



**SADI**

Find. Integrate.  
Analyze.

# SPARQL Assist

language-neutral query composer



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**SADI**

**Semantic Automated Discovery &  
Integration**

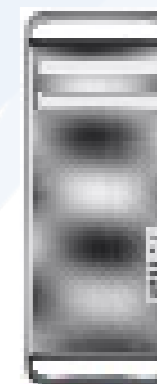
(Semantic Web Services)

# SADI

Find. Integrate.  
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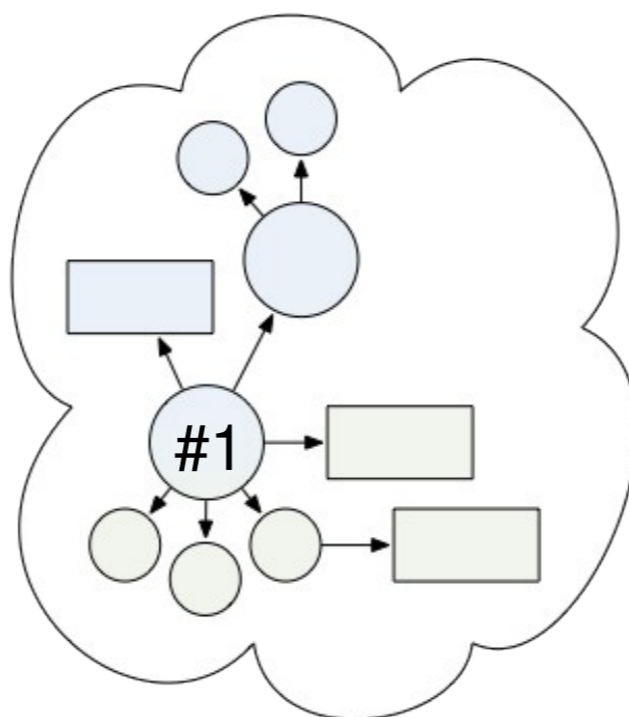
```
<rdf:RDF
  xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#"
  xmlns:regress="http://sadi.framework.org/examples/regression.owl#"
  <regress:PairedValueCollection rdf:about="http://sadi.framework.org/examples/input1">
    <regress:element>
      <regress:PairedValue>
        <regress:x rdf:datatype="http://www.w3.org/2001/XMLSchema#int">1</regress:x>
        <regress:y rdf:datatype="http://www.w3.org/2001/XMLSchema#int">2</regress:y>
      </regress:PairedValue>
    </regress:element>
    <regress:element>
      <regress:PairedValue>
        <regress:x rdf:datatype="http://www.w3.org/2001/XMLSchema#int">3</regress:x>
        <regress:y rdf:datatype="http://www.w3.org/2001/XMLSchema#int">5</regress:y>
      </regress:PairedValue>
    </regress:element>
  </regress:PairedValueCollection>
</rdf:RDF>
```



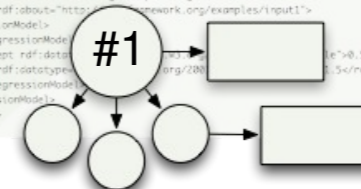
Service



Client



```
<rdf:RDF
  xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#"
  xmlns:regress="http://sadi.framework.org/examples/regression.owl#"
  <regress:OutputClass rdf:about="http://sadi.framework.org/examples/input1">
    <regress:hasRegressionModel>
      <regress:LinearRegressionModel>
        <regress:intercept rdf:datatype="http://www.w3.org/2001/XMLSchema#float">0.5</regress:intercept>
        <regress:slope rdf:datatype="http://www.w3.org/2001/XMLSchema#float">1.5</regress:slope>
      </regress:LinearRegressionModel>
    </regress:hasRegressionModel>
  </regress:OutputClass>
</rdf:RDF>
```





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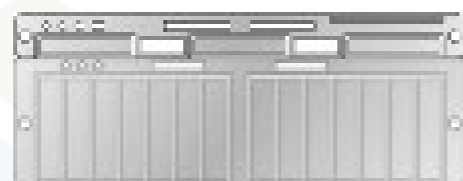
# SHARE

Semantic Health And Research Environment

# SADI

Find. Integrate.  
Analyze.

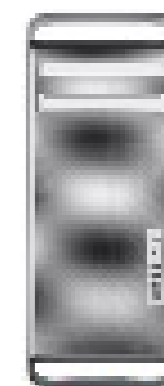
```
PREFIX sadi: <http://sadiframework.org/ontologies/predicates.owl#>  
PREFIX dumontier: <http://ontology.dumontierlab.com/>  
PREFIX kegg: <http://lsrn.org/KEGG\_PATHWAY:>  
SELECT ?gene ?protein ?seq  
WHERE {  
  kegg:hsa00232 dumontier:hasParticipant ?gene .  
  ?gene sadi:encodes ?protein .  
  ?protein sadi:hasSequence ?seq  
}
```



Service



Service



Service

# SADI

Find. Integrate.  
Analyze.

```
PREFIX rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX patients: <http://biordf.net/cardioSHARE/patients.owl#>
PREFIX bmi: <http://sadiframework.org/examples/bmi.owl#>
  SELECT ?patient ?bmi FROM <http://biordf.net/cardioSHARE/patients.rdf>
WHERE {
?patient rdf:type patients:AtRiskPatient . ?patient bmi:BMI ?bmi
}
```

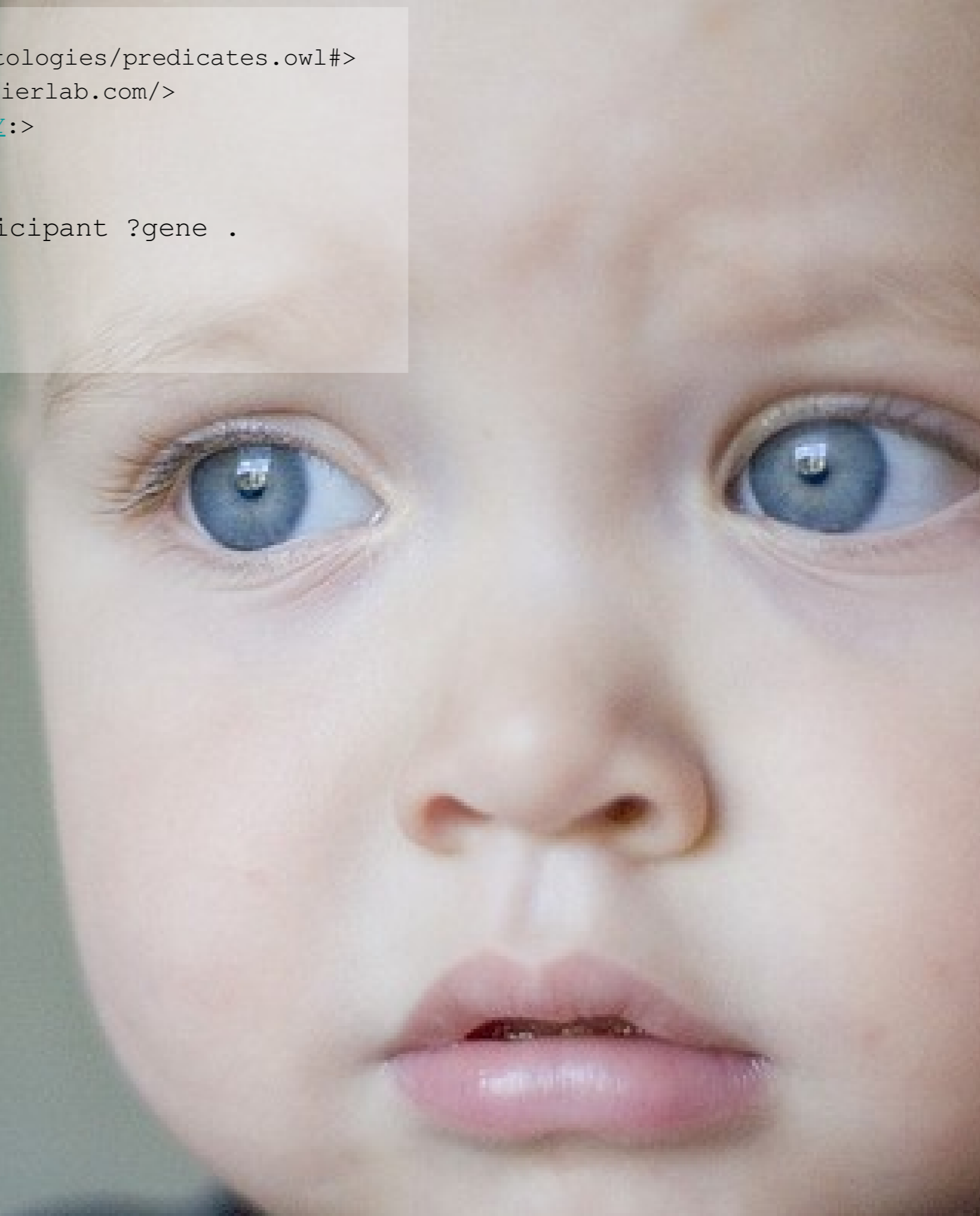


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# Problem

```
PREFIX sadi: <http://sadiframework.org/ontologies/predicates.owl#>
PREFIX dumontier: <http://ontology.dumontierlab.com/>
PREFIX kegg: <http://lsrn.org/KEGG\_PATHWAY:>
SELECT ?gene ?protein ?seq
WHERE {
    kegg:hsa00232 dumontier:hasParticipant ?gene .
    ?gene sadi:encodes ?protein .
    ?protein sadi:hasSequence ?seq
}
```







```
PREFIX rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#>
PREFIX sio: <http://semanticscience.org/resource/>
PREFIX kegg: <http://lsrn.org/KEGG\_PATHWAY:>
SELECT ?gene ?protein ?seq
WHERE {
    kegg:hsa00232 sio:SI0_000132 ?gene .
    ?gene sio:SI0_010078 ?protein .
    ?protein sio:SI0_000008 ?attr .
    ?attr rdf:type sio:SI0_010015 ?seq
}
```



# SADI

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## ...SPARQL assist

jQuery plugin for SPARQL-specific typeahead

two-stage suggestion

local (client-side) data

remote (server-side) data



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# Demo

<http://sadiframework.org/sparql-assist/demo>



# SADI

Find. Integrate.  
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...more information

<http://bit.ly/sparql-assist>

explore the demo, download the distribution

<http://slidesha.re/sadi-owled2010>

introduction to SADI + SHARE

<http://sadiframe.org/>

everything else

# SADI

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canarie



HEART &  
STROKE  
FOUNDATION

*Finding answers. For life.*



**NSERC**  
**CRSNG**



CIHR IRSC

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Photos

#8

<http://www.flickr.com/photos/jonaldinger/2263487963/>

#9 <http://www.flickr.com/photos/treacletart/2300241452/>

Translations

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# Acknowledgements