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2	BBSRC	BBE0249121	Informatics tools for analysis of quantitative proteomics data	1
3	BBSRC	BBS/B/13497	Chicken genome annotation and analysis	2
4	BBSRC	BBS/B/17204	ISPIDER - a pilot grid for integrative proteomics	6
5	BBSRC	BIO10517	Software tools for complex mixture analysis of proteome proteins	3
6	BBSRC	BIO14433	Prediction of functional properties of proteases from sequence and structure	0
7	BBSRC	EGM17685	Improved identification of proteins from fragment ion spectra using machine learning in proteomics	4

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BMC Genomics 2009; 10: 61
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BBSRC - CFB17723
Abstract
-  Upstream sequence elements direct post-transcriptional regulation of gene expression under stress conditions in yeast.
Lawless C, Pearson RD, Selley JN, Smirnova JB, Grant CM, Ashe MP, Pavitt GD, **Hubbard SJ**
BMC Genomics 2009; 10: 7
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Abstract
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Wright JC, Sugden D, Francis-McIntyre S, Riba-Garcia I, Gaskell SJ, Grigoriev IV, Baker SE, Beynon RJ, **Hubbard SJ**
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152

132

121

polymorphisms.

Wong GK, Liu B, Wang J, Zhang Y, Yang X, Zhang Z, Meng Q, Zhou J, Li D, Zhang J, Ni P, Li S, Ran L, Li H, Zhang J, Li R, Li S, Zheng H, Lin W, Li G, Wang X, Zhao W, Li J, Ye C, Dai M, Ruan J, Zhou Y, Li Y, He X, Zhang Y, Wang J, Huang X, Tong W, Chen J, Ye J, Chen C, Wei N, Li G, Dong L, Lan F, Sun Y, Zhang Z, Yang Z, Yu Y, Huang Y, He D, Xi Y, Wei D, Qi Q, Li W, Shi J, Wang M, Xie F, Wang J, Zhang Wang P, Zhao Y, Li N, Yang N, Dong W, Hu S, Zeng C, Zheng W, Hao B, Hillier LW, Yang SP, Warren WC, Wilson RK, Brandström M, Ellegren H, Crooijmans RF van der Poel JJ, Bovenhuis H, Groenen MA, Ovcharenko I, Gordon L, Stubbs L, Lucas S, Glavina T, Aerts A, Kaiser P, Rothwell L, Young JR, Rogers S, Walker B, van Hateren A, Kaufman J, Bumstead N, Lamont SJ, Zhou H, Hocking PM, Morrice D, de Koning DJ, Law A, Bartley N, Burt DW, Hunt H, Cheng HH, Gunnarsson U, Wahlberg P, Andersson L, Kindlund E, Tammi MT, Andersson B, Webber C, Ponting CP, Overton IM, Boardman PE, Tang H, **Hubbard SJ**, Wilson SA, Yu J,

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