

**Macquarie University**

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**Latrobe University**

Richard Simpson

**UNSW**

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**QIMR**

Jeff Gorman

**Garvan Institute**

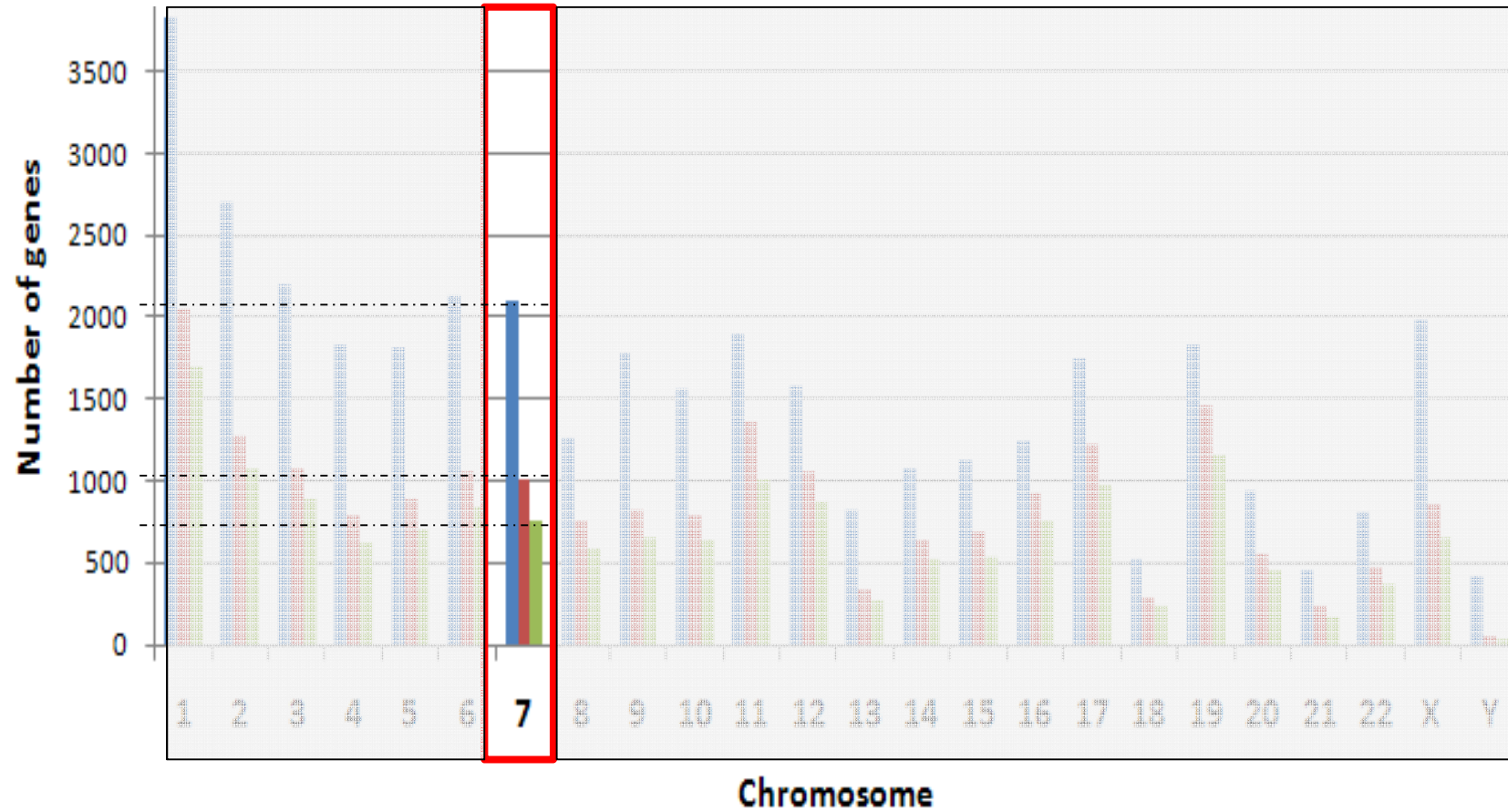
John Mattick, David James

**Bioplatforms Australia**

Andrew Gilbert, Anna Fitzgerald

**HPP WORKSHOPS**

1. Monash University, 29<sup>th</sup> July, 2011
2. Lorne, 2-5<sup>th</sup> February, 2012
3. Macquarie University, 9<sup>th</sup> March, 2012



■ Total genes   
 ■ Number of protein coding genes   
 ■ Identified proteins by MSMS

## C7-HPP Initiatives Currently Underway

1. Proteome Browser Visualization Tool Project
2. Chr7 "Missing Proteins" Bioinformatics Project
3. Chr7 Colon Cancer Cell Line Project
4. Chr7 Membrane Proteome Project
5. "Missing Proteins" MAb Project
6. Chromosome 17/7 Collaboration (USA/Australia/NZ)
7. B/D-HPP Projects (discussions in progress)

# AP32 - The Proteome Browser v1.0

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## Home

Project Definition  
AP32 - The Proteome Browser v1.0 - Project updates  
Key Technologies and Features  
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# 291

days until  
**Project Due Date**

## Join Our Discussion



[Join the Discussion](#)

## Home

## Vision



The Proteome Browser v1.0  
"Putting the pieces together"

FOR WHO  
IS A THAT  
UNLIKE OUR PRODUCT WILL

the Global Omics Community need an intuitive interface to interrogate and integrate existing and emerging proteomics data

**The Proteome Browser v1.0** visualisation tool enables comprehensive in-depth analysis shows proteins that are mapped in the context of the particular chromosome

publicly available tools delineate the complex proteome in the context of the linear genome

be a portal to the human proteome provide a genome based organisation of proteomics data

## Project Summary

This project will integrate protein data from multiple sources to produce an analysis resource that will help elucidate biological and molecular function and advance diagnosis and treatment of diseases.

It will be relevant to a range of government portfolios, including Health and Ageing and Innovation, Industry, Science and Research; and will engage with a variety of national research capabilities (including Bioplatforms Australia).

Data collections from this resource and their associated activities, parties, & services will be made available to ANDS's Research Data Australia.

## Messages

[3rd Australian & New Zealand Human Proteome Project Workshop in Sydney](#) We had the 3rd Australian & New Zealand Human Proteome Project Workshop in Sydney on Friday, 9-Mar-2012 at Macquarie University. The attendees were: Mark Molloy, Shoba Ranganathan, Mark Baker ...  
Posted Mar 15, 2012 6:12 PM by Wiki Team @ The Proteome Browser v1

[We have completed a first cut of the Project Backlog](#) We have identified a first cut of the epics and we are slowly breaking them down into user stories. We are also doing planning for Sprint 1.  
Posted Mar 4, 2012 7:33 PM by Wiki Team @ The Proteome Browser v1

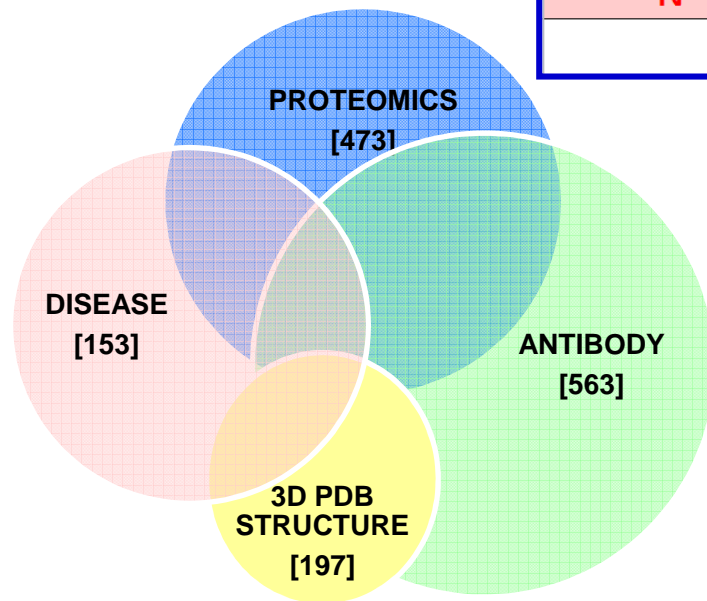
Showing posts 1 - 2 of 2. [View more »](#)

# Latest neXtProt Chromosome 7 Report

Release 2012-01-13



PROTEOMICS	ANTIBODY	3D STRUCTURE	NUMBER	CUMULATIVE	
Y	Y	Y	110		
Y	Y	N	215		
Y	N	Y	22		
Y	N	N	127	474	50%
N	Y	Y	37		
N	Y	N	202		
N	N	Y	28	741	78%
N	N	N	205		22%
			946		



1.	Acylglycerol hydrolase	52.	Leucine zipper protein 6	101.	Putative phosphoserine phosphatase-like protein	151.	STAG3-like protein 3
2.	ADP-ribosylation factor-like protein 4A	53.	Leucine-rich repeat and death domain-containing protein 1	102.	Putative postmeiotic segregation increased 2-like protein 1	152.	STAT3-interacting protein as a repressor
3.	Amiloride-sensitive cation channel 3	54.	Leucine-rich repeat neuronal protein 3	103.	Putative postmeiotic segregation increased 2-like protein 11	153.	Stimulated by retinoic acid gene 8 protein homolog
4.	Ankyrin repeat and MYND domain-containing protein 2	55.	Lipoma HMGIC fusion partner-like 3 protein	104.	Putative postmeiotic segregation increased 2-like protein 2	154.	Taste receptor type 2 member 16
5.	Ankyrin repeat and SOCS box protein 4	56.	Metabotropic glutamate receptor 8	105.	Putative postmeiotic segregation increased 2-like protein 3	155.	Taste receptor type 2 member 3
6.	Autophagy-related protein 9B	57.	Monocyte to macrophage differentiation factor 2	106.	Putative protein cTAGE-6	156.	Taste receptor type 2 member 4
7.	B-cell CLL/lymphoma 7 protein family member B	58.	Motor neuron and pancreas homeobox protein 1	107.	Putative protein RNF216-like	157.	Taste receptor type 2 member 40
8.	Beta-1,3-N-acetylglucosaminyltransferase lunatic fringe	59.	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial	108.	Putative protein unc-93 homolog B1-like protein	158.	Taste receptor type 2 member 41
9.	Brorin	60.	Neurogenic differentiation factor 6	109.	Putative protein ZNF815	159.	Taste receptor type 2 member 5
10.	CATR tumorigenic conversion 1 protein	61.	Nuclear factor erythroid 2-related factor 3	110.	Putative speedy protein E2-like protein	160.	T-cell receptor gamma chain C region 1
11.	Chloride channel protein 1	62.	Olfactory receptor 2A1/2A2	111.	Putative speedy protein E2-like protein	161.	Testis-specific gene 13 protein
12.	Class A basic helix-loop-helix protein 15	63.	Olfactory receptor 2A1/2A2	112.	Putative speedy protein E5	162.	TLR4 interactor with leucine rich repeats
13.	Claudin-15	64.	Olfactory receptor 2A12	113.	Putative speedy protein E6	163.	TP53-target gene 1 protein
14.	Cutaneous T-cell lymphoma-associated antigen 4	65.	Olfactory receptor 2A14	114.	Putative speedy protein E7	164.	Transcription factor NF-E4
15.	Cutaneous T-cell lymphoma-associated antigen 8	66.	Olfactory receptor 2A2	115.	Putative speedy protein-like protein 2	165.	Transcription factor Sp8
16.	Cytochrome P450 3A5	67.	Olfactory receptor 2A25	116.	Putative speedy protein-like protein 3	166.	Transmembrane protein 120A
17.	Cytochrome P450 3A7	68.	Olfactory receptor 2A5	117.	Putative speedy protein-like protein LOC442572	167.	Transmembrane protein 194A
18.	Diacylglycerol kinase iota	69.	Olfactory receptor 2A7	118.	Putative T-complex protein 1 subunit theta-like 1	168.	Transmembrane protein 213
19.	DNA repair protein XRCC2	70.	Olfactory receptor 2F1	119.	Putative transmembrane protein LOC401397	169.	Transmembrane protein 229A
20.	Equilibrative nucleoside transporter 4	71.	Olfactory receptor 2F2	120.	Putative uncharacterized protein C7orf40	170.	Transmembrane protein 60
21.	ETS translocation variant 1	72.	Olfactory receptor 6B1	121.	Putative uncharacterized protein C7orf71	171.	Transmembrane protein PVRIG
22.	Fascin-3	73.	Olfactory receptor 6V1	122.	Putative uncharacterized protein encoded by LINC00174	172.	tRNA wybutosine-synthesizing protein 1 homolog B
23.	F-box only protein 24	74.	Olfactory receptor 9A2	123.	Putative uncharacterized protein FLJ11871	173.	Twist-related protein 1
24.	F-box/LRR-repeat protein 13	75.	Pleckstrin homology domain-containing family A member 8	124.	Putative uncharacterized protein FLJ33307	174.	UDP-xylose and UDP-N-acetylglucosamine transporter
25.	Fez family zinc finger protein 1	76.	Postmeiotic segregation increased 2-like protein 5	125.	Putative uncharacterized protein FLJ38264	175.	Uncharacterized protein C7orf13
26.	Frizzled-9	77.	Prestin	126.	Putative uncharacterized protein FLJ40288	176.	Uncharacterized protein C7orf26
27.	Gamma-crystallin N	78.	PRKR-interacting protein 1	127.	Putative uncharacterized protein FLJ45340	177.	Uncharacterized protein C7orf33
28.	HERV-F(c)2_7q36.2 provirus ancestral Env polyprotein	79.	Probable alpha-ketoglutarate-dependent dioxygenase ABH4	128.	Putative uncharacterized protein FLJ92257	178.	Uncharacterized protein C7orf61
29.	HERV-K_7p22.1 provirus ancestral Env polyprotein	80.	Probable G-protein coupled receptor 141	129.	Putative uncharacterized protein LOC389458	179.	Uncharacterized protein C7orf63
30.	HERV-K_7p22.1 provirus ancestral Gag polyprotein	81.	Probable G-protein coupled receptor 146	130.	Putative uncharacterized protein PNAS-138	180.	Uncharacterized protein C7orf65
31.	HERV-K_7p22.1 provirus ancestral Pol protein	82.	Prolin-rich protein 15	131.	Putative uncharacterized protein PRO1854	181.	Uncharacterized protein C7orf66
32.	HERV-K_7p22.1 provirus ancestral Pro protein	83.	Prolin-rich transmembrane protein 4	132.	Putative Williams-Beuren syndrome chromosomal region 23 protein	182.	Uncharacterized protein C7orf73
33.	HERV-K_7q22.1 provirus Rec protein	84.	Protein ACN9 homolog, mitochondrial	133.	Putative zinc finger protein 727	183.	Uncharacterized protein C7orf74
34.	HERV-R_7q21.2 provirus ancestral Env polyprotein	85.	Protein dpy-19 homolog 2-like 1	134.	Putative zinc-alpha-2-glycoprotein-like 2	184.	Uncharacterized protein encoded by SND1-IT1
35.	Histone deacetylase complex subunit SAP25	86.	Protein orai-2	135.	Radial spoke head 10 homolog B	185.	Uncharacterized protein KIAA1908
36.	Histone-lysine N-methyltransferase MLL5	87.	Protein phosphatase 1 regulatory subunit 17	136.	Radial spoke head 10 homolog B2	186.	Uncharacterized protein LOC154872
37.	Homeobox even-skipped homolog protein 1	88.	Protein phosphatase 1 regulatory subunit 3A	137.	Receptor activity-modifying protein 3	187.	Uncharacterized protein LOC389493
38.	Homeobox protein GBX-1	89.	Protein ZNF767	138.	Rho guanine nucleotide exchange factor 35	188.	UPF0562 protein C7orf55
39.	Homeobox protein Hox-A7	90.	Putative DBH-like monoxygenase protein 2	139.	RING finger protein 32	189.	Uroplakin-3b-like protein
40.	Homeobox protein Hox-A9	91.	Putative diacylglycerol O-acyltransferase 2-like protein 7	140.	Scavenger receptor cysteine-rich domain-containing group B protein	190.	Uroplakin-3b-like protein
41.	Homeobox protein MOX-2	92.	Putative FKS06-binding protein 9-like protein	141.	Sclerostin domain-containing protein 1	191.	Williams-Beuren syndrome chromosomal region 28 protein
42.	Homeobox protein NOBOX	93.	Putative griffin	142.	Serine protease 58	192.	Zinc finger protein 117
43.	Homeobox protein unc-4 homolog	94.	Putative homeodomain transcription factor 2	143.	Solute carrier family 13 member 1	193.	Zinc finger protein 12
44.	Humanin-like protein 6	95.	Putative IQ and AAA domain-containing protein 1-like	144.	Solute carrier family 13 member 4	194.	Zinc finger protein 138
45.	Hyccin	96.	Putative maltase-glucoamylase-like protein FLJ16351	145.	Sorting nexin-13	195.	Zinc finger protein 212
46.	Insulin-induced gene 1 protein	97.	Putative maltase-glucoamylase-like protein LOC93432	146.	Speedy protein E1	196.	Zinc finger protein 394
47.	Integrator complex subunit 4-like protein 2	98.	Putative olfactory receptor 10AC1	147.	Speedy protein E2	197.	Zinc finger protein 398
48.	Kell blood group glycoprotein	99.	Putative olfactory receptor 9A1	148.	Speedy protein E3	198.	Zinc finger protein 425
49.	Kielin/chordin-like protein	100.	Putative oncomodulin-2	149.	STAG3-like protein 1	199.	Zinc finger protein 498
50.	Laminin subunit beta-4			150.	STAG3-like protein 2	200.	Zinc finger protein 736
51.	Leliomodrin-2					201.	Zinc finger protein 746

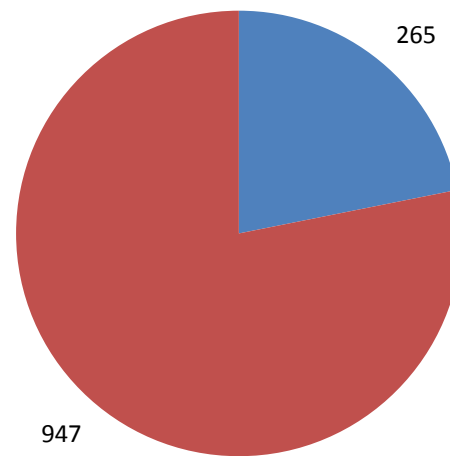


BLAST shows there are 3 duplicated entries (203 missing)

Some protein families have couple of members on the list

1.		protein 6	101.	Putative phosphoserine phosphatase-like protein	151.	STAG3-like protein 3
2.		and death domain-	102.	Putative postmeiotic segregation increased 2-like protein 1	152.	STAT3-interacting protein as a repressor
3.		neuronal protein 3	103.	Putative postmeiotic segregation increased 2-like protein 11	153.	Stimulated by retinoic acid gene 8 protein homolog
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51.	Leiomodin-2				201.	Zinc finger protein 746
					202.	Zinc finger protein 775
					203.	Zinc finger protein 786
					204.	Zinc finger protein 853
					205.	Zona pellucida sperm-binding protein 3
					206.	Zonahesin

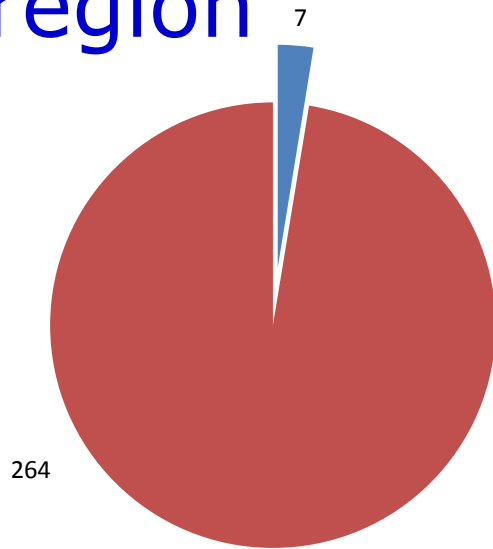
265 (28%) of *Homo sapiens* Chr7 proteins contain trans-membrane domains



Predicted using TMHMM  
(<http://www.cbs.dtu.dk/services/TMHMM-2.0>, a Hidden Markov Model topology prediction algorithm)



Of those 265, only 7 (2.6%) are predicted to contain a GPI-anchor region

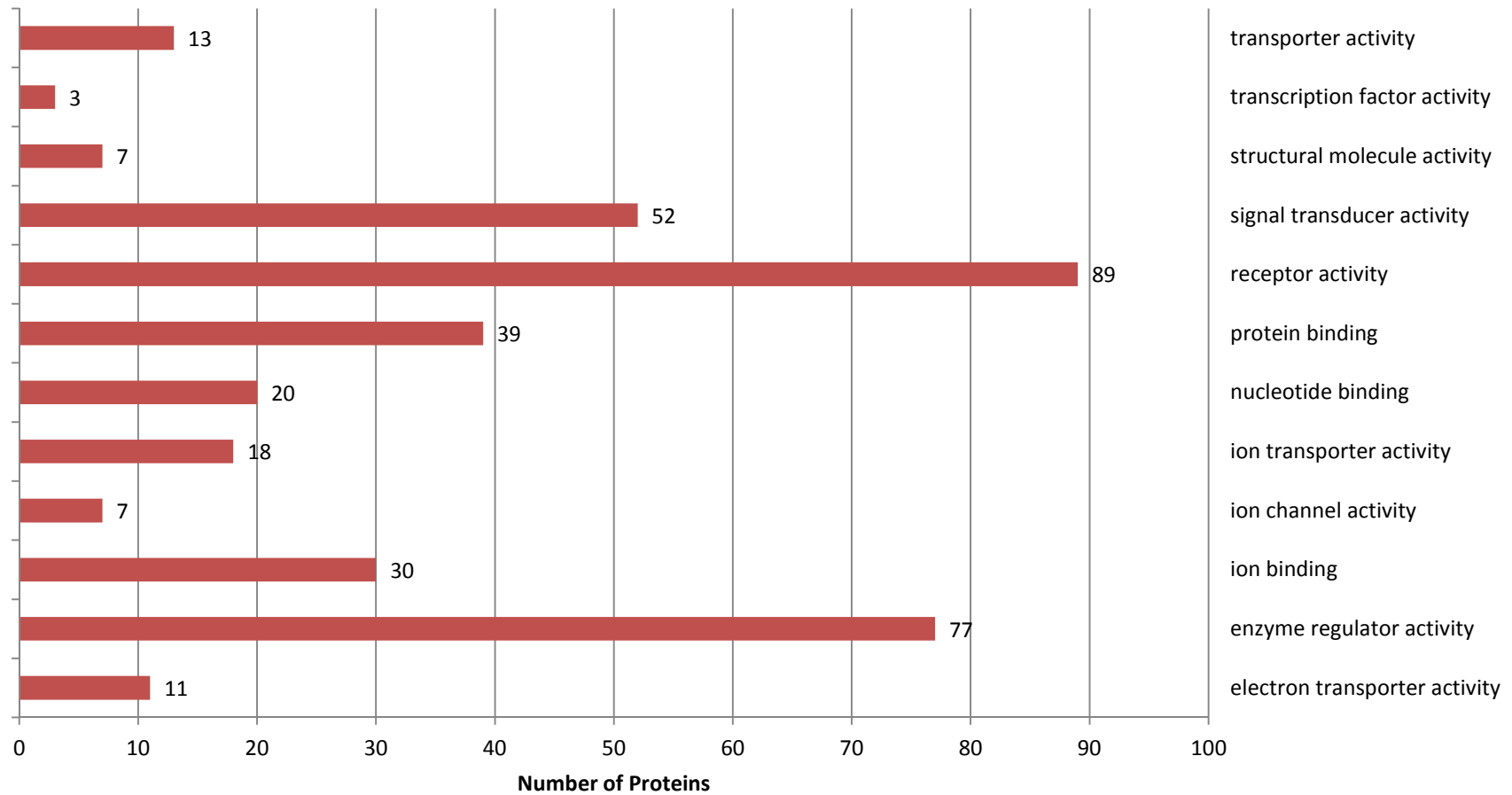


- STX1A\_HUMAN Syntaxin-1A
- FIS1\_HUMAN Mitochondrial fission 1 protein
- T2R41\_HUMAN Taste receptor type 2 member 41
- TMUB1\_HUMAN Transmembrane and ubiquitin-like domain-containing protein
- MSPD3\_HUMAN Motile sperm domain-containing protein 3
- HYALP\_HUMAN Hyaluronidase PH-20
- VTM2A\_HUMAN V-set and transmembrane domain-containing protein 2A

Predicted using FragAnchor  
(a combined neural network and Hidden Markov Model algorithm)

Chr7 transmembrane domain containing proteins categorised by GO (EBI) and assigned molecular function, biological process and cellular component  
*[Some proteins have multiple assignments to each class]*

### Molecular Function



Low scoring categories have been excluded

## Chr7 - ANZ Lab Colorectal Cancer Cell Line Study

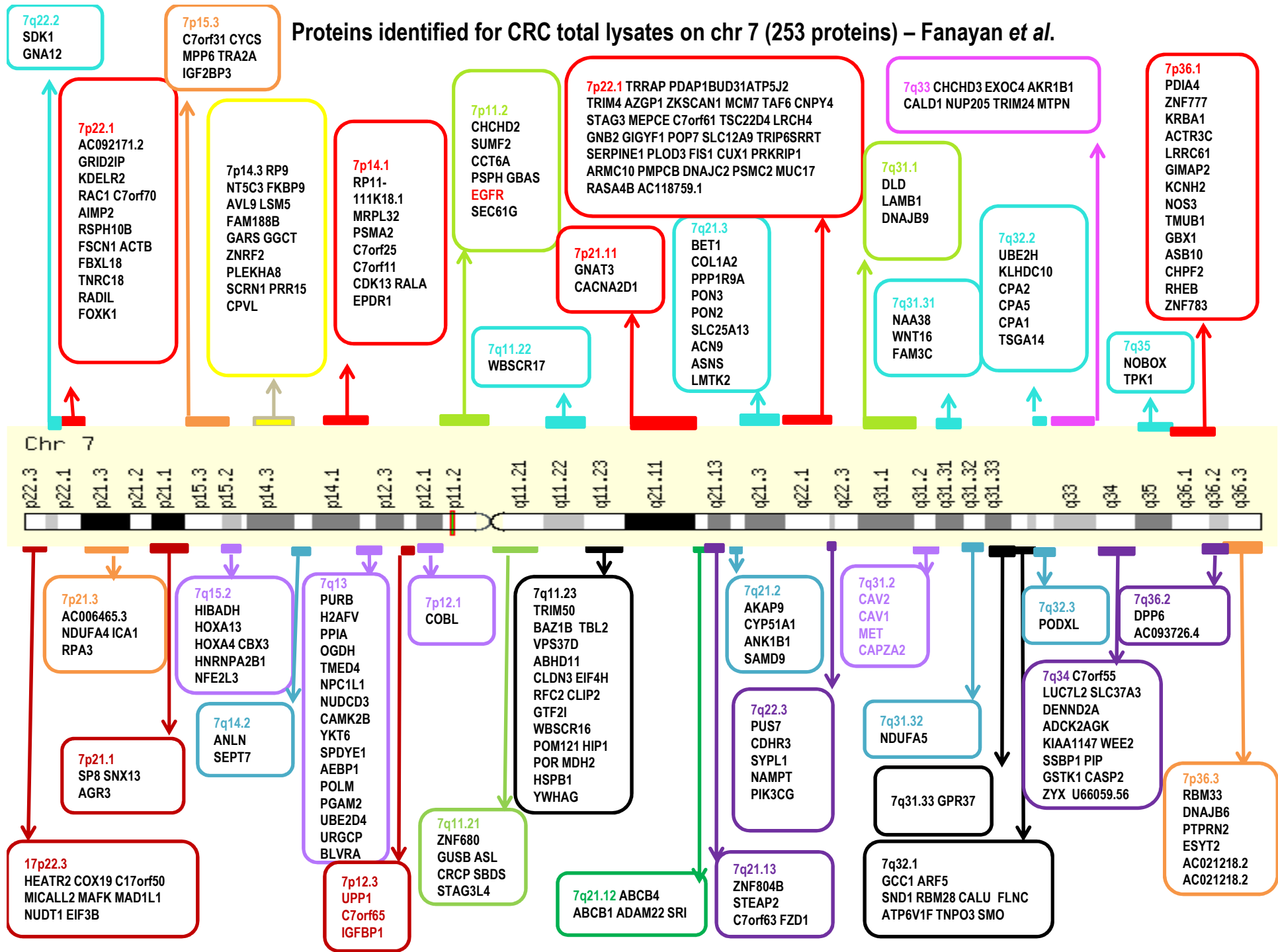
Sample	Sample Prep	Mass Spec.	No. of Chr. 7 Proteins Identified
4 CRC Cell Lines ( <b>Total Lysate</b> ) <b>Susan Fanayan/Bill Hancock</b>	Slice and Dice	LTQ-Thermo	253
24 CRC Cell Lines ( <b>Secretome, Exosome, Total &amp; Membrane Prep</b> ) <b>Rob Goode/Richard Simpson</b>	Slice and Dice	LTQ-Orbi	210
SW480 & SW480 $\beta$ 6 OE ( <b>Membrane Prep</b> ) <b>Mark Baker</b>	IPG-IEF	LTQ-Thermo	135
HCT116(WT) & HCT116 (UPAR antisense), ( <b>Membrane Prep</b> ) <b>Mark Baker</b>	IPG-IEF	LTQ-Thermo	95

Number of identified proteins on chromosome 7 = **948** (<http://www.uniprot.org>)

Total number of Chromosome 7 proteins from our merged non-redundant database = **374**

**~ 574 proteins yet to be observed experimentally**

Proteins identified for CRC total lysates on chr 7 (253 proteins) – Fanayan et al.



# Australian & New Zealand Human Proteome Project

## ARC Human Proteome Centre of Excellence

### Theme 1

#### Human Chromosome 7 Proteome Strand

*To map Chr 7 proteins translated from the human genome & catalogue and/or produce proteomic (i.e., MRM- or antibody-based) assays to all human Chr 7 translated proteins*

### Theme 2

#### Human Epithelial Biology Proteome Mapping Strand

*To map the cellular, phospho-, glyco- and membrane proteomes of healthy normal human epithelia*

### Theme 3

#### Proteomic Technologies Development Strand

*MRMs  
Quantitative Proteomics  
Membrane Proteomics  
Sample Preparation  
PTMs*

*To produce innovative, novel, commercialisable technologies that will advance our depth of understanding of the human proteome in health & disease*

## ANDS/NECTAR HPP e-Research

### Theme 4 [International e-Research Integration]

*Nodes to be hosted at Macquarie University (NSW) & Monash University (Melbourne)*

*[See Expanded Organisational Structure]*

# International e-Research Integration

*(ANDS/NECTAR HPP e-Research Laboratory)*

*Aim: To provide e-research support for all aspects of Australia and New Zealand's contribution to the Chromosomal and Biology/Disease Arms of the Human Proteome Project*

## Universities/Institutes A,B & C

### *Existing Infrastructure/Personnel*

*APAF NCRIS Facility  
NCRIS/EIF Bioinformatics Support  
MQ Professor of Proteomics  
MQ Professor of Bioinformatics  
APAF Bioinformaticians*

### **NECTAR VIRTUAL Lab**

*(to be requested)*

e-Research NECTAR Virtual Lab Manager  
E-research Coordinator  
NextProt Programmer  
Senior Mass Spectrometry Data Analyst

## Universities/Institute A,B & C

### *Existing Infrastructure/Personnel*

*MATF NCRIS Facility  
EIF Bioinformatics Support  
MATF Director  
DVC(Research Infrastructure)*

### **NECTAR VIRTUAL Lab**

*(to be requested)*

Human Protein Atlas Coordinator  
Antibody Expression Data Analyst