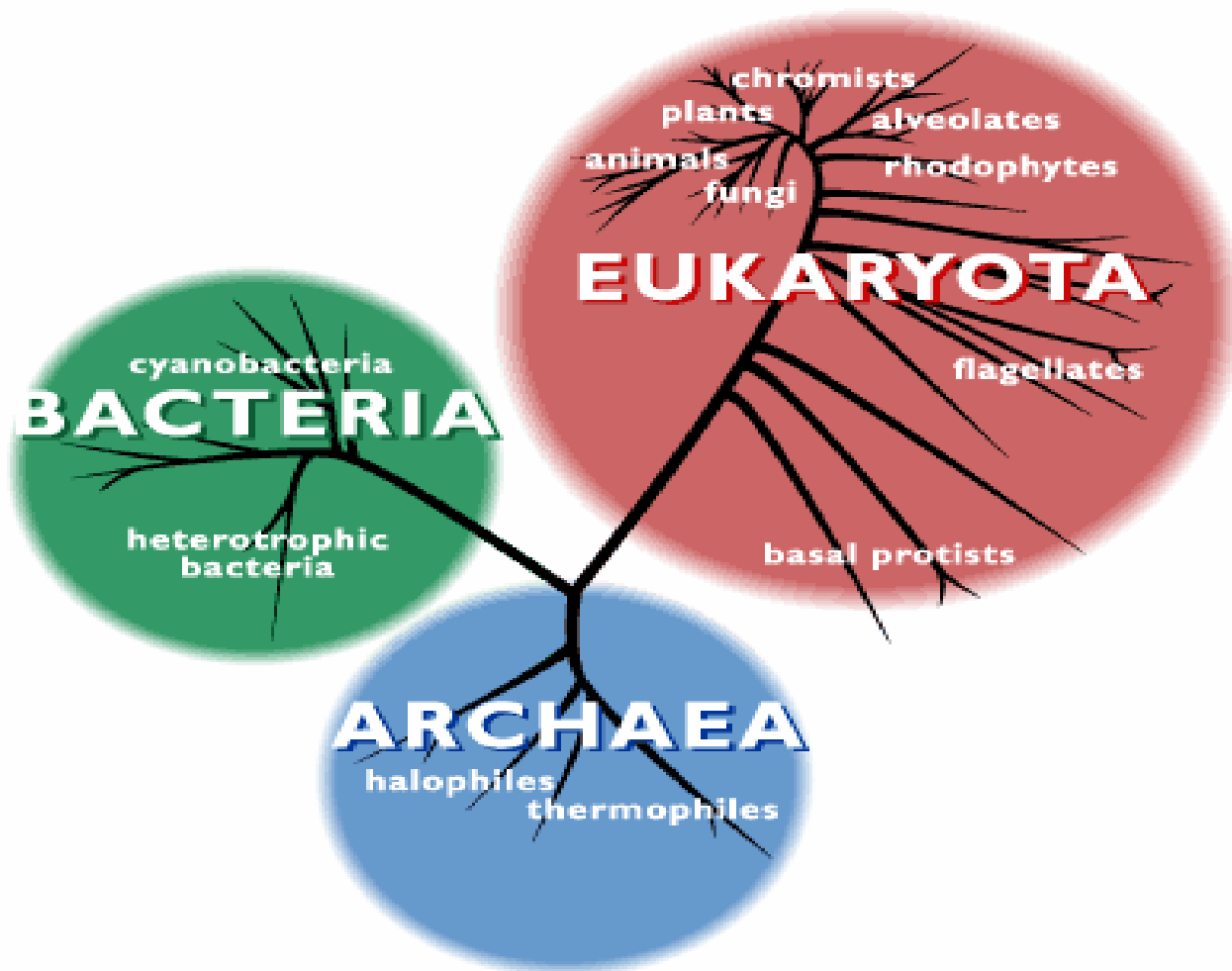


Proteome analysis of *Halobacterium* sp. NRC-1
facilitated by a biomodules analysis tool *BMSorter*

Wailap Victor Ng

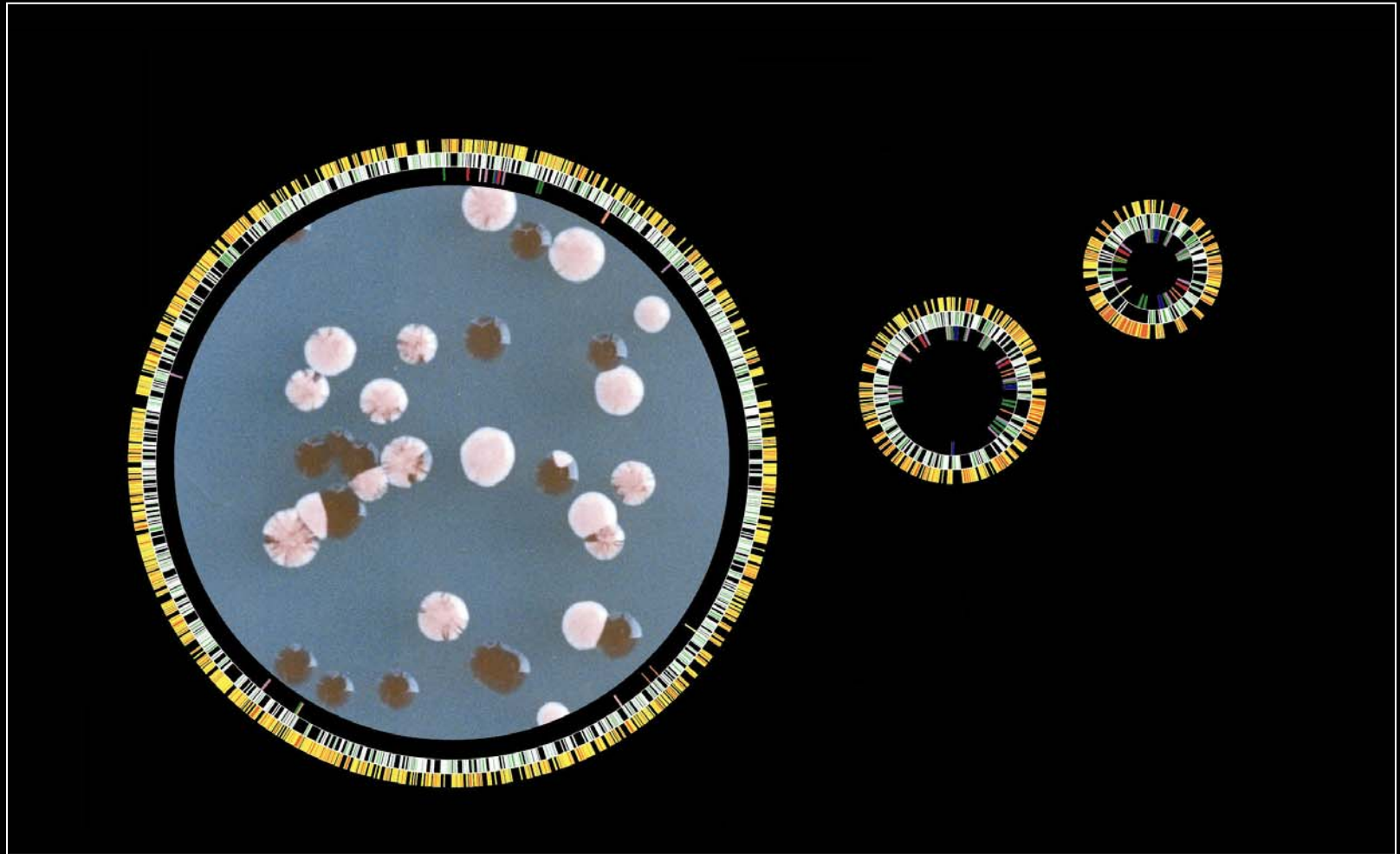
吳韋訥

Associate Professor
Institute of Biotechnology in Medicine
Institute of Bioinformatics
Dept of Biotechnology and Lab Science in Medicine
National Yang Ming University





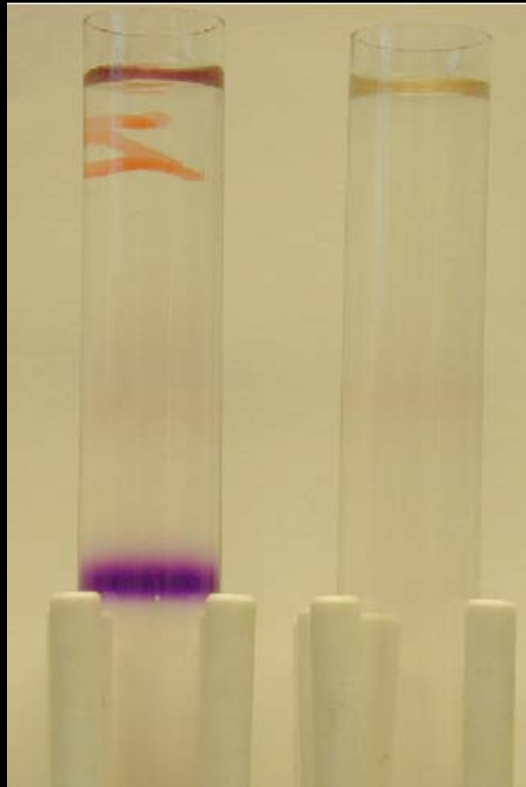
Halobacterium sp. NRC-1 (2,571,010 bp)



Halobacterium sp. NRC-1

- Genome size: 2.57 Mbp
- **2,630 putative protein coding genes**
 - 1,067 named function genes
 - 591 conserved hypothetical genes
 - 1,024 hypothetical genes

Proteome Analysis I



Membrane

Soluble

**Soluble/Membrane
Proteome**



Trypsin Digestion



C18-HPLC



MS/MS



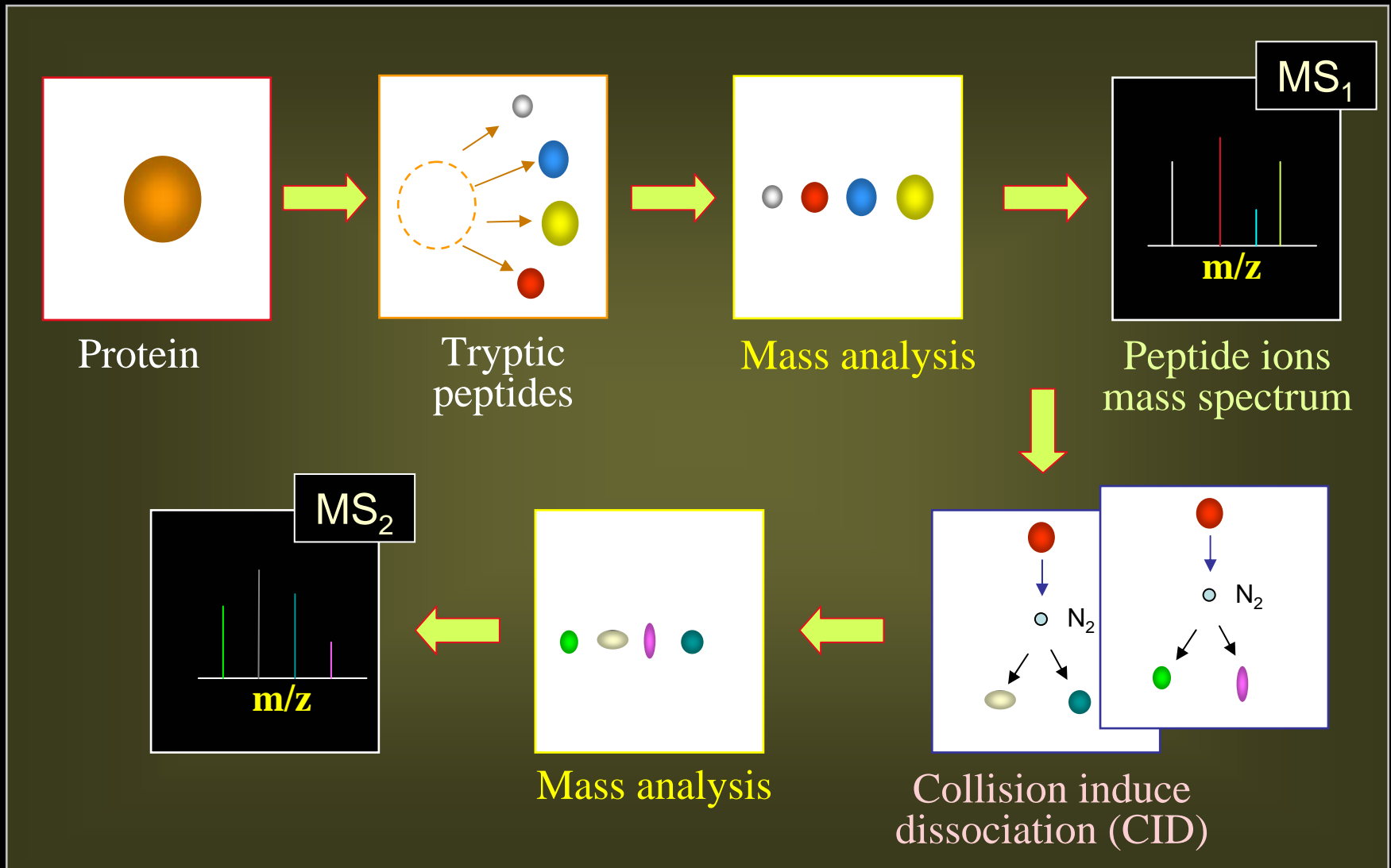
Sequest

Interact

PeptideProphet

ProteinProphet

Peptide Sequencing



Nomenclature of fragmented PEPTIDE IONS

S-P-A-F-D-S-I-M-A-E-T-L-K

E. coli oligopeptide binding protein
(MH+ 1410.6)

	<u>b-ions</u> ⁺			<u>y-ions</u> ⁺	
B1	88.1	S	PAFDSIMAETLK	1323.6	Y12
B2	185.2	SP	AFDSIMAETLK	1226.4	Y11
B3	256.3	SPA	FDSIMAETLK	1155.4	Y10
B4	403.5	SPAF	DSIMAETLK	1008.2	Y9
B5	518.5	SPAFD	SIMAETLK	893.1	Y8
B6	605.6	SPAFDS	IMAETLK	806.0	Y7
B7	719.3	SPAFDSI	MAETLK	692.3	Y6
B8	850.0	SPAFDSIM	AETLK	561.7	Y5
B9	921.1	SPAFDSIMA	ETLK	490.6	Y4
B10	1050.2	SPAFDSIMAE	TLK	361.5	Y3
B11	1151.3	SPAFDSIMAET	LK	260.4	Y2
b12	1264.4	SPAFDSIMAETL	K	147.2	Y1

描寫

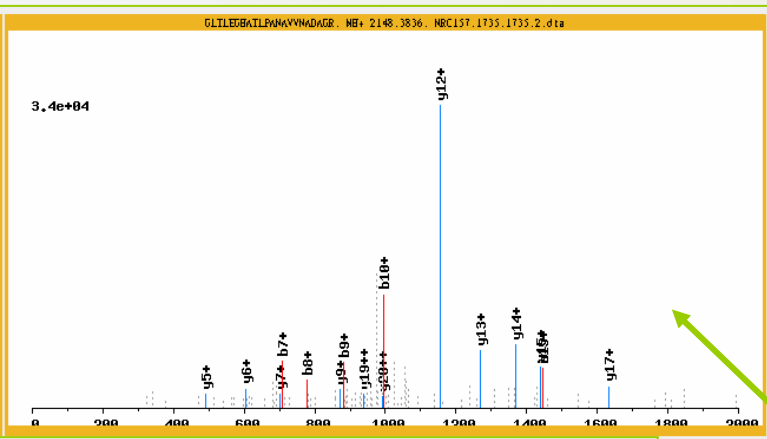
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GO

1 2
 Label:
 I M -
 Ions:
 a + 2+ 3+
 b + 2+ 3+
 c + 2+ 3+
 x + 2+ 3+
 y + 2+ 3+
 z + 2+ 3+



b ⁺	#	AA	#	y ⁺	y ²⁺
58.0599	1	G	22		
171.2193	2	L	21	2091.3317	1046.1698
272.3244	3	T	20	1978.1722	989.5901
385.4838	4	L	19	1877.0671	939.0375
514.5993	5	E	18	1763.9077	882.4578
571.6512	6	G	17	1634.7922	817.9001
708.7923	7	H	16	1577.7403	789.3741
779.8711	8	A	15	1440.5992	720.8036
880.9762	9	T	14	1369.5204	685.2642
994.1356	10	L	13	1268.4153	634.7116
1091.2523	11	P	12	1155.2559	578.1319
1162.3311	12	A	11	1058.1392	529.5736
1276.4349	13	N	10	987.0604	494.0342
1347.5137	14	A	9	872.9566	436.9823
1446.6463	15	V	8	801.8778	401.4429
1545.7789	16	V	7	702.7452	351.8766
1659.8827	17	N	6	603.6127	302.3103
1730.9615	18	A	5	489.5088	245.2584
1846.0501	19	D	4	418.4300	209.7190
1917.1289	20	A	3	303.3414	152.1747
1974.1808	21	G	2	232.2626	116.6353
	22	R	1	175.2107	88.1093

```

/ 0.56 ntt 2, nsp 5, tot 1
/ 0.35 ntt 0, nsp 5, tot 1
/ 0.22 ntt 1, nsp 5, tot 1

/ 1.00 ntt 2, nsp 5, tot 3
/ 1.00 ntt 2, nsp 5, tot 1
/ 1.00 ntt 1, nsp 5, tot 1
/ 1.00 ntt 1, nsp 5, tot 1
1.00 / 0.99 ntt 1, nsp 5, tot 1
    
```

se/halobacterium_092602.prot

63c

EVVHVR
VFNADAGR
VDDDESA

/interact-data.htm:

4 (+0.6)	2.8246	0.375	564.9	1	20 / 42	VNG0283C
4 (+1.4)	2.5061	0.342	452.4	1	17 / 42	VNG0283C
4 (+1.7)	1.9010	0.229	314.2	1	15 / 42	VNG0283C

R_GLTLEGHATLPANA
R_GLTLEGHATLPANA
R_GLTLEGHATLPANA

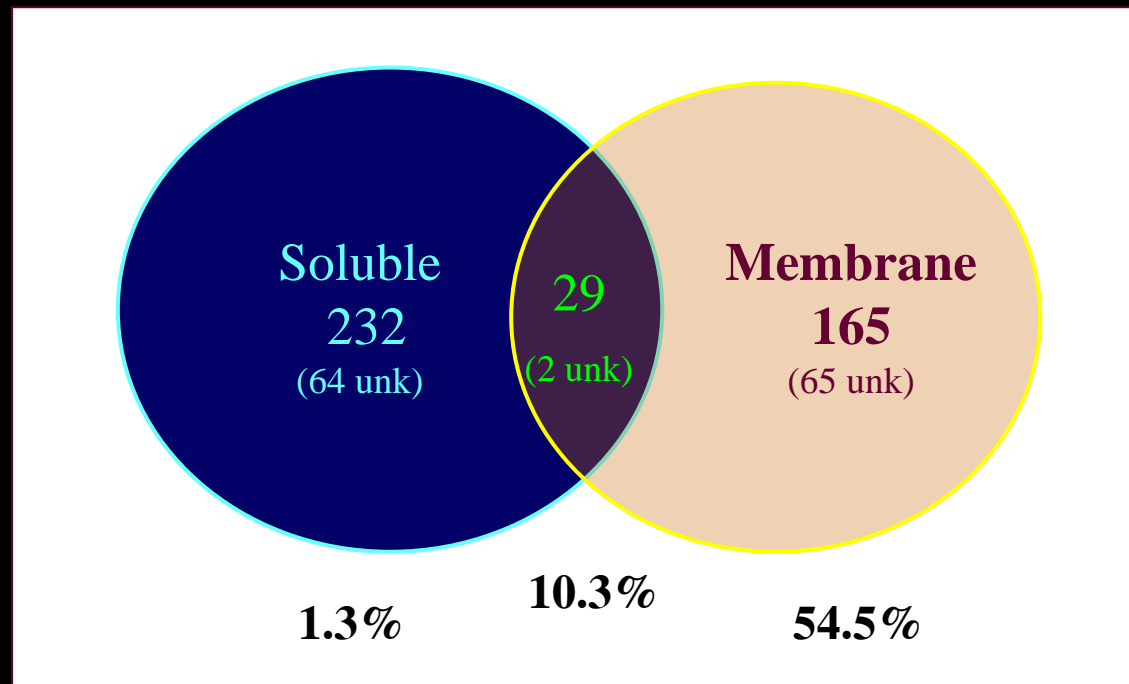
Pos Mass Seq pI

InclAA MarkAA cys unmodified

NxS/T MassRange 800.0 - 4000.0

ues) Mass 49.8% (7668 / 15383 Da)

***Halobacterium* sp. NRC-1 Proteome analysis -
% identified proteins containing *TMHMM* predicted
membrane spanning regions**

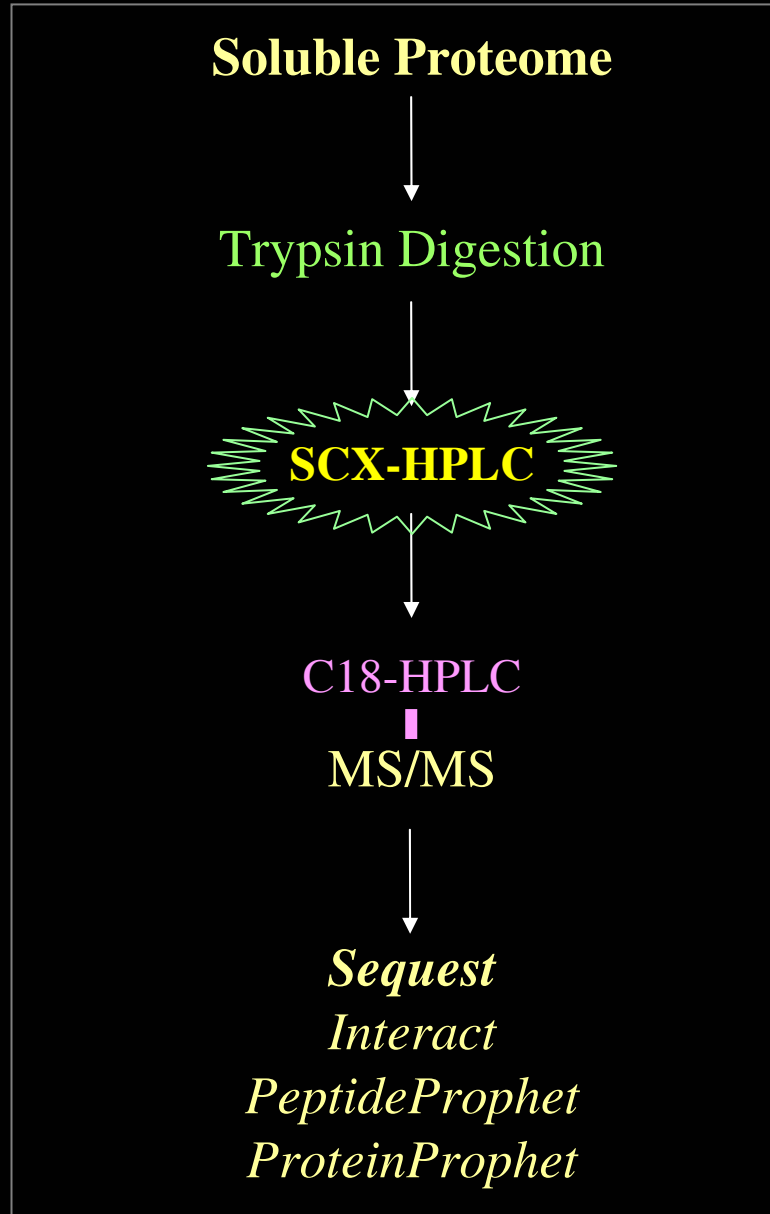


Total: 426

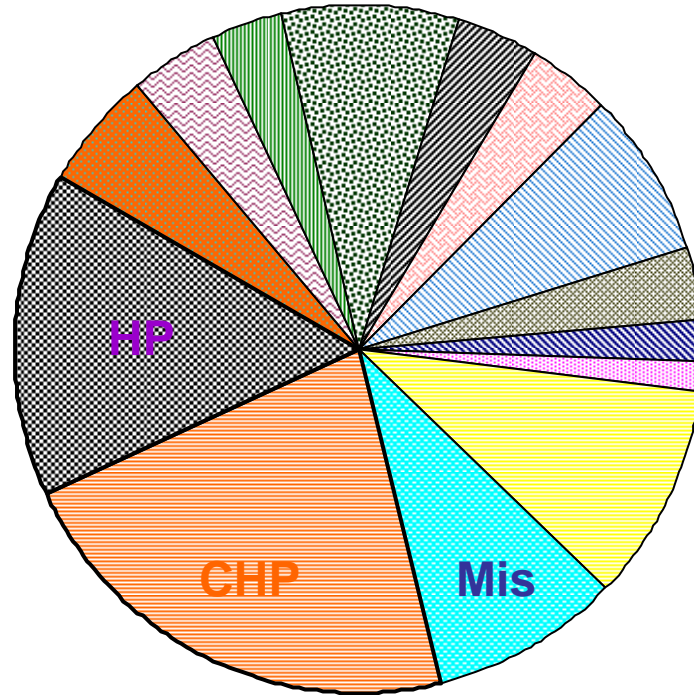
Metabolic Reconstruction

Purine metabolism	26	10	<p>VNG0414G PurH; phosphoribosylaminoimidazole-succinocarboxamide formyltransferase</p> <p>VNG0559G Apt; adenine phosphoribosyltransferase</p> <p>VNG0632G PurK; phosphoribosylaminoimidazole carboxylase ATP binding subunit</p> <p>VNG1001G GuaB; inosine monophosphate dehydrogenase</p> <p>VNG1089G PurA; adenylosuccinate synthase</p> <p>VNG1160G Ndk; nucleoside diphosphate kinase</p> <p>VNG1305G PurD; phosphoribosylglycinamide synthetase</p> <p>VNG1644G NrdB2; ribonucleoside reductase large chain</p> <p>VNG1724G Adk; adenylate kinase</p> <p>VNG6316G ArcC; carbamate kinase</p>
Pyrimidine metabolism	26	10	<p>VNG0448G PyrE1; orotate phosphoribosyl transferase</p> <p>VNG0893G Udp2; uridine phosphorylase</p> <p>VNG1160G Ndk; nucleoside diphosphate kinase</p> <p>VNG1644G NrdB2; ribonucleoside reductase large chain</p> <p>VNG1814G CarB; carbamoyl-phosphate synthase large subunit</p> <p>VNG1830G PyrG; CTP synthase</p> <p>VNG2118G PyrE2; orotate phosphoribosyl transferase</p> <p>VNG2507G PyrD; dihydroorotate dehydrogenase</p> <p>VNG6309G PyrB; aspartate carbamoyltransferase catalytic subunit</p> <p>VNG6311G PyrI; aspartate carbamoyltransferase regulatory chain</p>
Glutamate metabolism	18	6	<p>VNG0161G GdhB; glutamate dehydrogenase</p> <p>VNG0628G GdhA1; glutamate dehydrogenase</p> <p>VNG0629G AspB2; aspartate aminotransferase</p> <p>VNG1814G CarB; carbamoyl-phosphate synthase large subunit</p> <p>VNG2093G GlnA; glutamine synthetase</p> <p>VNG6316G ArcC; carbamate kinase</p>

In Depth Proteome Analysis II



Relative abundance of identified proteins



- Amino acid metabolism
- Cofactor metabolism
- Cell envelope components
- Cellular processes
- Transcription
- Translation
- Conserved Hypothetical

- Nucleotide metabolism
- Energy metabolism
- Transport
- DNA replication, repair & recombination
- Regulation
- Miscellaneous
- Hypothetical

888 proteins

BMSorter

Protein Prop

108
297

Curre

Citrat

E

num

1.1

Gly

1.1

Cit

Per

1.2

Fru

Gal

Asc

1.3

Fat

1.8

2.3

Halobacterium sp. NRC-1 loading or [List loaded ProteinProphet](#)

Current session:31, organism : **Halobacterium sp. NRC-1** , 1447 identified proteins, 681 with prob 1.00 , 456 with prob0

467 [VNG0627G](#) [citE](#) 1.00 **Acceptance:** Accept
 >VNG0627G_citE Q9HRM8 (Q9HRM8) Citrate (pro-3S)-lyase
 *wt-1.00 [2_VNPVGSAGDDVDAVLSGGGFDVVVVK](#) 1.00 / 1.00 nsp 5, tot 6
 *wt-1.00 [2_LAIHPAQVDPINDAYTPTEADTAW](#) 1.00 / 1.00 nsp 5, tot 9
 *wt-1.00 [1_FAADLGFDDGK](#) 0.85 / 0.83 nsp 5, tot 1
 *wt-1.00 [1_KAPTTGADVVVF](#) 0.57 / 0.54 nsp 5, tot 1
 *wt-1.00 [2_LMRKAPTTGADVVFVLEDAVAPARK](#) 0.22 / 0.22 nsp 5, tot 1

468 [VNG1957G](#) [tgtA2](#) 1.00 **Acceptance:** Accept
 >VNG1957G_tgtA2 Q9HNT2 (Q9HNT2) Archaeosine tRNA-ribosyltransferase
 *wt-1.00 [2_LSEPVTPTLTDVVIADAGSR](#) 1.00 / 1.00 nsp 4, tot 3
 *wt-1.00 [2_TVADHPTTDES LGELNAALAGEDK](#) 1.00 / 1.00 nsp 4, tot 1
 *wt-1.00 [2_EFTVADHPTTDES LGELNAALAGEDK](#) 0.96 / 0.96 nsp 4, tot 1

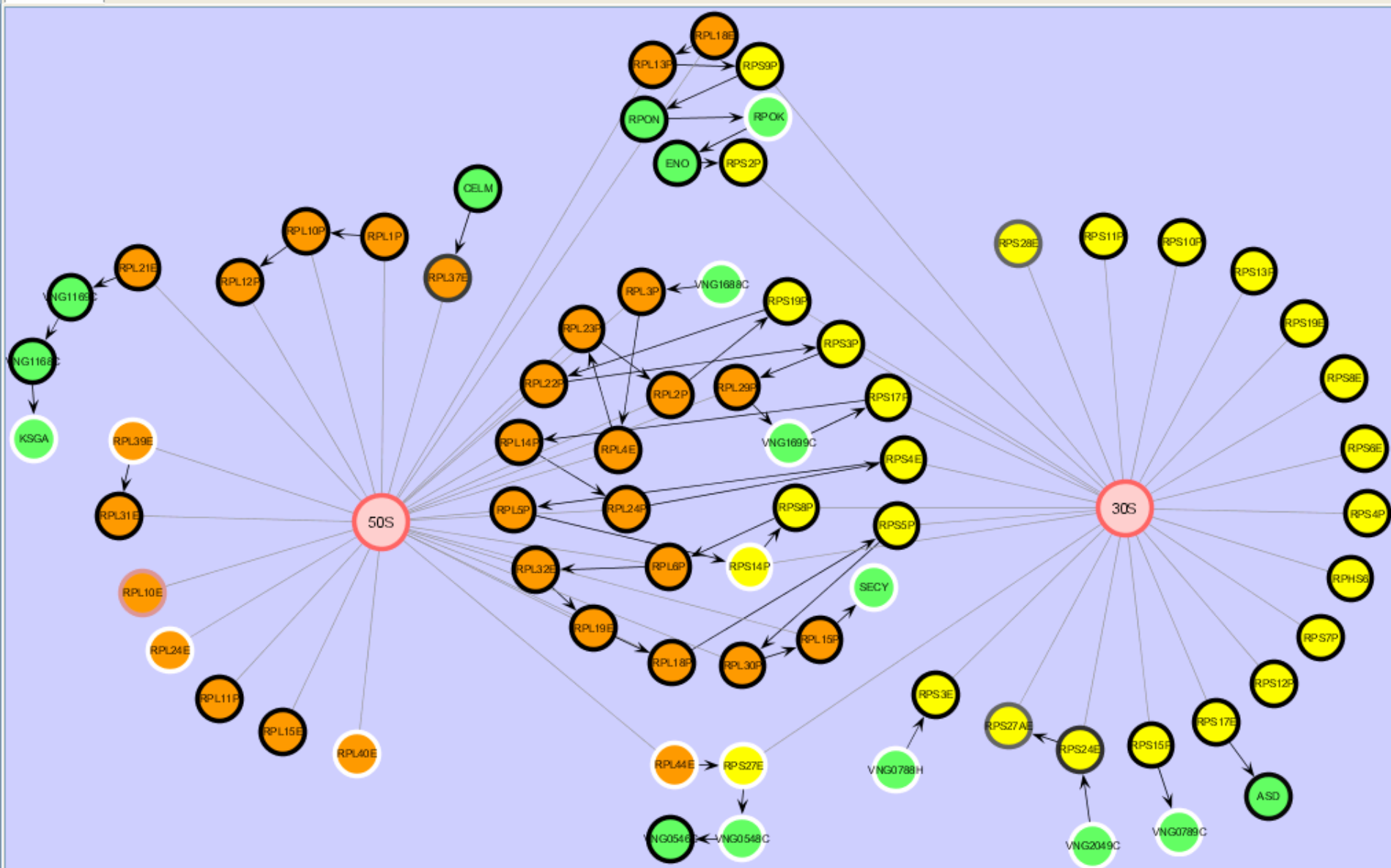
469 [VNG1201G](#) [fucA](#) 1.00 **Acceptance:** Accept
 >VNG1201G_fucA Q9HQE3 (Q9HQE3) Fuculose-1-phosphate aldolase
 *wt-1.00 [2_HGDPDILTDDQLAAVER](#) 1.00 / 1.00 nsp 4, tot 1
 *wt-1.00 [2_PDTLTDDQLAAVER](#) 1.00 / 1.00 nsp 4, tot 1
 *wt-1.00 [1_RVPVAEYAPY](#) 0.97 / 0.97 nsp 4, tot 1

470 [VNG2394G](#) [tssB](#) 1.00 **Acceptance:** Accept
 >VNG2394G_tssB Q9HMT6 (Q9HMT6) Thiosulfate sulfurtransferase
 *wt-1.00 [2_SDNWVVTPDWLDEQDDASVR](#) 1.00 / 1.00 nsp 4, tot 5
 *wt-1.00 [2_DPGEFADGHIPDAVNVTV](#) 1.00 / 1.00 nsp 4, tot 1
 *wt-1.00 [2_EHETTTGTPEVDETTYPGER](#) 0.99 / 0.99 nsp 4, tot 1

**Network analysis of Amino
Acid Metabolisms AND
Citrate Cycle**



op_ribos.gml



Nodes: 74 (0 selected) Edges: 101 (0 selected)



陽明大學 生物醫學資訊研究所



生物醫學資訊研究所將遷入圖書資訊大樓的四、五樓

Mass Spectrometry

David Goodlett (University of Washington)

Ruedi Aebersold (Inst. for Systems Biology, Seattle)

BMSorter

Rueichi Gan

Cytoscape

Yue-chieh Kao