Supplementary Materials for
Identification and validation of predictive factors for progression to severe COVID-19 pneumonia by proteomics

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Data S1. List of LC-MS/MS detected peptides and proteins from sera of 23 COVID-19 patients (Development group) and 10 healthy controls
Materials and Methods

Study Oversight and Participants
Guangzhou Center for Disease Control and Prevention (Guangzhou CDC) has been authorized for laboratory testing for SARS-CoV-2 infections since the official announcement of COVID-19 breakout, according to Chinese Law for Infectious Disease and Law for Health and Quarantine. All the patients with laboratory confirmed SARS-CoV-2 infection were referred to the No. 8 People’s Hospital of Guangzhou, which specializes in infectious diseases and has been designated as one of the major designated hospitals to treat COVID-19 patients in the province.

Between January 27 and March 3, 2020, we recruited 73 adult COVID-19 patients who were laboratory confirmed at Guangzhou CDC laboratory and then were referred to the No. 8 People’s Hospital of Guangzhou for treatment. All patients were divided into development group (Group I: 23 patients recruited between January 27 and February 10) and validation group (Group II: 50 patients recruited between February 13 and March 3). A total of 10 healthy volunteers were recruited as control group. The diagnosis of COVID-19 was made following the Protocol for Novel Coronavirus Pneumonia Diagnosis and Treatment issued by the National Health Commission of the People’s Republic of China. Written informed consent was obtained from each participant and the present study was approved by the Ethical Committee of Guangzhou CDC (GZCDC-ECHR-2020A0002).

Sample and Clinical Data collection
For all included COVID-19 patients (both Group I and Group II), serum samples and a panel of epidemiological, clinical, radiological and laboratory data were collected within 24 hours after admission. In addition, infection with other respiratory pathogens such as influenza A virus (H1N1, H3N2, H7N9), influenza B virus, respiratory syncytial virus (RSV), parainfluenza virus, adenovirus, SARS coronavirus and middle east respiratory syndrome (MERS) coronavirus were ruled out by real time - polymerase chain reaction (RT-PCR) assays approved by the China Food and Drug Administration. In addition, blood serum samples of group I and healthy control were collected for quantitative data-independent acquisition (DIA) proteomics analysis (Supplementary Fig. 1a). The serum samples were deactivated at 56 °C for 30 minutes before proteomics analysis.

Proteomics data analysis and confirmation
For deeper proteomic analysis, the proteins extracted from 100uL serum by 8 M urea (which can denature all proteins) and vortexed for 5 min. And then 10 mM dithiothreitol (DTT) was added to the mixture of serum and urea at 37°C for 1 h followed by added 55 mM iodoacetamide (IAM) and incubated for 45 min in a dark room. Finally, the mixture was centrifuged at 25,000 × g for 20 min at 4°C, and the 1ml supernatant get through the Cleantar PEP96 wellplate inserted with 30mg C18 individual columns (Agela Technologies, China) that bind with the lower abundance serum proteins with higher hydrophobicity and expel the high-abundance proteins in the flowthrough. The bound lower abundance proteins were finally eluted with 75% ACN (Acetonitrile) (10.1021/acs.jproteome.9b00353). Sample was dehydrated in vacuum and re-dissolved in 50 mM Ammonium bicarbonate (ABC), digested with FASP (Sartorius, U.K.), at the ratio of 50:1 (protein to enzyme), subsequently eluted with 70% ACN and dehydrated in a vacuum centrifuge. DIA proteomic strategy was adopted to quantify the serum protein changes between the patients and health controls, initiating in a data dependent acquisition (DDA) spectral library established by the separation of peptide mixtures from the 23 development cohort samples and 10 control samples (10 µg/sample) into 10 fractions on an high performance liquid chromatography
(HPLC) system (Shimadzu, Japan) linked with Gemini high pH C18 column (4.6 × 250 mm, 5 μm) under a basic condition (pH 9.8). The peptides of each fraction pooled with iRT peptides were analyzed by Orbitrap Fusion Lumos Mass Spectrometer (Thermo Fisher Scientific, CA, USA) and identified by database searching software Maxquant (version 15.3.30) against human uniport protein database. The data acquisition of individual serum peptide sample pooled with the same amount of iRT peptides was performed under the DIA mode as reported and the data analysis was completed by Spectronaut (12.0.20491.14.21367) software referenced as the DDA library above. The proteins quantified with no less than 1.5-fold changes and P-value < 0.05 (Wilcoxon rank sum test) between case and control were defined as the differential proteins. To confirm the alterations of these differential proteins, a target quantification approach, PRM (Parallel Reaction Monitoring), was adopted for further analysis. For PRM confirmation, the 72 peptide precursors of selected differential proteins and iRT precursors were scheduled with 16-min retention time windows using Q-Exactive HF mass spectrometer (Thermo Fisher Scientific, CA, USA). The PRM quantification was performed by Skyline software and the intensities of three iRT peptides DGLDAASYAPVR, GAGSSEPVTGLDAK, TPVISGGPYEYR were used to normalize the sample loading.

Validation of predictive factor performance
The accuracy of predictive factor panel was validated in the sera from group II and healthy controls by an ELISA assay. These ELISA kits are purchased from Beijing Andy Gene Co., Ltd and their commercial catalogue number are S100A8 (Cat: AD11500Hu), OAF (Cat: AD12688Hu), RPS28 (Cat: AD12692Hu), SOD2 (Cat: AD12691Hu), MB (Cat: AD12155Hu), GSTO1 (Cat: AD12018Hu), DDT (Cat: AD10014Hu) and CAPNS1 (Cat: AD12690Hu) respectively. The concentrations of these three proteins were determined according to the manufacturer’s protocols. Absorbance was measured at 450 nm using HydroFlex microplate washer. All samples were analyzed in triplicate, and the average concentration for each patient was calculated.

Statistical analysis and machine-learning
Based on the disease progression, all 73 patients were classified as progression to severe group and moderate group. Categorical variables were summarized in percentage and compared between progression to severe group and moderate group using χ² test and Fisher’s exact test. Continuous variables were expressed as median and interquartile range (IQR), whichever deemed appropriate. All data were analyzed with R (v3.5) and analysis of differentially expressed proteins was performed with MSstats R package which includes log2 transformation, normalization and P-value calculation on the Spectronaut and skyline quantitative data. PCA was performed with pcaMethods R package. GO enrichment analysis was performed with topGO R package with default parameters.

An iterative random forest machine-learning with 5-fold cross-validation approach was designed to identify the optimal panel of clinical and proteomic features for early detection of severe patient. Briefly, selected clinical and proteomic features from the patients were extracted for random forest modeling with 5-fold cross-validation, using disease severity as the response variable. Five-fold cross-validation was employed to eliminate potential overfitting of the random forest model. To reduce potential variability of the random forest models, each round of random sampling for training and testing dataset in model building was iteratively repeated for 100 times, and all reported results were averaged. All possible combinations of the selected clinical and proteomic features were exhaustively tested by this iterative machine-learning process, and the predictive power of each combination was recorded and ranked according to the AUC value by receiver operating characteristic (ROC) analysis. The average sensitivity and specificity scores
from each feature combination were also recorded. The combination of features with the highest AUC value was considered the best for distinguishing severe from moderate patients, and individual feature can be ranked according to the importance score in the corresponding random forest model.
Figure. S1. Overall study design and data reproducibility assessment.

a Identification of proteomic predictive factors for severe COVID-19 patient screening. b Pearson’s correlation of LC-MS/MS proteomics data among all 33 samples. P: Patient. N: Normal control.
Figure. S2. PRM validation results for up-regulated proteins in COVID-19 patients.

a Validation of target peptides of SAA2, CRP, ATP6V1G2 and H2AC4 by PRM. b Cumulative bar plots of peak area of retention curves in a for patients and controls. Color code is same as a. c Boxplots of PRM detection intensity of SAA2, CRP, ATP6V1G2 and H2AC4 in patients and controls. * P-value < 0.05, ** P-value < 0.01, Wilcoxon Rank Sum test.
**Figure S3.** PRM validation results for down-regulated proteins in COVID-19 patients.

- **a** Validation of targeted peptide of MST1, SHBG, PRG2 and F12 by PRM.
- **b** Cumulative bar plots of peak area of retention curves in **a** for patients and controls. Color code is same as **a**.
- **c** Boxplots of PRM detection intensity of MST1, SHBG, PRG2 and F12 in patients and controls.

**P-value** < 0.01, *****P-value** < 0.001, Wilcoxon Rank Sum test.
Figure. S4. Boxplots of PRM intensity for the 10 DE proteins between severe and moderate patients.

Data from the normal controls are also shown. All of these 10 proteins showed significant up-regulation in severe vs. moderate patient comparison. However, 7 of these proteins showed insignificant change between moderate patients and normal controls, and 3 even showed significant up-regulation in normal. * P-value < 0.05, ** P-value < 0.01, ns: not significant, Wilcoxon Rank Sum test.
Figure. S5. MS/MS spectra for target peptides identified for DTT, OAF, MB, CAPNS1, SOD2, GSTO1, RPS28 and S100A8 by PRM.
Figure S6. PRM validation results for selected up-regulated proteins in severe COVID-19 patients.

a Validation of target peptides of DDT, OAF and MB by PRM. b Cumulative bar plots of peak area of retention curves in A for severe and moderate patients. Color code is same as a. Dashed vertical lines separates severe and moderate patients.
Figure. S7. PRM validation results for selected up-regulated proteins in severe COVID-19 patients.

**a** Validation of target peptides of CAPNS1, SOD2, GSTO1, RPS28 and S100A8 by PRM. **b** Cumulative bar plots of peak area of retention curves in a for severe and moderate patients. Color code is same as a. **c** Boxplots of PRM detection intensity of CAPNS1, SOD2, GSTO1, RPS28 and S100A8 in severe and moderate patients. * P-value < 0.05, ** P-value < 0.01, Wilcoxon Rank Sum test.
Figure. S8. Summary of random forest machine-learning results for selected DE proteins between severe and moderate COVID-19 patients.

a Importance ranking for the 8 selected severe patient specific proteins used for random forest model. b ROC of the random forest machine-learning model using proteomics data of the 8 selected proteins for screening severe patients among all patients. The AUC is quoted with the 95% confidence interval values in brackets.
Figure. S9. Summary of the iterative random forest machine-learning leveraging proteomics data of distinct protein combinations.

a Workflow of the iterative random forest machine-learning approach. AUC (b), Sensitivity (c) and Specificity (d) ranking of all 255 random forest models with different number of features. The dashed lines indicate the fitted lines showing the AUC, sensitivity and specificity trend. The color-code indicates the number of features used for each random forest model building.
Figure. S10. ELISA and Random forest machine-learning summary on ELISA validation results of DDT, MB and OAF with 50 COVID-19 patients in Validation group.

a Boxplots of ELISA detection values of GST01, RPS28, SOD2, S100A8 and CAPNS1 between moderate (n=21) and severe (n=29) COVID-19 patients. b ROC of the random forest model built with the ELISA data of DDT, MB and OAF. The AUC is quoted with the 95% confidence interval values in brackets. c Confusion matrix showing the classification result by random forest analysis with 5-fold cross-validation on the ELISA data. Majority of moderate (n=18) and severe (n=25) samples were correctly classified, indicating the ELISA results of DDT, MB and OAF were reliable in screening severe COVID-19 patients. ** P-value < 0.01, ns: not significant, Wilcoxon Rank Sum test.
Table S1. Clinical Characteristics at admission of 23 COVID-19 patients (Development group)

| Characteristics                        | All Patients (n=23) | Moderate * (n=8) | Severe* (n=15) | P     |
|----------------------------------------|---------------------|------------------|----------------|-------|
| Age, median (IQR), year                | 56.00(43.00-62.00)  | 46.00(43.00-58.00) | 61.00(37.00-64.00) | 0.39  |
| Female sex                             | 9(39.1%)            | 4(50.0%)         | 5(33.3%)       | 0.44  |
| Coexisting disorder#                   | 10(43.5%)           | 3(37.5%)         | 7(46.7%)       | 0.67  |
| Clinical signs and symptoms            |                     |                  |                |       |
| Fever                                  | 18(78.3%)           | 6(75.0%)         | 12(80.0%)      | 1.00  |
| Cough                                  | 18(78.3%)           | 7(87.5%)         | 11(73.3%)      | 0.62  |
| Chilly                                 | 6(28.6%)            | 2(28.6%)         | 4(28.6%)       | 1.00  |
| Myalgia                                | 9(42.9%)            | 3(42.9%)         | 6(42.9%)       | 1.00  |
| Fatigue                                | 11(52.4%)           | 5(71.4%)         | 6(42.9%)       | 0.36  |
| Rhinorrhoea                            | 4(19.0%)            | 2(28.6%)         | 2(14.3%)       | 0.57  |
| Shortness of breath                    | 6(28.6%)            | 1(14.3%)         | 5(35.7%)       | 0.61  |
| Sore throat                            | 5(21.7%)            | 3(37.5%)         | 2(13.3%)       | 0.30  |
| Nausea or vomiting                     | 3(14.3%)            | 2(28.6%)         | 1(7.1%)        | 0.25  |
| Diarrhea                               | 2(8.7%)             | 0(0%)            | 2(13.3%)       | 0.53  |
| Chest CT findings                      |                     |                  |                |       |
| Ground-glass opacity                   | 10(43.5%)           | 4(50.0%)         | 6(40.0%)       | 0.69  |
| Local mottling shadow                  | 4(17.4%)            | 1(12.5%)         | 3(20.0%)       | 1.00  |
| Bilateral mottling shadow              | 11(47.8%)           | 4(50.0%)         | 7(46.7%)       | 1.00  |
| Laboratory parameters                  |                     |                  |                |       |
| Leucocytes(x10⁹/L; NR:3.5-7.0)         | 4.48(3.93-6.31)     | 4.54(4.08-6.95)  | 4.29(3.90-6.31) | 0.87  |
| Lymphocytes(x10⁹/L; NR:1.1-3.7)        | 1.07(0.86-1.56)     | 1.35(1.03-2.53)  | 0.99(0.62-1.53) | 0.08  |
| Neutrophils(x10⁹/L; NR:1.8-7.5)        | 2.96(2.23-4.94)     | 2.66(2.27-4.57)  | 3.17(2.16-4.94) | 0.39  |
| Platelets(x10⁹/L; NR:125.0-450.0)      | 193.00(145.00-333.00) | 208.00(187.75-218.00) | 173.00(134.00-208.00) | 0.19  |
| HGB(g/L; NR:130.0-175.0)               | 138.00(119.00-203.00) | 141.00(124.50-205.00) | 133.00(116.00-147.00) | 0.36  |
| APTT(s; NR:21.0-37.0)                  | 40.20(36.10-42.40)  | 38.90(36.50-40.18) | 40.70(36.10-43.10) | 0.12  |
| PT(s; NR:10.5-13.5)                    | 13.70(13.30-14.50)  | 13.60(13.25-14.05) | 13.80(13.30-14.70) | 0.68  |
| D-dimer(mg/L; NR:0-500)                | 1240.00(910.00-1700.00) | 950.00(625.00-1500.00) | 1560.00(1150.00-2080.00) | 0.03  |
| Albumin(g/L; NR:40.0-55.0)             | 37.70(35.30-41.50)  | 40.95(36.50-43.65) | 36.20(32.50-40.80) | 0.13  |
| ALT (U/L; NR:9.0-50.0)                 | 26.30(18.30-41.00)  | 24.10(19.98-37.33) | 33.30(18.20-44.90) | 0.83  |
| AST (U/L; NR:15.0-40.0)                | 22.40(17.40-33.70)  | 19.15(16.10-20.65) | 25.30(19.00-39.40) | 0.06  |
| TB (μmol/L; NR:0.0-21.0)               | 11.02(8.76-17.50)   | 13.73(10.62-20.77) | 17.30(7.31-17.50) | 0.43  |
| BUN (mmol/L; NR:3.6-9.5)               | 4.21(3.18-5.22)     | 4.33(3.31-4.86)   | 3.54(3.18-5.78)  | 0.94  |
| Scr (μmol/L; NR:57.0-111.0)            | 64.70(51.40-72.00)  | 65.50(60.20-73.83) | 63.30(48.60-72.00) | 0.51  |
| CK (U/L; NR:50.0-310.0)                | 58.00(44.00-100.50) | 51.00(43.00-84.00) | 61.50(44.00-151.75) | 0.32  |
| LDH (U/L; NR:120.0-250.0)              | 208.00(155.50-220.00) | 158.00(139.00-223.00) | 192.50(407.50-410.50) | 0.06  |
| CRP (mg/L; NR:0.0-5.0)                 | 4.90(4.90-32.46)    | 4.90(4.90-21.39)  | 4.90(4.90-43.96) | 0.59  |
*Classification of COVID-19 severity is based on whether the patient required intensive care during treatments.

Data are presented in median (IQR), or n (%);

$P$ values are derived from Rank sum test, $\chi^2$ test, or Fisher’s exact test;

#including Hypertension, Diabetes, and Hyperlipemia;

Abbreviations: NR=Normal Range, HGB=Haemoglobin, APTT=activated partial thromboplastin time, PT=prothrombin time, ALT=alanine aminotransferase, AST=aspartate aminotransferase, TB=Total bilirubin, BUN=blood urea nitrogen, Scr=serum creatinine, CK=creatine kinase, LDH=lactate dehydrogenase, CRP=C reactive protein.
| Characteristics                                      | All Patients (n=50) | Moderate (n=21) | Severe (n=29) | P       |
|-----------------------------------------------------|---------------------|----------------|---------------|---------|
| Age, median (IQR), year                             | 56.00(44.00-62.00)  | 47.00(44.00-59.00) | 29.00(37.00-63.50) | 0.38    |
| Female sex                                          | 31(62.00%)          | 11(52.38%)      | 20(68.97%)     | 0.23    |
| Coexisting disorder*                                | 26(52.00%)          | 9(42.86%)       | 17(58.62%)     | 0.27    |
| Clinical signs and symptoms                         |                     |                |               |         |
| Fever                                               | 39(78.00%)          | 15(71.43%)      | 24(82.76%)     | 0.54    |
| Cough                                               | 40(80.00%)          | 19(90.48%)      | 21(72.41%)     | 0.22    |
| Chilly                                              | 11(22.00%)          | 3(14.29%)       | 8(27.59%)      | 0.52    |
| Myalgia                                             | 19(38.00%)          | 7(33.33%)       | 12(41.38%)     | 0.71    |
| Fatigue                                             | 25(50.00%)          | 14(66.67%)      | 11(37.93%)     | 0.01    |
| Rhinorrheoa                                         | 9(18.00%)           | 6(28.57%)       | 3(10.34%)      | 0.14    |
| Shortness of breath                                 | 6(12.00%)           | 0               | 6(20.69%)      | 0.03    |
| Sore throat                                         | 12(24.00%)          | 9(42.86%)       | 3(10.34%)      | 0.00    |
| Nausea or vomiting                                  | 8(16.00%)           | 6(28.57%)       | 2(6.90%)       | 0.02    |
| Diarrhea                                            | 4(8.00%)            | 0               | 4(13.79%)      | 0.07    |
| Chest CT findings                                   |                     |                |               |         |
| Ground-glass opacity                                | 23(46.00%)          | 12(57.10%)      | 11(37.90%)     | 0.25    |
| Local mottling shadow                               | 7(14.00%)           | 2(9.50%)        | 5(17.20%)      | 0.68    |
| Bilateral mottling shadow                           | 24(48.00%)          | 10(47.60%)      | 14(48.30%)     | 1.00    |
| Laboratory parameters                               |                     |                |               |         |
| Leucocytes$x\times 10^9$/L; NR:3.5-11.0 (n=17)      | 4.54(4.02-6.31)     | 4.60(4.05-6.52) | 4.29(3.92-6.31) | 0.82    |
| Lymphocytes$x\times 10^9$/L; NR:0.8-1.5 (n=17)      | 1.07(0.88-1.61)     | 1.32(1.02-2.79) | 0.99(0.62-1.53) | 0.00    |
| Neutrophils$x\times 10^9$/L; NR:1.8-11.0 (n=17)     | 2.93(2.23-4.94)     | 2.83(2.23-4.01) | 3.17(2.16-4.94) | 0.09    |
| Platelets$x\times 10^9$/L; NR:125.0-350.0 (n=17)    | 193.00(145.00-257.0) | 220.00(186.00-257.0) | 173.00(134.00-225.75) | 0.04    |
| HGB(g/L; NR:130.0-175.0)                            | 138.00(119.75-183.75) | 140.00(120.00-183.75) | 133.00(116.50-166.20) | 0.16    |
| APTT(s; NR:21.0-37.0)                                | 40.10(36.25-41.43)  | 38.90(37.30-40.10) | 40.70(36.20-43.10) | 0.10    |
| PT(s; NR:10.5-13.5)                                 | 13.65(13.28-14.30)  | 13.50(13.20-13.90) | 13.80(13.30-14.70) | 0.36    |
| D-dimer(mg/L; NR:0.0-500)                           | 1195.00(910.00-1230.00) | 990.00(700.00-1560.00) | 1560.00(1196.00-1620.00) | 0.05    |
| Albumin (g/L; NR:40.0-55.0)                         | 37.90(35.30-41.63)  | 41.00(35.30-43.10) | 36.20(32.50-40.80) | 0.02    |
| ALT (U/L; NR:9.0-50.0)                              | 26.30(19.28-41.00)  | 25.40(21.43-41.00) | 33.30(18.25-44.90) | 0.22    |
| AST (U/L; NR:15.0-40.0)                             | 21.60(18.60-33.40)  | 19.20(16.70-20.80) | 25.30(20.70-39.40) | 0.00    |
| TB (μmol/L; NR:0.0-21.0)                            | 11.36(8.99-18.47)   | 14.59(10.75-22.45) | 10.73(8.04-17.50) | 0.41    |
| BUN (mmol/L; NR:3.6-9.5)                            | 4.33(3.19-5.32)     | 4.35(4.09-4.86)  | 3.54(3.18-5.78)  | 0.22    |
| Scr (μmol/L; NR:57.0-111.0)                         | 64.90(55.30-72.33)  | 66.10(58.70-76.30) | 63.30(48.60-72.00) | 0.47    |
| CK (U/L; NR:50.0-310.0)                             | 57.00(44.00-97.00)  | 51.00(43.00-84.00) | 63.00(44.00-139.00) | 0.00    |
| LDH (U/L; NR:120.0-250.0)                           | 208.00(158.00-342.00) | 173.50(149.50-225.00) | 225.00(198.00-257.00) | 0.00    |
| CRP (mg/L; NR:0.0-5.0)                              | 4.90(4.90-32.46)    | 4.90(4.90-20.73)  | 4.90(4.90-43.96)  | 0.15    |

Data are presented in median (IQR), or n (%); 
P values are derived from t test, χ² test, or Fisher’s exact test; 
*including Hypertension, Diabetes, and Hyperlipemia; 
Abbreviations: NR=normal range, HGB=haemoglobin, APTT=activated partial thromboplastin time, PT=prothrombin time, ALT=alanine aminotransferase, AST=aspartate aminotransferase, TB=total bilirubin, BUN=blood urea nitrogen, Scr=serum creatinine, CK=creatine kinase, 
LDH=lactate dehydrogenase, CRP= C reactive protein. 

Table S2. Clinical Characteristics at admission of 50 COVID-19 patients (Validation group)
Table S3. 90 differentially expressed proteins between COVID-19 patient group I and controls.

| Gene name  | Protein Accession | Ratio(Pati ent/Contr ol) | Up Or Down | Adjusted P-value | Protein Description |
|------------|------------------|--------------------------|------------|------------------|---------------------|
| SAA2       | P0DU9            | 11.448                   | UP         | 0.0066           | Serum amyloid A-2 protein |
| SAA1       | P0DU8            | 5.874                    | UP         | 0.0098           | Serum amyloid A-1 protein |
| CRP        | P02741           | 5.059                    | UP         | 0.0179           | C-reactive protein    |
| ATP6V1G2   | Q95670           | 3.573                    | UP         | 0.0397           | V-type proton ATPase subunit G 2 |
| H2AC4      | P04908           | 3.147                    | UP         | 0.0125           | Histone H2A type 1-B/E |
| HBB        | Q0GZL9           | 2.896                    | UP         | 0.0012           | Beta-globin (Fragment) |
| KRT6B      | P04259           | 2.747                    | UP         | 0.0331           | Keratin, type II cytoskeletal 6B |
| PSMB2      | P49721           | 2.735                    | UP         | 0.0092           | Proteasome subunit beta type-2 |
| H3-2       | Q5TEC6           | 2.690                    | UP         | 0.0143           | Histone H3            |
| H4C1       | P62805           | 2.651                    | UP         | 0.0382           | Histone H4            |
| H28C12     | O60814           | 2.645                    | UP         | 0.0178           | Histone H2B type 1-K  |
| MYH7       | P12883           | 2.393                    | UP         | 0.0227           | Myosin-7              |
| DDT        | P30046           | 2.352                    | UP         | 0.0143           | D-opochromal decarboxylase |
| S10A09     | P06702           | 2.340                    | UP         | 0.0015           | Protein S100-A         |
| S10A08     | P05109           | 2.290                    | UP         | 0.0006           | Protein S100-A8        |
| ACTA2      | P62736           | 2.115                    | UP         | 0.0078           | Actin, aortic smooth muscle |
| YWHAG      | P61981           | 2.020                    | UP         | 0.0020           | 14-3-3 protein gamma  |
| OSBPL7     | Q9FBF2           | 2.011                    | UP         | 0.0293           | Oxysterol-binding protein-related protein 7 |
| A0A068LKQ8 | A0A068LKQ8       | 1.988                    | UP         | 0.0310           | Ig heavy chain variable region (Fragment) |
| ORM1       | P02763           | 1.985                    | UP         | 0.0001           | Alpha-1-acid glycoprotein 1 |
| C21orf59-TC10L | F8VZ95             | 1.893                    | UP         | 0.0056           | Uncharacterized protein (Fragment) |
| R528       | P62857           | 1.835                    | UP         | 0.0115           | 40S ribosomal protein S28 |
| UBB        | P0CG47           | 1.823                    | UP         | 0.0179           | Polyubiquitin-B         |
| HBA2       | G3V1N2           | 1.810                    | UP         | 0.0114           | HCG1745306, isoform CRA_a |
| ACS6       | P02743           | 1.744                    | UP         | 0.0159           | Serum amyloid P-component |
| P5MB3      | P49720           | 1.728                    | UP         | 0.0036           | Proteasome subunit beta type-3 |
| ORM2       | P19652           | 1.698                    | UP         | 0.0024           | Alpha-1-acid glycoprotein 2 |
| LgI        | A0A2UBJ9D05      | 1.675                    | UP         | 0.0068           | Ig heavy chain variable region (Fragment) |
| CA1        | P00915           | 1.650                    | UP         | 0.0279           | Carbonic anhydrase 1    |
| VASP       | P05552           | 1.631                    | UP         | 0.0065           | Vasodilator-stimulated phosphoprotein |
| Q0ZCI1     | Q0ZCI1           | 1.626                    | UP         | 0.0404           | Immunglobulin heavy chain variable region (Fragment) |
| HBA2       | A0A15SU239       | 1.615                    | UP         | 0.0201           | Hemoglobin subunit alpha |
| GNA12      | P04B99           | 1.606                    | UP         | 0.0004           | Guanine nucleotide-binding protein G(i) subunit alpha-2 |
| SAA2-SA3   | A0A066AOA8       | 1.598                    | UP         | 0.0423           | Serum amyloid A protein |
| CSTB       | P04080           | 1.595                    | UP         | 0.0328           | Cystatin-B             |
| KHNYN      | O15037           | 1.592                    | UP         | 0.0038           | Protein KHNYN          |
| A0A125QY7  | A0A125QY7        | 1.574                    | UP         | 0.0382           | IBM-B1 heavy chain variable region (Fragment) |
| SERPINA3   | P01011           | 1.573                    | UP         | 0.0038           | Alpha-1-antichymotrypsin |
| B721F8     | B721F8           | 1.566                    | UP         | 0.0477           | cDNA FLJ53025, highly similar to Complement C4-B |
| EEF2       | P13639           | 1.552                    | UP         | 0.0331           | Elongation factor 2    |
| H6PD       | O95479           | 1.547                    | UP         | 0.0311           | GDH/6PGl endoplasmic bifunctional protein |
| C4BPB      | P20851           | 1.533                    | UP         | 0.0125           | C4b-binding protein beta chain |
| C4A        | P0CD4L           | 1.509                    | UP         | 0.0251           | Complement C4-A         |
| CBP2       | Q96Y4I           | 0.666                    | DOWN       | 0.0201           | Carboxypeptidase B2    |
| AFM        | P43652           | 0.664                    | DOWN       | 0.0201           | Afpamin                |
| EFCAB7     | A8K855           | 0.663                    | DOWN       | 0.0466           | EF-hand calcium-binding domain-containing protein 7 |
| TMEM198    | Q66K66           | 0.662                    | DOWN       | 0.0311           | Transmembrane protein 198 |
| C3orf85    | A0A1B0GTC6       | 0.660                    | DOWN       | 0.0039           | Uncharacterized protein C3orf85 |
| PPBP       | P02775           | 0.657                    | DOWN       | 0.0125           | Platelet basic protein  |
| CDS5       | D43866           | 0.654                    | DOWN       | 0.0098           | CDS antigen-like       |
| CHS1       | P0DML2           | 0.649                    | DOWN       | 0.0351           | Chorionic somatomammotropin hormone 1 |
| SELL       | P14151           | 0.649                    | DOWN       | 0.0143           | L-selectin             |
| NME3       | Q13232           | 0.648                    | DOWN       | 0.0125           | Nucleoside diphosphate kinase 3 |
| V4-2       | Q5NBV2           | 0.641                    | DOWN       | 0.0125           | V4-2 protein (Fragment) |
| Gene          | Name/Description                                                                 | Log2 Fold Change | p-value   |
|---------------|-----------------------------------------------------------------------------------|------------------|-----------|
| MMRN1         | Multimerin-1                                                                      | 0.633            | 0.0311    |
| PROC          | Vitamin K-dependent protein C                                                     | 0.630            | 0.0103    |
| APOL1         | Apolipoprotein L1                                                                 | 0.623            | 0.0251    |
| DKFZp686C15213| Uncharacterized protein DKFZp686C15213                                            | 0.622            | 0.0102    |
| IGLV7-43      | Immunoglobulin lambda variable 7-43                                              | 0.622            | 0.0225    |
| TGFβ1         | Transforming growth factor beta-1 proprotein                                      | 0.611            | 0.0293    |
| PSMC2         | Apolipoprotein A-I                                                                | 0.608            | 0.0102    |
| IHG           | Keratin, type I cytoskeletal 9                                                    | 0.607            | 0.0423    |
| IGKV1D-43     | Immunoglobulin kappa variable 1D-43                                              | 0.601            | 0.0028    |
| CGB1          | Heparanase                                                                        | 0.600            | 0.0102    |
| V1-11         | V1-11 protein (Fragment)                                                          | 0.559            | 0.0279    |
| IGKV6-21      | Immunoglobulin kappa variable 6-21                                               | 0.559            | 0.0015    |
| IGKV1D-43     | Immunoglobulin kappa variable 1D-43                                              | 0.545            | 0.0029    |
| CGB1          | Keratin, type I cytoskeletal 9                                                    | 0.542            | 0.0143    |
| SAR1A         | GTP-binding protein SAR1a                                                         | 0.542            | 0.0360    |
| CCL5          | Leptin                                                                            | 0.516            | 0.0327    |
| RBP4          | C-C motif chemokine 5                                                             | 0.516            | 0.0201    |
| HPSE          | Retinol-binding protein 4                                                          | 0.515            | 0.0423    |
| HECW1         | Heparanase                                                                        | 0.497            | 0.0086    |
| PTGDS         | E3 ubiquitin-protein ligase HECW1                                                 | 0.449            | 0.0378    |
| ITHH4         | Prostaglandin-H2 D-isomerase                                                      | 0.431            | 0.0000    |
| B4DPP8        | Inter-alpha-trypsin inhibitor heavy chain H4                                      | 0.424            | 0.0159    |
| MT1           | Hepatocyte growth factor like protein                                             | 0.393            | 0.0397    |

**Note:** The p-values indicate the significance of the fold change, with lower values indicating a more significant change. The Log2 Fold Change represents the fold change in expression compared to the reference condition.
Table S4. Significantly enriched GO biological process terms for COVID-19 patient-specific proteins.

| GO.ID    | Term                        | GO:0006953 | GO:0002526 | GO:0006954 | GO:0002443 | GO:0006952 | GO:0002376 | GO:0006955 | GO:0006950 | GO:0002682 | GO:0045087 | GO:0002252 | GO:0043312 | GO:0070488 | GO:0002283 | GO:0002446 | GO:0042119 | GO:0016192 |
|----------|-----------------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| GO:0006953 | acute-phase response        | 47         | 7          | 47         | 7          | 47         | 7          | 47         | 7          | 47         | 7          | 47         | 7          | 47         | 7          | 47         | 7          | 47         |
| GO:0002526 | acute inflammatory response | 218        | 10         |            | 10         |            |            |            |            |            |            |            |            |            |            |            |            |            |
| GO:0006954 | inflammatory response       | 875        | 12         | 875        | 12         | 875        | 12         | 875        | 12         | 875        | 12         | 875        | 12         | 875        | 12         | 875        | 12         | 875        |
| GO:0006955 | defense response            | 878        | 12         | 878        | 12         | 878        | 12         | 878        | 12         | 878        | 12         | 878        | 12         | 878        | 12         | 878        | 12         | 878        |
| GO:0002376 | immune system process       | 3229       | 20         |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| GO:0006950 | response to stress          | 4178       | 22         |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| GO:0002682 | regulation of immune system process | 1686 | 14 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| GO:0045087 | innate immune response      | 1015       | 11         |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| GO:0002252 | immune effector process     | 1276       | 12         |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| GO:0043312 | neutrophil degranulation    | 483        | 8          |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| GO:0070488 | neutrophil aggregation      | 2          | 2          |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| GO:0002283 | neutrophil activation       | 486        | 8          |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| GO:0002446 | neutrophil mediated immunity| 496        | 8          |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| GO:0042119 | neutrophil activation       | 497        | 8          |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| GO:0016192 | vesicle-mediated transport  | 2117       | 15         |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| GO:0036230 | granulocyte activation | 504 | 8 | 1 | 5.10E-06 | 0.00051 | CSTB,EEF2,HBB,ORM1,ORM2,S100A8,S100A9,SERPINA3 |
|-----|------------------------|-----|----|---|-----------|---------|-----------------------------------------------|
| GO:0006959 | humoral immune response | 361 | 7 | 0.72 | 5.90E-06 | 0.00059 | APCS,C4A,C4BPs,CRP,H2BC1,2,S100A8,S100A9 |
| GO:0031347 | regulation of defense response | 907 | 10 | 1.81 | 7.20E-06 | 0.00072 | APCS,C4A,C4BPs,DDT,PSMB2,PSMB3,S100A8,S100A9,SAA1,UBB |
| GO:0043299 | leukocyte degranulation | 531 | 8 | 1.06 | 7.50E-06 | 0.00075 | CSTB,EEF2,HBB,ORM1,ORM2,S100A8,S100A9,SERPINA3 |
| GO:0002253 | activation of immune response | 717 | 9 | 1.43 | 8.10E-06 | 0.00081 | APCS,C4A,C4BPs,CRP,PSMB2,PSMB3,S100A8,S100A9,UBB |
| GO:0002275 | myeloid cell activation involved in immune response | 541 | 8 | 1.08 | 8.60E-06 | 0.00086 | CSTB,EEF2,HBB,ORM1,ORM2,S100A8,S100A9,SERPINA3 |
| GO:0002444 | myeloid leukocyte mediated immunity | 547 | 8 | 1.09 | 9.30E-06 | 0.00093 | CSTB,EEF2,HBB,ORM1,ORM2,S100A8,S100A9,SERPINA3 |
| GO:0050896 | response to stimulus | 9377 | 31 | 18.66 | 9.70E-06 | 0.00097 | ACTA2,APCS,ATP6V1G2,C4A,C4BPs,CA1,CRP,CSTB,DDT,EEF2,GNAI2,HBB,H2BC12,H4-16,H4C11,H6PD,HBA2,HBB,MHY7,ORM1,ORM2,OSBPL7,PSMB2,PSMB3,S100A8,S100A9,SAA1,SAA2,SERPINA3,UBB,VASP,YWHAG |
| GO:0045055 | regulated exocytosis | 792 | 9 | 1.58 | 1.80E-05 | 0.0018 | CSTB,EEF2,GNAI2,HBB,ORM1,ORM2,S100A8,S100A9,SERPINA3 |
| GO:0002274 | myeloid leukocyte activation | 656 | 8 | 1.31 | 3.50E-05 | 0.0035 | CSTB,EEF2,HBB,ORM1,ORM2,S100A8,S100A9,SERPINA3 |
| GO:0050778 | positive regulation of immune response | 888 | 9 | 1.77 | 4.40E-05 | 0.0044 | APCS,C4A,C4BPs,CRP,PSMB2,PSMB3,S100A8,S100A9,UBB |
| GO:0050727 | regulation of inflammatory response | 502 | 7 | 1 | 5.00E-05 | 0.005 | APCS,C4A,C4BPs,DDT,S100A8,S100A9,UBB |
| GO:0006887 | exocytosis | 903 | 9 | 1.8 | 5.00E-05 | 0.005 | CSTB,EEF2,GNAI2,HBB,ORM1,ORM2,S100A8,S100A9,SERPINA3 |
| GO:0006810 | transport | 5239 | 22 | 10.43 | 5.10E-05 | 0.0051 | ATP6V1G2,C4A,C4BPs,CA1,CRP,CSTB,EEF2,GNAI2,HBA2,HBB,ORM1,ORM2,OSBPL7,PSMB2,PSMB3,PSMB5,PSMB8,S100A8,S100A9,SAA1,SERPINA3,UBB,YWHAG |
| GO:0002366 | leukocyte activation involved in immune response | 704 | 8 | 1.4 | 5.70E-05 | 0.0057 | CSTB,EEF2,HBB,ORM1,ORM2,S100A8,S100A9,SERPINA3 |
| GO:0002263 | cell activation involved in immune response | 708 | 8 | 1.41 | 5.90E-05 | 0.0059 | CSTB,EEF2,HBB,ORM1,ORM2,S100A8,S100A9,SERPINA3 |
| GO:0050716 | positive regulation of interleukin-1 secretion | 39 | 3 | 0.08 | 6.30E-05 | 0.0063 | ORM1,ORM2,SAA1 |
| GO:0051234 | establishment of localization | 5362 | 22 | 10.67 | 7.60E-05 | 0.0076 | ATP6V1G2,C4A,C4BPB,CA1,CRP,CSTB,EFF2,GNAI2,HBA2,HBB,ORM1,ORM2,OSBPL7,PSMB2,PSMB3,RPS28,S100A8,S100A9,SAA1,SERPINA3,UBB,YWHAG |
|-------------|--------------------------------|------|-----|--------|-----------|--------|--------------------------------|
| GO:0015701 | bicarbonate transport | 42 | 3 | 0.08 | 7.90E-05 | 0.0079 | CA1,HBA2,HBB |
| GO:0065008 | regulation of biological quality | 4129 | 19 | 8.22 | 8.00E-05 | 0.0089 | ACTA2,ATP6V1G2,C4BPB,CRP,GNAI2,H4-16,H4C1,H6PD,HBB,MYH7,PSMB2,PSMB3,S100A8,S100A9,SAA1,SERPINA3,UBB,YWHAG |
| GO:0031323 | regulation of cellular metabolic process | 6329 | 24 | 12.6 | 8.90E-05 | 0.0080 | ACTA2,APCS,ATP6V1G2,C4A,C4BPB,CRP,CSTB,DDT,EFF2,GNAI2,H2AC4,H4-16,H4C1,H6PD,HBB,OSBPL7,PSMB2,PSMB3,S100A8,S100A9,SAA1,SERPINA3,UBB,YWHAG |
| GO:0032119 | sequestering of zinc ion | 8 | 2 | 0.02 | 0.0001 | 0.0111 | S100A8,S100A9 |
| GO:0019222 | regulation of metabolic process | 6988 | 25 | 13.91 | 0.0001 | 0.0144 | ACTA2,APCS,ATP6V1G2,C4A,C4BPB,CRP,CSTB,DDT,EFF2,GNAI2,H2AC4,H4-16,H4C1,H6PD,HBB,OSBPL7,PSMB2,PSMB3,S100A8,S100A9,SAA1,SERPINA3,UBB,YWHAG |
| GO:0032940 | secretion by cell | 1563 | 11 | 3.11 | 0.0001 | 0.0152 | CRP,CSTB,EFF2,GNAI2,HBB,ORM1,ORM2,S100A8,S100A9,SAA1,SERPINA3 |
| GO:0006958 | complement activation, classical pathway | 140 | 4 | 0.28 | 0.0001 | 0.0178 | APCS,C4A,C4BPB,CRP |
| GO:0030162 | regulation of proteolysis | 839 | 8 | 1.67 | 0.0001 | 0.0199 | C4A,C4BPB,CSTB,OSBPL7,PSMB2,PSMB3,S100A8,S100A9,SAA1,SERPINA3,UBB,YWHAG |
| GO:0050704 | regulation of interleukin-1 secretion | 59 | 3 | 0.12 | 0.0002 | 0.0221 | ORM1,ORM2,SAA1 |
| GO:0002455 | humoral immune response mediated by circulating immunoglobulin | 154 | 4 | 0.31 | 0.0002 | 0.0248 | APCS,C4A,C4BPB,CRP |
| GO:0032732 | positive regulation of interleukin-1 production | 61 | 3 | 0.12 | 0.0002 | 0.0240 | ORM1,ORM2,SAA1 |
| GO:0009605 | response to external stimulus | 2595 | 14 | 5.16 | 0.0002 | 0.0241 | ACTA2,APCS,C4A,C4BPB,CRP,DDT,EFF2,GNAI2,H2BC12,S100A8,S100A9,SAA1,SAA2,VP |
| GO:2001244 | positive regulation of intrinsic apoptotic signaling pathway | 62 | 3 | 0.12 | 0.0002 | 0.0255 | S100A8,S100A9,UBB |
| GO:0050776 | regulation of immune response | 1116 | 9 | 2.22 | 0.0002 | 0.0258 | APCS,C4A,C4BPB,CRP,PSMB2,PSMB3,S100A8,S100A9,UBB,YWHAG |
| GO:0070887 | cellular response to chemical stimulus | 3327 | 16 | 6.62 | 0.0002 | 0.027 | ATP6V1G2,CA1,DDT,EEF2,GNAI2,HBA2,HBB,OSBP17,PSMB2,PSMB3,S100A8,S100A9,SA1,SA2,UBB,YWHAG |
| GO:0002758 | innate immune response-activating signal transduction | 294 | 5 | 0.59 | 0.0002 | 0.027 | PSMB2,PSMB3,S100A8,S100A9,UBB |
| GO:0035821 | modification of morphology or physiology of other organism | 162 | 4 | 0.32 | 0.0002 | 0.029 | APCS,CRP,H2BC12,S100A9 |
| GO:0008228 | opsonization | 13 | 2 | 0.03 | 0.0003 | 0.03 | C4BPB,CRP |
| GO:0044793 | negative regulation by host of viral process | 13 | 2 | 0.03 | 0.0003 | 0.03 | APCS,CRP |
| GO:0070486 | leukocyte aggregation | 13 | 2 | 0.03 | 0.0003 | 0.03 | S100A8,S100A9 |
| GO:0002758 | innate immune response-activating signal transduction | 294 | 5 | 0.59 | 0.0002 | 0.027 | PSMB2,PSMB3,S100A8,S100A9,UBB |
| GO:0035821 | modification of morphology or physiology of other organism | 162 | 4 | 0.32 | 0.0002 | 0.029 | APCS,CRP,H2BC12,S100A9 |
| GO:0008228 | opsonization | 13 | 2 | 0.03 | 0.0003 | 0.03 | C4BPB,CRP |
| GO:0044793 | negative regulation by host of viral process | 13 | 2 | 0.03 | 0.0003 | 0.03 | APCS,CRP |
| GO:0070486 | leukocyte aggregation | 13 | 2 | 0.03 | 0.0003 | 0.03 | S100A8,S100A9 |
| GO:0060326 | cell chemotaxis | 303 | 5 | 0.6 | 0.0003 | 0.031 | DDT,S100A8,S100A9,SAA1,SAA2 |
| GO:0046903 | secretion | 1703 | 11 | 3.39 | 0.0003 | 0.032 | CRP,CTST,EEF2,GNAI2,HBB,ORM1,ORM2,S100A8,S100A9,SAA1,SERPIN3 |
| GO:0051179 | localization | 6792 | 24 | 13.52 | 0.0003 | 0.032 | ATP6V1G2,CA1,CA4,CRP,CSTB,DDT,EEF2,GNAI2,HBB,OSBP17,PSMB2,PSMB3,PSMB9,RPS28,S100A8,S100A9,SAA1,SERPIN3,UBB,YWHAG |
| GO:0002218 | activation of innate immune response | 316 | 5 | 0.63 | 0.0003 | 0.038 | S100A8,S100A9 |
| GO:0006956 | complement activation | 175 | 4 | 0.35 | 0.0003 | 0.039 | APCS,CA4,C4BPB,CRP |
| GO:0002523 | leukocyte migration involved in inflammatory response | 15 | 2 | 0.03 | 0.0004 | 0.04 | S100A8,S100A9 |
| GO:0015671 | oxygen transport | 15 | 2 | 0.03 | 0.0004 | 0.04 | HBA2,HBB |
| GO:0017014 | protein nitrosylation | 15 | 2 | 0.03 | 0.0004 | 0.04 | S100A8,S100A9 |
| GO:0018119 | peptidyl-cysteine S-nitrosylation | 15 | 2 | 0.03 | 0.0004 | 0.04 | S100A8,S100A9 |
| GO:0051238 | sequestering of metal ion | 15 | 2 | 0.03 | 0.0004 | 0.04 | S100A8,S100A9 |
| GO:0044419 | interspecies interaction between organisms | 937 | 8 | 1.86 | 0.0004 | 0.041 | APCS,CRP,H2BC12,PSMB2,PSMB3,PSMB9,RPS28,S100A9,UBB |
| GO:0002684 | positive regulation of immune system process | 1194 | 9 | 2.38 | 0.0004 | 0.042 | APCS,CA4,C4BPB,CRP,PSMB2,PSMB3,S100A8,S100A9,UBB |
| GO:0031349 | positive regulation of defense response | 507 | 6 | 1.01 | 0.0004 | 0.044 | DDT,PSMB2,PSMB3,S100A8,S100A9,UBB |
| GO:2001235 | positive regulation of apoptotic signaling pathway | 182 | 4 | 0.36 | 0.00045 | 0.045 | S100A8,S100A9,UBB,YWHAG |
|------------|--------------------------------------------------|-----|---|------|----------|------|------------------|
| GO:0061418 | regulation of transcription from RNA polymerase II promoter in response to hypoxia | 78  | 3 | 0.16 | 0.0005  | 0.05  | PSMB2,PSMB3,UBB  |
Table S5. 24 differentially expressed proteins between severe and moderate COVID-19 cases.

| Gene name | Protein Accession | Ratio (Severe/Mild) | Up Or Down | Adjusted P-value | Protein Description |
|-----------|-------------------|---------------------|------------|------------------|---------------------|
| DDT       | P30046            | 3.584               | UP         | 0.0024           | D-dopachrome decarboxylase |
| CAPNS1    | P04632            | 2.996               | UP         | 0.0155           | Calpain small subunit 1 |
| IgH       | A0A2U8J946        | 2.790               | UP         | 0.0416           | Ig heavy chain variable region (Fragment) |
| TMSB4X    | P62328            | 2.709               | UP         | 0.0473           | Thymosin beta-4 |
| COL6A3    | P12111            | 2.645               | UP         | 0.0140           | Collagen alpha-3(VI) chain |
| UBB       | P0CG47            | 2.443               | UP         | 0.0235           | Polyubiquitin-B |
| VASP      | P50552            | 2.319               | UP         | 0.0221           | Vasodilator-stimulated phosphoprotein |
| SOD2      | P04179            | 2.228               | UP         | 0.0025           | Superoxide dismutase [Mn], mitochondrial |
| CSTB      | P04080            | 2.156               | UP         | 0.0098           | Cystatin-B |
| H4C1      | P62805            | 2.045               | UP         | 0.0473           | Histone H4 |
| MB        | P02144            | 1.976               | UP         | 0.0075           | Myoglobin |
| GSTO1     | P78417            | 1.967               | UP         | 0.0235           | Glutathione S-transferase omega-1 |
| ACTB      | P60709            | 1.953               | UP         | 0.0282           | Actin, cytoplasmic 1 |
| F8        | P09451            | 1.899               | UP         | 0.0137           | Coagulation factor VIII |
| RPS28     | P62857            | 1.770               | UP         | 0.0154           | 40S ribosomal protein S28 |
| S100A8    | P05109            | 1.733               | UP         | 0.0235           | Protein S100-A8 |
| S6C4Q9    | S6C4Q9            | 1.733               | UP         | 0.0173           | IgG L chain |
| OAF       | Q86UD1            | 1.608               | UP         | 0.0282           | Out at first protein homolog |
| S100A9    | P06702            | 1.536               | UP         | 0.0282           | Protein S100-A9 |
| TNFRSF17  | Q02223            | 1.530               | UP         | 0.0401           | Tumor necrosis factor receptor superfamily member 17 |
| CA6       | P23280            | 0.636               | DOWN       | 0.0336           | Carbonic anhydrase 6 |
| IGFALS    | P35858            | 0.604               | DOWN       | 0.0282           | Insulin-like growth factor-binding protein complex acid labile subunit |
| HSPB1     | P04792            | 0.436               | DOWN       | 0.0084           | Heat shock protein beta-1 |
| VCPIP1    | Q963H7            | 0.242               | DOWN       | 0.0303           | Deubiquitinating protein VCIP135 |
Table S6. Significantly enriched GO biological process terms for severe COVID-19 patient-specific proteins.

| GO.ID   | Term                          | Annotated | Significant | Expected | P value   | Adjusted P | Significant genes                                      |
|---------|-------------------------------|-----------|-------------|----------|-----------|------------|-------------------------------------------------------|
| GO:0070488 | neutrophil aggregation       | 2         | 2           | 0        | 1.10E-06  | 0.00011    | S100A8,S100A9                                         |
| GO:0042592 | homeostatic process          | 1950      | 10          | 2.11     | 9.90E-06  | 0.00099    | ACTB,GSTO1,H4-16,H4C1,MB,S100A8,S100A9,SO2,TNFRSF17,UBB |
| GO:0060326 | cell chemotaxis               | 303       | 5           | 0.33     | 1.40E-05  | 0.0014     | DDT,S100A8,S100A9,SA2,TMSB4X                          |
| GO:0051262 | protein tetramerization       | 145       | 4           | 0.16     | 1.60E-05  | 0.0016     | H4-16,H4C1,SO2,TMSB4X                                 |
| GO:0009636 | response to toxic substance   | 544       | 6           | 0.59     | 1.60E-05  | 0.0016     | ACTB,GSTO1,MB,S100A8,S100A9,SO2                         |
| GO:2001242 | regulation of intrinsic apoptotic signaling pathway | 168       | 4           | 0.18     | 2.80E-05  | 0.0028     | S100A8,S100A9,SO2,TMSB4X                              |
| GO:0032119 | sequestering of zinc ion      | 8         | 2           | 0.01     | 3.10E-05  | 0.0031     | S100A8,S100A9                                         |
| GO:2001244 | positive regulation of intrinsic apoptotic signaling pathway | 62        | 3           | 0.07     | 3.90E-05  | 0.0039     | S100A8,S100A9,UBB                                     |
| GO:0065008 | regulation of biological quality | 4129      | 13          | 4.46     | 4.10E-05  | 0.0041     | ACTB,F8,GSTO1,H4-16,H4C1,MB,S100A8,S100A9,SO2,TNFRSF17,UBB,VASP |
| GO:0006935 | chemotaxis                    | 647       | 6           | 0.7      | 4.40E-05  | 0.0044     | DDT,S100A8,S100A9,SA2,TMSB4X,VASP                     |
| GO:0042330 | taxis                         | 649       | 6           | 0.7      | 4.40E-05  | 0.0044     | DDT,S100A8,S100A9,SA2,TMSB4X,VASP                     |
| GO:0032501 | multicellular organismal process | 7828     | 17          | 8.46     | 6.00E-05  | 0.006      | ACTB,CAPN51,Col6A3,CSTB,DDT,F8,GSTO1,H4-16,H4C1,MB,S100A8,S100A9,SO2,TNFRSF17,UBB,VASP |
| GO:0070486 | leukocyte aggregation         | 13        | 2           | 0.01     | 8.60E-05  | 0.0086     | S100A8,S100A9                                         |
| GO:0002523 | leukocyte migration involved in inflammatory response | 15        | 2           | 0.02     | 0.0001    | 0.012      | S100A8,S100A9                                         |
| GO:0017014 | protein nitrosylation         | 15        | 2           | 0.02     | 0.0001    | 0.012      | S100A8,S100A9                                         |
| GO:0018119 | peptidyl-cysteine S-nitrosylation | 15       | 2           | 0.02     | 0.0001    | 0.012      | S100A8,S100A9                                         |
| GO:0051238 | sequestering of metal ion     | 15        | 2           | 0.02     | 0.0001    | 0.012      | S100A8,S100A9                                         |
| GO:0043044 | ATP-dependent chromatin remodeling | 90       | 3           | 0.1      | 0.0001    | 0.012      | ACTB,H4-16,H4C1                                       |
| GO:0097237 | cellular response to toxic substance | 254       | 4           | 0.27     | 0.0001    | 0.014      | ACTB,GSTO1,S100A9,SO2                                 |
| GO:0045653 | negative regulation of megakaryocyte differentiation | 18        | 2           | 0.02     | 0.0001    | 0.017      | H4-16,H4C1                                            |
| GO:0098869 | cellular oxidant detoxification | 103       | 3           | 0.11     | 0.0001    | 0.018      | GSTO1,S100A9,SO2                                      |
| GO:006954  | inflammatory response         | 875       | 6           | 0.95     | 0.0002    | 0.023      | DDT,F8,S100A8,S100A9,SA2,TMSB4X                       |
| GO:0097193 | intrinsic apoptotic signaling pathway | 291       | 4           | 0.31     | 0.0002    | 0.023      | S100A8,S100A9,SO2,TMSB4X                              |
| GO:1990748 | cellular detoxification       | 114       | 3           | 0.12     | 0.0002    | 0.024      | GSTO1,S100A9,SO2                                      |
| GO:006928  | movement of cell or subcellular component | 2239      | 9           | 2.42     | 0.0002    | 0.024      | ACTB,DDT,S100A8,S100A9,SA2,SO2,TMSB4X,UBB,VASP       |
| GO:0006950 | response to stress | 4178 | 12 | 4.51 | 0.00029 | 0.029 | ACTB, DDT, F8, H4-16, H4C1, MB, S100A8, S100A9, SAA2, SOD2, TMSB4X, UBB |
|-------------|------------------|------|----|------|---------|-------|-------------------------------------------------------------|
| GO:0065003  | protein-containing complex assembly | 1824 | 8  | 1.97 | 0.00035 | 0.035 | F8, H4-16, H4C1, RPS28, SOD2, TMSB4X, UBB, VASP |
| GO:0032103  | positive regulation of response to external stimulus | 325  | 4  | 0.35 | 0.00036 | 0.036 | DDT, S100A8, S100A9, TMSB4X |
| GO:0098754  | detoxification   | 132  | 3  | 0.14 | 0.00037 | 0.037 | GSTO1, S100A9, SOD2 |
| GO:0051235  | maintenance of location | 347  | 4  | 0.37 | 0.00046 | 0.046 | GSTO1, S100A8, S100A9, TMSB4X |
Table S7. Average AUCs for random forest model built with different combinations of proteins.

| Rank | Combinations                  | AUC       |
|------|-------------------------------|-----------|
| 1    | DDT OAF MB                     | 0.90728306|
| 2    | DDT OAF                        | 0.907392305|
| 3    | DDT MB                         | 0.907187658|
| 4    | DDT                            | 0.898882144|
| 5    | DDT OAF MB CAPNS1              | 0.866322447|
| 6    | DDT OAF GST01                  | 0.866028503|
| 7    | DDT OAF MB S100A8              | 0.860263131|
| 8    | DDT MB CAPNS1                  | 0.859293179|
| 9    | DDT MB GST01                   | 0.857223134|
| 10   | DDT GST01                      | 0.855488793|
| 11   | DDT OAF RPS28                  | 0.850739227|
| 12   | DDT MB SOD2                    | 0.850694994|
| 13   | DDT MB RPS28                   | 0.850470514|
| 14   | DDT OAF CAPNS1                 | 0.847262665|
| 15   | DDT OAF MB RPS28               | 0.845455766|
| 16   | DDT SOD2                       | 0.839511921|
| 17   | DDT MB S100A8                  | 0.83535057|
| 18   | DDT OAF SOD2                   | 0.834446108|
| 19   | DDT OAF MB GST01               | 0.827705407|
| 20   | DDT OAF MB RPS28 CAPNS1        | 0.818725293|
| 21   | DDT MB GST01 CAPNS1            | 0.814385897|
| 22   | OAF                            | 0.81427454|
| 23   | DDT GST01 CAPNS1               | 0.813774859|
| 24   | DDT MB RPS28 CAPNS1            | 0.813433477|
| 25   | DDT OAF MB S100A8 CAPNS1       | 0.812423929|
| 26   | DDT OAF MB GST01 RPS28         | 0.811800361|
| 27   | DDT GST01 SOD2                 | 0.810711752|
| 28   | DDT GST01 S100A8               | 0.809104178|
| 29   | DDT OAF MB GST01 CAPNS1        | 0.808917272|
| 30   | DDT RPS28                      | 0.807156987|
| 31   | DDT GST01 RPS28                | 0.804156987|
| 32   | DDT OAF S100A8                 | 0.8039121|
| 33   | DDT OAF GST01 CAPNS1           | 0.802585903|
| 34   | OAF MB                         | 0.801273896|
| 35   | DDT OAF MB GST01 S100A8        | 0.801249975|
| 36   | DDT MB GST01 S100A8            | 0.800129009|
| 37   | DDT OAF MB RPS28 S100A8        | 0.80071682|
| 38   | DDT MB S100A8 CAPNS1           | 0.800632488|
| 39   | DDT CAPNS1                     | 0.79805591|
|   |     |     |     |   |
|---|---|---|---|---|
| 42 | DDT | OAF | RPS28 | CAPNS1 | 0.798017799 |
| 43 | DDT | MB | SOD2 | CAPNS1 | 0.797005413 |
| 44 | DDT | MB | GST01 | RPS28 | CAPNS1 | 0.793985771 |
| 45 | DDT | OAF | MB | GST01 | RPS28 | CAPNS1 | 0.791182509 |
| 46 | DDT | OAF | MB | SOD2 | 0.78920716 |
| 47 | DDT | MB | RPS28 | S100A8 | 0.788673194 |
| 48 | DDT | MB | GST01 | SOD2 | CAPNS1 | 0.78818287 |
| 49 | DDT | OAF | MB | SOD2 | CAPNS1 | 0.78658846 |
| 50 | DDT | MB | S100A8 | SOD2 | 0.785652593 |
| 51 | DDT | OAF | MB | GST01 | S100A8 | 0.78439076 |
| 52 | DDT | MB | RPS28 | SOD2 | CAPNS1 | 0.782316285 |
| 53 | DDT | MB | GST01 | RPS28 | CAPNS1 | 0.781208386 |
| 54 | DDT | MB | S100A8 | SOD2 | CAPNS1 | 0.779990675 |
| 55 | DDT | MB | GST01 | RPS28 | S100A8 | 0.779888098 |
| 56 | DDT | MB | GST01 | S100A8 | 0.779545906 |
| 57 | DDT | MB | GST01 | S100A8 | CAPNS1 | 0.778763405 |
| 58 | DDT | MB | GST01 | S100A8 | 0.777923523 |
| 59 | DDT | MB | GST01 | SOD2 | 0.77719597 |
| 60 | DDT | MB | RPS28 | SOD2 | CAPNS1 | 0.7764239 |
| 61 | DDT | GST01 | S100A8 | 0.77600073 |
| 62 | DDT | OAF | MB | GST01 | SOD2 | 0.77583797 |
| 63 | DDT | OAF | MB | GST01 | SOD2 | CAPNS1 | 0.77496733 |
| 64 | DDT | MB | GST01 | RPS28 | SOD2 | 0.774755867 |
| 65 | DDT | MB | GST01 | RPS28 | S100A8 | 0.77467737 |
| 66 | DDT | OAF | MB | S100A8 | SOD2 | 0.774385323 |
| 67 | DDT | OAF | MB | S100A8 | CAPNS1 | 0.77385323 |
| 68 | DDT | OAF | MB | GST01 | RPS28 | SOD2 | CAPNS1 | 0.7728787 |
| 69 | DDT | OAF | MB | GST01 | RPS28 | SOD2 | 0.77218107 |
| 70 | DDT | OAF | SOD2 | CAPNS1 | 0.77186035 |
| 71 | DDT | MB | GST01 | S100A8 | SOD2 | CAPNS1 | 0.771374648 |
| 72 | DDT | RPS28 | SOD2 | 0.771257077 |
| 73 | DDT | OAF | MB | GST01 | S100A8 | SOD2 | CAPNS1 | 0.771216931 |
| 74 | DDT | MB | GST01 | S100A8 | SOD2 | 0.770652557 |
| 75 | DDT | OAF | MB | GST01 | RPS28 | S100A8 | CAPNS1 | 0.770219141 |
| 76 | OAF | MB | CAPNS1 | 0.770145595 |
| 77 | DDT | OAF | MB | S100A8 | SOD2 | CAPNS1 | 0.768799286 |
| 78 | DDT | OAF | GST01 | SOD2 | CAPNS1 | 0.768390196 |
| 79 | DDT | OAF | MB | RPS28 | SOD2 | 0.768064725 |
| 80 | DDT | OAF | GST01 | RPS28 | SOD2 | CAPNS1 | 0.767692241 |
| 81 | DDT | OAF | MB | GST01 | S100A8 | SOD2 | 0.767256989 |
| 82 | DDT | GST01 | SOD2 | CAPNS1 | 0.766782623 |
| 83 | DDT | MB | RPS28 | SOD2 | 0.76596032 |
| 84 | DDT | MB | RPS28 | S100A8 | CAPNS1 | 0.76537624 |
| 85 | DDT | OAF | GST01 | S100A8 | CAPNS1 | 0.765200862 |
|   |     |     |     |     |     |     |
|---|-----|-----|-----|-----|-----|-----|
| 86| OAF | MB  | GST01|     |     |     |
| 87| DDT | MB  | GST01| RPS28| S100A8 | SOD2 | CAPNS1 | 0.765165319 |
| 88| DDT | OAF | MB  | RPS28| SOD2  | CAPNS1 |     |     | 0.763594523 |
| 89| DDT | GST01| RPS28| S100A8 | SOD2 | CAPNS1 |     |     | 0.762486769 |
| 90| OAF | MB  | RPS28|     |     |     |     |     | 0.76155365  |
| 91| MB  | SOD2| CAPNS1|     |     |     |     |     | 0.761505403 |
| 92| DDT | MB  | GST01| RPS28| S100A8 | SOD2 | CAPNS1 |     |     | 0.761381743 |
| 93| DDT | GST01| RPS28|     |     |     |     |     | 0.761367147 |
| 94| DDT | OAF | GST01| RPS28| S100A8 | SOD2 | CAPNS1 |     |     | 0.761367147 |
| 95| MB  | GST01|     |     |     |     |     |     | 0.761505403 |
| 96| DDT | OAF | MB  | GST01| RPS28| S100A8 | SOD2 | CAPNS1 |     |     | 0.759636725 |
| 97| DDT | OAF | GST01| RPS28| S100A8 |     |     |     | 0.759603073 |
| 98| OAF | GST01|     |     |     |     |     |     | 0.758995502 |
| 99| DDT | OAF | RPS28| S100A8|     |     |     |     | 0.758562101 |
|100| DDT | MB  | GST01| RPS28| S100A8 | SOD2 |     |     | 0.758597773 |
|101| GST01| SOD2| CAPNS1|     |     |     |     |     | 0.758495814 |
|102| MB  | GST01| CAPNS1|     |     |     |     |     | 0.758293499 |
|103| DDT | OAF | MB  | RPS28| S100A8 | SOD2 |     |     | 0.757665422 |
|104| DDT | OAF | GST01| RPS28| SOD2  |     |     |     | 0.757631278 |
|105| DDT | GST01| RPS28| SOD2  |     |     |     |     | 0.756429686 |
|106| DDT | MB  | GST01| RPS28| S100A8 | CAPNS1|     |     | 0.755988465 |
|107| DDT | OAF | MB  | RPS28| S100A8 | SOD2 | CAPNS1|     |     | 0.755074714 |
|108| DDT | OAF | GST01| S100A8| SOD2 | CAPNS1|     |     | 0.754574388 |
|109| MB  | GST01| SOD2|     |     |     |     |     | 0.754538492 |
|110| DDT | MB  | RPS28| S100A8| SOD2  |     |     |     | 0.753637157 |
|111| DDT | S100A8| SOD2|     |     |     |     |     | 0.753364958 |
|112| MB  | RPS28| CAPNS1|     |     |     |     |     | 0.752189511 |
|113| DDT | GST01| RPS28| S100A8|     |     |     |     | 0.751629626 |
|114| DDT | OAF | GST01| S100A8| SOD2  |     |     |     | 0.751552636 |
|115| DDT | S100A8| SOD2 | CAPNS1|     |     |     |     | 0.75094518  |
|116| DDT | RPS28| SOD2  | CAPNS1|     |     |     |     | 0.750049667 |
|117| DDT | OAF | GST01| RPS28| S100A8 | CAPNS1|     |     | 0.749478134 |
|118| DDT | RPS28| CAPNS1|     |     |     |     |     | 0.749255807 |
|119| DDT | GST01| S100A8| CAPNS1|     |     |     |     | 0.74894135  |
|120| MB  | CAPNS1|     |     |     |     |     |     | 0.748651683 |
|121| DDT | GST01| S100A8| SOD2 | CAPNS1|     |     |     | 0.748463113 |
|122| OAF | MB  | SOD2 |     |     |     |     |     | 0.747652571 |
|123| DDT | OAF | RPS28| SOD2  | CAPNS1|     |     |     | 0.747425259 |
|124| DDT | OAF | GST01| RPS28| S100A8 | SOD2 |     |     | 0.747315783 |
|125| MB  | GST01| SOD2 | CAPNS1|     |     |     |     | 0.747281721 |
|126| DDT | OAF | GST01| RPS28| S100A8 | SOD2 | CAPNS1|     |     | 0.746879118 |
|127| DDT | GST01| RPS28| S100A8| SOD2 | CAPNS1|     |     | 0.746689155 |
|128| OAF | GST01| CAPNS1|     |     |     |     |     | 0.746449756 |
|129| DDT | GST01| S100A8| SOD2  |     |     |     |     | 0.746043516 |
|   |   |   |   |   |   |
|---|---|---|---|---|---|
| 130 | MB | GST01 | RPS28 | SOD2 | CAPNS1 |
| 131 | OAF | GST01 | SOD2 |   |   |
| 132 | GST01 | SOD2 |   |   |   |
| 133 | OAF | GST01 | RPS28 |   |   |
| 134 | DDT | OAF | S100A8 | SOD2 | CAPNS1 |
| 135 | OAF | MB | RPS28 | CAPNS1 |   |
| 136 | OAF | MB | S100A8 |   |   |
| 137 | DDT | OAF | S100A8 | SOD2 |   |
| 138 | DDT | GST01 | RPS28 | S100A8 | SOD2 |
| 139 | OAF | MB | GST01 | RPS28 | CAPNS1 |
| 140 | GST01 | RPS28 | SOD2 |   |   |
| 141 | MB | GST01 | S100A8 | SOD2 | CAPNS1 |
| 142 | MB | S100A8 | SOD2 |   |   |
| 143 | MB | GST01 |   |   |   |
| 144 | MB | S100A8 | SOD2 |   |   |
| 145 | OAF | MB | GST01 | S100A8 | SOD2 | CAPNS1 |
| 146 | OAF | MB | GST01 | RPS28 |   |
| 147 | OAF | MB | GST01 | CAPNS1 |   |
| 148 | DDT | GST01 | RPS28 | S100A8 | CAPNS1 |
| 149 | MB | SOD2 |   |   |   |
| 150 | OAF | MB | GST01 | RPS28 | SOD2 | CAPNS1 |
| 151 | DDT | OAF | RPS28 | SOD2 |   |
| 152 | OAF | MB | GST01 | SOD2 | CAPNS1 |
| 153 | DDT | OAF | RPS28 | S100A8 | CAPNS1 |
| 154 | MB | GST01 | RPS28 |   |   |
| 155 | GST01 | RPS28 | SOD2 |   |   |
| 156 | OAF | MB | GST01 | RPS28 | S100A8 | SOD2 | CAPNS1 |
| 157 | DDT | S100A8 |   |   |   |
| 158 | MB | GST01 | RPS28 | S100A8 | SOD2 | CAPNS1 |
| 159 | MB | GST01 | S100A8 | SOD2 |   |
| 160 | OAF | GST01 | RPS28 | SOD2 | CAPNS1 |
| 161 | MB | RPS28 | S100A8 | SOD2 | CAPNS1 |
| 162 | MB | RPS28 | SOD2 |   |   |
| 163 | MB | RPS28 | SOD2 |   |   |
| 164 | OAF | GST01 | SOD2 | CAPNS1 |   |
| 165 | SOD2 | CAPNS1 |   |   |   |
| 166 | MB | GST01 | RPS28 | SOD2 |   |
| 167 | GST01 | S100A8 | SOD2 | CAPNS1 |   |
| 168 | OAF | MB | GST01 | RPS28 | SOD2 |
| 169 | OAF | GST01 | RPS28 | CAPNS1 |   |
| 170 | MB | GST01 | RPS28 | S100A8 | SOD2 |
| 171 | MB | GST01 | RPS28 | CAPNS1 |   |
| 172 | OAF | MB | S100A8 | CAPNS1 |   |
| 173 | DDT | OAF | RPS28 | S100A8 | SOD2 | CAPNS1 |

**Values:**

|   |   |   |   |   |   |
|---|---|---|---|---|---|
| 130 | 0.745296681 |   |   |   |   |
| 131 | 0.745122392 |   |   |   |   |
| 132 | 0.743928723 |   |   |   |   |
| 133 | 0.742934045 |   |   |   |   |
| 134 | 0.742768755 |   |   |   |   |
| 135 | 0.742620926 |   |   |   |   |
| 136 | 0.742014086 |   |   |   |   |
| 137 | 0.739350821 |   |   |   |   |
| 138 | 0.738499927 |   |   |   |   |
| 139 | 0.738324161 |   |   |   |   |
| 140 | 0.738161587 |   |   |   |   |
| 141 | 0.737049953 |   |   |   |   |
| 142 | 0.736947435 |   |   |   |   |
| 143 | 0.736216019 |   |   |   |   |
| 144 | 0.735943563 |   |   |   |   |
| 145 | 0.735549474 |   |   |   |   |
| 146 | 0.735418516 |   |   |   |   |
| 147 | 0.73503149 |   |   |   |   |
| 148 | 0.730503149 |   |   |   |   |
| 149 | 0.730130349 |   |   |   |   |
| 150 | 0.729909588 |   |   |   |   |
| 151 | 0.729572855 |   |   |   |   |
| 152 | 0.72950707 |   |   |   |   |
| 153 | 0.72910109 |   |   |   |   |
| 154 | 0.728582071 |   |   |   |   |
| 155 | 0.723532184 |   |   |   |   |
| 156 | 0.723532184 |   |   |   |   |
| 157 | 0.723532184 |   |   |   |   |
| 158 | 0.723532184 |   |   |   |   |
| 159 | 0.723532184 |   |   |   |   |
| 174 | DDT | RPS28 | S100A8 | SOD2 | CAPNS1 | 0.722744025 |
| 175 | OAF | GST01 | S100A8 | SOD2 | CAPNS1 | 0.72204772 |
| 176 | OAF | MB | GST01 | RPS28 | S100A8 | CAPNS1 | 0.72127119 |
| 177 | OAF | MB | GST01 | RPS28 | S100A8 | SOD2 | 0.721173752 |
| 178 | GST01 | RPS28 | S100A8 | SOD2 | CAPNS1 | 0.720651138 |
| 179 | MB | RPS28 | S100A8 | SOD2 | CAPNS1 | 0.72053427 |
| 180 | RPS28 | SOD2 | CAPNS1 | 0.72017485 |
| 181 | OAF | MB | GST01 | S100A8 | CAPNS1 | 0.72017485 |
| 182 | OAF | MB | GST01 | S100A8 | SOD2 | 0.72005345 |
| 183 | OAF | MB | GST01 | S100A8 | SOD2 | 0.719627805 |
| 184 | OAF | MB | GST01 | S100A8 | SOD2 | 0.71836364 |
| 185 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.718116321 |
| 186 | OAF | GST01 | S100A8 | SOD2 | 0.717488293 |
| 187 | OAF | MB | GST01 | S100A8 | SOD2 | 0.717304779 |
| 188 | OAF | MB | GST01 | S100A8 | SOD2 | 0.716795394 |
| 189 | OAF | MB | GST01 | S100A8 | SOD2 | 0.716425914 |
| 190 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.716150743 |
| 191 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.713946598 |
| 192 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.713669951 |
| 193 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.713218999 |
| 194 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.712189325 |
| 195 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.710813923 |
| 196 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.709831808 |
| 197 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.709577328 |
| 198 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.708240183 |
| 199 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.707955067 |
| 200 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.706656125 |
| 201 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.70633461 |
| 202 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.70507851 |
| 203 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.703650996 |
| 204 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.70229492 |
| 205 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.70149475 |
| 206 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.701237406 |
| 207 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.700669463 |
| 208 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.699990067 |
| 209 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.69853489 |
| 210 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.698259442 |
| 211 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.69584734 |
| 212 | OAF | GST01 | RPS28 | S100A8 | SOD2 | 0.69584734 |
|   |   |   |   |   |   |
|---|---|---|---|---|---|
| 218 | OAF | GST01 | RPS28 | S100A8 | 0.695156196 |
| 219 | MB | RPS28 | S100A8 | CAPNS1 | 0.693648361 |
| 220 | RPS28 | S100A8 | SOD2 | CAPNS1 | 0.692696791 |
| 221 | OAF | RPS28 | SOD2 | CAPNS1 | 0.69199092 |
| 222 | DDT | S100A8 | CAPNS1 | 0.690732274 |
| 223 | OAF | MB | RPS28 | S100A8 | SOD2 | 0.690238322 |
| 224 | OAF | RPS28 | SOD2 | 0.690130755 |
| 225 | MB | S100A8 | 0.687923939 |
| 226 | OAF | MB | RPS28 | SOD2 | 0.68632042 |
| 227 | GST01 | RPS28 | CAPNS1 | 0.685641141 |
| 228 | S100A8 | SOD2 | 0.684085364 |
| 229 | RPS28 | SOD2 | 0.683179063 |
| 230 | OAF | S100A8 | SOD2 | CAPNS1 | 0.683168897 |
| 231 | MB | RPS28 | S100A8 | 0.673454096 |
| 232 | DDT | RPS28 | S100A8 | CAPNS1 | 0.67250715 |
| 233 | OAF | RPS28 | S100A8 | SOD2 | CAPNS1 | 0.671234771 |
| 234 | GST01 | RPS28 | S100A8 | CAPNS1 | 0.670242251 |
| 235 | OAF | S100A8 | SOD2 | 0.669742342 |
| 236 | GST01 | RPS28 | 0.66859089 |
| 237 | GST01 | S100A8 | CAPNS1 | 0.663921623 |
| 238 | GST01 | RPS28 | S100A8 | 0.66354692 |
| 239 | GST01 | RPS28 | S100A8 | 0.65875525 |
| 240 | GST01 | S100A8 | 0.658302824 |
| 241 | OAF | RPS28 | S100A8 | SOD2 | 0.651892801 |
| 242 | SOD2 | 0.650667291 |
| 243 | RPS28 | S100A8 | SOD2 | 0.650095372 |
| 244 | OAF | S100A8 | 0.649221612 |
| 245 | GST01 | 0.648652382 |
| 246 | OAF | RPS28 | S100A8 | CAPNS1 | 0.643721138 |
| 247 | OAF | S100A8 | CAPNS1 | 0.639571907 |
| 248 | RPS28 | CAPNS1 | 0.621672444 |
| 249 | OAF | RPS28 | S100A8 | 0.618244035 |
| 250 | CAPNS1 | 0.598815887 |
| 251 | RPS28 | 0.547484022 |
| 252 | RPS28 | S100A8 | CAPNS1 | 0.506007866 |
| 253 | S100A8 | CAPNS1 | 0.47393857 |
| 254 | RPS28 | S100A8 | 0.448705771 |
| 255 | S100A8 | 0.359768098 |
Data S1. (separate file)
List of LC-MS/MS detected peptides and proteins from sera of 23 COVID-19 patients (Development group) and 10 healthy controls