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Supporting Information

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for

Improved Catalytic Activity of a Purified Multienzyme from a Modular Polyketide Synthase after Coexpression with *Streptomyces* Chaperonins in *Escherichia coli*

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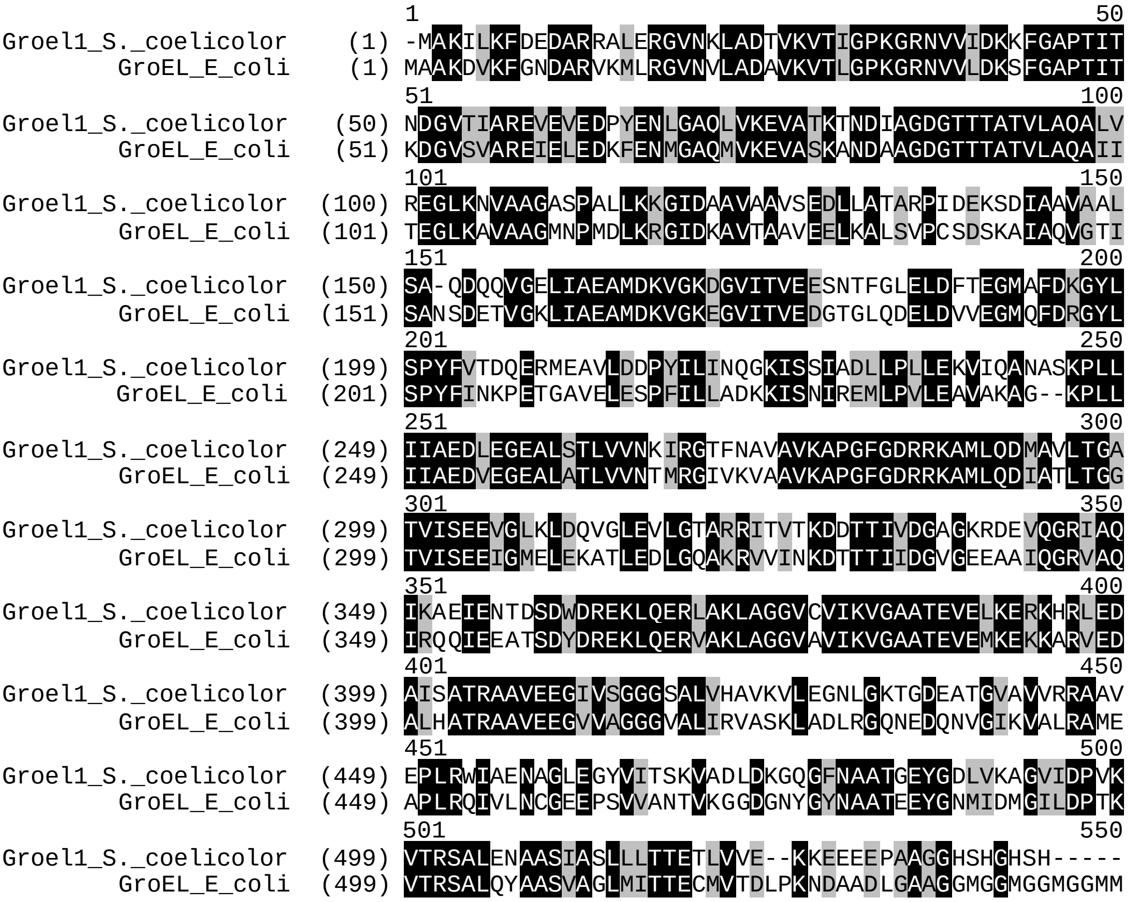
Table S1. Summary of the purification of DEBS 3, expressed with and without chaperonins.

Purification fraction	Protein conc. (mg mL^{-1})		Total protein (mg)	
	(–)	(+)	(–)	(+)
Clear lysate	29.1	32.1	877 ± 3	965 ± 3
Nickel-IDA	1.2	1.6	26.4 ± 0.4	35.0 ± 0.2
Ion exchange	0.79	1.3	6.2 ± 0.1	10.7 ± 0.2
Gel filtration	1.7	2.8	5.1 ± 0.1	8.4 ± 0.2

(+): With chaperonins, (–): Without chaperonins. The values given are the means of at least three independent measurements, together with their standard deviation.

GroEL1 (*S. coelicolor*) against GroEL

Similarity: 70.4%, identity: 57.6%



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                             1                                               50
Groel1_S._coelicolor     (1) -MAKILKFDEDARRALERGVNKLADTVKVTIGPKGRNVVIDKKFGAPTIT
        GroEL_E_coli     (1) MAAKDVKFGNDARVKMLRGVNVLADAVKVTLGPKGRNVVLDKSFGAPTIT
                             51                                             100
Groel1_S._coelicolor    (50) NDGVTIAREVEVEDPYENLGAQLVKEVATKTNDIAGDGTTTATVLAQALV
        GroEL_E_coli    (51) KDGVSVAREIELEDKFENMGAQMVKEVASKANDAAGDGTTTATVLAQAII
                             101                                            150
Groel1_S._coelicolor   (100) REGLKNVAAGASPALLKKGIDAAVAAVSEDLLATARPIDEKSDIAAVAAL
        GroEL_E_coli   (101) TEGLKAVAAGMNPMDLKRGIDKAVTAAVEELKALSVPCSDSKAIAQVGTI
                             151                                            200
Groel1_S._coelicolor   (150) SA-QDQQVGELIAEAMDKVGKDGVITVEESNTFGLELDFTEGMAFDKGYL
        GroEL_E_coli   (151) SANSDETVGKLIAEAMDKVGKEGVITVEDGTGLQDELDVVEGMQFDRGYL
                             201                                            250
Groel1_S._coelicolor   (199) SPYFVTDQERMEAVLDDPYILINQGKISSIADLLPLLEKVIQANASKPLL
        GroEL_E_coli   (201) SPYFINKPETGAVELESPFILLADKKISNIREMLPVLEAVAKAG--KPLL
                             251                                            300
Groel1_S._coelicolor   (249) IIAEDLEGEALSTLVVNKIRGTFNAVAVKAPGFGDRRKAMLQDMAVLTGA
        GroEL_E_coli   (249) IIAEDVEGEALATLVVNTMRGIVKVAAVKAPGFGDRRKAMLQDIATLTGG
                             301                                            350
Groel1_S._coelicolor   (299) TVISEEVGLKLDQVGLEVLGTARRITVTKDDTTIVDGAGKRDEVQGRIAQ
        GroEL_E_coli   (299) TVISEEIGMELEKATLEDLGQAKRVVINKDTTTIIDGVGEEAAIQGRVAQ
                             351                                            400
Groel1_S._coelicolor   (349) IKAEIENTDSDWDREKLQERLAKLAGGVCVIKVGAATEVELKERKHRLED
        GroEL_E_coli   (349) IRQQIEEATSDYDREKLQERVAKLAGGVAVIKVGAATEVEMKEKKARVED
                             401                                            450
Groel1_S._coelicolor   (399) AISATRAAVEEGIVSGGGSALVHAVKVLEGNLGKTGDEATGVAVVRRAAV
        GroEL_E_coli   (399) ALHATRAAVEEGVVAGGGVALIRVASKLADLRGQNEDQNVGIKVALRAME
                             451                                            500
Groel1_S._coelicolor   (449) EPLRWIAENAGLEGYVITSKVADLDKGQGFNAATGEYGDLVKAGVIDPVK
        GroEL_E_coli   (449) APLRQIVLNCGEEPSVVANTVKGGDGNYGYNAATEEYGNMIDMGILDPTK
                             501                                            550
Groel1_S._coelicolor   (499) VTRSALENAASIASLLLTTETLVVE--KKEEEEPAAGGHSHGHSH-----
        GroEL_E_coli   (499) VTRSALQYAASVAGLMITTECMVTDLPKNDAADLGAAGGMGGMGGMGGMM
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GroES (*S. coelicolor*) – GroES (*E. coli*)

Similarity: 54.8%, identity: 40.4%

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                            1                                                 52
GroeES_S_coelicolor     (1) MTTTSSKVAIKPLEDRIVVQPLDAEQTTASGLVIPDTAKEKPQEGVVLAVGP
       GroES_E_coli     (1) -------MNIRPLHDRVIVKRKEVETKSAGGIVLTGSAAAKSTRGEVLAVGN
                            53                                               104
GroeES_S_coelicolor    (53) G-RFEDGNRLPLDVSVGDVVLYSK-YGGTEVKYNGEEYLVLSARDVLAIVEK
       GroES_E_coli    (46) GRILENGEVKPLDVKVGDIVIFNDGYGVKSEKIDNEEVLIMSESDILAIVEA
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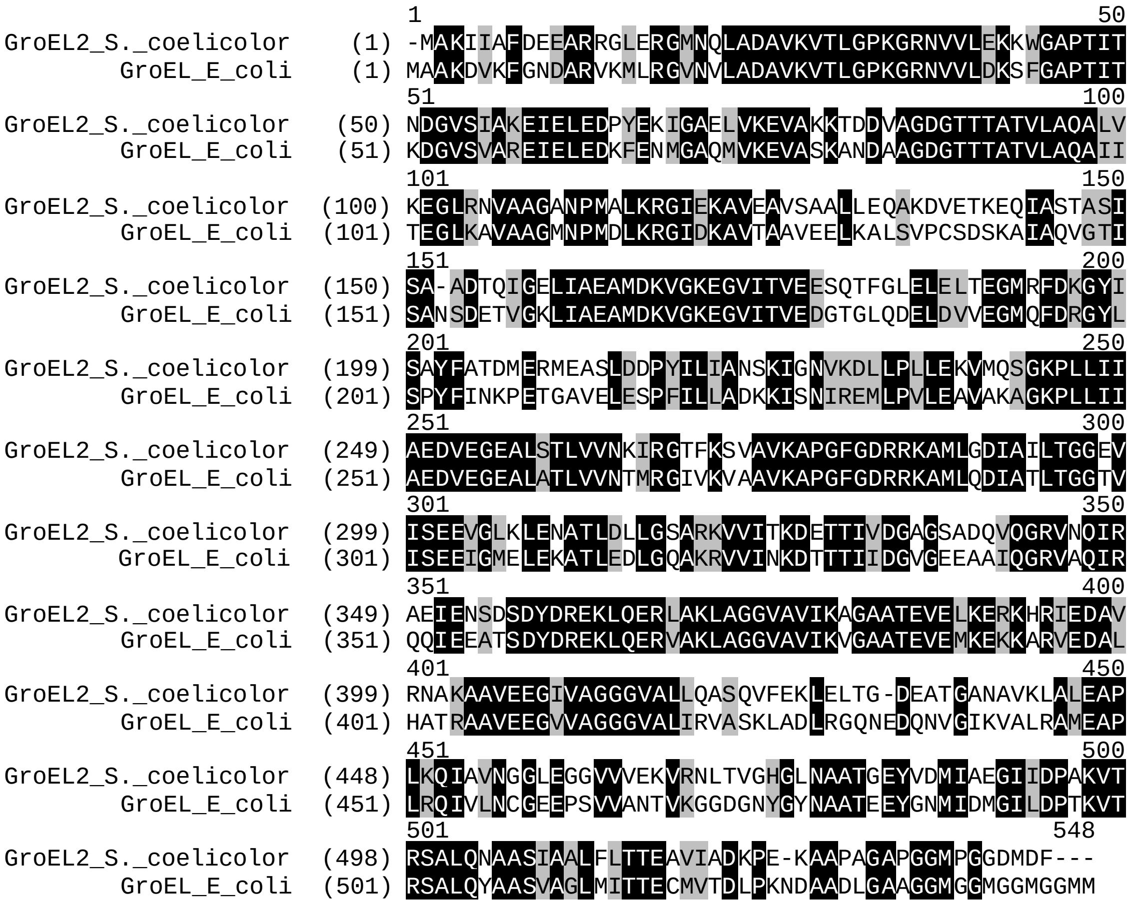
Figure S1. Alignment of GroEL and GroES chaperonins from *Streptomyces coelicolor* with their counterparts from *Escherichia coli*:

GroEL2 (*S. coelicolor*) against GroEL

Similarity: 70.8%, identity: 59.1%



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                                    1                                                50
GroEL2_S._coelicolor    (1) -MAKIIAFDEEARRGLERGMNQLADAVKVTLGPKGRNVVLEKKWGAPTIT
       GroEL_E_coli    (1) MAAKDVKFGNDARVKMLRGVNVLADAVKVTLGPKGRNVVLDKSFGAPTIT
                            51                                              100
GroEL2_S._coelicolor   (50) NDGVSIAKEIELEDPYEKIGAELVKEVAKKTDDVAGDGTTTATVLAQALV
       GroEL_E_coli   (51) KDGVSVAREIELEDKFENMGAQMVKEVASKANDAAGDGTTTATVLAQAII
                            101                                             150
GroEL2_S._coelicolor  (100) KEGLRNVAAGANPMALKRGIEKAVEAVSAALLEQAKDVETKEQIASTASI
       GroEL_E_coli  (101) TEGLKAVAAGMNPMDLKRGIDKAVTAAVEELKALSVPCSDSKAIAQVGTI
                            151                                             200
GroEL2_S._coelicolor  (150) SA-ADTQIGELIAEAMDKVGKEGVITVEESQTFGLELELTEGMRFDKGYI
       GroEL_E_coli  (151) SANSDETVGKLIAEAMDKVGKEGVITVEDGTGLQDELDVVEGMQFDRGYL
                            201                                             250
GroEL2_S._coelicolor  (199) SAYFATDMERMEASLDDPYILIANSKIGNVKDLLPLLEKVMQSGKPLLII
       GroEL_E_coli  (201) SPYFINKPETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLLII
                            251                                             300
GroEL2_S._coelicolor  (249) AEDVEGEALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLGDIAILTGGEV
       GroEL_E_coli  (251) AEDVEGEALATLVVNTMRGIVKVAAVKAPGFGDRRKAMLQDIATLTGGTV
                            301                                             350
GroEL2_S._coelicolor  (299) ISEEVGLKLENATLDLLGSARKVVITKDETTIVDGAGSADQVQGRVNQIR
       GroEL_E_coli  (301) ISEEIGMELEKATLEDLGQAKRVVINKDTTTIIDGVGEEAAIQGRVAQIR
                            351                                             400
GroEL2_S._coelicolor  (349) AEIENSDSDYDREKLQERLAKLAGGVAVIKAGAATEVELKERKHRIEDAV
       GroEL_E_coli  (351) QQIEEATSDYDREKLQERVAKLAGGVAVIKVGAATEVEMKEKKARVEDAL
                            401                                             450
GroEL2_S._coelicolor  (399) RNAKAAVEEGIVAGGGVALLQASQVFEKLELTG-DEATGANAVKLALEAP
       GroEL_E_coli  (401) HATRAAVEEGVVAGGGVALIRVASKLADLRGQNEDQNVGIKVALRAMEAP
                            451                                             500
GroEL2_S._coelicolor  (448) LKQIAVNGGLEGGVVVEKVRNLTVGHGLNAATGEYVDMIAEGIIDPAKVT
       GroEL_E_coli  (451) LRQIVLNCGEEPSVVANTVKGGDGNYGYNAATEEYGNMIDMGILDPTKVT
                            501                                           548
GroEL2_S._coelicolor  (498) RSALQNAASIAALFLTTEAVIADKPE-KAAPAGAPGGMPGGDMDF---
       GroEL_E_coli  (501) RSALQYAASVAGLMITTECMVTDLPKNDAADLGAAGGMGGMGGMGGMM
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Figure S1. (cont.)