELL
TVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLDVEVDLMADQISRRTPPRPTYESF
SRDSLDEDEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLMDDAYNYMRTQAEQGKKFLFVGT
KRQAAGIIAQEANRCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREENGALDLLPKKEASMLRREMSKLQKYLGGIKNM
RKVPDVVIIVDQRREYNAVQECQKLGIPIVSMLDTNCDPDTVDIPIPANDDAIRSIKLIVGKLADAIYEGRHGQLEVESDYEDYES
AEEDYEYDESEFVDSFSDDDDEEMGQKIHPVGFRLGITQEHQSLWFAVPDRYPELLQEDHKLRQYIEQKLGRNAQNNAGISEIH
IERKADQVDLELRTARPGVVVGRGGQGIEALRTGLQQLLGSHRQVRINVVEVQKVDADAYLIAEYIAQQLERRVSFRRVVRQA
IQRAQRAGVQGIKVQVSGRLNGAEIARTEWTREGRVPLHTLRADIDYSYCTAQTVYGILGIKVWVFKGEIIPGQEDIVSQPVTRE
REPRRRQQQRRRQQFEDRSNEAMATGRRKASKAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAIVIVGNERGQVGVGVGKA
SDVIGAVKKGVADGKKHLIEIPITKSNSIPHPIDGVGGGAKVIMRPAAPGTGVIAGGAVRTVLELAGVRNVLAKQLGSNNPLNN
ARAAVNALSTLRTFAEVAEDRGIAVENLYIMATVAENNSGRALYWGTGRRKSAVAQVRLVPGEGKFVVNGKEGELYFQYNP
NYLGVIKAPLETLGLENEYDILVKAKGGGLTGQADSIRLGVARALCQLDPDNRSPLKIEGYLTRDPRAKERKKYGLHKARKAP
QYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTHRRIIDIHQP
SSKTIDALMKLDLPSGVDIEVKLMARQPTKKTGSKKQKKNVPNGIAYIQSTFNNSIVTITDQNGDVISWASAGSSGFKGAKKGT
PFAAQTAAESAGRRAIDQGMRQIQVMVSGPGAGRETAIRALQGAGLEITLIRDVTPIPHNGCRPPKRRRVMARIAGVDLPRDKR
VEIGLTYIYGIGLTRSQDILAATDVNPDTRVKDLTDADLAALRAEIESNYQVEGDLRRLEAMNIKRLVDIGCYRGRRHRMGLPV

RGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLSKIEKLNANNEKQVIKTWSRASTILPLMVGHTIAVHNG
KQHVPVFVNEQMVGHKLGEFAPTRTYRGHGKTDKKSGRMSDKNEGYKIISDNRQARYLYEILETYEAGIQLTGTEVKSIRAGK
VNLQDGYALLRNGEAWLINAHISPYTASGQYFNHEPRRTRKLLLHRLEIRKLIGKVEQQGLTLIPLKMYFKRGWVKISIGLCRG
KKVHDKREDLKRRQDQRDIQRAMKNYMAEISAKLVQELRQKTGAGMMDCKKALSETQGNIDEAIDWLRKKGIASAGKKSDR
VTAEGLVDIYTTPDGNRGVLIEVNCQTDFVARNDAFKLLVKNLAKQAINANNVTSLLAQPYIENASVTVDEYIKETIATLGENIQ
VRRFVNFSLEDAPGAIDGYIHTGGRVGVLVSIIVDTGTAAANEEVKSLAKNTAMQVAACPNVEYVSVDKIPDQVVQKEKEIEM
GKEDLGNKPANIKEKIVQGRIDKRLREMTLLDQPYIRDQNISVADLIRQVESQVSGKIKVHEFVRYILGEGIEKQESNFAEEVAA
QIGTK
>Cylindrospermopsis_raciborskii_CENA302
MQIPRLHPDTVEEVKHRADIVDVISDYVVLRRRGKDFVGLCPFHEEKTPSFTVSPNKQIYYCFGCQASGNAIRFIMDLNKRKFAE
VVLDLAKRYQVPVKTLAPEQRQELQRQLSLREQLFEVLASTSQFYQHVLRQDIGQQALQYLQKKRFLKTETVEKFALGYAPPG
WETLYHYLVENKSYPAQLVEKAGLIKPRKEGGGYYDVFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFDKSKTLF
ALDVAKDAISKLDQAVVVEGYFDAIALHANGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATERAIGEISNL
AYKGEVRLKILHIPDGKDADEYLKNHSVTDYEQLLVEAPLWLDWQIAQVIQGRDLKQPTDFQLVSREFVKLLQKILNSDTLNY
YISHCAEILSLGDTRLIPLRVENLITQVAPRRTPTPILRPPASPNTHQISHPQPSLLEQAEGLLLRIFLHCPQERQVIIETLGSSNLEFS
VSHYRFLWEKSLQFPSQTLDLISQLQNLYLETQNDLGPVEHIFQLNEKNKQEILLRTNQLVQAAIACMEKVFRENRYRHFLELW
QKTDPSTDPDQYNLYAQTIYADKMRIQELSKQRQLSISDLINMKLAEAESTMNKTVEATQRAFNSIRTGRANASLLDKVQVDY
YGSPTPLKSLTNITTPDASTILIQPYDRSSLNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKELVKLAAKYAEEGRVGIRNIR
RDALDSIRKQEKAGEISEDESRDQQDKLQKITGKYTAKIDELLTEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDSEGAQL
GIMAPLEALRLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVKQAE
RFLKDGDKVKATVMFRGREIQHSDLAETLLNRMATDLEPFGEIQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIEKISLERN
LPRLAVQSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIDGEGFRVLSTKTIVEEVTNGDHQISLDEVQQVAPEAQS
GDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSFGQPEVEAELPK
REQLPNDTYRSNATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAVD
TLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIGKEG
QNVRLAARLTGWKIDIKDQAKYDYGAEDAKFAAVRANYQEESNQPDNQFEIIEEGYEDDPDEGEDDFNSMEEENMSKKSLAS
LSATDISDKRALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLISKGAKVILASHFGRPKGVDEKLRLTPVAKRLSELLGQEVIKT
DDCIGDDVTAQVAALEKGQVLLLENVRFYKEEEKNDPNFARQLAANADFYVNDAFGTAHRAHASTEGVTKYLSPSVAGYLV
EKELQYLQAAIEVPQRPLAAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEQDKLELASSLEKKAAERG
VTLLLPTDIVAADKFAPDADAVTVSIENIPDDRMGLDIGPKSVKLFQDALADCKTVIWNGPMGVFEFDKFAVGTEAIAQTLAEI
GKTGATTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGTVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKS
RDYSVSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGGTVQV

IPHITNEIKERVIRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGKQNVLYMHVTLLPWIASAGEMKTKPTQHSVKELR
SIGIQPDILVCRCDRPIPVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQREPDLTHWETMVERMSH
PQSPVEIAIVGKYVRLGDAYLSVVESLRHAAIATYGDLRLRWVNSEILEVEPPDNYLLGVDGIIVPGGFGIRGVDGKISAIEYARN
RQIPFLGLCLGMQCSIIEWARNVEGLVGANSAEFDPKTDYPVINLLPEQQDVIDMGGTMRLGLYPCHVQPNTLAFDLYQEEVIY
ERHRHRYEFNNLYRNHLLNSGYVISGTSPDGRLVEIVEYPQHPFFIACQFHPEFQSRPSHPHPLFKGFMEAAISHTHQGKKQLPQ
GFPQFPMVKKVSRRLQALQAKVEERDYAPLEALALLKETATAKFPEAAEAHIRLGIDPKYTDQQLRTTVVLPKGTGQIVRVAVI
ARGEKVTEATNAGADIAGSEELIDEIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDIASAISEFKAGKLE
FRADRTGIVHVMFGKASFSSEDLLVNLKALQETIDRNRPSGAKGRYWRTFYISSTMGPSIKVDINALRDLKTTDAAMGTRSYRP
YTPSTRQVTISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRDITATVIAVEYDPNRNARIALL
EYEDGEKRYILHPNGLKVGAKVTAGPQAPFEDGNALPLSNIPLGTNVHNVEMTPGKGGQIVRAAGATAQLMAKEGNYVTLKL
PSGEVRMVRRECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPALGA
KTRKRKKASSKLIVRRRRKSSKRGRGGRQSMSVGILGTKLGMTQIFDEAGVSIPVTVIKAGPCTVTQVKTQPTDGYCAIQVGYG
EVKPKALNKPKLGHLAKSSAVPVRYLNEYRTDAAGDYALGQEIKADIFSVGQIVDVIGTSIGRGFAGNQKRNNFGRGPMSHGS
KNHRAPGSIGAGTTPGRVYPGKRMAGRLGGSRVTVRKLTVVKVDAERNLILIKGAIPGKPGGLVNVVPTTKVGNKMVESIVKN
WQGEEVGQTSFELRVAKEETASHIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIF
GPKPREFNIKLNRKERRLALRTAFVSRREDLIVVEEFTDQLQRPKSKELVAALARWGATADQKTLLILSEIGQSTETISLSARNVE
NIKVIAADQLNVFDLLHADKIVVTSSALTKIQEVYSAMATTRLKTLYGQTIVPKLTQQFQYTNVHQVPKVLKVTVNRGLGEAA
QNAKALEASLSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSAKSFDGRGNYT
LGVREQLIFPEIEYDRIDQIRGLDISIITTAKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGTKVVVKGPKGELSRD
LPTHVTVSQSGETLLVTRRDDTRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGANLVLNIGYSHQVQIEPPA
GVQFAVENNTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRKAGKTGGKGKKMAKKVVAVIKLALNAGKA
NPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSDQPNKKKVGSITR
TQLREIAQTKLPDLNANDIEAAMNIVEGTAKNMGVTVKDMSTATDQILEQLKVLTLLEAAELVKQIEEAFGVSAAAPAGGMM
VMAAPGAAAAEPVEEQTEFNVVLEEVPADRKIAVLKIVREITGLGLKEAKELVESTPKAVKEGVNKESAEEISKKIADAGGKVV
IKMSSKTYLPPEEEIKRDWYVVDAADKRLGRLASEIAMVLRGKRKAEYTPHLDTGDFVVVINAEKVVVTGKKPSQKLYRRHS
GRPGGMKTETFAKLQQRLPERIVEHAVKGMLPKNSLGRQLFTKLKVYSGSTHPHTAQKPKELIINTIPGENMIQPQTYLNVADN
SGARKLMCIRVLGAGNRRYGGVGDRIIAVVKDAQPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKEGNPKGT
RVFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRRAMTRYI
RRGGKIWIRIFPDKPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQPQEQEMN
AQEIIRSIEAEQLKSDLPQIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSPRIDNIKI
MRRGKVRRAKLYYLRQLSGKATRIKQRFDRALMTRVKRGNVARNRRNKILKLAKGFRGSHSTLFRTANQQVMKALRSAYRD
RKKKKRDFRRLWITRINAASRQQGLSYSQLIGNLKKANVELNRKMLAQLAVLDPATFAKVAELASSVKGMAHKKGTGSTRNG

RDSNAQRLGVKRFGGQVVRAGNILVRQRGTKFHPGNNVGIGNDDTLFALIDGVVTFERKGKSRKKVSVYPSVTEEAVASMNN
ENYTEPSFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGHNYKLKEPKYSVEESKRRDSTYGVQMYVPTRLLN
KETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDLVWVRID
KTRKLSIQVLLKALGLSDNEILDALRHPEYFQKTIEKEGQFSEEEALLELYRKLRPGEPPTVMGGQQLLESRFFDPKRYDLGRVG
RYKLNKKLRLSVPDTTRVLTPGDILSAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRERMTVSDAEV
LTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEGPNAGLI
GSLATHARVNQYGFLETPFRPVENGRVCYEKPAVYMTADEEDDLRVAPGDIPVDDNGQILGIQVPVRYRQEFSTTTPEQVDYV
AVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSGMVIVSRTDGDVVYVDATEIRVR
VKEKAALTNRESETIPHKPQEIKYVLSKYQRSNQDTCLNQKPLVRIGEKVIAGQVLADGSSTEGGELALGQNVIVAYMPWEGY
NYEDAILISERLVQEDVYTSIHIEKFEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRVGAWVESGDILVGKVTPKGESDQPP
EEKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKGIISRI
LPLEDMPYLPDGTPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGEESSRRIVHGKLWEAREETSRDWV
YNPENPGKIMVYDGRTGEPFDRAVTVGIAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWALEAFG
AAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLDVEVDLMADQVSRR
TPPRPTYESFSRDSLDEDEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLMDDAYNYMRSQAEQ
GKKFLFVGTKRQAAGIIAQEANRCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREENGALDLLPKKEASMLRREMSKLQ
KYLGGIKNMRKVPDVVIIVDQRREYNAVQECQKLSIPIVSMLDTNCDPDTVDVPIPANDDAIRSIKLIVGKLADAIYEGRHGQLE
VEPDDEDYDIPEEDYEYNESEMGQKIHPVGFRLGITQEHQSLWFAVPGRYPELLQEDHKLRQYIEQKLGRNAQNNAGLSEIHIE
RKADQVDLELRTARPGVVVGRGGQGIEALRTGLQQLLGSHRQVRINVVEVQKVDADAYLIAEYIAQQLERRVSFRRVVRQAIQ
RAQRAGVQGIKVQVSGRLNGAEIARTEWTREGRVPLHTLRADIDYSYCTAQTVYGILGIKVWVFKGEIIPGQEDIVSQPVTRER
EPRRRQQQRRRQQFEDRSNEAMATGRRKASKAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAIVIVGNERGQVGVGVGKAS
DVIGAVKKGVADGKKHLIEIPITKSNSIPHPIDGVGGGAKVIMRPAAPGTGVIAGGAVRTVLELAGVRNVLAKQLGSNNPLNNA
RAAVNALSTLRTFAEVAEDRGIAVENLYIMATVAETNSGRALYWGTGRRKSAVAQVRLVPGEGKFVVNGKEGELYFQYNPN
YLGVIKAPLETLGLENEYDILVKAKGGGLTGQADSIRLGVARALCQLDPDNRSPLKIEGYLTRDPRAKERKKYGLHKARKAPQ
YSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTHRRIIDIHQPS
SKTIDALMKLDLPSGVDIEVKLMARQPTKKTGSKKQKKNVPNGVAYIQSTFNNSIVTITDQNGDVISWASAGSSGFKGAKKGTP
FAAQTAAESAGRRAIDQGMRQIQVMVSGPGAGRETAIRALQGAGLEITLIRDVTPIPHNGCRPPKRRRVMARIAGVDLPRDKRV
EIGLTYIYGIGLRRSQDILAATDVNPDTRVKDLTDADLAALRAEIESNYQVEGDLRRLEAMNIKRLVDIGCYRGRRHRMGLPVR
GQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLSKLEKLNANNEKQVIKTWSRASTILPLMVGHTIAVHNGK
QHVPVFVNEQMVGHKLGEFAPTRTYRGHGKTDKKSGRMSDKNEGYKIISDNRQARYLYEILETYEAGIQLTGTEVKSIRAGKV
NLQDGYALLRDGEAWLINAHISPYTASGQYFNHEPRRTRKLLLHGLEIRKLIGKVEQQGLTLIPLKMYFKRGWVKISIGLCRGK
KVHDKREDLKRRQDQRDIQRAMKNYMAEISAKLVQDLRQKTGAGIMDCKKALNETQGNIDEAIDWLRKKGIASAGKKSDRV

TAEGLVEIYTTPDRSGGVLIEVNCQTDFVARNDAFKLLVKNLAKQAVNADNVTSLLAQPYIENTAVTVDEYIKETIATLGENIQ
VRRFVNFSLEGSPGAIDGYIHTGGRVGVLISIGVDTETAAKNEEVQSLAKNTAMQVAACPNVEYVSVDKIPDQVVQKEKEIEM
GKEDLGNKPENIKEKIVQGRIDKRLKEMTLLDQPYIRDQSISVAELIKQVESKVSEPIKVHQFVRYILGEGIEKQESNFAQEVAAQ
IGAK
>Cylindrospermopsis_raciborskii_CENA303
MQIPRLHPDTVEEVKHRADIVDVISDYVVLRRRGKDFVGLCPFHEEKTPSFTVSPNKQIYYCFGCQASGNAIRFIMDLNKRKFAE
VVLDLAKRYQVPVKTLAPEQRQELQRQLSLREQLFEVLASTSQFYQHVLRQDIGQQALQYLQKKRFLKTETVEKFALGYAPPG
WETLYHYLVENKSYPAQLVEKAGLIKPRKEGGGYYDVFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFDKSKTLF
ALDVAKDAISKLDQAVVVEGYFDAIALHANGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATERAIGEISNL
AYKGEVRLKILHIPDGKDADEYLKNHSVTDYEQLLVEAPLWLDWQIAQVIQGRDLKQPTDFQLVSREFVKLLQKILNSDTLNY
YISHCAEILSLGDTRLIPLRVENLITQVAPRRTPTPILRPPASPNTHQISHPQPSLLEQAEGLLLRIFLHCPQERQVIIETLGSSNLEFS
VSHYRFLWEKSLQFPLQTLDLISQLQNLYLETQNDLGPVEHIFQLNEKNKQEILLRTNQLVQAAIACMEKVFRENRYRHFLELW
QKTDPSTDPDQYNLYAQTIYADKMRIQELSKQRQLSISDLINMKLAEAESTMNKTVEATQRAFNSIRTGRANASLLDKVQVDY
YGSPTPLKSLSNITTPDASTILIQPYDRSSLNIVEKAISLSDVGLTPSNDGSVVRLNIPPLTSDRRKELVKLAAKYAEEGRVGIRNIR
RDALDSIRKQEKAGEISEDESRDQQDKLQKITGKYTAKIDELLAEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDNEGAQ
LGIMAPLEALRLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVKQA
ERFLKDGDKVKATVMFRGREIQHSDLAETLLNRMATDLEPFGEIQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIEKISLER
NLPRLAVQSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIDGEGFRVLSTKIIVEEVTNSDHQISLDEVQQVAPEAQS
GDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSFGQPEVEAELPK
REQLPNDTYRSNATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAVD
TLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIGKEG
QNVRLAARLTGWKIDIKDQAKYDYGAEDAKFAAVRANYQEESNQFEVIEEEYERDPDEGEDDFNSMEEENMSKKSLASLSAA
DISDKRALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLISKGAKVILASHFGRPKGVDEKFRLTPVAKRLSELLGQEVIKTNDCI
GDDVTARVAALEQGQVLLLENVRFHKEEEKNDPEFARQLAANADFYVNDAFGTAHRAHASTEGVTKYLSPSVAGYLVEKEL
QYLQAAIEFPQRPLAAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEQDKLELASSLEKKAAERGVTLL
LPTDIVAADKFAPDADAVTVSIENIPDDRMGLDIGPDSVKLFQDALADCKTVIWNGPMGVFEFDKFAVGTEAIAQTLAEIGKTG
ATTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGTVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRDYS
VSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTYMSRLNSVTTGLIYQSVINKERRGDYNGGTVQVIPHIT
NEIKERVIRVAKETNPAALITEIGGTVGDIESLPFLEAIRQLRKEVGKQNVLYMHVTLLPWIASAGEMKTKPTQHSVKELRSIGIQ
PDILVCRCDRPIPVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQREPDLTHWETMVERMSHPQSP
VEIAIVGKYVRLGDAYLSVVESLRHAAIATYGDLRLRWVNSEILEVEPPDNYLLGVDGIIVPGGFGIRGVDGKISAIEYARNRQIP
FLGLCLGMQCSIIEWARNVEGLVGANSAEFDPKTDYPVINLLPEQQDVIDIGGTMRLGLYPCHVQPNTLAFDLYQEEVIYERHR

HRYEFNNLYRNHLLNSGYVISGTSPDGRLVEIVEYPQHPFFIACQFHPEFQSRPSHPHPLFKGFMEAAISHTHQGKKQLPHGFPQF
PMVKKVSRRLQALQAKVEERDYAPLEALSLLKETATAKFPEAAEAHIRLGIDPKYTDQQLRTTVVLPKGTGQIVRVAVIARGE
KVTEATNAGADIAGSEELIDEIQRGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDIASAISEFKAGKLEFRAD
RTGIVHVMFGKASFSSEDLLVNLKALQETIDRNRPSGAKGRYWRTFYISSTMGPSIKVDINALRDLKTTDAAMGTRSYRPYTPS
TRQVTISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRDITATVIAVEYDPNRNARIALLEYED
GEKRYILHPNGLKVGAKVTAGPQAPFEDGNALPLSNIPLGTNVHNVEMTPGKGGQIVRAAGATAQLMAKEGNYVTLKLPSGE
VRMVRRECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPALGAKTR
KRKKASSKLIVRRRRKSSKRGRGGRQSMSVGILGTKLGMTQIFDEAGVSIPVTVIKAGPCTVTQVKTQPTDGYCAIQVGYGEVK
PKALNQPKLGHLAKSSAGPVRYLNEYRTDAAGDYALGQEIKADIFSVGQIVDVIGTSIGRGFAGNQKRNNFGRGPMSHGSKNH
RAPGSIGAGTTPGRVYPGKRMAGRLGGSRVTVRKLTVVKVDAERNLILIKGAIPGKPGGLVNVVPTTKVGNKMVESIVKNWQ
GEEVGQTSFELRIAKEETASHIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFGPK
PRDFNIKLNRKERRLALRTAFVSRREDLIVVEEFTDQLQRPKSKELVAALARWGATAEQKTLLILSEIGQSTETISLSARNVENIK
VIAADQLNVFDLLHADKIVVTSSALNKIQEVYSAMATTRLKTLYGQTIVPKLTQQFQYTNVHQVPKVLKVTVNRGLGEAAQN
AKALEASLSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSAKSFDGRGNYTLG
VREQLIFPEIEYDRIDQIRGLDISIITTAKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGTKVVVKGPKGELSRDLP
THVTVSQSGETLLVTRRDDTRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGANLVLNIGYSHQVQIEPPAG
VQFVVENNTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRKAGKTGGKGKKMAKKVVAVIKLALNAGKAN
PAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSDQPNKKKVGSITRT
QLKEIAQTKLPDLNANDIEAAMNIVEGTAKNMGVTVKDMSTATDQILEQLKVLTLLEAAELVKQIEEAFGVSAAAPAGGMMV
MAAPGAAAAEPVEEQTEFNVVLEEVPADKKIAVLKIVREITGLGLKEAKELVESTPKAVKEGVNKESAEEISKKIAEAGGKVVI
KMSSKTYLPPEEEIKRDWYVVDAADKRLGRLASEIAMVLRGKRKAEYTPHLDTGDFVVVINAEKVVVTGKKPSQKLYRRHSG
RPGGMKTETFAKLQQRLPERIVEHAVKGMLPKNSLGRQLFTKLKVYSGSTHPHTAQKPKELIINTIPGENMIQPQTYLNVADNS
GARKLMCIRVLGAGNRRYGGVGDRIIAVVKDAQPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKEGNPKGTR
VFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRRAMTRYIR
RGGKIWIRIFPDKPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQPQEQEMNA
QEIIRSIEAEQLKSDLPQIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSPRIDNIKIM
RRGKVRRAKLYYLRQLSGKATRIKQRFDRALMTRVKRGNVARNRRNKILKLAKGFRGSHSTLFRTANQQVMKALRSAYRDR
KKKKRDFRRLWITRINAASRQQGLSYSQLIGNLKKANVELNRKMLAQLAVLDPATFAKVAELASSVKGMAHKKGTGSTRNGR
DSNAQRLGVKRFGGQVVRAGNILVRQRGTKFHPGNNVGIGNDDTLFALIDGVVTFERKGKSRKKVSVYPRVTEEAVASMNNE
NYMEPSFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGHNYKLKEPKYSVEESKRRDSTYGVQMYVPTRLLNK
ETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDLVWVRIDK
TRKLSIQVLLKALGLSDNEILDALRHPEYFQKTIEKEGQFSEEEALLELYRKLRPGEPPTVMGGQQLLESRFFDPKRYDLGRVGR

YKLNKKLRLSVPDTTRVLTPGDILSAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRERMTVSDAEVL
TPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEGPNAGLIG
SLATHARVNQYGFLETPFRPVENGRVCYEKPAVYMTADEEDDLRVAPGDIPVDDNGQILGIQVPVRYRQEFSTTTPEQVDYVA
VSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSGMVIVSRTDGDVVYVDATEIRVRV
KEKAALTNRESESIPHKPQEVKYVLSKYQRSNQDTCLNQKPLVRIGEKVIAGQVLADGSSTEGGELALGQNVIVAYMPWEGYN
YEDAILISERLVQEDVYTSIHIEKFEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRVGAWVESGDILVGKVTPKGESDQPPE
EKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKGIISRILP
LEDMPYLPDGTPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGEESSRRIVHGKLWEAREETSRDWVY
NPENPGKIMVYDGRTGEPFDRAVTVGIAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWALEAFGA
AYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLDVEVDLMADQVSRRT
PPRPTYESFSRDSLDEDEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLMDDAYNYMRSQAEQG
KKFLFVGTKRQAAGIIAQEANRCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREENGALDLLPKKEASMLRREMSKLQK
YLGGIKNMRKVPDVVIIVDQRREYNAVQECQKLSIPIVSMLDTNCDPDTVDIPIPANDDAIRSIKLIVGKLADAIYEGRHGQLEVE
PDYEDYDIPEEDYEDEEPGYVDHFSDDDDEEMGQKIHPVGFRLGITQEHQSLWFAVPGRYPELLQEDHKLRQYIEQKLGRNAQ
NNAGLSEIHIERKADQVDLELRTARPGVVVGRGGQGIEALRTGLQQLLGSHRQVRINVVEVQKVDADAYLIAEYIAQQLERRV
SFRRVVRQAIQRAQRAGVQGIKVQVSGRLNGAEIARTEWTREGRVPLHTLRADIDYSYCTAQTVYGILGVKVWVFKGEIIPGQE
DIVSQPVTREREPRRRQQQRRRQQFEDRSNEAMATGRRKASKAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAIVIVGNERG
QVGVGVGKASDVIGAVKKGVADGKKHLIEIPITKSNSIPHPIDGVGGGAKVIMRPAAPGTGVIAGGAVRTVLELAGVRNVLAK
QLGSNNPLNNARAAVNALSTLRTFAEVAEDRGIAVENLYIMATVAETNSGRALYWGTGRRKSAVAQVRLVPGEGKFVVNGK
EGELYFQYNPNYLGVIKAPLETLGLENEYDILVKAKGGGLTGQADSIRLGVARALCQLDPDNRSPLKIEGYLTRDPRAKERKKY
GLHKARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETR
THRRIIDIHQPSSKTIDALMKLDLPSGVDIEVKLMARQPTKKTGSKKQKKNVPNGVAYIQSTFNNSIVTITDQNGDVISWASAGS
SGFKGAKKGTPFAAQTAAESAGRRAIDQGMRQIQVMVSGPGAGRETAIRALQGAGLEITLIRDVTPIPHNGCRPPKRRRVMARI
AGVDLPRDKRVEIGLTYIYGIGLRRSQDILAATDVNPDTRVKDLTDADLAALRAEIESNYQVEGDLRRLEAMNIKRLVDIGCYR
GRRHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLSKLEKLNANNEKQVIKTWSRASTILPL
MVGHTIAVHNGKQHVPVFVNEQMVGHKLGEFAPTRTYRGHGKTDKKSGRMSDKNEGYKIISDNRQARYLYEILETYEAGIQL
TGTEVKSIRAGKVNLQDGYALLRDGEAWLINAHISPYTASGQYFNHEPRRTRKLLLHGLEIRKLIGKVEQQGLTLIPLKMYFKR
GWVKISIGLCRGKKVHDKREDLKRRQDQRDIQRAMKNYMAEISAKLVQDLRQKTGAGMMDCKKALNETQGNIDEAIDWLRK
KGIASAGKKSDRVTAEGLVDIYTTPDRSGGVLIEVNCQTDFVARNDAFKLLVKNLAKQAVNADNVTSLLAQPYIENTDVTVTV
DDYIKETIATLGENIQVRRFVNFSLEGAPGVIDGYIHTGGRVGVLVSIGVYTETAAKNEEVQSLARNTAMQVAACPNVEYVSVD
KIPDQVVQKEKEIEMGKEDLGNKPENIKEKIVQGRIDKRLKEMTLLDQPYIRDQNISVAELIKQVESKLSEPIIVHQFVRYILGEGI
EKQESNFAQEVAAQIGAK

>Cylindrospermopsis_raciborskii_CHAB3438
MQIPRLHPDTVEEVKHRADIVDVISDYVVLRRRGKDFVGLCPFHEEKTPSFTVSPTKQIYYCFGCQASGNAIKFMMDLNKRQFA
EVVLDLAKRYQVPVKTLAPEQRQELQRQLSLREQLFEVLASTSQFYQHVLRQDIGQQALQYLQKKRFLKTETVEKFALGYAPP
GWETLYHYLVENKNYPAQLVEKAGLIKPRKEGGGYYDVFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFDKSKT
LFALDVSKDAISKLDQAVVVEGYFDAIALHANGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATERAIGEIS
NLAYKGEVQLKILHIPDGKDADEYLKNHSVTDYGQLLVDAPLWLDWQIAQVIQGRDLRQPTDFQLVSREFVKLLQKILNSDTL
NYYISHCAEILSLGDTRLIPLRVENLITQVAPRRTPTPRPPQPDSTTSPNTHPISHPQPSLLEQAEGLLLRIFLHCPQERQVIIETLGSS
NLEFSVSHHRFLWEKSLQFPSQTLDLISQLQNLYLETQNDLGPVQHIFQLNEKNKQEILLRTSQLVQAAIACMEKVFRENRYRHF
LELWQKTDPSTDPDQYSLYAQTIYADKMRIQELSKRQLSIADLINMNKTVEATQRAFNSIRTGRANASLLDKVQVDYYGSPTS
LKSLANITTPDATTILIQPYDRTSLNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKELVKLAAKYAEEGRVGIRNIRRDALDS
IRKQEKAGEVSEDESRDQQDKLQKITSKYTAKIDELLAEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDSEGAQLGIMAPL
EALRLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVKQAERFLKDG
DKVKATVMFRGREIQHSDLAETLLNRMATDLEPFGEVQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIEKISLERNLPRLAV
QSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIDGEGFRVLSTKTIVEEVTNGDHQISLDEVQQVAPEAQSGDSVVL
DVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSFGQPEVEAELPKREQLPN
DTYRSNATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAVDTLDRDV
DPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIGKEGQNVRLA
ARLTGWKIDIKDQAKYDYGAEDAKFAAVRANYQEESNQLDNQFEVIEEEYEDDPDAGEDDFNSMEEENMSKKSLASLSAADI
SGKRALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLISKGAKVILASHFGRPKGVDEKLRLTPVAKRLSELLGQEVIKTDDCIG
DDVTTQVAALEKGQVLLLENVRFYKEEEKNDPEFARQLAANADFYVNDAFGTAHRAHASTEGVTKYLSPSVAGYLVEKELQ
YLQGAIEVPQRPLVAIIGGSKVSSKITVIETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEDDKLVLASSLEKKAAERGVALLL
PTDIVAADRFAPDADAVTVSIDSIPDDRMGLDIGPDSVKVFQAALADCKTVIWNGPMGVFEFDKFAVGTEAIAQTLAEISKTGA
TTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGKVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRDYSV
SILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGGTVQVIPHITN
EIKERVIRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGKQNVLYMHVTLLPWIASAGEMKTKPTQHSVKELRSIGIQP
DILVCRCDRPIPVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQREPDLTHWETMVERMSHPQSPV
EIAIVGKYVRLGDAYLSVVESLRHAAIATYGDLRLRWVNSEILEVPPDNYLLGVDGIIVPGGFGIRGVDGKISAIEYARNRQIPF
LGLCLGMQCSIIEWARNVEGLVGANSAEFNPQTDYPVINLLPEQQDVIDLGGTMRLGLYPCHVQPNTLAFDLYQEEVIYERHRH
RYEFNNLYRNHLLNSGYVISGTSPDGRLVEIVEYPQHPFFIACQFHPEFQSRPSHPHPLFKGFMEAAISHTHQGKKPNYPLRVSSV
PMVKKVSRRLQALQAKVEERDYTPLEALALLKETATAKFAEAAEAHIRLGIDPKYTDQQLRTTVVLPKGTGQIVRVAVIARGE
KVTEATNAGADIAGSEELIDEIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDIASAISEFKAGKLEFRAD
RTGIVHVMFGKASFSSEDLLVNLKALQETIDRNRPSGAKGRYWRTFYISSTMGPSIKIDINALRDFKTTDVAMGTRSYRPYTPST

RQVTISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRDITATVIAVEYDPNRNARIALVEYEDG
EKRYILHPNGLKVGAKITAGPQAPFEDGNALPLSNIPLGTNVHNVEMTPGKGGQIVRAAGATAQLMAKEGNYVTLKLPSGEVR
MVRRECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPALGAKTRKR
KKASSKLIVRRRRKSSKRGRGGRQSMSVGILGTKLGMTQIFDEAGVSIPVTVIQAGPCTVTQVKTQPTDGYCAIQVGYGEVKPK
ALNKPKLGHLAKSSAGPVRYLNEYRTDAAGDYALGQEIKADIFSVGQIVDVIGTSIGRGFAGNQKRNNFGRGPMSHGSKNHRA
PGSIGAGTTPGRVYPGKRMAGRLGGSRVTVRKLTVVKVDAERNLILIKGAIPGKPGGLVNVVPTTKVGNKMVESTVKNWQGE
EVGQTSFELRVAKEETASHIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFGPKPR
DFNIKLNRKERRLALRTAFVSRREDLIVVEEFTDQLQRPKSKELVAALARWGATADQKTLLILSEIGQNTETISLSARNVENIKVI
AADQLNVFDLLHADKIVVTSSALTKIQEVYSAMATTRLKTLYGQTIVPKLTQQFQYTNVHQVPKVLKVTVNRGLGEAAQNAK
ALEASLSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSAKSFDGRGNYTLGVR
EQLIFPEIEYDRIDQIRGLDISIITTAKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGTKVVVKGPKGELSRDLPAH
VTVSQSGETLLVTRRDDTRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGANLVLNIGYSHQVQIEPPAGVQ
FVVENNTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRKAGKTGGKGKKMAKKVVAVIKLALNAGKANPA
PPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSDQPNKKKVGSITRTQL
KEIAQTKLPDLNANDIEAAMNIVEGTAKNMGVTIKDMSTATDQILEQLKSLTLLEAAELVKQIEEAFGVSAAAPAGGMMMMA
APGGAAAAEVVEEKTEFDVILEEVPADKKIAVLKIVREITGLGLKEAKELVESTPKAVKEGVNKEAAEDISKKITEAGGKVAIK
MSSKTYLPPEEEIKRDWYVVDAADKRLGRLASEIAMVLRGKRKAEYTPHLDTGDFVVINAEKVVVTGKKQSQKLYRRHSGR
PGGMKTETFAKLQQRLPERIVEHAVKGMLPKNSLGRQLFTKLKVYSGATHPHTAQKPKELIINTIPGENMIQPQTYLNVADNSG
ARKLMCIRVLGAGNRRYGGVGDRIIAVVKDAQPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKEGNPKGTRV
FGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRRAMTRYIRR
GGKIWIRIFPDKPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQPQEQEMNA
QEIIRSIEAEQLKSDLPQIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSPRIDNIKIM
RRGKVRRAKLYYLRQLSGKATRIKQRFDRALMTRVKRGNVARNRRNKILKLAKGFRGSHSTLFRTANQQVMKALRSAYRDR
KKKKRDFRRLWITRINAASRQQGLSYSQLIGNLKKANVELNRKMLAQLAVLDPTTFAKVAELASSVKGNMAHKKGTGSTRNG
RDSNAQRLGVKRFGGQVVRAGNILVRQRGTKFHPGNNVGIGNDDTLFALIDGVVTFERKGKSRKKVSVYPRVTEEAVASMNN
ENYMEPSFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGHNYKLKEPKYSVEESKRRDSTYGVQMYVPTRLLN
KETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDLVWVRID
KTRKLSIQVLLKALGLLDNEILDALRHPEYFQKTIEKEGQFSEEEALLELYRKLRPGEPPTVMGGQQLLESRFFDPKRYDLGRVG
RYKLNKKLRLSVPDTTRVLTPGDILSAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRERMTVSDAEV
LTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEGPNAGLI
GSLATHARVNQYGFLETPFRPVENGRVCYEKPAVYMTADEEDDLRVAPGDIPVDDNGQILGIQVPVRYRQEFSTTTPEQVDYV
AVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSGMVIVSRTDGDVVYVDATEIRVR

VKEKAALTNRESESIPHKPQEIKYVLSKYQRSNQDTCLNQKPLVRIGEKVIAGQVLADGSSTEGGELALGQNVIVAYMPWEGY
NYEDAILISERLVQEDVYTSIHIEKFEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRVGAWVESGDILVGKVTPKGESDQPP
EEKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKGIISRI
LPLEDMPYLPDGTPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGEESSRRIVHGKLWEAREETSKDWV
YNPENPGKIMVYDGRTGEPFDRAVTVGIAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWALEAFG
AAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLDVEVDLMADQVSRR
TPPRPTYESFSRDSLDEDEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLMDDAYNYMRSQAEQ
GKKFLFVGTKRQAAGIIAQEANRCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREENGALDLLPKKEASMLRREMSKLQ
KYLGGIKNMRKVPDVVIIVDQRREYNAVQECQKLSIPIVSMLDTNCDPDTVDIPIPANDDAIRSIKLIVGKLADAIYEGRHGQLE
VESDYEEYESAEEDYEYDESEFVDSFSDDDDEEMGQKIHPVGFRLGITQEHQSLWFAVPGRYPELLQEDHKLRQYIEQKLGRNA
QNNAGLSEIHIERKADQVDLELRTARPGVVVGRGGQGIEALRTGLQQLLGSHRQVRINVVEVQKVDADAYLIAEYIAQQLERR
VSFRRVVRQAIQRAQRAGVQGIKVQVSGRLNGAEIARTEWTREGRVPLHTLRADIDYSYCTAQTVYGILGIKVWVFKGEIIPGQ
EDIVSQPVTREREPRRRQQQRRRQQFEDRSNEAMATGRRKASKAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAIVIVGNER
GQVGVGVGKASDVIGAVKKGVADGKKHLIEIPITKSNSIPHPIDGVGGGAKVIMRPAAPGTGVIAGGAVRTVLELAGVRNVLA
KQLGSNNPLNNARAAVNALSTLRTFAEVAEDRGIAVENLYIMATVAETNSGRALYWGTGRRKSAVAQVRLVPGEGKFVVNG
KEGELYFQYNPNYLGVIKAPLETLGLENEYDILVKAKGGGLTGQADSIRLGVARALCQLDPDNRSPLKIEGYLTRDPRAKERKK
YGLHKARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFET
RTHRRIIDIHQPSSKTIDALMKLDLPSGVDIEVKLMARQPTKKTGSKKQKKNVPNGVAYIQSTFNNSIVTITDQNGDVISWASAG
SSGFKGAKKGTPFAAQTAAESAGRRAIDQGMRQIQVMVSGPGAGRETAIRALQGAGLEITLIRDVTPIPHNGCRPPKRRRVMAR
IAGVDLPRDKRVEIGLTYIYGIGLRRSQDILAATDVNPDTRVKDLTDADLAALRAEIESNYQVEGDLRRLEAMNIKRLVDIGCYR
GRRHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLSKIEKLNANNEKQVIKTWSRASTILPLM
VGHTIAVHNGKQHVPVFVNEQMVGHKLGEFAPTRSYRGHGKTDKKSGRMSDKNEGYKIISDNRQARYLYEILETYEAGIQLTG
TEVKSIRAGKVNLQDGYALLRDGEAWLINAHISPYTASGQYFNHEPRRTRKLLLHGLEIRKLIGKVEQQGLTLIPLKMYFKRGW
VKISIGLCRGKKVHDKREDLKRRQDQRDIQRAMKNYMAEISAKLVQDLRQKTGAGMMDCKKALNETQGNIDEAIDWLRKKG
IASAGKKSDRVTAEGLVDIYTTPDKSGGVIIEVNCQTDFVARNDAFKLLVKNLAKQAVNADNVASLLAQPYIEKTDVTVDEYIK
ETIATLGENIQVRRFVNFSLEGAPGAIDGYIHTGGRVGVLVSIGVDTETAAKNEELQSLAKNTAMQVAACPNVEYVSVDKIPDQ
VVEKEKEIEMGKEDLGNKPANIKEKIVQGRIDKRLKEMTLLDQPYIRDQNISVAELIKQVESKVSEPIKVHQFVRYILGEGIEKQE
SNFAEEVAAQIGAK
>Cylindrospermopsis_raciborskii_Cr2010
MQIPRLHPDTVEEVKHRADIVDVISDYVVLRRRGKDFVGLCPFHEEKTPSFTVSPTKQIYYCFGCQASGNAIKFMMDLNKRQFA
EVVLDLAKRYQVPVKTLAPEQRQELQRQLSLREQLFEVLASTSQFYQHVLRQDIGQQALQYLQKKRFLKTETVEKFALGYAPP
GWETLYHYLVENKNYPAQLVEKAGLIKPRKEGGGYYDVFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFDKSKT

LFALDVSKDAISKLDQAVVVEGYFDAIALHANGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATERAIGEIS
NLAYKGEVQLKILHIPDGKDADEYLKNHSVTDYGQLLVDAPLWLDWQIAQVIQGRDLRQPTDFQLVSREFVKLLQKILNSDTL
NYYISHCAEILSLGDTRLIPLRVENLITQVAPRRTPTPRPPQPDSTTSPNTHQISHPQPSLLEQAEGLLLRIFLHCPQERQVIIETLGF
SNLEFSVSHHRFLWEKSLQFPSQTLDLISQLQNLYLETQNDLGPVQHIFQLNEKNKQEILLRTSQLVQAAIACMEKVFRENRYRH
FLELWQKTDPSTDPDQYSLYAQTIYADKMRIQELSKQRQLSIADLINMKLAEAESTMNKTVEATQRAFNSIRTGRANASLLDKV
QVDYYGSPTSLKSLANITTPDATTILIQPYDRTSLNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKELVKLAAKYAEEGRVG
IRNIRRDALDSIRKQEKAGEVSEDESRDQQDKLQKITSKYTAKIDELLAEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDS
EGAQLGIMAPLEALRLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVR
VKQAERFLKDGDKVKATVMFRGREIQHSDLAETLLNRMATDLEPFGEVQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIEK
ISLERNLPRLAVQSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIDGEGFRVLSTKTIVEEVTNGDHQISLDEVQQVA
PEAQSGDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSFGQPEVE
AELPKREQLPNDTYRSNATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRT
KIAVDTLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLA
IGKEGQNVRLAARLTGWKIDIKDQAKYDYGAEDAKFAAVRANYQEESNQLDHQFEVMEEEYEDDPDAGEDDFNSMEEENMS
KKSLASLSAADISDKRALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLISKGAKVILASHFGRPKGVDEKLRLTPVAKRLSELL
GQEVIKTDDCIGDDVTAQVAALEKGQVLLLENVRFYKEEENNDPEFARQLAANADFYVNDAFGTAHRAHASTEGVTKYLSPS
VAGYLVEKELQYLQGAIEVPQRPLVAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEQDKLGLASSLEK
KAAERGVTLLLPTDIVAADKFGPDADAVTVSIDHIPDDRMGLDIGPDSVKVFQAALADCKTVIWNGPMGVFEFDKFAVGTEAI
AQTLAEISKTGATTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGKVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAAS
LGRLLKSRDYSVSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDY
NGGTVQVIPHITNEIKERVIRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGKQNVLYMHVTLLPWIASAGEMKTKPT
QHSVKELRSIGIQPDILVCRCDRPIPVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQREPDLTHWE
TMVERMSHPQSPVEIAIVGKYVRLGDAYLSVVESLRHAAIATYGDLRLRWVNSEILEVEPPDNYLLGVDGIIVPGGFGIRGVDG
KISAIEYARNQQIPFLGLCLGMQCSIIEWARNVEGLVGANSAEFDPKTDYPVINLLPEQQDVIDLGGTMRLGLYPCHVQPNTLAF
DLYQEEVIYERHRHRYEFNNLYRNHLLNSGYVISGTSPDGRLVEIVEYPQHPFFIACQFHPEFQSRPSHPHPLFKGFMEAAISHTH
QGSTPMVKKVSRRLQALQAKVEERDYTPLEALALLKETATAKFAEAAEAHIRLGIDPKYTDQQLRTTVVLPKGTGQIVRVAVI
ARGEKVTEATNAGADIAGSEELIDEIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDIASAISEFKAGKLE
FRADRTGIVHVMFGKASFSSEDLLVNLKALQETIDRNRPSGAKGRYWRTFYISSTMGPSIKIDINALRDFKTTDVAMGTRSYRPY
TPSTRQVTISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRDITATVIAVEYDPNRNARIALVE
YEDGEKRYILHPNGLKVGAKITAGPQAPFEDGNALPLSNIPLGTNVHNVEMTPGKGGQIVRAAGATAQLMAKEGNYVTLKLPS
GEVRMVRRECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPALGAK
TRKRKKASSKLIVRRRRKSSKRGRGGRQSMSVGILGTKLGMTQIFDEAGVSIPVTVIQAGPCTVTQVKTQPTDGYCAIQVGYGE

VKPKALNKPKLGHLAKSSAGPVRYLNEYRTDAAGDYALGQEIKADIFSVGQIVDVIGTSIGRGFAGNQKRNNFGRGPMSHGSK
NHRAPGSIGAGTTPGRVYPGKRMAGRLGGSRVTVRKLTVVKVDAERNLILIKGAIPGKPGGLVNVVPTTKVGNKMVESTVKN
WQGEEVGQTSFELRVAKEETASHIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIF
GPKPRDFNIKLNRKERRLALRTAFVSRREDLIVVEEFTDQLQRPKSKELVAALARWGATADQKTLLILSEIGQNTETISLSARNV
ENIKVIAADQLNVFDLLHADKIVVTSSALTKIQEVYSAMATTRLKTLYGQTIVPKLTQQFQYTNVHQVPKVLKVTVNRGLGEA
AQNAKALEASLSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSAKSFDGRGN
YTLGVREQLIFPEIEYDRIDQIRGLDISIITTAKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGTKVVVKGPKGELS
RDLPAHVTVSQSGETLLVTRRDDTRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGANLVLNIGYSHQVQIE
PPAGVQFVVENNTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRKAGKTGGKGKKMAKKLVAVIKLALNA
GKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSDQPNKKKVGS
ITRTQLKEIAQTKLPDLNANDIEAAMNIVEGTAKNMGVTIKDMSTATDQILEQLKSLTLLEAAELVKQIEEAFGVSAAAPVGGM
AVIAAPGGAAAAEVVEEQTEFDVILQEVPADKKIAVLKIVREITGLGLKEAKELVESTPKAVKEGVNKEAAEDISKKITEAGGK
VAIKMSSKTYLPPEEEIKRDWYVVDAADKRLGRLASEIAMVLRGKRKAEYTPHLDTGDFVVVINAEKVVVTGKKQSQKLYRR
HSGRPGGMKTETFAKLQQRLPERIVEHAVKGMLPKNSLGRQLFTKLKVYSGATHPHTAQKPKELIINTIPGENMIQPQTYLNVA
DNSGARKLMCIRVLGAGNRRYGGVGDRIIAVVKDAQPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKEGNPK
GTRVFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRRAMT
RYIRRGGKIWIRIFPDKPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQPQEQ
EMNAQEIIRSIEAEQLKSDLPQIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSPRID
NIKIMRRGKVRRAKLYYLRQLSGKATRIKQRFDRALMTRVKRGNVARNRRNKILKLAKGFRGSHSTLFRTANQQVMKALRSA
YRDRKKKKRDFRRLWITRINAASRQQGLSYSQLIGNLKKANVELNRKMLAQLAVLDPTTFAKVAELASSVKGNMAHKKGTGS
TRNGRDSNAQRLGVKRFGGQVVRAGNILVRQRGTKFHPGNNVGIGNDDTLFALIDGVVTFERKGKSRKKVSVYPRVTEEAVA
SMNNENYMEPSFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGHNYKLKEPKYSVEESKRRDSTYGVQMYVP
TRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDLV
WVRIDKTRKLSIQVLLKALGLLDNEILDALRHPEYFQKTIEKEGQFSEEEALLELYRKLRPGEPPTVMGGQQLLESRFFDPKRYD
LGRVGRYKLNKKLRLSVPDTTRVLTPGDILSAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRERMTV
SDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEGP
NAGLIGSLATHARVNQYGFLETPFRPVENGRVCYEKPAVYMTADEEDDLRVAPGDIPVDDNGQILGIQVPVRYRQEFSTTTPEQ
VDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSGMVIVSRTDGDVVYVDATE
IRVRVKEKAALTNRESESIPHKPQEIKYVLSKYQRSNQDTCLNQKPLVRIGEKVIAGQVLADGSSTEGGELALGQNVIVAYMPW
EGYNYEDAILISERLVQEDVYTSIHIEKFEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRVGAWVESGDILVGKVTPKGESD
QPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRIVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKGIIS
RILPLEDMPYLPDGTPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGEESSRRIVHGKLWEAREETSKD

WVYNPENPGKIMVYDGRTGEPFDRAVTVGIAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWALEA
FGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLDVEVDLMADQVS
RRTPPRPTYESFSRDSLDEDEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLMDDAYNYMRSQA
EQGKKFLFVGTKRQAAGIIAQEANRCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREENGALDLLPKKEASMLRREMSK
LQKYLGGIKNMRKVPDVVIIVDQRREYNAVQECQKLSIPIVSMLDTNCDPDTVDIPIPANDDAIRSIKLIVGKLADAIYEGRHGQ
LEVESDYEEYESAEEDYEYDESEFVDSFSDDDDEEMGQKIHPVGFRLGITQEHQSLWFAVPGRYPELLQEDHKLRQYIEQKLGR
NAQNNAGLSEIHIERKADQVDLELRTARPGVVVGRGGQGIEALRTGLQQLLGSHRQVRINVVEVQKVDADAYLIAEYIAQQLE
RRVSFRRVVRQAIQRAQRAGVQGIKVQVSGRLNGAEIARTEWTREGRVPLHTLRADIDYSYCTAQTVYGILGIKVWVFKGEIIP
GQEDIVSQPVTREREPRRRQQQRRRQQFEDRSNEAMATGRRKASKAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAIVIVGN
ERGQVGVGVGKASDVIGAVKKGVADGKKHLIEIPITKSNSIPHPIDGVGGGAKVIMRPAAPGTGVIAGGAVRTVLELAGVRNVL
AKQLGSNNPLNNARAAVNALSTLRTFAEVAEDRGIAVENLYIMATVAETNSGRALYWGTGRRKSAVAQVRLVPGEGKFVVN
GKEGELYFQYNPNYLGVIKAPLETLGLENEYDILVKAKGGGLTGQADSIRLGVARALCQLDPDNRSPLKIEGYLTRDPRAKERK
KYGLHKARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFE
TRTHRRIIDIHQPSSKTIDALMKLDLPSGVDIEVKLMARQPTKKTGSKKQKKNVPNGVAYIQSTFNNSIVTITDQNGDVISWASA
GSSGFKGAKKGTPFAAQTAAESAGRRAIDQGMRQIQVMVSGPGAGRETAIRALQGAGLEITLIRDVTPIPHNGCRPPKRRRVMA
RIAGVDLPRDKRVEIGLTYIYGIGLRRSQDILAATDVNPDTRVKDLTDADLAALRAEIESNYQVEGDLRRLEAMNIKRLVDIGCY
RGRRHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLSKIEKLNANNEKQVIKTWSRASTILPL
MVGHTIAVHNGKQHVPVFVNEQMVGHKLGEFAPTRSYRGHGKTDKKSGRMSDKNEGYKIISDNRQARYLYEILETYEAGIQL
TGTEVKSIRAGKVNLQDGYALLRDGEAWLINAHISPYTASGQYFNHEPRRTRKLLLHGLEIRKLIGKVEQQGLTLIPLKMYFKR
GWVKISIGLCRGKKVHDKREDLKRRQDQRDIQRAMKNYMAEISAKLVQDLRQKTGAGMMDCKKALNETQGNIDEAIDWLRK
KGIASAGKKSDRVTAEGLVDIYTTPDKSGGVIIEVNCQTDFVARNDAFKLLVKNLAKQAVNADNVASLLDQPYIEKTDVTVDE
YIKETIATLGENIQVRRFVNFSLEGAPGAIDGYIHTGGRVGVLVSIGVDTETAAKNEELQSLAKNTAMQVAACPNVEYVSVDKI
PDQVVEKEKEIEMGKEDLGNKPANIKEKIVQGRIDKRLKEMTLLDQPYIRDQNISVAELIKQVESKVSEPIKVHQFVRYILGEGIE
KQESNFAEEVAAQIGAK
>Cylindrospermopsis_raciborskii_CS_505
MQIPRLHPDTVEEVKHRADIVDVISDYVVLRRRGKDFVGLCPFHEEKTPSFTVSPTKQIYYCFGCQASGNAIKFMMDLNKRQFA
EVVLDLAKRYQVPVKTLAPEQRQELQRQLSLREQLFEVLASTSQFYQHVLRQDIGQQALQYLQKKRFLKTETVEKFALGYAPP
GWETLYHYLVENKNYPPQLVEKAGLIKPRKEGGGYYDVFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFDKSKTL
FALDVSKDAISKLDQAVVVEGYFDAIALHANGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATERAIGEISN
LAYKGEVQLKILHIPDGKDADEYLKNHSVTDYGQLLVDAPLWLDWQIAQVIQGRDLRQPTDFQLVSREFVKLLQKILNSDTLN
YYISHCAEILSLGDTRLIPLRVENLITQVAPRRTPTPRPPQPDSTTSPNTHQISHPQPSLLEQAEGLLLRIFLHCPQERQVIIETLGSS
NLEFSVSHHRFLWEKSLQFPSQTLDLISQLQNLYLETQNDLGPVQHIFQLNEKNKQEILLRTSQLVQAAIACMEKVFRENRYRHF

LELWQKTDPSTDPDQYSLYTQTIYADKMRIQELSKQRQLSIADLINMKLAEAESTMNKTVEATQRAFNSIRTGRANASLLDKVQ
VDYYGSPTSLKSLANITTPDATTILIQPYDRTSLNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKELVKLAAKYAEEGRVGI
RNIRRDALDSIRKQEKAGEVSEDESRDQQDKLQKITSKYTAKIDELLAEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDSE
GAQLGIMAPLEALRLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRV
KQAERFLKDGDKVKATVMFRGREIQHSDLAETLLNRMATDLEPFGEVQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIEKI
SLERNLPRLAVQSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIDGEGFRVLSTKTIVEEVTNGDHQISLDEVQQVAP
EAQSGDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSFGQPEVEA
ELPKREQLPNDTYRSNATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKI
AVDTLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIG
KEGQNVRLAARLTGWKIDIKDQAKYDYGAEDAKFAAVRANYQEESNQLDNQFEVIEEEYEDDPDAGEDEFNSMEEENMSKK
SLASLSAADISDKRALVRVDFNVPVDNQGNITDDTRIRAALPTIQDLISKGAKVILASHFGRPKGVDEKLRLTPVAKRLSELLGQ
EVIKTDDCIGDDVTTQVAALEKGQVLLLENVRFYKEEEKNDPEFARQLAANADFYVNDAFGTAHRAHASTEGVTKYLSPSVA
GYLVEKELQYLQGAIEVPQRPLVAIIGGSKVSSKITVIETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEDDKLVLASSLEKKA
AERGVTLLLPTDIVAANTFAPDADAVTVSIDHIPDDRMGLDIGPDSVKVFQAALADCKTVIWNGPMGVFEFDKFAVGTEAIAQT
LAEISKNGATTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGKVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGR
LLKSRDYSVSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGG
TVQVIPHITNEIKERVIRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGKQNVLYMHVTLLPWIASAGEMKTKPTQHSV
KELRSIGIQPDILVCRCDRPIPVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQREPDLTHWETMVE
RMSHPQSPVEIAIVGKYVRLGDAYLSVVESLRHAAIATYGDLRLRWVNSEILEVEPPDNYLLGVDGIIVPGGFGIRGVDGKISAIE
YARNRQIPFLGLCLGMQCSIIEWARNVEGLVGANSAEFNPQTDYPVINLLPEQQDVIDLGGTMRLGLYPCHVQPNTLAFDLYQE
EVIYERHRHRYEFNNLYRNHLLNSGYVISGTSPDGRLVEIVEYPQHPFFIACQFHPEFQSRPSHPHPLFKGFMEAAISHTHQGKKP
NYPLRVSSVPMVKKVSRRLQALQAKVEERDYTPLEALALLKETATAKFAEAAEAHIRLGIDPKYTDQQLRTTVVLPKGTGQIV
RVAVIARGEKVTEATNAGADIAGSEELIDEIQKGMMDFDKLIATPDVMPVAKLGKLLGPRGLMPSPKGGTVTFDIASAISEFK
AGKLEFRADRTGIVHVMFGKASFSSEDLLVNLKALQETIDRNRPSGAKGRYWRTFYISSTMGPSIKIDINALRDFKTTDVAMGT
RSYRPYTPSTRQVTISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRDITATVIAVEYDPNRNA
RIALVEYEDGEKRYILHPNGLKVGAKITAGPQAPFEDGNALPLSNIPLGTNVHNVEMTPGKGGQIVRAAGATAQLMAKEGNYV
TLKLPSGEVRMVRRECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKP
ALGAKTRKRKKASSKLIVRRRRKSSKRGRGGRQSMSVGILGTKLGMTQIFDEAGVSIPVTVIQAGPCTVTQVKTQPTDGYCAIQ
VGYGEVKPKALNKPKLGHLAKSSAGPVRYLNEYRTDAAGDYALGQEIKADIFSVGQIVDVIGTSIGRGFAGNQKRNNFGRGPM
SHGSKNHRAPGSIGAGTTPGRVYPGKRMAGRLGGSRVTVRKLTVVKVDAERNLILIKGAIPGKPGGLVNVVPTTKVGNKMVES
TVKNWQGEEVGQTSFELRVAKEETASHIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRG
GGVIFGPKPRDFNIKLNRKERRLALRTAFVSRREDLIVVEEFTDQLQRPKSKELVAALARWGATADQKTLLILSEIGQNTETISLS

ARNVENIKVIAADQLNVFDLLHADKIVVTSSALTKIQEVYSAMATTRLKTLYGQTIVPKLTQQFQYTNVHQVPKVLKVTVNRG
LGEAAQNAKALEASLSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSAKSFDG
RGNYTLGVREQLIFPEIEYDRIDQIRGLDISIITTAKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGTKVVVKGPK
GELSRDLPAHVTVSQSGETLLVTRRDDTRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGANLVLNIGYSHQ
VQIEPPAGVQFVVENNTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRKAGKTGGKGKKMAKKVVAVIKLA
LNAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSDQPNKK
KVGSITRTQLKEIAQTKLPDLNANDIEAAMNIVEGTAKNMGVTIKDMSTATDQILEQLKSLTLLEAAELVKQIEEAFGVSAAAP
VGGMAVIAAPGGAAAAEVVEEQTEFDVILQEVPADKKIAVLKIVREITGLGLKEAKELVESTPKAVKEGVNKEAAEDISKKITE
AGGKVAIKMSSKTYLPPEEEIKRDWYVVDAADKRLGRLASEIAMVLRGKRKAEYTPHLDTGDFVVVINAEKVVVTGKKQSQK
LYRRHSGRPGGMKTETFAKLQQRLPERIVEHAVKGMLPKNSLGRQLFTKLKVYSGATHPHTAQKPKELIINTIPGENMIQPQTY
LNVADNSGARKLMCIRVLGAGNRRYGGVGDRIIAVVKDAQPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKE
GNPKGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRR
AMTRYIRRGGKIWIRIFPDKPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQP
QEQEMNAQEIIRSIEAEQLKSDLPQIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSP
RIDNIKIMRRGKVRRAKLYYLRQLSGKATRIKQRFDRALMTRVKRGNVARNRRNKILKLAKGFRGSHSTLFRTANQQVMKAL
RSAYRDRKKKKRDFRRLWITRINAASRQQGLSYSQLIGNLKKANVELNRKMLAQLAVLDPTTFAKVAELASSVKGNMAHKKG
TGSTRNGRDSNAQRLGVKRFGGQVVRAGNILVRQRGTKFHPGNNVGIGNDDTLFALIDGVVTFERKGKSRKKVSVYPRVTEE
AVASMNNENYMEPSFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGHNYKLKEPKYSVEESKRRDSTYGVQM
YVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRN
DLVWVRIDKTRKLSIQVLLKALGLLDNEILDALRHPEYFQKTIEKEGQFSEEEALLELYRKLRPGEPPTVMGGQQLLESRFFDPK
RYDLGRVGRYKLNKKLRLSVPDTTRVLTPGDILSAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRER
MTVSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIET
PEGPNAGLIGSLATHARVNQYGFLETPFRPVENGRVCYEKPAVYMTADEEDDLRVAPGDIPVDDNGQILGIQVPVRYRQEFSTT
TPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSGMVIVSRTDGDVVYV
DATEIRVRVKEKAALTNRESESIPHKPQEIKYVLSKYQRSNQDTCLNQKPLVRIGEKVIAGQVLADGSSTEGGELALGQNVIVA
YMPWEGYNYEDAILISERLVQEDVYTSIHIEKFEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRVGAWVESGDILVGKVTP
KGESDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRIVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHG
NKGIISRILPLEDMPYLPDGTPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGEESSRRIVHGKLWEARE
ETSKDWVYNPENPGKIMVYDGRTGEPFDRAVTVGIAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEV
WALEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLDVEVDL
MADQVSRRTPPRPTYESFSRDSLDEDEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLMDDAYN
YMRSQAEQGKKFLFVGTKRQAAGIIAQEANRCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREENGALDLLPKKEASML

RREMSKLQKYLGGIKNMRKVPDVVIIVDQRREYNAVQECQKLSIPIVSMLDTNCDPDTVDIPIPANDDAIRSIKLIVGKLADAIYE
GRHGQLEVESDYEEYESAEEDYEYDESEFVDSFSDDDDEEMGQKIHPVGFRLGITQEHQSLWFAVPGRYPELLQEDHKLRQYIE
QKLGRNAQNNAGLSEIHIERKADQVDLELRTARPGVVVGRGGQGIEALRTGLQQLLGSHRQVRINVVEVQKVDADAYLIAEYI
AQQLERRVSFRRVVRQAIQRAQRAGVQGIKVQVSGRLNGAEIARTEWTREGRVPLHTLRADIDYSYCTAQTVYGILGIKVWVF
KGEIIPGQEDIVSQPVTREREPRRRQQQRRRQQFEDRSNEAMATGRRKASKAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAI
VIVGNERGQVGVGVGKASDVIGAVKKGVADGKKHLIEIPITKSNSIPHPIDGVGGGAKVIMRPAAPGTGVIAGGAVRTVLELAG
VRNVLAKQLGSNNPLNNARAAVNALSTLRTFAEVAEDRGIAVENLYIMATVAETNSGRALYWGTGRRKSAVAQVRLVPGEG
KFVVNGKEGELYFQYNPNYLGVIKAPLETLGLENEYDILVKAKGGGLTGQADSIRLGVARALCQLDPDNRSPLKIEGYLTRDPR
AKERKKYGLHKARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKD
SREHFETRTHRRIIDIHQPSSKTIDALMKLDLPSGVDIEVKLMARQPTKKTGSKKQKKNVPNGVAYIQSTFNNSIVTITDQNGDVI
SWASAGSSGFKGAKKGTPFAAQTAAESAGRRAIDQGMRQIQVMVSGPGAGRETAIRALQGAGLEITLIRDVTPIPHNGCRPPKR
RRVMARIAGVDLPRDKRVEIGLTYIYGIGLRRSQDILAATDVNPDTRVKDLTDADLAALRAEIESNYQVEGDLRRLEAMNIKRL
VDIGCYRGRRHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLSKIEKLNANNEKQVIKTWSR
ASTILPLMVGHTIAVHNGKQHVPVFVNEQMVGHKLGEFAPTRSYRGHGKTDKKSGRMSDKNEGYKIISDNRQARYLYEILETY
EAGIQLTGTEVKSIRAGKVNLQDGYALLRDGEAWLINAHISPYTASGQYFNHEPRRTKLLLHGLEIRKLIGKVEQQGLTLIPLK
MYFKRGWVKISIGLCRGKKVHDKREDLKRRQDQRDIQRAMKNYMAEISAKLVQDLRQKTGAGMMDCKKALNETQGNIDEAI
DWLRKKGIASAGKKSDRVTAEGLVDIYTTPDKSGGVIIEVNCQTDFVARNDAFKLLVKNLAKQAVNADNVASLLAQPYIEKTD
VTVDEYIKETIATLGENIQVRRFVNFSLEGAPGAIDGYIHTGGRVGVLVSIGVDTETAAKNEELQSLAKNTAMQVAACPNVEYV
SVDKIPDQVVEKEKEIEMGKEDLGNKPANIKEKIVQGRIDKRLKEMTLLDQPYIRDQNISVAELIKQVESKVSEPIKVHQFVRYIL
GEGIEKQESNFAEEVAAQIGAK
>Cylindrospermopsis_raciborskii_CS_508
MQIPRLHPDTVEEVKHRADIVDVISDYVVLRRRGKDFVGLCPFHEEKTPSFTVSPTKQIYYCFGCQASGNAIKFMMDLNKRQFA
EVVLDLAKRYQVPVKTLAPEQRQELQRQLSLREQLFEVLASTSQFYQHVLRQDIGQQALQYLQKKRFLKTETVEKFALGYAPP
GWETLYHYLVENKNYPPQLVEKAGLIKPRKEGGGYYDVFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFDKSKTL
FALDVSKDAISKLDQAVVVEGYFDAIALHANGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATERAIGEISN
LAYKGEVQLKILHIPDGKDADEYLKNHSVTDYGQLLVDAPLWLDWQIAQVIQGRDLRQPTDFQLVSREFVKLLQKILNSDTLN
YYISHCAEILSLGDTRLIPLRVENLITQVAPRRTPTPRPPQPDSTTSPNTHQISHPQPSLLEQAEGLLLRIFLHCPQERQVIIETLGSS
NLEFSVSHHRFLWEKSLQFPSQTLDLISQLQNLYLETQNDLGPVQHIFQLNEKNKQEILLRTSQLVQAAIACMEKVFRENRYRHF
LELWQKTDPSTDPDQYSLYTQTIYADKMRIQELSKQRQLSIADLINMKLAEAESTMNKTVEATQRAFNSIRTGRANASLLDKVQ
VDYYGSPTSLKSLANITTPDATTILIQPYDRTSLNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKELVKLAAKYAEEGRVGI
RNIRRDALDSIRKQEKAGEVSEDESRDQQDKLQKITSKYTAKIDELLAEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDSE
GAQLGIMAPLEALRLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRV

KQAERFLKDGDKVKATVMFRGREIQHSDLAETLLNRMATDLEPFGEVQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIEKI
SLERNLPRLAVQSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIDGEGFRVLSTKTIVEEVTNGDHQISLDEVQQVAP
EAQSGDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSFGQPEVEA
ELPKREQLPNDTYRSNATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKI
AVDTLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIG
KEGQNVRLAARLTGWKIDIKDQAKYDYGAEDAKFAAVRANYQEESNQLDNQFEVIEEEYEDDPDAGEDEFNSMEEENMSKK
SLASLSAADISDKRALVRVDFNVPVDNQGNITDDTRIRAALPTIQDLISKGAKVILASHFGRPNGVDEKLRLTPVAKRLSELLGQ
EVIKTDDCIGDDVTTQVAALEKGQVLLLENVRFYKEEEKNDPEFARQLAANADFYVNDAFGTAHRAHASTEGVTKYLSPSVA
GYLVEKELQYLQGAIEVPQRPLVAIIGGSKVSSKITVIETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEDDKLVLASSLEKKA
AERGVTLLLPTDIVAANTFAPDADAVTVSIDHIPDDRMGLDIGPDSVKVFQAALADCKTVIWNGPMGVFEFDKFAVGTEAIAQT
LAEISKTGATTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGKVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGR
LLKSRDYSVSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGG
TVQVIPHITNEIKERVIRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGKQNVLYMHVTLLPWIASAGEMKTKPTQHSV
KELRSIGIQPDILVCRCDRPIPVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQREPDLTHWETMVE
RMSHPQSPVEIAIVGKYVRLGDAYLSVVESLRHAAIATYGDLRLRWVNSEILEVEPPDNYLLGVDGIIVPGGFGIRGVDGKISAIE
YARNRQIPFLGLCLGMQCSIIEWARNVEGLVGANSAEFNPQTDYPVINLLPEQQDVIDLGGTMRLGLYPCHVQPNTLAFDLYQE
EVIYERHRHRYEFNNLYRNHLLNSGYVISGTSPDGRLVEIVEYPQHPFFIACQFHPEFQSRPSHPHPLFKGFMEAAISHTHQGKKP
NYPLRVSSVPMVKKVSRRLQALQAKVEERDYTPLEALALLKETATAKFAEAAEAHIRLGIDPKYTDQQLRTTVVLPKGTGQIV
RVAVIARGEKVTEATNAGADIAGSEELIDEIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDIASAISEFK
AGKLEFRADRTGIVHVMFGKASFSSEDLLVNLKALQETIDRNRPSGAKGRYWRTFYISSTMGPSIKIDINALRDFKTTDVAMGT
RSYRPYTPSTRQVTISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRDITATVIAVEYDPNRNA
RIALVEYEDGEKRYILHPNGLKVGAKITAGPQAPFEDGNALPLSNIPLGTNVHNVEMTPGKGGQIVRAAGATAQLMAKEGNYV
TLKLPSGEVRMVRRECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKP
ALGAKTRKRKKASSKLIVRRRRKSSKRGRGGRQSMSVGILGTKLGMTQIFDEAGVSIPVTVIQAGPCTVTQVKTQPTDGYCAIQ
VGYGEVKPKALNKPKLGHLAKSSAGPVRYLNEYRTDAAGDYALGQEIKADIFSVGQIVDVIGTSIGRGFAGNQKRNNFGRGPM
SHGSKNHRAPGSIGAGTTPGRVYPGKRMAGRLGGSRVTVRKLTVVKVDAERNLILIKGAIPGKPGGLVNVVPTTKVGNKMVES
TVKNWQGEEVGQTSFELRVAKEETASHIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRG
GGVIFGPKPRDFNIKLNRKERRLALRTAFVSRREDLIVVEEFTDQLRPKSKELVAALARWGATADQKTLLILSEIGQNTETISLS
ARNVENIKVIAADQLNVFDLLHADKIVVTSSALTKIQEVYSAMATTRLKTLYGQTIVPKLTQQFQYTNVHQVPKVLKVTVNRG
LGEAAQNAKALEASLSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSAKSFDG
RGNYTLGVREQLIFPEIEYDRIDQIRGLDISIITTAKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGTKVVVKGPK
GELSRDLPAHVTVSQSGETLLVTRRDDTRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGANLVLNIGYSHQ

VQIEPPAGVQFVVENNTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRKAGKTGGKGKKMAKKVVAVIKLA
LNAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSDQPNKK
KVGSITRTQLKEIAQTKLPDLNANDIEAAMNIVEGTAKNMGVTIKDMSTATDQILEQLKSLTLLEAAELVKQIEEAFGVSAAAP
VGGMAVIAAPGGAAAAEVVEEQTEFDVILQEVPADKKIAVLKIVREITGLGLKEAKELVESTPKAVKEGVNKEAAEDISKKITE
AGGKVAIKMSSKTYLPPEEEIKRDWYVVDAADKRLGRLASEIAMVLRGKRKAEYTPHLDTGDFVVVINAEKVVVTGKKQSQK
LYRRHSGRPGGMKTETFAKLQQRLPERIVEHAVKGMLPKNSLGRQLFTKLKVYSGATHPHTAQKPKELIINTIPGENMIQPQTY
LNVADNSGARKLMCIRVLGAGNRRYGGVGDRIIAVVKDAQPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKE
GNPKGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRR
AMTRYIRRGGKIWIRIFPDKPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQP
QEQEMNAQEIIRSIEAEQLKSDLPQIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSP
RIDNIKIMRRGKVRRAKLYYLRQLSGKATRIKQRFDRALMTRVKRGNVARNRRNKILKLAKGFRGSHSTLFRTANQQVMKAL
RSAYRDRKKKKRDFRRLWITRINAASRQQGLSYSQLIGNLKKANVELNRKMLAQLAVLDPTTFAKVAELASSVKGNMAHKKG
TGSTRNGRDSNAQRLGVKRFGGQVVRAGNILVRQRGTKFHPGNNVGIGNDDTLFALIDGVVTFERKGKSRKKVSVYPRVTEE
AVASMNNENYMEPSFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGHNYKLKEPKYSVEESKRRDSTYGVQM
YVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRN
DLVWVRIDKTRKLSIQVLLKALGLLDNEILDALRHPEYFQKTIEKEGQFSEEEALLELYRKLRPGEPPTVMGGQQLLESRFFDPK
RYDLGRVGRYKLNKKLRLSVPDTTRVLTPGDILSAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRER
MTVSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIET
PEGPNAGLIGSLATHARVNQYGFLETPFRPVENGRVCYEKPAVYMTADEEDDLRVAPGDIPVDDNGQILGIQVPVRYRQEFSTT
TPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSGMVIVSRTDGDVVYV
DATEIRVRVKEKAALTNRESESIPHKPQEIKYVLSKYQRSNQDTCLNQKPLVRIGEKVIAGQVLADGSSTEGGELALGQNVIVA
YMPWEGYNYEDAILISERLVQEDVYTSIHIEKFEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRVGAWVESGDILVGKVTP
KGESDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRIVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHG
NKGIISRILPLEDMPYLPDGTPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGEESSRRIVHGKLWEARE
ETSKDWVYNPENPGKIMVYDGRTGEPFDRAVTVGIAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEV
WALEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLDVEVDL
MADQVSRRTPPRPTYESFSRDSLDEDEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLMDDAYN
YMRSQAEQGKKFLFVGTKRQAAGIIAQEANRCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREENGALDLLPKKEASML
RREMSKLQKYLGGIKNMRKVPDVVIIVDQRREYNAVQECQKLSIPIVSMLDTNCDPDTVDIPIPANDDAIRSIKLIVGKLADAIYE
GRHGQLEVESDYEEYESAEEDYEYDESEFVDSFSDDDDEEMGQKIHPVGFRLGITQEHQSLWFAVPGRYPELLQEDHKLRQYIE
QKLGRNAQNNAGLSEIHIERKADQVDLELRTARPGVVVGRGGQGIEALRTGLQQLLGSHRQVRINVVEVQKVDADAYLIAEYI
AQQLERRVSFRRVVRQAIQRAQRAGVQGIKVQVSGRLNGAEIARTEWTREGRVPLHTLRADIDYSYCTAQTVYGILGIKVWVF

KGEIIPGQEDIVSQPVTREREPRRRQQQRRRQQFEDRSNEAMATGRRKASKAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAI
VIVGNERGQVGVGVGKASDVIGAVKKGVADGKKHLIEIPITKSNSIPHPIDGVGGGAKVIMRPAAPGTGVIAGGAVRTVLELAG
VRNVLAKQLGSNNPLNNARAAVNALSTLRTFAEVAEDRGIAVENLYIMATVAETNSGRALYWGTGRRKSAVAQVRLVPGEG
KFVVNGKEGELYFQYNPNYLGVIKAPLETLGLENEYDILVKAKGGGLTGQADSIRLGVARALCQLDPDNRSPLKIEGYLTRDPR
AKERKKYGLHKARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKD
SREHFETRTHRRIIDIHQPSSKTIDALMKLDLPSGVDIEVKLMARQPTKKTGSKKQKKNVPNGVAYIQSTFNNSIVTITDQNGDVI
SWASAGSSGFKGAKKGTPFAAQTAAESAGRRAIDQGMRQIQVMVSGPGAGRETAIRALQGAGLEITLIRDVTPIPHNGCRPPKR
RRVMARIAGVDLPRDKRVEIGLTYIYGIGLRRSQDILAATDVNPDTRVKDLTDADLAALRAEIESNYQVEGDLRRLEAMNIKRL
VDIGCYRGRRHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLSKIEKLNANNEKQVIKTWSR
ASTILPLMVGHTIAVHNGKQHVPVFVNEQMVGHKLGEFAPTRSYRGHGKTDKKSGRMSDKNEGYKIISDNRQARYLYEILETY
EAGIQLTGTEVKSIRAGKVNLQDGYALLRDGEAWLINAHISPYTASGQYFNHEPRRTRKLLLHGLEIRKLIGKVEQQGLTLIPLK
MYFKRGWVKISIGLCRGKKVHDKREDLKRRQDQRDIQRAMKNYMAEISAKLVQDLRQKTGAGMMDCKKALNETQGNIDEAI
DWLRKKGIASAGKKSDRVTAEGLVDIYTTPDKSGGVIIEVNCQTDFVARNDAFKLLVKNLAKQAVNADNVASLLAQPYIEKTD
VTVDEYIKETIATLGENIQVRRFVNFSLEGAPGAIDGYIHTGGRVGVLVSIGVDTETAAKNEELQSLAKNTAMQVAACPNVEYV
SVDKIPDQVVEKEKEIEMGKEDLGNKPANIKEKIVQGRIDKRLKEMTLLDQPYIRDQNISVAELIKQVESKVSEPIKVHQFVRYIL
GEGIEKQESNFAEEVAAQIGAK
>Cylindrospermopsis_raciborskii_CYLP
MQIPRLHPDTVEEVKHRADIVDVISDYVVLRRRGKDFVGLCPFHEEKTPSFTVSPNKQIYYCFGCQASGNAIRFIMDLNKRKFAE
VVLDLAKRYQVPVKTLAPEQRQELQRQLSLREQLFEVLASTSQFYQHVLRQDIGQQALQYLQKKRFLKTETVEKFALGYAPPG
WETLYHYLVENKSYPAQLVEKAGLIKPRKEGGGYYDVFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFDKSKTLF
ALDVAKDAISKLDQAVVVEGYFDAIALHANGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATERAIGEISNL
AYKGEVRLKILHIPDGKDADEYLKNHSVTDYEQLLVEAPLWLDWQIAQVIQGRDLKQPTDFQLVSREFVKLLQKILNSDTLNY
YISHCAEILSLGDTRLIPLRVENLITQVAPRRTPTPILRPPASPNTHQISHPQPSLLEQAEGLLLRIFLHCPQERQVIIETLGSSNLEFS
VSHYRFLWEKSLQFPSQTLDLISQLQNLYLETQNDLGPVEHIFQLNEKNKQEILLRTNQLVQAAIACMEKVFRENRYRHFLELW
QKTDPSTDPDQYNLYAQTIYADKMRIQELSKQRQLSISDLINMKLAEAESTMNKTVEATQRAFNSIRTGRANASLLDKVQVDY
YGSPTPLKSLTNITTPDASTILIQPYDRSSLNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKELVKLAAKYAEEGRVGIRNIR
RDALDSIRKQEKAGEISEDESRDQQDKLQKITGKYTAKIDELLTEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDSEGAQL
GIMAPLEALRLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVKQAE
RFLKDGDKVKATVMFRGREIQHSDLAETLLNRMATDLEPFGEIQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIEKISLERN
LPRLAVQSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIDGEGFRVLSTKTIVEEVTNGDHQISLDEVQQVAPEAQS
GDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSFGQPEVEAELPK
REQLPNDTYRSNATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAVD

TLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIGKEG
QNVRLAARLTGWKIDIKDQAKYDYGAEDAKFAAVRANYQEESNQPDNQFEIIEEGYEDDPDEGEDDFNSMEEENKKVIASLSA
TDISDKRALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLISKGAKVILASHFGRPKGVDEKLRLTPVAKRLSELLGQEVIKTDD
CIGDDVTAQVAALEKGQVLLLENVRFYKEEEKNDPNFARQLAANADFYVNDAFGTAHRAHASTEGVTKYLSPSVAGYLVEKE
LQYLQAAIEVPQRPLAAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEQDKLELASSLEKKAAERGVTL
LLPTDIVAADKFAPDADAVTVSIENIPDDRMGLDIGPKSVKLFQDALADCKTVIWNGPMGVFEFDKFAVGTEAIAQTLAEIGKT
GATTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGTVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRDY
SVSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGGTVQVIPHI
TNEIKERVIRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGKQNVLYMHVTLLPWIASAGEMKTKPTQHSVKELRSIGI
QPDILVCRCDRPIPVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQREPDLTHWETMVERMSHPQS
PVEIAIVGKYVRLGDAYLSVVESLRHAAIATYGDLRLRWVNSEILEVEPPDNYLLGVDGIIVPGGFGIRGVDGKISAIEYARNRQI
PFLGLCLGMQCSIIEWARNVEGLVGANSAEFDPKTDYPVINLLPEQQDVIDMGGTMRLGLYPCHVQPNTLAFDLYQEEVIYERH
RHRYEFNNLYRNHLLNSGYVISGTSPDGRLVEIVEYPQHPFFIACQFHPEFQSRPSHPHPLFKGFMEAAISHTHQGKKQLPQGFP
QFPMVKKVSRRLQALQAKVEERDYAPLEALALLKETATAKFPEAAEAHIRLGIDPKYTDQQLRTTVVLPKGTGQIVRVAVIAR
GEKVTEATNAGADIAGSEELIDEIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDIASAISEFKAGKLEFR
ADRTGIVHVMFGKASFSSEDLLVNLKALQETIDRNRPSGAKGRYWRTFYISSTMGPSIKVDINALRDLKTTDAAMGTRSYRPYT
PSTRQVTISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRDITATVIAVEYDPNRNARIALLEY
EDGEKRYILHPNGLKVGAKVTAGPQAPFEDGNALPLSNIPLGTNVHNVEMTPGKGGQIVRAAGATAQLMAKEGNYVTLKLPS
GEVRMVRRECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPALGAK
TRKRKKASSKLIVRRRRKSSKRGRGGRQSMSVGILGTKLGMTQIFDEAGVSIPVTVIKAGPCTVTQVKTQPTDGYCAIQVGYGE
VKPKALNKPKLGHLAKSSAVPVRYLNEYRTDAAGDYALGQEIKADIFSVGQIVDVIGTSIGRGFAGNQKRNNFGRGPMSHGSK
NHRAPGSIGAGTTPGRVYPGKRMAGRLGGSRVTVRKLTVVKVDAERNLILIKGAIPGKPGGLVNVVPTTKVGNKMVESIVKN
WQGEEVGQTSFELRVAKEETASHIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIF
GPKPREFNIKLNRKERRLALRTAFVSRREDLIVVEEFTDQLQRPKSKELVAALARWGATADQKTLLILSEIGQSTETISLSARNVE
NIKVIAADQLNVFDLLHADKIVVTSSALTKIQEVYSAMATTRLKTLYGQTIVPKLTQQFQYTNVHQVPKVLKVTVNRGLGEAA
QNAKALEASLSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSAKSFDGRGNYT
LGVREQLIFPEIEYDRIDQIRGLDISIITTAKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGTKVVVKGPKGELSRD
LPTHVTVSQSGETLLVTRRDDTRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGANLVLNIGYSHQVQIEPPA
GVQFAVENNTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRKAGKTGGKGKKMAKKVVAVIKLALNAGKA
NPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSDQPNKKKVGSITR
TQLREIAQTKLPDLNANDIEAAMNIVEGTAKNMGVTVKDMSTATDQILEQLKVLTLLEAAELVKQIEEAFGVSAAAPAGGMM
VMAAPGAAAAEPVEEQTEFNVVLEEVPADRKIAVLKIVREITGLGLKEAKELVESTPKAVKEGVNKESAEEISKKIADAGGKVV

IKMSSKTYLPPEEEIKRDWYVVDAADKRLGRLASEIAMVLRGKRKAEYTPHLDTGDFVVVINAEKKVVVTGKKPSQKLYRRH
MIQPQTYLNVADNSGARKLMCIRVLGAGNRRYGGVGDRIIAVVKDAQPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDN
AAVIINKEGNPKGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITS
RQIEASRRAMTRYIRRGGKIWIRIFPDKPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKT
KFIVRSQPQEQEMNAQEIIRSIEAEQLKSDLPQIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVE
RVFLLHSPRIDNIKIMRRGKVRRAKLYYLRQLSGKATRIKQRFDRALMTRVKRGNVARNRRNKILKLAKGFRGSHSTLFRTAN
QQVMKALRSAYRDRKKKKRDFRRLWITRINAASRQQGLSYSQLIGNLKKANVELNRKMLAQLAVLDPATFAKVAELASSVKG
MAHKKGTGSTRNGRDSNAQRLGVKRFGGQVVRAGNILVRQRGTKFHPGNNVGIGNDDTLFALIDGVVTFERKGKSRKKVSV
YPSVTEEAVASMYVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNR
GAWLKFETDRNDLVWVRIDKTRKLSIQVLLKALGLSDNEILDALRHPEYFQKTIEKEGQFSEEEALLELYRKLRPGEPPTVMGG
QQLLESRFFDPKRYDLGRVGRYKLNKKLRLSVPDTTRVLTPGDILSAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVR
VGLNRLERIIRERMTVSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDI
HPSHYGRICPIETPEGPNAGLIGSLATHARVNQYGFLETPFRPVENGRVCYEKPAVYMTADEEDDLRVAPGDIPVDDNGQILGIQ
VPVRYRQEFSTTTPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSGMVI
VSRTDGDVVYVDATEIRVRVKEKAALTNRESETIPHKPQEIKYVLSKYQRSNQDTCLNQKPLVRIGEKVIAGQVLADGSSTEGG
ELALGQNVIVAYMPWEGYNYEDAILISERLVQEDVYTSIHIEKFEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRVGAWVE
SGDILVGKVTPKGESDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQ
VGDKMAGRHGNKGIISRILPLEDMPYLPDGTPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGEESSRRI
VHGKLWEAREETSRDWVYNPENPGKIMVYDGRTGEPFDRAVTVGIAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQ
GGQRFGEMEVWALEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTD
GSSLDVEVDLMADQVSRRTPPRPTYESFSRDSLDEDEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQT
AQLMDDAYNYMRSQAEQGKKFLFVGTKRQAAGIIAQEANRCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREENGALD
LLPKKEASMLRREMSKLQKYLGGIKNMRKVPDVVIIVDQRREYNAVQECQKLSIPIVSMLDTNCDPDTVDVPIPANDDAIRSIK
LIVGKLADAIYEGRHGQLEVPDDEDYDIPEEDYEYNESEMGQKIHPVGFRLGITQEHQSLWFAVPGRYPELLQEDHKLRQYIE
QKLGRNAQNNAGLSEIHIERKADQVDLELRTARPGVVVGRGGQGIEALRTGLQQLLGSHRQVRINVVEVQKVDADAYLIAEYI
AQQLERRVSFRRVVRQAIQRAQRAGVQGIKVQVSGRLNGAEIARTEWTREGRVPLHTLRADIDYSYCTAQTVYGILGIKVWVF
KGEIIPGQEDIVSQPVTREREPRRRQQQRRRQQFEDRSNEAMATGRRKASKAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAI
VIVGNERGQVGVGVGKASDVIGAVKKGVADGKKHLIEIPITKSNSIPHPIDGVGGGAKVIMRPAAPGTGVIAGGAVRTVLELAG
VRNVLAKQLGSNNPLNNARAAVNALSTLRTFAEVAEDRGIAVENLYIMATVAETNSGRALYWGTGRRKSAVAQVRLVPGEG
KFVVNGKEGELYFQYNPNYLGVIKAPLETLGLENEYDILVKAKGGGLTGQADSIRLGVARALCQLDPDNRSPLKIEGYLTRDPR
AKERKKYGLHKARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKD
SREHFETRTHRRIIDIHQPSSKTIDALMKLDLPSGVDIEVKLLRGQKKGTPFAAQTAAESAGRRAIDQGMRQIQVMVSGPGAGRE

TAIRALQGAGLEITLIRDVTPIPHNGCRPPKRRRVMARIAGVDLPRDKRVEIGLTYIYGIGLRRSQDILAATDVNPDTRVKDLTDA
DLAALRAEIESNYQVEGDLRRLEAMNIKRLVDIGCYRGRRHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLK
KGPFVADHLLSKLEKLNANNEKQVIKTWSRASTILPLMVGHTIAVHNGKQHVPVFVNEQMVGHKLGEFAPTRTYRGHGKTDK
KSGRMSDKNEGYKIISDNRQARYLYEILETYEAGIQLTGTEVKSIRAGKVNLQDGYALLRDGEAWLINAHISPYTASGQYFNHE
PRRTRKLLLHGLEIRKLIGKVEQQGLTLIPLKMYFKRGWVKISIGLCRGKKVHDKREDLKRRQDQRDIQRAMKNYMDCKKAL
NETQGNIDEAIDWLRKKGIASAGKKSDRVTAEGLVEIYTTPDRSGGVLIEVNCQTDFVARNDAFKLLVKNLAKQAVNADNVTS
LLAQPYIENTDVTVDEYIKGTITTLGENIQVRRFVNFSLEGSPGAIDGYIHTGGRVGVLISIGVDTENAAKNEEVQSLAKNTAMQ
VAACPNVEYVSVDKIPDQVVQKEKEIEMGKEDLGNKPENIKEKIVQGRIDKRLKEMTLLDQPYIRDQSISVAELIKQVESKVSEP
IKVHQFVRYILGEGIEKQESNFAQEVAAQIGAK
>Cylindrospermopsis_raciborskii_CYRF
MQIPRLHPDTVEEVKHRADIVDVISDYVVLRRRGKDFVGLCPFHEEKTPSFTVSPNKQIYYCFGCQASGNAIRFIMDLNKRKFAE
VVLDLAKRYQVPVKTLAPEQRQELQRQLSLREQLFEVLASTSQFYQHVLRQDIGQQALQYLQKKRFLKTETVEKFALGYAPPG
WETLYHYLVENKSYPAQLVEKAGLIKPRKEGGGYYDAFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFDKSKTLF
ALDVAKDAISKLDQAVVVEGYFDAIALHANGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATERAIGEISNL
AYKGEVRLKILHIPDGKDADEYLKNHSVTDYEQLLVEAPLWLDWQIAQVIQGRDLKQPTDFQLVSREFVKLLQKILNSDTLNY
YISHCAEILSLGDTRLIPLRVENLITQVAPRRTPTPILRPPASPNTHQISHPQPSLLEQAEGLLLRIFLHCPQERQVIIETLGSSNLEFS
VSHYRFLWEKKFAVPMKLAEAESTMNKTVEATQRAFNSIRTGRANASLLDKVQVDYYGSPTPLKSLTNITTPDASTILIQPYDR
SSLNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKELVKLAAKYAEEGRVGIRNIRRDALDSIRKQEKAGEISEDESRDQQDK
LQKITGKYTAKIDELLTEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDSEGAQLGIMAPLEALRLAEEKELDLVLLSDKAD
PPVCRIMDYGKYKFEQEKKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVKQAERFLKDGDKVKATVMFRGREIQHSDLA
ETLLNRMATDLEPFGEIQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIEKISLERNLPRLAVQSSIREALLKGYERYRRAQNL
ERRQFDENYFDNFEVELDIDGEGFRVLSTKTIVEEVTNGDHQISLDEVQQVAPEAQSGDSVVLDVTPDQGEFGRMAAMQTKQV
LAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSFGQPEVEAELPKREQLPNDTYRSNATFKVYLKKVSQGQQ
RGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAVDTLDRDVDPVGACIGARGSRIQVVVNELR
GEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIGKEGQVKKKSLASLSATDISDKRALVRVDFNV
PVDDQGNITDDTRIRAALPTIQDLISKGAKVILASHFGRPKGVDEKLRLTPVAKRLSELLGQEVIKTDDCIGDDVTAQVAALEKG
QVLLLENVRFYKEEEKNDPDFARQLAANADFYVNDAFGTAHRAHASTEGVTKYLSPSVAGYLVEKELQYLQAAIEVPQRPLA
AIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEQDKLELASSLEKKAAERGVTLLLPTDIVAADKFAPDA
DAVTVSIENIPDDRMGLDIGPKSVKLFQDALADCKTVIWNGPMGVFEFDKFAVGTEAIAQTLAEIGKTGATTIIGGGDSVAAVE
KVGLADQMSHISTGGGASLELLEGTVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRDYSVSILKLDPYINVDPG
TMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGGTVQVIPHITNEIKERVIRVAKETN
PAAVITEIGGTVGDIESLPFLEAIRQLRKEVGKQNVLYMHVTLLPWIASAGEMKTKPTQHSVKELRSIGIQPDILVCRCDRPIPVG

LKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQREPDLTHWETMVERMSHPQSPVEIAIVGKYVRLGD
AYLSVVESLRHAAIATYGDLRLRWVNSEILEVEPPDNYLLGVDGIIVPGGFGIRGVDGKISAIEYARNRQIPFLGLCLGMQCSIIE
WARNVEGLVGANSAEFDPKTDYPVINLLPEQQDVIDIGGTMRLGLYPCHVQPNTLAFDLYQEEVIYERHRHRYEFNNLYRNHL
LNSGYVISGTSPDGRLVEIVEYPQHPFFIACQFHPEFQSRPSHPHPLFKGFMEAAISHTHQGKKQLPHGFPQFPMVKKVSRRLQA
LQAKVEERDYAPLEALALLKETATAKFPEAAEAHIRLGIDPKYTDQQLRTTVVLPKGTGQIVRVAVIARGEKVTEATNSGADIA
GSEELIDEIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDIASAISEFKAGKLEFRADRTGIVHVMFGKAS
FSSEDLLVNLKALQETIDRNRMGTRSYRPYTPSTRQVTISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRII
DFKRDKRDITATVIAVEYDPNRNARIALLEYEDGEKRYILHPNGLKVGAKVTAGPQAPFEDGNALPLSNIPLGTNVHNVEMTPG
KGGQIVRAAGATAQLMAKEGNYVTLKLPSGEVRMVRRECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVD
HPHGGGEGRAPIGRSGPVTPWGKPALGAKTRKRKKASSKLIVRRRRKSSKRGRGGRQSMSVGILGTKLGMTQIFDEAGVSIPVT
VIKAGPCTVTQVKTQPTDGYCAIQVGYGEVKPKALNKPKLGHLAKSSAVPVRYLNEYRTDAAGDYALGQEIKADIFSVGQIVD
VIGTSIGRGFAGNQKRNNFGRGPMSHGSKNHRAPGSIGAGTTPGRVYPGKRMAGRLGGSRVTVRKLTVVKVDAERNLILIKGA
IPGKPGGLVNVVPTTKVGNKMVESIVKNWQGEEVGQTSFELRVAKEETASHIVHRALVRQMTNSRQGTASTKTRAEVRGGGR
KPWRQKGTGRARAGSIRSPLWRGGGVIFGPKPREFNIKLNRKERRLALRTAFVSRREDLIVVEEFTDQLQRPKSKELVAALARW
GATADQKTLLILSEIGQSTETISLSARNVENIKVIAADQLNVFDLLHADKIVVTSSALTKIQEVYSAMATTRLKTLYGQTIVPKLT
QQFQYTNVHQVPKVLKVTVNRGLGEAAQNAKALEASLSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAF
LDRLISLALPRIRDFRGVSAKSFDGRGNYTLGVREQLIFPEIEYDRIDQIRGLDISIITTAKTDEEGRALLKEMGMPFRDQMSRIGK
RPITIPAKVQVAIDGTKVVVKGPKGELSRDLPTHVTVSQSGETLLVTRRDDTRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQ
GVGYRAQVQGANLVLNIGYSHQVQIEPPAGVQFAVENNTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRK
AGKTGGKGKKMAKKVVAVIKLALNAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLK
TPPASVLIRKAAKIERGSDQPNKKKVGSITRTQLREIAQTKLPDLNANDIEAAMNIVEGTAKNMGVTVKDMSTATDQILEQLKV
LTLLEAAELVKQIEEAFGVSAAAPAGGMMVMAAPGAAAAEPVEEQTEFNVVLEEVPADKKIAVLKIVREITGLGLKEAKELVE
STPKAVKEGVNKESAEEISKKIAEAGGKVVIKMVVTGKKPSQKLYRRHSGRPGGMKTETFAKLQQRLPERIVEHAVKGMLPKN
SLGRQLFTKLKVYSGSTHPHTAQKPKELIINTIPGENMIQPQTYLNVADNSGARKLMCIRVLGAGNRRYGGVGDRIIAVVKDAQ
PNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKEGNPKGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKF
RKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRRAMTRYIRRGGKIWIRIFPDKPVTMRPAETRMGSGKGNPEF
WVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQPQEQEMNAQEIIRSIEAEQLKSDLPQIYVGDTVRVGVKIKEG
DKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSPRIDNIKIMRRGKVRRAKLYYLRQLSGKATRIKQRFDRALM
TRVKRGNVARNRRNKILKLAKGFRGSHSTLFRTANQQVMKALRSAYRDRKKKKRDFRRLWITRINAASRQQGLSYSQLIGNL
KKANVELNRKMLAQLAVLDPATFAKVAELASSVKGMAHKKGTGSTRNGRDSNAQRLGVKRFGGQVVRAGNILVRQRGTKF
HPGNNVGIGNDDTLFALIDGVVTFERKGKSRKKVSVYPPVTEESVASMNNENYTEPSFLLPDLIEIQRSSFRWFLEEGLIEELNSF
SPITDYTGKLELHFLGHNYKLKEPKYSVEESKRRDSTYGVQMYVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIV

NQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDLVWVRIDKTRKLSIQVLLKALGLSDNEILDALRHPEYFQKTI
EKEGQFSEEEALLELYRKLRPGEPPTVMGGQQLLESRFFDPKRYDLGRVGRYKLNKKLRLSVPDTTRVLTPGDILSAVDYLINL
EYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRERMTVSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNP
LAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEGPNAGLIGSLATHARVNQYGFLETPFRPVENGRVCYEKPA
VYMTADEEDDLRVAPGDIPVDDNGQILGIQVPVRYRQEFSTTTPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQ
RQAVPLLKPERPLVGTGLEAQGARDSGMVIVSRTDGDVVYVDATEIRVRVKEKAALTNRESETIPHKPQEIKYVLSKYQRSNQ
DTCLNQKPLVRIGEKVIAGQVLADGSSTEGGELALGQNVIVAYMPWEGYNYEDAILISERLVQEDVYTSIHIEKFEIEARQTKLG
PEEITREIPNVGEDALRQLDEQGIIRVGAWVESGDILVGKVTPKGESDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDV
RLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKGIISRILPLEDMPYLPDGTPVDIVLNPLGVPSRMNVGQVFE
CLLGWAGHNLGVRFKITPFDEMYGEESSRRIVHGKLWEAREETSRDWVYNPENPGKIMVYDGRTGEPFDRAVTVGIAYMLKL
VHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWALEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRP
GTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLDVEVDLMADQVSRRTPPRPTYESFSRDSLDEDEMPVVSLAQMMESGVHF
GHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLMDDAYNYMRSQAEQGKKFLFVGTKRQAAGIIAQEANRCGSHYINQRWL
GGMLTNWATIKTRADRLKDLERREENGALDLLPKKEASMLRREMSKLQKYLGGIKNMRKVPDVVIIVDQRREYNAVQECQK
LSIPIVSMLDTNCDPDTVDVPIPANDDAIRSIKLIVGKLADAIYEGRHGQLEVEPDDEDYDIPEEDYEYNESEMGQKIHPVGFRLG
ITQEHQSLWFAVPGRYPELLQEDHKLRQYIEQKLGRNAQNNAGLSEIHIERKADQVDLELRTARPGVVVGRGGQGIEALRTGL
QQLLGSHRQVRINVVEVQKVDADAYLIAEYIAQQLERRVSFRRVVRQAIQRAQRAGVQGIKVQVSGRLNGAEIARTEWTREGR
VPLHTLRADIDYSYCTAQTVYGILGIKVWVFKGEIIPGQEDIVSQPVTREREPRRRQQQRRQQFEDRSNEAMATGRRKASKAK
KEETNWQERVIQIRRVSKVVKGGKKLSFRAIVIVGNERGQVGVGVGKASDVIGAVKKGVADGKKHLIEIPITKSNSIPHPIDGVG
GGAKVIMRPAAPGTGVIAGGAVRTVLELAGVRNVLAKQLGSNNPLNNARAAVNALSTLRTFAEVAEDRGIAVENLYIMATVA
ETNSGRALYWGTGRRKSAVAQVRLVPGEGKFVVNGKEGELYFQYNPNYLGVIKAPLETLGLENEYDILVKAKGGGLTGQADS
IRLGVARALCQLDPDNRSPLKIEGYLTRDPRAKERKKYGLHKARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTA
NRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTHRRIIDIHQPSSKTIDALMKLDLPSGVDIEVKLMRQIQVMVSGPGA
GRETAIRALQGAGLEITLIRDVTPIPHNGCRPPKRRRVMARIAGVDLPRDKRVEIGLTYIYGIGLRRSQDILAATDVNPDTRVKDL
TDADLAALRAEIESNYQVEGDLRRLEAMNIKRLVDIGCYRGRRHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGR
SLKKGPFVADHLLSKLEKLNANNEKQVIKTWSRASTILPLMVGHTIAVHNGKQHVPVFVNEQMVGHKLGEFAPTRTYRGHGK
TDKKSGRMSDKNEGYKIISDNRQARYLYEILETYEAGIQLTGTEVKSIRAGKVNLQDGYALLRDGEAWLINAHISPYTASGQYF
NHEPRRTRKLLLHGLEIRKLIGKVEQQGLTLIPLKMYFKRGWVKISIGLCRGKKVHDKREDLKRRQDQRDIQRAMKNYMAEIS
AKLVQDLRQKTGAGMMDCKKALNETQGNIDEAIDWLRKKGIASAGKKSDRVTAEGLVDIYTTPDRSGGVLIEVNCQTDFVAR
NDAFKLLVKNLAKQAVNADNVTSLLAQPYIENTDVTVDEYIKETIATLGENIQVRRFVNFSLEGSPGAIDGYIHTGGRVGVLISI
GVDTETAAKNEEVQSLAKNTAMQVAACPNVEYVSVDKIPDR

>Cylindrospermopsis_raciborskii_DSH_PROT
MQIPRLHPDTVEEVKHRADIVDVISDYVVLRRRGKDFVGLCPFHEEKTPSFTVSPTKQIYYCFGCQASGNAIKFMMDLNKRQFA
EVVLDLAKRYQVPVKTLAPEQRQELQRQLSLREQLFEVLASTSQFYQHVLRQDIGQQALQYLQKKRFLKTETVEKFALGYAPP
GWETLYHYLVENKNYPAQLVEKAGLIKPRKEGGGYYDVFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFDKSKT
LFALDVSKDAISKLDQAVVVEGYFDAIALHANGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATERAIGEIS
NLAYKGEVQLKILHIPDGKDADEYLKNHSVTDYGQLLVDAPLWLDWQIAQVIQGRDLRQPTDFQLVSREFVKLLQKILNSDTL
NYYISHCAEILSLGDTRLIPLRVENLITQVAPRRTPTPRPPQPDSTTSPNTHQISHPQPSLLEQAEGLLLRIFLHCPQERQVIIETLGS
TNLEFSVSHHRFLWEKSLQFPSQTLDLISQLQNLYLETQNDLGPVQHIFQLNEKNKQEILLRTSQLVQAAIACMEKVFRENRYRH
FLELWQKTDPSTDPDQYSLYAQTIYADKMRIQELSKQRQLSIADLINMKLAEAESTMNKTVEATQRAFNSIRTGRANASLLDKV
QVDYYGSPTSLKSLANITTPDATTILIQPYDRTSLNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKELVKLAAKYAEEGRVG
IRNIRRDALDSIRKQEKAGEVSEDESRDQQDKLQKITSKYTAKIDELLAEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDS
EGAQLGIMAPLEALRLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVR
VKQAERFLKDGDKVKATVMFRGREIQHSDLAETLLNRMATDLEPFGEVQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIEK
ISLERNLPRLAVQSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIDGEGFRVLSTKTIVEEVTNGDHQISLDEVQQVA
PEAQSGDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSFGQPEVE
AELPKREQLPNDTYRSNATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRT
KIAVDTLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLA
IGKEGQNVRLAARLTGWKIDIKDQAKYDYGAEDAKFAAVRANYQEESNQLDNQFEVMEEEYEDDPDAGEDDFNSMEEENMS
KKSLASLSAADISDKRALVRVDFNVPVDNQGNITDDTRIRAALPTIQDLISKGAKVILASHFGRPKGVDEKLRLTPVAKRLSELL
GQEVIKTDDCIGDDVTAQVAALEKGQVLLLENVRFYKEEEKNNPEFARQLAANADFYVNDAFGTAHRAHASTEGVTKYLSPS
VAGYLVEKELQYLQGAIEVPQRPLVAIIGGSKVSSKITVIETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEDDKLVLASSLEE
KAAERGVTLLLPTDIVAADKFAPDADCRTVSIDHIPDDRMGLDIGPDSVKVFQAALADCKTVIWNGPMGVFEFDKFAVGTEAI
AQTLAEISKTGATTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGKVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAAS
LGRLLKSRDYSVSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDY
NGGTVQVIPHITNEIKERVIRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGKQNVLYMHVTLLPWIASAGEMKTKPT
QHSVKELRSIGIQPDILVCRCDRPIPVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQREPDLTHWE
TMVERMSHPQSPVEIAIVGKYVRLGDAYLSVVESLRHAAIATYGDLRLRWVNSEILEVPPDNYLLGVDGIIVPGGFGIRGVDG
KISAIEYARNQQIPFLGLCLGMQCSIIEWARNVEGLVGANSAEFDPQTDYPVINLLPEQQDVIDLGGTMRLGLYPCHVQPNTLAF
DLYQEEVIYERHRHRYEFNNLYRNHLLNSGYVISGTSPDGRLVEIVEYPQHPFFIACQFHPEFQSRPSHPHPLFKGFMEAAISHTH
QGSTPMVKKVSRRLQALQAKVEERDYTPLEALALLKETATAKFAEAAEAHIRLGIDPKYTDQQLRTTVVLPKGTGQIVRRVAVI
ARGEKVTEATNAGADIAGSEELIDEIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDIASAISEFKAGKLE
FRADRTGIVHVMFGKASFSSEDLLVNLKALQETIDRNRPSGAKGRYWRTFYISSTMGPSIKIDINALRDFKTTDVAMGTRSYRPY

TPSTRQVTISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRDITATVIAVEYDPNRNARIALVE
YEDGEKRYILHPNGLKVGAKITAGPQAPFEDGNALPLSNIPLGTNVHNVEMTPGKGGQIVRAAGATAQLMAKEGNYVTLKLPS
GEVRMVRRECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPALGAK
TRKRKKASSKLIVRRRRKSSKRGRGGRQSMSVGILGTKLGMTQIFDEAGVSIPVTVIQAGPCTVTQVKTQPTDGYCAIQVGYGE
VKPKALNKPKLGHLAKSSAGPVRYLNEYRTDAAGDYALGQEIKADIFSVGQIVDVIGTSIGRGFAGNQKRNNFGRGPMSHGSK
NHRAPGSIGAGTTPGRVYPGKRMAGRLGGSRVTVRKLTVVKVDAERNLILIKGAIPGKPGGLVNVVPTTKVGNKMVESTVKN
WQGEEVGQTSFELRVAKEETASHIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIF
GPKPRDFNIKLNRKERRLALRTAFVSRREDLIVVEEFTDQLQRPKSKELVAALARWGATADQKTLLILSEIGQNTETISLSARNV
ENIKVIAADQLNVFDLLHADKIVVTSSALTKIQEVYSAMATTRLKTLYGQTIVPKLTQQFQYTNVHQVPKVLKVTVNRGLGEA
AQNAKALEASLSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSAKSFDGRGN
YTLGVREQLIFPEIEYDRIDQIRGLDISIITTAKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGTKVVVKGPKGELS
RDLPAHVTVSQSGETLLVTRRDDTRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGANLVLNIGYSHQVQIE
PPAGVQFVVENNTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRKAGKTGGKGKKMAKKVVAVIKLALNA
GKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSDQPNKKKVGS
ITRTQLKEIAQTKLPDLNANDIEAAMNIVEGTAKNMGVTIKDMSTATDQILEQLKSLTLLEAAELVKQIEEAFGVSAAAPAGGM
MMMAAPGGAAAAEVVEEQTEFDVILQEVPADKKIAVLKIVREITGLGLKEAKELVESTPKAVKEGVNKEAAEDISKKITEAGG
KVAIKMSSKTYLPPEEEIKRDWYVVDAADKRLGRLASEIAMVLRGKRKAEYTPHLDTGDFVVVINAEKVVVTGKKQSQKLYR
RHSGRPGGMKTETFAKLQQRLPERIVEHAVKGMLPKNSLGRQLFTKLKVYSGATHPHTAQKPKELIINTIPGENMIQPQTYLNV
ADNSGARKLMCIRVLGAGNRRYGGVGDRIIAVVKDAQPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKEGNP
KGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRRAM
TRYIRRGGKIWIRIFPDKPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQPQE
QEMNAQEIIRSIEAEQLKSDLPQIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSPRI
DNIKIMRRGKVRRAKLYYLRQLSGKATRIKQRFDRALMTRVKRGNVARNRRNKILKLAKGFRGSHSTLFRTANQQVMKALRS
AYRDRKKKKRDFRRLWITRINAASRQQGLSYSQLIGNLKKANVELNRKMLAQLAVLDPTTFAKVAELASSVKGNMAHKKGT
GSTRNGRDSNAQRLGVKRFGGQVVRAGNILVRQRGTKFHPGNNVGIGNDDTLFALIDGVVTFERKGKSRKKVSVYPRVTEEA
VASMNNENYMEPSFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGHNYKLKEPKYSVEESKRRDSTYGVQMY
VPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDL
VWVRIDKTRKLSIQVLLKALGLLDNEILDALRHPEYFQKTIEKEGQFSEEEALLELYRKLRPGEPPTVMGGQQLLESRFFDPKRY
DLGRVGRYKLNKKLRLSVPDTTRVLTPGDILSAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRERMT
VSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEG
PNAGLIGSLATHARVNQYGFLETPFRPVENGRVCYEKPAVYMTADEEDDLRVAPGDIPVDDNGQILGIQVPVRYRQEFSTTTPE
QVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSGMVIVSRTDGDVVYVDAT

EIRVRVKEKAALTNRESESIPHKPQEIKYVLSKYQRSNQDTCLNQKPLVRIGEKVIAGQVLADGSSTEGGELALGQNVIVAYMP
WEGYNYEDAILISERLVQEDVYTSIHIEKFEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRVGAWVESGDILVGKVTPKGE
SDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRIVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKG
IISRILPLEDMPYLPDGTPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGEESSRRIVHGKLWEAREETSK
DWVYNPENPGKIMVYDGRTGEPFDRAVTVGIAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWALE
AFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLDVEVDLMADQ
VSRRTPPRPTYESFSRDSLDEDEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLMDDAYNYMRS
QAEQGKKFLFVGTKRQAAGIIAQEANRCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREENGALDLLPKKEASMLRREM
SKLQKYLGGIKNMRKVPDVVIIVDQRREYNAVQECQKLSIPIVSMLDTNCDPDTVDIPIPANDDAIRSIKLIVGKLADAIYEGRHG
QLEVESDYEEYESAEEDYEYDESEFVDSFSDDDDEEMGQKIHPVGFRLGITQEHQSLWFAVPGRYPELLQEDHKLRQYIEQKLG
RNAQNNAGLSEIHIERKADQVDLELRTARPGVVVGRGGQGIEALRTGLQQLLGSHRQVRINVVEVQKVDADAYLIAEYIAQQL
ERRVSFRRVVRQAIQRAQRAGVQGIKVQVSGRLNGAEIARTEWTREGRVPLHTLRADIDYSYCTAQTVYGILGIKVWVFKGEII
PGQEDIVSQPVTREREPRRRQQQRRRQQFEDRSNEAMATGRRKASKAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAIVIVG
NERGQVGVGVGKASDVIGAVKKGVADGKKHLIEIPITKSNSIPHPIDGVGGGAKVIMRPAAPGTGVIAGGAVRTVLELAGVRN
VLAKQLGSNNPLNNARAAVNALSTLRTFAEVAEDRGIAVENLYIMATVAETNSGRALYWGTGRRKSAVAQVRLVPGEGKFV
VNGKEGELYFQYNPNYLGVIKAPLETLGLENEYDILVKAKGGGLTGQADSIRLGVARALCQLDPDNRSPLKIEGYLTRDPRAKE
RKKYGLHKARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSRE
HFETRTHRRIIDIHQPSSKTIDALMKLDLPSGVDIEVKLMARQPTKKTGSKKQKKNVPNGVAYIQSTFNNSIVTITDQNGDVISW
ASAGSSGFKGAKKGTPFAAQTAAESAGRRAIDQGMRQIQVMVSGPGAGRETAIRALQGAGLEITLIRDVTPIPHNGCRPPKRRR
VMARIAGVDLPRDKRVEIGLTYIYGIGLRRSQDILAATDVNPDTRVKDLTDADLAALRAEIESNYQVEGDLRRLEAMNIKRLVD
IGCYRGRRHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLSKIEKLNANNEKQVIKTWSRAST
ILPLMVGHTIAVHNGKQHVPVFVNEQMVGHKLGEFAPTRSYRGHGKTDKKSGRMSDKNEGYKIISDNRQARYLYEILETYEAG
IQLTGTEVKSIRAGKVNLQDGYALLRDGEAWLINAHISPYTASGQYFNHEPRRTRKLLLHGLEIRKLIGKVEQQGLTLIPLKMYF
KRGWVKISIGLCRGKKVHDKREDLKRRQDQRDIQRAMKNYMAEISAKLVQDLRQKTGAGMMDCKKALNETQGNIDEAIDWL
RKKGIASAGKKSDRVTAEGLVDIYTTPDKSGGVIIEVNCQTDFVARNDAFKLLVKNLAKQAVNADNVASLLDQPYIEKTDVTV
DEYIKETIATLGENIQVRRFVNFSLEGAPGAIDGYIHTGGRVGVLVSIGVDTETAAKNEELQSLAKNTAMQVAACPNVEYVSVD
KIPDQVVEKEKEIEMGKEDLGNKPANIKEKIVQGRIDKRLKEMTLLDQPYIRDQNISVAELIKQVESKVSEPIKVHQFVRYILGEG
IEKQESNFAEEVAAQIGAK

>Cylindrospermopsis_raciborskii_GIHE_2018
MQIPRLHPDTVEEVKHRADIVDVISDYVVLRRRGKDFVGLCPFHEEKTPSFTVSPTKQIYYCFGCQASGNAIKFMMDLNKRQFA
EVVLDLAKRYQVPVKTLAPEQRQELQRQLSLREQLFEVLASTSQFYQHVLRQDIGQQALQYLQKKRFLKTETVEKFALGYAPP
GWETLYHYLVENKNYPAQLVEKAGLIKPRKEGGGYYDVFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFDKSKT
LFALDVSKDAISKLDQAVVVEGYFDAIALHANGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATERAIGEIS
NLAYKGEVQLKILHIPDGKDADEYLKNHSVTDYGQLLVDAPLWLDWQIAQVIQGRDLRQPTDFQLVSREFVKLLQKILNSDTL
NYYISHCAEILSLGDTRLIPLRVENLITQVAPRRTPTPRPPQPDSTTSPNTHQISHPQPSLLEQAEGLLLRIFLHCPQERQVIIETLGS
TNLEFSVSHHRFLWEKSLQFPSQSLDLISQLQNLYLETQNDLGPVQHIFQLNEKNKQEILLRTSQLVQAAIACMEKVFRENRYRH
FLELWQKTDPSTDPDQYSLYAQTIYADKMRIQELSKQRQLSIADLINMKLAEAESTMNKTVEATQRAFNSIRTGRANASLLDKV
QVDYYGSPTSLKSLANITTPDATTILIQPYDRTSLNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKELVKLAAKYAEEGRVG
IRNIRRDALDSIRKQEKAGEVSEDESRDQQDKLQKITSKYTAKIDELLAEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDS
EGAQLGIMAPLEALRLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVR
VKQAERFLKDGDKVKATVMFRGREIQHSDLAETLLNRMATDLEPFGEVQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIEK
ISLERNLPRLAVQSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIDGEGFRVLSTKTIVEEVTNGDHQISLDEVQQVA
PEAQSGDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSFGQPEVE
AELPKREQLPNDTYRSNATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRT
KIAVDTLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLA
IGKEGQNVRLAARLTGWKIDIKDQAKYDYGAEDAKFAAVRANYQEESNQLDNQFEVMEEEYEDDPDAGEDDFNSMEEENMS
KKSLASLSAADISDKRALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLISKGAKVILASHFGRPKGVDEKLRLTPVAKRLSELL
GQEVIKTDDCIGDDVTAQVAALEKGQVLLLENVRFYKEEENNDPEFARQLAANADFYVNDAFGTAHRAHASTEGVTKYLSPS
VAGYLVEKELQYLQGAIEVPQRPLVAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEQDKLGLASSLEK
KAAERGVTLLLPTDIVAADKFGPDADAVTVSIDHIPDDRMGLDIGPDSVKVFQAALADCKTVIWNGPMGVFEFDKFAVGTEAI
AQTLAEISKTGATTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGKVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAAS
LGRLLKSRDYSVSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDY
NGGTVQVIPHITNEIKERVIRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGKQNVLYMHVTLLPWIASAGEMKTKPT
QHSVKELRSIGIQPDILVCRCDRPIPVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQREPDLTHWE
TMVERMSHPQSPVEIAIVGKYVRLGDAYLSVVESLRHAAIATYGDLRLRWVNSEILEVPPDNYLLGVDGIIVPGGFGIRGVDG
KISAIEYARNQQIPFLGLCLGMQCSIIEWARNVEGLVGANSAEFDPQTDYPVINLLPEQQDVIDLGGTMRLGLYPCHVQPNTLAF
DLYQEEVIYERHRHRYEFNNLYRNHLLNSGYVISGTSPDGRLVEIVEYPQHPFFIACQFHPEFQSRPSHPHPLFKGFMEAAISHTH
QGSTPMVKKVSRRLQALQAKVEERDYTPLEALALLKETATAKFAEAAEAHIRLGIDPKYTDQQLRTTVVLPKGTGQIVRVAVI
ARGEKVTEATNAGADIAGSEELIDEIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDIASAISEFKAGKLE
FRADRTGIVHVMFGKASFSSEDLLVNLKALQETIDRNRPSGAKGRYWRTFYISSTMGPSIKIDINALRDFKTTDVAMGTRSYRPY

TPSTRQVTISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRDITATVIAVEYDPNRNARIALVE
YEDGEKRYILHPNGLKVGAKITAGPQAPFEDGNALPLSNIPLGTNVHNVEMTPGKGGQIVRAAGATAQLMAKEGNYVTLKLPS
GEVRMVRRECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPALGAK
TRKRKKASSKLIVRRRRKSSKRGRGGRQSMSVGILGTKLGMTQIFDEAGVSIPVTVIQAGPCTVTQVKTQPTDGYCAIQVGYGE
VKPKALNKPKLGHLAKSSAGPVRYLNEYRTDAAGDYALGQEIKADIFSVGQIVDVIGTSIGRGFAGNQKRNNFGRGPMSHGSK
NHRAPGSIGAGTTPGRVYPGKRMAGRLGGSRVTVRKLTVVKVDAERNLILIKGAIPGKPGGLVNVVPTTKVGNKMVESTVKN
WQGEEVGQTSFELRVAKEETASHIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIF
GPKPRDFNIKLNRKERRLALRTAFVSRREDLIVVEEFTDQLQRPKSKELVAALARWGATADQKTLLILSEIGQNTETISLSARNV
ENIKVIAADQLNVFDLLHADKIVVTSSALTKIQEVYSAMATTRLKTLYGQTIVPKLTQQFQYTNVHQVPKVLKVTVNRGLGEA
AQNAKALEASLSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSAKSFDGRGN
YTLGVREQLIFPEIEYDRIDQIRGLDISIITTAKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGTKVVVKGPKGELS
RDLPAHVTVSQSGETLLVTRRDDTRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGANLVLNIGYSHQVQIE
PPAGVQFVVENNTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRKAGKTGGKGKKMAKKLVAVIKLALNA
GKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSDQPNKKKVGS
ITRTQLKEIAQTKLPDLNANDIEAAMNIVEGTAKNMGVTIKDMSTATDQILEQLKSLTLLEAAELVKQIEEAFGVSAAAPAGGM
MMMAAPGGAAAAEVVEEQTEFDVILQEVPADKKIAVLKIVREITGLGLKEAKELVESTPKAVKEGVNKEAAEDISKKITEAGG
KVAIKMSSKTYLPPEEEIKRDWYVVDAADKRLGRLASEIAMVLRGKRKAEYTPHLDTGDFVVVINAEKVVVTGKKQSQKLYR
RHSGRPGGMKTETFAKLQQRLPERIVEHAVKGMLPKNSLGRQLFTKLKVYSGATHPHTAQKPKELIINTIPGENMIQPQTYLNV
ADNSGARKLMCIRVLGAGNRRYGGVGDRIIAVVKDAQPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKEGNP
KGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRRAM
TRYIRRGGKIWIRIFPDKPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQPQE
QEMNAQEIIRSIEAEQLKSDLPQIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSPRI
DNIKIMRRGKVRRAKLYYLRQLSGKATRIKQRFDRALMTRVKRGNVARNRRNKILKLAKGFRGSHSTLFRTANQQVMKALRS
AYRDRKKKKRDFRRLWITRINAASRQQGLSYSQLIGNLKKANVELNRKMLAQLAVLDPTTFAKVAELASSVKGNMAHKKGT
GSTRNGRDSNAQRLGVKRFGGQVVRAGNILVRQRGTKFHPGNNVGIGNDDTLFALIDGVVTFERKGKSRKKVSVYPRVTEEA
VASMNNENYMEPSFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGHNYKLKEPKYSVEESKRRDSTYGVQMY
VPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDL
VWVRIDKTRKLSIQVLLKALGLLDNEILDALRHPEYFQKTIEKEGQFSEEEALLELYRKLRPGEPPTVMGGQQLLESRFFDPKRY
DLGRVGRYKLNKKLRLSVPDTTRVLTPGDILSAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRERMT
VSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEG
PNAGLIGSLATHARVNQYGFLETPFRPVENGRVCYEKPAVYMTADEEDDLRVAPGDIPVDDNGQILGIQVPVRYRQEFSTTTPE
QVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSGMVIVSRTDGDVVYVDAT

EIRVRVKEKAALTNRESESIPHKPQEIKYVLSKYQRSNQDTCLNQKPLVRIGEKVIAGQVLADGSSTEGGELALGQNVIVAYMP
WEGYNYEDAILISERLVQEDVYTSIHIEKFEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRVGAWVESGDILVGKVTPKGE
SDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRIVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKG
IISRILPLEDMPYLPDGTPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGEESSRRIVHGKLWEAREETSK
DWVYNPENPGKIMVYDGRTGEPFDRAVTVGIAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWALE
AFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLDVEVDLMADQ
VSRRTPPRPTYESFSRDSLDEDEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLMDDAYNYMRS
QAEQGKKFLFVGTKRQAAGIIAQEANRCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREENGALDLLPKKEASMLRREM
SKLQKYLGGIKNMRKVPDVVIIVDQRREYNAVQECQKLSIPIVSMLDTNCDPDTVDIPIPANDDAIRSIKLIVGKLADAIYEGRHG
QLEVESDYEEYESAEEDYEYDESEFVDSFSDDDDEEMGQKIHPVGFRLGITQEHQSLWFAVPGRYPELLQEDHKLRQYIEQKLG
RNAQNNAGLSEIHIERKADQVDLELRTARPGVVVGRGGQGIEALRTGLQQLLGSHRQVRINVVEVQKVDADAYLIAEYIAQQL
ERRVSFRRVVRQAIQRAQRAGVQGIKVQVSGRLNGAEIARTEWTREGRVPLHTLRADIDYSYCTAQTVYGILGIKVWVFKGEII
PGQEDIVSQPVTREREPRRRQQQRRRQQFEDRSNEAMATGRRKASKAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAIVIVG
NERGQVGVGVGKASDVIGAVKKGVADGKKHLIEIPITKSNSIPHPIDGVGGGAKVIMRPAAPGTGVIAGGAVRTVLELAGVRN
VLAKQLGSNNPLNNARAAVNALSTLRTFAEVAEDRGIAVENLYIMATVAETNSGRALYWGTGRRKSAVAQVRLVPGEGKFV
VNGKEGELYFQYNPNYLGVIKAPLETLGLENEYDILVKAKGGGLTGQADSIRLGVARALCQLDPDNRSPLKIEGYLTRDPRAKE
RKKYGLHKARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSRE
HFETRTHRRIIDIHQPSSKTIDALMKLDLPSGVDIEVKLMARQPTKKTGSKKQKKNVPNGVAYIQSTFNNSIVTITDQNGDVISW
ASAGSSGFKGAKKGTPFAAQTAAESAGRRAIDQGMRQIQVMVSGPGAGRETAIRALQGAGLEITLIRDVTPIPHNGCRPPKRRR
VMARIAGVDLPRDKRVEIGLTYIYGIGLRRSQDILAATDVNPDTRVKDLTDADLAALRAEIESNYQVEGDLRRLEAMNIKRLVD
IGCYRGRRHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLSKIEKLNANNEKQVIKTWSRAST
ILPLMVGHTIAVHNGKQHVPVFVNEQMVGHKLGEFAPTRSYRGHGKTDKKSGRMSDKNEGYKIISDNRQARYLYEILETYEAG
IQLTGTEVKSIRAGKVNLQDGYALLRDGEAWLINAHISPYTASGQYFNHEPRRTRKLLLHGLEIRKLIGKVEQQGLTLIPLKMYF
KRGWVKISIGLCRGKKVHDKREDLKRRQDQRDIQRAMKNYMAEISAKLVQDLRQKTGAGMMDCKKALNETQGNIDEAIDWL
RKKGIASAGKKSDRVTAEGLVDIYTTPDKSGGVIIEVNCQTDFVARNDAFKLLVKNLAKQAVNADNVASLLDQPYIEKTDVTV
DEYIKETIATLGENIQVRRFVNFSLEGAPGAIDGYIHTGGRVGVLVSIGVDTETAAKNEELQSLAKNTAMQVAACPNVEYVSVD
KIPDQVVEKEKEIEMGKEDLGNKPANIKEKIVQGRIDKRLKEMTLLDQPYIRDQNISVAELIKQVESKVSEPIKVHQFVRYILGEG
IEKQESNFAEEVAAQIGAK

>Cylindrospermopsis_raciborskii_isolate_1523720_PROT
MQIPRLHPDTVEEVKHRADIVDVISDYVVLRRRGKDFVGLCPFHEEKTPSFTVSPTKQIYYCFGCQASGNAIKFMMDLNKRQFA
EVVLDLAKRYQVPVKTLAPEQRQELQRQLSLREQLFEVLASTSQFYQHVLRQDIGQQALQYLQKKRFLKTETVEKFALGYAPP
GWETLYHYLVENKNYPAQLVEKAGLIKPRKEGGGYYDVFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFDKSKT
LFALDVSKDAISKLDQAVVVEGYFDAIALHANGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATERAIGEIS
NLAYKGEVQLKILHIPDGKDADEYLKNHSVTDYGQLLVDAPLWLDWQIAQVIQGRDLRQPTDFQLVSREFVKLLQKILNSDTL
NYYISHCAEILSLGDTRLIPLRVENLITQVAPRRTPTPRPPQPDSTTSPNTHPISHPQPSLLEQAEGLLLRIFLHCPQERQVIIETLGSS
NLEFSVSHHRFLWEKSLQFPSQTLDLISQLQNLYLETQNDLGPVQHIFQLNEKNKQEILLRTSQLVQAAIACMEKVFRENRYRHF
LELWQKTDPSTDPDQYSLYAQTIYADKMRIQELSKQRQLSIADLINMKLAEAESTMNKTVEATQRAFNSIRTGRANASLLDKV
QVDYYGSPTSLKSLANITTPDATTILIQPYDRTSLNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKELVKLAAKYAEEGRVG
IRNIRRDALDSIRKQEKAGEVSEDESRDQQDKLQKITSKYTAKIDELLAEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDS
EGAQLGIMAPLEALRLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVR
VKQAERFLKDGDKVKATVMFRGREIQHSDLAETLLNRMATDLEPFGEVQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIEK
ISLERNLPRLAVQSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIDGEGFRVLSTKTIVEEVTNGDHQISLDEVQQVA
PEAQSGDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSFGQPEVE
AELPKREQLPNDTYRSNATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRT
KIAVDTLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLA
IGKEGQNVRLAARLTGWKIDIKDQAKYDYGAEDAKFAAVRANYQEESNQLDNQFEVIEEEYEDDPDAGEDDFNSMEEENMSK
KSLASLSAADISGKRALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLISKGAKVILASHFGRPKGVDEKLRLTPVAKRLSELLG
QEVIKTDDCIGDDVTTQVAALEKGQVLLLENVRFYKEEEKNDPEFARQLAANADFYVNDAFGTAHRAHASTEGVTKYLSPSV
AGYLVEKELQYLQGAIEVPQRPLVAIIGGSKVSSKITVIETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEDDKLVLASSLEKK
AAERGVALLLPTDIVAADRFAPDADAVTVSIDSIPDDRMGLDIGPDSVKVFQAALADCKTVIWNGPMGVFEFDKFAVGTEAIA
QTLAEISKTGATTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGKVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASL
GRLLKSRDYSVSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYN
GGTVQVIPHITNEIKERVIRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGKQNVLYMHVTLLPWIASAGEMKTKPTQ
HSVKELRSIGIQPDILVCRCDRPIPVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQREPDLTHWET
MVERMSHPQSPVEIAIVGKYVRLGDAYLSVVESLRHAAIATYGDLRLRWVNSEILEVEPPDNYLLGVDGIIVPGGFGIRGVDGKI
SAIEYARNRQIPFLGLCLGMQCSIIEWARNVEGLVGANSAEFNPQTDYPVINLLPEQQDVIDLGGTMRLGLYPCHVQPNTLAFD
LYQEEVIYERHRHRYEFNNLYRNHLLNSGYVISGTSPDGRLVEIVEYPQHPFFIACQFHPEFQSRPSHPHPLFKGFMEAAISHTHQ
GKKPNYPLRVSSVPMVKKVSRRLQALQAKVEERDYTPLEALALLKETATAKFAEAAEAHIRLGIDPKYTDQQLRTTVVLPKGT
GQIVRVAVIARGEKVTEATNAGADIAGSEELIDEIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDIASAI
SEFKAGKLEFRADRTGIVHVMFGKASFSSEDLLVNLKALQETIDRNRPSGAKGRYWRTFYISSTMGPSIKIDINALRDFKTTDVA

MGTRSYRPYTPSTRQVTISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRDITATVIAVEYDPN
RNARIALVEYEDGEKRYILHPNGLKVGAKITAGPQAPFEDGNALPLSNIPLGTNVHNVEMTPGKGGQIVRAAGATAQLMAKEG
NYVTLKLPSGEVRMVRRECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPW
GKPALGAKTRKRKKASSKLIVRRRRKSSKRGRGGRQSMSVGILGTKLGMTQIFDEAGVSIPVTVIQAGPCTVTQVKTQPTDGYC
AIQVGYGEVKPKALNKPKLGHLAKSSAGPVRYLNEYRTDAAGDYALGQEIKADIFSVGQIVDVIGTSIGRGFAGNQKRNNFGR
GPMSHGSKNHRAPGSIGAGTTPGRVYPGKRMAGRLGGSRVTVRKLTVVKVDAERNLILIKGAIPGKPGGLVNVVPTTKVGNK
MVESTVKNWQGEEVGQTSFELRVAKEETASHIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPL
WRGGGVIFGPKPRDFNIKLNRKERRLALRTAFVSRREDLIVVEEFTDQLQRPKSKELVAALARWGATADQKTLLILSEIGQNTE
TISLSARNVENIKVIAADQLNVFDLLHADKIVVTSSALTKIQEVYSAMATTRLKTLYGQTIVPKLTQQFQYTNVHQVPKVLKVT
VNRGLGEAAQNAKALEASLSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSA
KSFDGRGNYTLGVREQLIFPEIEYDRIDQIRGLDISIITTAKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGTKVVV
KGPKGELSRDLPAHVTVSQSGETLLVTRRDDTRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGANLVLNIG
YSHQVQIEPPAGVQFVVENNTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRKAGKTGGKGKKMAKKVVA
VIKLALNAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSDQ
PNKKKVGSITRTQLKEIAQTKLPDLNANDIEAAMNIVEGTAKNMGVTIKDMSTATDQILEQLKSLTLLEAAELVKQIEEAFGVS
AAAPAGGMMMMAAPGGAAAAEVVEEKTEFDVILEEVPADKKIAVLKIVREITGLGLKEAKELVESTPKAVKEGVNKEAAEDI
SKKITEAGGKVAIKMSSKTYLPPEEEIKRDWYVVDAADKRLGRLASEIAMVLRGKRKAEYTPHLDTGDFVVVINAEKVVVTGK
KQSQKLYRRHSGRPGGMKTETFAKLQQRLPERIVEHAVKGMLPKNSLGRQLFTKLKVYSGATHPHTAQKPKELIINTIPGENMI
QPQTYLNVADNSGARKLMCIRVLGAGNRRYGGVGDRIIAVVKDAQPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAA
VIINKEGNPKGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQ
IEASRRAMTRYIRRGGKIWIRIFPDKPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFI
VRSQPQEQEMNAQEIIRSIEAEQLKSDLPQIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERV
FLLHSPRIDNIKIMRRGKVRRAKLYYLRQLSGKATRIKQRFDRALMTRVKRGNVARNRRNKILKLAKGFRGSHSTLFRTANQQ
VMKALRSAYRDRKKKKRDFRRLWITRINAASRQQGLSYSQLIGNLKKANVELNRKMLAQLAVLDPTTFAKVAELASSVKGN
MAHKKGTGSTRNGRDSNAQRLGVKRFGGQVVRAGNILVRQRGTKFHPGNNVGIGNDDTLFALIDGVVTFERKGKSRKKVSV
YPRVTEEAVASMNNENYMEPSFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGHNYKLKEPKYSVEESKRRDS
TYGVQMYVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLK
FETDRNDLVWVRIDKTRKLSIQVLLKALGLLDNEILDALRHPEYFQKTIEKEGQFSEEEALLELYRKLRPGEPPTVMGGQQLLES
RFFDPKRYDLGRVGRYKLNKKLRLSVPDTTRVLTPGDILSAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRL
ERIIRERMTVSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYG
RICPIETPEGPNAGLIGSLATHARVNQYGFLETPFRPVENGRVCYEKPAVYMTADEEDDLRVAPGDIPVDDNGQILGIQVPVRYR
QEFSTTTPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSGMVIVSRTDG

DVVYVDATEIRVRVKEKAALTNRESESIPHKPQEIKYVLSKYQRSNQDTCLNQKPLVRIGEKVIAGQVLADGSSTEGGELALGQ
NVIVAYMPWEGYNYEDAILISERLVQEDVYTSIHIEKFEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRVGAWVESGDILV
GKVTPKGESDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKM
AGRHGNKGIISRILPLEDMPYLPDGTPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGEESSRRIVHGKL
WEAREETSKDWVYNPENPGKIMVYDGRTGEPFDRAVTVGIAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRF
GEMEVWALEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLD
VEVDLMADQVSRRTPPRPTYESFSRDSLDEDEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLM
DDAYNYMRSQAEQGKKFLFVGTKRQAAGIIAQEANRCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREENGALDLLPK
KEASMLRREMSKLQKYLGGIKNMRKVPDVVIIVDQRREYNAVQECQKLSIPIVSMLDTNCDPDTVDIPIPANDDAIRSIKLIVGK
LADAIYEGRHGQLEVESDYEEYESAEEDYEYDESEFVDSFSDDDDEEMGQKIHPVGFRLGITQEHQSLWFAVPGRYPELLQEDH
KLRQYIEQKLGRNAQNNAGLSEIHIERKADQVDLELRTARPGVVVGRGGQGIEALRTGLQQLLGSHRQVRINVVEVQKVDAD
AYLIAEYIAQQLERRVSFRRVVRQAIQRAQRAGVQGIKVQVSGRLNGAEIARTEWTREGRVPLHTLRADIDYSYCTAQTVYGIL
GIKVWVFKGEIIPGQEDIVSQPVTREREPRRRQQQRRRQQFEDRSNEAMATGRRKASKAKKEETNWQERVIQIRRVSKVVKGG
KKLSFRAIVIVGNERGQVGVGVGKASDVIGAVKKGVADGKKHLIEIPITKSNSIPHPIDGVGGGAKVIMRPAAPGTGVIAGGAV
RTVLELAGVRNVLAKQLGSNNPLNNARAAVNALSTLRTFAEVAEDRGIAVENLYIMATVAETNSGRALYWGTGRRKSAVAQ
VRLVPGEGKFVVNGKEGELYFQYNPNYLGVIKAPLETLGLENEYDILVKAKGGGLTGQADSIRLGVARALCQLDPDNRSPLKIE
GYLTRDPRAKERKKYGLHKARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVL
RSPHVDKDSREHFETRTHRRIIDIHQPSSKTIDALMKLDLPSGVDIEVKLMARQPTKKTGSKKQKKNVPNGVAYIQSTFNNSIVTI
TDQNGDVISWASAGSSGFKGAKKGTPFAAQTAAESAGRRAIDQGMRQIQVMVSGPGAGRETAIRALQGAGLEITLIRDVTPIPH
NGCRPPKRRRVMARIAGVDLPRDKRVEIGLTYIYGIGLRRSQDILAATDVNPDTRVKDLTDADLAALRAEIESNYQVEGDLRRL
EAMNIKRLVDIGCYRGRRHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLSKIEKLNANNEK
QVIKTWSRASTILPLMVGHTIAVHNGKQHVPVFVNEQMVGHKLGEFAPTRSYRGHGKTDKKSGRMSDKNEGYKIISDNRQAR
YLYEILETYEAGIQLTGTEVKSIRAGKVNLQDGYALLRDGEAWLINAHISPYTASGQYFNHEPRRTRKLLLHGLEIRKLIGKVEQ
QGLTLIPLKMYFKRGWVKISIGLCRGKKVHDKREDLKRRQDQRDIQRAMKNYMAEISAKLVQDLRQKTGAGMMDCKKALNE
TQGNIDEAIDWLRKKGIASAGKKSDRVTAEGLVDIYTTPDKSGGVIIEVNCQTDFVARNDAFKLLVKNLAKQAVNADNVASLL
AQPYIEKTDVTVDEYIKETIATLGENIQVRRFVNFSLEGAPGAIDGYIHTGGRVGVLVSIGVDTETAAKNEELQSLAKNTAMQV
AACPNVEYVSVDKIPDQVVEKEKEIEMGKEDLGNKPANIKEKIVQGRIDKRLKEMTLLDQPYIRDQNISVAELIKQVESKVSEPI
KVHQFVRYILGEGIEKQESNFAEEVAAQIGAK

>Cylindrospermopsis_raciborskii_ITEP_A1
MQIPRLHPDTVEEVKHRADIVDVISDYVVLRRRGKDFVGLCPFHEEKTPSFTVSPNKQIYYCFGCQASGNAIRFIMDLNKRKFAE
VVLDLAKRYQVPVKTLAPEQRQELQRQLSLREQLFEVLASTSQFYQHVLRQDIGQQALQYLQKKRFLKTETVEKFALGYAPPG
WETLYHYLVENKSYPAQLVEKAGLIKPRKEGGGYYDAFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFDKSKTLF
ALDVAKDAISKLDQAVVVEGYFDAIALHANGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATERAIGEISNL
AYKGEVRLKILHIPDGKDADEYLKNHSVTDYEQLLVEAPLWLDWQIAQVIQGRDLKQPTDFQLVSREFVKLLQKILNSDTLNY
YISHCAEILSLGDTRLIPLRVENLITQVAPRRTPTPILRPPASPNTHQISHPQPSLLEQAEGLLLRIFLHCPQERQVIIETLGSSNLEFS
VSHYRFLWEKSLQFPSQTLDLISQLQNLYLETQNDLGPVEHIFQLNEKNKQEILLRTNQLVQAAIACMEKVFRENRYRHFLELW
QKTDPSTDPDQYNLYAQTIYADKMRIQELSKQRQLSISDLINMKLAEAESTMNKTVEATQRAFNSIRTGRANASLLDKVQVDY
YGSPTPLKSLTNITTPDASTILIQPYDRSSLNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKELVKLAAKYAEEGRVGIRNIR
RDALDSIRKQEKAGEISEDESRDQQDKLQKITGKYTAKIDELLTEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDSEGAQL
GIMAPLEALRLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKQHTADVKEVKMRYKIEEHDYNVRVKQAE
RFLKDGDKVKATVMFRGREIQHSDLAETLLNRMATDLEPFGEIQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIEKISLERN
LPRLAVQSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIDGEGFRVLSTKTIVEEVTNGDHQISLDEVQQVAPEAQS
GDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSFGQPEVEAELPK
REQLPNDTYRSNATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAVD
TLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIGKEG
QNVRLAARLTGWKIDIKDQAKYDYGAEDAKFAAVRANYQEESNQPDNQFEIIEEGYEDDPDEGEDDFNSMEEENMSKKSLAS
LSATDISDKRALVRVDFNPVDDQGNITDDTRIRAALPTIQDLISKGAKVILASHFGRPKGVDEKLRLTPVAKRLSELLGQEVIKT
DDCIGDDVTAQVAALEKGQVLLLENVRFYKEEEKNDPDFARQLAANADFYVNDAFGTAHRAHASTEGVTKYLSPSVAGYLV
EKELQYLQAAIEVPQRPLAAIIGGSKVSSKIGVIETLLKKCDKLIIGGGMIFTFYKARGLNVGKSLVEQDKLELASSLEKKAAERG
VTLLLPTDIVAADKFAPDADAVTVSIENIPDDRMGLDIGPDSVKLFQDALADCKTVIWNGPMGVFEFDKFAVGTEAIAQTLAEI
GKTGATTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGTVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKS
RDYSVSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGGTVQV
IPHITNEIKERVIRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGKQNVLYMHVTLLPWIASAGEMKTKPTQHSVKELR
SIGIQPDILVCRCDRPIPVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQREPDLTHWETMVERMSH
PQSPVEIAIVGKYVRLGDAYLSVVESLRHAAIATYGDLRLRWVNSEILEVEPPDNYLLGVDGIIVPGGFGIRGVDGKISAIEYARN
RQIPFLGLCLGMQCSIIEWARNVEGLVGANSAEFDPKTDYPVINLLPEQQDVIDIGGTMRLGLYPCHVQPNTLAFDLYQEEVIYE
RHRHRYEFNNLYRNHLLNSGYVISGTSPDGRLVEIVEYPQHPFFIACQFHPEFQSRPSHPHPLFKGFMEAAISHTHQGKKQLPHG
FPQFPMVKKVSRRLQALQAKVEERDYAPLEALALLKETATAKFPEAAEAHIRLGIDPKYTDQQLRTTVVLPKGTGQIVRVAVIA
RGEKVTEATNSGADIAGSEELIDEIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDIASAISEFKAGKLEF
RADRTGIVHVMFGKASFSSEDLLVNLKALQETIDRNRPSGAKGRYWRTFYISSTMGPSIKVDINALRDLKTTDAAMGTRSYRPY

TPSTRQVTISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRDITATVIAVEYDPNRNARIALLE
YEDGEKRYILHPNGLKVGAKVTAGPQAPFEDGNALPLSNIPLGTNVHNVEMTPGKGGQIVRAAGATAQLMAKEGNYVTLKLP
SGEVRMVRRECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPALGA
KTRKRKKASSKLIVRRRRKSSKRGRGGRQSMSVGILGTKLGMTQIFDEAGVSIPVTVIKAGPCTVTQVKTQPTDGYCAIQVGYG
EVKPKALNKPKLGHLAKSSAVPVRYLNEYRTDAAGDYALGQEIKADIFSVGQIVDVIGTSIGRGFAGNQKRNNFGRGPMSHGS
KNHRAPGSIGAGTTPGRVYPGKRMAGRLGGSRVTVRKLTVVKVDAERNLILIKGAIPGKPGGLVNVVPTTKVGNKMVESIVKN
WQGEEVGQTSFELRVAKEETASHIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIF
GPKPREFNIKLNRKERRLALRTAFVSRREDLIVVEEFTDQLQRPKSKELVAALARWGATADQKTLLILSEIGQSTETISLSARNVE
NIKVIAADQLNVFDLLHADKIVVTSSALTKIQEVYSAMATTRLKTLYGQTIVPKLTQQFQYTNVHQVPKVLKVTVNRGLGEAA
QNAKALEASLSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSAKSFDGRGNYT
LGVREQLIFPEIEYDRIDQIRGLDISIITTAKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGTKVVVKGPKGELSRD
LPTHVTVSQSGETLLVTRRDDTRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGANLVLNIGYSHQVQIEPPA
GVQFAVENNTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRKAGKTGGKGKKMAKKVVAVIKLALNAGKA
NPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSDQPNKKKVGSITR
TQLREIAQTKLPDLNANDIEAAMNIVEGTAKNMGVTVKMSTATDQILEQLKVLTLLEAAELVKQIEEAFGVSAAAPAGGMMV
MAAPGAAAAEPVEEQTEFNVVLEEVPADKKIAVLKIVREITGLGLKEAKELVESTPKAVKEGVNKESAEEISKKIAEAGGKVVI
KMSSKTYLPPEEEIKRDWYVVDAADKRLGRLASEIAMVLRGKRKAEYTPHLDTGDFVVINAEKVVVTGKKPSQKLYRRHSG
RPGGMKTETFAKLQQRLPERIVEHAVKGMLPKNSLGRQLFTKLKVYSGSTHPHTAQKPKELIINTIPGENMIQPQTYLNVADNS
GARKLMCIRVLGAGNRRYGGVGDRIIAVVKDAQPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKEGNPKGTR
VFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRRAMTRYIR
RGGKIWIRIFPDKPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQPQEQEMNA
QEIIRSIEAEQLKSDLPQIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSPRIDNIKIM
RRGKVRRAKLYYLRQLSGKATRIKQRFDRALMTRVKRGNVARNRRNKILKLAKGFRGSHSTLFRTANQQVMKALRSAYRDR
KKKKRDFRRLWITRINAASRQQGLSYSQLIGNLKKANVELNRKMLAQLAVLDPATFAKVAELASSVKGMAHKKGTGSTRNGR
DSNAQRLGVKRFGGQVVRAGNILVRQRGTKFHPGNNVGIGNDDTLFALIDGVVTFERKGKSRKKVSVYPPVTEESVASMNNE
NYTEPSFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGHNYKLKEPKYSVEESKRRDSTYGVQMYVPTRLLNK
ETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDLVWVRIDK
TRKLSIQVLLKALGLSDNEILDALRHPEYFQKTIEKEGQFSEEEALLELYRKLRPGEPPTVMGGQQLLESRFFDPKRYDLGRVGR
YKLNKKLRLSVPDTTRVLTPGDILSAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRERMTVSDAEVL
TPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEGPNAGLIG
SLATHARVNQYGFLETPFRPVENGRVCYEKPAVYMTADEEDDLRVAPGDIPVDDNGQILGIQVPVRYRQEFSTTTPEQVDYVA
VSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSGMVIVSRTDGDVVYVDATEIRVRV

KEKAALTNRESETIPHKPQEIKYVLSKYQRSNQDTCLNQKPLVRIGEKVIAGQVLADGSSTEGGELALGQNVIVAYMPWEGYN
YEDAILISERLVQEDVYTSIHIEKFEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRVGAWVESGDILVGKVTPKGESDQPPE
EKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKGIISRILP
LEDMPYLPDGTPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGEESSRRIVHGKLWEAREETSRDWVY
NPENPGKIMVYDGRTGEPFDRAVTVGIAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWALEAFGA
AYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLDVEVDLMADQVSRRT
PPRPTYESFSRDSLDEDEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLMDDAYNYMRSQAEQG
KKFLFVGTKRQAAGIIAQEANRCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREENGALDLLPKKEASMLRREMSKLQK
YLGGIKNMRKVPDVVIIVDQRREYNAVQECQKLSIPIVSMLDTNCDPDTVDVPIPANDDAIRSIKLIVGKLADAIYEGRHGQLEV
EPDDEDYDIPEEDYEYNESEMGQKIHPVGFRLGITQEHQSLWFAVPGRYPELLQEDHKLRQYIEQKLGRNAQNNAGLSEIHIER
KADQVDLELRTARPGVVVGRGGQGIEALRTGLQQLLGSHRQVRINVVEVQKVDADAYLIAEYIAQQLERRVSFRRVVRQAIQR
AQRAGVQGIKVQVSGRLNGAEIARTEWTREGRVPLHTLRADIDYSYCTAQTVYGILGIKVWVFKGEIIPGQEDIVSQPVTREREP
RRRQQQRRRQQFEDRSNEAMATGRRKASKAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAIVIVGNERGQVGVGVGKASD
VIGAVKKGVADGKKHLIEIPITKSNSIPHPIDGVGGGAKVIMRPAAPGTGVIAGGAVRTVLELAGVRNVLAKQLGSNNPLNNAR
AAVNALSTLRTFAEVAEDRGIAVENLYIMATVAETNSGRALYWGTGRRKSAVAQVRLVPGEGKFVVNGKEGELYFQYNPNYL
GVIKAPLETLGLENEYDILVKAKGGGLTGQADSIRLGVARALCQLDPDNRSPLKIEGYLTRDPRAKERKKYGLHKARKAPQYS
KRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTHRRIIDIHQPSSK
TIDALMKLDLPSGVDIEVKLMARQPTKKTGSKKQKKNVPNGVAYIQSTFNNSIVTITDQNGDVISWASAGSSGFKGAKKGTPFA
AQTAAESAGRRAIDQGMRQIQVMVSGPGAGRETAIRALQGAGLEITLIRDVTPIPHNGCRPPKRRRVMARIAGVDLPRDKRVEI
GLTYIYGIGLRRSQDILAATDVNPDTRVKDLTDADLAALRAEIESNYQVEGDLRRLEAMNIKRLVDIGCYRGRRHRMGLPVRG
QRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLSKLEKLNANNEKQVIKTWSRASTILPLMVGHTIAVHNGKQ
HVPVFVNEQMVGHKLGEFAPTRTYRGHGKTDKKSGRMSDKNEGYKIISDNRQARYLYEILETYEAGIQLTGTEVKSIRAGKVN
LQDGYALLRDGEAWLINAHISPYTASGQYFNHEPRRTRKLLLHGLEIRKLIGKVEQQGLTLIPLKMYFKRGWVKISIGLCRGKK
VHDKREDLKRRQDQRDIQRAMKNYMAEISAKLVQDLRQKTGAGMMDCKKALNETQGNIDEAIDWLRKKGIASAGKKSDRV
TAEGLVDIYTTPDRSGGVLIEVNCQTDFVARNDAFKLLVKNLAKQAVNADNVTSLLAQPYIENTDVTVDEYIKETIATLGENIQ
VRRFVNFSLEGSPGAIDGYIHTGGRVGVLISIGVDTETAAKNEEVQSLAKNTAMQVAACPNVEYVSVDKIPDQVVQKEKEIEM
GKEDLGNKPENIKEKIVQGRIDKRLKEMTLLDQPYIRDQSISVAELIKQVESKVSEPIKVHQFVRYILGEGIEKQESNFAQEVAAQ
IGAK

>Cylindrospermopsis_raciborskii_KL1
MQIPRLHPDTVEEVKHRADIVDVISDYVVLRRRGKDFVGLCPFHEEKTPSFTVSPNKQIYYCFGCQASGNAIKFIMDLNKRKFAE
VVLDLAKRYQVPVKTLAPEQRQELQRQLSLREQLFEVLASTSQFYQHVLRQDIGQQALQYLQRKRFLKTETVEKFALGYAPPG
WETLYHYLVESKNYPAQLLEKAGLIKPRKEGGGYYDVFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFDKSKTLF
ALDVAKDAISKLDQAVVVEGYFDAITLHANGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATERAIGEISNL
AYKGEVRLKILHIPDGKDADEYLKNHSVTDYEQLLVDAPLWLDWQIAQVIQGRDLKQPTDFQLVSREFVKLLQKILNSDTLNY
YISHCAEILSLGDTRLIPLRVENLITQVAPRHSTTSPKTHQISHPQPSLLEQAEGLLLRIFLHCPQERQVIIETLQSSNLEFSVSHHRF
LWEKSLQFPSQTLDLISQLQNLYLETQNDLGPVEHIFQLNEKNKQEILLRTNQLVQAAIACMEKVFRENRYRHFLELWQKTDPS
TDPDQYNLYAQTIYADKMRIQELSKQRQLSISDLINMKLAEAESTMNKTVEATQRAFNSIRTGRANASLLDKVQVDYYGSPTPL
KSLANITTPDATTIYIQPYDRSSLNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKELVKLAAKYAEEGRVGIRNIRRDALDSI
RKQEKAGEISEDESRDQQDKLQKITGKYTAKIDELLAEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDSEGAQLGIMAPL
EALRLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVKQAERFLKDG
DKVKATVMFRGREIQHSDLAETLLNRMATDLEPFGEIQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIEKISLERNLPRLAV
QSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIDGEGFRVLSTKTIVEEVTNGDHQISLDEVQQVAPEAQSGDSVVL
DVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSFGQPEVEAELPKREQLPN
DTYRSNATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAVDTLDRDV
DPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIGKEGQNVRLA
ARLTGWKIDIKDQAKYDYGAEDAKFAAVRANYQEESNQPDNQFEVIEEEYEDDPDEGGDDFNSMEEKNMSKKSLASLSATDIS
DKRALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLISKGAKVILASHFGRPKGVDEKLRLTPVAKRLSELLGQEVIKTDDCIGD
DVTTQVAALEKGQVLLLENVRFYKEEEKNPDFARQLAANADFYVNDAFGTAHRAHASTEGVTKYLSPSVAGYLVEKELQY
LQAAIEDPQRPLAAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEQDKLELASSLEKKAAERGVTLLLP
TDIVAADKFAPDANAVTVSIDNIPDDRMGLDIGPDSVKVFQAALADCKTVIWNGPMGVFEFDKFAVGTEAIAQTLAEISKTGAT
TIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGKVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRDYSVS
ILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGGTVQVIPHITNE
IKERVIRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGKQNVLYMHVTLLPWIASAGEMKTKPTQHSVKELRSIGIQPD
ILVCRCDRPIPVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQREPDLTHWETMVERMSHPQSPVE
IAIVGKYVRLGDAYLSVVESLRHAAIATYGDLRLRWVNSEILEVEPPDNYLLGVDGIIVPGGFGIRGVDGKISAIEYARNQQIPFL
GLCLGMQCSIIEWARNVEGLVGANSAEFDPKTDYPVINLLPEQQDVIDLGGTMRLGLYPCHVQPNTLAFDLYQEEVIYERHRH
RYEFNNLYRNHLLNSGYVISGTSPDGRLVEIVEYPQHPFFIACQFHPEFQSRPSHPHPLFKGFMEAAISHTHQGKKQVPHGFPQFP
MVKKVSRRLQALQAKVEERDYAPLEALALLKETATAKFPEAAEAHIRLGIDPKYTDQQLRTTVVLPKGTGQIVRVAVIARGEK

VTEATNAGADIAGSEELIDEIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDIASAISEFKAGKLEFRADR
TGIVHVMFGKASFSSEDLLVNLKALQETIDRNRPSGAKGRYWRTFYISSTMGPSIKVDINALRDLKTTDAAMGTRSYRPYTPST
RQVTISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRDITATVIAVEYDPNRNARIALVEYEDG
EKRYILHPNGLKVGAKVTAGPQAPFEDGNALPLSNIPLGTNVHNVEMTPGKGGQIVRAAGATAQLMAKEGNYVTLKLPSGEV
RMVRRECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPALGAKTRK
RKKASSKLIVRRRRKSSKRGRGGRQSMSVGILGTKLGMTQIFDEAGVSIPVTVIKAGPCTVTQVKTQPTDGYCAIQVGYGEVKP
KALNKPKLGHLAKSSAGPVRYLNEYRTDAAGDYALGQEIKADIFSVGQIVDVIGTSIGRGFAGNQKRNNFGRGPMSHGSKNHR
APGSIGAGTTPGRVYPGKRMAGRLGGSRVTVRKLTVVKVDAERNLILIKGAIPGKPGGLVNVVPTTKVGNKMVESIVKNWQG
EEVGQTSFELRVAKEETASHIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFGPKP
RDFNIKLNRKERRLALRTAFVSRREDLIVVEEFTDQLQRPKSKELVAALARWGATAEQKTLLILSEIGQSTETISLSARNVENIKV
IAADQLNVFDLLHADKIIVTSSALTKIQEVYSAMATTRLKTLYGQTIVPKLTQQFQYTNVHQVPKVLKVTVNRGLGEAAQNAK
ALEASLSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSAKSFDGRGNYTLGVR
EQLIFPEIEYDRIDQIRGLDISIITTAKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGTKVVVKGPKGELSRDLPAH
VTVSQSGETLLVTRRDDTRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGANLVLNIGYSHQVQIEPPAGVQ
FAVENNTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRKAGKTGGKGKKMAKKVVAVIKLALNAGKANPA
PPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSDQPNKKKVGSITRTQL
REIAQTKLPDLNANDIEAAMNIVEGTAKNMGVTVKDMSTATDQILEQLKVLTLLEAAELVKQIEEAFGVSAAAPAGGMMVMA
APGGAAAAEVVEEQTEFNVILEEVPADKKIAVLKIVREITGLGLKEAKELVESTPKAVKEGVNKESAEEISKKIAEAGGKVAIKM
SSKTYLPPEEEIKRDWYVVDAADKRLGRLASEIAMVLRGKRKAEYTPHLDTGDFVVVINAEKVVVTGKKPSQKLYRRHSGRP
GGMKTETFAKLQQRLPERIVEHAVKGMLPKNSLGRQLFTKLKVYSGSTHPHTAQKPKELIINTIPGENMIQPQTYLNVADNSGA
RKLMCIRVLGAGNRRYGGVGDRIIAVVKDAQPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKEGNPKGTRVF
GPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRRAMTRYIRRG
GKIWIRIFPDKPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQPQEQEMNAQE
IIRSIEAEQLKSDLPQIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSPRIDNIKIMRR
GKVRRAKLYYLRQLSGKATRIKQRFDRALMTRVKRGNVARNRRNKILKLAKGFRGSHSTLFRTANQQVMKALRSAYRDRKK
KKRDFRRLWITRINAASRQQGLSYSQLIGNLKKSNVELNRKMLAQLAVLDPATFAKVAELASSVKGMAHKKGTGSTRNGRDS
NAQRLGVKRFGGQVVRAGNILVRQRGTKFHPGNNVGIGNDDTLFALIDGVVTFERKGKSRKKVSVYPRVTEEAVASMNNENY
TEPSFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGHNYKLKEPKYSVEESKRRDSTYGVQMYVPTRLLNKET
GDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDLVWVRIDKTR
KLSIQVLLKALGLSDNEILDALRHPEYFQKTIEKEGQFSEEEALLELYRKLRPGEPPTVMGGQQLLESRFFDPKRYDLGRVGRYK
LNKKLRLSVPDTTRVLTPGDILSAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRERMTVSDAEVLTP
ASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEGPNAGLIGSL

ATHARVNQYGFLETPFRPVENGRVCYEKPAVYMTADEEDDLRVAPGDIPVDDNGQILGIQVPVRYRQEFSTTTPEQVDYVAVS
PVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSGMVIVSRTGDVVYVDATEIRVRVKE
KAALTNRESETIPHKPQEVKYVLSKYQRSNQDTCLNQKPLVRIGEKVIAGQVLADGSSTEGGELALGQNVIVAYMPWEGYNYE
DAILISERLVQEDVYTSIHIEKFEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRVGAWVESGDILVGKVTPKGESDQPPEEK
LLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKGIISRILPLE
DMPYLPDGTPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGEESSRRIVHGKLWEAREETSRDWVYNP
ENPGKIMVYDGRTGEPFDRAVTVGIAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWALEAFGAAY
TLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLDVEVDLMADQVSRRTPP
RPTYESFSRDSLDEDEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLMDDAYNYMRSQAEQGK
KFLFVGTKRQAAGIIAQEANRCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREENGALDLLPKKEASMLRREMSKLQKY
LGGIKNMRKVPDVVIIVDQRREYNAVQECQKLSIPIVSMLDTNCDPDTVDIPIPANDDAIRSIKLIVGKLADAIYEGRHGQLEVEP
DHEDYDIPEEDYEYDESEFVDSFSDDDDEEMGQKIHPVGFRLGITQEHQSLWFAVPGRYPELLQEDHKLRQYIEQKLGRNAQN
NAGLSEIHIERKADQVDLELRTARPGVVVGRGGQGIEALRTGLQQLLGSHRQVRINVVEVQKVDADAYLIAEYIAQQLERRVSF
RRVVRQAIQRAQRAGVQGIKVQVSGRLNGAEIARTEWTREGRVPLHTLRADIDYSYCTAQTVYGILGIKVWVFKGEIIPGQEDI
VSQPVTREREPRRRQQQRRQQFEDRSNEAMATGRRKASKAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAIVIVGNERGQV
GVGVGKASDVIGAVKKGVADGKKHLIEIPITKSNSIPHPIDGVGGGAKVIMRPAAPGTGVIAGGAVRTVLELAGVRNVLAKQL
GSNNPLNNARAAVNALSTLRTFAEVAEDRGIAVENLYIMATVAETNSGRALYWGTGRRKSAVAQVRLVPGEGKFVVNGKEG
ELYFQYNPNYLGVIKAPLETLGLENEYDILVKAKGGGLTGQADSIRLGVARALCQLDPDNRSPLKIEGYLTRDPRAKERKKYGL
HKARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTH
RRIIDIHQPSSKTIDALMKLDLPSGVDIEVKLMARQPTKKTGSKKQKKNVPNGVAYIQSTFNNSIVTITDQNGDVISWASAGSSG
FKGAKKGTPFAAQTAAESAGRRAIDQGMRQIQVMVSGPGAGRETAIRALQGAGLEITLIRDVTPIPHNGCRPPKRRRVMARIAG
VDLPRDKRVEIGLTYIYGIGLRRSQDILAATDVNPDTRVKDLTDADLAALRAEIESNYQVEGDLRRLEAMNIKRLVDIGCYRGR
RHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLSKLEKLNANNEKQVIKTWSRASTILPLMV
GHTIAVHNGKQHVPVFVNEQMVGHKLGEFAPTRTYRGHGKTDKKSGRMSDKNEGYKIISDNRQARYLYEILETYEAGIQLTGT
EVKSIRAGKVNLQDGYALLRDGEAWLINAHISPYTASGQYFNHEPRRTRKLLLHGLEIRKLIGKVEQQGLTLIPLKMYFKRGWV
KISIGLCRGKKVHDKREDLKRRQDQRDIQRAMKNYMAEISAKLVQDLRQKTGAGIMDCKKALNETQGNIDEAIDWLRKKGIA
SAGKKSDRVTAEGLVDIYTTPDRSGGVLIEVNCQTDFVARNDAFKLLVKNLAKQAVNADNVTSLLAQPYIENTDVTVDDYIKE
TIATLGENIQVRRFVNFSLEGAPGAIDGYIHTGGRVGVLVSIGVDTETAAKNEEVQSLARNAAMQVAACPNVEYVSVDKIPDQV
VQKEKEIEMGKEDLGNKPDNIKEKIVQGRIDKRLKEMTLLDQPYIRDQNISVAELINQVQSKVSEPIKVHQFVRYILGEGIEKQES
NFAEEVAAQIGTK

>Cylindrospermopsis_raciborskii_KLL07
MQIPRLHPDTVEEVKHRADIVDVISDYVVLRRRGKDFVGLCPFHEEKTPSFTVSPTKQIYYCFGCQASGNAIKFMMDLNKRQFA
EVVLDLAKRYQVPVKTLAPEQRQELQRQLSLREQLFEVLASTSQFYQHVLRQDIGQQALQYLQKKRFLKTETVEKFALGYAPP
GWETLYHYLVENKNYPAQLVEKAGLIKPRKEGGGYYDVFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFDKSKT
LFALDVSKDAISKLDQAVVVEGYFDAIALHANGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATERAIGEIS
NLAYKGEVQLKILHIPDGKDADEYLKNHSVTDYGQLLVDAPLWLDWQIAQVIQGRDLRQPTDFQLVSREFVKLLQKILNSDTL
NYYISHCAEILSLGDTRLIPLRVENLITQVAPRRTPTPRPPQPDSTTSPNTHQISHPQPSLLEQAEGLLLRIFLHCPQERQVIIETLGF
SNLEFSVSHHRFLWEKSLQFPSQTLDLISQLQNLYLETQNDLGPVQHIFQLNEKNKQEILLRTSQLVQAAIACMEKVFRENRYRH
FLELWQKTDPSTDPDQYSLYAQTIYADKMRIQELSKQRQLSIADLINMKLAEAESTMNKTVEATQRAFNSIRTGRANASLLDKV
QVDYYGSPTSLKSLANITTPDATTILIQPYDRTSLNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKELVKLAAKYAEEGRVG
IRNIRRDALDSIRKQEKAGEVSEDESRDQQDKLQKITSKYTAKIDELLAEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDS
EGAQLGIMAPLEALRLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVR
VKQAERFLKDGDKVKATVMFRGREIQHSDLAETLLNRMATDLEPFGEVQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIEK
ISLERNLPRLAVQSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIDGEGFRVLSTKTIVEEVTNGDHQISLDEVQQVA
PEAQSGDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSFGQPEVE
AELPKREQLPNDTYRSNATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRT
KIAVDTLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLA
IGKEGQNVRLAARLTGWKIDIKDQAKYDYGAEDAKFAAVRANYQEESNQLDHQFEVMEEEYEDDPDAGEDDFNSMEEENMS
KKSLASLSAADISDKRALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLISKGAKVILASHFGRPKGVDEKLRLTPVAKRLSELL
GQEVIKTDDCIGDDVTAQVAALEKGQVLLLENVRFYKEEENNDPEFARQLAANADFYVNDAFGTAHRAHASTEGVTKYLSPS
VAGYLVEKELQYLQGAIEVPQRPLVAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEQDKLGLASSLEK
KAAERGVTLLLPTDIVAADKFGPDADAVTVSIDHIPDDRMGLDIGPDSVKVFQAALADCKTVIWNGPMGVFEFDKFAVGTEAI
AQTLAEISKTGATTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGKVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAAS
LGRLLKSRDYSVSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDY
NGGTVQVIPHITNEIKERVIRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGKQNVLYMHVTLLPWIASAGEMKTKPT
QHSVKELRSIGIQPDILVCRCDRPIPVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQREPDLTHWE
TMVERMSHPQSPVEIAIVGKYVRLGDAYLSVVESLRHAAIATYGDLRLRWVNSEILEVPPDNYLLGVDGIIVPGGFGIRGVDG
KISAIEYARNQQIPFLGLCLGMQCSIIEWARNVEGLVGANSAEFNPQTDYPVINLLPEQQDVIDLGGTMRLGLYPCHVQPNTLAF
DLYQEEVIYERHRHRYEFNNLYRNHLLNSGYVISGTSPDGRLVEIVEYPQHPFFIACQFHPEFQSRPSHPHPLFKGFMEAAISHTH
QGSTPMVKKVSRRLQALQAKVEERDYTPLEALALLKETATAKFAEAAEAHIRLGIDPKYTDQQLRTTVVLPKGTGQIVRVAVI
ARGEKVTEATNAGADIAGSEELIDEIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDIASAISEFKAGKLE
FRADRTGIVHVMFGKASFSSEDLLVNLKALQETIDRNRPSGAKGRYWRTFYISSTMGPSIKIDINALRDFKTTDVAMGTRSYRPY

TPSTRQVTISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRDITATVIAVEYDPNRNARIALVE
YEDGEKRYILHPNGLKVGAKITAGPQAPFEDGNALPLSNIPLGTNVHNVEMTPGKGGQIVRAAGATAQLMAKEGNYVTLKLPS
GEVRMVRRECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPALGAK
TRKRKKASSKLIVRRRRKSSKRGRGGRQSMSVGILGTKLGMTQIFDEAGVSIPVTVIQAGPCTVTQVKTQPTDGYCAIQVGYGE
VKPKALNKPKLGHLAKSSAGPVRYLNEYRTDAAGDYALGQEIKADIFSVGQIVDVIGTSIGRGFAGNQKRNNFGRGPMSHGSK
NHRAPGSIGAGTTPGRVYPGKRMAGRLGGSRVTVRKLTVVKVDAERNLILIKGAIPGKPGGLVNVVPTTKVGNKMVESTVKN
WQGEEVGQTSFELRVAKEETASHIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIF
GPKPRDFNIKLNRKERRLALRTAFVSRREDLIVVEEFTDQLQRPKSKELVAALARWGATADQKTLLILSEIGQNTETISLSARNV
ENIKVIAADQLNVFDLLHADKIVVTSSALTKIQEVYSAMATTRLKTLYGQTIVPKLTQQFQYTNVHQVPKVLKVTVNRGLGEA
AQNAKALEASLSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSAKSFDGRGN
YTLGVREQLIFPEIEYDRIDQIRGLDISIITTAKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGTKVVVKGPKGELS
RDLPAHVTVSQSGETLLVTRRDDTRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGANLVLNIGYSHQVQIE
PPAGVQFVVENNTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRKAGKTGGKGKKMAKKLVAVIKLALNA
GKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSDQPNKKKVGS
ITRTQLKEIAQTKLPDLNANDIEAAMNIVEGTAKNMGVTIKDMSTATDQILEQLKSLTLLEAAELVKQIEEAFGVSAAAPAGGM
MMMAAPGGAAAAEVVEEQTEFDVILQEVPADKKIAVLKIVREITGLGLKEAKELVESTPKAVKEGVNKEAAEDISKKITEAGG
KVAIKMSSKTYLPPEEEIKRDWYVVDAADKRLGRLASEIAMVLRGKRKAEYTPHLDTGDFVVVINAEKVVVTGKKQSQKLYR
RHSGRPGGMKTETFAKLQQRLPERIVEHAVKGMLPKNSLGRQLFTKLKVYSGATHPHTAQKPKELIINTIPGENMIQPQTYLNV
ADNSGARKLMCIRVLGAGNRRYGGVGDRIIAVVKDAQPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKEGNP
KGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRRAM
TRYIRRGGKIWIRIFPDKPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQPQE
QEMNAQEIIRSIEAEQLKSDLPQIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSPRI
DNIKIMRRGKVRRAKLYYLRQLSGKATRIKQRFDRALMTRVKRGNVARNRRNKILKLAKGFRGSHSTLFRTANQQVMKALRS
AYRDRKKKKRDFRRLWITRINAASRQQGLSYSQLIGNLKKANVELNRKMLAQLAVLDPTTFAKVAELASSVKGNMAHKKGT
GSTRNGRDSNAQRLGVKRFGGQVVRAGNILVRQRGTKFHPGNNVGIGNDDTLFALIDGVVTFERKGKSRKKVSVYPRVTEEA
VASMNNENYMEPSFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGHNYKLKEPKYSVEESKRRDSTYGVQMY
VPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDL
VWVRIDKTRKLSIQVLLKALGLLDNEILDALRHPEYFQKTIEKEGQFSEEEALLELYRKLRPGEPPTVMGGQQLLESRFFDPKRY
DLGRVGRYKLNKKLRLSVPDTTRVLTPGDILSAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRERMT
VSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEG
PNAGLIGSLATHARVNQYGFLETPFRPVENGRVCYEKPAVYMTADEEDDLRVAPGDIPVDDNGQILGIQVPVRYRQEFSTTTPE
QVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSGMVIVSRTDGDVVYVDAT

EIRVRVKEKAALTNRESESIPHKPQEIKYVLSKYQRSNQDTCLNQKPLVRIGEKVIAGQVLADGSSTEGGELALGQNVIVAYMP
WEGYNYEDAILISERLVQEDVYTSIHIEKFEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRVGAWVESGDILVGKVTPKGE
SDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRIVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKG
IISRILPLEDMPYLPDGTPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGEESSRRIVHGKLWEAREETSK
DWVYNPENPGKIMVYDGRTGEPFDRAVTVGIAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWALE
AFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLDVEVDLMADQ
VSRRTPPRPTYESFSRDSLDEDEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLMDDAYNYMRS
QAEQGKKFLFVGTKRQAAGIIAQEANRCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREENGALDLLPKKEASMLRREM
SKLQKYLGGIKNMRKVPDVVIIVDQRREYNAVQECQKLSIPIVSMLDTNCDPDTVDIPIPANDDAIRSIKLIVGKLADAIYEGRHG
QLEVESDYEEYESAEEDYEYDESEFVDSFSDDDDEEMGQKIHPVGFRLGITQEHQSLWFAVPGRYPELLQEDHKLRQYIEQKLG
RNAQNNAGLSEIHIERKADQVDLELRTARPGVVVGRGGQGIEALRTGLQQLLGSHRQVRINVVEVQKVDADAYLIAEYIAQQL
ERRVSFRRVVRQAIQRAQRAGVQGIKVQVSGRLNGAEIARTEWTREGRVPLHTLRADIDYSYCTAQTVYGILGIKVWVFKGEII
PGQEDIVSQPVTREREPRRRQQQRRRQQFEDRSNEAMATGRRKASKAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAIVIVG
NERGQVGVGVGKASDVIGAVKKGVADGKKHLIEIPITKSNSIPHPIDGVGGGAKVIMRPAAPGTGVIAGGAVRTVLELAGVRN
VLAKQLGSNNPLNNARAAVNALSTLRTFAEVAEDRGIAVENLYIMATVAETNSGRALYWGTGRRKSAVAQVRLVPGEGKFV
VNGKEGELYFQYNPNYLGVIKAPLETLGLENEYDILVKAKGGGLTGQADSIRLGVARALCQLDPDNRSPLKIEGYLTRDPRAKE
RKKYGLHKARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSRE
HFETRTHRRIIDIHQPSSKTIDALMKLDLPSGVDIEVKLMARQPTKKTGSKKQKKNVPNGVAYIQSTFNNSIVTITDQNGDVISW
ASAGSSGFKGAKKGTPFAAQTAAESAGRRAIDQGMRQIQVMVSGPGAGRETAIRALQGAGLEITLIRDVTPIPHNGCRPPKRRR
VMARIAGVDLPRDKRVEIGLTYIYGIGLRRSQDILAATDVNPDTRVKDLTDADLAALRAEIESNYQVEGDLRRLEAMNIKRLVD
IGCYRGRRHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLSKIEKLNANNEKQVIKTWSRAST
ILPLMVGHTIAVHNGKQHVPVFVNEQMVGHKLGEFAPTRSYRGHGKTDKKSGRMSDKNEGYKIISDNRQARYLYEILETYEAG
IQLTGTEVKSIRAGKVNLQDGYALLRDGEAWLINAHISPYTASGQYFNHEPRRTRKLLLHGLEIRKLIGKVEQQGLTLIPLKMYF
KRGWVKISIGLCRGKKVHDKREDLKRRQDQRDIQRAMKNYMAEISAKLVQDLRQKTGAGMMDCKKALNETQGNIDEAIDWL
RKKGIASAGKKSDRVTAEGLVDIYTTPDKSGGVIIEVNCQTDFVARNDAFKLLVKNLAKQAVNADNVASLLDQPYIEKTDVTV
DEYIKETIATLGENIQVRRFVNFSLEGAPGAIDGYIHTGGRVGVLVSIGVDTETAAKNEELQSLAKNTAMQVAACPNVEYVSVD
KIPDQVVEKEKEIEMGKEDLGNKPANIKEKIVQGRIDKRLKEMTLLDQPYIRDQNISVAELIKQVESKVSEPIKVHQFVRYILGEG
IEKQESNFAEEVAAQIGAK

>Cylindrospermopsis_raciborskii_MVCC14
VLRRRGKDFVGLCPFHEEKTPSFTVSPNKQIYYCFGCQASGNAIRFIMDLNKRKFAEVVLDLAKRYQVPVKTLAPEQRQELQRQ
LSLREQLFEVLASTSQFYQHVLRQDIGQQALQYLQKKRFLKTETVEKFALGYAPPGWETLYHYLVENKSYPAQLVEKAGLIKP
RKEGGGYYDVFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFDKSKTLFALDVAKDAISKLDQAVVVEGYFDAIAL
HANGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATERAIGEISNLAYKGEVRLKILHIPDGKDADEYLKNHS
VTDYEQLLVEAPLWLDWQIAQVIQGRDLKQPTDFQLVSREFVKLLQKILNSDTLNYYISHCAEILSLGDTRLIPLRVENLITQVA
PRRTPTPILRPPASPNTHQISHPQPSLLEQAEGLLLRIFLHCPQERQVIIETLGSSNLEFSVSHYRFLWEKSLQFPSQTLDLISQLQNL
YLETQNDLGPVEHIFQLNEKNKQEILLRTNQLVQAAIACMEKVFRENRYRHFLELWQKTDPSTDPDQYNLYAQTIYADKMRIQ
ELSKQRQLSISDLINMKLAEAESTMNKTVEATQRAFNSIRTGRANASLLDKVQVDYYGSPTPLKSLTNITTPDASTILIQPYDRSS
LNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKELVKLAAKYAEEGRVGIRNIRRDALDSIRKQEKAGEISEDESRDQQDKL
QKITGKYTAKIDELLTEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDSEGAQLGIMAPLEALRLAEEKELDLVLLSDKADP
PVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVKQAERFLKDGDKVKATVMFRGREIQHSDLAET
LLNRMATDLEPFGEIQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIEKISLERNLPRLAVQSSIREALLKGYERYRRAQNLER
RQFDENYFDNFEVELDIDGEGFRVLSTKTIVEEVTNGDHQISLDEVQQVAPEAQSGDSVVLDVTPDQGEFGRMAAMQTKQVLA
QKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSFGQPEVEAELPKREQLPNDTYRSNATFKVYLKKVSQGQQRG
PQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAVDTLDRDVDPVGACIGARGSRIQVVVNELRGE
KIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIGKEGQNVRLAARLTGWKIDIKDQAKYDYGAEDA
KFAAVRANYQEESNQPDNQFEIIEEGYEDDPDEGEDDFNSMEEENMSKKSLASLSATDISDKRALVRVDFNVPVDDQGNITDDT
RIRAALPTIQDLISKGAKVILASHFGRPKGVDEKLRLTPVAKRLSELLGQEVIKTDDCIGDDVTAQVAALEKGQVLLLENVRFYK
EEEKNDPNFARQLAANADFYVNDAFGTAHRAHASTEGVTKYLSPSVAGYLVEKELQYLQAAIEVPQRPLAAIIGGSKVSSKIGV
IETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEQDKLELASSLEKKAAERGVTLLLPTDIVAADKFAPDADAVTVSIENIPDD
RMGLDIGPKSVKLFQDALADCKTVIWNGPMGVFEFDKFAVGTEAIAQTLAEIGKTGATTIIGGGDSVAAVEKVGLADQMSHIS
TGGGASLELLEGTVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRDYSVSILKLDPYINVDPGTMSPFQHGEVFV
TQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGGTVQVIPHITNEIKERVIRVAKETNPAAVITEIGGTV
GDIESLPFLEAIRQLRKEVGKQNVLYMHVTLLPWIASAGEMKTKPTQHSVKELRSIGIQPDILVCRCDRPIPVGLKQKLSEFCDVP
VECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQREPDLTHWETMVERMSHPQSPVEIAIVGKYVRLGDAYLSVVESLRHA
AIATYGDLRLRWVNSEILEVEPPDNYLLGVDGIIVPGGFGIRGVDGKISAIEYARNRQIPFLGLCLGMQCSIIEWARNVEGLVGA
NSAEFDPKTDYPVINLLPEQQDVIDMGGTMRLGLYPCHVQPNTLAFDLYQEEVIYERHRHRYEFNNLYRNHLLNSGYVISGTSP
DGRLVEIVEYPQHPFFIACQFHPEFQSRPSHPHPLFKGFMEAAISHTHQGKKQLPQGFPQFPMVKKVSRRLQALQAKVEERDYA
PLEALALLKETATAKFPEAAEAHIRLGIDPKYTDQQLRTTVVLPKGTGQIVRVAVIARGEKVTEATNAGADIAGSEELIDEIQKG
MMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDIASAISEFKAGKLEFRADRTGIVHVMFGKASFSSEDLLVNLK
ALQETIDRNRPSGAKGRYWRTFYISSTMGPSIKVDINALRDLKTTDAAMGTRSYRPYTPSTRQVTISDFAEITKTEPEKSLTESVH

RPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRDITATVIAVEYDPNRNARIALLEYEDGEKRYILHPNGLKVGAKVTAGPQA
PFEDGNALPLSNIPLGTNVHNVEMTPGKGGQIVRAAGATAQLMAKEGNYVTLKLPSGEVRMVRRECYATIGQVGNTDARNLS
AGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPALGAKTRKRKKASSKLIVRRRRKSSKRGRGGR
QSMSVGILGTKLGMTQIFDEAGVSIPVTVIKAGPCTVTQVKTQPTDGYCAIQVGYGEVKPKALNKPKLGHLAKSSAVPVRYLN
EYRTDAAGDYALGQEIKADIFSVGQIVDVIGTSIGRGFAGNQKRNNFGRGPMSHGSKNHRAPGSIGAGTTPGRVYPGKRMAGR
LGGSRVTVRKLTVVKVDAERNLILIKGAIPGKPGGLVNVVPTTKVGNKMVESIVKNWQGEEVGQTSFELRVAKEETASHIVHR
ALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFGPKPREFNIKLNRKERRLALRTAFVSRR
EDLIVVEEFTDQLQRPKSKELVAALARWGATADQKTLLILSEIGQSTETISLSARNVENIKVIAADQLNVFDLLHADKIVVTSSAL
TKIQEVYSAMATTRLKTLYGQTIVPKLTQQFQYTNVHQVPKVLKVTVNRGLGEAAQNAKALEASLSEIALITGQKPVVTRAKK
AIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSAKSFDGRGNYTLGVREQLIFPEIEYDRIDQIRGLDISIITTA
KTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGTKVVVKGPKGELSRDLPTHVTVSQSGETLLVTRRDDTRTSRQ
MHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGANLVLNIGYSHQVQIEPPAGVQFAVENNTNVIVSGYDKEVVGNTA
AKIRAVRPPEPYKGKGIRYAGEVVRRKAGKTGGKGKKMAKKVVAVIKLALNAGKANPAPPVGPALGQHGVNIMMFCKEYNA
KTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSDQPNKKKVGSITRTQLREIAQTKLPDLNANDIEAAMNIVEG
TAKNMGVTVKDMSTATDQILEQLKVLTLLEAAELVKQIEEAFGVSAAAPAGGMMVMAAPGAAAAEPVEEQTEFNVVLEEVP
ADRKIAVLKIVREITGLGLKEAKELVESTPKAVKEGVNKESAEEISKKIADAGGKVVIKMSSKTYLPPEEEIKRDWYVVDAADK
RLGRLASEIAMVLRGKRKAEYTPHLDTGDFVVVINAEKVVVTGKKPSQKLYRRHSGRPGGMKTETFAKLQQRLPERIVEHAV
KGMLPKNSLGRQLFTKLKVYSGSTHPHTAQKPKELIINTIPGENMIQPQTYLNVADNSGARKLMCIRVLGAGNRRYGGVGDRII
AVVKDAQPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKEGNPKGTRVFGPVARELRDKNFTKIVSLAPEVLM
LSPRRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRRAMTRYIRRGGKIWIRIFPDKPVTMRPAETRMGS
GKGNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQPQEQEMNAQEIIRSIEAEQLKSDLPQIYVGDTVRV
GVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSPRIDNIKIMRRGKVRRAKLYYLRQLSGKATRIKQ
RFDRALMTRVKRGNVARNRRNKILKLAKGFRGSHSTLFRTANQQVMKALRSAYRDRKKKKRDFRRLWITRINAASRQQGLSY
SQLIGNLKKANVELNRKMLAQLAVLDPATFAKVAELASSVKGMAHKKGTGSTRNGRDSNAQRLGVKRFGGQVVRAGNILVR
QRGTKFHPGNNVGIGNDDTLFALIDGVVTFERKGKSRKKVSVYPSVTEEAVASMNNENYTEPSFLLPDLIEIQRSSFRWFLEEGL
IEELNSFSPITDYTGKLELHFLGHNYKLKEPKYSVEESKRRDSTYGVQMYVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIING
AERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDLVWVRIDKTRKLSIQVLLKALGLSDNEILDALRHPE
YFQKTIEKEGQFSEEEALLELYRKLRPGEPPTVMGGQQLLESRFFDPKRYDLGRVGRYKLNKKLRLSVPDTTRVLTPGDILSAV
DYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRERMTVSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFM
DQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEGPNAGLIGSLATHARVNQYGFLETPFRPVENGRVC
YEKPAVYMTADEEDDLRVAPGDIPVDDNGQILGIQVPVRYRQEFSTTTPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALM
GSNMQRQAVPLLKPERPLVGTGLEAQGARDSGMVIVSRTDGDVVYVDATEIRVRVKEKAALTNRESETIPHKPQEIKYVLSKY

QRSNQDTCLNQKPLVRIGEKVIAGQVLADGSSTEGGELALGQNVIVAYMPWEGYNYEDAILISERLVQEDVYTSIHIEKFEIEAR
QTKLGPEEITREIPNVGEDALRQLDEQGIIRVGAWVESGDILVGKVTPKGESDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKG
RVVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKGIISRILPLEDMPYLPDGTPVDIVLNPLGVPSRMNV
GQVFECLLGWAGHNLGVRFKITPFDEMYGEESSRRIVHGKLWEAREETSRDWVYNPENPGKIMVYDGRTGEPFDRAVTVGIA
YMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWALEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKG
KAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLDVEVDLMADQVSRRTPPRPTYESFSRDSLDEDEMPVVSLAQMME
SGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLMDDAYNYMRSQAEQGKKFLFVGTKRQAAGIIAQEANRCGSHYIN
QRWLGGMLTNWATIKTRADRLKDLERREENGALDLLPKKEASMLRREMSKLQKYLGGIKNMRKVPDVVIIVDQRREYNAVQ
ECQKLSIPIVSMLDTNCDPDTVDVPIPANDDAIRSIKLIVGKLADAIYEGRHGQLEVEPDDEDYDIPEEDYEYNESEMGQKIHPVG
FRLGITQEHQSLWFAVPGRYPELLQEDHKLRQYIEQKLGRNAQNNAGLSEIHIERKADQVDLELRTARPGVVVGRGGQGIEALR
TGLQQLLGSHRQVRINVVEVQKVDADAYLIAEYIAQQLERRVSFRRVVRQAIQRAQRAGVQGIKVQVSGRLNGAEIARTEWTR
EGRVPLHTLRADIDYSYCTAQTVYGILGIKVWVFKGEIIPGQEDIVSQPVTEREPRRRQQQRRRQQFEDRSNEAMATGRRKAS
KAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAIVIVGNERGQVGVGVGKASDVIGAVKKGVADGKKHLIEIPITKSNSIPHPID
GVGGGAKVIMRPAAPGTGVIAGGAVRTVLELAGVRNVLAKQLGSNNPLNNARAAVNALSTLRTFAEVAEDRGIAVENLYIMA
TVAETNSGRALYWGTGRRKSAVAQVRLVPGEGKFVVNGKEGELYFQYNPNYLGVIKAPLETLGLENEYDILVKAKGGGLTGQ
ADSIRLGVARALCQLDPDNRSPLKIEGYLTRDPRAKERKKYGLHKARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIV
DTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTHRRIIDIHQPSSKTIDALMKLDLPSGVDIEVKLMARQPTKKTG
SKKQKKNVPNGVAYIQSTFNNSIVTITDQNGDVISWASAGSSGFKGAKKGTPFAAQTAAESAGRRAIDQGMRQIQVMVSGPGA
GRETAIRALQGAGLEITLIRDVTPIPHNGCRPPKRRRVMARIAGVDLPRDKRVEIGLTYIYGIGLRRSQDILAATDVNPDTRVKDL
TDADLAALRAEIESNYQVEGDLRRLEAMNIKRLVDIGCYRGRRHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGR
SLKKGPFVADHLLSKLEKLNANNEKQVIKTWSRASTILPLMVGHTIAVHNGKQHVPVFVNEQMVGHKLGEFAPTRTYRGHGK
TDKKSGRMSDKNEGYKIISDNRQARYLYEILETYEAGIQLTGTEVKSIRAGKVNLQDGYALLRDGEAWLINAHISPYTASGQYF
NHEPRRTRKLLLHGLEIRKLIGKVEQQGLTLIPLKMYFKRGWVKISIGLCRGKKVHDKREDLKRRQDQRDIQRAMKNYMAEIS
AKLVQDLRQKTGAGIMDCKKALNETQGNIDEAIDWLRKKGIASAGKKSDRVTAEGLVEIYTTPDRSGGVLIEVNCQTDFVARN
DAFKLLVKNLAKQAVNADNVTSLLAQPYIENTDVTVDEYIKGTITTLGENIQVRRFVNFSLEGSPGAIDGYIHTGGRVGVLISIG
VDTENAAKNEEVQSLAKNTAMQVAACPNVEYVSVDKIPDQVVQKEKEIEMGKEDLGNKPENIKEKIVQGRIDKRLKEMTLLD
QPYIRDQSISVAELIKQVESKVSEPIKVHQFVRYILGEGIEKQESNFAQEVAAQIGAK

>Cylindrospermopsis_raciborskii_MVCC19
MQIPRLHPDTVEEVKHRADIVDVISDYVVLRRRGKDFVGLCPFHEEKTPSFTVSPNKQIYYCFGCQASGNAIRFIMDLNKRKFAE
VVLDLAKRYQVPVKTLAPEQRQELQRQLSLREQLFEVLASTSQFYQHVLRQDIGQQALQYLQKKRFLKTETVEKFALGYAPPG
WETLYHYLVENKSYPAQLVEKAGLIKPRKEGGGYYDVFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFDKSKTLF
ALDVAKDAISKLDQAVVVEGYFDAIALHANGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATERAIGEISNL
AYKGEVRLKILHIPDGKDADEYLKNHSVTDYEQLLVEAPLWLDWQIAQVIQGRDLKQPTDFQLVSREFVKLLQKILNSDTLNY
YISHCAEILSLGDTRLIPLRVENLITQVAPRRTPTPILRPPASPNTHQISHPQPSLLEQAEGLLLRIFLHCPQERQVIIETLGSSNLEFS
VSHYRFLWEKSLQFPSQTLDLISQLQNLYLETQNDLGPVEHIFQLNEKNKQEILLRTNQLVQAAIACMEKVFRENRYRHFLELW
QKTDPSTDPDQYNLYAQTIYADKMRIQELSKRQLSISDLINMNKTVEATQRAFNSIRTGRANASLLDKVQVDYYGSPTPLKSL
TNITTPDASTILIQPYDRSSLNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKELVKLAAKYAEEGRVGIRNIRRDALDSIRKQ
EKAGEISEDESRDQQDKLQKITGKYTAKIDELLTEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDSEGAQLGIMAPLEALR
LAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVKQAERFLKDGDKVK
ATVMFRGREIQHSDLAETLLNRMATDLEPFGEIQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIEKISLERNLPRLAVQSSIR
EALLKGYERYRRAQNLERRQFDENYFDNFEVELDIDGEGFRVLSTKTIVEEVTNGDHQISLDEVQQVAPEAQSGDSVVLDVTPD
QGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSFGQPEVEAELPKREQLPNDTYRS
NATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAVDTLDRDVDPVGA
CIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIGKEGQNVRLAARLTG
WKIDIKDQAKYDYGAEDAKFAAVRANYQEESNQPDNQFEIIEEGYEDDPDEGEDDFNSMEEENMSKKSLASLSATDISDKRAL
VRVDFNVPVDDQGNITDDTRIRAALPTIQDLISKGAKVILASHFGRPKGVDEKLRLTPVAKRLSELLGQEVIKTDDCIGDDVTAQ
VAALEKGQVLLLENVRFYKEEEKNDPNFARQLAANADFYVNDAFGTAHRAHASTEGVTKYLSPSVAGYLVEKELQYLQAAIE
VPQRPLAAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEQDKLELASSLEKKAAERGVTLLLPTDIVAA
DKFAPDADAVTVSIENIPDDRMGLDIGPKSVKLFQDALADCKTVIWNGPMGVFEFDKFAVGTEAIAQTLAEIGKTGATTIIGGG
DSVAAVEKVGLADQMSHISTGGGASLELLEGTVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRDYSVSILKLDP
YINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGGTVQVIPHITNEIKERVI
RVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGKQNVLYMHVTLLPWIASAGEMKTKPTQHSVKELRSIGIQPDILVCR
CDRPIPVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQREPDLTHWETMVERMSHPQSPVEIAIVG
KYVRLGDAYLSVVESLRHAAIATYGDLRLRWVNSEILEVEPPDNYLLGVDGIIVPGGFGIRGVDGKISAIEYARNRQIPFLGLCL
GMQCSIIEWARNVEGLVGANSAEFDPKTDYPVINLLPEQQDVIDMGGTMRLGLYPCHVQPNTLAFDLYQEEVIYERHRHRYEF
NNLYRNHLLNSGYVISGTSPDGRLVEIVEYPQHPFFIACQFHPEFQSRPSHPHPLFKGFMEAAISHTHQGKKQLPQGFPQFPMVK
KVSRRLQALQAKVEERDYAPLEALALLKETATAKFPEAAEAHIRLGIDPKYTDQQLRTTVVLPKGTGQIVRVAVIARGEKVTEA
TNAGADIAGSEELIDEIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDIASAISEFKAGKLEFRADRTGIV
HVMFGKASFSSEDLLVNLKALQETIDRNRPSGAKGRYWRTFYISSTMGPSIKVDINALRDLKTTDAAMGTRSYRPYTPSTRQVT

ISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRDITATVIAVEYDPNRNARIALLEYEDGEKRY
ILHPNGLKVGAKVTAGPQAPFEDGNALPLSNIPLGTNVHNVEMTPGKGGQIVRAAGATAQLMAKEGNYVTLKLPSGEVRMVR
RECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPALGAKTRKRKKAS
SKLIVRRRKSSKRGRGGRQSMSVGILGTKLGMTQIFDEAGVSIPVTVIKAGPCTVTQVKTQPTDGYCAIQVGYGEVKPKALNK
PKLGHLAKSSAVPVRYLNEYRTDAAGDYALGQEIKADIFSVGQIVDVIGTSIGRGFAGNQKRNNFGRGPMSHGSKNHRAPGSIG
AGTTPGRVYPGKRMAGRLGGSRVTVRKLTVVKVDAERNLILIKGAIPGKPGGLVNVVPTTKVGNKMVESIVKNWQGEEVGQT
SFELRVAKEETASHIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFGPKPREFNIK
LNRKERRLALRTAFVSRREDLIVVEEFTDQLQRPKSKELVAALARWGATADQKTLLILSEIGQSTETISLSARNVENIKVIAADQ
LNVFDLLHADKIVVTSSALTKIQEVYSAMATTRLKTLYGQTIVPKLTQQFQYTNVHQVPKVLKVTVNRGLGEAAQNAKALEAS
LSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSAKSFDGRGNYTLGVREQLIFP
EIEYDRIDQIRGLDISIITTAKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGTKVVVKGPKGELSRDLPTHVTVSQ
SGETLLVTRRDDTRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGANLVLNIGYSHQVQIEPPAGVQFAVEN
NTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRKAGKTGGKGKKMAKKVVAVIKLALNAGKANPAPPVGP
ALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSDQPNKKKVGSITRTQLREIAQT
KLPDLNANDIEAAMNIVEGTAKNMGVTVKDMSTATDQILEQLKVLTLLEAAELVKQIEEAFGVSAAAPAGGMMVMAAPGAA
AAEPVEEQTEFNVVLEEVPADRKIAVLKIVREITGLGLKEAKELVESTPKAVKEGVNKESAEEISKKIADAGGKVVIKMSSKTYL
PPEEEIKRDWYVVDAADKRLGRLASEIAMVLRGKRKAEYTPHLDTGDFVVVINAEKVVVTGKKPSQKLYRRHSGRPGGMKTE
TFAKLQQRLPERIVEHAVKGMLPKNSLGRQLFTKLKVYSGSTHPHTAQKPKELIINTIPIGENMIQPQTYLNVADNSGARKLMCI
RVLGAGNRRYGGVGDRIIAVVKDAQPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKEGNPKGTRVFGPVARE
LRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRRAMTRYIRRGGKIWIRI
FPDKPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQPQEQEMNAQEIIRSIEA
EQLKSDLPQIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSPRIDNIKIMRRGKVRR
AKLYYLRQLSGKATRIKQRFDRALMTRVKRGNVARNRRNKILKLAKGFRGSHSTLFRTANQQVMKALRSAYRDRKKKKRDF
RRLWITRINAASRQQGLSYSQLIGNLKKANVELNRKMLAQLAVLDPATFAKVAELASSVKGMAHKKGTGSTRNGRDSNAQRL
GVKRFGGQVVRAGNILVRQRGTKFHPGNNVGIGNDDTLFALIDGVVTFERKGKSRKKVSVYPSVTEEAVASMNNENYTEPSFL
LPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGHNYKLKEPKYSVEESKRRDSTYGVQMYVPTRLLNKETGDIKEQ
EVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDLVWVRIDKTRKLSIQV
LLKALGLSDNEILDALRHPEYFQKTIEKEGQFSEEEALLELYRKLRPGEPPTVMGGQQLLESRFFDPKRYDLGRVGRYKLNKKL
RLSVPDTTRVLTPGDILSAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRERMTVSDAEVLTPASLVNP
KPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEGPNAGLIGSLATHARV
NQYGFLETPFRPVENGRVCYEKPAVYMTADEEDDLRVAPGDIPVDDNGQILGIQVPVRYRQEFSTTTPEQVDYVAVSPVQIVSV
ATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSGMVIVSRTDGDVVYVDATEIRVRVKEKAALTNR

ESETIPHKPQEIKYVLSKYQRSNQDTCLNQKPLVRIGEKVIAGQVLADGSSTEGGELALGQNVIVAYMPWEGYNYEDAILISERL
VQEDVYTSIHIEKFEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRVGAWVESGDILVGKVTPKGESDQPPEEKLLRAIFGEK
ARDVRDNSLRVPNGEKGRVVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKGIISRILPLEDMPYLPDG
TPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGEESSRRIVHGKLWEAREETSRDWVYNPENPGKIMV
YDGRTGEPFDRAVTVGIAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWALEAFGAAYTLQELLTV
KSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLDVEVDLMADQVSRRTPPRPTYESFSR
DSLDEDEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLMDDAYNYMRSQAEQGKKFLFVGTKR
QAAGIIAQEANRCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREENGALDLLPKKEASMLRREMSKLQKYLGGIKNMRK
VPDVVIIVDQRREYNAVQECQKLSIPIVSMLDTNCDPDTVDVPIPANDDAIRSIKLIVGKLADAIYEGRHGQLEVEPDDEDYDIPE
EDYEYNESEMGQKIHPVGFRLGITQEHQSLWFAVPGRYPELLQEDHKLRQYIEQKLGRNAQNNAGLSEIHIERKADQVDLELRT
ARPGVVVGRGGQGIEALRTGLQQLLGSHRQVRINVVEVQKVDADAYLIAEYIAQQLERRVSFRRVVRQAIQRAQRAGVQGIKV
QVSGRLNGAEIARTEWTREGRVPLHTLRADIDYSYCTAQTVYGILGIKVWVFKGEIIPGQEDIVSQPVTREREPRRRQQQRRRQ
QFEDRSNEAMATGRRKASKAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAIVIVGNERGQVGVGVGKASDVIGAVKKGVAD
GKKHLIEIPITKSNSIPHPIDGVGGGAKVIMRPAAPGTGVIAGGAVRTVLELAGVRNVLAKQLGSNNPLNNARAAVNALSTLRTF
AEVAEDRGIAVENLYIMATVAETNSGRALYWGTGRRKSAVAQVRLVPGEGKFVVNGKEGELYFQYNPNYLGVIKAPLETLGL
ENEYDILVKAKGGGLTGQADSIRLGVARALCQLDPDNRSPLKIEGYLTRDPRAKERKKYGLHKARKAPQYSKRMATLQQQKIR
IRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTHRRIIDIHQPSSKTIDALMKLDLPS
GVDIEVKLMARQPTKKTGSKKQKKNVPNGVAYIQSTFNNSIVTITDQNGDVISWASAGSSGFKGAKKGTPFAAQTAAESAGRR
AIDQGMRQIQVMVSGPGAGRETAIRALQGAGLEITLIRDVTPIPHNGCRPPKRRRVMARIAGVDLPRDKRVEIGLTYIYGIGLRR
SQDILAATDVNPDTRVKDLTDADLAALRAEIESNYQVEGDLRRLEAMNIKRLVDIGCYRGRRHRMGLPVRGQRTRTNARTRR
GRRQTVAGKKKAPGKMGRSLKKGPFVADHLLSKLEKLNANNEKQVIKTWSRASTILPLMVGHTIAVHNGKQHVPVFVNEQM
VGHKLGEFAPTRTYRGHGKTDKKSGRMSDKNEGYKIISDNRQARYLYEILETYEAGIQLTGTEVKSIRAGKVNLQDGYALLRD
GEAWLINAHISPYTASGQYFNHEPRRTRKLLLHGLEIRKLIGKVEQQGLTLIPLKMYFKRGWVKISIGLCRGKKVHDKREDLKR
RQDQRDIQRAMKNYMAEISAKLVQDLRQKTGAGIMDCKKALNETQGNIDEAIDWLRKKGIASAGKKSDRVTAEGLVEIYTTP
DRSGGVLIEVNCQTDFVARNDAFKLLVKNLAKQAVNADNVTSLLAQPYIENTDVTVDEYIKGTITTLGENIQVRRFVNFSLEGS
PGAIDGYIHTGGRVGVLISIGVDTENAAKNEEVQSLAKNTAMQVAACPNVEYVSVDKIPDQVVQKEKEIEMGKEDLGNKPENI
KEKIVQGRIDKRLKEMTLLDQPYIRDQSISVAELIKQVESKVSEPIKVHQFVRYILGEGIEKQESNFAQEVAAQIGAK

>Cylindrospermopsis_raciborskii_N8
MQIPRLHPDTVEEVKHRADIVDVISDYVVLRRRGKDFVGLCPFHEEKTPSFTVSPTKQIYYCFGCQASGNAIKFMMDLNKRQFA
EVVLDLAKRYQVPVKTLAPEQRQELQRQLSLREQLFEVLASTSQFYQHVLRQDIGQQALQYLQKKRFLKTETVEKFALGYAPP
GWETLYHYLVENKNYPAQLVEKAGLIKPRKEGGGYYDVFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFDKSKT
LFALDVSKDAISKLDQAVVVEGYFDAIALHANGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATERAIGEIS
NLAYKGEVQLKILHIPDGKDADEYLKNHSVTDYGQLLVDAPLWLDWQIAQVIQGRDLRQPTDFQLVSREFVKLLQKILNSDTL
NYYISHCAEILSLGDTRLIPLRVENLITQVAPRRTPTPRPPQPDSTTSPNTHQISHPQPSLLEQAEGLLLRIFLHCPQERQVIIETLGS
TNLEFSVSHHRFLWEKSLQFPSQTLDLISQLQNLYLETQNDLGPVQHIFQLNEKNKQEILLRTSQLVQAAIACMEKVFRENRYRH
FLELWQKTDPSTDPDQYSLYAQTIYADKMRIQELSKQRQLSIADLINMKLAEAESTMNKTVEATQRAFNSIRTGRANASLLDKV
QVDYYGSPTSLKSLANITTPDATTILIQPYDRTSLNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKELVKLAAKYAEEGRVG
IRNIRRDALDSIRKQEKAGEVSEDESRDQQDKLQKITSKYTAKIDELLAEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDS
EGAQLGIMAPLEALRLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVR
VKQAERFLKDGDKVKATVMFRGREIQHSDLAETLLNRMATDLEPFGEVQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIEK
ISLERNLPRLAVQSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIDGEGFRVLSTKTIVEEVTNGDHQISLDEVQQVA
PEAQSGDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSFGQPEVE
AELPKREQLPNDTYRSNATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRT
KIAVDTLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLA
IGKEGQNVRLAARLTGWKIDIKDQAKYDYGAEDAKFAAVRANYQEESNQLDNQFEVMEEEYEDDPDAGEDDFNSMEEENMS
KKSLASLSAADISDKRALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLISKGAKVILASHFGRPKGVDEKLRLTPVAKRLSELL
GQEVIKTDDCIGDDVTAQVAALEKGQVLLLENVRFYKEEENNDPEFARQLAANADFYVNDAFGTAHRAHASTEGVTKYLSPS
VAGYLVEKELQYLQGAIEVPQRPLVAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEQDKLGLASSLEK
KAAERGVTLLLPTDIVAADKFGPDADAVTVSIDHIPDDRMGLDIGPDSVKVFQAALADCKTVIWNGPMGVFEFDKFAVGTEAI
AQTLAEISKTGATTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGKVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAAS
LGRLLKSRDYSVSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDY
NGGTVQVIPHITNEIKERVIRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGKQNVLYMHVTLLPWIASAGEMKTKPT
QHSVKELRSIGIQPDILVCRCDRPIPVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQREPDLTHWE
TMVERMSHPQSPVEIAIVGKYVRLGDAYLSVVESLRHAAIATYGDLRLRWVNSEILEVPPDNYLLGVDGIIVPGGFGIRGVDG
KISAIEYARNQQIPFLGLCLGMQCSIIEWARNVEGLVGANSAEFDPKTDYPVINLLPEQQDVIDLGGTMRLGLYPCHVQPNTLAF
DLYQEEVIYERHRHRYEFNNLYRNHLLNSGYVISGTSPDGRLVEIVEYPQHPFFIACQFHPEFQSRPSHPHPLFKGFMEAAISHTH
QGKKPNYPLRVSSVPMVKKVSRRLQALQAKVEERDYTPLEALALLKETATAKFAEAAEAHIRLGIDPKYTDQQLRTTVVLPKG
TGQIVRVAVIARGEKVTEATNAGADIAGSEELIDEIQKGMMDFDKLIATPDVMPVAKLGKLLGPRGLMPSPKGGTVTFDIASA
ISEFKAGKLEFRADRTGIVHVMFGKASFSSEDLLVNLKALQETIDRNRPSGAKGRYWRTFYISSTMGPSIKIDINALRDFKTTDV

AMGTRSYRPYTPSTRQVTISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRDITATVIAVEYDP
NRNARIALVEYEDGEKRYILHPNGLKVGAKITAGPQAPFEDGNALPLSNIPLGTNVHNVEMTPGKGGQIVRAAGATAQLMAKE
GNYVTLKLPSGEVRMVRRECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTP
WGKPALGAKTRKRKKASSKLIVRRRRKSSKRGRGGRQSMSVGILGTKLGMTQIFDEAGVSIPVTVIQAGPCTVTQVKTQPTDG
YCAIQVGYGEVKPKALNKPKLGHLAKSSAGPVRYLNEYRTDAAGDYALGQEIKADIFSVGQIVDVIGTSIGRGFAGNQKRNNF
GRGPMSHGSKNHRAPGSIGAGTTPGRVYPGKRMAGRLGGSRVTVRKLTVVKVDAERNLILIKGAIPGKPGGLVNVVPTTKVG
NKMVESTVKNWQGEEVGQTSFELRVAKEETASHIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIR
SPLWRGGGVIFGPKPRDFNIKLNRKERRLALRTAFVSRREDLIVVEEFTDQLQRPKSKELVAALARWGATADQKTLLILSEIGQN
TETISLSARNVENIKVIAADQLNVFDLLHADKIVVTSSALTKIQEVYSAMATTRLKTLYGQTIVPKLTQQFQYTNVHQVPKVLK
VTVNRGLGEAAQNAKALEASLSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGV
SAKSFDGRGNYTLGVREQLIFPEIEYDRIDQIRGLDISIITTAKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGTKV
VVKGPKGELSRDLPAHVTVSQSGETLLVTRRDDTRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGANLVLN
IGYSHQVQIEPPAGVQFVVENNTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRKAGKTGGKGKKMAKKVV
AVIKLALNAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSD
QPNKKKVGSITRTQLKEIAQTKLPDLNANDIEAAMNIVEGTAKNMGVTIKDMSTATDQILEQLKSLTLLEAAELVKQIEEAFGV
SAAAPAGGMMMMAAPGGAAAAEVVEEQTEFDVILQEVPADKKIAVLKIVREITGLGLKEAKELVESTPKAVKEGVNKESADD
ISKKITEAGGKVTIKMSSKTYLPPEEEIKRDWYVVDAADKRLGRLASEIAMVLRGKRKAEYTPHLDTGDFVVVINAEKVVVTG
KKQSQKLYRRHSGRPGGMKTETFAKLQQRLPERIVEHAVKGMLPKNSLGRQLFTKLKVYSGATHPHTAQKPKELIINTIPGEN
MIQPQTYLNVADNSGARKLMCIRVLGAGNRRYGGVGDRIIAVVKDAQPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDN
AAVIINKEGNPKGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITS
RQIEASRRAMTRYIRRGGKIWIRIFPDKPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKT
KFIVRSQPQEQEMNAQEIIRSIEAEQLKSDLPQIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVE
RVFLLHSPRIDNIKIMRRGKVRRAKLYYLRQLSGKATRIKQRFDRALMTRVKRGNVARNRRNKILKLAKGFRGSHSTLFRTAN
QQVMKALRSAYRDRKKKKRDFRRLWITRINAASRQQGLSYSQLIGNLKKANVELNRKMLAQLAVLDPTTFAKVAELASSVKG
NMAHKKGTGSTRNGRDSNAQRLGVKRFGGQVVRAGNILVRQRGTKFHPGNNVGIGNDDTLFALIDGVVTFERKGKSRKKVS
VYPRVTEEAVASMNNENYMEPSFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGHNYKLKEPKYSVEESKRRD
STYGVQMYVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWL
KFETDRNDLVWVRIDKTRKLSIQVLLKALGLLDNEILDALRHPEYFQKTIEKEGQFSEEEALLELYRKLRPGEPPTVMGGQQLLE
SRFFDPKRYDLGRVGRYKLNKKLRLSVPDTTRVLTPGDILSAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNR
LERIIRERMTVSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHY
GRICPIETPEGPNAGLIGSLATHARVNQYGFLETPFRPVENGRVCYEKPAVYMTADEEDDLRVAPGDIPVDDNGQILGIQVPVRY
RQEFSTTTPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSGMVIVSRTD

GDVVYVDATEIRVRVKEKAALTNRESESIPHKPQEIKYVLSKYQRSNQDTCLNQKPLVRIGEKVIAGQVLADGSSTEGGELALG
QNVIVAYMPWEGYNYEDAILISERLVQEDVYTSIHIEKFEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRVGAWVESGDIL
VGKVTPKGESDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRIVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDK
MAGRHGNKGIISRILPLEDMPYLPDGTPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGEESSRRIVHGK
LWEAREETSKDWVYNPENPGKIMVYDGRTGEPFDRAVTVGIAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQR
FGEMEVWALEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLD
VEVDLMADQVSRRTPPRPTYESFSRDSLDEDEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLM
DDAYNYMRSQAEQGKKFLFVGTKRQAAGIIAQEANRCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREENGALDLLPK
KEASMLRREMSKLQKYLGGIKNMRKVPDVVIIVDQRREYNAVQECQKLSIPIVSMLDTNCDPDTVDIPIPANDDAIRSIKLIVGK
LADAIYEGRHGQLEVESDYEEYESAEEDYEYDESEFVDSFSDDDDEEMGQKIHPVGFRLGITQEHQSLWFAVPGRYPELLQEDH
KLRQYIEQKLGRNAQNNAGLSEIHIERKADQVDLELRTARPGVVVGRGGQGIEALRTGLQQLLGSHRQVRINVVEVQKVDAD
AYLIAEYIAQQLERRVSFRRVVRQAIQRAQRAGVQGIKVQVSGRLNGAEIARTEWTREGRVPLHTLRADIDYSYCTAQTVYGIL
GIKVWVFKGEIIPGQEDIVSQPVTREREPRRRQQQRRRQQFEDRSNEAMATGRRKASKAKKEETNWQERVIQIRRVSKVVKGG
KKLSFRAIVIVGNERGQVGVGVGKASDVIGAVKKGVADGKKHLIEIPITKSNSIPHPIDGVGGGAKVIMRPAAPGTGVIAGGAV
RTVLELAGVRNVLAKQLGSNNPLNNARAAVNALSTLRTFAEVAEDRGIAVENLYIMATVAETNSGRALYWGTGRRKSAVAQ
VRLVPGEGKFVVNGKEGELYFQYNPNYLGVIKAPLETLGLENEYDILVKAKGGGLTGQADSIRLGVARALCQLDPDNRSPLKIE
GYLTRDPRAKERKKYGLHKARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVL
RSPHVDKDSREHFETRTHRRIIDIHQPSSKTIDALMKLDLPSGVDIEVKLMARQPTKKTGSKKQKKNVPNGVAYIQSTFNNSIVTI
TDQNGDVISWASAGSSGFKGAKKGTPFAAQTAAESAGRRAIDQGMRQIQVMVSGPGAGRETAIRALQGAGLEITLIRDVTPIPH
NGCRPPKRRRVMARIAGVDLPRDKRVEIGLTYIYGIGLRRSQDILAATDVNPDTRVKDLTDADLAALRAEIESNYQVEGDLRRL
EAMNIKRLVDIGCYRGRRHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLSKIEKLNANNEK
QVIKTWSRASTILPLMVGHTIAVHNGKQHVPVFVNEQMVGHKLGEFAPTRSYRGHGKTDKKSGRMSDKNEGYKIISDNRQAR
YLYEILETYEAGIQLTGTEVKSIRAGKVNLQDGYALLRDGEAWLINAHISPYTASGQYFNHEPRRTRKLLLHGLEIRKLIGKVEQ
QGLTLIPLKMYFKRGWVKISIGLCRGKKVHDKREDLKRRQDQRDIQRAMKNYMAEISAKLVQDLRQKTGAGMMDCKKALNE
TQGNIDEAIDWLRKKGIASAGKKSDRVTAEGLVDIYTTPDKSGGVIIEVNCQTDFVARNDAFKLLVKNLAKQAVNADNVASLL
DQPYIEKTDVTVDEYIKETIATLGENIQVRRFVNFSLEGAPGAIDGYIHTGGRVGVLVSIGVDTETAAKNEELQSLAKNTAMQV
AACPNVEYVSVDKIPDQVVEKEKEIEMGKEDLGNKPANIKEKIVQGRIDKRLKEMTLLDQPYIRDQNISVAELIKQVESKVSEPI
KVHQFVRYILGEGIEKQESNFAEEVAAQIGAK

>Cylindrospermopsis_raciborskii_PAMP2012_PROT
MQIPRLHPDTVEEVKHRADIVDVISDYVVLRRRGKDFVGLCPFHEEKTPSFTVSPNKQIYYCFGCQASGNAIRFIMDLNKRKFAE
VVLDLAKRYQVPVKTLAPEQRQELQRQLSLREQLFEVLASTSQFYQHVLRQDIGQQALQYLQKKRFLKTETVEKFALGYAPPG
WETLYHYLVENKSYPAQLVEKAGLIKPRKEGGGYYDAFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFDKSKTLF
ALDVAKDAISKLDQAVVVEGYFDAIALHANGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATERAIGEISNL
AYKGEVRLKILHIPDGKDADEYLKNHSVTDYEQLLVEAPLWLDWQIAQVIQGRDLKQPTDFQLVSREFVKLLQKILNSDTLNY
YISHCAEILSLGDTRLIPLRVENLITQVAPRRTPTPILRPPASPNTHQISHPQPSLLEQAEGLLLRIFLHCPQERQVIIETLGSSNLEFS
VSHYRFLWEKSLQFPSQTLDLISQLQNLYLETQNDLGPVEHIFQLNEKNKQEILLRTNQLVQAAIACMEKVFRENRYRHFLELW
QKTDPSTDPDQYNLYAQTIYADKMRIQELSKRQLSISDLINMKLAEAESTMNKTVEATQRAFNSIRTGRANASLLDKVQVDY
YGSPTPLKSLTNITTPDASTILIQPYDRSSLNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKELVKLAAKYAEEGRVGIRNIR
RDALDSIRKQEKAGEISEDESRDQQDKLQKITGKYTAKIDELLTEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDSEGAQL
GIMAPLEALRLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKQHTADVKEVKMRYKIEEHDYNVRVKQAE
RFLKDGDKVKATVMFRGREIQHSDLAETLLNRMATDLEPFGEIQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIEKISLERN
LPRLAVQSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIDGEGFRVLSTKTIVEEVTNGDHQISLDEVQQVAPEAQS
GDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSFGQPEVEAELPK
REQLPNDTYRSNATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAVD
TLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIGKEG
QNVRLAARLTGWKIDIKDQAKYDYGAEDAKFAAVRANYQEESNQPDNQFEIIEEGYEDDPDEGEDDFNSMEEENKCDKLIIGG
GMIFTFYKARGLNVGKSLVEQDKLELASSLEKKAAERGVTLLLPTDIVAADKFAPDADAVTVSIENIPDDRMGLDIGPDSVKLF
QDALADCKTVIWNGPMGVFEFDKFAVGTEAIAQTLAEIGKTGATTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGTV
LPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRDYSVSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHY
ERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGGTVQVIPHITNEIKERVIRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLR
KEVGKQNVLYMHVTLLPWIASAGEMKTKPTQHSVKELRSIGIQPDILVCRCDRPIPVGLKQKLSEFCDVPVECVITCQDASSIYE
VPLILEKEGLAQQTLDLLQMEQREPDLTHWETMVERMSHPQSPVEIAIVGKYVRLGDAYLSVVESLRHAAIATYGDLRLRWVN
SEILEVEPPDNYLLGVDGIIVPGGFGIRGVDGKISAIEYARNRQIPFLGLCLGMQCSIIEWARNVEGLVGANSAEFDPKTDYPVINL
LPEQQDVIDMGGTMRLGLYPCHVQPNTLAFDLYQEEVIYERHRHRYEFNNLYRNHLLNSGYVISGTSPDGRLVEIVEYPQHPFF
IACQFHPEFQSRPSHPHPLFKGFMEAAISHTHQGKKQLPHGFPQFPMVKKVSRRLQALQAKVEERDYAPLEALALLKETATAKF
PEAAEAHIRLGIDPKYTDQQLRTTVVLPKGTGQIVRVAVIARGEKVTEATNSGADIAGSEELIDEIQKGMMDFDKLIATPDVMP
QVAKLGKLLGPRGLMPSPKGGTVTFDIASAISEFKAGKLEFRADRTGIVHVMFGKASFSSEDLLVNLKALQETIDRNRPSGAKG
RYWRTFYISSTMGPSIKVDINALRDLKTTDAAMGTRSYRPYTPSTRQVTISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRR
GGGHKQLYRIIDFKRDKRDITATVIAVEYDPNRNARIALLEYEDGEKRYILHPNGLKVGAKVTAGPQAPFEDGNALPLSNIPLGT
NVHNVEMTPGKGGQIVRAAGATAQLMAKEGNYVTLKLPSGEVRMVRRECYATIGQVGNTDARNLSAGKAGRNRWKGRRPK

VRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPALGAKTRKRKKASSKLIVRRRRKSSKRGRGGRQSMSVGILGTKLGMTQ
IFDEAGVSIPVTVIKAGPCTVTQVKTQPTDGYCAIQVGYGEVKPKALNKPKLGHLAKSSAVPVRYLNEYRTDAAGDYALGQEI
KADIFSVGQIVDVIGTSIGRGFAGNQKRNNFGRGPMSHGSKNHRAPGSIGAGTTPGRVYPGKRMAGRLGGSRVTVRKLTVVKV
DAERNLILIKGAIPGKPGGLVNVVPTTKVGNKMVESIVKNWQGEEVGQTSFELRVAKEETASHIVHRALVRQMTNSRQGTAST
KTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFGPKPREFNIKLNRKERRLALRTAFVSRREDLIVVEEFTDQLQRPK
SKELVAALARWGATADQKTLLILSEIGQSTETISLSARNVENIKVIAADQLNVFDLLHADKIVVTSSALTKIQEVYSAMATTRLK
TLYGQTIVPKLTQQFQYTNVHQVPKVLKVTVNRGLGEAAQNAKALEASLSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIM
VTLRGERMYAFLDRLISLALPRIRDFRGVSAKSFDGRGNYTLGVREQLIFPEIEYDRIDQIRGLDISIITTAKTDEEGRALLKEMG
MPFRDQMSRIGKRPITIPAKVQVAIDGTKVVVKGPKGELSRDLPTHVTVSQSGETLLVTRRDDTRTSRQMHGLSRTLVANMVE
GVSQGFQRRLEIQGVGYRAQVQGANLVLNIGYSHQVQIEPPAGVQFAVENNTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGK
GIRYAGEVVRRKAGKTGGKGKKMAKKVVAVIKLALNAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEIS
VFEDRSFTFVLKTPPASVLIRKAAKIERGSDQPNKKKVGSITRTQLREIAQTKLPDLNANDIEAAMNIVEGTAKNMGVTVKDMS
TATDQILEQLKVLTLLEAAELVKQIEEAFGVSAAAPAGGMMVMAAPGAAAAEPVEEQTEFNVVLEEVPADKKIAVLKIVREIT
GLGLKEAKELVESTPKAVKEGVNKESAEEISKKIAEAGGKVVIKMSSKTYLPPEEEIKRDWYVVDAADKRLGRLASEIAMVLR
GKRKAEYTPHLDTGDFVVVINAEKVVVTGKKPSQKLYRRHSGRPGGMKTETFAKLQQRLPERIVEHAVKGMLPKNSLGRQLF
TKLKVYSGSTHPHTAQKPKELIINTIPGENMIQPQTYLNVADNSGARKLMCIRVLGAGNRRYGGVGDRIIAVVKDAQPNMAVK
KSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKEGNPKGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRG
RMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRRAMTRYIRRGGKIWIRIFPDKPVTMRPAETRMGSGKGNPEFWVAVVK
PGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQPQEQEMNAQEIIRSIEAEQLKSDLPQIYVGDTVRVGVKIKEGDKYRVQ
PYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSPRIDNIKIMRRGKVRRAKLYYLRQLSGKATRIKQRFDRALMTRVKRG
NVARNRRNKILKLAKGFRGSHSTLFRTANQQVMKALRSAYRDRKKKKRDFRRLWITRINAASRQQGLSYSQLIGNLKKANVE
LNRKMLAQLAVLDPATFAKVAELASSVKGMAHKKGTGSTRNGRDSNAQRLGVKRFGGQVVRAGNILVRQRGTKFHPGNNV
GIGNDDTLFALIDGVVTFERKGKSRKKVSVYPPVTEESVASMNNENYTEPSFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYT
GKLELHFLGHNYKLKEPKYSVEESKRRDSTYGVQMYVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSP
GVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDLVWVRIDKTRKLSIQVLLKALGLSDNEILDALRHPEYFQKTIEKEGQFS
EEEALLELYRKLRPGEPPTVMGGQQLLESRFFDPKRYDLGRVGRYKLNKKLRLSVPDTTRVLTPGDILSAVDYLINLEYDIGSID
DIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRERMTVSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHK
RRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEGPNAGLIGSLATHARVNQYGFLETPFRPVENGRVCYEKPAVYMTADE
EDDLRVAPGDIPVDDNGQILGIQVPVRYRQEFSTTTPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLK
PERPLVGTGLEAQGARDSGMVIVSRTDGDVVYVDATEIRVRVKEKAALTNRESETIPHKPQEIKYVLSKYQRSNQDTCLNQKPL
VRIGEKVIAGQVLADGSSTEGGELALGQNVIVAYMPWEGYNYEDAILISERLVQEDVYTSIHIEKFEIEARQTKLGPEEITREIPN
VGEDALRQLDEQGIIRVGAWVESGDILVGKVTPKGESDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQG

DELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKGIISRILPLEDMPYLPDGTPVDIVLNPLGVPSRMNVGQVFECLLGWAG
HNLGVRFKITPFDEMYGEESSRRIVHGKLWEAREETSRDWVYNPENPGKIMVYDGRTGEPFDRAVTVGIAYMLKLVHLVDDKI
HARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWALEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKV
LMRELQSLGLDIAVHKVETQTDGSSLDVEVDLMADQVSRRTPPRPTYESFSRDSLDEDEMPVVSLAQMMESGVHFGHQTRRW
NPKMSPYIYTARNGVHIIDLVQTAQLMDDAYNYMRSQAEQGKKFLFVGTKRQAAGIIAQEANRCGSHYINQRWLGGMLTNW
ATIKTRADRLKDLERREENGALDLLPKKEASMLRREMSKLQKYLGGIKNMRKVPDVVIIVDQRREYNAVQECQKLSIPIVSML
DTNCDPDTVDVPIPANDDAIRSIKLIVGKLADAIYEGRHGQLEVEPDDEDYDIPEEDYEYNESEMGQKIHPVGFRLGITQEHQSL
WFAVPGRYPELLQEDHKLRQYIEQKLGRNAQNNAGLSEIHIERKADQVDLELRTARPGVVVGRGGQGIEALRTGLQQLLGSHR
QVRINVVEVQKVDADAYLIAEYIAQQLERRVSFRRVVRQAIQRAQRAGVQGIKVQVSGRLNGAEIARTEWTREGRVPLHTLRA
DIDYSYCTAQTVYGILGIKVWVFKGEIIPGQEDIVSQPVTREREPRRRQQQRRRQQFEDRSNEAMATGRRKASKAKKEETNWQ
ERVIQIRRVSKVVKGGKKLSFRAIVIVGNERGQVGVGVGKASDVIGAVKKGVADGKKHLIEIPITKSNSIPHPIDGVGGGAKVIM
RPAAPGTGVIAGGAVRTVLELAGVRNVLAKQLGSNNPLNNARAAVNALSTLRTFAEVAEDRGIAVENLYIMATVAETNSGRA
LYWGTGRRKSAVAQVRLVPGEGKFVVNGKEGELYFQYNPNYLGVIKAPLETLGLENEYDILVKAKGGGLTGQADSIRLGVAR
ALCQLDPDNRSPLKIEGYLTRDPRAKERKKYGLHKARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNAT
AIGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTHRRIIDIHQPSSKTIDALMKLDLPSGVDIEVKLMARQPTKKTGSKKQKKNVP
NGVAYIQSTFNNSIVTITDQNGDVISWASAGSSGFKGAKKGTPFAAQTAAESAGRRAIDQGMRQIQVMVSGPGAGRETAIRALQ
GAGLEITLIRDVTPIPHNGCRPPKRRRVMARIAGVDLPRDKRVEIGLTYIYGIGLRRSQDILAATDVNPDTRVKDLTDADLAALR
AEIESNYQVEGDLRRLEAMNIKRLVDIGCYRGRRHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVA
DHLLSKLEKLNANNEKQVIKTWSRASTILPLMVGHTIAVHNGKQHVPVFVNEQMVGHKLGEFAPTRTYRGHGKTDKKSGRMS
DKNEGYKIISDNRQARYLYEILETYEAGIQLTGTEVKSIRAGKVNLQDGYALLRDGEAWLINAHISPYTASGQYFNHEPRRTRK
LLLHGLEIRKLIGKVEQQGLTLIPLKMYFKRGWVKISIGLCRGKKVHDKREDLKRRQDQRDIQRAMKNYMAEISAKLVQDLRQ
KTGAGMMDCKKALNETQGNIDEAIDWLRKKGIASAGKKSDRVTAEGLVDIYTTPDRSGGVLIEVNCQTDFVARNDAFKLLVK
NLAKQAVNADNVTSLLAQPYIENTDVTVDEYIKETIATLGENIQVRRFVNFSLEGSPGAIDGYIHTGGRVGVLISIGVDTETAAK
NEEVQSLAKNTAMQVAACPNVEYVSVDKIPDQVVQKEKEIEMGKEDLGNKPENIKEKIVQGRIDKRLKEMTLLDQPYIRDQSIS
VAELIKQVESKVSEPIKVHQFVRYILGEGIEKQESNFAQEVAAQIGAK

>Cylindrospermopsis_sp_CR12
MQIPRLHPDTVEEVKHRADIVDVISDYVVLRRRGKDFVGLCPFHEEKTPSFTVSPTKQIYYCFGCQASGNAIKFMMDLNKRQFA
EVVLDLAKRYQVPVKTLAPEQRQELQRQLSLREQLFEVLASTSQFYQHVLRQDIGQQALQYLQKKRFLKTETVEKFALGYAPP
GWETLYHYLVENKNYPAQLVEKAGLIKPRKEGGGYKEGGGYYDVFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETEL
FDKSKTLFALDVSKDAISKLDQAVVVEGYFDAIALHANGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATER
AIGEISNLAYKGEVQLKILHIPDGKDADEYLKNHSVTDYGQLLVDAPLWLDWQIAQVIQGRDLRQPTDFQLVSREFVKLLQKIL
NSDTLNYYISHCAEILSLGDTRLIPLRVENLITQVAPRRTPTPRPPQPDSTTSPNTHQISHPQPSLLEQAEGLLLRIFLHCPQERQVII
ETLGSTNLEFSVSHHRFLWEKSLQFPSQTLDLISQLQNLYLETQNDLGPVQHIFQLNEKNKQEILLRTSQLVQAAIACMEKVFRE
NRYRHFLELWQKTDPSMDPDQYSLYAQTIYADKMRIQELSKQRQLSIADLINMKLAEAESTMNKTVEATQRAFNSIRTGRANA
SLLDKVQVDYYGSPTSLKSLANITTPDATTILIQPYDRTSLNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKELVKLAAKYA
EEGRVGIRNIRRDALDSIRKQEKAGEVSEDESRDQQDKLQKITSKYTAKIDELLAEKEKDITTVMPVIEKKRTRDLPQINERIRFP
KIRVIDSEGAQLGIMAPLEALRLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEH
DYNVRVKQAERFLKDGDKVKATVMFRGREIQHSDLAETLLNRMATDLEPFGEVQQAPKKEGRNMMMLISPKKMSMVTLPGL
KDLIEKISLERNLPRLAVQSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIDGEGFRVLSTKTIVEEVTNGDHQISLDE
VQQVAPEAQSGDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSF
GQPEVEAELPKREQLPNDTYRSNATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSR
YVGPRTKIAVDTLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAE
DQLSLAIGKEGQNVRLAARLTGWKIDIKDQAKYDYGAEDAKFAAVRANYQEESNQLDNQFEVMEEEYEDDPDAGEDDFNSM
EEENMSKKSLASLSAADISDKRALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLISKGAKVILASHFGRPKGVDEKLRLTPVAK
RLSELLGQEVIKTDDCIGDDVTAQVAALEKGQVLLLENVRFYKEEENNDPEFARQLAANADFYVNDAFGTAHRAHASTEGVT
KYLSPSVAGYLVEKELQYLQGAIEVPQRPLVAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEQDKLGL
ASSLEKKAAERGVTLLLPTDIVAADKFGPDADAVTVSIDHIPDDRMGLDIGPDSVKVFQAALADCKTVIWNGPMGVFEFDKFA
VGTEAIAQTLAEISKTGATTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGKVLPGIAALDEAMTKFIFVTGGVVSSIGK
GIVAASLGRLLKSRDYSVSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKE
RRGDYNGGTVQVIPHITNEIKERVIRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGKQNVLYMHVTLLPWIASAGEM
KTKPTQHSVKELRSIGIQPDILVCRCDRPIPVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQREPDL
THWETMVERMSHPQSPVEIAIVGKYVRLGDAYLSVVESLRHAAIATYGDLRLRWVNSEILEVEPPDNYLLGVDGIIVPGGFGIR
GVDGKISAIEYARNQQIPFLGLCLGMQCSIIEWARNVEGLVGANSAEFDPKTDYPVINLLPEQQDVIDLGGTMRLGLYPCHVQP
NTLAFDLYQEEVIYERHRHRYEFNNLYRNHLLNSGYVISGTSPDGRLVEIVEYPQHPFFIACQFHPEFQSRPSHPHPLFKGFMEA
AISHTHQGSTPMVKKVSRRLQALQAKVEERDYTPLEALALLKETATAKFAEAAEAHIRLGIDPKYTDQQLRTTVVLPKGTGQIV
RVAVIARGEKVTEATNAGADIAGSEELIDEIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDIASAISEFK
AGKLEFRADRTGIVHVMFGKASFSSEDLLVNLKALQETIDRNRPSGAKGRYWRTFYISSTMGPSIKIDINALRDFKTTDVAMGT

RSYRPYTPSTRQVTISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRDITATVIAVEYDPNRNA
RIALVEYEDGEKRYILHPNGLKVGAKITAGPQAPFEDGNALPLSNIPLGTNVHNVEMTPGKGGQIVRAAGATAQLMAKEGNYV
TLKLPSGEVRMVRRECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKP
ALGAKTRKRKKASSKLIVRRRRKSSKRGRGGRQSMSVGILGTKLGMTQIFDEAGVSIPVTVIQAGPCTVTQVKTQPTDGYCAIQ
VGYGEVKPKALNKPKLGHLAKSSAGPVRYLNEYRTDAAGDYALGQEIKADIFSVGQIVDVIGTSIGRGFAGNQKRNNFGRGPM
SHGSKNHRAPGSIGAGTTPGRVYPGKRMAGRLGGSRVTVRKLTVVKVDAERNLILIKGAIPGKPGGLVNVVPTTKVGNKMVES
TVKNWQGEEVGQTSFELRVAKEETASHIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRG
GGVIFGPKPRDFNIKLNRKERRLALRTAFVSRREDLIVVEEFTDQLQRPKSKELVAALARWGATADQKTLLILSEIGQNTETISLS
ARNVENIKVIAADQLNVFDLLHADKIVVTSSALTKIQEVYSAMATTRLKTLYGQTIVPKLTQQFQYTNVHQVPKVLKVTVNRG
LGEAAQNAKALEASLSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSAKSFDG
RGNYTLGVREQLIFPEIEYDRIDQIRGLDISIITTAKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGTKVVVKGPK
GELSRDLPAHVTVSQSGETLLVTRRDDTRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGANLVLNIGYSHQ
VQIEPPAGVQFVVENNTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRKAGKTGGKGKKMAKKVVAVIKLA
LNAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSDQPNKK
KVGSITRTQLKEIAQTKLPDLNANDIEAAMNIVEGTAKNMGVTIKDMSTATDQILEQLKSLTLLEAAELVKQIEEAFGVSAAAP
AGGMMMMAAPGGAAAAEVVEEQTEFDVILQEVPADKKIAVLKIVREITGLGLKEAKELVESTPKAVKEGVNKESADDISKKIT
EAGGKVTIKMSSKTYLPPEEEIKRDWYVVDAADKRLGRLASEIAMVLRGKRKAEYTPHLDTGDFVVVINAEKVVVTGKKQSQ
KLYRRHSGRPGGMKTETFAKLQQRLPERIVEHAVKGMLPKNSLGRQLFTKLKVYSGATHPHTAQKPKELIINTIPGENMIQPQT
YLNVADNSGARKLMCIRVLGAGNRRYGGVGDRIIAVVKDAQPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIIN
KEGNPKGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEAS
RRAMTRYIRRGGKIWIRIFPDKPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRS
QPQEQEMNAQEIIRSIEAEQLKSDLPQIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLL
HSPRIDNIKIMRRGKVRRAKLYYLRQLSGKATRIKQRFDRALMTRVKRGNVARNRRNKILKLAKGFRGSHSTLFRTANQQVMK
ALRSAYRDRKKKKRDFRRLWITRINAASRQQGLSYSQLIGNLKKANVELNRKMLAQLAVLDPTTFAKVAELASSVKGNMAHK
KGTGSTRNGRDSNAQRLGVKRFGGQVVRAGNILVRQRGTKFHPGNNVGIGNDDTLFALIDGVVTFERKGKSRKKVSVYPRVT
EEAVASMNNENYMEPSFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGHNYKLKEPKYSVEESKRRDSTYGVQ
MYVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDR
NDLVWVRIDKTRKLSIQVLLKALGLLDNEILDALRHPEYFQKTIEKEGQFSEEEALLELYRKLRPGEPPTVMGGQQLLESRFFDP
KRYDLGRVGRYKLNKKLRLSVPDTTRVLTPGDILSAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRE
RMTVSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIE
TPEGPNAGLIGSLATHARVNQYGFLETPFRPVENGRVCYEKPAVYMTADEEDDLRVAPGDIPVDDNGQILGIQVPVRYRQEFST
TTPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSGMVIVSRTDGDVVY

VDATEIRVRVKEKAALTNRESESIPHKPQEIKYVLSKYQRSNQDTCLNQKPLVRIGEKVIAGQVLADGSSTEGGELALGQNVIV
AYMPWEGYNYEDAILISERLVQEDVYTSIHIEKFEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRVGAWVESGDILVGKVT
PKGESDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRIVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRH
GNKGIISRILPLEDMPYLPDGTPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGEESSRRIVHGKLWEAR
EETSKDWVYNPENPGKIMVYDGRTGEPFDRAVTVGIAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEME
VWALEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLDVEVDL
MADQVSRRTPPRPTYESFSRDSLDEDEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLMDDAYN
YMRSQAEQGKKFLFVGTKRQAAGIIAQEANRCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREENGALDLLPKKEASML
RREMSKLQKYLGGIKNMRKVPDVVIIVDQRREYNAVQECQKLSIPIVSMLDTNCDPDTVDIPIPANDDAIRSIKLIVGKLADAIYE
GRHGQLEVESDYEEYESAEEDYEYDESEFVDSFSDDDDEEMGQKIHPVGFRLGITQEHQSLWFAVPGRYPELLQEDHKLRQYIE
QKLGRNAQNNAGLSEIHIERKADQVDLELRTARPGVVVGRGGQGIEALRTGLQQLLGSHRQVRINVVEVQKVDADAYLIAEYI
AQQLERRVSFRRVVRQAIQRAQRAGVQGIKVQVSGRLNGAEIARTEWTREGRVPLHTLRADIDYSYCTAQTVYGILGIKVWVF
KGEIIPGQEDIVSQPVTREREPRRRQQQRRRQQFEDRSNEAMATGRRKASKAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAI
VIVGNERGQVGVGVGKASDVIGAVKKGVADGKKHLIEIPITKSNSIPHPIDGVGGGAKVIMRPAAPGTGVIAGGAVRTVLELAG
VRNVLAKQLGSNNPLNNARAAVNALSTLRTFAEVAEDRGIAVENLYIMATVAETNSGRALYWGTGRRKSAVAQVRLVPGEG
KFVVNGKEGELYFQYNPNYLGVIKAPLETLGLENEYDILVKAKGGGLTGQADSIRLGVARALCQLDPDNRSPLKIEGYLTRDPR
AKERKKYGLHKARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGIPIPLPTKRKIYCVLRSPHVDKD
SREHFETRTHRRIIDIHQPSSKTIDALMKLDLPSGVDIEVKLMARQPTKKTGSKKQKKNVPNGVAYIQSTFNNSIVTITDQNGDVI
SWASAGSSGFKGAKKGTPFAAQTAAESAGRRAIDQGMRQIQVMVSGPGAGRETAIRALQGAGLEITLIRDVTPIPHNGCRPPKR
RRVMARIAGVDLPRDKRVEIGLTYIYGIGLRRSQDILAATDVNPDTRVKDLTDADLAALRAEIESNYQVEGDLRRLEAMNIKRL
VDIGCYRGRRHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLSKIEKLNANNEKQVIKTWSR
ASTILPLMVGHTIAVHNGKQHVPVFVNEQMVGHKLGEFAPTRSYRGHGKTDKKSGRMSDKNEGYKIISDNRQARYLYEILETY
EAGIQLTGTEVKSIRAGKVNLQDGYALLRDGEAWLINAHISPYTASGQYFNHEPRRTRKLLLHGLEIRKLIGKVEQQGLTLIPLK
MYFKRGWVKISIGLCRGKKVHDKREDLKRRQDQRDIQRAMKNYMAEISAKLVQDLRQKTGAGMMDCKKALNETQGNIDEAI
DWLRKKGIASAGKKSDRVTAEGLVDIYTTPDKSGGVIIEVNCQTDFVARNDAFKLLVKNLAKQAVNADNVASLLDQPYIEKTD
VTVDEYIKETIATLGENIQVRRFVNFSLEGAPGAIDGYIHTGGRVGVLVSIGVDTETAAKNEELQSLAKNTAMQVAACPNVEYV
SVDKIPDQVVEKEKEIEMGKEDLGNKPANIKEKIVQGRIDKRLKEMTLLDQPYIRDQNISVAELIKQVESKVSEPIKVHQFVRYIL
GEGIEKQESNFAEEVAAQIGAK

>Raphidiopsis_brookii_D9
MQIPRLHPDTVEEVKHRADIVDVISDYVVLRRRGKDFVGLCPFHEEKTPSFTVSPNKQIYYCFGCQASGNAIRFIMDLNKRKFAE
VVLDLAKRYQIPVKTLAPEQRQELQRQLSLRDQLFEVLASTSQFYQHVLRQDIGQQALQYLQKKRFLKTETVEKFALGYAPPG
WETLYHYLVENKSYPAQLVEKAGLIKPRKEGGGYYDVFRNRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFDKSKTLF
ALDVAKDAISKLDQAVVVEGYFDAIALHANGINNVVASLGTALSLEQVRLLLRYSESKQLVLNFDGDKAGINATERAIGEISNL
AYKGEVRLKILHIPDGKDADEYLKNHSVTDYEQLLVEAPLWLDWQIAQVIQGRDLKQPTDFQLVSREFVKLLQKILNSDTLNY
YISHCAEILSLGDTRLIPLRVENLITQVAPRRTPTPILRPPASPNTHQISHPQPSLLEQAEGLLLRIFLHCPQERQVIIETLGSSNLEFS
VSHYRFLWEKSLQFPSQTLDLISQLQNLYLETQNDLGPVEHIFQLNEKNKQEILLRTNQLVQAAIACMEKVFRENRYRHFLELW
QKTDPSTDPDQYNLYAQTIYADKMRIQELSKQRQLSISDLINMKLAEAESTMNKTVEATQRAFNSIRTGRANASLLDKVQVDY
YGSPTPLKSLSNITTPDASTILIQPYDRSSLNIVEKAISLSDVGLTPSNDGSVVRLNIPPLTSDRRKELVKLAAKYAEEGRVGIRNIR
RDALDSIRKQEKAGEISEDESRDQQDKLQKITGKYTAKIDELLAEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDNEGAQ
LGIMAPLEALRLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVKQA
ERFLKDGDKVKATVMFRGREIQHSDLAETLLNRMATDLEPFGEIQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIEKISLER
NLPRLAVQSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIDGEGFRVLSTKIIVEEVTNSDHQISLDEVQQVAPEAQS
GDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSSFGQPEVEAELPK
REQLPNDTYRSNATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAVD
TLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIGKEG
QNVRLAARLTGWKIDIKDQAKYDYGAEDAKFAAVRANYQEESNQFEVIEEEYERDPDEGEDDFNSMEEENMSKKSLASLSAA
DISDKRALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLISKGAKVILASHFGRPKGVDEKFRLTPVAKRLSELLGQEVIKTNDCI
GDDVTARVAALEQGQVLLLENVRFHKEEEKNDPEFARQLAANADFYVNDAFGTAHRAHASTEGVTKYLSPSVAGYLVEKEL
QYLQAAIEFPQRPLAAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEQDKLELASSLEKKAAERGVTLL
LPTDIVAADKFAPDADAVTVSIENIPDDRMGLDIGPKSVKLFQDALADCKTVIWNGPMGVFEFDKFAVGTEAIAQTLAEIGKTG
ATTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGTVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRDYS
VSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTYMSRLNSVTTGLIYQSVINKERRGDYNGGTVQVIPHIT
NEIKERVIRVAKETNPAALITEIGGTVGDIESLPFLEAIRQLRKEVGKQNVLYMHVTLLPWIASAGEMKTKPTQHSVKELRSIGIQ
PDILVCRCDRPIPVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQREPDLTHWETMVERMSHPQSP
VEIAIVGKYVRLGDAYLSVVESLRHAAIATYGDLRLRWVNSEILEVPPDNYLLGVDGIIVPGGFGIRGVDGKISAIEYARNRQIP
FLGLCLGMQCSIIEWARNVEGLVGANSAEFDPKTDYPVINLLPDQQDVIDIGGTMRLGLYPCHVQPNTLAFDLYQEEVIYERHR
HRYEFNNLYRNHLLNSGYVISGTSPDGRLVEIVEYPQHPFFIACQFHPEFQSRPSHPHPLFKGFMEAAISHTHQGKKQLPHGFPQF
PMVKKVSRRLQALQAKVEERDYAPLEALSLLKETATAKFPEAAEAHIRLGIDPKYTDQQLRTTVVLPKGTGQIVRVAVIARGE
KVTEATNAGADIAGSEELIDEIQRGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDIASAISEFKAGKLEFRAD
RTGIVHVMFGKASFSSEDLLVNLKALQETIDRNRPSGAKGRYWRTFYISSTMGPSIKVDINALRDLKTTDAAMGTRSYRPYTPS

TRQVTISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRDITATVIAVEYDPNRNARIALLEYED
GEKRYILHPNGLKVGAKVTAGPQAPFEDGNALPLSNIPLGTNVHNVEMTPGKGGQIVRAAGATAQLMAKEGNYVTLKLPSGE
VRMVRRECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPALGAKTR
KRKKASSKLIVRRRRKSSKRGRGGRQSMSVGILGTKLGMTQIFDEAGVSIPVTVIKAGPCTVTQVKTQPTDGYCAIQVGYGEVK
PKALNQPKLGHLAKSSAGPVRYLNEYRTDAAGDYALGQEIKADIFSVGQIVDVIGTSIGRGFAGNQKRNNFGRGPMSHGSKNH
RAPGSIGAGTTPGRVYPGKRMAGRLGGSRVTVRKLTVVKVDAERNLILIKGAIPGKPGGLVNVVPTTKVGNKMVESIVKNWQ
GEEVGQTSFELRIAKEETASHIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFGPK
PRDFNIKLNRKERRLALRTAFVSRREDLIVVEEFTDQLQRPKSKELVAALARWGATAEQKTLLILSEIGQSTETISLSARNVENIK
VIAADQLNVFDLLHADKIVVTSSALNKIQEVYSAMATTRLKTLYGQTIVPKLTQQFQYTNVHQVPKVLKVTVNRGLGEAAQN
AKALEASLSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSAKSFDGRGNYTLG
VREQLIFPEIEYDRIDQIRGLDISIITTAKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGTKVVVKGPKGELSRDLP
THVTVSQSGETLLVTRRDDTRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGANLVLNIGYSHQVQIEPPAG
VQFVVENNTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRKAGKTGGKGKKMAKKVVAVIKLALNAGKAN
PAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSDQPNKKKVGSITRT
QLKEIAQTKLPDLNANDIEAAMNIVEGTAKNMGVTVKDMSTATDQILEQLKVLTLLEAAELVKQIEEAFGVSAAAPAGGMMV
MAAPGAAAAEPVEEQTEFNVVLEEVPADKKIAVLKIVREITGLGLKEAKELVESTPKAVKEGVNKESAEEISKKIAEAGGKVVI
KMSSKTYLPPEEEIKRDWYVVDAADKRLGRLASEIAMVLRGKRKAEYTPHLDTGDFVVINAEKVVVTGKKPSQKLYRRHSG
RPGGMKTETFAKLQQRLPERIVEHAVKGMLPKNSLGRQLFTKLKVYSGSTHPHTAQKPKELIINTIPGENMIQPQTYLNVADNS
GARKLMCIRVLGAGNRRYGGVGDRIIAVVKDAQPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKEGNPKGTR
VFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRRAMTRYIR
RGGKIWIRIFPDKPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQPQEQEMNA
QEIIRSIEAEQLKSDLPQIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSPRIDNIKIM
RRGKVRRAKLYYLRQLSGKATRIKQRFDRALMTRVKRGNVARNRRNKILKLAKGFRGSHSTLFRTANQQVMKALRSAYRDR
KKKKRDFRRLWITRINAASRQQGLSYSQLIGNLKKANVELNRKMLAQLAVLDPATFAKVAELASSVKGMAHKKGTGSTRNGR
DSNAQRLGVKRFGGQVVRAGNILVRQRGTKFHPGNNVGIGNDDTLFALIDGVVTFERKGKSRKKVSVYPRVTEEAVASMNNE
NYMEPSFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGHNYKLKEPKYSVEESKRRDSTYGVQMYVPTRLLNK
ETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDLVWVRIDK
TRKLSIQVLLKALGLSDNEILDALRHPEYFQKTIEKEGQFSEEEALLELYRKLRPGEPPTVMGGQQLLESRFFDPKRYDLGRVGR
YKLNKKLRLSVPDTTRVLTPGDILSAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRERMTVSDAEVL
TPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEGPNAGLIG
SLATHARVNQYGFLETPFRPVENGRVCYEKPAVYMTADEEDDLRVAPGDIPVDDNGQILGIQVPVRYRQEFSTTTPEQVDYVA
VSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSGMVIVSRTDGDVVYVDATEIRVRV

KEKAALTNRESETIPHKPQEVKYVLSKYQRSNQDTCLNQKPLVRIGEKVIAGQVLADGSSTEGGELALGQNVIVAYMPWEGYN
YEDAILISERLVQEDVYTSIHIEKFEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRVGAWVESGDILVGKVTPKGESDQPPE
EKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKGIISRILP
LEDMPYLPDGTPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGEESSRRIVHGKLWEAREETSRDWVY
NPENPGKIMVYDGRTGEPFDRAVTVGIAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWALEAFGA
AYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLDVEVDLMADQVSRRT
PPRPTYESFSRDSLDEDEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLMDDAYNYMRSQAEQG
KKFLFVGTKRQAAGIIAQEANRCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREENGALDLLPKKEASMLRREMSKLQK
YLGGIKNMRKVPDVVIIVDQRREYNAVQECQKLSIPIVSMLDTNCDPDTVDIPIPANDDAIRSIKLIVGKLADAIYEGRHGQLEVE
PDYEDYDIPEEDYEDEEPGYVDHFSDDDDEEMGQKIHPVGFRLGITQEHQSLWFAVPGRYPELLQEDHKLRQYIEQKLGRNAQ
NNAGLSEIHIERKADQVDLELRTARPGVVVGRGGQGIEALRTGLQQLLGSHRQVRINVVEVQKVDADAYLIAEYIAQQLERRV
SFRRVVRQAIQRAQRAGVQGIKVQVSGRLNGAEIARTEWTREGRVPLHTLRADIDYSYCTAQTVYGILGVKVWVFKGEIIPGQE
DIVSQPVTREREPRRRQQQRRRQQFEDRSNEAMATGRRKASKAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAIVIVGNERG
QVGVGVGKASDVIGAVKKGVADGKKHLIEIPITKSNSIPHPIDGVGGGAKVIMRPAAPGTGVIAGGAVRTVLELAGVRNVLAK
QLGSNNPLNNARAAVNALSTLRTFAEVAEDRGIAVENLYIMATVAETNSGRALYWGTGRRKSAVAQVRLVPGEGKFVVNGK
EGELYFQYNPNYLGVIKAPLETLGLENEYDILVKAKGGGLTGQADSIRLGVARALCQLDPDNRSPLKIEGYLTRDPRAKERKKY
GLHKARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETR
THRRIIDIHQPSSKTIDALMKLDLPSGVDIEVKLMARQPTKKTGSKKQKKNVPNGVAYIQSTFNNSIVTITDQNGDVISWASAGS
SGFKGAKKGTPFAAQTAAESAGRRAIDQGMRQIQVMVSGPGAGRETAIRALQGAGLEITLIRDVTPIPHNGCRPPKRRRVMARI
AGVDLPRDKRVEIGLTYIYGIGLRRSQDILAATDVNPDTRVKDLTDADLAALRAEIESNYQVEGDLRRLEAMNIKRLVDIGCYR
GRRHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLSKLEKLNANNEKQVIKTWSRASTILPL
MVGHTIAVHNGKQHVPVFVNEQMVGHKLGEFAPTRTYRGHGKTDKKSGRMSDKNEGYKIISDNRQARYLYEILETYEAGIQL
TGTEVKSIRAGKVNLQDGYALLRDGEAWLINAHISPYTASGQYFNHEPRRTRKLLLHGLEIRKLIGKVEQQGLTLIPLKMYFKR
GWVKISIGLCRGKKVHDKREDLKRRQDQRDIQRAMKNYMAEISAKLVQDLRQKTGAGMMDCKKALNETQGNIDEAIDWLRK
KGIASAGKKSDRVTAEGLVDIYTTPDRSGGVLIEVNCQTDFVARNDAFKLLVKNLAKQAVNADNVTSLLAQPYIENTDVTVDD
YIKETIATLGENIQVRRFVNFSLEGAPGVIDGYIHTGGRVGVLVSIGVYTETAAKNEEVQSLARNTAMQVAACPNVEYVSVDKI
PDQVVQKEKEIEMGKEDLGNKPENIKEKIVQGRIDKRLKEMTLLDQPYIRDQNISVAELIKQVESKLSEPIIVHQFVRYILGEGIE
KQESNFAQEVAAQIGAK

>Sphaerospermopsis_kisseleviana_NIES_73
MQIPRLHPDTIEEVKHRADIVDVVSDYVVLRRRGKDFVGLCPFHDEKTPSFTVSPSKQMYYCFGCQAAGNAIKFVMDLNKRHF
AEVVLDLAKRYQVPVKTLAPEQRQELQRQISLREQLYEILASTAQFYQHALRQNLGQKAMQYLQENRQLKIETIQQFGLGYAP
PGWETLHRYLVENKNYPVQLVEKAGLIKPRKEGGGYYDVFRDRLMIPIHDVQGRVIAFGGRTLTDEQPKYLNSPETELFSKGK
TLFALDQAKDGISKSDQGVVVEGYFDAIALHAAGINNVVASLGTALSIEQVRLLLRYSDSKQLILNFDADNAGINAAERAIGEIA
TLAYKGEVQLKILNIPDGKDADEYLQTHTAAEYQQLLTNAPLWLNWQIEEIIKDRDLKQATNFQIVTKEMVKILQKIVNSDTLN
YYISYCAEILSLGDARLIPLRVENLLTQIAPASVQTPPLRLRKPESKTPKLSLVTTERSLLEQAEALLLRIFLHCPEQRQIIFEELEER
NLEFSLSHHRFLWQKSLEFPLEEVDLISNLQNRYLELEEDLKIVSHVFHLNEKNKQEILRTPQVVQATLACMEIVLREKRYRHFM
ELWEKVDPQIEPEKNKSYYDNAIAEKRRIQELDKQRQFSIAELMKLAEAESTMQKTVEATQRAFNTIRTGRANASLLDKVQVD
YYGSPTPLKSLANISTPDASTILIQPYDKKSLNMVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKEFAKLAAKYAEEGRVGIRN
IRRDALDSIRKQEKNAEISEDESRDQQDKLQKLTNKYTAKIDDLLAEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDTDG
GQLGIMPPHEALKLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVK
QAERFLKDGDKVKATVMFRGREIQHSDLAEDLLKRMATDLEPFGEVQQAPKKEGRNMMMLISPKKMVTLPGLKDLIESISRER
NLPRLAVQSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIEGEGFRVLSTKTIVEEVTNTDHQISLDEVQQVAPEAQS
GDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLESTVLQARVLRFERQSVILAVSSGFGQPEVEAELPK
REQLPNDTYRSNTTFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAVD
TLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIGKEG
QNVRLAARLTGWKIDIKDQAKYDYAAEDAKFAAVRAKYQAENDETEMEQLEDEYQDKLELENDNFETNEEETMSKKSLASL
SAADISGKRALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLTQKGAKVILTSHFGRPKGVDDKLRLTPVAKRLSELLGQEVVK
TDDCIGDDVAAKVAALENGQVLLLENVRFYKEEEKNDPEFAQKLAANADFYVNDAFGTAHRAHASTEGVTKYLSPSVAGYL
VEKELQYLQSAIEVPQRPLAAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLSVGKSLVEEDKLELAKSLEAKAKER
GVTFLLPTDIVAADKFAPDANATTVSIENIPADGMGLDIGPDSVKVFQDALADCKTVIWNGPMGVFEFDQFAVGTEAIAHTLAE
IGKTGTTTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGKVLPGIAALDEADLGHYERFTDTSMSRLNSVTTGLIYQSVI
NKERRGDYNGGTVQVIPHITNEIKDRILRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGRQNVLYMHVTLLPWIASA
GEMKTKPTQHSVKELRSIGIQPDILVCRCDRPIGVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQR
QPDLSQWETMVERMYSPKYSVEIAIVGKYVRLSDAYLSVVESLRHAAISTYGDLRIRWVNSETLETESAENYLAGVDGILVPGG
FGSRGIDGKIAAIKFARDRQIPFLGLCLGMQCSVIEWARNVEGLADANSAEFDPYTTNPIINLLPEQQDVVDLGGTMRLGLYPCR
VQPGTIAFDLYQEEVIYERHRHRYEFNNLYRNALLESGYVVSGTSPDGRLVEIVEYPKHPFFIACQFHPEFQSRPSTPHPLFKGFM
EAAISRTHHSKNTSKPVQVSMGKKISRRLQALLEKVEDRDYAPLDALALLKETATAKFPEAAEAHIRLGIDPKYTDQQLRTTVA
LPKGTGQVVRVAVIARGEKVTEATNAGADIAGSEELIDEIQGMMDFDKLIATPDVMPVAKLGKLLGPRGLMPSPKGGTVTF
DVASAIAEFKAGKLEFRADRTGIVHVMFGKASFTPEDLLVNLKALQETIDRNRPSGAKGRYWRTFYVSATMGPSIKVDINALRD
LKVTDAAMGTRSYRPYTPSTRQVTISDFAEITKTEPEKSLTESVHRAKGRNNQGRITSRRRGGGHKKLYRIIDFKRDKRNIAATV

TAIEYDPNRNARIALVQYEDGEKRYILHPNGLKVGAKIIAGSEAPFEDGNALPLSNIPLGTNVHNVELTAGKGGQIVRAAGATA
QVVAKEGNYVTLKLPSGEVRMIRKECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGR
SGPVTPWGKPALGAKTRKRKKASTKLIVMSVGILGTKLGMTQIFDEAGVAIPVTVIKAGPCTVTQVKTKQTDGYSAIQVGYGE
VKPKALNQPKLGHLAKSSAPALRHLNEYRTDTASEYALGQEIKADIFSEGQIVDVIGTSIGRGFAGNQKRNNFGRGPMSHGSKN
HRAPGSIGAGTTPGRVYPGKRMAGRLGGTRVTIRKLTVVKVDAERNLILVKGAIPGKPGGLVNVVPTNKVGNKMVESVVKNW
QGEEVGQTSFELRVAKEETAAHIVHRALVRQMTNSRQGTVSTKTRSEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFG
PKPRDFNIKLNRKERRLALRTAFVSRAEDLIVVEEFSNELQRPKTKELVAALARWGAVPEQKTLLILSEIAENVNLSARNVENLK
VIAADQLNVFDLLHAGKIVVTSSALTKIQEVYSAMATTRLKTVYQETIVPKLTQQFQYTNVHQVPKVVKITVNRGLGEAAQNA
KALEASLNEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSPKSFDGRGNYTLGV
REQLIFPEVEYDSIDQIRGLDISIITTAKNDEEGRALLKEMGMPFRDQMSRIGKRPITVPAKVQVAIDGTKVVVKGPKGELSRDLP
ANVIVSQEGETLLVTRRDETRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGRNLVLNIGYSHQVQIEPPDGI
QFAVENNTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRMAKKVVAVIKLALNAGKANPAPPVGPALGQHG
VNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSEQPNKKKVGSITKAQLREIAQTKLPDLN
ANDIDAAMNIVAGTAKNMGVTITDMSTATDQILEQLKSLTLLEAAELVKQIEEAFGVSAAAPAGGMMMMAAPGAAAPAEAV
EEKTEFDAILESVPADKKIAVLKIVREITGLGLKEAKDLVEAAPKPVKEGVNKEAAEDIKKRIAEAGGTVTIKMSSKTYLPPQEK
LEREWYVVDATDKRLGRLASEIAMVLRGKRKAEYTPHLDTGDFVVVINAEKVAVTGKKRTQKVYRRHSGRPGGMKTETFAK
LQQRLPERIVEHAVKGMLPKNSLGKQLFTKLKVYAGPTHPHAAQKPKELIVNTIPGENMIQPQTYLNVADNSGAKKLMCIRVL
GAGNRRYGGVGDKIIAVVKESNPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKDGNPRGTRVFGPVARELRD
KNFTKIVSLAPEVLMLSPKRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRRAMTRYIRRGGKIWIRIFPD
KPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQPQEQEMNVQEVIRSIEAEHL
KSDLPEIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSPRIDNIKVVRRGKVRRAKL
YYLRQLSGKATRIKQRFDRALMTRVKRGNVARKRRNKILKLAKGFRGSHSTLFRTANQQVMKALRSAYRDRKKKKRDFRRL
WITRINAASRQHGLSYSQLIGNLKKANVDLNRKMLAQLAVLDPASFAKVAELANSAKGMAHKKGTGSTRNGRDSNAQRLGV
KRFGGQTVLAGNILVRQRGTKFHPGNNVGIGSDDTLFALVDGVVTFERKGKSRKKVSVYPAIAAEAVASMTNETYMEPAFLLP
DLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFIGQNYKLKEPKYSVEESKRRDSTYAVQMYVPTRLLNKETGDIKEQEV
FIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDLVWVRIDKTRKLSAQVLL
KALGLSDNEIFDALRHPEYFQKTIEKEGQFSEEEALMELYRKLRPGEPPTVLGGQQLLDSRFFDPKRYDLGRVGRYKLNKKLRL
SVPDTMRVLTPGDILAAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRERMTVSDAEVLTPASLVNPK
PLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEGPNAGLIGSLATHARVN
QYGFLETPFRPVENGRVCYEKAAVYMTADEEDDLRVAPGDIPVDENGHIIGPQVPVRYRQEFSTTTPEQVDYVAVSPVQIVSVA
TSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQAARDSGMVIVSRTDGDVVYADANEIRVRVRERTGDRLQV
TGDSEETSSFPVSKPQEIKYVLSKYQRSNQDTCLNQKPLVRIGEKVVAGQVLADGSSTEGGELALGQNIVVAYMPWEGYNYED

AILISERLVQDDVYTSIHIEKYEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRIGAWVESGDILVGKVTPKGESDQPPEEKLL
RAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKGIISRILPAED
MPYLPDGSPVDIVLNPLGVPSRMNVGQVFECLLGWAGQNLGVRFKITPFDEMYGEESSRRIVHGKLQEARDETGKTWVYNPD
DSGKIMVYDGRTGEPFDRPVTVGVAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWALEAFGAAYT
LQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQADGSSLDVEVDLMADQGSRRTPPR
PTYESLSRESLEEDEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLMDDAYNYMRTQAEQGKK
FLFVGTKRQAAGIIAQEANRCGSHYINQRWLGGMLTNWATIKTRAERLKDLERREENGALDLLPKKEASMLRREMAKLQKYL
GGIKNMRKVPDIVVIVDQRREYNAVQECQKLGIPIVSMLDTNCDPDVVDIPIPANDDAIRSIKLIVGKLADAIYEGRHGQLEVEE
DYEDYEGAEEEYDYDESEYTDSMMSDDDEEMGQKIHPVGFRLGITQEHQSRWFAVPDRYPALLQEDHKLRQYIEKKLGRTAQ
NNAGISEIRIERKADQIDLELRTARPGVVVGRGGQGIESLRTGLQDLLGGQRQIRINVVEVQKVDADAYLIAEYIAQQLERRVSF
RRVVRQAIQRAQRAGVQGIKVQVGGRLNGAEIARTEWTREGRVPLHTLRADIDYSYCTAQTIYGILGIKVWVFKGEIIPGQEEA
PQPSGREREPRRRDQKRRRQQFEDRSNEAMATGRRKASKAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAIVIVGNERGQVG
VGVGKASDVIGAVKKGVADGKKHLIEIPITKSNSIPHPIDGIGGGAKVIMRPAAPGTGVIAGGAVRTVLELAGVRNVLAKQLGS
SNPLNNARAAVNALSTLRTFAEVAEDRGIAVENLYIMATVAEANSGRAVYWGTGRRKSAVAQVRLVPGEGKFTVNGKDGEL
YFQFNANYLGAIKAPLETLGLESEYDILVKAEGGGLTGQADSIRLGVARALCQLDPDNRSPLKIEGYLTRDPRAKERKKYGLHK
ARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTHRRI
IDIYQPSSKTIDALMKLDLPSGVDIEVKLMARQPTKKTGSKKQKRNVPNGIAYIQSTFNNSIVTITDQNGDVISWASAGSSGFKG
AKKGTPFAAQTAAESAGRRAMDQGMRQIEVMVSGPGAGRETAIRALQGAGLEITLIRDITPIPHNGCRPPKRRRVMARISGVDL
PRDKRVEIGLTYIYGIGLTRSQEILAATGVNPDTRVKDLSDADVAALRAEIESNYQVEGDLRRLEAMSIKRLVDIGCYRGRRHR
MGLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLSKIEKLNEKNEKQVIKTWSRASTIIPVMVGHTIA
VHNGKQHVPVFVNEQMVGHKLGEFAPTRTYRGHGKSDKKSGRMSDKNEGYKVISDNRQARYLYEILETYEAGIQLAGTEVKS
IRAGKANLQDGYALIRNGEAWLINVHISPYTSSGQYFNHEPRRTRKLLLHRQELRKLIGKVEQQGLTLVPLKMYLKRGWVKVSI
GLCKGKKIHDKRESLKRRQDQRDIQRAMKNYMAEISAKLVQELRQKTGAGMMDCKKALKENDGNIDAAIDWLRKKGIASAG
KKSDRVAAEGLVDTYIQPDGKVGVLIEVNCQTDFVARNDAFKTLVKNLAQQAATADSVESLLAQPYIEKAEVTVDEFIKESIAT
LGENIQVRRFVNFSLGDTPGVVDSYIHTGGRVGVLLQVIAKTDDAAGNEEFKKFAKNAAMQVAACPNVEYVSVDQIPAETVQ
KEKDIEMGKEDLANKPENIREKIVQGRIEKRLKELTLLDQPYIRDQSISVADLVKQVQSKVGEDITVHGFVRYVLGEGIEKQESN
FAEEVAAQMGAK

>Sphaerospermopsis_sp_FACHB_1194
MQIPRLHPDTIEEVKHRADIVDVVSDYVVLRRRGKDFVGLCPFHDEKTPSFTVSPSKQMYYCFGCQAAGNAIKFVMDLNKRHF
AEVVLDLAKRYQVPVKTLAPEQRQELQRQISLREQLYEILASTAQFYQHALRQNLGQKAMQYLQENRQLKIETIQQFGLGYAP
PGWETLHRYLVENKNYPVQLVEKAGLIKPRKEGGGYYDVFRDRLMIPIHDVQGRVIAFGGRTLTDEQPKYLNSPETELFSKGK
TLFALDQAKDGISKSDQGVVVEGYFDAIALHAAGINNVVASLGTALSIEQVRLLLRYSDSKQLILNFDADNAGINAAERAIGEIA
TLAYKGEVQLKILNIPDGKDADEYLQTHTAAEYQQLLTNAPLWLNWQIEEIIKDRDLKQATNFQIVTKEMVKILQKIVNSDTLN
YYISYCAEILSLGDARLIPLRVENLLTQIAPASVQTPPLRLRKPESKTPKLSLVTTERSLLEQAEALLLRIFLHCPEQRQIIFEELEER
NLEFSLSHHRFLWQKSLEFPLEEVDLISNLQNRYLELEEDLKIVSHVFHLNEKNKQEILRTPQVVQATLACMEIVLREKRYRHFM
ELWEKVDPQIEPEKNKSYYDNAIAEKRRIQELDKQRQFSIAELMQKTVEATQRAFNTIRTGRANASLLDKVQVEYYGNPTPLKS
LANISTPDATTILIQPYDKKSLNMVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKEFAKLAAKYAEEGRVGIRNIRRDALDSIR
KQEKNAEISEDESRDQQDKLQKLTNKYTAKIDDLLAEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDTDGGQLGIMPPHE
ALKLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVKQAERFLKDGD
KVKATVMFRGREIQHSDLAEDLLKRMATDLEPFGEVQQAPKKEGRNMMMLISPKKMSMVALPGLKDLIESISRERNLPRLAVQ
SSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIEGEGFRVLSTKTIVEEVTNTDHQISLDEVQQVAPEAQSGDSVVLDV
TPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLESTVLQARVLRFERQSVILAVSSGFGQPEVEAELPKREQLPNDT
YRSNTTFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAVDTLDRDVDP
VGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIGKEGQNVRLAAR
LTGWKIDIKDQAKYDYAAEDAKFAAVRAKYQAENDETEMEQLEDEYQDKLELENDNFETNEEETVSKKSLASLSAADISGKR
ALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLTQKGAKVILTSHFGRPKGVDEKLRLTPVAKRLSELLGQEVVKTDDCIGDDV
AAKVAALENGQVLLLENVRFYKEEEKNDPEFAQKLAANADFYVNDAFGTAHRAHASTEGVTKYLSPSVAGYLVEKELQYLQ
SAIEVPQRPLAAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLSVGKSLVEEDKLELAKSLEAKAKERGVALLLPTD
VVLADNFAADANSQTVTIEAIPDGWMGLDIGPDSVKVFQEALADCKTVIWNGPMGVFEFDKFAAGTEAIAHTLAEIGKTGTTTI
IGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGKVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRDYSVSIL
KLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGGTVQVIPHITNEIK
DRILRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGRQNVLYMHVTLLPWIASAGEMKTKPTQHSVKELRSIGIQPDIL
VCRCDRPIGVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQRQPDLSQWETMVERMYSPKYSVEI
AIVGKYVRLSDAYLSVVESLRHAAISTYGDLRIRWVNSETLETESAENYLAGVDGILVPGGFGSRGIDGKIAAIKFARDRQIPFLG
LCLGMQCSVIEWARNVEGLADANSAEFDPYTTNPIINLLPEQQDVVDLGGTMRLGLYPCRVQPGTIAFDLYQEEVIYERHRHRY
EFNNLYRNALLGSGYVVSGTSPDGRLVEIVEYPKHPFFIACQFHPEFQSRPSTPHPLFKGFMEAAISRTHHSKNTSKPVQVSMGK
KISRRLQALLEKVEDRDYAPLDALALLKETATAKFPEAAEAHIRLGIDPKYTDQQLRTTVALPKGTGQVVRVAVIARGEKVTEA
TNAGADIAGSEELIDEIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDVASAIAEFKAGKLEFRADRTGIV
HVMFGKASFTPEDLLVNLKALQETIDRNRPSGAKGRYWRTFYVSATMGPSIKVDINALRDLKVTDAAMGTRSYRPYTPSTRQV

TISDFAEITKTEPEKSLTESVHRAKGRNNQGRITSRRRGGGHKKLYRIIDFKRDKRNIAATVTAIEYDPNRNARIALVQYEDGEK
RYILHPNGLKVGAKIIAGPEAPFEDGNALPLSNIPLGTNVHNVELTAGKGGQIVRAAGATAQVVAKEGNYVTLKLPSGEVRMIR
KECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPALGAKTRKRKKAS
TKLIVMSVGILGTKLGMTQIFDEAGVAIPVTVIKAGPCTVTQVKTQQTDGYSAIQVGYGEVKPKALNQPKLGHLAKSSAPALRH
LNEYRTDTASEYALGQEIKADIFSEGQIVDVIGTSIGRGFAGNQKRNNFGRGPMSHGSKNHRAPGSIGAGTTPGRVYPGKRMAG
RLGGTRVTIRKLTVVKVDAERNLILVKGAIPGKPGGLVNVVPTNKVGNKMVESVVKNWQGEEVGQTSFELRVAKEETAAHIV
HRALVRQMTNSRQGTVSTKTRSEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFGPKPRDFNIKLNRKERRLALRTAFVS
RAEDLIVVEEFSNELQRPKTKELVAALARWGAVPEQKTLLILSEIAENVNLSARNVENLKVIAADQLNVFDLLHADKIVVTSSA
LTKIQEVYSAMATTRLKTVYQETIVPKLTQQFQYTNVHQVPKVVKITVNRGLGEAAQNAKALEASLNEIALITGQKPVVTRAK
KAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSPKSFDGRGNYTLGVREQLIFPEVEYDSIDQIRGLDISIIT
TAKNDEEGRALLKEMGMPFRDQMSRIGKRPITVPAKVQVAIDGTKVVVKGPKGELSRDLPANVIVSQEGETLLVTRRDETRTS
RQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGRNLVLNIGYSHQVQIEPPDGIQFAVENNTNVIVSGYDKEVVGN
TAAKIRAVRPPEPYKGKGIRYAGEVVRRMAKKVVAVIKLALNAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMV
IPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSEQPNKKKVGSITKAQLREIAQTKLPDLNANDIDAAMNIVAGTAKNMGVTI
TDMSTATDQILEQLKSLTLLEAAELVKQIEEAFGVSAAAPAGGMMMMAAPGAAAPAEAVEEKTEFDAILESVPADKKIAVLKI
VREITGLGLKEAKDLVEAAPKPVKEGVNKEAAEDIKKRIAEAGGTVTIKMSSKTYLPPQEKLEREWYVVDATDKRLGRLASEI
AMVLRGKRKAEYTPHLDTGDFVVVINAEKVAVTGKKRTQKVYRRHSGRPGGMKTETFAKLQQRLPERIVEHAVKGMLPKNS
LGKQLFTKLKVYAGPTHPHAAQKPKELIVNTIPGENMIQPQTYLNVADNSGAKKLMCIRVLGAGNRRYGGVGDKIIAVVKESN
PNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKDGNPRGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPKRTKF
RKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRRAMTRYIRRGGKIWIRIFPDKPVTMRPAETRMGSGKGNPEF
WVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQPQEQEMNVQEVIRSIEAEHLKSDLPEIYVGDTVRVGVKIKE
GDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSPRIDNIKVVRRGKVRRAKLYYLRQLSGKATRIKQRFDRAL
MTRVKRGNVARKRRNKILKLAKGFRGSHSTLFRTANQQVMKALRSAYRDRKKKKRDFRRLWITRINAASRQHGLSYSQLIGN
LKKANVDLNRKMLAQLAVLDPASFAKVAELANSAKGMAHKKGTGSTRNGRDSNAQRLGVKRFGGQTVLAGNILVRQRGTK
FHPGNNVGIGSDDTLFALVDGVVTFERKGKSRKKVSVYPAIAAEAVASMTNETYMEPAFLLPDLIEIQRSSFRWFLEEGLIEELN
SFSPITDYTGKLELHFIGQNYKLKEPKYSVEESKRRDSTYAVQMYVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVI
VNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDLVWVRIDKTRKLSAQVLLKALGLSDNEIFDALRHPEYFQK
TIEKEGQFSEEEALMELYRKLRPGEPPTVLGGQQLLDSRFFDPKRYDLGRVGRYKLNKKLRLSVPDTMRVLTPGDILAAVDYLI
NLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRERMTVSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQT
NPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEGPNAGLIGSLATHARVNQYGFLETPFRPVENGRVCYEK
AAVYMTADEEDDLRVAPGDIPVDENGHIIGPQVPVRYRQEFSTTTPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSN
MQRQAVPLLKPERPLVGTGLEAQAARDSGMVIVSRTDGDVVYADANEIRVRVRERTGDRLQVTGDSEETSSFPVSKPQEIKYV

LSKYQRSNQDTCLNQKPLVRIGEKVVAGQVLADGSSTEGGELALGQNIVVAYMPWEGYNYEDAILISERLVQDDVYTSIHIEK
YEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRIGAWVESGDILVGKVTPKGESDQPPEEKLLRAIFGEKARDVRDNSLRVP
NGEKGRVVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKGIISRILPAEDMPYLPDGSPVDIVLNPLGVP
SRMNVGQVFECLLGWAGQNLGVRFKITPFDEMYGEESSRRIVHGKLQEARDETGKTWVYNPNDSGKIMVYDGRTGEPFDRPV
TVGVAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWALEAFGAAYTLQELLTVKSDDMQGRNEAL
NAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQADGSSLDVEVDLMADQGSRRTPPRPTYMPVVSLAQMMESGVHF
GHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLMDDAYNYMRTQAEQGKKFLFVGTKRQAAGIIAQEANRCGSHYINQRWL
GGMLTNWATIKTRAERLKDLERREENGALDLLPKKEASMLRREMAKLQKYLGGIKNMRKVPDIVVIVDQRREYNAVQECQK
LGIPIVSMLDTNCDPDVVDIPIPANDDAIRSIKLIVGKLADAIYEGRHGQLEVEEDYEDYEGAEEEYDYDESEYTDSMMSDDDEE
MGQKIHPVGFRLGITQEHQSRWFAVPDRYPALLQEDHKLRQYIEKKLGRTAQNNAGISEIRIERKADQIDLELRTARPGVVVGR
GGQGIESLRTGLQDLLGGQRQIRINVVEVQKVDADAYLIAEYIAQQLERRVSFRRVVRQAIQRAQRAGVQGIKVQVGGRLNGA
EIARTEWTREGRVPLHTLRADIDYSYCTAQTIYGILGIKVWVFKGEIIPGQEEAPQPSGREREPRRRDQKRRRQQFEDRSNEAMA
TGRRKASKAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAIVIVGNERGQVGVGVGKASDVIGAVKKGVADGKKHLIEIPITK
SNSIPHPIDGIGGGAKVIMRPAAPGTGVIAGGAVRTVLELAGVRNVLAKQLGSSNPLNNARAAVNALSTLRTFAEVAEDRGIAV
ENLYIMATVAEANSGRAVYWGTGRRKSAVAQVRLVPGEGKFTVNGKDGELYFQFNANYLGAIKAPLETLGLESEYDILVKAE
GGGLTGQADSIRLGVARALCQLDPDNRSPLKIEGYLTRDPRAKERKKYGLHKARKAPQYSKRMATLQQQKIRIRLQAFDRRLL
DTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTHRRIIDIYQPSSKTIDALMKLDLPSGVDIEVKLMAR
QPTKKTGSKKQKRNVPNGIAYIQSTFNNSIVTITDQNGDVISWASAGSSGFKGAKKGTPFAAQTAAESAGRRAMDQGMRQIEV
MVSGPGAGRETAIRALQGAGLEITLIRDITPIPHNGCRPPKRRRVMARISGVDLPRDKRVEIGLTYIYGIGLTRSQEILAATGVNPD
TRVKDLSDADVAALRAEIESNYQVEGDLRRLEAMSIKRLVDIGCYRGRRHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAP
GKMGRSLKKGPFVADHLLSKIEKLNEKNEKQVIKTWSRASTIIPVMVGHTIAVHNGKQHVPVFVNEQMVGHKLGEFAPTRTYR
GHGKSDKKSGRMSDKNEGYKVISDNRQARYLYEILETYEAGIQLAGTEVKSIRAGKANLQDGYALIRNGEAWLINVHISPYTSS
GQYFNHEPRRTRKLLLHRQELRKLIGKVEQQGLTLVPLKMYLKRGWVKVSIGLCKGKKIHDKRESLKRRQDQRDIQRAMKNY
MAEISAKLVQELRQKTGAGMMDCKKALKENDGNIDAAIDWLRKKGIASAGKKSDRVAAEGLVDTYIQPDGKVGVLIEVNCQ
TDFVARNDAFKTLVKNLAQQAATADSVESLLAQPYIEKAEVTVDEFIKESIATLGENIQVRRFVNFSLGDTPGVVDSYIHTGGR
VGVLLQVIAKTDDAAGNEEFKKFAKNAAMQVAACPNVEYVSVDQIPAETVQKEKDIEMGKEDLANKPENIREKIVQGRIEKRL
KELTLLDQPYIRDQSISVADLVKQVQSKVGEDITVHGFVRYVLGEGIEKQESNFAEEVAAQMGAK

>Sphaerospermopsis_sp_LEGE_00249
MQIPRLHPDTIEEVKHRADIVDVVSDYVVLRRRGKDFVGLCPFHDEKTPSFTVSPSKQMYYCFGCQAAGNAIKFVMDLNKRHF
TEVVLDLAKRYQVPVKTLAPEQRQELQRQISLREQLYEILASTAQFYQHALRQNLGQKAMQYLQEKRLFKIETIQQFGLGYAPP
GWETLYRYLVDNKNYPVQLVEKAGLIKPRKEGGSYYDVFRDRLMIPIRDIQGRVIAFGGRTLTEEQPKYLNSPETELFSKGKTL
FALDQAKDGISKSDQGVVVEGYFDAIALHAAGINNVVASLGTALSIEQVRLLLRYSDSKQLILNFDADKAGINAAERAIGEIATL
AYKGEVQLKILNIPDGKDADEYLHSHTATEYQQLLANAPLWLNWQIEEIIKDRDLKQAANFQIVTKEMVKLLQKIVNSDTLNY
YISYCAEILSLGDARLIPLRVENLLTQIAPANVQTPPLRPRKPESKTPKLSLVTTERSLLEQAEALLLRIFLHCPEQRKVVFAELEE
RNLEFSLSHHRFLWQQSLEFPLEEVDLISNLQNRYLELEEDLKIVSHVFHLNEKNKTEILRTPQVVQATLACMERVLREKRYRHF
MELWKKIDPQAEPDKYKSYADAIYADKMRIQELDKQRQFPISELFMQKTVEATQRAFNTIRTGRANASLLDKVQVDYYGSPTP
LKSLANISTPDASTILIQPYDKKSLNMVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRREFAKLAAKYAEEGRVGIRNIRRDALD
SIRKQEKAAEISEDESRDQQDKLQKLTNKYTAKIDDLLAEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDTDGGQLGIMP
PHEALKLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVKQAERFLK
DGDKVKATVMFRGREIQHSDLAEDLLKRMATDLEPFGEVQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIESISRERNLPRL
AVQSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIEGEGFRVLSTKTIVEEVTNTDHQISLDEVQQVAPEAQSGDSV
VLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLESTVLQARVLRFERQSVILAVSSGFGQPEVEAELPKREQL
PNDTYRSNTTFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAVDTLDR
DVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIGKEGQNVR
LAARLTGWKIDIKDQAKYDYAAEDAKFAAVRAKYQAENDETEMEQLEDEYQDKLELENDNFETNEEETVSKKSLASLSAADI
SGKRALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLTQKGAKVILTSHFGRPKGVDDKLRLTPVAKRLSELLGQEVVKTDDCI
GDDVAAKVAALENGQVLLLENVRFYKEEEKNDPEFAQKLAANADFYVNDAFGTAHRAHASTEGVTKYLSPSVAGYLVEKEL
QYLQSAIEVPQRPLAAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLSVGKSLVEEDKLELAKSLEAKAKERGVALL
LPTDVVLADNFAADANSQTVSIEAIPDGWMGLDIGPDSVKVFQEALADCKTVIWNGPMGVFEFDKFAVGTEAIAHTLAEIGKT
GTTTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGKVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRDY
SVSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGGTVQVIPHI
TNEIKDRILRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGRQNVLYMHVTLLPWIASAGEMKTKPTQHSVKELRSIGI
QPDILVCRCDRPIGVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEREGLAQQTLDLLQMEQRQPDLSQWETMVERMYSPK
YSVEIAIVGKYVRLSDAYLSVVESLRHAAISTYGDLRIRWVNSETLETESAENYLAGVDGILVPGGFGSRGIDGKIAAIKFARDR
QIPFLGLCLGMQCSVIEWARNVEGLADANSAEFDPYTTNPIINLLPEQQDVVDLGGTMRLGLYPCRVQPGTIAFDLYQEEVIYER
HRHRYEFNNLYRNALLESGYVVSGTSPDGRLVEIVEYPKHPFFIACQFHPEFQSRPSTPHPLFKGFMEAAISRTHHSKNTSKPVQ
VSMGKKISRRLQALLEKVEDRDYAPLDALALLKETATAKFPEAAEAHIRLGIDPKYTDQQLRTTVALPKGTGQVVRVAVIARG
EKVTEATNAGADIAGSEELIDEIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDVASAIAEFKAGKLEFR
ADRTGIVHVMFGKASFTPEDLLVNLKALQETIDRNRPSGAKGRYWRTFYVSATMGPSIKVDINALRDLKVTDAAMGTRSYRPY

TPSTRQVTISDFAEITKTEPEKSLTESVHRAKGRNNQGRITSRRRGGGHKKLYRIIDFKRDKRNIAATVTAIEYDPNRNARIALVQ
YEDGEKRYILHPNGLKVGAKIIAGSEAPFEDGNALPLSNIPLGTNVHNVELTAGKGGQIVRAAGATAQVVAKEGNYVTLKLPS
GEVRMIRKECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPALGAKT
RKRKKASTKLIVMSVGILGTKLGMTQIFDEAGVAIPVTVIKAGPCTVTQVKTKQTDGYSAIQVGYGEVKPKALNQPKLGHLAK
SSAPALRHLNEYRTDTASEYALGQEIKADIFSEGQIVDVIGTSIGRGFAGNQKRNNFGRGPMSHGSKNHRAPGSIGAGTTPGRVY
PGKRMAGRLGGTRVTIRKLTVVKVDAERNLILVKGAIPGKPGGLVNVVPTNKVGNKMVESVVKNWQGEEVGQTSFELRVAK
EETAAHIVHRALVRQMTNSRQGTVSTKTRSEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFGPKPRDFNIKLNRKERRL
ALRTAFVSRAEDLIVVEEFSNELQRPKTKELVAALARWGAVPEQKTLLILSEIAENVNLSARNVENLKVIAADQLNVFDLLHAD
KIVVTSSALTKIQEVYSAMATTRLKTVYQETIVPKLTQQFQYTNVHQVPKVVKITVNRGLGEAAQNAKALEASLNEIALITGQK
PVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLALPRIRDFRGVSPKSFDGRGNYTLGVREQLIFPEVEYDSIDQIR
GLDISIITTAKNDEEGRALLKEMGMPFRDQMSRIGKRPITVPAKVQVAIDGTKVVVKGPKGELSRDLPANVIVSQEGETLLVTRR
DETRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGRNLVLNIGYSHQVQIEPPDGIQFAVENNTNVIVSGYDK
EVVGNTAAKIRAVRPPEPYKGKGIRYSGEVVRRMAKKVVAVIKLALNAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTAD
QAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSEQPNKKKVGSITKAQLREIAQTKLPDLNANDIDAAMNIVAGTAK
NMGVTITDMSTATDQILEQLKSLTLLEAAELVKQIEEAFGVSAAAPAGGMMMMAAPGAAAPAEAVEEKTEFDAILESVPADK
KIAVLKIVREITGLGLKEAKDLVEAAPKPVKEGVNKEAAEDIKKRIAEAGGTVTIKMSSKTYLPPQEKLEREWYVVDATDKRLG
RLASEIAMVLRGKRKAEYTPHLDTGDFVVVINAEKVAVTGKKRTQKVYRRHSGRPGGMKTETFAKLQQRLPERIVEHAVKGM
LPKNSLGKQLFTKLKVYAGPTHPHAAQKPKELIVNTIPGENMIQPQTYLNVADNSGAKKLMCIRVLGAGNRRYGGVGDKIIAV
VKESNPNMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKDGNPRGTRVFGPVARELRDKNFTKIVSLAPEVLMLSP
KRTKFRKQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRRAMTRYIRRGGKIWIRIFPDKPVTMRPAETRMGSGK
GNPEFWVAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQPQEQEMNVQEVIRSIEAEHLKSDLPEIYVGDTVRVG
VKIKEGDKYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSPRIDNIKVVRRGKVRRAKLYYLRQLSGKATRIKQR
FDRALMTRVKRGNVARKRRNKILKLAKGFRGSHSTLFRTANQQVMKALRSAYRDRKKKKRDFRRLWITRINAASRQHGLSYS
QLIGNLKKANVDLNRKMLAQLAVLDPASFAKVAELANSAKGMAHKKGTGSTRNGRDSNAQRLGVKRFGGQTVLAGNILVRQ
RGTKFHPGNNVGIGSDDTLFALVDGVVTFERKGKSRKKVSVYPAIAAEAVASMTNETYMEPAFLLPDLIEIQRSSFRWFLEEGLI
EELNSFSPITDYTGKLELHFIGQNYKLKEPKYSVEESKRRDSTYAVQMYVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGA
ERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDLVWVRIDKTRKLSAQVLLKALGLSDNEIFDALRHPE
YFQKTIEKEGQFSEEEALMELYRKLRPGEPPTVLGGQQLLDSRFFDPKRYDLGRVGRYKLNKKLRLSVPDTMRVLTPGDILAAV
DYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRERMTVSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFM
DQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEGPNAGLIGSLATHARVNQYGFLETPFRPVENGRVC
YEKAAVYMTADEEDDLRVAPGDIPVDENGHIIGPQVPVRYRQEFSTTTPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALM
GSNMQRQAVPLLKPERPLVGTGLEAQAARDSGMVIVSRTDGDVVYADANEIRVRVRERTGDRLQVTGDSEETSSSPVSKPQEI

KYVLSKYQRSNQDTCLNQKPLVRIGEKVVAGQVLADGSSTEGGELALGQNIVVAYMPWEGYNYEDAILISERLVQDDVYTSIH
IEKYEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRIGAWVESGDILVGKVTPKGESDQPPEEKLLRAIFGEKARDVRDNSLR
VPNGEKGRVVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKGIISRILPAEDMPYLPDGSPVDIVLNPLG
VPSRMNVGQVFECLLGWAGQNLGVRFKITPFDEMYGEESSRRIVHGKLQEARDETGKTWVYNPDDSGKIMVYDGRTGEPFDR
PVTVGVAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWALEAFGAAYTLQELLTVKSDDMQGRNE
ALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQADGSSLDVEVDLMADQGSRRTPPRPTYESLSRESLEEDEMPV
VSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLMDDAYNYMRTQAEQGKKFLFVGTKRQAAGIIAQEA
NRCGSHYINQRWLGGMLTNWATIKTRAERLKDLERREENGALDLLPKKEASMLRREMAKLQKYLGGIKNMRKVPDIVVIVDQ
RREYNAVQECQKLGIPIVSMLDTNCDPDVVDIPIPANDDAIRSIKLIVGKLADAIYEGRHGQLEVEEDYEDYEGAEEEYDYDESE
YTDSMMSDDDEEMGQKIHPVGFRLGITQEHQSRWFAVPDRYPALLQEDHKLRQYIEKKLGRTAQNNAGISEIRIERKADQIDLE
LRTARPGVVVGRGGQGIESLRTGLQDLLGGQRQIRINVVEVQKVDADAYLIAEYIAQQLERRVSFRRVVRQAIQRAQRAGVQG
IKVQVGGRLNGAEIARTEWTREGRVPLHTLRADIDYSYCTAQTIYGILGIKVWVFKGEIIPGQEEAPQPSGREREPRRRDQKRRR
QQFEDRSNEAMATGRRKASKAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAIVIVGNERGQVGVGVGKASDVIGAVKKGVA
DGKKHLIEIPITKSNSIPHPIDGIGGGAKVIMRPAAPGTGVIAGGAVRTVLELAGVRNVLAKQLGSSNPLNNARAAVNALSTLRT
FAEVAEDRGIAVENLYITVAEANSGRAVYWGTGRRKSAVAQVRLVPGEGKFTVNGKDGELYFQFNANYLGSIKAPLETLGLES
EYDILVKAEGGGLTGQADSIRLGVARALCQLDPDNRSPLKIEGYLTRDPRAKERKKYGLHKARKAPQYSKRMATLQQQKIRIR
LQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTHRRIIDIYQPSSKTIDALMKLDLPSGV
DIEVKLMARQPTKKTGSKKQKRNVPNGIAYIQSTFNNSIVTITDQNGDVISWASAGSSGFKGAKKGTPFAAQTAAESAGRRAM
DQGMRQIEVMVSGPGAGRETAIRALQGAGLEITLIRDITPIPHNGCRPPKRRRVMARISGVDLPRDKRVEIGLTYIYGIGLTRSQEI
LAATGVNPDTRVKDLSDADVAALRAEIESNYQVEGDLRRLEAMSIKRLVDIGCYRGRRHRMGLPVRGQRTRTNARTRRGRRQ
TVAGKKKAPGKMGRSLKKGPFVADHLLSKIEKLNEKNEKQVIKTWSRASTIIPVMVGHTIAVHNGKQHVPVFVNEQMVGHKL
GEFAPTRTYRGHGKSDKKSGRMSDKNEGYKVISDNRQARYLYEILETYEAGIQLAGTEVKSIRAGKANLQDGYALIRNGEAWL
INVHISPYTSSGQYFNHEPRRTRKLLLHRQELRKLIGKVEQQGLTLVPLKMYLKRGWVKVSIGLCKGKKIHDKRESLKRRQDQR
DIQRAMKNYMAEISAKLVQELRQKTGAGMMDCKKALKENDGNIDAAIDWLRKKGIASAGKKSDRVAAEGLVDTYIQPDGKV
GVLIEVNCQTDFVARNDAFKTLVKNLAQQAATADSVESLLAQPYIEKAEVTVDEFIKESIATLGENIQVRRFVNFSLGDTPGVV
DSYIHTGGRVGVLLQVIAKTDDAAGNEEFKKFAKNAAMQVAACPNVEYVSVDQIPAETVQKEKDIEMGKEDLANKPENIREKI
VQGRIEKRLKELTLLDQPYIRDQSISVADLVKQVQSKVGEDITVHGFVRYVLGEGIEKQESNFAEEVAAQMGAK

>Sphaerospermopsis_sp_LEGE_08334
MQIPRLHPDTIEEVKHRADIVDVVSDNVVLRRRGKDFVGLCPFHDEKTPSFTVSPSKQMYYCFGCQAAGNAIKFVMDLNKRHF
AEVVLDLAKRYQVPVKTLAPEQRQELQRQISLREQLYEILASTAQFYQHALRQNLGQKAMQYLQENRQFKIETIQQFGLGYAP
PGWETLYRYLVDNKNYPVQLVEKAGLIKPRKEGGGCYDVFRDRLMIPIRDVQGRVIAFGGRTLTDEQPKYLNSPETELFSKGK
TLFALDQAKDGISKSDQGVVVEGYFDAIALHAAGINNVVASLGTALSIEQVRLLLRYSDSKQLILNFDADKAGINAAERAIGEIA
TLAYKGEVQLKILNIPDGKDADEYLHSHTAADYQQLLANAPLWLNWQIEEIIKDRDLKQATDFQIVTKEIVKLLQKIVNSDTLN
YYISYCAEILSLGDTRLIPLRVENLLTQIAPASVQTPPLRLRKPESKTPKLSLVTTERSLLEQAEALLLRIFLHCAEQRQVIFEELEE
RNLEFSLSHHRFLWQQSLEFPLQELDLISKLQNRYLELEEDLKIVSHVFHLNEKNKTEILRTPQVVQATLACMERVLREKRYRHF
MELWKKIDPQAEPDKYKSYADAIYADKMRIQELDKQRQFPISELFMQKTVEATQRAFNTIRTGRANASLLDKVQVEYYGTPTP
LKSLANISTPDASTILIQPYDKSSLNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKEFVKLAAKYAEEGRVGIRNIRRDALDS
IRKQEKAAEISEDESRDQQDKLQKLTNKYTTRIDELLAEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDTDGGQLGIMPPH
EALKLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVKQAERFLKDG
DKVKATVMFRGREIQHSDLAEDLLKRMATDLEPFGEVQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIESISRERNLPRLAV
QSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIEGEGFRVLSTKTIVEEVTNSDHQISLDEVQQVAPEAQSGDSVVLD
VTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLESTVLQARVLRFERQSVILAVSSGFGQPEVEAELPKREQLPND
TYRSNTTFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAVDTLDRDVD
PVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIGKEGQNVRLAA
RLTGWKIDIKDQAKYDYAAEDAKFAAVRANYQAENDETEMEQLEDEYQDKLELENDNFETNEEETMSKKSLASLSAADISGK
RALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLTQKGAKVILTSHFGRPKGVDEKLRLTPVAKRLSELLGQEVVKTDDCIGDE
VAAKVAALDNGQVLLLENVRFYKEEEKNDPEFAQKLAANADFYVNDAFGTAHRAHASTEGVTKFLSPSVAGYLVEKELQYL
QSAIEAPQRPLAAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLSVGKSLVEEDKLELAKTLEAKAKERGVALLLPT
DIVAADKFAPDANATTVSIENIPADGMGLDIGPDSVKVFQEALADCKTVIWNGPMGVFEFDKFAVGTEAIAHTLAEIGKTGAITI
IGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGKVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRDYSVSIL
KLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGEYNGGTVQVIPHITNEIK
DRILRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGRQNVLYMHVTLLPWIASAGEMKTKPTQHSVKELRSIGIQPDIL
VCRCDRPIGVGLKQKLSEFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQRQPDLSQWETMVERMYSPKYSVEI
AIVGKYVRLSDAYLSVVESLRHAAISTYGDLRIRWVNSETLETESAENYLAGVDGILVPGGFGSRGIDGKIAAIKFARDRQIPFLG
LCLGMQCSVIEWARNVEGLADANSAEFDPYTTNPIINLLPEQQDVVDLGGTMRLGLYPCRVQPDTLAFDLYQEEVIYERHRHR
YEFNNLYRNALLESGYVVSGTSPDGRLVEIVEYPKHPFFIACQFHPEFQSRPSTPHPLFKGFMEAAISRTHHSKNTSKPVQVSMG
KKISRRLQALLEKVEDRDYAPLDALALLKETATAKFPEAAEAHIRLGIDPKYTDQQLRTTVALPKGTGQVVRVAVIARGEKVTE
ATNAGADIAGSEELIDEIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDVASAIAEFKAGKLEFRADRTGI
VHVMFGKASFTPEDLLVNLKALQETIDRNRPSGAKGRYWRTFYVSATMGPSIRIDINALRDLKVTDAAMGTRSYRPYTPSTRQ

VTISDFAEITKTEPEKSLTESVHRAKGRNNQGRITSRRRGGGHKKLYRIIDFKRDKRDIAATVTAIEYDPNRNARIALVQYEDGE
KRYILHPNGLKVGAKIIAGPEAPFEDGNALPLSNIPLGTNVHNVELTAGKGGQIVRAAGATAQVVAKEGNYVTLKLPSGEVRMI
RRECYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPALGAKTRKRKKA
STKLIVMSVGILGTKLGMTQIFDEAGVAIPVTVIKAGPCTVTQVKTKQTDGYSAIQVGYGEVKPKALNQPKLGHLAKSSAPALR
HLNEYRTDAASEYALGQEIKADIFSEGQIVDVIGTSIGRGFAGNQKRNNFGRGPMSHGSKNHRAPGSIGAGTTPGRVYPGKRMA
GRLGGTRVTIRKLTVVKVDAERNLILIKGAIPGKPGGLVNVVPTNKVGNKMVESVVKNWQGEEVGQTSFELRVAKEETAAHIV
HRALVRQMTNSRQGTASTKTRSEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFGPKPRDFNLKLNRKERRLALRTAFV
SRAEDLIVVEEFSNELQRPKTKELVAALARWGAAPEQKTLLILSEIAENVNLSARNVENLKVIAADQLNVFDLLHADKIVVTSS
ALTKIQEVYSAMATTRLKTVYQETIVPKLTQQFQYTNVHQVPKVVKITVNRGLGEAAQNAKALEASLNEIALITGQKPVVTRA
KKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLISLSLPRIRDFRGVSPKSFDGRGNYTLGVREQLIFPEVEYDSIDQIRGLDISIIT
TAKNDEEGRALLKEMGMPFRDQMSRIGKRPITVPAKVQVAIDGTKVVVKGPKGELSRDLPANVIVSQEGETLLVTRRDETRTS
RQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQVQGRNLVLNIGYSHQVQIEPPDGVQFAVENNTNVIVSGYDKEVVGN
TAAKIRAVRPPEPYKGKGIRYAGEVVRRMAKKVVAVIKLALNAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMV
IPVEISVFEDRSFTFVLKTPPASVLIRKAAKIERGSEQPNQKKVGSITKAQLREIAQTKLPDLNANDIDAAMNIVAGTAKNMGVTI
TDMSAATDQILEQLKSLTLLEASELVKQIEEAFGVSAAAPAGGMMMMAAPGAAAPAEAVEEKTEFDAILESVPADKKIAVLKI
VREITGLGLKEAKDLVEATPKPVKEGVNKEAAEDIKKRIAEAGGTVTIKMSSKTYLPPQEKLEREWYVVDATDKRLGRLASEIA
MVLRGKRKAEYTPHLDTGDFVVVINAEKVAVTGKKRTQKVYRRHSGRPGGMKTETFAKLQQRLPERILEHAVKGMLPKNSL
GKQLFTKLKVYAGPTHPHAAQKPKELIVNTIPGENMIQPQTYLNVADNSGAKKLMCIRVLGAGNRRYGGVGDKIIAVVKESNP
NMAVKKSDVVEAVIVRTKKSINRDSGMSIRFDDNAAVIINKDGNPRGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPKRTKFR
KQQRGRMEGLAHRGSTLNFGDFALQAQEPCWITSRQIEASRRAMTRYIRRGGKIWIRIFPDKPVTMRPAETRMGSGKGNPEFW
VAVVKPGRILFEIAGVSEEIAREAMRLAAYKLPIKTKFIVRSQPQEQEMNVQEVIRSIEAEHLKSDLPEIYVGDTVRVGVKIKEGD
KYRVQPYEGVVIGKRNGGINETITVRRVFQGVGVERVFLLHSPRIDNIKVVRRGKVRRAKLYYLRQLSGKATRIKQRFDRALM
TRVKRGNVARKRRNKILKLAKGFRGSHSTLFRTANQQVMKALRSAYRDRKKKKRDFRRLWITRINAASRQHGLSYSQLIGNL
KKANVDLNRKMLAQLAVLDPASFAKVAELANSVKAMAHKKGTGSTRNGRDSNAQRLGVKRFGGQTVLAGNILVRQRGTKF
HPGNNVGIGSDDTLFALVDGVVTFERKGKSRKKVSVYPAVAAEAVASMTNETYMEPAFLLPDLIEIQRSSFRWFLEEGLIEELN
SFSPITDYTGKLELHFIGQNYKLKEPKYSVEESKRRDSTYAVQMYVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVI
VNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDLVWVRIDKTRKLSAQVLLKALGLSDNEIFDALRHPEYFQK
TIEKEGQFSEEEALMELYRKLRPGEPPTVLGGQQLLDSRFFDPKRYDLGRVGRYKLNKKLRLSVPDTLRVLTPGDILAAVDYLI
NLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRERMTVSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQT
NPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEGPNAGLIGSLATHARVNQYGFLETPFRPVENGRVCYEK
AAVYMTADEEDDLRVAPGDIPVDENGHIIGPQVPVRYRQEFSTTTPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSN
MQRQAVPLLKPERPLVGTGLEAQAARDSGMVIVSRTDGDVVYADANEIRVRVREKALTTGEETSSAKPQEIRYVLSKYQRSNQ

DTCLNQKPLVRIGEKVVAGQVLADGSSTEGGELALGQNIVVAYMPWEGYNYEDAILISERLVQDDVYTSIHIEKYEIEARQTKL
GPEEITREIPNVGEDALRQLDEQGIIRIGAWVESGDILVGKVTPKGESDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRVVD
VRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKGIISRILPAEDMPYLPDGSPVDIVLNPLGVPSRMNVGQVF
ECLLGWAGQNLGVRFKITPFDEMYGEESSRRIVHGKLQEARDETGKTWVYNPDDSGKIMVYDGRTGEPFDRPVTVGVAYMLK
LVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWALEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPR
PGTPESFKVLMRELQSLGLDIAVHKVETQADGSSLDVEVDLMADQGSRRTPPRPTYESLSRESLEEDEMPVVSLAQMMESGVH
FGHQTRRWNPKMSPYIYTSRNGVHIIDLVQTAQLMDNAYNYMRTQAEQGKKFLFVGTKRQAAGIIAQEANRCGSHYINQRWL
GGMLTNWATIKTRAERLKDLERREENGALDLLPKKEASMLRREMAKLQKYLGGIKNMRKVPDIVVIVDQRREYNAVQECQK
LGIPIVSMLDTNCDPDVVDIPIPANDDAIRSIKLIVGKLADAIYEGRHGQLEVEEDYEDYEGAEEEYDYDESEYTDSMMSDDDEE
MGQKIHPVGFRLGITQEHQSRWFAVPDRYPALLQEDHKLRQYIEKKLGRNAQNNAGISEIRIERKADQIDLELRTARPGVVVGR
GGQGIESLRTGLQDLLGGQRQIRINVVEVQKVDADAYLIAEYIAQQLERRVSFRRVVRQAIQRAQRAGVQGIKVQVGGRLNGA
EIARTEWTREGRVPLHTLRADIDYSYCTAQTIYGILGIKVWVFKGEIIPGQEEAPQPSGREREPRRRDQKRRRQQFEDRSNETMA
TGRRKASKAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAIVIVGNERGQVGVGVGKASDVIGAVKKGVADGKKHLIDIPITK
SNSIPHPIDGIGGGAKVIMRPAAPGTGVIAGGAVRTVLELAGVRNVLAKQLGSNNPLNNARAAVNALSTLRTFAEVAEDRGISV
ENLYITVAEANSGRAVYWGTGRRKSAVAQVRLVPGEGKFTVNGKDGELYFQFNANYLGAIKAPLETLGLESEYDILVKAEGG
GLTGQADSIRLGVARALCQLDPDNRSPLKTEGYLTRDPRAKERKKYGLHKARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDT
SCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTHRRIIDIYQPSSKTIDALMKLDLPSGVDIEVKLMARQP
TKKTGSKKQKRNVPNGMAYIQSTFNNSIVTITDQNGDVISWASAGSSGFKGAKKGTPFAAQTAAESAGRRAMDQGMRQIEVM
VSGPGAGRETAIRALQGAGLEITLIRDITPIPHNGCRPPKRRVMARISGVDLPRDKRVEIGLTYIYGIGLTRSQEILAATGVNPDT
RVKDLSDADVAALRAEIESNYQVEGDLRRLEAMNIKRLVDIGCYRGRRHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAP
GKMGRSLKKGPFVADHLLSKIEKLNEKNEKQVIKTWSRASTIIPVMVGHTIAVHNGKQHVPVFVNEQMVGHKLGEFAPTRTYR
GHGKSDKKSGRMSDKNEGYKVISDNRQARYLYEILETYEAGIQLAGTEVKSIRAGKANLQDGYALIRNGEAWLINVHISPYTSS
GQYFNHEPRRTRKLLLHRQELRKLIGKVEQQGLTLVPLKMYLKRGWVKVSIGLCKGKKIHDKRESLKRRQDQRDIQRAMKNY
MAEISAKLVQELRQKTGAGMMDCKKALKETEGNIEEAINWLRKKGIASAGKKSDRVAAEGLVETYIQPDGKVGVLIEVNCQT
DFVARNDAFKSLVKNLAQQAATADSVESLLAQPYIEKADVTVDEFIKESIATLGENIQVRRFVNFSLGDTPGVVDSYIHTGGRV
GVLVQINANTAAAAGNEEFKILAKNTAMQVAACPNVEYVSVDQIPAETVQKEKDIEMGKEDLANKPENIREKIVQGRIEKRLK
ELTLLDQPYIRDQSISVADLVKQVQSKVDEDIKVHGFVRYVLGEGIEKQETNFAEEVAAQMGAK

>Sphaerospermopsis_sp_SIO1G1
MQIPRIHPDTIEEVKSRADIVEVVSDYVVLKKRGKDFVGLCPFHNEKTPSFTVSPGKQIYYCFGCQAGGNAIKFIMELDKRNFGD
VVLGLAQRYQVPVKSLAPEQRQELQRQISLRDQLYEVLASAAQFYQHALRQSLGQKAMLYLQEERKLTTETIQQFGLGYAPAG
WETLYRYLVENKNYPVQLVDKAGLIKPRKEDKGYYDVFRDRLMIPIRDVQGRVIAFGGRTLTEEQPKYLNSPETELFLKGKTLF
ALDQAKDGVSKLDQAVVVEGYFDAIALHAAGVNNVVASLGTALSIEQIRLLLRYCDSKQLILNFDADKAGTNATERAIGEIAN
LAYQGEVQLKILNLPNGKDADEYLQNHTVENYQQLLANAPLWLNWQIEEIIKDRDLKQATDFQIVTKEIVKILQNIGNSDTLNY
YISYCAEILSLGDTRLIPLRVENLLTQIAPSHFKTPARPRKQESKKPKFTVATTEKSLLEQAEALLLRIFLHCPEQREMIFAELEDR
NLEFSLSHHRLLWQQSLVFPLEDNDLISKLENRYLELAEDLNILSHVFHLDEKNKLEIIRTPQVVQATLACMEKVFREKRHRYF
MEQWEKVDSKTEPEKERLYYENAMGEKRRIQELEKQRQFSIIELFMKLDESESKMKSSVEATQRDFNTVRTGRANSSLLDKVE
VEYYGTPTPLKSLASVSTPDASTIMIQPYDKGTLNIIEKAISLSDVGITPNNDGSSIRLNIPPLTSERRQEFVKLASKYAEDGKVAIR
NIRRETVDSIRKREKAGEISEDESRDEQDKLQKLTNKYTAKIDDLLAEKEKDITKVMPVIEKKRARDLPQINERIRFPKIRVIDTD
GAQLGILTPSEAIRLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVK
QAERFLKDGDKVKATVMFRGREIQHSDLAEELLKRMANDLQAIGEVQQAPKKEGRNMMMLISPKKMVTLPGLKDLIEKISQE
RNLPRLAVQSSIREALLKGYERYRRAQNLERKQFDEDYFENFEVELDIEGEGFRVLSTKTIVEEVSNSDHQISLEEVQQVAPEAQ
SGDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLESTVLQARVLRFERQSVILAVSSGFGQPEVEAELP
KREQLPNDTYRSNTAFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAV
DTLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIGKE
GQNVRLAARLTGWKIDIKDKAKYDYAAEDAKFAEVRAKYQMSKKSLASLSAADIAGKRALVRVDFNVPMDEGKITDDTRIRA
ALPTIQDLTQKGAKVILASHFGRPKGKVKDEFRLTPVAKRLSELLGQEVVKTDDCIGDDVATKVAALQNGQVLLLENVRFYPG
EEENDPQFAEKLAANADFYVNDAFGTAHRAHASTEGVTKYLSPSVAGYLVEKELQYLQGAIEEPKRPLAAIIGGSKVSSKIGVIE
TLLEKCDKLIIGGGMIFTFYKARGLSVGKSLVEDDKLELAKSLEAKAKEKGVTFLLPTDIVSADKFDKDANATTVSIENIPADGM
GLDIGPDSVKVFQEALADCKTVIWNGPMGVFEFDKFAVGTEAIARTLAEISQTGTTTIIGGGDSVAAVEKVGLAEKMSHISTGG
GASLELLEGKVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRDYSVSILKLDPYINVDPGTMSPFQHGEVFVTQD
GAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGGTVQVIPHITNEIKDRILRVAKESNPAAVITEIGGTVGDIE
SLPFLEAIRQLRKEVGRQNVLYMHVTLLPWIASAGEMKTKPTQHSVKELRSIGIQPDILVCRSDRPIPVGLKRKLSEFCDVPVKC
VITAQDASSIYEVPLILEREGLAQQTLDLLQMEQRQPDLTQWANMVERMYSPKYSVEIAIVGKYVRLSDAYLSVVESLRHAAIS
TYGDLRIRWVNSELLENEPADNYLSGVDGIIVPGGFGSRGIDGKINAIKYARDRQIPFLGLCLGMQCSVIEWARNVKGLDTANS
AEVDPYTEHPVINLLPEQQDVVDLGGTMRLGLYPCSIQPGTLAHNLYQEDIIYERHRHRYEFNNFYRQALLDSGYVVSGTSPDG
RLVEIVEYPNHPFFIACQFHPEFQSRPNTPHPLFQGLMQAAISRTHHAPSTPKPVQVSMGKKISKRLKALLEKVEDRDYAPEEAL
ALLKETATAKFPEAAEAHIRLGIDPKYTDQQLRTTVALPKGTGQDVRVAVIARGEKVTEATNAGANIAGSEELINDIQKGMMD
FDKLIATPDVMPQVAKLGKMLGPRGLMPSPKGGTVTFDIAGAIAEFKAGKLEFRADRTGIVHVMFGKASFSPDDLLVNLKALQ
ETIDRNRPSGAKGRYWRTVYVSATMGPSIRVDINALRDLKITDAAMGTRSYRPYTPSTRQVTISDFAEITKSKPEKSLTEFIHRAK

GRNNQGRITSRRRGGGHKKLYRIIDFKRDKRDIPATVKAVEYDPNRNARIALVQYEDGEKRYILHPNGLKVGTTIIAGVDSPIED
GNALPLYRIPTGTSVHNVEMTPGKGGQIVRAAGATAQVMAKDGDYVTLKLPSGEFRMIRRECYATIGQVGNTEARNLSAGKA
GRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPALGAKTRKRKKASSKFIVMSVGILGTKLGMTQVFTEE
GVAIPVTVVKVGPCTVTQVKTRQTDGYSAIQVGYGEVKPKALNKPKMGHLAKSNAPALRHLKEYRTDTAGDYNIGQEIKADIF
SEGQIVDVAGTSIGRGFAGNQKRHNFGRGPMSHGSKNHREPGSIGAGTTPGRVYPGKRMAGRLGGSSVTIRKLTVVKVDAERN
LLLIKGAIPGKPGGLVDVSPTNKVGNKMVESVVKNWQGDQVGQTNFDLKVAKEETAAHIVHRALVRQMTNSRQGTASTKTR
SEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFGPKPREFNIKLNRKERRLALRTAFVSRAEDLIVVEEFSSELQRPKTKEL
VAALVRWGAAPEQKTLLILSEIAENVNLSARNVENLKLIAADQLNVYDILHADKIVVTPASLEKIQEVYSAMATTRLKTLYQET
IVPKLTQQFQYTNIHQVPKLVKITVNRGLGEAAQNAKALEASLSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRSER
MYAFLDRLISLALPRIRDFRGISPKSFDGRGNYTLGVREQLIFPEVEYDSIDQIRGLDISIITTAKNDEEGRALLKEMGMPFRDMSR
IGKRPITIPAKVQVTINGTQVAVKGPKGELSREISNTIAISQEGETLRVTRRDETRVARQMHGLSRTLIANMVEGVSNGFERRLE
MQGVGYRAQMQGTKLVLNIGYSHQIQVEPPAGVNFKVENNTNIIVSGYDKEVVGNTAAKIRDYRPPEPYKGKGIRYVGEVVR
RMAKKVVAVIKLALSAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIRKA
AKIDKGSSEPNKKKVGSITTEQLKEIAQTKLPDLNANDIEAAMNIVAGTARNMGVTVKDMSAATEQILEQLKSLTLLEAAELVK
EIEEAFGVSAAAPAGGMMMMAAPGAGGGAAEAVEEKTEFDVVLESVPADKKIAILKIVREITGLGLKEAKDLVESAPKAIKEGI
AKDAAEDIKKRITDAGGTVSVKMSSKTYLPPQASLERDWYIVDATDKRLGRLASEIAMVLRGKRKAEYTPHLDTGDFVVVINA
EKVAVTGKKRSQKLYRRHSGRPGGMKTETFAKLQQRIPERIVEKAVKGMLPKNSLGRQLFTKLKVYAGSTHPHAAQKPKELII
NTIPGDMIQPQTYLNVADNSGAKKLMCIRVLGAGNRRYGGVGDRIIAVVKESSPNMAVKKSDVVEAVIVRTKKNINRDSGMSI
RFDDNAAVIINKEGNPRGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPKRTKFRKQQRGRMEGLAHRGSSINFGDFALQAQEP
SWITSRQIEAARRAMTRYIRRGGKIWIRIFPDKPITMRPAETRMGSGKGNPEFWVAVVKPGRILFEISGVSEEVAREAMRLASHK
LPIKTKFIVRPKVQEQMNVQEIIRSIEAEHLKSDIPQIYVGDTVRVGVKIKEGNKYRVQPYEGVVIGKRNGGINETITVRKVFQGV
GVERVFLLHSPRIDNIKVVRRGKVRRAKLYYLRNRTGKATRIKQRFDRPLMTRVKRGNVARKRRNKILKLAKGFRGSHSTLFR
TANQQVMKALRSAYRDRKKKKRDFRRLWIARINAASRQQGLSYSQLIGNLKKANVELNRKMLAQLAVLDPDSFVKVTELANS
VKMAHKKGTGSTRNGRDSNSQRLGVKRYGGQSVIAGNILVRQRGTKFHPGNNVGIGSDDTLFALVDGIVTFERKGKTRKKVS
VYPVATEAVAMTNETYMEPAFLLPDLIEIQRSSFRWFLEEGLIEELSSFSPITDYTGKLELHFLGHNYRLKEPKYSVEESKRRDST
YAVQMYVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKF
ETDRNDLVWVRIDKTRKLSAQVLLKALGLSDNEIFDALRHPEYFQKTIEKEGQFSEEEALMELYRKLRPGEPPTVLGGQQLLES
RFFDPKRYDLGRVGRYKLNKKLRLSVPDSVRVLTPGDILAAIDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLE
RIIRERMTVSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRI
CPIETPEGPNAGLIGSLATHARVNKYGFLETPFRPVENGKVKFDIPPVYMTADEEDDLRTATGDVPLDENGYIKGPQVPVRYRQ
DWTTTSPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQAARDSGMVIVSRTDG
DVVYVDANEIRVRVREKTITSGTEISEPPKHQEIRYPLSKYQRSNQDTCLNQKPLVRIGEKVVTGQVLADGSSTEGGELALGQNI

IVTYMPWEGYNYEDAILISERLVQDDIYTSIHIEKYEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRIGAWVEAGDILVGKV
TPKGESDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGR
HGNKGIISRILPIEDMPYLPDGSPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGEESSRRIVHGKLQEAR
DETGKDWLYNPDNAGKIMVYDGRTGEPFDHPVTVGVAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEM
EVWALEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQADGSSLDVEVD
LMADQNSRRTPPRPTYQMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTARNGVHIIDLVQTAQLIDQAYNYMRSESEQGK
RFLFVGTKRQAAGIIAQEAARCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREESGALDLLPKKEASMLRREMAKLQKY
LGGIKNMRKVPDVVVIVDQKREYNAVQECQKLNIPIVSMLDTNCDPDVVDIPIPANDDAIRSIKLIVGKLADAIYEGRHGQLESE
NDYEDYEGAEEDYDYDEGEYTDSMGMGQKIHPVGFRLGITKEHQSRWFAVPDRYPELLQEDYKLRQYIDQKLGKKAQNNAGI
SEVRIERKADQIDLEVRTARPGVVVGRGGQGIEALRTGLQELLGSNRQIRINVVEVQRVDADAYLIGEYIAQQLERRVSFRRVV
RQAIQRAQRAGVQGIKVQVSGRLNGAEIARTEWTREGRVPLHTLRANIDYAYCTAQTIYGILGIKVWVFTGEIIPGQEEAPAQPA
NREREPRRRQQQRRRQQFEDRSNETMATGRRKANRAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAIVVIGNERGQVGVGV
GKASDVIGAVKKGVADGKKHLIDIPITKSNSIPHPIDGIGGGAKVIMRPASPGTGVIAGGAVRTVLELAGVRNVLAKQLGSNNPL
NNARAAVNALSTLRTLSEVAEDRGIALENLYFATEANSGRAIYWGTGRRKSSVARVRLIPGEGKFSVNGKDGELYFQFNANYL
GSIKAPLETLGLESEYDIVVKAEGGGLTGQADSIRLGVARALCQLDPDNRLPLKTEGYLTRDPRAKERKKYGLHKARKAPQYS
KRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTHRRIIDIYQPSSK
TIDALMKLDLPSGVDIEVKLMARQPTKKSGSKKQKKNVPNGIAYIQSTFNNSIVTITDQNGDVISWASAGSSGFKGAKKGTPFA
AQTAAESAGRRAIDQGMRQIEVMVSGPGAGRETAIRALQGAGLEITLIRDITPIPHNGCRPPKRRRVMARISGIDLPRDKRIEYGL
TYIYGIGLTSSHQILAATGVNPDTRVKDLSDADVAALRAEIESNYQVEGDLRRLEAMNIKRLVDIGCYRGRRHRMGLPVRGQR
TRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLSKIEKLNANNDKQVIKTWSRASTIIPIMVGHTIAVHNGKQHVP
VFVNEQMVGHKLGEFAPTRPYRGHGRSDKKSGRMSDKNNSDGYKVITDNRQARYLYQILETYEAGIQLAGTEVKSIRAGKVN
LQDGYALLRNGEAWLINAHISPYTSSGQYFNHEPRRTRKLLLHRQELRKLIGKVEQQGLTLIPLKMYLKRGWVKVSIGLCKGK
KIHDKREDLKRRQDQRDIQRALKRYMAEISAKLVQELRQKTGAGMMDCKKALKENDGSIEAATDWLRKKGIAKADKASSRV
AAEGLVENYIQPDGKVGVIIEVNCQTDFVARNEAFKALVKTLAKQAANADSVEALLAQPYIENSSVTVDEAIKQTTATLGENIQ
VRRFVTFAPASTPGIVDSYIHTGGRVGVLVELGSKTEDTTGKEEFQGLAKNIAMQVAACPNVEYVNIGQIPAEFVQKEKEIEMG
KDDLGKKPENIREKIVQGRIDKRLKEITLLDQPYIRDQSISVEDLVKQVKSQVGDEIEVNRFVRYVLGEGIDKQEVSFAEEVAAQ
MG

>Sphaerospermopsis_torques_reginae_ITEP_024
MQIPRLHPDTIEEVKHRADIVDVVSDYVVLRRRGKDFVGLCPFHDEKTPSFTVSPTKQMYYCFGCQAAGNAIKFVMDLNKRHF
AEVVLDLAKRYQVPVKTLAPEQRQELQRQLSLREQLYEILASTAQFYQHALRQNLGQKAMQYLQENRQFKIETIQQFGLGYAP
PGWETLYRYLVDNKNYPVQLVEKAGLIKPRKEGGSYYDVFRDRLMIPIRDVQGRVIAFGGRTLTEEQPKYLNSPETELFSKGKT
LFALDQAKDGISKSDQGVVVEGYFDAIALHAAGINNVVASLGTALSIEQVRLLLRYTDSKQLILNFDADKAGINAAERAIGEIAT
LAYKGEVQLKILNIPDGKDADEYLHSHTAADYQQLLANAPLWLNWQIEEIIKDRDLKQATDFQIVTKEMVKLLQKIVNSDTLN
YYISYCAEILSLGETRLIPLRVENLLTQIAPASVQTPPLRLRKPESKTPKLSLVTTERSLLEQAEALLLRIFLHCAEQRQVIFEELEE
RNLEFSLSHHRFLWQKSLEFPLEELDLISKLQNRYLELEEDLKIVSHVFHLNEKNKTEILRTPQVVQATLACMERVLREKRYRHF
MELWKKIDPQAEPDKYKSYADAIYADKMRIQELDKQRQFPISELFMKLAEAESTMQKTVEATQRAFNTIRTGRANASLLDKVQ
VEYYGTPTPLKSLANISTPDASTILIQPYDKGSLNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKEFVKLAAKYAEEGRVGI
RNIRRDALDSIRKQEKAAEISEDESRDQQDKLQKLTNKYTTRIDELLAEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDTD
GGQLGIMPPHEALKLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRV
KQAERFLKDGDKVKATVMFRGREIQHSDLAEDLLKRMATDLEPFGEVQQAPKKEGRNMMMLISPKKMSMVTLPGLKDLIESI
SRERNLPRLAVQSSIREALLKGYERYRRAQNLERRQFDENYFDNFEVELDIEGEGFRVLSTKTIVEQVSNSDHQISLEEVQQVAP
EAQSGDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLESTVLQARVLRFERQSVILAVSSGFGQPEVEA
ELPKREQLPNDTYRSNTTFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKI
AVDTLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIG
KEGQNVRLAARLTGWKIDIKDKAKYDYAAEDAKFAAVRAQYQSEDDENDMSKKSLASLSAADISGKRALVRVDFNVPVDDQ
GNITDDTRIRAALPTIQDLTQKGAKVILTSHFGRPKGVDEKLRLTPVAKRLSELLGQEVIKTDDCIGDDVAAKVAALDNGQVLL
LENVRFYKEEEKNEPEFAQKLAANADFYVNDAFGTAHRAHASTEGVTKFLSPSVAGYLVEKELQYLQSAIEVPQRPLAAIIGGS
KVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLDVGKSLVEEDKLELAKSLEAKAKERGVTFLLPTDIVAADKFAPDANATTV
SIENIPADGMGLDIGPDSVKVFQAALADCKTVIWNGPMGVFEFDKFAVGTEAIAHTLAEIGKTGAITIIGGGDSVAAVEKVGLA
DQMSHISTGGGASLELLEGKVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRDYSVSILKLDPYINVDPGTMSPFQ
HGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGEYNGGTVQVIPHITNEIKDRILRVAKETNPAAVIT
EIGGTVGDIESLPFLEAIRQLRKEVGRQNVLYMHVTLLPWIASAGEMKTKPTQHSVKELRSIGIQPDILVCRCDRPIGVGLKQKLS
EFCDVPVECVITCQDASSIYEVPLILEKEGLAQQTLDLLQMEQRQPDLSQWETMVERMYSPKYSVEIAIVGKYVRLSDAYLSVV
ESLRHAAISTYGDLRIRWVNSETLETESAENYLAGVDGILVPGGFGSRGIDGKIAAIKFARDRQIPFLGLCLGMQCSVIEWARNV
EGLADANSAEFDPYTTNPIINLLPEQQDVVDLGGTMRLGLYPCRVQPGTLAFDLYQEEVIYERHRHRYEFNNLYRNALLESGYV
VSGTSPDGRLVEIVEYPKHPFFIACQFHPEFQSRPSTPHPLFKGFMEAAISRTHHSKNTSKPVQVSMGKKISRRLQALLEKVEDRD
YAPLEALALLKETATAKFPEAAEAHIRLGIDPKYTDQQLRTTVALPKGTGQVVRVAVIARGEKVTEATNAGADIAGSEELIDDI
QKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDVASAIAEFKAGKLEFRADRTGIVHVMFGKASFTPEDLL
VNLKALQETIDRNRPSGAKGRYWRTFYVSATMGPSIRIDINALRDLKVTDAAMGTRSYRPYTPSTRQVTISDFAEITKTEPEKSL

TESVHRAKGRNNQGRITSRRRGGGHKKLYRIIDFKRDKRDIAATVTAIEYDPNRNARIALVQYEDGEKRYILHPNGLKVGAKIIA
GPEAPFEDGNALPLSNIPLGTNVHNVELTAGKGGQIVRAAGATAQVVAKEGNYVTLKLPSGEVRMIRKECYATIGQVGNTDAR
NLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPALGAKTRKRKKASTKLIVMSVGILGTKLG
MTQIFDEAGVAIPVTVIKAGPCTVTQVKTKQTDGYSAIQVGYGEVKPKALNQPKLGHLAKSSAPALRHLNEYRTDAASEYALG
QEIKADIFSEGQIVDVIGTSIGRGFAGNQKRNNFGRGPMSHGSKNHRAPGSIGAGTTPGRVYPGKRMAGRLGGTRVTIRKLTVV
KVDAERNLILIKGAIPGKPGGLVNVVPTNKVGNKMVESVVKNWQGEEVGQTSFELRVAKEETAAHIVHRALVRQMTNSRQGT
ASTKTRSEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFGPKPRDFNLKLNRKERRLALRTAFVSRAEDLIVVEEFSNELQ
RPKTKELVAALARWGAAPEQKTLLILSDIAENVNLSARNVENLKVIAADQLNVFDLLHADKIVVTSSALTKIQEVYSAMATTRL
KTVYQETIVPKLTQQFQYTNVHQVPKVVKITVNRGLGEAAQNAKALEASLNEIALITGQKPVVTRAKKAIAGFKIRQGMPVGI
MVTLRGERMYAFLDRLISLSLPRIRDFRGVSPKSFDGRGNYTLGVREQLIFPEVEYDSIDQIRGLDISIITTAKNDEEGRALLKEM
GMPFRDQMSRIGKRPITVPAKVQVAIDGTKVVVKGPKGELSRDLPANVIVSQEGETLLVTRRDETRTSRQMHGLSRTLVANMV
EGVSQGFQRRLEIQGVGYRAQVQGRNLVLNIGYSHQVQIEPPDGVQFAVENNTNVIVSGYDKEVVGNTAAKIRAVRPPEPYKG
KGIRYAGEVVRRMAKKVVAVIKLALNAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVL
KTPPASVLIRKAAKIERGSEQPNKKKVGSITKAQLREIAQTKLPDLNANDIDAAMNIVAGTAKNMGVTITDMSAATDQILEQLK
SLTLLEAAELVKQIEEAFGVSAAAPAGGMMMMAAPGAAAPAEAAEEKTEFDAILESVPADKKIAVLKIVREITGLGLKEAKDL
VEAAPKPIKEGVNKEAAEDIKKRIAEAGGTVTIKMSSKTYLPPQEKLEREWYVVDATDKRLGRLASEIAMVLRGKRKAEYTPH
LDTGDFVVVINAEKVAVTGKKRTQKVYRRHSGRPGGMKTETFAKLQQRLPERILEHAVKGMLPKNSLGKQLFTKLKVYAGPT
HPHAAQKPKELIVNTIPGENMIQPQTYLNVADNSGAKKLMCIRVLGAGNRRYGGVGDKIIAVVKESNPNMAVKKSDVVEAVIV
RTKKSINRDSGMSIRFDDNAAVIINKDGNPRGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPKRTKFRKQQRGRMEGLAHRGS
TLNFGDFALQAQEPCWITSRQIEASRRAMTRYIRRGGKIWIRIFPDKPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVS
EEIAREAMRLAAYKLPIKTKFIVRSQPQEQEMNVQEVIRSIEAEHLKSDLPEIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRN
GGINETITVRRVFQGIGVERVFLLHSPRIDNIKVVRRGKVRRAKLYYLRQLSGKATRIKQRFDRALMTRVKRGNVARKRRNKIL
KLAKGFRGSHSTLFRTANQQVMKALRSAYRDRKKKKRDFRRLWITRINAASRQHGLSYSQLIGNLKKANVDLNRKMLAQLAV
LDPASFAKVAELANSVKGMAHKKGTGSTRNGRDSNAQRLGVKRFGGQTVLAGNILVRQRGTKFHPGNNVGIGSDDTLFALVD
GVVTFERKGKSRKKVSVYPAVAAEAVASMTNETYMEPAFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFIGQN
YKLKEPKYSVEESKRRDSTYAVQMYVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKN
GRRTYSASLIPNRGAWLKFETDRNDLVWVRIDKTRKLSAQVLLKALGLSDNEIFDALRHPEYFQKTIEKEGQFSEEEALMELYR
KLRPGEPPTVLGGQQLLDSRFFDPKRYDLGRVGRYKLNKKLRLSVPDTLRVLTPGDILAAVDYLINLEYDIGSIDDIDHLGNRRV
RSVGELLQNQVRVGLNRLERIIRERMTVSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGL
TRERAGFAVRDIHPSHYGRICPIETPEGPNAGLIGSLATHARVNQYGFLETPFRPVENGRVCYEKAAVYMTADEEDDLRVAPGD
IPVDENGHIIGPQVPVRYRQEFSTTTPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGL
EAQAARDSGMVIVSRTDGDVVYADANEIRVRVRERTGDRSQVLRHGDSEETSSLPVSKPQEIKYVLSKYQRSNQDTCLNQKPL

VRIGEKVVAGQVLADGSSTEGGELALGQNIIVAYMPWEGYNYEDAILISERLVQDDVYTSIHIEKYEIEARQTKLGPEEITREIPN
VGEDALRQLDEQGIIRIGAWVESGDILVGKVTPKGESDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQGD
ELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKGIISRILPAEDMPYLPDGSPVDIVLNPLGVPSRMNVGQVFECLLGWAGQ
NLGVRFKITPFDEMYGEESSRRIVHGKLQEARDETGKNWVYNPDDPGKIMVYDGRTGEPFDRPVTVGVAYMLKLVHLVDDKI
HARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWALEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKV
LMRELQSLGLDIAVHKVETQADGSSLDVEVDLMADQGSRRTPPRPTYESLSRESLEEDEMPVVSLAQMMESGVHFGHQTRRW
NPKMSPYIYTARNGVHIIDLVQTAQLMDDAYNYMRTQAEQGKKFLFVGTKRQAAGIIAQEATRCGSHYINQRWLGGMLTNW
ATIKTRAERLKDLERREENGALDLLPKKEASMLRREMTKLQKYLGGIKNMRKVPDIVVIVDQRREYNAVQECQKLGIPIVSML
DTNCDPDVVDIPIPANDDAIRSIKLIVGKLADAIYEGRHGQLEVEEDYEDYEGAEEEYDYDESEYTDSMMSDDDEEMGQKIHPV
GFRLGITQEHQSRWFAVPDRYPALLQEDHKLRQYIEQKLGRNAQNNAGISEIRIERKADQIDLELRTARPGVVVGRGGQGIESLR
TGLQDLLGGQRQIRINVVEVQKVDADAYLIAEYIAQQLERRVSFRRVVRQAIQRAQRAGVQGIKVQVGGRLNGAEIARTEWTR
EGRVPLHTLRADIDYSYCTAQTIYGILGIKVWVFKGEIIPGQEEAPQPSGREREPRRRDQKRRRQQFEDRSNEAMATGRRKASK
AKKEETNWQERVIQIRRVSKVVKGGKKLSFRAIVIVGNERGQVGVGVGKASDVIGAVKKGVADGKKHLIDIPITKSNSIPHPIDG
IGGGAKVIMRPAAPGTGVIAGGAVRTVLELAGVRNVLAKQLGSNNPLNNARAAVNALSTLRTFAEVAEDRGISVENLYIMATV
AEANSGRAVYWGTGRRKSAVAQVRLVPGEGKFTVNGKDGELYFQFNANYLGAIKAPLETLGLESEYDILVKAEGGGLTGQAD
SIRLGVARALCQLDPDNRSPLKIEGYLTRDPRAKERKKYGLHKARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDT
ANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTHRRIIDIYQPSSKTIDALMKLDLPSGVDIEVKLMARQPTKKTGSK
KQKRNVPNGIAYIQSTFNNSIVTITDQNGDVISWASAGSSGFKGAKKGTPFAAQTAAESAGRRAMDQGMRQIEVMVSGPGAGR
ETAIRALQGAGLEITLIRDITPIPHNGCRPPKRRVMARISGVDLPRDKRVEIGLTYIYGIGLTRSQEILAATGVNPDTRVKDLSDA
DVAALRAEIESNYQVEGDLRRLEAMNIKRLVDIGCYRGRRHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLK
KGPFVADHLLSKIEKLNEKNEKQVIKTWSRASTIIPVMVGHTIAVHNGKQHVPVFVNEQMVGHKLGEFAPTRTYRGHGKSDKK
SGRMSDKNEGYKVISDNRQARYLYEILETYEAGIQLAGTEVKSIRAGKANLQDGYALIRNGEAWLINVHISPYTSSGQYFNHEP
RRTRKLLLHRQELRKLIGKVEQQGLTLVPLKMYLKRGWVKVSIGLCKGKKIHDKRESLKRRQDQRDIQRAMKNYMAEISAKL
VQELRQKTGAGMMDCKKALKENDGNIDAAIDWLRKKGIASAGKKSDRVAAEGLVDTYIQPDGKVGVLIEVNCQTDFVARND
AFKSLVKNLAQQAATADSIESLLAQPYIEKAEVTVDEFIKESIATLGENIQVRRFVNFSLGDTPGVVDSYIHTGGRVGVLLQVSA
KTDAAADNEEFKNLAKNAAMQVAACPNVEYVSVDQIPAETVQKEKDIEMGKEDLANKPENIREKIVQGRIEKRLKELTLLDQP
YIRDQSISVADLVKQVQSKVGADITVQGFVRYVLGEGIEKQESNFAEEVAAQMGAK

>Anabaena_cylindrica_PCC_7122
MEIPRLHPDTIEEVKLRADIVDVVSEYVVLRKRGKDFVGLCPFHDEKSPSFTVSPSKQMFYCFGCQAGGNAIKFVMDLGKRHFT
EVVLDLARRYQVPVQTLEPEQKQELQRQLSLREQLYEVLASTAQFYQHALRHTQQQKVMQYLRENRQLREETIQQFGLGYAP
AGWETLHRYLVEDKHYPVQLVEKAGLIKPRKEGGGYYDVFRDRLMIPIRDVQGRVIAFGGRTLTEEQPKYLNSPETELFSKGK
TLFALDQAKDGIAKLDQAVVEGYFDAIALHAAGINNAVASLGTALSIEQVRLLLRYTDSKQLILNFDADKAGTNAAERAIGEI
ATLAYKGEVQLKILNLPNGKDADEYLQSHTSADYQQLLATAPLWLNWQIDQIIQNRDLRQATDFQQVTQQIVKLLQNIVNGDT
LNYYISYCAEILSLGDSRIIPLRVENLLTQIAPASVQTPPSRFRKQESKTPKLSLVNTERSLLEQAEALLLQIYLHCPEQRQLIINELE
ERNLELSLTHHRFLWLQISELTDEADLISNLQNRYLELSEELGLISHLFHLNEKTNKEILRTPQVVQATLACMEIVLREKRYRHF
MELWENIDIQAEPDKYKSYADAIYAEKMRIQELDKQRQFPITELLMKLDEAESKMQHTVEATQRAFNTIRTGRANASLLDKVQ
VEYYGTPTGLKSLANISTPDASTILIQPYDKGSLNIVEKAISLSDIGITPSNDGSVIRLNIPPLTSDRRKEFVKMAAKYAEEGRVGIR
NIRRDALDSIRKQEKAAEVSEDESRDQQDKLQKLTNKYTARIDDLLTEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDTD
GAQLGIMPPQEALQLAEDKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYLVRV
KQAERFLKDGDKVKATVMFRGREIQHSDLAETLLKRMATDLDALGEVQQAPKKEGRNMMMLISPKKMSMVTLPGLKELIESI
SRERNLPRLAVQSSIREALLKGYERYRRAQNLERRQFDEEYFDNFEVELDIEGEGFRVLSTKTIVDEVSNTDHQISLEEVQQVAP
EAQSGDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSGFGQPEVE
AELPKREQLPNDNYRANATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRT
KIAVDTLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPETRQTHVLVAEDQLSLA
IGKEGQNVRLAARLTGWKIDIKDKAKYDYAAEDAKFVAVRAKYQMSKKSLASLSAADVSGKRALVRVDFNVPVDDQGSITD
DTRIRAALPTIQDLTKKGAKVILASHFGRPKGVDDKLRLTPVAKRLSELLGQEVVKTDDCIGDDVAAKVAALQNGQVLLLENV
RFYKEEEKNEPEFAKKLAANADFYVNDAFGTAHRAHASTEGVTKFLSPSVAGYLVEKELQYLQSAIEEPKRPLAAIIGGSKVSS
KIGVIETLLEKCDKLIIGGGMIFTFYKARGLSVGKSLVEEDKLELAKALEAKAKERGVALLLPTDIVSADKFAPDANATTVSIENI
PADGMGLDIGPDSIKVFQAALADCKTVIWNGPMGVFEFDKFAAGTEAIAHTLAEIGKTGTTTIIGGGDSVAAVEKVGLADQMS
HISTGGGASLELLEGKILPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRDYSVSILKLDPYINVDPGTMSPFQHGEV
FVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGGTVQVIPHITNEIKDRILRVAKETNPSAVITEIGGT
VGDIESLPFLEAIRQLRKEVGRQNVLYMHVTLLPWIASAGEMKTKPTQHSVKELRSIGIQPDILVCRSDRTIPVGLKQKLSEFCD
VPVECVITCQDASSIYEVPLILEREGLAQQALDLLQMEQRQPNLTQWETMVERMYSPKHSIEIAIVGKYVRLSDAYLSVVESLR
HAAIATHGDLRLRWVNSEALENEPPENYLAGVDGIVVPGGFGSRGIDGKIAAIKYARDRQIPFLGLCLGMQCSVIEWARNVAGL
VDANSAEFDPYTSDPVINLLPEQQDVVDLGGTMRLGLYPCRVIPGTLAFDLYQEEVIYERHRHRYEFNNVYRNPLLDSGYVVS
GTSPDGRLVEIVELPNHPFFLACQFHPEFQSRPSSPHPLFKGFMQATISMGKKLSRRLQALQEKVEDRDYTPVEALALLKETATA
KFAEAVEAHIRLGIDPKYTDQQLRTTVALPKGTGQIVRVAVIARGEKVTEATNAGADIAGSEELIEDIQKGMMDFDKLIATPDV
MPMVAKLGKLLGPRGLMPSPKGGTVTFDVASAIAEFKAGKLEFRADRTGIVHVMFGKASFAPEDLLVNLKALQETIDRNRPSG
AKGRYWRTLYVSATMGPSIKIDISALRDLKLTDAAMGTRSYRPYTPSTRQVIVSDFAEITKTEPEKSLTESVHRPKGRNNQGRIT

SRRRGGGHKQLYRIIDFKRDKRDIPATVTAIEYDPNRNARIALLLYEDGEKRYILHPNGLKVGTTIIAGADAPFEDGNALPLFKIP
LGTSVHNVEMTPGKGGQIVRAAGAEAQVVAKEGNYVTLKLPSGEVRLIRRDCYATIGKVGNTDARNLSAGKAGRNRWKGRR
PKVRGSVMNPVDHPHGGGEGRAPIGRAGPVTPWGKPTLGAKTRKRKKASSKLIVMSVGILGTKLGMTQIFDDAGRAIPVTVIQ
AGPCTVTQVKTKQTDGYAAIQVGYGEVKPKALNRPLLGHLAKSSAPALRHLNEYRTDASGDYALGQELKADIFSEGQIVDVIG
TSIGRGFAGNQKRNNFGRGPMSHGSKNHRAPGSIGAGTTPGRVYPGKRMAGRLGGTRVTIRKLTVVRVDAERNLILIKGAIPGK
PGALVNVVPTNKVGNKMVESVVKNWQGEQVGETTFDLRVAKAETAAHIVHRALVRQMTNSRQGTASTKTRSEVRGGGRKP
WRQKGTGRARAGSIRSPLWRGGGVIFGPKPRDFNLKLNRKERRLALRTAFVSRAEDLIVVEEFSNELQRPKTKELVAALARWG
ALPEQKSLLILSEIAENVLLSARNIENLKLIAADQLNVYDLLHADKIILTSAALAKIQEVYSAMAKTRLKNLYQETIVPKLINQFQ
YTNVHQVPKVVKITINRGLGEAAQNAKSLEASLNEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLVS
LSLPRIRDFRGISPKSFDGRGNYTLGVREQLIFPEVEYDSIDQIRGLDISIITTAKNDEEGRALLKEMGMPFRDQMSRIGKRPITVPA
KVQVAIDGSKVVVKGPKGELSRVLPSNVIVSQEGETLLVTRRDETRTSRQLHGLSRTLVANMVEGVSLGFQRRLEIQGVGYRA
QVQGRNLVLNMGYSHQVQIEPPEGIQFAVEGTTNVIVSGYDKEIVGNTAAKVRGVRPPEPYKGKGIRYAGEVVRRKAGKTGKS
GKKMAKKVVAVIKLALNAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKTPPASVLIR
KAAKIERGSNEPNKKKVGSITRVQLREIAQTKLPDLNANDIDAAMNIVEGTAKNMGVTITDMSAATEQILEQLKTLTLLEASEL
VKQIEEAFGVSAAPAAGGMMMMAAPGAAAAEVVEEKTEFDAVLESVPADKKIAVLKIVREITGLGLKEAKDLVEAAPKAIKE
AVAKEAAEDIKKRVEEAGGKVVIKMSSKTYLPPQATLERDWYVVDATDKRLGRLASEIAMILRGKKKPEYTPHMDTGDFVVV
INAEKVAVTGKKRTQKIYRRHSGRPGGMKTETFAKLQQRLPERILEHAVKGMLPKNSLGKQLFTKLKVYAGPTHPHAAQQPK
ELVINTIPGENMIQPQTYLNVADNSGAKKLMCIRVLGAGNRRYGGVGDKIIAVVKESTPNMAVKKSDVVEAVIVRTRKAINRD
SGMCIRFDDNAAVIINKDGNPRGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLATRGSTLNFGDFAL
QAQEPAWITSRQIEASRRAMTRYIRRGGKIWIRIFPDKPVTMRPAETRMGSGKGNPEFWVAVVKPGRILFEIAGVTEEIAREAMR
LAAYKLPIKTKFIIRSQPQEQEMNAQEIIRSIEAEHLKSDIPIIYVGDTVRVGVKIKEGDKYRVQPYEGVVIGKRNGGINETITVRR
VFQGVGVERVFLLHSPRIDNIKVLRRGRVRRAKLYYLRDRVGKATRIKQRFDRALMTRVKRGNVARKRRNKILKIAKGFRGSH
STLFRTANQQVMKALRSSYRDRKKKKRDFRRLWITRINAASRQHGLSYSQLIGNLKKANIELNRKMLAQLAVLDPASFAKVAE
MANAVKGMAHKKGTGSTRNGRDSNAQRLGVKRFGGQVVRAGNILIRQRGTKIHPGNNVGIGNDDTLFALVDGVVTFERKGK
TRKKVSVYPVVAVEALASMTNETYMEPAFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGNNYKLKEPKYSV
EESKRRDSTYAVQMYVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIP
NRGAWLKFETDRNDLVWVRIDKTRKLSAQVLLKALGLSDNEIFDALRHPEYFQKTIEKEGQFSEEEALMELYRKLRPGEPPTVL
GGQQLLDSRFFDPKRYDLGRVGRYKLNKKLRLSVPDTMRVLTPGDILAAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELLQNQ
VRVGLNRLERIIRERMTVSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVR
DIHPSHYGRICPIETPEGPNAGLIGSLATHARVNLYGFLETPFRPVENGKVRFDVQPVYMTADEEDDLRTATGDIPVDENGYIKG
PQVPVRYRQDWATTTPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSG
MVIVSRTDGDVVYVDAAEIRVRVREQTTDKNLTQLPASLKESPTGKPPEVTYYLSKYQRSNQDTCLNQKPLVRIGEKVVAGQV

LADGSSTEGGELALGQNIVVAYMPWEGYNYEDAILISERLVQDDVYTSIHIEKYEIEARQTKLGPEEITREIPNVGEDALRQLDE
QGIIRIGAWVEAGDILVGKVTPKGESDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQGDELPPGANMVV
RVYVAQKRKIQVGDKMAGRHGNKGIISRILPAEDMPYLPDGSPVDIVLNPLGVPSRMNVGQVFECLLGWAGQNLGVRFKITPF
DEMYGEESSRRIVHGKLQEARDETGKNWVYNPDDPGKIMVYDGRTGEPFDRPITIGVAYMLKLVHLVDDKIHARSTGPYSLVT
QQPLGGKAQQGGQRFGEMEVWALEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDI
AVHKVETQADGSSLDVEVDLMADQATRRTPPRPTYESLSRESLEEEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTSRN
GVHIIDLVQTAQLMDNAYNYMRSQSEQGKKFLFVGTKRQAAGIIAQEAARCGSHYINQRWLGGMLTNWATIKTRADRLKDLE
RREENGALDLLPKKEASMLRREMTKLQKYLGGIKNMRKVPDVVIIVDQRREYNAVQECEKLGIPIVSMLDTNCDPDVVDIPIPA
NDDAIRSIKLIVGKLADAIYEGRHGQLEAEGDYDDYEGAEGDYDYDESEYTDAVIPDEEEEMGQKIHPVGFRLGITQEHQSRWF
AVPDRYPELLQEDHKLRKYIEQKLGRYAQNNAGISEVRIERKADQIDLEVRTARPGVVVGRGGQGIESLRTGLQDLLGSNRQIRI
NVVEVQRVDADAYLIAEYIAQQLERRVSFRRVVRQAIQRAQRAGVQGIKVQVGGRLNGAEIARTEWTREGRVPLHTLRADIDY
SYCTAQTIYGILGIKVWVFKGEIIPGQEETPSAPTTREPRRQQQRRRQQFEDRSNEGMATGRRKTNRAKKEETNWQERVIQIRR
VSKVVKGGKKLSFRAIVVVGNERGQVGVGVGKASDVIGAVKKGVADGKKHLIDIPITKSNSIPHPIDGIGGGAKVMMRPAAPG
TGVIAGGAVRTVLELAGVRNVLAKQLGSNNPLNNARAAVNALSTLRTFAEVAEDRGIPIESLYIVAEANSGRAVYWGTGRRKS
AVARVRLVPGEGKFVVNGKDGELYFQFNANYLGAIKAPLETLGLESEYDILVKAEGGGLTGQADSIRLGVARALCQLDPDNRP
PLKTEGYLTRDPRAKERKKYGLHKARKAPQYSKRMATLQQQKIRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRRI
YCVLRSPHVDKDSREHFETRTHRRIIDIYQPSSKTIDALMKLDLPSGVDIEVKLMARQPTKKSGSKKQKRNVPNGMAYIQSTFN
NSIVTITDQNGDVISWASAGSSGFKGAKKGTPFAAQTAAESAGRRAIDQGMRQIEVMVSGPGAGRETAIRALQGAGLEITLIRDI
TPIPHNGCRPPKRRRVMARISGVDLPRDKRVEIGLTYIYGIGLSRSQEILAATGVNPDTRVKDLSDADVAALRGEIESNYQVEGD
LRRLEAMNIKRLVDIGSYRGRRHRMGLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLSKIEKLNAK
NEKQVIKTWSRASTILPMMVGHTIAVHNGRQHVPVFVNEQMVGHKLGEFSPTRTYRGHGKSDKKSGRMSDKKEGFKVISDNR
QARYLYEIIETYEAGIQLTGTEVKSIRAGKVNLQDGYALLRNGEAWLINIHISPYTSSGQYFNHEPRRTRKLLLHRQELRKLIGKV
EQQGLTLVPLKMYLQRGWVKVSIALGKGKKLHDKRESLKRRQDQRDIQRAMKSYMAEISAKLVQELRQKTGAGMMDCKKA
LKETEGNIEEAVDWLRKKGIASAGKKSDRIAAEGLVDTYIQSGGQVGVLIEVNCQTDFVARNDAFKSLVKNLAQQAATADSVE
SLLAQPYLEKSSVSVDEFIKETMATLGENIQVRRFVNFALSAATPGVVDSYIHTGGRVGVLLELNAQTESAAGNEDFQNLAKNA
AMQVAACPNVEYVTIEQIPAEFVQKEKDIEMGKDDLGNKPENIKEKIVQGRIDKRLKEITLLDQPYIRDQAISVEELVKQVKSKV
GEEIKINRFVRYVLGEGIDKQEISFADEVAAQMGAK

>Anabaena_sp_90
MQIPRLHPDTIEEVKLRADIVDVVSEYVVLRKRGKDFLGLCPFHDEKSPSFSVSPNKQMYYCFGCQAAGNAIKFVMDLGKRQF
ADVVLDLAKRYQVPVKTLEPEQRQELQRQISLRDQLYTVLATAAQFYQHTLRQSQGQKALEYLEQTRQFKQGTIQQFGLGYAP
AGWETLYRYLVESKHYPVQLVEQAGLIKPRKEGGGYYDVFRDRLMIPIRDIQGRVIAFGGRTLTDEQPKYLNSPETELFSKGKM
LFALDEAKDGISKVDQAVVVEGYFDAIALHAAGINNAVASLGTALSIEQVRLLLRYTESKQLILNFDADKAGTNATERAIGEIA
NLAYAGEVQLKILNLPNGKDADEYLHSHTSADYQKLLTNAPLWLDWQIQNIIKNRDLKQATDFQQVTQQIVKLLQNIVNSDTL
NYYVSSCAEILSLGDTRLIPLRVENLLTQIKPGRIKSLNPRTSNPATKTPKLSLVNTERSLLERAEALLLIIYLHSSQQRQIIIEDLEN
RNLEFSLSHHRFLWQQMAEFTVDEVDLISSVQNRYLELAEELEIVSHIFHLNEKNKTEILRTPHVIQAALACMERVFREKRYRYF
MEQWEKIDPEAEPEKDKYYAEAIYIEKLHLQDLEKQRQFSITDLIMKLAEAESMMQKTVESTQRAFNTIRTGRANASLLDKVQ
VEYYGTPTSLKALTNISTPDSSTILIQPYDKGSLNIIEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKEFVKLAAKYAEEGRVAIR
NIRRDANDSIRKQEKSAEISEDESRDQQDKLQKLTNKHTEKIDHLLVEKEKEITTVMPVIEKKRTRDLPQINERIRFPKIRVIDTDG
AQLGIITPQEAIQLAEEKELDLVLISDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVKQA
ERFLKDGDKVKATVMFRGREIQHSDLAETLLKRMATDLEPFGELQQAPKKEGRNMMMLISPKKMSMVTLSGLKELIESISQER
NLPRLAVQAAIREALIKGYERYRRAQNLERRQFDEEYFNNFEVELDIEGEGFRVLSTKTIVEAVANTDHQISLDEVQQVAPEAQ
LGDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVVLAVSSGFGQSEVEAEL
PKREQLPNDNYRANATFKVYLKKVSQGQQRGPQLMVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIA
VDTLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPAKVDEVRLMDPESRQTHVLVAEDQLSLAIGK
EGQNVRLAARLTGWKIDIKDQAKYDEEAENTKFAAVRAQYQSQNDRDDRSDREDAMAEELELDEDRFDNSEEDMSKKSLAS
LSAADISGKRALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLTQKGAKVILTSHFGRPKGVDEKLRLTPVAKRLSELLGQEVIK
TDDCIGDDVAAKVAALDNGQVLLLENVRFYKEEEKNDREFAQKLAANADFYVNDAFGTAHRAHASTEGVTEFLSPSVAGYL
VEKELQYLQSAIEEPKRPLAAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEEDKLELARELEAKAKER
GVALLLPTDIVSADKFAPDANATTVSIENIPADGMGLDIGPDSIKVFQAALADCQTVIWNGPMGVFEFDKFAAGTEAIAHTLAEI
GKTGATTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGKVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKS
RDYSVSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGGTVQV
IPHITNEIKERILRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGKRNVLYMHVTLLPWIAAAGEMKTKPTQHSVKELR
SIGIQPDILVCRSDRPIPVGLKQKLSEFCDVPVECVITSPDARSIYEVPVILEREGLAEQVLNLLQMEQRQPNMTQWENMVDRMY
NPKYTVEIAIVGKYVRLGDAYLSVVESLRHAAIATHGDLRLRWINSEVLENEPPENYLAGVDGIIVPGGFGSRGIDGKIAAIKYA
RDRQIPFLGLCLGMQCSVIEWARNVEGLSNANSAEFDPYTDNPVINLLPEQQDVVDLGGTMRLGLYPCRVLPNSLAFQLYQEE
VIYERHRHRYEFNNVYRSQLLDSGYLVSGTSPDGRLVEIIEYPKHPFFIACQFHPEFQSRPNAPHPLFKGFMTAAISQFHSTTTTPK
PVQVSMAKKVSRRLQALLEKVEDRDYTPLEALALLKETATAKFAEAAEAHIRLGIDPKYTDQQLRTTVALPKGTGQIIRVAVIA
RGEKVTEATNAGADIAGSEELIEDIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDVASAIAEFKAGKLE
YRADRTGIVHVMFGKTAFSPEDLLINLKALQESIDRNRPSGAKGRYWRSVYISSTMGPSIAIDISALRELKITDAAMGTRSYRPYT

SSTRQVIISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRNMSATVTAIEYDPNRNARIALVLY
EDGEKRYILQTNGMTVGTKIIAGPESPIEDGNALPLSNMPLGTSVHNVEMTPGKGGQIVRAAGAVAQVVAKEGNYVTLKLPSG
EVRLIRRDCYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSAMNPVDHPHGGGEGRAPIGRAGPVTPWGKPTLGAKTR
NRKKASTKLIIMSVGILGTKLGMTQIFDEAGVSIPVTVIKAGPCTVTQVKTKQTDGYSAIQVGYGEVKPKSLNRPLLGHLAKSSA
PPVRHLNEYRTDSTGDYALGQEIKADIFSVGEIVDVVGTSIGRGFAGNQKRNNFARGPMSHGSKNHRAPGSIGAGTTPGRVYPG
KRMAGRLGGTRVTIRKLTVIRVDAERNLIIIKGAIPGKPGALVSVVPATIVGKKMVESVIKNWQGEQVGETSFDLRVAKETTAA
HIVHRALVRQMTNSRQGTVSTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFGPKPRDFDLKMNRKERRLALRT
AFVGRAEDLIVVEEFSNELQRPKTKDLVAALARWGATSEQKTLLILSEIAENVLLSARNIENLKLIPADQLNVYDLLHADKIIVTS
STLDKIQEVYSAMAKTRLKTVYQETITPKLTTQFEYTNVHQVPKVIKITINRGLGESAQNAKSLEASISEIALITGQKPVVTRAKK
AIAGFKIRQGMPVGIMVTLRGERMYAFLDRLINLTLPRIRDFRGVSPKSFDGRGNYTLGVREQLIFPEVEYDRIDQVRGLDISIITT
AKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGVKVVVKGPKGELSRQLPKNVIVSQEGETLIVTRRDETRTSRQ
MHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQLQGSNLVLNMGYSHQVQIEPPAGIQFAVEGTTNVIVSGYDKEIVGNTA
AKIRAVRPPEPYKGKGIRYAGEVVRRMAKKVVAVIKLALNAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIP
VEISVYEDRSFTFVLKTPPASVLIRKAAKIERGSSEPNKTKVGSISRTQLREIAQTKLPDLNANDIDAAMNIVEGTAKNMGVTITD
MSAATEQILDQLKSLTLLEASELVKQIEEAFGVSAAPTGGGMMMMAAPGAVAEVVEEKTEFDAILDSVPADKKIAVLKIVREIT
GLGLKEAKDLVEAAPKAVKEAVTKEAAEDIKKRIEEAGGKVTVKTKTYLPPQASIERDWYLVDATDKRLGRLATEVAMILRG
KKKPEFTPHMDTGDFVIIINAEKVAVTGKKRTQKVYRRHSGRPGGMKTETFAKLQQRLPERILEHAIKGMLPKNSLGKQLFTKL
KVYAGPTHPHAAQLPKEITISTIPGENMIQPQSYLNVADNSGAKKLMCIRVLGAGNRRYGGVGDRIIAVVKESSPNMAVKKSDV
VEAVIVRTRKAISRDSGMAIRFDDNAAVIINKEGNPRGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEG
LASRGSTLNFGDFGLQAQEPSWITSRQIEASRRAMTRYIRRGGKIWIRIFPDKPITMRPAETRMGSGKGNPEFWVAVVKPGRIMF
EIGGVTEEIAREAMRLADSKLPIKTKFITRSQPQEQEMNAQEIIRSIEAEQMKSDLPDIYVGDTVKVGIKIQEGTKFRVQPYEGVVI
ARRNGGINETITVRKVFQGVGVERVFLLHSPLVESIKVLRRGKVRRAKLYYLRALVGKATRIKQRFDRPLMTRVKRGNVARKR
RNKILKLAKGFRGSHSTLFRTANQQVMKALRSAYRDRKKKKRDFRRLWIARINAASRQHGLSYSRLIGNLKKANVELNRKML
AQLAILDPASFAKIAELANSVNGMAHKKGTGSTRNGRDSNAQRLGVKRYGGQTVRAGNILVRQRGTKVHPGNNVGIGSDDTL
FALIDGVVTFERRGKSQKKVSVYAVAAELVEAVANDDKYMESAFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELH
FLGNNYKLKEPKYSVEESKRRDSTYAVQMYVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKS
EIDKNGRRTYSASLIPNRGAWLKFETDRNDLVWVRIDKTRKLSAQVLLKALGLSDNEIFDALRHPEYFQKTIEKEGQFSEEEAL
MELYRKLRPGEPPTVLGGQQLLDSRFFDPKRYDLGKVGRYKLNKKLRLSAPDTMRVLTPGDILAAIDYLINLEYDIGSIDDIDHL
GNRRVRSVGELLQNQVRVGLNRLERIIRERMTVSDAESLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSAL
GPGGLTRERAGFAVRDIHPSHYGRICPIETPEGPNAGLIGSLATHARVNLYGFLETPFRPVENGKVLFDVLPVYMTADEEDDLRT
ATGDVPLDENGYIKGPHVPVRYRQDWTTTGPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLRPERP
LVGTGLEAQAARDSGMVIVSRTDGDVVYVDATEIRVRASGQLSAASGSQVIEKGQELKYKLSKYQRSNQDTCLNQKPLVRIGE

KVVAGQVLADGSSTEGGELALGQNIVVAYMPWEGYNYEDAILISERLVQEDVYTSIHIEKYEIEARQTKLGPEEITREIPNVGED
ALRQLDEQGIIRIGAWVDAGDILVGKVTPKGESDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQGDELPP
GANMVVRVYVAQKRKIQVGDKMAGRHGNKGIISRILAAEDMPYLADGSPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLG
VRFKITPFDEMYGEETSRRLVHGKLQEARDETTKDWIYNPDNAGKIMVYDGRTGEPFDRAITVGVAYMLKLVHLVDDKIHAR
STGPYSLVTQQPLGGKAQQGGQRFGEMEVWALEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMR
ELQSLGLDIAVHKVETQADGSSLDVEVDLMADQAARRTPPRPTYESLSRESLEGEEMPVVSLAQMMESGVHFGHQTRRWNPK
MAPYIYTSRNGVHIIDLVQTAQLMDNAYNYMRTQSEQGKKFLFVGTKRQAAGIIAQEALRCGSHYINQRWLGGMLTNWATIK
TRAERLKDLERREETGALDLLPKKEASMLRREMTKLQKYLGGIKNMRKVPDIVVIVDQKREYNAVQECEKLGIPIVSMLDTNC
DPDVVDIPIPANDDAIRSIKLIVGKLADAIYEGRHGQLMGQKIHPVGFRLGITQEHQSRWFAEPDRYPELLQEDYKLRQYIEQKL
GRYAQNNAGISEVRIERKADQIDLEVRTARPGVVVGRGGQGIESLRLGLQGALGGNRQIRINVVEVQRVDADAYLIAEYIAQQL
ERRVSFRRVVRQAIQRAQRAGVQGIKVQVGGRLNGAEIARSEWTREGRVPLHTLRADIDYSGCTAKTVYGILGIKVWVFKGEII
PGQEQAPAQPAMVTGRRKASRTKKEETTWQERVIQIRRVSKVVKGGKKLSFRAIVVVGNERGQVGVGVGKASDVIGAVKKG
VADGKKHLIDIPITKSNSIPHPIDGVGGGAKVMMRPAAPGTGVIAGGAVRTVLELAGIRNILAKQLGSNNPLNNARAAVNALST
LRTLSEVAEDRGISIEKLYIVAETTSGRAVYWGTGRRKCSVASVRLVPGEGKMTVNGKDGDLYFQFNPNYLGAIKAPLETLGLE
SEYDILVKAEGGGLTGQADSIRLGVARALCQLDPDNRSPLKTEGYLTRDPRAKERKKYGLHKARKAPQYSKRMATLQQQKIRI
RLKAFDRRLLDTSCEKIVETANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTHRRIIDIYQPSSKTIDALMKLDLPSG
VDIEVKLMARQPTKKSGSKKQKRNVPNGVAYIQSTFNNSIVTITDQNGDVISWASAGSSGFKGAKKGTPFAAQTAAESAARRA
TDQGMRQIEVMVSGPGAGRETAIRALQGAGLEITLIRDITPIPHNGCRPPKRRRVMARISGVDLPRDKRVEIGLTYIYGIGLTRSH
QILAATGVNPDIRVKDLSDADVAALRGEIESNYQVEGDLRRLEGLNIKRLVDIGCYRGRRHRMGLPVRGQRTRTNARTRRGRR
QTVAGKKKAPGKMGRSLKKGPFVADHLLKKIEKLNAKDEKQVVKTWSRASTILPLMVGHTIAVHNGRQHIPVFNEQMVGH
KLGEFAPTRTYRGHGKSDKKSGRMSDKQSEGYKVICDNRQARFLYEIIETYEAGVQLTGTEVKSIRAGKANLQDGYALLRDGE
AWLINVHISPYASSGAYFNHEPRRTRKLLLHKQELRKLIGRVQQEGLTLVPLKMYLKRGWVKIVIALGKGKKLHDKRESLKRR
DDQRDMQRAMKRYMAEISAKLVQELRQKTGAGMMDCKKALKENNGDVEESITWLRQKGIAKADKGSARIAAEGLVDTYIQ
ADGHIGVLIEVNCQTDFVARNEAFKALVKNLAQQAATTDSVESLLAQPYLEKSSVTVDEFIKETIATLGENIQVRRFVNFSLTTD
TPGIADSYIHTGGRVGVLLELTAQSASAAANEEFQSLAKNAAMQVAACPNVEYVSVDQIPAEIVTKEKGIEMGKDDLGNKPENI
KEKIVQGRIDKRLKEMTLLDQPYIRDQSISVEELVKQVKSKVGEEIQVSRFVRYVLGEGIEKNEMSFADEVAAQMGAK

>Aphanizomenon_flos_aquae_DEX188
MQIPRLHPDTIEEVKIRADIVDVVSEYVVLRKRGKDFVGLCPFHNEKSPSFTVSPNKQMYYCFGCQAAGNAIKFVMDLGKRQF
ADVVLDLAKRYQVPIKTLEPEQRQELQRQISLRDQLYTVLAAAAQFYQHTLRQSQGQKALEYLEKIRQFQQGTIQQFGLGYAP
AGWETLYRYLVESKHYPVQLLEQAGLIKPRKEGGGYYDVFRDRLMIPIRDIQGRVIAFGGRTLTDEQPKYLNSPETELFSKGKIL
FALDEAKEGISKVDQSVVVEGYFDAISLHAAGINHVVASLGTALSIEQVRLLLRYTESKQLILNFDADKAGINATEKAIGEIANL
AYTGEVQLKILNLPNGKDADEYLHGHTSDDYQQLLTNAPLWLDWQIQKIIENRDLKQATDFQQVTQQIVKLLQNIVNSDTLNY
YVSYCAEILSLGDSRLKPLRVENLLTQIKPSSVKSLSPRTTNPQPKTPKLSLVTTERSLLERAEALLLIIYLHSFEQRQIIIEDLEARN
LEFSLSHHRFLWQQMAEFTIDEIDLISSVQNRYLELGEELDIVSHIFHLNEKNKTEILRTPHVIQAALACMERVFREKRYRYFMEQ
WEKIDPETEPEKDKYYAEAMYIEKIHLHDLEKQRQFSITDLIMKLAEAQETMQKTVEATQRSFNTIRTGRANASLLDKVQVEYY
GTPTSLKSLANITTPDSSIILIQPYDKGSLNIIEKAISLSDVGLTPSNDGVVIRLNIPPLTSDRRKEFVKLAAKYAEEGRVAIRNIRRD
AIDAIRKQEKSAEISEDEARDQQDKLQKLTNKHTEKIDHLFAEKEKEITTVMPVIEKKRTRDLPQINERIRFPKIRVIDTDGAQLGI
ITPQEAIQLAEEKELDLVLISDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVKQAERFLK
DGDKVKATVMFRGREIQHSDLAETLLKRMATDLEPFGELQQAPKKEGRNMMMLISPKKMVTLSGLKELIESISQERNLPRVAV
QAAIREALIKGYERYRRAQNLERRQFDEEYFNNFEVELDIDGEGFRVLSTKTIVDTVSNTDHQISLDEVQQVAPEAQLGDSVVL
DVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVVLAVTSGFGQSEVEAELPKREQLP
NDNYRANATFKVYLKKVSQGQQRGPQLMVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAVDTLDR
DVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPAKVDEVRLMDPESRQTHVLVAEDQLSLAIGKEGQNVR
LAARLTGWKIDIKDQAKYDQEAEDIKFAAVRAQNQPQNDHDDRSNREDKMEEELELEEDRFDSREEDMSKKSLASLSAADISG
KRALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLTQKGAKVILTSHFGRPKGVDEKLRLTPVAKRLSELLGQEVIKTDDCIGD
DVAAKVAALDNGQVLLLENVRFYKEEEKNDREFAQKLAANADFYVNDAFGTAHRAHASTEGVTKFLSPSVAGYLVEKELQY
LQSAIEAPQRPLAAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLSVGKSLVEEDKLELAKSLEAKAKERGVALLLPT
DIVSADKFAPDANATTVSIENIPADGMGLDIGPDSVKVFQAALADCKTVIWNGPMGVFEFDKFAAGTEAIAHTLAEISKTGAITII
GGGDSVAAVEKVGLADQMSHISTGGGASLELLEGKVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRDYSVSIL
KLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINRERRGDYNGGTVQVIPHITNEIK
ERILRVAKETNPSAVITEIGGTVGDIESLPFLEAIRQLRKEVGKRNVLYMHVTLLPWIAAAGEMKTKPTQHSVKELRSIGIQPDIL
VCRSDRPIPVGLKQKLSEFCDVAVECVITSPDARSIYEVPVILEREGLAEQVLNLLQMEQRQPNMSQWEMMVERMYNPKYSVE
IAIVGKYVRLSDAYLSVVESLRHAAIATHSDLRLRWVNSEALETEPAENYLSGVDGIIVPGGFGSRGIDGKIAAIKYARTRQIPFL
GLCLGMQCSVIEWARNVEGLSHADSAEFNPYTEDPVINLLPEQQDVVDLGGTMRLGLYPCRILPNTLAFQLYQEEVIYERHRHR
YEFNNIYRNQLLDSGYLVSGTSPDGRLVEIVEYSQHPFFIACQFHPEFQSRPNAPHPLFKGFITAAISQSMAKKVSRRLQALLDKV
EDRDYSPLEALALLKETATAKFSEAAEAHVRLGIDPKYTDQQLRTTVALPKGTGQIIRVAVIARGEKVTEATNAGADIAGSEELI
DQIQKGFMEFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDIASAIAEFKAGKLEYRADRTGIVHVMFGKAAFSPEDL
LINLKALQESIDRNRPSGAKGRYWRSLYISSTMGPSIAIDISALRDLKLTEAAMGTRSYRPYTPSTRQVIISDFAEITKTEPEKSLTE

SVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRNMTATVTAIEYDPNRNARIALLLYEDGEKRYILQPNGMTVGTKVIAG
PDSPIEDGNALPLANMPLGTGVHNVEMTPGKGGQIVRAAGAVAQVVAKEGNYVTLRLPSGEVRLIRRDCYATIGQVGNTDAR
NLSAGKAGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPTLGAKTRNRKKSSTKLILMSVGILGTKLGM
TQIFDEAGVSIPITIIQAGPCTVTQVKTKQTDGYSAIQVGYGEVKPKALNKPLLGHLAKSSAPALRHLNEYRTDSAGDYTPGQEI
KADIFSAGEIVDVVGTSIGRGFAGNQKRNNFGRGPMSHGSKNHRAPGSIGAGTTPGRVYPGKRMAGRLGGTRVTIRKLTVVRV
DTERNLILIKGAIPGKPGALVSVVPATIVGKKMVESVIKNWQGEQVGETSFDLPVAKETTAAHIVHRALVRQMTNSRQGTASTK
TRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFGPKPRDFDLKMNRKERRLALRTALIGRAEDIIIVEEFSNELQRPKT
KDLVAALARWGAVPEQKTLLILSEIAENVLLSARNIENLKLIPADQLNVYDLLHADKIVVTSSTLEKIQEVYSAMAITRLKTVYQ
ETITPKLITQFQYTNVHQVPKVTKITINRGLGEAAQNAKSLEASISEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGER
MYAFLDRLINLTLPRIRDFRGVSAKSFDGRGNYTLGVREQLIFPEVEYDKIDQVRGLDISIITTAKTDEEGRALLKEMGMPFRDQ
MSRIGKRPITIPAKVQVAIDGVKVVVKGPKGELSRQLPNNVIVSQEGETLLVTRRDETRTSRQMHGLSRTLVANMVEGVSQGFQ
RRLEIQGVGYRAQLQGSNLVLNMGYSHQVQIEPPPGIKFAVEGTTNVIVSGYDKEIVGNTAAKIRAVRPPEPYKGKGIRYAGEV
VRRMAKKVVAVIKLALNAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVYEDRSFTFVLKTPPASVLIR
KAAKIERGSNEPNKKKVGSISRTQLREIAQTKLPDLNANDIDAAMNIVEGTAKNMGVTVTDMSAATEQILEQLKSLTLLEASEL
VKQIEEAFGVSAAAPAGGMMMMAPGAGAAAEEVVEKTEFDAILDSVPADKKIAVLKIVREITGLGLKEAKDLVEAAPKAVKE
AVTKDAAEDIKKRIEEAGGKVTVKMSSKTYLPPQASLERDWYLVDATDKRLGRLASEVAMILRGKRKAEYTPHLDTGDFVIII
NAEKVAVTGKKRTQKLYRRHSGRPGGMKTETFAKLQQRLPERILEHAIKGMLPKNSLGKQLFTKLKVYAGPTHPHEAQQPKEI
TISTIPGENMIQPQSYLNVADNSGAKKLMCIRVLGAGNRRYGGVGDRIIAVVKESSPNMAVKKSDVVEAVIVRTRKAISRDSGM
TIRFDDNAAVIINKEGNPRGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLASRGSTLNFGDFGLQAQ
EPSWITSRQIEASRRAMTRYIRRGGKIWIRIFPDKPITMRPAETRMGSGKGNPEFWVAVVKPGRIMFEIGGVTEEIAREAMRLAD
AKLPIKTKFIVRSQPQEQEMNAQEIIRSIEAEQMKSNLPDIYVGDTVKVGVKIQEGNKFRVQPYEGVVIAMRNGGINETITVRKV
FQGVGVERVFLLHSPLIETIKVLRRGKVRRAKLYYLRALVGKATRIKQRFDRPLMTRVKRGNVARKRRNKILKLAKGFRGSHS
TLFRTANQQVMKALRSAYRDRKKKKRDFRRLWIARINAASRQHGLSYSRLIGNLKKANVELNRKMLAQLAILDPTSFAKIAEL
AQSVNGMAHKKGTGSTRNGRDSNAQRLGVKRYGGQTVRAGNILVRQRGTKVHPGNNVGIGSDDTLFALVDGVVTFERKGKS
QKKVSVYPNDDKYMESAFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGNNYKLKEPKYSVEESKRRDSTYA
VQMYVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFET
DRNDLVWVRIDKTRKLSAQVLLKALGLSDNEIFDALRHPEYFQKTIEKEGQFSEEEALMELYRKLRPGEPPTVLGGQQLLDSRF
FDPKRYDLGKVGRYKLNKKLRLSAPDTMRVLSSSDILAAIDYLINLEFDIGNIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERI
IRERMTVSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRIC
PIETPEGPNAGLIGSLATHARVNLYGFLETPFRPVENGKVLFHLPPVYMTADEEDDLRTATGDIPLDEYGFIKGPNVPVRYRQD
WTTTPPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQAARDSGMVIVSRTDGD
VVYVDATEIRVRVGGQRLVAGDNEKTGDREQLRTDKPQELKYKLSKYQRSNQDTCLNQKPLVRIGEKVVAGQVLADGSSTEG

GELALGQNIVVAYMPWEGYNYEDAILISERLVQEDVYTSIHIEKYEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRVGAW
VDAGDILVGKVTPKGESDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQGDELPPGANMVVRAYVAQKR
KIQVGDKMAGRHGNKGIISRILPAEDMPYLSDGSPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGEETS
RRLVHGKLEEAREETGRDWVYNPDNAGKITVYDGRTGEAFDRDVTVGVAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGK
AQQGGQRFGEMEVWALEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDVAVHKVE
TQTDGSSLDVEVDLMIDQATRRTPPRPTYESLSRESLDEEEMPVVSLAQMMESGVHFGHQTRRWNPKMAPYIYTSRNGVHIIDL
VQTAQLMDDAYNYMRTQSEQGKKFLFVGTKRQAAGIIAQEALRCGSHYINQRWLGGMLTNWATIKTRAERLKDLERREETG
ALDLLPKKEASMLRREMTKLQKYLGGIKNMRKVPDIVVIVDQKREYNAVQECEKLGIPIVSMLDTNCDPDVVDIPIPANDDAIR
SIKLIVGKLADAIYEGRHGQLEVMGQKIHPVGFRLGITQEHQSLWFAEPDRYPELLQEDYKLRQYIEQKLGRYAQNNAGISEVRI
ERKADQIDLEVRTARPGVVVGRGGQGIESLRLGLQGALGGNRQIRINVVEVQRVDADAYLIAEYIAQQLERRVSFRRVVRQAIQ
RAQRAGVQGIKVQVGGRLNGAEIARSEWTREGRVPLHTLRADIDYSGCTAKTIYGILGIKVWVFKGEIIPGQEQAPAQPARERD
RDRDRGDREREPRRRQQQRRRQQFEDRSNETMVTGRRKASRTKKEETTWQERVIQIRRVSKVVKGGKKLSFRAIVVVGNERG
QVGVGVGKASDVIGAVKKGVADGKKHLIDIPITKSNSIPHPIDGIGGGAKVMMRPAAPGTGVIAGGAVRTVLELAGIRNILAKQ
LGSNNPLNNARAAVNALSTLRTLTEVAEDRGIAIEKLYIIAEINSGRAVYWGTGRRKASVARVRLVPGEGKMIVNGKDGELYF
QFNPNYLGSIKAPLETLGLENEYDILVKAEGGGLTGQADSIRLGVARALCELDPDNRSPLKTEGYLTRDPRAKERKKYGLHKAR
KAPQYSKRMATLQQQKIRIRLKAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTHRRIIDI
YQPSSKTIDALMKLDLPSGVDIEVKLMARQPTKKTGSKKQKRNVPNGVAYIQSTFNNSIVTITDQNGDVISWASAGSSGFKGAK
KGTPFAAQTAAESAARRATDQGMRQVEVMVSGPGAGRETAIRALQGAGLEITLIRDITPIPHNGCRPPKRRRVMARISGVDLPR
DKRIEIGLTYIYGIGLTRSHQILAATGVNPDTRVKDLSDADVTALRGEIESNYQVEGDLRRLEGLNIKRLVDIGCYRGRRHRMGL
PVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLKKIEKLNAKDEKQVVKTWSRASTILPLMVGHTIAVH
NGRQHVPVFVNEQMVGHKLGEFAPTRTYRGHGKSDKKSGRMSEKQSEGYKVICDNRQARFLYEIIETYEAGVQLTGTEVKSIR
AGKANLQDGYALLRDGEAWLINVHISPYTSSGAYFNHEPRRTRKLLLHKQELRKLIGRVQQEGLTLVPLKMYLKRGWVKIVIA
LGKGKKLHDKRESMKRRDDQRDMQRAMKRYMAEISAKLVQELRQKTGAGMMDCKKALKENDGDIEAATTWLRQKGIAKA
DKGSSRIAAEGLVDTYIRPDGQVGVLIEVNCQTDFVARNDAFKDLVKKLAQQAATTDSVESLLAQPYIGKESVSVDEFIKETIAT
LGENIQVRRFVNFSFTSDTPGIADSYIHTGGRVGVLVELTTPGALAGTNEDLQGLAKNAAMQVAACPNVEYVSVDQIPVEVVQ
KEKDIEMGKDDLANKPVNIREKIVQGRIDKRLKEMTLLDQPYIRDQSISVEDLVKQVKSKVDREIQVSRFVRYILGEGIEKKEISF
ADEVAAQIGAK

>Aphanizomenon_flos_aquae_KM1D3
MQIPRLHPDTIEEVKLRADIVDVVSEYVVLRKRGKDFVGLCPFHDEKSPSFTVSPNKQMYYCFGCQAAGNAIKFVMDLGKRQF
ADVVLDLAKRYQVPVKTLEPEQRQELQRQISLRDQLYTVLASAAQFYQHTLRQSQGQKALEYLEKTRQFQQGTIQQFGLGYAP
AGWETLYRYLVESKHYPVQLVEQAGLIKPRKEGGGYYDVFRDRLMIPIRDIQGRVIAFGGRTLTEEQPKYLNSPETELFSKGKT
LFALDEAKDGISKVDQAVVEGYFDAIALHAAGINNAVASLGTALSLEQVRLLLRYTESKQLILNFDADKAGTTATERAIGEIA
NLAYTGEVQLKILNLPNGKDADEYLHSHTPADYQQLLTNAPLWLDWQIQNIIKNRDLKQATDFQQVTQQIVKLLQNIVNSDTL
NYYVSYCAEILSLGDTRLIPLRVENLLTQIKPGSIKPSIPRTSRPPTKTPKLSLVTTERSLLERAEALLLIIYLHSSQQRQIIIEDLETR
NLEFSLSHHRFLWQQMAEFIVDEVDLISSVQNRYLELGEELDIVSHIFHLNEKNKTEILRTPHVIQAALACMERVFREKRYRYFM
EQWEKIDPQTEPEKDKYYAEAIYIEKIHLHDLEKQRQFSITDLIMKLAEAESTMQKTVESTQRAFNTIRTGRANSSLLDKVQVDY
YGSPTSLKSLANITTPDSSTILIQPYDRNALNIVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKEFVKLAAKYAEEGRVAIRNIR
RDALDTIRKQEKSAEISEDEARDQQDKLQKLTNKHIVKIDELLREKEQEISTVMPVIEKKRTRDLPQINERIRFPKIRVIDTDGAQL
GIITPQEAIQLAEEKELDLVLISDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVKQAERF
LKDGDKVKATVMFRGREIQHSDLAETLLKRMATDLEPFGELQQAPKKEGRNMMMLISPKKMVTLSGLKELIESISKERNLPRL
AVQAAIREALIKGYERYRRAQNLERRQFDEEYFNNFEVELDIEGEGFRVLSTKTIVDAVSNTDHQISLDEVQQVAPEAQLGDSV
VLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVSSGFGQSEVDAELPKREQL
PNDNYRANATFKVYLKKVSQGQQRGPQLMVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAVDTLD
RDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIGKEGQNV
RLAARLTGWKIDIKDQAKYDQEAEDIKFAAVRAQNQPRNDEDDRSDREYEMAEELELDEDRFNNREEDMSKKSLASLSAADIS
GKRALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLTQKGAKVILTSHFGRPKGVDEKLRLTPVAKRLSELLGQEVIKTDDCIG
DDVAAKVAALDNGQVLLLENVRFYKEEEKNDPEFAQKLAANADFYVNDAFGTAHRAHASTEGVTKFLSPSVAGYLVEKELQ
YLQSAIEVPQRPLAAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLSVGKSLVEEDKLELAKSLEAKAKERGVALLL
PTDIVSADKFAPDANATTVSIENIPADGMGLDIGPDSIKVFQAALADCKTVIWNGPMGVFEFDKFAAGTEAIAHTLAEIGKTGAT
TIIGGGDSVAAVEKVGLADKMSHISTGGGASLELLEGKILPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRDYSVSI
LKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGGTVQVIPHITNEI
KDRILRVAKETNPSAVITEIGGTVGDIESLPFLEAIRQLRKEVGKRNVLYMHVTLLPWIAAAGEMKTKPTQHSVKELRSIGIQPDI
LVCRSDRPIPVGLKQKLSEFCDVPVECVITSPDARSIYEVPVILEREGLAEQVLNLLQMEQRQPNMTQWETMVDRMYNPQHTV
EIAIVGKYVRLGDAYLSVVESLRHAAIATHGDLRLRWVNSEVLENEPPENYLSGVDGIIVPGGFGSRGIDGKIAAIKYARDRQIPF
LGLCLGMQCSVIEWARNVEGLSNANSAEFDPYTDNPVINLLPEQQDVVDLGGTMRLGLYPCRVLPNTLAFQLYQEEVIYERHR
HRYEFNNVYRSQLLDSGYLVSGTSPDGRLVEIVEYPKHPFFIACQFHPEFQSRPNAPHPLFKGLMTAAISQSHSATATPKPVQVM
AKKVSRRLQALLEKVEDKDYTPLEALALLKETATAKFPEAAEAHIRLGIDPKYTDQQLRTTVALPKGTGQIIRVAVIARGEKVT
EATNAGADIAGSEELIEDIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDVASAIAEFKAGKLEYRADRT
GIVHVMFGKTAFSPEDLLINLKALQESIDRNRPSGAKGRYWRSLYISSTMGPSIAIDISALRELKLTDAAMGTRSYRPYTPSTRQV

IISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRNIPATVTAIEYDPNRNARIALLLYEDGEKRY
ILQPNGMTVGTKIIAGPESPIEDGNALPLSNIPLGTGVHNVEMTPGKGGQIVRAAGAVAQVVAKEGNYVTLKLPSGEVRLIRRD
CYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSAMNPVDHPHGGGEGRAPIGRSGPVTPWGKPTLGAKTRKRKKASTK
LIIMSVGILGTKLGMTQIFDEAGVSIPVTVVKAGPCTVTQVKTKQTDGYSAIQVGYGEVKPKALNKPLLGHLAKSSAPAVRHLN
EYRTDSAGDYALGQEIKADIFSAGEIVDVVGTSIGRGFAGNQKRNNFGRGPMSHGSKNHRAPGSIGAGTTPGRVYPGKRMAGR
LGGTRVTIRKLTVVRVDTERNLILIKGAIPGKPGALVSVVPATIVGKKMVESVIKNWQGEQVGETNFDLRVAKETTAAHIVHRA
LVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFGPKPRDFDLKMNRKERRLALRTAFISRA
EDLIVVEEFSNELQRPKTKDLVAALARWGAAPEQKALLILSEIAENVLLSARNIENLKLIPADQLNVYDLLHADKIIVTSSTLEKI
QEVYSAMAITRLKTVYQETITPKLINQFQYTNVHQVPKVIKVTINRGLGEAAQNAKSLEASISEIALITGQKPVVTRAKKAIAGF
KIRQGMPVGIMVTLRGERMYAFLDRLINLTLPRIRDFRGVSPKSFDGRGNYTLGVREQLIFPEVEYDRIDQVRGLDISIITTAKTD
EEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGVKVVVKGPKGELSRQLPNNVILSLDGETLLVTRRDETRTSRQMHGL
SRTLVANMVEGVSQGFQRRLEIQGVGYRAQLEGRNLVLNMGYSHKVQIEPPEGIQFAVEGTTNVIVSGYDKEIVGNTAAKIRA
VRPPEPYKGKGIRYAGEVVRRMAKKVVAVIKLALNAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISV
YEDRSFTFVLKTPPASVLIRKAAKIERGSNEPNKKKVGSISRTQLREIAQTKLPDLNANDIDAAMNIVEGTAKNMGVTVTDMSA
ATEQILEQLKSLTLLEASELVKQIEEAFGVSAAATGGGMMMMAAPGGAAAEVVEEKTEFDAILDSVPADKKIAVLKIVREITGL
GLKEAKDLVEAAPKAVKEAVTKDAAEDIKKRIEEAGGKVTVKMSSKTYLPPQASLERDWYLVDATDKRLGRLASEVAMILRG
KRKAEYTPHLDTGDFVIIINAEKVAVTGKKRTQKLYRRHSGRPGGMKTETFAKLQQRLPERILEHAIKGMLPKNSLGKQLFTKL
KVYAGPTHPHAAQQPKEITISTIPGENMIQPQSYLNVADNSGAKKLMCIRVLGAGNRRYGGVGDRIIAVVKESSPNMAVKKSD
VVEAVIVRTRKAISRDSGMCIRFDDNAAVIINKEGNPRGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRME
GLASRGSTLNFGDFGLQAQEPSWITSRQIEASRRAMTRYIRRGGKIWIRIFPDKPITMRPAETRMGSGKGNPEFWVAVVKPGRIM
FEIGGVTEEIAREAMRLADAKLPIKTKFIVRSQPQEQEMNAQEIIRSIEAEQMKSDLPEIYVGDTVKVGVKIQEGTKFRVQPYEGV
VIARRNGGINETITVRKVFQGVGVERVFLLHSPLVESIKVLRRGKVRRAKLYYLRKLVGKATRIKQRFDRPLMTRVKRGNVAR
KRRNKILKLAKGFRGSHSTLFRTANQQVMKALRSAYRDRKKKKRDFRRLWIARINAASRQHGLSYSRLIGNLKKANVELNRK
MLAQLAILDPASFAKIAELANSVNGMAHKKGTGSTRNGRDSNAQRLGVKRYGGQTVRAGNILVRQRGTKVHPGNNVGIGSDD
TLFALVDGVVTFERRGKSQKKVSVYPVAVELVEAVASNDDKYMESAFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKL
ELHFLGNNYKLKEPKYSVEESKRRDSTYAVQMYVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVY
YKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDLVWVRIDKTRKLSAQVLLKALGLSDNEIFDALRHPEYFQKTIEKEGQFSEEE
ALMELYRKLRPGEPPTVLGGQQLLDSRFFDPKRYDLGKVGRYKLNKKLRLSAPDTMRVLTPGDILAAIDYLINLEYDIGSIDDID
HLGNRRVRSVGELLQNQVRVGLNRLERIIRERMTVSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRL
SALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEGPNAGLIGSLATHARVNLYGFLETPFRPVENGKVLFDVPPVYMTADEEDD
LRTATGDVPLDENGYIKGPQVPVRYRQDWTTTGPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKP
ERPLVGTGLEAQAARDSGMVIVSRTDGDVVYVDATEIRVRSSGQLSAASGSQVIEKGQELKYKLSKYQRSNQDTCLNQKPLVR

IGEKVVAGQVLADGSSTEGGELALGQNIVVAYMPWEGYNYEDAILISERLVQEDVYTSIHIEKYEIEARQTKLGPEEITREIPNV
GEDALRQLDEQGIIRIGAWVDAGDILVGKVTPKGESDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQGD
ELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNKGIISRILPAEDMPYLADGSPVDIVLNPLGVPSRMNVGQVFECLLGWAGH
NLGVRFKITPFDEMYGEETSRRLVHGKLQEARDETAKDWVYNPDNAGKIMVYDGRTGEPFDRAITVGVAYMLKLVHLVDDKI
HARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWALEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKV
LMRELQSLGLDIAVHKVETQADGSSLDVEVDLMADQAARRTPPRPTYESLSRESLEGDDMPVVSLAQMMESGVHFGHQTRR
WNPKMAPYIYTSRNGVHIIDLVQTAQLMDNAYNYMRTQSEQGKKFLFVGTKRQAAGIIAQEALRCGSHYINQRWLGGMLTN
WATIKTRAERLKDLERREESGALDLLPKKEASMLRREMTKLQKYLGGIKNMRKVPDIVVIVDQKREYNAVQECEKLGIPIVSM
LDTNCDPDVVDIPIPANDDAIRSIKLIVGKLADAIYEGRHGQLMGQKIHPVGFRLGITQEHQSRWFAEPDRYPELLQEDYKLRQY
IEQKLGRYAQNNAGISEVRIERKADQIDLEVRTARPGVVVGRGGQGIESLRLGLQGALGGNRQIRINVVEVQRVDADAYLIAEY
IAQQLERRVSFRRVVRQAIQRAQRAGVQGIKVQVGGRLNGAEIARSEWTREGRVPLHTLRADIDYSGCTAKTIYGILGIKVWVF
KGEIIPGQEQAPAQPAMVTGRRKASRTKKEETTWQERVIQIRRVSKVVKGGKKLSFRAIVVVGNERGQVGVGVGKASDVIGAV
KKGVADGKKHLIDIPITKSNSIPHPIDGIGGGAKVMMRPAAPGTGVIAGGAVRTVLELAGIRNILAKQLGSNNPLNNARAAVNA
LSTLRTLSEVAEDRGIAIEKLYIVAEITSGRAVYWGTGRRKASVARVRLVPGEGKMTVNGKDGDLYFQFNPNYLGAIKAPLETL
GLESEYDIVVKAEGGGLTGQADSIRLGVARALCQLDPDNRSPLKTEGYLTRDPRAKERKKYGLHKARKAPQYSKRMATLQQQ
KIRIRLKAFDRRLLDTSCEKIVETANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTHRRIIDIYQPSSKTIDALMKLDL
PSGVDIEVKLMARQPTKKSGSKKQKRNVPNGVAYIQSTFNNSIVTITDQNGDVISWASAGSSGFKGAKKGTPFAAQTAAESAA
RRATDQGMRQIEVMVSGPGAGRETAIRALQGAGLEITLIRDITPIPHNGCRPPKRRRVMARISGVDLPRDKRIEIGLTYIYGIGLT
RSHQILAATGVNPDTRVKELSDADVAALRGEIESNYQVEGDLRRLEGLNIKRLVDIGCYRGRRHRMGLPVRGQRTRTNARTRR
GRRQTVAGKKKAPGKMGRSLKKGPFVADHLLKKIEKLNAKDEKQVVKTWSRASTILPLMVGHTIAVHNGRQHVPVFVNEQM
VGHKLGEFAPTRTYRGHGKSDKKSGRMSDKQSEGYKVICDNRQARFLYEIIETYEAGIQLTGTEVKSIRAGKANLQDGYALLR
DGEAWLINVHISPYTSSGAYFNHEPRRTRKLLLHKQELRKLIGRVQQEGLTLVPLKMYLKRGWVKIVIALGKGKKLHDKRESL
KRRDDQRDMQRAMKRYMAEISAKLVQELRQKTGAGMMDCKKALKENEGDVEAATTWLRQKGIAKADKGSARIAAEGLVD
TYIRPDGQVGVLIEVNCQTDFVARNEAFKALVKNLAKQAANADTVESLLAQPYTEKSSVTVDEFIKETIATLGENIQVRRFVNF
SLTTDKPGIVDSYIHTGGRVGVLLELNSQTDAPATQEEFQNLARNAAMQVAACPNVEYVNIDQIPVEVVTKEKDIEMGKDDLG
NKPENIKEKIVQGRIEKRLKEMTLLDQPFIRDQSISVEDLVKQVEKIVGEGIQVSRFVRYVLGEGIERKEMSFADEVAAQIGAK

>Dolichospermum_circinale_AWQC310F
MQIPRLHPDTIEEVKLRADIVDVISEYVVLRKRGKDFVGLCPFHDEKTPSFTVSPYKQMYYCFGCQAAGNAIKFVMDLGKRQF
AEVVLDLAKRYQVPVKTLEPEQRQELQRQISLRDQLYTVLASAAQFYQHTLRQSQGQKAREYLTKIRQFQEETIQQFGLGYAPP
GWETLYRYLVESKHYPLQLVEQAGLIKPRKEGGGYYDVFRDRLMIPIRDLQGRVIAFGGRTLTEEQPKYLNSPETELFSKGKTL
FALDAAKNAISKVDQAVVVEGYFDVISLHAAGINNAVASLGTALSIEQVRLLLRYTESKQLILNFDADKAGINATEKAIGEVSNL
VYTGEVQLKILNLPHSKDADEYLHDHTSSDYQQLLKDAPLWLDWQIQNIIKNRDLKQATDFQQVTQQIIKLLQNIVNSDTLNYY
VSYCAEILSLGDSRLKPLRVENLLTQIRPNSLKSLSPRINKPQPQKLKLSLVNTERTLLERAEASLLIIYIHFSEQRQIIIDELETRNL
EFSLSHHRFLWQQMLEFSLDELDLISHVQNRYLELGEELDIISHLFHLNEKNKKEDILRISYIIQVALACMERVFREKRCRYFIEQ
WEKINPQTEPEKDKYYAEAIYIEKIHLQDLEKQQMKLAEAESTMQKTVESTQRAFNTIRTGRANASLLDKVQVEYYGTPTSLKS
LANISTPDASTILIQPYDKSSLNIVEKAISLSDVGLTPSNDGIVIRLNIPPLTTDRRKEFVKLAAKYAEEGRVAIRNIRRDAIESIRKQ
EKNAEIPEDEARDQQDKLQKLTNKYTAKIDELLAEKEKDISTVMPVIEKKRTRDLPQINERIRFPKIRVIDTDGAQLGIITPQEAIQ
LAEEKELDLVLISDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVKQAERFLKDGDKVK
ATVMFRGREIQHSDLAETLLKRMATDLEPFGELQQAPKKEGRNMMMLISPKKMSMVTLSGLKELIESISQERNLPRLAVQAAIR
EALLKGYERYRRAQNLERKQFDEEYFKNFEVELDIEGEGFRVLSTKNIVETVSNTDHQISLDEVQQVAPEAQLGDSVVLDVTPD
QGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVVLAVSSGFGQSEVEAELPKREQLPNDNYR
ANATFKVYLKKVSQGQQRGPQLMVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAVDTLDRDVDPV
GACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPAKVDEVRLMDPESRQTHVLVAEDQLSLAIGKEGQNVRLAARL
TGWKIDIKDQAKYDYEAENTKFAAVRAQYQSQNMSKKSLASLSAADISGKRALVRVDFNVPVDDQGNITDDTRIRAALPTIQD
LTQKGAKVILTSHFGRPKGVDEKLRLTPVAKRLSALLGQEVIKTDDCIGDDVAAKVAALDNGQVLLLENVRFYAEEEKNDPEF
AQKLAANADFYVNDAFGTAHRAHASTEGVTKFLSPSVAGYLVEKELQYLQSAIEAPQRPLAAIVGGSKVSSKIGVIETLLEKCD
KLIIGGGMIFTFYKARGLSVGKSLVEEDKLELAKSLEAKAKERGVALLLPTDVVLADKFAPDADSQTVNIDAIPDGWMGLDIGP
DSVKVFQAALADCKTVIWNGPMGVFEFDKFAKGTEAIAHTLADISKTGAITIIGGGDSVAAVEKVGLADQMSHISTGGGASLEL
LEGKILPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRDYSVSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDL
DLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGGTVQVIPHITNEIKDRIVRVAKETNPSAVITEIGGTVGDIESLPFLEA
IRQLRKEVGRRNVLYMHVTLLPWIASAGEMKTKPTQHSVKELRSIGIQPDILVCRSDRPIPVGLKQKLSEFCDVAVECVIPAPDA
RSIYEVPVILEREGLAEQVLDLLQMEQRQPNLQEWETMVERMYTPKYSVEIAIVGKYVRLSDAYLSVVESLRHAAIATHGDLRL
RWVNSEALETEPAENYLSGVDGIIVPGGFGSRGIDGKIAAIKYARDRQIPFLGLCLGMQCSVIEWARNVEGLSHANSAEFDPNTN
DPVINLLPEQQDVVDLGGTMRLGLYPCRILPNTLAFQLYQEEVIYERHRHRYEFNNVYRSQLLDSGYLVSGTSPDGRLVEIVEY
SQHPFFIACQFHPEFQSRPNAPHPLFKGFVNAAISQAHSTTNIPKPLKVSMAKKVSRRLRALLEKVEDRDYTPLEGLALLKETAT
AKFAEAAEAHIRLGIDPKYTDQQLRTTVALPKGTGQIIRVAVIARGEKVTEATNAGADIAGSEELIEQIQKGFMDFDKLIATPDV
MPQVAKLGKLLGPRGLMPSPKGGTVTFDIGSAIAEFKAGKLEYRADRTGIVHVMFGKAGFSPEDLLINLKALQESIDRNRPSGA
KGRYWRSLYVSSTMGPSIAIDISALRELKLTEAAMGTRSYRPYTPSTRQVTISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSR

RRGGGHKQLYRIIDFKRDKRNIPATVTAIEYDPNRNARIALLLYEDGEKRYILQPNGMTVGTKVIAGPDSPIEDGNALPLSNIPLG
SNVHNVEMTPGKGGQIVRAAGATAQVVAKEGNYVTLKLPSGEVRLIRRDCYATIGQVGNTDARNLSAGKAGRNRWKGRRPK
VRGSVMNPVDHPHGGGEGRAPIGRSGPVTPWGKPTLGAKTRKRKKASTKLIIMSVGILGTKLGMTQIFDEEGVSIPVTVIQAGP
CTVTQVKTKQTDGYAAIQVGYGEVKPKALNRPLLGHLAKSSAPAVRHLNEYRTDSAGDYALGQEIKADIFSAGEIVDVVGTSI
GRGFAGNQKRNNFGRGPMSHGSKNHRAPGSIGAGTTPGRVYPGKRMAGRLGGTRVTIRKLTVVRVDTERNLIIIKGAIPGKPG
ALVNVLPAKKVGKKMVESVIKNWQGEQVGETSFDLRVAKETTAAHIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWR
QKGTGRARAGSIRSPLWRGGGVIFGPKPRDFNLQMNRKERRLALRTAFISRAEDLIIVEEFSNELQRPKTKELVAALARWGAAP
EQKTLLILSEIAENVLLSARNIENLKLIPANQLNVYDLLHADKIVVTSSTIDKIQEVYSAMATTRLKTVYQETITPKLISQFQYTNV
HQVPKVTKITVNRGLGEAAQNAKSLEASLSEIALITGQKPVVTRAKKAIAGFKIRQGMPVGIMVTLRGERMYAFLDRLINLTLP
RIRDFRGVSPKSFDGRGNYTLGVREQLIFPEVEYDKIDQVRGLDISIITTAKTDEEGRALLKEMGMPFRDQMSRIGKRPITVPAKV
QVAIDGVKVVVKGPKGELSRQLPNNVIVSQEGETLLVTRRDETRTSRQMHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQI
QGRNLVLNMGYSHQVQIEPPEGIQFAVEGTTNVIVSGYDKEIVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRMAKKLVAVIK
LALNAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVYEDRSFTFVLKTPPASVLIRKAAKIERGSNEPNK
KKVGSISRNQLREIAQTKLPDLNANDIDAAMKIVAGTAKNMGVTVTDMSAATEQILEQLKALTLLEASELVKQIEEAFGVSAA
ATGGMMMVAPGAAAPAEEVVEKTEFDAILDSVPADKKIAVLKIVREITGLGLKEAKELVEAAPKAVKEGVAKEAAEDIKKRIE
EAGGKVVIKMSSKTYLPPQASLERDWYLVDATDKRLGRLASEVAMILRGKRKAEYTPHLDTGDFVIIINAEKVAVTGKKRTQK
IYRRHSGRPGGMKTETFAKLQQRLPERILEHAIKGMLPKNSLGKQLFTKLKVYAGPTHPHAAQQPKEITISTIPGENMIQPQSYL
NVADNSGAKKLMCIRVLGAGNRRYGGVGDRIIAVVKESSPNMAVKKSDVVEAVIVRTRKAINRDSGMTIRFDDNAAVIINKEG
NPRGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEGLASRGSTLNFGDFGLQAQEPSWITSRQIEASRRA
MTRYIRRGGKIWIRIFPDKPITMRPAETRMGSGKGNPEFWVAVVKPGRIMFEIAGVAEEIAREAMRLADAKLPIKTKFIVRSQPQ
EQEMNAQEIIRSIEAEQLKSDLPDIYVGDTVKVGVKIKEGTKYRVQPYEGVVIAMRNGGINETITVRKVFQGVGVERVFLLHSPR
IESIKVLRRGKVRRAKLYYLRALVGKATRIKQRFDRALMTRVKRGNVARKRRNKILKLAKGFRGSHSTLFRTANQQVMKALR
SAYRDRKKKKRDFRRLWIARINAASRQHGLSYSRLIGNLKKANVELNRKMLAQLAILDPASFAKIAELAQSVMAHKKGTGSTR
NGRDSNAQRLGVKSYGGQTVRAGNILVRQRGTKVHPGNNVGIGSDDTLFALVDGVVTFERKGKSRKKVSVYPVVVAEVEAM
TNDKYMESAFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGNNYKLKEPKYSVEESKRRDSTYAVQMYVPTR
LLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLKFETDRNDLVWV
RIDKTRKLSAQVLLKALGLSDNEIFDALRHPEYFQKTIEKEGQFSEEEALMELYRKLRPGEPPTVLGGQQLLDSRFFDPKRYDLG
KVGRYKLNKKLRLSAPDTMRVLTSGDILAAIDYLINLEFDIGSIDDIDHLGNRRVRSVGELLQNQVRVGLNRLERIIRERMTVSD
AEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSHYGRICPIETPEGPNA
GLIGSLATHARVNQYGFLETPFRPVENGKVLFDVPPVYMTADEEDDLRTATGDVPLDENGYIKGPQVPVRYRQDWTTTGPEQV
DYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQAARDSGMVIVSRTDGEVVYVDATEIR
VRVSSQWSVISGQSSLAEKRTTDNEQLTTDKPQEIRYNLSKYQRSNQDTCLNQKPLVRIGEKVVAGQVLADGSSTEGGELALG

QNIVVAYMPWEGYNYEDAILISERLVQEDIYTSIHIEKYEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRIGAWVDAGDILV
GKVTPKGESDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKM
AGRHGNKGIISRILPAEDMPYLADGSPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKVTPFDEMYGEETSRRLVHGK
LQEARDETGRDWVYNPENCGKIMVYDGRTGEPFDRAVTVGVAYMLKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQR
FGEMEVWALEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKVETQVDGSSLD
VEVDLMADLAPRRTPPRPVYESLSYESLEDDDMPVVSLAQLMESGVHFGHQTRRWNPKMDPYIYTSRNGVHIIDLVQTAQLM
DNAYNYMRTQSEQGKKFLFVGTKRQAAGIIAQEALRCGSHYINQRWLGGMLTNWATIKTRAERLKDLERREETGALDLLPKK
EASMLRREMTKLQKYLGGIKNMRKVPDIVIIVDQKREYNAVQECEKLGIPIVSMLDTNCDPDVVDIPIPANDDAIRSIKLIVGKL
ADAIYEGRHGQLMGQKIHPVGFRLGITQEHQSRWFAEPDRYPELLQEDYKLRQYIEQKLGRYAQNNAGISEVRIERKADQIDLE
VRTARPGVVVGRGGQGIESLRLGLQGALGGNRQIRINVVEIQRVDADAYLIAEYIAQQLERRVSFRRVVRQAIQRAQRAGVQGI
KIQVGGRLNGAEIARSEWTREGRVPLHTLRADIDYSGCTAKTIYGILGIKVWVFKGEIIPGQEQAPVQPARDRDRDRDRGDRER
EPRRRQQQRRRQQFEDRSNEAMVTGRRKASRAKKEETNWQERVIQIRRVSKVVKGGKKLSFRAIVVVGNERGQVGVGVGKA
SDVIGAVKKGVADGKKHLIDIPITKSNSIPHPIDGIGGGAKVMMRPAAPGTGVIAGGAVRTVLELAGIRNILAKQLGSNNPLNNA
RAAVNALSTLRTLSEVAEDRGVAIEKLYIVAEINSGRAVYWGTGRRKCSVARVRLVPGAGKMTVNGKDGELYFQFNPNYLGA
IKAPLETLGLENEYDIVVKAEGGGLTGQADSIRLGVARALCELDPDNRSPLKTEGYLTRDPRAKERKKYGLHKARKAPQYSKR
MATLQQQKIRIRLKAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTHRRIIDIYQPSSKTI
DALMKLDLPSGVDIEVKLMARQPTKKTGSKKPKRNVPNGIAYIQSTFNNSIVTITDQKGDVISWASAGSSGFKGAKKGTPFAAQ
TAAESAARRATDQGMRQIEVMVSGPGAGRETAIRALQGAGLEITLIRDITPIPHNGCRPPKRRRVIKRLVDIGCYRGRRHRMGLP
VRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFIADHLLKKIEKLNAKNEKQVVKTWSRASTILPLMVGHTIAVHN
GRQHVPVFVNEQMVGHKLGEFAPTRTYRGHGKSDKKSGRMSDKQSEGYKTICDNRQARFRYEILETYEAGIELTGTEVKSIRG
GKANLQDGYALIRDGEAWLINVHISPYTSSGAYFNHEPRRTKLLLHKQELRKLIGKVEQEGLTLVPLKMYLKRGWVKVVIAL
GRGKKLHDKRESIKRRDDQRSMQRAMKRFMAEISAKLVQELRQKTGAGMMDCKKALKENDGNIEAATTWLRQKGIAKADK
GSSRIAAEGLVDTYIQPGGQVGVLIEVNCQTDFVARNEAFKALVKNLAQQAATADSVESLLAQPYIENSSVTVEEFIKETIATLG
ENIQVRRFVNFSLANGTPGVADSYIHTGGRVGVLLELTTESDSAVANEEFQGLAKNAAMQVAACPNVEYVSVDKIPAELVQKE
KDIEMGKDDLANKPENIREKIVQGRIEKRLKEMTLLDQPYIRDQSILVEDLVRQVKSIGEEVQVSRFVRYVLGEGIEKKEISFAE
EVAAQMGAK

>Dolichospermum_sp_DET69
MQIPRLHPDTIEEVKLRADIVDVVSEYVVLRKRGKDFVGLCPFHDEKSPSFTVSPNKQMYYCFGCQAAGNAIKFVMDLGKRQF
ADVVLDLAKRYQVPVKTLEPEQRQELQRQISLRDQLYTVLASAAQFYQHTLRQSQGQKALEYLEKSRQFQQGTIQQFGLGYAP
AGWETLYRYLVESKHHPVQLVEQAGLIKPRKEGGGYYDVFRDRLMIPIRDIQGRVIAFGGRTLTDEQPKYLNSPETELFSKGKT
LYALDEAKDGISKVDQAVVVEGYFDAIALHAAGINNAVASLGTALSIEQVRLLLRYSESKQLILNFDADKAGTNATERAIGEIA
NLAYAGEVQLKILNLPNGKDADEYLHSHTSADYQQLLVNAPLWLDWQIQKIIENRDLKQATDFQQVTQQIVKLLQNIVNSDTL
NYYVSSCAEILSLGDTRLIPLRVENLLTQIKPGRIKSSPQQIRNQQPKTSKLSLVTTERSLLERAEALLLIIYLHSSRQRQIIIEDLET
RNLEFSLSHHRFLWQQMAEFTVDEVDLISSVQNRYLELAEELEVVSHLFHLNEKNKTEILRTPHVIQAALACMERVFREKRYRY
FMEQWEKIDPETEPEKDKYFAEAIYIEKIHLQDLEKQRQFSITDLIMKLAEAQETMEKTVESTQRAFNTIRTGRANASLLDKVQV
EYYGTPTALKSLASISTPDSSTILIQPYDKGSLNIIEKALSLSDVGLTPSNDGVVIRLNIPPLTSDRRKQFVKLAAKYAEEGRVAIR
NIRRDAIESIRKQEKSAEISEDESRDQQDKLQKLTNKHTEKIDHLLVEKEKEISTVMPVIEKKRTRDLPQINERIRFPKIRVIDTDG
AQLGIITPQEAIQLAEEKELDLVLISDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVKQA
ERFLKDGDKVKATVMFRGREIQHSDLAETLLKRMATDLEPFGELQQAPKKEGRNMMMLISPKKMSMVTLSGLKELIESISQDR
NLPRLAVQAAIREALIKGYERYRRAQNLERRQFDEEYFNNFEVELDIDGEGFRVLSTKTIVEAVSNTDHQISLDEVQQVAPEAQL
GDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVVLAVSSGFGQSEVEAELP
KREQLPNDNYRANATFKVYLKKVSQGQQRGPQLMVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIA
VDTLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPARVDEVRLMDPESRQTHVLVAEDQLSLAIGK
EGQNVRLAARLTGWKIDIKDQAKYDEAAENTKFAAVRAQYQSHNNENDRSNREDEIQEQLELDEDRFDSREEDMSKKSLASL
SAAEISGKRALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLTQKGAKVILASHFGRPKGVDEKLRLTPVAKRLSELLKQEVVK
TDDCIGDDVAAKVAALQNGQVLLLENVRFYPEEEKNEPEFAKKLAANADFYVNDAFGTAHRAHASTEGVTKFLSPSVAGYLV
EKELQYLQSAIESPQRPLVAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLSVGKSLVEEDKLELAKALEAKAKERG
VALLLPTDIVSADKFSPDANATTVSIENIPADGMGLDIGPDSIKVFQAALADCKTVIWNGPMGVFEFDKFAAGTEAIAHTLADIS
KTGAITIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGKILPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRD
YSVSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGGTVQVIP
HITNEIKERILRVAKETNPSAVITEIGGTVGDIESLPFLEAIRQLRKEVGRRNVLYHVTLLPWIAAAGEMKTKPTQHSVKELRSIG
IQPDILVCRSDRPIPTGLKQKLSEFCDVPVECVITSPDARSIYEVPVLLEREGLAEQVLNLLQMEQRQPNMTQWEMMVDRMYNP
KYTVEIAIVGKYVRLSDAYLSVVESLRHAAIATHGDLRLRWVNSEVLENEPPENYLSGVDGIIVPGGFGNRGIDGKIAAIKYARD
RQIPFLGLCLGMQCSVIEWARNVEGLSNANSAEFDQYTKNPVINLLPEQQDVVDLGGTMRLGLYPCRVLPNTLAFQLYQEEVI
YERHRHRYEFNNVYRSQLLNSGYLVSGTSPDGRLVEIIEYPKHPFFIACQFHPEFQSRPNAPHPLFKGFMTAALSQSHSTTTIPKP
VEVSMAKKVSRRLQALLEKVEDRDYTPLEALALLKETATAKFPEAAEAHIRLGIDPKYTDQQLRTTVALPKGTGQIIRVAVIAR
GEKVTEATNAGADLAGSEELIDQIQKGFMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDVASAIAEFKAGKLEY
RADRTGIVHVMFGKTAFSPEDLLINLKALQESVDRNRPSGAKGRYWRSLYISSTMGPSIAIDISALRDLKLTDAAMGTRSYRPYT

PSTRQVIISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRNISATVTAIEYDPNRNARIALLLYE
DGEKRYILQPNGMTVGTKIIAGPESPIEDGNALPLSNIPLGTGVHNVEMIPGKGGQIVRAAGAVAQVVAKDGNYVTLKLPSGEV
RLIRRDCYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSAMNPVDHPHGGGEGRAPIGRAGPVTPWGKPTLGAKTRKK
KKASSKLIIMSVGILGTKLGMTQIFDEAGVAIPVTVIKAGPCTVTQVKTKQTDGYAAIQVGYGEVKPKALNRPLLGHLAKSSAP
ALRHLNEYRTDNSGDYTLGQELKADLFSAGEIVDVAGTSIGRGFAGNQKRNNFARGPMSHGSKNHRAPGSIGAGTTPGRVYPG
KRMAGRLGGTRVTIRKLTVIRVDVERNLILIKGAIPGKPGALVSIIPANLVGRKMVESVIKNWQGEQVGQTSFELRVAKETTAA
HIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFGPKPRDFNINMNRKERRLALRT
AFIGRAEDLIVVEEFSNELQRPKTKDLVAALGRWGATPEQKTLLILSEIAENVLLSARNIENLKLIPADQLNVYDLLHADKIIVTS
STLDKIQEVYSAMAKTRLKTVYQETITPKLITQFEYTNVHQVPKVTKITINRGLGEAAQNAKSLEASISEIALITGQKPVVTRAKK
AIAGFKIRQGMPVGIMVTLRGERMYAFLDRLINLTLPRIRDFRGISPKSFDGRGNYTLGVREQLIFPEVEYDRIDQVRGLDISIITT
AKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGLKVVVKGPKGELSRQLPRNVILSQEGETLLVTRRDETRTSRQ
MHGLSRTLVANMVEGVSLGFQRRLEIQGVGYRAQLEGRNLVLNMGFSHKVQIEPPEGIQFAVEGTTNVIVSGYDKEIVGNTAA
KIRAVRPPEPYKGKGIRYAGEVVRRMAKKVVAVIKLALNAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPV
EISVYEDRSFTFVLKTPPASVLIRKAAKIEKGSNEPNKTKVGSISRTQLREIAQTKLPDLNANDIDAAMNIVEGTAKNMGVTITEM
SAATETILEQLKSLSLLEASELVKQIEEAFGVSAAPAAGGMMMMAAPGAVAEAVEEKVEFDAILDSVPADKKIAVLKIVREITG
LGLKEAKDLVEAAPKAIKEAVTKDAAEDIKKRVEEAGGKVTVKTKTYLPPQASIERDWYLVDATDKRLGRLATEVAMILRGK
KKPEFTPHMDTGDFVIIINAEKVAVTGKKRTQKLYRRHSGRPGGMKTETFAKLQQRLPERIIEHAVKGMLPKCSLGKQLFTKLK
VYAGPTHPHAAQLPKEITINTIPGENMIQPQSYLNVADNSGAKKLMCIRVLGAGNRRYGGVGDKIIAVVKESTPNMAVKKSDV
VEAVIVRTRKAISRDNGMCIRFDDNAAVIINKDGNPRGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEG
LASRGSTLNFGDFGLQAQEPSWITSRQIEASRRAMTRYIRRGGKIWIRIFPDKPITMRPAETRMGSGKGNPEFWVAVVKPGRIMF
EIGGVTEEIAREAFRLADAKLPIKTKFMARSQPQEQEMNAQEIIRSIEAEQMKSDLPDIYVGDTVKVGVKIQEGTKFRVQPYEGV
VIARRNGGINETITVRKVFQGVGVERVFLLHSPLVESIKVLRRGKVRRAKLYYLRDLVGKATRIKQRFDRPLMTRVKRGNVAR
KRRNKILKLAKGFRGSHSTLFRTANQQVMKALRSAYRDRKKKKRDFRRLWIARINAASRQHGLSYSRLIGNLKKANVELNRK
MLAQLAILDPASFAKIAELANSVNGMAHKKGTGSTRNGRDSNAQRLGVKRYGGQTVRAGNILVRQRGTKVHPGNNVGIGSDD
TLFALIDGVVTFERRGKSQKKNDDKYMESAFLLPDLIEIQRSSFRWFLEEGLVEELNSFSPITDYTGKLELHFLGNNYKLKEPKY
SVEESKRRDSTYAVQMYVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSAS
LIPNRGAWLKFETDRNDLVWVRIDKTRKLSAQVLLKALGLSDNEIFDALRHPEYFQKTIEKEGQFSEEEALMELYRKLRPGEPP
TVLGGQQLLDSRFFDPKRYDLGKVGRYKLNKKLRLSAPDTMRVLTPGDILAAVDYLINLEYDIGSIDDIDHLGNRRVRSVGELL
QNQVRVGLNRLERIIRERMTVSDAESLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGF
AVRDIHPSHYGRICPIETPEGPNAGLIGSLATHARVNLYGFLETPFRAVENGKVLFNVAPVYMTADEEDDLRTATGDVPLDENG
YIKGPSVPVRYRQDWTTTNPEQVDYVAVSPVQIISVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQAAR
DSGMVIVSRTDGDVIYVDATEIRVRASGQLSAASGSQPIEKGQELKYKLSKYQRSNQDTCLNQKPLVRIGEKVVAGQVLADGS

STEGGELALGQNIVVAYMPWEGYNYEDAILISERLVQEDVYTSIHIEKYEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRIG
AWVDAGDILVGKVTPKGESDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQGDELPPGANMVVRVYVAQ
KRKIQVGDKMAGRHGNKGIISRILPAEDMPYLADGSPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVRFKITPFDEMYGE
ETSRRLVHGKLQEARDETSKDWIYNPDNAGKIMVYDGRTGEPFDRAITVGVAYMLKLVHLVDDKIHARSTGPYSLVTQQPLG
GKAQQGGQRFGEMEVWALEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQSLGLDIAVHKV
ETQADGSSLDVEVDLMADQAARRTPSRPTYESLSRESLEGEEMPVVSLAQMMESGVHFGHQTRRWNPKMAPYIYTSRNGVHII
DLVQTAQLMDNAYNYMRTQSEQGKKFLFVGTKRQAAGIIAQEALRCGSHYINQRWLGGMLTNWATIKTRAERLKDLERREE
TGALDLLPKKEASMLRREMTKLQKYLGGIKNMKKVPDIVVIVDQKREYNAVQECEKLGIPIVSMLDTNCDPDVVDIPIPANDD
AIRSIKLIVGKLADAIYEGRHGQLMGQKIHPVGFRLGITQEHQSRWFAEPDRYPELLQEDYKLRQYIEQKLGRYAQNNAGISEV
RIERKADQIDLEVRTARPGVVVGRGGQGIESLRLGLQGALGGNRQIRINVVEIQRVDADAYLIAEYIAQQLERRVSFRRVVRQSI
QRAQRAGVQGIKVQVGGRLNGAEIARSEWTREGRVPLHTLRADIDYSSCSAKTTYGILGIKVWVFKGEIIPGQEQAPEQPARDR
DRDRDRDRGDRDREPRRKQQRRQQFEDRSNESMVTGRRKQARAKKEETTWQERVIQIRRVSKVVKGGKKLSFRAIVVVGNE
RGQVGVGVGKASDVIGAVKKGVADGKKHLIDIPITKANSIPHPIDGIGGGAKVMMRPAAPGTGVIAGGAVRTVLELAGIKNILA
KQLGSNNPLNNARAAVNALSTLRTLSEVAEDRGIAIEKLYVAETTSGRAVYWGTGRRKCSVASVRLVPGEGKMTVNGKDGDL
YFQFNPNYLGAIKAPLETLGLESEYDILVKAEGGGLTGQADSIRLGVARALCQLDPDNRSPLKTEGYLTRDPRAKERKKYGLHK
ARKAPQYSKRMATLQQQKIRIRLKAFDRRLLDTSCEKIVETANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTHRRI
IDIYQPSSKTIDALMKLDLPSGVDIEVKLMARQPTKKSGSKKQKRNVPSGVAYIQSTFNNSIVTITDQNGDVISWASAGSSSGFKG
AKKGTPFAAQTAAESAARRATDQGMRQIEVMVSGPGAGRETAIRALQGAGLEITLIRDITPIPHNGCRPPKRRRVMARISGVDL
PRDKRVEIGLTYIYGIGLTRSHQILAATGVNPDIRVKDLSDADVAALRGEIESNYQVEGDLRRLEGLNIKRLIDIGCYRGRRHRM
GLPVRGQRTRTNARTRRGRRQTVAGKKKAPGKMGRSLKKGPFVADHLLKKIEKLNAKDEKQVVKTWSRASTILPLMVGHTIA
VHNGRQHIPVFVNEQMVGHKLGEFAPTRTYRGHGKSDKKSGRMSDKQSDGYKVICDNRQARFLYEIIETYEVGIQLTGTEVKSI
RAGKANLQDGYALLRDGEAWLINVHISPYASSGAYFNHEPRRTRKLLLHKQELRKLIGRVQQEGLTLVPLKMYLKRGWVKIVI
ALGKGKKLHDKRESLKRRDDQRDMQRAMKRYMAEISAKLVQELRQKTGAGMMDCKKALKENDGNVDESIDWLRKKGIAK
ADKGSSRIAAEGLVDTYIQPDGQVGVLIEVNCQTDFVARNEAFKALVKNLAQQAATTDSVESLLAQSYAEKPSVTVDEFIKETI
ATLGENIQVRRFVNYSLTSTPGIADSYIHTGGRVGVLMELTAQSASAAANAEFQSLAKNAAMQVAACPNVEYVSVDQIPVEVV
TKEKSIEMGKDDLGNKPENIKEKIVQGRIDKRLKEMTLLDQPYIRDQSISVEDLVKQVKSTVGEEIQVNRFVRYILGEGIEKNEM
SFADEVAAQIGAK

>Dolichospermum_sp_DL01
MQIPRLHPDTIEEVKLRADIVDVVSEYVVLRKRGKDFLGLCPFHDEKSPSFSVSPNKQMYYCFGCQAAGNAIKFVMDLGKRQF
ADVVLDLAKRYQVPVKTLEPEQRQELQRQISLRDQLYTVLATAAQFYQHTLRQSQGQKALEYLEQTRQFKQGTIQQFGLGYAP
AGWATLYRYLVESKHYPVQLVEQAGLIKPRKEGGGYYDVFRDRLMIPIRDIQGRVIAFGGRTLTEEQPKYLNSPETELFSKGKM
LFALDEAKDGISKVDQAVVVEGYFDAIALHAAGINNAVASLGTALSIEQVRLLLRYTESKQLILNFDADKAGTNATERAIGEIA
NLAYAGEVQLKILNLPNGKDADEYLHSHTSADYQQLLTNAPLWLDWQIQNIIKNRDLKQATDFQKVTQQIVKLLQNIVNSDTL
NYYVSSCAEILSLGDTRLIPLRVENLLTQIKPGRIKSLNPRTSNPATKTPKLSLVNTERSLLERAEALLLIIYLHSSQQRQIIIEDLEN
RNLEFSLSHHRFLWQQMAEFTVDEVDLISSVQNRYLELAEELEIVSHIFHLNEKNKTEILRTPHVIQAALACMERVFREKRYRYF
MEQWEKIDPEAEPEKDKYYAEAIYIEKLHLQDLEKQRQFSITDLIMKLAEAESMMQKTVESTQRAFNTIRTGRANASLLDKVQ
VEYYGTPTSLKALTNISTPDSSTILIQPYDKGSLNIIEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKEFVKLAAKYAEEGRVAIR
NIRRDANDSIRKQEKSAEISEDESRDQQDKLQKLTNKHTEKIDHLLVEKEKEITTVMPVIEKKRTRDLPQINERIRFPKIRVIDTDG
AQLGIITPQEAIQLAEEKELDLVLISDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVKQA
ERFLKDGDKVKATVMFRGREIQHSDLAETLLKRMATDLEPFGELQQAPKKEGRNMMMLISPKKMVTLSGLKELIESISQERNL
PRLAVQAAIREALIKGYERYRRAQNLERRQFDEEYFNNFEVELDIEGEGFRVLSTKTIVEAVANTDHQISLDEVQQVAPEAQLG
DSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVVLAVSSGFGQSEVEAELPK
REQLPNDNYRANATFKVYLKKVSQGQQRGPQLMVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKIAV
DTLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPATYIANALSPAKVDEVRLMDPESRQTHVLVAEDQLSLAIGKE
GQNVRLAARLTGWKIDIKDQAKYDEEAENTKFAAVRAQYQSQNDRDDRSDREDAMAEELELDEDRFDNSEEDMSKKSLASL
SAADISGKRALVRVDFNVPVDDQGNITDDTRIRAALPTIQDLTQKGAKVILTSHFRRPKGVDEKLRLTPVAKRLSELLGQEVIKT
DDCIGDDVAAKVAALDNGQVLLLENVRFYKEEEKNDPEFAQKLAANADFYVNDAFGTAHRAHASTEGVTKFLSPSVAGYLV
EKELQYLQSAIEEPKRPLAAIIGGSKVSSKIGVIETLLEKCDKLIIGGGMIFTFYKARGLNVGKSLVEEDKLELARELEAKAKERG
VALLLPTDIISADKFAPDANATTVSIENIPADGMGLDIGPDSIKVFQAALADCQTVIWNGPMGVFEFDKFAAGTEAIAHTLAEIG
KTGATTIIGGGDSVAAVEKVGLADQMSHISTGGGASLELLEGKVLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSR
DYSVSILKLDPYINVDPGTMSPFQHGEVFVTQDGAETDLDLGHYERFTDTSMSRLNSVTTGLIYQSVINKERRGDYNGGTVQVI
PHITNEIKERILRVAKETNPAAVITEIGGTVGDIESLPFLEAIRQLRKEVGKRNVLYMHVTLLPWIAAAGEMKTKPTQHSVKELRS
IGIQPDILVCRSDRPIPVGLKQKLSEFCDVPVECVITSPDARSIYEVPVILEREGLAEQVLNLLQMEQRQPNMTQWENMVDRMYN
PKYTVEIAIVGKYVRLGDAYLSVVESLRHAAIATHGDLRLRWVNSEVLENEPPENYLAGVDGIIVPGGFGSRGIDGKIAAIKYAR
DRQIPFLGLCLGMQCSVIEWARNVEGLSNANSAEFDPYTDNPVINLLPEQQDVVDLGGTMRLGLYPCRVLPNTLAFQLYQEEVI
YERHRHRYEFNNVYRSQLLDSGYLVSGTSPDGRLVEIIEYPKHPFFIACQFHPEFQSRPNAPHPLFKGFMTAAISQFHSTTTTPKP
VQVSMAKKVSRRLQALLEKVEDRDYTPLEALALLKETATAKFAEAAEAHIRLGIDPKYTDQQLRTTVALPKGTGQIIRVAVIAR
GEKVTEATNAGADIAGSEELIEDIQKGMMDFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDVASAIAEFKAGKLEY
RADRTGIVHVMFGKTAFSPEDLLINLKALQESVDRNRPSGAKGRYWRSLYISSTMGPSISIDISALRELKLTDAAMGTRSYRPYT

SSTRQVIISDFAEITKTEPEKSLTESVHRPKGRNNQGRITSRRRGGGHKQLYRIIDFKRDKRNMPATVTAIEYDPNRNARIALVLY
EDGEKRYILQTNGMTVGTKIIAGPESPIEDGNALPLSNMPLGTSVHNVEMTPGKGGQIVRAAGAVAQVVAKEGNYVTLKLPSG
EVRLIRRDCYATIGQVGNTDARNLSAGKAGRNRWKGRRPKVRGSAMNPVDHPHGGGEGRAPIGRAGPVTPWGKPTLGAKTR
NRKKASTKLIIMSVGILGTKLGMTQIFDEAGVSIPVTVIKAGPCTVTQVKTKQTDGYSAIQVGYGEVKPKSLNRPLLGHLAKSSA
PPVRHLNEYRTDSTGDYALGQEIKADIFSAGEIVDVVGTSIGRGFAGNQKRNNFARGPMSHGSKNHRAPGSIGAGTTPGRVYPG
KRMAGRLGGTRVTIRKLTVIRVDAERNLIIIKGAIPGKPGALVSVVPATIVGKKMVESVIKNWQGEQVGETSFDLRVAKETTAA
HIVHRALVRQMTNSRQGTASTKTRAEVRGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFGPKPRDFDLKMNRKERRLALRT
AFVGRAEDLIVVEEFSNELQRPKTKDLVAALARWGAAPEQKTLLILSEIAENVLLSARNIENLKLIPADQLNVYDLLHADKIIVT
SSTLDKIQEVYSAMAKTRLKTVYQETITPKLITQFEYTNVHQVPKVIKITINRGLGESAQNAKSLEASISEIALITGQKPVVTRAKK
AIAGFKIRQGMPVGIMVTLRGERMYAFLDRLINLTLPRIRDFRGISPKSFDGRGNYTLGVREQLIFPEVEYDRIDQVRGLDISIITT
AKTDEEGRALLKEMGMPFRDQMSRIGKRPITIPAKVQVAIDGVKVVVKGPKGELSRQLPKNVIVSQEGETLIVTRRDETRTSRQ
MHGLSRTLVANMVEGVSQGFQRRLEIQGVGYRAQLQGSNLVLNMGYSHQVQIEPPAGVQFAVEGTTNVIVSGYDKEIVGNTA
AKIRAVRPPEPYKGKGIRYAGEVVRRMAKKVVAVIKLALNAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIP
VEISVYEDRSFTFVLKTPPASVLIRKAAKIERGSSEPNKTKVGRISRTQLREIAQTKLPDLNANDIDAAMNIVEGTAKNMGVTITD
MSAATEQILEQLKSLTLLEASELVKQIEEAFGVSAAAPVGVAIAAPGAAAAEVVEEKTEFDAILDSVPADKKIAVLKIVREITGL
GLKEAKDLVEAAPKAVKEAVTKEAAEDIKKRIEEAGGKVKVKMTSKTYLPPQQSIERDWYLVDATDKRLGRLATEVAMILRG
KKKPEFTPHMDTGDFVIIINAEKVAVTGKKRTQKVYRRHSGRPGGMKTETFAKLQQRLPERILEHAIKGMLPKNSLGKQLFTKL
KVYAGPTHPHAAQLPKEITISTIPGENMIQPQSYLNVADNSGAKKLMCIRVLGAGNRRYGGVGDRIIAVVKESSPNMAVKKSDV
VEAVIVRTRKAISRDSGMAIRFDDNAAVIINKEGNPRGTRVFGPVARELRDKNFTKIVSLAPEVLMLSPRRTKFRKQQRGRMEG
LASRGSTLNFGDFGLQAQEPSWITSRQIEASRRAMTRYIRRGGKIWIRIFPDKPITMRPAETRMGSGKGNPEFWVAVVKPGRIMF
EIGGVTEEIAREAMRLADSKLPIKTKFITRSQPQEQEMNAQEIIRSIEAEQMKSDLPDIYVGDTVKVGIKIQEGTKFRVQPYEGVVI
ARRNGGINETITVRKVFQGVGVERVFLLHSPLVESIKVLRRGKVRRAKLYYLRALVGKATRIKQRFDRPLMTRVKRGNVARKR
RNKILKLAKGFRGSHSTLFRTANQQVMKALRSAYRDRKKKKRDFRRLWIARINAASRQHGLSYSRLIGNLKKANVELNRKML
AQLAILDPASFAKIAELANSVNGMAHKKGTGSTRNGRDSNAQRLGVKRYGGQTVRAGNILVRQRGTKVHPGNNVGIGSDDTL
FALIDGVVTFERRGKTQKKVSVYAVAAVEPVEANDDKYMESAFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFL
GNNYKLKEPKYSVEESKRRDSTYAVQMYVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEI
DKNGRRTYSASLIPNRGAWLKFETDRNDLVWVRIDKTRKLSAQVLLKALGLSDNEIFDALRHPEYFQKTIEKEGQFSEEEALME
LYRKLRPGEPPTVLGGQQLLDSRFFDPKRYDLGKVGRYKLNKKLRLSAPDTMRVLTPGDILAAIDYLINLEYDIGSIDDIDHLGN
RRVRSVGELLQNQVRVGLNRLERIIRERMTVSDAESLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGP
GGLTRERAGFAVRDIHPSHYGRICPIETPEGPNAGLIGSLATHARVNLYGFLETPFRPVENGKVLFDVLPVYMTADEEDDLRTAT
GDVPLDENGYIKGPHVPVRYRQDWTTTGPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLRPERPLV
GTGLEAQAARDSGMVIVSRTDGDVVYVDATEIRVRASGQLSAASGSQVIEKGQELKYKLSKYQRSNQDTCLNQKPLVRIGEKV

VAGQVLADGSSTEGGELALGQNIVVAYMPWEGYNYEDAILISERLVQEDVYTSIHIEKYEIEARQTKLGPEEITREIPNVGEDAL
RQLDEQGIIRIGAWVDAGDILVGKVTPKGESDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQGDELPPGA
NMVVRVYVAQKRKIQVGDKMAGRHGNKGIISRILAAEDMPYLADGSPVDIVLNPLGVPSRMNVGQVFECLLGWAGHNLGVR
FKITPFDEMYGEETSRRLVHGKLQEARDETTKDWIYNPDNAGKIMVYDGRTGEPFDRAITVGVAYMLKLVHLVDDKIHARSTG
PYSLVTQQPLGGKAQQGGQRFGEMEVWALEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKAIPRPGTPESFKVLMRELQ
SLGLDIAVHKVETQADGSSLDVEVDLMADQAARRTPPRPTYESLSRESLEGEEMPVVSLAQMMESGVHFGHQTRRWNPKMAP
YIYTSRNGVHIIDLVQTAQLMDNAYNYMRTQSEQGKKFLFVGTKRQAAGIIAQEALRCGSHYINQRWLGGMLTNWATIKTRA
ERLKDLERREETGALDLLPKKEASMLRREMTKLQKYLGGIKNMRKVPDIVVIVDQKREYNAVQECEKLGIPIVSMLDTNCDPD
VVDIPIPANDDAIRSIKLIVGKLADAIYEGRHGQLMGQKIHPVGFRLGITQEHQSRWFAEPDRYPELLQEDYKLRQYIEQKLGRY
AQNNAGISEVRIERKADQIDLEVRTARPGVVVGRGGQGIESLRLGLQGALGGNRQIRINVVEVQRVDADAYLIAEYIAQQLERR
VSFRRVVRQAIQRAQRAGVQGIKVQVGGRLNGAEIARSEWTREGRVPLHTLRADIDYSGCTAKTVYGILGIKVWVFKGEIIPGQ
EQAPAQPAMVTGRRKASRTKKEETTWQERVIQIRRVSKVVKGGKKLSFRAIVVVGNERGQVGVGVGKASDVIGAVKKGVAD
GKKHLIDIPITKSNSIPHPIDGVGGGAKVMMRPAAPGTGVIAGGAVRTVLELAGIRNILAKQLGSNNPLNNARAAVNALSTLRTL
SEVAEDRGIAIEKLYIVAETTSGRAVYWGTGRRKCSVASVRLVPGEGKMTVNGKDGDLYFQFNPNYLGAIKAPLETLGLESEY
DILVKAEGGGLTGQADSIRLGVARALCQLDPDNRSPLKTEGYLTRDPRAKERKKYGLHKARKAPQYSKRMATLQQQKIRIRLK
AFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTHRRIIDIYQPSSKTIDALMKLDLPSGVDI
EVKLMARQPTKKSGSKKQKRNVPNGVAYIQSTFNNSIVTITDQNGDVISWASAGSSGFKGAKKGTPFAAQTAAESAARRATDQ
GMRQIEVMVSGPGAGRETAIRALQGAGLEITLIRDITPIPHNGCRPPKRRVMARISGVDLPRDKRVEIGLTYIYGIGLTRSHQILA
ATGVNPDTRVKDLSDADVAALRGEIESNYQVEGDLRRLEGLNIKRLVDIGCYRGRRHRMGLPVRGQRTRTNARTRRGRRQTV
AGKKKAPGKMGRSLKKSPFVADHLLKKIEKLNAKDEKQVVKTWSRASTILPLMVGHTIAVHNGRQHIPVFVNEQMVGHKLGE
FAPTRTYRGHGKSDKKSGRMSDKQSEGYKVICDNRQARFLYEIIETYEAGVQLTGTEVKSIRAGKANLQDGYALLRDGEAWLI
NVHISPYASSGAYFNHEPRRTRKLLLHKQELRKLIGRVQQEGLTLVPLKMYLKRGWVKIVIALGKGKKLHDKRESLKRRDDQR
DMQRAMKRYMAEISAKLVQELRQKTGAGMMDCKKALKENNGDVEESITWLRQKGIAKADKGSARIAAEGLVDTYIQPGGQV
GVLIEVNCQTDFVARNDAFKALVKNLAQQAATTDSVESLLAQPYLEKSSVTVDEFIKETIATLGENIQVRRFVNFSLTTDTPGIA
DSYIHTGGRVGVLLELNSQTDAAATNEEFQNLARNAAMQVAACPNVEYVSVDQIPAEIVTKEKDIEMGKDDLGNKPENIKEKI
VQGRIDKRLKEMTLLDQPYIRDQSISVEELVKQVKSKVGEEIQVSRFVRYVLGEGIEKNEMSFADEVAAQIGAK

>Nodularia_sphaerocarpa_UHCC_0038
MQIPRLHPDTIEEIKQRADIVDVVSDHVVLRKRGKDFVGLCPFHDEKSPSFTVSQTKQMYYCFGCQAGGNAIKFLMDVGKHSF
AEVVLDLARRYQVPVQTLAPEQRQELQRQISLREQLYEVLASTGQFYQHALRQSQGQKAYQYLQSERQLKEETIQQFGLGYAP
AGWETLHRYLVEDKRYPVHLVEKAGLIKPRKEGGGYYDVFRDRLMIPICDIQGRVIAFGGRTLSDEQPKYLNSPETELFSKGKT
LFALDHAKDGISKLDQAVVEGYFDAIALHAAGINNAVASLGTALSIEQVRLILRYTESKQLVLNFDADKAGNIAAERAIGEIAA
LAYKGEVQLKIVNIPDGKDADEYLHTHTPFDYEQLLANAPLWLNWQIDQIIQNRDLKQATDFQQVSQQLVKLLKNIDNSDTRN
YYVSHCAEILSLGDTRLIPLRVENLLTQIAPTTATRNKPLSSKKKFTQSPVPGDKSLLELAEALLLRIYLHCPEQRQVIFNILEERN
LEFSFSHHRLLWQKILGATGDELDFVSSLQDRYLELAEEIESVSHLFHVNEKSKQEMLRTPQVVQAAVACMERVLIEKRYRYFL
ELWEQTDSEAEPEKWQSYYQSFYNEKMRLQELDRQRQFSITDLIMKLSEAKSTMEKTVEATQRAFNSIRTGRANASLLDKVSV
DYHGTPTSLKSLANISTPDATTILIQPYDKGSLNIVEKAISLSDIGLTPSNDGSVIRLNIPPLTSDRRKEFVKIAAKYAEEGRVAIRNI
RRDVQDTIRKEEKASEISKDESKDQQDQLQKLTNKYTSRIDDLLAEKEKDITTVMPVIEKKRTRDLPQINERIRFPKIRVIDNDGA
QLGIMPPQEALQLADEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNVRVKQ
AERFLKDGDKVKATVMFRGREIQHSDLAEHLLKRMAKDLEPLGELQQAPKKEGRNMMMLISPKKMSMVSLPGLKELIESISRE
RNLPRLAVQSAIREALLKGYERYRRAQNLERRQFDEEYFDNFEVELDIEGEGFRVLSTKSIVEAVENSDHQISLEEVQQVAQEA
QLGDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVASNFGQPEVEAE
LPKREQLPNDNYRANATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKI
AVDTLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPSTYIANALSPARVDEVRLMDPETRQTHVLVAEDQLSLAIG
KEGQNVRLAARLTGWKIDIKDKAKYDYAGEDTKFAAARAKYQMSKKTLANLSAADISGKRALVRVDFNVPLDDQGNITDDT
RIRAALPTIKDLMQKGAKVILASHFGRPKGVDDKLRLTPVAQRLSELLGQEVVKTDDCIGDAVAAQVGALQNGQVLLLENVRF
YKEEEKNDPEFAKKLAANADFYVNDAFGTAHRAHASTEGVTHYLSPSVGGYLIEKELQYLQNAIENPQRPLVAIIGGSKVSSKI
GVIETLLEKCDKLIIGGGMIFTFYKARGLSVGKSLVEEDKLELAKTLEAKAKERGVALLLPTDIVSADKFAPDANATTVSIENIPA
DGMGLDIGPDSIKVFQAALADCKTVIWNGPMGVFEFDKFAAGTEAIAHTLAEISKTGTTTIIGGGDSVAAVEKVGLADQMSHIS
TGGGASLELLEGKILPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRDYSVSILKLDPYINIDPGTMSPFQHGEVFVTE
DGAETDLDLGHYERFTDTSMSRLNSVTTGSIYQAVINKERRGDYNGGTVQVIPHITNEIKERILSVAQETNPSVLITEIGGTVGDI
ESLPFLEAIRQLRKEVGRQNVLYMHVTLIPWIASAGEMKTKPTQHSVKELRSIGIQPDILVCRCDRAIPLGLKRKLSEFCDVPQEC
VITAQDASSIYEVPLIVEREGLAEQVLDLLQMEQRQPNLVQWQTMVERLYSPKYTVEIAIVGKYVRLSDAYLSVVEALRHAAIS
TYGDLRLRWVNSEDIENESPETYLAGVDGILVPGGFGVRGVDGKIAAIKYARDRQIPFLGLCLGMQCSVIEWARNVEGLIGANS
AEFDSETQYPVINLLPEQQDVVDLGGTMRLGLYPCHLVPNTMAANLYQKEVVNERHRHRYEFNNTYRNMMLESGYVISGTSP
DGRLVEIVEFPEHPFFLACQFHPEFHSRPSTPHPLFKGFMEAAINRTNPMSNLPTPVEVSMGKKISRRFQALLEKVEDRDYAPLD
ALNLLKETATAKFAEAAEAHIRLGIDPKYTDQQLRTTVTLPKGTGQTVRVAVIARGEKVTEASNAGADIVGSDELINEIQQGML
DFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDVASAIAEFKAGKLEFRADRTGIVHVMFGKASFSSEDLLVNLKAL
QETIDRNRPSGAKGRYWRTIYVTSTMGPSIKVDINALRDLKLSELAMGTRSYRPYTPSTRQVTVSDFAEITKSKPEKSLTEYVHR

PKGRNNQGRITSRRRGGGHKQMYRIIDFKRDKRNIPAQVIAIEYDPNRNARIALVLYQDGEKRYILHPNKLPVGATIIAGPDSPFE
DGNALPLLNIPLGTSVHNVELTPGKGGQIVRAAGANAQVVAKEGQYVTLKLPSGEVRMIRRECYATIGQVGNTDARNLSAGK
AGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRPGPVTPWGKPTLGAKTRKPKKASSKLIVMSVGILGTKLGMTQVFDE
SGVSIPVTVVQAGPCTVTQVKTKQTDGYSAIQLGYGEVKPKALNRPLLGHLAKSSAPALRHLNEYHTDSPSDYALGQELKADIF
TEGQIVDVVGTSIGRGFAGNQKRNNFSRGPMSHGSKNHRAPGSIGAGTTPGRVYPGKRMAGRLGGTRVTIRKLTVVRVDLERN
LLLIKGAIPGKPGSLVNILPAKKVGMVESVVKNWQGEQVGETTFELRVAKESTASHIVHRALVRQMTNSRQGTASTKTRSEVR
GGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFGPKPRDYNQKLNRKERRLALRTALVSRAEDLIVVQDFSNELSRPKTKELVA
ALARWGAAPENKALLIMPAISSEDNVYLSARNIQNLKLIAADQLNVYDLLHADKIVITASALAKIQEVYSAMPTTRLKNLYQET
IVPKLTNQFQYTNVHQVPKVIKITINRGLGEAAQNAKSLEASLNEIAVITGQKPVVTRAKKAIAGFKIREGMPVGIMVTLRGERM
YAFLDRLISLSLPRIRDFRGISPKSFDGRGNYTLGVREQLIFPEVEYDSIDQIRGMDISIITTAKNDEEGRALLKEMGMPFRDQMSR
IGKQPITIPAKVEVTIDGPKVLVKGPKGQLSRTLSANVIVSQEGEILNVTRRDETRVSRQMHGLSRTLVANMVEGVSQGFKRRLE
IQGVGYRAQLQGRNLVLNIGYSHQVHIVPPDGVEFVVETNTSIVVSGYDKEIVGNTAAKIRAVRPPEPYKGKGIRYAGEVVRRK
AGKTGKSGKKMAKKVVAVIKLALNAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTFVLKT
PPASVLIRKAAKIERGSNEPNKKKVGSITKAQLQEIAQTKMPDLNANDIEAAMRIVEGTANNMGVTISDMSATTDQILEQLKTLS
LLEASELVKQIEEAFGVSAAAPAGGMMMMAPGAAAAAEPVEEKTEFDVVLDSVPADKKIAVLKIVRELTGLGLKEAKDLVEA
APKAVKEAITKDAAEDAKKRIEEAGGKVTIKMTTKTYLPPQATLEREWYVVDATDKRLGRLATEIAMILRGKKKAEFTPHMDT
GDFVIVINAEKIAVTGKKRTQKLYRRHSGRPGGMKTETFAKLQQRLPERILEHAVKGMLPKNSLGKQLFTKLKVYAGPTHPHE
AQQPKELKINTIPGEMIQTQTYLNVADNSGAKKIMCIRVLGGGNRRYGFIGDRIIAVVKDAIPNMAVKKSDVIEAVIVRTRHSIR
RDSGMTIRFDDNAAVIINKDGNPRGTRVFGPVARELREKSFTKIVSLAPEVLMLSPRRTKFRKQQRGRMQGLATRGCNIDFGDF
ALQAQEPSWITARQIEASRRAMTRYIRRGGQIWIRIFPDKPITMRAAETRMGSGKGNPEYWVAVVKPGRIMFEIAGVTEEIAREA
MRLAANKLPIKTKFIVRSQPKEQEMSAQEIIRSIEAEQLKSDLPIIYVGDTVKVGVKIKEGEKFRVQPYEGVVIAKRNGGINETITV
RRVFQGIGVERVFLLHSPRIDNIKILRRGKVRRAKLYYLRGRVGKATRIKQRFDRALMTRVKRGNVARKRRNKILKLAKGFRGS
HSTLFRTANQQVMKALRSSYRDRKKKKRDFRRLWIARINAAARQHGLSYSQLIGNLKKADIQLNRKMLAQLAVLDPASFGKV
AELALQAKGMAHKKGTGSTRNGRDSNAQRLGVKRFGGQKVIAGNILVRQRGTKVHPGNNVGIGSDDTLFALIEGVVTFERKG
KSRKKVSVYMTTDTYNMESAFLLPDLIEIQRASFRWFLEEGLIEELNSFSPITDYTGKLELHFLGNNYKLKEPKYSVEESKRRDS
TYAVQMYVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNRGAWLK
FETDRNDLVWVRIDKTRKLSAQVLLKALGLSDNEIFDALRHPEYFQKTIEKEGQFSEEEALMELYRKLRPGEPPTVLGGQQLLD
SRFFDPKRYDLGRVGRYKLNKKLRLSVPDTMRVLTPGDILAAVDYLINLEYDIGNIDDIDHLGNRRVRSVGELLQNQVRVGLN
RLERIIRERMTVSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRDIHPSH
YGRICPIETPEGPNAGLIGSLATHARVNLYGFLETPFRPVENGRVRFDLPPVYMTADEEDDLRTATGDIPVDENGYIKGPQVPVR
YRQDWATTTPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSGMVVVS
RTDGDVTYVDATEIRVRPKGGNSETRYRLSKYQRSNQDTCLNQKPLVRIGERVVAGQVLADGSATEGGELALGQNIVLAYMP

WEGYNYEDAILISERLVQDDVYTSIHIEKYEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRIGAWVEAGDILVGKVTPKGE
SDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHGNK
GIISRILPVEDMPYLADGSTVDIVLNPLGVPSRMNVGQVFECMLGWAAHTLGVRFKITPFDEMYGEETSRSIVHGKLQEARDET
GKDWVYNPDNPGKIMVFDGRTGEAFDRPITVGVAYILKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVWA
LEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKSIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLDVEVDLMAD
QSARRTPPRPTYESLSRDSLEEEEMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTSRNGVHIIDLVQTAQLMDNAYNYMR
SQSEQGKKFLFVGTKRQAAGIIAQEAARCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREENGALDLLPKKEASMLRRE
MTKLQKYLGGIKNMRKVPDVVVIVDQRREYNAVQECQKLGLPIVSMLDTNCDPDVVDIPIPANDDAIRSIKLIVGKLADAIYEG
RGGKLEGEDDYEDYDGSEYDDEYDDGEYAQASTSDEEMGQKIHPVGFRLGITREHQSRWFAIPERYPELLQEDYKLRQYIEQK
LGKLAQNNAGISEVRIERKADQIDLEVRTARPGVVVGRGGQGIESLRIGLQEVLGGNRQIRINVVEVQKVDADASLIGEYIAQQL
ERRVSFRRVVRQAIQRAQRAGVQGIKIQVSGRLNGAEIARTEWTREGRVPLHTLRADIDYAYCTAKTIYGILGIKVWVFKGEIIP
GQEETPAPPSTMATGRRKANRTKKEETTWQERVIQIRRVSKVVKGGKKLSFRAIVVVGNERGQVGVGVGKASDVIGAVKKGV
ADGKKHLIDIPMTKSNSIPHPIDGVGGGAKVMMRPAAPGTGVIAGGAVRTVLELAGVRNILAKQLGSNNPLNNARAAVNALST
LRTLSEVAEDRGIPIEKLYIVVADSNSGRAVYWGTGRRKCAVARVRLVPGEGKLTVNGKDGELYFQFNANYLGVIKNPLETLG
LENEYDILVKAEGGGLTGQADSIRLGVARALCQLDPDNRPPLKTEGYLTRDPRAKERKKYGLHKARKAPQYSKRMATLQQQK
IRIRLQAFDRRLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDAREHFETRTHRRIIDIYQPSSKTIDALMKLDLP
SGVDIEVKLMARQPTKKGGSKKQKRNVPNGMAYIQSTFNNSIVTITDQNGDVISWASAGSSGFKGAKKGTPFAAQTAAESAAR
RAMDQGMRQIEVMVSGPGAGRETAIRAIQGAGLEITLIRDITPIPHNGCRPPKRRRVMARISGVDLPRDKRVEIGLTYIYGIGLTR
SLEILAATGVNPDTRVKDLSDADVAALRGEIESNYQVEGDLRRLEAMSIKRLVDIGCYRGRRHRMGLPVRGQRTRTNARTRRG
RRQTVAGKKKAPGKMGRSLKKGPFVADHLLTKIEKLNAKNEKQVIKTWSRASTILPLMIGHTIAVHNGRQHVPVFVNEQMVG
HKLGEFAPTRTYRGHGKSDKKAGRMSEKSQSYKVISDNRQARYLYEILETFEAGVELVGTEVKSIRAGRVNLQDGYALIRNGE
AWLINVHISPYNASGQYFNHEPRRTRKLLLHRQEIRKLIGKVEQEGLTLVPLKMYLKRGWVKVSIALGKGKKLHDKRESLKRR
QDQRDMQRAMKSYMAEISAKLVQELRQKTGAGMMDCKKALKENDGDIEKGIEWLRQKGIASAGKKSDRIAAEGLVDTYIQP
GGRVGVLIEVNCQTDFVARNEAFKVLVKNLAQQAATADSVESLLAQPYIEETSVTVDQFIKQTIAQLGENIQVRRFINFALEGK
QGIVDSYIHTGGRVGVLVEVNAQTESPAQNEEFQTLAKNAAMQVAACPNVEYVSVDEIPAEFAQKETEIEMGRDDLGNKPQNI
KEKIVQGRIEKRLKELTLLDQPFIRDQSISVEDLVKQVKGKVGEEIKVNRFVRYILGEGIEKQESNFAEEVAAQMG

>Nodularia_spumigena_CCY9414
MQIPRLHPDTIEEIKQRADIVDVVSDHVVLRKRGKDFVGLCPFHDEKTPSFTVSQTKQMYYCFGCQAGGNAIKFLMDLGKHSF
AEVVLDLARRYQVPVQTLAPEQRQELQRQISLREQLYEVLASTGQFYQHALRQSQGQKAYQYLQSERQLKEETIQQFGLGYAP
AGWETLHRYLVEDKRYPVQLVEKAGLIKPRKEGGGYYDVFRDRLMIPIRDIQGRVIAFGGRTLSEEQPKYLNSPETELFSKGKT
LFALDIAKDGISQLDQAVVVEGYFDAIALHAAGINNAVASLGTALSIEQVRLILRYTESKQLVLNFDADKAGNIAAERAIGEIAT
LAYKGEVQLKILNIPDGKDADEYLYTHTPFDYEQLLANAPLWLNWQIEQIIQNRDLKQATDFQQVSQQVVKLLKNIDNSDTRN
YYVSYCAEILSLGDARLIPLRVENLLTQIAPTTATRNKPLSSKKKFTQSPIPGDKSLLELAEALLLRIYLHCPEQRQIIFNTLEERNL
EFSLSHHRLLWQKILGSTGEEVDFVSSLQDRYLELSEEIASISHLFHLNEKSQKEILRTPQAVQAAVACMERVLIEKRYRYFLEL
WEKTDSQAEPEKWQSYYQSFYHEKMRLQELDRQRQFSITDLLMKLSEAESTMQKTVEATQRAFNTIRTGRANASLLDKVSVD
YYGSPTPLKSLANISTPDASTILIQPYDKGSLNVVEKAISLSDVGLTPSNDGSVIRLNIPPLTSDRRKEFVKMASKYAEEGRVAIRN
IRRDVQDTIRKEEKASEISEDESKDQQDQLQKLTNKYTARIDDLLAEKEKDISTVMPVIEKKRTRDLPQINERIRFPKIRVIDTDGA
QLGIMPPQEALQLAEEKELDLVLLSDKADPPVCRIMDYGKYKFEQEKKAREARKKQHTADVKEVKMRYKIEEHDYNRVKQ
AERFLKDGDKVKATVMFRGREIQHSDLAEHLLKRMAKDLEPLGELQQAPKKEGRNMMMLISPKKMSMVSLPGLKELIESISRE
RNLPRLAVQTAIREALLKGYERYRRAQNLEKRQFDEEYFDNFEVELDIEGEGFRVLSTKSIVEAVDNTDHQISLEEVQQVAPEA
QLGDSVVLDVTPDQGEFGRMAAMQTKQVLAQKLRDQQRQMVQEEFQDLEGTVLQARVLRFERQSVILAVASGFGQPEVEAE
LPKREQLPNDNYRANATFKVYLKKVSQGQQRGPQLLVSRADAGLVVYLFANEVPEIEDEVVRIVAVAREANPPSRYVGPRTKI
AVDTLDRDVDPVGACIGARGSRIQVVVNELRGEKIDVIRWSPDPSTYIANALSPARVDEVRLMDPETRQTHVLAEDQLSLAIG
KEGQNVRLAARLTGWKIDIKDKAKYDYAGEDTKFAAARAKYQMSKKTLANLSAADISGKRALVRVDFNVPVDDNGNITDDT
RIRAALPTIQDLMEKGAKVILASHFGRPKGVDDKLRLTPVAQRLSELLGQEVVKTDDCIGDAVTAQVGALQNGQVLLLENVRF
YKEEEKNDPEFAKKLAANADFYVNDAFGTAHRAHASTEGVTHYLSPSVGGYLIEKELQYLQSAIENPQRPLAAIIGGSKVSSKI
GVIETLLDKCDKLIIGGGMIFTFYKARGLSVGKSLVEEDKLELAKTLEAKAKERGVALLLPTDIVSADKFAPDANATTVSIENIPA
DGMGLDIGPDSIKVFQAALADCKTVIWNGPMGVFEFDKFAAGTEAIAHTLAEIGKTGTTTIIGGGDSVAAVEKVGLADQMSHIS
TGGGASLELLEGKTLPGIAALDEAMTKFIFVTGGVVSSIGKGIVAASLGRLLKSRDYSVSILKLDPYINIDPGTMSPFQHGEVFVT
EDGAETLDLGHYERFTDTSMSRLNSVTTGSIYQAVINKERRGDYNGGTVQVIPHITNEIKERILRVAQDTNPSVLITEIGGTVGD
IESLPFLEAIRQLRKEVGRQNVLYMHVTLIPWIASAGEMKTKPTQHSVKELRSIGIQPDILVCRCDRAIPLGLKRKLSEFCDVPQE
CVITAQDASSIYEVPLIVEREGLAEQALDLLQMEQRQPNLVQWQTMVERLYSPKYTVEIAIVGKYVRLSDAYLSVVEALRHAAI
STYGDLRLRWVNSEDLENESAETYLAGVDGILVPGGFGIRGVDGKIAAIKYARDRQIPFLGLCLGMQCSVIEWARNVEGLNGA
NSAEFDPETKYPVINLLPEQQDVVDLGGTMRLGLYPCHLLPNTLAANLYQQEVVDERHRHRYEFNNNYRNLLLESGYVISGTS
PDGRLVEIVEFPQHPFFLACQFHPEFHSRPSTPHPLFKGFMEASINRTHSISNLPTPVEVSMGKKISRRFQALLEKVEDRDYTPLEA
LNLLKETATAKFPEAAEAHIRLGIDPKYTDQQLRTTVTLPKGTGQTVRVAVIARGEKVTEASNAGADVVGSDELINEIQQGMM
DFDKLIATPDVMPQVAKLGKLLGPRGLMPSPKGGTVTFDVASAIAEFKAGKLEFRADRTGIVHVMFGKASFSPEDLLVNLKAL
QETIDRNRPSGAKGRYWRTIYVTSTMGPSIKVDINALRDLKLSELAMGTRSYRPYTPSTRQVTVSDFAEITKSKPEKSLTEYVHR

PKGRNNQGRITSRRRGGGHKQMYRIIDFKRDKRNIPAQVIAIEYDPNRNARIALVLYQDGEKRYILHPNKLPVGATIIAGPDSPFE
DGNALPLLNIPLGTSVHNVELTPGKGGQIVRAAGANAQVVAKEGQYVTLKLPSGEVRMIRRECYATIGQVGNTDARNLSAGK
AGRNRWKGRRPKVRGSVMNPVDHPHGGGEGRAPIGRPGPVTPWGKPTLGAKTRKPKKASSKLIVMSVGILGTKLGMTQVFDE
AGVSIPVTVVQAGPCTVTQVKTKQTDGYSAIQLGYGEVKPKALNRPLLGHLAKSSAPALRHLNEYHTDSPSDYALGQELKADI
FSEGQIVDVVGTSIGRGFAGNQKRNNFGRGPMSHGSKNHRAPGSIGAGTTPGRVYPGKRMAGRLGGTRVTIRKLTVVRVDLER
NLLLIKGAIPGKPGSLVNILPAKKVGMVESVVKNWQGEQVGETTFELRVAKESTASHIVHRALVRQMTNSRQGTASTKTRSEV
RGGGRKPWRQKGTGRARAGSIRSPLWRGGGVIFGPKPRDYNQKLNRKERRLALRTAFVSRADDLIVVQDFSNELSRPKTKELV
AALARWGAAPENKALLIMPIISSEDNVYLSARNIQNLKLIAADQLNVYDLLHADKIVITASALAKIQEVYSAMPTTRLKNLYQE
TIVPKLTNQFQYTNVHQVPKVIKITINRGLGEAAQNAKSLEASLNEIAVITGQKPVVTRAKKAIAGFKIREGMPVGIMVTLRGER
MYAFLDRLISLSLPRIRDFRGISPKSFDGRGNYTLGVREQLIFPEVEYDSIDQIRGMDISIITTAKNDEEGRALLKEMGMPFRDQM
SRIGKQPITIPAKVEVTIDGPKVVVKGPKGQLSRTLSANVIVSQEGGILNVTRRDETRVSRQMHGLSRTLVANMVEGVSQGFKR
RLEIQGVGYRAQLQGRNLVLNIGYSHQVNIVPPDGVEFLVETNTNIVVSGYDKEIVGNTAAKIRAVRPPEPYKGKGIRYAGEVV
RRKAGKTGKSGKKMAKKVVAVIKLALNAGKANPAPPVGPALGQHGVNIMMFCKEYNAKTADQAGMVIPVEISVFEDRSFTF
VLKTPPASVLIRKAAKIERGSNEPNKKKVGSITKAQLQEIAQTKMPDLNANDIEAAMRIVEGTANNMGVTISDMSATTDQILEQ
LKTLSLLEASELVKQIEEAFGVSAAAPAGGMMMMAPGAAAAAEPVEEKTEFDVILDSVPADKKIAVLKIVRELTGLGLKEAKD
LVEAAPKAVKEGIAKDAAEDAKKRIEEAGGKVTVKMTTKTYLPPQATLEREWYVVDATDKRLGRLATEIAMILRGKKKAEFT
PHMDTGDFVIVINAEKIAVTGKKRTQKLYRRHSGRPGGMKTETFAKLQQRLPERILEHAVKGMLPKNSLGKQLFTKLKVYAGP
THPHEAQQPKELKINTIPGEMIQTQTYLNVADNSGAKKIMCIRVLGGGNRRYGFIGDRIIAVVKDAIPNMAVKKSDVIEAVIVRT
RHSIRRDSGMTIRFDDNAAVIINKDGNPRGTRVFGPVARELREKSFTKIVSLAPEVLMLSPRRTKFRKQQRGRMQGLATRGCNI
DFGDFALQAQEPSWITARQIEASRRAMTRYIRRGGQIWIRIFPDKPITMRAAETRMGSGKGNPEYWVAVVKPGRIMFEIAGVTE
EIAREAMRLAANKLPIKTKFIVRSQPKEQEMSAQEIIRSIEAEQLKSDLPIIYVGDTVKVGVKIKEGQKFRVQPYEGVVIAKRNGG
INETITVRRVFQGIGVERVFLLHSPRIDNIKIIRRGKVRRAKLYYLRGRVGKATRIKQRFDRALMTRVKRGNVARKRRNKILKLA
KGFRGSHSTLFRTANQQVMKALRSSYRDRKKKKRDFRRLWIARINAAARQHGLSYSQLIGNLKKADIQLNRKMLAQLAVLDP
ASFGKVAELALQAKGMAHKKGTGSTRNGRDSNAQRLGVKRYGGQTVLAGNILVRQRGTKVHPGNNVGIGSDDTLFALIEGV
VTFERKGKSRKKVSVYMTTDTYMESAFLLPDLIEIQRSSFRWFLEEGLIEELNSFSPITDYTGKLELHFLGNNYKLKEPKYSVEES
KRRDSTYAVQMYVPTRLLNKETGDIKEQEVFIGDLPLMTDRGTFIINGAERVIVNQIVRSPGVYYKSEIDKNGRRTYSASLIPNR
GAWLKFETDRNDLVWVRIDKTRKLSAQVLLKALGLSDNEIFDALRHPEYFQKTIEKEGQFSEEEALMELYRKLRPGEPPTVLGG
QQLLDSRFFDPKRYDLGRVGRYKLNKKLRLSVPDTMRVLTPGDILAAVDYLINLEYDIGNIDDIDHLGNRRVRSVGELLQNQV
RVGLNRLERIIRERMTVSDAEVLTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRLSALGPGGLTRERAGFAVRD
IHPSHYGRICPIETPEGPNAGLIGSLATHARVNLYGFLETPFRPVENGRVRFDLPPVYMTADEEDDLRTATGDIPLDENGYIKGPQ
VPVRYRQDWATTTPEQVDYVAVSPVQIVSVATSMIPFLEHDDANRALMGSNMQRQAVPLLKPERPLVGTGLEAQGARDSGM
VIVSRTGDVTYVDATEIRVRPKDGNSEIRYRLSKYQRSNQDTCLNQKPLVRIGERVVAGQVLADGSSTEGGELALGQNIVIAY

MPWEGYNYEDAILISEKLVQDDVYTSIHIEKYEIEARQTKLGPEEITREIPNVGEDALRQLDEQGIIRIGAWVEAGDILVGKVTPK
GESDQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRLFTREQGDELPPGANMVVRVYVAQKRKIQVGDKMAGRHG
NKGIISRILPVEDMPYLADGSTVDIVLNPLGVPSRMNVGQVFECMLGWAAHTLGVRFKITPFDEMYGEETSRSIVHGKLQEARD
ETGKDWVYNPDNPGKIMVFDGRTGEPFDRPITVGVAYILKLVHLVDDKIHARSTGPYSLVTQQPLGGKAQQGGQRFGEMEVW
ALEAFGAAYTLQELLTVKSDDMQGRNEALNAIVKGKSIPRPGTPESFKVLMRELQSLGLDIAVHKVETQTDGSSLDVEVDLMA
DQSARRTPPRPTYMPVVSLAQMMESGVHFGHQTRRWNPKMSPYIYTSRNGVHIIDLVQTAQLMDNAYNYMRSQSEQGKKFLF
VGTKRQAAGIIAQEAARCGSHYINQRWLGGMLTNWATIKTRADRLKDLERREENGALDLLPKKEASMLRREMTKLQKYLGGI
KNMRKVPDVVVIVDQRREYNAVQECQKLGLPIVSMLDTNCDPDVVDIPIPANDDAIRSIKLIVGKLADAIYEGRGGTLEGEDDY
EDYDGSEYDDDYDESEYAQGSSDESSDEMGQKIHPVGFRLGITREHQSRWFAVPERYPELLQEDYKLRQYIEKKLGKLAQNNA
GISEVRIERKADQIDLEVRTARPGVVVGRGGQGIESLRLGLQEVLGGNRQIRINVVEVQKVDADASLIGEYIAQQLERRVSFRRV
VRQAIQRAQRAGVQGIKIQVSGRLNGAEIARTEWTREGRVPLHTLRADIDYAYCTAKTIYGILGIKVWVFKGEIIPGQEEIPAPPS
TMATGRRKANRTKKEETTWQERVIQIRRVSKVVKGGKKLSFRAIVVVGNERGQVGVGVGKASDVIGAVKKGVADGKKHLIDI
PMTKSNSIPHPIDGVGGGAKVMMRPAAPGTGVIAGGAVRTVLELAGVRNILAKQLGSNNPLNNARAAVNALSTLRTLSEVAED
RGIPIEKLYIVVAQSNSGRAVYWGTGRRKSAVARVRLVPGEGKLTVNGKDGELYFQFNANYLGVIKNPLETLGLENEYDILVK
AEGGGLTGQADSIRLGVARALCQLDPDNRPPLKTEGYLTRDPRAKERKKYGLHKARKAPQYSKRMATLQQQKIRIRLQAFDR
RLLDTSCEKIVDTANRTNATAIGPIPLPTKRKIYCVLRSPHVDKDAREHFETRTHRRIIDIYQPSSKTIDALMKLDLPSGVDIEVKL
MARQPTKKGGSKKQKRNVPNGMAYIQSTFNNSIVTITDQNGDVISWASAGSSGFKGAKKGTPFAAQTAAESAARRAMDQGM
RQIEVMVSGPGAGRETAIRAIQGAGLEITLIRDITPIPHNGCRPPKRRRVMARISGVDLPRDKRVEIGLTYIYGIGLTRSLEILAATG
VNPDTRVKDLSDAEVAALRGEIESNYQVEGDLRRLEAMSIKRLVDIGCYRGRRHRMGLPVRGQRTRTNARTRRGRRQTVAGK
KKAPGKMGRSLKKGPFVADHLLTKIEKLNAKNEKQVIKTWSRASTILPLMIGHTIAVHNGRQHVPVFVNEQMVGHKLGEFAPT
RTYRGHGKSDKKAGRMSEKSQSYKVISDNRQARYLYEILETFEAGVELTGTEVKSIRAGRVNLQDGYALIRNGEAWLINVHISP
YNASGQYFNHEPRRTRKLLLHRQEIRKLIGKVEQEGLTLVPLKMYLKRGWVKVSIALGKGKKLHDKRESLKRRQDQRDMQRA
MKNYMAEISAKLVQELRQKTGAGMMDCKKALKENDGDIEKAIEWLRQKGIASAGKKSDRIAAEGLVDTYIQPGGRVGVLIEV
NCQTDFVARNEAFKALVKNLAQQATTADSVESLLAQPYIEETSVTVDQFIKQTIAQLGENIQVRRFINFALPEGQQGVVDSYIHT
GGRVGVLVELNAQTETAAQNEEFQTLAKNAAMQVAACPNVEYVSVDEIPAEFAQKETEIEMGRDDLGNKPQNIKEKIVQGRIE
KRLKELTLLDQPFIRDQSISVEDLVKQVKTKVGEDIKVNRFVRYILGEGIEKQEISFAEEVAAQMGSK

>Synechocystis_sp_PCC_6803
RLHPDTIQEIKQRIDIVEIIGDYVVLKKRGRDHLGLCPFHDEKSPSFSVSPAKQMYYCFGCGAGGNAFNFLMELGKRSFTDVALD
LARRYQIQIQTLEPAQKQELQRQLSLREQLYEIMAVAAGFYHHTLFQPQGQEALTYLDQKRCLSSATIQEFQLGYAPAGWETLY
RYLVEQKRYPVAAVEQAGLIKARQSGTGYYDQFRHRLMIPIRDVQGKTIAFGSRTLGNDEPKYLNSPETPLFHKSKTLFGLDQA
KTAIQKVDEAILVEGYFDVIALHESGIKQTVAALGIALSRDQVQSLMRFSQSKQIIFNFDADKAGINATQRAIQEIEPLVYSGQVN
LRILNLPAGKDADEFIHSSAENKEIYQTLVKQAPLWVDWQIQQLLKQKNLKDPLDFEQVARGMVDILKRLTDQNKRAYYLQLC
GEILSQGDSRLISLQVNNLSSQLTYGDRPGKNGSRHWQAKDPTSSLLEKAEALLLKIYLHCPQERPTIDQILTENDLLFSFAHHRL
LWQKIDQVREYFNLDSDPDNQLPLLVQLAYLEQEGDFNSVESLFQLTETSAEDLFRANLRIPEAIAIMEKVPWESYQKHCFGKL
QQLDPRTQAEDFRYYQEQWQKAHQEIQRLESQRMKLAELKDHMQKSVEATQRSFNTIRTGRANASLLDRITVEYYGAETPLKS
LATIGTPDASTIVIQPFDMGSIGTIEKAISLSDLGLTPNNDGKVIRLNIPPLTAERRKELVKVAGKLAEEGKVAIRNIRRDAVDEVR
KQEKNSDISEDEARDLQEEIQKLTDQSTKRIDELLAAKEKDITTVRDLPQINERIRFPEIRVIDSDGAQLGIITPNEAMEIADERGLD
LVLVSETADPPVCRIMDYGKYKFEQEKKAREAKKKQHTADVKEVKMRYKIDEHDYQVRINQAKRFLKAGDKVKATVNFRGR
EIQHAHLAKELLDRMATDLATEADIQQAPKREGRNMMMFLSPKKMSLVSLPGLPAMISEISKRNNLPTTAVEEALREALLKGY
ERFRRSQLMGHQFPEEYFNNFEVELDTEEEGFRVLSTKRIVEEVENSDQQISLKEVLEVAEEAQLGDEVVLDVTPEQKDFGRMA
AIQTKQVLLQKLRDQQRKIIQEEFQDLEGTVLNARALRFERQSIIVAVQSSFGQPEVEAELPKREQLPNDNYRANSTFRVYLKRV
REGSQRGPQLVVSRAAAGLVVDLFSVEVPEIEEEVVRIVAVAREAKPPSPSVGPRTKIAVDTLERDVDPVGACIGARGSRIHAVV
NELRGEKIDVIRWSPDPATYIAQALSPARVDQVYLIHAEERHALVIVAEDQLSLAIGKEGQNVRLAARLTGWKIDIKDPETYMS
KQSIANLTEADLAGKRVFVRVDFNVPLDNGSITDDTRIRAALPTIKDLLSKGAKVILGSHFGRPKGKVVDSMRLTPVGDRLGEL
LGQPVVKCDDCIGAEVTAKIASLPNGGVALLENLRFHAGEEGNDAEFAKALAANADLYVNDAFGTAHRAHASTEGVTHFLSP
NVAGYLIEKELQFLQGAIEAPKRPLVAIVGGSKVSSKIGVIETLLDKCDKLIIGGGMIFTFYKAQGLNTGKSLVEEDKLDLAKSL
MAKAKEKGVEFLLPTDVVVADNFAPDANAQTVGVDAIPDGWMGLDIGPDSVKTFQDALAGCGTVIWNGPMGVFEFDKFAVG
TEAIACSLAELTASGTVTIIGGGDSVAAVEKVGVAEKMSHISTGGGASLELLEGKVLPGIAALDDMSKFVFVTGGVVSSIGKGIV
AASLGRLLKSRHYSVSILKLDPYINVDPGTMSPFQHGEVFVTEDGAETDLDLGHYERFTDTSMSRLNSVTTGSIYQAVINKERR
GAYMGGTVQVIPHITNEIKERILRVAQNTNPDVVITEIGGTVGDIESLPFLEAIRQFRKEVGRHNVIYMHVTLIPWIPAAKEMKTK
PTQHSVKELRSIGIQPDILVCRCDRPLHPGMKEKLSEFCDVPVESVITCQDASSIYEVPLILEKEGLAHQTLELLRMENRSPDLSQ
WQSLVEKMQSPHHDITVALVGKYVQLSDAYLSVVEALGHAAIASDSKLHLRWISAEEIEAQGAATFLKDVDGVLVPGGFGIRG
VDGKVQAIEYARENQLPFLGLCLGMQCSVIEWARNVAKLPEANSAEFETETPNPVINLLPEQQDVVDLGGTMRLGLYPCRIAP
DTLAFSLYQKEVVYERHRHRYEFNNSYRTQFTDTGFVVSGTSPDGRLVEIVEYPHHPFFIACQFHPEFHSRPNQAHPLFSGFINA
VLKRRNAPAKIAMTKKLSKRMQAAIAKVDDSKLYSPLEAMELLKETATAKFDETAEAHIRLGIDPKYSDQQIRTTVSLPKGTGQ
TVRVAVLARGEKVKEATDAGADIAGSEELIEEIQKGMMDFDVLIATPDMMPKIARLGKQLGPRGLMPSPKGGTVTADLAAAV
NEFKAGKLEFRADRTGIVHVMFGKASFSADDLLANLKALQETIDRNRPSGAKGRFWRTVFVSSSMGPSIPVDINALRDLKFEDM
GIRNYRPMTPGTRQASVSDFTEITKSKPEKSLTTNRHDQKGRNNRGVITSRHRGGGHKKLYRIIDFKRNKQNIPARVAAIEYDPN

RNARIALLFYTDGEKRYILAPAGLQVGMTVIAGEEAPFEIGNTLPLSRIPLGSEIHNVELVAGRGGQMVRSAGAFAQVVAKEGD
YVTIKLPSKEVRMVRKECVATLGRVSNAEFRNLKLGKAGRKRHLGRRPHVRGSVMNPCDHPHGGGEGRAPIGRSGPVSPWGK
PALGAKTRNKKKRSSALIVRRRTKMSIGILGTKLGMTQIFDQESGISIPVTVVQAGPCPVTQVKTQDTDGYNAIQVGFLPVKEKA
LSKPELGHLKKSNTDPMRHLKEYRLTDAPNLQPGDAVTADIFQAGDLVDVAGQSMGRGFAGYQKRHNFRRGNMTHGSKNHR
LPGSTGAGTTPGRVYPGKRMAGQYGASQVTVRRLTVVRVDAERNLLIIKGALPGKPGTLLNITPAKTVGMVDCIVKNWQGEE
VGNASLTLRVAKEENAAHIVHRALVRQQNNARQGNASAKTRAEVRGGGRKPWKQKGTGRARAGSIRSPLWRGGGVIFGPKP
RDYSQKMNRKERRLALRTAIASRADNMVVVEAFGDQFSQPKTKELATALTRWGAKPEKRVLLILDEIPENVFLSGRNIPYLKIL
RADNLNIYDVLVADTIVATATALEKIQEVYTQRLKTLYQETILPKLQEEFGYKNIHQVPKLTKVTVNRGLGEASQNAKALESSL
TELATITGQKPVVTRARKAIAGFKIREGMPVGVMVTLRSERMYAFLDRLINLALPRIRDFRGISPNSFDGRGNYSLGIREQLIFPEI
DYDTIDQIRGMDVSIITSAQTDEEGRALLKALGMPFRMSRIGKRPIPLPAKVSVDIQGSHLSVKGPKGSLERQLPEKVIVAQEGET
ITVTRQDESRTARERHGLVRTLVANMVDGVAQGFERRLEIQGVGYRAQAQGNKLTLNVGYSKPVEMTMPQGIEVKVENNTQ
VIVSGIDKELLGNTAAKIRAVRPPEPYKGKGIRYQGEYVRRKAGKTGKKMAKKVVALIKLALPAGKANPAPPVGPALGQHGV
NIMAFCKEYNAKTADKPGMIIPVEISVFEDRSFTFILKTPPASVLIRKAAGVEKGSSEPNKNKVASITREQLREIAQTKLPDLNAN
DIDAAMNIIEGTARNMGITVMSAATDQILEQLKSLSLLEASELVKQIEEAFGVSAAAPVGGMVMAAAAAAPAEAAEEKTEFDVI
LEEVPADKKIAVLKVVRTITGLGLKEAKELVESTPKAIKEATGKDDAEAIKKQIEEAGGKAAVKNKTVLPTIDNLDHKWYVIDA
EGQRLGRLATEVATILRGKNKPTFTPHMDTGDFVIINAEKIEVTGRKREQKLYRRHSGRPGGMKEETFEKLQVRLPERIVESAV
RGMLPKNSLGRKLFTKLKVYAGPSHPHAAQQPETLVINTIPAMIQQQTYLNVADNSGARKLMCLRVLGTGNCTYGGIGDQIIA
VVKDALPNMPIKKSDVVRAVIVRTKQPLRRASGMSIRFDDNAAVIINAEGNPRGTRVFGPVARELRDKNFTKIVSLAPEVLMLS
PRRTKFRKQQRGRMRGLAERGSTLNFGDYALQATEPCWITSRQIEAARRAMTRYIRRGGKIWIRIFPDKPVTMRPAETRMGSG
KGSPEYWVAVVKPGRVMFELAGVSEEVAREAMRLAAQKLPIKTKFISRQEMNAQAIINSIEAEFLKEDLPTIHVGDTIKVGVKIV
EGGKERIQPYEGTVIAKRNGGISETITVRKIFQGVGVERVFLLHSPRVASIKVLRRGKVRRAKLYYLRDRVGKATRIKQRFDRAL
MTRVKRGNVARKRRKKILKLAKGFRGSHSKLFRTANQQVMKALRNAYRDRRKRKRDFRRLWITRINAAARQEGMSYSKLTG
QLKKANIEINRKMLAQLAVLDPAAFSEVVKVAATAKMAHKKGTGSTRNGRDSNAQRLGVKRYGGQTVTAGSIIVRQRGTQV
HPGNNVGRGKDDTLFALIDGVVKFEHKTRSRRKVSVYPATAEMLPDLIEIQHASFHWFLEEGLIEELNSFSPISDYTGKLELHFL
GKDYKLKQPKYDVDESKRRDASYSVQMYVPTRLINKETGEIKEQEVFIGDLPLMTERGTFIINGAERVIVNQIVRSPGVYYKKE
LDKNGRRTYSASLIPNRGAWLKFETDKNGLVYVRIDKTRKLSAQVLLKAIGLSDNEILDSLSHPEFYQKTLDKEGNPTEEEALV
ELYKKLRPGEPPTVSGGQQLLESRFFDPKRYDLGRVGRYKLNKKLRLNEADTTRVLTPQDILAAINYLINLEFDVGTTDDIDHL
GNRRVRSVGELLQNQIRVGLNRLERIIRERMTVSESDALTPASLVNPKPLVAAIKEFFGSSQLSQFMDQTNPLAELTHKRRISAL
GPGGLTRERAGFAVRDIHPSHHGRICPVETPEGPNAGLIGSLATCARVNDYGFIETPYFRVESGRVRKDLDPVYLTADEEDDMR
VAPGDIPTDEEGNIIGESVPIRYRQEFSTTSPEQVDYVAVSPVQIISVATSMIPFLEHDDANRALMGSNMQRQAVPLLRPERPLVG
TGLEAQAARDSGMVIVSRTHGIVTYVDATEIRVQPHSPDNPAEKGEEIVYPIQKYQRSNQDTCLNQRPLVYAGEDVVPGQVLA
DGSATEGGELALGQNILVAYMPWEGYNYEDAILISERLVYDDVYTSIHIEKFEIEARQTKLGPEEITREIPNVGEDALRNLDEHGI

IRIGAWVESGDILVGKVTPKGEADQPPEEKLLRAIFGEKARDVRDNSLRVPNGEKGRVVDVRVFTREKGDELPPGANMVVRIY
VAQKRKIQVGDKMAGRHGNKGIISRILPIEDMPYLPDGRPIDIALNPLGVPSRMNVGQVFECLLGWAGENLGVRFKITPFDEMY
GEEASRDTVHGLLEEASQRPNKDWVFNENHPGKIQVFDGRTGEPFDRPITVGQAYMLKLVHLVDDKIHARSTGPYSLVTQQPL
GGKAQQGGQRFGEMEVWALEAYGAAYILQELLTVKSDDMQGRNEALNAIVKGKSIPRPGTPESFKVLMRELQSLGLDIAAHK
VQLSEDGESADAEVDLMIDSQRRAPNRPTYESLMPVVSLADLLESGVHFGHQTRRWNPRMDQYIYTARNGVHIIDLVQTAQL
MEDAYEYVRSSTINGKKFLFVGTKRQAAGIISQEAQRCGAHYVNQRWLGGMLTNWETIRKRVDRLKELEALEASGGIDRRGK
KEGSMLRRELGKLQKYLGGIKNMRKLPDVVVIVDQRREHNAIHECQKLGIPIIAMLDTNCDPDVVDVPIPANDDAIRSIKLIVGK
LADAIYEGRHGQPDVSDDYEEFDEGMGQKIHPVGFRLGITKDHKSCWYADPKRYPELLQEDHKIRQYIEKTLNNAGISDIRIER
KAEQIELGIHTARPGVVVGRGGSGIEQLREGLQKLLGSARQIRVNVIEVPNADADAALMAEYIGQQLERRVSFRRVVRQALQR
AERAEVKGIKIQVSGRLNGAEIARTEWVREGRVPLHTLRADIDYAYRTALTTYGILGIKVWIFKGEVIPGQEAAIVAPPSQPRRK
SRRQQFDDRSQDRRKTSREKKEDTNWQERVIQIRRVSKVVKGGKKLSFRAIVVVGNETGQVGVGVGKAGDVIGAVRKGVAD
GKKQLIEVPLTKSNSITHITNGVSGGAKVVVRPAAPGTGVIAGGAVRTVLELAGVKNILAKQLGSNNPLNNARAAINALETLRT
FSEVAEERGVSVEHLYANDSSNKVVYWGTGRRKAAIARVRLVPGQGEVIVNGKPGEIYFNRIANYIQSLKAPLETLGLEGEYNI
LVNAHGGGLTGQADAVKLGVARALCQLSPENRQPLKAEGYLTRDPRAKERKKYGLHKARKAPQYSKRMATLQQQKIRIRLK
AFDRRLLDTSCDKIVDTANRTNAAAVGPIPLPTKRKIYCVLRSPHVDKDSREHFETRTHRRIIDIYQPSSKTIDALMKLDLPAGVD
IEVKLMARPTRKTGPKKAKKNVPSGVAHIQSTFNNTIVTISDIRGDVISWASAGSSGFKGAKKGTPYAAQTAADSAARRAMEQ
GMRQLEVMVSGPGAGRETAIRALQGAGLEITLIRDVTPIPHNGCRPPKRRRVMARIAGVDLPRDKRVEIALTYLYGIGLSRSHEI
LDATGVSPDVRVKDLSDEDALKLRTYIDENYEIEGDLRRWEAMNIKRLGDIGTYRGRRHRQGLPVRGQRTRTNARTRRGRRLT
VAGKKKTPAKMGRSLKKGPFVAASLLRKIDKLNDKGDKQVVKTWSRASTILPQMVGHTIAVHNGRQHVPVFVSEQMVGHKL
GEFAPTRTFRSHSKSDKKAMAKEKERIKVVSDNRQARFLYEILETYEAGIELQGTEVKSIRAGKVNLRDGFALLRDGEVWLMN
VHISPYDKSSLFFNHDPRRTRRLLMHNWEIRKLIGQVEQKGLTLVPLKMYFKGSWVKVALGLGKGKKLHDKRETLKRRQDDR
DMARAMKAEGLVHSYIHFGGRIGVLVEVNCETDFVARGDRFKDLVNDVAMQIAACPNVEYVSVADIPQEMVAKEKEIEMGR
DDLGKKPANIKEKIVQGRIDKRLKELSLLDQPYIKDQNLTIEELVKQAIAELGENIQVRRFIRFNLGEGIEKAETNFAEEVAA

Suplementary Table S4. Summary of NRPS, PKS, NRPS/PKS, terpene synthase, and phytoene synthase genes analyzed in this research.

Strain	NRPS	PKS	Hybrid NRPS/PKS	Terpene synthase	Phytoene synthase	Total
C. raciborskii KLL07	4	12	1	1	2	20
C. raciborskii N8	4	8	0	1	2	15
C. raciborskii Cr2010	4	12	1	1	2	20
C. curvispora GIHE G1	1	4	0	1	2	8
C. raciborskii GIHE 2018	6	3	0	1	2	12
C. raciborskii CS-505	4	10	0	1	2	17
R. brookii D9	3	9	0	1	2	15
C. raciborskii CENA 302	0	9	0	1	2	12
C. raciborskii CENA 303						
C. raciborskii MVCC14						
C. raciborskii KL1						
C. sp. CR12						
C. raciborskii MVCC 19						
C. raciborskii CS508						

C. raciborskii CYRF						
C. raciborskii CYLP						
C. raciborskii CHAB3438						
C. raciborskii ITEPA-A1						
C. raciborskii DSH						
C. raciborskii PAMP2012						
C. raciborskii 1523720						
S. torques-reginae ITEP-024						
S. kisseleviana NIES-73						
S. sp. SIO1G1						
S. sp. FACHB-1194						
S. sp. LEGE 08334						
S. sp. LEGE 00249						

Suplementary Table S5. Proposed function of the proteins encoded by heterocyte glycolipid biosynthetic gene cluster and two proteins involved in the regulation of heterocyte differentiation in the genomes of the *S. torques reginae* ITEP-024, *S. kisseleviana* NIES-73, *S.* SIO1G1, *S.* FACHB-1194 and *S.* LEGE 00249.

Protein	Aminoacids	Product	Strain	Organism	Identity (%)	Function	Acession number
HglA	556	2-nitropropane dioxygenas	*S. torques reginae ITEP024*	*S. LEGE 08334*	99	2-nitropropane dioxygenas	WP_194054992.1
	556		*S. Kisseleviana NIES 73*	*S. LEGE 00249*	99	family polyunsaturated fatty acid	MBC5793826.1
	556		*S. sp SIO1G1*	*S. torques reginae ITEP024*	88		WP_220610685.1
	556		*S. FACHB 1194*	*S. LEGE 08334*	99		WP_194054992.1
	556		*S. LEGE 08334*	*S. LEGE 00249*	99		MBC5793826.1
	556		*S. FACHB 1194*	*S. LEGE 08334*	99		WP_194054992.1
	556		*S. LEGE 08334*	*S. LEGE 00249*	99		MBC5793826.1
	556		*S. sp. LEGE 00249*	*S. Kisseleviana NIES 73*	99		WP_096572229.1
	556		*S. torques reginae ITEP024*	*S. LEGE 08334*	99		WP_194054992.1
	556		*S. Kisseleviana NIES 73*	*S. LEGE 00249*	99		MBC5793826.1

HglB	497	Polyketide synthase	*S. sp SIO1G1*	*S. FACHB 1194*	84	thioester reductase	WP_190647549.1
	505		*S. FACHB 1194*	*S. Kisseleviana NIES 73*	100		WP_096572228.1
	505		*S. LEGE 08334*	*S. torquesreginaeITEP024*	98		WP_220610686.1
	505		*S. sp. LEGE 00249*	*S. Kisseleviana NIES 73*	99		WP_096572228.1
HglC	1106	omega-3	*S. Kisseleviana NIES 73*	*S. FACHB 1194*	99	polyketide synthase	WP_242027320.1
	1106		*S. FACHB 1194*	*S. Kisseleviana NIES 73*	100		WP_272109449.1
	1106		*S. torques reginae ITEP024*	*S. LEGE 08334*	97		WP_194054993.1
	1106		*S. LEGE 08334*	*S. torques reginae ITEP024*	98		WP_220610684.1
	1106		*S. sp. LEGE 00249*	*S. Kisseleviana NIES 73*	98		WP_272109449.1
	1089		*S. sp SIO1G1*	*S. torques reginae ITEP024*	85		WP_220610684.1
HglD	450	polyketide synthase	*S. torques reginae ITEP024*	*S. LEGE 08334*	98	polyketide synthase	WP_194054994
	450		*S. Kisseleviana NIES 73*	*S. sp. LEGE 00249*	99		MBC5793824.1
	451		*S. sp SIO1G1*	*S. LEGE 08334*	89		WP_194054994.1
	450		*S. FACHB 1194*	*S. sp. LEGE 00249*	99		MBC5793824.1
	450		*S. LEGE 08334*	*S. torques reginae ITEP024*	98		WP_220610683
	450		*S. sp. LEGE 00249*	*S. torques reginae ITEP024*	98		WP_220610683
	450		*S. sp. LEGE 00249*	*S. torques reginae ITEP024*	98		WP_220610683

HglE	1826	polyketide synthase	S. torques reginae ITEP024	S. LEGE 08334	99	polyketide synthase	WP_220611797.1
	1807		S.Kisseleviana NIES 73	S.Aphanizomenoids	99		WP_193941129.1
	1788		S. sp SIO1G1	S. torques reginae ITEP024	80		WP_220611797.1
	1801		S. FACHB 1194	S.Kisseleviana NIES 73	99		WP_096572232.1
	1793		S. LEGE 08334	S. torques ITEP024	99		WP_220611797.1
	1802		S. sp. LEGE 00249	S.kisseleviana NIES73	99		WP_096572232.1
HglG	334	Polyketide synthase	S. torques reginae ITEP024	S. LEGE 08334	99	NAD-dependent epimerase/dehyd ratase	WP_194054998.1
	334		S. Kisseleviana NIES 73	S. sp. LEGE 00249	100		WP_18703495.1
	334		S. sp SIO1G1	S. sp. LEGE 00249	85		WP_187038495.1
	334		S. FACHB 1194	S. LEGE 00249	100		WP_187038495.1
	334		S. LEGE 08334	S. torques reginae ITEP024	99		WP_220610678.1
	334		S. sp. LEGE 00249	S. LEGE 08334	99		WP_194054998.1
HetR	299	Heterocyst differentiation control protein	S. torques reginae ITEP024	S. sp. LEGE 08334	100	Heterocyst differentiation control protein	QYX31586.1
	299		S. torques reginae ITEP024	S. LEGE 00249	99	Heterocyst differentiation control protein	MBC5794768.1
	299		S. torques reginae ITEP024	S. sp. SIO1G1	96	Heterocyst differentiation	NET01886.1

HetN		SDR family NAD(P)-dependent oxidoreductase				control protein	
	263		S. torques reginae ITEP024	S. LEGE 08334	99	SDR family NAD(P)-dependent oxidoreductase	WP_194057199.1
	263		S. torques reginae ITEP024	S. LEGE 08334	99		WP_194057199.1
	267		S. torques reginae ITEP024	S. Kisseleviana NIES 73	95		WP_096572227.1
	267		S. Kisseleviana NIES 73	S. torques reginae ITEP024	94		WP_220610687.1
	267		S. sp SIO1G1	S. LEGE 08334	80		WP_194054985.1
	267		S. FACHB 1194	S. Kisseleviana NIES 73	99		WP_096572227.1
	267		S. LEGE 08334	S. Kisseleviana NIES 73	94		WP_096572227.1
	267		S. sp. LEGE 00249	S. Kisseleviana NIES 73	100		WP_096572227.1

Supplementary Table S6. Proposed function of the proteins encoded by the nitrogen fixation biosynthetic gene cluster in the genomes of Sphaerospermopsis strains.

Protein	Aminoacids	Proposed function	Strain	Organism	Identity (%)	Function	Acession number
FeoA	90	FeoA family protein	*S. LEGE 00249*	*S. kisseleviana NIES-73*	93	Iron transporter FeoA	BAZ80902.1
	115	FeoA family protein	S. kisseleviana NIES-73	S. LEGE 00249	93	Iron transporter FeoA	MBC5796910.1
	83	FeoA family protein	S. sp. SIO1G1	S. LEGE 00249	75	Iron transporter FeoA	MBC5796910.1
	99	Ferrodixin (2Fe-2S)	*S. torquees reginae ITEP-024*	*S. LEGE 08334*	99	Iron transporter FeoA	MBE9054910.1
	99	Ferrodixin (2Fe-2S)	*S. torquees reginae ITEP-024*	*S. sp. SIO1G1*	82	Iron transporter FeoA	NET00481.1
FdxH	99	Ferrodixin (2Fe-2S)	*S. LEGE 08334*	*S. torquees reginae ITEP-024*	*99*	Ferredoxin (2Fe-2S)	QYX31309.1
	99	Ferrodixin (2Fe-2S)	*S. torquees reginae ITEP-024*	S. LEGE 08334	*99*	Ferredoxin (2Fe-2S)	MBE9054910.1
FdxN	112	4Fe-4S binding protein	S. Kisseleviana NIES 73	S. sp SIO1G1	85	Ferredoxin(4Fe-4S)	NET02523.1

HesA	259	UBA/THIF-type NAD/FAD binding protein	*S. torques ITEP024*	*S. LEGE 08334*	100	HesA/MoeB	MBE9054908.1
	259	UBA/THIF-type NAD/FAD binding protein	*S. torques ITEP024*	*S. sp SIO1G1*	95	HesA/MoeB	NET00479.1
HesB	121	Iron-sulfur cluster assembly acessory protein	*S. sp. SIO1G1*	S. LEGE 00249	85	Fe-S cluster assembly protein HesB	MBC5796912.1
NifD	460	Nitrogenase molybdenum-ion protein alpha chain	*S. torques reginae ITEP-024*	*S.* LEGE *00249*	99	Nitrogenase molybdenum-iron protein alpha chain	MBC5795059.1
NifE	455	Nitrogenase MoFe cofactor biosynthesis protein	*S. torques reginae ITEP-024*	*S.* kisseleviana NIES-73	99	Nitrogenase molybdenum-cofactor biosynthesis protein NifE	BAZ80912.1
	455	Nitrogenase MoFe cofactor biosynthesis protein	*S. torques reginae ITEP-024*	*S. sp.* LEGE 08334	99	Nitrogenase MoFe cofactor biosynthesis protein NifE	MBE9054902.1
	455	Nitrogenase MoFe cofactor biosynthesis protein	*S. torques reginae ITEP-024*	*S.* sp. FACHB 1194	99	Nitrogenase MoFe cofactor biosynthesis protein NifE	MBD2144569.1
	455	Nitrogenase MoFe cofactor biosynthesis protein	*S. torques reginae ITEP-024*	*S.* LEGE *00249*	99	Nitrogenase MoFe cofactor biosynthesis protein NifE	MBC5796919.1

	455	Nitrogenase MoFe cofactor biosynthesis protein	*S. torques reginae ITEP-024*	*S.* sp SIO1G1	99	Nitrogenase MoFe cofactor biosynthesis protein NifE	NET02491.1
NifB	478	Nitrogenase cofactor biosynthesis protein	*S. torques ITEP024*	*S. LEGE 08334*	100	Nitrogenase cofactor biosynthesis protein NifB	MBE9059234.1
	478	Nitrogenase cofactor biosynthesis protein	*S. torques ITEP024*	*S. sp. LEGE 00249*	99	Nitrogenase cofactor biosynthesis protein NifB	MBC5795050.1
	478	Nitrogenase cofactor biosynthesis protein	*S. torques ITEP024*	*S.* sp SIO1G1	94	Nitrogenase cofactor biosynthesis protein NifB	NET02524.1
NifW	105	Nitrogen fixation protein	*S. torques* ITEP024	*S. sp. LEGE 00249*	98	Nitrogenase stabilizing/protective protein	MBC5796914.1
	105	Nitrogen fixation protein	*S. torques* ITEP024	*S.* sp SIO1G1	78	Nitrogenase stabilizing/protective protein	NET00478.1
NifX	139	Nitrogen fixation protein	*S. sp SIO1G1*	*S. sp. LEGE 00249*	88	Dinitrogenase iron-molybdenum cofactor biosynthesis	MBC5796917.1
NifN	442	Nitrogenase molybdenum-ion	*S. torques* ITEP024	*S. sp.* LEGE 08334	100	Nitrogenase molybdenum-	MBE9054903.1

		cofactor biosynthesis protein NifN				cofactor biosynthesis protein NifN	
	442	Nitrogenase molybdenum-ion cofactor biosynthesis protein NifN	*S. torques* ITEP024	*S. sp*. LEGE 00249	98	Nitrogenase molybdenum-cofactor biosynthesis protein NifN	MBC5796918.1
	442	Nitrogenase molybdenum-ion cofactor biosynthesis protein NifN	*S. torques* ITEP024	*S.* FACHB-1194	98	Nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	MBD2144570.1
	442	Nitrogenase molybdenum-ion cofactor biosynthesis protein NifN	*S. torques ITEP024*	*S.* sp SIO1G1	91	Nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	NET02490.1
NifK	511	Nitrogenase molybdenum-ion protein beta chain	*S. torques* ITEP024	S. sp LEGE 08334	100	Nitrogenase molybdenum-iron protein subunit beta	MBE9054900.1
NifU	300	Fe-S cluster assembly protein NifU	*S. torques ITEP024*	*S. sp. LEGE 08334*	100	Fe-S cluster assembly protein NifU	MBE9059231.1
	308	Fe-S cluster assembly protein NifU	*S. torques ITEP024*	*S. sp SIO1G1*	92	Fe-S cluster assembly protein NifU	NET02521.1
NifS	403	Nitrogenase metalloclusters biosynthesis protein NifS	*S. torques ITEP024*	*S. sp. LEGE 08334*	99	Cysteine desulfurase NifS	MBE9059232.1

	403	Nitrogenase metalloclusters biosynthesis protein NifS	*S. torques ITEP024*	*S. kisseleviana NIES-73*	99	Cysteine desulfurase NifS	BAZ80945.1
	403	Nitrogenase metalloclusters biosynthesis protein NifS	*S. torques ITEP024*	*S. sp.* LEGE 00249	98	Cysteine desulfurase NifS	MBC5795052.1
	403	Nitrogenase metalloclusters biosynthesis protein NifS	*S. torques ITEP024*	S. sp SIO1G1	94	Cysteine desulfurase NifS	NET02522.1

Suplementary Table S7. Proposed function of the proteins encoded by anabaenopeptin biosynthetic gene cluster of the Sphaerospermopsis group.

Protein	Amino acids	Product	Strain	Organism	Identity (%)	Function	Acession number
aptA1	4161	Siderophore biosynthesis non-ribosomal peptide synthetase modules	*S. torques ITEP024*	*Aphanizomenon flos-aquae*	90	non-ribosomal peptide synthetase	WP_190382984.1
	4109		*S. Kisseleviana NIES 73*	*Dolichospermum sp. LEGE 00246*	83		WP_1939621
aptA2	2208	Polyketide synthase	*S. torques ITEP024*	*S. LEGE 08334*	97	Polyketide synthase	WP_194056036.1
	2226		*S. Kisseleviana NIES 73*	*S. FACHB 1194*	95		WP_190346674.1
	2186		*S. sp SIO1G1*	*S. LEGE 08334*	74		WP_194056036.1
	2224		*S. FACHB 1194*	*S. Kisseleviana NIES 73*	96		WP_096571779.1
	2212		*S. LEGE 08334*	*S. torques reginae ITEP024*	97		WP_220609901.1

aptB	1069	Siderophore biosynthesis non-ribosomal peptide	*S. torques ITEP024*	*S. LEGE 08334*	95	non-ribosomal peptide synthetase	WP_194056038.1
	1087		*S. Kisseleviana NIES 73*	*S. FACHB 1194*	95	amino acid adenylation	WP_242052557.1
	1074		*S. sp SIO1G1*	*S. torques ITEP024*	72	non-ribosomal peptide synthetase	WP_220609902.1
	1088		*S. FACHB 1194*	*S. Kisseleviana NIES 73*	95	non-ribosomal peptide synthetase	WP_096571778.1
	1073		*S. LEGE 08334*	*S. torques reginae ITEP024*	95	non-ribosomal peptide synthetase	WP_220609902.1
aptC	2576	Siderophore biosynthesis non-ribosomal peptide synthetase modules	*S. torques ITEP024*	*Nodularia spumigena*	90	non-ribosomal peptide synthetase	WP_063874470.1
	2587		*S. Kisseleviana NIES 73*	*Dolichospermum sp. LEGE 00246*	97	non-ribosomal peptide synthetase	WP_193962698.1
	2562		*S. sp SIO1G1*	*Aphanizomenonacea e cyanobacterium TIOX110*	74	amino acid adenylation	WZB86541.1
	2570		*S. FACHB 1194*	*S. Kisseleviana NIES 73*	81	non-ribosomal peptide synthetase	WP_096571777.1
	2200		*S. LEGE 08334*	*S. FACHB 1194*	78		WP_190346675.1

aptD	1415	Siderophore biosynthesis non-ribosomal peptide	*S. torques ITEP024*	*S. LEGE 08334*	88		WP_194056042.1
	1363		*S. Kisseleviana NIES 73*	*Dolichospermum*	93		WP_193962697.1
	1397		*S. sp SIO1G1*	*Aphanizomenonacea e cyanobacterium TIOX110*	74	amino acid adenylation	WZB86542.1
	1419		*S. FACHB 1194*	*S. Kisseleviana NIES 73*	84		WP_272110476.1
	1420		*S. LEGE 08334*	*S. torques reginae ITEP024*	88	non-ribosomal peptide synthetase	WP_220609905.1
aptE	392	2-isopropylmalate synthase	*S. torques ITEP024*	*S. FACHB 1194*	98	2-isopropylmalate synthase	WP_190346677.1
	392		*S. LEGE 08334*	*S. Kisseleviana NIES 73*	93		WP_272110474.1
	253		*S. Kisseleviana NIES 73*	*S. FACHB 1194*	100		MBD2144629.1
	392		*S. LEGE 08334*	*S. Kisseleviana NIES 73*	93		WP_272110474.1
aptF	813	ATP-binding cassette	*S. FACHB 1194*	*Sphaerospermopsis reniformis*	95	ATP-binding cassette	GCL35044.1
	761		*S. sp SIO1G1*	*Okeanomitos corallinicola*	73		WZB86544.1
	803		*S. torques ITEP024*	*S. FACHB 1194*	86		WP_190346678
	761		*S. Kisseleviana NIES 73*	*S. LEGE 08334*	94		MBE9057071.1
	769		*S. LEGE 08334*	*S. Kisseleviana NIES 73*	94		BAZ82708.1

Suplementary Table S8. Proposed function of the proteins encoded by Sphaerociclamida biosynthetic gene cluster

Protein	Amino acids	Product	Strain	Organism	Identity (%)	Function	Acession number
sphG	710	cyanobactin maturation protease	*S. sp. LEGE 00249*	*Aphanizomenon gracile PMC638.10*	95	cyanobactin maturation protease	MDM3844803.1
sphF	290	LynF/TruF/PatF family peptide O-prenyltransferase	*S. sp. LEGE 00249*	*Chrysosporum ovalisporum Ak1311*	99	LynF/TruF/PatF family peptide O-prenyltransferase	MDH6088854.1
sphE	47	anacyclamide/piricyclamide	*S. sp. LEGE 00249*	*Dolichospermum sp. JUN01*	97	anacyclamide/piricyclamide	MBO1057685.1
sphA	667	cyanobactin maturation protease	*S. sp. LEGE 00249*	*Sphaerospermopsis aphanizomenoides*	95	cyanobactin maturation protease	MBE9236410.1

Suplementary Table S9. Proposed function of the proteins encoded by Nocuolin biosynthetic gene cluster

Protein	Aminoacids	Product	Strain	Organism	Identity (%)	Function	Acession number
nocT	597	AarF/ABC1/UbiB kinase family protein	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	99	AarF/ABC1/UbiB kinase family protein	MBE9236862.1
nocS	2101	tectonin domain-containing protein	*S. sp. LEGE 00249*	*S. FACHB 1194*	96	tectonin domain-containing protein	WP_242052555.1
nocR	426	NocR	*S. sp. LEGE 00249*	*Nostoc sp. CCAP 1453/38*	82	NocR	AKL71651.1
nocQ	2325	Oxidoreductase	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	99	oxidoreductase	MBE9235326.1
nocP	1286	Polyketide synthase	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	99	polyketide synthase	MBE9235325.1
nocO	452	hypothetical protein	*S. sp. LEGE*	*S. Aphanizomenoids*	87	Hypothetical protein	MBE9235324.1

			00249				
nocM	92	acyl carrier protein	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	92	*acyl carrier protein*	MBE9235322.1
nocN	471	hypothetical protein	*S. sp. LEGE 00249*	*Anabaena sp. PCC 7108*	87	Hypothetical protein	WP_016949101.1
nocK	397	DUF3419 family protein	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	99	DUF3419 family protein	MBE9235319
nocJ	349	NocJ	*S. sp. LEGE 00249*	*Nostoc sp. CCAP 1453/38*	89	NocJ	AKL71643.1
nocI	372	acyl-CoA dehydrogenase	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	100	acyl-CoA dehydrogenase	MBE9235317.1
nocH	698	AMP-binding protein	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	100	AMP-binding protein	MBE9235316.1
nocG	347	3-oxoacyl-[acyl-carrier-protein] synthase	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	99	3-oxoacyl-[acyl-carrier-protein] synthase III	MBE9235315.1
nocF	872	aminotransferase	*S. sp. LEGE 00249*	*S. aphanizomenoides BCCUSP55*	89	aminotransferase	MBK1987674
nocE	486	NAD(P)-binding	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	100	NAD(P)-binding	MBE9235313.1
nocD	231	Isoprenylcysteine carboxylmethyltransferase	*S. sp. LEGE 00249*	*S. Aphanizomenoids*	100	Isoprenylcysteine carboxylmethyltransferase	MBE9235312.1
nocB	184	NocB	*S. sp. LEGE 00249*	*Nostoc sp. CCAP 1453/38*	89	NocB	AKL71634.1
nocA	214	NocA	*S. sp. LEGE 00249*	*Nostoc sp. CCAP 1453/38*	90	NocA	AKL71633.1

Suplementary Table S10. Proposed function of the proteins encoded by the saxitoxin biosynthetic gene cluster from the *Sphaerospermopsis* group.

Protein	Amino acids	Product	Strain	Organism	Identity (%)	Function	Acession number
	266	Phytanoyl-CoA dioxygenase	*S. torques ITEP024*	*S. LEGE 08334*	100	phytanoyl-CoA dioxygenase	WP_194055575.1
sxtJ	747	carbamoyltransferase	*S. torques ITEP024*	*S. LEGE 08334*	100	carbamoyltransferase	MBE9056840.1
sxtK	54	DUF5989	*S. torques ITEP024*	*Nostoc sp. ChiQUE01a*	89	DUF5989	MDZ8239473.1
sxtJ	747	carbamoyltransferase	*S. LEGE 08334*	*S. torques ITEP024*	100	carbamoyltransferase	QYX30560.1
sxtK	54	DUF5989	*S. LEGE 08334*	*Nostoc sp. ChiQUE01a*	89	DUF5989	MDZ8239473.1
	747	Nodulation protein nolO	*S. torques ITEP024*	*S. LEGE 08334*	100	SxtJ family membrane protein	WP_194055576
	108	hypothetical protein	*S. torques ITEP024*	*S. LEGE 08334*	100	macrolide family glycosyltransferase	WP_194055579.1
	385	Carbamoyl-phosphate synthase small chain	*S. torques ITEP024*	*S. LEGE 08334*	99	glutamine-hydrolyzing carbamoyl-phosphate	WP_194055594.1

Supplementary Table S11. Proposed function of the proteins encoded by heterocyte glycolipid biosynthetic gene cluster and two proteins involved in the regulation of heterocyte differentiation in the genomes of the *C. raciborskii* .

Protein	Aminoacids	Product	Strain	Organism	Identity (%)	Function	Acession number
HglA	577	2-nitropropane dioxygenase	*C. raciborskii CS-505*	*C. raciborskii CS-505*	99	2-nitropropane dioxygenase, NPD	EFA69444.1
	577		*C. raciborskii CS-508*	*C. raciborskii CS-505*	99		EFA69444.1
	577		*C. raciborskii CR12*	*C. raciborskii CS-505*	99		EFA69444.1
	577		*C. raciborskii CENA302*	*C. raciborskii MVCC14*	99		OHY31851.1
	577		*C. raciborskii ITEP-A1*	*C. raciborskii MVCC14*	99		OHY31851.1

	577		*C. raciborskii MVCC14*	*C. raciborskii CR12*	97		EFA69444.1
	577		*C. raciborskii CR12*	*C. raciborskii CHAB3438*	100		MCH4905695.1
	577		*C. raciborskii CR12*	*C. curvispora GIHE-G8*	98		QNP28543.1
	577		*C. raciborskii CR12*	*S. SIO1G1*	80		NET02811.1
	577		*C. raciborskii CR12*	*S. kisseleviana NIES-73*	84		BAZ83237.1
	577		*C. raciborskii CR12*	*S. torques reginae ITEP-024*	84		QYX32837.1
	577		*C. raciborskii CR12*	*S. LEGE 08334*	84		MBE9056527.1
	577		*C. raciborskii CR12*	*S. LEGE 00249*	84		MBC5793826.1
HglB	507	Polyketide synthase	*C. raciborskii CS-508*	*C. raciborskii CS-505*	100	Polyketide synthase HetM	EFA69445.1
	507		*C. raciborskii CS-508*	*C. raciborskii CS-505*	99	Polyketide synthase HetM	<u>EFA69445.1</u>
	507		*C. raciborskii CR12*	*C. raciborskii CS-505*	100	Polyketide synthase HetM	EFA69445.1
	507		*C. raciborskii CENA302*	*C. raciborskii MVCC14*	100	Polyketide synthase	OHY31850.1
	507		*C. raciborskii ITEP-A1*	*C. raciborskii MVCC14*	99	Polyketide synthase	OHY31850.1
	507		*C. raciborskii MVCC14*	*C. raciborskii CS-505*	96	Polyketide synthase HetM	EFA69445.1
HglC	1104	Polyketide synthase	*C. raciborskii CS-508*	*C. raciborskii CS-505*	100	HglC (Beta-ketoacyl synthase)	EFA69443.1
	1104		*C. raciborskii CS-508*	*C. raciborskii CR12*	99	Polyketide synthase	KRH97007.1
	1104		*C. raciborskii CR12*	*C. raciborskii CS-508*	99		OHY37860.1
	1100		*C. raciborskii CENA302*	*C. raciborskii MVCC14*	99		OHY31852.1
	1100		*C. raciborskii ITEP-A1*	*C. raciborskii MVCC14*	99		OHY31852.1
	1100		*C. raciborskii MVCC14*	*C. raciborskii CS-508*	97		OHY37860.1

HglD	453	Polyketide synthase	*C. raciborskii CS-508*	*C. raciborskii CS-505*	100	Heterocyst glycolipid synthase HglD	EFA69442.1
	453		*C. raciborskii CS-508*	*C. raciborskii CS-505*	99	Heterocyst glycolipid synthase HglD	EFA69442.1
	453		*C. raciborskii CR12*	*C. raciborskii CS-505*	100	Heterocyst glycolipid synthase HglD	EFA69442.1
	453		*C. raciborskii CENA302*	*C. raciborskii CS-505*	98	Heterocyst glycolipid synthase HglD	EFA69442.1
	453		*C. raciborskii ITEP-A1*	*C. raciborskii MVCC14*	99	Polyketide synthase	OHY31853.1
	453		*C. raciborskii MVCC14*	*C. raciborskii CS-505*	98	Heterocyst glycolipid synthase HglD	EFA69442.1
HglE	1771	Polyketide synthase	*C. raciborskii CS-508*	*C. raciborskii CS-505*	100	Beta-ketoacyl synthase	EFA69440.1
	1771		*C. raciborskii CS-508*	*C. raciborskii CS-505*	99	Beta-ketoacyl synthase	EFA69440.1
	1771		*C. raciborskii CR12*	*C. raciborskii CS-505*	98	Beta-ketoacyl synthase	EFA68870.1
	1751		*C. raciborskii CENA302*	*C. raciborskii MVCC14*	99	Beta-ketoacyl synthase	OHY34297.1
	1751		*C. raciborskii ITEP-A1*	*R. brookii D9*	95	Beta-ketoacyl synthase	EFA74388.1
	1751		*C. raciborskii MVCC14*	*R. brookii D9*	96	Beta-ketoacyl synthase	EFA74388.1

HglG	585	Polyketide synthase	*C. raciborskii CS-508*	*C. raciborskii CS-505*	100	Putative ketoreductase and dehydrase (HglG)	EFA69441.1
	585		*C. raciborskii CS-508*	*C. raciborskii CS-505*	99	Putative ketoreductase and dehydrase (HglG)	EFA69441.1
	585		*C. raciborskii CR12*	*C. raciborskii CS-508*	99	Polyketide synthase	OHY37862.1
	585		*C. raciborskii CENA302*	*C. raciborskii MVCC14*	100	Polyketide synthase	OHY31854.1
	585		*C. raciborskii ITEP-A1*	*C. raciborskii MVCC14*	100	Polyketide synthase	OHY31854.1
	585		*C. raciborskii MVCC14*	*C. raciborskii CS-508*	97	Polyketide synthase	OHY37862.1
HetR	299	Heterocyte differentiation control protein	*C. raciborskii CS-505*	*C. raciborskii CS-505*	100	Heterocyst differentiation control protein	EFA68362.1
	299		*C. raciborskii CS-508*	*C. raciborskii CS-505*	100	Heterocyst differentiation control protein	EFA683621
	299		*C. raciborskii CR12*	*C. raciborskii CS-505*	100	Heterocyst differentiation control protein	EFA68362.1
	299		*R. brookii D9*	*C. raciborskii CENA303*	99	Heterocyst differentiation control	OSO91885.1

					protein	
299		*C. raciborskii CENA303*	*R. brookii D9*	99	Heterocyst differentiation control protein	EFA73115.1
299		*C. raciborskii CENA302*	*C. raciborskii CS-505*	100	Heterocyst differentiation control protein	EFA68362.1
299		*C. raciborskii ITEP-A1*	*C. raciborskii CS-505*	100	Heterocyst differentiation control protein	EFA68362.1
299		*C. raciborskii MVCC14*	*C. raciborskii CS-505*	100	Heterocyst differentiation control protein	EFA68362.1
299		*C. raciborskii CS-505*	*C. curvispora GIHE-G8*	100	Heterocyst differentiation control protein	QNP30904.1
299		*C. raciborskii CS-505*	*S. LEGE 08334*	90	Heterocyst differentiation control protein	MBE9057199.1
299		*C. raciborskii CS-505*	*S. torques reginae ITEP-024*	90	Heterocyst differentiation control protein	QYX31586.1
299		*C. raciborskii CS-505*	*S. LEGE 00249*	89	Heterocyst differentiation control protein	MBC5794768.1
299		*C. raciborskii CS-505*	*S. SIO1G1*	88	Heterocyst differentiation control protein	NET01886.1
241		*C. raciborskii CS-505*	*C. raciborskii CS-505*	100	SDR family NAD(P)-dependent oxidoreductase	EFA70572.1

HetN	241	SDR family NAD(P)-dependent oxidoreductase	*C. raciborskii CS-508*	*C. raciborskii CS-505*	100	SDR family NAD(P)-dependent oxidoreductase	EFA70572.1
	241		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	SDR family NAD(P)-dependent oxidoreductase	EFA70572.1
	241		*R. brookii D9*	*C. raciborskii CENA303*	99	Short-chain dehydrogenase	OSO94107.1
	241		*C. raciborskii CENA303*	*R. brookii D9*	99	Short-chain dehydrogenase/reductase SDR	EFA73007.1
	241		*C. raciborskii CENA302*	*C. raciborskii MVCC14*	100	Short-chain dehydrogenase	OHY31780.1
	241		*C. raciborskii ITEP-A1*	*C. raciborskii MVCC14*	99	Short-chain dehydrogenase	OHY31780.1
	241		*C. raciborskii MVCC14*	*C. raciborskii CENA302*	100	Short-chain dehydrogenase	OPH09154.1

Supplementary Table S12. Proposed function of the proteins encoded by the nitrogen fixation biosynthetic gene cluster in the genomes of the Cylindrospermopsis strains.

Protein	Aminoacids	Proposed function	Strain	Organism	Identity (%)	Function	Acession number
FeoA	86	FeoA family protein	*C. raciborskii CS-505*	*R. brookii CR12*	99	Iron transporter FeoA	KRH97483.1
	86		*C. raciborskii CS-508*	*R. brookii CR12*	100	Iron transporter FeoA	KRH97483.1
	86		C. raciborskii GIHE 2018	*R. brookii CR12*	99	Iron transporter FeoA	TPX29624.1
	86		C. raciborskii CR2010	*R. brookii CR12*	99	Iron transporter FeoA	UJL32789.1
	86		C. raciborskii KLL07	*R. brookii CR12*	99	Iron transporter FeoA	UJS05248.1

	86		C. raciborskii CHAB3438	*R. brookii CR12*	99	Iron transporter FeoA	MCH4904046.1
	86		*C. raciborskii CS-508*	*R. brookii CR12*	100	Iron transporter FeoA	KRH97483.1
	86		C. raciborskii DSH	*R. brookii CR12*	99	Iron transporter FeoA	WP_057177527.1
	86		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	Iron transporter FeoA	EFA68726.1
	86		*C. raciborskii CENA302*	*C. raciborskii CS-505*	99	Iron transporter FeoA	EFA68726.1
	86		*C. raciborskii CS-505*	*S. sp SIO1G1*	71	Iron transporter FeoA	NET00482.1
	86		*C. raciborskii CS-505*	*S. LEGE 00249*	72	Iron transporter FeoA	MBC5796910.1
	86		*C. raciborskii CS-505*	*C. raciborskii DSH*	99	Iron transporter FeoA	MEE6161293.1
FdxH	99	Ferrodixin (2Fe-2S)	*C. raciborskii CS-505*	*C. raciborskii CR12*	100	Ferredoxin	KRH97484.1
	99		*C. raciborskii CS-508*	*C. raciborskii CS-505*	100	Ferredoxin (2Fe-2S)	EFA68727.1
	99		*C. raciborskii CR12*	*C. raciborskii CS-505*	100	Ferredoxin (2Fe-2S)	EFA68727.1
	99		*C. raciborskii CENA302*	*C. raciborskii CS-505*	99	Ferredoxin (2Fe-2S)	EFA68727.1
	99		*C. raciborskii ITEP-A1*	*C. raciborskii MVCC14*	100	Ferredoxin	OHY36357.1
	99		*C. raciborskii MVCC14*	*C. raciborskii CS-505*	99	Ferredoxin (2Fe-2S)	EFA68727.1
	99		*C. raciborskii CHAB 3438*	*C. raciborskii CS-505*	99	Ferredoxin (2Fe-2S)	MCH4904045.1
	99		*C. raciborskii DSH*	*C. raciborskii CS-505*	99	Ferredoxin (2Fe-2S)	MEE6161294.1

	99		*C. raciborskii GIHE 2018*	*C. raciborskii CS-505*	99	Ferredoxin (2Fe-2S)	TPX29625
	99		*C. raciborskii KLL07*	*C. raciborskii CS-505*	99	Ferredoxin (2Fe-2S)	UJS05249.1
	99		*C.raciboskii CR2010*	*C. raciborskii CS-505*	99	Ferredoxin (2Fe-2S)	UJL32790.1
fdxN	130	Ferrodixin (2Fe-2S)	*C. raciborskii CS-505*	*C. raciborskii CR12*	100	Ferredoxin	KRH97498.1
	130		*C. raciborskii CS-508*	*C. raciborskii CS-505*	100	Ferredoxin-like protein in nif region protein, fdxN	EFA68741.1
	130		*C. raciborskii CR12*	*C. raciborskii CS-505*	100	Ferredoxin-like protein in nif region protein, fdxN	EFA68741.1
	112		*C. raciborskii CENA302*	*C. raciborskii CS-505*	94	Ferredoxin-like protein in nif region protein, fdxN	EFA68741.1
	112		*C. raciborskii ITEP-A1*	*C. raciborskii CS-505*	94	Ferredoxin-like protein in nif region protein, fdxN	EFA68741.1
	112		*C. raciborskii MVCC14*	*C. raciborskii CS-505*	94	Ferredoxin-like protein in nif region protein, fdxN	EFA68741.1
	112		*C. raciborskii DSH*	*C. curvispora GIHE G1*	96	Ferredoxin-like protein in nif region protein, fdxN	MEE6161308.1
	112		*C. raciborskii CR12*	*S. Kisseleviana NIES 73*	85	Ferredoxin-like protein in nif region protein, fdxN	BAZ80946.1

	112		*C. raciborskii CR12*	*S. sp SIO1G1*	*80*	Ferredoxin-like protein in nif region protein, fdxN	NET02523.1
HesA	259	UBA/THIF-type NAD/FAD binding protein	*C. raciborskii CS-505*	*C. raciborskii CR12*	100	Protein hesA	KRH97486.1
	259		*C. raciborskii CS-508*	*C. raciborskii CS-505*	100	MoeZ/MoeB	EFA68729.1
	259		*C. raciborskii CR12*	*C. raciborskii CS-505*	100	MoeZ/MoeB	EFA68729.1
	259		*C. raciborskii CENA302*	*C. raciborskii CS-505*	99	MoeZ/MoeB	EFA68729.1
	259		*C. raciborskii ITEP-A1*	*C. raciborskii CS-505*	98	MoeZ/MoeB	EFA68729.1
	259		*C. raciborskii MVCC14*	*C. raciborskii CS-505*	99	MoeZ/MoeB	EFA68729.1
	259		*C. raciborskii DSH*	*C. curvispora GIHE G1*	99	HesA/MoeB	MEE6161296.1
	259		*C. raciborskii CHAB 3438*	*C. curvispora GIHE G1*	99	Protein hesA	MCH4904043.1
	259		*C. raciborskii GIHE 2018*	*C. curvispora GIHE G1*	99	HesA/MoeB	TPX29627.1
	259		*C.raciboskii CR2010*	*C. curvispora GIHE G1*	99	HesA/MoeB	UJL32792.1
	259		*C. raciborskii KLL07*	*C. curvispora GIHE G1*	99	HesA/MoeB	UJS05251.1
	259		*C. raciborskii CR12*	*S. LEGE 08334*	94	HesA/MoeB	MBE9054908
	259		*C. raciborskii CR12*	*S. torques ITEP024*	93	HesA/MoeB	CP080598.1
	259		*C. raciborskii CR12*	*S. sp SIO1G1*	93	HesA/MoeB	NET00479.1
HesB	121		*C. raciborskii CS-505*	*C. raciborskii CR12*	99	Fe-S cluster assembly protein HesB	KRH97485.1

	121		C. raciborskii CS-508	C. raciborskii CR12	100	Fe-S cluster assembly protein HesB	KRH97485.1
	121		C. raciborskii CR12	C. raciborskii CS-505	99	HesB/YadR/YfhF	EFA68728.1
	121		C. raciborskii CENA302	C. raciborskii CR12	97	Fe-S cluster assembly protein HesB	KRH97485.1
	138		C. raciborskii ITEP-A1	C. raciborskii MVCC14	100	Fe-S cluster assembly protein HesB	OHY36358.1
	121	Iron-sulfur cluster assembly acessory protein	C. raciborskii MVCC14	C. raciborskii CR12	97	Fe-S cluster assembly protein HesB	KRH97485.1
	121		C. raciborskii CHAB 3438	C. curvispora GIHE G1	92	Fe-S cluster assembly protein HesB	MCH4904044.1
	121		C. raciborskii DSH	C. curvispora GIHE G1	92	Fe-S cluster assembly protein HesB	MEE6161295.1
	121		C.raciboskii CR2010	C. curvispora GIHE G1	92	Fe-S cluster assembly protein HesB	UJL32791.1
	121		C. raciborskii KLL07	C. curvispora GIHE G1	92	Fe-S cluster assembly protein HesB	UJS05250
	121		C. raciborskii GIHE 2018	C. curvispora GIHE G1	92	Fe-S cluster assembly protein HesB	TPX29626.1
NifD	501	Nitrogenase molybdenum-ion protein alpha chain	C. raciborskii CS-505	C. raciborskii CR12	99	Nitrogenase molybdenum-iron protein alpha chain	KRH97494.1
	501	Nitrogenase molybdenum-ion protein alpha chain	C. raciborskii CS-508	C. raciborskii CS-505	100	Nitrogenase molybdenum-iron protein alpha chain	EFA68737.1
	501	Nitrogenase	C. raciborskii CR12	C. raciborskii	99	Nitrogenase	EFA68737.1

		molybdenum-ion protein alpha chain		*CS-505*		molybdenum-iron protein alpha chain	
	501	Nitrogenase molybdenum-ion protein alpha chain	*C. raciborskii CENA302*	*C. raciborskii CS-505*	99	Nitrogenase molybdenum-iron protein alpha chain	EFA68737.1
	501	Nitrogenase molybdenum-ion protein alpha chain	*C. raciborskii ITEP-A1*	*C. raciborskii MVCC14*	100	Nitrogenase molybdenum-iron protein alpha chain	OHY36367.1
	501	Nitrogenase molybdenum-ion protein alpha chain	*C. raciborskii MVCC14*	*C. raciborskii CS-505*	99	Nitrogenase molybdenum-iron protein alpha chain	EFA68737.1
	501	Nitrogenase molybdenum-ion protein alpha chain	*C. raciborskii DSH*	*C. curvispora GIHE G1*	100	Nitrogenase molybdenum-iron protein alpha chain	MEE6161304.1
	501	Nitrogenase molybdenum-ion protein alpha chain	*C. raciborskii GIHE 2018*	*C. curvispora GIHE G1*	100	Nitrogenase molybdenum-iron protein alpha chain	TPX29635.1
	501	Nitrogenase molybdenum-ion protein alpha chain	*C. raciborskii CR12*	*S. torques ITEP024*	96	Nitrogenase molybdenum-iron protein alpha chain	QYX31286.1
	501	Nitrogenase molybdenum-ion protein alpha chain	*C. raciborskii CR12*	*S. LEGE 00249*	96	Nitrogenase molybdenum-iron protein alpha chain	MBC5795059.1
	501						
NifE	460	Nitrogenase MoFe cofactor biosynthesis protein	*C. raciborskii CS-505*	*C. raciborskii CR12*	99	Nitrogenase molybdenum-cofactor biosynthesis protein NifE	KRH97492.1
	460		*C. raciborskii CS-508*	*C. raciborskii*	100	Nitrogenase MoFe	EFA68735.1

			CS-505		cofactor biosynthesis protein NifE	
460		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	Nitrogenase MoFe cofactor biosynthesis protein NifE	EFA68735.1
460		*C. raciborskii CENA302*	*C. raciborskii CR12*	99	Nitrogenase molybdenum-cofactor biosynthesis protein NifE	KRH97492.1
460		*C. raciborskii ITEP-A1*	*C. raciborskii CS-505*	99	Nitrogenase MoFe cofactor biosynthesis protein NifE	EFA68735.1
460		*C. raciborskii MVCC14*	*C. raciborskii CS-505*	99	Nitrogenase MoFe cofactor biosynthesis protein NifE	EFA68735.1
460		*C. raciborskii DSH* *C. curvispora GIHE-G1*		98	Nitrogenase MoFe cofactor biosynthesis protein NifE	MEE6161302.1
460		*C. raciborskii GIHE 2018*	*S. FACHB 1194*	95	Nitrogenase MoFe cofactor biosynthesis protein NifE	TPX29633.1
460		*C. raciborskii CR2010*	*C. curvispora GIHE- G1*	98	Nitrogenase MoFe cofactor biosynthesis protein NifE	UJL32798.1
460		*C. raciborskii KLL07*	*C. curvispora GIHE- G1*	98	Nitrogenase MoFe cofactor biosynthesis protein NifE	UJS05257.1
295	Nitrogenase iron protein NifH	*C. raciborskii CS-505*	*C. raciborskii CR12*	99	Nitrogenase reductase	KRH97495.1
295		*C. raciborskii CS-508*	*C. raciborskii*	100	Nitrogenase iron	EFA68738.1

Gene	Length	Description	Strain	Closest match	%	Protein	Accession
				CS-505		protein	
NifH	295		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	Nitrogenase iron protein	EFA68738.1
	295		*C. raciborskii CENA302*	*C. raciborskii CR12*	99	Nitrogenase reductase	KRH97495.1
	295		*C. raciborskii ITEP-A1*	*C. raciborskii CR12*	99	Nitrogenase reductase	KRH97495.1
	295		*C. raciborskii MVCC14*	*C. raciborskii CR12*	99	Nitrogenase reductase	KRH97495.1
	295		*C. raciborskii DSH*	*C. curvispora GIHE G1*	99	Nitrogenase reductase	MEE6161305.1
	295		*C. raciborskii GIHE 2018*	*C. curvispora GIHE G1*	99	Nitrogenase reductase	TPX29636.1
	295		*C. raciborskii CR2010*	*C. curvispora GIHE G1*	99	Nitrogenase reductase	UJL32801.1
	295						
	295		*C. raciborskii KLL07*	*C. curvispora GIHE G1*	99	Nitrogenase reductase	UJS05260.1
NifB	477	Nitrogenase cofactor biosynthesis protein	*C. raciborskii CS-505*	*C. raciborskii CR12*	100	Nitrogen fixation protein NifB	KRH97499.1
	477		*C. raciborskii CS-508*	*C. raciborskii CS-505*	100	Nitrogenase cofactor biosynthesis protein NifB	EFA68742.1

	477		C. raciborskii CR12	C. raciborskii CS-505	100	Nitrogenase cofactor biosynthesis protein NifB	EFA68742.1
	478		C. raciborskii CENA302	C. raciborskii MVCC14	100	Nitrogenase cofactor biosynthesis protein NifB	OHY36372.1
	478		C. raciborskii ITEP-A1	C. raciborskii CS-505	99	Nitrogenase cofactor biosynthesis protein NifB	EFA68742.1
	478		C. raciborskii MVCC14	C. raciborskii CS-505	99	Nitrogenase cofactor biosynthesis protein NifB	EFA68742.1
	477		C. curvispora GIHE G1	C. raciborskii DSH	99	Nitrogenase cofactor biosynthesis protein NifB	MEE6161309.1
	477		C. curvispora GIHE G1	C. raciborskii CS-508	98	Nitrogenase cofactor biosynthesis protein NifB	OHY32534.1
	477		C. curvispora GIHE G1	C. raciborskii CR2010	98	Nitrogenase cofactor biosynthesis protein NifB	UJL32805.1
	477		C. curvispora GIHE G1	C. raciborskii KLL07	98	Nitrogenase cofactor biosynthesis protein NifB	UJS05264.1
	477		S. LEGE 08334	S. torques ITEP024	100	Nitrogenase cofactor biosynthesis protein NifB	WP_220609327.1
	477		S. torques ITEP024	S. LEGE 00834	100	Nitrogenase cofactor biosynthesis protein NifB	WP_194059990.1
	477		S. LEGE 08334	S. sp. LEGE 00249	99	Nitrogenase cofactor biosynthesis	WP_187039462

						protein NifB	
			S. torques ITEP024	*S. sp SIO1G1*	94	Nitrogenase cofactor biosynthesis protein NifB	NET02524.1
NifW	105	Nitrogen fixation protein	*C. raciborskii CS-505*	*C. raciborskii CR12*	100	Nitrogenase stabilizing/protective protein	KRH97487.1
	105		*C. raciborskii CS-508*	*C. raciborskii CS-505*	100	Nitrogen fixation protein NifW	EFA68730.1
	105		*C. raciborskii CR12*	*C. raciborskii CS-505*	100	Nitrogen fixation protein NifW	EFA68730.1
	105		*C. raciborskii CENA302*	*C. raciborskii CS-505*	96	Nitrogen fixation protein NifW	EFA68730.1
	105		*C. raciborskii ITEP-A1*	*C. raciborskii CS-505*	96	Nitrogen fixation protein NifW	EFA68730.1
	105		*C. raciborskii MVCC14*	*C. raciborskii CS-505*	96	Nitrogen fixation protein NifW	EFA68730.1
	105		*C. curvispora GIHE G1*	*C. raciborskii CHAB 3438*	94	Nitrogenase stabilizing/protective protein	KRH97487.1
	105		*C. curvispora GIHE G1*	*C. raciborskii DSH*	94	Nitrogenase stabilizing/protective protein	MEE6161297
	105		*C. curvispora GIHE G1*	*C. raciborskii CS-508*	94	Nitrogenase stabilizing/protective protein	OHY32546.1
	105		*C. curvispora GIHE G1*	C. raciborskii GIHE 2018	94	Nitrogenase stabilizing/protective protein	TPX29628.1
	105		*C. curvispora GIHE G1*	C. raciborskii CR2010	94	Nitrogenase stabilizing/protective protein	UJL32793.1

	105		*C. curvispora GIHE G1*	*C. raciborskii KLL07*	94	Nitrogenase stabilizing/protective protein	UJS05252.1
	105		*S. torques ITEP024*	*S. sp. LEGE 00249*	98	Nitrogenase stabilizing/protective protein	WP_187040960.1
	105		*S. sp. LEGE 00249*	*S. torques ITEP024*	98	Nitrogenase stabilizing/protective protein	WP_220609369.1
NifX	139	Nitrogen fixation protein	*C. raciborskii CS-505*	*C. raciborskii CR12*	100	Nitrogen fixation protein NifX	KRH97490.1
	139		*C. raciborskii CS-508*	*C. raciborskii CS-505*	100	Dinitrogenase iron-molybdenum cofactor biosynthesis	EFA68733.1
	139		*C. raciborskii CR12*	*C. raciborskii CS-505*	100	Dinitrogenase iron-molybdenum cofactor biosynthesis	EFA68733.1
	139		*C. raciborskii CENA302*	*C. raciborskii CS-505*	97	Dinitrogenase iron-molybdenum cofactor biosynthesis	EFA68733.1
	139		*C. raciborskii ITEP-A1*	*C. raciborskii CS-505*	97	Dinitrogenase iron-molybdenum cofactor biosynthesis	EFA68733.1
	139		*C. raciborskii MVCC14*	*C. raciborskii CS-505*	97	Dinitrogenase iron-molybdenum cofactor biosynthesis	EFA68733.1
	139		*C. curvispora GIHE G1*	*C. raciborskii CHAB 3438*	97	Nitrogen fixation protein NifX	MCH4904039
	139		*C. curvispora GIHE G1*	*C. raciborskii DSH*	97	Nitrogen fixation protein NifX	MEE6161300.1
	139		*C. curvispora GIHE G1*	*C. raciborskii*	97	Nitrogen fixation	UJL32796.1

			CR2010		protein NifX		
	139		*C. curvispora GIHE G1*	*C. raciborskii KLL07*	97	Nitrogen fixation protein NifX	UJS05255.1
	139		*C. curvispora GIHE G1*	*S. sp SIO1G1*	85	Nitrogen fixation protein NifX	NET02489.1
	139		*C. curvispora GIHE G1*	*S. sp. LEGE 00249*	92	Nitrogen fixation protein NifX	WP_187040961.1
NifN	443	Nitrogenase molybdenum-ion cofactor biosynthesis protein NifN	*C. raciborskii CS-505*	*C. raciborskii CR12*	100	Nitrogenase molybdenum-cofactor biosynthesis protein NifN	KRH97491.1
	443		*C. raciborskii CS-508*	*C. raciborskii CR12*	100	Nitrogenase molybdenum-cofactor biosynthesis protein NifN	KRH97491.1
	443		*C. raciborskii CR12*	*C. raciborskii CR12*	100	Nitrogenase molybdenum-cofactor biosynthesis protein NifN	KRH97491.1
	443		*C. raciborskii CENA302*	*C. raciborskii CR12*	100	Nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	KRH97491.1
	443		*C. raciborskii ITEP-A1*	*C. raciborskii CR12*	100	Nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	KRH97491.1
	443		*C. raciborskii MVCC14*	*C. raciborskii*	99	Nitrogenase iron-	KRH97491.1

	443			CR12		molybdenum cofactor biosynthesis protein NifN	
	443		*C. raciborskii CS-505*	*C. raciborskii CR12*	*100*	Nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	KRH97493.1
	443		*C. raciborskii CR12*	*C. raciborskii CHAB 3438*	100	Nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	MCH4904038.1
	443		*C. raciborskii CR12*	*C. raciborskii DSH*	100	Nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	MEE6161301.1
	443		*C. raciborskii CR12*	C. raciborskii GIHE 2018	100	Nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	TPX29632.1
	443		*C. raciborskii CR12*	C. raciborskii CR2010	100	Nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	UJL32797.1
	443		*C. raciborskii CR12*	C. raciborskii KLL07	100	Nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	UJS05256.1
	443		*C. curvispora GIHE G1*	*C. raciborskii CHAB 3438*	99	Nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	MCH4904038.1
	443		*C. curvispora GIHE G1*	*C. raciborskii*	99	Nitrogenase iron-	MEE6161301.1

			DSH		molybdenum cofactor biosynthesis protein NifN	
443		*C. curvispora GIHE G1*	C. raciborskii GIHE 2018	99	Nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	TPX29632.1
443		*C. curvispora GIHE G1*	C. raciborskii CR2010	99	Nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	UJL32797.1
443		*C. curvispora GIHE G1*	C. raciborskii KLL07	99	Nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	UJS05256.1
442		S. sp. LEGE 00249	S. torques reginae ITEP024	99	Nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	WP_220609367.1
442		S. sp. LEGE 00249	S. FACHB 1194	99	Nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	WP_190346642.1
442		S. torques reginae ITEP024	S. LEGE 08334	99	Nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	WP_194051913.1
442		S. FACHB 1194	S. sp. LEGE 00249	99	Nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	WP_187040962.1
511		*C. raciborskii CS-508*	C. raciborskii	100	Nitrogenase	EFA68736.1

			CS-505		molybdenum-iron protein beta chain	
511		C. raciborskii CR12	C. raciborskii CS-505	100	Nitrogenase molybdenum-iron protein beta chain	EFA68736.1
511		C. raciborskii CENA302	C. raciborskii CS-505	99	Nitrogenase molybdenum-iron protein beta chain	EFA68736.1
511		C. raciborskii ITEP-A1	C. raciborskii CS-505	99	Nitrogenase molybdenum-iron protein beta chain	EFA68736.1
511		C. raciborskii MVCC14	C. raciborskii CS-505	99	Nitrogenase molybdenum-iron protein beta chain	EFA68736.1
511		C. curvispora GIHE G1	C. raciborskii DSH	99	Nitrogenase molybdenum-iron protein beta chain	MEE6161303.1
511		C. curvispora GIHE G1	C. raciborskii GIHE 2018	99	Nitrogenase molybdenum-iron protein beta chain	TPX29634.1
511		C. curvispora GIHE G1	C. raciborskii CR2010	99	Nitrogenase molybdenum-iron protein beta chain	UJL32799.1
511		C. curvispora GIHE G1	C. raciborskii KLL07	99	Nitrogenase molybdenum-iron protein beta chain	UJS05258.1
511		S. LEGE 08334	S. torques reginae ITEP024	100	Nitrogenase molybdenum-iron protein beta chain	WP_220609365.1
511		S. torques reginae ITEP024	S. LEGE 08334	100	Nitrogenase molybdenum-iron protein beta chain	WP_194051907.1

NifU	308	Fe-S cluster assembly protein NifU	*C. raciborskii CS-505*	*C. raciborskii CR12*	99	Fe-S cluster assembly protein NifU	KRH97496.1
	308		*C. raciborskii CS-508*	*C. raciborskii CS-505*	100	Fe-S cluster assembly protein NifU	EFA68739.1
	308		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	Fe-S cluster assembly protein NifU	EFA68739.1
	308		*C. raciborskii CENA302*	*C. raciborskii CS-505*	97	Fe-S cluster assemblyprotein NifU	EFA68739.1
	308		*C. raciborskii ITEP-A1*	*C. raciborskii CS-505*	97	Fe-S cluster assembly protein NifU	EFA68739.1
	308		*C. raciborskii MVCC14*	*C. raciborskii CS-505*	97	Fe-S cluster assembly protein NifU	EFA68739.1
	308		*C. curvispora GIHE G1*	*C. raciborskii DSH*	97	Fe-S cluster assembly protein NifU	MEE6161306.1
	308		*S. LEGE 08334*	*S. torques reginae ITEP024*	100	Fe-S cluster assembly protein NifU	WP_220609329.1
	308		*S. torques reginae ITEP024*	*S. LEGE 08334*	100	Fe-S cluster assembly protein NifU	WP_194059988.1
	308		*S. LEGE 08334*	*S. sp SIO1G1*	92	Fe-S cluster assembly protein NifU	NET02521.1

	401			C. raciborskii CS-505	C. raciborskii CR12	100	Cysteine desulfurase NifS	KRH97497.1
	401			C. raciborskii CS-508	C. raciborskii CR12	100	Cysteine desulfurase NifS	KRH97497.1
	401			C. raciborskii CR12	C. raciborskii CS-505	100	Aromatic amino acid beta-eliminating lyase/threonine aldolase	EFA68740.1
NifS	401	Nitrogenase metalloclusters biosynthesis protein NifS		C. raciborskii CENA302	C. raciborskii CS-505	99	Aromatic amino acid beta-eliminating lyase/threonine aldolase	EFA68740.1
	401			C. raciborskii ITEP-A1	C. raciborskii CS-505	99	Aromatic amino acid beta-eliminating lyase/threonine aldolase	EFA68740.1
	401			C. raciborskii MVCC14	C. raciborskii CS-505	99	Aromatic amino acid beta-eliminating lyase/threonine aldolase	EFA68740.1
	401			C. curvispora GIHE G1	C. raciborskii DSH	99	Cysteine desulfurase NifS	MEE6161307.1
	401			C. curvispora GIHE G1	C. raciborskii GIHE 2018	99	Cysteine desulfurase NifS	TPX29638

	401		C. curvispora GIHE G1	C. raciborskii CR2010	99	Cysteine desulfurase NifS	UJL32803.1
	401		C. curvispora GIHE G1	C. raciborskii KLL07	99	Cysteine desulfurase NifS	UJS05262.1
	403		S. LEGE 08334	S. torques reginae ITEP024	99	Cysteine desulfurase NifS	WP_220609328.1
	403		S. Kisseleviana NIES 73	S. sp SIO1G1	94	Cysteine desulfurase NifS	NET02522.1
	403		S. torques reginae ITEP024	S. LEGE 08334	99	Cysteine desulfurase NifS	WP_194059993.1

Supplementary Table S13. Proposed function of proteins encoded by hassallidin gene cluster identified in the genomes of the C. raciborskii strains CENA303, PAMP 2012, KL1, KLL07, CR 2010, CS-505, CS-508, GIHE-2018, GIHE-G1, DSH, N8, CR12, 1523720, CYRF and S. torques reginae ITEP-024 como a única do gênero Sphaerospermopsis.

Protein	Aminoacids	Proposed function	Strain	Organism	Identity (%)	Function	Acession number
HasA	555	*ABC-transporter*	C. raciborskii CS-505	C. raciborskii CR12	99	ABC transporter ATP-binding protein	KRH96585.1
	555		C. raciborskii CS-508	C. raciborskii CS-505	99	ABC transporter-like protein	EFA70507.1
	555		C. raciborskii CR12	C. raciborskii CS-505	99	ABC transporter-like protein	EFA70507.1
	555		C. raciborskii CENA303	C. raciborskii CR12	88	ABC transporter ATP-binding protein	KRH96585.1
	555		C. raciborskii CR12	C. raciborskii CR2010	99	ABC transporter ATP-binding protein	UJL33519.1

	555			C. raciborskii CR12	C. raciborskii KLL07	99	ABC transporter ATP-binding protein	UJS03222.1
HasB	670	Alpha amylase	C. raciborskii CS-505	C. raciborskii CR12	97	Alpha amylase	KRH96572.1
	670		C. raciborskii CS-508	C. raciborskii CS-505	99	Alpha-amylase	EFA70488.1
	670		C. raciborskii CR12	C. raciborskii CS-505	97	Alpha amylase	EFA70488.1
	571		R. brookii D9	C. raciborskii CR12	79	Alpha amylase	KRH96572.1
	670		C. raciborskii CENA303	R. brookii D9	99	Alpha amylase	EFA73364.1
	329		C. raciborskii CENA302	C. raciborskii CR12	79	Alpha-amylase	KRH96572.1
	670		C. raciborskii CR12	C. curvispora GIHE G1	98	Alpha-amylase	WP_187706034.1
	210		C.raciboskii PAMP2012	C. raciborskii CR12	73	Alpha-amylase	KRH96572.1
	571		R. brookii D9	C.raciboskii PAMP2012	98	Alpha-amylase	MCZ2202904.1
	670		C. raciborskii GIHE 2018	C. curvispora GIHE G1	99	Alpha-amylase	WP_187706034.1
	670		C. raciborskii GIHE 2018	C. raciborskii CR12	98	Alpha-amylase	WP_057178215.1
	670		C. curvispora GIHEG1	C. raciborskii CR12	99	Alpha-amylase	WP_057178215.1
	670		C. raciborskii KLL07	C. raciborskii CR12	98	Alpha-amylase	WP_057178215.1

	670		*C. raciborskii KLL07*	*C. curvispora GIHEG1*	98	Alpha-amylase	WP_187706034.1
	670		*C. raciborskii N8*	*C. raciborskii CR12*	100	Alpha-amylase	WP_057178215.1
	670		*C. raciborskii N8*	*C. curvispora GIHEG1*	99	Alpha-amylase	WP_187706034.1
	502		*C. raciborskii PAMP2012*	*C. curvispora GIHEG1*	81	Alpha-amylase	WP_187706034.1
	502		*C. raciborskii PAMP2012*	*C. raciborskii CR12*	81	Alpha-amylase	WP_057178215.1
	523		*C. raciborskii 1523720*	*C. raciborskii CR12*	98	Alpha-amylase	WP_057178215.1
	523		*C. raciborskii 1523720*	*C. curvispora GIHEG1*	98	Alpha-amylase	WP_187706034.1
HasC	342	Methyltransferase	*C. raciborskii CS-505*	*C. raciborskii CR12*	95	Methyltransferase domain-containing protein	KRH96618.1
	342		*C. raciborskii CS-508*	*C. raciborskii CS-505*	98	Hypothetical protein	EFA70501.1
	361		*C. raciborskii CR12*	*C. raciborskii CS-505*	95	Hypothetical protein	EFA70501.1
	342		*R. brookii D9*	*C. raciborskii CS-505*	83	Methyltransferase domain-containing protein	OBU78171.1
	357		*C. raciborskii CENA303*	*C. raciborskii CR12*	95	Methyltransferase domain-containing protein	KRH96618.1
	344		*C. raciborskii CENA302*	*R. brookii D9*	93	Hypothetical protein	EFA73367.1
	342		*C. raciborskii CR12*	*C. raciborskii CHAB 3438*	99	Methyltransferase domain-containing protein	MCH4903615.1
	342		*C. raciborskii CS-508*	*C. raciborskii CHAB 3438*	97	Methyltransferase	MCH4903615.2

						domain-containing protein	
	71		*C.raciboskii PAMP2012*	*C. raciborskii CHAB 3438*	100	Methyltransferase domain-containing protein	MCH4903615.1
	372	acetylglucosamine	*C. raciborskii CR2010*	*C. curvispora GIHEG1*	97	acetylglucosamine	WP_187706020.1
	372		*C. raciborskii GIHE 2018*	*C. raciborskii CR12*	100	acetylglucosamine	WP_057178233.1
	372		*C. raciborskii GIHE 2018*	*C. curvispora GIHE G1*	97	acetylglucosamine	WP_187706020.1
	372		*C. curvispora GIHEG1*	*C. raciborskii CR12*	97	acetylglucosamine	WP_057178233.1
	372		*C. raciborskii N8*	*C. raciborskii CR12*	99	undecaprenyldiphospho-muramoylpentapeptide	WP_057178233
	372		*C. raciborskii N8*	*C. curvispora GIHEG1*	97	undecaprenyldiphospho-muramoylpentapeptide	WP_187706020.1
HasD	265	Glycosyl transferase family	*C. raciborskii CS-505*	*C. raciborskii CR12*	99	Glycosyl transferase family 2	KRH96581.1
	265		*C. raciborskii CS-508*	*C. raciborskii CS-505*	99	Glycosyl transferase family 2	EFA70500.1
	275		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	Glycosyl transferase family 2	EFA70500.1
	267		*C. raciborskii ITEP-A1*	*Anabaena sp. 90*	83	Glycosyl transferase family 2	AFW95739.1
	266		*C. raciborskii CR12*	*C. curvispora GIHE G1*	100	Glycosyl transferase family 2	QNP29407.1
	266		*C. raciborskii CR12*	*C. raciborskii GIHE 2018*	100	Glycosyl transferase family 2	TPX27091.1
	266	Dolichol-phosphate mannosyltransferase	*C. raciborskii GIHE 2018*	*C. raciborskii CENA303*	76	polyprenol monophosphomannose synthase	OSO97128.1

	266		*C. raciborskii GIHE 2018*	*C. raciborskii KL1*	76	polyprenol monophosphomannose synthase	MBG0742668.1
	266		*C. raciborskii GIHE 2018*	*C. raciborskii KL1*	76	polyprenol monophosphomannose synthase	MBG0742668.1
	266		*C. raciborskii GIHE 2018*	*C. raciborskii CENA303*	76	polyprenol monophosphomannose synthase	OSO97128.1
	266		*C. curvispora GIHEG1*	*C. raciborskii CENA303*	76	polyprenol monophosphomannose synthase	WP_141303791.1
	266	Dolichol-phosphate mannosyltransferase	*C. curvispora GIHEG1*	*C. raciborskii KL1*	76	polyprenol monophosphomannose synthase	MBG0742668.1
	265	Dolichol-phosphate mannosyltransferase	*C. raciborskii KLL07*	*C. raciborskii KL1*	77	polyprenol monophosphomannose synthase	MBG0742668.1
	265	Dolichol-phosphate mannosyltransferase	*C. raciborskii KLL07*	*C. raciborskii CENA303*	77	polyprenol monophosphomannose synthase	OSO97128.1
	266	Dolichol-phosphate mannosyltransferase	*C. raciborskii N8*	*C. raciborskii KL1*	76	polyprenol monophosphomannose synthase	MBG0742668.1
	266	Dolichol-phosphate mannosyltransferase	*C. raciborskii N8*	*C. raciborskii CENA303*	76	polyprenol monophosphomannose synthase	OSO97128.1
HasE	154	GtrA family protein	*C. raciborskii CS-505*	*C. raciborskii CR12*	100	Hypothetical protein	KRH96580.1
	151	GtrA family protein	*C. raciborskii CS-508*	*C. raciborskii CR12*	99	Hypothetical protein	KRH96580.1
	151		*C. raciborskii CR12*	*C. raciborskii CS-505*	100	Hypothetical protein	OBU77708.1

	184		*C. raciborskii CENA303*	*Scytonema hofmanni UTEX B 1581*	70	Hypothetical protein	WP_051502819.1
	184		*C. raciborskii ITEP-A1*	*Anabaena sp. 90*	68	GtrA-like protein	AFW95740.1
	197	Polyketide synthase	*C. raciborskii 1523720*	*C. raciborskii CR12*	96	non-ribosomal peptide synthetase	WP_057178252.1
	197	Polyketide synthase	*C. raciborskii 1523720*	*C. curvispora GIHEG1*	96	non-ribosomal peptide synthetase	WP_187706030.1
HasF	547	Putative membrane protein	*C. raciborskii CS-505*	*C. raciborskii CR12*	99	Dolichyl-phosphate-mannose-protein mannosyltransferase	KRH96579.1
	547		*C. raciborskii CS-508*	*C. raciborskii CS-505*	99	Dolichyl-phosphate-mannose-protein mannosyltransferase	OBU77709.1
	547		*C. raciborskii CR12*	*C. curvispora GIHEG1*	99	Dolichyl-phosphate-mannose-protein mannosyltransferase	WP_187706028.1
	547		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	Conserved hypothetical protein	EFA70498.1
	545		*C. raciborskii CENA303*	*Anabaena sp. 90*	68	Putative membrane protein	AFW95741.1
	62		*C. raciborskii CENA302*	*Anabaena sp. Syke748*	75	Putative membrane protein	AHZ20765.1
	547		*C. curvispora GIHEG1*	*C. raciborskii CR12*	99	Dolichyl-phosphate-mannose-protein mannosyltransferase	KRH96579.1
HasG	312	AMP-dependent synthetase/ligase	*C. raciborskii CENA303*	*Anabaena sp. 90*	87	AMP-dependent synthase/ligase	AFW95742.1
	452	Major facilitator transporter	*C. raciborskii CS-505*	*C. raciborskii CR12*	98	MFS transporter	KRH96587.1
	456		*C. raciborskii CR12*	*C. raciborskii CR2010*	98	MFS transporter	UJL33521.1
HasK	456		*C. raciborskii CR12*	*C. raciborskii CS- 508*	97	MFS transporter	OHY34101.1

	456		*C. raciborskii CR12*	*C. raciborskii CHAB 3438*	97	MFS transporter	MCH4903619.1
	456		*C. raciborskii CR12*	*C. curvispora GIHEG1*	96	MFS transporter	TPX27098.1
	456		*C. raciborskii CS-508*	*C. raciborskii CS-505*	99	Hypothetical protein	EFA70509.1
	452		*C. raciborskii CR12*	*C. raciborskii CS-505*	98	MFS transporter	OBU77700.1
	449		*R. brookii D9*	*C. raciborskii CS-505*	66	MFS transporter	OBU77700.1
	449		*C. raciborskii CENA303*	*C. raciborskii CS-505*	66	MFS transporter	OBU77700.1
	449		*C. raciborskii ITEP-A1*	*R. brookii D9*	96	Major facilitator superfamily MFS_1	EFA73366.1
	445	Long-chain-fatty-acid--CoA ligase	*C. raciborskii KLL07*	*Nostocaceae cyanobacterium*	92	MAG TPA: fatty acid-CoA ligase family protein	HLO88498
	444	hypothetical protein	*C. raciborskii KLL07*	*Nostocaceae cyanobacterium*	80	alpha/beta hydrolase-fold protein	HLO88501.1
HasL	254	3-oxoacyl-acyl-carrier-protein reductase	*C. raciborskii CS-505*	*C. raciborskii CR12*	99	3-oxoacyl-ACP reductase	KRH96575.1
	254		*C. raciborskii CS-508*	*C. raciborskii CS-505*	100	3-oxoacyl-ACP reductase	EFA70493.1
	254		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	3-oxoacyl-ACP reductase	EFA70493.1
	254		*C. raciborskii CENA303*	*C. raciborskii CS-505*	87	3-oxoacyl-ACP reductase	EFA70493.1
	254		*C. raciborskii CR12*	*S. torques reginae ITEP024*	87	3-oxoacyl-ACP reductase	WP_220609295.1
	254		*C. raciborskii CS-505*	*S. torques reginae ITEP024*	87	3-oxoacyl-ACP reductase	WP_220609295.1
	254		*C. raciborskii CR2010*	*S. torques ITEP024*	87	3-oxoacyl-ACP reductase	WP_220609295.1
	254		*C. raciborskii GIHE 2018*	*S. torques ITEP024*	87	3-oxoacyl-ACP reductase	WP_220609295.1
	254		*C. raciborskii KLL07*	*S. torques ITEP024*	87	3-oxoacyl-ACP reductase	WP_220609295.1

	254		*C. raciborskii N8*	*S. torques ITEP024*	87	3-oxoacyl-ACP reductase	WP_220609295.1
	254		*C. raciborskii PAMP2012*	*S. torques ITEP024*	89	3-oxoacyl-ACP reductase	WP_220609295.1
	254		*C. raciborskii 1523720*	*S. torques ITEP024*	87	oxidoreductase	WP_220609295.1
	254		*S. torques ITEP024*	*Cronbergia sp. UHCC 0137]*	95	oxidoreductase	WP_323283647
HasM	192	Aspartyl/asparaginyl beta-hydroxylase	*C. raciborskii CS-505*	*C. raciborskii CR12*	99	Hydroxylase	KRH96574.1
	192		*C. raciborskii CS-508*	*C. raciborskii CS-505*	99	Aspartyl/asparaginyl beta-hydroxylase	EFA70492.1
	192		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	Hydroxylase	OBU77714.1
	204		*C. raciborskii CENA303*	*Anabaena sp. 90*	73	Aspartyl/asparaginyl beta-hydroxylase	AFW95748.1
	192		*C. raciborskii CR12*	*S. torques reginae ITEP024*	70	Aspartyl/asparaginyl beta-hydroxylase	WP_220609294.1
	197	Polyketide synthase	*C. raciborskii 1523720*	*C. raciborskii CR12*	96	Non-ribosomal peptide synthetase	WP_057178252.1
	197	Polyketide synthase	*C. raciborskii 1523720*	*C. curvispora GIHEG1*	96	Non-ribosomal peptide synthetase	WP_187706030.1
	3051		*C. raciborskii CS-505*	*C. raciborskii CR12*	98	Non-ribosomal peptide	KRH96616.1

						synthetase	
	2824	NRPS	*C. raciborskii CS-508*	*C. raciborskii CR12*	96	Non-ribosomal peptide synthetase	KRH96616.1
	3049		*C. raciborskii CR12*	*C. raciborskii CS-505*	98	Non-ribosomal peptide synthetase	OBU77715.1
	3050		*C. raciborskii CENA303*	*C. raciborskii CS-505*	71	Non-ribosomal peptide synthetase	OBU77715.1
	3049		*C. raciborskii CR2010*	*C. raciborskii CR12*	99	Non-ribosomal peptide synthetase	WP_072149121.1
	3049		*C. raciborskii CR2010*	*C. raciborskii CS505*	97	Non-ribosomal peptide synthetase	EFA70490.1
	3049		*C. raciborskii CR2010*	*S. torques ITEP024*	70	Non-ribosomal peptide synthetase	WP_220609293.1
	3049		*C. raciborskii GIHE 2018*	*C. curvispora GIHE G1*	99	Non-ribosomal peptide synthetase	WP_187706032.1
	3049		*C. raciborskii GIHE 2018*	*C. raciborskii CR12*	99	Non-ribosomal peptide synthetase	WP_072149121.1
	3049		*C. curvispora GIHEG1*	*C. raciborskii CR12*	99	Non-ribosomal peptide synthetase	WP_072149121.1
HasN	3049	NRPS	*C. curvispora GIHEG1*	*C. raciborskii CS505*	97	Non-ribosomal peptide synthetase	EFA70490.1
	3050		*C. raciborskii KLL07*	*C. curvispora GIHEG1*	99	Non-ribosomal peptide synthetase	WP_187706032.1
	3050		*C. raciborskii KLL07*	*C. raciborskii CR12*	98	Non-ribosomal peptide synthetase	WP_072149121.1
	3050		*C. raciborskii KLL07*	*C. raciborskii CS505*	96	Non-ribosomal peptide synthetase	EFA70490
	3050		*C. raciborskii KLL07*	*S. torques ITEP024*	71	Non-ribosomal peptide synthetase	WP_220609293.1
	3049		*C. raciborskii N8*	*C. curvispora GIHEG1*	99	Non-ribosomal peptide synthetase	WP_187706032.1

	3049		*C. raciborskii N8*	*C. raciborskii CR12*	100	Non-ribosomal peptide synthetase	WP_072149121.1
	3049		*C. raciborskii N8*	*C. raciborskii CS505*	98	Non-ribosomal peptide synthetase	EFA70490.1
	3050		*C. raciborskii PAMP2012*	*C. curvispora GIHEG1*	*71*	Non-ribosomal peptide synthetase	WP_187706032.1
	3050		*C. raciborskii PAMP2012*	*C. raciborskii CR12*	*71*	Non-ribosomal peptide synthetase	*WP_072149121.1*
	3055		*C. raciborskii 1523720*	*C. raciborskii CR12*	*94*	Non-ribosomal peptide synthetase	*WP_072149121.1*
	3055		*C. raciborskii 1523720*	*C. raciborskii CS505*	*95*	Non-ribosomal peptide synthetase	*EFA70490.1*
	3056		*S. torques ITEP024*	*Cronbergia sp. UHCC 0137]*	*85*	Non-ribosomal peptide synthetase	WP_323283649.1
HasO	3661	NRPS	*C. raciborskii CR12*	*C. raciborskii CS-505*	100	Non-ribosomal peptide synthase	EFA70489.1
	3670		*C. raciborskii CENA303*	*C. raciborskii CR12*	72	Non-ribosomal peptide synthase	KRH96573.1
	3049		*C. raciborskii CR12*	*C. curvispora GIHEG1*	97	Non-ribosomal peptide synthase	WP_187706032.1
	3049		*C. raciborskii CR12*	*C. raciborskii CS-505*	100	Non-ribosomal peptide synthase	EFA70490.1
	3049		*C. raciborskii CR12*	*S. torques reginae ITEP024*	71	Non-ribosomal peptide synthase	WP_220609293.1
	3662		*C. raciborskii CR2010*	*C. raciborskii CR12*	97	Non-ribosomal peptide synthase	WP_057178216.1
	3659		*C. raciborskii GIHE 2018*	*C. raciborskii CR12*	97	Non-ribosomal peptide synthase	WP_057178216.1
	3659		*C. curvispora GIHEG1*	*C. raciborskii CR12*	97	Non-ribosomal peptide synthase	WP_057178216.1
	3662		*C. raciborskii KLL07*	*C. curvispora GIHEG1*	99	Non-ribosomal peptide	WP_187706033.

						synthase	1
	3662		*C. raciborskii KLL07*	*C. raciborskii CR12*	97	Non-ribosomal peptide synthase	WP_057178216.1
	3661		*C. raciborskii N8*	*C. raciborskii CR12*	100	Non-ribosomal peptide synthase	WP_057178216.1
	3661		*C. raciborskii N8*	*C. curvispora GIHEG1*	97	Non-ribosomal peptide synthase	WP_057178216.1
	3670		*C. raciborskii PAMP2012*	C. raciborskii CR12	72	Non-ribosomal peptide synthase	*WP_057178216.1*
	3670		*C. raciborskii PAMP2012*	C. curvispora GIHEG1	72	Non-ribosomal peptide synthase	*WP_187706033.1*
	3660		*C. raciborskii 1523720*	C. raciborskii CR12	95	non-ribosomal peptide synthetase	*WP_057178216.1*
	3660		*C. raciborskii 1523720*	C. curvispora GIHEG1	94	non-ribosomal peptide synthetase	*WP_187706033*
HasP	354	NAD-dependent epimerase dTDP-glucose 4,6-dehydratase	*C. raciborskii CS-505*	*C. raciborskii CR12*	99	NAD-dependent epimerase	KRH96583.1
	354		*C. raciborskii CR12*	*C. curvispora GIHEG1*	100	NAD-dependent epimerase/dehydratase	WP_187706027.1
	354		*C. raciborskii CS-505*	*C. curvispora GIHEG1*	99	NAD-dependent epimerase/dehydratase	WP_187706027.1
	354		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	NAD-dependent epimerase/dehydratase	EFA70505.1
	352		*C. raciborskii CENA303*	*Anabaena sp. 90*	84	NAD dependent epimerase/dehydratase	AFW95751.1
	370		*C. raciborskii CR2010*	C. raciborskii CR12	99	NAD-dependent epimerase/dehydratase	WP_057178224.1
	370		*C. raciborskii GIHE 2018*	C. raciborskii CR12	99	NAD-dependent epimerase/dehydratase	WP_057178224.1
	370		*C. raciborskii GIHE 2018*	C. curvispora GIHE G1	99	NAD-dependent epimerase/dehydratase	WP_187706027.1
	370		*C. curvispora*	*C. raciborskii CR12*	94	NAD-dependent	WP_057178224.

			GIHEG1			epimerase/dehydratase	1
	370		*C. raciborskii KLL07*	*C. curvispora GIHEG1*	100	NAD-dependent epimerase/dehydratase	WP_187706027
	370		*C. raciborskii KLL07*	*C. raciborskii CR12*	100	NAD-dependent epimerase/dehydratase	WP_057178224.1
	354		*C. raciborskii N8*	*C. raciborskii CR12*	100	NAD dependent epimerase/dehydratase	WP_057178224.1
	354		*C. raciborskii N8*	*C. curvispora GIHEG1*	99	NAD dependent epimerase/dehydratase	WP_187706027.1
	352		*C. raciborskii PAMP2012*	*Anabaena cylindrica*	82	NAD-dependent epimerase/dehydratase	WP_323309738.1
HasQ	402	Glycosyltransferase	*C. raciborskii CS-505*	*C. raciborskii CR12*	99	MGT family glycosyltransferase	KRH96584.1
	402		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	Hypothetical protein	EFA70506.1
	73		*C. raciborskii CENA303*	*C. raciborskii CS-505*	90	MGT family glycosyltransferase	OBU77703.1
	402		*C. raciborskii CS-505*	*S. torques reginae ITEP024*	83	MGT family glycosyltransferase	WP_220609292.1
	402		*C. raciborskii CR2010*	*S. torques ITEP024*	82	Glycosyl transferase	WP_220609292.1
	402		*C. raciborskii GIHE 2018*	*S. torques ITEP024*	72	Glycosyl transferase	WP_220609292.1
	402		*C. curvispora GIHEG1*	*S. torques ITEP024*	83	Glycosyl transferase	WP_220609292.1
	402		*C. raciborskii KLL07*	*S. torques ITEP024*	83	Glycosyl transferase	WP_220609292.1
	402		*C. raciborskii CR12*	*S. torques reginae ITEP024*	83	Glycosyl transferase	WP_220609292.1
	402		*C. raciborskii*	*S. torques ITEP024*	82	Glycosyl transferase	WP_220

			N8				609292.1
	408	Putative acyltransferase	*S. torques ITEP024*	*Dolichospermum sp. UHCC 0352*	91	Glycosyl transferase	WP_168 652019.1
HasR	206		*C. raciborskii CENA303*	*Anabaena sp. 90*	68	Hypothetical protein	WP_015080900.1
HasT	245	Glycosyl transferase	*C. raciborskii CS-505*	*C. raciborskii CR12*	99	Glycosyl transferase	KRH96578.1
	245		*C. raciborskii CS-508*	*C. raciborskii CS-505*	100	Glycosyl transferase	EFA70497.1
	245		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	Putative glycosyltransferase	EFA70497.1
	245		*C. raciborskii CR12*	*C. curvispora GIHEG1*	99	Glycosyl transferase	WP_187706029.1
	258		*C. raciborskii CENA303*	*C. raciborskii CR12*	79	Glycosyl transferase	KRH96578.1
	258		*C. raciborskii CR12*	*C. raciborskii PAMP2012*	79	Glycosyl transferase	MCZ2202044.1
	315		*S. torques ITEP024*	*C. raciborskii*	88	Glycosyl transferase	WP_324140027.1
HasU	72	Putative MbtH-like protein	*C. raciborskii CS-505*	*C. raciborskii CR12*	100	Antibiotic synthesis protein MbtH	KRH96576.1
	72		*Cylindrospermopsis CR12*	*S. torques reginae ITEP024*	84	Antibiotic synthesis protein MbtH	WP_220609290.1
	72		*C. raciborskii CS-508*	*C. raciborskii CS-505*	98	Putative MbtH-like protein	EFA70494.1
	72		*C. raciborskii CS-505*	*C. raciborskii DSH*	100	Putative MbtH-like protein	MEE6162471
	72		*C. raciborskii CS-505*	*C. raciborskii CR12*	100	Putative MbtH-like protein	KRH96576.1
	72		*C. raciborskii CS-505*	*C. raciborskii CS-508*	100	Antibiotic synthesis protein MbtH	OHY35853.1

	72		*C. raciborskii CS-505*	*C. curvispora GIHEG1*	100	Putative MbtH-like protein	TPX27085.1
	72		*C. raciborskii CS-505*	*C. raciborskii CR2010*	100	MbtH family NRPS accessory protein	UJL33506.1
	72		*C. raciborskii CS-505*	*C. raciborskii KLL07*	100	MbtH family NRPS accessory protein	UJS03236.1
	72		*C. raciborskii CR12*	*C. raciborskii CS-505*	100	Putative MbtH-like protein	EFA70494.1
	73		*C. raciborskii CENA303*	*Anabaena sp. 90*	87	MbtH-like protein	AFW95756.1
	72		*C. raciborskii CR2010*	*S. torques ITEP024*	84	MbtH family protein	WP_220609290.1
	72		*C. raciborskii GIHE 2018*	*S. torques ITEP024*	72	MbtH family protein	WP_220609290.1
	72		*C. curvispora GIHEG1*	*S. torques ITEP024*	84	MbtH family protein	WP_220609290.1
	72		*C. raciborskii KLL07*	*S. torques ITEP024*	84	MbtH family protein	WP_220609290.1
	72		*C. raciborskii N8*	*S. torques ITEP024*	84	MbtH family protein	WP_220609290.1
	73		*C. raciborskii PAMP2012*	*S. torques ITEP024*	94	MbtH family protein	WP_220609290
	72		*C. raciborskii 1523720*	*S. torques ITEP024*	84	MbtH family protein	WP_220609290.1
	71		*S. torques ITEP024*	*Cronbergia sp. UHCC 0137]*	96	MbtH-like NRPS chaperone	WP_323283663.1
HasV	2153	NRPS	*C. raciborskii CS-505*	*C. raciborskii CR12*	97	Non-ribosomal peptide synthase	KRH96577.1
	2127		*C. raciborskii CS-508*	*C. raciborskii CR12*	99	Non-ribosomal peptide synthase	KRH96577.1
	2153		*C. raciborskii CR12*	*C. curvispora GIHEG1*	99	Non-ribosomal peptide synthase	WP_187706031.1

	2153			C. raciborskii CR12	C. raciborskii CR2010	99	amino acid adenylation domain-containing protein	UJL33507.1
	2153			C. raciborskii CR12	C. raciborskii KLL07	99	amino acid adenylation domain-containing protein	UJS06337.1
	2153			C. raciborskii CR12	S. torques reginae ITEP024	74	Non-ribosomal peptide synthase	WP_220609291.1
	2153			C. raciborskii CR12	C. raciborskii KL1	98	amino acid adenylation domain-containing protein	MBG0742686.1
	2153			C. raciborskii CR12	C. raciborskii CS-505	97	Non-ribosomal peptide synthase	EFA70495.1
	2147			C. raciborskii CENA303	Anabaena sp. 90	73	Non-ribosomal peptide synthase	AFW95757.1
	2153			C. raciborskii GIHE 2018	C. raciborskii CR2010	100	amino acid adenylation	UJL33507.1
	2153			C. raciborskii GIHE 2018	C. raciborskii CR12	99	Non-ribosomal peptide synthase	WP_057178219
	2153			C. raciborskii GIHE 2018	C. curvispora GIHE G1	99	Non-ribosomal peptide synthase	WP_187706031.1
	2153			C. raciborskii GIHE 2018	C. raciborskii KLL07	100	Non-ribosomal peptide synthase	UJS06337.1
	2153			C. raciborskii GIHE 2018	S. torques ITEP024	74	Non-ribosomal peptide synthase	WP_220609291.1
	2153			C. curvispora GIHEG1	C. raciborskii CR12	100	Non-ribosomal peptide synthase	WP_057178219.1
	2153			C. curvispora GIHEG1	C. raciborskii CR2010	100	Non-ribosomal peptide synthase	UJL33507.1
	2153			C. curvispora GIHEG1	C. raciborskii KLL07	99	Non-ribosomal peptide synthase	UJS06337.1
	2153			C. curvispora	S. torques ITEP024	74	Non-ribosomal peptide	WP_220609291.

			GIHEG1			synthase	1
	2153		*C. raciborskii KLL07*	*C. raciborskii CR2010*	100	Non-ribosomal peptide synthase	UJL33507.1
	2153		*C. raciborskii KLL07*	*C. raciborskii CR12*	99	Non-ribosomal peptide synthase	WP_057178219.1
	2153		*C. raciborskii KLL07*	*C. curvispora GIHEG1*	99	Non-ribosomal peptide synthase	WP_187706031.1
	2153		*C. raciborskii KLL07*	*S. torques ITEP024*	74	Non-ribosomal peptide synthase	WP_220609291.1
	2153		*C. raciborskii N8*	*C. raciborskii CR12*	100	Non-ribosomal peptide synthase	WP_057178219.1
	2153		*C. raciborskii N8*	*C. curvispora GIHEG1*	99	Non-ribosomal peptide synthase	WP_187706031.1
	2153		*C. raciborskii N8*	*C. raciborskii CR2010*	99	amino acid adenylation domain-containing protein	UJL33507.1
	2153		*C. raciborskii N8*	*C. raciborskii KLL07*	99	amino acid adenylation domain-containing protein	UJS06337.1
	2153		*C. raciborskii N8*	*S. torques ITEP024*	74	Non-ribosomal peptide synthase	WP_220609291.1
	2147		*C. raciborskii PAMP2012*	*C. raciborskii KL1*	98	amino acid adenylation	MBG0742686.1
	2147		*C. raciborskii PAMP2012*	*S. torques ITEP024*	77	Non-ribosomal peptide synthase	WP_220609291.1
	2153		*C. raciborskii 1523720*	*C. curvispora GIHEG1*	96	Non-ribosomal peptide synthase	WP_187706031.1
	2153		*C. raciborskii 1523720*	*C. raciborskii CR12*	95	Non-ribosomal peptide synthase	WP_057178219.1
	2153		*C. raciborskii 1523720*	*C. raciborskii CR2010*	95	amino acid adenylation	UJL33507.1

	2153		*C. raciborskii 1523720*	*C. raciborskii KLL07*	95	amino acid adenylation	UJS06337.1
	2142		*S. torques ITEP024*	*C. raciborskii KL1*	76	Non-ribosomal peptide synthase	WP_220609288.1
	1961		*S. torques ITEP024*	*C. curvispora GIHEG1*	74	Non-ribosomal peptide synthase	WP_187706033.1
	1961		*S. torques ITEP024*	*C. raciborskii CR12*	74	Non-ribosomal peptide synthase	WP_057178216.1
HasX	310	Glycosyltransferase	*C. raciborskii CR12*	*Anabaena sp. 90*	73	Glycosyl transferase family 2	AFW95759.1
	310		*C. raciborskii N8*	*S. torques ITEP024*	88	Glycosyltransferase	WP_220609289.1
	267		*C. raciborskii CENA303*	*Anabaena sp. 90*	83	Family 2 glycosyl transferase	AFW95739.1
	82	Hypothetical protein	*C. raciborskii CENA302*	*Scytonema hofmanni UTEX B 1581*	74	Hypothetical protein	WP_051502821.1
	82	Glycosyltransferase	*C. raciborskii PAMP2012*	*S. torques ITEP024*	83	Glycosyltransferase	WP_220609289.1
HasY	2874	NRPS	*C. raciborskii CS-505*	*C. raciborskii CR12*	90	Non-ribosomal peptide synthase	KRH96617.1
	2870		*C. raciborskii CS-508*	*C. raciborskii CR12*	96	Non-ribosomal peptide synthase	KRH96617.1
	2864		*C. raciborskii CR12*	*C. raciborskii CS-505*	90	Non-ribosomal peptide synthase	EFA70496.1
	2864		*C. raciborskii CR12*	*S. torques reginae ITEP024*	76	Non-ribosomal peptide synthase	WP_220609288.1
	2864		*C. raciborskii CR12*	*C. raciborskii KL1*	72	Non-ribosomal peptide	MBG0742682.1

					synthase	
2864		*C. raciborskii CR12*	*C. raciborskii CENA303*	72	Non-ribosomal peptide synthase	OSO88008.1
2863		*C. raciborskii CENA303*	*C. curvispora GIHEG1*	72	Non-ribosomal peptide synthase	WP_187706030.1
2864		*C. raciborskii GIHE 2018*	*C. curvispora GIHEG1*	100	Non-ribosomal peptide synthase	WP_187706030.1
2864		*C. raciborskii GIHE 2018*	*C. raciborskii CR12*	97	Non-ribosomal peptide synthase	WP_057178252.1
2864		*C. raciborskii GIHE 2018*	*C. raciborskii KL1*	72	Non-ribosomal peptide synthase	MBG0742682.1
2864		*C. raciborskii GIHE 2018*	*S. torques ITEP024*	76	Non-ribosomal peptide synthase	WP_220609288.1
2864		*C. raciborskii GIHE 2018*	*C. raciborskii CENA303*	72	Non-ribosomal peptide synthase	OSO88008.1
2864		*C. curvispora GIHEG1*	*C. raciborskii CR12*	97	Non-ribosomal peptide synthase	WP_057178252.1
2864		*C. curvispora GIHEG1*	*S. torques ITEP024*	76	Non-ribosomal peptide synthase	WP_220609288.1
2864		*C. raciborskii KLL07*	*C. curvispora GIHEG1*	100	Non-ribosomal peptide synthase	WP_220609288.1
2864		*C. raciborskii KLL07*	*C. raciborskii CR12*	98	Non-ribosomal peptide synthase	WP_220609288.1
2864		*C. raciborskii KLL07*	*S. torques ITEP024*	76	Non-ribosomal peptide synthase	WP_220609288.1
2864		*C. raciborskii N8*	*C. curvispora GIHEG1*	99	Non-ribosomal peptide synthase	WP_220609288.1
2864		*C. raciborskii N8*	*C. raciborskii CR12*	97	Non-ribosomal peptide synthase	WP_220609288.1
2864		*C. raciborskii N8*	*S. torques ITEP024*	76	Non-ribosomal peptide synthase	WP_220609288.1
2864		*C. raciborskii N8*	*C. raciborskii KL1*	72	amino acid adenylation	MBG0742682.1

						domain-containing protein	
	2864		*C. raciborskii N8*	*C. raciborskii CENA303*	72	Non-ribosomal peptide synthase	OSO88008.1
	2862		*C. raciborskii PAMP2012*	*S. torques ITEP024*	84	Non-ribosomal peptide synthase	WP_220609288.1
	2862		*C. raciborskii PAMP2012*	*C. raciborskii KL1*	98	Non-ribosomal peptide synthase	MBG0742682.1
	2862		*C. raciborskii PAMP2012*	*C. raciborskii CENA303*	99	Non-ribosomal peptide synthase	OSO88008.1
	2855		*S. torques ITEP024*	*C. raciborskii KL1*	84	Non-ribosomal peptide synthase	MBG0742686.1
	2855		*S. torques ITEP024*	*C. raciborskii CENA303*	84	Non-ribosomal peptide synthase	OSO88008.1
	2855		*S. torques ITEP024*	*C. curvispora GIHEG1*	76	Non-ribosomal peptide synthase	WP_187706030.1
	2855		*S. torques ITEP024*	*C. raciborskii CR12*	76	Non-ribosomal peptide synthase	WP_057178252.1
HasZ	431	Transporter	*C. raciborskii CS-505*	*Cylindrospermopsis CR12*	97	MFS transporter	KRH96586.1
	431		*C. raciborskii CS-505*	*C. curvispora GIHE G1*	97	MFS transporter	QNP29400.1
	431		*C. raciborskii CS-505*	*C. curvispora GIHE G1*	97	MFS transporter	QNP29400.1
	431		*C. raciborskii CS-505*	*C. curvispora GIHE G1*	97	Major facilitator superfamily MFS_0	QNP29400.1
	427		*C. raciborskii CS-508*	*C. raciborskii CS-505*	96	Major facilitator superfamily MFS_1	EFA70508.1
	431		*C. raciborskii CR12*	*C. raciborskii CS-505*	97	Major facilitator superfamily MFS_1	EFA70508.1
	431		*C. raciborskii CS-505*	*C. raciborskii CR12*	97	MFS transporter	WP_057178227.1
	429		C. raciborskii CENA303	*C. raciborskii CS-505*	68	MFS transporter	OBU77701.1

Supplementary Table S14. Proposed function of the proteins encoded by cylindrospermopsin biosynthetic gene cluster in the genomes of the *C. raciborskii* strains CS-505, CR12, DSH and CHAB-3438.

Protein	Amino acids	Proposed function	Strain	Organism	Identity(%)	Function	Acession number
CyrA	391	Amidinotransferase	*C. raciborskii CS-505*	*C. raciborskii AWT205*	100	Amidinotransferase	ABX60160.1
	391		*C. raciborskii CR12*	*C. raciborskii AWT205*	99	Amidinotransferase	ABX60160.1
	391		*C. raciborskii CHAB3438*	*C. raciborskii AWT205*	100	Amidinotransferase	ABX60160.1
CyrB	2917	NRPS/PKS	*C. raciborskii CS-505*	*C. raciborskii AWT205*	100	Mixed NRPS/PKS	ABX60161.1
	2917		*C. raciborskii CR12*	*C. raciborskii AWT205*	100	Mixed NRPS/PKS	ABX60161.1
	2917		*C. raciborskii CHAB3438*	*Raphidiopsis curvata HB1*	100	Mixed NRPS/PKS	AHN91606.1
CyrC	1667	PKS	*C. raciborskii CS-505*	*C. raciborskii AWT205*	99	Polyketide synthase	ABX60163.1
	1667		*C. raciborskii CR12*	*C. raciborskii AWT205*	99	Polyketide synthase	ABX60163.1
	1667		*C. raciborskii CHAB3438*	*Raphidiopsis curvata HB1*	100	Polyketide synthase	AHN91608.1
CyrD	1851	PKS	*C. raciborskii CS-505*	*C. raciborskii AWT205*	100	Polyketide synthase	ABX60152.1
	1876		*C. raciborskii*	*C. raciborskii*	99	Polyketide synthase	ABX60152.1

			CR12	AWT205			
	1876		*C. raciborskii CHAB3438*	*Raphidiopsis curvata HB1*	100	Polyketide synthase	AHN91609.1
CyrE	1888	PKS	*C. raciborskii CS-505*	*C. raciborskii AWT205*	99	Polyketide synthase	ABX60162.1
	1888		*C. raciborskii CR12*	*C. raciborskii AWT205*	99	Polyketide synthase	ABX60162.1
	1888		*C. raciborskii CHAB3438*	*Raphidiopsis curvata HB1*	100	Polyketide synthase	AHN91607.1
CyrF	1357	PKS	*C. raciborskii CS-505*	*C. raciborskii AWT205*	100	Polyketide synthase	ABX60153.1
	1357		*C. raciborskii CR12*	*C. raciborskii AWT205*	99	Polyketide synthase	ABX60153.1
	1357		*C. raciborskii CHAB3438*	*Raphidiopsis curvata CHAB1150*	100	Polyketide synthase	AFC35246.1
CyrG	478	Uracil ring formation	*C. raciborskii CS-505*	*C. raciborskii AWT205*	100	Putative uracil ring formation	ABX60154.1
	478		*C. raciborskii CR12*	*C. raciborskii AWT205*	99	Putative uracil ring formation	ABX60154.1
	478		*C. raciborskii CHAB3438*	*Raphidiopsis curvata HB1*	99	Putative uracil ring formation	AHN91611.1
CyrI	276	Hydroxylation of C-7	*C. raciborskii CS-505*	*C. raciborskii CHAB3438*	100	Putative 2-oxoglutarate-dependent iron oxygenase	AHN91588.1
	276		*C. raciborskii CS-505*	*C. raciborskii CR12*	99	Putative 2-oxoglutarate-dependent iron oxygenase	WP_057178790
	278		*C. raciborskii CR12*	*C. raciborskii CHAB3438*	99	Putative 2-oxoglutarate-dependent iron oxygenase	AHN91588.1
	276		*C. raciborskii CHAB3438*	*C. raciborskii CR12*	99	Putative 2-oxoglutarate-dependent iron oxygenase	WP_057178790.1

CyrK	465	Exporter	*C. raciborskii CS-505*	*C. raciborskii AWT205*	99	Multidrug exporter MatE	ABX60156.1
	465		*C. raciborskii CR12*	*C. raciborskii CS-505*	99	MATE family efflux transporter	OBU75962.1
	451		*C. raciborskii CHAB3438*	*Raphidiopsis curvata CHAB1150*	100	Multidrug exporter MatE	AFC35248.1
CyrL	249	Transposase	C. raciborskii CS-505	*C. raciborskii AWT205*	100	Transposase	ABX60157.1
	153		C. raciborskii CHAB3438	*C. raciborskii CR12*	98	Transposase	WP_161808566.1
CyrH	476	Uracil ring formation	*C. raciborskii CS-505*	*C. raciborskii AWT205*	100	Amidohydrolase	ABX60158.1
	476		*C. raciborskii CR12*	*C. raciborskii AWT205*	99	Amidohydrolase	ABX60158.1
	476		*C. raciborskii CHAB3438*	*Raphidiopsis curvata CHAB1150*	100	Amidohydrolase	AHN91614.1
CyrJ	259	Sulfotransferase	C. raciborskii CS-505	*C. raciborskii AWT205*	100	Putative sulfotransferase	ABX60159.1
	259		*C. raciborskii CR12*	*C. raciborskii AWT205*	99	Putative sulfotransferase	ABX60159.1
	261		*C. raciborskii CHAB3438*	*Raphidiopsis curvata HB1*	100	Putative sulfotransferase	AHN91615
CyrM	105	Transposase	*C. raciborskii CS-505*	*C. raciborskii AWT205*	97	Transposase protein	ABX60157.1
CyrN	219	Adenylyl-sulfate kinase	C. raciborskii CS-505	*C. raciborskii AWT205*	100	Adenylylsulfate kinase	ABX60164.1

CyrO	515	Regulator	*C. raciborskii CS-505*	*C. raciborskii AWT205*	99	Hypothetical protein	AHN91599.1

Supplementary Table S15. Proposed function of the proteins encoded by saxitoxin biosynthetic gene cluster in the genomes of the *C. raciborskii* strains *R. brookii* D9 , MVCC14, MVCC19,CENA302, ITEP-A1, and the CYRF.

Protein	Amino acids	Product	Strains	Organism	Identity(%)	Function	Acession number
SxtA	1245	PKS	*R. brookii D9*	*C. raciborskii T3*	99	Polyketide synthase-related protein	ABI75094.1
	1245		*C. raciborskii CENA302*	*C. raciborskii T3*	100	Polyketide synthase-related protein	ABI75094.1
	1245		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	100	Polyketide synthase-related protein	ABI75094.1
	1245		*C. raciborskii MVCC14*	*C. raciborskii T3*	100	Polyketide synthase-related protein	ABI75094.1
	1245		*C. raciborskii MVCC19*	*C. raciborskii T3*	99	Polyketide synthase-related protein	ABI75094.1
	860		*C. raciborskii CYRF*	*C. raciborskii T3*	99	polyketide synthase-related protein	ABI75094.1
SxtB	318	Cytidine deaminase	*R. brookii D9*	*C. raciborskii T3*	100	Cytidine deaminase	ABI75093.1
	318		*C. raciborskii CENA302*	*R. brookii D9*	100	SxtB	EFA72782.1
	318		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	100	Cytidine deaminase	ABI75093.1
	318		*C. raciborskii MVCC14*	*C. raciborskii T3*	100	Cytidine deaminase	ABI75093.1
	318		*C. raciborskii MVCC19*	*C. raciborskii T3*	89	Cytidine deaminase	WP_254011061.1

	318		*C. raciborskii CYRF*	*Heteroscytonema crispum UCFS10*	92	SxtB	AYN62266.1
SxtC	117	Regulatory	*R. brookii D9*	*C. raciborskii T3*	100	SxtC	ABI75092.1
	94		*C. raciborskii CENA302*	*C. raciborskii T3*	100	SxtC	ABI75092.1
	94		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	100	sxtC	ABI75092.1
	117		*C. raciborskii MVCC14*	*C. raciborskii T3*	100	sxtC	ABI75092.1
	94		*C. raciborskii MVCC19*	*Heteroscytonema crispum UCFS10*	91	sxtC	AYN62265.1
	117		*C. raciborskii CYRF*	*C. raciborskii T3*	100	sxtC	AYN62265.1
SxtD	252	Sterole desaturase-like protein	*R. brookii D9*	*C. raciborskii T3*	99	Sterole desaturase	ABI75089.1
	252		*C. raciborskii CENA302*	*R. brookii D9*	100	SxtD	EFA72785.1
	252		*C. raciborskii ITEP-A1*	*R. brookii D9*	100	SxtD	EFA72785.1
	252		*C. raciborskii MVCC14*	*R. brookii D9*	100	SxtD	EFA72785.1
SxtE	128	Unknown protein	*R. brookii D9*	*C. raciborskii T3*	99	SxtE	ABI75095.1
	45		*C. raciborskii CENA302*	*C. raciborskii T3*	100	SxtE	ABI75095.1
	45		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	100	SxtE	ABI75095.1
	128		*C. raciborskii MVCC14*	*C. raciborskii T3*	100	SxtE	ABI75095.1
	127		*C. raciborskii MVCC19*	*Microseira wollei*	88	SxtE	ACZ26228.1
	120		*C. raciborskii CYRF*	*Microseira wollei*	92	SxtE	ACZ26228.1

SxtF	471	MATE	*R. brookii D9*	*C. raciborskii T3*	99	Sodium-driven multidrug and toxic compound extrusion protein	ABI75096.1
	471		*C. raciborskii CENA302*	*C. raciborskii T3*	100	Sodium-driven multidrug and toxic compound extrusion protein	ABI75096.1
	471		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	100	Sodium-driven multidrug and toxic compound extrusion protein	ABI75096.1
	471		*C. raciborskii MVCC14*	*C. raciborskii T3*	100	Sodium-driven multidrug and toxic compound extrusion protein	ABI75096.1
	471		*C. raciborskii MVCC19*	*C. raciborskii T3*	100	Sodium-driven multidrug and toxic compound extrusion protein	ABI75096.1
	220		*C. raciborskii CYRF*	*Heteroscytonema crispum UCFS10*	83	SxtM1	AYN62272.1
SxtG	377	Amidinotransferase	*R. brookii D9*	*C. raciborskii T3*	100	Amidinotransferase	ABI75097.1
	377		*C. raciborskii CENA302*	*C. raciborskii T3*	100	Amidinotransferase	ABI75097.1
	377		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	100	Amidinotransferase	ABI75097.1
	377		*C. raciborskii MVCC14*	*C. raciborskii T3*	100	Amidinotransferase	ABI75097.1
	377		*C. raciborskii*	*C. raciborskii T3*	100	Amidinotransferase	ABI75097.1

			MVCC19				
	377		*C. raciborskii CYRF*	*C. raciborskii T3*	100	Amidinotransferase	ABI75097.1
SxtH	334	Phenylpropionate dioxygenase	*R. brookii D9*	*C. raciborskii T3*	100	Phenylpropionate dioxygenase	ABI75098.1
	334		*C. raciborskii CENA302*	*C. raciborskii T3*	100	Phenylpropionate dioxygenase	ABI75098.1
	334		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	100	Phenylpropionate dioxygenase	ABI75098.1
	334		*C. raciborskii MVCC14*	*C. raciborskii T3*	100	Phenylpropionate dioxygenase	ABI75098.1
	334		*C. raciborskii MVCC19*	*C. raciborskii T3*	100	Phenylpropionate dioxygenase	ABI75098.1
	334		*C. raciborskii CYRF*	*C. raciborskii T3*	100	Phenylpropionate dioxygenase	ABI75098.1
SxtI	612	Carbamoyltransferase	*R. brookii D9*	*C. raciborskii T3*	100	NodU/CmcH-related carbamoyltransferase	ABI75099.1
	596		*C. raciborskii CENA302*	*C. raciborskii T3*	99	NodU/CmcH-related carbamoyltransferase	ABI75099.1
	612		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	100	NodU/CmcH-related carbamoyltransferase	ABI75099.1
	612		*C. raciborskii MVCC19*	*C. raciborskii T3*	99	NodU/CmcH-related carbamoyltransferase	ABI75099.1
	612		*C. raciborskii CYRF*	*C. raciborskii T3*	99	NodU/CmcH-related carbamoyltransferase	ABI75099.1

SxtJ	147	Regulatory	*R. brookii D9*	*C. raciborskii T3*	100	SxtJ	ABI75100.1
	134		*C. raciborskii MVCC14*	*C. raciborskii T3*	99	SxtJ	ABI75100.1
	147		*C. raciborskii MVCC19*	*C. raciborskii MVCC14*	100	SxtJ	OHY34958.1
	147		*C. raciborskii CENA302*	*C. raciborskii MVCC14*	100	SxtJ	OHY34958.1
	147		*C. raciborskii CYRF*	*C. raciborskii MVCC14*	100	SxtJ	OHY34958.1
SxtK	54	Unknown protein	*C. raciborskii CENA302*	*C. raciborskii T3*	100	SxtK	ABI75101.1
	54		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	100	SxtK	ABI75101.1
	54		*C. raciborskii MVCC19*	*C. raciborskii T3*	100	SxtK	ABI75101.1
	54		*C. raciborskii CYRF*	*C. raciborskii T3*	100	SxtK	ABI75101.1
	54		*C. raciborskii MVCC14*	*C. raciborskii T3*	100	SxtK	ABI75101.1

SxtL	435	GDSL-lipase	*R. brookii D9*	*C. raciborskii T3*	100	GDSL-lipase	ABI75102.1
	407		*C. raciborskii CENA302*	*C. raciborskii T3*	99	GDSL-lipase	ABI75102.1
	420		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	99	GDSL-lipase	ABI75102.1
	419		*C. raciborskii MVCC14*	*C. raciborskii T3*	99	GDSL-lipase	ABI75102.1
	419		*C. raciborskii MVCC19*	*C. raciborskii T3*	99	GDSL-lipase	ABI75102.1
	432		*C. raciborskiiCYRF*	*C. raciborskii T3*	99	GDSL-lipase	ABI75102.1
SxtM	475	MATE	*R. brookii D9*	*C. raciborskii MVCC14*	99	SxtM, partial	AFQ99040.1
	429		*C. raciborskii CENA302*	*C. raciborskii MVCC14*	99	SxtM, partial	AFQ99040.1
	482		*C. raciborskii ITEP-A1*	*C. raciborskii T3*	99	Sodium-driven multidrug and toxic compound extrusion protein	ABI75103.1
	475		*C. raciborskii MVCC14*	*R. brookii D9*	99	SxtSUL	EFA72771.1
	475		*C. raciborskii MVCC19*	*C. raciborskii MVCC14*	99	SxtM	AFQ99040.1
	182		*C. raciborskii CYRF*	*C. raciborskii T3*	99	Sodium-driven multidrug and toxic compound extrusion protein	ABI75103.1

SxtN	302	Sulfotransferase	*R. brookii D9*	*Microseira wollei*	89	SxtSUL	ACG63834.1
	302		*C. raciborskii CENA302*	*R. brookii D9*	100	SxtSUL	EFA72773.1
	302		*C. raciborskii MVCC14*	*R. brookii D9*	100	SxtSUL	EFA72773.1
	270		*C. raciborskii CYRF*	*C. raciborskii T3*	100	SxtSUL	EFA72773.1
SxtO	200	Adenylylsulfate kinase	*R. brookii D9*	*C. raciborskii T3*	100	Adenylylsulfate kinase	ABI75115.1
	159		*C. raciborskii CENA302*	*R. brookii D9*	100	Adenylylsulfate kinase	EFA72764.1
	200		*C. raciborskii MVCC14*	*R. brookii D9*	100	Adenylylsulfate kinase	EFA72764.1
	200		*C. raciborskii MVCC19*	*C. raciborskii MVCC14*	100	Adenylylsulfate kinase	OHY34903.1
	200		*C. raciborskii MVCC19*	*C. raciborskii CENA302*	100	Adenylylsulfate kinase	OPH09277
	200		*C. raciborskii MVCC19*	*C. raciborskii T3*	100	Adenylylsulfate kinase	ABI75115.1
	200		*C. raciborskii CYRF*	*C. raciborskii T3*	100	Adenylylsulfate kinase	ABI75115.1
SxtP	408	RTX toxin	*R. brookii D9*	*C. raciborskii T3*	99	Putative saxitoxin-binding protein	ABI75114.1
	408		*C. raciborskii CENA302*	*C. raciborskii T3*	100	Putative saxitoxin-binding protein	ABI75114.1
	408		*C. raciborskii MVCC14*	*C. raciborskii T3*	100	Putative saxitoxin-binding protein	ABI75114.1
	408		*C. raciborskii MVCC19*	*C. raciborskii T3*	100	Putative saxitoxin-binding protein	ABI75114.1
	408		*C. raciborskii*	*C. raciborskii T3*	100	Putative saxitoxin-	ABI75114.1

			CYRF			binding protein	
SxtQ	258	Unknown protein	*R. brookii D9*	*C. raciborskii T3*	99	SxtQ	ABI75113.1
	239		*C. raciborskii CENA302*	*R. brookii D9*	100	SxtQ	EFA72766.1
	239		*C. raciborskii MVCC14*	*R. brookii D9*	100	SxtQ	EFA72766.1
	239		*C. raciborskii MVCC19*	*C. raciborskii T3*	100	SxtQ	EFA72766.1
	239		*C. raciborskii CYRF*	*C. raciborskii T3*	100	SxtQ	EFA72766.1
SxtR	258	Acyl transferase	*R. brookii D9*	*C. raciborskii T3*	100	Acyl-CoA N-acyltransferase	ABI75112.1
	258		*C. raciborskii CENA302*	*C. raciborskii T3*	100	Acyl-CoA N-acyltransferase	ABI75112.1
	258		*C. raciborskii MVCC14*	*C. raciborskii T3*	100	Acyl-CoA N-acyltransferase	ABI75112.1
	258		*C. raciborskii MVCC19*	*C. raciborskii T3*	100	Acyl-CoA N-acyltransferase	ABI75112.1
	258		*C. raciborskii CYRF*	*C. raciborskii T3*	100	Acyl-CoA N-acyltransferase	ABI75112.1
SxtS	241	Phytanoyl-CoA dioxygenase	*R. brookii D9*	*C. raciborskii T3*	99	Phytanoyl-CoA dioxygenase	ABI75110.1
	241		*C. raciborskii CENA302*	*R. brookii D9*	100	SxtS	EFA72768.1
	241		*C. raciborskii MVCC14*	*R. brookii D9*	100	SxtS	EFA72768.1
	241		*C. raciborskii MVCC19*	*C. raciborskii T3*	99	Phytanoyl-CoA dioxygenase	ABI75110
	241		*C. raciborskii CYRF*	*C. raciborskii T3*	100	Phytanoyl-CoA dioxygenase	ABI75110

SxtT	334	Phenylpropionate dioxygenase	*R. brookii D9*	*C. raciborskii T3*	99	Phenylpropionate dioxygenase	ABI75109.1
	334		*C. raciborskii CENA302*	*R. brookii D9*	100	SxtT	EFA72769.1
	334		*C. raciborskii MVCC14*	*R. brookii D9*	100	SxtT	EFA72769.1
	334		*C. raciborskii MVCC19*	*R. brookii D9*	100	SxtT	EFA72769.1
	334		*C. raciborskii CYRF*	*C. raciborskii T3*	100	Phenylpropionate dioxygenase	EFA72769.1
SxtU	248	Alcohol dehydrogenase	*R. brookii D9*	*C. raciborskii T3*	100	Short-chain alcohol dehydrogenase	ABI75108.1
	248		*C. raciborskii CENA302*	*R. brookii D9*	100	SxtU	EFA72770.1
	248		*C. raciborskii MVCC14*	*R. brookii D9*	100	SxtU	EFA72770.1
	248		*C. raciborskii MVCC19*	*R. brookii D9*	93	SxtU	EFA72770.1
	249		*C. raciborskii CYRF*	*C. raciborskii T3*	100	Short-chain alcohol dehydrogenase	ABI75108.1
SxtDIOX	334	(2Fe-2S)-binding protein	*R. brookii D9*	*Microseira wollei*	86	SxtDIOX	ACG63835.1
	334		*C. raciborskii CENA302*	*R. brookii D9*	99	SxtDIOX	EFA72772.1
	334		*C. raciborskii MVCC14*	*R. brookii D9*	99	SxtDIOX	EFA72772.1