

# BV-BRC Test Report

## D12. Domains and Motifs Data Tab

<b>Item to test</b>	<b>Domains and Motifs Data Tab</b>
<b>URL</b>	<a href="https://www.bv-brc.org/view/Taxonomy/234#view_tab=proteinFeatures&amp;filter=false">https://www.bv-brc.org/view/Taxonomy/234#view_tab=proteinFeatures&amp;filter=false</a>
<b>Prerequisites</b>	None
<b>References</b>	<a href="https://www.bv-brc.org/docs/quick_references/organisms_menu.html#browsing-bv-brc-by-taxon">https://www.bv-brc.org/docs/quick_references/organisms_menu.html#browsing-bv-brc-by-taxon</a>
<b>Tester(s)</b>	Rebecca Wattam, Ron Kenyon
<b>Test date</b>	6-Jan-2022 (original – passed), 9-May-2022 (follow-up-passed)
<b>Test result</b>	<b>Passed</b>

### Overview

- Test the Specialty Genes Tab with example bacterial data.
- Verify display of Domain Source categories
- Test filtering by a Source.

### Test Results

- Test results were verified by examination of returned data via inspection and filters.
- All operations performed as expected

# Brucella:

Taxon View  
 Bacteria » Proteobacteria » Alphaproteobacteria » Hyphomicrobiales » Brucellaceae » **Brucella** ( 1192 Genomes )

Overview Phylogeny Taxonomy Genomes AMR Phenotypes Sequences Proteins Protein Structures Specialty Genes **Domains and Motifs** Epitopes Pathways

DOWNLOAD KEYWORDS ADV Search HIDE

- Source** Evidence
- CDD (27597)
  - Coils (5340)
  - Gene3D (67334)
  - Hamap (8506)
  - MobiDBLite (11989)
  - PANTHER (67606)
  - PIRSF (7542)
  - PRINTS (33916)
  - Pfam (66800)
  - ProSitePatterns (12870)
  - ProSiteProfiles (18885)
  - SFLD (1328)
  - SMART (13565)
  - SUPERFAMILY (54603)
  - TIGRFAM (17624)

<input type="checkbox"/>	BRC ID	RefSeq Locus Tag	Gene	Product	Source	Source ID	Description	E Value	Evidence
<input type="checkbox"/>	fig 359391.4.peg.191	BAB1_1845		Carboxyl-terminal protease (EC 3.4.21.102)	SUPERFAM	SSF50156	PDZ domain-like	6.59E-19	InterProScan
<input type="checkbox"/>	fig 439375.7.peg.223	Oant_2125		NAD(FAD)-utilizing dehydrogenases	Gene3D	G3DSA:3.50-		3.5E-59	InterProScan
<input type="checkbox"/>	fig 359391.4.peg.124	BAB1_1193		D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	SUPERFAM	SSF110997	Sporulation related repeat	1.83E-5	InterProScan
<input type="checkbox"/>	fig 439375.7.peg.304	Oant_2902		Transketolase (EC 2.2.1.1)	ProSitePatt	PS00801	Transketolase signature 1.	-	InterProScan
<input type="checkbox"/>	fig 359391.4.peg.313	BAB2_0844		Thioesterase	CDD	cd03443	Paal_thioesterase	8.50788E-37	InterProScan
<input type="checkbox"/>	fig 444178.3.peg.289	BOV_1498	hemF	Coproporphyrinogen III oxidase, aerobic (EC 1.3.3.3)	PRINTS	PR00073	Coprogen oxidase signature	1.4E-50	InterProScan
<input type="checkbox"/>	fig 444178.3.peg.312	BOV_1707	phbA-1	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Gene3D	G3DSA:3.40-		0.0	InterProScan
<input type="checkbox"/>	fig 1437448.3.peg.49			hypothetical protein	PIRSF	PIRSF02048	BAP	5.0E-45	InterProScan
<input type="checkbox"/>	fig 520459.3.peg.326	BAIG_03090		Thioredoxin reductase (EC 1.8.1.9)	PRINTS	PR00368	FAD-dependent pyridine nucleotide reductase	1.9E-38	InterProScan
<input type="checkbox"/>	fig 439375.7.peg.113	Oant_1087	purH	IMP cyclohydrolase (EC 3.5.4.10) / Phosphoribosylamin	ProSiteProfil	PS51855	MGS-like domain profile.	18.597057	InterProScan
<input type="checkbox"/>	fig 520461.7.peg.214	BPI_I2213		Metal-dependent hydrolase YbeY, involved in rRNA and	PANTHER	PTHR46986	ENDORIBONUCLEASE YBEY, CHLOROPL	1.1E-24	InterProScan
<input type="checkbox"/>	fig 439375.7.peg.119	Oant_1137	rpoH2	RNA polymerase sigma factor RpoH-related protein	MobiDBLite	mobidb-lite	consensus disorder prediction	-	InterProScan
<input type="checkbox"/>	fig 568815.3.peg.303	BMI_I1830	sun	16S rRNA (cytosine(967)-C(5))-methyltransferase (EC 2	PRINTS	PR02008	RNA (C5-cytosine) methyltransferase signat	5.7E-24	InterProScan
<input type="checkbox"/>	fig 419475.3.peg.121	A8A54_05855		Translation elongation factor Tu	Pfam	PF03143	Elongation factor Tu C-terminal domain	5.3E-38	InterProScan
<input type="checkbox"/>	fig 483179.4.peg.282	BCAN_B0606	mnr	3'-to-5' exoribonuclease RNase R	Coils	Coil	Coil	-	InterProScan
<input type="checkbox"/>	fig 359391.4.peg.244			Sarcosine oxidase alpha subunit (EC 1.5.3.1)	Pfam	PF01571	Aminomethyltransferase folate-binding dome	2.9E-68	InterProScan
<input type="checkbox"/>	fig 520459.3.peg.260	BAIG_02747		Myo-inositol 2-dehydrogenase 2 (EC 1.1.1.18)	PANTHER	PTHR43818	BCDNA.GH03377	2.2E-64	InterProScan
<input type="checkbox"/>	fig 419475.3.peg.211	A8A54_10170		Uncharacterized protein YhiN	Gene3D	G3DSA:1.10-		0.0	InterProScan
<input type="checkbox"/>	fig 520448.3.peg.212	BAZG_00237		Phosphoribosylanthranilate isomerase (EC 5.3.1.24)	Pfam	PF00697	N-(5-phosphoribosyl)anthranilate (PRA) isom	5.1E-44	InterProScan
<input type="checkbox"/>	fig 520461.7.peg.102	BPI_I1056	gltX-1	Glutamyl-tRNA(Gln) synthetase (EC 6.1.1.24)	Pfam	PF00749	tRNA synthetases class I (E and Q), catalytic	1.6E-70	InterProScan
<input type="checkbox"/>	fig 568815.3.peg.335	BMI_I2153	gshb	Glutathione synthetase (EC 6.3.2.3)	Pfam	PF02955	Prokaryotic glutathione synthetase, ATP-gra	2.9E-73	InterProScan

1 - 200 of 415505 results

< 1 2 3 ... 2078 >

Filter: Hamap

Taxon View  
 Bacteria » Proteobacteria » Alphaproteobacteria » Hyphomicrobiales » Brucellaceae » **Brucella** (1192 Genomes)

Overview | Phylogeny | Taxonomy | Genomes | AMR Phenotypes | Sequences | Proteins | Protein Structures | Specialty Genes | **Domains and Motifs** | Epitopes | Pathways

DOWNLOAD | KEYWORDS | ADV Search | **Hamap** | SOURCE x | HIDE

**Source** Evidence

- Hamap (8506)**
- InterProScan (8506)
- CDD (27597)
- Coils (5340)
- Gene3D (67334)
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<input type="checkbox"/>	BRC ID	RefSeq Locus Tag	Gene	Product	Source	Source ID	Description	E Value	Evidence
<input type="checkbox"/>	fig 262698.4.peg.120	BruAb1_1140	pyrG	CTP synthase (EC 6.3.4.2)	Hamap	MF_01227	CTP synthase [pyrG].	49.597736	InterProSc
<input type="checkbox"/>	fig 1437448.3.peg.57			ATP synthase F0 sector subunit c (EC 3.6.3.14)	Hamap	MF_01396	ATP synthase subunit c [atpH].	13.630615	InterProSc
<input type="checkbox"/>	fig 204722.5.peg.912	BR0898	tig	Cell division trigger factor (EC 5.2.1.8)	Hamap	MF_00303	Trigger factor [tig].	20.971195	InterProSc
<input type="checkbox"/>	fig 520456.3.peg.262	BANG_01644		tRNA dimethylallyltransferase (EC 2.5.1.75)	Hamap	MF_00185	tRNA dimethylallyltransferase [miaA].	26.318653	InterProSc
<input type="checkbox"/>	fig 1437448.3.peg.27			SSU ribosomal protein S16p	Hamap	MF_00385	30S ribosomal protein S16 [rpsP].	24.72127	InterProSc
<input type="checkbox"/>	fig 483179.4.peg.281	BCAN_B0600	pyrB	Aspartate carbamoyltransferase (EC 2.1.3.2)	Hamap	MF_00001	Aspartate carbamoyltransferase [pyrB].	39.519802	InterProSc
<input type="checkbox"/>	fig 444178.3.peg.255	BOV_1187	rpsQ	SSU ribosomal protein S17p (S11e)	Hamap	MF_01345	30S ribosomal protein S17 [rpsQ].	23.160061	InterProSc
<input type="checkbox"/>	fig 483179.4.peg.139	BCAN_A1388	ureG	Urease accessory protein UreG	Hamap	MF_01389	Urease accessory protein UreG [ureG].	45.141979	InterProSc
<input type="checkbox"/>	fig 1437448.3.peg.24			Helicase PriA essential for oriC/DnaA-independent DNA	Hamap	MF_00983	Probable primosomal protein N' [priA].	23.669815	InterProSc
<input type="checkbox"/>	fig 224914.11.peg.28	BMEII0510		Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9) / I	Hamap	MF_01576	Bifunctional protein FolD [folD].	38.863281	InterProSc
<input type="checkbox"/>	fig 483179.4.peg.970	BCAN_A0959	valS	Valyl-tRNA synthetase (EC 6.1.1.9)	Hamap	MF_02004	Valine-tRNA ligase [valS].	15.713161	InterProSc
<input type="checkbox"/>	fig 1437448.3.peg.21			Ketol-acid reductoisomerase (NADP(+)) (EC 1.1.1.86)	Hamap	MF_00435	Ketol-acid reductoisomerase (NADP(+)) [livC].	45.639172	InterProSc
<input type="checkbox"/>	fig 568815.3.peg.151	BMI_II154	figl	Flagellar P-ring protein Figl	Hamap	MF_00416	Flagellar P-ring protein [figl].	36.264591	InterProSc
<input type="checkbox"/>	fig 483179.4.peg.494	BCAN_A0483	thrB	Homoserine kinase (EC 2.7.1.39)	Hamap	MF_00301	Homoserine kinase [thrB].	174.984268	InterProSc
<input type="checkbox"/>	fig 262698.4.peg.198	BruAb1_1882	leuC	3-isopropylmalate dehydratase large subunit (EC 4.2.1.1)	Hamap	MF_01026	3-isopropylmalate dehydratase large subunit	58.473816	InterProSc
<input type="checkbox"/>	fig 520448.3.peg.54	BAZG_03065		Adenylosuccinate synthetase (EC 6.3.4.4)	Hamap	MF_00011	Adenylosuccinate synthetase [purA].	209.594574	InterProSc
<input type="checkbox"/>	fig 359391.4.peg.121	BAB1_1167	lexA	SOS-response repressor and protease LexA (EC 3.4.21)	Hamap	MF_00015	LexA repressor [lexA].	34.375248	InterProSc
<input type="checkbox"/>	fig 444178.3.peg.197	BOV_0644		DNA-directed RNA polymerase omega subunit (EC 2.7.7.6)	Hamap	MF_00366	DNA-directed RNA polymerase subunit omega	16.243128	InterProSc
<input type="checkbox"/>	fig 520459.3.peg.318	BAIG_03010		ATP synthase gamma chain (EC 3.6.3.14)	Hamap	MF_00815	ATP synthase gamma chain [atpG].	33.426765	InterProSc
<input type="checkbox"/>	fig 359391.4.peg.367	BAB1_0348	mscL	Large-conductance mechanosensitive channel	Hamap	MF_00115	Large-conductance mechanosensitive chan	24.322998	InterProSc
<input type="checkbox"/>	fig 419475.3.peg.273	A8A54_13200		Glutamine-fructose-6-phosphate aminotransferase [iso	Hamap	MF_00164	Glutamine-fructose-6-phosphate aminotrans	38.531483	InterProSc

1 - 200 of 8506 results

< 1 2 3 ... 43 >