Accession	Protein	Modifications/function	nI	MW	#Alt	Scores	SC	RMS90
Accession	littem	Wioumcations/Tunction	hī	[kDa]	Protein	Scores	SC [%]	[ppm]
AACT_HUMAN	Alpha-l- antichymotrypsin sapiens	Oxidation (inhibitor)	5.3	47.6	1	339.6 (M:339.6 )	16.5	40.27
ANT3_HUMAN	Antithrombin-III	Nonvitamin K-dependent protease	6.3	52.6	1	56.2 (M:56.2)	2.6	39.85
AIBG_HUMAN	Alpha-lB-glycoprotein	Upregulated in adenocarcinoma-unknown function	5.6	54.2	1	21.1 (M:21.1)	1.6	41.8
APOA1_HUMA N	Apolipoprotein A-I	Cholesterol metabolism	5.6	30.8	1	172 (M:172.0 )	22.5	23.66
AIBG_HUMAN	Alpha-lB-glycoprotein	Carbamidomethyl/Upregulate d in adenocarcinoma-unknown function	5.6	54.2	1	705.7 (M:705.7 )	38.2	9.87
CO9_HUMAN	Complement component C9 C4b- binding protein alpha	Complement cascade	5.4	63.1	1	50.3 (M:50.3)	2.1	39.23
C4BPA_HUMA N	chain	Complement cascade	7.2	67	1	15.1 (M:15.1)	1.8	40.78
CO3_HUMAN	Complement C3	Oxidation/Complement cascade	6	187	1	313.7 (M:313.7	4.1	24.23
CSN2_HUMAN	COP9 signalosome complex subunit 2	Ubiquitin regulator	5.4	51.6	1	) 17.0 (M:17.0)	2.3	763.59
EFCB7HUMAN	EF-hand calcium- binding domain-containing proteir	Carbamidomethy Ucytoplasmic calcium sensor 17	6	71.9	1	31.6 (M:31.6)	1.6	44.1
FIBA_HUMAN	Fibrinogen alpha chain	Act as DAMPs	5.7	94.9	1	82.0 (M·82.0)	3.1	40.02
HBB_HUMAN	Hemoglobin subunit beta	Oxidation/blood pigment	6.7	16	5	(M:187.8 )	28.6	14.73
HEMO_HUMA N	Hemopexin	Carbamidomethyl, Oxidation/inflammation	6.5	51.6	1	) 381.8 (M:381.8 )	32.7	39.92
		induced acute phase protein						
HRG_HUMAN	Histidine-rich glycoprotein	Carbamidomethyl/roles in immunity, coagulation	7.1	59.5	1	169.3 (M:169.3	10.1	39.27
IGHA1_HUMA N	Ig alpha-1 chain C region	Carbamidomethyl/immunity	6.1	37.6	2	235.4 (M:235.4	21.8	40.36
KV311_HUMA N	Ig kappa chain V-III region IARC/BL41	immunity	6.2	14.1	1	90.6 (M:80.6)	12.5	23.77
IGHG1_HUMA N	Ig gamma-1 chain C region	Carbamidomethyl/immunity	8.5	36.1	2	61.5 (M:61.5)	7.9	23.62
LV_102_HUMA N	Ig lambda chain V-I region HA	Immunity	9.1	11.9	2	56.3 (M:56.3)	18.8	24.64
TRFM_HUMAN	Melanotransferrin	Carbamidomethyl/Role in melanoma cell proliferation and tumorigenesis	5.6	80.2	1	41.6 (M:41.6)	1.8	780.36
OSGI2_HUMA N	Oxidative stress- induced growth inhibitor 2	Oxidation/apoptotic regulator	7	56.6	1	16.2 (M:16.2)	1.6	1076.69
THRB_HUMAN	Prothrombin	Blood clotting	5.6	70	1	31.5	1.6	7.97

Annexture 1 Proteins identified from OA samples along with their structural and functional characteristics

						(M:31.5)		
KS6A3_HUMA N	Ribosomal protein S6 kinase alpha 3	Oxidation/Mediates cell survival	6.4	83.7	1	17.4 (M:17.4)	1.2	31.89
RMD2_HUMA N	Regulator of microtubule dynamics protein 2	Role in signaling	6.1	47.4	1	16.5 (M:16.5)	4.6	4.1
RABXS_HUMA N	Rab5 GDP/GTP exchange factor	Involved in signaling	6.4	79.3	1	17.2 (M:17.2)	1.8	632.58
RB27B_HUMA N	Ras-related protein Rab-27B	Involved in vesicular fusion and trafficking	5.4	24.6	1	15.1 (M:15.1)	5	774.92
ARRS_HUMAN	S-arrestin	Role in retinal photoreceptorcells	6.1	45.1	1	16.4 (M:16.4)	3.2	48.05
TRFE_HUMAN	Serotransferrin	Oxidation/uptake of transferring bound iron	6.8	77	1	4161.6 (M:4161. 6)	63.8	10.29
TMM78_HUMA N	Transmembrane protein 78	-	4.9	15.2	1	18.1 (M:18.1)	5.9	1229.9
VTDB_HUMAN	Vitamin D binding protein	Bone metabolism	5.4	52.9	1	19.5 (M:19.5)	2.3	10.76

[(PE: protein existence, SV: sequence version, MW [kDa], pI: isoelectric point, Score: Mascot score, SC: sequence coverage, RMS90 [ppm]: root mean square (RMS.)]

Annexture 2 List of OA disease-associated proteins and their classification

Serine protease inhibitors/signalling proteins	Bone metabolism/ pathway regulators	Inflammation and immunologic cascade	Oxidative stress	Cholesterol metabolism
Alpha 1	Vitamin D	Alpha 1B glycoprotein	Hemopexin	Apolipoprotein A
antichymotrypsin Antithrombin III	protein Zinc finger and BTB	Apolipoprotein A1 Fibrinogen alpha chain	Transmembrane protein78	EF hand calcium binding domain
Hemopexin	domain protein 45	Rab5 GDP/GTP exchange	Oxidative	
Prothrombin		factor	stress-induced	
Serotransferrin		S-arrestin	growth	
Melanotransferrin		Complement C3	inhibitor 2	
COP9 signalosome		Complement		
complex subunit 2		component C9 C4 binding protein α chain		

Serine protease inhibitors/signalling proteins	Bone metabolism/ pathway regulators	Inflammation and immunologic cascade	Oxidative stress	Cholesterol metabolism
Alpha 1	Vitamin D binding	Alpha 1B glycoprotein	Hemopexin	Apolipoprotein A
antichymotrypsin	protein	Apolipoprotein A1	Transmembrane	EF hand
Antithrombin III	Zinc finger and BTB	Fibrinogen alpha chain	protein78	calcium binding domain
Hemopexin	domain protein 45	Rab5 GDP/GTP exchange	Oxidative	
Prothrombin		factor	stress-induced	
Serotransferrin		S-arrestin	growth	
Melanotransferrin		Complement C3	inhibitor 2	
COP9 signalosome		Complement component C9		
complex subunit 2		C4 binding protein α chain		

Annexture 3 List of OA disease-associated proteins and their classification

[The terms 'up' and 'down' denote elevated and reduced metabolite levels in OA patients compared to normal controls. (AUC: Area under curve (receiver operating characteristic curve), VIP: Variable importance in projection (for quantitative estimation of discriminatory power of each individual feature).