

Surface-exposed protein moieties of *Burkholderia cenocepacia* J2315 in microaerophilic and aerobic conditions

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Table S5 – Predicted moonlight proteins identified in *B. cenocepacia* J2315 by using the “surface shaving” strategy followed by LC-MS/MS (Threshold score: ≥ 2 peptides).

ORF	Description	Canonical Function	Moonlight Function in other bacteria ²	PSM ¹	Peptides ¹	References
BCAL0201	N-acetyl-gamma-glutamyl-phosphate reductase (ArgC)	Cytoplasm: Catalyzes the conversion of N-acetyl-L-glutamate to N-acetyl-L-glutamate 5-phosphate (EC 1.2.1.38).	Cell surface: Binds mucus and Caco-2 cells, and human ABO blood group antigens (<i>Lactobacillus plantarum</i>).	34	7	[1]
BCAL0219/ BCAL0232*	Elongation factor Tu (TufA)	Cytoplasm: Elongation factor in protein synthesis.	Cell surface: Attachment to human cells and mucins (<i>Lactobacillus johnsonii</i>). Fibronectin binding (<i>Mycoplasma pneumoniae</i>). Factor H and plasminogen binding (<i>Pseudomonas aeruginosa</i>).	76	10	[2][3][4]
BCAL0226	DNA-directed RNA polymerase subunit beta (RpoB)	Cytoplasm: Beta subunit of DNA-directed RNA polymerase (EC 2.7.7.6)	Cell surface: Salivary mucin binding protein Muc7 (<i>Streptococcus gordonii</i>).	15	7	[5]
BCAL0231	Elongation factor G (FusA)	Cytoplasm: Elongation factor in translation.	Cell surface: Binds salivary mucin MUC7(<i>S. gordonii</i>)	38	14	[5]
BCAL0739	Phosphoglyceromutase (GpmA)	Cytoplasm: Phosphoglycerate mutase (EC 5.4.2.11)	Cell surface: Plasminogen binding (<i>Bifidobacterium lactis</i> , <i>Bifidobacterium bifidum</i> , <i>Bifidobacterium longum</i>).	15	5	[6]
(BCAL1001/ BCAL2869)*/ BCAL2829	Serine endoprotease DegP-like (MucD2/ MucD1/ HtrA)	Periplasm: Serine endoprotease (EC 3.4.21.107).	Extracellular: Cleaves E-cadherin to disrupt intercellular adhesion (<i>Helicobacter pylori</i>).	71 / 28	18 / 7	[7]
BCAL1070/ BCAL3192	Peroxiredoxin, AhpC-type	Cytoplasm: Cell redox homeostasis (EC 1.11.1.24).	Cell surface: Binds plasminogen (<i>Neisseria meningitidis</i>).	17 / 42	6 / 8	[8]
BCAL1919	Heat shock protein ClpB	Cytoplasm: Part of a stress-induced multi-chaperone system, it is involved in the recovery of the cell from heat-induced damage, in cooperation with DnaK, DnaJ and GrpE.	Extracellular: Interact with host macrophages and mediates inflammatory immune response (<i>Mycobacterium tuberculosis</i>).	4	2	[9]

BCAL1990	Glucose-6-phosphate isomerase	Cytoplasm: Catalyzes interconversion of glucose-6-phosphate and fructose-6-phosphate in glycolysis and gluconeogenesis (EC 5.3.1.9).	Cell Surface: Laminin, collagen I binding (<i>Lactobacillus crispatus</i>).	15	8	[10]
BCAL1996	ATP-dependent Clp protease proteolytic subunit (ClpP)	Cytoplasm: Hydrolysis of proteins to small peptides in the presence of ATP and magnesium (EC 3.4.21.92).	Cell Surface: Binding of plasmin(ogen), fibronectin and binding and invasion to epithelial and endothelial cells (<i>Streptococcus pneumoniae</i>).	25	5	[11]
BCAL2013	AhpC/TSA family protein	Cytoplasm: Hydroxyperoxidase activity, antioxidant (EC 1.11.1.-).	Cell surface: Plasminogen binding (<i>N. meningitidis</i>).	29	6	[8]
BCAL2122	Malate synthase (AceB)	Cytoplasm: Catalyzes the condensation and subsequent hydrolysis of acetyl-CoA and glyoxylate to form malate and CoA (EC 2.3.3.9)	Cell surface: Binds fibronectin, laminin and A549 lung epithelial cells (<i>M. tuberculosis</i>).	4	2	[12]
BCAL2152/ BCAL2153/ BCAM0088	Peptidyl-prolyl cis-trans isomerase (PpiA/ PpiB)	Periplasm / Cytoplasm: Catalyzes the cis-trans isomerization of proline imidic peptide bonds in oligopeptides (EC 5.2.1.8)	Extracellular: Induces gastric epithelial cell apoptosis in a TLR4-dependent manner (<i>H. pylori</i>).	92 / 24 /14	17 / 6 / 4	[13]
BCAL2179	Enolase	Cytoplasmic Membrane: Catalyzes the reversible conversion of 2-phosphoglycerate into phosphoenolpyruvate. (EC. 4.2.1.11)	Cell surface: Plasminogen binding (<i>Aeromonas hydrophila</i> , <i>Borrelia burgdorferi</i> , <i>N. meningitidis</i>).	37	7	[14]
BCAL2224	Glutamine synthetase (GlnA)	Cytoplasm: Synthesis of glutamine (EC 6.3.1.2)	Cell surface: Binds fibronectin (<i>M. tuberculosis</i>). Binding laminin (<i>L. crispatus</i>). Plasminogen binding (<i>M. tuberculosis</i> ; <i>L. crispatus</i> ; <i>B. lactis</i>). Binds collagen I and other bacterial species (<i>L. crispatus</i>).	10	2	[10][15][6]
BCAL2346	Triosephosphate isomerase (TpiA)	Cytoplasm: Catalyzes the reversible interconversion of dihydroxyacetone phosphate and D-glyceraldehyde 3-phosphate (glycolysis) (EC 5.3.1.1).	Cell surface: Plasminogen binding (<i>Streptococcus anginosus</i> , <i>Streptococcus oralis</i>). Adhesin, contact-mediated killing of <i>Cryptococcus</i> (<i>Staphylococcus aureus</i>).	9	4	[16][17]

BCAL2433	Transaldolase B (TalB)	Cytoplasm: Important for the balance of metabolites in the pentose-phosphate pathway (EC 2.2.1.2)	Extracellular: Binds mucin (<i>B. longum</i>).	62	13	[18]
BCAL2730	Putative ATP-dependent Clp protease ATP-binding subunit (ClpA)	Cytoplasm: Protease ATP-dependent protein. Chymotrypsin-like activity. Major role in the degradation of misfolded proteins.	Cell surface: Binding of plasminogen and fibronectin. Adhesion and invasion of epithelial and endothelial cells (<i>S. pneumoniae</i>).	12	4	[11]
BCAL2757	Superoxide dismutase (SodB)	Periplasm: Superoxide dismutase (EC 1.15.1.1)	Cell surface: Adhesin binding mucus-associated proteins. Binding to epithelial cell aldolase, GAPDH and cyclophilin A (<i>Mycobacterium avium</i>).	42	5	[19]
BCAL2767	Ornithine carbamoyltransferase (ArgF)	Cytoplasm: Reversibly catalyzes the transfer of the carbamoyl group from carbamoyl phosphate to the N(epsilon) atom of ornithine to produce L-citrulline (EC 2.1.3.3).	Cell surface: Binds fibronectin (<i>Staphylococcus epidermidis</i>).	11	2	[20]
BCAL2777	N-acetylmuramoyl-L-alanine amidase	Periplasm: Autolysin that hydrolyzes the amide bond between N-acetylmuramoyl and L-amino acids in certain cell wall glycopeptides (EC 3.5.1.28).	Extracellular: Fibrinogen and fibronectin binding (<i>S. aureus</i>).	18	6	[21]
BCAL2839	Fructose-1,6-bisphosphate aldolase (CbbA)	Cytoplasm: Glycolysis and gluconeogenesis (EC 4.1.2.13).	Cell surface: Adhesion to host (<i>N. meningitidis</i>). Binds to host Flamingo cadherin receptor (FCR) (<i>S. pneumoniae</i>).	30	7	[22][23]
BCAL2841	Phosphoglycerate kinase	Cytoplasm: Phosphoglycerate kinase (EC 2.7.2.3).	Cell surface: Plasminogen binding (<i>S. anginosus</i> , <i>S. oralis</i> , <i>S. pneumoniae</i>). Cell surface virulence factor (<i>A. hydrophila</i>).	60	11	[16][24][25]
BCAL3004	Chorismate mutase	Periplasm: Key enzyme in the shikimate pathway (EC 5.4.99.5).	Extracellular: Involved in virulence, being important in bacterium-rice interactions (<i>Xanthomonas oryzae</i>).	8	3	[26]

BCAL3146	Chaperonin GroEL	Cytoplasm: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions.	Extracellular: Adhesion to host (<i>Salmonella typhimurium</i>).	241	27	[27]
BCAL3270	Molecular chaperone DnaK	Cytoplasm: Chaperone	Cell surface: Binds plasminogen (<i>N. meningitidis</i>).	23	6	[8]
BCAL3272	Heat shock protein GrpE	Cytoplasm: Part of the HSP70 chaperone complex (GrpE, DnaJ, and DnaK), which is important for protein folding and helps to protect cells from stress.	Cell surface: Interaction with Salivary Proline-rich Proteins of Pharyngeal Epithelial Cell (<i>Streptococcus pyogenes</i>)	11	4	[28]
BCAL3388	Glyceraldehyde-3-phosphate (G-3-P) dehydrogenase 1 (GapA)	Cytoplasm: Glycolytic enzyme that catalyses the conversion of G-3-P to 1, 3-bisphosphoglycerate (EC 1.2.1.-).	Cell surface: Binds plasminogen and Fibrinogen (<i>Escherichia coli</i> ; <i>Francisella tularensis</i> ;). Binds fibronectin (<i>F. tularensis</i>)	84	13	[29]
BCAL3453	Preprotein translocase subunit SecA	Cytoplasm: Part of the Sec protein translocase complex.	Cell surface: Binds salivary mucin (<i>S. gordonii</i>)	22	6	[5]
BCAM0941	6-phosphogluconate dehydrogenase (6PGD)	Cytoplasm: Produces NADPH by converting 6-phosphogluconate to ribulose 5-phosphate in the pentose phosphate pathway (EC 1.1.1.44).	Cell surface: Adhesin (<i>S. pneumoniae</i>).	76	7	[30]
BCAM0965	Malate dehydrogenase	Cytoplasm: Tricarboxylic acid cycle (TCA) (EC 1.1.1.37).	Cell surface: Binds fibronectin and plasminogen (<i>Brucella abortus</i>).	88	16	[31]
BCAM1309	γ -glutamyltransferase precursor 2 (Ggt2)	Periplasm: Converts glutamine into glutamate and ammonia, and converts glutathione into glutamate and cysteinylglycine (EC 2.3.2.2).	Extracellular: Causes glutamine and glutathione consumption in the host cells. Inhibition of T cell-mediated immunity and dendritic cell differentiation (<i>H. pylori</i>)	66	17	[32]
BCAM2821	Malate synthase G (GlcB)	Cytoplasm: Malate synthase, glyoxylate cycle (EC 2.3.3.9).	Cell surface: Binds fibronectin, laminin and A549 lung epithelial cells (<i>M. tuberculosis</i>).	9	4	[12]

¹Peptides identified using surface-shaving with trypsin and LC-MS/MS analysis.

²"Moonlight proteins" in other bacteria with secondary function at the Outer membrane or Extracellular. Information retrieved from Database MoonProt 3.0 and MultitaskProtDBII.

* In-paralogs.

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Table S6 – Predicted surface-exposed proteins identified in *B. cenocepacia* J2315 by using the “surface shaving” strategy followed by LC-MS/MS (Threshold score: ≥2 peptides) and their predicted B cell epitopes. HP – hypothetical protein.

ORF (Description)	Peptides identified ¹			B cell epitopes average ²	Predicted B cell epitopes ^{2,3}
	Aerobic conditions	Microaerophilic condition	Both conditions		
BCAL0076 (Putative lipoprotein)			⁸⁶ QEANDMSAQHNGGLSGDEQR ¹⁰⁵ ¹⁰⁶ VLNQELDTAAR ¹¹⁶	0.510	⁸⁵ RQEANDMSAQHNGGLSGDEQRL NQ ¹⁰⁹
BCAL0151 (Extracellular ligand binding protein)	³³ IGHVAPLTGGIAHLGK ⁴⁸ ⁹⁶ LVDDKVVAVVGHLNSGTSIP ASK ¹¹⁸ ¹⁹⁹ VMSHDATNDKAVD FR ²¹³ ³⁵⁵ GDLQHGVISLYNYK ³⁶⁸		⁵⁶ LAVEEINAK ⁶⁴ ⁷³ ITLQLDPQDDAADPR ⁸⁷ ⁷³ ITLQLDPQDDAADPRQATQVAQK ⁹⁵ ¹⁰¹ VVAVVGHLNSGTSIPASK ¹¹⁸ ¹¹⁹ IYSDAGVVQISPSATNPAYTQQGFK ¹⁴³ ¹⁴⁸ VVATDAQQGPALADYAHSK ¹⁶⁶ ¹⁷⁰ SVAVVDDS ¹⁷⁷ ¹⁷⁰ SVAVVDDSTAYGQGLANEFEK ¹⁹⁰ ²¹⁹ IKGENPDAIMYGGMDATGGPFAK ²⁴¹ ²⁸⁶ MPGGAAFK ²⁹³ ³²⁵ ANSTDPAKILAAMPATK ³⁴¹ ³³³ ILAAMPATK ³⁴¹ ³⁴² YTGVI GTTTFDSK ³⁵⁴ ³⁷³ SLLDEVK ³⁷⁹	0.439	⁶⁴ KGLTIGGQK ⁷² ⁸² DAADPRQATQV ⁹² ¹³⁶ AYTQQG ¹⁴¹ ²⁰² HDATNDKAVD ²¹¹ ²⁶² KLADLAGD ²⁶⁹ ²⁸² SLEKMPGG ²⁸⁹ ²⁹⁷ EKRFGQP ³⁰³ ³²⁶ NSTDPAK ³³² ³⁵³ SKGDLQ ³⁵⁸ ³⁷² KSLLD ³⁷⁶
BCAL0304 (VacJ-like lipoprotein)	¹⁹⁵ ANLLGAGDVLDAALDK ²¹¹		²³² GEAAVTSNNDALPK ²⁴⁵	0.469	²⁷ VQTPTKGDPLE ³⁷ ¹²⁵ KLPKHTADF ¹³³ ¹⁷⁵ YVKPDG ¹⁸⁰ ¹⁹⁴ RANLLGAGDV ²⁰³
BCAL0343 (Putative type VI secretion system protein -TssD)		³⁰ SWDHSIVQPR ³⁹ ⁹⁹ VQYLEVK ¹⁰⁵ ¹⁴⁴ IGGNQGGNTQGAWSL TK ¹⁶⁰	⁴⁰ SATASTAGGHTMTR ⁵³	0.503	¹³ VKGESADKDHQ ²³ ³¹ WDHSIVQPRSATASTAGGHTMTR C ⁵⁴ ⁹² ADGEGKRV ⁹⁹ ¹¹⁶ PSVREEGLP ¹²⁴
BCAL0349	¹⁹⁵ VSASEQGVLDQTLAN			0.516	⁵ IQVRRAR ¹¹

(Type VI secretion system-associated protein TagL)	R ²¹⁰ ²⁵⁷ TSNIALSQAR ²⁶⁶				⁴⁰ GATVTPVGN ⁴⁸ ¹⁸⁴ NPTYTIKNGLRV VSASEQGVL ²⁰³ ²¹³ EFETGSATLTPQ ²²⁴ ²⁵¹ DNSGNRT SNIAL ²⁶² ²⁹⁰ GPDQPIAPNDTADGRARN ³⁰⁷
BCAL0360 (HP)		⁴⁸ DNAPLDER ⁵⁵ ⁷² AANHQVIGTSETYSSVQ AR ⁹⁰	²¹ SANGEILASER ³²	0.488	⁸ KKATNGQ ¹⁴ ³¹ ERYEEKSG ³⁸ ⁴⁹ NAPLDERYERKLAHN ⁶³ ⁸⁰ TSETYSSVQA ⁸⁹ ⁹⁹ RDAPIAET ¹⁰⁶
BCAL0389 (Thiol:disulfide interchange protein - DsbC)	²²⁴ RLPGAVSADQLNQALAS SK ²⁴²		⁴⁰ LGNDAPIK ⁴⁷	0.481	²⁴ QADQTTDK ³¹ ³³ KATLQARLGND APIKSVSKSPVA ⁵⁵ ²²³ RRLPGAVSADQL ²³⁴
BCAL0562 (Flagellin synthesis anti-sigma-28 factor - FglM)		²² APSGTAQSSAQAGDAGSTGG DTTVNLSGLSGQLR ⁵⁵ ⁸⁹ IADGVLNTAR ⁹⁸	³ IDSTPKPSPLAPTGNGAAR ²¹	0.553	⁵¹ SGQLRSVSASGDADIDTG ⁶⁸ ⁹⁹ ELLQRQR ¹⁰⁵
BCAL0565 (Flagellar basal body rod protein FlgC)		⁴⁷ QVVFATDPMGGAR ⁵⁹ ⁶⁰ TASGQGVGGVR ⁷⁰ ¹¹⁸ SYQANVETLNTAK ¹³⁰		0.485	³² ADSATGPDGKPY ⁴³ ⁵⁴ PMGGARTASGQGVGGV ⁶⁹
BCAL0577 (Flagellar hook-associated protein - FlgL)		¹⁰⁸ SALSTQLQGYR ¹¹⁸ ¹⁴¹ TATAPFSNAPGGGVTYSGDT GSR ¹⁶³	¹⁶⁴ EVQIADTR ¹⁷¹	0.535	¹⁷ SDQQAQLSQLYQQISSGVSLATPA ⁴⁰ ⁹⁸ GDGSLSDSNR SA ¹⁰⁹ ⁴⁰³ LSLFQ ⁴⁰⁷
BCAL0849 (Metallo peptidase, subfamily M48B)		¹⁴⁷ AMQTAYAVSAAR ¹⁵⁸ ¹⁵⁹ SAAGAASPGVAALSSSQLGDI TEK ¹⁸²		0.469	²³ QSLDANSLTSAGT ³⁵ ³⁹ KAATLSDS D ⁴⁷ ⁶⁰ DAESKIAPANSAYAKR ⁷⁵ ⁸⁵ DMTLNGQK ⁹² ¹⁷² SSSQLGDIT ¹⁸⁰ ²⁰⁶ QKGMSQK ²¹² ²²³ QMDGGQSSMMSSHPSASRAQ ²⁴³

BCAL1105 (HP)		³⁷ DAMGHDAMAK ⁴⁶ ⁶³ DAMGHDAMK ⁷¹	0.504	²³ QNDAMSKDGMMSKD DAMGH ⁴¹
BCAL1390 (Glucanase)	²⁶⁷ ADPLAAPLLAK ²⁷⁷ ³⁶⁵ FGADGTLDTR ³⁷⁴		0.461	¹⁷ TGAADAAGAGCSVAWPRWDA ³⁶ ⁸⁸ NNLAQGDLSAH ⁹⁸ ¹⁰⁷ APDGAWRVLDA ¹¹⁷ ¹³⁸ WRERSY ¹⁴³ ¹⁵⁸ ETATVPG ¹⁶⁴ ¹⁷⁵ GFKLADG ¹⁸¹ ²⁰³ PDDRR ²⁰⁷ ²³⁴ YRACKGFGPDPDTHA ²⁴⁸ ²⁶⁷ ADPLA ²⁷¹ ²⁸⁹ GAPPERVDTTTGVAGPND ³⁰⁶ ³²⁵ HALADA ³³⁰ ³³² AARVDTLARQSAP ³⁴⁴ ³⁷⁰ TLDTRW GDRS ³⁷⁹
BCAL1848 (HP)		⁹⁸ APQALVVTTR ¹⁰⁷ ¹⁰⁸ SAGSGGYVGAQAYVTTSR ¹²⁵	0.489	²¹ AADECGFVKKVELPSR ³⁶ ⁴⁵ GALEPCSTGS ⁵⁴ ⁶⁰ YSTAHAAPGFDTDDY ⁷⁴ ⁹¹ TADLGAR AP ⁹⁹ ¹⁰⁷ RSAGSGGYVG ¹¹⁶ ¹³² SVDGLAPDVD ¹⁴¹
BCAL1849 (HP)		⁷² GGGTGQLEYTVK ⁸³ ⁸⁸ TFGNTQETR ⁹⁶ ¹⁵³ GVANVQLSFQAAAPK ¹⁶⁷	0.520	⁶¹ FAAPPVKGSLK GGGTGQ ⁷⁷ ¹⁴³ VRLAPSVDAK GVA ¹⁵⁵ ¹⁶⁴ AAPK GTRSVTAGGKSLQCPDVVS ¹⁸⁸ VS ¹⁸⁸ ¹⁹⁸ NGGSKSVTM ²⁰⁶
BCAL1893 (Family M23 peptidase)	²⁰¹ GVNIGGTAGEAVK ²¹³	⁸⁵ IALENGQNYR ⁹⁴ ²²⁹ GYGNI IIIK ²³⁷	0.523	⁵ SMLRAMQNRSREPLTLA ²² ¹⁹¹ LNGFDDAK ¹⁹⁸ ²⁵¹ ALMVKEGDAVTK ²⁶² ²⁸⁷ GKPVDPLKY ²⁹⁵
BCAL1938 (Cysteine peptidase, family C40)	³⁴⁶ TSTADDPIAR ³⁵⁵	³²⁴ SIEPAPVQVLR ³³⁴	0.532	¹⁰⁹ GRGVSIEPD ¹¹⁷ ¹⁶¹ LTNPYWAK ¹⁶⁸ ³³⁴ RASTQ SAPVSPRT STADDPIARFA ³⁵⁷

BCAL1961 (HP)	⁸² VAAAIATTPNVDLEK ⁹⁶	⁴³ FDDIADIGK ⁵¹	0.472	⁵⁸ LDPNTLAPNG ⁶⁷
	¹⁷⁴ GNHASTVTLLLDQGADPQV K ¹⁹³	⁵⁸ LDPNTLAPNGDPILVIAAR ⁷⁶ ⁸² VAAAIATTPNVDLEKEDK ⁹⁹ ¹³¹ GWAPLHYAATNGQDAVVK ¹⁴⁸ ¹⁹⁴ NQLGITALEFAK ²⁰⁵ ²⁰⁶ HYNAPDAIEILSK ²¹⁸ ²²³ IGASTPADAQK ²³³		⁹² VDLEKEDKAG ¹⁰¹ ¹²⁵ AEVSKKG ¹³¹ ¹⁵⁵ AYIDTASPNI ¹⁶³ ¹⁸⁷ GADPQVKNQLGIT ¹⁹⁹ ²¹⁹ RTTRIGASTPADAQK ²³³
BCAL1985 (Putative exported isomerase)		⁶⁸ EILMQEAIR ⁷⁶ ⁷⁷ EGIPNRPDVK ⁸⁶ ⁸⁷ AQVAVAQQTVVLR ⁹⁹ ¹⁸⁶ AYVPEFAAAAQK ¹⁹⁷ ²³⁵ AQIAQQLVQQK ²⁴⁵ ²⁴⁶ LQAFEELR ²⁵⁴	0.494	⁴⁵ LVQQGQTDGPQLQQAVRQELVN RE ⁶⁸ ⁷⁸ GIPNRPD ⁸⁴ ¹⁹⁸ LQKGQMTDT ²⁰⁶ ²²¹ DIRDIAPPPF ²³⁰ ²⁴⁰ QLVQQKLQAFEEL ²⁵²
		¹³ GLLNDAADSVQDPSR ²⁷ ³⁵ ELDDSIGR ⁴² ⁷⁸ ALQGGDEALAR ⁸⁸ ¹⁵⁰ DVAASALGGIGGK ¹⁶² ¹⁶³ NLSEDFQK ¹⁷⁰		²⁰ DSVQDPSRD ²⁸ ¹⁵⁶ LGGIGGKNLSEDFQKLEDK ¹⁷⁴ ²¹⁵ AALKKQLD ²²²
BCAL2022 (PspA/IM30 family protein)			0.503	
BCAL2229 (HP)	¹¹⁰ WFAAAGLR ¹¹⁷	⁴⁶ EVVSTMPTGK ⁵⁵	0.427	⁶ SLGRT ¹⁰
	³¹¹ SPHGIYFYDR ³²⁰	¹²¹ VDIYGYDGR ¹²⁹ ¹³⁷ VPLAVMPSHLAFTK ¹⁵⁰ ¹⁸⁴ VPAGLWLTPDDK ¹⁹⁵ ²³² SLADGTHVAVTNR ²⁴⁴ ²⁹¹ KVGIIDLASR ³⁰⁰ ²⁹² VGIIDLASR ³⁰⁰ ³⁰¹ KLVQTIAVGR ³¹⁰ ³⁰² LVQTIAVGR ³¹⁰		⁸⁷ GKLQRTVE ⁹⁴ ¹³⁰ DLKLVKRVPLA ¹⁴⁰ ¹⁷⁴ TVKWKMK ¹⁸⁰ ²¹⁵ QKVVKQIY ²²² ²⁵⁷ LTNVGDITGLLP ²⁶⁸ ³⁰⁰ RKLVQ ³⁰⁴
BCAL2413 (HP)		⁷⁰ QMLFVDTVSASGAR ⁸³	0.474	²² AQLTVEEIDADARQQ ³⁶
		⁹⁷ EATLRDEIADPK ¹⁰⁸ ¹⁰² DEIADPK ¹⁰⁸		⁷⁹ ASGARYQAGRYTWWTKGKEA ⁹⁸ ¹⁰¹ RDEIADPKSPP ¹¹¹ ¹¹⁹ VEKKK ¹²³
BCAL2476 (HP)	⁵ YYTSLDLSTGK ¹⁵	³⁸ SYITELLSK ⁴⁶	0.526	⁶¹ SNGKPAECRERKFIIDD ⁷⁷
	¹⁶ DLNSLDMFSSNGK ²⁸	⁷² KFIIDNLIK ⁸⁰		⁸⁶ NSFSSC ⁹¹

BCAL2645 (Putative OmpA family protein)	⁷⁹ LAPSAAQGTGTQVTEQPDGS LK ⁹⁹	¹⁶¹ AQSVVNALVQR ¹⁷¹ ¹⁷⁸ LSAQGMGASNPIADNATEAGR ¹⁹⁸	0.502	⁸⁸ TQVTEQ ⁹³ ¹⁰⁹ ATNQYAITPA ¹¹⁸ ¹⁴⁵ DSTGSAQLNQTL ¹⁵⁶ ¹⁸³ MGASNPIADNATEAGRAQN ²⁰¹
BCAL2820 (RND-4 efflux system outer membrane protein - oprM)	⁸⁹ VSVLNIEAAR ⁹⁸ ¹²³ LPNSLTAVPGR ¹³³	⁴⁰¹ GTYDQQIAALER ⁴¹²	0.519	¹⁵² FGRVQSLKDQAL ¹⁶³ ¹⁶⁷ LSTSY ¹⁷² ²⁴¹ ANQQAQARARAQ ²⁵² ²⁹⁷ PDVMQAEQ ³⁰⁴ ³¹⁴ GAARAAFFPK ³²³ ³²⁹ AFGTASPTLGGLFKAGTA ³⁴⁶ ⁴⁴⁶ YAAQQ ⁴⁵⁰
BCAL2958 (Putative ompA family protein)	¹²³ IEGMNTEVVVATGYTDR ¹³⁹	⁵⁶ DAFWTPATANAK ⁶⁷ ⁹³ ITYQADALFDFDK ¹⁰⁵ ¹⁰⁶ ATLKPLGK ¹¹³ ¹¹⁴ QKDELASK ¹²² ¹¹⁶ LDELASK ¹²² ¹²³ IEGMNTEVVVATGYTDR ¹³⁹ * ¹⁴⁰ IGSDKYNDR ¹⁴⁸ ²⁰³ RVEVEVVGTTQQVQK ²¹⁶ ²⁰⁴ VEVEVVGTTQQVQK ²¹⁶	0.512	¹⁰¹ DFFDKATLKPLGKQ ¹¹⁴ ¹³⁹ RIGSDKYNDRL ¹⁴⁹ ²¹¹ TQQVQKTTV ²¹⁹
BCAL3149 (HP)		⁴³ DGEHTEIR ⁵⁰ ⁶¹ MDFVSPHR ⁶⁸ ⁶⁹ GAVLAYDPGDGK ⁸⁰ ¹²² NVHALQQGGATVTEGEEAVGGR ¹⁴³	0.483	¹¹ IGASMTADPV ²⁰ ⁴⁰ SARDGEH ⁴⁶ ¹⁰¹ PLVRDRTGHRVDRSDVG ¹¹⁷ ¹²⁴ HALQQGGATVTEGEEAVGG ¹⁴² ¹⁵² GAPAHAVDGV ¹⁶¹ ¹⁸⁰ SYASDDDT ¹⁸⁷
BCAL3203 (Tol-Pal system protein - TolB)		⁹⁶ GANAFVAGSVNR ¹⁰⁷ ¹⁷⁶ YQLQISDSGQNAR ¹⁸⁹ ²¹⁰ VAYVSFER ²¹⁷ ³²⁶ VTFTGSYNTSPR ³³⁷	0.454	⁴⁷ FTNEANLPQQVTS ⁵⁹ ¹²³ VKQQSLG ¹²⁹ ¹⁵⁰ YIYQKLLGVRGVF ¹⁶² ¹⁸⁵ GQNARIA ¹⁹¹ ²²⁹ TGRRYMVSDQKG ²⁴⁰ ²⁷⁴ GGLRRLTQS ²⁸² ³¹⁶ QGESAGAAQRV ³²⁶ ³⁶⁴ TGAANAITNTNRD ³⁷⁶

BCAL3204 (Putative OmpA family lipoprotein)																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
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BCAM1576 (Phosphoesterase family protein)	62 HIVVIYAENR 71	104 TPLPVLPK 111	0.489	126 TAPYRLSP 133
	145ITDAQGKPLPNGV	134 DIDKLPNAPFR 144		146 ARGP SCPDANAS 157
	ITR160	166 FYQNQMQUIAGGR177		169 RIRPV 173
	489 IPALVISPFAK 499	256 VEGDDPAGTR 265		180 GWVSVEGDACGPGAGDARSE 199
	520 VHGLAPLDGVVLR 532	268 LADDSPASALDGPPK 282		208 EKTSSHG 214
	533 DNAFAAR 539			225 TKTQRKNGDYSDTGKRTA 242
BCAM1761 (Putative lipoprotein)	52LSGTEQSQHNGVTDIAVGSN	91 GSGSEPAEEAMR 102	0.484	254 GIDMFRNFWYSPTAM 268
	SYFVTLTPSGNGSVIK87			5 PDRPDDLPAADPD 16
				40 AGNAPRSAADLRIDEALRQ 58
				147 DAQGKPL 153
				181FAAWADSGGLVMGHYRNSAD
BCAM1876 (HP)		41 TFGGLAAQANK 51	0.503	TLR203
		41 TFGGLAAQANKK 52		241 PDAHKHPHA 249
		59 FKDV TAR 65		256 VEGDDPAG 263
				273 PASALDGPPKFAVD 286
				310 PPDPGNAAYADPADHRVMPPQ 330
BCAM1920 (HP)	1MAVTIDLGSGK11	13 ATLSSDSGSIR 23	0.520	470 GWWDHVAPPVGDRWG 484
				500 KGFVDHTL 507
				17 GSAPSSDSAGSGAA30
				38 QRPAY 42
				53 SGTEQSQHNGVTD 65
BCAM1921 (Putative phage membrane protein)		240 NNPALMTDTLDASMR 254	0.495	90 RSGSGSEPAEEAMR 102
		330 LGGQVSNDVVYAR 342		9 SASAQQS 15
				24 QAQLQNNATDQ 34
				96 GITDESDGIAE 106
				8 GSGKRATLSSDSGSIRTAEQRA 29
				39 PRYPGL 44
				56 GLAGSLSGD 64
				219 KDANDLGG 226
				39 GGSVPFGQIDSR 50
				67 MVEFRPIKTKRG 78
				97 NAAPSDNE 104
				110 FQDMRFPPGTDESMC 124

[illegible]

(Multidrug efflux system outer membrane protein OpcM)	253AKNELASAQADAVGV			264AVGVARRRAA	273
	AR ²⁶⁹			286PADFAFKETPIVPVAVKIPPGL	307
	396AQYDEQVANYR ⁴⁰⁶			316PDVSA	320
	415EVEDNLADLR ⁴²⁴			332IGLAKSAYFPK	342
				346TGSFGYEASTLGNLFLWSSRTFLLG	370
			421ADLRLLDDQIRAQEA AVNASRR		
			AAT ⁴⁴⁵		
			448RTQYQEGEVAYL	459	
			466RSVLQSQLQANQ	477	
			495GGWGNAPAPTAVGDAASGKAD	515	
BCAM2603 (HP)	19YDGLTALNAYDEDGR ³³		37YAITEGPYAGAK ⁴⁸	0.507	5TQRPPFAGK ¹³
			73ATVVHIDDFEAAGTSR ⁸⁷		21GLTALNAYDEDGR ³³
					40TEGPYAGAKGEVE ⁵²
					56QRIAGE ⁶¹
					65ISWQEAD ⁷¹
				80DFAAGTSRS ⁸⁸	
				97FYRLDGS ¹⁰³	
BCAM2686 (HP)		118TVESQAADAEAAQPAVEAA	108LQAADGVAAR ¹¹⁷	0.543	318HLKQDVATKQQRIDR ³³²
		VVK ¹³⁹			351HEALLSQ ³⁵⁷
		76LAAQAADLPAGAGA			359DRLQRNANREAAVAKRV ³⁷⁵
		ATK ⁹²			
BCAM2761 (Giant cable pilus - CblA)			80LATAPALK ⁸⁷	0.501	67IFTNDKAKD ⁷⁵
			80LATAPALKNQTSPGAAEIPLSVK ¹⁰²		85ALKNQTSPGAA ⁹⁵
			88NQTSPGAAEIPLSVK ¹⁰²		
			102LGETELTTTAATLK ¹¹⁶		
BCAS0104 (A-type flagellar hook-associated protein 2 - FliD2)		52VATLAASQASGNTR ⁶⁵	439TTALNADLK ⁴⁴⁷	0.517	57ASQASGNT ⁶⁴
		386DGTLNVDSAK ³⁹⁵	449VAQQQSDLSDYAAQLTK ⁴⁶⁵		84TSLKNGALQSTFNAVASG ¹⁰¹
		396LDSALSANPSGVAR ⁴⁰⁹			129ALSSSGFNGSKALGT ¹⁴³
		421LADQITQFTR ⁴³⁰			201KTGSANAI ²⁰⁸
		481MNTNSQYLTR ⁴⁹⁰			302DTKSQAA ³⁰⁸
	491LFGGANSNGTLSK ⁵⁰³			326ALSSYTAGASSQGALIGDST ³⁴⁵	
				358ARGVDGGGATEKGNHVN ³⁷⁵	
				483TNSQYLTR ⁴⁹⁰	
				494GANSNGTL ⁵⁰¹	

BCAS0151 (HP)		¹¹ SPLADSGVTANAPAATSSSGG TTDAASTTGTTGATGATDTTR ⁴⁴ ⁵⁸ DSTGATGETLGAAGASSEDPA VAQLK ⁸³	¹ MQIDFSTTAR ¹⁰	0.567	⁹⁴ ATLERQ ⁹⁹ ¹⁰⁴ AQRAKDDPAAAVEQQSLSA ¹²² ¹⁴⁴ KSGGSPSGGLV ¹⁵⁴
BCAS0236 (Trimeric autotransporter adhesin)	¹⁰⁵⁷ QITNVADGTGQQDAVT VR ¹⁰⁷⁴		¹⁰¹⁷ AVVPSSGILR ¹⁰²⁶	0.667	-
BCAS0522 (HP)			³ THQPILTTSVTAAAGLNR ²⁰ ⁸⁵ ATGASNGYALDAATAAGDVIR ¹⁰⁵	0.501	¹⁹ NRFQFVGFDGGV ³⁰ ⁴³ TTADVGEQA ⁵¹
BCAS0750 (HP)		¹⁷¹ GSASAQGGAL ¹⁸⁰	¹³⁰ SHAQGAVSTAGDVAGGAK ¹⁴⁷ ¹⁵⁰ AGEALEGATNAVQGGASVGVK ¹⁷⁰	0.568	-

¹Peptides identified using surface-shaving with trypsin and LC-MS/MS analysis.

²<http://tools.iedb.org/bcell/>. Threshold used of 0.5.

³Epitopes shorter than 5 or larger than 25 amino acids were not considered. At bold are the predicted B cell epitopes found by the Surface-shaving approach.

*Peptide has an oxidation in the fourth amino acid (Methionine)