

Supplementary Table 3: GO analysis

HES CELLULAR LOCATION SUMMARY		count	% total
none detected		300	80.2
GO:0005576	extracellular region	44	11.8
GO:0005615	extracellular space	12	3.2
GO:0005737	cytoplasm	5	1.3
GO:0000786	nucleosome	3	0.8
GO:0005634	nucleus	3	0.8
GO:0005783	endoplasmic reticulum	3	0.8
GO:0000015	phosphopyruvate hydratase complex	2	0.5
GO:0005622	intracellular	2	0.5
GO:0016020	membrane	2	0.5

HES MOLECULAR FUNCTION SUMMARY		count	% total
none detected		205	54.8
GO:0004222	metalloendopeptidase activity	21	5.6
GO:0003824	catalytic activity	19	5.1
GO:0004190	aspartic-type endopeptidase activity	12	3.2
GO:0004867	serine-type endopeptidase inhibitor activity	10	2.7
GO:0005509	calcium ion binding	10	2.7
GO:0005515	protein binding	10	2.7
GO:0043169	cation binding	10	2.7
GO:0005319	lipid transporter activity	9	2.4
GO:0005506	iron ion binding	9	2.4
GO:0020037	heme binding	9	2.4
GO:0005488	binding	8	2.1
GO:0005524	ATP binding	7	1.9
GO:0005544	calcium-dependent phospholipid binding	7	1.9
GO:0008236	serine-type peptidase activity	7	1.9
GO:0019825	oxygen binding	7	1.9
GO:0005529	sugar binding	5	1.3
GO:0004197	cysteine-type endopeptidase activity	4	1.1
GO:0005198	structural molecule activity	4	1.1
GO:0008289	lipid binding	4	1.1

HES BIOLOGICAL PROCESS SUMMARY		count	% total
none detected		257	68.7
GO:0006508	proteolysis	48	12.8
GO:0005975	carbohydrate metabolic process	14	3.7
GO:0006869	lipid transport	9	2.4
GO:0008152	metabolic process	8	2.1
GO:0015671	oxygen transport	7	1.9
GO:0006096	glycolysis	6	1.6
GO:0055114	oxidation-reduction process	6	1.6
GO:0006457	protein folding	4	1.1
GO:0045454	cell redox homeostasis	4	1.1
GO:0006334	nucleosome assembly	3	0.8
GO:0006030	chitin metabolic process	2	0.5
GO:0006629	lipid metabolic process	2	0.5
GO:0006662	glycerol ether metabolic process	2	0.5
GO:0006801	superoxide metabolic process	2	0.5
GO:0007155	cell adhesion	2	0.5
GO:0006004	fucose metabolic process	1	0.3

HEX CELLULAR LOCATION SUMMARY		coun	%
	t		total
none detected	290		65.0
GO:0005622 intracellular	70		15.7
GO:0005840 ribosome	60		13.5
GO:0005737 cytoplasm	27		6.1
GO:0005576 extracellular region	11		2.5
GO:0005615 extracellular space	10		2.2
GO:0005839 proteasome core complex	6		1.3
GO:0005783 endoplasmic reticulum	5		1.1
GO:0005874 microtubule	4		0.9
GO:0005634 nucleus	3		0.7

HEX MOLECULAR FUNCTION SUMMARY		coun	%
	t		total
none detected	105		23.5
GO:0003735 structural constituent of ribosome	61		13.7
GO:0005524 ATP binding	46		10.3
GO:0003824 catalytic activity	44		9.9
GO:0005488 binding	32		7.2
GO:0016491 oxidoreductase activity	29		6.5
GO:0005515 protein binding	22		4.9
GO:0000166 nucleotide binding	18		4.0
GO:0003676 nucleic acid binding	16		3.6
GO:0003723 RNA binding	16		3.6
GO:0005525 GTP binding	15		3.4
GO:0005198 structural molecule activity	14		3.1
GO:0020037 heme binding	13		2.9
GO:0005506 iron ion binding	13		2.9
GO:0051082 unfolded protein binding	12		2.7
GO:0003924 GTPase activity	11		2.5
GO:0019825 oxygen binding	11		2.5
GO:0005319 lipid transporter activity	9		2.0
GO:0008289 lipid binding	8		1.8
GO:0009055 electron carrier activity	8		1.8

HEX BIOLOGICAL PROCESS SUMMARY		coun	%
	t		total
none detected	184		41.3
GO:0006412 translation	68		15.2
GO:0008152 metabolic process	44		9.9
GO:0055114 oxidation-reduction process	35		7.8
GO:0006457 protein folding	16		3.6
GO:0006508 proteolysis	13		2.9
GO:0005975 carbohydrate metabolic process	12		2.7
GO:0015671 oxygen transport	11		2.5
GO:0006096 glycolysis	10		2.2
GO:0006886 intracellular protein transport	10		2.2
GO:0006869 lipid transport	9		2.0
GO:0044267 cellular protein metabolic process	9		2.0
GO:0006414 translational elongation	7		1.6
GO:0045454 cell redox homeostasis	7		1.6
GO:0006418 tRNA aminoacylation for protein translation	6		1.3
GO:0044262 cellular carbohydrate metabolic process	6		1.3
GO:0051603 proteolysis involved in cellular protein catabolic process	6		1.3