

Genome annotation
by **UNIPROT**

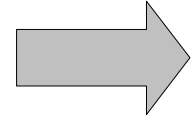
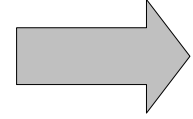
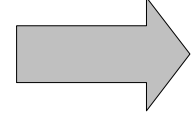
Genome annotation
by **NCBI**

Genome annotation
by **KEGG**

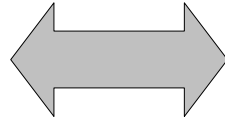
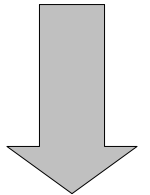
Genome annotation
by **PEDANT**

⋮

UNIPROT



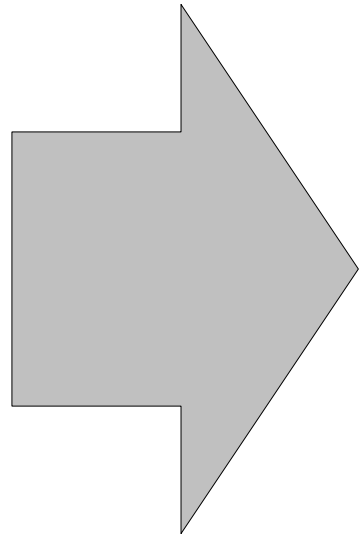
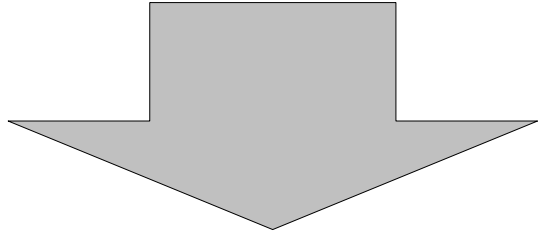
Genes and
annotations of the
organism of interest



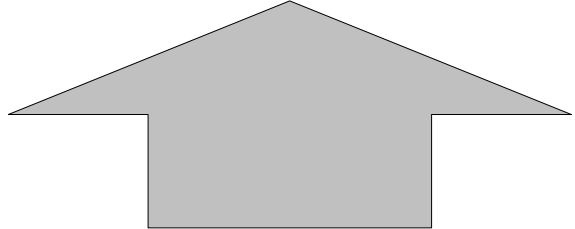
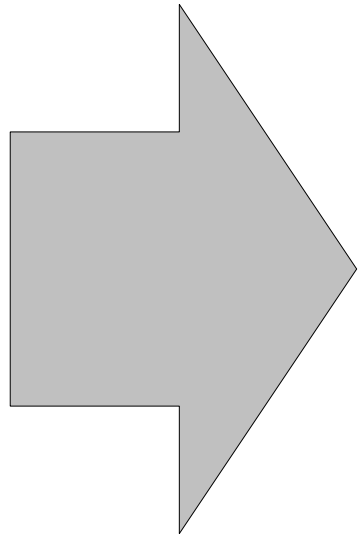
BLAST-search

**BRENDA
AMENDA**

BREPS

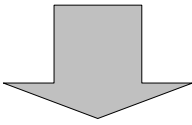


**Enzyme function
datapool for the
organism of interest**



BLAST-based annotation

Intern result database



EnzymeDetector

Results | Statistics | Comparison | Visualization

organism: Escherichia coli strain: K12 NC-Number: NC_009413

minimal overall-relevance the entries should have: 0

maximal E-value the entries should have: 15

SEARCH results for: [SEARCH]

RELOAD DATA Show full entries

gene-position	gene-position	GI	EC-number	recommended-name	e-value	AMENDA	BRENDA	BREPS	KEGG	NCBI	PEDANT	UNIPROT	ownBLAST	overall-relevance	selection	
681161	802951	14569230	3.6.-		2e-106									+3	3	✓
798945	799798	14569233	4.2.1.1	carbonate dehydratase	3e-35	+2	+4							+1	7	✓
864743	868614	14569235	3.6.3.27	phosphate-transporting ATPase	0.0	+2	+4							+4	10	
			3.6.3.25	sulfate-transporting ATPase	2e-151	+2	+4							+4	10	
			3.6.3.24	nucleic acid-transporting ATPase	2e-115			+5							8	
			3.6.3.-					+10							10	
1028002	1029192	14569239	2.1.1.4	acetylserine O-methyltransferase	3e-100									+3	3	
			2.1.1.52	RNA (guanine-N2)-methyltransferase	8e-49									+8	8	
			2.1.1.-					+10							10	
1481085	1484987	14569235	3.6.4.13	RNA helicase	0.0	+2	+4							+8	14	
			3.6.1.15	nucleoside-triphosphatase	0.0	+2	+4							+5	11	
			3.6.2.14	nuclear inclusions assembly	0.0	+2	+4							+4	5	
			3.6.1.-					+10	+2						12	
1494880	1496535	14569236	2.4.1.-		2e-92									+3	3	✓
1661792	1661844	14569242	2.7.7.65	lipopolysaccharase	0.0	+2	+4	+10	+2					+8	39	✓
1680183	1680982	14569248	3.1.1.81	protein-glutamate methyltransferase	2e-33	+2	+4							+1	7	✓
1724047	1724646	14569269	1.8.99.3	NADH dehydrogenase	3e-38	+2								+1	3	✓
1781055	1782701	14569273	6.2.1.26	Quercetinyl benzoyl-CoA ligase	5e-49	+2	+4							+4	10	
			6.2.1.3	Long-chain fatty acyl-CoA ligase	3e-75	+2	+4							+4	18	
			2.7.7.38	(2,3-dihydroxy benzoyl) synthase	2e-67									+6	6	
			6.2.1.12	6-Coumarate-CoA ligase	4e-55									+6	6	
			1.13.12.7	Phenylacetylserine 4-aminotransferase (ATP-hydrolyzing)	8e-50									+6	6	
			6.2.1.25	Benzoyl-CoA ligase	4e-45			+6						+6	6	

DOWNLOAD SELECTED DATA DOWNLOAD ALL DATA