<table>
<thead>
<tr>
<th><strong>Target ID</strong></th>
<th>GO.13081</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Source Organism</strong></td>
<td><em>Arabidopsis thaliana</em></td>
</tr>
<tr>
<td><strong>Target Name</strong></td>
<td>At3g17210.1</td>
</tr>
<tr>
<td><strong>PDB Entry</strong></td>
<td>1Q53 (replaced 1NWJ)</td>
</tr>
<tr>
<td><strong>Deposition</strong></td>
<td>06-Aug-2003</td>
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<td><strong>BMRB Entry</strong></td>
<td>5843</td>
</tr>
<tr>
<td><strong>Deposition</strong></td>
<td>07-Aug-2003</td>
</tr>
<tr>
<td><strong>Function</strong></td>
<td>unknown (FF/Refine: 2Q3P)</td>
</tr>
<tr>
<td><strong>Produced From</strong></td>
<td><em>E. coli</em> Rosetta(DE3)/pLysS</td>
</tr>
<tr>
<td><strong>Structure by NMR</strong></td>
<td>Restraints/Residue: 18.4</td>
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<tr>
<td></td>
<td>No. of Residues: 224</td>
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<tr>
<td></td>
<td>Backbone RMSD: 0.95 Å</td>
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<tr>
<td><strong>Data Collected At</strong></td>
<td>Medical College of Wisconsin, Milwaukee, WI</td>
</tr>
<tr>
<td><strong>Authors</strong></td>
<td>B.L. Lytle, F.C. Peterson, B.F. Volkman</td>
</tr>
</tbody>
</table>

**Structural Features**

The most similar structure in the PDB to homodimeric (112 residues/monomer) At3g17210.1 shows 35% identity over 108 aligned residues (1RJJ). Additionally, ActVA-Orf6, a bacterial monooxygenase from *Streptomyces coelicolor* (1LQ9) and a protein of unknown function from *Thermus thermophilus* (1IUJ) show structural similarity. Although the two proteins, ActVA-Orf6 and At3g17210.1, share only 10% sequence identity, their tertiary and quaternary structures are very similar. Because none of the active site residues of ActVA-Orf6 are retained in At3g17210.1, the latter protein probably has a different function, which remains to be elucidated. This target aligns to Pfam-B domain of Pfam-B_3438 over residues 8–102.


**Percent Identity with Nearest PDB Structure at Time Solved**

| Pfam Cluster | 10% over 109 aa (1LQ9) |

**Protonet Cluster Size : Structures in PDB**

| B_3438 | 67 : 0 |

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