

Level 3

Physical Entity State

Physical Entity State

- From Transpath docs:
 - Protein can be:
 - de-phosphorylated in the cytosol
 - phosphorylated in the cytosol or
 - phosphorylated and bound to DNA in the nucleus
- Some BioPAX Conversions are state transitions e.g. phosphorylation reaction
- PhysicalEntityParticipant = state

BioPAX Level 2

biochemicalReaction	
<input type="radio"/>	SPONTANEOUS
<input type="radio"/>	RIGHT
<input type="radio"/>	LEFT
<input type="radio"/>	INTERACTION-TYPE
<input type="radio"/>	PARTICIPANTS
<input type="radio"/>	NEGATIVE
<input type="radio"/>	HAS-SUPPORT
<input type="radio"/>	NAME
<input type="radio"/>	SHORT-NAME
<input type="radio"/>	SYNONYMS
<input type="radio"/>	COMMENT
<input type="radio"/>	DATA-SOURCE
<input type="radio"/>	XREF
<input type="radio"/>	AVAILABILITY
<input checked="" type="radio"/>	EC-NUMBER
<input checked="" type="radio"/>	DELTA-G
<input checked="" type="radio"/>	DELTA-H
<input checked="" type="radio"/>	KEQ
<input checked="" type="radio"/>	DELTA-S

physicalEntityParticipant	
<input type="radio"/>	COMMENT
<input checked="" type="radio"/>	CELLULAR-LOCATION
<input checked="" type="radio"/>	STOICHIOMETRIC-COEFFICIENT
<input checked="" type="radio"/>	PHYSICAL-ENTITY
<input checked="" type="radio"/>	XREF

physicalEntity	
<input type="radio"/>	NAME
<input type="radio"/>	SHORT-NAME
<input type="radio"/>	SYNONYMS
<input type="radio"/>	COMMENT
<input type="radio"/>	DATA-SOURCE
<input type="radio"/>	XREF
<input type="radio"/>	AVAILABILITY

Unique per reaction

proteinParticipant	
<input type="radio"/>	CELLULAR-LOCATION
<input type="radio"/>	STOICHIOMETRIC-COEFFICIENT
<input type="radio"/>	PHYSICAL-ENTITY
<input type="radio"/>	XREF
<input type="radio"/>	COMMENT
<input checked="" type="radio"/>	SEQUENCE-FEATURE-LIST

protein	
<input type="radio"/>	NAME
<input type="radio"/>	SHORT-NAME
<input type="radio"/>	SYNONYMS
<input type="radio"/>	COMMENT
<input type="radio"/>	DATA-SOURCE
<input type="radio"/>	XREF
<input type="radio"/>	AVAILABILITY
<input checked="" type="radio"/>	SEQUENCE
<input checked="" type="radio"/>	ORGANISM

BioPAX Level 2

biochemicalReaction	
0	SPONTANEOUS
0	RIGHT
0	LEFT
0	INTERACTION-TYPE
0	PARTICIPANTS
0	NEGATIVE
0	HAS-SUPPORT
0	NAME
0	SHORT-NAME
0	SYNONYMS
0	COMMENT
0	DATA-SOURCE
0	XREF
0	AVAILABILITY
0	EC-NUMBER
0	DELTA-G
0	DELTA-H
0	KEQ
0	DELTA-S

physicalEntityParticipant	
0	COMMENT
0	CELLULAR-LOCATION
0	STOICHIOMETRIC-COEFFICIENT
0	PHYSICAL-ENTITY
0	XREF

physicalEntity	
0	NAME
0	SHORT-NAME
0	SYNONYMS
0	COMMENT
0	DATA-SOURCE
0	XREF
0	AVAILABILITY

Unique per reaction

proteinParticipant	
0	CELLULAR-LOCATION
0	STOICHIOMETRIC-COEFFICIENT
0	PHYSICAL-ENTITY
0	XREF
0	COMMENT
0	SEQUENCE-FEATURE-LIST

protein	
0	NAME
0	SHORT-NAME
0	SYNONYMS
0	COMMENT
0	DATA-SOURCE
0	XREF
0	AVAILABILITY
0	SEQUENCE
0	ORGANISM

?

Level 3 State

- Class: **State** = set of participants that provider defines as a single state
- People may differ on the definition of state e.g. localization change defines a new state?
- Issues: information duplication (data in participants e.g. location, PTM)
 - Maybe can fix by having participant and state subclass on

State Attributes

- Constant: protein sequence, domains
- Variable: location, post-translational modification
- Level 2: No differentiation!
Thus, can't represent states

proteinParticipant	
<input type="checkbox"/>	CELLULAR-LOCATION
<input type="checkbox"/>	STOICHIOMETRIC-COEFFICIENT
<input type="checkbox"/>	PHYSICAL-ENTITY
<input type="checkbox"/>	XREF
<input type="checkbox"/>	COMMENT
<input checked="" type="checkbox"/>	SEQUENCE-FEATURE-LIST

State Attributes

- Add differentiation between constant and variable features to support states
- sequenceFeature subclasses with different definitions (restrictions on use of external CVs?)

- ① sequenceFeature
 - ① variableSequenceFeature
 - ① constantSequenceFeature
- ① sequenceInterval
- ① sequenceSite

proteinParticipant	
①	CELLULAR-LOCATION
①	STOICHIOMETRIC-COEFFICIENT
①	PHYSICAL-ENTITY
①	XREF
①	COMMENT
①	SEQUENCE-FEATURE-LIST