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Title

Serum amyloid A1 and plasminogen as predictory proteins to monitor the progression of preleukemic diseases towards acute lymphoblastic leukaemia.

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Keywords

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E. mail: musharraf1977@yahoo.com <u>musharraf@iccs.edu</u> **Table S 1:** KEGG pathways involved by differentially regulated proteins in acute

 lymphoblastic leukaemia and preleukemic diseases.

Pathway	False discovery rate
Complement and coagulation cascades	1.6e-59
Staphylococcus aureous infection	2.47e-09
Platelet activation	2.59e-06
Pertussis	0.000422
ECM-receptor interaction	0.00899
PI3K-Akt signaling pathway	0.00899
Transcriptional misregulation in cancer	0.00185
Proteoglycans in cancer	0.00665
African trypanosomiasis	0.000422
p53 signaling pathway	0.0368
Rap1 signaling pathway	0.0225
Inflammatory mediator regulation of TRP channels	0.011
Systemic lupus erythematosus	0.011
Neuroactive ligand-receptor interaction	0.00307
Malaria	0.0159
Cell cycle	0.0227



Figure S 1: Chromatogram of fast protein liquid chromatography (FPLC) during depletion of top seven abundant proteins using MARS hu-7 column.



Figure S 2: Checking depletion efficiency of MARS column. Fractions loaded were equivalent to 0.1 μ L original crude human plasma on 12 % SDS-PAGE. 1: Protein ladder 2: Blank 3: Crude plasma (MDS pool) 3: unbound portion (MDS pool) 5: bound portion (MDS pool).



Figure S 3: Checking enrichment efficiency of unbound fraction through MARS column by 5Kda MWCO tubes. Fractions loaded were equivalent to 0.1 μ L original crude human plasma on 12 % SDS-PAGE 1: Protein ladder, 2: Crude plasma (ALL pool) 3: Fraction-2, unbound portion (ALL pool) before cut off tube 4: unbound portion (ALL pool) after cut off tube.



Figure S 4: IEF fractions after ZOOM_IEF of ALL pool. 15 μ L (Max load) of each fractionwas loaded onto 12%, 10 well's gel. 1: Protein ladder 2: Blank 3: unbound fraction withoutZOO-IEF, 4: Fraction-1 (pH 3.0-4.6) 5: Fraction-2 (pH 4.6-5.4) 6: Fraction-3 (pH 5.4-6.2) 7:Fraction-4 (pH 6.2-7.0)8: Fraction-5 (pH 7.0-10.0).



Figure S 5: Master gel created from PDQuest software by combining all spots from ALL, APA, MDS and healthy pool's gels



Figure S 6: KEGG pathway of eight differentially expressed proteins in acute lymphoblastic leukaemia and preleukemic diseases in comparison to healthy, acquired from online STRING database. Balls with structures show that their 3D structures are also available in database.



Figure S 7: Quantity graph report of differentially expressed proteins in the unbound portion of ALL, preleukemic diseases and healthy pool. Green colour is for healthy, orange colour for ALL, purple colour is for APA, and yellow colour is for MDS. Spots number are those, which are highlighted in Figure 3 with green crosses and are those assigned by PDQuest software



Acute lymphoblastic leukemia (ALL) (Precursor T lymphoblastic leukemia)

Acute lymphoblastic leukemia (ALL) (Precursor B lymphoblastic leukemia)



Figure S 8: Transcriptional misregulation in cancer.