Revised Supplemental Figures for GYCO-2008-00148

```
Gl              SIKSVIRDSQHITHGPIFSYDRALITLARSKHSSKCPISYIDIVNLKSPLRLGVLCDDIN
Dr              ---NLCLDKINALHKPAYEHP-------------------KDLKASSGRLRVGYISSDFG
                   .:  *. :  * * :.:                     *:   .. **:* :..*:.

Gl              SIPIGCILESWLRNIDPKVASLSIYSTVASDKSALRTSLEAHCSNFIDFTNYKYQNNPFL
Dr              NHPTSHLMQSIPGMHNSEKFEVFCYALSPDDGTNFRVKVMAEAHHFIDLSQIPCNG---K
                . * . :::*     :.:  .:  *:  ..* : :*..: *.. :***:::   :.

Gl              CAQRINGDGICIMISMCQHNCGLEGRILAMRPAPIQISYWTHGGTTNSNYLDYILADQYC
Dr              AADRIHQDGIHILVNMNGYTKGARNELFALRPAPIQAMWLAYPGTSGAPFMDYIVSDKAT
                .*:**: *** *::.*  :. * ...::*:******  : :: **:.: ::***::*:

Gl              IPPGYAHLYSEHVITMPGCFICPSHSMHYSNAILLEEHADILKVTVEEVRSLIQDSKPDI
Dr              SPIEVAEQYSEKLAYMPNTFFIGDHANMFP----------------------HLKKKAVI
                 *   *. ***::  **. *:  .*:  :.                        ..*. *
```

GAP

```
Gl              KKMEPLLKAIYPLQRIASEAAVPASMEKSENNSDLTSHRVCLELPLYRKNIRALYGIPAN
Dr              ---------GLATTQINNKAATGEEVPR-----------------TIVVTTRSQYGLPED
                           .  :* .:**.  .: :                     . *: **:* :

Gl              CFLFCTFNQVYKFDMGTLGIIAALLRSVPNAYYALLKFPPASQLHIEAFFRHKAPDILDR
Dr              SIVYCNFNQLYKIDPPTLQMWANILKRVPNSVIWLLRFPAVGEPNIQQYAQNLG--LPAS
                .:::*.***:**:*  ** : * :*: ***:   **:**...: :*: : :: .  :

Gl              VIFLSMLPMKVEHIRRYLAVDVFVDTLKCNGSTIVLDALWSGVPVVGFVGEYILSRKTLS
Dr              RIIFSPVAPKEEHVRRGQLADVCLDTPLCNGHTTGMDVLWAGTPMVTMPGETLASRVAAS
                 *::* :. * **:**   .** :**  *** *  :*.**:*.*:* : ** : ** : *

Gl              FLSVLECKDLICASQGEAVLLCTRLAVDSGYYFSVRKRILKNRSN--LFNISRWCDNFVL
Dr              QLTCLGCPELIAQSRQEYEDVAVKLGTDMEFLKKVRARVWKQRICSPLFNTKQYTMDLEK
                 *: * * :**. *: *   :..:*..*  :  .** *: *:*    *** .::  ::

Gl              TMMLAYKNWIFGGKPTSFSTERVIANVKSQGFSWPLKSTGAQ
Dr              LYLQMWENHASGGKPDHLVKMQSLETSEST------------
                  :  ::*   ****  : . : : . :*
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Supplemental Fig. 1. Alignment of the catalytic “spy” domain of the *Giardia lamblia* (Gl) OGT with that of *Danio rerio* (Dr). Stars indicate identity, while periods and colons indicate similarity. In the alignable portions of the sequences there is a 29% amino acid identity and a 65% amino acid similarity. Note there is a gap in the alignment, because there is a large insert in the “spy“ domain of the *Giardia* OGT.

```
Cp              LGFIDQAILCYERISRINQNCITTLNVIAALYGNIGKIDESYEYFKRCIEVNQGVPDVYN
Ph              RDNLDKAVECYQMALTIKPNFSQSLNNLGVVYTVQGKMDAAASMIEKAIIANPTYAEAYN
                 . :*:*: **:    *: *   :** :..:*   **:* : . :::.* .*   .:.**

Cp              NLGVLYRDCGNFLMAKNCFLVALELDPNHTLAFQNLLYILNYFIPLDNPKLIGNIRNNSI
Ph              NLGVLYRDAGNISLAIEAYEQCLKIDPDSRNAGQNRLLAMNYINEGSDDKLYEAHR----
                ********.**: :* :.:  .*::**:   * ** *  :**:   .: **    *

Cp              ESIINNLKDSEKSLCLDISSTPESYVCESQIWINNSDYYINYQDMYDLSLEWGDKFIEIH
Ph              --------------------------------------------------DWGWRFMRLY
                                                                  :** :*:.::

Cp              REIKNRLDDLIPIAEIPDIESTSDKQLINIGFVGAEYFHHAVAFFILAPIKFLIKNFSKN
Ph              QQYN------------SWDNSKDPERQLVIGYVSPDYFTHSVSYFIEAPLAYHDYAN---
                :: :            .  :*.. :: : **:*..:** *:*::** **: :

Cp              STRDCNIEGNSQVKLNIFIYDNSPHHDYYSCFFKDLIPSEN--WRYIHGKDIEFSSKLIR
Ph              --------------YKVVIYSAVVKADAKTNRFRDKVLKKGGVWRDIYGIDEKKVSSMIR
                               ::.**.   : *  :  *:* : .:.  ** *:* * :  *.:**

Cp              SDNIHILFDLSGHTVNNCLALFALKNSPIQISWIGYPNTTGLKYIDYRITDKIVDPLHTK
Ph              EDKVDIMIELTGHTANNKLGMMACRPAPVQVTWIGYPNTTGLPTIDYRITDSMADPPSTK
                .*::.*:::*:***.** *.::* : :*:*::**********  *******.:.**  **

Cp              QKYSEKLLYLPNCFLCYTLPKIQHPPISEPPMKKNGFITFGSFNRVTKLHPLTIELWGEV
Ph              QKHVEELVRLPDSFLCYTP-SPEAGPVSPAPALTNGFVTFGSFNNLAKITPKVLQVWARI
                **: *:*: **:.*****  . :  *:* .*  .***:******.::*: * .:::*..:

Cp              LKSVPESHLLLKSKAFSSQSCCNFYLEIFKSKYNIQPHRISLIPLSNSYYSHLELYNDID
Ph              LCAVPHSRLIVKCKPFGCDSVRQRFLSILEQLG-LEPQRVDLVPLILLNHDHMQAYSLMD
                * :**.*:*::*.*.*..:*  : :*.*::.   ::*:*:.*:**    :.*:: *. :*

Cp              ISLDTFPYAGTTTTFECIFMGVPLITLSIDQSENSQIDSSDIYTEISSFHSQNVGRSILT
Ph              ISLDTFPYAGTTTTCESLYMGVPCVTMGG-----------------SVHAHNVGVSLLK
                ************** *.::**** :*:.                   *.*::*** *:*.

Cp              NLNLNELIASNKKEFIKAALSLANDTERLIYYRSNLRRILTESKLCDGEKFSRDFFELIL
Ph              TVGLRKLVARNEDEYVELAIQLASDVTSLSNLRMSLRELMAKSPLCDGAQFTQNLESTYR
                .:.*.:*:* *:.*::: *:.**.*.  *   * .**.::::* **** :*:::: .
```

Supplemental Fig. 2. Alignment of the catalytic “spy” domain of the *Cryptosporidium parvum* (Cp) OGT with that of *Petunia hybrida* (Ph). Stars indicate identity, while periods and colons indicate similarity. In the alignable portions of the sequences there is a 39% amino acid identity and a 76% amino acid similarity.