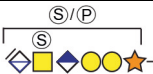



Protein name ^{a, b}	Peptide sequence ^c	Glycan modification ^d	Mass / charge and precursor charge	Accuracy (ppm) ^e	Sample type
Cell Surface CSPGs					
⁹ Brain-specific angiogenesis inhibitor 2	²⁵⁰ ALVPGGPAPPAAEADLHSGSSNDLFTTEM ²⁷⁸		1310.910; 3+	+ 7.5	CSF
CD44 antigen	¹⁶³ TNPEDIYPSNPTDDDVS ¹⁸⁶		1188.130; 3+	+ 4.2	Urine
			1214.782; 3+	+ 3.4	
^{a, b} CD99L2 protein	¹³² YGSNDDPGSGGFLNPEAPVGHVK ¹⁵⁶		1103.128; 3+	+ 4.7	CSF
CSPG5	³⁵ EAGSAVEAEELVK ⁴⁶		775.659; 3+	+ 5.4	CSF
HLA class II histocompatibility antigen gamma chain	²⁷⁵ LELEDPSGLGVT ²⁸⁸		1259.506; 2+	+ 5.7	Urine
⁹ Plexin domain-containing protein	²⁴ GAGHDEGPGSGWAAK ³⁸		797.306; 3+	- 1.1	CSF and Urine
			823.959; 3+	- 3.6	
Receptor-type tyrosine-protein phosphatase R	²² FSGNNDHFLAINQK ³⁵		866.695; 3+	+ 2.6	CSF
Extracellular Matrix CSPGs					
Basement membrane-specific heparan sulfate proteoglycan core protein	⁴¹⁸⁷ DWHLEGSGGN ⁴¹⁹⁶		1032.876; 3+	+ 6.9	CSF and Urine
Brevican core protein	⁴⁰³ GAIYSIPIMEDGGGSSTPEDPAEAPR ⁴²⁹		1249.832; 3+	+ 3.9	CSF
Collagen alpha-1 (XV) chain	²³¹ TPEELCDPEESSASGETSGLQE ²⁵¹		1142.413; 3+	+ 5.5	Urine
Decorin	³¹ DEASGIGPEVPDDR ⁴⁴		1265.455; 3+	+ 4.0	CSF and Urine
⁹ Laminin subunit alpha-4	²⁸ DDNAFPFDIEGSSAVGR ⁴⁴		930.704; 3+	+ 2.9	Urine
			957.359; 3+	+ 5.2	
⁹ Matrix-remodeling-associated protein 5	⁶⁹¹ VREDIVEDEGGSGMGDEENTSR ⁷¹²		1125.445; 3+	+ 7.1	CSF
Neurocan core protein	³⁵⁸ AHHPTSQHGDLETPSSGDEGEILSAEGPPVR ³⁸⁸		840.964; 5+	+ 3.5	CSF
			1070.936; 4+	- 1.7	
			1299.275; 4+ (without modifications)	+ 4.5	

Neurocan core protein	³⁸⁹ ELEPTLEEEVVTPDFQEPLVSSGEEETLILEEK ⁴²²		1220.800; 4+	4.4	CSF
³ Osteopontin	²²³ DSYETSQLDDQSAETHSHK ²⁴¹		793.557; 4+	+ 1.5	CSF and Urine
			1084.394; 3+	+ 2.7	
³ Osteopontin	³⁰² ISHELDSASSEVN ³¹⁴		1230.941; 2+	+ 1.2	CSF and Urine
Versican core protein	¹⁵²⁶ DTEVGHQAHEHTEPVSLFPEESSGGEIAIDQESQK ¹⁵⁵⁹		951.610; 5+	+ 4.0	CSF and Urine
Intracellular Granules CSPGs					
Bone marrow proteoglycan	⁵³ ELEEEEWGSGSEDASK ⁶⁹		1452.545; 3+	+ 8.1	Urine
			1492.512; 3+	- 2.2	
³ Cholecystokinin	²¹ QPVPADPAGSGLQR ³⁵		822.683; 3+	+ 1.4	CSF and Urine
Chromogranin-A	⁴¹⁹ KEEEGSANR ⁴²⁷		671.587; 3+	- 4.6	CSF and Urine
			698.242; 3+	- 5.3	
³ Collagen and calcium-binding EGF domain-containing protein 1	³⁸² DLGSGDDHPR ³⁹¹		687.921; 3+	- 2.2	Urine
			1071.358; 3+	+ 0.1	
³ Dermcidin	²⁰ YDPEAASAPGSGNPCHEASAAQK ⁴²		1103.433; 3+	+ 1.0	Urine
			1130.084; 3+	+ 0.5	
³ Neuropeptide W	¹²⁰ APEPALEPESLDFSGAGQR ¹³⁸		988.752; 3+	+ 4.9	CSF and Urine
			1015.405; 3+	+ 2.9	
³ Secretogranin-1	⁸⁸ DPADASEAHSSSR ¹⁰¹		817.970; 3+	+ 2.0	CSF and Urine
			844.625; 3+	+ 1.0	
³ Secretogranin-1	²³⁵ SSQESGEETGSQENHPQESK ²⁵⁴		1046.734; 3+	+ 3.6	CSF
³ Secretogranin-3	³⁵ ELSAERPLNEQIAEAEEDK ⁵³		1055.451; 3+	+ 3.4	Urine
Miscellaneous CSPGs					
Bikunin	²⁰⁶ AVLPQEEEGSGGGQLVTEVTK ²²⁶		1041.125; 3+	+ 0.4	CSF and Urine
			1067.779; 3+	- 2.1	
			1094.437; 3+	+ 4.7	

Bikunin	²⁰⁶ AVLPQEEEG <u>SGGG</u> QLVTEVTK ²²⁶		1094.432; 3+	+ 2.7	CSF and Urine
^a Neuroserpin	³⁹⁴ VMHPETMNT <u>SG</u> HDFEEL ⁴¹⁰		989.718; 3+	+ 6.8	CSF

^aIndicate novel CSPGs identified in this study.

^bIdentified in searches against NCBI nr.

^cBold and underlined serine residues depict established attachment sites while bold depict probable attachment sites.

^dThe CS-hexasaccharide were identified either without or with sulfate (SO₃⁻) and/or phosphate (PO₃⁻) modifications and their positions on the hexasaccharide structure are indicated. The positioning and distinction of sulfate- (79.9663 Da) and phosphate (79.9568 Da) modifications were made by manually evaluating the MS2-spectra. When the expected modifications could not be identified a bracket including the whole hexasaccharide structure is presented as the expected modification could be, in theory, anywhere on the glycan.

^eThe accuracy denotes the difference between the theoretical and the measured mass for a randomly selected precursor ion of each CS-glycopeptide. For CS-glycopeptides where the nature of the expected modification could not be determined (i.e. sulfate- or phosphate) the theoretical mass is calculated based on the assumption of a sulfate modification.