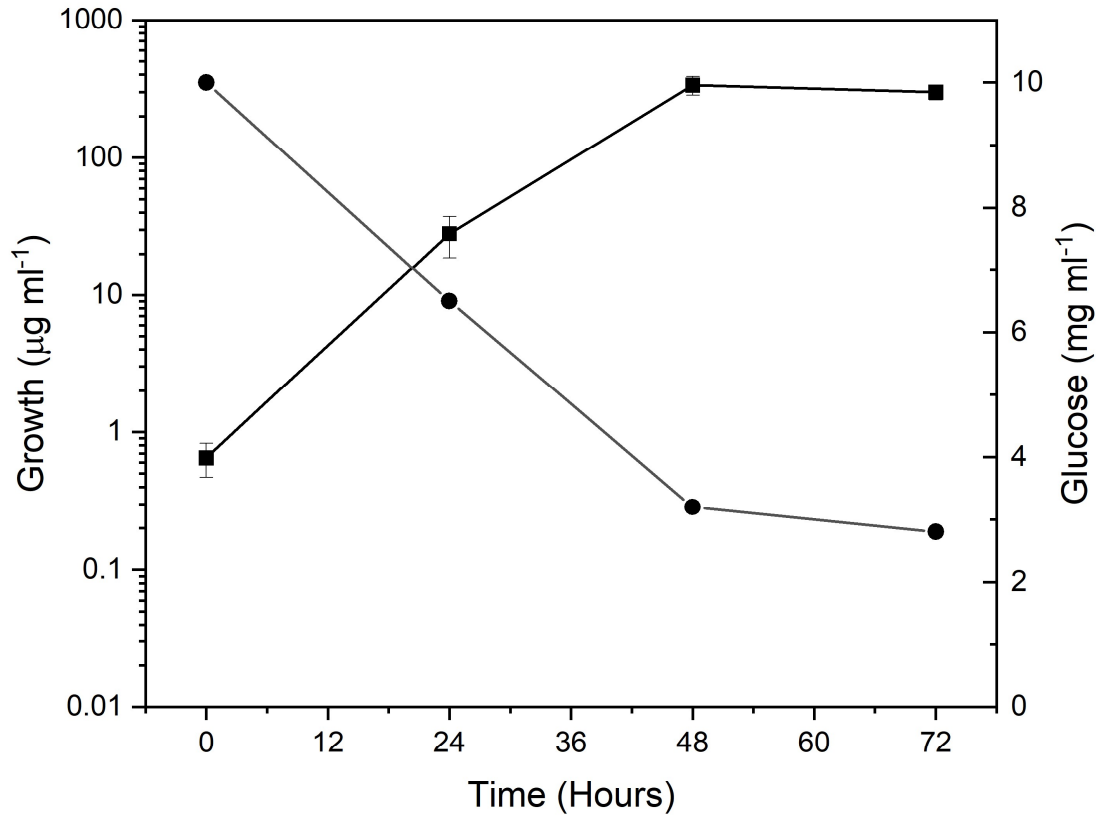


## Supplementary figures



Supplementary Fig 1. Biomass (■) and residual glucose (●) of *Streptomyces coelicolor* M145 grown in MM with 1% glucose. Samples were taken at the indicated times, and growth was quantified as described in the “Materials and methods” section. Bars represent the standard deviation, and all measurements were performed at least in triplicate.

|                                                                                 |                                                                |                                                              |     |
|---------------------------------------------------------------------------------|----------------------------------------------------------------|--------------------------------------------------------------|-----|
| SCO5059                                                                         |                                                                | -----MQIFGVDIGGSIGKAPVLDLDRGL                                | 25  |
| SCO0063                                                                         |                                                                | -----MIT-----ATTRHASRPVPVLDIGGTHVTAALVDPTASRP                | 35  |
| SCO4285                                                                         |                                                                | -----MKAALAGPGGELL                                           | 13  |
| SCO6110                                                                         |                                                                | -----MSGPGAPVFAGVDIGGTTTQVVLCDEELKVL                         | 31  |
| SCO1077                                                                         |                                                                | -----MHTDLVAALDIGGTKIAGALVDGHGRIO                            | 28  |
| SCO6260                                                                         |                                                                | MSTYRDFTAPIGSRRAPVLRVTGTRERRSHLTAPRVPTVGIDIGGTKVMAGVVDADGNIL | 60  |
| SCO2126                                                                         |                                                                | -----MGLTIGVDIGGTKIAAGVVDDEGNIL                              | 26  |
| 3VGM_1 SgG1k                                                                    |                                                                | -----MGLTIGVDIGGTKIAAGVVDDEEGRIL                             | 26  |
|                                                                                 |                                                                |                                                              |     |
| SCO5059                                                                         | AQER-CKVLTPHPATPD----                                          | GVADGVKQVVEH----FGWTRGVGLTFPGVVTGGATVR                       | 75  |
| SCO0063                                                                         | VSPSVIRRLRAHADAD----                                           | AVLDAIARAALA--LP-AGHSRWGVAMPGPFDYATGVG                       | 88  |
| SCO4285                                                                         | HQA---RRATGRERGPEAVVAGILDFAAELRAYGADRFGEPARAAGVAVPGIVDABRGVA   |                                                              | 70  |
| SCO6110                                                                         | DRA---DTATPARSGGRAMIAATLDALAV--VR--ARTPGRLAAVGVGAAGVVDASGHI    |                                                              | 84  |
| SCO1077                                                                         | ARA---QRATPAREDGDTVMRAVEDVLAELTV--SPLWGRASAVGIGSAGPVDDASAGTV   |                                                              | 82  |
| SCO6260                                                                         | EKL---RTETPKSKSPK--VVEDTIVELVLD--LSDRHDVHAVGIGAAGVVDADRNRV     |                                                              | 112 |
| SCO2126                                                                         | STH---KVPTPTT---PE---AIVDAIASAVEG--ARVGHEIVAVGIGAAGVYNRQRSTV   |                                                              | 75  |
| 3VGM_1 SgG1k                                                                    | STF---KVATPPT---AE---GIVDAICAAVAG--ASEGHDVEAVGIGAAGVVDVKRATV   |                                                              | 75  |
| *                               *:      *                                       |                                                                |                                                              |     |
|                                                                                 |                                                                |                                                              |     |
| SCO5059                                                                         | TAAN--VDKGWV----DTDARALFAERLGGLDVTVVNDADAAGVAEMHFAGAGRGRKGTVV  |                                                              | 129 |
| SCO0063                                                                         | RFADVGFESLNGVDVGAGLRERLADRC--ERLRLNDADAFVGEYGSGAAAGHD-HVV      |                                                              | 145 |
| SCO4285                                                                         | VYAA--NL-GWR----DVPLRTLGERLGSIPVALGHDVRTGGLAEGRIGAGRGAD-RFL    |                                                              | 122 |
| SCO6110                                                                         | LVASDSFT-DWA----GFPVTAALRTA-LGVP AFLDNVDNAFLRGEIACGAAADEE-DVL  |                                                              | 137 |
| SCO1077                                                                         | SPVN--VP-GWR----DYPLVRRVQAAAGGLPVELIGDGVAITAAEHWQGAARGHD-NAL   |                                                              | 134 |
| SCO6260                                                                         | LFAP--HL-SWR----NEPLRDIAGR-LAVPVLVDNDANTAAWAEWRFGAGRGED-HLV    |                                                              | 163 |
| SCO2126                                                                         | YFAP--NI-DWR----QEPLKEKVEAR-VGLPVVENDANAAAWGEYKFGGGKGHR-NVI    |                                                              | 126 |
| 3VGM_1 SgG1k                                                                    | LFAP--NI-DWR----HEPLKDKVEQR-VGLPVVENDANAAAWGEYRFAGQGQHD-DVI    |                                                              | 126 |
| .                               .*     *. . . :                               : |                                                                |                                                              |     |
|                                                                                 |                                                                |                                                              |     |
| SCO5059                                                                         | LLTFTGTIGSAVFTDGLLVPN-----TELGHLELD--GHDA-----EKASS---         |                                                              | 169 |
| SCO0063                                                                         | CLTLGTGVGSSFLSGGRP VHS GPL-----VPPGGHAYRLTVHGRPLEDTVSRRI       |                                                              | 195 |
| SCO4285                                                                         | FVPLGTGIAGAIGIDGRVEA-GAHGFAGEIGHVVVRPGGIACPCGQRG-CLERFASASAV   |                                                              | 180 |
| SCO6110                                                                         | GMTLTGTGVGGALWTGGELRT-GAHGAAGEIGHIPG-FGDL PCTCGGRG-HLETLASARSL |                                                              | 194 |
| SCO1077                                                                         | CMVVSTGVGGGLVLGGR LHP-GPTGNAGHIGHISVDLDGDGPCPGARG-CVERIASGPNI  |                                                              | 192 |
| SCO6260                                                                         | MITLTGTIGGAILEDGQVKR-KGYGVAGEFGHMQVVPVGGHRCPCGNRG-CWEQYSSGNAL  |                                                              | 221 |
| SCO2126                                                                         | CITLTGTGLGGGIIIGNKLRR-GHFGVAAEFGHIRMVPDGLLCGCSQG-CWEQYASGRAL   |                                                              | 184 |
| 3VGM_1 SgG1k                                                                    | CITLTGTGLGGGIIIGNKLRR-GRFGVAAEFGHIRVVPDGLLCGCSQG-CWEQYASGRAL   |                                                              | 184 |
| : ..**:. . . . .                               *     *                          |                                                                |                                                              |     |
|                                                                                 |                                                                |                                                              |     |
| SCO5059                                                                         |                                                                | -----KVKDD---HMSWEHWHAHRVQKYL                                | 190 |
| SCO0063                                                                         | RAHYARLT-----SATGDQHLPDVRDIAARARKGDAAAQEA FRYAFDALGOAL         |                                                              | 243 |
| SCO4285                                                                         | SQAWAQAC-----GDPGADAADCAKAVESGDARALAVWQDAVDALADGL              |                                                              | 224 |
| SCO6110                                                                         | RARYGER-----TGRELTAREVAEAARDGDADAHGVFAAAGAGIARAI               |                                                              | 237 |
| SCO1077                                                                         | ARRALEAG-----WLPGPDGDT SAAVAASARLGDPVAVASFERA AQALAGI          |                                                              | 240 |
| SCO6260                                                                         | VREARELAAADSPVAYGIIIEHVKSIGDITGPMITELAREGDAMCVELLQDIGQWLGVGI   |                                                              | 281 |
| SCO2126                                                                         | VRYAKQRANATPERAEVLLALGDGTPD GIEGKHISVAARQQCPVAVDSYRELARWAGAGL  |                                                              | 244 |
| 3VGM_1 SgG1k                                                                    | VRYAKQRANATPENAAVLLGLGDGSVDGIEGKHISEAARQQDPVAVDSFRELARWAGAGL   |                                                              | 244 |
| . . .                               :                                           |                                                                |                                                              |     |
|                                                                                 |                                                                |                                                              |     |
| SCO5059                                                                         | AHVEMLFSPELFIIGGVSRK SQKFLPHIKDV-----RAEIVPAQLQN NAGIV         |                                                              | 238 |
| SCO0063                                                                         | APWIDRFEATAV VIGGSMARSWDLIHPALT TGRAP---A--DGPDPVLPARPQPEEAPLL |                                                              | 298 |
| SCO4285                                                                         | VTALTLLDPRVLIIGGLAEAGETLFTPLRDAVRRRVTF---QKLP EIVPAALGDTAGCL   |                                                              | 281 |
| SCO6110                                                                         | VMTAGLV DIGTVVIGGGVSGAWT LLEPLIREPLAEPPISG--HPVKLLRAALGPDAVPL  |                                                              | 295 |
| SCO1077                                                                         | AATATLVEIDI AVVGGGVGKAGDVLFAPLRKALTDYATL-SFVQRLAVVPAQMGT DAGLV |                                                              | 299 |
| SCO6260                                                                         | ANLAAALDFPSCFVIGGGVSAADDLLIGPARD AFKRQLTGRGVRPEARIVRAQLGPEAGMV |                                                              | 341 |
| SCO2126                                                                         | ADLASLDFPSAFIVGGGLSDEGDLVDPI RKS YKRWLVGGNNWRPVAVIAAQLGNKAGLV  |                                                              | 304 |
| 3VGM_1 SgG1k                                                                    | ADLASLDFPSAFIVGGGVSDEGELVLDPI RKSFRWLIGGEWRPHAQVLA AQLGGKAGLV  |                                                              | 304 |

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      .      ..      ::**.:.      .      :: *      *      :
SC05059      GAAMHAAG----- 246
SC00063      GAAHWAQGTPDAP----- 311
SC04285      GAGLMAWDLLDTAAPSAPSAPSAPSASTASTAATAATPPEVTT 326
SC06110      GAAARARHELTAR----- 308
SC01077      GAAAAALTRTADVTAHV----- 317
SC06260      GAADLSRLVARRFRRAKRRRVERYERYERYA--EARRESRESL-- 382
SC02126      GAADLAREPDPI----- 317
3VGM_1|SgG1k| GAADLARQGLEHHHHHH----- 321
      ** .      :

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Supplementary fig 2 Multiple alignment of amino acid sequences of the probable glucokinases from *S. coelicolor* and Glk from *S. griseus* (pdb\_00003vgm). Amino acids involved in the ATP-binding motifs (underlined). The alignment was performed using CLUSTAL O (1.2.4) Multiple sequence alignment.

|         |     |                                                     |     |
|---------|-----|-----------------------------------------------------|-----|
| sco1942 | 1   | MNADGRTRLHQTPWEAALVKH-REQLGEVRLREMFAADPGRGTGWTLRVG  | 49  |
| sco6659 | 1   | --MSDTPKLNQRPEWTALADHAKGTLPHPDRLRELFQDPGRAERYVVRVG  | 48  |
| sco1942 | 50  | DLHVDYSKHLVTDETLALLQELAAATGVSGLRDAMFRGERINITEDRAVL  | 99  |
| sco6659 | 49  | DLRIDYSKHLVTDETLALLQELAAATGVSGLRDAMFRGERINITEDRAVL  | 98  |
| sco1942 | 100 | HTALRAPRDAVIEVDGENVVPQVHAVLDMAGFADRVRTGEWTGHTGRRI   | 149 |
| sco6659 | 99  | HTALRAPRDAVIEVDGENVVPQVHAVLDMAGFADRVRSGEWTGHTGRRI   | 148 |
| sco1942 | 150 | RNVVNIGIGGSDLGPAMAYEALRAFTDRSLTLRFVSNVDGADLHEAVRDL  | 199 |
| sco6659 | 149 | RNVVNIGIGGSDLGPAMAYEALRAFTDRSLTLRFVSNVDGADLHEAVRDL  | 198 |
| sco1942 | 200 | DPAETLFIIASKTFTTITETITNATSARSWLLAGLGDEKAVAKHFVALST  | 249 |
| sco6659 | 199 | DPAETLFIIASKTFTTITETITNATSARSWLLDGLGDEKAVAKHFVALST  | 248 |
| sco1942 | 250 | NAEKVADFGIDTANMFEFWDWVGGRYSFDSAIGLSLMIAIGPDRFREMLD  | 299 |
| sco6659 | 249 | NAEKVADFGIDTANMFEFWDWVGGRYSFDSAIGLSLMIAIGPDRFREMLD  | 298 |
| sco1942 | 300 | GFHLVDEHFRTAPAESNVPLLMGLLGWVYGSFLGAQSHAVLPYSHYLSKF  | 349 |
| sco6659 | 299 | GFRIVDEHFRNAEAPANAPLLLGLLGWVYGDFLGAQSHAVLPYSHYLSKF  | 348 |
| sco1942 | 350 | TAYLQQLDMESNGKSVSDREGKPVQWQTGPVVWGTPGTNGQHAYYQLIHQG | 399 |
| sco6659 | 349 | TAYLQQLDMESNGKSVSDREGNPVQWQTGPVVWGTPGTNGQHAYYQLIHQG | 398 |
| sco1942 | 400 | TKLIPADFIGFARPVDELSEELKSQHDLLMANFFAQTQALAFGKTPDEV   | 449 |
| sco6659 | 399 | TKLIPADFIGFARPVDELSEELKAQHDLLMANFFAQTQALAFGKTPDEV   | 448 |
| sco1942 | 450 | AEGVPEELVPHKTFPGDHPTTILARELTPSVLGQLVALYEHKVFVQGAI   | 499 |
| sco6659 | 449 | AEGVPEELVPHKTFRGNHPTTTVLAAELTPSVLGQLIALYEHKVFVQGAI  | 498 |
| sco1942 | 500 | WNIDSFDQWGVELGKVLAKRVEPALTEGADVPGLDPSTGALVAAYREL    | 549 |
| sco6659 | 499 | WNIDSFDQWGVELGKVLAKRVEPALTEGADVPGLDPSTAALVAAYRELKE  | 548 |
| sco1942 | 550 | RR                                                  | 551 |
| sco6659 | 549 | VH                                                  | 550 |

Supplementary Fig 3 Pairwise Sequence alignment paired between the protein sequences of *S. coelicolor* M145 phosphoglucosomerases (SCO1942, SCO6659). The alignment was performed with the EMBOSS Needle program.

```

SCO2119      MKVGVLTGGGDCPGLNAVIRAVVRKGVQEYGYDFTGFRDGRGPLEGDTVPLDIPAVRGI 60
SCO1214      MRIGVLTSGGDCPGLNAVIRSVVHRAVVDHGDEVIGFRDGWKGLLECDYLLKLDLDAVGGI 60
SCO5426      MRIGVLTAGGDCPGLNAVIRSVVHRAVDNYGDEVIGFEDGYAGLLDGRYRALDLNAVSGI 60
              *: : ****.*****: *: : . * : * : . **.*: * * :      **: ** **

SCO2119      LPRGGTVLGSSRTNPLKQRDGIRRIKDNLALGVEALITIGGEDTLGVATRLADEYGVPC 120
SCO1214      LARGGTILGSSRVRPEHLRDGVERARGHVEELGLDAIIPIGGEGTLKAA-RLLSDNGLPI 119
SCO5426      LARGGTILGSSRLERDRLREACENAGDMIQNFIDALIPIGGEGTLTAA-RMLSDAGLPV 119
              * ****:***** . : *: . . . : :*:*: * ***,** . * *: .: *: *

SCO2119      VGVPKTIDNDLSATDYTFGFDTAVGIATEAIDRLHTTAESHMRVLVVEVMGRHAGWIALH 180
SCO1214      VGVPKTIDNDIAVTDVTFGFDTAVTVATEALDRLKTTAESHQRVLIVEVMGRHTGWIALH 179
SCO5426      VGVPKTIDNDISSTDRTFGFDTAVGVATEAMDRLKTTAESHQRMVVEVMGRHAGWIALE 179
              *****: : ** ***** :****:***:***** **: :*****:*****.

SCO2119      SGLAGGANVILIPEQRFQVCSWVTSRFRASY-APIVVVAEGAMPDGMVLKDESLD 239
SCO1214      SGMAAGAHAVVPERPFDIDELTAKVGERFSAGKRFAIVVAAEGAKPKAGTMDFDEGGKD 239
SCO5426      SGMAAGAHGICLPERPFDPADLVKMVEERFSRGKKFAVVCVAEGAHPAEGSMDYGKGAID 239
              **:*.**: : :*: ** : : * .** . : * .***** * * * . . *

SCO2119      SYGHVRLSGVGEWLAKQIEKRTGNEARTTVLGHVQRGGTPSAFDRWLATRFGHLHAVDCVH 299
SCO1214      VYGHERFAGIARQLSIELEERLGKEARPVILGHVQRGGTPAYDRVLATRFGWHAVEAVH 299
SCO5426      KFGHERFQGIGTALAFELERRLGKEAKPVILGHVQRGGVPTAYDRVLATRFGWHAVEAAH 299
              :** *: *: . *: :*. * *: **: .:*****. *: *: ** ***** **: :. *

SCO2119      DGDFGKMVALRGTDIVRVPIAEATARLKTVPALYEEVGVFFG 342
SCO1214      RGEFGKMTALRGTDIEMVSLADAVESLKTVPDARYAEAECVL- 341
SCO5426      RGDFGRMTALRGTDVVMVPLAEAVTELKTVPKDRMDEAESVF- 341
              *: **: *.*****: * *: *. **** * . .:

```

Supplementary Fig 4 Multiple Sequence alignment paired between the protein sequences of *S. coelicolor* M145 phosphofructokinases (SCO1214, SCO2119, SCO5426). The alignment was performed using CLUSTAL O (1.2.4) Multiple sequence alignment.

|         |     |                                                     |     |
|---------|-----|-----------------------------------------------------|-----|
| sco3649 | 1   | MP-IATPEVYNEMLDRAKAGKFAYPAINVTSSQTLHAALRGFAEAEESDGI | 49  |
|         |     | :. .: :  :. .:  :. .:  :. .:  :. .:  :. .:  :. .:   |     |
| sco5852 | 1   | MPLVPTRELVSE---AAVAGR-AVAAFNVITLEHAEAIASGAQAAGAPVI  | 46  |
| sco3649 | 50  | VQISTGGAEFLGGQHNDKDMVTGAVALAEFAHIVAEKYDVTVALHTDHCPK | 99  |
|         |     | :   ..... .:  :.: .: .: .: .: .: .: .: .:           |     |
| sco5852 | 47  | LQISENAVRFHGGR-----VEPIARAAAEVGKACGVDVALHLDH---     | 85  |
| sco3649 | 100 | DKLDGYVRPLIIVSEERVKAG-RNPLFQSHMWGSAETLADNLSIAQELL   | 148 |
|         |     | : .: .:  :.: .: .: .: .: .: .: .: .: .:             |     |
| sco5852 | 86  | -----VTDPRLLHGAADAGFSSAMFDAGAQPYAENLAATRAAA         | 123 |
| sco3649 | 149 | ARARAARIILEVEITPTGGEEDGVSHEINDSLYTTVDDAVRTVEALGLGE  | 198 |
|         |     | .. .. .: .: .: .: .: .: .: .: .: .: .: .: .:        |     |
| sco5852 | 124 | QWAHGAGLWLEAELGYVGGKPDAPASAAAGVRTDPQEAARYVADTGVD-   | 172 |
| sco3649 | 199 | KGRYLLAASFGNVHGVYKPGNVVLRPELLKELNEGIASKYGQPAGSKPFD  | 248 |
|         |     | . .: .: .: .:  :.: .: .: .: .: .:  : ..             |     |
| sco5852 | 173 | ----ALAVAVGSSHAMTE-RSASLDHALIERLREAV-----PVP        | 206 |
| sco3649 | 249 | FVFHGGSGSTAEEIATALENGVVKMNIDTDTQYAFTRPVVDHMFERNYDGV | 298 |
|         |     | . .: .: .: .: .: .: .: .: .: .: .: .: .: .:         |     |
| sco5852 | 207 | LVLHGSSGVGDDELRRRAVRAGILKVNVTALNIAFTGAVRETLAARPD--  | 254 |
| sco3649 | 299 | LKVDGEVGNKKTYDPRTWGKLAEGMA----ARVVEACGHLRSAGQKIK    | 343 |
|         |     | .. .: .: .: .:  :  :.: .:                           |     |
| sco5852 | 255 | -----LTDPRPYVARGREAMAETVRALLAVVSG-----              | 282 |

Supplementary Fig 5 Pairwise Sequence alignment paired between the protein sequences of *S. coelicolor* M145 aldolases (SCO3649, SCO5852). The alignment was performed with the EMBOSS Needle program.

|         |                                                        |     |
|---------|--------------------------------------------------------|-----|
| sco1945 | 1 --MTTRTPLMAG--NWKMNLNHLEAIAHVQKLAFALADKDYDAVEVAVLAP  | 47  |
|         | ..... :::  :  ... :.....:    :: :  .....               |     |
| sco0578 | 1 MPAPAPSPVLLGVSLKMYFGHHQTLNWSRRIA-ALAER-HPAVTSGAARL   | 48  |
| sco1945 | 48 FTDLRVQTLVDGDKLKIY----GAQDISAHDGGAYTGEISGPMLAKLK    | 93  |
|         | .  ::...  .....:      :.. . .    :.. : ::              |     |
| sco0578 | 49 FV-LPTFPALVPATGILAPYGVALGAQDIATEDSGPYTGEVGGPVLKEIG  | 97  |
| sco1945 | 94 CTYVAVGHSERRQYHAETDEIVNAKVKAAYKHGLTPILCVGEELDVREAG  | 143 |
|         | .. ..   :    :.. . .:. .  ..  :..:    :    .  .....    |     |
| sco0578 | 98 CRYAEVGHAEERRLYGEGDTVVAAKTAAALRNGLTPVLCVGER-DAADPA  | 146 |
| sco1945 | 144 NHVEHTLAQVE---GGLKDLAAEQAESVVIAYEPVWAIGTGKVCGADDAQ | 190 |
|         | :..... : ::      :::  :    .    ..... ...              |     |
| sco0578 | 147 DAASRTVAEAERLLGGL-----SGAVVLAYEPQWAIGAPEPASADHIA   | 189 |
| sco1945 | 191 EVCAAIRGKLAELYSQELADKVRIQYGGSVKSGNVAEIMAKPDIDGALVG | 240 |
|         | .  .  : ..  ::::.....  .    ... :..... :.: ...         |     |
| sco0578 | 190 TVCTALRGWL-DSHPRHAGSTV--IYGGSAGPGLLTRLAG--TAEGLFLG | 234 |
| sco1945 | 241 -----GASLDSDEFVKIVRFRDQ-----                       | 258 |
|         | ..  .. ..                                              |     |
| sco0578 | 235 RFAHDPANVGAILD-----EIRSPAPAAVA                     | 259 |

Supplementary Fig 6 Pairwise Sequence alignment paired between the protein sequences of *S. coelicolor* M145 triose phosphate isomerases (SCO1945, SCO0578). The alignment was performed with the EMBOSS Needle program.

```

SCO7040      MTVNDDSFNTWKHREETAESMIPMIGKLHREQDVTILLHSRSLVNKSVVSILKTHRFRARQ 60
SCO1947      ----- 0
SCO7511      ----- 0

SCO7040      IAGAELSVTETMPFLRALTALDLGPSQIDIGMLAATYRTDDRGLSVEEFTAEAVAGATGA 120
SCO1947      ----- 0
SCO7511      ----- 0

SCO7040      NKIDRREGRDVVLYGFGRIGRILVARLLIEKAGSGNGLRLRAIVVRGGGEQDLVKRASLLR 180
SCO1947      -----MTIRVGINGFGRIGRNYFRALLEQGADIE-----IVAVND--LGD TATT A H L L K 47
SCO7511      -----MTRIGINGFGRIGRNVLRALLERDTKLE-----V V A V N D--L T E P A T L A R L L A 46
                  : : ***** * *: : . : : . * . : . . * * *

SCO7040      RDSVHGQFQGTITVDEDNSTILANGNAIKVIYADDP AQVDYTAYGIKDAILIDNTGKWRD 240
SCO1947      YDTILGRLKAEVSHTE--DTITVDGKTIKVLSE RNPADIPWGELGV--DIVIESTGIFTK 103
SCO7511      FDSTAGRLGRPVTVDG--DTLVVDGHR IKVLAERE PARLPWAE LGV--DIVLEATGRFTS 102
                  *: *: : : .*: .*: *: : **: : : *: *::: ** : .

SCO7040      REGLSKHLRPGIDKVVLTAPGKGDPNIVHGVNHDTIKPDE-RILSCASCTTNAIVPPLK 299
SCO1947      KADAEKHIAGGAKKVLISAPAKDEDITIVMGVNQDKYDPANHHVISNASCTTNCVAPMAK 163
SCO7511      ADAARAHLTAGARKVLVSAPSSGADVTLAYGVNTDAYDPAHTIVSNASCTTNALAPLAA 162
                  *: * **:::**... .:. *** * .* ::* *****..*

SCO7040      AMEDEYGVLRGHVETVHSFTNDQNLLDNYHKSDRRGRSAPLNMVITETGAASAVAKALPD 359
SCO1947      VLDENFGIVKGLMTTVHAYTNDQRILDFPHKDLRRARAAAENIIP TTTGA AKAT ALVLPQ 223
SCO7511      VLDELAGIEHGFM TTVHAYTQE QNLQDGP HRDARRARAAGVNIVPTTTGA AKAI GLVLPG 222
                  .::: *: *: : **:::*:*: * *: . **.*:* *: * ***** . . **

SCO7040      LKARITGSSIRVPVPDVSIAILNLQLAREASREEVVDHLREVS L TSPLKRQIDFIGAPDA 419
SCO1947      LKGKLDGIAMRVPVP TGSATDLVVELQREVT KDEVNAAFKKAADDGDLKGILFYTE-DAI 282
SCO7511      LDGKLSGDSIRVPVPVGSIVELNTTVARDVTREDVLAAYRA-AADGPLAGVLEYS D-DPL 280
                  *...: * :***** * . * : *:::*: : : . * : :

SCO7040      VSSDFIGSRHASIVDAGALKV-EGDNAILYLWYDNEFGYSCQVVRV VQH VSGVEYPTYP A 478
SCO1947      VSSDITGDPASCTFDSSLTMVQEGKSVKILGWYDNEWGYSNRLVDLT V FVG N Q L----- 336
SCO7511      VSSDITGNPASSIFDSALTRV-EGRHIKVVAWYDNEWGFSNRVIDTLALLATR----- 332
                  ****: *. :. .*: . * ** : *****:*: : : :.

SCO7040      PAV      481
SCO1947      ---      336
SCO7511      ---      332

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Supplementary Fig 7 Multiple Sequence alignment paired between the protein sequences of *S. coelicolor* M145 glyceraldehyde 3-phosphat e dehydrogenases (SCO7040, SCO1947, SCO7511). The alignment was performed using CLUSTAL O (1.2.4) Multiple sequence alignment.

|         |     |                                                     |     |
|---------|-----|-----------------------------------------------------|-----|
| sco4209 | 1   | MADAPYKLILLRHGESEWNEKNLFTGWVDVNLTpkgekeatrGGELLKDA  | 50  |
| sco6818 | 1   | -----                                               | 0   |
| sco4209 | 51  | GLLPDVVHTSVQKRAIRTAQLALEAADRHWIPVHRHWRLNERHYGALQGK  | 100 |
| sco6818 | 1   | -----                                               | 0   |
| sco4209 | 101 | DKAQTLAEFGEEQFMLWRRSYDTPPPALDRDAEYSQFSDPRYAMLPPELR  | 150 |
| sco6818 | 1   | -----MSTPEPVLAGPGIL                                 | 14  |
| sco4209 | 151 | PQTECLKDVVGRMLPYWFDIAIVPD---LLTGRT---VLVAAHGNSLR--  | 191 |
| sco6818 | 15  | -----LVLDGWSADAADDNALSLARTPVLDELVAQHPSTLAEA         | 53  |
| sco4209 | 192 | --ALVKHLDG-ISDADIAGLNIPGTGIPLSYELNAEFKPLNPGGTYLDPDA | 238 |
| sco6818 | 54  | SGEAVGLLPGTVGNSEIGHMVIGAGRPLPYDSLVLVQQAIDSGALRSHPR  | 103 |
| sco4209 | 239 | AAAAIEAVKNQGKKK-----                                | 253 |
| sco6818 | 104 | DAVLNEVAATSGALHLIGLCSDGQIHAHVEHSELLAAAATHQVERVFIH   | 153 |
| sco4209 | 254 | -----                                               | 253 |
| sco6818 | 154 | AITDGRDVADHTGEAYLTRVAELAAAAGTGQIATVIGRGYAMDKAGDLDL  | 203 |
| sco4209 | 254 | -----                                               | 253 |
| sco6818 | 204 | TERAVALVADGRGSPADSAHSAVHSSERGDEWVPASVLTEAGDARVADGD  | 253 |
| sco4209 | 254 | -----                                               | 253 |
| sco6818 | 254 | AVLWFNFRSDRIQQFADRLHEHLTASGRTVNMVSLAQYDTRTAIPALVKR  | 303 |
| sco4209 | 254 | -----                                               | 253 |
| sco6818 | 304 | ADASGGLADELQEAGLRSVRIAETEKFEHVTTYINGRDATVRDGEEHVRI  | 353 |
| sco4209 | 254 | -----                                               | 253 |
| sco6818 | 354 | TGEGKADYVAHPHMLNDRVTDVVEAAGRVDVDLVIANLANIDVVGHTGN   | 403 |
| sco4209 | 254 | -----                                               | 253 |
| sco6818 | 404 | LAATVTACEATDAAVDQILQAARNSGRWVAVGDHGNAERMTKQAPDGSV   | 453 |
| sco4209 | 254 | -----                                               | 253 |
| sco6818 | 454 | RPYGGHTTNPVPLVIVPNRTDTPAPTLPGTATLADVAPTILHLLGHKPGP  | 503 |
| sco4209 | 254 | -----                                               | 253 |
| sco6818 | 504 | AMTGRPLL                                            | 511 |

Supplementary Fig 8 Pairwise Sequence alignment paired between the protein sequences of *S. coelicolor* M145 phosphoglycerate mutases (SCO4209, SCO6818). The alignment was performed with the EMBOSS Needle program.

[illegible]

Supplementary Fig 9 Pairwise Sequence alignment paired between the protein sequences of *S. coelicolor* M145 enolases (SCO3096, SCO7638). The alignment was performed with the EMBOSS Needle program.

|         |     |                                                         |     |
|---------|-----|---------------------------------------------------------|-----|
| Sco2014 | 1   | MRRAKIVCTLGPPATDSYDQIKDLVDAGMDIARFNFSHGTHAEHEERYHRV     | 50  |
|         |     | :       .  : :.. : : : : : : : : : : : : : : : :        |     |
| Sco5423 | 1   | MRRSKIVCTLGPAVDSHEQLVTLIEAGMNVARFNFSHGTHAEHQGRYDRV      | 50  |
| Sco2014 | 51  | RKASDETGSRVSGALADLQGPKIRLGHFGEGPVLLERGDSFTITVEEGVEG     | 100 |
|         |     | .:.    : .       .. .     .     .    : .                |     |
| Sco5423 | 51  | RAAAKETGRAIGVLADLQGPKIRLETFAEGPVELVRGDEFTITAED-VPG      | 99  |
| Sco2014 | 101 | DRYICGTTYAGLAEDVTPGERVLVDDGKVCLEVTGVDGTRVTRVIEGGM       | 150 |
|         |     | .     .  ..   .  : : : : . .  : .  : .   : :    :       |     |
| Sco5423 | 100 | DRTICGTTYKGLPGDVTKGDQVLINDGNVELKVTEVEGPRVKTIIEGGV       | 149 |
| Sco2014 | 151 | VSDHKGLNLPGVAVSVPALSKKDEDDLRLWALRAGFDVVALSFVRSGRDIL     | 200 |
|         |     | :    :     .  :    : : : : : .  :     .  :     .  : :.. |     |
| Sco5423 | 150 | ISDHKGINLPGAAVNVPALSEKDVEDLRFALRMGCDLVALSFVRDAKDVA      | 199 |
| Sco2014 | 201 | DVHRIMDEEGRRLPVIKVEKPQAVENIEDIVAAFDGMVARGDLGVEMP        | 250 |
|         |     | :     : : : : : : : : : : : : : : : : : : : :           |     |
| Sco5423 | 200 | DVHRVMDEEGRVPVIKVEKPQAVDNMEDVMAFDGVMVARGDLAVEYP         | 249 |
| Sco2014 | 251 | LEQVPTVQKRAVKLAKRNAKPVIVATQMLDSMIDNARPTRAEASDVANAV      | 300 |
|         |     | : .    .: : : : : : : : : : : : : : : : : : : :         |     |
| Sco5423 | 250 | LEKVPVQKRLIELCRRNAKPVIVATQMMESMITNSRPTRAEASDVANAI       | 299 |
| Sco2014 | 301 | IDGTDVAMLSGETSVGKHPTDVTVMARIVEAAEEDILAKGLPPLTERNK       | 350 |
|         |     | :  .     .  : : : : : : : : : : : : : : : : : : :       |     |
| Sco5423 | 300 | LDGADAVMLSAESSVGAYPIETVKTMSKIVTAAEQELLSKGLQPLVPGKK      | 349 |
| Sco2014 | 351 | PRTQGGAVARAAAEMGDFLGAKFLVAFTQSGDTPVRLSRYSPIPLLAFT       | 400 |
|         |     | :     : .     .       ..     :.. :                      |     |
| Sco5423 | 350 | PRTQGGSVARAAEIADFLGKGLVAFTQSGDTARRLSRYRAAQPILAFT        | 399 |
| Sco2014 | 401 | PEPATRSQSLTWGVETFLGPHADSTDAMVDQVDELLTRYGRCEKGDVVV       | 450 |
|         |     | ..: : : : : : : : : : : : : : : : : : : : : : :         |     |
| Sco5423 | 400 | TDESTRNQLALSWGVEPHVVPFVNTTDEMVDLVDQETARLGRFSDGDTV       | 449 |
| Sco2014 | 451 | ITAGSPPGVSGTTNLVRVHHIGEDDIPK                            | 478 |
|         |     | : : : : : : : : : : : : : : : : : : :                   |     |
| Sco5423 | 450 | ITAGSPPGVSGTTNMVRVLHLGETRRG-                            | 476 |

Supplementary Fig 10 Pairwise Sequence alignment paired between the protein sequences of *S. coelicolor* M145 pyruvate kinases (SCO1214, SCO5423). The alignment was performed with the EMBOSS Needle program.