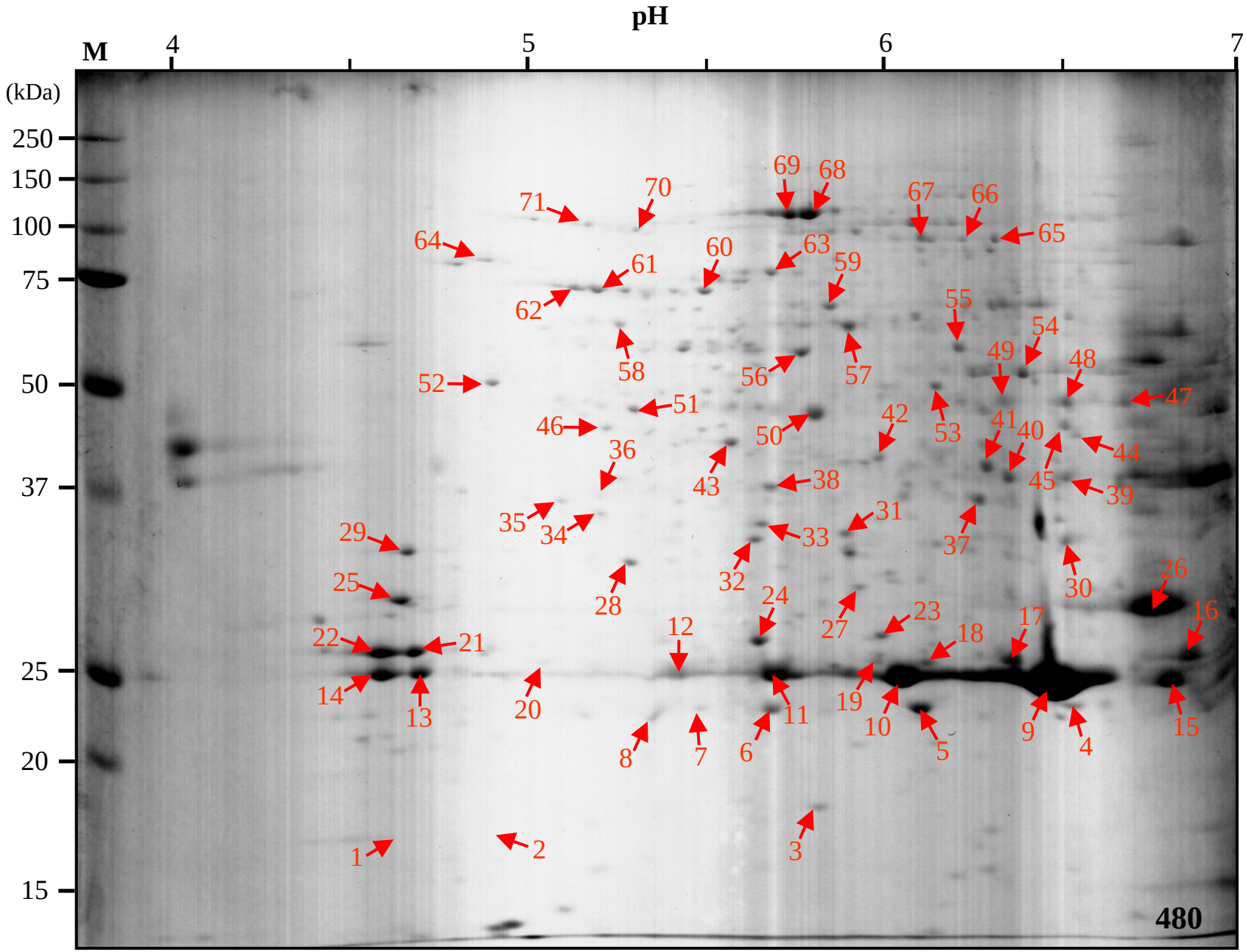
pH
M
4
5
6
7
(kDa)
250
150
100
75
50
37
25
20
15
480

Figure 3. Development of 2-D gel reference map of fruiting body in *S. crispa*. The total soluble proteins were separated on pre-cast IPG strips (18 cm, pH 4-7) in the first dimension followed by 12.5% SDS-PAGE in the second dimension. Molecular masses were determined by running standard protein markers (2.5 ml/gel; Bio-Rad), and separated proteins stained with colloidal CBB G-250. Total spot numbers (ImageMaster 2D platinum software 5.0) detected on gel is given at the bottom right-hand corner. The electroblotted proteins onto PVDF membrane were sequenced on an Applied Biosystems 494 protein sequencer. The obtained sequences were used to interrogate databases with Web accessible search programs Fasta3 (EMBL Outstation of the European Bioinformatics Institute) to identify homology to proteins already present in the protein and nucleic acid databases.

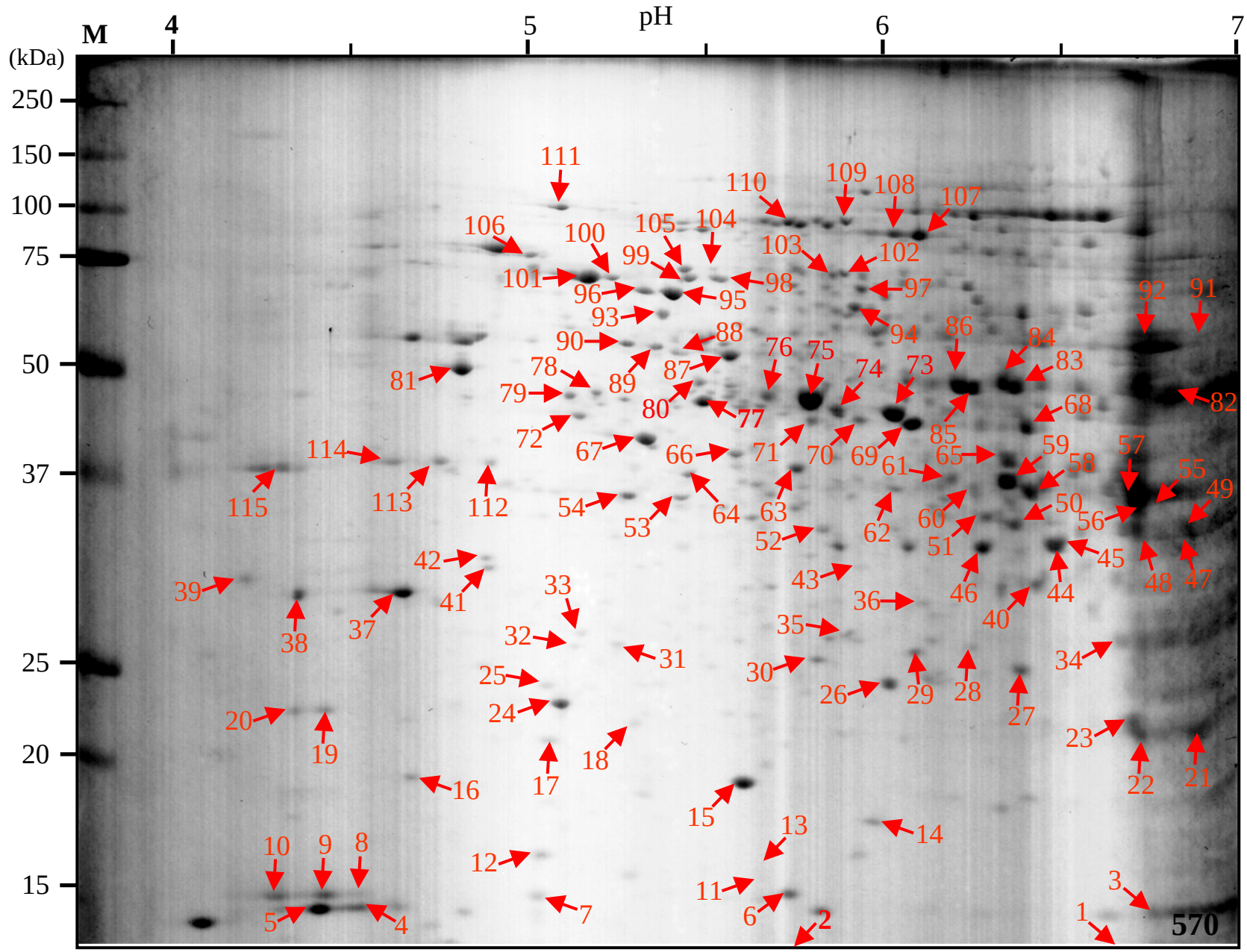
M
4
5
pH
6
7
(kDa)
250
150
100
75
50
37
25
20
15
570

Figure 4. Development of 2-D gel map of *H. erinaceum* fruiting body proteins.
2-DGE was carried out as described in Figure 3.