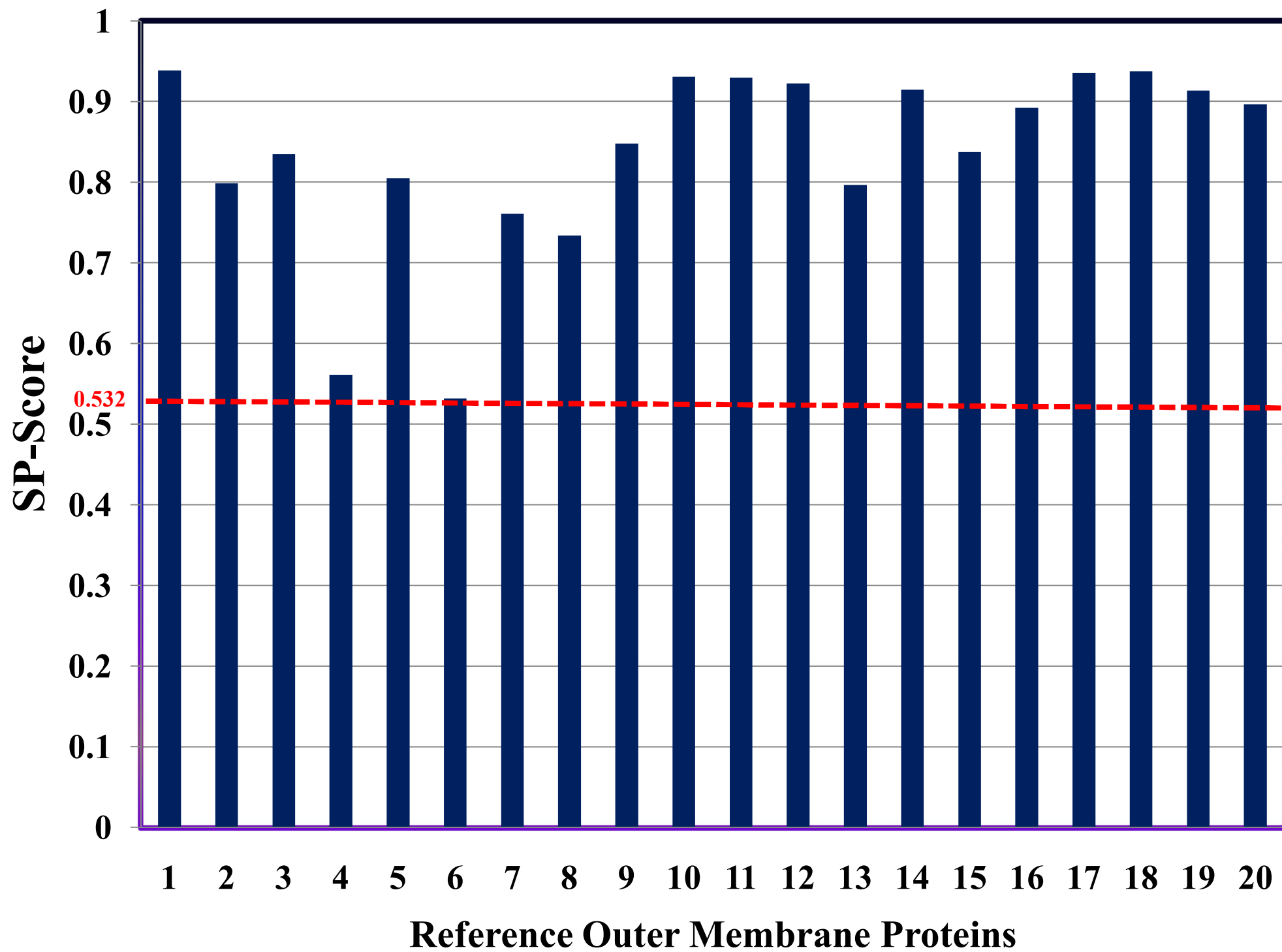


## **SUPPORTING INFORMATION**

### **Supplementary Figure Legends:**

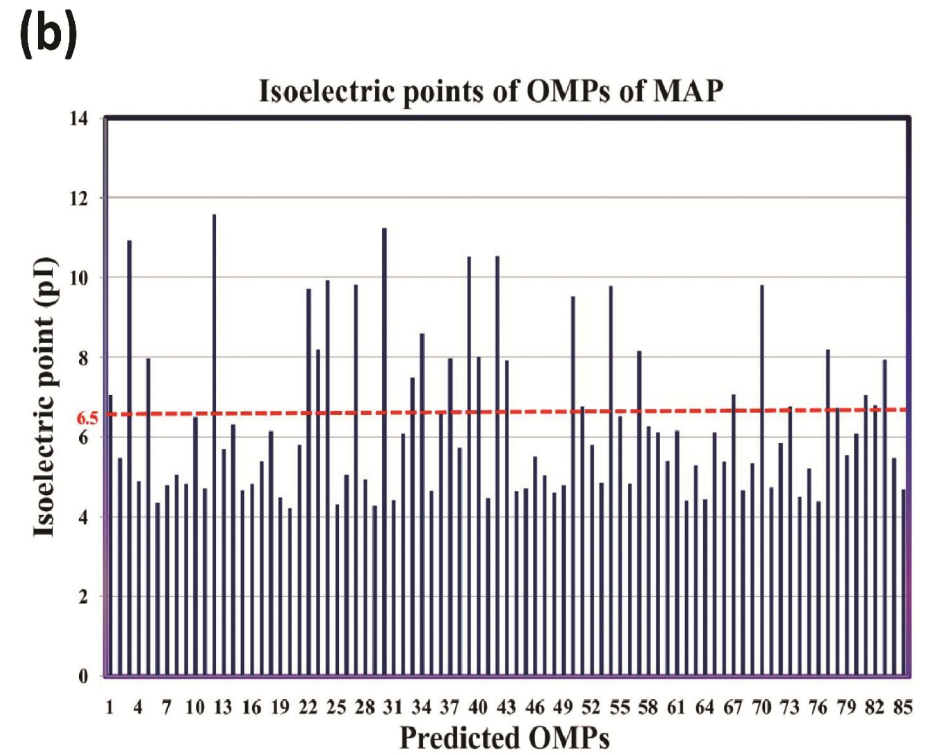
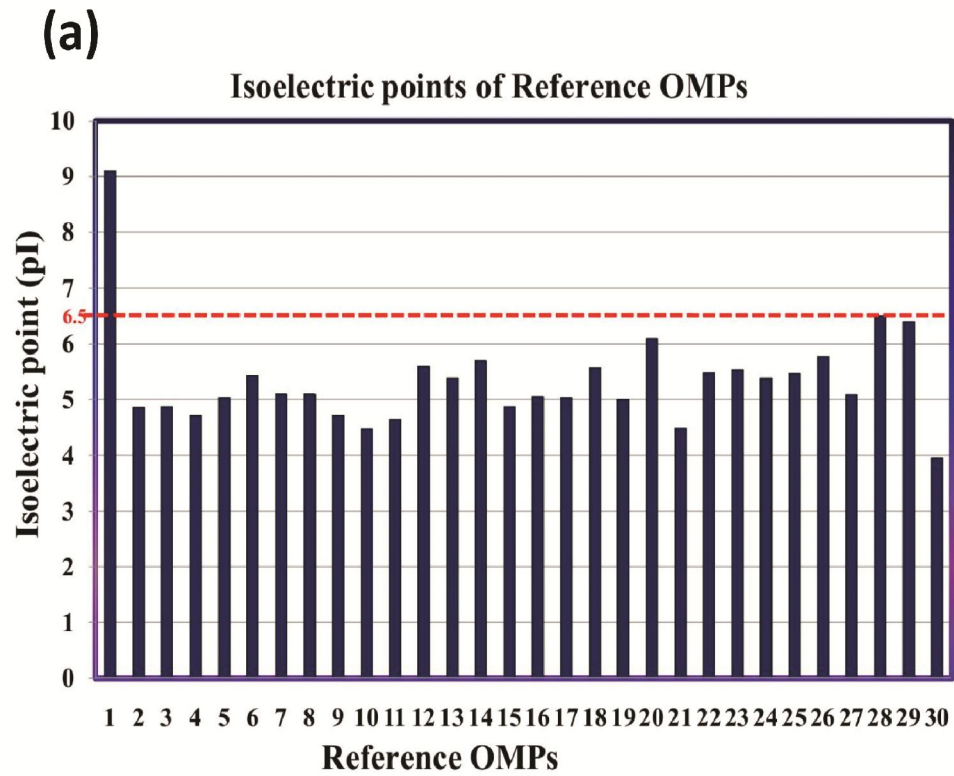
**Figure S1: Signal Peptide scores of reference OMPs.** Reference Outer Membrane Proteins with SP-Score as predicted using TargetP 1.1 program. Catecholate siderophore receptor FliC of *Escherichia coli* (K12) scored the lowest value of SP score as 0.532.



**Figure S2: Theoretical Isoelectric points.** Theoretical pI was computed using ProtParam tool .

**(a)** All the 30 well characterized reference OMPs were found to be rich in acidic amino acid residues and scored a pI of less than 6.5; **(b)** Out of 85 predicted OMPs, 58 proteins scored a minimum pI of 6.5 and were found to be rich in acidic residues.

**FIGURE S2**



**Supplementary Table 1: Predicted putative 85 OMPs of MAP**

SERIAL NO.	GI	DESCRIPTION	LENGTH	% $\beta$ -STRAND	AMPHIPHILICITY	pI	FUNCTIONAL CATEGORY
<b>1</b>	<b>41406112</b>	<b>HYPOTHETICAL PROTEIN MAP0014</b>	<b>214</b>	<b>0.14</b>	<b>0.9</b>	<b>7.07</b>	<b>3</b>
2	41406117	Pencillin Binding Protein A	462	0.14	0.7	5.47	3
3	41406120	Hypothetical Protein MAP0022c	125	0.29	0.42	10.95	9
4	41406207	MCE1B	338	0.14	1.43	4.89	0
<b>5</b>	<b>41406245</b>	<b>HYPOTHETICAL PROTEIN MAP0147c</b>	<b>232</b>	<b>0.22</b>	<b>0.96</b>	<b>7.98</b>	<b>7</b>
6	41406325	Hypothetical Protein MAP0227C	141	0.3	0.4	4.36	3
7	41406378	Hypothetical Protein MAP0280	298	0.1	1.74	4.78	7
8	41406379	Hypothetical Protein MAP0281	135	0.16	0.77	5.06	10
9	41406476	Hypothetical Protein MAP0378C	111	0.11	1.25	4.82	10
10	41406499	Hypothetical Protein MAP0401	191	0.17	0.66	6.51	7
11	41406504	Hypothetical Protein MAP0406	204	0.31	0.59	4.72	7
12	41406518	Hypothetical Protein MAP0420	67	0.19	0.38	11.6	10
13	41406534	Hypothetical Protein MAP0436	433	0.13	1.5	5.7	0
<b>14</b>	<b>41406560 *</b>	<b>HYPOTHETICAL PROTEIN MAP0462 *</b>	<b>36</b>	<b>0.14</b>	<b>0.6</b>	<b>6.32</b>	<b>7</b>

15	41406593	Hypothetical Protein MAP0495C	152	0.3	0.42	4.67	10
16	41406662	MCE4	364	0.15	1.18	4.82	0
17	41406663	Hypothetical Protein MAP0565	315	0.15	0.76	5.4	0
18	41406664	Hypothetical Protein MAP0566	321	0.15	0.96	6.15	0
19	41406678	Hypothetical Protein MAP0580C	60	0.35	0.19	4.48	0
20	41406681	Hypothetical Protein MAP0583	194	0.36	0.29	4.22	7
21	41406793	3-(2,3-Dihydroxyphenyl)Propionat edioxygenase	299	0.09	1.5	5.8	7
<b>22</b>	<b>41406858</b>	<b>HYPOTHETICAL PROTEIN MAP0760</b>	<b>311</b>	<b>0.18</b>	<b>0.86</b>	<b>9.72</b>	<b>0</b>
<b>23</b>	<b>41406859</b>	<b>HYPOTHETICAL PROTEIN MAP0761</b>	<b>342</b>	<b>0.13</b>	<b>1.26</b>	<b>8.211</b>	<b>0</b>
24	41406860	Hypothetical Protein MAP0762	219	0.21	0.91	9.95	0
25	41406864	Hypothetical Protein MAP0766C	150	0.4	0.25	4.32	1
26	41407047	Hypothetical Protein MAP0949	596	0.16	0.91	5.06	10
<b>27</b>	<b>41407050</b>	<b>HYPOTHETICAL PROTEIN MAP0952</b>	<b>459</b>	<b>0.14</b>	<b>0.89</b>	<b>9.83</b>	<b>7</b>
28	41407072	Hypothetical Protein MAP0974	342	0.34	0.3	4.94	3
29	41407140	Preprotein Translocase Subunit YAJC	92	0.35	0.28	4.28	3
<b>30</b>	<b>41407215</b>	<b>Hypothetical protein MAP1117</b>	<b>149</b>	<b>0.23</b>	<b>0.68</b>	<b>11.25</b>	<b>3</b>

31	41407310	Hypothetical Protein MAP1212C	294	0.11	1.23	4.41	10
<b>32</b>	<b>41407321</b>	<b>HYPOTHETICAL PROTEIN MAP1223c</b>	<b>243</b>	<b>0.32</b>	<b>0.42</b>	<b>6.09</b>	<b>10</b>
33	41407332	HYPOTHETICAL PROTEIN MAP1234	251	0.1	1.65	7.5	7
34	41409411	HYPOTHETICAL PROTEIN MAP3313	371	0.33	0.44	8.59	10
35	41409479	Hypothetical Protein MAP3381	465	0.13	1.11	4.66	10
<b>36</b>	<b>41409526</b>	<b>HYPOTHETICAL PROTEIN MAP3428c</b>	<b>189</b>	<b>0.17</b>	<b>0.91</b>	<b>6.64</b>	<b>3</b>
<b>37</b>	<b>41409618</b>	<b>HYPOTHETICAL PROTEIN MAP3520c</b>	<b>505</b>	<b>0.35</b>	<b>0.45</b>	<b>7.98</b>	<b>3</b>
38	41409826	Hypothetical Protein MAP3728	325	0.1	1.42	5.74	10
<b>39</b>	<b>41409830</b> *	<b>HYPOTHETICAL PROTEIN MAP3732c*</b>	<b>129</b>	<b>0.39</b>	<b>4.2</b>	<b>10.54</b>	<b>7</b>
<b>40</b>	<b>41409848</b>	<b>MmpS1</b>	<b>121</b>	<b>0.4</b>	<b>0.27</b>	<b>8.026</b>	<b>3</b>
41	41407435	Hypothetical Protein MAP1337C	95	0.16	0.8	4.46	3
<b>42</b>	<b>41407445</b>	<b>HYPOTHETICAL PROTEIN MAP1347c</b>	<b>272</b>	<b>0.13</b>	<b>0.83</b>	<b>10.55</b>	<b>10</b>
<b>43</b>	<b>41407531</b>	<b>3-KETOSTEROID- DELTA-1- DEHYDROGENASE</b>	<b>550</b>	<b>0.11</b>	<b>1.06</b>	<b>7.92</b>	<b>7</b>
44	41407574	Hypothetical Protein MAP1476C	192	0.17	0.97	4.65	3
45	41407624	Hypothetical Protein MAP1526	205	0.33	0.49	4.72	10
46	41407660	Hypothetical Protein MAP1562C	105	0.23	0.5	5.51	unknown
47	41407709	Hypothetical Protein MAP1611	364	0.13	0.72	5.05	10

48	41407722	Hypothetical Protein MAP1624	86	0.09	1.89	4.61	10
49	41407760	Hypothetical Protein MAP1662C	194	0.15	0.66	4.78	3
<b>50</b>	<b>41407810</b>	<b>HYPOTHETICAL PROTEIN MAP1712</b>	<b>245</b>	<b>0.11</b>	<b>1.22</b>	<b>9.54</b>	<b>1</b>
<b>51</b>	<b>41407835</b>	<b>MmpS5</b>	<b>118</b>	<b>0.39</b>	<b>0.35</b>	<b>6.78</b>	<b>0</b>
52	41407950	Hypothetical Protein MAP1852	330	0.15	1.18	5.8	0
53	41407952	Hypothetical Protein MAP1854	351	0.17	1.02	4.85	0
<b>54</b>	<b>41408018</b>	<b>HYPOTHETICAL PROTEIN MAP1920c</b>	<b>216</b>	<b>0.11</b>	<b>1.5</b>	<b>9.79</b>	<b>10</b>
<b>55</b>	<b>41408190</b>	<b>UspC</b>	<b>420</b>	<b>0.09</b>	<b>1.51</b>	<b>6.52</b>	<b>3</b>
56	41408211	Hypothetical Protein MAP2113C	421	0.1	1.38	4.83	0
<b>57</b>	<b>41408213</b>	<b>HYPOTHETICAL PROTEIN MAP2115c</b>	<b>311</b>	<b>0.15</b>	<b>1.04</b>	<b>8.17</b>	<b>0</b>
58	41408268	MBTG	411	0.12	1.27	6.27	1
59	41408288	Hypothetical Protein MAP2190	311	0.15	1	6.13	0
60	41408289	Hypothetical Protein MAP2191	329	0.14	1.4	5.41	0
61	41408290	Hypothetical Protein MAP2192	422	0.11	1.51	6.16	0
62	41408332	Hypothetical Protein MAP2234	357	0.14	1.33	4.4	3
63	41408564	Homoserine Kinase	295	0.18	0.81	5.29	7
64	41408575	Hypothetical Protein MAP2477C	180	0.3	0.38	4.43	2
65	41408692	Hypothetical Protein MAP2594	507	0.13	1.18	6.13	10



66	41408890	Hypothetical Protein MAP2792	492	0.11	1.21	5.39	7
<b>67</b>	<b>41408931</b>	<b>HYPOTHETICAL PROTEIN MAP2833c</b>	<b>136</b>	<b>0.5</b>	<b>0.3</b>	<b>7.08</b>	<b>10</b>
68	41408940	Hypothetical Protein MAP2842C	209	0.14	0.63	4.67	10
69	41409023	Hypothetical Protein MAP2925	356	0.13	1.22	5.35	7
<b>70</b>	<b>41409055</b>	<b>HYPOTHETICAL PROTEIN MAP2957</b>	<b>147</b>	<b>0.25</b>	<b>0.46</b>	<b>9.82</b>	<b>10</b>
71	41409071	LPPW	293	0.99	1.64	4.74	3
72	41409116	Hypothetical Protein MAP3018	155	0.11	1.53	5.84	3
<b>73</b>	<b>41409148</b>	<b>HYPOTHETICAL PROTEIN MAP3050c</b>	<b>88</b>	<b>0.17</b>	<b>0.73</b>	<b>6.78</b>	<b>3</b>
74	41409154	LPQA	185	0.14	0.32	4.5	3
75	41409165	Hypothetical Protein MAP3067C	213	0.34	0.6	5.21	10
76	41409221	Hypothetical Protein MAP3123C	203	0.43	0.33	4.38	3
<b>77</b>	<b>41409966</b>	<b>HYPOTHETICAL PROTEIN MAP3868</b>	<b>285</b>	<b>0.13</b>	<b>0.68</b>	<b>8.21</b>	<b>6</b>
<b>78</b>	<b>41410080</b>	<b>SenX3</b>	<b>384</b>	<b>0.11</b>	<b>1.05</b>	<b>6.74</b>	<b>0</b>
79	41410107	Hypothetical Protein MAP4009	208	0.12	1.37	5.54	3
80	41410120	Hypothetical Protein MAP4022	175	0.18	0.75	6.09	7
<b>81</b>	<b>41410183</b>	<b>HYPOTHETICAL PROTEIN MAP4085</b>	<b>314</b>	<b>0.15</b>	<b>1.04</b>	<b>7.06</b>	<b>0</b>
82	41410243	Hypothetical Protein MAP4145	224	0.14	1.06	6.81	3
<b>83</b>	<b>41410334</b>	<b>HYPOTHETICAL PROTEIN MAP4236c</b>	<b>181</b>	<b>0.18</b>	<b>0.94</b>	<b>7.94</b>	<b>3</b>

84	41410386	LPQP		284	0.2	0.92	5.47	3
85	41410387	Hypothetical Protein MAP4289		404	0.15	0.95	4.69	10

- Length: Length represents the mature protein obtained after deleting the predicted signal peptide sequence.
- \*Single  $\beta$ -stranded proteins.
- Protein showing a pI above 6.5 not considered as member of core set of OMPs (Shown in bold).

**Supplementary Table 2:** List of Potential N-linked and O-linked Glycosylated sites among 57 OMPs with GO terms.

S. NO	GI	GO IDENTIFIER	GO TERM NAME	DESCRIPTION	LENGTH	N-LINKED		O-LINKED	
						POSITION	RESIDUE	POSITION	RESIDUE
1	41406117	GO:0008658	Penicillin Binding	Pencillin Binding Protein A	462	22	NAT	92	<b>S</b>
								125	<b>T</b>
						109	NGS	136	<b>T</b>
								181	<b>S</b>
					463	NGA	230	<b>T</b>	
							241	<b>T</b>	
2	41406120	GO:0005515	Protein Binding	Hypothetical Protein MAP0022c	125	-	-	92	<b>T</b>
								108	<b>T</b>
4	41406325	-	-	Hypothetical Protein MAP0227C	141	73	NGS	-	-
5	41406378	GO:0030245	Cellulose Catabolic Process	Hypothetical Protein MAP0280	298	187	NAA	72	<b>T</b>
								91	<b>T</b>
		267	NWC			164	<b>S</b>		
						181	<b>T</b>		
		270	NPS			241	<b>S</b>		
326	NVG	284	<b>T</b>						
		GO:0004553	Hydrolase Activity, Hydrolyzing O-Glycosyl						

			Compounds						
6	41406379	-	-	Hypothetical Protein MAP0281	135	71	NGV	-	-
						131	NCG		
7	41406476	-	-	Hypothetical Protein MAP0378C	111	-	-	-	-
8	41406499	GO:0055114	Oxidation - Reduction Process	Hypothetical Protein MAP0401	191	115	NFW	80	T
		GO:0016209	Antioxidant Activity					154	T
		GO:0045454	Cell Redox Homeostasis					190	T
		GO:0006662	Glycerol Ether Metabolic Process					202	T
		GO:0015035	Protein Disulfide Oxidoreductase Activity					208	S
9	41406504	GO:0003824	Catalytic Activity	Hypothetical Protein MAP0406	204	117	NGF	-	-
						190	NLP		
						218	NAK		
10	41406518	-	-	Hypothetical Protein MAP0420	67	-	-	-	-
11	41406534	GO:0006508	Proteolysis	Hypothetical Protein MAP0436	433	145	NAQ	137	T
						239	NSR	326	T
						443	NGR	336	T

						446	NAM		
12	41406593	-	-	Hypothetical Protein MAP0495C	152	173	NIT	-	-
13	41406662	-	-	MCE4	364	66	NSK	-	-
						76	NAT		
						140	NGT		
						320	NCR		
14	41406663	-	-	Hypothetical Protein MAP0565	315	162	NTI	96	S
						289	NND	130	T
						324	NGP	166	S
15	41406664	-	-	Hypothetical Protein MAP0566	321	145	NAS	240	S
						148	NLN		
						150	NKP		
						308	NVY		
16	41406678	-	-	Hypothetical Protein MAP0580C	60	-	-	-	-
17	41406681	GO:0003824	Catalytic Activity	Hypothetical Protein MAP0583	194	182	NPD	112	S
18	41406793	GO:0008198	Ferrous Iron Binding	3-(2,3-Dihydroxyphenyl)Propionatedioxygenase	299	237	NPT	-	-
		GO:0055114	Oxidation - Reduction Process						
		GO:0019439	Aromatic Compound Catabolic Process						
		GO:0047070	3-Carboxyethylcatech						

			ol 2,3-Dioxygenase Activity								
19	41406860	-	-	Hypothetical Protein MAP0762	219	23	NTF	179	S		
						56	NIK	209	S		
						167	NGD				
						187	NGS				
						191	NIV				
						228	NDS				
20	41406864	-	-	Hypothetical Protein MAP0766C	150	130	NEY	-	-		
21	41407047	GO:0005515	Protein Binding	Hypothetical Protein MAP0949	596	308	NCT	95	S		
								194	T		
								246	S		
								95	S		
								329	NQT	194	T
										246	T
		277	T								
		278	T								
		285	T								
		294	S								
		346	NDI	303		T					
				310		S					
				334		S					
				335		T					
				440		NVS	339	T			
397	T										
442	T										
454	T										
22	41407072	GO:0005576	Extracellular Region	Hypothetical Protein MAP0974	342	7	NPS	125	T		
						131	NRG				
						219	NAR	167	T		
						254	NGV				
						329	NGG				
23	414071	-	-	Preprotein	92	-	-	38	S		

	40			Translocase Subunit YAJC				54	<b>T</b>
								59	<b>T</b>
								62	<b>T</b>
								73	<b>T</b>
								98	<b>S</b>
24	414073 10	-	-	Hypothetical Protein MAP1212C	294	27	<b>NAW</b>	162	<b>T</b>
						100	<b>NVV</b>		
						133	<b>NPH</b>		
25	414094 79	-	-	Hypothetical Protein MAP3381	465	28	<b>NVR</b>	226	<b>S</b>
						363	<b>NDT</b>	251	<b>S</b>
						440	<b>NDY</b>		
26	414098 26	GO:000 5488	Binding	Hypothetical Protein MAP3728	325	100	<b>NAE</b>	68	<b>T</b>
								83	<b>T</b>
								88	<b>T</b>
								136	<b>T</b>
								168	<b>T</b>
								197	<b>T</b>
								198	<b>T</b>
								207	<b>T</b>
								253	<b>S</b>
27	414074 35	0016020	Membran e	Hypothetical Protein MAP1337C	95	-	-	183	<b>S</b>
28	414075 74	GO:001 6787	Hydrolase Activity	Hypothetical Protein MAP1476C	192	210	<b>NPA</b>	81	<b>S</b>
								97	<b>T</b>
								103	<b>S</b>
29	414076 24	GO:000 3824	Catalytic Activity	Hypothetical Protein MAP1526	205	172	<b>NGD</b>	-	-
30	414076 60	GO:000 8152	Metabolic Process	Hypothetical Protein MAP1562C	105	83	<b>NAS</b>	72	<b>S</b>
		GO:001 6787	Hydrolase Activity						
31	414077 09	-	-	Hypothetical Protein MAP1611	364	-	-	141	<b>S</b>

32	414077 22	-	-	Hypothetical Protein MAP1624	86	36	NKT	32	<b>S</b>		
								72	<b>S</b>		
33	414077 60	-	-	Hypothetical Protein MAP1662C	194	33	NCT	49	<b>S</b>		
								46	NES	91	<b>S</b>
								67	NRT	160	<b>T</b>
								151	NGS		
								163	NPT		
								167	NDR		
34	414079 50	-	-	Hypothetical Protein MAP1852	330	90	NTL	78	<b>S</b>		
								99	NIV	94	<b>S</b>
								157	NLT	130	<b>T</b>
								214	NLD	181	<b>S</b>
35	414079 52	-	-	Hypothetical Protein MAP1854	351	68	NPR	190	<b>S</b>		
								207	NLS	327	<b>S</b>
								245	NTG		
								264	NRD		
								276	NDT		
36	414082 11	-	-	Hypothetical Protein MAP2113C	421	48	NGL	-	-		
								171	NLR		
								206	NLQ		
								301	NFL		
								321	NFA		
								369	NPF		
37	414082 68	-	-	MBTG	411	177	NPR	-	-		
								383	NLS		
								395	NLS		
38	414082 88	-	-	Hypothetical Protein MAP2190	311	101	NLV	131	<b>T</b>		
39	414082 89	-	-	Hypothetical Protein MAP2191	329	162	NQS	243	<b>S</b>		
								248	NVS	257	<b>T</b>
								263	NES		
								284	NRD		

						287	NLS		
						308	NGF		
40	414082 90	-	-	Hypothetical Protein MAP2192	422	192	NGS	63	S
						196	NIV		
						215	NQQ		
						245	NLS	184	S
						287	NIL		
						298	NGY		
						318	NLS		
						321	NPV		
						335	NVT	229	S
						359	NYL		
						410	NGD		
41	414083 32	-	-	Hypothetical Protein MAP2234	357	255	NPS	-	-
						269	NSR		
42	414085 64	GO:000 5524	ATP Binding	Homoserine Kinase	295	22	NLG	41	T
								45	T
								47	S
								157	T
								190	S
								195	T
						211	NVS	213	S
								264	T
								266	S
								279	S
								295	T
43	414085 75	GO:001 6787	Hydrolase Activity	Hypothetical Protein MAP2477C	180	-	-	120	T
44	414086 92	-	-	Hypothetical Protein MAP2594	507	170	NDE	161	S
						369	NRS	281	S
45	414088 90	-	-	Hypothetical Protein MAP2792	492	121	NQT	112	S
						212	NCT	140	S
						343	NAI	210	T



						358	NAT		
46	414089 40	-	-	Hypothetical Protein MAP2842C	209	-	-	-	-
47	414090 23	GO:000 3824	Catalytic Activity	Hypothetical Protein MAP2925	356	239	NAA	-	-
		GO:000 8152	Metabolic Process						
48	414090 71	-	-	LPPW	293	235	NGV	155	<b>S</b>
								227	<b>S</b>
49	414091 16	-	-	Hypothetical Protein MAP3018	155	181	NPG	-	-
50	414091 54	-	-	LPQA	185	152	NGS	-	-
51	414091 65	-	-	Hypothetical Protein MAP3067C	213	-	-	97	<b>S</b>
								101	<b>S</b>
52	414092 21	-	-	Hypothetical Protein MAP3123C	203	40	NPP	-	-
						201	NRV		
53	414101 07	GO:001 6787	Hydrolase Activity	Hypothetical Protein MAP4009	208	69	NEG	-	-
54	414101 20	GO:001 6491	Oxidored uctase Activity	Hypothetical Protein MAP4022	175	85	NIW	42	<b>T</b>
								50	<b>S</b>
								71	<b>S</b>
								159	<b>T</b>
								164	<b>S</b>
55	414102 43	-	-	Hypothetical Protein MAP4145	224	74	NGV	-	-
						129	NAR		
						138	NPT		
						168	NTT		
						190	NNI		
56	414103	-	-	LPQP	284	142	NAV	125	<b>T</b>

	86							135	<b>T</b>
						227	<b>NGS</b>	162	<b>T</b>
								202	<b>S</b>
57	414103 87	GO:001 6042	Lipid Catabolic Process	Hypothetical Protein MAP4289	404	-	-	341	<b>S</b>
		GO:000 4806	Triglyceri de Lipase Activity						

a) GI: Gene Identifier

b) "-": Absent

## **Abbreviations**

BLAST, Basic Local Alignment Search Tool; EMBL, European Molecular Biology Laboratory; FASTA, FAST-ALL; GSP, General Secretory Pathway; HMMTOP, Hidden Markov Model for Topology Prediction; IMP, Inner Membrane Protein; MAP, *Mycobacterium avium* subsp. *paratuberculosis*; MATLAB, Matrix Laboratory; NCBI, National Centre For Biotechnology Information; OMPs, Outer Membrane Proteins; OmpATb, OMP A of *Mycobacterium tuberculosis*; PEDANT, Protein Extraction Description and Analysis Tool; pI, Isoelectric Point; SCL, Sub-cellular Localization; SRP, Signal Recognition Particle; TMHMM, Transmembrane Hidden Markov Model.