Genome sequencing and analysis of the versatile cell factory Aspergillus niger CBS 513.88

Pel, Herman J.; de Winde, Johannes H.; Archer, David B.; Dyer, Paul S.; Hofmann, Gerald; Schaap, Peter J.; Turner, Geoffrey; Albang, Richard; Albermann, Kaj; Andersen, Mikael R.

Published in:
Nature Biotechnology

DOI:
10.1038/nbt1282

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version
Publisher's PDF, also known as Version of record

Publication date:
2007

Link to publication in University of Groningen/UMCG research database

Citation for published version (APA):

Copyright
Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

The publication may also be distributed here under the terms of Article 25fa of the Dutch Copyright Act, indicated by the "Taverne" license. More information can be found on the University of Groningen website: https://www.rug.nl/library/open-access/self-archiving-pure/taverne-amendment.

Take-down policy
If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): http://www.rug.nl/research/portal. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.
<table>
<thead>
<tr>
<th>PFAM domain</th>
<th>hmm description</th>
<th>A. niger</th>
<th>A. nidulans</th>
<th>A. fumigatus</th>
<th>A. oryzae</th>
<th>N. crassa</th>
<th>S. cerevisiae</th>
</tr>
</thead>
<tbody>
<tr>
<td>PF00096</td>
<td>Zn_C2H2</td>
<td>66</td>
<td>60</td>
<td>52</td>
<td>42</td>
<td>54</td>
<td>38</td>
</tr>
<tr>
<td>PF00642</td>
<td>Zn_CCCCH</td>
<td>14</td>
<td>10</td>
<td>12</td>
<td>10</td>
<td>10</td>
<td>7</td>
</tr>
<tr>
<td>PF00170</td>
<td>bZIP</td>
<td>13</td>
<td>9</td>
<td>12</td>
<td>7</td>
<td>9</td>
<td>11</td>
</tr>
<tr>
<td>PF00249</td>
<td>myb_DNA-binding</td>
<td>13</td>
<td>18</td>
<td>16</td>
<td>14</td>
<td>16</td>
<td>14</td>
</tr>
<tr>
<td>PF00098</td>
<td>Zn_CCHC</td>
<td>12</td>
<td>22</td>
<td>12</td>
<td>13</td>
<td>10</td>
<td>10</td>
</tr>
<tr>
<td>PF00333</td>
<td>BRCT</td>
<td>12</td>
<td>10</td>
<td>11</td>
<td>11</td>
<td>10</td>
<td>10</td>
</tr>
<tr>
<td>PF02178</td>
<td>AT_hook</td>
<td>11</td>
<td>6</td>
<td>7</td>
<td>7</td>
<td>16</td>
<td>6</td>
</tr>
<tr>
<td>PF00010</td>
<td>HLH</td>
<td>10</td>
<td>12</td>
<td>9</td>
<td>10</td>
<td>14</td>
<td>7</td>
</tr>
<tr>
<td>PF01336</td>
<td>IRSN</td>
<td>10</td>
<td>9</td>
<td>9</td>
<td>9</td>
<td>11</td>
<td>8</td>
</tr>
<tr>
<td>PF02037</td>
<td>SAP</td>
<td>10</td>
<td>7</td>
<td>7</td>
<td>7</td>
<td>5</td>
<td>5</td>
</tr>
<tr>
<td>PF00046</td>
<td>homeobox</td>
<td>8</td>
<td>6</td>
<td>6</td>
<td>7</td>
<td>7</td>
<td>8</td>
</tr>
<tr>
<td>PF00498</td>
<td>FHA</td>
<td>8</td>
<td>8</td>
<td>6</td>
<td>8</td>
<td>8</td>
<td>14</td>
</tr>
<tr>
<td>PF05225</td>
<td>HTH_psq</td>
<td>8</td>
<td>21</td>
<td>30</td>
<td>1</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>PF00320</td>
<td>GATA</td>
<td>7</td>
<td>7</td>
<td>7</td>
<td>7</td>
<td>6</td>
<td>10</td>
</tr>
<tr>
<td>PF00439</td>
<td>brodomomain</td>
<td>7</td>
<td>6</td>
<td>6</td>
<td>5</td>
<td>6</td>
<td>10</td>
</tr>
<tr>
<td>PF00505</td>
<td>HMG_box</td>
<td>7</td>
<td>7</td>
<td>7</td>
<td>3</td>
<td>11</td>
<td>7</td>
</tr>
<tr>
<td>PF02463</td>
<td>SMC_N</td>
<td>7</td>
<td>7</td>
<td>7</td>
<td>7</td>
<td>7</td>
<td>7</td>
</tr>
<tr>
<td>PF00488</td>
<td>Mus_S</td>
<td>6</td>
<td>4</td>
<td>5</td>
<td>6</td>
<td>5</td>
<td>6</td>
</tr>
<tr>
<td>PF00493</td>
<td>MCM</td>
<td>6</td>
<td>6</td>
<td>6</td>
<td>6</td>
<td>7</td>
<td>6</td>
</tr>
<tr>
<td>PF01529</td>
<td>zf-DHHC</td>
<td>6</td>
<td>6</td>
<td>5</td>
<td>3</td>
<td>5</td>
<td>7</td>
</tr>
<tr>
<td>PF00250</td>
<td>Fork_head</td>
<td>5</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td>3</td>
<td>4</td>
</tr>
<tr>
<td>PF01753</td>
<td>zf_MYND</td>
<td>5</td>
<td>2</td>
<td>3</td>
<td>2</td>
<td>5</td>
<td>1</td>
</tr>
<tr>
<td>PF02146</td>
<td>SIR2</td>
<td>5</td>
<td>5</td>
<td>6</td>
<td>6</td>
<td>7</td>
<td>5</td>
</tr>
<tr>
<td>PF00136</td>
<td>DNA_pol_B</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td>PF00730</td>
<td>HhH-GPD</td>
<td>4</td>
<td>4</td>
<td>3</td>
<td>3</td>
<td>6</td>
<td>4</td>
</tr>
<tr>
<td>PF01096</td>
<td>TFIIIS</td>
<td>4</td>
<td>1</td>
<td>4</td>
<td>4</td>
<td>3</td>
<td>4</td>
</tr>
<tr>
<td>PF01624</td>
<td>MuS_I</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td>PF00192</td>
<td>KE2</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td>3</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td>PF02292</td>
<td>APSES</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td>2</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td>PF02854</td>
<td>MIF4G</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td>6</td>
</tr>
<tr>
<td>PF00047</td>
<td>HSF_DNA-bind</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>3</td>
<td>3</td>
<td>5</td>
</tr>
<tr>
<td>PF03178</td>
<td>CPSF_A</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>3</td>
<td>3</td>
<td>2</td>
</tr>
<tr>
<td>PF04675</td>
<td>DNA_ligase_A_N</td>
<td>3</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>3</td>
<td>1</td>
</tr>
<tr>
<td>PF05190</td>
<td>MuS_IV</td>
<td>3</td>
<td>2</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
</tr>
<tr>
<td>PF05224</td>
<td>NDT80_PhoG</td>
<td>3</td>
<td>2</td>
<td>3</td>
<td>2</td>
<td>3</td>
<td>1</td>
</tr>
<tr>
<td>PF00319</td>
<td>SRF-TF</td>
<td>2</td>
<td>2</td>
<td>3</td>
<td>2</td>
<td>2</td>
<td>4</td>
</tr>
<tr>
<td>PF00565</td>
<td>SNAse</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>PF00633</td>
<td>HhH</td>
<td>2</td>
<td>3</td>
<td>2</td>
<td>1</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>PF01388</td>
<td>ARID</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>3</td>
<td>2</td>
</tr>
<tr>
<td>PF01422</td>
<td>zf-NF-X1</td>
<td>2</td>
<td>1</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>PF01424</td>
<td>R3H</td>
<td>2</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>2</td>
</tr>
<tr>
<td>PF01997</td>
<td>Translin</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>1</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>PF02735</td>
<td>ku</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>0</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>PF02891</td>
<td>zf-MIZ</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>1</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>PF07529</td>
<td>HAS</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>PF08265</td>
<td>YL1_C</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>PF00165</td>
<td>HTH_AraC</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>2</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>PF00352</td>
<td>TBP</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>PF00436</td>
<td>SBS</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>PF00649</td>
<td>Copper-fist</td>
<td>1</td>
<td>1</td>
<td>2</td>
<td>0</td>
<td>2</td>
<td>3</td>
</tr>
<tr>
<td>PF01035</td>
<td>DNA_binding_1</td>
<td>1</td>
<td>1</td>
<td>2</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>PF01285</td>
<td>TEA</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>3</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>PF01381</td>
<td>HTH 3</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>PF01426</td>
<td>BAH</td>
<td>1</td>
<td>2</td>
<td>3</td>
<td>0</td>
<td>3</td>
<td>5</td>
</tr>
<tr>
<td>PF01833</td>
<td>TIC</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>PF01984</td>
<td>dsDNA_bind</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>PF02045</td>
<td>CBFB_NFYA</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>PF02257</td>
<td>RFX_DNA_binding</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>PF02671</td>
<td>PAH</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>2</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>PF02795</td>
<td>RPEL</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>PF02765</td>
<td>Telo_bind</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>PF02791</td>
<td>DDT</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>PF02805</td>
<td>Ada_Zn_binding</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>2</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>PF Code</td>
<td>Description</td>
<td>Match Count</td>
<td>Identity</td>
<td>Similarity</td>
<td>E-value</td>
<td>Query Coverage</td>
<td></td>
</tr>
<tr>
<td>---------</td>
<td>------------------------------------------------------------------------------</td>
<td>-------------</td>
<td>----------</td>
<td>------------</td>
<td>---------</td>
<td>----------------</td>
<td></td>
</tr>
<tr>
<td>PF02919</td>
<td>Topoisom_I_N - Eukaryotic DNA topoisomerase I, DNA binding fragment</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>PF03126</td>
<td>Plus-3 domain</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>PF03871</td>
<td>RNA_pol_Rpb5_N - RNA polymerase Rpb5, N-terminal domain</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>PF04152</td>
<td>Mre11_DNA_bind - Mre1 DNA-binding presumed domain</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>PF04406</td>
<td>TP6A_N - Type IIB DNA topoisomerase</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>PF04769</td>
<td>MAT_Alpha1 - Mating-type protein MAT alpha 1</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>1</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td>PF04921</td>
<td>XAP5 - XAP5 protein</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>PF05181</td>
<td>XPA C - XPA protein C-terminus</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>PF05764</td>
<td>YL1 - YL1 nuclear protein</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>PF06420</td>
<td>Mgm101p - Mitochondrial genome maintenance MGM101</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>PF06831</td>
<td>H2TH - Formamidopyrimidine-DNA glycosylase H2TH</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>PF08221</td>
<td>HTH 9 - RNA polymerase III subunit RPC82 helix-turn-helix domain</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>PF00196</td>
<td>GerE - Bacterial regulatory proteins, luxR family</td>
<td>0</td>
<td>7</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>PF01498</td>
<td>Transposase 5 - Transposase</td>
<td>0</td>
<td>4</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>PF02186</td>
<td>TFIIE_betas - TFIIE beta subunit core domain</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>PF02229</td>
<td>PC4 - Transcriptional Coactivator p15 (PC4)</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>PF02892</td>
<td>zt-BED - BED zinc finger</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>PF04090</td>
<td>RNA_pol_I_TF - RNA polymerase I specific initiation factor</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>PF04684</td>
<td>BAF1_ABF1 - BAF1 / ABF1 chromatin reorganising factor</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>PF06839</td>
<td>zt-GRF - GRF zinc finger</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td>PF07453</td>
<td>NUMOD1 - NUMOD1 domain</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td></td>
</tr>
</tbody>
</table>

Total PF hits: 1018 831 740 364 525 407