

Automatic Annotation in UniProtKB

Alan Bridge, Automation and Enhancements, Swiss-Prot group

alan.bridge@isb-sib.ch



Fourth International Biocuration Conference,
Tokyo, Japan
October 12th 2010



Swiss Institute of
Bioinformatics

Talk outline

- Introduction

- What?

What we annotate in UniProtKB, and what we propagate

- Why?

Need for automatic annotation in UniProtKB

- How?

Automatic annotation systems for UniProtKB

- Current status and future plans

Talk outline

- **Introduction**

- What?

What we annotate in UniProtKB, and what we propagate

- Why?

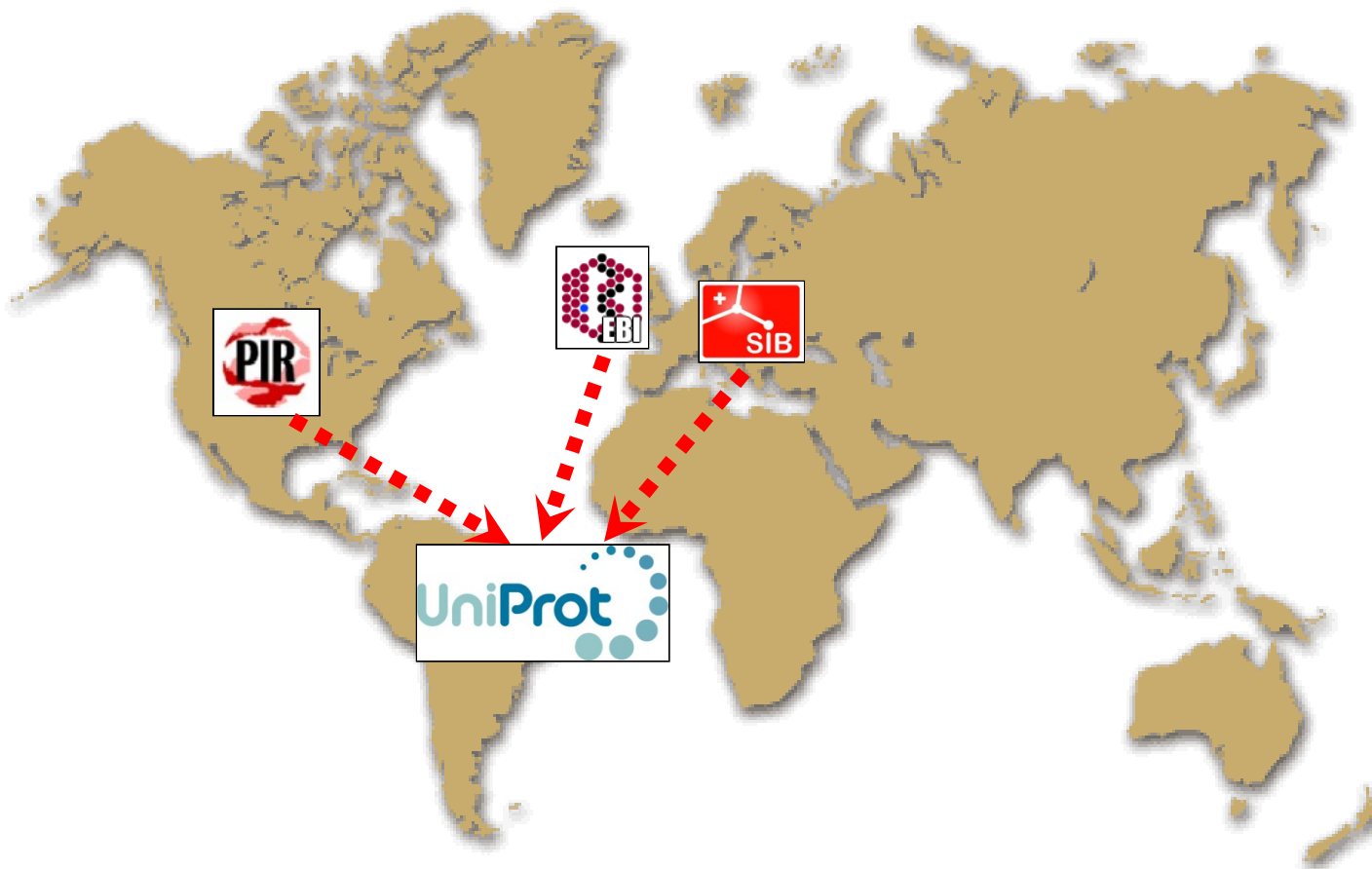
Need for automatic annotation in UniProtKB

- How?

Automatic annotation systems for UniProtKB

- Current status and future plans

The UniProt consortium



The mission of **UniProt** is to provide the scientific community with a comprehensive, high-quality and freely accessible resource of **protein sequence** and **functional information**.



Swiss Institute of
Bioinformatics





UniRef
Sequence clusters

UniRef100
UniRef90
UniRef50



UniProtKB

Protein knowledgebase

UniProtKB/Swiss-Prot

Reviewed ★
Manual annotation



UniProtKB/TrEMBL

Unreviewed ★
Automatic annotation

UniMES

Metagenomic
and environmental
sample sequences



UniParc - Sequence archive
Current and obsolete sequences



EMBL/GenBank/DDBJ, Ensembl,
RefSeq, PDB, other resources



Talk outline

- Introduction
- **What?**

What we annotate in UniProtKB, and what we propagate

- Why?

Need for automatic annotation in UniProtKB

- How?

Automatic annotation systems for UniProtKB

- Current status and future plans

What? UniProtKB annotation content

Nature Precedings : doi:10.1038/npre.2010.5247.1 : Posted 12 Nov 2010

UniProt > UniProtKB Downloads · Contact · Documentation/Help

Search Blast * Align Retrieve ID Mapping *

Search in **Query**
Protein Knowledgebase (UniProtKB) [Fields »](#)

Q16719 (KYNU_HUMAN) ★ Reviewed, UniProtKB/Swiss-Prot [Contribute](#)
[Send feedback](#)
[Read comments \(0\) or add your own](#)

Last modified October 5, 2010. Version 94. [History...](#)

[Clusters with 100%, 90%, 50% identity](#) | [Documents \(7\)](#) | [Third-party data](#) [text](#) [xml](#) [rdf/xml](#) [gff](#) [fasta](#)

[Names](#) · [Attributes](#) · [General annotation](#) · [Ontologies](#) · [Sequence annotation](#) · [Sequences](#) · [References](#) · [Cross-refs](#) · [Entry info](#) · [Documents](#) [Customize order](#)

Names and origin

Protein names	<i>Recommended name:</i> Kynureninase EC=3.7.1.3 <i>Alternative name(s):</i> L-kynurenine hydrolase
Gene names	Name:KYNU
Organism	Homo sapiens (Human) [Complete proteome]
Taxonomic identifier	9606 [NCBI]
Taxonomic lineage	Eukaryota > Metazoa > Chordata > Craniata > Vertebrata > Euteleostomi > Mammalia > Eutheria > Euarchontoglires > Primates > Haplorrhini > Catarrhini > Hominidae > Homo

What? UniProtKB annotation content

General annotation (Comments)

Function	Catalyzes the cleavage of L-kynurenine (L-Kyn) and L-3-hydroxykynurenine (L-3OHKyn) into anthranilic acid (AA) and 3-hydroxyanthranilic acid (3-OHAA), respectively. Has a preference for the L-3-hydroxy form. Also has cysteine-conjugate-beta-lyase activity.
Catalytic activity	L-kynurenine + H ₂ O = anthranilate + L-alanine. (Ref.1) (Ref.2) (Ref.6) (Ref.7) L-3-hydroxykynurenine + H ₂ O = 3-hydroxyanthranilate + L-alanine. (Ref.1) (Ref.2) (Ref.6) (Ref.7)
Cofactor	Pyridoxal phosphate.
Enzyme regulation	Inhibited by o-methoxybenzoylalanine (OMBA). (Ref.1) (Ref.2)
Pathway	Amino-acid degradation; L-kynurenine degradation; L-alanine and anthranilate from L-kynurenine: step 1/1. Cofactor biosynthesis; NAD(+) biosynthesis; quinolinate from L-kynurenine: step 2/3.
Subunit structure	Homodimer. (Ref.7)
Subcellular location	Cytoplasm (Ref.1).
Tissue specificity	Expressed in all tissues tested (heart, brain placenta, lung, liver, skeletal muscle, kidney and pancreas). Highest levels found in placenta, liver and lung. Expressed in all brain regions. (Ref.1) (Ref.2)
Induction	Increased levels in several cerebral and systemic inflammatory conditions. (Ref.1) (Ref.2)
Involvement in disease	Defects in KYNU may be a cause of hydroxykynureninuria [MIM:236800]; also known as kynureninase deficiency. Hydroxykynureninuria is characterized by urinary excretion of large amounts of kynurenine, 3-hydroxykynurenine and xanthurenic acid. This suggests a block in the conversion of kynurenine and 3-hydroxykynurenine to anthranilate and 3-hydroxyanthranilate, respectively, which leads to impaired niacin biosynthesis. Hydroxykynureninuria can be associated with psychomotor retardation and non-progressive encephalopathy. (Ref.8)
Sequence similarities	Belongs to the kynureninase family .
Caution	It has been reported that this enzyme possesses no measurable activity against L-kynurenine and is subject to inhibition by both L-kynurenine and D-kynurenine at pH 7.9 (Ref.6).
Biophysicochemical properties	<u>Kinetic parameters:</u>

What? UniProtKB annotation content

Ontologies

Keywords

Biological process	Pyridine nucleotide biosynthesis
Cellular component	Cytoplasm
Coding sequence diversity	Polymorphism
Disease	Disease mutation
Ligand	Pyridoxal phosphate
Molecular function	Hydrolase
PTM	Acetylation
Technical term	3D-structure Complete proteome

Gene Ontology (GO)

Biological process	NAD biosynthetic process Inferred from electronic annotation. Source: InterPro anthranilate metabolic process Inferred from direct assay (Ref.6). Source: UniProtKB quinolinate biosynthetic process Inferred from direct assay. Source: UniProtKB response to interferon-gamma Inferred from direct assay. Source: UniProtKB response to vitamin B6 Inferred from mutant phenotype. Source: UniProtKB
Cellular component	cytosol Inferred from direct assay. Source: UniProtKB

What? UniProtKB annotation content

Sequence annotation (Features)						
	Feature key	Position(s)	Length	Description	Graphical view	Feature identifier
Molecule processing						
<input type="checkbox"/>	Chain	1 – 465	465	Kynureninase		PRO_0000218657
Regions						
<input type="checkbox"/>	Region	165 – 168	4	Pyridoxal phosphate binding		
Sites						
<input type="checkbox"/>	Binding site	137	1	Pyridoxal phosphate; via amide nitrogen <small>(By similarity)</small>		
<input type="checkbox"/>	Binding site	138	1	Pyridoxal phosphate		
<input type="checkbox"/>	Binding site	250	1	Pyridoxal phosphate		
<input type="checkbox"/>	Binding site	253	1	Pyridoxal phosphate		
<input type="checkbox"/>	Binding site	275	1	Pyridoxal phosphate		
<input type="checkbox"/>	Binding site	305	1	Pyridoxal phosphate		
<input type="checkbox"/>	Binding site	333	1	Pyridoxal phosphate		
Amino acid modifications						
<input type="checkbox"/>	Modified residue	1	1	N-acetylmethionine <small>(By similarity)</small>		
<input type="checkbox"/>	Modified residue	276	1	N6-(pyridoxal phosphate)lysine		
Natural variations						
<input type="checkbox"/>	Natural variant	188	1	R → Q. [dbSNP:rs2304705]		VAR_049724

What? Annotation propagation in UniProtKB

General annotation

Annotation	Propagated?
RecName	Yes
AltName	Yes
Function	Yes
Catalytic activity	Yes
Pathway	Yes
Subunit	Yes
Subcellular location	Yes
Disease	No
Disruption phenotype	No
Polymorphism	No
Alternative products	No

Feature annotation

Annotation	Propagated?
KW	Yes
GO	Yes
Regions of interest	Yes
Active site	Yes
Ligand-binding	Yes
Processing	Yes
PTMs	Yes
Ambiguities	No
Conflicts	No
Natural variants	No
Isoforms	No

Talk outline

- Introduction
- What?

What we annotate in UniProtKB, and what we propagate

- **Why?**

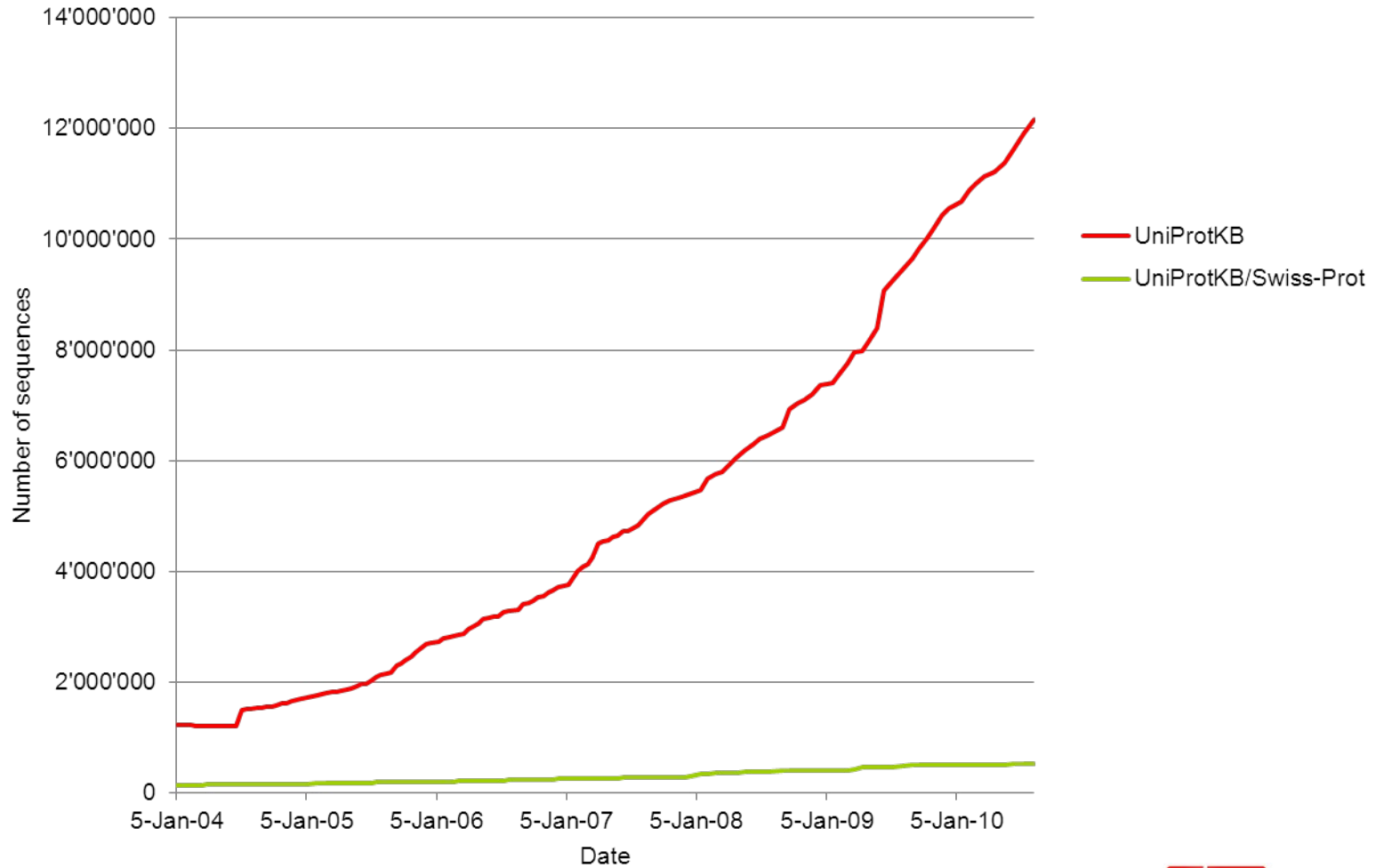
Need for automatic annotation in UniProtKB

- How?

Automatic annotation systems for UniProtKB

- Current status and future plans

Why? Data increase in UniProtKB



Talk outline

- Introduction
- What?

What we annotate in UniProtKB, and what we propagate

- Why?

Need for automatic annotation in UniProtKB

- **How?**

Automatic annotation systems for UniProtKB

- Current status and future plans

How? Automatic annotation in UniProtKB/TrEMBL

- Based on **annotation rules**
- Rules are linked to specific signatures - InterPro
- Annotation rules have
 - annotations
 - conditions
- Rules are tested and validated against UniProtKB/Swiss-Prot
- Rules and annotations are updated each UniProtKB release

How? Automatic annotation in UniProtKB

System		Rule creation	Trigger	Annotations	Scope
SAAS (Spearmin)		automatic	InterPro	comments, KW	all taxa
UniRules	RuleBase	manual	InterPro	protein names, comments, KW	all taxa
	PIR name / site rules	manual	PIRSF*	protein names, comments, features, KW	all taxa
	HAMAP	manual	HAMAP*	protein names, comments, features, KW, GO	Archaea Bacteria plastids

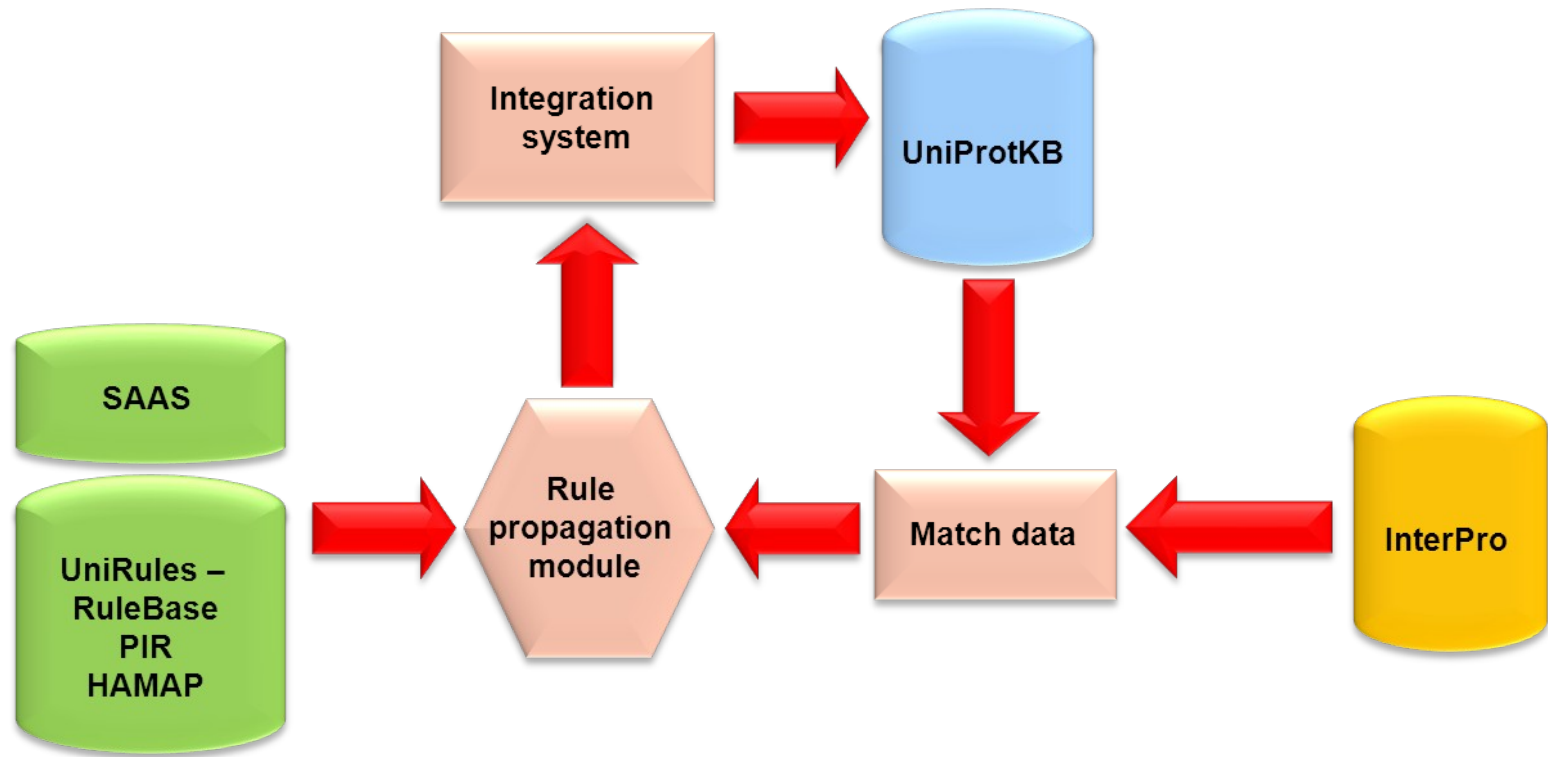
* Signatures produced by UniProt consortium members and submitted to InterPro

How? Automatic annotation in UniProtKB

System	Rule creation	Trigger	Annotations	Scope
SAAS	automatic	InterPro	comments, KW	all taxa
UniRules	manual	InterPro*	protein names, comments, features, KW, GO terms	all taxa

* Flexibility to create custom signatures for InterPro as required

How? Automatic annotation in UniProtKB



How? SAAS – C4.5 algorithm

Proteins	Attributes			Annotations
	Prosite PS00847	Pfam PF01493	Mammalia	FAD
Q9ZN27	-	yes	-	yes
Q9JI00	-	-	yes	-
Q9ZL14	yes	-	-	-
Q9NYQ3	-	-	yes	-
Q9UJM8	-	-	yes	-
Q9NYQ2	-	-	yes	-
Q43155	-	yes	-	yes
Q9T0P4	-	yes	-	yes
Q9WU19	-	-	yes	-

- At each node of the tree, C4.5 chooses one attribute of the entries that most effectively splits them into subsets enriched in the desired annotation.
- The split criterion used by C4.5 is based on Shannon entropy.

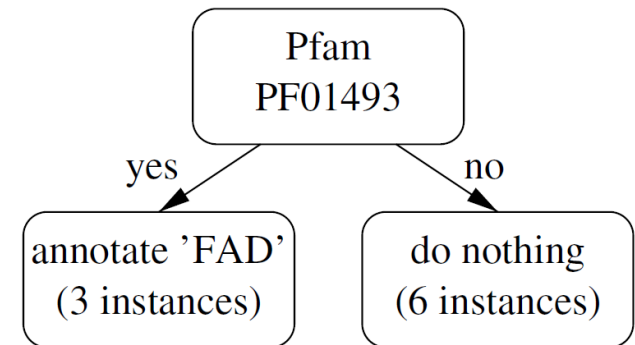
How? SAAS – C4.5 algorithm

Proteins	Attributes			Annotations
	Prosite PS00847	Pfam PF01493	Mammalia	FAD
Q9ZN27	-	yes	-	yes
Q9JI00	-	-	yes	-
Q9ZL14	yes	-	-	-
Q9NYQ3	-	-	yes	-
Q9UJM8	-	-	yes	-
Q9NYQ2	-	-	yes	-
Q43155	-	yes	-	yes
Q9T0P4	-	yes	-	yes
Q9WU19	-	-	yes	-

- At each node of the tree, C4.5 chooses one attribute of the entries that most effectively splits them into subsets enriched in the desired annotation.
- The split criterion used by C4.5 is based on Shannon entropy.

How? SAAS – C4.5 algorithm

Proteins	Attributes			Annotations
	Prosite PS00847	Pfam PF01493	Mammalia	FAD
Q9ZN27	-	yes	-	yes
Q9JI00	-	-	yes	-
Q9ZL14	yes	-	-	-
Q9NYQ3	-	-	yes	-
Q9UJM8	-	-	yes	-
Q9NYQ2	-	-	yes	-
Q43155	-	yes	-	yes
Q9T0P4	-	yes	-	yes
Q9WU19	-	-	yes	-



- At each node of the tree, C4.5 chooses one attribute of the entries that most effectively splits them into subsets enriched in the desired annotation.
- The split criterion used by C4.5 is based on Shannon entropy.

How? SAAS – validation

- 4-fold cross validation is performed on UniProtKB/Swiss-Prot – true and false positives are measured on this training/test set
- Performance on UniProtKB/TrEMBL is estimated using a standard Bernoulli-process based method, assuming a normal distribution:

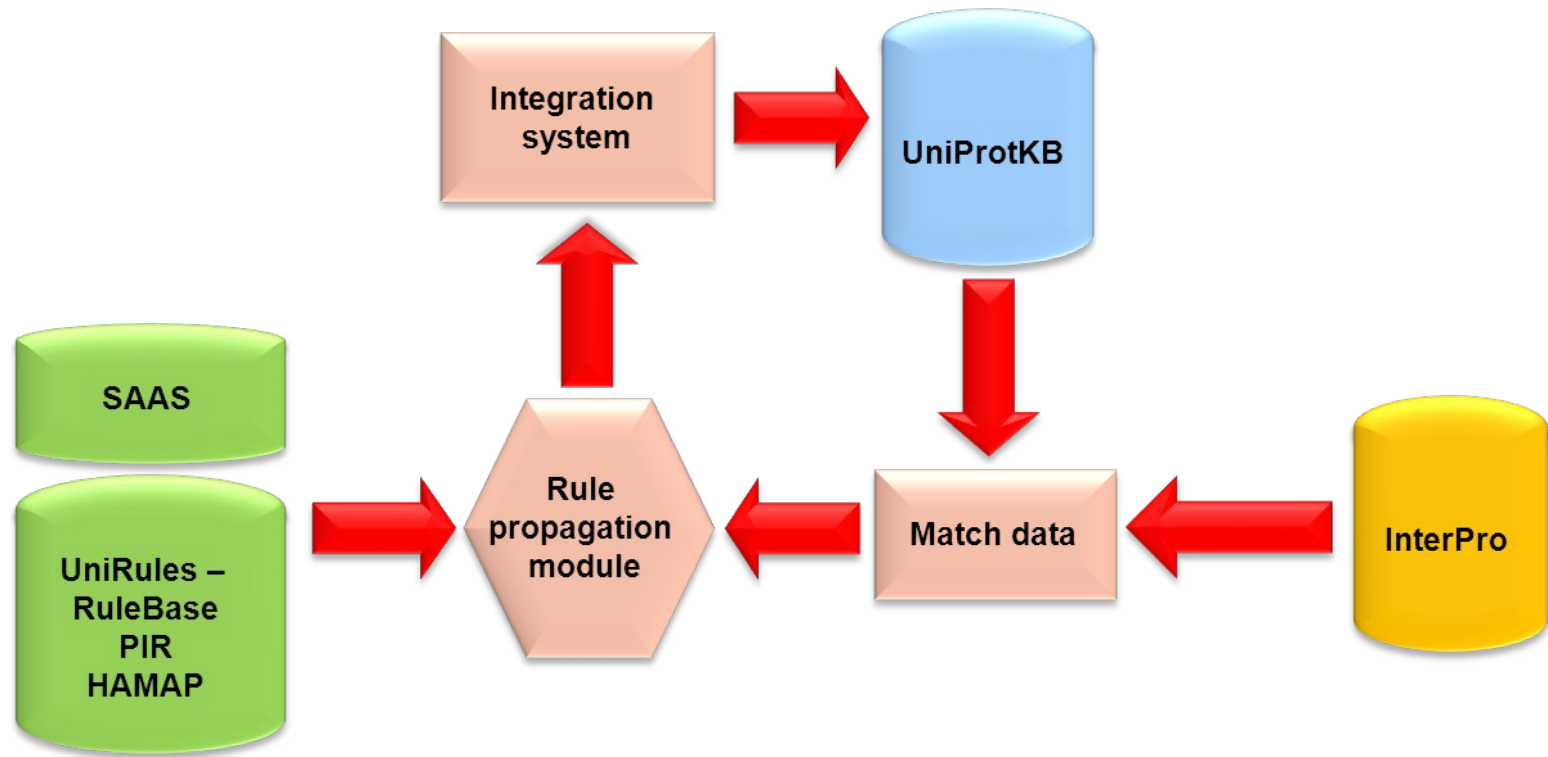
$$p = \frac{\left(f + \frac{z^2}{2N} \pm z \sqrt{\frac{f}{N} - \frac{f^2}{N} + \frac{z^2}{4N^2}} \right)}{(1 + z^2/N)}$$

f - observed success rate
 N - number of predictions

p - estimated success rate
 z - confidence limit

- Only SAAS rules with 99% or greater estimated confidence generate annotation. Rules are produced and validated each release.

How? Automatic annotation in UniProtKB



How - UniRules

- Rules of varying complexity: annotation varies from simple KW attribution to complete annotation as for UniProtKB/Swiss-Prot
- Curation:
 - From SAAS rules as input
 - From UniProtKB/Swiss-Prot annotation and InterPro match data, taxonomy information – continuously reported to curators
 - From literature based curation of characterized families - with the possibility to create new signatures for specific functional groups
- Validation: rules are continuously monitored – validation on UniProtKB/Swiss-Prot – 97% confidence

How? UniRule – rule complexity (HAMAP)

Propagated annotation

Identifier, protein and gene names

Identifier IDI

Protein name RecName: Full=Isopentenyl-diphosphate Delta-isomerase;
Short=IPP isomerase;
EC=5.3.3.2;

Comments

FUNCTION: Catalyzes the 1,3-allylic rearrangement of the homoallylic substrate isopentenyl (IPP) to its highly electrophilic allylic isomer, dimethylallyl diphosphate (DMAPP) (By similarity).

CATALYTIC ACTIVITY: Isopentenyl diphosphate = dimethylallyl diphosphate.

case <FTGroup:1>

COFACTOR: Binds 1 manganese ion per subunit (By similarity).

end case

case <Property:PHOTOSYN>

PATHWAY: Porphyrin biosynthesis; chlorophyll biosynthesis.

end case

Features

From: IDI_ECOLI (Q46822)

Key	From	To	Description	Condition	FTGroup
ACT_SITE	67	67	By similarity	C	
ACT_SITE	116	116	By similarity	E	
METAL	25	25	Manganese (By similarity)	H	1
METAL	32	32	Manganese (By similarity)	H	1
METAL	69	69	Manganese (By similarity)	H	1

How? UniRule – rule complexity (HAMAP)

Propagated annotation

Identifier, protein and gene names

Identifier IDI

Protein name RecName: Full=Isopentenyl-diphosphate Delta-isomerase;
Short=IPP isomerase;
EC=5.3.3.2;

Comments

FUNCTION: Catalyzes the 1,3-allylic rearrangement of the homoallylic substrate isopentenyl (IPP) to its highly electrophilic allylic isomer, dimethylallyl diphosphate (DMAPP) (By similarity).
CATALYTIC ACTIVITY: Isopentenyl diphosphate = dimethylallyl diphosphate.

case <FTGroup:1>

COFACTOR: Binds 1 manganese ion per subunit (By similarity).

end case

case <Property:PHOTOSYN>

PATHWAY: Porphyrin biosynthesis; chlorophyll biosynthesis.

end case

Features

From: IDI_ECOLI (Q46822)

Key	From	To	Description	Condition	FTGroup
ACT_SITE	67	67	By similarity	C	
ACT_SITE	116	116	By similarity	E	

METAL	25	25	Manganese (By similarity)	H	1
METAL	32	32	Manganese (By similarity)	H	1
METAL	69	69	Manganese (By similarity)	H	1

How? UniRule – curator tool

Nature Precedings : doi:10.1038/npre.2010.5247.1 : Posted 12 Nov 2010

The screenshot shows the UniRule curator tool interface. At the top, there is a search bar with 'All Databases' selected and a search input field containing 'Enter Text Here'. Navigation tabs include 'Databases', 'Tools', 'EBI Groups', 'Training', 'Industry', 'About Us', and 'Help'. A sidebar on the left lists various UniProt services like 'UniProt Home', 'UniProt Website', and 'Searches/ Tools', with 'UNIRULE' currently selected. The main content area displays the UniRule 'RU003777' page. It features a search bar with 'RU003777' entered and a 'Search!' button. Below this are buttons for 'View rule statistics', 'Edit this rule', and 'Copy this rule'. The page is divided into several tabs: 'Rule Information', 'Conditions', 'Actions', 'Triggers', 'Flat File', and 'Relationships'. The 'Rule Information' tab is active, showing a table of rule details:

Version	0.93	Old rule num	Related
Creator	john	ID	
Created	2004-05-04	DC	Protein Template
Updater	mindy	Names	
Updated	2010-07-06	Size	
Pack	InterPro	Fusion Nter	
Status	Apply	Fusion Cter	Duplicate
Comments	<input type="text"/>		Plasmid
			GO

At the bottom of the 'Rule Information' section, there is a 'Rule Stats' section showing a star icon, 'Confidence 98.72%', and 'Error Rate 2.13%'. The footer contains 'Terms of Use', 'EBI Funding', 'Contact EBI', and copyright information for the European Bioinformatics Institute 2010.

How? UniRule – curator tool

Nature Precedings : doi:10.1038/npre.2010.5247.1 : Posted 12 Nov 2010

The screenshot displays the UniRule curator tool interface. At the top, there is a search bar with the text "All Databases" and "Enter Text Here", along with "Go", "Reset", and "Give us feedback" buttons. Below the search bar is a navigation menu with options: Databases, Tools, EBI Groups, Training, Industry, About Us, Help, and Site Index. The main content area shows the breadcrumb "EBI > Databases > Databases > UniProt > UNIRULE" and a search input field containing "RU003777". Below the search field are three buttons: "View rule statistics", "Edit this rule", and "Copy this rule". A tabbed interface below these buttons shows "Rule Information", "Conditions", "Actions", "Triggers", "Flat File", and "Relationships". The "Triggers" tab is active, displaying a table with two rows of InterPro IDs: "IPR002616" and "IPR004803". The footer contains the text: "Terms of Use | EBI Funding | Contact EBI | © European Bioinformatics Institute 2010. EBI is an Outstation of the European Molecular Biology Laboratory."

How? UniRule – curator tool

Nature Precedings : doi:10.1038/npre.2010.5247.1 : Posted 12 Nov 2010

The screenshot displays the UniRule curator tool interface. At the top, there is a navigation bar with 'EMBL-EBI' and 'EB-eye Search' logos, a search input field with 'All Databases' selected, and buttons for 'Go', 'Reset', and 'Advanced Search'. Below this is a menu with 'Databases', 'Tools', 'EBI Groups', 'Training', 'Industry', 'About Us', and 'Help'. A sidebar on the left lists various UniProt services, with 'UNIRULE' highlighted. The main content area shows the UniProt UNIRULE page for 'RU003777'. It includes a search bar, a 'Login' link, and a toolbar with 'View rule statistics', 'Edit this rule', and 'Copy this rule' buttons. Below the toolbar are tabs for 'Rule Information', 'Conditions', 'Actions', 'Triggers', 'Flat File', and 'Relationships'. The 'Rule Information' tab is active, displaying a table of annotations:

Type	Annotation	Note
DEEC	2.4.2.29	
DEPN	Queuine tRNA-ribosyltransferase	
CCFU	Exchanges the guanine residue with 7-aminomethyl-7-deazaguanine in tRNAs with GU(N) anticodons (tRNA-Asp, -Asn, -His and -Tyr). After this exchange, a cyclopentendiol moiety is attached to the 7-aminomethyl group of 7-deazaguanine, resulting in the hypermodified nucleoside queuosine (Q) (7-(((4,5-cis-dihydroxy-2-cyclopenten-1-yl)amino)methyl)-7-deazaguanosine)	
CCCA	[tRNA]-guanine + queuine = [tRNA]-queuine + guanine	
CCCO	Binds 1 zinc ion per subunit	
CCSI	Belongs to the queuine tRNA-ribosyltransferase family	
SPKW	Transferase	
SPKW	Zinc	
SPKW	Glycosyltransferase	
SPKW	tRNA processing	
SPKW	Queuosine biosynthesis	

At the bottom of the page, there is a footer with 'Terms of Use', 'EBI Funding', 'Contact EBI', and '© European Bioinformatics Institute 2010. EBI is an Outstation of the European Molecular Biology Laboratory.'

How? UniRule – curator tool

Nature Precedings : doi:10.1038/npre.2010.5247.1 : Posted 12 Nov 2010

The screenshot shows the UniRule curator tool interface. At the top, there is a search bar with 'All Databases' selected and a search input field containing 'Enter Text Here'. Below the search bar are navigation tabs for 'Databases', 'Tools', 'EBI Groups', 'Training', 'Industry', 'About Us', and 'Help'. A left sidebar contains a menu with items like 'UniProt Home', 'UniProt Website', 'About UniProt', 'Searches/ Tools', 'UNIRULE', 'UniProtJAPI', 'Search/Tools', 'Text Search [SRS]', 'UniProt Text Search', 'Blast', 'Useful Tools/ Links', 'UniSave', 'Submissions', 'Downloads', 'Documentation', 'Publications', 'People', and 'Help'. The main content area shows the breadcrumb 'EBI > Databases > Databases > UniProt > UNIRULE' and a search input for 'RU003777'. Below this are buttons for 'View rule statistics', 'Edit this rule', and 'Copy this rule'. A tabbed interface shows 'Rule Information', 'Conditions', 'Actions', 'Triggers', 'Flat File', and 'Relationships'. The 'Conditions' tab is active, displaying a table for rule S0068815. The table has columns for 'Type', 'Negative', 'Signature', and 'Note'. The table contains the following rows:

Type	Negative	Signature	Note
IPRO	yes	IPR000398	
IPRO	yes	IPR004804	
IPRO	yes	IPR008471	
PFAC		PF01702	
TGAC		TIGR00430	
PSTX		A?EP?	

At the bottom of the page, there is a footer with 'Terms of Use', 'EBI Funding', 'Contact EBI', and '© European Bioinformatics Institute 2010. EBI is an Outstation of the European Molecular Biology Laboratory.'

How? UniRule – curator tool

Nature Precedings : doi:10.1038/npre.2010.5247.1 : Posted 12 Nov 2010

EMBL-EBI All Databases

Databases | Tools | EBI Groups | Training | Industry | About Us | Help | Site Index

- UniProt Home
- UniProt Website
- About UniProt
- Searches/ Tools
 - UNIRULE**
 - UniProtJAPI
 - Search/Tools
 - Text Search [SRS]
 - UniProt Text Search
 - Blast
 - Useful Tools/ Links
- UniSave
- Submissions
- Downloads
- Documentation
- Publications
- People
- Help

EBI > Databases > Databases > UniProt > UNIRULE

Statistics: RU003777 Logged in as: udw_dev ([Log out](#))

Stats last run: 2010-10-05 at 01:40

Swiss-Prot

Total Number Hits	Confidence/Error	Positives	Negatives
470	Confidence 98.72% Error Rate 2.13%	True 460 False 10	True 518,878 False 0

Rating Adjusted Results (based on rule exceptions)

Confidence/Error	Positives	Negatives
Confidence 98.72% Error Rate 2.13%	True 460 False 10	True 518,878 False 0

TrEMBL

Positive Hits	Exported Predictions
1,535	16,885

Terms of Use | [EBI Funding](#) | [Contact EBI](#) | © European Bioinformatics Institute 2010. EBI is an Outstation of the [European Molecular Biology Laboratory](#).



How? UniRule – output

Nature Precedings : doi:10.1038/npre.2010.5247.1 : Posted 12 Nov 2010

UniProt > UniProtKB Downloads · Contact · Documentation/Help

Search Blast * Align Retrieve ID Mapping *

Search in Query [Fields »](#)

Q54E51 (Q54E51_DICDI) ★ Unreviewed, UniProtKB/TrEMBL
Last modified August 10, 2010. Version 45. [History...](#)

[Contribute](#)
[Send feedback](#)
[Read comments \(0\) or add your own](#)

[Clusters with 100%, 90%, 50% identity](#) | [Third-party data](#) [text](#) [xml](#) [rdf/xml](#) [gff](#) [fasta](#)

[Customize display](#) [Names](#) · [Attributes](#) · [General annotation](#) · [Ontologies](#) · [Sequences](#) · [References](#) · [Cross-refs](#) · [Entry info](#)

Names and origin

Protein names	<i>Recommended name:</i> Queuine tRNA-ribosyltransferase (RuleBase RU003777V0) EC=2.4.2.29 (RuleBase RU003777V0)
Gene names	Name: qtrt1 (EMBL EAL61522.1) ORF Names: DDB_0184073, DDB_G0291802 (EMBL EAL61522.1)
Organism	Dictyostelium discoideum (Slime mold) [Complete proteome]
Taxonomic identifier	44689 [NCBI]
Taxonomic lineage	Eukaryota > Amoebozoa > Mycetozoa > Dictyostelida > Dictyostelium

How? UniRule – output

General annotation (Comments)

Function	Exchanges the guanine residue with 7-aminomethyl-7-deazaguanine in tRNAs with GUN anticodons (tRNA-Asp, -Asn, -His and -Tyr). After this exchange, a cyclopentendiol moiety is attached to the 7-aminomethyl group of 7-deazaguanine, resulting in the hypermodified nucleoside queuosine (Q) (7-(((4,5-cis-dihydroxy-2-cyclopenten-1-yl)amino)methyl)-7-deazaguanosine) (By similarity) . RuleBase RU003777V0
Catalytic activity	[tRNA]-guanine + queuine = [tRNA]-queuine + guanine. RuleBase RU003777V0
Cofactor	Binds 1 zinc ion per subunit (By similarity) . RuleBase RU003777V0
Sequence similarities	Belongs to the queuine tRNA-ribosyltransferase family . RuleBase RU003777V0
Caution	The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

Ontologies

Keywords

Biological process	Queuosine biosynthesis RuleBase RU003777V0 tRNA processing RuleBase RU003777V0
Ligand	Zinc RuleBase RU003777V0
Molecular function	Glycosyltransferase RuleBase RU003777V0 Transferase
Technical term	Complete proteome

How? UniRule – output

Nature Precedings : doi:10.1038/npre.2010.5247.1 : Posted 12 Nov 2010

★ Unreviewed, UniProtKB/TrEMBL [Q54E51 \(Q54E51_DICDI\)](#)

Documents

Predictions

Proteinname	2.4.2.29 Predicted Queuine tRNA-ribosyltransferase Predicted
Comment	Exchanges the guanine residue with 7-aminomethyl-7-deazaguanine in tRNAs with GU(N) anticodons (tRNA-Asp, -Asn, -His and -Tyr). After this exchange, a cyclopentendiol moiety is attached to the 7-aminomethyl group of 7-deazaguanine, resulting in the hypermodified nucleoside queuosine (Q) (7-(((4,5-cis-dihydroxy-2-cyclopenten-1-yl)amino)methyl)-7-deazaguanosine) (By similarity) Predicted [tRNA]-guanine + queuine = [tRNA]-queuine + guanine Predicted Binds 1 zinc ion per subunit (By similarity) Predicted Belongs to the queuine tRNA-ribosyltransferase family Predicted
Keyword	Transferase Predicted Zinc Predicted Glycosyltransferase Predicted tRNA processing Predicted Queuosine biosynthesis Predicted

How? UniRule – output

Prediction rules

Nature Precedings : doi:10.1038/npre.2010.5247.1 : Posted 12 Nov 2010

Unreviewed, UniProtKB/TrEMBL **Q54E51 (Q54E51_DICDI)**

Documents

Predictions

Proteinname	2.4.2.29 Predicted Queuine tRNA-ribosyltransferase Predicted
Comment	Exchanges the guanine residue with 7-aminomethyl-7 and -Tyr). After this exchange, a cyclopentadiol moiety is attached to the hypermodified nucleoside queuosine (Q) (7-((4,5-dihydroxy-7-methyl-2-thiohydropyridin-4-yl)methyl)uracil) Predicted [tRNA]-guanine + queuine = [tRNA]-queuine + guanine Predicted Binds 1 zinc ion per subunit (By similarity) Predicted Belongs to the queuine tRNA-ribosyltransferase family Predicted
Keyword	Transferase Predicted Zinc Predicted Glycosyltransferase Predicted tRNA processing Predicted Queuosine biosynthesis Predicted

RuleBase
RU003777V0.92S0068815

Condition:
Not InterProGroup
IPR000398

|

Condition:
Not InterProGroup
IPR004804

|

Condition:
Not InterProGroup
IPR008471

|

Condition:
PFAM PF01702

|

Condition:
TIGRFAMs TIGR00430

|

Condition:
Taxonomy: Eukaryota

.sn, -His
resulting in
iosine) (By

How? Automatic annotation in UniProtKB/TrEMBL - Summary

- Manual annotation cannot keep pace with current or projected rates of growth of UniProtKB -> automatic annotation
- SAAS – automatically generated annotation rules for comments, KWs
- UniRule – manually curated annotation rules
 - annotation varies from simple KWs to full annotation
 - start point can be SAAS rules, InterPro reports, literature-based curation of protein families
 - possibility to create custom signatures -> InterPro
- Automatic annotation of UniProtKB/TrEMBL is **refreshed**, and **validated**, each UniProtKB release – validation using UniProtKB/Swiss-Prot as reference
- The source of each annotation is indicated - users can access rule logic

Talk outline

- Introduction

- What?

What we annotate in UniProtKB, and what we propagate

- Why?

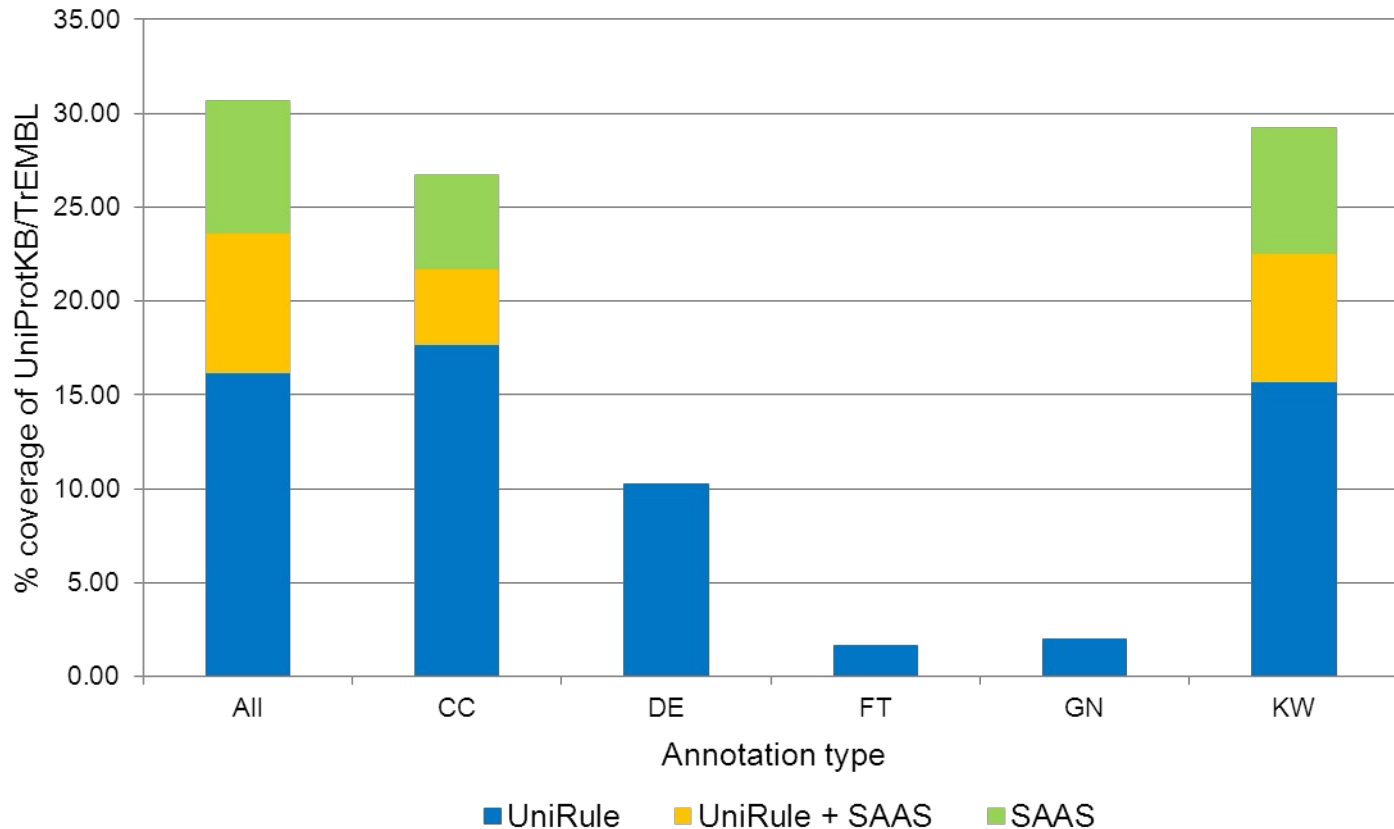
Need for automatic annotation in UniProtKB

- How?

Automatic annotation systems for UniProtKB

- **Current status and future plans**

Current status - coverage of UniProtKB/TrEMBL



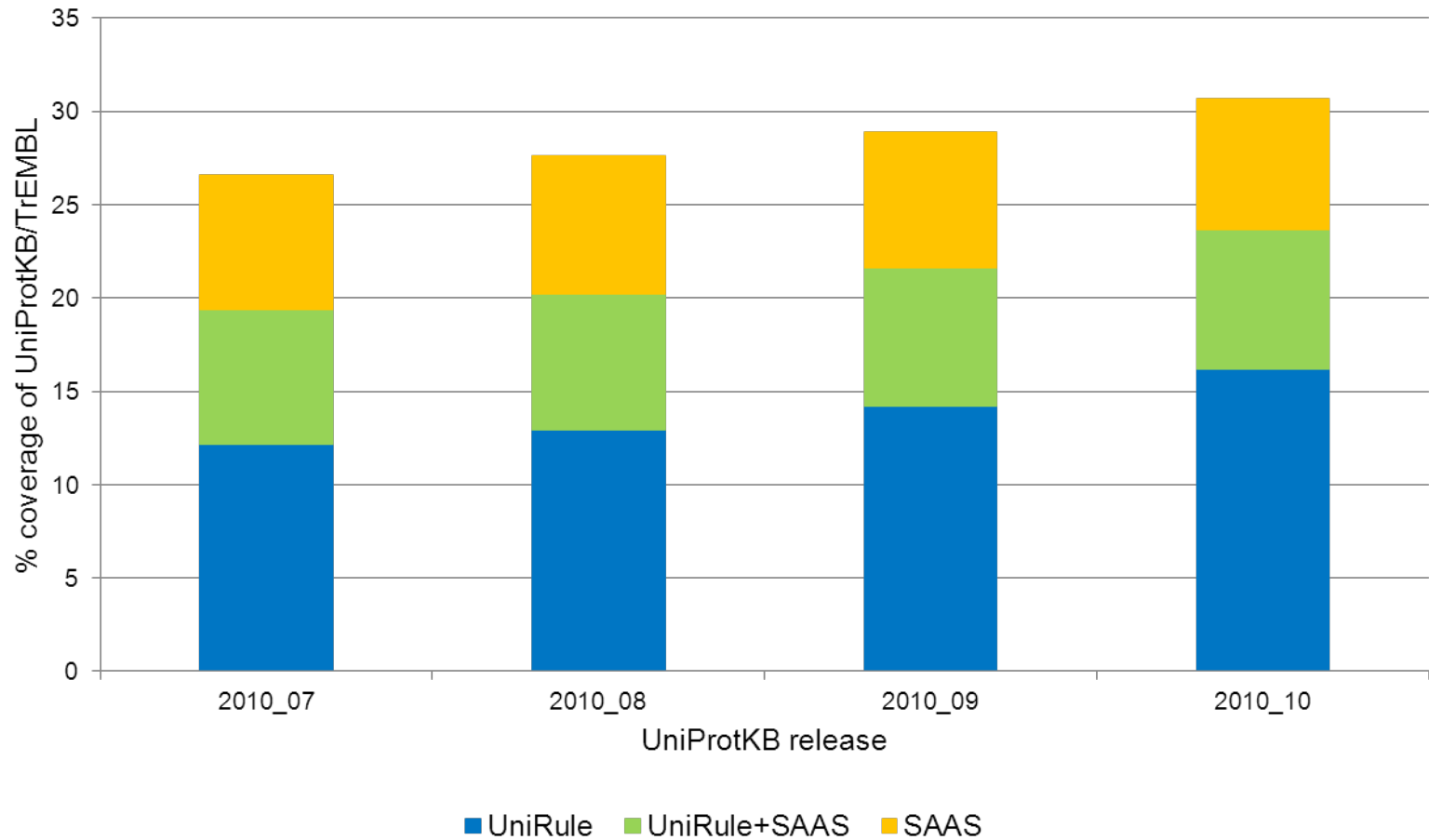
UniProt release 2010_10 included annotations from 7767 SAAS rules, 1814 UniRules



Swiss Institute of
Bioinformatics

Current status – coverage of UniProtKB/TrEMBL

Nature Precedings : doi:10.1038/npre.2010.5247.1 : Posted 12 Nov 2010



Future plans

- Complete integration of all existing rules into one unified system
- Improve presentation and access – including prediction server similar to that currently provided for HAMAP rules
- Collaborative exchange of annotations with other groups – to improve coverage and quality

Acknowledgements

- ✓ **Curators and developers at EBI:**
Ricardo Antunes, Mark Bingley, Alan da Silva, Kati Laiho, Sam Patient, Klemens Pichler, **Diego Poggioli**, Mindi Sehra, Tony Wardell, Maria Jesus Martin, **Claire O'Donovan**
- ✓ **Curators and developers at SIB:**
Andrea Auchincloss, Delphine Baratin, Edouard de Castro, Elisabeth Coudert, Thomas Kappler, Guillaume Keller, Corinne Lachaize, Tania Lima, Karine Michoud, Isabelle Phan, Nicole Redaschi, Catherine Rivoire
- ✓ **Curators and developers at PIR:**
Chuming Chen, Hongzhan Huang, Peter McGarvey, Natalia Petrova, Cecilia Arighi, Winona C. Barker, Raja Mazumder, Darren Natale, C.R. Vinayaka, Lai-Su L. Yeh, Qinghua Wang, Uzoamaka Ugochukwu
- ✓ **The rest of the UniProt production team**
- ✓ **Prosite team:**
Nicolas Hulo, Christian Sigrist, Lorenzo Cerutti, Beatrice Cuče
- ✓ **InterPro team**
- ✓ **National Institutes of Health (NIH), Swiss Federal Government through the Federal Office of Education and Science; European Commission**

Thanks for your attention