Supplementary Table S1. An example BioPAX file describing the phosphorylation and activation of CHK2 by ATM in human. Data was originally obtained from the Reactome database<sup>8</sup>.

```
<?xml version="1.0"?>
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            xmlns="http://www.biopax.org/examples/myExample#"
           xmlns:bp="http://www.biopax.org/release/biopax-level3.owl#" xmlns:rd="http://www.w3.org/1999/02/22-rdf-syntax-ns#"
           xmlns:rul= http://www.w3.org/2001/xMLSchema#"
xmlns:rdfs="http://www.w3.org/2000/01/rdf-schema#"
xmlns:owl="http://www.w3.org/2002/07/owl#"
     </owl:Ontology>
      <rdf:Property rdf:about="http://www.biopax.org/release/biopax-
level3.owl#direction"/>
  <bp:Protein rdf:ID="Protein_5">
             <br/>
<br/>
dataSource>
                   .
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                         .
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                                    <bp:year rdf:datatype="http://www.w3.org/2001/XMLSchema#int"</pre>
                                    >2003</brigger>
                                     <bp:db rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                    >pubmed</bp:db>
                                     <bp:title rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                    >The Genome Knowledgebase: a resource for biologists and
bioinformaticists.</bp:title>
                                    <bp:id rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                    >15338623</bp:id>
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                         </br:xref>
                   </br></bp:Provenance>
             </br></br></dataSource>
             <bp:cellularLocation>
                   <br/><br/><br/><br/><br/>CellularLocationVocabulary rdf:ID="CellularLocationVocabulary_6">
                        <br/>
<
                         <bp:xref>
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                               </br>
</br>
                         </bp:xref>
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             </br></bp:cellularLocation>
             <bp:entityReference>
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                         <bp:organism>
                               .
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                                     <bp:taxonXref>
                                           .
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                                                  <br/>
<
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>9606</bp:id>
                                           </br></bp:UnificationXref>
                                     </br></bp:taxonxref>
                                     <bp:standardName rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                    >Homo sapiens</br>
                                     <bp:displayName rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                    >Human</br/>
/bp:displayName>
                              </br></bp:BioSource>
```

```
</bp:organism>
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                                        >see-also</bp:term>
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                              >IUBMB</bp:db>
                              <bp:id rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                              >EC 2.7.1.37</bp:id>
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                    <bp:xref>
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                              >096017</bp:id>
                              <bp:db rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                              >uniprot</bp:db>
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                    </bp:xref>
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          </bp:entityReference>
          <br/>
<
          >Serine/threonine-protein kinase Chk2 (Cds1)</br><br/>
<br/>
<br/>
tandardName><br/>
<br/>
<br/>
<br/>
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          >CHEK2</bp:name>
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>EMBO J 22:2860-71 
          <br/><br/><br/>datatype="http://www.w3.org/2001/XMLSchema#string"
          >Foray, N </bp:author>
          <bp:author rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
          >Jeggo, P </bp:author
          <bp:id rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
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         <bp:author rdf:datatype="http://www.w3.org/2001/XMLSchema#string"
>Perricaudet, M </bp:author>
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<
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          <bp:author rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
          >Randrianarison, V </bp:author>
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          >A subset of ATM- and ATR-dependent phosphorylation events requires the BRCA1
protein./bp:title>
          <br/>hp:author rdf:datatype="http://www.w3.org/2001/XMLSchema#string"
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          <bp:author rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
          >Marot, D</bp:author>
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```

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               <br/>
<
               <bp:xref>
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                            >CHEBI:2342</bp:id>
                            <bp:db rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                            >ChEBI</bp:db>
                       </br:UnificationXref>
               </bp:xref>
               <bp:entityReference>
                      charter | Comparison | Com
                            >ADP</bp:displayName>
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>Adenosine 5'-diphosphate/bp:standardName>
                       </bp:SmallMoleculeReference>
               </bp:entityReference>
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        </br></bp:SmallMolecule>
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<br/>
<br/>
displayName rdf:datatype="http://www.w3.org/2001/XMLSchema#string"
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               <bp:standardName rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
              >Serine-protein kinase ATM (Ataxia telangiectasia mutated) (A-T,
<bp:xref>
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                            >uniprot
                       </br>
</bp:UnificationXref>
               </br></ref>
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        </bp:ProteinReference>
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                                           <bp:id rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                    >MI:0355</bp:id>
</bp:UnificationXref>
                              </bp:xref>
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               </bp:relationshipType>
        </br></br></re></re></re>
        <br/>
<
               <bp:controlled>
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```

```
<bp:right>
                             .
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                                                                    <bp:id rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                                                    >MI:0176</bp:id>
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                                                        >o-phospho-serine</br:term>
                                                    </bp:SequenceModificationVocabulary>
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                                        </br></bp:ModificationFeature>
                                  </br>
</br>
</br>

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                                  <bp:dataSource rdf:resource="#Provenance_3"/>
<bp:displayName rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                  >CHK2</bp:displayName>
                                  <bp:cellularLocation rdf:resource="#CellularLocationVocabulary_6"/>
                             </bp:Protein>
                       </bp:right>
                       <br/>
<
>1.0</bp:stoichiometricCoefficient>
                                  <bp:physicalEntity>
                                        .
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                                             >Ataxia telangiectasia mutated) (A-T, mutated) </bp:name>
                                             <bp:standardName</pre>
rdf:datatype="http://www.w3.org/2001/XMLSchema#string"
                                             >Serine-protein kinase AT(Ataxia telangiectasia mutated) (A-T,
mutated)/bp:standardName>
                                              <bp:cellularLocation rdf:resource="#CellularLocationVocabulary_6"/>
                                             <bp:comment rdf:datatype="http://www.w3.org/2001/XMLSchema#string"
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repair. May function as a tumor suppressor. Necessary for activation of ABL1 and
SAPK"</bp:comment>
                                             <bp:xref rdf:resource="#UnificationXref_28"/>
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                                        </bp:Protein>
                                  </br></br/>physicalEntity>
                            </br></br>files.
                       </bp:participantStoichiometry>
<bp:left rdf:resource="#Protein_5"/>
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<br/>
left>
                             .
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                                        .
<bp:SmallMoleculeReference rdf:ID="SmallMoleculeReference 15">
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                                             <bp:xref>
                                                    <bp:UnificationXref rdf:ID="UnificationXref_14">
```

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                                                                                           >ChEBI</bp:db>
                                                                                   </br></bp:UnificationXref>
                                                                          </bp:xref>
                                                                         <bp:standardName</pre>
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                                                                  </bp:SmallMoleculeReference>
                                                        </br></bp:entityReference>
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<br/>
| StandardName><br/>
| Stand
                                                        >ATP</bp:displayName>
                                               </br></bp:SmallMolecule>
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                                     <br/>
<
                                                        <bp:stoichiometricCoefficient</pre>
rdf:datatype="http://www.w3.org/2001/XMLSchema#float"
                                                       >1.0</br>>1.0</pr
                                      </br>
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</pr>
</pr>
</pr>
</pr>
</pr>

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                                               .
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                                                      <bp:db rdf:datatype="http://www.w3.org/2001/XMLSchema#string"
>reactome</bp:db>
                                                        <bp:comment rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                               >http://www.reactome.org </bp:comment>
</bp:UnificationXref>
                                      </bp:xref>
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>Phosphorylation and activation of CHK2 by ATMbp:displayName>
                                     <bp:conversionDirection rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                    >LEFT-TO-RIGHT</bp:conversionDirection>
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                                     <br/>
<
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                                               </br:Stoichiometry>
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  <br/><br/>cbp:author rdf:datatype="http://www.w3.org/2001/XMLSchema#string"
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                                                        <br/>
<
                                                        >Laus, MC </bp:author>
                                                        <bp:author rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                                      >Luyten, WH </bp:author> <br/> <br/> <br/> <br/> chitle rdf:datatype="http://www.w3.org/2001/XMLSchema#string"
>A human homologue of the checkpoint kinase Cds1 directly inhibits Cdc25 phosphatase.</br>
                                                      <bp:source rdf:datatype="http://www.w3.org/2001/XMLSchema#string"
>Curr Biol 9:1-10 
                                                        <bp:author rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                                       >Parker, AE </bp:author>
                                                        <bp:author rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                                       >de Weyer, IV </bp:author>
                                                        <bp:author rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                                       >Blasina, A </bp:author>
                                                        <bp:id rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                                       >9889122</bp:id>
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         </br></ref>
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           </br></br>cli>
         </bp:participantStoichiometry>
<br/>
<br/>
<br/>
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         >false</br>>false
       </bp:BiochemicalReaction>
     </bp:controlled>
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    >ACTIVATION</bp:controlType>
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    >ATM phosphorylates and activates CHK2</bp:displayName>
<br/>
<br/>
<br/>
<br/>
<br/>
<br/>
>ATM phosphorylates and activates CHK2</br/>
/bp:displayName>
<br/>
<br/>
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<br/>
<br/>
<br/>
<br/>
>ATM phosphorylates and activates CHK2</br/>
/bp:displayName>
<bp:catalysisDirection rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
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  </br></bp:Catalysis>
</rdf:RDF>
<!-- Created with Protege (with OWL Plugin 3.3.1, Build 430)
http://protege.stanford.edu -->
```

Supplementary Table S2. An example BioPAX file describing the two reactions involved in glucose metabolism in *Escherichia coli*. Data was originally obtained from the EcoCyc database<sup>14</sup>.

```
<?xml version="1.0"?>
<rdf:RDF
            xmlns="http://www.biopax.org/examples/myExample#"
           xmlns:bp="http://www.biopax.org/release/biopax-level3.owl#"
xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#"
xmlns:xsd="http://www.w3.org/2001/xMLSchema#"
xmlns:xsd="http://www.w3.org/2001/xMLSchema#"
           xmlns:rdfs="http://www.w3.org/2000/01/rdf-schema#"
xmlns:owl="http://www.w3.org/2002/07/owl#"
           xmlns:p1="http://www.owl-ontologies.com/assert.owl#"
     </owl:Ontology>
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            <bp:xref>
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  <br:id rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
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                       <bp:comment rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                      >PMID: 15608167//bp:comment>
<bp:db rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                       >uniprot</bp:db>
                  </bp:UnificationXref>
            </bp:xref>
            <bp:entityReference>
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MKKNLGFSHLEIINDFTAVSMAIPMLKKEHLIOFGGAEPVEGKPIAVYGAGTGLGVAHLVHVDKRWVSLPGEGGHVDFAPNSEEEA
IILEILRAEIGHVSAERVLSGPGLVNLYRAIVKADNRLPENLKPKDITERALADSCTDCRRALSLFCVIMGRFGGNLALNLGTFGG
VFIAGGIVPRFLEFFKASGFRAAFEDKGRFKEYVHDIPVYLIVHDNPGLLGSGAHLRQTLGHIL</br>
                       <br/>
<
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                       >GLK</bp:standardName>
                        <br/>bp:organism>
                             <bp:BioSource rdf:ID="Escherichia_coli">
                                   <bp:taxonXref>
                                         .
<bp:UnificationXref rdf:ID="taxon_562">
                                               <br/>
<
                                              >562</bp:id>
                                               <bp:db rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                               >taxonomy</bp:db>
                                         </br></bp:UnificationXref>
                                   </br></bp:taxonxref>
                                   <bp:displayName_rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                   >Escherichia coli</bp:displayName>
                             </br></bp:BioSource>
                        </br>
</br>
</br>
                  </br></bp:ProteinReference>
            </bp:entityReference>
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            >GLK_ECOLI</bp:name>
            <bp:cellularLocation>
                  .
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                             .
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```

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                                        >PMID: 11483584 </bp:comment>
<br/>

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</bp:UnificationXref>
                             </bp:xref>
                           <br/>
<
should be filled; it is not intended to provide useful (or even accurate) biological
information
                                            </br></bp:comment>
                            <bp:term rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                           >cytoplasm</br:term>
                      </bp:CellularLocationVocabulary>
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> [CH] 3(n1(c2(c(nc1)c(N)ncn2)))(0[CH]([CH](0)[CH](0)3)COP(=0)(0)OP(0)(=0)OP(0)(=0)0>(/b
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                                         >C00668</bp:id>
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</br>
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                            <bp:displayName rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
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                            <bp:entityReference>
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                                         >260.14</br>molecularweight>
                                         <bp:chemicalFormula rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
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       </bp:SmallMolecule>
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         <bp:physicalEntity>
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   <br:>bp:name rdf:datatype="http://www.w3.org/2001/XMLSchema#string"
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>C(OP(0)(0)=0)[CH]1([CH](0)[CH](0)C(0)(01)C0)</bp:structureData>
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>260.14</br>molecularWeight>
>C6H1309P</bp:chemicalFormula>
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<br/>
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<
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                               >SMILES</bp:structureFormat>
                               <bp:structureData rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
>c12(n(cnc(c(N)ncn1)2)[CH]3(0[CH]([CH](0)[CH](0)3)COP(=0)(0)OP(0)(=0)0))</br>
Data>
                               <rdfs:comment rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
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<t
                        >kegg compound</bp:db>
</br>

                </br:xref>
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<br/>
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                >C10H16N5O13P3</bp:chemicalFormula>
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                              >Adenosine 5'-diphosphate</bp:displayName>
<br/>
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                             <br/>
<
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                                <bp:stepProcess>
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p_to_beta-D-fruc-6-p
                                                              <bp:controller>
                                                                            controller

<br/>
<b
                                                                                           >glucose-6-phosphate isomerase</br/>hp:name>
                                                                                            <bp:entityReference>
                                                                                                           .
<bp:ProteinReference rdf:ID="ProteinReference_16">
                                                                                                                           .
-kpp:comment rdf:datatype="http://www.w3.org/2001/XMLSchema#string"
>This example is meant to provide an illustration of how various
BioPAX slots should be filled; it is not intended to provide useful (or even accurate)
biological information
                                                                                                                                                                                                        </br></bp:comment>
                                                                                                                          <bp:name rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                                                                                                         >PHI</bp:name>
                                                                                                                          <bp:sequence rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
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QETMTNAHSARDWFLKAAGDEKHVAKHFAALSTNAKAVGEFGIDTANMFEFWDWVGGRYSLWSAIGLSIVLSIGFDNFVELLSGAH
 AMDKHFSTTPAEKNLPVLLALIGIWYNNFFGAETEAILPYDQYMHRFAAYFQQGNMESNGKYVDRNGNVVDYQTGPIIWGEPGTNG
 QHAFYQLIHQGTKMVPCDFIAPAITHNPLFDHHQKLLSKFFAQTEALAFGKSREVVEQEYRDQGKDPAT</bp:sequence>
                                                                                                                         <br/>
<
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                                                                                                                         >PGI</bp:standardName>
                                                                                                                         <br/>
<
                                                                                                                       <bp:displayName rdf:datatype="http://www.w3.org/2001/XMLSchema#string"
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                                                                                                                        >glucose-6-phosphate isomerase</br/>
<br/>
<br/>
<br/>
| op:organism rdf:resource="#Escherichia_coli"/><br/>
<br/>
| op:name rdf:datatype="http://www.w3.org/2001/XMLSchema#string"
                                                                                                                          >GPI</bp:name>
                                                                                                            </br></bp:ProteinReference>
                                                                                            </br></br</pre>
                                                                                         <br/>
<
                                                                                           >PHI</bp:name>
                                                                                         <hr/>
<br/>
<b
                                                                                            <bp:name rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                                                                         >phosphohexose isomerase//p:name>
<bp:standardName rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                                                                           >PGI</bp:standardName>
```

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                      </bp:Protein>
                 </br></bp:controller>
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                <br/>
<
>The source of this data did not store catalyses of reactions as separate objects, so there are no unification x-refs pointing to the source of these BioPAX
                            </br></bp:comment>
instances.
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>PMID: 9847135 /bp:comment>
                     </br></bp:UnificationXref>
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                 <bp:displayName rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
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<bp:dataSource rdf:resource="#KEGG"/>
                 <bp:datasource 'dillesource= #REGG //
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                 <bp:name rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                 ><FONT FACE="Symbol"&gt;a&lt;/FONT&gt;-D-glucose </bp:name>
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                         <bp:structure>
                             <br/><br/><br/><br/><br/><br/>comment rdf:ID="ChemicalStructure_5"><br/><rdfs:comment rdf:datatype="http://www.w3.org/2001/XMLSchema#string"><alpha-D-glucose</rdfs:comment>
                                  <br/>bp:structureData
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>C1(C(0)C(0)C(0)C(01)C0)(0)</br>
>SMILES</bp:structureFormat>
</bp:ChemicalStructure>
                          </br:structure>
                         >beta-D-glucose</bp:displayName>
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                         >C6H12O6</bp:chemicalFormula>
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                         >180.16</bp:molecularWeight>
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                                       </br></br></d>
                              </bp:SmallMolecule>
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          </br></br>figure </br/>/bp:Stoichiometry>
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<br/>
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                    </br></br>physicalEntity>
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</bp:Stoichiometry>
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<
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<br/>
<br/>
<br/>
<br/>
<br/>
<br/>
>beta-D-glu-6-p + ADP</br/>
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<
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                    </br>
</bp:participantStoichiometry></br
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                  <br/>
<
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information
                                                            </br></bp:comment>
                    <bp:displayName rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
```

```
>Glycolysis Pathway</bp:displayName>
<bp:availability rdf:datatype="http://www.w3.org/2001/XMLSchema#string"
>see http://www.amaze.ulb.ac.be/</bp:availability>
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                     <bp:availability rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
>All data within the pathway has the same availability</bp:availability>
<br/>
<br/>
<br/>
data within the pathway has the same availability</br/>
<br/>
<br/>
<br/>
cbp:pathwayComponent rdf:resource="#phosphoglucose_isomerase_converts_alpha-D-gluc-6-p_to_beta-D-fruc-6-p"/>
                    >ACTIVATION</bp:controlType>
                                       >ACTIVATION</pp:Controllype>
<bp:displayName rdf:datatype="http://www.w3.org/2001/XMLSchema#string"
>catalysis of (alpha-D-glu &lt;=&gt; alpha-D-glu-6-p)</bp:displayName>
<bp:dataSource rdf:resource="#aMAZE"/>
<bp:dataSource rdf:resource="#KEGG"/>
<bp:controlled rdf:resource="#glucokinase"/>

                                         <bp:comment rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
>The source of this data did not store catalyses of reactions as separate objects, so there are no unification x-refs pointing to the source of these BioPAX
                                                                   </br></bp:comment>
 instances.
                                        <br/>
<
                                       >GLK -> (a-D-glu <=&gt; a-D-glu-6-p)</bp:standardName>
                                         <br/>
<
                                         >LEFT-TO-RIGHT</bp:catalysisDirection>
                               </br></bp:Catalysis>
                      </br></bp:pathwayComponent>
                     ></bp:comment>
                      <bp:pathwayComponent rdf:resource="#glucokinase"/>
                    <bp:name rdf:datatype="http://www.w3.org/2001/XMLSchema#string"
>Embden-Meyerhof pathway
                    <br/>

                      <br/>bp:pathwayOrder>
                               <bp:stepDirection rdf:datatype="http://www.w3.org/2001/XMLSchema#string"</pre>
                                       >LEFT-TO-RIGHT</bp:stepDirection>
<br/>
<br/>
<br/>
<br/>
<br/>
<br/>
<br/>
>bp:stepProcess rdf:resource="#glucokinase_converts_alpha-D-glu_to_alpha-D-
glu-6-p"/>
                                .
</bp:BiochemicalPathwayStep>
                       </bp:pathwayOrder>
           </br></bp:Pathway>
 </rdf:RDF>
```

## Supplementary Table S3: BioPAX covers five main types of biological pathways and coverage has increased over time with new levels of the ontology.

Type of	Main BioPAX Classes Used	Introduced
Biological Pathway		
Metabolic pathways	All types of physical entities (most common use of protein, small molecule, complex), All types of conversion events (most common use of BiochemicalReaction, ComplexAssembly and Transport), Catalysis, Modulation and Pathway	Level 1
Signaling pathways	All types of physical entities (most common use of protein, complex), All types of conversion events (most common use of BiochemicalReaction, ComplexAssembly, Transport and Degradation), Control, Catalysis, Modulation, MolecularInteraction, Pathway	Level 2
Molecular interactions	All types of physical entities (most common use of protein, complex, small molecule), MolecularInteraction, Pathway	Level 2
Gene regulatory networks	All types of physical entities, TemplateReaction, TemplateReactionRegulation	Level 3
Genetic interactions	Gene, GeneticInteraction	Level 3

## Supplementary Table S4: Databases and software supporting BioPAX. Note, PSI-MI data sources can be converted to BioPAX Level 2 using the PSI-MI to BioPAX converter.

Database	Type	URL	Format	License	Statistics
BIND 1	Protein	http://tap.med.utoron	PSI-MI	Free to	>85,000 interactions
	interactions	to.ca/~bind/	Level 1	all	
BioCyc	Metabolic and	http://biocyc.org	BioPAX	Free to	~500 mostly
databases	signaling		Level 3	all	computationally predicted pathway databases
BioGRID 4,5	Protein- protein and genetic interactions	http://www.thebiogri d.org/	PSI-MI Level 1 and 2.5	Free to all	>265,000 interactions
BioModels <sup>6</sup>	Metabolic and signaling	http://biomodels.net/	SBML, BioPAX Level 2	Free to all	>450 pathways, >240 curated pathways, >40,000 interactions
Cancer Cell Map	Signaling Pathways	http://cancer.cellmap .org	BioPAX Level 2	Free to all	Pathways: 10 Interactions: 2,104 Physical Entities: 899
DIP 7,8	Protein- protein interactions	http://dip.doe- mbi.ucla.edu/	PSI-MI Level 1	Free for Academi cs	>57,000 interactions
Ecocyc <sup>9</sup>	Metabolic and Signaling Pathways	http://ecocyc.org/	BioPAX, Level 3	Free to all	Pathways: 246 Regulatory interactions: 5,000 Metabolic reactions: 1400 Physical Entities: 3,606
HPRD 10	Protein- protein interactions	http://hprd.org/	PSI-MI Level 2.5	Free for Academi cs	>38,000 interactions
IMID	Signaling	http://www.sbcny.org /data.htm	BioPAX Level 2	Free to all	>2000 interactions
INOH	Signaling	http://www.inoh.org/	BioPAX Level 2	Free to all	>60 pathways
IntAct 11	Protein- protein interactions	http://www.ebi.ac.uk/ intact	PSI-MI Level 1 and 2.5	Free to all	>200,000 interactions
KEGG Pathway 12	Metabolic	http://www.genome.j p/kegg/	BioPAX Level 1	Free for Academi cs	>330 reference pathways
MetaCyc 13	Metabolic and signaling	http://metacyc.org/	BioPAX Level 3	Free to all	1399 curated pathways, >8,100 reactions
MINT 14	Protein- protein interactions	http://mint.bio.uniro ma2.it/mint	PSI-MI Level 1 and 2.5	Free to all	>80,000 interactions
MIPS MPact <sup>15</sup>	Protein- protein interactions	http://mips.gsf.de/ge nre/proj/mpact/	PSI-MI Level 1 and 2.5	Free to all	>12,000 interactions
NCI/Nature Pathway	Signaling	http://pid.nci.nih.gov/	BioPAX Level 2	Free to all	>400 curated pathways >12800 interactions

1.6			I	1	T
Interaction					
Database 16					
NetPath 17	Signaling	http://netpath.org/	BioPAX Level 2	Free to all	20 large curated pathways
OPHID <sup>18</sup>	Protein- protein interaction	http://ophid.utoronto. ca	PSI-MI Level 1	Free for Academi cs	>424,000 interactions
Pathway Commons	Pathways and interactions	http://www.pathwayc ommons.org	BioPAX Level 2	Free to all	>1,400 collected pathways >421,000 interactions
Reactome 19	Metabolic and Signaling Pathways	http://reactome.org/	BioPAX, Level 2	Free to all	>50 curated pathways
RegulonDB 20	Regulatory Network	http://regulondb.ccg. unam.mx	BioPAX Level 3	Free to all	Regulatory interactions: 2,594 Physical Entities: 18,371 Pathways: 2,660
Rhea	Metabolic Reactions	http://www.ebi.ac.uk/ rhea	BioPAX, Level 2	Free to all	>11,000 reactions
Software	Туре	URL	Format	License	Language
BiNoM <sup>21</sup>	Editor/Convert er	http://bioinfo- out.curie.fr/projects/ binom/	BioPAX Level 1 and 2	Free to all (open source)	Java
BioPAX validator	Validator	http://www.ohsucanc er.com/biopaxvalidat or/index.html	BioPAX Level 1 and 2	Free to all (open source)	Java
BioPAX	Validator	http://www.biopax.or	BioPAX	Free to	Java
validator	Validatoi	g/biopax-validator/	Level 3	all (open source)	Java
BioUML	Editor/Simulat or	http://www.biouml.or g/	BioPAX Level 2	Free to all (open source)	Java
Biowarehou se	Biological data warehouse software	http://biowarehouse. ai.sri.com/	BioPAX Level 1 and 2	Free to all (open source)	C and Java
ChiBE 79	Visualization and analysis	http://www.bilkent.ed u.tr/~bcbi/chibe.html	BioPAX Level 1 and 2	Free for Academi	Java
cPath <sup>22</sup>	Pathway database software	http://cbio.mskcc.org /dev_site/cpath/	BioPAX Level 1 and 2	Free to all (open source)	Java
Cytoscape 23	Visualization and analysis	http://cytoscape.org	BioPAX Level 1, 2, 3	Free to all (open source)	Java
ExPlain Analysis System	Pathway analysis	http://www.biobase- international.com/pa ges/index.php?id=28 6	BioPAX Level 1 and 2	Commerc ial	
GeneSpring GX	Pathway analysis	http://www.agilent.co m/chem/genespring	BioPAX Level 1 and 2	Commerc	Java
Navigator <sup>24</sup>	Visualization and analysis	http://ophid.utoronto. ca/navigator/	BioPAX Level 1 and 2	Free for Academi cs	Java
Pathway Tools <sup>25</sup>	Pathway prediction,	http://bioinformatics. ai.sri.com/ptools/	BioPAX Level 3	Free for Academi	Lisp

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•			cs	
visualization,				
network				
analysis, gene				
expression				
analysis				
Visualization	http://web.patika.org	BioPAX	Free for	Java
and analysis		Level 1	Academi	
,		and 2	cs	
BioPAX	http://www.biopax.or	BioPAX	Free to	Java
input/export		Level	all (open	
		1,2,3	` .	
BioPAX			Free to	Java
translator		Level	all (open	
		2,3	` '	
Gene	https://cabig.nci.nih.	BioPAX	Free to	Java
expression		Level 1	all	
•	<b>3</b>	and 2		
BioPAX	http://www.ebi.ac.uk/	BioPAX	Free to	Java
translator	•	Level 2	all (open	
	•		` .	
Pathway		BioPAX	Free to	Java
visualizer	atics.leeds.ac.uk/sha	Level 1	all	
	rk/	and 2		
Pathway	http://jlab.calumet.pu	BioPAX	Free to	Java
•	rdue.edu/theGatewa	Level 1	all	
service	v/	and 2		
	,			
Visualization	http://visant.bu.edu/	BioPAX	Free to	Java
		Level 1	all	
	analysis, gene expression analysis Visualization and analysis BioPAX input/export library BioPAX translator Gene expression analysis BioPAX translator  Pathway visualizer  Pathway query web	visualization, network analysis, gene expression analysis  Visualization and analysis  BioPAX http://www.biopax.or g/paxtools/ library BioPAX translator  Gene https://cabig.nci.nih. gov/tools/QPACA analysis  BioPAX http://www.ebi.ac.uk/ compneur-srv/sbml/convertors/SBMLtoBioPax.html  Pathway visualizer http://www.bioinform atics.leeds.ac.uk/shark/ Pathway query web service v/sualization http://visant.bu.edu/	visualization, network analysis, gene expression analysis  Visualization and analysis  BioPAX http://www.biopax.or g/paxtools/ library	visualization, network analysis, gene expression analysis  Visualization and analysis  BioPAX   http://www.biopax.or g/paxtools/ library   BioPAX translator   https://cabig.nci.nih. gxpression analysis   BioPAX translator   http://www.ebi.ac.uk/ translator   http://www.ebi.ac.uk/ translator   http://www.ebi.ac.uk/ translator   http://www.ebi.ac.uk/ compneur-srv/sbml/convertors/ SBMLtoBioPax.html   Pathway visualizer   http://www.bioinform atics.leeds.ac.uk/sha rk/   http://ijlab.calumet.pu rdue.edu/theGatewa y/   http://visant.bu.edu/   BioPAX   Free to all open source)   Free to all open source)   http://www.bioinform and analysis   http://www.bioinform atics.leeds.ac.uk/sha rk/   http://www.bioinform atics.leeds

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## References

- Bader, G. D., Betel, D. & Hogue, C. W. BIND: the Biomolecular Interaction Network Database. Nucleic Acids Res. 31, 248-250, (2003).
- 2 Karp, P. D. *et al.* Expansion of the BioCyc collection of pathway/genome databases to 160 genomes. Nucleic Acids Res 33, 6083-6089, (2005).
- Romero, P. *et al.* Computational prediction of human metabolic pathways from the complete human genome. Genome Biol 6, R2, (2005).
- Breitkreutz, B. J., Stark, C. & Tyers, M. The GRID: the General Repository for Interaction Datasets. Genome Biol. 4, R23, (2003).
- 5 Stark, C. *et al.* BioGRID: a general repository for interaction datasets. Nucleic Acids Res 34, D535-539, (2006).
- Le Novere, N. *et al.* BioModels Database: a free, centralized database of curated, published, quantitative kinetic models of biochemical and cellular systems. Nucleic Acids Res 34, D689-691, (2006).
- Xenarios, I. *et al.* DIP, the Database of Interacting Proteins: a research tool for studying cellular networks of protein interactions. Nucleic Acids Res. 30, 303-305, (2002).
- 8 Salwinski, L. *et al.* The Database of Interacting Proteins: 2004 update. Nucleic Acids Res 32, D449-451, (2004).
- 9 Keseler, I. M. *et al.* EcoCyc: a comprehensive view of Escherichia coli biology. Nucleic Acids Res 37, D464-470, (2009).
- Peri, S. *et al.* Development of Human Protein Reference Database as an initial platform for approaching systems biology in humans. Genome Res 13, 2363-2371, (2003).
- Hermjakob, H. *et al.* IntAct: an open source molecular interaction database. Nucleic Acids Res 32, D452-455, (2004).
- 12 Kanehisa, M., Goto, S., Kawashima, S., Okuno, Y. & Hattori, M. The KEGG resource for deciphering the genome. Nucleic Acids Res 32 Database issue, D277-280, (2004).
- Caspi, R. *et al.* The MetaCyc database of metabolic pathways and enzymes and the BioCyc collection of pathway/genome databases. Nucleic Acids Res 38, D473-479, (2010).
- Zanzoni, A. *et al.* MINT: a Molecular INTeraction database. FEBS Lett. 513, 135-140, (2002).
- Guldener, U. *et al.* MPact: the MIPS protein interaction resource on yeast. Nucleic Acids Res 34, D436-441, (2006).
- Schaefer, C. F. *et al.* PID: the Pathway Interaction Database. Nucleic Acids Res 37, D674-679, (2009).
- 17 Kandasamy, K. *et al.* NetPath: a public resource of curated signal transduction pathways. Genome Biol 11, R3, (2010).
- Brown, K. R. & Jurisica, I. Online predicted human interaction database. Bioinformatics 21, 2076-2082, (2005).
- Joshi-Tope, G. *et al.* Reactome: a knowledgebase of biological pathways. Nucleic Acids Res 33, D428-432, (2005).

- Gama-Castro, S. *et al.* RegulonDB (version 6.0): gene regulation model of Escherichia coli K-12 beyond transcription, active (experimental) annotated promoters and Textpresso navigation. Nucleic Acids Res 36, D120-124, (2008).
- Zinovyev, A., Viara, E., Calzone, L. & Barillot, E. BiNoM: a Cytoscape plugin for manipulating and analyzing biological networks. Bioinformatics 24, 876-877, (2008).
- Babur, O., Dogrusoz, U., Demir, E. & Sander, C. ChiBE: interactive visualization and manipulation of BioPAX pathway models. Bioinformatics 26, 429-431, (2010).
- Cerami, E. G., Bader, G. D., Gross, B. E. & Sander, C. cPath: open source software for collecting, storing, and querying biological pathways. BMC Bioinformatics 7, 497, (2006).
- Shannon, P. *et al.* Cytoscape: a software environment for integrated models of biomolecular interaction networks. Genome Res 13, 2498-2504, (2003).
- Brown, K. R. *et al.* NAViGaTOR: Network Analysis, Visualization and Graphing Toronto. Bioinformatics 25, 3327-3329, (2009).
- Karp, P. D. *et al.* Pathway Tools version 13.0: integrated software for pathway/genome informatics and systems biology. Brief Bioinform 11, 40-79, (2010).
- Demir, E. *et al.* PATIKA: an integrated visual environment for collaborative construction and analysis of cellular pathways. Bioinformatics. 18, 996-1003, (2002).
- Novak, B. A. & Jain, A. N. Pathway recognition and augmentation by computational analysis of microarray expression data. Bioinformatics 22, 233-241, (2006).
- Pinney, J. W., Shirley, M. W., McConkey, G. A. & Westhead, D. R. metaSHARK: software for automated metabolic network prediction from DNA sequence and its application to the genomes of Plasmodium falciparum and Eimeria tenella. Nucleic Acids Res 33, 1399-1409, (2005).
- Hu, Z. *et al.* VisANT 3.0: new modules for pathway visualization, editing, prediction and construction. Nucleic Acids Res 35, W625-632, (2007).
- Hu, Z., Mellor, J., Wu, J. & DeLisi, C. VisANT: an online visualization and analysis tool for biological interaction data. BMC Bioinformatics 5, 17, (2004).

