

1 **Rapid identification of SARS-CoV-2-infected patients at the emergency**
2 **department using routine testing**

3

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42 **Keywords:**

43 COVID-19, coronavirus, prediction-model, algorithm, emergency department,

44 pandemic, SARS-CoV-2

45

46 **List of Abbreviations**

47 ALC Absolute lymphocyte count

48 AMP Amphia Hospital

49 ANC Absolute neutrophil count

50 AUROC Area under the receiver operating characteristic

51	BHZ	Bernhoven Hospital
52	COVID-19	Coronavirus disease 19
53	CRP	C-reactive protein
54	CXR	Chest X-ray
55	ED	Emergency department
56	EQA	External quality assessment
57	ETZ	Elizabeth TweeSteden Hospital
58	JBZ	Jeroen Bosch Hospital
59	LDH	Lactate dehydrogenase
60	SKML	Dutch Foundation for Quality Assessment in Medical
61		Laboratories

62 **ABSTRACT**

63 **Background:**

64 The novel coronavirus disease 19 (COVID-19), caused by SARS-CoV-2,
65 spreads rapidly across the world. The exponential increase in the number of
66 cases has resulted in overcrowding of emergency departments (ED).
67 Detection of SARS-CoV-2 is based on an RT-PCR of nasopharyngeal swab
68 material. However, RT-PCR testing is time-consuming and many hospitals
69 deal with a shortage of testing materials. Therefore, we aimed to develop an
70 algorithm to rapidly evaluate an individual's risk of SARS-CoV-2 infection at
71 the ED.

72 **Methods:** In this multicenter retrospective study, routine laboratory
73 parameters (C-reactive protein, lactate dehydrogenase, ferritin, absolute
74 neutrophil and lymphocyte counts), demographic data and the chest X-ray/CT
75 result from 967 patients entering the ED with respiratory symptoms were
76 collected. Using these parameters, an easy-to-use point-based algorithm,
77 called the corona-score, was developed to discriminate between patients that
78 tested positive for SARS-CoV-2 by RT-PCR and those testing negative.
79 Computational sampling was used to optimize the corona-score. Validation of
80 the model was performed using data from 592 patients.

81 **Results:** The corona-score model yielded an area under the receiver
82 operating characteristic curve of 0.91 in the validation population. Patients
83 testing negative for SARS-CoV-2 showed a median corona-score of 3 versus
84 11 (scale 0-14) in patients testing positive for SARS-CoV-2 ($p < 0.001$). Using
85 cut-off values of 4 and 11 the model has a sensitivity and specificity of 96%
86 and 95%, respectively.

87 **Conclusion:** The corona-score effectively predicts SARS-CoV-2 RT-PCR
88 outcome based on routine parameters. This algorithm provides the means for
89 medical professionals to rapidly evaluate SARS-CoV-2 infection status of
90 patients presenting at the ED with respiratory symptoms.

91

92 **INTRODUCTION**

93 In December 2019 the novel coronavirus disease 2019 (COVID-19), caused
94 by SARS-CoV-2, spread rapidly from its origin in Wuhan, China (1).
95 Symptoms can range from mild, common cold-like, to life threatening with
96 intensive care unit admission and extensive mechanical ventilation (2, 3). On
97 February 27th 2020 the first patient was identified in the Netherlands, and
98 thousands of new patients were diagnosed within the first month.

99

100 The subsequent exponential increase in prevalence has resulted in
101 overcrowding of emergency departments (ED) and has led to a shortage of
102 isolation rooms (4). For correct triaging of patients diagnostic testing is of key
103 importance. The leading standard test for detecting SARS-CoV-2 is an RT-
104 PCR of nasopharyngeal swab material (5). However, RT-PCR testing is time-
105 consuming and shortage of testing materials and capacity imposes a serious
106 threat (6).

107

108 Doctors at the ED are required to assess the probability of SARS-CoV-2
109 infection in each patient entering the ED. To accelerate the triage process at
110 the ED, we integrated routine demographic, laboratory and imaging data of
111 patients presenting at the ED with COVID-19-like symptoms to develop a

112 point-based algorithm. This algorithm can assess whether a person,
113 presenting at the ED with respiratory symptoms, is likely to have COVID-19.
114 In case of a shortage of testing capacity, adoption of this algorithm could
115 reduce the number of patients for whom RT-PCR testing is required.
116 Moreover, implementation of the corona-score enables rapid decision making
117 at the ED, lowering pressure on isolation rooms.

118

119 **METHODS**

120 **Patient population**

121 In this retrospective multicenter study, 375 patients from three different
122 hospitals presenting at the ED with respiratory symptoms and subsequent
123 SARS-CoV-2 RT-PCR testing were included (Figure 1 and Table 2). Patients
124 from other departments and patients without any respiratory symptoms or
125 suspicion of COVID-19 were excluded. An independent cohort of 592 patients
126 from four hospitals was used to validate the model (Figure 1 and Table 2). For
127 the validation population, patients with missing values or hemolytic samples
128 were excluded (n=97).

129

130 **Measurements**

131 For clinical chemistry analyses and RT-PCR, venous blood and pharyngeal
132 plus nasal swab specimens, respectively, were collected. Clinical chemistry
133 parameters (C-reactive protein (CRP), ferritin, lactate dehydrogenase (LDH),
134 absolute lymphocyte and neutrophil counts (ALC and ANC)) were obtained on
135 routine analyzers from Siemens (Jeroen Bosch Hospital and the (immuno-
136)chemistry of Bernhoven Hospital), Sysmex (Elisabeth TweeSteden Hospital

137 and the hematology of Amphia Hospital), Roche (Elisabeth TweeSteden
138 Hospital and the (immuno-)chemistry of Amphia Hospital) and Abbott
139 (hematology of Bernhoven Hospital). SARS-CoV-2 RT-PCR testing at Amphia
140 Hospital and Elizabeth TweeSteden Hospital was performed using tests from
141 Microvida Laboratory (the Netherlands), whereas Jeroen Bosch Hospital and
142 Bernhoven Hospital used in-house developed tests. Chest X-rays (CXR) and
143 chest CT-scans were imaged using Siemens, GE Healthcare and Philips
144 equipment. External quality assessment (EQA) in commutable materials by
145 Dutch Foundation for Quality Assessment in Medical Laboratories (SKML)
146 demonstrated that ferritin measured on Roche analyzers is on average 20%
147 higher than on Siemens analyzers. For building the model and calculating
148 corona-scores ferritins measured on Siemens analyzers were therefore
149 multiplied by 1.2. All other measurands in the scoring system had no
150 significant inter-method differences for Roche, Siemens and Sysmex in the
151 particular SKML EQA schemes.

152

153 **Corona-score algorithm**

154 A scoring-based algorithm was developed using laboratory measurands
155 (CRP, ALC, ANC, LDH and ferritin), age, sex and CXR/CT as input. Scores
156 were assigned to each parameter according to Table 1 (or see www.corona-score.nvkc.nl) for more information). The corona-score is obtained by the
157 summation of the score for each parameter. The final score is clamped from a
158 minimum of 0 to a maximum of 14 points. Cut-off points and weights of
159 demographic, laboratory and imaging parameters were computationally
160 sampled using Python (v3.7.0, Python Software Foundation, USA) to optimize
161

162 for a maximum area under the receiver operating characteristic (AUROC)
163 curve. When values were missing in the data of the model population (n=3 for
164 ALC and ANC, n=31 for LDH and n=4 for ferritin) the median of the total
165 population was used.

166

167 **Statistical analyses**

168 Data were analyzed using the Excel 2010 (Microsoft Corporation, USA) plugin
169 'Analyse-it v5.11' (Analyse-it Software, Ltd, UK) and SPSS statistics v22 (IBM,
170 USA). Continuous variables were tested for normal distribution using a
171 Kolmogorov-Smirnov test. In case of non-normal distribution, a Mann-Whitney
172 U test was performed to compare the medians. Categorical variables were
173 compared by a chi square test. A p -value <0.05 was considered statistically
174 significant.

175

176 **RESULTS**

177 Using a cohort of 375 ED patients with respiratory symptoms a point-based
178 algorithm was created and subsequently validated using a separate
179 independent cohort of 592 patients (Table 2). At the time of presentation at
180 the ED the parameters sex, age, CRP, ferritin, LDH, ALC, ANC and CXR
181 were significantly different between the COVID-19 positive and negative
182 patients (Figure 2 and Table 2). Together, these parameters were used to
183 develop an algorithm, named 'corona-score'. Inclusion of albumin,
184 procalcitonin or clinical parameters such as fever, cough and dyspnea did not
185 sufficiently improve the performance of the algorithm (data not shown). The
186 corona-score resulted in a model with an AUROC of 0.94 (Figure 3A, 95% CI

187 0.91 – 0.96). Patients with a negative RT-PCR test had a median of 4
188 compared to a median of 11 for SARS-CoV-2 positive patients (Figure 3B and
189 Table 2). The corona-score algorithm was validated with data from 592
190 patients, yielding an AUROC of 0.91 (Figure 3C, 95% CI 0.89-0.94). In the
191 validation population SARS-CoV-2 negative patients had a median of 3
192 versus a median of 11 for SARS-CoV-2 positive patients (Figure 3D and
193 Table 2).

194

195 By using different cut-off values the desired sensitivity and specificity for the
196 test can be found (Table 3). Using corona-score cut-offs of 4 (96% sensitivity)
197 and 11 (95% specificity) at a 70% prevalence, this model showed negative
198 and positive predictive values of 88% and 96% (Figure 3E). The total false
199 rate given these conditions is 4% (Figure 3E).

200

201 RT-PCR testing for SARS-CoV-2 is hampered by significant numbers of false
202 negatives as the sensitivity of RT-PCR is estimated at approximately 70-90%
203 (7). Indeed, many doctors request multiple COVID-19 tests when the RT-PCR
204 result does not match the clinical presentation of the patient. Patients from the
205 validation population of the JBZ hospital that showed positivity for SARS-CoV-
206 2 after repeated RT-PCR testing (n=13) had an initial median corona-score of
207 12, while patients that remained negative (n=12) had an initial median corona-
208 score of 4 (Figure 3F). This shows that the corona-score is able to distinguish
209 between true and false negatives.

210

211 **DISCUSSION**

212 Using a cohort of 967 patients we developed and validated a point-based
213 algorithm to predict the likelihood of SARS-CoV-2 infection in patients
214 presenting at the ED with respiratory symptoms. Validation of the model
215 resulted in an AUROC of 0.91 with a 96% sensitivity and 95% specificity,
216 using corona-score cut-offs of 4 and 11. Such an algorithm can be used to, 1)
217 accelerate determination of isolation needs and 2) reduce RT-PCR testing: a
218 reduction of about 60% can be achieved if cut-offs of 4 and 11, yielding 125
219 true negative and 219 true positive patients in the validation cohort of 592
220 patients, are used.

221

222 Our algorithm is optimized to predict the outcome of the SARS-CoV-2 RT-
223 PCR test, which has limited (70-90%) sensitivity (7). Inclusion of patients
224 having false negative RT-PCR tests into the validation population results in an
225 underestimation of the performance of the algorithm. Interestingly, for twenty-
226 five patients that received multiple COVID-19 tests our algorithm could predict
227 which patients were initially false negatives. Therefore, the sensitivity of the
228 corona-score appears to exceed the sensitivity of the initial SARS-CoV-2 RT-
229 PCR.

230

231 In a minority of cases, our model produces a corona-score of 0 – 5 in patients
232 that tested positive for SARS-CoV-2 by RT-PCR. There are two common
233 underlying reasons for this phenomenon. Firstly, the corona-score performed
234 poorly in patients with a gastro-intestinal presentation of COVID-19, but
235 without respiratory symptoms. Therefore, this algorithm should only be used
236 for patients at the ED with respiratory symptoms. Secondly, patients that only

237 have mild respiratory symptoms, and therefore do not have large alterations in
238 their laboratory parameters, generally have a low corona-score. However, in
239 most cases the patients with a mild presentation were not hospitalized.
240 Therefore, we consider that the low corona-score corresponds with the clinical
241 findings. On the other hand, some negatively-tested patients received a high
242 corona-score. This could be due to false-negative RT-PCR testing or possibly
243 other viral infections. Interestingly, four patients that were positive for
244 influenza and negative for SARS-CoV-2 had a low corona-score (2 – 6).
245 During this COVID-19 pandemic, the prevalence of other respiratory viruses
246 appears very low; hence, the discriminative potential of the corona-score in
247 patients infected by such viruses could not be systematically established.
248 Notably, in case of any viral outbreak, a similar modelling approach could be
249 considered to develop an algorithm as described here.

250

251 The four laboratories involved in this study deploy different instruments from
252 the major *in-vitro* diagnostic device providers. Most measurands that were
253 included in the algorithm have an identical metrological traceability and hence
254 comparable results in the commutable EQA scheme of the SKML (8).
255 However, there is no reference method for ferritin (9). The different
256 calibrations lead to approximately 20% difference in ferritin results between
257 the methods employed by the laboratories in this study. Therefore, a 1.2
258 harmonization factor was applied to the ferritin values obtained from Siemens
259 instruments, before calculating corona-scores, correcting the lack of
260 standardization. Generally, methodological harmonization between

261 laboratories should be encouraged for better comparison of laboratory results
262 (10).

263

264 To our knowledge, our algorithm is the first available validated tool to rapidly
265 evaluate COVID-19 status in ED patients with respiratory symptoms based on
266 routine laboratory tests. The model has already been implemented at the ED
267 of several hospitals in the Netherlands. Implementation of this algorithm will
268 accelerate the triage of patients and reduce the number of RT-PCR tests
269 required.

270

271 **Author Contributions**

272 All authors confirmed they have contributed to the intellectual content of this
273 paper and have met the following 4 requirements: (a) significant contributions
274 to the conception and design, acquisition of data, or analysis and
275 interpretation of data; (b) drafting or revising the article for intellectual content;
276 (c) final approval of the published article; and (d) agreement to be
277 accountable for all aspects of the article thus ensuring that questions related
278 to the accuracy or integrity of any part of the article are appropriately
279 investigated and resolved.

280

281 **Conflict of Interest Disclosure**

282 All authors have read the journal's policy on disclosure of potential conflicts of
283 interest and have none to declare.

284

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291

292 **Statement of ethics**

293 The study was conducted according to the declaration of Helsinki, Guidelines
294 for Good Clinical Practice and the Dutch Medical Research Involving Human
295 Subjects Act. The execution of this retrospective observational study of
296 patient records was approved by the local review board of the Jeroen Bosch
297 Hospital. This study had no effect on the behaviour of patients or medical
298 decision-making.

299

300 **Data availability**

301 The data that support the findings of this study are available from the
302 corresponding author upon reasonable request. More information can be
303 obtained at www.corona-score.nvkc.nl.

304

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337
338

339 **Figure legends**

340 **Figure 1. Flow diagram of the study setup for the model and validation population.** (A)

341 A flow diagram depicting the inclusion and exclusion of patients that were used to develop the
342 algorithm. A total of 375 patients were included. (B) A flow diagram depicting the inclusion
343 and exclusion of patients that were used to validate the algorithm. A total of 592 patients were
344 included.

345

346 **Figure 2. Difference in demographic and routine laboratory parameters between**
347 **COVID-19 positive and negative patients.** Box plots depicting the median and interquartile

348 range of continuous variables included in our model, (A) age, (B) C-reactive protein (CRP),

349 (C) lactate dehydrogenase (LDH), (D) ferritin, (E) absolute lymphocyte count (ALC), (F)

350 absolute neutrophil count (ANC). Data are taken from the model population presented in

351 Table 2. * indicates a p -value ≤ 0.05 .

352

353 **Figure 3. Performance of the corona-score to predict RT-PCR outcome.** (A) ROC-curve

354 (AUROC = 0.94, 95% CI 0.91 – 0.96) of the model, created using data from 375 patients from

355 3 different hospitals. Points were attributed to each patient based on demographic, laboratory

356 and CXR data (the range of the corona-score is clamped from 0 – 14). (B) Box-plot displaying

357 the difference in the median between the SARS-CoV-2 negative and positive patients from

358 the model population obtained using the corona-score. (C) The model was validated using

359 592 patients (AUROC = 0.91, 95% CI 0.89-0.94). (D) Box-plot displaying the difference in the

360 median between the SARS-CoV-2 negative and positive patients from the validation

361 population obtained using the corona-score. (E) Positive (triangle) and negative (square)

362 predictive values and false rate (circle) at several different prevalences, using a corona-score

363 of four and eleven as lower and upper cut-offs, respectively. (F) Box-plot depicting the median

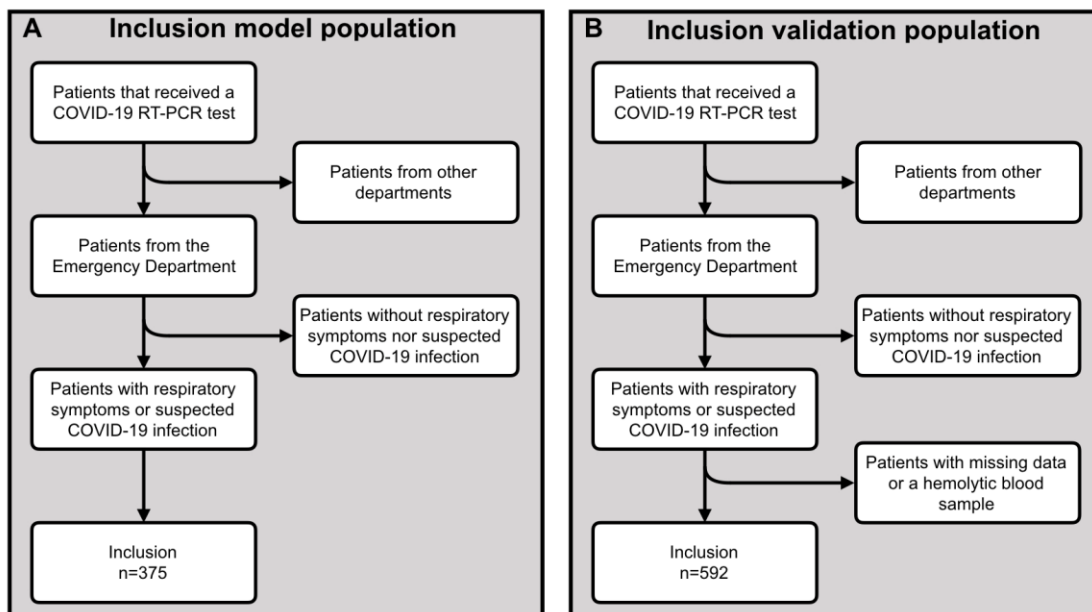
364 corona-score of patients that received multiple SARS-CoV-2 RT-PCR tests, for whom the

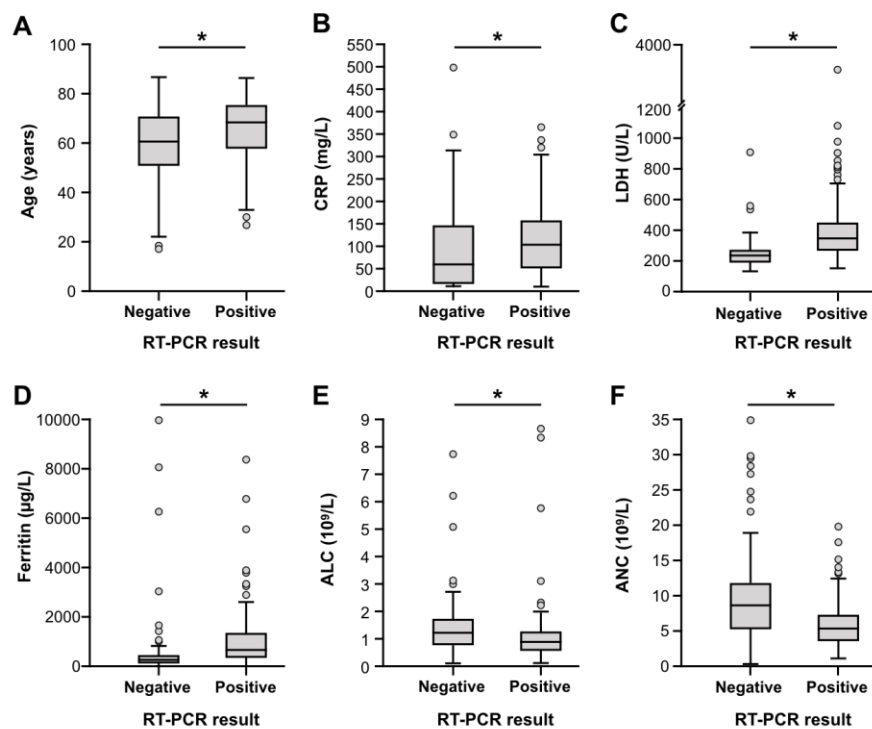
365 latest RT-PCR (material obtained from either nasopharyngeal, fecal or sputum) was positive

366 (n=13) or remained negative (n=12). * indicates a p -value ≤ 0.05 .

367

368





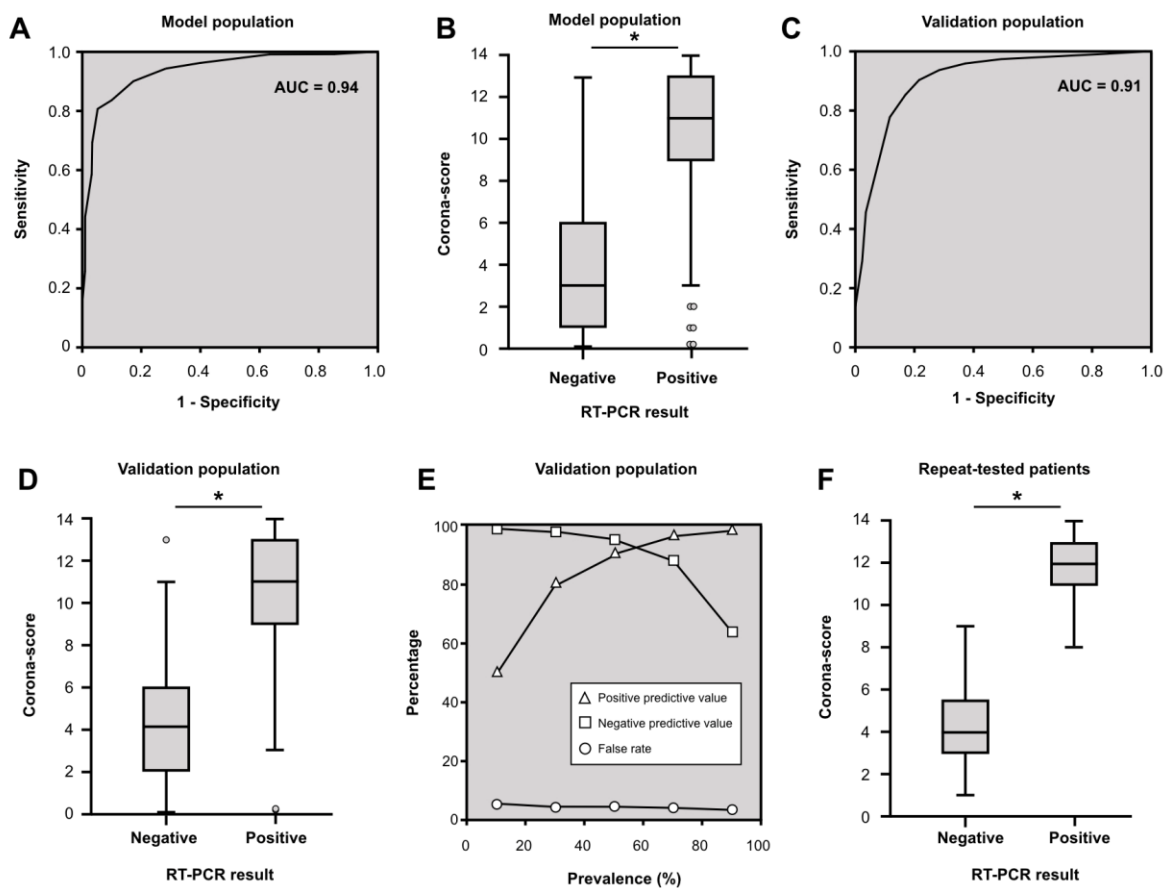


Table 1. The point-based scoring system for the calculation of the corona-score. The final score is clamped from a minimum of 0 to a maximum of 14 points. More information can also be found at www.corona-score.com.

Age (years)	≤75	76-79	80+				
Points	0	1	2				
Sex	Female	Male					
Points	0	1					
CRP (mg/L)	0-9	10-14	15-38	39-69	70-193	194-303	304+
Points	0	1	2	3	2	1	0
Ferritin (µg/L)	≤15	16-179	180-301	302-538	≥539		
Points	-1	0	1	2	3		
LDH (U/L)	≤257	258-265	266-397	≥398			
Points	0	1	2	3			
ALC (10⁹/L)	≤1.2	≥1.3					
Points	1	0					
ANC (10⁹/L)	≤5.1	5.2-7.9	8.0-9.0	9.1-10.3	≥10.4		
Points	0	-1	-2	-3	-4		
CXR	No infiltrate		Unilateral infiltrate		Bilateral infiltrate		
Points	0		1		4		

CRP, C-reactive protein; LDH, lactate dehydrogenase; ALC, absolute lymphocyte count; ANC, absolute neutrophil count; CXR, chest X-ray.

Table 2. Overview of the demographic, clinical chemistry and chest x-ray parameters of the patients included in the model development and validation.

Model population		COVID-19 negative (n = 99)		COVID-19 positive (n = 276)		p-value
		Mean ± SD	Median (25 th – 75 th percentile)	Mean	Median (25 th – 75 th percentile)	
Age (years)		62 ± 16	64 (52 – 74)	70 ± 12	72 (61 – 79)	<0.001*
CRP (mg/L)		84 ± 97	47 (8 – 138)	106 ± 72	98 (46 – 153)	<0.001*
LDH (U/L)		251 ± 111	233 (186 – 270)	391 ± 254	346 (270 – 449)	<0.001*
Ferritin (µg/L)		617 ± 1457	222 (111 – 517)	933 ± 960	633 (363 – 1291)	<0.001*
Lymphocytes (*10 ⁹ /L)		1.5 ± 1.1	1.2 (0.8 – 1.7)	1.0 ± 0.8	0.90 (0.6 – 1.2)	<0.001*
Neutrophils (*10 ⁹ /L)		9.5 ± 6.9	7.7 (5.1 – 11.4)	5.7 ± 3.0	5.20 (3.5 – 7.1)	<0.001*
Corona-score (0 – 14)		3.9 ± 2.9	4.0 (2.0 – 6.0)	10.5 ± 2.8	11.0 (9.0 – 13.0)	<0.001*
Sex	Male	43.0%		64.1%		<0.001**
CXR	No infiltrate	50%		13%		<0.001**
	Unilateral infiltrate	33%		13%		
	Bilateral infiltrate	17%		74%		
Hospital† (n)		JBZ (69); BHZ (20); ETZ (10); AMP (0)		JBZ (107); BHZ (136); ETZ (43); AMP (0)		
Validation population		COVID-19 negative (n = 199)		COVID-19 positive (n = 393)		p-value
		Mean ± SD	Median (25 th – 75 th percentile)	Mean ± SD	Median (25 th – 75 th percentile)	
Age (years)		63 ± 17	67 (51 – 76)	69 ± 12	71 (61 – 77)	0.001*
CRP (mg/L)		78 ± 97	32 (9 – 127)	107 ± 70	95 (54 – 147)	<0.001*
LDH (U/L)		279 ± 242	228 (190 – 296)	401 ± 155	371 (292 – 464)	<0.001*
Ferritin (µg/L)		419 ± 552	211 (91 – 529)	1195 ± 1288	796 (394 – 1431)	<0.001*
Lymphocytes (*10 ⁹ /L)		1.5 ± 1.0	1.3 (0.7 – 2.0)	1.4 ± 4.6	0.9 (0.7 – 1.3)	<0.001*
Neutrophils (*10 ⁹ /L)		8.5 ± 5.3	7.0 (4.9 – 10.9)	6.0 ± 3.0	5.5 (3.8 – 7.4)	<0.001*
Corona-score (0 – 14)		3.9 ± 3.4	3.0 (1.0 – 6.0)	10.5 ± 2.9	11.0 (9.0 – 13.0)	<0.001*
Sex	Male	53.3%		63.8%		<0.05**
CXR	No infiltrate	64%		13%		<0.001**
	Unilateral infiltrate	20%		18%		
	Bilateral infiltrate	16%		69%		
Hospital† (n)		JBZ (66); BHZ (15); ETZ (80); AMP (38)		JBZ (136); BHZ (20); ETZ (139); AMP (98)		

*: Mann-Whitney U test ($\alpha = 0.05$)

** : Chi square test

† : JBZ = Jeroen Bosch Hospital; BHZ = Bernhoven Hospital; ETZ = Elisabeth-TweeSteden Hospital; AMP = Amphia Hospital

Table 3. Sensitivity and specificity at different lower and upper cut-off values for the corona-score (value included, \leq for 2 to 5 and \geq for 9 to 12) determined using the validation population (n = 592). The right column depicts the number of true and false negative and positive patients.

Corona-score cut-off value	Sensitivity (95% CI)	Specificity (95% CI)	True false negative (n)
2	98% (0.96 – 0.99)	42% (0.35 – 0.49)	83 7
3	98% (0.95 – 0.99)	53% (0.46 – 0.60)	105 10
4	96% (0.94 – 0.98)	63% (0.56 – 0.70)	125 15
5	94% (0.91 – 0.96)	72% (0.66 – 0.78)	144 25
Corona-score cut-off value	Sensitivity (95% CI)	Specificity (95% CI)	True false positive (n)
9	78% (0.73 – 0.82)	89% (0.84 – 0.93)	305 22
10	68% (0.63 – 0.72)	92% (0.87 – 0.95)	267 17
11	56% (0.51 – 0.61)	95% (0.90 – 0.97)	219 11
12	45% (0.40 – 0.50)	97% (0.94 – 0.99)	177 6