Producing a database of protein expression changes in human Alzheimer's Disease

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1824
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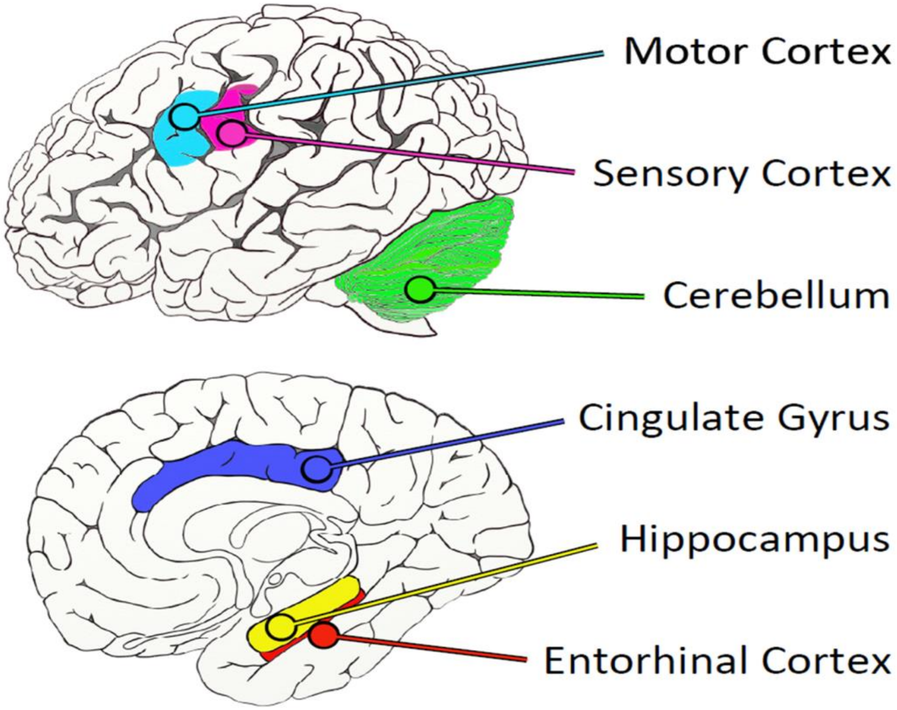
Alzheimer’s Disease

- Aim: To perform a proteomic, metabolomic and metallomic analysis of human brain tissue from patient with AD and age-matched healthy controls.
- Collaboration with Jingshu Xu and Richard Faull (Auckland).
- Analyse SIX distinct tissue regions in Alzheimer's:



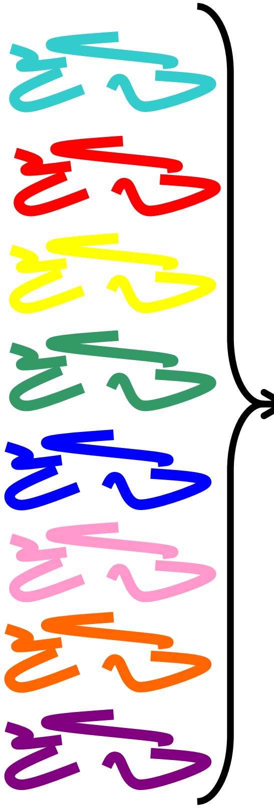
MCx
SCx
Relatively Unaffected

CB
Spared

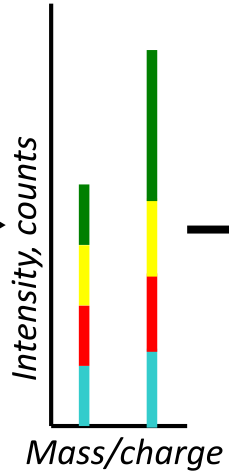
CG
HP
ENT
Heavily Affected

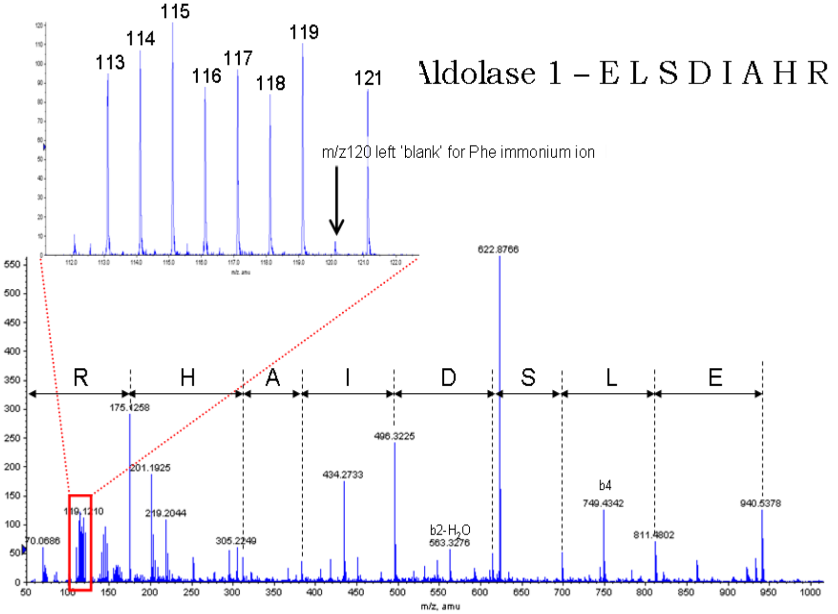
iTRAQ for relative quantification

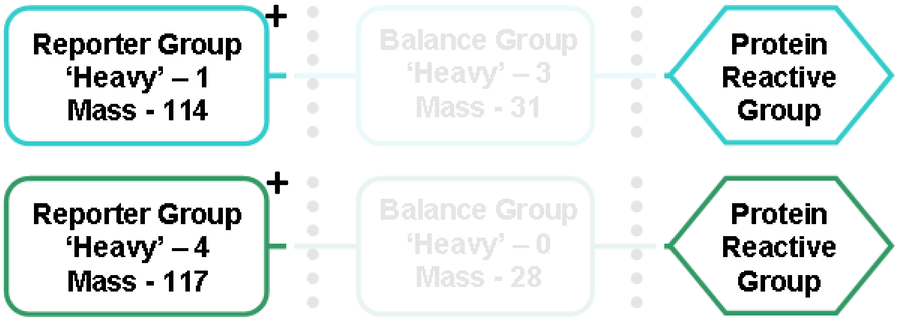
- isobaric Tags for Relative and Absolute Quantification (c.f. TMT 10-plex)
- Used for comparing 8 samples simultaneously



Mix and analyse by LC-MS/MS







BayesProt

- To overcome difficulties merging ratiometric data from individual 8-plexes, we have developed a Bayesian framework for combining data from multiple 8plexes and samples into a single statistical model:

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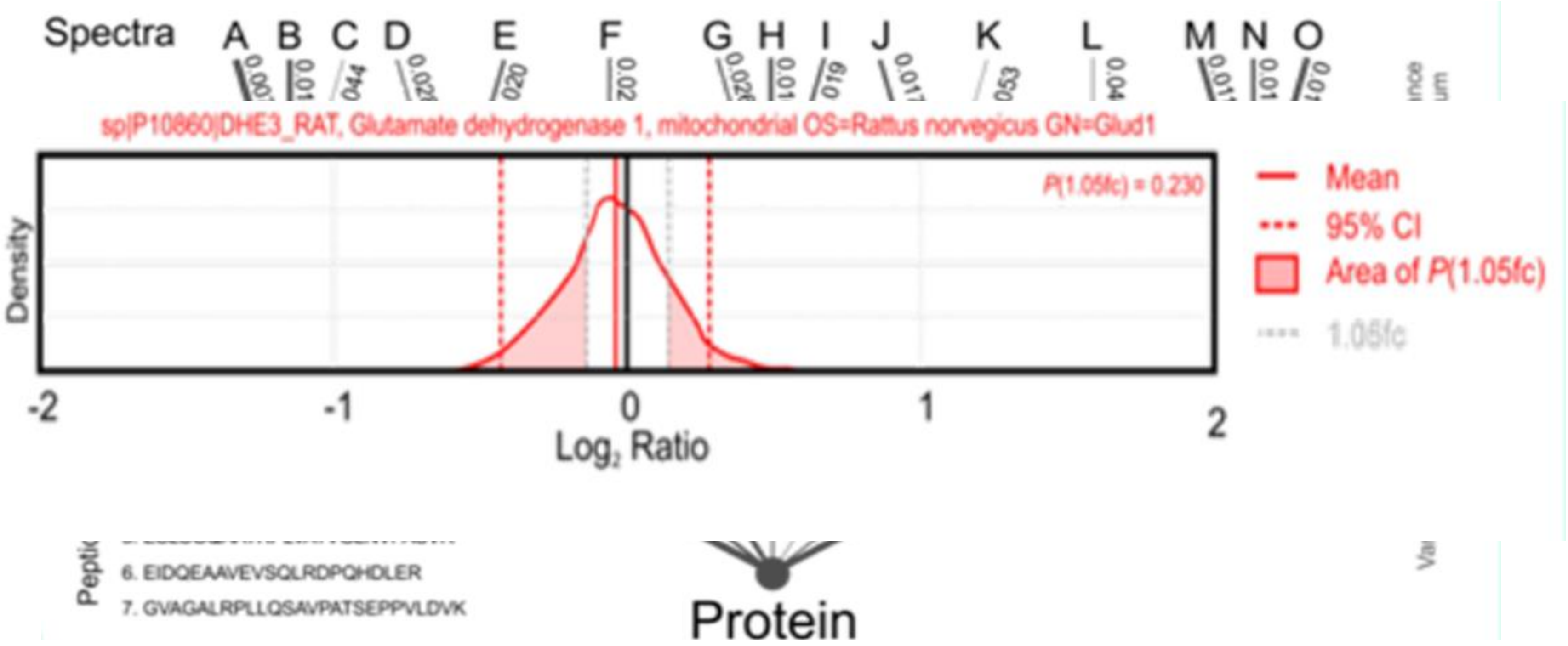
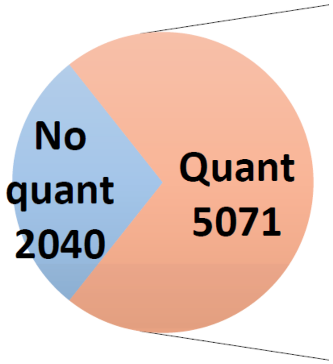
- Collaboration with Prof Andrew Dowsey, University of Bristol.



Data summary

Region	#Proteins quantified	#Proteins quantified spectra>3
Hippocampus	4444	3548
Motor Cortex	2992	2188
Sensory Cortex	4362	3412
Cerebellum	5279	4198
Entorhinal Cortex	4641	3241
Cingulate Gyrus	3900	2722

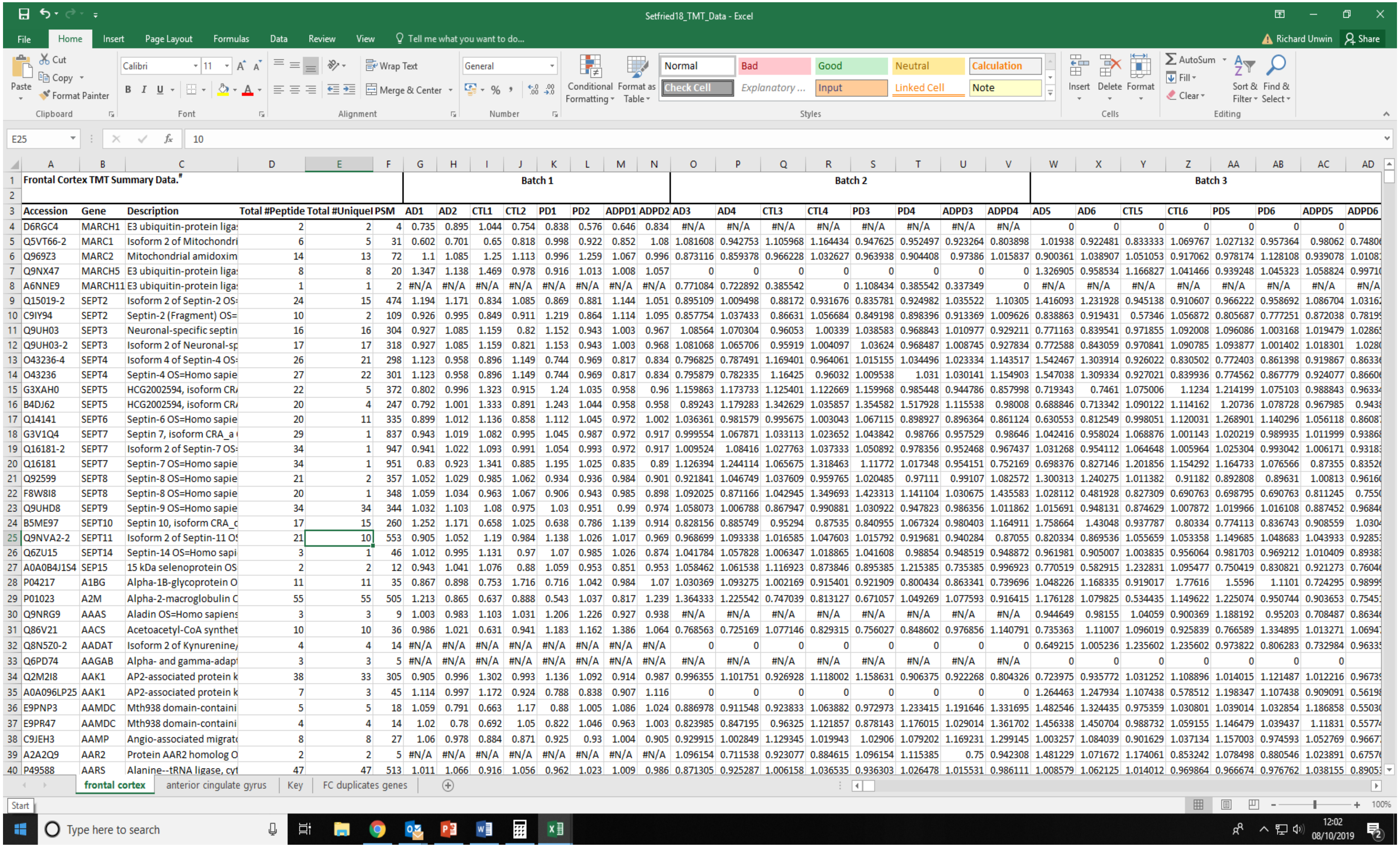
>25,000 datapoints



Data sharing

- This study provides a large amount of data that is useful to may groups. It needs to be freely available, not least because:
  - There’s no way we can follow up all of the leads
  - It provides extra information for researchers studying specific disease aspects.
  - Might help garner extra citations.
  - The funders would like to see it used.
  - Journal will expect all data to be shared.
  - We spend 3+ years gathering it – WE’d like to see it used.

The ‘usual’ way



	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	AD
1	**Frontal Cortex TMT Summary Data.#**						**Batch 1**								**Batch 2**								**Batch 3**							
2																														
3	**Accession**	**Gene**	**Description**	**Total #Peptide**	**Total #UniqueI**	**PSM**	**AD1**	**AD2**	**CTL1**	**CTL2**	**PD1**	**PD2**	**ADPD1**	**ADPD2**	**AD3**	**AD4**	**CTL3**	**CTL4**	**PD3**	**PD4**	**ADPD3**	**ADPD4**	**AD5**	**AD6**	**CTL5**	**CTL6**	**PD5**	**PD6**	**ADPD5**	**ADPD6**
4	D6RGC4	MARCH1	E3 ubiquitin-protein liga	2	2	4	0.735	0.895	1.044	0.754	0.838	0.576	0.646	0.834	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	0	0	0	0	0	0	0	
5	Q5VT66-2	MARC1	Isoform 2 of Mitochondri	6	5	31	0.602	0.701	0.65	0.818	0.998	0.922	0.852	1.08	1.081608	0.942753	1.105968	1.164434	0.947625	0.952497	0.923264	0.803898	1.01938	0.922481	0.833333	1.069767	1.027132	0.957364	0.98062	0.7480
6	Q969Z3	MARC2	Mitochondrial amidoxim	14	13	72	1.1	1.085	1.25	1.113	0.996	1.259	1.067	0.996	0.873116	0.859378	0.966228	1.032627	0.963938	0.904408	0.97386	1.015837	0.900361	1.038907	1.051053	0.917062	0.978174	1.128108	0.939078	1.0108
7	Q9NX47	MARCH5	E3 ubiquitin-protein liga	8	8	20	1.347	1.138	1.469	0.978	0.916	1.013	1.008	1.057	0	0	0	0	0	0	0	0	1.326905	0.958534	1.166827	1.041466	0.939248	1.045323	1.058824	0.9971
8	A6NNE9	MARCH11	E3 ubiquitin-protein liga	1	1	2	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	0.771084	0.722892	0.385542	0	1.108434	0.385542	0.337349	0	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A
9	Q15019-2	SEPT2	Isoform 2 of Septin-2 OS	24	15	474	1.194	1.171	0.834	1.085	0.869	0.881	1.144	1.051	0.895109	1.009498	0.88172	0.931676	0.835781	0.924982	1.035522	1.10305	1.416093	1.231928	0.945138	0.910607	0.966222	0.958692	1.086704	1.0316
10	C9IY94	SEPT2	Septin-2 (Fragment) OS=	10	2	109	0.926	0.995	0.849	0.911	1.219	0.864	1.114	1.095	0.857754	1.037433	0.86631	1.056684	0.849198	0.898396	0.913369	1.009626	0.838863	0.919431	0.57346	1.056872	0.805687	0.777251	0.872038	0.7819
11	Q9UH03	SEPT3	Neuronal-specific septin	16	16	304	0.927	1.085	1.159	0.82	1.152	0.943	1.003	0.967	1.08564	1.070304	0.96053	1.00339	1.038583	0.968843	1.010977	0.929211	0.771163	0.839541	0.971855	1.092008	1.096086	1.003168	1.019479	1.0286
12	Q9UH03-2	SEPT3	Isoform 2 of Neuronal-sp	17	17	318	0.927	1.085	1.159	0.821	1.153	0.943	1.003	0.968	1.081068	1.065706	0.95919	1.004097	1.03624	0.968487	1.008745	0.927834	0.772588	0.843059	0.970841	1.090785	1.093877	1.001402	1.018301	1.028
13	O43236-4	SEPT4	Isoform 4 of Septin-4 OS	26	21	298	1.123	0.958	0.896	1.149	0.744	0.969	0.817	0.834	0.796825	0.787491	1.169401	0.964061	1.015155	1.034496	1.023334	1.143517	1.542467	1.303914	0.926022	0.830502	0.772403	0.861398	0.919867	0.8633
14	O43236	SEPT4	Septin-4 OS=Homo sapie	27	22	301	1.123	0.958	0.896	1.149	0.744	0.969	0.817	0.834	0.795879	0.782335	1.16425	0.96032	1.009538	1.031	1.030141	1.154903	1.547038	1.309334	0.927021	0.839936	0.774562	0.867779	0.924077	0.8660
15	G3XAH0	SEPT5	HCG2002594, isoform CR	22	5	372	0.802	0.996	1.323	0.915	1.24	1.035	0.958	0.96	1.159863	1.173733	1.125401	1.122669	1.159968	0.985448	0.944786	0.857998	0.719343	0.7461	1.075006	1.1234	1.214199	1.075103	0.988843	0.9633
16	B4DJ62	SEPT5	HCG2002594, isoform CR	20	4	247	0.792	1.001	1.333	0.891	1.243	1.044	0.958	0.958	0.89243	1.179283	1.342629	1.035857	1.354582	1.517928	1.115538	0.98008	0.688846	0.713342	1.090122	1.114162	1.20736	1.078728	0.967985	0.943
17	Q14141	SEPT6	Septin-6 OS=Homo sapie	20	11	335	0.899	1.012	1.136	0.858	1.112	1.045	0.972	1.002	1.036361	0.981579	0.995675	1.003043	1.067115	0.898927	0.896364	0.861124	0.630553	0.812549	0.998051	1.120031	1.268901	1.140296	1.056118	0.8608
18	G3V1Q4	SEPT7	Septin 7, isoform CRA_a	29	1	837	0.943	1.019	1.082	0.995	1.045	0.987	0.972	0.917	0.999554	1.067871	1.033113	1.023652	1.043842	0.98766	0.957529	0.98646	1.042416	0.958024	1.068876	1.001143	1.020219	0.989935	1.011999	0.9386
19	Q16181-2	SEPT7	Isoform 2 of Septin-7 OS	34	1	947	0.941	1.022	1.093	0.991	1.054	0.993	0.972	0.917	1.009524	1.08416	1.027763	1.037333	1.050892	0.978356	0.952468	0.967437	1.031268	0.954112	1.064648	1.005964	1.025304	0.993042	1.006171	0.9318
20	Q16181	SEPT7	Septin-7 OS=Homo sapie	34	1	951	0.83	0.923	1.341	0.885	1.195	1.025	0.835	0.89	1.126394	1.244114	1.065675	1.318463	1.11772	1.017348	0.954151	0.752169	0.698376	0.827146	1.201856	1.154292	1.164733	1.076566	0.87355	0.8352
21	Q92599	SEPT8	Septin-8 OS=Homo sapie	21	2	357	1.052	1.029	0.985	1.062	0.934	0.936	0.984	0.901	0.921841	1.046749	1.037609	0.959765	1.020485	0.97111	0.99107	1.082572	1.300313	1.240275	1.011382	0.91182	0.892808	0.89631	1.00813	0.9616
22	F8W8I8	SEPT8	Septin-8 OS=Homo sapie	20	1	348	1.059	1.034	0.963	1.067	0.906	0.943	0.985	0.898	1.092025	0.871166	1.042945	1.349693	1.423313	1.141104	1.030675	1.435583	1.028112	0.481928	0.827309	0.690763	0.698795	0.690763	0.811245	0.755
23	Q9UHD8	SEPT9	Septin-9 OS=Homo sapie	34	34	344	1.032	1.103	1.08	0.975	1.03	0.951	0.99	0.974	1.058073	1.006788	0.867947	0.990881	1.030922	0.947823	0.986356	1.011862	1.015691	0.948131	0.874629	1.007872	1.019966	1.016108	0.887452	0.9684
24	B5ME97	SEPT10	Septin 10, isoform CRA_c	17	15	260	1.252	1.171	0.658	1.025	0.638	0.786	1.139	0.914	0.828156	0.885749	0.95294	0.87535	0.840955	1.067324	0.980403	1.164911	1.758664	1.43048	0.937787	0.80334	0.774113	0.836743	0.908559	1.030
25	Q9NVA2-2	SEPT11	Isoform 2 of Septin-11 O	21	10	553	0.905	1.052	1.19	0.984	1.138	1.026	1.017	0.969	0.968699	1.093338	1.016585	1.047603	1.015792	0.919681	0.940284	0.87055	0.820334	0.869536	1.055659	1.053358	1.149685	1.048683	1.043933	0.9285
26	Q6ZU15	SEPT14	Septin-14 OS=Homo sapi	3	1	46	1.012	0.995	1.131	0.97	1.07	0.985	1.026	0.874	1.041784	1.057828	1.006347	1.018865	1.041608	0.98854	0.948519	0.948872	0.961981	0.905007	1.003835	0.956064	0.981703	0.969212	1.010409	0.8938
27	A0A0B4J1S4	SEP15	15 kDa selenoprotein OS	2	2	12	0.943	1.041	1.076	0.88	1.059	0.953	0.851	0.953	1.058462	1.061538	1.116923	0.873846	0.895385	1.215385	0.735385	0.996923	0.770519	0.582915	1.232831	1.095477	0.750419	0.830821	0.921273	0.7604
28	P04217	A1BG	Alpha-1B-glycoprotein O	11	11	35	0.867	0.898	0.753	1.716	0.716	1.042	0.984	1.07	1.030369	1.093275	1.002169	0.915401	0.921909	0.800434	0.863341	0.739696	1.048226	1.168335	0.919017	1.77616	1.5596	1.1101	0.724295	0.9899
29	P01023	A2M	Alpha-2-macroglobulin C	55	55	505	1.213	0.865	0.637	0.888	0.543	1.037	0.817	1.239	1.364333	1.225542	0.747039	0.813127	0.671057	1.049269	1.077593	0.916415	1.176128	1.079825	0.534435	1.149622	1.225074	0.950744	0.903653	0.7545
30	Q9NRG9	AAAS	Aladin OS=Homo sapiens	3	3	9	1.003	0.983	1.103	1.031	1.206	1.226	0.927	0.938	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	0.944649	0.98155	1.04059	0.900369	1.188192	0.95203	0.708487	0.8634
31	Q86V21	AACS	Acetoacetyl-CoA synthet	10	10	36	0.986	1.021	0.631	0.941	1.183	1.162	1.386	1.064	0.768563	0.725169	1.077146	0.829315	0.756027	0.848602	0.976856	1.140791	0.735363	1.11007	1.096019	0.925839	0.766589	1.334895	1.013271	1.0694
32	Q8N5Z0-2	AADAT	Isoform 2 of Kynurenine/	4	4	14	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	0	0	0	0	0	0	0	0	0.649215	1.005236	1.235602	1.235602	0.973822	0.806283	0.732984	0.9633
33	Q6PD74	AAGAB	Alpha- and gamma-adapt	3	3	5	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	0	0	0	0	0	0	0	
34	Q2M2I8	AAK1	AP2-associated protein k	38	33	305	0.905	0.996	1.302	0.993	1.136	1.092	0.914	0.987	0.996355	1.101751	0.926928	1.118002	1.158631	0.906375	0.922268	0.804326	0.723975	0.935772	1.031252	1.108896	1.014015	1.121487	1.012216	0.9673
35	A0A096LP25	AAK1	AP2-associated protein k	7	3	45	1.114	0.997	1.172	0.924	0.788	0.838	0.907	1.116	0	0	0	0	0	0	0	0	1.264463	1.247934	1.107438	0.578512	1.198347	1.107438	0.909091	0.5619
36	E9PNP3	AAMDC	Mth938 domain-containi	5	5	18	1.059	0.791	0.663	1.17	0.88	1.005	1.086	1.024	0.886978	0.911548	0.923833	1.063882	0.972973	1.233415	1.191646	1.331695	1.482546	1.324435	0.975359	1.030801	1.039014	1.032854	1.186858	0.5503
37	E9PR47	AAMDC	Mth938 domain-containi	4	4	14	1.02	0.78	0.692	1.05	0.822	1.046	0.963	1.003	0.823985	0.847195	0.96325	1.121857	0.878143	1.176015	1.029014	1.361702	1.456338	1.450704	0.988732	1.059155	1.146479	1.039437	1.11831	0.5577
38	C9JEH3	AAMP	Angio-associated migrat	8	8	27	1.06	0.978	0.884	0.871	0.925	0.93	1.004	0.905	0.929915	1.002849	1.129345	1.019943	1.02906	1.079202	1.169231	1.299145	1.003257	1.084039	0.901629	1.037134	1.157003	0.974593	1.052769	0.9667
39	A2A2Q9	AAR2	Protein AAR2 homolog O	2	2	5	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	1.096154	0.711538	0.923077	0.884615	1.096154	1.115385	0.75	0.942308	1.481229	1.071672	1.174061	0.853242	1.078498	0.880546	1.023891	0.6757
40	P49588	AARS	Alanine--tRNA ligase, cyt	47	47	513	1.011	1.066	0.916	1.056	0.962	1.023	1.009	0.986	0.871305	0.925287	1.006158	1.036535	0.936303	1.026478	1.015531	0.986111	1.008579	1.062125	1.014012	0.969864	0.966674	0.976762	1.038155	0.8905
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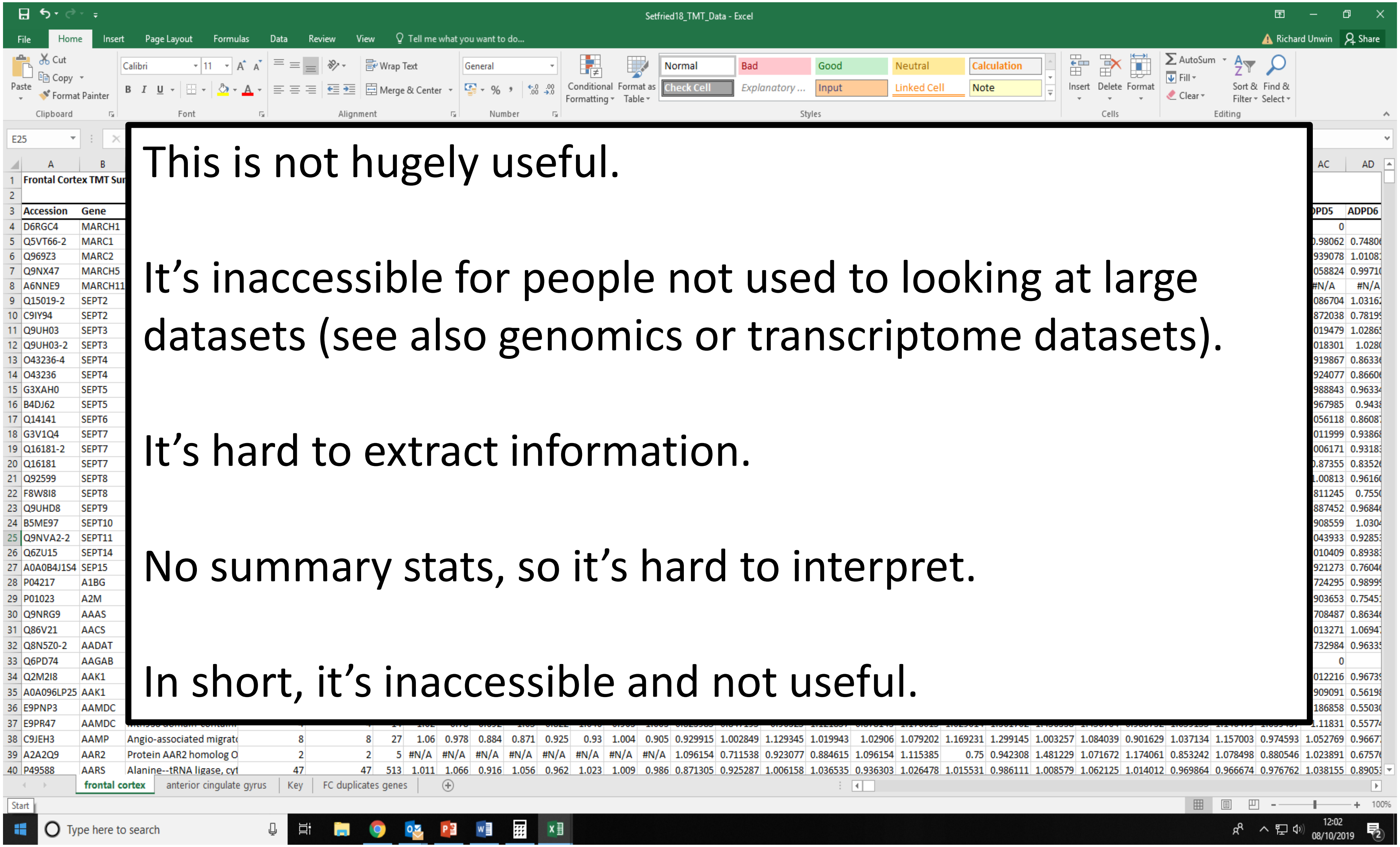
The ‘usual’ way



	A	B
1	**Frontal Cortex TMT Sur**	
2		
3	**Accession**	**Gene**
4	D6RGC4	MARCH1
5	Q5VT66-2	MARC1
6	Q969Z3	MARC2
7	Q9NX47	MARCH5
8	A6NNE9	MARCH11
9	Q15019-2	SEPT2
10	C9IY94	SEPT2
11	Q9UH03	SEPT3
12	Q9UH03-2	SEPT3
13	O43236-4	SEPT4
14	O43236	SEPT4
15	G3XAH0	SEPT5
16	B4DJ62	SEPT5
17	Q14141	SEPT6
18	G3V1Q4	SEPT7
19	Q16181-2	SEPT7
20	Q16181	SEPT7
21	Q92599	SEPT8
22	F8W8I8	SEPT8
23	Q9UHD8	SEPT9
24	B5ME97	SEPT10
25	Q9NVA2-2	SEPT11
26	Q6ZU15	SEPT14
27	A0A0B4J1S4	SEP15
28	P04217	A1BG
29	P01023	A2M
30	Q9NRG9	AAAS
31	Q86V21	AACS
32	Q8N5Z0-2	AADAT
33	Q6PD74	AAGAB
34	Q2M2I8	AAK1
35	A0A096LP25	AAK1
36	E9PNP3	AAMDC
37	E9PR47	AAMDC
38	C9JEH3	AAMP
39	A2A2Q9	AAR2
40	P49588	AARS

38	C9JEH3	AAMP	Angio-associated migrat	8	8	27	1.06	0.978	0.884	0.871	0.925	0.93	1.004	0.905	0.929915	1.002849	1.129345	1.019943	1.02906	1.079202	1.169231	1.299145	1.003257	1.084039	0.901629	1.037134	1.157003	0.974593	1.052769
39	A2A2Q9	AAR2	Protein AAR2 homolog O	2	2	5	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	#N/A	1.096154	0.711538	0.923077	0.884615	1.096154	1.115385	0.75	0.942308	1.481229	1.071672	1.174061	0.853242	1.078498	0.880546	1.023891
40	P49588	AARS	Alanine--tRNA ligase, cyt	47	47	513	1.011	1.066	0.916	1.056	0.962	1.023	1.009	0.986	0.871305	0.925287	1.006158	1.036535	0.936303	1.026478	1.015531	0.986111	1.008579	1.062125	1.014012	0.969864	0.966674	0.976762	1.038155

This is not hugely useful.

It’s inaccessible for people not used to looking at large datasets (see also genomics or transcriptome datasets).

It’s hard to extract information.

No summary stats, so it’s hard to interpret.

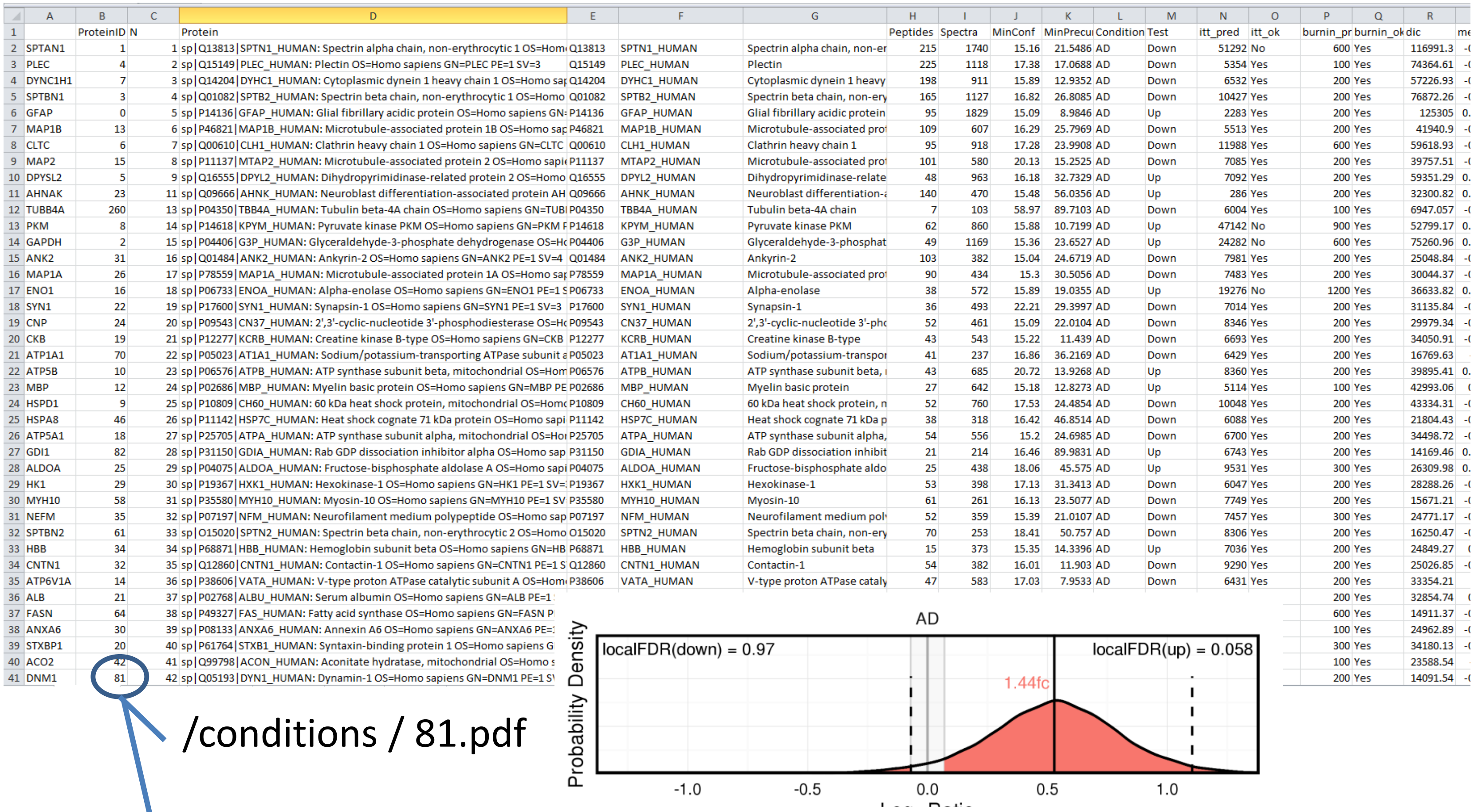
In short, it’s inaccessible and not useful.

Research IT brief

Build a way to make this more accessible.

- Web accessible via a unique UoM URL.
- Searchable, so that researchers can easily find proteins of interest.
- Provide an immediate and easily interpretable result.
- Provide the ability to ‘delve deeper’ into a result to see the underlying data.

Research IT – Our data



	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	
1		ProteinID	N	Protein				Peptides	Spectra	MinConf	MinPrecu	Condition	Test	itt_pred	itt_ok	burnin_pr	burnin_ok	dic	me
2	SPTAN1	1	1	sp|Q13813|SPTN1_HUMAN: Spectrin alpha chain, non-erythrocytic 1 OS=Hom	Q13813	SPTN1_HUMAN	Spectrin alpha chain, non-er	215	1740	15.16	21.5486	AD	Down	51292	No	600	Yes	116991.3	-
3	PLEC	4	2	sp|Q15149|PLEC_HUMAN: Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3	Q15149	PLEC_HUMAN	Plectin	225	1118	17.38	17.0688	AD	Down	5354	Yes	100	Yes	74364.61	-
4	DYNC1H1	7	3	sp|Q14204|DYHC1_HUMAN: Cytoplasmic dynein 1 heavy chain 1 OS=Homo sa	Q14204	DYHC1_HUMAN	Cytoplasmic dynein 1 heavy	198	911	15.89	12.9352	AD	Down	6532	Yes	200	Yes	57226.93	-
5	SPTBN1	3	4	sp|Q01082|SPTB2_HUMAN: Spectrin beta chain, non-erythrocytic 1 OS=Homo	Q01082	SPTB2_HUMAN	Spectrin beta chain, non-ery	165	1127	16.82	26.8085	AD	Down	10427	Yes	200	Yes	76872.26	-
6	GFAP	0	5	sp|P14136|GFAP_HUMAN: Glial fibrillary acidic protein OS=Homo sapiens GN	P14136	GFAP_HUMAN	Glial fibrillary acidic protein	95	1829	15.09	8.9846	AD	Up	2283	Yes	200	Yes	125305	0.
7	MAP1B	13	6	sp|P46821|MAP1B_HUMAN: Microtubule-associated protein 1B OS=Homo sa	P46821	MAP1B_HUMAN	Microtubule-associated pro	109	607	16.29	25.7969	AD	Down	5513	Yes	200	Yes	41940.9	-
8	CLTC	6	7	sp|Q00610|CLH1_HUMAN: Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC	Q00610	CLH1_HUMAN	Clathrin heavy chain 1	95	918	17.28	23.9908	AD	Down	11988	Yes	600	Yes	59618.93	-
9	MAP2	15	8	sp|P11137|MTAP2_HUMAN: Microtubule-associated protein 2 OS=Homo sapi	P11137	MTAP2_HUMAN	Microtubule-associated pro	101	580	20.13	15.2525	AD	Down	7085	Yes	200	Yes	39757.51	-
10	DPYSL2	5	9	sp|Q16555|DPYL2_HUMAN: Dihydropyrimidinase-related protein 2 OS=Homo	Q16555	DPYL2_HUMAN	Dihydropyrimidinase-relate	48	963	16.18	32.7329	AD	Up	7092	Yes	200	Yes	59351.29	0.
11	AHNAK	23	11	sp|Q09666|AHNK_HUMAN: Neuroblast differentiation-associated protein AH	Q09666	AHNK_HUMAN	Neuroblast differentiation-	140	470	15.48	56.0356	AD	Up	286	Yes	200	Yes	32300.82	0.
12	TUBB4A	260	13	sp|P04350|TBB4A_HUMAN: Tubulin beta-4A chain OS=Homo sapiens GN=TUB	P04350	TBB4A_HUMAN	Tubulin beta-4A chain	7	103	58.97	89.7103	AD	Down	6004	Yes	100	Yes	6947.057	-
13	PKM	8	14	sp|P14618|KPYM_HUMAN: Pyruvate kinase PKM OS=Homo sapiens GN=PKM	P14618	KPYM_HUMAN	Pyruvate kinase PKM	62	860	15.88	10.7199	AD	Up	47142	No	900	Yes	52799.17	0.
14	GAPDH	2	15	sp|P04406|G3P_HUMAN: Glyceraldehyde-3-phosphate dehydrogenase OS=H	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphat	49	1169	15.36	23.6527	AD	Up	24282	No	600	Yes	75260.96	0.
15	ANK2	31	16	sp|Q01484|ANK2_HUMAN: Ankyrin-2 OS=Homo sapiens GN=ANK2 PE=1 SV=4	Q01484	ANK2_HUMAN	Ankyrin-2	103	382	15.04	24.6719	AD	Down	7981	Yes	200	Yes	25048.84	-
16	MAP1A	26	17	sp|P78559|MAP1A_HUMAN: Microtubule-associated protein 1A OS=Homo sa	P78559	MAP1A_HUMAN	Microtubule-associated pro	90	434	15.3	30.5056	AD	Down	7483	Yes	200	Yes	30044.37	-
17	ENO1	16	18	sp|P06733|ENOA_HUMAN: Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1	P06733	ENOA_HUMAN	Alpha-enolase	38	572	15.89	19.0355	AD	Up	19276	No	1200	Yes	36633.82	0.
18	SYN1	22	19	sp|P17600|SYN1_HUMAN: Synapsin-1 OS=Homo sapiens GN=SYN1 PE=1 SV=3	P17600	SYN1_HUMAN	Synapsin-1	36	493	22.21	29.3997	AD	Down	7014	Yes	200	Yes	31135.84	-
19	CNP	24	20	sp|P09543|CN37_HUMAN: 2',3'-cyclic-nucleotide 3'-phosphodiesterase OS=H	P09543	CN37_HUMAN	2',3'-cyclic-nucleotide 3'-ph	52	461	15.09	22.0104	AD	Down	8346	Yes	200	Yes	29979.34	-
20	CKB	19	21	sp|P12277|KCRB_HUMAN: Creatine kinase B-type OS=Homo sapiens GN=CKB	P12277	KCRB_HUMAN	Creatine kinase B-type	43	543	15.22	11.439	AD	Down	6693	Yes	200	Yes	34050.91	-
21	ATP1A1	70	22	sp|P05023|AT1A1_HUMAN: Sodium/potassium-transporting ATPase subunit	P05023	AT1A1_HUMAN	Sodium/potassium-transpo	41	237	16.86	36.2169	AD	Down	6429	Yes	200	Yes	16769.63	-
22	ATP5B	10	23	sp|P06576|ATPB_HUMAN: ATP synthase subunit beta, mitochondrial OS=Hom	P06576	ATPB_HUMAN	ATP synthase subunit beta,	43	685	20.72	13.9268	AD	Up	8360	Yes	200	Yes	39895.41	0.
23	MBP	12	24	sp|P02686|MBP_HUMAN: Myelin basic protein OS=Homo sapiens GN=MBP PE	P02686	MBP_HUMAN	Myelin basic protein	27	642	15.18	12.8273	AD	Up	5114	Yes	100	Yes	42993.06	
24	HSPD1	9	25	sp|P10809|CH60_HUMAN: 60 kDa heat shock protein, mitochondrial OS=Hom	P10809	CH60_HUMAN	60 kDa heat shock protein,	52	760	17.53	24.4854	AD	Down	10048	Yes	200	Yes	43334.31	-
25	HSPA8	46	26	sp|P11142|HSP7C_HUMAN: Heat shock cognate 71 kDa protein OS=Homo sap	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa p	38	318	16.42	46.8514	AD	Down	6088	Yes	200	Yes	21804.43	-
26	ATP5A1	18	27	sp|P25705|ATPA_HUMAN: ATP synthase subunit alpha, mitochondrial OS=Ho	P25705	ATPA_HUMAN	ATP synthase subunit alpha,	54	556	15.2	24.6985	AD	Down	6700	Yes	200	Yes	34498.72	-
27	GDI1	82	28	sp|P31150|GDIA_HUMAN: Rab GDP dissociation inhibitor alpha OS=Homo sap	P31150	GDIA_HUMAN	Rab GDP dissociation inhibit	21	214	16.46	89.9831	AD	Up	6743	Yes	200	Yes	14169.46	0.
28	ALDOA	25	29	sp|P04075|ALDOA_HUMAN: Fructose-bisphosphate aldolase A OS=Homo sapi	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldo	25	438	18.06	45.575	AD	Up	9531	Yes	300	Yes	26309.98	0.
29	HK1	29	30	sp|P19367|HXK1_HUMAN: Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=	P19367	HXK1_HUMAN	Hexokinase-1	53	398	17.13	31.3413	AD	Down	6047	Yes	200	Yes	28288.26	-
30	MYH10	58	31	sp|P35580|MYH10_HUMAN: Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV	P35580	MYH10_HUMAN	Myosin-10	61	261	16.13	23.5077	AD	Down	7749	Yes	200	Yes	15671.21	-
31	NEFM	35	32	sp|P07197|NFM_HUMAN: Neurofilament medium polypeptide OS=Homo sap	P07197	NFM_HUMAN	Neurofilament medium pol	52	359	15.39	21.0107	AD	Down	7457	Yes	300	Yes	24771.17	-
32	SPTBN2	61	33	sp|O15020|SPTN2_HUMAN: Spectrin beta chain, non-erythrocytic 2 OS=Homo	O15020	SPTN2_HUMAN	Spectrin beta chain, non-ery	70	253	18.41	50.757	AD	Down	8306	Yes	200	Yes	16250.47	-
33	HBB	34	34	sp|P68871|HBB_HUMAN: Hemoglobin subunit beta OS=Homo sapiens GN=HB	P68871	HBB_HUMAN	Hemoglobin subunit beta	15	373	15.35	14.3396	AD	Up	7036	Yes	200	Yes	24849.27	
34	CNTN1	32	35	sp|Q12860|CNTN1_HUMAN: Contactin-1 OS=Homo sapiens GN=CNTN1 PE=1 S	Q12860	CNTN1_HUMAN	Contactin-1	54	382	16.01	11.903	AD	Down	9290	Yes	200	Yes	25026.85	-
35	ATP6V1A	14	36	sp|P38606|VATA_HUMAN: V-type proton ATPase catalytic subunit A OS=Hom	P38606	VATA_HUMAN	V-type proton ATPase cataly	47	583	17.03	7.9533	AD	Down	6431	Yes	200	Yes	33354.21	
36	ALB	21	37	sp|P02768|ALBU_HUMAN: Serum albumin OS=Homo sapiens GN=ALB PE=1												200	Yes	32854.74	
37	FASN	64	38	sp|P49327|FAS_HUMAN: Fatty acid synthase OS=Homo sapiens GN=FASN P												600	Yes	14911.37	-
38	ANXA6	30	39	sp|P08133|ANXA6_HUMAN: Annexin A6 OS=Homo sapiens GN=ANXA6 PE=												100	Yes	24962.89	-
39	STXBP1	20	40	sp|P61764|STXB1_HUMAN: Syntaxin-binding protein 1 OS=Homo sapiens G												300	Yes	34180.13	-
40	ACO2	42	41	sp|Q99798|ACON_HUMAN: Aconitate hydratase, mitochondrial OS=Homo s												100	Yes	23588.54	-
41	DNM1	81	42	sp|Q05193|DYN1_HUMAN: Dynamin-1 OS=Homo sapiens GN=DNM1 PE=1 S												200	Yes	14091.54	-

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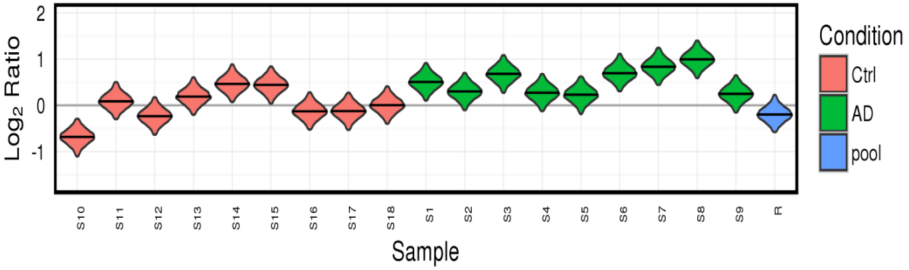

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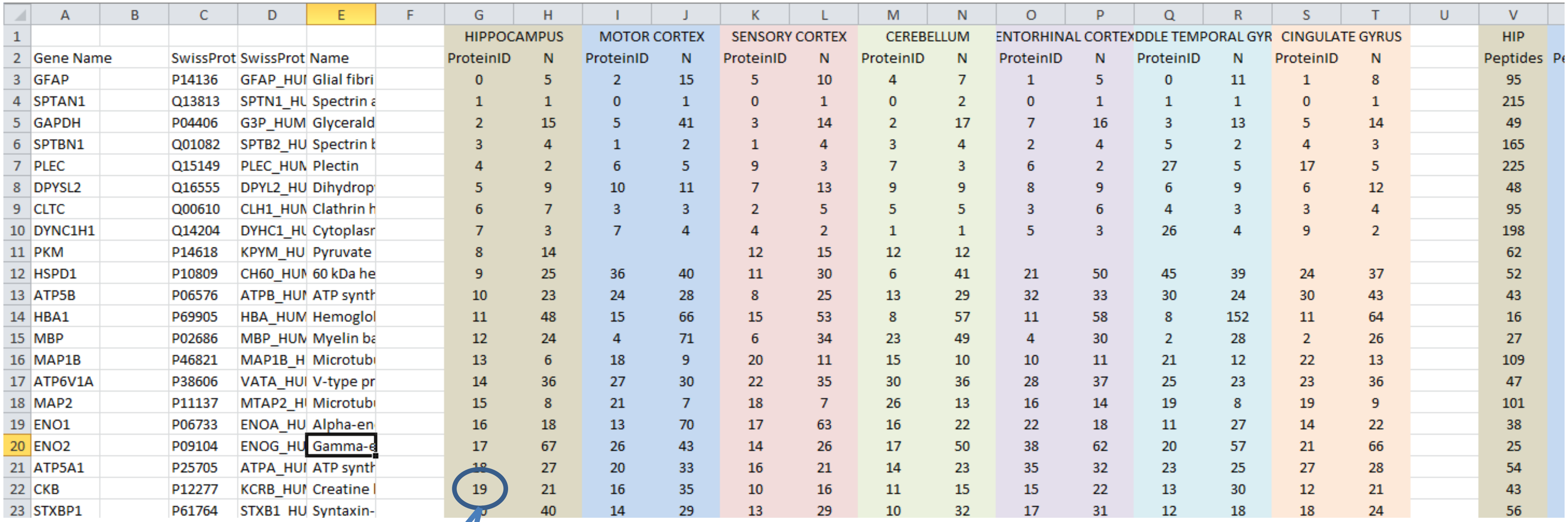
Research IT – Our data Take 2



	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	
1							HIPPOCAMPUS		MOTOR CORTEX		SENSORY CORTEX		CEREBELLUM		ENTORHINAL CORTEX		DDLE TEMPORAL GYR		CINGULATE GYRUS			HIP	
2	Gene Name		SwissProt	SwissProt	Name		ProteinID	N	ProteinID	N	ProteinID	N	ProteinID	N	ProteinID	N	ProteinID	N	ProteinID	N		Peptides	Pe
3	GFAP		P14136	GFAP_HUI	Glial fibri		0	5	2	15	5	10	4	7	1	5	0	11	1	8		95	
4	SPTAN1		Q13813	SPTN1_HU	Spectrin a		1	1	0	1	0	1	0	2	0	1	1	1	0	1		215	
5	GAPDH		P04406	G3P_HUM	Glycerald		2	15	5	41	3	14	2	17	7	16	3	13	5	14		49	
6	SPTBN1		Q01082	SPTB2_HU	Spectrin b		3	4	1	2	1	4	3	4	2	4	5	2	4	3		165	
7	PLEC		Q15149	PLEC_HUN	Plectin		4	2	6	5	9	3	7	3	6	2	27	5	17	5		225	
8	DPYSL2		Q16555	DPYL2_HU	Dihydrop		5	9	10	11	7	13	9	9	8	9	6	9	6	12		48	
9	CLTC		Q00610	CLH1_HUN	Clathrin h		6	7	3	3	2	5	5	5	3	6	4	3	3	4		95	
10	DYNC1H1		Q14204	DYHC1_HU	Cytoplasr		7	3	7	4	4	2	1	1	5	3	26	4	9	2		198	
11	PKM		P14618	KPYM_HU	Pyruvate		8	14			12	15	12	12								62	
12	HSPD1		P10809	CH60_HUN	60 kDa he		9	25	36	40	11	30	6	41	21	50	45	39	24	37		52	
13	ATP5B		P06576	ATPB_HUI	ATP synth		10	23	24	28	8	25	13	29	32	33	30	24	30	43		43	
14	HBA1		P69905	HBA_HUM	Hemoglol		11	48	15	66	15	53	8	57	11	58	8	152	11	64		16	
15	MBP		P02686	MBP_HUN	Myelin ba		12	24	4	71	6	34	23	49	4	30	2	28	2	26		27	
16	MAP1B		P46821	MAP1B_H	Microtubı		13	6	18	9	20	11	15	10	10	11	21	12	22	13		109	
17	ATP6V1A		P38606	VATA_HUI	V-type pr		14	36	27	30	22	35	30	36	28	37	25	23	23	36		47	
18	MAP2		P11137	MTAP2_HI	Microtubı		15	8	21	7	18	7	26	13	16	14	19	8	19	9		101	
19	ENO1		P06733	ENOA_HU	Alpha-en		16	18	13	70	17	63	16	22	22	18	11	27	14	22		38	
20	ENO2		P09104	ENOG_HU	Gamma-e		17	67	26	43	14	26	17	50	38	62	20	57	21	66		25	
21	ATP5A1		P25705	ATPA_HUI	ATP synth		18	27	20	33	16	21	14	23	35	32	23	25	27	28		54	
22	CKB		P12277	KCRB_HUI	Creatine I		19	21	16	35	10	16	11	15	15	22	13	30	12	21		43	
23	STXBP1		P61764	STXB1_HU	Syntaxin-		[illegible]	40	14	29	13	29	10	32	17	31	12	18	18	24		56	

x1

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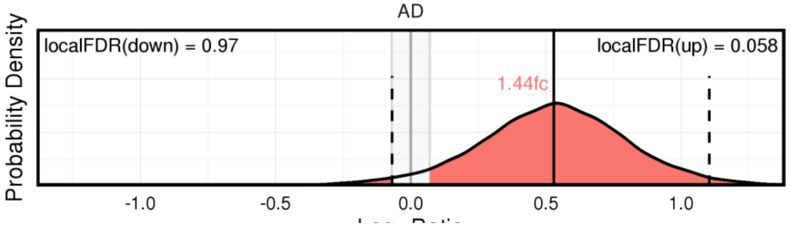

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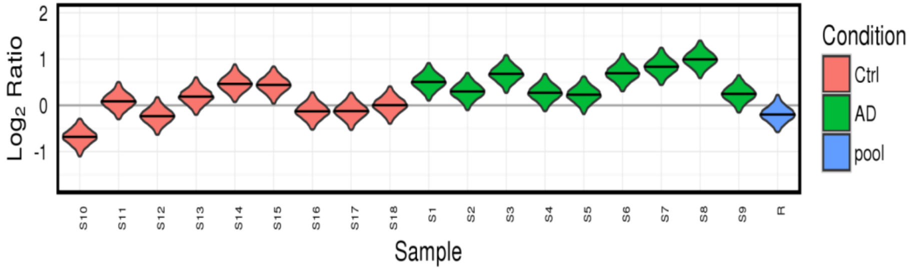
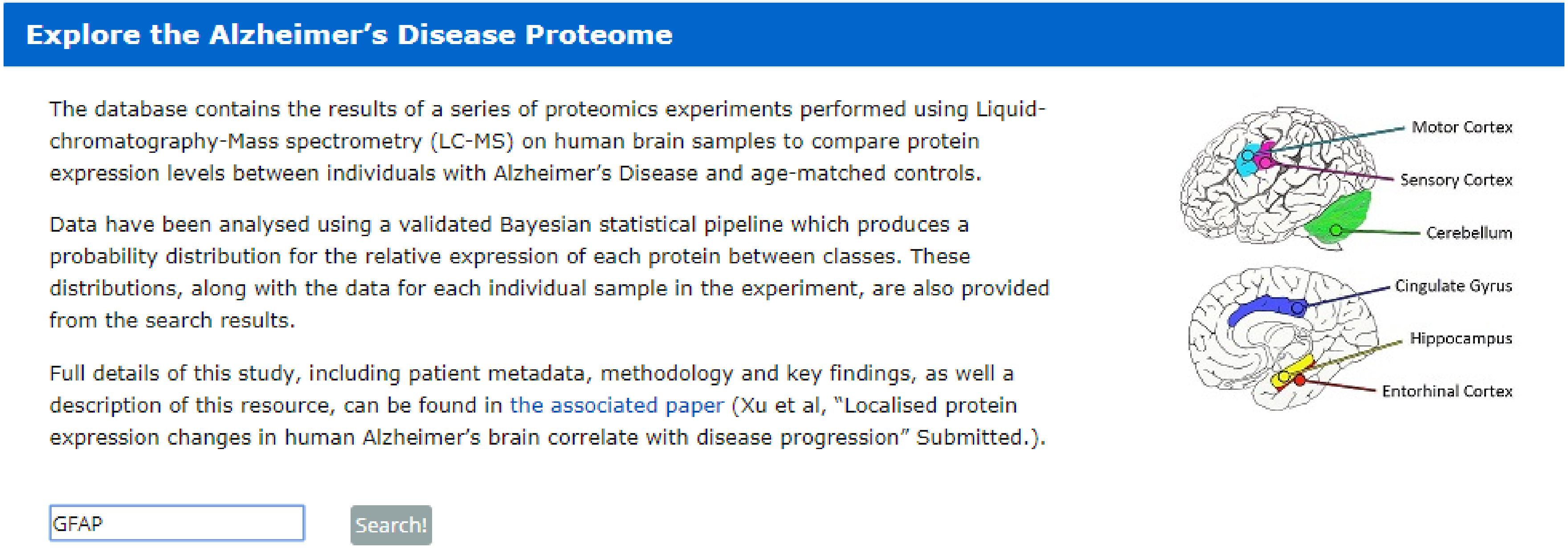


Online database

Developed in collaboration with Research IT

www.manchester.ac.uk/dementia-proteomes-project



Explore the Alzheimer's Disease Proteome

The database contains the results of a series of proteomics experiments performed using Liquid-chromatography-Mass spectrometry (LC-MS) on human brain samples to compare protein expression levels between individuals with Alzheimer's Disease and age-matched controls.

Data have been analysed using a validated Bayesian statistical pipeline which produces a probability distribution for the relative expression of each protein between classes. These distributions, along with the data for each individual sample in the experiment, are also provided from the search results.

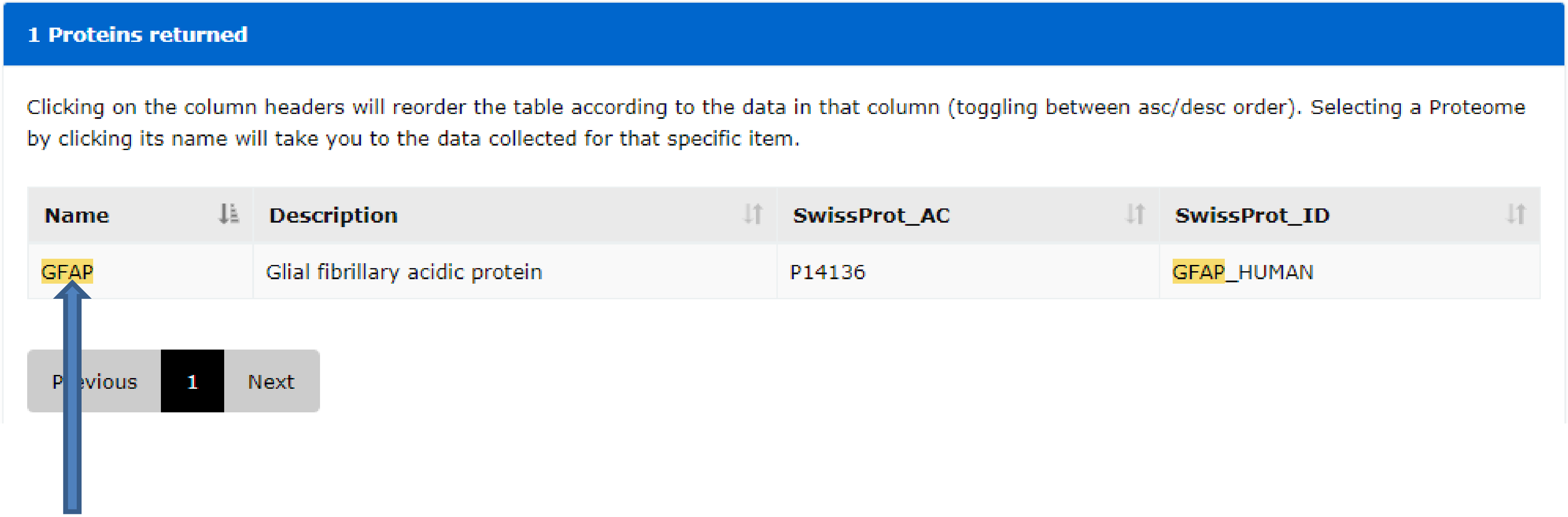
Full details of this study, including patient metadata, methodology and key findings, as well a description of this resource, can be found in the associated paper (Xu et al, "Localised protein expression changes in human Alzheimer's brain correlate with disease progression" Submitted.).

Enter your protein here – will search by gene name or free text in protein name

Online database

Developed in collaboration with Research IT

www.manchester.ac.uk/dementia-proteomes-project



1 Proteins returned

Clicking on the column headers will reorder the table according to the data in that column (toggling between asc/desc order). Selecting a Proteome by clicking its name will take you to the data collected for that specific item.

Name	Description	SwissProt_AC	SwissProt_ID
GFAP	Glial fibrillary acidic protein	P14136	GFAP_HUMAN

Select protein of interest from list

Online database

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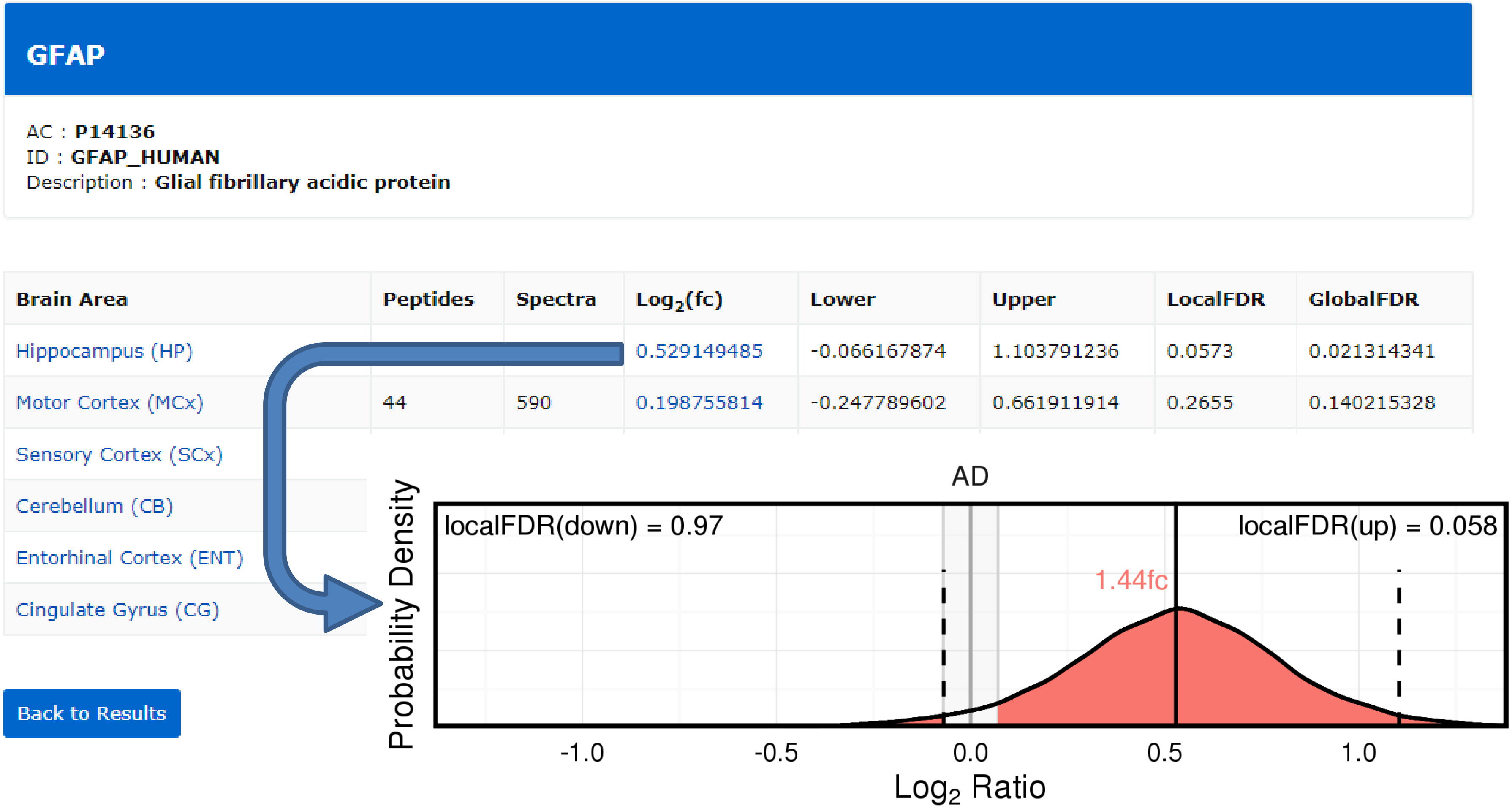

GFAP

AC : **P14136**
ID : **GFAP_HUMAN**
Description : **Glial fibrillary acidic protein**

Brain Area	Peptides	Spectra	Log_2(fc)	Lower	Upper	LocalFDR	GlobalFDR
Hippocampus (HP)			0.529149485	-0.066167874	1.103791236	0.0573	0.021314341
Motor Cortex (MCx)	44	590	0.198755814	-0.247789602	0.661911914	0.2655	0.140215328
Sensory Cortex (SCx)							
Cerebellum (CB)							
Entorhinal Cortex (ENT)							
Cingulate Gyrus (CG)							

Back to Results

Online database

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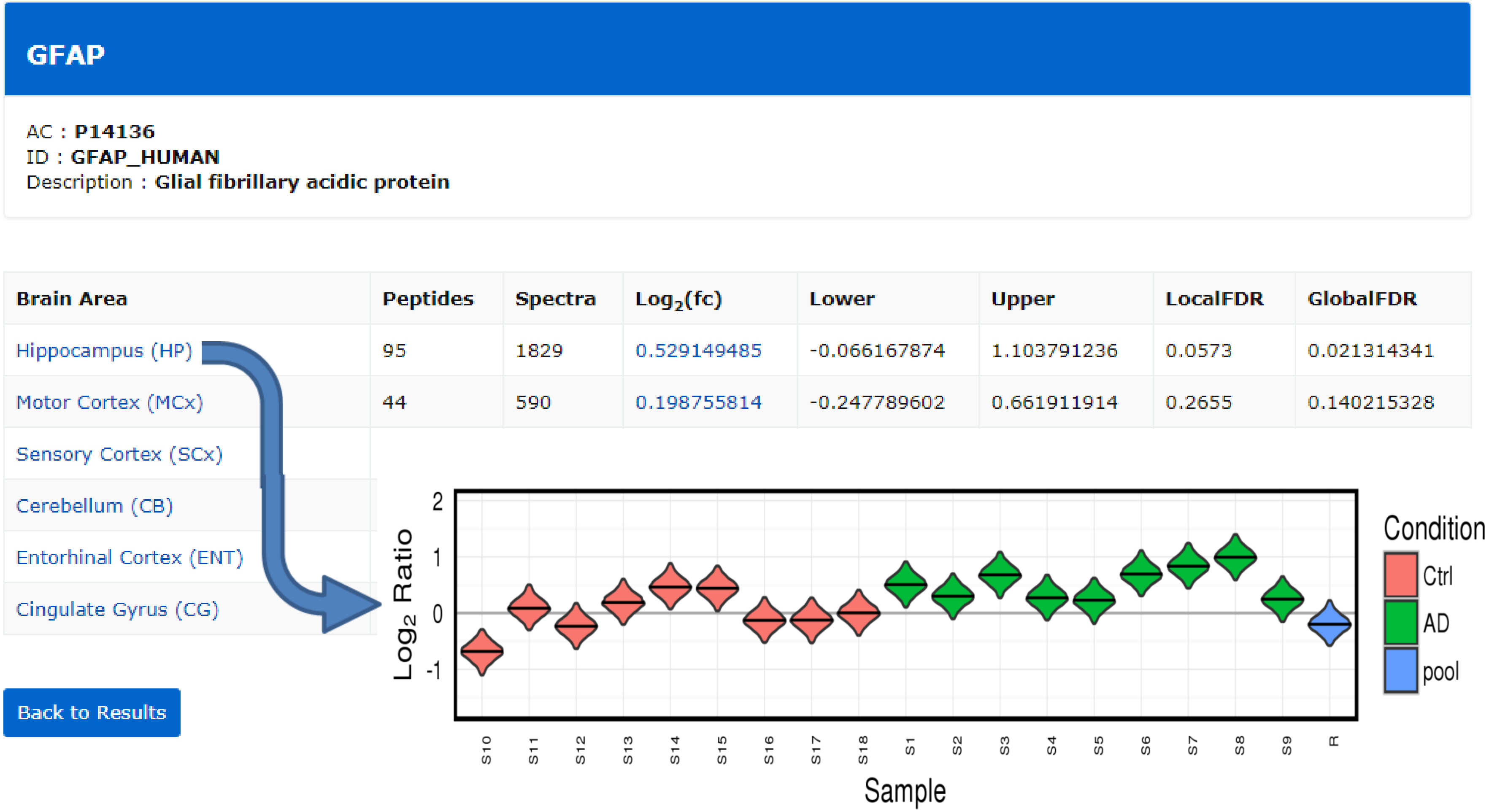

GFAP

AC : **P14136**
ID : **GFAP_HUMAN**
Description : **Glial fibrillary acidic protein**

Brain Area	**Peptides**	**Spectra**	**$Log_2(fc)$**	**Lower**	**Upper**	**LocalFDR**	**GlobalFDR**
Hippocampus (HP)	95	1829	0.529149485	-0.066167874	1.103791236	0.0573	0.021314341
Motor Cortex (MCx)	44	590	0.198755814	-0.247789602	0.661911914	0.2655	0.140215328
Sensory Cortex (SCx)							
Cerebellum (CB)							
Entorhinal Cortex (ENT)							
Cingulate Gyrus (CG)							

Outcomes

- Fantastic tool or me to be able get easy access to our data – web page works on my phone!

- Great feedback from reviewers of our paper. (Reviewer 2: “I was impressed with … the authors’ commitment to publicly sharing this data both in this paper and on the online resource they developed.“

- Great example for inclusion into future grant applications, and good feedback.

- Easy access to the data by others several other groups at UoM and round the UK I know are looking through this DB to get data to support their own work.

Lessons learned

- Approach Research IT early!
- We redesigned bits of our data output sheets to fit with their needs, including reformatting to only include key data columns, all on one sheet etc.
- Also reformatted data processing to output images as .png, not .pdf as originally written.
- Think about impact – we should have included a ‘counter’ for visits, or searches?
- Road test it. Made a few minor changes after feedback from lab members – image appearing in same rather than a new tab or as a file download, for example….

Acknowledgements

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University of
BRISTOL

Andrew Dowsey

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The Power to Defeat Dementia

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NHS Foundation Trust