SUPPLEMENTAL TUTORIALS

EFI-EST, EFI-GNT, and EFI-CGFP: Enzyme Function Initiative (EFI) Web Resource for Genomic Enzymology Tools

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Tutorial 1. Use of the Taxonomy Tool and Filter by Taxonomy: GRE Superfamily

This tutorial provides the details for the jobs described in the **Taxonomy Tool and Filter By Taxonomy: GRE Superfamily** section in the text. The web resource **Training** page (https://efi.igb.illinois.edu/training/example.php?id=2022) provides links to 1) the **Taxonomy Taxonomy Tool** jobs used to generate **Taxonomy Sunbursts** and 2) both the **DATASET COMPLETED** and **DOWNLOAD NETWORK FILES** pages for the EFI-EST jobs used for generating the taxonomy category-filtered SSNs.

Taxonomy Sunbursts: Taxonomy Tool Families Option

Complete Sequences and Fragments. The **Taxonomy Sunburst** for complete sequences and fragments was generated from the entries in UniProt Release 2022_04 by entering IPR004184 (pyruvate formate lyase domain) into the **Pfam and/or InterPro Families and/or Pfam clans** box on the **Taxonomy Tool Families Option** page (red arrow), entering the **Job name** (green arrow) and an **E-mail address** (magenta arrow), and clicking **"Submit analysis"** (black arrow).

	Pfam ar	d/or InterPro	Families and/or Pfam cla	ne:			
	IPR00	4184					
	11100						
		Family	Family Name	Full Size	UniRef90 Size	UniRef50 Size	
		IPR004184	PFL_dom	25,513	8,545	1,869	
			Total Computed:	25,513 25 513	8,545	1,869	
	The inpu PFxxxxx	ut format is a sin (five digits), IP	ngle family or comma/spac Rxxxxxx (six digits) or CLx	e separated lis xxx (four digits	t of families. Families) for Pfam clans.	should be specified as	
ilter by T	axonom	y can be used	to remove UniProt IDs that	do not match t	he specified taxonom	y categories.	
he rema	ining Ur	iProt IDs are u	sed to generate the sunbur	rst.			
JniRef90 ookup tal etained.	and Uni ple provi	Ref50 clusters ded by UniProt	that contain the UniProt ID /UniRef. Clusters for which	s are retrieved the cluster ID	from the UniRef90 ar (representative seque	ndUniRef50 databases using the notation of the databases using the notation of the list of families and the list of families of the list of families and the notation of the list of the notation of the notat	ne es are
i [°] he numb ooth UniR EFI-EST t	ers of L ef90 clu o gener	IniProt IDs and ister and UniRe ate SSNs.	both UniRef90 cluster and f50 cluster IDs are availab	UniRef50 clus le for download	ter IDs are displayed I and/or transfer to the	on the sunburst; the UniProt IE e Accession ID option (Option	Ds and D) of
f the list EST, the categorie	s of Uni lists she s (Filte	Ref90 or UniR ould (must!) be r by Taxonomy	ef50 cluster IDs are used e filtered with the same li /) used to generate the lis	to generate S st of families (sts.	SNs with the Acces Filter by Family) an	sion IDs option (Option D) of d any specified taxonomy	EFI-
This filteri are not m	ng remo embers	oves the UniRef of the specified	90 and UniRef50 clusters I families or have the selec	with cluster IDs ted taxonomy c	("representative seq ategories.	uences") or internal UniProt ID	s that
- Fragr	nent Op	otion					
UniP codo	rot desi ns; Frag	gnates a Seque gment if the sta	ence Status for each memb rt and/or stop codon is mis	er: Complete it sing. Approxim	the encoding DNA s ately 10% of the entri	equence has both start and sto es in UniProt are fragments.	р
Frag	ments:	Check to	exclude UniProt-defined fra	agments in the	results. (default: off)		
	F	or the UniRef90 fragment.	0 and UniRef50 databases	, clusters are e	xcluded if the cluster	ID ("representative sequence")) is
	L	IniProt IDs in U re fragments.	niRef90 and UniRef50 clus	ters with comp	lete cluster IDs are re	moved from the clusters if the	ý
	by Taxe	onomy					
▶ Filter	h Filter						
▸ Filter Lengt							
 Filter Lengt 		91_IPR0041	84_All		(required)		
 ▶ Filter ▶ Lengt Job name 	e: IP						
 Filter Lengt Job name E-mail addition 	e: <i>IP</i> :						

The results were available on the **DATASET COMPLETED** page. The **Taxonomy Sunburst** tab (below) is the interactive display that provides the numbers of UniProt, UniRef90 cluster, and UniRef50 cluster IDs (red arrow), downloads for IDs and FASTA sequences (blue arrow), and transfers of IDs to EFI-EST (green arrow) or EFI-GND viewer (magenta arrow).



Complete Sequences. The **Taxonomy Sunburst** for the complete sequences was generated by entering IPR004184 into the **Pfam and/or InterPro Families and/or Pfam clans** box on the **Taxonomy Tool Families Option** page (red arrow), checking the **Fragments** box in the **Fragment Option** to exclude fragments (blue arrow), entering the **Job name** (green arrow) and an **E-mail address** (magenta arrow), and clicking **"Submit analysis"** (black arrow).

	m and/or InterPro	Families and/or Pfam cla	ans:		
IP	R004184				
	Family	Family Name	Full Size	UniRef90 Size	UniRef50 Size
	IPR004184	PFL_dom	25,513	8,545	1,869
		Total	25,513	8,545	1,869
The PF:	e input format is a s xxxxx (five digits), ll	Total Computed: ingle family or comma/spa PRxxxxxx (six digits) or CL	: 25,513 ce separated lis xxxx (four digits	t of families. Families) for Pfam clans.	should be specified as
ilter by Taxe	onomy can be used	to remove UniProt IDs that	it do not match i	he specified taxonon	ny categories.
he remainir	ng UniProt IDs are u	used to generate the sunbu	ırst.		
IniRef90 an ookup table etained.	d UniRef50 clusters provided by UniPro	that contain the UniProt I t/UniRef. Clusters for whic	Ds are retrieved h the cluster ID	from the UniRef90 a (representative sequ	ndUniRef50 databases using the ence) matches the list of families are
he number oth UniRefs	s of UniProt IDs and 90 cluster and UniR generate SSNs.	d both UniRef90 cluster and ef50 cluster IDs are availa	d UniRef50 clus ble for download	ter IDs are displayed I and/or transfer to th	on the sunburst; the UniProt IDs and e Accession ID option (Option D) of
his filtering re not mem	removes the UniRe bers of the specifie	of90 and UniRef50 clusters d families or have the sele	with cluster IDs cted taxonomy o	("representative seq categories.	uences") or internal UniProt IDs that
	designates a Sequ	ence Status for each mem	ber: Complete i	f the encoding DNA s	equence has both start and stop
UniProt codons	; Fragment if the sta	an and/or stop codon is mis		atery 10% of the entr	les in UniProt are tragments.
UniProt codons Fragme	; Fragment if the sta	exclude UniProt-o	in the	results. (default: off)	les in UniProt are tragments.
UniProt codons Fragme	Fragment if the sta ents: ☑ Check to For the UniRefs a fragment.	exclude UniProt-5 00 and UniRef50 database	s, clusters are e	results. (default: off) xcluded if the cluster	ID ("representative sequence") is
UniProt codons Fragme	Fragment if the sta ents: C Check to For the UniRefs a fragment. UniProt IDs in I are fragments.	exclude UniProt-5 20 and UniRef50 database JniRef90 and UniRef50 clu	s, clusters are e	results. (default: off) xcluded if the cluster lete cluster IDs are re	es in UniProt are inagments.
UniProt codons Fragme	 Fragment if the statement if the statement if the statement if the statement is a fragment. UniProt IDs in the are fragments. Taxonomy 	exclude UniProt-5 30 and UniRef50 database JniRef90 and UniRef50 clu	s, clusters are e	results. (default: off) xcluded if the cluster lete cluster IDs are re	ID ("representative sequence") is emoved from the clusters if they
UniProt codons Fragme	 Fragment if the statement if the statement. For the UniRefs a fragment. UniProt IDs in I are fragments. Taxonomy Filter 	exclude UniProt-5 00 and UniRef50 database	s, clusters are e	results. (default: off) xcluded if the cluster lete cluster IDs are re	es in OniProt are inagments.
UniProt codons Fragme • Filter by • Length I	 Fragment if the statement: Check to For the UniRefs a fragment. UniProt IDs in I are fragments. Taxonomy Filter IP91_IPR004 	exclude UniProt-5 90 and UniRef50 database JniRef90 and UniRef50 clu	s, clusters are e	(required)	es in OniProt are inagments.
UniProt codons Fragme • Filter by • Length I lob name: E-mail addr	 Fragment if the stands: Check to For the UniReft a fragment. UniProt IDs in U are fragments. Taxonomy Filter IP91_IPR004 ess: 	exclude UniProt-6 10 and UniRef50 database 10 and UniRef50 database 184_NoFragments	s, clusters are e	lete cluster IDs are re	ID ("representative sequence") is amoved from the clusters if they

The results were available on the **DATASET COMPLETED** pages. The **Taxonomy Sunburst** tab (below) is the interactive display that provides the numbers of UniProt, UniRef90 cluster, and UniRef50 cluster IDs (red arrow), downloads for IDs and FASTA sequences (blue arrow), and transfers of IDs to EFI-EST (green arrow) or EFI-GND viewer (magenta arrow).



Complete Sequences, Minimum Length 650 Residues. The **Taxonomy Sunburst** for complete sequences with a minimum length of 650 residues ("full-length" sequences) was generated by entering IPR004184 into the **Pfam and/or InterPro Families and/or Pfam clans** box on the **Taxonomy Tool Families Option** page (red arrow), checking the **Fragments** box in the **Fragment Option** to exclude fragments (blue arrow), entering 650 for the **Minimum Length** in the **Length Filter** (orange arrow), entering the **Job name** (green arrow) and an **E-mail address** (magenta arrow), and clicking "**Submit analysis**" (black arrow).

Retrieve taxono	my for families	i.					
The UniProt IDs f	or family memb	ers are iden	tified in UniProtKB	with a list of Pl	am families, Inte	rPro families, and/or Pfam clans	
Pfam a	nd/or InterPro	Families an	d/or Pfam clans:				
IPR00	4184						
		-			ID (00 0)	U ID (54 0)	
	Family	PEL dom	ly Name F	UII SIZE U	0 EAE	Uniket50 Size	
	IPR004164	PFL_dom	Total	20,013	0,040	1,009	
		Tota	I Computed:	25,513	0,040	1,005	
The inp	ut format is a si	ngle family o	r comma/space se	eparated list of f	amilies. Families	should be specified as	
Filter by Taxonon	iy can be used	to remove U sed to gener	niProt IDs that do ate the sunburst.	not match the s	pecified taxonon	ny categories.	
UniRef90 and Un lookup table prov retained.	iRef50 clusters ided by UniProt	that contain /UniRef. Clu	the UniProt IDs a sters for which the	re retrieved fron cluster ID (rep	n the UniRef90 a resentative sequ	ndUniRef50 databases using the ence) matches the list of families	e s are
The numbers of l both UniRef90 cli EFI-EST to genei	JniProt IDs and uster and UniRe rate SSNs.	both UniRei af50 cluster I	90 cluster and Un Ds are available fo	iRef50 cluster li or download and	Ds are displayed d/or transfer to th	on the sunburst; the UniProt IDs e Accession ID option (Option D	s and) of
lf the lists of Un EST, the lists sh categories (Filte	Ref90 or UniR ould (must!) b r by Taxonom	ef50 cluster e filtered wi /) used to g	IDs are used to th the same list c enerate the lists.	generate SSNs of families (Filt	with the Acces er by Family) an	sion IDs option (Option D) of I d any specified taxonomy	EFI-
This filtering remo are not members	oves the UniRel of the specified	190 and UniF I families or	tef50 clusters with have the selected	cluster IDs ("re taxonomy categ	presentative seq jories.	uences") or internal UniProt IDs	that
 Fragment Op 	otion						
UniProt desi codons; Fra	gnates a Seque gment if the sta	ence Status rt and/or sto	for each member: o codon is missing	Complete if the . Approximately	encoding DNA s	equence has both start and stop ies in UniProt are fragments.)
Fragments:	Check to	exclude Unil	Prot-define	esu	lts. (default: off)		
F	or the UniRef9	0 and UniRe	f50 databases, clu	isters are exclu	ded if the cluster	ID ("representative sequence")	s
l	JniProt IDs in U re fragments.	niRef90 and	UniRef50 clusters	with complete	cluster IDs are re	emoved from the clusters if they	
Eilter by Tax	onomy						
- Filler by Tax	Shoriny			_	_		
- Length Filter							
- Length Filter			_				
- Length Filter Minimum L	ength: 650		•				
• Length Filter Minimum L Maximum L	ength: 650 ength:		+				
▪ Length Filter Minimum L Maximum L	ength: 650 ength:		+				
 Length Filter Minimum L Maximum L Job name: IP 	ength: 650 .ength: 91_ <i>IPR0041</i>	84_NoFra	ngments_Minle	n650	(required)	—	
Length Filter Minimum L Maximum L Job name: IP E-mail address:	ength: 650 .ength: 91_IPR0041	84_NoFra	rgments_Minle	n650	(required)	=	
Length Filter Minimum L Maximum L Job name: IP E-mail address: You will be notifie	ength: 650 .ength: 91_IPR0041 d by e-mail who	84_NoFra	ngments_Minle	m650 processed.	(required)	-	
Length Filter Minimum L Maximum L Job name: IP E-mail address: You will be notifie	ength: 650 .ength: 91_IPR0041 d by e-mail who	*84_NoFra	egments_Minle	n 650 processed. mit Analysis	(required)		

The results were available on the **DATASET COMPLETED** pages. The **Taxonomy Sunburst** tab (below) is the interactive display that provides the numbers of UniProt, UniRef90 cluster, and UniRef50 cluster IDs (red arrow), downloads for IDs and FASTA sequences (blue arrow), and transfers of IDs to EFI-EST (green arrow) or EFI-GND viewer (magenta arrow).



The UniProt ID SSN was generated for the complete UniProt entries in UniProt Release 2022_04 using the EFI-EST Families Option by entering IPR004184 into the Pfam and/or InterPro Families and/or Pfam clans box (red arrow), checking the Fragments box in the Fragment Option to exclude fragments (blue arrow), entering the Job name (green arrow) and an E-mail address (magenta arrow), and clicking "Submit analysis" (black arrow).

Previous Jobs	Sequence BLAS	ST Families	FASTA	Accession IDs	SSN Utilities	
Generate a SSN f	or a protein family	<i>y</i> .				
The members of t	ne input Pfam famil	ies, InterPro familie	s, and/or Pfa	m clans are selecte	d from the UniProt	, UniRef90, or UniRef50
Pfam an	d/or InterPro Fam	ilies and/or Pfam o	clans:			
IPR004	184					
Use	UniRef90 - cluste	r ID sequences inst	tead of UniPr	ot IDs (UniProt is de	fault).	
_ (Family	Family Name	Full Siz	e UniRef90 Si	ze UniRef50	Size
	IPR004184 PI	=L_dom	25,	513 8	,545	1,869
		Tota	al: 25,	513 8	,545	1,869
		Total Compute	d: 25,	513		
UniRef90 clusters cluster ("seed seq UniRef50 clusters the UniProt IDs in The sequences frr ("representative su not match the spe - Fragment Op UniProt desig codons; Frag Fragments:	contain UniProt ID: uence"); as a result contain UniProt ID: the cluster often ar orm the UniRef90 ar gquence") matches cliffed families are ne tion ment if the start an C Check to exclu or the UniRef90 and	s that share ≥90% s t, the UniPro IDs in its sthat share ≥50% s e functionally heterr ad UniRef90 databa the specified famili smoved from the cli Status for each me d/or stop codon is n und d UniRef50 databas	sequence ide the cluster u sequence ide ogeneous, e. sees are the U es. The UniF uster. ember: Comp nissing. Appr fragments in ses, clusters :	htity and have 80% sually are functiona g., paralogues. IniRef90 and UniRe rot members in thes ete if the encoding I oximately 10% of th the results. (defaul are excluded if the co	overlap with the lo ly homogeneous, overlap with the so (50 clusters for wh e UniRef90 and U DNA sequence has e entries in UniPro :: off) luster ID ("represe	ngest sequence in the i.e., orthologues. sed sequence; as a result ich the cluster ID ni/Ref50 clusters that do both start and stop t are fragments.
U ar	niProt IDs in UniRe re fragments.	f90 and UniRef50 c	clusters with o	complete cluster IDs	are removed from	the clusters if they
Filter by Taxo	nomy					
Protein Famil	y Size Options					
Family Doma	in Boundary Optic	on				
SSN Edge Ca	Iculation Option					
Job name: IPS E-mail address: You will be notified	91_IPR004184_	UniProt_NoFra	gments	(requi	red)	
			Submit An	alysis		

The SSN was finalized on the **SSN Finalization** tab of the **DATASET COMPLETED** page using 240 as the **Alignment Score Threshold** that separates the SwissProt-curated functions into different clusters (orange arrow) and 650 residues as the **Minimum** in the **Sequence Length Restriction** to remove truncated sequences (cyan arrow) [1], entering the **Network (SSN) name** (brown arrow), and clicking "**Create SSN**" (black arrow).

DATASET COMPLETED								
Submission Name: IP91_IPR004184_UniProt_NoFragments								
A minimum sequence similarity threshold that specifies the sequence pairs connected by edges is needed to generate the SSN. This threshold also determines the segregation of proteins into clusters. The threshold is applied to the edges in the SSN using the alignment score, an edge node attribute that is a measure of the similarity between sequence pairs.								
Dataset Summary Taxonomy Sunburst Dataset Analysis SSN Finalization								
This tab is used to specify the minimum "Alignment Score Threshold" (that is a measure of the minimum sequence similarity threshold) for drawing the edges that connect the proteins (nodes) in the SSN.								
Alignment Score Threshold: 240 ⑦								
This value corresponds to the lower limit for which an edge will be present in the SSN. The alignment score is similar in magnitude to the negative base-10 logarithm of a BLAST e-value.								
✓ Sequence Length Restriction Options								
Allows restriction of sequences in the generated SSN based on their length. 🕡								
Minimum: 650 (default: 0)								
Maximum: (default: 50000)								
Filter by Taxonomy								
Neighborhood Connectivity								
Fragment Option								
Network name: PR004184_UniProt_NoFragments_Minlen650_AS240 This national splayed in Cytoscape.								
You will be notified by e-mail when the SSN is ready for download.								
Create SSN								

The **Network Files** tab of the **DOWNLOAD NETWORK FILES** page provided the xgmml file for the **Full (SSN) Network** (red arrow; all UniProt nodes and edges) as well as the xgmml files for **Representative Node Networks** that conflate the UniProt nodes based on percent identity (blue arrow). The xgmml file for the full SSN was downloaded, opened with Cytoscape 3.9.1, and displayed with the yFiles Organic layout to obtain the SNN shown below.

SN Overview	Network Files	•				
Rémi Zall Leveraging Pathwa	lot, Nils Oberg Protein, Gen I ys . Biochemis	Pleas I, and John A. G I ome, and Met a stry 2019 58 (41	e cite your use of t erit, The EFI Web genome Databas), 4169-4182. http	he EFI tools: Resource for Genomic es to Discover Novel E is://doi.org/10.1021/acs	Enzymology Tools nzymes and Metab biochem.9b00735	s: ol
e panels below an approximate 0M edges can b 3 RAM, and ~12	provide files for e guide, SSNs w be opened with 6 0M edges can b	full and represent ith ~2M edges car 64 GB RAM, ~20M be opened with 76	ative node SSNs for d n be opened with 16 C I edges can be opene 8 GB RAM.	download with the indicated of BRAM, ~5M edges can be edges and a state of the edges can be edges and a state of the edges can be edges and a state of the e	numbers of nodes and o opened with 32 GB RA edges can be opened w	∍de \M ∕ith
es may be trans eighborhood Cor	ferred to the Ge nectivity utility.	nome Neighborhc	od Tool (GNT), the Co	olor SSN utility, the Cluster A	Analysis utility, or the	
Ill Network	?					
ich node in the r	network represer	nts a single protei	n sequence.			
		# N	lodes	# Edges		
Down	nload ZIP e Node Netwo node (RepNode) or example, for a gle node (meta r orks easier to loa zation is not cha	rorks ? networks, each n a 75% identity Reg node). Sequences ad in Cytoscape.	o,089 ode in the network rep Node network, all cor are collapsed togethe stering of sequences :	47,499,276 presents a collection of proto nnected sequences that sha er to reduce the overall num remains identical to the full	Transfer To: • eins grouped according re 75% or more identity ber of nodes, making fo	to rai
Dow epresentativer representativer crent identity. For suped into a sing mplicated networ we cluster organi	nload ZIP e Node Netwo node (RepNode) or example, for a gle node (meta r gle node (meta r rks easier to loa zation is not cha	orks ? networks, each n a 75% identity Rep ande). Sequences ad in Cytoscape. anged, and the clu	o,089 ode in the network rep Node network, all cor are collapsed togethe stering of sequences	47,499,276 presents a collection of prote nnected sequences that sha er to reduce the overall num remains identical to the full n	Transfer To: •	to 'ai prl
Dow epresentative representative r crent identity. Fc ouped into a sing mplicated networ e cluster organia	e Node Netwo node (RepNode) or example, for a gle node (meta r orks easier to loa zation is not cha	orks ⑦ networks, each n a 75% (dentity Reg identity Reg ad in Cytoscape. anged, and the clu % ID 100	o,089 ode in the network rep Node network, all cor are collapsed togethe stering of sequences # Nodes	47,499,276 presents a collection of prote nnected sequences that sha er to reduce the overall num remains identical to the full r # Edges	Transfer To: • eins grouped according re 75% or more identity ber of nodes, making fo network.	to 'ai
Down epresentative r rcent identity. Fr ouped into a sin mplicated netwo e cluster organia Downle	e Node Netwo node (RepNode) or example, for a gle node (meta r orks easier to loa zation is not cha	orks ⑦ networks, each n a 75% identity Reg node). Sequences ad in Cytoscape. Inged, and the clu % ID 100 05	0,089 ode in the network rep Node network, all cor are collapsed togethe stering of sequences # Nodes 15,986	47,499,276 presents a collection of proto nected sequences that sha er to reduce the overall num remains identical to the full r #Edges 27,061,467 4,012,155	Transfer To: •	to 'an >r I
Down epresentative r representative r reper identity. Fr upped into a st mplicated networ ie cluster organia Downlo Downlo	e Node Netwo node (RepNode) or example, for a gle node (met a reks easier to loa zation is not cha oad ZIP oad ZIP	orks ⑦ Inetworks, each n n a 75% identity Reg a 75% identity Reg node). Sequences ad in Cytoscape. Inged, and the clu % ID 100 95 90	o,089 odde in the network rep Node network, all cor are collapsed togethe stering of sequences # Nodes 15,986 7,879 6,623	47,499,276 presents a collection of proto nnected sequences that sha er to reduce the overall num remains identical to the full r #Edges 27,061,467 4,912,158 2,328,401	Transfer To:	to ran prl
Down epresentative r representative r r r r r r r r r r r r r r	e Node Netwo node (RepNode) or example, for a gle node (meta r orks easier to loa zation is not cha wad ZIP oad ZIP oad ZIP	orks ⑦ Inetworks, each n 75% identity Rej node). Sequences ad in Cytoscape. Inged, and the clu V ID 100 95 90 85	o,089 odde in the network reg Node network, all cor are collapsed togethe stering of sequences # Nodes 15,986 7,879 6,623 5,885	47,499,276 presents a collection of protonnected sequences that shaler to reduce the overall num remains identical to the full r #Edges 27,061,467 4,912,158 2,928,401 1,789,330	Transfer To:	to 'ai >r l
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Downlo Compresentative representative representati	e Node Netwo ande (RepNode) or example, for a gle node (metar gle node (metar gle node (metar prks easier to loa zation is not cha ad ZIP ad ZIP	Image: Control of the second	0,089	47,499,276	Transfer To:	
Downlor Compresentative representative representative representative representative representative representative representative recent dentity. For a second seco	e Node Netwo node (RepNode) or example, for a gle node (meta r rks easier to loa zation is not cha ad ZIP ad ZIP ad ZIP ad ZIP ad ZIP ad ZIP ad ZIP ad ZIP ad ZIP ad ZIP		0,089 odde in the network reprint Node network, all cor are collapsed together stering of sequences # Nodes 15,986 7,879 6,623 5,685 4,903 4,237 3,631 3,149 2,759	47,499,276	Transfer To:	
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Downlor Common Commo	e Node XIP e Node (RepNode) or example, for a gle node (RepNode) or example, for a gle node (metar rtxs easier to loa zation is not cha ad ZIP add ZIP		0,089 ode in the network region Node network, all cor are collapsed together # Nodes 1 5,986 7 ,879 6,623 5 ,685 4 ,903 4 ,237 3 ,631 3 ,149 2 ,759 2 ,461 2 ,247	47,499,276	Transfer To: ains grouped according re 75% or more identity ber of nodes, making for network. Transfer To:	to 'all' 'rl
Downlo Common	e Node ZIP e Node (RepNode) or example, for a gle node (metar prks easier to loa zation is not cha ad ZIP ad ZIP	••••••••••••••••••••••••••••••••••••	0,089 ode in the network reg are collapsed together stering of sequences # Nodes 15,986 15,986 4,903 4,237 3,631 3,149 2,759 2,461 2,247 2,113	47,499,276	Transfer To: • ains grouped according re 75% or more identity ber of nodes, making for network. • Transfer To: •	to rank and r



UniProt ID SSN for the GRE Superfamily. As described in the previous sections, the UniProt ID SSN for the GRE superfamily was generated using an alignment score threshold of 240 and a minimum length of 650 residues. The full SSN was opened with Cytoscape 3.9.1 and displayed with the yFiles Organic layout using a Mac Pro computer with 1.5TB RAM. The SSN contains 20,089 UniProt ID nodes and 47,499,276 edges.

The UniRef90 cluster SSN was generated for the complete UniProt entries with the EFI-EST Family Option by entering IPR004184 into the Pfam and/or InterPro Families and/or Pfam clans box (red arrow), selecting UniRef90 cluster ID sequences (orange arrow), checking the Fragments box in the Fragment Option to exclude fragments (blue arrow), entering the Job name (green arrow) and an E-mail address (magenta arrow), and clicking "Submit analysis" (black arrow).

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The SSN was finalized on the **SSN Finalization** tab of the **DATASET COMPLETED** page using 240 as the **Alignment Score Threshold** that separates the SwissProt-curated functions into different clusters (orange arrow) and 650 residues as the **Minimum** in the **Sequence Length Restriction** to remove truncated sequences (cyan arrow) [1], entering the **Network (SSN) name** (brown arrow), and clicking "**Create SSN**" (black arrow).

DATASET COMPLETED								
Submission Nam	e: IP91_IPR	004184_UniR	Ref90_NoFragment	s				
A minimum sequenc threshold also deterr score, an edge node	e similarity thre nines the segre attribute that is	shold that speci egation of proteir s a measure of t	fies the sequence pairs ns into clusters. The thre he similarity between se	connected by edges is eshold is applied to the equence pairs.	needed to generate the SSN. This edges in the SSN using the alignment			
Dataset Summa	ry Taxono	my Sunburst	Dataset Analysis	SSN Finalization				
This tab is used to threshold) for dra	o specify the m wing the edges	inimum "Alignme that connect the	ent Score Threshold" (the proteins (nodes) in the	nat is a measure of the e SSN.	minimum sequence similarity			
Alignment Score	Threshold:	240	?					
This v magni	alue correspon tude to the neg	ds to the lower I ative base-10 lo	imit for which an edge v ogarithm of a BLAST e-v	vill be present in the SS value.	SN. The alignment score is similar in			
- Sequence Le	ength Restrict	on Options						
Allows restri	ction of sequer	ices in the gene	rated SSN based on the	eir length. 🕡				
Minimum:	650	(default: 0)						
Maximum:		(default: 5000	00)					
▶ Filter by Tax	onomy							
▸ Neighborhoo	d Connectivit	у						
 Fragment Op 	otion							
Network name:	2004184_Ui	niRef90_NoF	ragments_Minlen6	50_AS240 This nar	haved in Cytoscape.			
You will be notifie	d by e-mail wh	en the SSN is re	ady for download.					
			Create SSI	٧				

The Network Files tab of the DOWNLOAD NETWORK FILES page provided the xgmml file for the Full (SSN) Network (red arrow; all UniProt nodes and edges) as well as the xgmml files for Representative Node Networks that conflate the UniProt nodes based on percent identity (blue arrow). These files are available for download and/or transfer to the Color SSNs utility, Cluster Analysis utility, Neighborhood Connectivity utility, and/or EFI-GNT using the "Transfer To" menus (green arrows).

V Overview Network Files	s			
Rémi Zallot, Nils Oberg Leveraging Protein, Gen Pathways. Biochemis	Please , and John A. Ge 10me, and Metag stry 2019 58 (41)	cite your use of th rlt, The EFI Web F Jenome Database , 4169-4182. https	e EFI tools: Resource for Genomi s to Discover Novel E s://doi.org/10.1021/act	c Enzymology Tools: Enzymes and Metabolic s.biochem.9b00735
panels below provide files for an approximate guide, SSNs w M edges can be opened with 6 RAM, and ~120M edges can b	full and representat ith ~2M edges can 64 GB RAM, ~20M o be opened with 768	ive node SSNs for do be opened with 16 G adges can be opened GB RAM.	wnload with the indicated B RAM, ~5M edges can be with 128 GB RAM, ~40M	numbers of nodes and edge e opened with 32 GB RAM, edges can be opened with 2
s may be transferred to the Ge ghborhood Connectivity utility.	nome Neighborhoo	d Tool (GNT), the Col	lor SSN utility, the Cluster	Analysis utility, one
h node in the network represer	nts a single protein	sequence.		•
	# N	odes	# Edges	
		801	2,133,174	Transfer To: -
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Download ZIP presentative Node Netw epresentative node (RepNode) ent identity. For example, for a upde into a single node (meta r uplicated networks easier to loa cluster organization is not cha	orks (2) networks, each no a 75% identity Reph node). Sequences a ad in Cytoscape. unged, and the clust % ID 100	te in the network reputed in the network, all common re collapsed together ering of sequences re # Nodes 5.801	resents a collection of prol nected sequences that shar to reduce the overall nun emains identical to the full # Edges 2.133.174	teins grouped activity are nober of nodes, n ng for les network.
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Download ZIP Do	• • • • • • • • • • • • • • • • • • •	te in the network replode network, all commerce collapsed together ering of sequences re 5,801 5,772 5,681 4,964 4,264 3,708 3,184 2,762 2,400 2,162	resents a collection of prof nected sequences that shar to reduce the overall num amains identical to the full #Edges 2,133,174 2,098,397 1,985,278 1,284,066 776,890 4444,354 228,973 110,675 46,366 25,507	teins grouped action ding to are 75% or more pentity are aber of nodes, n Transfer To: • Transfer To: •
Download ZIP	Instruction Instruction Instruction <td>le in the network replode network, all com recollapsed together ering of sequences re # Nodes 5,801 5,772 5,681 4,964 4,264 3,708 3,184 2,762 2,400 2,162 1,983</td> <td>resents a collection of prof nected sequences that shar to reduce the overall num amains identical to the full # Edges 2,133,174 2,098,397 1,985,278 1,284,066 776,890 444,354 228,973 110,675 46,366 25,507 17,835</td> <td>teins grouped activity are notwork. Transfer To: • Transfer To: •</td>	le in the network replode network, all com recollapsed together ering of sequences re # Nodes 5,801 5,772 5,681 4,964 4,264 3,708 3,184 2,762 2,400 2,162 1,983	resents a collection of prof nected sequences that shar to reduce the overall num amains identical to the full # Edges 2,133,174 2,098,397 1,985,278 1,284,066 776,890 444,354 228,973 110,675 46,366 25,507 17,835	teins grouped activity are notwork. Transfer To: • Transfer To: •
Download ZIP Do	• • • • • • • • • • • • • • • • • • •	te in the network replode network, all commerce collapsed together ering of sequences re # Nodes 5,801 5,772 5,681 4,964 4,264 3,708 3,184 2,762 2,400 2,162 1,983 1,879	resents a collection of prof nected sequences that shar to reduce the overall num amains identical to the full # Edges 2,133,174 2,098,397 1,985,278 1,284,066 776,890 444,354 228,973 110,675 46,366 25,507 17,835 15,914	teins grouped activity are notwork. Transfer To: • Transfer To: •

The xgmml file for the full UniRef90 cluster SSN was transferred from the **DOWNLOAD NETWORK FILES** page to the **Color SSN** utility of the **SSN Utilities** tab by clicking the "**Transfer To**" button and selecting the **Color SSN** option. This utility assigns unique numbers to each cluster (**Sequence Count Cluster Number** node attribute based on decreasing number of UniProt IDs and **Cluster Count Node Number** node attribute based on decreasing number of nodes in each cluster) and colors to the nodes in each cluster. The job was submitted by clicking "**Submit Analysis**" (black arrow).

Previous Jobs	Sequence BLAST	Families	FASTA	Acce	ssion IDs	SSN Utilities	
Color SSNs	Cluster Analysis	Neighborho	od Connec	tivity	Converge	nce Ratio	
Clusters in th	e submitted SSN are id	dentified, num	bered and	colored	. Summary ta	bles, sets of IDs a	and sequences per
cluster are pro	vided.						
The clusters and decreasing numerical nodes in the clusters and the cluste	re numbered and colore mber of UniProt IDs in th uster.	d using two co ne cluster; 2) N	nventions: 1 Iode Count) Seque Cluster	nce Count C Number ass	igned in order of c	ssigned in order of lecreasing number of
SSN	File: 7						
<u>ئە</u>	78201_IP91_IPR004184	4_UniRef90_N	oFragments_	_Minlen@	650_AS240_f	ull_ssn.xgmml.zip	•
A Cytr zip).	oscape-edited SNN can	serve as input	t. The accept	ted form	at is XGMML	(or compressed)	KGMML as
E-mail addres	s:						
You will be not	ified by e-mail when you	ur submission h	nas been pro	cessed.			
			Submit Ar	nalysis			•

The xgmml file for the Color SSN that was generated was downloaded from the Data File

Download tab of the DOWNLOAD COLORED SSN FILES page (red arrow), opened with

Cytoscape 3.9.1, and displayed with the yFiles Organic layout to obtain the Color SNN shown in

Figure 1B.

DOWNLOAD CO	LORED SSN FILES							
Uploaded Filename 90691_IP91_IPR004	:: I184_UniRef90_NoFragments_Minlen650_AS240_full_ssn.xgmml							
Six node attributes were added to the input SSN: Cluster Sequence Count, Sequence Count Cluster Number, Cluster Node Count, Vode Count Cluster Number, node.fillColor (according to Cluster Sequence Count, hexadecimal), and Node Count Fill Color according to Cluster Node Count, hexadecimal).								
"he Data File Download tab provides the Color SSN with the nodes colored according to Cluster Sequence Count (node.fillColor).								
To change the node colors in 0 Color Property; 3) select "Rem " Node Count Fill Color " as th Fill Color .	Cytoscape to Node Count Fill Color : 1) select all nodes; 2) on the Style Panel, click on the "?" in the Fill nove Bypass"; 4) deselect the nodes (now default node color); and 5) open the Fill Color Property and select the Column and "Passthrough Mapping" as the Mapping Type. The nodes will be colored with the Node Count							
The Data File Download tab each cluster, 3) cluster sizes, a	also provides files for 1) the UniProt ID-Color-Cluster Number mapping table, 2) ID Lists and FASTA Files for and 4) SwissProt annotations for clusters and singletons.							
Submission Summary	Data File Download							
	Please cite your use of the EFI tools:							
Rémi Zallot, Nils Leveraging Protei Pathways. Bio	Oberg, and John A. Gerlt, The EFI Web Resource for Genomic Enzymology Tools: n, Genome, and Metagenome Databases to Discover Novel Enzymes and Metabolic ochemistry 2019 58 (41), 4169-4182. https://doi.org/10.1021/acs.biochem.9b00735							
Colored SSN								
Each cluster in the submitte	ed SSN has been identified and assigned a unique number and color.							
Download ZIP (48 MB)								
Supplementary Files								
	Mapping Tables							
Download	UniProt ID-Color-Cluster number mapping table							
	ID Lists and FASTA Files per Cluster							
Download	UniProt ID lists per cluster							
Download	UniRef90 ID lists per cluster							
Download	FASTA files per UniProt cluster							
Download	FASTA files per UniRef90 cluster							
	Miscellaneous Files							
Download	Cluster sizes							
Download	Cluster-based convergence ratio for UniProt IDs							
Download	SwissProt annotations by cluster							
	Run CGFP on Colored SSN							



UniRef90 Cluster SSN for the GRE Superfamily. As described in the previous sections, the UniRef90 cluster SSN for the GRE superfamily was generated using an alignment score threshold of 240 and a minimum length of 650 residues. The nodes were colored using the **Color SSNs** utility. The SSN contains 5,801 UniRef90 cluster nodes and 2,133,174 edges.

The **DOWNLOAD COLORED SSN FILES** page provides other files for download, including the **UniProt ID-Color-Cluster number mapping table** (blue arrow) that can be used by the BridgeDb application in Cytoscape to color the nodes and assign cluster numbers in other SSNs that contain the same (or a subset of the same) UniProt/UniRef90/UniRef50 IDs; this file was used to color the SSNs for the taxonomy-filtered UniRef90 cluster SSNs described in the following sections.

Taxonomy Category-Specific UniRef90 SSNs: Taxonomy Tool Families Option, with transfer of UniRef90 cluster IDs to the EFI-EST Accession IDs Option

The **Taxonomy Sunburst** for complete sequences was used with the **Transfer to EFI-EST** feature (red arrow) to generate taxonomy category-specific UniRef90 SSNs. For superkingdom Bacteria; superkingdom Bacteria, phylum Actinobacteria; superkingdom Bacteria, phylum Bacteroidetes; superkingdom Bacteria, phylum Firmicutes; superkingdom Bacteria, Phylum proteobacteria; and superkingdom Archaea, the taxonomy categories were selected by clicking on the wedge (left panel). For **Preselected conditions** Fungi (four phyla within superkingdom Eukaryota), the Eukaryota taxonomy category was selected (right panel).



For the single taxonomy categories (left panel), in the EFI-EST Accession IDs Option pages that opened, the Fragment Option was used to exclude fragments (blue arrow), Filter by Family was used to select IPR004184 (green arrow), and Filter by Taxonomy was used to select the six single taxonomy categories (magenta arrow). For Fungi (right panel), Fungi was selected from the Preselected conditions menu (magenta arrow). As described in the text, Filter by Family and Filter by Taxonomy are used to ensure that the UniRef90 cluster IDs and internal UniProt IDs match the desired taxonomy category and family. The Job name (orange arrow) and an E-mail address (cyan arrow) were entered, and the job was started by clicking "Create SSN" (black arrow).



The SSNs were finalized on the **SSN Finalization** tabs of the **DATASET COMPLETED** pages using 240 as the **Alignment Score Threshold** that separates the SwissProt-curated functions into different clusters (orange arrow) and 650 residues as the **Minimum** in the **Sequence Length Restriction** to remove truncated sequences (cyan arrow) [1], entering the **Network (SSN) name** (brown arrow), and clicking "**Create SSN**" (black arrow).

DATASET COMPLETED								
Submission Name: I	P91_IPR004184_NoF	ragments_Bacteria	_UniRef90_NoFra	gments_IPR004184_Bacteria				
minimum sequence similarity threshold that specifies the sequence pairs connected by edges is needed to generate the SSN. This reshold also determines the segregation of proteins into clusters. The threshold is applied to the edges in the SSN using the alignment core, an edge node attribute that is a measure of the similarity between sequence pairs.								
Dataset Summary	Taxonomy Sunburst	Dataset Analysis	SSN Finalization					
This tab is used to spe threshold) for drawing	This tab is used to specify the minimum "Alignment Score Threshold" (that is a measure of the minimum sequence similarity threshold) for drawing the edges that connect the proteins (nodes) in the SSN.							
Alignment Score Th	reshold: 240	?						
This value magnitude	e corresponds to the lower l to the negative base-10 lo	imit for which an edge w ogarithm of a BLAST e-v	vill be present in the SS alue.	SN. The alignment score is similar in				
- Sequence Lengt	h Restriction Options							
Allows restriction	n of sequences in the gene	rated SSN based on the	ir length. 🕡					
Minimum: 65	50 (default: 0)							
Maximum:	(default: 5000	00)						
▶ Filter by Taxonor	my							
Neighborhood C	onnectivity							
Fragment Option	ı							
Network name: DFragments_IPR004184_Bacteria_Minlen650_AS240 This name played in Cytoscape.								
You will be notified by	e-mail when the SSN is re	ady for download.						
		Create SSN	N	←				

The Network Files tab of the DOWNLOAD NETWORK FILES pages provided the xgmml file for the Full (SSN) Network (red arrow; all UniProt nodes and edges) as well as the xgmml files for Representative Node Networks that conflate the UniProt nodes based on percent identity (blue arrow). The xgmml files for the full SSNs were download and opened with Cytoscape; the nodes were colored using the BridgeDb app and the UniProt ID-Color-Cluster number color mapping table obtained for the Color SSN in Figure 1B.

omission Name: IP91_I	PR004184_NoFragr	nents Bacteria l	JniRef90_NoFragmen	ts_IPR004184_Bacteria
work Name: 1 IPR004184 NoFrag	ments Bacteria U	niRef90 NoFrag	ments IPR004184 Ba	acteria Minlen650 AS2
SN Overview Networ	k Files			
	Please	e cite your use of t	he EFI tools:	
Rémi Zallot, Nils C	berg, and John A. G	erlt, The EFI Web	Resource for Genomic	c Enzymology Tools:
Leveraging Protein, Pathways. Bioc	, Genome, and Meta hemistry 2019 58 (41	genome Databas), 4169-4182. <mark>http</mark>	es to Discover Novel E os://doi.org/10.1021/acs	Enzymes and Metabolic s.biochem.9b00735
The panels below provide files an approximate guide, St 10M edges can be opened BB RAM, and ~120M edges	es for full and representa SNs with ~2M edges can with 64 GB RAM, ~20M can be opened with 768	tive node SSNs for a be opened with 16 a edges can be opene GB RAM.	download with the indicated GB RAM, ~5M edges can be d with 128 GB RAM, ~40M	numbers of nodes and edges e opened with 32 GB RAM, edges can be opened with 25
iles may be transferred to t leighborhood Connectivity ι	he Genome Neighborhoo utility.	od Tool (GNT), the C	olor SSN utility, the Cluster	Analysis utility, or the
ull Network 🕡				
ach node in the network re	presents a single protein	sequence.		
		Nodes	# Edges	
Download ZIP		110	2 021 043	Transfor To:
Download 21	5	,413	2,021,945	
Representative Node I n representative node (Rep ercent identity. For example rouped into a single node () omplicated networks easier	Networks ⑦ Node) networks, each no e, for a 75% identity Repi meta node). Sequences to load in Cytoscape	de in the network re Node network, all co are collapsed togeth	presents a collection of prot nnected sequences that sha er to reduce the overall nun	teins grouped according to are 75% or more identity are aber of nodes, making for less
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Taxonomy Category-Filtered UniRef90 Cluster SSNs for the GRE Superfamily. The SSNs were generated using an alignment score threshold of 240 and a minimum length of 650 residues. For Panel A, the nodes were colored using the Color SSNs utility; for Panels B through H, the clusters/nodes were colored using the UniProt ID-Color-Cluster number color mapping table for the Color SSN in Panel A to allow the clusters/nodes to be associated with the clusters/nodes in the SSN for the entire superfamily in panel A. Panel A, SSN for the entire GRE superfamily; the SSN contains 5,801 nodes and 2,133,174 edges. Panel B, Superkingdom Bacteria; the SSN contains 5,419 nodes and 2,021,943 edges. Panel C, Superkingdom Bacteria, phylum Actinobacteria; the SSN contains 333 nodes and 13,658 edges. Panel E, Superkingdom Bacteria, phylum Firmicutes; the SSN contains 2,467 nodes and 515,667 edges. Panel F, Superkingdom Bacteria, phylum Proteobacteria; the SSN contains 1,048 nodes and 50,190 edges. Panel G, Superkingdom Archaea; the SSN contains 262 nodes and 2,074 edges. Panel H, Superkingdom Eukaryota, Fungi only; the SSN contains 28 nodes

Taxonomy Category-Specific UniRef90 SSNs: EFI-EST Families Option, Filter by Taxonomy in the Analysis Step

The SSN Finalization tab of the DATASET COMPLETED page for the UniRef90 cluster SSN for the complete entries was used to generate the taxonomy category-filtered SSNs described in the previous section. The SSNs were finalized using 240 as the Alignment Score Threshold (red arrow) and 650 residues as the Minimum in the Sequence Length Restriction (blue arrow). For the single taxonomy categories (left panel), Filter by Taxonomy was used to select the single taxonomy categories (green arrow). For Fungi (right panel), Fungi was selected from the Preselected conditions menu (green arrow).



The Network Files tab of the DOWNLOAD NETWORK FILES pages provided the xgmml file for the Full (SSN) Network (red arrow; all UniProt nodes and edges) as well as the xgmml files for Representative Node Networks that conflate the UniProt nodes based on percent identity (blue arrow). The xgmml files for the full SSNs were downloaded and opened with Cytoscape; the nodes were colored using the BridgeDb app and the UniProt ID-Color-Cluster number color mapping table obtained for the Color SSN in Figure 1B.

	84_UniRef90_N	oFragments_Ba	cteria_Minlen650_AS	240
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e panels below provide files for an approximate guide, SSNs v OM edges can be opened with 3 RAM, and ~120M edges can I es may be transferred to the G eighborhood Connectivity utility.	full and representat <i>i</i> th ~2M edges can 64 GB RAM, ~20M i be opened with 768 shome Neighborhoo	ive node SSNs for do be opened with 16 G adges can be opened GB RAM. d Tool (GNT), the Co	ownload with the indicated B RAM, ~5M edges can be I with 128 GB RAM, ~40M Ior SSN utility, the Cluster.	numbers of nodes and edges. opened with 32 GB RAM, edges can be opened with 250 Analysis utility, or the
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Taxonomy Category-Specific UniRef90 SSNs: EFI-EST Families Option, Filter by Taxonomy in the Generate Step

The same taxonomy category-filtered UniRef90 SSNs were generated in separate jobs using the **EFI-EST Family Option** by specifying IPR004184 as the input family (red arrow), selecting UniRef90 cluster IDs (blue arrow), selecting **Fragment Option** to exclude fragments (green arrow), and selecting the taxonomy categories (magenta arrow; single categories in the left panel; Fungi in the right panel). The **Job name** (orange arrow) and an **E-mail address** (cyan arrow) were entered; the job was started by clicking **"Submit analysis"** (black arrow).

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Family Size UniRef90 Size UniRef50 Size	IPR004184 PFL_om 25,513 8,545 1,869 Total: 25,513 8,545 1,869
Total: 25,513 8,545 1,869	Total Computed: 8,545
Total Computed: 8,545	The input format is a single family or comma/space separated list of families. Families should be specified as PFxxxxx (five digits), IPRxxxxxxx (six digits) or CLxxxx (four digits) for Pfam clans.
The input format is a single family or commalispace apparated list of families. Families should be specified as PFxxxxx (live digits), IPFxxxxxx (gits) or CLxxxx (four digits) for Pfam clans.	UniReI90 clusters contain UniProt IDs that share >290% sequence identity and have 80% overlap with the longest sequence in the cluster ("seed sequence)", as a result, the UniProt IDs in the cluster usually are functionally homogeneous, i.e., orthologues. UniReI60 clusters contain UniProt IDs that share >250% sequence identity and have 80% overlap with the set sequence; as a result,
Omster doublete doublete doublet for an on the similar build requests down in the norm of the doublet	The uni-mot los in the custer often are functionary neterogeneous, e.g., paraiogues. The sequences from the Unified ion and Unified addatases are the Unified ion and Unified Dictators for which the duster ID ("representative sequences") matches the specified families. The UniFrot members in these Unified ion and Unified Dictators that do
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* Fragment Option	UniProt designates a Sequence Status for each member: Complete if the encoding DNA sequence has both start and stop codons; Fragment if the start and/or stop codon is missing, Approximately 10% of the entries in UniProt are fragments.
UniProt designates a Sequence Status for each member: Complete if the encoding DNA sequence has both start and stop codons; Fragment if the start and/or stop codon is missing. Approximately 10% of the entries in UniProt are fragments.	Fragments: Check to excent the control of the results. (default: off) For the UnRef50 and U_Ref50 databases, clusters are excluded if the cluster ID ("representative sequence") is forement
Fragments: Check to exclude ts in the results. (default: off)	a tragment. UniProt IDs in UniRef90 and UniRef50 clusters with complete cluster IDs are removed from the clusters if they
For the UniRef90 and UniRef50 databases, clusters are excluded if the cluster ID ("representative sequence") is a fragment.	are fragments.
UniProt IDs in UniRef90 and UniRef50 clusters with complete cluster IDs are removed from the clusters if they are fragments.	- Filter by Taxonomy
	From preselected conditions, the user can select "Bacteria, Archaea, Fungi", "Eukaryota, no Fungi", "Fungi", "Viruses",
- Filter by Taxonomy	bacteria, clushyola, or increase to resinct the reteneved sequences to these autonomy groups. "Bacteria, Archaea, Fungi", "Bacteria, "Archaea", and "Fungi" select organisms that may provide genome context (gene clusters/cencrea) used for inferring functions.
From preselected conditions, the user can select "Bacteria, Archaea, Fungi", "Eukaryota, no Fungi", "Fungi", "Viruses", "Bacteria", "Eukaryota", or "Archaea" to restrict the retrieved sequences to these taxonomy groups.	The retrieved sequences also can be restricted to taxonomy categories within the Superkingdom, Kingdom, Phylum, Class, Order, Family, Genus, and Species ranks. Multiple conditions are combined to be a union of each other.
"Bacteria, Archaea, Fungi", "Bacteria", "Archaea", and "Fungi" select organisms that may provide genome context (gene clusters/operons) useful for inferring functions.	The sequences from the UniRef90 and UniRef50 databases are the UniRef80 and UniRef50 clusters for which the cluster ID ("representative sequence") matches the specified taxonomy categories. The UniProt members in these clusters that do not match the secretified arrangement efforts are removed from the cluster.
The retrieved sequences also can be restricted to taxonomy categories within the Superkingdom, Kingdom, Phylum, Class, Order, Family, Genus, and Species ranks. Multiple conditions are combined to be a union of each other.	Preselected conditions: [Fungi -
The sequences from the UniRef30 and UniRef50 databases are the UniRef30 and UniRef50 clusters for which the cluster ID ("representative sequence") matches the specified taxonomy categories. The UniProt members in these clusters that do not moth the securities taxonomy categories are recovered in the cluster.	Phylum Ascomycota
Preselected conditions: Bacteria	Phylum Basidiomycota
Superkingdom - Bacteria	Phylum · Fungi incertae sedis
Reset	Phylum undassified fungi
Protein Family Size Options	Keset
Family Domain Boundary Option	Protein Family Size Options
SSN Edge Calculation Option	Family Domain Boundary Option
	SSN Edge Calculation Option
Job name: IP91_IPR004184_UniRef90_NoFragments_Bacteria (required)	Job name: IP91_IPR004184_UniRef90_NoFragments_Fungi (required)
E-mail address:	E-mail address:
You will be notified by e-mail when your submission has been processed.	You will be notified by e-mail when your submission has been processed.
Submit Analysis	Submit Analysis
	``````````````````````````````````````

As described previously for the UniProt ID and UniRef90 cluster SSNs, the SSNs were finalized (SSN Finalization tab on the DATASET COMPLETED pages) using 240 as the Alignment Score Threshold and 650 residues as the Minimum in the Sequence Length Restriction, entering the Network (SSN) name (brown arrow), and clicking "Create SSN" (black arrow).

DATASET (	COMPLE	TED			
Submission Nan	ne: IP91_IPR	004184_UniR	ef90_NoFragment	s_Bacteria	
A minimum sequent threshold also deter score, an edge node	ce similarity thre mines the segre a attribute that i	eshold that specifi egation of protein s a measure of th	ies the sequence pairs s into clusters. The thre e similarity between se	connected by edges is eshold is applied to the equence pairs.	needed to generate the SSN. This edges in the SSN using the alignment
Dataset Summa	ary Taxono	omy Sunburst	Dataset Analysis	SSN Finalization	
This tab is used threshold) for dra	to specify the m awing the edges	ninimum "Alignme s that connect the	nt Score Threshold" (the proteins (nodes) in the	nat is a measure of the e SSN.	minimum sequence similarity
Alignment Scor	e Threshold:	240			
This magr	value correspor hitude to the neg	nds to the lower lingative base-10 log	mit for which an edge v garithm of a BLAST e-v	vill be present in the SS alue.	SN. The alignment score is similar in
- Sequence L	ength Restrict	ion Options			
Allows restr	iction of seque	nces in the genera	ated SSN based on the	ir length. 🧿	
Minimum:	650	(default: 0)			
Maximum:		(default: 5000	0)		
▶ Filter by Ta	conomy				
▸ Neighborho	od Connectivi	ty			
<ul> <li>Fragment O</li> </ul>	ption				
Network name:	UniRef90_I	NoFragments_	Bacteria_Minlen6	50_AS240 This nar	ne w <b>ater and a set of the set of</b>
You will be notifi	ed by e-mail wh	en the SSN is rea	ady for download.		
			Create SSI	N	

The Network Files tab of the DOWNLOAD NETWORK FILES pages provided the xgmml file for the Full (SSN) Network (red arrow; all UniProt nodes and edges) as well as the xgmml files for Representative Node Networks that conflate the UniProt nodes based on percent identity (blue arrow). The xgmml files for the full SSNs were download and opened with Cytoscape; the nodes were colored using the BridgeDb app and the UniProt ID-Color-Cluster number color mapping table obtained for the Color SSN in Figure 1B.

Overview Network File	s			
Rémi Zallot, Nils Oberg Leveraging Protein, Ger Pathways. Biochemi	Please g, and John A. Ge <b>nome, and Metag</b> istry 2019 58 (41)	e cite your use of th erit, <b>The EFI Web I</b> genome Database I, 4169-4182. https	ne EFI tools: Resource for Genomi es to Discover Novel I s://doi.org/10.1021/ac:	c Enzymology Tools: Enzymes and Metaboli s.biochem.9b00735
panels below provide files for n approximate guide, SSNs w /l edges can be opened with f RAM, and ~120M edges can b	full and representa vith ~2M edges can 64 GB RAM, ~20M be opened with 768	tive node SSNs for de be opened with 16 G edges can be opened GB RAM.	ownload with the indicated B RAM, ~5M edges can b d with 128 GB RAM, ~40M	numbers of nodes and edg e opened with 32 GB RAM, edges can be opened with
may be transferred to the Ge	enome Neighborhoo	d Tool (GNT), the Co	lor SSN utility, the Cluster	Analysis utility, or the
hborhood Connectivity utility.				
Network ?				
node in the network represe	ents a single protein	sequence.		
	# N	lodes	# Edges	
Download ZIP	5	,419	2,021,943	Transfer To: 💌
presentative Node Netw presentative node (RepNode) ant identity. For example, for ped into a single node (meta i plicated networks easier to lo	orks (7) ) networks, each no a 75% identity Rep node). Sequences a ad in Cytoscape.	de in the network rep Vode network, all con are collapsed togethe	resents a collection of pro nected sequences that sh r to reduce the overall nun	teins grouped according to are 75% or more identity ar nber of nodes, making for le
presentative Node Netw presentative node (RepNode) ant identity. For example, for ped into a single node (meta plicated networks easier to loa cluster organization is not cha	orks (7) ) networks, each no a 75% identity Reph node). Sequences a ad in Cytoscape. anged, and the clusi % In	de in the network rep lode network, all con are collapsed togethe tering of sequences n # Nodes	resents a collection of pro nected sequences that shi r to reduce the overall nun emains identical to the full # Edges	teins grouped according to are 75% or more identity are nber of nodes, making for le network.
presentative Node Netw presentative node (RepNode) ant identity. For example, for a ped into a single node (meta plicated networks easier to loa cluster organization is not cha	) networks, each no a 75% identity Reph node). Sequences <i>i</i> ad in Cytoscape. anged, and the clus: % ID	de in the network rep lode network, all con are collapsed togethe tering of sequences r <b># Nodes</b> 5.419	resents a collection of pro nected sequences that sh r to reduce the overall nun emains identical to the full <b>#Edges</b> 2 021 043	teins grouped according to are 75% or more identity an ober of nodes, making for le network.
presentative Node Netw presentative node (RepNode) ent identity. For example, for i ped into a single node (meta plicated networks easier to loa cluster organization is not cha	) networks ⑦ ) networks, each no a 75% identity Reph node). Sequences a ad in Cytoscape. anged, and the clust % ID 100 05	de in the network rep Vode network, all con are collapsed togethe tering of sequences r <b># Nodes</b> 5,419 5,300	resents a collection of pro nected sequences that sh r to reduce the overall nun emains identical to the full <b>#Edges</b> 2,021,943 1 087 868	teins grouped according to are 75% or more identity are ber of nodes, making for le network. Transfer To: • Transfer To: •
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### Tutorial 2. Use of the Taxonomy Tool and Filter by Taxonomy: RS Superfamily

This tutorial provides the details for the jobs described in the **Taxonomy Tool and Filter By Taxonomy: RS Superfamily** section in the text. The web resource **Training** page (https://efi.igb.illinois.edu/training/example.php?id=2022) provides links to 1) the **Taxonomy Taxonomy Tool** jobs used to generate **Taxonomy Sunbursts** and 2) both the **DATASET COMPLETED** and **DOWNLOAD NETWORK FILES** pages for the EFI-EST jobs used for generating the taxonomy category-filtered SSNs.

### **Taxonomy Sunbursts: Taxonomy Tool Families Option**

**Complete Sequences and Fragments**. The **Taxonomy Sunburst** for complete sequences and fragments was generated from UniProt Release 2022_04 by entering a list of 211 Pfam and InterPro families and/or domains (**Tutorial Table 1**) into the **Pfam and/or InterPro Families and/or Pfam Clans** box on the **Taxonomy Tool Families Option** page (red arrow), entering the **Job name** (orange) and an **E-mail address** (cyan arrow), and clicking "**Submit analysis**" (black arrow). The Tool provides the list of input families/domains with the numbers of UniProt, UniRef90, and UniRef50 clusters in each, so the page is long (next page). The two boxed areas are enlarged on the following page to clearly show the input parameters.

Previous Jobs	Families FASTA Accession IDs	_		7						
						IPR024001 Cys-rich_pep_rSAM_mat_CcpM	231	130	67	IPR034ves sactenocnicropryt_L6_M1 4/ 33 1 170021605 Commonwhisteneen III oxidate 68.641 21.743 5.980
Retrieve taxonc	my for families.			,		IPR024007 FeFe-hyd_mat_nyou	3,483	1,754	78	ID0014508 Spectrometrin biosynthesis 8 7 5
The UniProt IDs	for family members are identified in UniProtKB with a	a list of Pfam farr	milles, InterPro fan	nilies and/or Pfam clans.		IPR024016 CHP04064_RSAM	20	14	4	1000/34514 TheK-like 11 3 1
Diam a	A satisfy house and reactions and the second s	IBL WY FRANK	1965, max	/805, senaror r m		IPR024017 Pep_cyd_forwi	40	160	2	1000/04515 Thei-like 8 4 2
Plana	dior InterPro Families:			/		IPRO24016 URPORUS_FORM	3.30	2.075	14	10001/519 TunB-like 11 6 1
45784	PF04055 PF06969 PF08497 PF12345 PF1318	36 PF16199 PF	-16881 PF19238	3 PF19288 PF19864		IPR024021 rere-ryo_ryot_rown	3,733	2,075	217	IPR034529 Form3-like 5 2 1
	Really Mana	Tott Plan 11	10.400 Piece 11e			IPR024025 COLE (SAM maturate	2,759	1 222	70	IPP/034530 HznP-like 3,559 1,910 158
	Family Family Name	Fun Size um	Refer size orm	Ret50 Size		IPR024020 OGFF_TOWE_maturase	1,002	1,202	142	IDP/04/531 Methylation of vatakemycin 9 4 1
	IPR000385 Moan_NITS_PQqt_Fe-S-bu_C-a	49,241	23,160	4,777		IPH024032 rown_pareo_msc	24.904	9.997	142	100/04/512 (2008-like 57 53 11
	IPR001989 Radical_activat_CS	26,935	9,907	1,836	11	IPR024177 Biotin_synthese	24,304	8,337	478	ID0034534 Durimitina methalfransferana 8 7 1
	IPR002684 Biotin_synth/BioAB	27,640	9,880	1,004		IPR024521 DUP3641	4,310	2,730	235	IPR0345a4 rymmune_menymaniserase o r .
	IPR003698 Lipoyl_synth	39,047	13,924	1,318		IPR024560 UPF0313_C	11,093	3,850	317	1PH034547 Tel 100a_matutate 21 3 5
	IPR003739 Lys_aminomutase/Glu_NH3_mut	20,775	10,372	1,278		IPR024924 7-CO-7-deazaguanine_synth-like	25,740	11,573	1,114	194034500 trove_wyouceme-symmetry 0,000 3,330 rvv
	IPR004383 rRNA_lsu_MTrfase_RimN/Cfr	39,944	15,429	1,455		IPR025895 LAM_C_dom	6,845	3,760	332	19R034557 (1024_10294_102310033389389 3,721 1,422 120
	IPR004558 Coprogen_oxidase_HemN	16,796	6,746	513	1	IPR026322 Geopep_mat_rSAM	106	95	26	IPR034559 Spore_PP_lysase_unamous 557 327 20
	IPR004559 HemW-like	38,255	17,990	2,765	1	IPR026332 HutW	1,392	438	75	IPR034560 Spore_PP_lysase_bacili 1,2/3 302 0
	IPR005839 Methylthiotransferase	87,716	37,295	4,127	1	IPR026335 SAM_SPASM_FxsB	1,394	895	82	IPR034687 ELP3-Iko 7,115 3,020 300
	IPR005840 Ribosomal_S12_MeSTrtase_Rimu	28,658	11,857	2,029		IPR026344 SCM_rSAM_ScmE	66	62	7	IPR038135 Methythiotranslerase_N_st 21,07.4 00,000 0,000
	IPR005909 RaSEA	2,035	1,022	229	11	IPR026346 SCM_rSAM_Scmi-	59	56	6	PR038651 ELP3 63,650 19,761 1,779
	IPR005911 YhcC-like	11,293	4,505	502		IPR026351 rSAM_SeCys	4,383	2,794	272	IPR040072 Methyltransterase_A 45,000 11,0% 6,000
	IPR005980 Nase_CF_NIfB	2,647	1,104	82		IPR026357 rSAM/SPASM_prot_GRRM_system	342	189	72	IPR040074 BssD/PfWYjW 9,191 3,899 962
	IPR006463 MiaB_methiclase	35,615	13,649	723		IPR026401 CXOX_matur	139	93	35	IPR040081 Cndl-like 1 2 1
	IPR006468 MiaB-like_B	4,407	2,226	506		IPR026404 rSAM_w_lipo	429	175	16	IPR040082 GenK-like 4 1 1
	IPR006467 MiaB-like_C	17,077	8,216	1,089		IPR026407 SAM_GG-Bacter	267	131	67	IPR040085 MJ0674-like 7,375 4,888 624
	IPR006638 Elp3/MiaA/NfB-like_rSAM	446,282	212,389	36,535		IPR026412 rSAM_Cxxx_rpt	171	108	34	IPR040086 MJ0683-like 22,149 11,842 1,979
	IPR007197 rSAM	722,535	355,669	70,723		IPR026423 rSAM_cobopep	190	138	15	IPR040087 MJ0021-like 1,943 1,037 231
	IPR010505 Mob_synth_C	38,361	16,635	1,682		IPR026426 rSAM_FibroRumin	18	18	5	IPR040088 MJ0103-like 747 535 117
	IPR010722 BATS_dom	39,852	14,953	1,222	11	IPR026429 MIA_synthase	13	10	1	IPR041582 Rim0_TRAM 25,468 10,202 1,260
	IPR010723 HemN_C	39,495	17,002	2,804	1	IPR026447 B12_SAM_Ta0216	457	325	66	IPR045375 Put_radical_SAM-like_N 4,615 2,655 513
	IPR011101 DUF5131	7,313	4,801	1,324	11	IPR026482 rSAM_nif11_3	129	44	1	IPR045567 CofHIMnqC-like_C 21,334 9,047 696
	IPR011843 PQQ_synth_PqqE_bac	5,549	1,835	59		IPR027492 RNA_MTrfsse_RimN	37,070	13,980	1,140	IPR045784 Radical_SAM_N2 11,865 6,446 1,460
		_	_	_	1	IPR027526 Lipoyl_synth_chipt	337	132	20	PF04055 Radical_SAM 672,681 327,815 62,850
	IPR012837 NrdG	11,645	4,135	630	1	IPR027527 Lipoy[_synth_mt	265	79	14	PF06969 HemN_C 39,495 17,002 2,804
	IPP012838 PFL1 activating	9,425	2,995	180		IPR027559 B12_rSAM_oligo	443	144	8	PF08497 Radical_SAM_N 12,479 4,760 404
	IDP012839 Omanic radical activase	16.374	5,941	1.127		IPR027564 HonR B12 rSAM	427	155	5	PF12345 DUF3841 4,310 2,730 235
	IPRO12029 Ulgani_uma_	33.719	14.394	0.74		PR027570 GeoRSP (SAM	60	51	2	PF13186 SPASM 47,292 26,993 9,996
	IDD013704 UDE0313 N	12,479	4 760	404		IDR027583 rSAM ACGX	154	98	8	PF16199 Radical_SAM_C 20,918 9,267 1,452
1	incorregate Multiplicitizate N	01 463	99,689	6 460		incorporate state mate	167	146	44	PF16881 LIAS N 25,755 8,384 724
	IPR013848 Matryaniatak analogy	9.013	4.009	5,460		PR027080 comm_metu_max	10.	7 712	94	PF10218 Padical SAM 2 4,615 2,655 513
1	IPR013917 IProv_wyoutcomercyne.	0,013	9,649	504		IPH027006 Animalwania.com	10,07 -	1,1 IA 960	840	DE10288 C-04 C 21.334 9.047 696
1	IPR014191 Anaer_KNK_activa	10.016	303	27		IPR027804 W_town_matur	901	477	101	DE10888 Daview CAM N2 11.885 6.446 1.460
1	IPR016431 Pyrv-formate_lyase-acury_pro	16,210	11,19/	1,144		IPR027808 Spiro_onvom	330	177	83	Total 4 055 068 1,898,245 336,149
1	IPR016771 Fe-S_0xRdiase_rsAM_1 wvs+o_pro	62	39	6		IPR027609 rSAM_Quet_Protectory	2,527	501	21	Tassi Pomovini A AEE 668
1	IPR016779 rSAM_MSMEG0568	1,825	751	63		IPR027621 rSAM_Quet_gams	3,644	1,315	28	The invest format is a sincle family or commarkance secarated list of families. Families should be specified as
i i	IPR016863 Desli	58	32	5		IPR027622 rSAM_Clo7bot	50	11	3	PFiconx (five digits), IPRicoccor (ski digits) or CLocox (four digits) for Plam clans.
1	IPR017200 PqqE-like	19,368	10,212	2,373		IPR027626 Pseudo_SAM_Halo	248	67	1	
1	IPR017672 MA_4551-like	433	209	15		IPR027633 rSAM_NirJ2	399	186	5	Filter by Taxonomy can be used to remove UniProt IDs that do not match the specified taxonomy categories.
1	IPR017742 Deazaguanine_synth	2,879	884	27		IPR030801 Glu_2_3_NH3_mut	266	178	2	The remaining UniProt IDs are used to generate the sunburst.
1	IPR017833 Hopanoid_synth-assoc_rSAM_HpnH	4,542	1,470	82		IPR030837 B12_rSAM_cona1	65	41	2	UniRef90 and UniRef50 clusters that contain the UniProt IDs are retrieved from the UniRef90 andUniRef50 databases using the
1	IPR017834 Hopenoid_synth-assoc_rSAM_HpnJ	1,453	448	14		IPR030894 Ahb_Proteobacteria	570	287	4	lookup table provided by UniProtUniRef. Clusters for which the cluster ID (representative sequence) matches the list of families are
1	IPR019939 CofG_family	6,705	3,144	254		IPR030896 rSAM_AhbD_hemeb	580	364	19	retained.
1	IPR019940 CofH_family	6,240	2,738	154		IPR030905 CutC_activ_rSAM	564	190	10	The numbers of UniProt IDs and both UniRet90 cluster and UniRet50 cluster IDs are displayed on the sunturst; the unimovirus and tools LiveRet90 cluster and UniRet90 cluster IDs are available for download and/or transfer to the Accession ID option (Option D) of
1	IPR020050 FO_synthase_su2	20,381	8,463	490		IPR030915 rSAM_SkfB	33	10	6	EFI-EST to generate SSNs.
1	IPR020612 Methylthiotransferase_CS	96,829	40,909	5,265		IPR030933 Non_iron_rSAM	34	21	4	If the lists of UniRef90 or UniRef50 cluster IDs are used to generate SSNs with the Accession IDs option (Option D) of EFI-
1	IPR022431 Cyclic_DHFL_synthase_mqnC	6,120	2,294	95		IPR030950 rSAM_PoyD	190	106	59	EST, the lists should (must) be filtered with the same list of families (Filter by Family) and any specified taxonomy
1	IPR022432 MgnE	5,864	2,259	97		IPR030959 B12_rSAM_trp_MT	74	46	2	categories (Fitter by Taxonomy) used to generate the insta-
1	IPR022447 Lys_aminomutase-rel	1,692	860	38		IPR030977 QueE_Cx14CoxC	3,947	1,835	23	This filtering removes the UniRe/90 and UniRe/50 clusters with cluster IDs ("representative sequences") or internal UniProt IDs that
1	IPR022459 Lysine_aminomutase	3,211	1,685	52		IPR030989 rSAM_XyeB	38	16	3	are not memours or the spectred lammers of memory an amount and another services
1	IPR022462 Epm8	5,760	2,170	180		IPR031003 BopO_PhpK_rSAM	97	75	29	- Fragment Option
1	IPR022881 rRNA_lau_MeTfrase_Cfr	256	54	2		IPR031004 rSAM_YIKAB	1,610	526	16	An analysis of the second
i i	IPR022948 UPF0313	13,008	5,108	563		IPR031010 rSAM_mob_pairA	702	29	4	UniProt designates a Sequence Status for each member: Compete in the encourag prevalence may poor state and way endour: Encourse if the start and/or stors codon is missing. Approximately 10% of the entries in UniProt are fragments.
1	IDP023404 rSAM horseshoe	197,532	100,156	21.993		IPR031012 rSAM mob pairB	902	101	4	COOMIS, Fragment in the solid and/or ship cooking inspirationality in the solid and solid
1	IPR023805 Uncharacterised_Spl-rel	1,028	422	9		IPR031014 rSAM_BlatE	39	23	1	Fragments: Check to exclude Univitor-Denned regments in the results. (Denaut: Of)
i i	IPR023807 Peptide mod_rSAM	116	104	37		IPR031015 Arg 2 3 am_muta	160	51	4	For the UniRef90 and UniRef30 databases, clusters are excluded if the cluster ID ("representative sequence") is
1	IPP023819 Pan-mod rSAM AF0577	682	468	66		PROVIDE ISAM VS C rich	11	11		a fragment.
	IPROZATO PROVINCIAL CONTRACTOR	219	33	1		PR031091 LIAS N	25,755	A 384	724	UniProt IDs in UniRef90 and UniRef50 clusters with complete cluster IDs are removed from the clusters if they
1	IPREZIGEN IDAM_GOL-MANN	2.039	1.236	1		Phoses Desired Sam C	20,000	0,004	1.459	are fragments.
1	IPR023821 ISAM_rear-assou	2,035	1,600	200	1	Phozesz ration_over_o	20,810	9,697	1,402	
1	IPR023822 rSAM_iatu-assoc_owo	430	1/0	22		IPR053971 Avlamyca_epimerase	9	3	1	- Filter by Taxonomy
1	IPR023858 RSAM_Hmas	100	0.004	8		IPR033974 Gycero_Genyurasase_sectors	3.0			
	IPR023862 CHP03960_rsAM	7,935	3,804	596		IPR033975 ThnP-like		3	1	This filter is annived to the UniProt IDs after they have been identified using the list of Pfam families, InterPro families,
	IPR023863 rSAM_PTO1314	82	36	5		IPR033976 GntE-like	9	1	1	and/or Pfam clans. The remaining UniProt IDs are used to generate the surburst.
	IPR023867 Sulphatase_maturase_rSAM	26,588	13,657	5,204	1	IPR034165 NI/B_C	2,248	884	94	Error mesetanteri monthione, the user can select "Bacteria, Archaea, Fundi", "Eukanyota, no Fundi", "Fundi", "Viruses",
	IPR023868 7-CO-7-deazaGua_synth_put_Clo	534	250	13		IPR034386 BtrN-like	3	2	2	"Bacteria", "Eukaryota", or "Archaea" to restrict the UniProt IDs in the surburst to these taxonomy groups.
	IPR023874 DNA_rSAM_put	8,922	3,282	228		IPR034391 Cmo-like_SPASM_containing	9,351	6,770	2,830	"Prysteria Aerhaea Funni" "Resteria" "Archaea", and "Funol" select organisms that may provide genome context (gene
	IPR023880 Benzylsucc_Synthase_activating	10	8	1		IPR034405 F420	26,713	12,035	1,325	clusters/operons) useful for inferring functions.
	IPR023885 4Fe4S-binding_SPASM_dom	60,484	34,788	13,238	1	IPR034422 HydE/Py(B-like	5,384	3,253	647	The LielBook De also can be contricted to taxonomy categories within the Superkingdom, Kingdom, Phylum, Class, Order,
	IPR023886 QH-AmDH_gsu_maturation	777	235	15		IPR034428 ThH/NoCL/HydG-like	10,820	4,489	454	Family, Genus, and Species ranks. Multiple conditions are combined to be a union of each other.
	IPR023891 Pyrrolys_PylB	266	172	23		IPR034436 NocNiNosN-like	11	9	1	
	IPR023897 Spore_PP_lysase	1,810	628	20		IPR034438 4-hPhe_decarboxylase_activase	15	1	1	Preselected conditions: select a preset to auto populate
	IPR023904 Pep_rSAM_mat_YydG	36	16	6		IPR034457 Organic_radical-activating	53,598	26,655	4,922	
	IPR023912 YjjW_bact	2,077	431	55		IPR034462 Benzylsuc_synthase_activase	21	4	2	Add Taxonomy callegory
	IPR023913 MRC	1,478	492	22		IPR034465 Pyruvate_for-lyase_activase	3,836	433	27	
	IPR023930 NrJ1	269	128	5		IPR034466 Methyltransferase_Class_B	32,110	22,738	7,891	
	IPR073969 CHP04072_B12-bd/tSAM	68	60	15		IPR034471 GDGT/MA_synthase	1.393	710	47	Length Filter
	IPR023079 CHP04014 B12-bd//SAM	212	108	15		IPR034474 Methyltransferase Class D	5,445	3,184	757	
1	IPR023080 CHP04013 B12-bd//SAM	910	558	151		IPR034479 AhbC-like	942	477	11	Internet Dec All (registed)
1	IPR023084 rSAM pcin 1	1.314	927	397		IPR034480 Herne garboxy lyase-like	344	262	37	Job name: H35_AW
	IPR023607 Israe_con	1.137	401	8		ID0054485 Anaemhin Custone suffatesetm	862	365	75	E-mail address
	PRO23652 Common _ opinio mo	1,107				Income in the second se	6.000	4 860	149	

Previous	s Jobs	Families	FASTA	Accession IDs				
Potriovo	taxonon	av for familie	0.6					
Retrieve	taxonon	iy for familie						
The UniF	rot IDs to	or family men	nbers are iden	tified in UniProtKB v	with a list of Pfam	families, InterPro	o families, and/or	Ptam clans.
	Pfam an	d/or InterPro	o Families:					
	45784	PF04055 P	F06969 PF0	3497 PF12345 PF	13186 PF16199	PF16881 PF1	9238 PF19288 I	PF19864
		Family	F	amily Name	Full Size	UniRef90 Size	UniRef50 Size	
		IPR000385	MoaA_NifB_	PqqE_Fe-S-bd_CS	49,241	23,160	4,777	
		IPR001989	Radical_activ	vat_CS	26,935	9,907	1,836	
		IPR002684	Biotin_synth/	BioAB	27,640	9,880	1,004	
		IPR003698	Lipoyl_synth		39,047	13,924	1,318	
		IPR003739	Lys_aminom	utase/Glu_NH3_mu	t 20,775	10,372	1,278	
		IPR004383	rRNA_lsu_M	Trfase_RImN/Cfr	39,944	15,429	1,455	
		IPR004558	Coprogen_o:	kidase_HemN	16,796	6,746	513	
		IPR004559	HemW-like		38,255	17,990	2,765	
		IPR005839	Methylthiotra	nsferase	87,716	37,295	4,127	
		IPR005840	Ribosomal_S	12_MeSTrfase_Rin	nO 28,658	11,857	2,029	
		IPR005909	RaSEA		2,035	1,022	229	
		IPR005911	YhcC-like		11,293	4,505	502	
		IPR005980	Nase_CF_Ni	fB	2,647	1,104	82	
		IPR006463	MiaB_methic	lase	35,615	13,649	723	
		IPR006466	MiaB-like_B		4,407	2,226	506	
		IPR006467	MiaB-like_C		17,077	8,216	1,089	
		IPR006638	Elp3/MiaA/Ni	fB-like_rSAM	446,282	212,389	36,535	
		IPR007197	rSAM		722,535	355,669	70,723	
		IPR010505	Mob_synth_0	0	38,361	16,635	1,682	
		IPR010722	BATS_dom		39,852	14,953	1,222	
		IPR010723	HemN_C		39,495	17,002	2,804	
		IPR011101	DUF5131		7,313	4,801	1,324	
		IPR011843	PQQ_synth_	PqqE_bac	5,549	1,835	59	

#### - Fragment Option

UniProt designates a Sequence Status for each member: Complete if the encoding DNA sequence has both start and stop codons; Fragment if the start and/or stop codon is missing. Approximately 10% of the entries in UniProt are fragments.

Fragments: Check to exclude UniProt-defined fragments in the results. (default: off)
For the UniRef90 and UniRef50 databases, clusters are excluded if the cluster ID ("representative sequence") is

a fragment.

UniProt IDs in UniRef90 and UniRef50 clusters with complete cluster IDs are removed from the clusters if they are fragments.

#### Filter by Taxonomy

This filter is applied to the UniProt IDs after they have been identified using the list of Pfam families, InterPro families, and/or Pfam clans. The remaining UniProt IDs are used to generate the sunburst.

From preselected conditions, the user can select "Bacteria, Archaea, Fungi", "Eukaryota, no Fungi", "Fungi", "Viruses", "Bacteria", "Eukaryota", or "Archaea" to restrict the UniProt IDs in the sunburst to these taxonomy groups.

"Bacteria, Archaea, Fungi", "Bacteria", "Archaea", and "Fungi" select organisms that may provide genome context (gene clusters/operons) useful for inferring functions.

The UniProt IDs also can be restricted to taxonomy categories within the Superkingdom, Kingdom, Phylum, Class, Order, Family, Genus, and Species ranks. Multiple conditions are combined to be a union of each other.

Preselected conditions: -- select a preset to auto populate -- -

	Add Taxonomy category			
→ Length F	ilter			
Job name:	IP91_RSS_All		(required)	
E-mail addre	ss:	as been processed.		
		Submit Analysis		

The results were available on the **DATASET COMPLETED** page. The **Taxonomy Sunburst** tab (below) is the interactive display that provides the numbers of UniProt, UniRef90 cluster, and UniRef50 cluster IDs (red arrow), downloads for IDs and FASTA sequences (blue arrow), and transfers of IDs to EFI-EST (green arrow) or EFI-GND viewer (magenta arrow).



**Complete Sequences.** The **Taxonomy Sunburst** for the complete sequences was generated from UniProt Release 2022_04 by entering a list of 211 Pfam and InterPro families and/or domains (**Tutorial Table 1**) into the **Pfam and/or InterPro Families and/or Pfam Clans** box on the **Taxonomy Tool Families Option** page (red arrow), selecting **Fragment Option** to exclude fragments (blue arrow), entering the **Job name** (orange arrow) and an **E-mail address** (cyan arrow), and clicking "**Submit analysis**" (black arrow). The Tool provides the list of input families/domains, so the page is long (next page). The two boxed areas are enlarged on the following page to clearly show the input parameters.

ם ה

				IPR024001 Cys-rich_pep_rSAM_mat_CopM	231	130	67	IPR054498 Bactandonordpnyii_C6_wi1 4/ 33 1
omy for families				IPR024007 FeFe-hyd_mat_HydG	3,483	1,754	78	100034505 Coproportingen-in_conduse 65,641 31,743 5,860
for family members are identified in LiniProfil'D with a	ist of Plans fam	villes InterBro fac	million and for Pfam class	IPR024016 CHP04064_SAM	20	14	4	IPR04514 TheK-like 11 3 1
for larity members are identified in oniProcks with a	st or Planniani	ines, interPro tan	miles, and/or Plan clans.	IPR024018 CHP04083 (SAM	40	159	14	IPR034515 ThnL-like 8 4 2
and/or InterPro Families:				IPR024021 Eallachart Hall +SAM	3,733	2.075	217	IPR034519 TunB-like 11 6 1
4 PF04055 PF06969 PF08497 PF12345 PF1318	PF16199 PF	16881 PF1923	8 PF19288 PF19864	IPR024023 rSAM paired HasB	1.143	625	125	IPR034529 Fom3-like 5 2 1
Family Family Many	Full Plan Ha	Define the	ID-000 Plan	IPR024025 SCIFF rSAM maturage	2.738	1.232	79	IPR034530 HpnP-like 3,569 1,910 158
IPR000385 MonA M/B Page En-S-bd CS	40 241	23.160	A 777	IPR024032 rSAM paired HxsC	1,002	526	142	IPR034531 Methylation_of_yatakemycin 9 4 1
IPR000355 Wda/_NIB_PqqE_P6-3-00_C3	26.035	0.007	4,777	IPR024177 Biotin synthese	24,304	8,337	476	IPR034532 Oxs8-like 57 53 11
IPR02684 Bintin swith/BinAB	27.640	9,880	1,004	IPR024521 DUF3841	4,310	2,730	235	IPR034534 Pyrimidine_methyltransferase 8 7 1
IPR03898 Linux swith	39.047	13,924	1,318	IPR024560 UPF0313_C	11,093	3,850	317	IPR034547 Tie1188a_maturase 21 3 3
IPR003739 Lvs aminomutase/Glu NH3 mut	20.775	10.372	1.278	IPR024924 7-CO-7-deazaguanine_synth-like	25,740	11,573	1,114	IPR034556 tRNA_wybutosine-synthase 6,265 3,336 768
IPR004353 rRNA isu MTrfase RimN/Cfr	39,944	15,429	1,455	IPR025895 LAM_C_dom	6,845	3,760	332	IPR034557 ThrcA_IRNA_MEthiotransferase 3,721 1,422 120
IPR004558 Coprogen oxidase HemN	16,796	6.746	513	IPR026322 Geopep_mat_rSAM	106	95	26	IPR034559 Spore_PP_lysase_Clostridia 537 327 20
IPR004559 HemW-like	38.255	17.990	2,765	IPR026332 HutW	1,392	438	75	IPR034560 Spore_PP_lysase_Badlli 1,273 302 6
IPR005839 Methylthiotransferase	87,716	37,295	4,127	IPR026335 SAM_SPASM_FxsB	1,394	895	82	IPR034687 ELP3-like 7,115 3,099 309
IPR005840 Ribosomal_S12_MeSTrfase_RimO	28,658	11,857	2,029	IPR026344 SCM_rSAM_ScmE	66	62	7	IPR038135 Methylthiotransferase_N_sf 91,072 39,494 5,392
IPR005909 RaSEA	2,035	1,022	229	IPR026346 SCM_rSAM_ScmF	59	56	6	IPR039661 ELP3 23,268 10,427 1,876
IPR005911 YhcC-like	11,293	4,505	502	IPR026351 rSAM_SeCys	4,383	2,794	272	IPR040072 Methyltransferase_A 43,050 17,542 2,586
IPR005980 Nase_CF_NifB	2,647	1,104	82	IPR026357 rSAM/SPASM_prot_GRRM_system	342	189	72	IPR040074 BaaD/PfWYjW 9,191 3,899 962
IPR006463 Mia8_methiolase	35,615	13,649	723	IPR026401 CXOX_matur	139	93	35	IPR040081 Cndi-like 1 2 1
IPR006466 Mia8-like_B	4,407	2,226	506	IPR026404 rSAM_w_lipo	429	175	16	IPR040082 GenK-like 4 1 1
IPR006467 Mia8-like_C	17,077	8,216	1,089	IPR026407 SAM_GG-Bacter	267	131	67	IPR040085 MJ0674-ike 7,375 4,888 824
IPR006638 Elp3/MiaA/NfB-like_rSAM	446,282	212,389	36,535	IPR026412 rSAM_Cxxx_rpt	171	108	34	IPR040086 MJ0683-like 22,149 11,842 1,979
IPR007197 rSAM	722,535	355,669	70,723	IPR026423 rSAM_cobopep	190	138	15	IPR040087 MJ0021-like 1,943 1,037 231
IPR010505 Mob_synth_C	38,361	16,635	1,682	IPR026426 rSAM_FibroRumin	18	18	5	In:R040088 MJ0103-like 747 535 117
IPR010722 BATS_dom	39,852	14,953	1,222	IPR026429 MIA_synthase	13	10	1	IPR041582 RimO_TRAM 25,468 10,202 1,260
IPR010723 HemN_C	39,495	17,002	2,804	IPR026447 B12_SAM_Ta0216	457	325	66	IPR045375 Put_radical_SAM-like_N 4,615 2,655 513
IPR011101 DUF5131	7,313	4,801	1,324	IPR026482 rSAM_nif11_3	129	44	1	IPR045567 CofHIMnqC-like_C 21,334 9,047 696
IPR011843 PQQ_synth_PqqE_bac	5,549	1,835	59	IPR027492 RNA_MTrfase_RimN	37,070	13,980	1,140	IrrR045784 Radical_SAM_N2 11,865 6,446 1,460
				IPR027526 Lipoyl_synth_chipt	337	132	20	Pr04055 Radical_SAM 672,681 327,815 62,860
IPR012837 NrdG	11,645	4,135	630	IPR027527 Lipoyl_synth_mt	265	79	14	17:06069 HemN_C 39,405 17,002 2,804
IPR012838 PFL1_activating	9,425	2,995	180	IPR027559 B12_rSAM_oligo	443	144	8	Pr/08497 Radical_SAM_N 12,479 4,760 404
IPR012839 Organic_radical_activase	16,374	5,941	1,127	IPR027564 HpnR_B12_rSAM	427	155	5	Ph12345 DUF3541 4,310 2,730 235
IPR013483 MoaA	33,719	14,394	976	IPR027570 GeoRSP_rSAM	60	51	2	Ph13188 SPASM 47,292 26,993 9,956
IPR013704 UPF0313_N	12,479	4,760	404	IPR027583 rSAM_ACGX	154	98	8	PF-16199 Radica_SAW_C 20,918 9,267 1,452
IPR013848 Methylthiotransferase_N	91,463	39,689	5,468	IPR027596 rSAM_metal_mat	167	146	44	PT10001 LVA5_N 220,750 0,394 724
IPR013917 tRNA_wybutosine-synth	8,013	4,099	552	IPR027596 AmmeMemoSam_rS	10,871	7,712	845	PF18238 R8888_SAW_2 4,615 2,656 513
IPR014191 Anaer_RNR_activator	584	303	27	IPR027604 W_rSAM_matur	481	350	101	PF18288 04H_0 21,334 6,041 656
IPR016431 Pyrv-formate_lyase-activ_prd	16,215	11,197	1,144	IPR027608 Spiro_SPASM	330	177	83	The ADD ADD ADD ADD ADD ADD ADD ADD ADD AD
IPR016771 Fe-S_0xRdtase_rSAM_TM0948_prd	62	39	6	IPR027609 rSAM_QueL_Proteobac	2,527	501	21	Table Commuted: 4.055.050 1,035,240 330,149
IPR016779 /SAM_MSMEG0568	1,825	751	63	IPR02r621 ISAM_QUBE_gams	3,044	1,315	28	The input format is a single family or comma/space separated list of families. Families should be specified
IPR016863 Desll	58	32	5	IPHUZ/622 ISAM_CIG/bet	50	11	3	PFxxxxx (five digits), IPRxxxxxx (six digits) or CLxxxx (four digits) for Pfam clans.
IPR017200 PqqE-like	19,368	10,212	2,373	IPR027625 Pseudo_SAM_Hato	248	67	1	Planck Territoria de la contra de Participa de la contra de
IPR017672 MA_4551-like	433	209	15	IPRO27633 F5AM_NFJ2	399	180	5	Priser by laconomy can be used to remove UniProt IUs that do not match the specified tationomy categories.
IPR017742 Deazaguanine_synth	2,879	884	27	IPR030801 GU_2_3_NH3_MU	200	1/0	2	The remaining UniProt IDs are used to generate the sunburst.
IPR017833 Hopanoid_synth-assoc_rSAM_HpnH	4,542	1,470	82	IPRO30637 B12_Taiwi_cola1	60	14		UniRef90 and UniRef50 clusters that contain the UniProt IDs are retrieved from the UniRef90 andUniRef50 database
IPR017834 Hopanoid_synth-assoc_rSAM_HpnJ	1,453	448	14	IPRO20004 AND Installation	690	201	19	retained.
IPR019939 ColG_tamly	6,705	3,144	254	IPROSOBILE CHE activ (SAM	564	190	10	The numbers of UniProt IDs and both UniRef90 cluster and UniRef50 cluster IDs are displayed on the sunburst; the
IPRO19940 Cont_amily	0,240	2,738	104	IPR030915 rSAM SkB	33	10	6	both UniRef90 cluster and UniRef50 cluster IDs are available for download and/or transfer to the Accession ID option EELERT to concerns SOM
IPR020000 PO_syllbase_soz	20,301	40,900	6 266	IPR030933 Non iron rSAM	34	21	4	The fact of the Borne to the Borne to the second to second to the state of the second se
IPR020612 Methylinibransinase_C5	8 120	40,909	0,200	IPR030950 rSAM PovD	190	106	59	If the lists of Unikel30 or Unikel30 cluster IDs are used to generate SSNs with the Accession IDs option (Op EST, the lists should (must!) be filtered with the same list of families (Filter by Family) and any specified taxe
IDD022437 Mare	6 984	2,244	07	IPR030959 B12 rSAM tro MT	74	46	2	categories (Filter by Taxonomy) used to generate the lists.
IPRO22402 Wight	4,600	2,2,09	39	IPR030977 Quie Cx14CxxC	3.947	1.835	23	This filtering removes the UniRef90 and UniRef50 clusters with cluster IDs ("representative sequences") or internal
IPRO22447 Lys_aminomolaseries	1,052	4.000	30	IPR030989 rSAM Xvn8	38	16	3	are not members of the specified families or have the selected taxonomy categories.
IPR022462 FomB	5 760	2 170	180	IPR031003 BopD_PhpK_rSAM	97	75	29	Fragment Option
IPR022881 (RNA Inc. MaTirasa Cfr	258	54	2	IPR031004 rSAM_YIKAB	1,610	526	16	
IDD022046_UDD0313	13.008	5 108	463	IPR031010 rSAM mob_pairA	702	29	4	UniProt designates a Sequence Status for each member: Complete if the encoding DNA sequence has both at codoos: Ecoment if the start and/or stop codoo is missing. Approximately 10% of the entries in LiniProt are free
IPB023404 (SAM borreshoe	197.532	100.156	21,993	IPR031012 rSAM_mob_pairB	902	101	4	Example:   Check to exclude the first defined foremula is the second of
IPR023805 Uncharacterised Sol-rel	1.028	422	9	IPR031014 rSAM_BisE	39	23	1	Programme. V Check to exclude UniProc-defined tragments in the results. (default: off)
IPR023807 Peptide mod rSAM	116	104	37	IPR031015 Arg_2_3_am_muta	160	51	4	For the UniRef90 and UniRef50 databases, clusters are excluded if the cluster ID ("representative s a framment
IPR023819 Pap-mod rSAM AF0577	682	468	66	IPR031019 rSAM_vs_C_rich	11	11	6	o roginati.
IPR023820 rSAM GDL-seaso:	219	33	1	IPR031691 LIAS_N	25,755	8,384	724	UniProt IDs in UniRef90 and UniRef50 clusters with complete cluster IDs are removed from the cluster are fragments.
IPR023821 rSAM TatD-assoc	2.039	1.236	206	IPR032432 Radical_SAM_C	20,918	9,267	1,452	o.o.o.ogunana.
IPR023822 rSAM TatD-assoc bac	438	178	22	IPR033971 Avilamycin_epimerase	9	3	1	
IPR023858 RSAM HmdB	135	61	8	IPR033974 Glycerol_dehydratase_activase	33	5	3	* Filter by Taxonomy
IPR023862 CHP03960 (SAM	7,935	3,804	598	IPR033975 ThnP-like	9	3	1	
	82	36	5	IPR033976 GntE-like	9	1	1	This filter is applied to the UniProt IDs after they have been identified using the list of Pfam families, InterPro fa and/or Pfam class. The remaining UniProt IDs are used to canarate the surfuur*
IPR023853 rSAM PT01314	25.558	13.657	5,204	IPR034165 NifB_C	2,248	884	94	and a second the first second of the first second s
IPR023863 rSAM_PT01314 IPR023867 Sulphatase_rSAM		250	13	IPR034386 BtrN-like	3	2	2	From presenced conditions, the user can select "Bacteria, Archaea, Fungi", "Eukaryota, no Fungi", "Fungi", "V "Bacteria", "Eukaryota", or "Archaea" to restrict the UniProt IDs in the surburst to these textmemu annuns.
IPR023863 rSAM_PTO1314 IPR023867 Sulphatase_maturase_rSAM IPR023868 7-CO-7-deazaGua_synth.out Clo	534			IPR034391 Cmo-like_SPASM_containing	9,351	6,770	2,830	Prototo Antone Proti Prototo Bankard and Proti Advantary State
IPR023863 rSAM_PT01314 IPR023867 Sulphatase_maturase_rSAM IPR023868 7-CO-7-deazaGua_synth_put_Clo IPR023874 DNA_rSAM_put	534 8,922	3,282	228	IPR034405 F420	26,713	12,035	1,325	bacterna, virchaea, Hungi", "dacterna", "Archaea", and "Hungi" select organisms that may provide genome contro clusters/operons) useful for inferring functions.
IPR023883 rSAM_PTO1314 IPR023867 Sulphatase_maturase_rSAM IPR023868 7-CO-7-deazaGua_synth_put_Clo IPR023874 DNA_rSAM_put IPR023880 Benzylsucc_Synthase_act/vatina	534 8,922 10	3,282	228	IDD024422 HadE/DVD like	6 284	0.050	047	The Uniform Parallel and the second state of the formation of the second state of the
IPR023883 ISAM_PT01314 IPR023863 TSubhatase_maturase_ISAM IPR023863 7-C0-7-dear26Gus_prith_put_Clo IPR023880 Benzysuucc_Syntase_activating IPR02388 densystuucc_Syntase_activating IPR02388 densystems	534 8,922 10 60,484	3,282 8 34,786	228 1 13,238	in noomaal injuuri yurinnii	0,004	3,203	047	Fine Uniterory IDA also can be restricted to taxonomy categories within the Superkingdom, Kingdom, Phylum, Cla Family, Genus, and Species ranks. Multiple conditions are combined to be a union of each other
IPR023865 rSAM_PT01314 IPR023867 Sulphatse_maturase_rSAM IPR023887 -CO-7-deataClus_pyth_put_Clo IPR023887 ADNA_rSAM_put IPR023886 eliments_pythase_activating IPR023886 eliments_clonding_SPASM_dom IPR023886 eliments_clonding_SPASM_dom	534 8,922 10 60,484 777	3,282 8 34,788 235	228 1 13,236 15	IPR034428 ThH/NoCL/HydG-like	10,820	4,489	454	
IPR02888 ISAM_PT01314 IPR02895 Sythate_maturase_ISAM IPR02895 Sythate_maturase_ISAM IPR028958 7-CO-7-dearaGue_ent_put_cto IPR02898 Bonduce_Sythates_activating IPR02888 ChildrenDit_gen_maturation IPR02898 ChildrenDit_gen_maturation IPR02898 ChildrenDit_gen_maturation	534 8,922 10 60,484 777 266	3,282 8 34,786 235 172	228 1 13,238 15 23	IPR034428 ThiH/NoCL/HydG-like IPR034438 NocNiNosN-like	10,820	4,489	454	
IPR023983 ISAM_PT01314 IPR023987 Syldnase_maturase_f6AM IPR023987 Syldnase_maturase_f6AM IPR023180 AVI_SAM_ptd IPR023180 Benzytsuzc_Synthase_activating IPR023880 Benzytsuzc_Synthase_activating IPR023980 Benzytsuzc_Synthase_activating IPR023987 Denthol_psg_maturation IPR023989 Pymsys_P18 IPR023987 Denthol_psg_maturation	534 8,922 10 60,484 777 266 1,810	3,282 8 34,786 235 172 628	228 1 13,236 15 23 20	IPR034428 ThHINoCLHydG-ike IPR034428 ToHINoCLHydG-ike IPR034438 AchPhe_decarboxylase_activase	10,820 11 15	4,489 9 1	454 1	Preselected conditions:
IPR02988 r5AAL/PTO1314 IPR02985 r5Abrase_mbrase_f5AM IPR02985 r5Co-7-desta3Gua_synth_put_Cib IPR02988 r5Co-7-desta3Gua_synth_put_Cib IPR02988 r5Abrase_sat/sating IPR02988 r5Abrase_sat/sating IPR02998 r5Abrase_sat/sating IPR02998 r5Abrase_sat/sating IPR02999 r5Abrase_sat/sating IPR02999 r5Abrase_sat/sating IPR02999 r5Abrase_sating IPR02999 r5Abrase_sating IPR0299 r5Abrase	534 8,922 10 60,484 777 255 1,810 36	3,282 8 34,786 235 172 628 16	228 1 13,238 15 23 20 6	IPR034428 ThiHNsCLHydG-like IPR034428 NochNosN-like IPR034438 4-hPhe_decarbox/lase_activase IPR034438 4-hPhe_decarbox/lase_activase	10,820 11 15 53,598	3,253 4,489 9 1 26,655	454 1 1 4,922	Preselected conditions:
19402388 3 AMJ 7101314 19402385 3 AMJ 7101314 19402385 3 AMJ 7013482, minutes, ISAM 19402385 7.00,74682,040, ymh, put, Clo 19402385 0 Amythus, Synhaas, adhrang 19402385 0 Amythus, Synhaas, adhrang 19402389 1 Amythus, Synhaas, adhrang 19402389 1 Amythus, Pyla 19402389 1	534 8,922 10 60,484 777 255 1,810 36 2,077	3,282 8 34,786 235 172 628 16 431	2228 1 13,236 15 23 20 6 55	IPR03442 ThiNNsCL/hydGHke IPR034435 NichNick/Hke IPR034438 Arbhe_decarboxy(ase_activase IPR034437 Organic_radical-activating IPR034462 Banctytus_ruthase_activase	10,820 11 15 53,598 21	3,253 4,489 9 1 26,655 4	454 1 1 4,922 2	Preselected conditions:
PH202865 (AMJ PT0-1314     PH202895 (AMJ PT0-1314     PH202895 (AMJ AMJ AMJ AMJ AMJ AMJ AMJ AMJ AMJ AMJ	534 8,922 10 60,484 7777 286 1,810 36 2,077 1,478	3,282 8 34,788 235 172 628 16 431 492	228 1 13,238 15 23 20 6 55 55 22	IPR03428 ThithAcL/hydG-like IPR03428 NocNIYash-like IPR03428 A-Pht-g-doctoxylase_activase IPR034457 Organic_radical-activating IPR034452 Benzyluc_sylthase_activase IPR034452 Pyrviva6_crysae_activase	10,820 11 15 53,598 21 3,838	3,253 4,489 9 1 26,655 4 433	454 1 4,922 2 27	Presolected conditions:
PH202865 (AMJ PT0114 PH202867 Systems, matures, FAM PH202867 Systems, matures, FAM PH20287 AM, Ang AL PH202885 Am, Ang AL PH202885 (Am, Ang AL) PH202885 (Am, AL) PH202885 (Am, AL) PH202815 (Am,	534 8,922 10 60,484 7777 286 1,810 36 2,077 1,478 209	3,282 8 34,786 235 172 628 16 431 462 128	228 1 13,236 15 23 20 6 55 22 5	in PIG3442 ThinkNoCLHyRGCHke IPRG34435 NocNNoN-ktke IPRG3435 NocNNoN-ktke IPRG34435 Organic_matical-activating IPRG34452 Benzytsuc_synthese_activase IPRG34452 Pyrovala_bc-hysea_activase IPRG3445 Motifythanferse_Class B	10,820 11 15 53,598 21 3,836 32,110	3,253 4,489 9 1 25,655 4 433 22,736	454 1 4,922 2 27 7,891	Preselected confidence select a preset to auto populate Add Texanomy category
PR02388 AVAL_PT00144 PR02387 Subhars PR02387 Subhars PR02387 Subhars PR02387 Subhars PR02388 AVAL PR02388 Subhars AVAL PR02388 Subhars PR0238 Subhars PR0238 Subhars PR0238 Subhars PR0238 Sub	534 8,922 10 60,484 7777 286 1,810 36 2,077 1,478 209 68	3,282 8 34,786 235 172 628 16 431 492 128 60	228 1 13,28 15 23 20 6 55 22 22 5 15	IP 102442 (F) (F)(J) (F)(J) (F)(J) IP 1024428 (F)(J)(J)(J)(J)(J)(J)(J)(J)(J)(J)(J)(J)(J)	10,820 11 15 53,598 21 3,838 32,110 1,383	3,253 4,489 9 1 25,655 4 433 222,736 710	454 1 4,922 2 27 7,891 47	Presidente constitues [selled a prevait to ado populate
PR02288         SetMar TOO 144           PR02288         SetMarkan SetMarkan (SMM)           PR02288	534 8,922 10 60,484 7777 286 1,810 36 2,077 1,478 209 68 212	3,282 8 34,786 235 172 628 16 431 462 128 60 108	228 1 13,238 23 20 6 55 22 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	In 100442 Tryster Parket C-Hea IPR004488 NochNeat-Hea IPR004488 NochNeat-Hea IPR004488 C-Hen, decartoroyster, schware IPR004487 Organic, and auto-activating IPR004487 Dirganic, and auto-activating IPR004488 Deryster, and auto-activating IPR004489 Deryster, and auto-activating IPR004491 Deryster, and auto-activating IPR004491 Deryster, and auto-activating IPR004491 Deryster, and auto-activation IPR004491 Deryster, and activation IPR004491 Deryster, and activation IPR00491 D	10,620 11 15 53,598 21 3,636 32,110 1,383 5,445	3,233 4,489 9 1 26,655 4 433 22,738 710 3,184	641) 454 1 4,822 2 27 7,891 47 757	Prevelected conditions:stated a prevail to also populate Add Taxonomy conlegney  - Length Filter
PR02088 34AM /T00144 PR02087 Solvabary Solvaba	534 8,922 10 60,484 7777 2555 1,810 36 2,077 1,478 259 68 212 910	3,282 8 34,786 235 172 628 16 431 462 128 60 108 598	228 1 13,238 23 20 6 55 22 5 5 15 15 15	PR02442         Ppc1/P042-File           PR02442         Pc0Mod2           PR02442         NooNhah-Hie           PR02442         NooNhah-Hie           PR02442         Digate_mode-administration           PR02442         Digate_mode-administration           PR02442         Digate_mode-administration           PR02442         Digate_mode-administration           PR02442         Digate_mode-administration           PR024442         Digate_mode-administration           PR024442         Digate_mode-administration           PR024442         Digate_mode-administration           PR024447         Digate_mode-administration           PR024447         Digate_mode-administration           PR024447         Moderadaministration           PR024447         Moderadaministration	10,820 11 15 53,598 21 3,838 32,110 1,393 5,445 842	3,233 4,489 9 1 26,655 4 4 33 22,736 710 3,184 477	641) 4654 1 4,822 2 27 7,891 47 7557 11	Presidente conditions = selled a presate to ado populate == Adil Teannomy collegory  Langth Filter  Johnson / DSS No/Finamente
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Previous Jobs	Families	FASTA	Accession IDs			
tetrieve taxonon	ny for famili	es.				
he UniProt IDs fo	or family men	nbers are ider	tified in UniProtKB w	ith a list of Pfam	families, InterPro	o families, and/or
Pfam an	d/or InterPro	o Families:				
45784	PF04055 P	F06969 PF0	8497 PF12345 PF	13186 PF16199	PF16881 PF1	9238 PF19288
	Family	F	amily Name	Full Size	UniRef90 Size	UniRef50 Size
	IPR000385	MoaA_NifB_	PqqE_Fe-S-bd_CS	49,241	23,160	4,777
	IPR001989	Radical_activ	vat_CS	26,935	9,907	1,836
	IPR002684	Biotin_synth/	BioAB	27,640	9,880	1,004
	IPR003698	Lipoyl_synth		39,047	13,924	1,318
	IPR003739	Lys_aminom	utase/Glu_NH3_mut	20,775	10,372	1,278
	IPR004383	rRNA_lsu_M	Trfase_RImN/Cfr	39,944	15,429	1,455
	IPR004558	Coprogen_o	xidase_HemN	16,796	6,746	513
	IPR004559	HemW-like		38,255	17,990	2,765
	IPR005839	Methylthiotra	insferase	87,716	37,295	4,127
	IPR005840	Ribosomal_S	S12_MeSTrfase_Rim	0 28,658	11,857	2,029
	IPR005909	RaSEA		2,035	1,022	229
	IPR005911	YhcC-like		11,293	4,505	502
	IPR005980	Nase_CF_N	ifB	2,647	1,104	82
	IPR006463	MiaB_methic	blase	35,615	13,649	723
	IPR006466	MiaB-like_B		4,407	2,226	506
	IPR006467	MiaB-like_C		17,077	8,216	1,089
	IPR006638	Elp3/MiaA/N	ifB-like_rSAM	446,282	212,389	36,535
	IPR007197	rSAM		722,535	355,669	70,723
	IPR010505	Mob_synth_	C	38,361	16,635	1,682
	IPR010722	BATS_dom		39,852	14,953	1,222
	IPR010723	HemN_C		39,495	17,002	2,804
	IPR011101	DUF5131		7,313	4,801	1,324
	IPR011843	PQQ_synth_	PqqE_bac	5,549	1,835	59

#### - Fragment Option

UniProt designates a Sequence Status for each member: Complete if the encoding DNA sequence has both start and stop codons; Fragment if the start and/or stop codon is missing. Approximately 10% of the entries in UniProt are fragments.

Fragments: Check to exclude Un ments in the results. (default: off)

For the UniRef90 and UniRef50 databases, clusters are excluded if the cluster ID ("representative sequence") is a fragment.

UniProt IDs in UniRef90 and UniRef50 clusters with complete cluster IDs are removed from the clusters if they are fragments.

#### Filter by Taxonomy

This filter is applied to the UniProt IDs after they have been identified using the list of Pfam families, InterPro families, and/or Pfam clans. The remaining UniProt IDs are used to generate the sunburst.

From preselected conditions, the user can select "Bacteria, Archaea, Fungi", "Eukaryota, no Fungi", "Fungi", "Viruses", "Bacteria", "Eukaryota", or "Archaea" to restrict the UniProt IDs in the sunburst to these taxonomy groups.

"Bacteria, Archaea, Fungi", "Bacteria", "Archaea", and "Fungi" select organisms that may provide genome context (gene clusters/operons) useful for inferring functions.

The UniProt IDs also can be restricted to taxonomy categories within the Superkingdom, Kingdom, Phylum, Class, Order, Family, Genus, and Species ranks. Multiple conditions are combined to be a union of each other.

Preselected conditions: -- select a preset to auto populate -- -

Fiesele	cied conditions.	select a preset to auto	populate ·		
	Add Taxon	omy category			
▸ Length F	Filter				
Job name:	IP91_RSS_	NoFragments		(required)	
E-mail addro	ess:				
You will be n	otified by e-mail	when your submission has	s been processed.		
			Submit Analysis		

The results were available on the **DATASET COMPLETED** page. The **Taxonomy Sunburst** tab (below) is the interactive display that provides the numbers of UniProt, UniRef90 cluster, and UniRef50 cluster IDs (red arrow), downloads for IDs and FASTA sequences (blue arrow), and transfers of IDs to EFI-EST (green arrow) or EFI-GND viewer (magenta arrow).



Complete Sequences, Minimum Length 140 Residues. The Taxonomy Sunburst for the complete sequences with a minimum length of 140 residues ("full-length" sequences) was generated by entering a list of 211 Pfam and InterPro families and/or domains (Tutorial Table 1) into the Pfam and/or InterPro Families and/or Pfam Clans box on the Taxonomy Tool Families Option page (red arrow), selecting Fragment Option to exclude fragments (blue arrow), entering 650 for the Minimum Length in the Length Filter (green arrow), entering the Job name (orange arrow) and an E-mail address (cyan arrow), and clicking "Submit analysis" (black arrow). The Tool provides the list of input families/domains, so the page is long (next page). The two boxed areas are enlarged on the following page to clearly show the input parameters.

										IPR034485 Anaerobic_Cys-type_sulfatase-m 662 365 75
						IPR023995 HemZ	3,639	1,607	322	IPR034491 Anaerob Ser sulfatase-maturase 5,937 1,729 148
Previous Jobs	Families FASTA Accession IDs					IPR024001 Cys-rich_pep_rSAM_mat_CcpM	231	130	67	100034407 Backadoobid C12 MT 55 37 1
						IPP024007 EaEa bud mat Hudg	3.493	1 754	79	IPR034467 Babelochorophyl_C12_M1 36 37 1
Retrieve taxon	omy for families.					I TREADED THE DRING THE OTHER	0,400	1,104	10	IPR034498 Bacteriochlorophyll_C8_MT 47 33 1
						IPR024016 CHP04064_rSAM	20	14	4	IPR034505 Coproporphyrinogen-III oxidase 68,641 31,743 5,880
The UniProt IDs	for family members are identified in UniProtKB with a	list of Ptam far	milies, InterPro tar	nilies, and/or Ptam clans	e. 📕	IPR024017 Pep_cycl_rSAM	45	6	2	IDD034508 Spartingments International B 7 5
Pfam	and/or InterPro Families and/or Pfam clans:					IPR024018 CHP04083 rSAM	330	159	14	
						IPR024021 FeFerbal HatE (SAM	3,733	2.075	217	IPR034514 ThmK-like 11 3 1
4578	4 PF04055 PF06969 PF08497 PF12345 PF1318	0 PF 10199 P	1-16881 PF 1923	8 PF19288 PF19864						IPR034515 ThnL-like 8 4 2
						IPR024023 F3AM_pared_HK88	1,143	625	120	IPR034519 TunB-like 11 6 1
	Family Family Name	Full Size U	IniRef90 Size Un	hiRef50 Size		IPR024025 SCIFF_rSAM_maturase	2,738	1,232	79	
	IPR000385 MoaA_NIB_PogE_Fe-S-bd_CS	49,241	23,160	4,777		IPR024032 rSAM_paired_HesC	1,002	525	142	IPR034529 F0003-1666 5 2 1
	IPR001989 Barlical activat CS	26.935	9 907	1.836		IPB024177 Biotin synthese	24.304	8.337	476	IPR034530 HpnP-like 3,569 1,910 158
		20,000				a respective sourceptotase			410	IPR034531 Methylation of vatakemycin 9 4 1
	IPR002684 Biotin_synth/BioAB	27,640	9,880	1,004		IPR024521 DUF3641	4,310	2,730	235	
	IPR003698 Lipoyl_synth	39,047	13,924	1,318		IPR024550 UPF0313_C	11,093	3,850	317	IPR034532 0X88-188 57 53 11
	IPR003739 Lvs aminomutase/Glu NH3 mut	20,775	10.372	1.278		IPR024924 7-CO-7-deazaguanine synth-like	25,740	11.573	1,114	IPR034534 Pyrimidine_methyltransferase 8 7 1
	IDD004383 (DNA los MTriture Direk)/Cfr	10.044	15.420	1.455		IDR025895 LAM C dom	6.045	3 780	332	IPR034547 Tie1186a maturase 21 3 3
	PR004363 PR00_B0_WITHabe_RITIVOT	30,044	10,420	1,400		IPR02000 DWI_C_0011	0,040	3,700	332	
	IPR004558 Coprogen_oxidase_HemN	16,795	6,745	513		IPR026322 Geopep_mat_rSAM	105	95	26	IPR034006 tRNA_Wybuosine-synmase 6,265 3,336 768
	IPR004559 HemW-like	38,255	17,990	2,765		IPR026332 HutW	1,392	438	75	IPR034557 ThrcA_IRNA_MEthiotransferase 3,721 1,422 120
	IPR005839 Methythiotransferase	87,716	37,295	4.127		IPR026335 SAM SPASM FxsB	1.394	895	82	IPR034559 Spore PP Ivaase Clostridia 537 327 20
	IDD005840 Disessed 640 McDTdees DieO	20.000	44.057	0.000		IDDODDA4, DOM, CAM, Camp			7	
	IPR000040 R0000001a_312_We311abe_R000	20,000	11,007	2,028		PR020344 acm_avm_autic	00	02	1	12/23 302 6
	IPR005909 RaSEA	2,035	1,022	229		IPR026346 SCM_rSAM_SomF	59	56	6	IPR034687 ELP3-like 7,115 3,099 399
	IPR005911 YhoC-like	11,293	4,505	502		IPR026351 rSAM_SeCys	4,383	2,794	272	IPR038135 Methylthiotransferase N sf 91.072 39.494 5.392
	IPR005980 Nase CF N/B	2.647	1,104	82		IPR026357 rSAM/SPASM prot GRRM syste	am 342	189	72	IDD030601 ELD2 22.308 10.437 1.978
	IDD000450 MinD methology	20.045	10.010	700		IDRODUCE CXXX makes	430			IPR030601 ELP3 23,206 10,427 1,876
	IPRODOVO3 MIAB_INDERIONADO	30,010	13,049	123		PR020401 CXXX_IIIau	139	85	30	IPR040072 Methytransferase_A 43,050 17,542 2,586
	IPR006466 MiaB-like_B	4,407	2,225	506		IPR026404 rSAM_w_lipo	429	175	16	IPR040074 BesD/PflA/YiW 9,191 3,899 962
	IPR006467 MiaB-like_C	17,077	8,216	1,089		IPR026407 SAM_GG-Bacter	267	131	67	IRR040081 Coultilion 1 2 1
	IPR006638 Elp3/MiaA/N/B-like rSAM	446,282	212,389	36.535		IPR026412 rSAM Goox rpt	171	108	34	
	IDE007107 (GAM	722.525	255 660	70 723		IPP026423 rSAM orbitate	192	138	15	IPR040082 GenK-like 4 1 1
	a rearran TOMM	122,030	300,009	10,120	<b>I</b>	invocosco rosse_orospep	190	100	10	IPR040085 MJ0674-like 7,375 4,888 824
	IPR010506 Mob_synth_C	38,361	16,635	1,682		IPR026426 rSAM_FibroRumin	18	18	5	IDD040086 M I0582-Iko 22 149 11 842 1 978
	IPR010722 BATS_dom	39,852	14,953	1,222		IPR026429 MIA_synthase	13	10	1	
	IPR010723 HereN C	39 495	17.002	2 804		IPR026447 B12 SAM Te0216	457	325	66	IPR040087 MJ0021-like 1,943 1,037 231
	I TOTOTES TRAINCO	53,455	17,502	2,004			407	060		IPR040088 MJ0103-like 747 535 117
	PROTION DOPOTAT	1,515	4,601	1,324		IPR026482_F8AW_0IT1_3	129	44	1	170044893 D-O TDAN 05 425 40 003 1 320
	IPR011843 PQQ_synth_PoqE_bac	5,549	1,835	59		IPR027492 RNA_MTrfase_RimN	37,070	13,900	1,140	PR041062 NINO_1NOW 20,408 10,202 1,200
	IPR012726 ThiH	6,704	2,297	125		IPR027526 Lipovi swith chipt	337	132	20	IPR045375 Put_redical_SAM-like_N 4,615 2,655 513
	100040003 Note	44.045	4.405	620		INTOXICIAL Land with at	007	70		IPR045567 CofH/MngC-like C 21.334 9.047 696
	IPR012831 WIDG	11,040	4,135	630		IPRO21021 CIPOy(Syntr)(Inc	200	10	14	100045796 Devided 24M M2 51 995 6446 1460
	IPR012838 PFL1_activating	9,425	2,995	180		IPR027559 B12_rSAM_oligo	443	144	8	IPR045764 P680(28_S4M_N2 11,005 6,446 1,460
	IPR012839 Organic_radical_activase	16,374	5,941	1,127		IPR027564 HpnR_B12_rSAM	427	155	5	PF04055 Radical_SAM 672,681 327,815 62,860
	IPR013483 MoaA	33,719	14 394	976		IPR027570 GeoRSP rSAM	60	51	2	PF06989 HemN C 39.495 17.002 2.804
										2000/07 Defect 044 N
	IPR013704_UPF0313_N	12,479	4,760	404		IPR027563 FSAM_ACGA	154	98	8	PT04497 P680E8L_SAM_N 12,479 4,780 404
	IPR013848 Methythiotransferase_N	91,463	39,689	5,468		IPR027586 rSAM_metal_mat	167	145	44	PF12345 DUF3641 4,310 2,730 235
	IPR013917 tRNA_wybutosine-synth	8,013	4,099	552		IPR027596 AmmeMemoSam_rS	10,871	7,712	845	PF13186 SPASM 47.292 26.993 9.956
	IPP014191 Anner PNP activator	50.4	303	27		IPRO27804 W (SAM matur	401	360	101	
	TOTAL PRINT PRINT PRINT	004	505	A.1		Traction Inclosed Chara	401	000	101	PP16199 Rubical_SAW_C 20,918 9,267 1,462
	IPR016431 Pyrv-formate_lyase-activ_prd	16,215	11,197	1,144		IPR027608 Spiro_SPASM	330	177	83	PF16881 LIAS_N 25,755 8,384 724
	IPR016771 Fe-S_OxRdtase_rSAM_TM0948_prd	62	39	6		IPR027609 rSAM_QueE_Protectac	2,527	501	21	PF19238 Radical SAM 2 4.615 2.655 513
	IPR016779 rSAM MSMEQ0568	1.825	751	63		IPR027621 rSAM QueE gams	3.644	1.315	28	
	IDD046050 Deall		22			IDD003E00 -CAM Cirther		.,		1111110 001 0
	IPR016863 Desli	58	32	5		IPR027622 rSAM_Clo7bot	50	11	3	PF19864 Radical_SAM_N2 11,865 6,446 1,460
	IPR016863 Desll IPR017200 PqgE-like	58 19,368	32 10,212	5 2,373		IPR027622 rSAM_Glo7bot IPR027626 Pseudo_SAM_Halo	50 248	11 67	3	PF19864 Ravicaj_SAM_N2 11,865 6,446 1,460 Tcvat: 4,055,668 1,982,246 336,149
	IPR016863 Desll IPR017200 PqgE-like IPR017672 MA_4551-like	58 19,368 433	32 10,212 209	5 2,373 15		IPR027622 rSAM_Clo7bot IPR027626 Pseudo_SAM_Halo IPR027633 rSAM_NirJ2	50 248 399	11 67 185	3 1 5	PF19864 Resical_SAM_N2 Total: 0.05568 1.898,246 336,149
	IPR016963 Desil IPR017200 PogE-like IPR017672 MA_4651-like IPR017672 DA_4651-like	58 19,368 433 2,879	32 10,212 209 884	5 2,373 15 27		IPR027622 rSAM_Clo7bot IPR027626 Psoudo_SAM_Halo IPR027633 rSAM_NixJ2 IPR030801 (u.2.3.NH3 mult	50 248 399 205	11 67 185 178	3 1 5 2	PP19864 Radical_SAM_N2 11.865 0.446 1.460 Total: 4,055,668 1.892,246 336,149 Total: Computer: 4,055,668
	IPR016863 Desil IPR017200 PqqE-lke IPR017672 MA_4551-lke IPR017742 Deazaguarine_synth	58 19,368 433 2,879	32 10,212 209 884	5 2,373 15 27		IPR027622 rSAM_Clo7bot IPR027626 Pseudo_SAM_Halo IPR027633 rSAM_NicJ2 IPR030601 Glu_2_3_MH_Smut	50 248 399 206	11 67 195 178	3 1 5 2	P11984 Redical_SAN_N2 11,685 6,644 1,460 P11984 Redical_SAN_N2 Total: 40,5568 1,898,249 338,149 Total: 40,5568 1,1898,249 338,149 Total form table a single tently or commaniques assemblated int of femilian. Families should be specified as
	IPR016963 Deall IPR017200 PqqE-like IPR017672 MA_4551-like IPR01742 Deazaguarine_synth IPR017833 Hopanoid_synth-assoc_rSAM_HprH	58 19,368 433 2,879 4,542	32 10,212 209 884 1,470	5 2,373 15 27 82		IPR027622 rSAM_Clo7bot IPR027626 Pseudo,SAM_Halo IPR027633 rSAM_NLJ2 IPR026001 Giu_2_NH3_mut IPR030601 Giu_2_NH3_mut	50 248 399 206 65	11 67 185 178 41	3 1 5 2 2	PTIALCO WONT_CLASS_ALL_XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
	IPR016683         Desili           IPR017200         PogE-like           IPR017672         MA_4561-like           IPR017742         Deszeguarine_synth           IPR017834         Hopanold_synth-assoc_rSAM_HpnJ           IPR017834         Hopanold_synth-assoc_rSAM_HpnJ	58 19,368 433 2,879 4,542 1,453	32 10,212 209 884 1,470 448	5 2,373 15 27 82 14		IPR027622 rSAM_Clo7bot IPR027628 Pseudo_SAM_Halo IPR027633 rSAM_VK1/2 IPR030601 Glu_2_3_VK1/2 IPR0306037 B12_rSAM_cofa1 IPR030684 Arb_pr0sobacteria	50 248 399 206 65 570	11 67 185 178 41 287	3 1 5 2 2 4	PP11864 Reduct_GML_V2 11,855 6.448 1460 PP11864 Reduct_GML_V2 11,855 6.448 1460 PT014.450568 1380,246 356,149 PT014 PT014 PT0144 PT014
	IPR016683 Destil IPR0176200 PqcE-kke IPR017672 Md-4551-kke IPR017782 Deazaguanine_synth IPR017833 Hopanold_synth-assoc_rSAM_HpnH IPR017834 Hopanold_synth-assoc_rSAM_HpnJ IPR019982 Octo_f_mith*	58 19,368 433 2,879 4,542 1,453 6,705	32 10,212 209 884 1,470 448 3,144	5 2,373 15 27 82 14 254		IPR027622 rSAM_Clo7bot IPR027625 Pseudo_SAM_Hab IPR027633 rSAM_Nrs2 IPR020607 Glu_2_3_Nrs1mst IPR020607 Glu_2_3_Nrs1mst IPR020607 Glu_2_6M_code1 IPR020696 rSAM_Arbb_hrenb	50 248 389 286 65 570 580	11 67 185 178 41 287 364	3 1 5 2 2 4 19	PF1984 Rudios_EML_N2 1185 6.448 1460 PF1984 Rudios_EML_N2 1185 Field Computer. 4595.469 PF1980 Computer. 4595.469 The input format is a single relify or communication asymptatic the formation asymptatic the splice (PF10000 CPR asymptatic the splice) PF10000 CPR asymptatic the splice (PF10000 CPR asymptatic the splice) PF10000 CPR asymptatic the splice (PF10000 CPR asymptatic the splice) PF10000 CPR asymptatic the splice (PF10000 CPR asymptatic the splice) PF10000 CPR asymptatic the splice (PF10000 CPR asymptatic the splice) PF10000 CPR asymptatic the splice (PF10000 CPR asymptatic the splice) PF10000 CPR asymptatic the splice (PF10000 CPR asymptatic the splice) PF10000 CPR asymptatic the splice (PF10000 CPR asymptatic the splice) PF10000 CPR asymptatic the splice (PF10000 CPR asymptatic the splice) PF10000 CPR asymptatic the splice (PF10000 CPR asymptatic the splice) PF10000 CPR asymptatic the splice (PF10000 CPR asymptatic the splice) PF10000 CPR asymptatic the splice (PF10000 CPR asymptatic the splice) PF10000 CPR asymptatic the splice) PF10000 CPR asymptatic the splice) PF10000 CPR asymptatic the splice (PF10000 CPR asymptatic the splice) PF10000 CPR asymptatic the splice) PF10000 CPR asymptatic the splice (PF10000 CPR asymptatic the splice) PF10000 CPR asymptatic th
	IPR016683 DextI IPR017672 MA_6514ke IPR017672 MA_6514ke IPR017742 Deazeguarine_synth IPR017883 Hopanold_synth-assoc_SAM_Ppr4 IPR017884 Hopanold_synth-assoc_SAM_Ppr4 IPR019898 CutS_family IPR019898 CutS_family	58 19,368 433 2,879 4,542 1,453 6,705 6,240	32 10,212 209 884 1,470 448 3,144 2,738	5 2,373 15 27 82 14 254 154		IPR027622 rSAM_Clo7bot IPR027629 Paedo_SAM_Hato IPR027635 rSAM_VRiz2 IPR030801 GW_2_3_NH3_mut IPR030801 B12_FSAM_cofn1 IPR030864 A/b_Pr05botatelia IPR030866 Cpt_ack_/SMM	50 248 399 286 65 570 580 544	11 67 185 178 41 287 364 190	3 1 5 2 2 4 19	The second
	IPR01688 Desti IPR01720 P26/E46 IPR017472 Deszgaaring_sym IPR017472 Deszgaaring_sym IPR01783 Hopanid_symh-assofSAM_HprH IPR01783 Hopanid_symh-assofSAM_HprH IPR01993 Cdt_stmly IPR01994 Cdt_stmly	58 19,368 433 2,879 4,542 1,453 6,705 6,240	32 10,212 209 884 1,470 448 3,144 2,738	5 2,373 15 27 82 14 254 154		IPROZIEZZ ISAM, Cushou IPROZIEGO Puedo, SAM, Halo IPROZIEGO ISAM, Ivaz IPRODORI SIL, Z.J. MAJ, mu IPRODORI SIL, Z.J. Mad, mu IPROZORIA AIb. Prostocatoria IPROZORIA AIb. Prostocatoria IPROZORIA (ALM, NAS), Demb	50 248 399 286 65 570 580 580 564	11 67 195 178 41 287 364 190	3 1 5 2 4 19 10	PF1064 Reduct_SML_N2 1185 6.448 1460     PF1064 Reduct_SML_N2 1185 6.448 1460     PT1044 CMC666 13812436     D514 500     T044 CMC966 13812436     D514 500     T044 CMC966 13812436     D514 500     T044 CMC966 1381243     D514 500     T044 CMC966 1381     PF2002 (fm dg)s, PF2002 (fm dg)s     PF2002 (fm dg)s, PF2002 (fm dg)s     PF2002 (fm dg)s, PF2002 (fm dg)s     PF2002 (fm dg)
	IPR016882         Dextl           IPR0177220         PagE-Me           IPR017772         Deazaguarine, synth           IPR017782         Deazaguarine, synth           IPR017823         Hopanold, synth-assoc, SAM_Hon4           IPR017833         Hopanold, synth-assoc, SAM_Hon4           IPR017834         Deazota, synth-assoc, SAM_Hon4           IPR017835         Caff_smith           IPR019940         Caff_smith           IPR019940         Caff_smith           IPR020050         For_synthase_su2	58 19,368 433 2,879 4,542 1,453 6,705 6,240 20,381	32 10,212 209 884 1,470 448 3,144 2,738 8,463	5 2,373 15 27 82 14 254 154 490		PR027022 r5AALControl PR027023 r5AAL540 PR02503 r5AAL540 PR02503 r5AAL542 PR025037 812_5AA1547 PR025037 812_5AA5_cota1 PR025034 AR2_https://action.org/ PR025034 AR2_https://action.org/ PR0250365 Cat2_cot_r5AA	50 248 309 206 55 570 580 564 33	11 67 195 178 41 287 384 190 10	3 1 5 2 2 4 19 10 6	These Gental Action and Acti
	IPR01500         Posl           IPR017502         Posl-fake           IPR017512         MA_45051460           IPR017524         Posl-gasarine_stymth           IPR0256521         Mosl-Posl-gasarine_stymtheastymtose_CS	58 19,368 433 2,879 4,542 1,453 6,705 6,240 20,381 96,829	32 10,212 209 884 1,470 448 3,144 2,738 8,463 40,909	5 2,373 15 27 82 14 254 154 154 480 5,265		PR027022 r5MA/LovText PR022033 r5MA/LovText PR022033 r5MA/LovZ PR0220037 B12_AM_cofst PR020047 B12_AM_cofst PR02008F r5MA/LovE_henete PR02008F r5MA/LovE_henete PR02008F r5MA/LovE_henete PR02008F r5MA/LovE	50 248 389 286 65 570 580 580 564 33 34	11 67 186 178 41 287 384 190 10 21	3 1 5 2 2 4 19 10 6 4	PF11864 Rudia_GM_V2 1185 448 1460     PR11864 GM_V2 1185 448 1460     PR11864 GM_V2 1886 GM_V2
	IPR010083         Deall           IPR0117202         P426/5146           IPR011722         P426/5146           IPR011742         Deadsolution, synth- assoc, ISAM_Hord           IPR011742         Deadsolution, synth- assoc, ISAM_Hord           IPR011742         Deadsolution, synth- IPR011943           IPR011943         Cold, Junity           IPR010943         Cold, Junity           IPR020054         FOL, Junity           IPR02005         FOL, Junity	58 19,368 433 2,879 4,542 1,453 6,705 6,240 20,381 96,829 6,120	32 10,212 209 884 1,470 448 3,144 2,738 8,463 40,909 2,294	5 2,373 15 27 82 14 254 154 490 5,285 95		PR027022 (SAM, CONtrol PR027020) (SAM, PAND) PR027030 (SAM, PAND) PR030001 (SAL, 3, 3, 4A) PR030001 (SAL, 3, 3, 4A) PR030001 A/ID, 2MA/AA) PR030001 (SAL, 2MA/AA) PR030005 (SAL, 2MA/AA) PR030005 (SAL, 2MA/AA) PR030005 (SAL, 2MA/AA) PR030005 (SAL, 2MA/AA) PR030005 (SAL, 2MA/AA) PR030005 (SAL, 2MA/AA)	50 248 399 206 65 65 670 580 584 33 34 190	11 67 185 178 41 287 384 190 10 20 10 21 105	3 1 5 2 2 4 19 10 6 4 59	PF1084 Reduce_EML_PI2 11.85 6.448 1460     PE1084
	IPR016083 Deall IPR017020 Pq2.Fie IPR017020 Pq2.Fie IPR017021 Pq2.fie IPR017021 Pq2.fie IPR017021 Occurs.field.ymfa.stocs.field.yFe/H IPR017031 Occurs.field.ymfa.stocs.field.yFe/H IPR017030 Cr0_stythase_su2 IPR019040 Coff.ymfa.stocs.field IPR019040 Coff.ymfa.stocs.field IPR019040 Coff.ymfa.stocs.field IPR019040 Coff.ymfa.stocs.field IPR019040 Coff.ymfa.stocs.field IPR019041 Coff.ymfa.stocs.field IPR019041 Coff.ymfa.stocs.field IPR020412 Myrtice.field IPR020412 Myrtice.field	58 19,368 433 2,879 4,542 1,463 6,705 6,240 20,381 96,829 6,120 5,964	32 10,212 209 884 1,470 448 3,144 2,738 8,463 40,909 2,294 2,294	5 2,373 15 27 82 14 254 490 5,285 95 95		PRECIFIC2 (SAM, CONTrol PRECIFIC2) (SAM, SAM) PRECIFIC3 (SAM, NAZ) PRECIFIC3 (SAM, NAZ) PRECIFIC3 (SAM, NAZ) PRECIFIC3 (SAM, SAM) PRECIFIC3 (SAM) PRECIFIC3	50 248 399 286 65 570 580 564 33 34 190 74	11 67 185 178 41 287 384 190 10 21 21 105 45	3 1 5 2 2 4 19 10 6 4 50 9	PF1984 Robics_SML_P2     Total 4.05.669     PF1984 Robics_SML_P2     Total 4.05.669
	PR010300         Deall           PR017020         PAgE-Like           PR017020         PAgE-Like           PR017020         PAgE-Like           PR017020         PAgE-Like           PR017020         PAgE-Like           PR017020         PAgE-Like           PR017024         PAge-Like           PR017024         PAge-Like           PR017024         PAge-Like           PR017024         PAge-Like           PR017024         Cold, LineNy           PR0200421         MAYR-Date-LineNy           PR0200421         MAYRID Cold, LineNy           PR0200421         MAYRID Cold, LineNy           PR0200421         MAYRID Cold, LineNy           PR0200421         MAYRID Cold, LineNy           PR020421         MAYRID Cold, LineNy           PR020423         MAYRID Cold, LineNy	58 19,368 433 2,879 4,542 1,453 6,705 6,240 20,381 96,829 6,120 5,864	32 10,212 209 884 1,470 448 3,144 2,738 8,463 40,909 2,294 2,259	5 2,373 15 27 82 14 254 154 490 5,285 95 95 97		PRETRIZ (MM, Chicha) PRETRIZ (MM, Chicha) PRETRIZ (MM, Via) PRETRIZ (MM, Via) PRETRIZ (MJ, Z, J, MA) PRETRIZ (MJ, Z, J, MA) PRETRIZ (MJ, Z, MA) PRETRIZ (MJ, MA) PRETRIZ (MJ, MA) PRETRIZ (MJ, MA) PRETRIZ (MJ, MA) PRETRIZ (J, Z, MA) PRE	50 248 399 286 65 570 580 564 33 34 190 74	11 67 195 178 41 287 384 190 10 21 21 105 45	3 1 5 2 2 4 19 10 6 4 509 2 2	PF1984 Reduct_GML_PG     Total 5.448 1480     PE1984     PF1984 Reduct_GML_PG     Total 4.565.88     Total 4.565     Total 4.565.88     Total 4.565     Total 4.56     Total 4.565     Total 4.56
	PROTECTION Deall     PROTECTION Deall     PROTECTION Deall     PROTECTION Deall     PROTECTION ALL, 656 Labe     PROTECTION ALL	58 19,368 433 2,879 4,542 1,453 6,705 6,240 20,381 96,829 6,120 5,864 1,692	32 10,212 209 884 1,470 448 3,144 2,738 8,463 40,909 2,294 2,259 860	5 2,373 15 27 82 14 254 154 480 5,285 96 96 97 38		PRETER (MM, ChoTra) PRETER (MM, ChoTra) PRETERS (MM, PAR) PRETERS (M, J, J, MA) PRESERS (J, J, J, MA), rul PRESERS (J, J, J, MA), rul PRESERS (J, J, MA), rule PRESERS (MM, PAR) PRESERS (MM, PAR)	50 248 399 206 65 650 580 564 33 34 190 74 3,947	11 67 185 178 41 287 384 190 10 21 2105 46 45 1,835	3 1 5 2 2 4 19 10 6 4 50 2 2 23	PF1984 Radius_EM_32 11.85 4.448 1.44     PF1984 Radius_EM_32 11.85     Fait Compare: 4.85.68     Text Compare: 4.85.6
	PR019580 Dell PR019720 PagElaa PR019727 Mu,456146 PR019727 Mu,456146 PR019728 Isapandi, pr01-asaci, GMU,9pH PR019781 Isapandi, pr01-asaci, GMU,9pH PR0197814 Gald, Pr01-asaci, GMU,9pH PR01978144 Gald, Pr01-asaci, GMU,9pH PR020051 GMU,9pHasaci, GMU,9pH PR020051 GMU,9PH PR0205	58 19,368 433 2,879 4,542 1,463 6,705 6,240 20,381 96,829 6,120 5,884 1,692 3,211	32 10.212 209 884 1.470 448 3.144 2.738 8.463 40,909 2.294 2.259 860 1.685	5 2.373 15 27 82 14 254 154 460 5.265 95 97 38 52		PRETREZ (MM, Cohar) PRETREZ (MM, Cohar) PRETRES (MM, Naz) PRETRES (MM, Naz) PRETRES (MJ, J, MM, Naz) PRETRES (MJ, J, MM, Naz) PRETRES (MJ, J, MM, J, MM, MM, MM, MM, MM, MM, MM	50 248 399 266 65 570 580 564 33 34 190 74 190 74 3,947 38	11 67 195 178 41 287 384 190 10 21 105 45 1,835 16	3 1 2 2 4 19 10 6 4 4 59 2 2 2 3	PF1984 Robics_SML_V2 1185 644 146     PF1984 Robics_SML_V2 1185 644 146     PF1984 Robics_SML_V2 1185 644     PF1985 148     PF1998     PF199     PF1
	PR019580 Deall PR0197220 PagE/ale PR019727 ML_45514e PR019727 ML_45514e PR019727 Deale PR019728 DealersC, Starthause, Jack PR019738 DealersC, Starthause, Jack PR019738 DealersC, Starthause, Jack PR019739 DealersC, Starthause, Jack PR019739 DealersC, Starthause, Jack PR019737 Ministrational Conf. PR019737 Ministrational Conf. PR	58 19,368 433 2,879 4,542 1,453 6,705 6,240 20,381 96,829 6,120 5,864 1,662 3,211 5,760	32 10,212 209 884 1,470 448 3,144 2,738 8,463 40,909 2,294 2,259 860 1,685 2,170	5 2.373 15 27 82 14 254 480 5,285 95 95 97 38 52 28 52 180		PRETERE (MM, CNoTo) PRETERE (MM, CNoTo) PRETERE (MM, PARO, SMM, PARO, PRETERE (MM, Z, Z, MA), PARO PRETERE (Z, Z, MA), PARO PRETERE (MM, Z, MA), PA)	50 248 399 205 55 570 580 564 33 34 190 74 3,947 3,947 38 97	11 67 185 178 41 287 384 190 10 10 21 06 46 1,835 16 75	3 1 5 2 4 19 6 4 50 2 2 3 3 3 29	PF1984 Reduce_SML_N2 to 11.85 6.448 1.469     PF1984 Reduce_SML_N2 to 11.85 6.448 1.469     Total 4.056.68 1.382.249 30.5149     Total 4.056.68 1.382.249 30.5149     Total 4.056.68 1.382.249     Total 4.056.68
	PR010502 Dell PR011722 PagE/ak PR011727 ML455148 PR011727 Dealer/ak PR011732 Dealer/ak PR011732 Dealer/ak PR011742 Deale	58 19,368 433 2,879 4,542 1,453 6,705 6,240 20,381 96,829 6,820 6,820 6,820 5,884 1,682 3,211 5,884	32 10,212 209 884 1,470 448 3,144 2,738 8,463 40,909 2,294 2,259 860 1,685 2,170	5 2.373 15 27 82 14 254 480 5,285 97 97 38 97 38 97 38 97		PRETERZ (MAL, CONTOR PRETERS) (MAL) (Mark) PRETERS) (MAL) (Mark) PRETERS) (MAL) (Mark) PRETERS) (MAL) (MAL) PRETERS) (MAL) (MAL	50 248 389 206 65 570 580 580 584 33 34 190 74 3,947 38 97 4,00	11 67 185 41 287 384 190 10 21 105 45 1,835 1,835 16 75	3 1 2 2 4 19 10 6 4 4 59 2 2 3 3 23 3 29	PF1984 Radias_EM_192 11.85 4.448 1440     PF1984 Radias_EM_192 11.85     Fait 4000000000000000000000000000000000000
	PR010502 Dell PR010727 DelLes PR010727 DelLes PR010727 MLASS Man, Symo PR010781 Name, Symo PR010783 Name, Symo PR010783 Name, Symo PR010783 Code, Janho San, SAN, Symo PR0107830 Code, Janho San, San, San, San, San, San, San, San,	58 19,388 433 2,879 4,542 1,463 6,705 6,240 20,381 96,829 6,120 5,884 1,692 5,884 1,692 13,221 5,760 256	32 10,212 209 884 1,470 448 4,63 40,909 2,294 2,259 860 1,685 2,170 54	5 2.373 15 27 82 440 5.285 96 96 97 38 62 88 62 80 2 2		PRETREZ (MM, ChoTra) PRETRES (MM, Valo) PRETRES (MM, Valo)	50 248 399 206 55 570 680 664 33 34 34 190 74 3,947 38 7 38 7 97	11 67 196 178 41 287 364 190 10 21 21 106 46 1,836 46 1,835 26	3 1 2 2 4 4 19 6 6 4 59 2 2 3 3 3 16	PP11864 Reduct_GML_PD     Field Control
	PR019582 Dell PR019722 Pp2EA PR019727 ML425146 PR019727 ML425146 PR019727 Delta Delta Delta Della ML426 PR019738 Anapolia Delta Delta Della ML426 PR019738 Anapolia Delta Delta Della ML426 PR019738 Delta Delta Delta Della D	58 19,388 433 2,879 4,542 1,453 6,705 6,240 20,31 6,200 5,864 1,602 5,864 1,602 3,211 5,700 2,256 13,008	32 10.212 209 884 1.470 448 3.144 2.738 8.463 40,909 2.294 2.259 860 1.685 2.170 54 5,108	5 2.373 15 27 82 14 480 5.265 99 97 38 52 180 2 563		PRETER IMA, CINIT PRETER IMAN, SAN JAN PRETER IMAN, SAN JAN PRE	50 248 389 206 570 580 554 33 34 190 74 34 74 38 97 38 97 702	11 67 196 41 287 364 190 10 21 100 21 100 21 100 6 5 5 6 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	3 1 2 2 4 4 10 6 6 4 59 2 23 23 23 23 23 23 4 4	PF1984 Radius_SM_32     1.185 6.448 1.40     PF1984 Radius_SM_32     Table Table STATES 1.1857     State STATES     PF1984 Radius_SM_32     Table STATES     PF1984 Radius_SM_32     Table STATES     PF1984 Radius_SM_32     PF1984     Table STATES     Table STATE     Table S
	PR019502 Dell PR019727 Delles PR019727 M.450146 PR019727 M.450146 PR01972 Delles PR01972 Delles PR01974	58 19,388 4,333 2,879 4,542 1,463 6,705 6,240 20,381 96,829 6,120 5,864 1,682 3,211 5,760 2,564 13,008 137,532	32 10,212 209 884 1,470 448 8,463 40,909 8,663 2,259 8,665 2,170 5,108 5,108 5,100	5 2.373 15 27 82 14 254 4400 5.265 95 95 95 95 95 95 95 95 25 180 2 2 863		PRETERZ (MAL, CONTOR PRETERS) (SAM, Valor) PRETERS) (SAM, VALOR)	50 248 399 286 65 670 680 664 33 34 190 74 3,947 3,947 3,947 3,947 72 38 97 1,510 702 902	11 67 196 41 287 364 190 10 21 106 46 4,1,335 106 46 5,26 29 20 101	3 1 5 2 2 4 4 9 10 6 4 4 2 2 2 3 3 29 5 6 4 4	PF1984 Rubus_EML_P2     1.185 4.448 1.440     Test Compare: 4.555.68
	PR019580 Deall           PR0197202 PugE-Bak           PR019727 ML_605146           PR019727 ML_605146           PR019728 Puganot2, Mythaasc, CMM_Port           PR019783 Regards, Dythaasc, CMM_Port           PR019784 Degards, Dythaasc, CMM_Port           PR019785 Degards, Dythaasc, CMM_Port           PR01986 Cold, Dythaasc, CMM_Port	58 19,388 4,333 4,542 1,453 6,754 6,240 20,381 96,829 6,829 6,829 6,829 6,829 6,829 5,884 1,692 3,211 5,780 2,566 13,008 197,525 1,028	32 10,212 209 884 1,470 4,48 3,144 2,738 8,403 2,234 2,259 880 1,685 2,170 5,108 5,108 4,22	5 2,373 15 27 82 14 254 154 480 5,285 97 38 5,285 97 38 5,285 97 38 5,285 97 38 5,285 97 38 5,285 97 38 5,285 97 38 5,295 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,297 5,20		PRETRIZ (MM, CNoTo) PRETRIZ (MM, CNoTo) PRETRIX (MM, Nato) PRETRIX (MM, Nato) PRET	50 248 399 206 65 650 656 33 34 190 7,4 3,947 38 97 1,610 702 202 39	11 67 106 1778 41 287 190 100 21 21 105 465 16 526 29 101 23	3 1 2 2 4 4 19 10 6 4 59 2 23 3 29 16 4 4 4 1	Image: Name         Number of the
	IPR010502         Deall           IPR017020         Deall           IPR017021         Mutual Schell           IPR017021         Mutual Sch	58 19,388 433 2,879 4,542 1,463 6,705 6,240 20,381 96,829 6,120 5,864 1,682 3,211 5,760 2,566 13,088 197,532 13,088	32 10,212 209 884 1,470 4,88 8,483 40,909 2,289 8,000 1,665 2,270 5,108 5,108 5,108 100,166 422	5 2.373 15 27 42 254 440 5.265 95 97 38 97 38 52 190 2 98 2 1993 9 7		PRETERZ IMAL, DONTO PRETERZ IMAL, SAM, Mark PRETERZ IMAL, SAM, SAM PRETERZ IMAL, SAM PRE	50 248 399 265 65 500 580 580 584 34 190 784 384 74 3,847 387 71,810 702 902 399 292 902	11 67 106 178 41 287 41 287 190 10 21 100 21 100 46 1,835 16 75 526 29 101 23 51	3 1 5 2 4 4 19 10 6 4 4 2 23 29 29 16 4 4 4 1 4 1 4 1 4	PF1084         Reduce_SML_P2         11.85         6.448         1.949           Text 407666         138.242         30.549         30.549           Text 407666         138.242         30.549         30.549           Text 507666         138.242         30.549         30.549           Text 507666         138.242         30.549         30.549           Text 5076666         138.242         30.549         30.549           Text 50766666         158.242         158.668         30.549           Text 50766667         158.242         158.668         30.549           Text 50766676         158.242         158.668         30.549           Text 50766767         158.242         158.668         30.549           Text 507667676         158.242         159.668         159.668           Text 50766767         158.242         159.668         159.668         159.668           Text 50766767         158.242         159.668         159.668         159.668         159.668           Text 50766767         159.242         159.668         159.668         159.668         159.668         159.668         159.668         159.668         159.668         159.668         159.668         159.668
	PR019502 Dell PR019727 Della PR019727 AL,450 Les PR019727 AL,450 Les PR019727 AL,450 Les PR01972 Les P	58 19,388 433 2,879 4,542 1,463 6,705 6,240 20,381 96,829 6,829 6,829 6,829 6,829 6,829 5,864 1,682 3,211 5,780 1,5780 13,008 197,528 1,028 116	32 10,212 209 884 1,470 4,48 8,463 8,463 8,463 4,0,009 2,294 8,600 2,294 8,600 2,295 8,600 2,2170 1,685 2,170 1,685 2,170 1,685 2,100 8,600 2,219 2,209 8,600 2,209 8,600 2,209 8,600 2,209 8,600 2,209 8,600 2,209 8,600 2,209 8,600 2,209 8,600 2,209 8,600 2,209 8,600 2,209 8,600 2,209 8,600 2,209 8,600 2,209 8,600 2,209 8,600 2,209 8,600 2,209 8,600 2,209 8,600 2,209 8,600 2,209 8,600 2,209 8,000 2,209 8,000 2,209 8,000 2,209 8,000 2,209 8,000 2,209 8,000 2,209 8,000 2,209 8,000 2,209 8,000 2,209 8,000 2,200 8,000 2,200 8,000 2,200 8,000 2,200 8,000 2,200 8,000 2,200 8,000 2,200 8,000 2,200 8,000 2,200 8,000 2,200 8,000 2,200 8,000 2,200 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,000 2,00	5 2,373 15 27 82 14 154 154 154 5,285 95 95 95 95 95 95 95 95 95 21,993 21,993 9 37		PRETERZ (MAL, CONTON PRETERS) (SAM, FAILE PRETERS) (SAM, FAILE PRETERS) (SAM, FAILE PRETERS) (SAM, FAILE PRETERS) (SAM, SAM, SAM) PRETERS) (SAM, SAM) PRETERS) (SAM) PRETERS) (SAM, SAM) PRETERS) (SAM) PRETERS) (SAM) PRE	50 248 205 65 570 500 664 33 34 4 3,947 74 3,947 38 97 1,807 702 902 902 902 902 902 902 902 902 902 9	11 67 106 1778 41 287 190 100 21 1005 465 21 1,835 16 755 6326 29 101 101 23 51	3 5 2 2 4 19 10 6 4 4 22 23 33 7 50 23 33 16 4 4 1 1 4	PF1984         Reduct_SML_92         11.85         4.44         1.464           Data         Cata
	PR019582 Deal PR019722 PagE-lake PR019727 ML-455146 PR019727 ML-455146 PR019727 Dealers, and an annual pro- PR019727 Dealers, and annual pro- PR019728 Dealers, annual pro- PR01978 Dealers, annual pro- PR01978 Dealers, annual p	58 19,388 433 2,879 4,542 1,453 6,705 6,240 20,381 96,829 6,120 5,884 1,682 3,211 5,760 2568 197,532 13,088 197,532 1,028 197,532	32 10,212 209 884 1,470 4,88 8,483 40,909 2,294 8,000 1,605 5,108 5,108 5,108 5,108 4,22 2,170 5,4 4,23 4,24 5,108 4,22 4,45 4,45	5 2.373 15 27 28 28 14 254 400 5.285 97 38 97 38 5.285 97 38 21,983 21,983 9 37 563		PRETERE (MM, CNoTo) PRETERE (MM, PAND, SMM) PRETERE (MM, PAND, SMM) PRETERE (MM, Z, Z, MA) PRETERE (MM, Z, Z, MA) PRETERE (MM, Z, Z, MA) PRETERE (MM, Z, MA) PRETERE (MM, PAND, SMM) PRETERE	50 248 265 570 580 564 33 34 190 747 38 57 38 57 1,810 702 292 39 180 101	11 67 106 178 41 287 364 190 21 106 1,835 16 526 29 101 23 51 01 23 51 101 23 51 11	3 5 2 2 4 19 10 6 4 59 2 2 3 3 29 16 4 4 4 1 4 4 0 6	Image         Adda         Adda <t< td=""></t<>
	IPR010500 Deall           IPR017020 Deall           IPR01702 ML_050146           IPR01702 ML_050146           IPR01702 Deallow, ph0           IPR01702 Deallow, ph0           IPR01702 Deallow, ph0           IPR01703 Deallow, ph0           IPR01704 Deallow, ph0           IPR01704 Deallow, ph0           IPR01705 De	58 19,388 433 2,879 4,542 1,453 6,705 6,240 20,381 96,829 6,120 5,884 1,682 3,211 5,780 2266 13,008 197,532 1,028 116 6,822 116 6,822 116	32 10,212 209 884 1,470 4,48 8,463 4,40,009 2,234 2,259 860 2,259 860 2,254 2,259 860 2,259 8,60 2,259 1,665 2,170 4,510 8,100 1,665 2,170 4,510 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,299 8,000 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500 2,500	5 2.373 15 27 82 440 524 440 526 96 97 38 52 180 2 56 52 52 58 52 38 52 38 52 37 66 37 60 37 60 51 52 51 52 51 52 52 52 52 52 52 52 52 52 52 52 53 52 54 52 54 52 54 52 52 52 52 52 52 52 52 52 52 52 52 52		PRETERZ (MAL, CONTOR PRETERS) (MAL), Make PRETERS) (MAL), MAL), MAL PRETERS) (MAL), MAL), MAL PRETERS) (MAL), MAL), MAL PRETERS) (MAL), MAL), MAL), MAL PRETERS) (MAL), MAL), MAL)	50 248 399 265 570 580 584 33 34 33 34 33 33 4 33 33 4 33 57 1,810 77 1,810 77 1,810 77 1,810 77 1,810 77 1,810 77 57 57 57 57 57 57 57 57 57 57 57 57	11 67 106 178 41 287 190 100 21 100 46 21 100 46 52 52 9 101 155 229 101 23 51 11 11 1 8,384	3 3 5 2 2 2 4 19 10 6 4 4 59 2 23 20 23 20 23 20 5 20 4 4 4 4 1 1 4 6 774	PF1004         Reduce_DML_92         11.85         4.44         14.94           Text 4200666         318.242         30.543           Text 5400666         318.242         30.543           Text 54006666         318.242         30.543           Text 54006666         318.242         30.543           Text 54006666         318.242         30.543           Text 54006666         318.242         30.543           Text 5400666         318.242         30.543           Text 5400666         318.242         30.543           Text 540066         318.242         10.5435           Text 540066         318.242         10.5436           Text 540066         318.242         10.5436           Text 5400666         318.242         10.5436           Text 5400666         318.242         10.5436           Text 54006666         318.242         10.5436           Text 54006666         318.242         10.5436           Text 5400
	PR010020 Dell PR011727 DelL PR011727 DelL PR011727 DelL PR011727 DelL PR011727 DelL PR011728 DelL PR	58 19,388 4,33 2,879 4,542 1,463 6,705 6,240 20,381 96,829 6,120 5,884 1,692 3,211 5,780 2568 197,532 1,028 197,532 1,028 197,532 1,028	32 10,212 209 884 1,470 4,48 3,144 2,738 8,463 40,909 2,294 2,294 2,299 800 1,685 2,170 54 5,168 5,168 54 100,166 44 422 104 483 333	5 2.373 15 27 82 44 480 524 480 524 90 7 38 62 90 7 38 62 180 2 1993 9 37 66 1 220 9		PRETERZ (MAL, Cholma) PRETERS (MAL, 2), Markon, SMA, Markon PRETERS (MAL, 2), Markon, SMA, Markon PRESERVE (MAL, 2), Markon, SMA, Markon PRESERVE (MAL, 2), Markon, SMA, Markon PRESERVE (MAL, 2), Markon, SMA, Parkon PRESERVE (MAL, 2), Markon PRESERVE (MAL,	50 248 399 266 550 570 564 33 4 190 564 33 4 34 34 34 34 34 34 34 74 74 702 597 702 902 39 97 100 702 2039 101 203,755 2039 2039 2039 2039 205 505 507 507 507 507 507 507 507 507 5	11 67 108 41 287 364 190 21 100 21 106 1,835 16 526 29 101 23 101 23 101 23 11 11 8,884 9,267	3 5 2 2 4 4 9 10 6 4 8 9 2 3 3 9 16 4 4 4 1 1 4 6 774	PF1904         Rudia_LSM_V2         11.85         4.44         Vote           PR1904         Rudia_LSM_V2         11.85         4.44         Vote         Vo
	PHISTISSO Dell PHISTISSO Public PHISTISSO Public PHISTISSO Public PHISTISSO Public PHISTISSO Phistopy Phistopy CAUCH PHISTISSO Color (Phistopy Phistopy CAUCH) PHISTISSO Color (Phistopy Phistopy CAUCH) PHISTISSO Color (Phistopy Phistopy CAUCH) PHISTISSO Color (Phistopy Phistopy Phistopy Cauch) PHISTISSO Color (Phistopy Phistopy Phisto	58 19,88 433 2,879 4,542 1,453 6,705 6,240 20,841 96,829 6,120 5,864 1,662 3,211 5,760 1,560 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,500 1,5	32 10.212 209 884 1.470 4.48 3.144 4.63 3.144 4.630 2.234 40.900 2.234 40.900 2.234 40.900 2.234 5.108 54 40.0156 44 4.022 104 4.022 104 4.033 33 1.236	6 2.373 15 27 27 44 284 40 554 400 554 400 554 400 563 563 563 563 21,993 37 563 21,993 30 7 664 12,293 20 7 865 21,293 20 7 86 20 7 86 20 7 86 20 7 86 20 20 20 20 20 20 20 20 20 20 20 20 20		PRETERE (MM, ChoRnel) PRETERE (MM, Parkon), SM, Marko PRETERE (MM, Parkon), SM, Marko PRETERE (MM, Z, Z, MA), mail PRETERE (MM, Z, Z, MA), mail PRETERE (MM, Z, Z, MA), mail PRETERE (MM, PARKON), marko PRETERE (MM, PARKON), markon PRETERE (MM, PARKON), m	50 248 399 265 670 884 33 4 39 74 74 74 74 74 75 75 77 1,8,10 707 797 1,8,10 707 1,8,10 707 1,8,10 707 1,8,10 707 1,8,10 707 1,8,10 707 70 802 30 902 309 100 70 70 70 70 70 70 70 70 70 70 70 70 7	11 67 196 178 41 287 364 190 201 21 100 46 46 46 46 46 528 100 101 23 51 51 101 23 51 11 8,384 8,267	3 5 2 2 4 19 10 6 4 20 22 3 3 29 5 6 4 4 4 4 4 4 1 1 4 6 724 4 52 5 2 2 3 3 29 5 6 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	mining         mining <thmining< th=""> <thmining< th=""> <thmining< t<="" td=""></thmining<></thmining<></thmining<>
	IPR010030 Deall           IPR017020 PagE-Bas           IPR01702 ValueSchart           IPR01702 ValueSchart           IPR01702 ValueSchart           IPR01703 ValueSchart           IPR01704 Descart           IPR01705 ValueSchart	58 19,268 4,33 2,879 4,542 1,453 6,705 6,240 20,381 96,829 6,120 2,884 1,682 3,211 5,760 2,266 197,532 13,008 197,532 1,008 197,532 1,008 197,532 1,008 197,532 1,008 197,532 1,008 197,532 1,008 197,532 1,008 197,532 1,008 197,532 1,008 197,532 1,008 197,532 1,008 197,532 1,008 197,55 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 1,008 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Dist         2015.608         2015.608         2015.608         2015.608           Dist         2015.608         2015.608         2015.608         2015.608         2015.608           Dist         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608         2015.608
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	IPR010030 Deall           IPR017020 PagE-Bas           IPR01702 ValueSchart           IPR01702 ValueSchart           IPR01702 ValueSchart           IPR01702 ValueSchart           IPR01702 ValueSchart           IPR01702 ValueSchart           IPR01703 ValueSchart           IPR01704 ValueSchart           IPR01705 ValueSchart	58 19,368 4,33 2,879 4,542 6,705 6,240 20,381 96,829 6,829 6,829 6,829 5,884 1,682 3,211 5,700 2256 13,068 197,532 116 6829 13,009 116 6829 116 6829 116 6829 116 6829 116 6829 116 6829 116 6829 116 6829 116 6829 116 6829 116 6829 116 6829 116 6829 116 7,555 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 116 884 116 884 116 884 116 884 116 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 884 116 885 116 884 116 884 116 884 116 884 116 884 116 884 116 885 116 884 116 884 116 884 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	PR010020 Dell PR010727 Dipelise PR010727 Dipelise PR010727 Dipelise PR010727 MLASS Market PR010781 Standard Standard Standard PR010781 Standard Standard Standard PR010782 Coll, Suntan Standard PR010782 Coll, Suntan Standard PR02020 Coll, S	58 19,368 433 2,379 4,542 1,463 6,705 6,200 20,381 96,829 6,120 5,864 1,662 3,211 5,700 2266 13,068 13,068 13,0752 2269 13,028 1107,532 2109 438 1357 7,935 82 82 82 82 82 82 82 82 82 82	32 10.212 209 844 1.470 448 8.463 8.463 2.234 8.000 1.685 2.234 8.000 1.685 4.229 8.000 1.685 4.229 1.04 4.685 3.125 1.015 1.015 3.100 1.026 3.128 1.026 3.128 1.026 3.128 1.026 3.128 1.026 3.128 1.026 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.128 3.1283 3.1283 3.1283 3.1283 3.1283 3.1283 3.1283 3.1283 3.1283 3.1283	6 5 2,273 15 22 24 44 440 544 440 645 440 645 440 645 440 645 440 645 440 645 445 446 645 445 445 445 445		PRETEZ (MA), Cholma PRETEZ (MA), Cholma PRETEX (MA), PARA PRETEX (M	50 244 349 266 55 55 56 56 56 56 56 56 56 57 57 57 57 57 57 57 57 57 57 57 57 57	111 67 1965 1978 41 190 100 21 190 21 190 21 190 46 4 525 29 101 101 23 51 101 23 51 11 8.384 9.267 3 6 3 3 6 3 3 3 5 3 3 4 5 25 525 525 525 525 525 525 525 525		Printer     Reading SML y2     1.18.6     4.44     1.04.9       Printer     Tate 4.04.06.3     3.03.4.9       Data 4.04.06.3     3.03.4.9     3.03.4.9       Printer     Tate 4.04.06.3     3.03.4.9       Data 4.04.06.3     3.03.4.9     3.03.4.9       Printer     Tate 4.04.06.3     1.04.0.9     3.03.4.9       Printer     Tate 4.04.06.0     1.04.0.9     1.04.0.9       Printer     Tate 4.04.06.0     1.04.0.0     1.04.0.9       Printer     Tate 4.04.06.0     1.04.0.0     1.04.0.0       Printer     Tate 4.04.06.00     1.04.0.0     1.04.0.0       Printer     Tate 4.04.06.00     1.04.0.0     1.04.0.0       Printer     Tate 4.04.06.00     1.04.0.0     1.04.0.0     1.04.0.0       Printer     Tate 4.04.06.00     1.04.0.0     1.04.0.0     1.04.0.0       Printer     Tate 4.04.06.00     1.04.0.0     1.04.0.0     1.04.0.0       Printer     Tate 4.04.00.00     1.04.0.0     1.04.0.0
	IPR010500 Dell           IPR01050 Dell           IPR01052 Dell           IPR02052 Dell           IPR02052 Multiple           IPR02052 Multiple           IPR02052 Dell           IPR02052 Dell<	58 19,368 433 2,879 4,542 1,463 6,705 6,240 20,341 6,200 6,240 6,240 6,240 6,240 3,211 5,760 2,266 13,008 197,532 13,008 116 6,622 197,532 116 6,622 13,009 148 135 7,005 2,249 1,35 135 7,005 2,249 1,35 1,35 1,35 1,35 1,35 1,35 1,35 1,35	32 10.212 209 864 4.463 8.463 8.463 8.463 8.463 8.463 8.229 8.80 1.865 2.209 8.80 1.865 4.45 5.108 4.22 1.015 5.108 4.22 1.015 5.108 1.235 6.1 1.235 6.1 1.235 6.1 1.235 6.1 1.235 6.1 1.235 6.1 1.235 6.1 1.235 6.1 1.235 6.1 1.235 6.1 1.235 6.1 1.235 6.1 1.235 6.1 1.235 6.1 1.235 6.1 1.235 6.1 1.235 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 7.125 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    10.45       10.45         P10010       Reduc_RM_10       Reduc_RM_10       Reduc_RM_10       Reduc_RM_10       10.45         P10010       Reduc_RM_10       Reduc_RM_1
	IPRIETISSO         Deall           IPRIETISSO         PageLinka           IPRIETISSO         PageLinka           IPRIETISSO         PageLinka           IPRIETISSO         PageLinka           IPRIETISSO         PageLinka           IPRIETISSO         PageLinka           IPRIETISSO         Cale, Samily           IPRIETISSO         Cale, Cale, Samily           IPRIETISSO         Cale, Ca	58 19.368 4.33 2.879 4.542 1.463 6.705 6.240 20.381 106 120 258 13.088 116 6.259 1.008 117.532 1.008 116 6.229 1.008 116 6.229 1.008 116 6.229 1.008 116 6.229 1.008 116 6.229 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 1.008 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	IPRIETISSO Dell	686 913,568 433 434 434 434 434 434 434 434 434 43	32 10.212 209 844 3.144 2.738 8.403 40.909 2.294 2.299 880 2.294 2.294 2.295 1.685 2.170 5.1 6 100.166 100.166 100.166 100.166 100.166 100.166 100.166 100.166 100.166 100.166 100.166 100.166 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.100 100.1000 100.1000 100.1000 100.1000 100.1000 100.1000 100.1000 100.1000 100.1000 100.1000 100.1000 100.1000 100.1000 100.1000 100.1000 100.1000 100.1000 100.1000 100.1000 100.1000 100.1000 100.10000 100.100000000	6 2.273 127 127 144 144 144 144 144 144 144 14		PRECTIZE (MM_CDNM           PRECTIZE (MM_CDNM)           PRECTIZE (MM_CDM_M)           PRECTIZE (	50 248 266 65 670 64 33 34 34 34 35 7 7 8 7 8 9 9 9 2 2 2 9 9 9 9 3 3 9 9 9 2 2 2 8 9 9 9 3 3 9 9 9 2 2 2 8 10 0 10 0 10 0 10 0 10 0 10 0 1	11 607 617 618 116 116 116 121 100 201 101 211 106 406 106 406 106 406 220 201 101 201 201 201 201 201		Printed     Reading_CML_192     1.18.65     1.44.16     1.04.01       Printed     District depticed     1.05.01     1.05.01       Printed     Printed     District depticed     1.05.01       Printed     Printed     Printed     District depticed     1.05.01       Printed     Printed     Printed     Printed     Printed
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	Pre11920 Dell Pre11927 Dell Pre11927 Della Pre11927 Della Pre11928 ALSA SA SA SA Pre11928 ALSA SA S	88         8           443         3           443         3           4542         3           4542         3           4562         2           8         4           6         3           7         5           8         3           1000         1000           1000         1000           1000         1000           1000         1000           1000         1000           1000         1000           1000         1000           1000         1000           1000         1000           1000         1000           1000         1000           1000         1000           1000         1000           1000         1000           1000         1000           1000         1000           1000         1000           1000         1000           1000         1000           1000         1000           1000         1000           1000         1000           1000         1000	32 32 32 32 32 32 32 32 32 32 32 32 32 3	6 6 7 7 7 8 7 7 8 7 8 7 8 7 8 7 8 7 8 7		PRECTIZE (MML, Chord)	90 248 399 266 64 30 30 34 34 30 34 30 34 30 34 30 34 30 30 30 30 30 30 30 30 30 30 30 30 30	11 11 10 10 10 11 12 13 14 13 14 13 14 14 14 15 15 15 15 15 15 15 15 15 15	3 5 2 2 2 4 4 10 10 6 4 9 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3	

Previous Jo	bs Families	FASTA	Accession IDs							
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Retrieve tax	onomy for familie									
The UniProt	IDs for family men	nbers are ident	ified in UniProtKB v	vith a list of Pfam	families, InterPro	families, and/or				
Pfa	m and/or InterPro	o Families and	l/or Pfam clans:							
45	45784 PF04055 PF06969 PF08497 PF12345 PF13186 PF16199 PF16881 PF19238 PF19288 PF19864									
	Family	F	amily Name	Full Size	UniRef90 Size	UniRef50 Size				
	IPR000385	MoaA_NifB_F	PqqE_Fe-S-bd_CS	49,241	23,160	4,777				
	IPR001989	Radical_activ	at_CS	26,935	9,907	1,836				
	IPR002684	Biotin_synth/8	BioAB	27,640	9,880	1,004				
	IPR003698	Lipoyl_synth		39,047	13,924	1,318				
	IPR003739	Lys_aminomu	itase/Glu_NH3_mul	20,775	10,372	1,278				
	IPR004383	rRNA_lsu_M1	rfase_RImN/Cfr	39,944	15,429	1,455				
	IPR004558	Coprogen_ox	idase_HemN	16,796	6,746	513				
	IPR004559	HemW-like		38,255	17,990	2,765				
	IPR005839	Methylthiotrar	nsferase	87,716	37,295	4,127				
	IPR005840	Ribosomal_S	12_MeSTrfase_Rim	10 28,658	11,857	2,029				
	IPR005909	RaSEA		2,035	1,022	229				
	IPR005911	YhcC-like		11,293	4,505	502				
	IPR005980	Nase_CF_Nif	В	2,647	1,104	82				
	IPR006463	MiaB_methiol	ase	35,615	13,649	723				
	IPR006466	MiaB-like_B		4,407	2,226	506				
	IPR006467	MiaB-like_C		17,077	8,216	1,089				
	IPR006638	Elp3/MiaA/Nif	B-like_rSAM	446,282	212,389	36,535				
	IPR007197	rSAM		722,535	355,669	70,723				
	IPR010505	Mob_synth_C	:	38,361	16,635	1,682				
	IPR010722	BATS_dom		39,852	14,953	1,222				

* Fragment Ontion								
UniProt designates a Sequence Status for each member: Complete if the encoding DNA sequence has both start and stop codons; Fragment if the start and/or stop codon is missing. Approximately 10% of the entries in UniProt are fragments.								
Fragments: I Check to								
For the UniRef90 and UniRef50 databases, clusters are excluded if the cluster ID ("representative sequence") is a fragment.								
UniProt IDs in UniRef90 and UniRef50 clusters with complete cluster IDs are removed from the clusters if they are fragments.								
Filter by Taxonomy								
✓ Length Filter								
Minimum Length: 140 Maximum Length:								
Job name: IP91_RSS_NoFragments_Minlen140 (required)								
E-mail address:								
You will be notified by e-mail when your submission has been processed.								
Submit Analysis								

The results were available on the **DATASET COMPLETED** page. The **Taxonomy Sunburst** tab (below) is the interactive display that provides the numbers of UniProt, UniRef90 cluster, and UniRef50 cluster IDs (red arrow), downloads for IDs and FASTA sequences (blue arrow), and transfers of IDs to EFI-EST (green arrow) or EFI-GND viewer (magenta arrow).



### **UniRef50 Cluster SSN**

The UniRef50 cluster SSN was generated for the complete UniRef50 cluster entries in the RSS using the **EFI-EST Families Option** by inserting the list of 211 Pfam and InterPro families and/or domains (**Tutorial Table 1**) into the **Pfam and/or InterPro Families and/or Pfam Clans** box (red arrow) and **UniRef50 cluster IDs** (blue arrow), checking the **Fragments** box in the **Fragment Option** to exclude fragments (green), entering the **Job name** (orange arrow) and an **E-mail address** (cyan arrow), and clicking "**Submit analysis**" (black arrow).

Previous Jobs	Sequence BLAST	Families F	FASTA Acc	ession IDs	SSN Utilities		<ul> <li>              Fragment Option      </li> </ul>
Generate a SSN	for a protein family.						UniProt designates a Sequence Status for each member: Complete if the encoding DNA sequence has both start and stop codons; Fragment if the start and/or stop codon is missing. Approximately 10% of the entries in UniProt are fragments.
The members of t	the input Pfam families,	InterPro families, a	and/or Pfam clar	ns are selected	from the UniPro	t, UniRef90, or UniRef50	Fragments: Check to exclude UniProt-
patabase. Pfam ar	nd/or InterPro Families	and/or Pfam clar	ns:				For the UniRef90 and UniRef50 databases, clusters are excluded if the cluster ID ("representative sequence") is a fragment.
45784	PF04055 PF06969 P	F08497 PF1234	5 PF13186 PF	16199 PF168	81 PF19238 PF	F19288 PF19864	UniProt IDs in UniRef90 and UniRef50 clusters with complete cluster IDs are removed from the clusters if they
🗸 Use	UniRef50 - cluster ID	seque	t IDs	(UniProt is de	fault).		are fragments.
	Family	Family Name	Full	Size UniRef	90 Size UniRef	f50 Size	* Filter by Taxonomy
	IPR000385 MoaA_Ni	fB_PqqE_Fe-S-bd	_CS 4	19,241	23,160	4,777	
	IPR001989 Radical_a	activat_CS	2	26,935	9,907	1,836	From preselected conditions, the user can select "Bacteria, Archaea, Fungi", "Eukarvota, no Fungi", "Fungi", "Viruses",
	IPR002684 Biotin_sy	nth/BioAB	2	27,640	9,880	1,004	"Bacteria", "Eukaryota", or "Archaea" to restrict the retrieved sequences to these taxonomy groups.
	IPR003698 Lipoyl_sy	nth	3	39,047	13,924	1,318	"Bacteria, Archaea, Fungi", "Bacteria", "Archaea", and "Fungi" select organisms that may provide genome context (gene
	IPR003739 Lys_amin	omutase/Glu_NH3	3_mut 2	20,775	10,372	1,278	clusters/operons) useful for inferring functions.
	IPR004383 rRNA_Isu	_MTrfase_RImN/C	Cfr 3	39,944	15,429	1,455	The retrieved sequences also can be restricted to taxonomy categories within the Superkingdom, Kingdom, Phylum, Class,
	IPR004558 Coproger	_oxidase_HemN	1	16,796	6,746	513	Order, Family, Genus, and Species ranks. Multiple conditions are combined to be a union of each other.
	IPR004559 HemW-lik	e	3	38,255	17,990	2,765	The sequences from the UniRef90 and UniRef50 databases are the UniRef90 and UniRef50 clusters for which the cluster
	IPR005839 Methylthic	otransferase	8	37,716	37,295	4,127	ID ("representative sequence") matches the specified taxonomy categories. The UniProt members in these clusters that do not match the specified taxonomy categories are removed from the cluster.
	IPR005840 Ribosoma	al_S12_MeSTrfase	e_RimO 2	28,658	11,857	2,029	
	IPR005909 RaSEA			2,035	1,022	229	Preselected conditions: select a preset to auto populate
	IPR005911 YhcC-like		1	11,293	4,505	502	
	IPR005980 Nase_CF	_NifB		2,647	1,104	82	Add Taxonomy category
	IPR006463 MiaB_me	thiolase	3	35,615	13,649	723	
	IPR006466 MiaB-like	_B		4,407	2,226	506	- Bendelle Freudlu Blan Belline
	IPR006467 MiaB-like	_c	1	17,077	8,216	1,089	Protein Family Size Options
	IPR006638 Elp3/Mia/	VNifB-like_rSAM	44	16,282	212,389	36,535	Family Domain Boundary Option
	IPR007197 rSAM		72	2,535	355,669	70,723	SSN Edge Calculation Option
	IPR010505 Mob_synt	th_C	3	38,361	16,635	1,682	
	IPR010722 BATS_do	m	3	39,852	14,953	1,222	
	IPR010723 HemN_C		3	39,495	17,002	2,804	Job name: IP91_RSS_UniRef50_NoFragments (required)
	IPR011101 DUF5131			7,313	4,801	1,324	E-mail address:
	IPR011843 PQQ_syn	th_PqqE_bac		5,549	1,835	59	
	IPR012726 ThiH			6,704	2,297	125	You will be notified by e-mail when your submission has been processed.
	IPR012837 NrdG		1	11,645	4,135	630	
	IPR012838 PFL1_act	ivating		9,425	2,995	180	Submit Analysis
	IPR012839 Organic_	radical_activase	1	16,374	5,941	1,127	
	IPR013483 MoaA		3	33,719	14,394	976	11

The SSN was finalized on the SSN Finalization tab of the DATASET COMPLETED page using 11 as the Alignment Score Threshold (orange arrow) and 140 residues as the Minimum in the Sequence Length Restriction to remove truncated sequences (cyan arrow), entering the Network (SSN) name (brown arrow), and clicking "Create SSN" (black arrow). We previously determined that the members of the anaerobic ribonucleotide reductase activating enzyme family have the shortest sequences ( $\geq$ 140 residues) [2]).

DATASET C	OMPLET	ED						
Submission Name	e: IP91_RSS_	_UniRef50_N	loFragments					
A minimum sequence threshold also detern score, an edge node	e similarity thres nines the segreg attribute that is a	hold that specif ation of protein a measure of th	ies the sequence pairs is into clusters. The thre ne similarity between se	connected by edges is shold is applied to the quence pairs.	needed to generate the SSN. This edges in the SSN using the alignment			
Dataset Summar	ry Taxonom	y Sunburst	Dataset Analysis	SSN Finalization				
This tab is used to specify the minimum "Alignment Score Threshold" (that is a measure of the minimum sequence similarity threshold) for drawing the edges that connect the proteins (nodes) in the SSN.								
Alignment Score	Threshold:	11 ?						
This va magni	alue correspond: tude to the nega	s to the lower lin tive base-10 log	mit for which an edge w garithm of a BLAST e-v	ill be present in the SS alue.	SN. The alignment score is similar in			
- Sequence Le	ength Restrictio	n Options						
Allows restrie	ction of sequenc	es in the genera	ated SSN based on the	ir length. 🕡				
Minimum:	140	(default: 0)		l				
Maximum:		(default: 5000	0)					
▶ Filter by Taxe	onomy							
▸ Neighborhoo	od Connectivity							
Fragment Op	otion							
Network name:	₽91_RSS_UI	niRef50_Nol	Fragments_Minlen	140_AS11 This nar	ne v red in Cytoscape.			
You will be notified	d by e-mail wher	n the SSN is rea	ady for download.					
			Create SSN					

The **Network Files** tab of the **DOWNLOAD NETWORK FILES** page provided the xgmml file for the **Full (SSN) Network** (red arrow; all UniRef50 cluster nodes and edges) as well as the xgmml files for **Representative Node Networks** that conflate the UniProt nodes based on percent identity (blue arrow). The xgmml files for the full SSN were downloaded, opened with Cytoscape 3.9.1, and displayed with the Prefuse Force Directed layout; the nodes were colored according to the Structure-Function Linkage Database (SFLD) subgroups [2, 3].

ork Name: IP91_R55_UI	– – niRef50_NoFrag	gments_Minlen14	40_AS11	
N Overview Network File	es			
	Pleas	e cite your use of t	he EFI tools:	
Rémi Zallot, Nils Ober Leveraging Protein, Ge Pathways. Biochem	g, and John A. G <b>nome, and Meta</b> iistry 2019 58 (41	erlt, <b>The EFI Web</b> genome Databas ), 4169-4182. http	Resource for Genomic es to Discover Novel E s://doi.org/10.1021/acs	Enzymology Tools: nzymes and Metabolic .biochem.9b00735
e panels below provide files fo an approximate guide, SSNs v 0M edges can be opened with 8 RAM, and ~120M edges can	r full and represent with ~2M edges car 64 GB RAM, ~20M be opened with 76	ative node SSNs for d n be opened with 16 C l edges can be opene 8 GB RAM.	lownload with the indicated r GB RAM, ~5M edges can be d with 128 GB RAM, ~40M e	numbers of nodes and edge opened with 32 GB RAM, edges can be opened with 2
es may be transferred to the G ighborhood Connectivity utility.	enome Neighborho	od Tool (GNT), the Co	olor SSN utility, the Cluster A	Analysis utility, or the
Ill Network 🧿				
ch node in the network represe	ents a single proteir	n sequence.		
	# N	lodes	# Edges	
Download ZIP	63	3,359	65,098,917	Transfer To: 💌
presentative Node Netw representative node (RepNode crent identity. For example, for puped into a single node (meta mplicated networks easier to lo	works (?) a) networks, each n a 75% identity Rep node). Sequences bad in Cytoscape.	ode in the network rep Node network, all cor are collapsed togethe	presents a collection of prote nected sequences that shar ar to reduce the overall numl	sins grouped according to re 75% or more identity are ber of nodes, making for les
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epresentative Node Netw representative node (RepNode rcent identity. For example, for upped into a single node (meta publicated networks easier to lo e cluster organization is not ch Download ZIP	works ⑦	ode in the network rep Node network, all cor are collapsed togethe stering of sequences in <b># Nodes</b> 63,359	presents a collection of prote nected sequences that sha er to reduce the overall numi remains identical to the full n # Edges 65,098,917	ins grouped according to re 75% or more identity are ber of nodes, making for les hetwork.
epresentative Node Netw representative node (RepNode crent identity. For example, for puped into a single node (meta mplicated networks easier to lo e cluster organization is not ch Download ZIP Download ZIP	works ⑦	ode in the network rej Node network, all cor are collapsed togethe stering of sequences I <b># Nodes</b> 63,359 63,352	presents a collection of prote nnected sequences that sha ar to reduce the overall numl remains identical to the full n # Edges 65,098,917 65,091,388	ins grouped according to re 75% or more identity are ber of nodes, making for les network. Transfer To: •
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Presentative Node Netw representative node (RepNode creat identity. For example, for puped into a single node (meta puped into a single node (meta ce cluster organization is not ch Download ZIP Download ZIP	works         ?           a) betworks, each not a 75% (dentify Reguences) and in Cytoscapes) and in Cytoscapes (dentify Reguences) and in Cytoscapes (dentify Reguen	Andee         Ite network region           Node         network, all contract of sequences of	acceleration of protein exercision of reduce the overail number of reduce the overai number of reduce the overail number of reduce	Ans grouped according bar re 75% or more identity are ber of nodes, making for les thetwork. Transfer To: • Transfer To: •



**UniRef50 Cluster SSN for the RS Superfamily**. The UniRef50 cluster SSN for the RS superfamily was generated using a minimum length of 140 residues and an alignment score threshold of 11, opened with Cytoscape 3.9.1, and displayed with the Prefuse Force Directed layout using a Mac Pro computer with 1.5TB RAM. The nodes are colored according to the subgroups defined by the Structure-Function Linkage Database (SFLD) [2, 3]. The SSN contains 63,359 nodes and 65,098,917 edges.

### **UniRef90 Cluster SSN**

The UniRef90 cluster SSN was generated for the complete UniRef90 cluster entries in the RSS using the **EFI-EST Families Option** by specifying the list of 211 Pfam and InterPro families and/or domains (**Tutorial Table 1**) into the **Pfam and/or InterPro Families and/or Pfam Clans** box (red arrow) and **UniRef90 cluster IDs** (blue arrow), checking the **Fragments** box in the **Fragment Option** to exclude fragments (green arrow), entering the **Job name** (orange arrow) and an **E-mail address** (cyan arrow), and clicking "**Submit analysis**" (black arrow).

Previous Jobs	Sequence BLAST	Families F/	ASTA Accession II	SSN Utilities		* Fragment Option
Generate a SSN	for a protein family.					UniProt designates a Sequence Status for each member: Complete if the encoding DNA sequence has both start and stop codons; Fragment if the start and/or stop codon is missing. Approximately 10% of the entries in UniProt are fragments.
The members of	the input Pfam families, I	nterPro families, ar	nd/or Pfam clans are sel	ected from the UniPr	ot, UniRef90, or UniRef50	Fragments: Z Check to exclude the state of the results. (default: off)
database. Pfam ar	nd/or InterPro Families	and/or Pfam clans	s:			For the UniRef90 and UniRef50 databases, clusters are excluded if the cluster ID (*representative sequence*) is a fragment.
45784	PE04055 PE06969 PE	08497 PE12345	PE13186 PE16199 P	E16881 PE19238 F	F19288 PF19864	IniProt IDs in UniRef90 and UniRef50 clusters with complete cluster IDs are removed from the clusters if they
				1000111102001	1102001110001	are fragments.
🗸 Use	UniRef90 - cluster ID	sequence	)s (UniProt	is default).		
	Family	Family Name	Full Size U	niRef90 Size UniRe	ef50 Size	* Filter by Taxonomy
	IPR000385 MoaA_Nifl	B_PqqE_Fe-S-bd_	CS 49,241	23,160	4,777	
	IPR001989 Radical_a	ctivat_CS	26,935	9,907	1,836	From preselected conditions, the user can select "Bacteria, Archaea, Fungi", "Eukaryota, no Fungi", "Fungi", "Viruses",
	IPR002684 Biotin_syn	th/BioAB	27,640	9,880	1,004	"Bacteria", "Eukaryota", or "Archaea" to restrict the retrieved sequences to these taxonomy groups.
	IPR003698 Lipoyl_syn	ith	39,047	13,924	1,318	"Bacteria, Archaea, Fungi", "Bacteria", "Archaea", and "Fungi" select organisms that may provide genome context (gene
	IPR003739 Lys_amino	mutase/Glu_NH3_	mut 20,775	10,372	1,278	clusters/operons) useful for inferring functions.
	IPR004383 rRNA_lsu_	MTrfase_RImN/Cf	r 39,944	15,429	1,455	The retrieved sequences also can be restricted to taxonomy categories within the Superkingdom, Kingdom, Phylum, Class,
	IPR004558 Coprogen	_oxidase_HemN	16,796	6,746	513	Order, Family, Genus, and Species ranks. Multiple conditions are combined to be a union of each other.
	IPR004559 HemW-like	)	38,255	17,990	2,765	The sequences from the UniRef90 and UniRef50 databases are the UniRef90 and UniRef50 clusters for which the cluster
	IPR005839 Methylthio	transferase	87,716	37,295	4,127	ID ("representative sequence") matches the specified taxonomy categories. The UniProt members in these clusters that do not match the specified taxonomy categories are removed from the cluster.
	IPR005840 Ribosoma	_S12_MeSTrfase_	RimO 28,658	11,857	2,029	
	IPR005909 RaSEA		2,035	1,022	229	Preselected conditions: select a preset to auto populate
	IPR005911 YhcC-like		11,293	4,505	502	
	IPR005980 Nase_CF_	NifB	2,647	1,104	82	Add Taxonomy category
	IPR006463 MiaB_met	hiolase	35,615	13,649	723	
	IPR006466 MiaB-like_	В	4,407	2,226	506	
	IPR006467 MiaB-like_	c	17,077	8,216	1,089	Protein Family Size Options
	IPR006638 Elp3/MiaA	/NifB-like_rSAM	446,282	212,389	36,535	Family Domain Boundary Option
	IPR007197 rSAM		722,535	355,669	70,723	> SSN Edge Calculation Option
	IPR010505 Mob_synth	1_C	38,361	16,635	1,682	
	IPR010722 BATS_dor	n	39,852	14,953	1,222	
	IPR010723 HemN_C		39,495	17,002	2,804	Job name: IP91_RSS_UniRef90_NoFragments (required)
	IPR011101 DUF5131		7,313	4,801	1,324	
	IPR011843 PQQ_synt	h_PqqE_bac	5,549	1,835	59	E-mail address:
	IPR012726 ThiH		6,704	2,297	125	You will be notified by e-mail when your submission has been processed.
	IPR012837 NrdG		11,645	4,135	630	
	IPR012838 PFL1_acti	vating	9,425	2,995	180	Submit Analysis
	IPR012839 Organic_ra	adical_activase	16,374	5,941	1,127	
	IPR013483 MoaA		33,719	14,394	976	

The SSN was finalized on the SSN Finalization tab of the DATASET COMPLETED page using 11 as the Alignment Score Threshold and 140 residues as the Minimum in the Sequence Length Restriction to remove truncated sequences, entering the Network (SSN) name (brown arrow), and clicking "Create SSN" (black arrow). We previously determined that the members of the anaerobic ribonucleotide reductase activating enzyme family have the shortest sequences ( $\geq$ 140 residues) [2].

DATASET (	COMPLET	ED			
Submission Nan	ne: IP91_RSS	_UniRef90_I	NoFragments		
A minimum sequen threshold also deter score, an edge node	ce similarity thres mines the segreg a attribute that is	hold that specif ation of protein a measure of th	fies the sequence pairs is into clusters. The thre ne similarity between se	connected by edges is eshold is applied to the equence pairs.	enceded to generate the SSN. This edges in the SSN using the alignment
Dataset Summa	ary Taxonom	ıy Sunburst	Dataset Analysis	SSN Finalization	
Alignment S	core Threshold				
This tab is us threshold) for	ed to specify the drawing the edge	minimum "Aligr es that connect	nment Score Threshold the proteins (nodes) in	" (that is a measure of the SSN.	the minimum sequence similarity
Alignment S	core Threshold:	11			
TI si	nis value correspo milar in magnitud	onds to the lowe e to the negativ	er limit for which an edg /e base-10 logarithm of	e will be present in the a BLAST e-value.	e SSN. The alignment score is
- Sequence L	ength Restrictio	n Options			
Allows rest	iction of sequenc	es in the gener	ated SSN based on	ir longth. ?	
Minimum:	140	(default: 0)			
Maximum:		(default: 5000	)0)		
▶ Filter by Tax	conomy				
Neighborho	od Connectivity				
Fragment O	ption				
→ Dev Site Op	tions				
Network name:	₽91_RSS_U	niRef90_No	Fragments_Minlen	140_AS11 This nar	me will be displayed in Cytoscape.
You will be notified	ed by e-mail whe	n the SSN is re	ady for download.		
			Create SSI	Ν	

The DOWNLOAD NETWORK FILES page did not provide the xgmml file for the full

SSN or the representative node networks (348,446 nodes and 2,583,616,067 edges); the edge

maximum for generating an SSN is 200,000,000.

	Network Files							
		Please cite your use of the EFI tools:						
Rémi Zallot, Nils Oberg, and John A. Gerlt, <b>The EFI Web Resource for Genomic Enzymology Tools:</b> Leveraging Protein, Genome, and Metagenome Databases to Discover Novel Enzymes and Metabolic Pathways. Biochemistry 2019 58 (41), 4169-4182. https://doi.org/10.1021/acs.biochem.9b00735								
[™] he panels belov \s an approxima -10M edges can 3B RAM, and ~1	w provide files for full te guide, SSNs with be opened with 64 ( 20M edges can be c	and representative node SSNs for download with the indicated numbers of nodes and edges. 2M edges can be opened with 16 GB RAM, ~5M edges can be opened with 32 GB RAM, B RAM, ~20M edges can be opened with 128 GB RAM, ~40M edges can be opened with 256 bened with 768 GB RAM.						
[:] iles may be trar √eighborhood Co	nsferred to the Genor onnectivity utility.	e Neighborhood Tool (GNT), the Color SSN utility, the Cluster Analysis utility, or the						
ull Network	?							
Each node in the	e network represents	single protein sequence.						
he output file v lifferent alignm	was too large (edge ent score.	=2,583,616,067) to be generated by EST. Please use a repnode below or choose a						
Representativ	ve Node Networ	S 🕐						
n representative percent identity. I prouped into a si complicated netv	node (RepNode) ne For example, for a 75 ngle node (meta nod vorks easier to load i	works, each node in the network represents a collection of proteins grouped according to % identity RepNode network, all connected sequences that share 75% or more identity are b). Sequences are collapsed together to reduce the overall number of nodes, making for less Cytoscape.						
he cluster organ	nization is not change	d, and the clustering of sequences remains identical to the full network.						
% ID		Nodes #Edges						
	,	in Edges						
100	Th	e output file was too large (edges=2,583,616,067) to be generated by EST.						
100 95	Th Th	e output file was too large (edges=2,583,616,067) to be generated by EST.						
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100 95 90 85	, Th Th Th Th	e output file was too large (edges=2,583,616,067) to be generated by EST. e output file was too large (edges=2,569,142,064) to be generated by EST. e output file was too large (edges=2,526,601,854) to be generated by EST.						
100 95 90 85 80	, Th Th Th Th Th	<ul> <li>a output file was too large (edges=2,569,142,064) to be generated by EST.</li> <li>a output file was too large (edges=2,566,142,064) to be generated by EST.</li> <li>a output file was too large (edges=2,526,601,854) to be generated by EST.</li> <li>a output file was too large (edges=2,165,619,179) to be generated by EST.</li> <li>a output file was too large (edges=1,846,597,151) to be generated by EST.</li> </ul>						
100       95       90       85       80       75	, Th Th Th Th Th Th	<ul> <li>a output file was too large (edges=2,569,142,064) to be generated by EST.</li> <li>a output file was too large (edges=2,569,142,064) to be generated by EST.</li> <li>b output file was too large (edges=2,526,601,854) to be generated by EST.</li> <li>c output file was too large (edges=2,165,619,179) to be generated by EST.</li> <li>c output file was too large (edges=1,846,597,151) to be generated by EST.</li> <li>c output file was too large (edges=1,577,543,078) to be generated by EST.</li> </ul>						
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# Taxonomy Category-Specific UniRef90 SSNs: Taxonomy Tool Families Option, with Transfer of UniRef90 cluster IDs to the EFI-EST Accession IDs Option

The **Taxonomy Sunburst** for the entire RSS with complete sequences was used with the Transfer to EFI-EST feature to generate taxonomy category-specific UniRef90 SSNs that could be analyzed with Cytoscape. For superkingdom Bacteria, phylum Actinobacteria; superkingdom Bacteria, phylum Bacteroidetes; superkingdom Bacteria, phylum Firmicutes; superkingdom Bacteria, phylum Proteobacteria; and superkingdom Archaea, the indicated taxonomy categories were selected by clicking on the wedge (left panel). For **Preselected conditions** Fungi (a combination of four phyla within superkingdom Eukaryota), the Eukaryota taxonomy category was selected (right panel).



The UniRef90 cluster SSN for superkingdom Bacteria, phylum Proteobacteria is too large to be analyzed with Cytoscape (102,114 nodes and 250,587,566 edges). However, UniRef90 cluster SSNs were generated for Classes within the Proteobacteria that can be analyzed with Cytoscape: class Alphaproteobacteria, class Betaproteobacteria, class Gammaproteobacteria, class Deltaproteobacteria, and Class Epsilonproteobacteria.

For the single taxonomy categories (left panel), in the EFI-EST Accession IDs Option pages that opened, the Fragment Option was used to exclude fragments (blue arrow), Filter by Family was used with the list of 211 Pfam and InterPro families and/or domains (Tutorial Table 1) (green arrow), and Filter by Taxonomy was used to select the taxonomy category (magenta arrow). For Fungi, Fungi was selected from the Preselected conditions menu in Filter by Taxonomy; for Eukaryota, no Fungi, Eukaryota, no Fungi was selected from the Preselected conditions menu in Filter by Taxonomy. As described in the text, Filter by Family and Filter by Taxonomy are used to ensure that the UniRef90 cluster IDs and internal UniProt IDs match the desired taxonomy category and family. The Job name (orange arrow) and an E-mail address were entered (cyan arrow), and the job was started by clicking "Create SSN" (black arrow).



Fragment	agment in the start and/or stop codol, is missing. Approximately to a of the entries in only for are nagments.
	s: Z Check to exclude UniProt
	For the UniRef90 and UniRef50 databases, clusters are excluded if the cluster ID ("representative sequence") is a fragment.
	UniProt IDs in UniRef90 and UniRef50 clusters with complete cluster IDs are removed from the clusters if they are fragments.
Filter by Fa	mily
The input InterPro f	list of UniRef90 or UniRef50 cluster IDs should (must!) be filtered with the same list of Pfam families, amilies, and/or Pfam clans used to generate the IDs, if:
The input I (Option B) Tool.	ist of UniRef90 or UniRef50 IDs is obtained from 1) the Color SSN or Cluster Analysis utility for a Families option EFI-EST SSN, 2) the Families option of the Taxonomy Tool, or 3) the Accession IDs option of the Taxonomy
Input a list these fami	of Pfam families, InterPro families, and/or Pfam clans to restrict the UniProt and/or UniRef IDs in the SSN to lies.
Family(s):	5 PF06969 PF08497 PF12 199 PF16881 PF19238 PF19288 PF19864
	The input format is a single family or comma/space separated list of families. Families should be specified as PFxxxxxx (five digits), IPRxxxxxxx (digits) or CLxxxx (four digits) for Pfam clans.
For input li match the families ar	sts of UniRe/90 and UniRe/90 clusters, the cluster ID (representative sequence) is used to identify those that list of families and are included in the SSN. The UniProt members in these clusters that do not match the input removed from the cluster and are not included in the SSN node attributes.
Filter by Ta	, xonomy
The input	list of UniRef90 or UniRef50 cluster IDs should (must!) be filtered with the same taxonomy categories
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Previous Jobs Sequence BLAST Families FASTA Accession IDs SSN Utilities

An all-by-all BLAST (?) is performed to obtain the similarities between sequence pairs to calculate edge values to generate the SSN.

Generate a SSN from a list of UniProt, UniRef, NCBI, or Genbank IDs.

Use UniProt IDs Use UniRef50 or UniRef90 Cluster IDs

Accession IDs:

Accession ID File: (7) ARSS_NoFragments

Input a list of UniRef50 or UniRef90 cluster accession IDs, or upload a text file.

Input accession IDs are: UniRef90 cluster IDs 🚽 💿

• Fragment Option

E-mail address: You will be notified by e-mail when your submission has been processed. Submit Analysis The SSNs were finalized on the SSN Finalization tab of the DATASET COMPLETED page using 11 as the Alignment Score Threshold and 140 residues as the Minimum in the Sequence Length Restriction to remove truncated sequences (orange arrow), entering the Network (SSN) name (brown arrow), and clicking "Create SSN" (black arrow). We previously determined that the members of the anaerobic ribonucleotide reductase activating enzyme family have the shortest sequences ( $\geq$ 140 residues) [2].

DATASET CO	MPLETED			
Submission Name: I	P91_RSS_NoFragmer	nts_Actinobacteria	_UniRef90_NoFra	agments_RSS_Actinobacteria
A minimum sequence sir threshold also determine score, an edge node attr	milarity threshold that specif is the segregation of protein ibute that is a measure of th	ies the sequence pairs is into clusters. The thre ne similarity between se	connected by edges is shold is applied to the quence pairs.	needed to generate the SSN. This edges in the SSN using the alignment
Dataset Summary	Taxonomy Sunburst	Dataset Analysis	SSN Finalization	
This tab is used to sp threshold) for drawing	ecify the minimum "Alignme g the edges that connect the	ent Score Threshold" (th proteins (nodes) in the	at is a measure of the SSN.	minimum sequence similarity
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- Sequence Lengt	h Restriction Options			
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Network name: No	Fragments_RSS_Acti	nobacteria_Minlen ⁻	140_AS11 This nar	ne version in Cytoscape.
You will be notified by	/ e-mail when the SSN is rea	ady for download.		
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The **Network Files** tab of the **DOWNLOAD NETWORK FILES** page provided the xgmml file for the **Full (SSN) Network** (red arrow; all UniProt nodes and edges) as well as the xgmml files for **Representative Node Networks** that conflate the UniProt nodes based on percent identity (blue arrow). The xgmml files for the full SSN was downloaded, opened with Cytoscape 3.9.1, and displayed with the Prefuse Force Directed layout. The nodes were colored according to the subgroups defined by the Structure-Function Linkage Database (SFLD) [2, 3].

_RSS_NoFragments_Ac	tinobacteria_U	niRef90_NoFrag	gments_RSS_Actinoba	cteria_Minlen140_AS
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e panels below provide files fo an approximate guide, SSNs 0M edges can be opened with 8 RAM, and ~120M edges can es may be transferred to the G ighthorboot Connectivity utility	r full and representa with ~2M edges can 64 GB RAM, ~20M be opened with 768 enome Neighborhoo	tive node SSNs for be opened with 16 edges can be open GB RAM. od Tool (GNT), the 0	download with the indicated GB RAM, ~5M edges can be ed with 128 GB RAM, ~40M Color SSN utility, the Cluster /	numbers of nodes and edge e opened with 32 GB RAM, edges can be opened with 2 Analysis utility, or the
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Taxonomy Category-Filtered UniRef 90 Cluster SSNs for the RS Superfamily. The SSNs were generated as described in the text. The SSNs were generated using a minimum length of 140 residues and an alignment score threshold of 11. The nodes are colored according to the subgroups defined by the Structure-Function Linkage Database (SFLD) [2, 3]. Panel A, Superkingdom Bacteria, phylum Actinobacteria; the SSN contains 27,953 nodes and 20,427,984 edges. Panel B, Superkingdom Bacteria, phylum Bacteroidetes; the SSN contains 27,028 nodes and 21,948,018 edges. Panel C, Superkingdom Bacteria, phylum Firmicutes; the SSN contains 52,451 nodes and 61,254,499 edges. Panel D, Superkingdom Archaea; the SSN contains 36,996 nodes and 27,905,053 edges. Panel E, Superkingdom Eukaryota, Fungi only; the SSN contains 3,341 nodes and 715,572 edges. Panel F, Superkingdom Eukaryota, no Fungi; the SSN contains 8,2661 nodes and 3,859,619 edges.



# **E** Epsilonproteobacteria



Taxonomy Category-Filtered UniRef 90 Cluster SSNs for Taxonomy Classes in the Proteobacteria Phylum in the Radical SAM Superfamily. The SSNs were generated using the Families option of the Taxonomy Tool with transfer of UniRef90 cluster IDs to Option D pipeline described in the text. The SSNs were generated using a minimum length of 140 residues and an alignment score threshold of 11. The nodes are colored according to the subgroups defined by the Structure-Function Linkage Database (SFLD) [2, 3]. Panel A, Class Alphaproteobacteria; the SSN contains 27,868 nodes and 29,935,838 edges. Panel B, Class Betaproteobacteria; the SSN contains 11,936 nodes and 4,364,852 edges. Panel C, Class Gammaproteobacteria; the SSN contains 28,350 nodes and 24,151,979 edges. Panel D, Class Deltaproteobacteria; the SSN contains 26,875 nodes and 15,107,300 edges. Panel E, Class Epsilonproteobacteria; the SSN contains 3,830 nodes and 513,294 edges.

# Taxonomy Category-Specific UniRef90 SSNs: EFI-EST Families Option, Filter by Taxonomy in the Analysis Step

The SSN Finalization tab of the **DATASET COMPLETED** page for the UniRef90 cluster SSN for the complete entries was used to generate the category-filtered SSNs described in the **Taxonomy Tool Families Option, with transfer of UniRef90 cluster IDs to the EFI-EST Accession IDs Option** section. The SSNs were finalized using 11 as the **Alignment Score Threshold** and 140 residues as the **Minimum** in the **Sequence Length Restriction** to remove truncated sequences. As described previously, for the single taxonomy categories, **Filter by Taxonomy** was used to select the single taxonomy categories. For Fungi, **Fungi** was selected from the **Preselected conditions** menu. For Eukaryota, no Fungi, **Eukaryota, no Fungi** was selected from the **Preselected conditions** menu.

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The xgmml files for the full UniRef90 cluster SSNs (all UniRef90 cluster nodes and edges with alignment scores  $\geq 11$ ) as well as representative node networks that conflate UniRef90 clusters nodes based on percent identity were available for download on the **DOWNLOAD NETWORK FILES** page. The xgmml files for the full SSNs were downloaded and opened with Cytoscape; the nodes were colored according to the subgroups defined by the Structure-Function Linkage Database (SFLD) [2, 3].

Notework Files         Please cite your use of the EFI tools:         Rémi Zallot, Nils Oberg, and John A. Gerlt, The EFI Web Resource for Genomic Enzymology Tools:         Leveraging Protein, Genome, and Metagenome Databases to Discover Novel Enzymes and Metabol Pathways. Biochemistry 2019 56 (41), 4169-4182. https://doi.org/10.1021/acs.biochem.9b00735         tep anels below provide files for full and representative node SSNs for download with the indicated numbers of nodes and edg as an approximate guide, SSNs with ~20M edges can be opened with 12 GB RAM, ~5M edges can be opened with 32 GB RAM         Old Medges can be opened with 768 GB RAM.       20M edges can be opened with 128 GB RAM, ~40M edges can be opened with 18 GB RAM, ~40M edges can be opened with 82 GB RAM.         Ise may be transferred to the Genome Neighborhood Tool (GNT), the Color SSN utility, the Cluster Analysis utility, or the sighborhood Connectivity utility.         ull Network (?)         ach node in the network represents a single protein sequence.         ************************************	Network Files Please cite your use of the EFI tools: ot, Nils Oberg, and John A. Gerlt, The EFI Web Resource for Genomic Enzymology Tools: Protein, Genome, and Metagenome Databases to Discover Novel Enzymes and Metabolic vs. Biochemistry 2019 58 (41) 4169-4182. https://doi.org/10.1021/acs.biochem.9h00735	SN Overview Network Files					
Please cite your use of the EFI tools:         Rémi Zallot, Nils Oberg, and John A. Gerlt, The EFI Web Resource for Genomic Enzymology Tools:         Leveraging Protein, Genome, and Metagenome Databases to Discover Novel Enzymes and Metagol Pathways. Biochemistry 2019 58 (41), 4169–4182. https://doi.org/10.1021/acs.biochem.9b00735         ne panels below provide files for full and representative node SNs for download with the indicated numbers of nodes and edi as an approximate guide, SNs with ~2M edges can be opened with 16 GB RAM, ~5M edges can be opened with 28 GB RAM, and ~120M edges can be opened with 786 GB RAM.         Nodes and edges can be opened with 126 GB RAM, ~40M edges can be opened with 28 GB RAM, and ~120M edges can be opened with 786 GB RAM.         Ide may be transferred to the Genome Neighborhood Tool (GNT), the Color SSN utility, the Cluster Analysis utility, or the eighborhood connectivity utility.         Ide Nodes         # Nodes         # Rodes         # Rodes         # Edges         Download ZIP         27,953       20,397,534         Transfer To: •         * Nodes         # Edges         Transfer To: •         Paresentative Node Networks, each node in the network represents a collection of proteins grouped according to rorent identity. For example, for a 75% identity RepNode network, all c	Please cite your use of the EFI tools: ot, Nils Oberg, and John A. Gerlt, <b>The EFI Web Resource for Genomic Enzymology Tools:</b> Protein, Genome, and Metagenome Databases to Discover Novel Enzymes and Metabolic vs. Biochemistry 2019 58 (41) 4169-4182. https://doi.org/10.1021/acs.biochem.9h00735						
Leveraging Protein, Genome, and Metagenome Databases to Discover Novel Enzymes and Metabol Pathways. Biochemistry 2019 58 (41), 4169-4182. https://doi.org/10.1021/acs.biochem.9b00735         he panels below provide files for full and representative node SSNs for download with the indicated numbers of nodes and edis an approximate guide, SSNs with ~2M edges can be opened with 16 GB RAM. ~5M edges can be opened with 28 GB RAM.         10M edges can be opened with 768 GB RAM.         10B RAM, and ~120M edges can be opened with 768 GB RAM.         10B random ZiP         27,953         20,397,534         Transfer To: •         *         *         Pownload ZIP         27,953         20,397,534         Transfer To: •         *         *         *         *         *         *         *         *         *         *         *         *         *         *         *         *         *         *         *         *         *         *         *         *         *         * <t< th=""><th>Protein, Genome, and Metagenome Databases to Discover Novel Enzymes and Metabolic ys. Biochemistry 2019 58 (41) 4169-4182. https://doi.org/10.1021/acs.biochem.9b00735</th><th colspan="6">Please cite your use of the EFI tools:</th></t<>	Protein, Genome, and Metagenome Databases to Discover Novel Enzymes and Metabolic ys. Biochemistry 2019 58 (41) 4169-4182. https://doi.org/10.1021/acs.biochem.9b00735	Please cite your use of the EFI tools:					
the panels below provide files for full and representative node SSNs for download with the indicated numbers of nodes and edgs an approximate guide, SSNs with ~2M edges can be opened with 12 GB RAM, ~5M edges can be opened with 23 GB RAM.         10M edges can be opened with 64 GB RAM, ~20M edges can be opened with 128 GB RAM, ~40M edges can be opened with 768 GB RAM.         12B RAM, and ~120M edges can be opened with 768 GB RAM.         12B RAM, and ~120M edges can be opened with 768 GB RAM.         12B RAM, and ~120M edges can be opened with 768 GB RAM.         12B RAM, and ~120M edges can be opened with 768 GB RAM.         12B RAM, and ~120M edges can be opened with 768 GB RAM.         12B RAM, and ~120M edges can be opened with 768 GB RAM.         12B RAM, and ~120M edges can be opened with 768 GB RAM.         12B RAM, and ~120M edges can be opened with 768 GB RAM.         12B RAM, and ~120M edges can be opened with 768 GB RAM.         12B RAM, and ~120M edges can be opened with 768 GB RAM.         12B RAM, and ~120M edges can be opened with 768 GB RAM.         12B RAM, and ~120M edges can be opened with 768 GB RAM.         12B RAM, and ~120M edges can be opened with 768 GB RAM.         12B RAM, and ~120M edges can be opened with 768 GB RAM.         12B RAM, and ~120M edges can be opened with 768 GB RAM.         12B Commoad ZIP       27,953         12B Commoad ZIP       90         12F 7,810       20,397,534         12B Commoad ZIP		Leveraging Protein, Genome Pathways. Biochemistry 2					
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Moles       # Edges         ack node in the network represents a single protein sequence.         Download ZIP       27,953       20,397,534       Transfer To: •         epresentative Node Networks, each node in the network represents a collection of proteins grouped according to protein single node (Meta node). Sequences are collapsed together to reduce the overall number of nodes, making for a 75% identity RepNode network, all connected sequences that share 75% or more identity arouped into a single node (meta node). Sequences are collapsed together to reduce the overall number of nodes, making for a male cluster organization is not change, and the clustering of sequences remains identical to the full network.         Nownload ZIP       100       27,810       20,397,534       Transfer To: •         Download ZIP       95       27,810       20,397,534       Transfer To: •         Download ZIP       95       27,810       20,397,534       Transfer To: •         Download ZIP       90       27,810       20,397,534       Transfer To: •         Download ZIP       90       27,810       20,397,534       Transfer To: •         Download ZIP	ferred to the Genome Neighborhood Tool (GNT), the Color SSN utility, the Cluster Analysis utility, or the nectivity utility.	les may be transferred to the Genome eighborhood Connectivity utility.					
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Download ZIP       27,953       20,397,534       Transfer To:         Perpresentative Node Networks each node in the network represents a collection of proteins grouped according to procent identity. For example, for a 75% identity RepNode network, all connected sequences that share 75% or more identity an upped into a single node (meta node). Sequences are collapsed toender to reduce the overall nutworks easier to load in Cytoscape.         the cluster organization is not changed, and the clustering of sequences that share 75% or more identity an Download ZIP       90       27,953       20,397,534       Transfer To:       •         Download ZIP       90       27,953       20,397,534       Transfer To:       •         Download ZIP       90       27,432       19,568,000       Transfer To:       •         Download ZIP       85       24,941       15,842,539       Transfer To:       •         Download ZIP       80       22,566       12,682,765       Transfer To:       •         Download ZIP       75       20,347       9,893,597       Transfer To:       •	# Nodes # Edges						
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% ID         # Nodes         # Edges           Download ZIP         100         27,953         20,397,534         Transfer To:         •           Download ZIP         95         27,810         20,180,999         Transfer To:         •           Download ZIP         90         27,432         19,568,000         Transfer To:         •           Download ZIP         85         24,941         15,842,539         Transfer To:         •           Download ZIP         80         22,566         12,682,765         Transfer To:         •           Download ZIP         75         20,347         9,893,597         Transfer To:         •	zation is not changed, and the clustering of sequences remains identical to the full network.	e cluster organization is not changed					
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# Taxonomy Category-Specific UniRef90 SSNs: EFI-EST Families Option, Filter by Taxonomy in the Generate Step

The same taxonomy category-filtered UniRef90 SSNs described in the previous sections were generated in separate jobs using the **EFI-EST Family Option** by specifying the list of 211 Pfam and InterPro families and/or domains (**Tutorial Table 1**) (red arrow) and UniRef50 cluster IDs (blue arrow), selecting **Fragment Option** to exclude fragments (green arrow), and selecting the taxonomy category (magenta arrow). The **Job name** (orange arrow) and an **E-mail address** (cyan arrow) were entered; the job was started by clicking **"Submit analysis"** (black arrow).

Cencere as SNB for a protein family.         Using the designation as Sequence SNB bas for advancement protein structure complete life encoding. PMA expanse has howed has all address of doors. Fragment in the standard structure complete fire encoding. PMA expanse has howed has all address of doors. Fragment in the standard structure of mathins. Reference and the structure of the security.           STATE PF00055P Pr0056P / PF12335 PF13285 PF132855 PF13285 PF13285 PF13285 PF13285 PF13285 PF132855	Previous Jobs	Sequence BLAS	T Families	FASTA	Accession II	Ds SSN Util	ities	* Fragment Option
The members of the liquel Plant families, Indiver families, and/or Plant datas are selected from the UniProt, UniReffo, or UNIR650.       Fragments: © check to capacity and the merculas, (cafault of)         Afrida PErdosos P	Generate a SSN	for a protein family						UniProt designates a Sequence Status for each member: Complete if the encoding DNA sequence has both start and stop codons; Fragment if the start and/or slop codon is missing. Approximately 10% of the entries in UniProt are fragments.
Utabalantic       Prof Indian and/or InterPro Pamilies or Prof 2017 PF12345 PF16159 PF16258 PF19228 PF19258       Frid Builder Stater Discount Prof Prof Prof Prof Prof Prof Prof Prof	The members of t	the input Pfam famili	es, InterPro families	s, and/or Pfa	m clans are sel	ected from the U	IniProt, UniRef90, or UniRef5	) Fragments: 🗹 Check to exclude the pents in the results. (default: off)
46744       PF04055       PF04055       PF12454       PF11245	database. Pfam ar	nd/or InterPro Fami	lies ar					For the UniRef90 and UniRef50 databases, clusters are excluded if the cluster ID ("representative sequence") is a fragment.
Image: Strategy         Event Do. (UniProt is default).           Finally         Finally Kame         Finally Kame         Final Size         UniRed50 Size           IPPO00358         Moad_NIR_PROC_FS-S-6.4 C.S         40,241         23,160         4,777           IPPO00358         Moad_NIR_PROC_FS-S-6.4 C.S         40,241         23,160         4,777           IPPO00358         Signature         58,800         1,004         47,872           IPPO00358         Signature         30,972         1,278         1,378           IPPO00358         Signature         30,974         1,342         1,452           IPPO0358         Signature         30,974         1,372         1,278           IPPO0358         IPMO1488         33,255         17,990         2,764         513           IPPO0358         Next_ST_MAR_max         37,255         2,029         19,800         1,802         2,025           IPPO03588         Name_GF_NIME         1,232         1,104         82         1,014         82           IPPO03588         Name_GF_NIM         1,232         5,056         1,022         2,203         1,002         2,004         1,014         82         1,014         1,014         1,014         1,014	45784	PF04055 PF0696	9 PF08497 PF123	345 PF1318	6 PF16199 P	F16881 PF192	38 PF19288 PF19864	UniProt IDs in UniRef90 and UniRef50 clusters with complete cluster IDs are removed from the clusters if they
Family         Panily Name         Full Size         UnRetPO Size           IPR00385         MaA, NIE, Poet, Fe-S-bu, CS         40,241         23,160         4,777           IPR00386         Biotin, synth/BiokA         27,640         9,880         1,004           IPR00386         Lipov, synth         30,447         13,224         1,318           IPR00386         Lipov, synth         30,447         13,624         1,4155           IPR00386         Lipov, synth         30,447         13,624         1,4555           IPR00456         Gorgon_coldase_Herm         16,766         513           IPR00556         Reproduction         2,776         37,205         4,127           IPR005659         Reproduction         2,765         1,022         229           IPR005690         Rasce, CP_NIB         2,674         1,104         82           IPR005690         Rasce, CP_NIB         2,674         1,104         82           IPR005690         Rasce, CP_NIB         2,674         1,104         82           IPR005690         Rasce, CP_NIB         2,625         1,022         229           IPR005690         Rasce, CP_NIB         2,447         1,014         82           IPR005690<	🗸 Use	UniRef90 - cluster	r ID se	hiPr	ot IDs (UniProt	is default).		are fragments.
IPR00338       MosA_NMB_PqqE_Fe-S-bd_CS       49,241       23,160       4.777         IPR003385       MosA_NMB_PqqE_Fe-S-bd_CS       28,335       9,307       1,388         IPR002648       Biolong_synth/BioAB       27,404       9,808       1,004         IPR002648       Biolong_synth/BioAB       27,404       9,808       1,004         IPR002648       Biolong_synth/BioAB       27,404       9,808       1,004         IPR003736       Lys_aminonudase/Biu_JMH3 mut       20,775       1,322       1,372         IPR004583       RMA_Mut/Infrase_RimO/Cr       19,444       1,425       1,455         IPR005585       Corgen_coddsse_HernN       16,796       6,746       513         IPR005585       Corgen_coddsse_HernN       16,796       4,127         IPR005586       Rinz Park       2,825       17,909       2,785         IPR005580       Rinz Park       2,825       17,909       2,785         IPR005580       Rinz Park       2,8265       513       3,4407       2,226         IPR005580       Nale_C F_MMB       2,647       1,104       722       506       1,777       6,716       1,227       1,986       1,835       1,6822       1,8353       1,6823       1,8		Family	Family Name		Full Size U	niRef90 Size U	niRef50 Size	
IPR001989       Radical_actival_CS       26,935       9,907       1,836         IPR002648       Biolin_synth®loA8       27,640       9,880       1,004         IPR003686       Lipo/Lipo/Lynth       30,447       1,318         IPR004387       RNA_lsu_MTAss_MINUCIr       33,944       1,318         IPR004587       River, Name       30,947       1,324         IPR004587       River, Name       30,944       1,429         IPR004587       River, Name       Statural, Accharas, Hory River, Statural, Accharas, Funy River, Statural, Name, Human River, Thurgit, Youngit, Y		IPR000385 MoaA	_NifB_PqqE_Fe-S-t	bd_CS	49,241	23,160	4,777	· Filter by laxonomy
IPR002684       Biolin_synth/BioAB       27,60       9,880       1,004         IPR002684       Biolin_synth/BioAB       27,60       9,880       1,004         IPR002684       Lipvi_synth       39,047       13,324       1,318         IPR003783       Lys_aminomutase/oliu_N13, mut       20,075       10,372       1,278         IPR00483       rRNA_Isu_MTrfase_RImVCfr       39,944       15,429       1,455         IPR00585       Coprogen_oxidase_HemN       16,766       6,746       513         IPR00583       Methylthotransferase       87,716       37,295       4,127         IPR005891       Nace_CF_NIB       2,045       10,22       229         IPR005891       Nace_CF_NIB       2,647       1,104       82         IPR005891       Nace_CF_NIB       2,647       1,049       82         IPR005891       Nace_CF_NIB       2,647       1,049       82         IPR005891       Nace_S_C       17,077       8,216       1,089         IPR005891       Nace_S_CA       2,035       1,022       229         IPR005891       Nace_S_CA       2,035       1,022       226         IPR005951       Nace_S_CA       1,035       1,636		IPR001989 Radic	al_activat_CS		26,935	9,907	1,836	Free enveloped an differentia constant and the state of Archaele Free 2 (Free 2 (Free 2 (Free 2 (Free 2 (Free 2
IPR003998       Lipoyl_synth       39,047       13,324       1,318         IPR003939       Lys_aminomutase/Gu_NH3_mut       20,775       10,372       1,278         IPR004337       Lys_aminomutase/Gu_NH3_mut       20,775       10,372       1,278         IPR004587       Korpoge_oxidase_HemN       16,796       6,746       513         IPR004589       HemW-Hite       38,255       7,799       2,775         IPR00589       Methythiotransferase       8,7,716       37,295       4,127         IPR00589       Methythiotransferase       8,7,716       37,295       4,127         IPR00589       Methythiotransferase       8,7,716       37,295       4,127         IPR00589       MasExe_C       2,035       11,267       2,029         IPR00589       MasExe_C       2,035       11,223       229         IPR00580       Nase_CF_NHB       2,647       1,104       82         IPR00581       IPR00584       MaB_metric.       8,535       16,924       1,936         IPR005845       MaB_metric.       11,037       8,535       1,927       Add Taxonomy categories       IProtein Family Size Options         IPR00584       IPR01702       HemN_L       39,845       1,702 <td></td> <td>IPR002684 Biotin</td> <td>_synth/BioAB</td> <td></td> <td>27,640</td> <td>9,880</td> <td>1,004</td> <td>"From preselected conditions, the user can select "Bacteria, Archaea, Fungi", "Eukaryota, no Fungi", "Fungi", "Viruses", "Bacteria", "Eukaryota", or "Archaea" to restrict the retrieved sequences to these taxonomy groups.</td>		IPR002684 Biotin	_synth/BioAB		27,640	9,880	1,004	"From preselected conditions, the user can select "Bacteria, Archaea, Fungi", "Eukaryota, no Fungi", "Fungi", "Viruses", "Bacteria", "Eukaryota", or "Archaea" to restrict the retrieved sequences to these taxonomy groups.
IPR00379       Lys_aminomutase/Glu_NH3_mut       20,775       10,372       1,278         IPR00333       RNA_lsu_Intrase_Rim/VCr       39,944       15,429       1,455         IPR004585       Corpogen_oxidase_HemN       16,766       513         IPR00589       HemW-like       38,255       17,990       2,765         IPR00589       Methythiotransferase       87,716       37,295       4,127         IPR00590       Nade_Cr_Mill B       2,035       1,022       229         IPR00591       YhcC-ike       11,293       4,505       502         IPR005961       Nade_metholicate       38,515       13,649       723         IPR005961       MaB_metholate       38,517       1,3649       723         IPR005961       MaB_metholate       38,565       1,869       1,867       1,228         IPR005961       Synch_C       38,862       1,6635       1,683       1,869       1,224         IPR005961       Synch_C       38,862       1,6353       1,869       1,224       506         IPR005961       Synch_G       38,862       1,865       1,885       1,885       1,885       1,885       1,885         IPR005961       Synch_G       38,862		IPR003698 Lipoyl	_synth		39,047	13,924	1,318	"Bacteria Archaea Fundi" "Bacteria" "Archaea" and "Fundi" select organisms that may provide genome context (gene
IPR004383       RNA_Jsu_MTrfæse_RimNCfr       39,844       15,429       1,455         IPR004583       Coprogen_oddase_HernN       16,796       6,746       513         IPR004583       MehWilkie       38,255       17,990       2,7755         IPR005939       Methythiotransferase       87,716       37,295       4,127         IPR005939       Methythiotransferase       87,716       37,295       4,127         IPR005930       Nase_C       2,085       10,22       229         IPR005931       Yhc-Cilke       11,233       4,505       502         IPR005930       Nase_C_/MiB       2,447       1,104       82         IPR005947       MaB-Mke_C       17,077       8,216       1,099         IPR005958       Eps/MiAn/MiTe-Kike_SAM       466,222       12,239       36,535         IPR001967       NaM       722,353       55669       7,723         IPR010591       Hmk_C       39,8452       14,853       18,824         IPR001967       MaB-Mke_C       39,8452       14,963       1,822         IPR001973       McM       722,535       35669       7,723         IPR010724       Hmm C       39,8452       14,963       1,822		IPR003739 Lys_a	minomutase/Glu_Ni	H3_mut	20,775	10,372	1,278	clusters/operons) useful for inferring functions.
IPR004559       Corrogen_oxidase_HemN       16,796       6,746       513         IPR004559       MemW-like       38,255       17,990       2,765         IPR00559       MemW-like       38,255       17,990       2,765         IPR005590       Methythoitansferase       87,716       37,225       4,127         IPR00590       Rase_CF_/INFS       2,035       1,022       229         IPR00590       Nase_CF_/INFS       2,035       1,022       229         IPR00590       Nase_CF_/INFS       2,455       502         IPR00590       Nase_CF_/INFS       2,455       502         IPR00590       Nase_KFDIMB       2,447       1,104       52         IPR00591       YncC-Kike       11,357       4,505       502         IPR005947       MaB-Kike_D       4,407       2,226       5066         IPR00595       Hole Sike_D       17,077       8,216       1,089         IPR00596       MaB-Kike_D       17,077       8,216       1,685         IPR01055       Mob_synth_C       38,381       16,855       1,892         IPR01056       Mob_synth_C       38,381       1,824       1,933       1,222         IPR01056		IPR004383 rRNA	_lsu_MTrfase_RImN	l/Cfr	39,944	15,429	1,455	The retrieved sequences also can be restricted to taxonomy categories within the Superkingdom, Kingdom, Phylum, Class,
IPR004559       HemW-like       38,255       17,900       2,765         IPR004559       MemV-like       37,255       4,127         IPR00549       Meby(hito/ansferase       87,716       37,295       4,127         IPR005490       Rasca_       2,035       1,022       229         IPR005491       Yhc-Like       11,293       4,505       502         IPR005496       MaB-Ike_D       2,647       1,104       82         IPR005460       MaB-Ike_D       3,647       1,104       82         IPR005466       MaB-Ike_D       4,407       2,228       506         IPR005466       MaB-Ike_D       1,707       8,218       1,089         IPR005797       rSAM       722,55       355,669       70,723         IPR007197       rSAM       722,55       355,669       70,723         IPR01722       HemN_C       39,495       17,002       2,804         IPR01723       FMI_D       7,731       4,801       1,324         IPR01723       FMI       6,704       1,324       S9         IPR01723       Protein Family Size Options       *Family Demain Boundary Option       *SN Edge Calculation Option         IPR01723       FMI		IPR004558 Copro	gen_oxidase_HemN	N	16,796	6,746	513	Order, Family, Genus, and Species ranks. Multiple conditions are combined to be a union of each other.
IPR005839       Methythiotransferase       87,716       37,295       4,127         IPR005840       Ribosomal, S12_MeSTráse_RimO       28,686       11,857       2,029         IPR005991       NasSEA       2,035       1,022       229         IPR005991       Nas_CF_NIB       2,647       1,104       82         IPR005990       Nas_C, C_NIB       2,647       1,104       82         IPR006461       MaB-Mike_D       3,647       7,23       506         IPR006477       MaB-Mike_D       17,077       8,216       1,089         IPR007197       rSAM       722,533       355,669       70,723         IPR007197       rSAM       722,533       355,669       70,723         IPR01702       Bros, dom       39,852       1,822       iProtein Family Size Options       * Protein Family Size Options         IPR01702       Hern C       38,361       1,824       iprotein Family Size Options       * SN Edge Calculation Option         IPR01702       Hern C       5,549       1,827       122       iprotein Family Size Options       * SN Edge Calculation Option         IPR01703       Hern C       5,549       1,827       122       iprotein Family Size Options       * SN Edge Calculation Option		IPR004559 HemV	V-like		38,255	17,990	2,765	The sequences from the UniRef90 and UniRef50 databases are the UniRef90 and UniRef50 clusters for which the cluster
IPR00540       Ribosomal_S12_MeSTrfase_RimO       28,658       11,857       2,029         IPR00590       RasEA       2,033       1,022       229         IPR00590       Nase_CF_MIB       2,647       1,104       620         IPR005940       Nase_CF_MIB       2,647       1,104       620         IPR00540       MaB-Inke_D       36,615       13,649       723         IPR006467       MaB-Inke_C       17,077       8,216       1,089         IPR006467       MaB-Inke_C       17,077       8,216       1,089         IPR006467       MaB-Inke_C       17,077       8,216       1,089         IPR007197       75AM       722,555       356,669       77,723         IPR010505       Mob_synth_C       38,861       16,855       1,882         IPR010722       RAT3_dom       39,455       1,702       2,804         IPR011010       DUF5131       7,313       4,801       1,324         IPR012837       FinH       6,704       2,297       125         IPR012830       FinH       6,374       5,941       1,127         IPR012830       Finali address:		IPR005839 Methy	Ithiotransferase		87,716	37,295	4,127	ID ("representative sequence") matches the specified taxonomy categories. The UniProt members in these clusters that do
IPR005909       RasEA       2,035       1,022       229         IPR005901       YhcC-ike       11,233       4,505       502         IPR006463       MaB_methiolase       35,615       13,649       723         IPR006466       MaB-ike_D       4,407       2,226       506         IPR006467       MaB-ike_D       4,407       2,226       506         IPR006467       MaB-ike_D       1,077       8,216       1,089         IPR006467       MaB-ike_D       723,355       355,659       70,723         IPR010767       FSAM       722,535       355,659       70,723         IPR010723       HemN_C       39,462       11,683       1,682         IPR010723       HemN_C       39,465       17,002       2,804         IPR010723       HemN_C       39,465       17,002       2,804         IPR01101       DUFS131       7,313       4,801       1,324         IPR012728       ThiH       6,704       2,297       125         IPR01283       Pit1_activating       4,435       630         IPR01283       Pit1_activating       4,245       1,127         IPR01283       Pit1_activating       6,544       1,127 <td></td> <td>IPR005840 Ribos</td> <td>omal_S12_MeSTrfa</td> <td>ise_RimO</td> <td>28,658</td> <td>11,857</td> <td>2,029</td> <td>not match the specified taxonomy categories are removed from the cluster.</td>		IPR005840 Ribos	omal_S12_MeSTrfa	ise_RimO	28,658	11,857	2,029	not match the specified taxonomy categories are removed from the cluster.
IPR005911       YheC-lke       11.283       4.505       502         IPR005980       Nase_CF_MiB       2.647       1.104       82         IPR006464       MaB_methiolase       35.615       13.649       723         IPR006466       MaB_methiolase       35.615       13.649       723         IPR006467       MaB-like_C       17.077       8.216       1.089         IPR0067197       ISAM       46.282       22.1239       36.535         IPR007197       ISAM       722.555       355.669       70.723         IPR010723       MemN_C       38.451       16.635       1.682         IPR010723       MemN_C       39.452       17.002       2.2804         IPR010723       MemN_C       39.459       17.002       2.804         IPR01101       DUF5131       7.731       4.801       1.324         IPR01283       Pinti_mathing_back       5.549       1.832         IPR01283       Find       6.304       1.324         IPR01283       Pinti_mathing_back       5.549       1.832         IPR01283       Pinti_mathing_back       5.549       1.832         IPR01283       Pinti_mathing_back       4.135       6.30 <td></td> <td>IPR005909 RaSE</td> <td>A</td> <td></td> <td>2,035</td> <td>1,022</td> <td>229</td> <td>Preselected conditions: - select a preset to auto populate</td>		IPR005909 RaSE	A		2,035	1,022	229	Preselected conditions: - select a preset to auto populate
IPR005800       Nase, CF, MIB       2,647       1,104       52         IPR005840       MaB_methiolase       35,615       13,649       723         IPR005464       MaB-ike, D       4,407       2226       506         IPR005467       MaB-ike, C       17,077       8,216       1,089         IPR005467       MaB-ike, C       17,077       8,216       1,089         IPR00547       MiB-ike, C       17,077       8,216       1,089         IPR001505       Mo, Synth, C       38,381       16,635       1,882         IPR017022       ATS, dom       39,852       14,953       1,222         IPR01702       MaTS, dom       39,852       14,953       1,222         IPR01702       MaTS, dom       39,852       14,953       1,222         IPR01702       MaTS, dom       39,852       17,002       2,804         IPR01704       UPA       6,704       1,324       59         IPR01728       ThH       6,704       2,297       125         IPR017283       FMiH       6,374       5,594       1,127         IPR01728       PT1_activating       9,422       2,995       180         IPR017283       Proiner, calci		IPR005911 YhcC-	like		11,293	4,505	502	Phylum - Actinobacteria
IPR000463       MiaB_methiolase       35,615       13,649       723         IPR004646       MiaB-like_C       44,07       2226       506         IPR00466       MiaB-like_C       17,077       82,165       506         IPR00466       MiaB-like_C       17,077       82,166       1089         IPR006058       Elp3/MiaA/MIB-like_SAM       446,222       212,389       36,535         IPR001675       KAM       722,535       355,669       70,723         IPR010725       Minb_C       38,861       16,825       1,822         IPR010723       HemN_C       39,862       14,953       1222         IPR010723       HemN_C       39,485       17,002       2,804         IPR011723       Dog. synth-PoqE_bac       5,541       1,224         IPR012726       ThiH       6,704       2,297       125         IPR012728       ThiH       6,704       2,297       125         IPR01283       Ph1_activating       9,425       2,995       180         IPR01283       Ph1_activating       9,425       5,941       1,127		IPR005980 Nase_	CF_NifB		2,647	1,104	82	
IPR006466       MaB-like_B       4.407       2.226       506         IPR006466       MaB-like_G       17,077       8.216       1,089         IPR006467       MaB-like_GSAMMAN/HE-like_GSAM       462,82       221,239       365,655         IPR007197       rSAM       722,535       355,669       70,723         IPR010705       Mosymth_C       38,861       16,835       1,893         IPR010723       HemN_C       39,895       17,002       2,804         IPR01101       DUF5131       7,713       4,801       1,324         IPR01123       FmH       6,704       2,297       125         IPR01238       FU1_activating       9,425       2,995       180         IPR01238       PL1_activating       9,425       2,995       180         IPR01283       Profine_raine_iactivating_extreme       9,429       1,837         IPR01283       Profine_raine_raine_iactivating_extreme       6,374       5,594         IPR01283       Profine_raine_raine_iactivating_extreme       9,429       1,837         IPR01283       Profine_raine_raine_iactivating_extreme       1,324       1,837         IPR01283       Profine_raine_raine_iactivating_extreme       6,374       5,594 <td< td=""><td></td><td>IPR006463 MiaB</td><td>methiolase</td><td></td><td>35,615</td><td>13,649</td><td>723</td><td></td></td<>		IPR006463 MiaB	methiolase		35,615	13,649	723	
IPR000667 Mia-luke_C       17,077       8,216       1,089         IPR006687 Mia-luke_SAM       446,282       212,389       36,535         IPR01055 Mob_synth_C       38,361       16,635       1,682         IPR01055 Mob_synth_C       38,361       16,635       1,682         IPR010722 BATS_Join       39,852       14,953       1,222         IPR010731 HemN_C       39,495       17,002       2,804         IPR01101 DUF5131       7,313       4,801       1,324         IPR01273 ThH       6,704       2,297       125         IPR01283 PTH_L_activating       9,425       2,995       180         IPR01283 PTL_activating       9,425       5,541       1,127		IPR006466 MiaB-	like_B		4,407	2,226	506	Add Taxonomy category
IPR000638       Ejg3Mila/NifB-like_rSAM       446,282       212,389       36,535         IPR001797       FSAM       722,535       355,669       70,723         IPR01797       FSAM       722,535       355,669       70,723         IPR017022       ATS_dom       39,852       14,953       1,222         IPR017023       HenN_C       39,465       17,002       2,804         IPR01101       DUF5131       7,313       4,801       1,324         IPR011282       FNH       6,704       2,297       125         IPR012837       NrdG       11,455       4,135       630         IPR012838       PCI_astrivations       14,955       180         IPR012838       PCI_astrivations       16,374       5,941       1,127		IPR006467 MiaB-	like_C		17,077	8,216	1,089	
IPR001797       rSAM       722,535       355,669       70,723         IPR01050       Mob_synth_C       38,361       16,635       1,682         IPR010722       ISTS, dom       39,495       17,002       2,804         IPR010723       HemN_C       39,495       17,002       2,804         IPR01101       DUF5131       7,313       4,801       1,324         IPR011226       ThiH       6,704       2,297       125         IPR012837       NrdG       11,445       4,135       630         IPR012838       PC1_mathixating       9,495       1,807       180         IPR012838       PC1_mathixating       6,374       5,941       1,127		IPR006638 Elp3/M	/liaA/NifB-like_rSAM	4	446,282	212,389	36,535	
IPR010055       Mob_synth_C       38,361       16.635       1.682         IPR010722       BATS_dom       39,852       14,953       1,222         IPR010723       HemN_C       39,852       14,953       1,222         IPR01101       DUF5131       7,012       2,2844         IPR011141       DUF5131       7,313       4,801       1,324         IPR011243       PQ_synth_PqqE_bac       5,549       1,835       59         IPR012726       ThH       6,704       2,297       125         IPR01283       PK1_activating       9,425       2,995       180         IPR01283       Pril_activating       9,627       1,127		IPR007197 rSAM			722,535	355,669	70,723	Protein Family Size Options
IPR010722       BATS_dom       39,852       14,953       1,222         IPR010723       HenN_C       39,455       17,002       2,804         IPR011011       DUF5131       7,313       4,801       1,324         IPR011726       ThIH       6,704       2,297       125         IPR012726       ThIH       6,704       2,297       125         IPR012837       NrdG       11,845       4,135       650         IPR012838       PL1_adtivating       9,425       2,995       180         IPR012839       Organic_radical_activase       16,374       5,941       1,127		IPR010505 Mob_s	synth_C		38,361	16,635	1,682	Family Domain Boundary Option
IPR010723       HemN_C       39.495       17.002       2.804         IPR01101       DUF5131       7.313       4.801       1.324         IPR01124       FOLMO Synth_PqqE_bac       5.549       1.835       569         IPR01226       ThiH       6.704       2.297       125         IPR012337       NrdG       11.645       4.135       630         IPR012838       PFL_activation       9.455       2.995       180         IPR012839       Organic_radical_activase       16.374       5.941       1.127		IPR010722 BATS	_dom		39,852	14,953	1,222	1 CON Edge Option Option
IPR011101       DUF5131       7,313       4,801       1,324         IPR011843       PQQ_synth_PqqE_bac       5,549       1,835       59         IPR012726       ThH       6,704       2,297       125         IPR012383       Prol.       11,645       4,135       630         IPR012383       PL1_activating       9,425       2,995       180         IPR012383       Pin1_activating       16,374       5,941       1,127		IPR010723 HemN	I_C		39,495	17,002	2,804	· Son Edge Calculation Option
IPR011843         PQQ_synth_PqqE_bac         5,549         1,835         59           IPR012726         ThH         6,704         2,297         125           IPR012726         ThH         6,704         2,297         125           IPR012837         MrdG         11,645         4,135         630           IPR012838         PFL1_activating         9,425         2,995         180           IPR012839         Organic_radical_activase         16,374         5,941         1,127		IPR011101 DUF5	131		7,313	4,801	1,324	
IPR012726         Thi H         6,704         2,297         125           IPR012726         Thi H         6,704         2,297         125           IPR012837         Trug G         11,645         4,135         630           IPR012838         PFL1_activating         9,425         2,995         180           IPR012839         Organic_radical_activase         16,374         5,941         1,127		IPR011843 PQQ_	synth_PqqE_bac		5,549	1,835	59	Job name: IP91_RSS_UniRef90_NoFragments_Actinobacteria (required)
IPR012837         NtdG         11.645         4.135         6.30         E-mail address:           IPR012838         PFL1_activating         9.425         2.995         180         You will be notified by e-mail when your submission has been processed.           IPR012839         Organic_radical_activase         16.374         5.941         1.127		IPR012726 ThiH			6,704	2,297	125	
IPR012838     PFL1_activating     9,425     2,995     180       IPR012839     Organic_radical_activase     16,374     5,941     1,127		IPR012837 NrdG			11,645	4,135	630	E-mail address:
IPR012839 Organic_radical_activase 16,374 5,941 1,127		IPR012838 PFL1	_activating		9,425	2,995	180	You will be notified by e-mail when your submission has been processed.
		IPR012839 Organ	ic_radical_activase		16,374	5,941	1,127	
IPR013483 Moa 33,719 14,394 976 Submit Analysis		IPR013483 MoaA			33,719	14,394	976	Submit Analysis
IPR013704 UPF0313_N 12,479 4,760 404		IPR013704 UPF0	313_N		12,479	4,760	404	
IPR013848 Methylthiotransferase_N 91,463 39,689 5,468		IPR013848 Methy	Ithiotransferase_N		91,463	39,689	5,468	

The SSNs were finalized (SSN Finalization tab on the DATASET COMPLETED pages) using 11 as the Alignment Score Threshold (orange arrow) and 140 residues as the Minimum in the Sequence Length Restriction to remove truncated sequences (cyan arrow), entering the Network (SSN) name (brown arrow), and clicking "Create SSN" (black arrow). We previously determined that the members of the anaerobic ribonucleotide reductase activating enzyme family have the shortest sequences ( $\geq$ 140 residues) [2].

DATASET C	OMPLE	TED				
Submission Nam	e: IP91_RS	S_UniRef90_N	NoFragments_Acti	nobacteria		
minimum sequence similarity threshold that specifies the sequence pairs connected by edges is needed to generate the SSN. This hreshold also determines the segregation of proteins into clusters. The threshold is applied to the edges in the SSN using the alignment core, an edge node attribute that is a measure of the similarity between sequence pairs.						
Dataset Summa	ry Taxon	omy Sunburst	Dataset Analysis	SSN Finalization		
This tab is used t threshold) for dra	This tab is used to specify the minimum "Alignment Score Threshold" (that is a measure of the minimum sequence similarity threshold) for drawing the edges that connect the proteins (nodes) in the SSN.					
Alignment Scor	e Threshold:	11				
This v magn	alue correspo itude to the ne	nds to the lower li gative base-10 lo	mit for which an edge w garithm of a BLAST e-v	rill be present in the SS alue.	SN. The alignment score is similar in	
- Sequence L	ength Restric	tion Options				
Allows restr	iction of seque	nces in the gener	ated SSN based on the	ir length. 🕡		
Minimum:	140	(default: 0)		I		
Maximum:		(default: 5000	00)			
▶ Filter by Tax	onomy					
Neighborhood Connectivity						
Fragment Option						
Network name: 'ef90_NoFragments_Actinobacteria_Minlen140_AS11 This name with the base of the second						
You will be notifie	You will be notified by e-mail when the SSN is ready for download.					
			Create SSN		<b></b>	
					٦	

The **Network Files** tab of the **DOWNLOAD NETWORK FILES** pages provided the xgmml file for the **Full (SSN) Network** (red arrow; all UniProt nodes and edges) as well as the xgmml files for **Representative Node Networks** that conflate the UniProt nodes based on percent identity (blue arrow). The xgmml files for the full SSNs were downloaded, opened with Cytoscape 3.9.1, and displayed with the Prefuse Force Directed layout; the nodes were colored according to the Structure-Function Linkage Database subgroups [2, 3].

SN Overview Network Files						
Please cite your use of the EFI tools: Rémi Zallot, Nils Oberg, and John A. Gerlt, <b>The EFI Web Resource for Genomic Enzymology Tools:</b> Leveraging Protein, Genome, and Metagenome Databases to Discover Novel Enzymes and Metabolic Pathways. Biochemistry 2019 58 (41), 4169-4182. https://doi.org/10.1021/acs.biochem.9b00735						
e panels below provide files for an approximate guide, SSNs w M edges can be opened with RAM, and ~120M edges can	r full and representa with ~2M edges car 64 GB RAM, ~20M be opened with 76	ative node SSNs for d n be opened with 16 G l edges can be opene 8 GB RAM.	lownload with the indicated r GB RAM, ~5M edges can be d with 128 GB RAM, ~40M d	numbers of nodes and edges opened with 32 GB RAM, edges can be opened with 25		
as may be transferred to the Ge ghborhood Connectivity utility.	enome Neighborho	ood Tool (GNT), the Co	olor SSN utility, the Cluster A	Analysis utility, or the		
ch node in the network represe	ents a single proteir	n sequence.	# Edgos			
Download ZIP	27 27	7.052	# Euges	Transfor To:		
presentative Node Netw epresentative node (RepNode cent identity. For example, for uped into a single node (meta nplicated networks easier to lo	vorks ⑦ e) networks, each n a 75% identity Rep node). Sequences bad in Cytoscape.	ode in the network rep Node network, all cor are collapsed togethe	presents a collection of prote nnected sequences that sha er to reduce the overall num	eins grouped according to re 75% or more identity are ber of nodes, making for less		
presentative Node Netw epresentative node (RepNode cent identity. For example, for uped into a single node (meta nplicated networks easier to lo e cluster organization is not ch	vorks () ) networks, each n a 75% identity Rep node). Sequences ad in Cytoscape. anged, and the clus	ode in the network reg Node network, all cor are collapsed togethe stering of sequences i	presents a collection of proto nected sequences that sha er to reduce the overall num remains identical to the full r	ins grouped according to re 75% or more identity are ber of nodes, making for less network.		
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	Chart Name	10	Chart Name
IPR000385	MOAA_NIB_PQQE_FE-S-DO_CS	IPR026423	rSAM_cobopep
IPR001989	Radical_actival_CS	IPR026426	
IPR002684	BIOTIN_SYNTN/BIOAB	IPR026429	MIA_synthase
IPR003698	Lipoyi_synth	IPR026447	B12_SAIVI_Ta0216
IPR003739	Lys_aminomutase/Glu_NH3_mut	IPR026482	rSAM_nif11_3
IPR004383	rRNA_Isu_MTrtase_RImN/Cfr	IPR027492	RNA_MTrfase_RImN
IPR004558	Coprogen_oxidase_HemN	IPR027526	Lipoyl_synth_chlpt
IPR004559	HemW-like	IPR027527	Lipoyl_synth_mt
IPR005839	Methylthiotransferase	IPR027559	B12_rSAM_oligo
IPR005840	Ribosomal_S12_MeSTrfase_RimO	IPR027564	HpnR_B12_rSAM
IPR005909	RaSEA	IPR027570	GeoRSP_rSAM
IPR005911	YhcC-like	IPR027583	rSAM_ACGX
IPR005980	Nase_CF_NifB	IPR027586	rSAM_metal_mat
IPR006463	MiaB_methiolase	IPR027596	AmmeMemoSam_rS
IPR006466	MiaB-like_B	IPR027604	W_rSAM_matur
IPR006467	MiaB-like_C	IPR027608	Spiro_SPASM
IPR006638	Elp3/MiaB/NifB	IPR027609	rSAM_QueE_Proteobac
IPR007197	rSAM	IPR027621	rSAM_QueE_gams
IPR010505	Mob_synth_C	IPR027622	rSAM_Clo7bot
IPR010722	BATS_dom	IPR027626	Pseudo_SAM_Halo
IPR010723	HemN_C	IPR027633	rSAM_NirJ2
IPR011101	DUF5131	IPR030801	Glu_2_3_NH3_mut
IPR011843	PQQ_synth_PqqE_bac	IPR030837	B12_rSAM_cofa1
IPR012726	ThiH	IPR030894	Ahb_Proteobacteria
IPR012837	NrdG	IPR030896	rSAM_AhbD_hemeb
IPR012838	PFL1_activating	IPR030905	CutC_activ_rSAM
IPR012839	Organic_radical_activase	IPR030915	rSAM_SkfB
IPR013483	МоаА	IPR030933	Non_iron_rSAM
IPR013704	UPF0313_N	IPR030950	rSAM_PoyD
IPR013848	Methylthiotransferase N	IPR030969	B12 rSAM trp MT
IPR013917	tRNA_wybutosine-synth	IPR030977	QueE_Cx14CxxC
IPR014191	Anaer RNR activator	IPR030989	rSAM XyeB
IPR016431	Pyrv-formate lyase-activ prd	IPR031003	BcpD PhpK rSAM
IPR016771	Fe-S OxRdtase rSAM TM0948 prd	IPR031004	rSAM YfkAB
IPR016779	 rSAM_MSMEG0568	IPR031010	rSAM mob pairA
IPR016863	Desll	IPR031012	rSAM mob pairB
IPR017200	PqqE-like	IPR031014	rSAM_BlsE

### Tutorial Table 1. Pfam and IntePro Families Used to Identify Member of the RSS.

IPR017672	MA_4551-like	IPR031015	Arg_2_3_am_muta
IPR017742	Deazaguanine_synth	IPR031019	rSAM_vs_C_rich
IPR017833	Hopanoid_synth-assoc_rSAM_HpnH	IPR031691	LIAS_N
IPR017834	Hopanoid_synth-assoc_rSAM_HpnJ	IPR032432	Radical_SAM_C
IPR019939	CofG_family	IPR033971	Avilamycin_epimerase
IPR019940	CofH_family	IPR033974	Glycerol_dehydratase_activase
IPR020050	FO_synthase_su2	IPR033975	ThnP-like
IPR020612	Methylthiotransferase_CS	IPR033976	GntE-like
IPR022431	Cyclic_DHFL_synthase_mqnC	IPR034165	NifB_C
IPR022432	MqnE	IPR034386	BtrN-like
IPR022447	Lys_aminomutase-rel	IPR034391	Cmo-like_SPASM_containing
IPR022459	Lysine_aminomutase	IPR034405	F420
IPR022462	EpmB	IPR034422	HydE/PylB-like
IPR022881	rRNA_lsu_MeTfrase_Cfr	IPR034428	ThiH/NoCL/HydG-like
IPR022946	UPF0313	IPR034436	NocN/NosN-like
IPR023404	rSAM_horseshoe	IPR034438	4-hPhe_decarboxylase_activase
IPR023805	Uncharacterised_Spl-rel	IPR034457	Organic_radical-activating
IPR023807	Peptide_mod_rSAM	IPR034462	Benzylsuc_synthase_activase
IPR023819	Pep-mod_rSAM_AF0577	IPR034465	Pyruvate_for-lyase_activase
IPR023820	rSAM_GDL-assoc	IPR034466	Methyltransferase_Class_B
IPR023821	rSAM_TatD-assoc	IPR034471	7_8-dihydro-6-hydroxymethylpte
IPR023822	rSAM_TatD-assoc_bac	IPR034474	Methyltransferase_Class_D
IPR023858	RSAM_HmdB	IPR034479	AhbC-like
IPR023862	CHP03960_rSAM	IPR034480	Heme_carboxy_lyase-like
IPR023863	rSAM_PTO1314	IPR034485	Anaerobic_Cys-type_sulfatase-m
IPR023867	Sulphatase_maturase_rSAM	IPR034491	Anaerob_Ser_sulfatase-maturase
IPR023868	7-CO-7-deazaGua_synth_put_Clo	IPR034497	Bacteriochlorophyll_C12_MT
IPR023874	DNA_rSAM_put	IPR034498	Bacteriochlorophyll_C8_MT
IPR023880	Benzylsucc_Synthase_activating	IPR034505	Coproporphyrinogen-III_oxidase
IPR023885	4Fe4S-binding_SPASM_dom	IPR034508	Spectinomycin_biosynthesis
IPR023886	QH-AmDH_gsu_maturation	IPR034514	ThnK-like
IPR023891	Pyrrolys_PylB	IPR034515	ThnL-like
IPR023897	Spore_PP_lysase	IPR034519	TunB-like
IPR023904	Pep_rSAM_mat_YydG	IPR034529	Fom3-like
IPR023912	YjjW_bact	IPR034530	HpnP-like
IPR023913	MftC	IPR034531	Methylation_of_yatakemycin
IPR023930	NirJ1	IPR034532	OxsB-like
IPR023969	CHP04072_B12-bd/rSAM	IPR034534	Pyrimidine_methyltransferase
IPR023979	CHP04014_B12-bd/rSAM	IPR034547	Tte1186a_maturase
IPR023980	CHP04013_B12-bd/rSAM	IPR034556	tRNA_wybutosine-synthase

IPR023984	rSAM_ocin_1	IPR034557	ThrcA_tRNA_Methiotransferase
IPR023992	HemeD1_Synth_NirJ	IPR034559	Spore_PP_lysase_Clostridia
IPR023993	TYW1_archaea	IPR034560	Spore_PP_lysase_Bacilli
IPR023995	HemZ	IPR034687	ELP3-like
IPR024001	Cys-rich_pep_rSAM_mat_CcpM	IPR038135	Methylthiotransferase_N_sf
IPR024007	FeFe-hyd_mat_HydG	IPR039661	ELP3
IPR024016	CHP04064_rSAM	IPR040072	Methyltransferase_A
IPR024017	Pep_cycl_rSAM	IPR040074	BssD/PfIA/YjjW
IPR024018	CHP04083_rSAM	IPR040081	Cndl-like
IPR024021	FeFe-hyd_HydE_rSAM	IPR040082	GenK-like
IPR024023	rSAM_paired_HxsB	IPR040085	MJ0674-like
IPR024025	SCIFF_rSAM_maturase	IPR040086	MJ0683-like
IPR024032	rSAM_paired_HxsC	IPR040087	MJ0021-like
IPR024177	Biotin_synthase	IPR040088	MJ0103-like
IPR024521	DUF3641	IPR041582	RimO_TRAM
IPR024560	UPF0313_C	IPR045375	Put_radical_SAM-like_N
IPR024924	7-CO-7-deazaguanine_synth-like	IPR045567	CofH/MnqC-like_C
IPR025895	LAM_C_dom	IPR045784	Radical_SAM_N2
IPR026322	Geopep_mat_rSAM	PF04055	Radical_SAM
IPR026332	HutW	PF06969	HemN_C
IPR026335	SAM_SPASM_FxsB	PF08497	Radical_SAM_N
IPR026344	SCM_rSAM_ScmE	PF12345	DUF3641
IPR026346	SCM_rSAM_ScmF	PF13186	SPASM
IPR026351	rSAM_SeCys	PF16199	Radical_SAM_C
IPR026357	rSAM/SPASM_prot_GRRM_system	PF16881	LIAS_N
IPR026401	CXXX_matur	PF19238	Radical_SAM_2
IPR026404	rSAM_w_lipo	PF19288	CofH_C
IPR026407	SAM_GG-Bacter	PF19864	Radical_SAM_N2
IPR026412	rSAM_Cxxx_rpt		

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