

### 3.2.2.2 Prediction of proteins

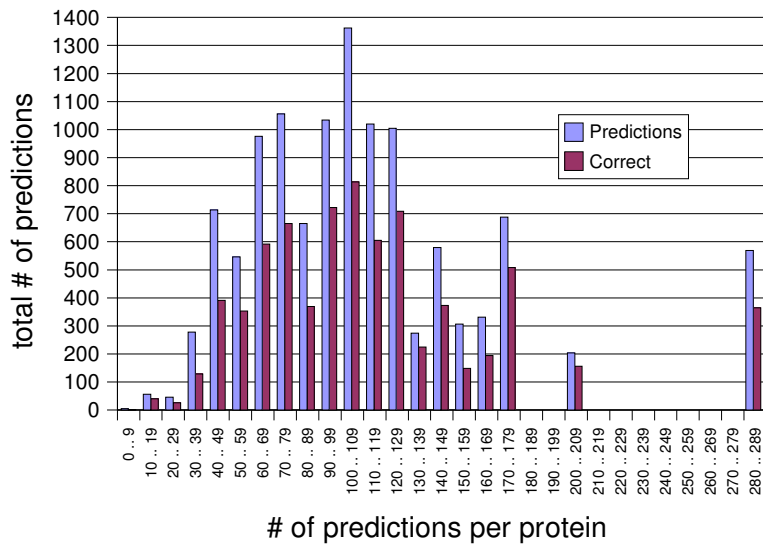
The results of the evaluations of proteins has been represented in a very similar way than the results for the GO terms. There are two sections corresponding to tasks 2.1 and 2.2. In each of these sections the first two diagrams show the proteins according to how many predictions have been made for each protein and diagram 3 and 4 show, for each individual protein, what fraction of the predictions were correct (i.e. marked with "high" by the evaluators).

The results indicate that there is no obvious difference between tasks 2.1 and 2.2, precision does not depend on how many times a protein appears in the results and in general precision for the correct prediction of proteins is above 50%.

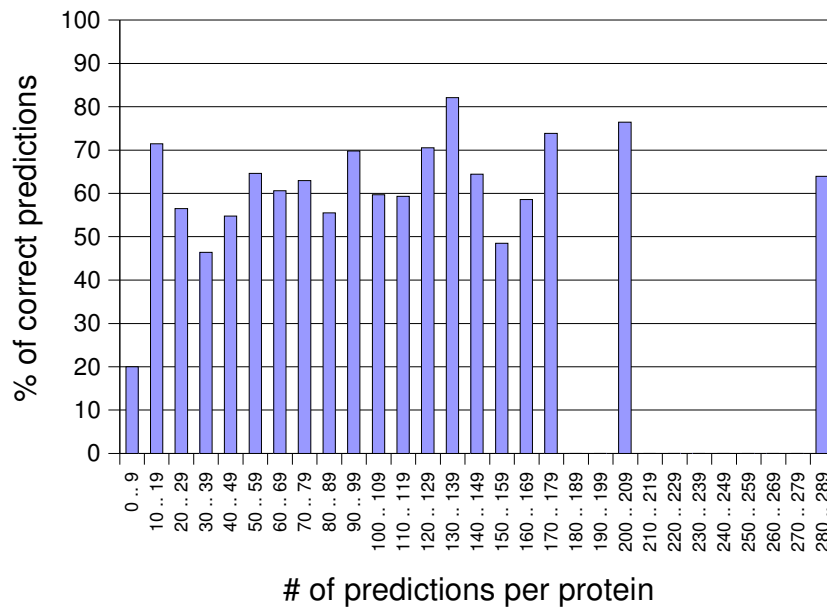
Some examples for proteins with "good" predictions and "bad" predictions.

| Accession number | times predicted | correct predictions | %     | Swiss-Prot/TREMBL description   |
|------------------|-----------------|---------------------|-------|---|
| Q9NP80           | 74              | 46                  | 0.62  | AC Q9NP80;<br>DE Calcium-independent phospholipase A2 (Intracellular membrane-associated calcium-independent phospholipase A2 gamma).<br>GN IPLA2.        |
| O15023           | 102             | 40                  | 0.39  | AC O15023;<br>DE Hypothetical protein KIAA0305 (Endofin).<br>GN KIAA0305.   |
| O75612           | 89              | 31                  | 0.35  | AC O75612;<br>DE Bile salt-dependent lipase oncofetal isoform (Fragment).   |
| Q9NYK7           | 44              | 15                  | 0.34  | AC Q9NYK7;<br>DE CCK-B/gastrin receptor.  |
| Q8WY32           | 91              | 12                  | 0.13  | AC Q8WY32;<br>DE TAR RNA-binding protein TRBP1 (Fragment).<br>GN TARBP2.  |
| P51993           | 38              | 2                   | 0.053 | AC P51993;<br>DE Alpha-(1,3)-fucosyltransferase (EC 2.4.1.65) (Galactoside 3-L-fucosyltransferase) (Fucosyltransferase 6) (FUCT-VI).<br>GN FUT6 OR FCT3A. |
| O60547           | 46              | 1                   | 0.022 | AC O60547; O75357; Q9UGZ3; Q9UJK9;<br>DE GDP-mannose 4,6 dehydratase (EC 4.2.1.47) (GDP-D-mannose dehydratase)<br>DE (GMD).<br>GN GMDS.                   |
| Q9Y231           | 68              | 1                   | 0.015 | AC Q9Y231;<br>DE Alpha-3-fucosyltransferase (Fucosyltransferase 9) (Alpha (1,3) fucosyltransferase).<br>GN FUT9   |
| Q8TDF8           | 83              | 1                   | 0.012 | AC Q8TDF8;<br>DE Laminin alpha5 chain precursor.  |
| Q8TE43           | 106             | 1                   | 0.009 | AC Q8TE43;<br>DE Putative alpha 1,3-fucosyl transferase.<br>GN FUT10.   |

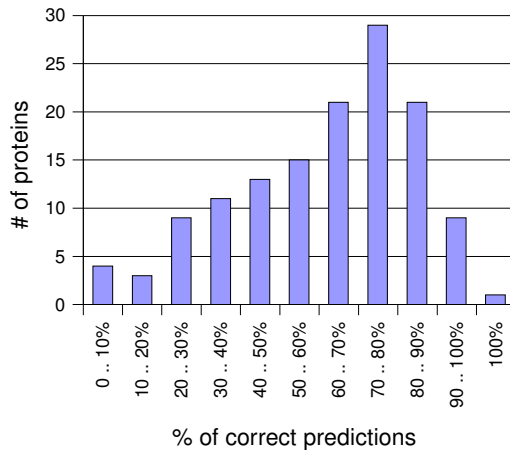
### Task 2.1: proteins



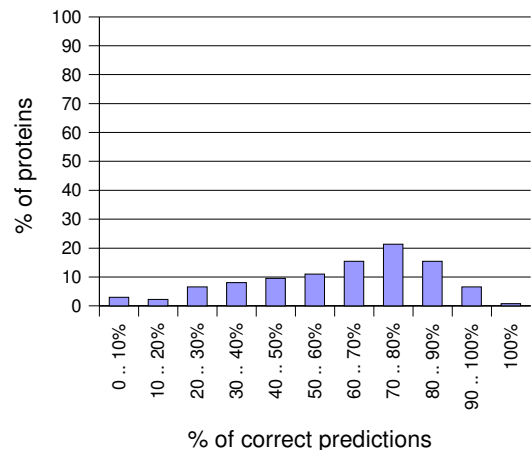
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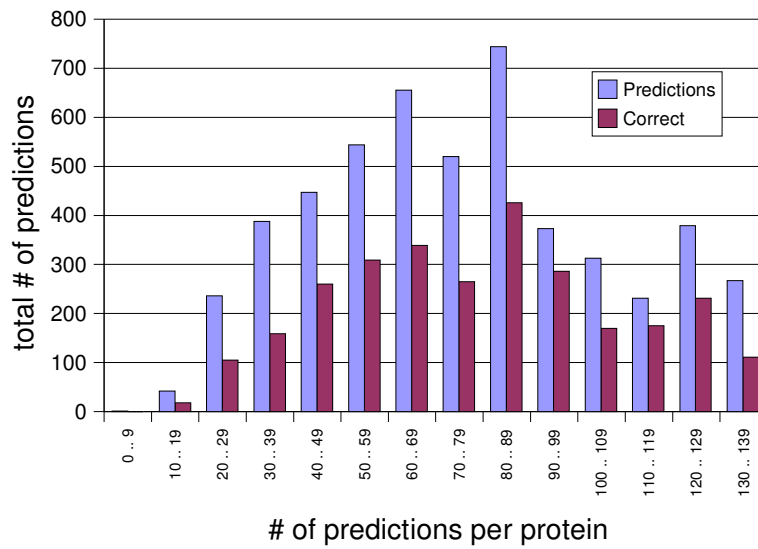
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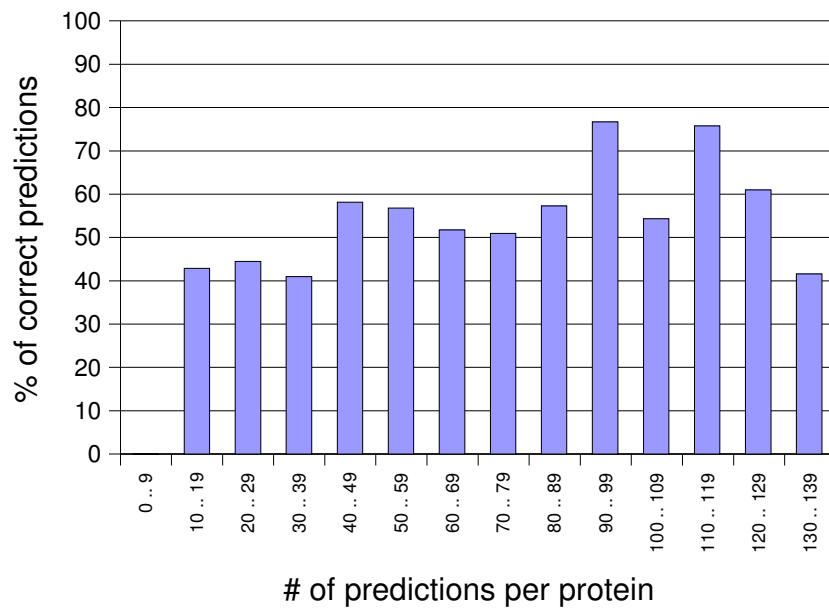
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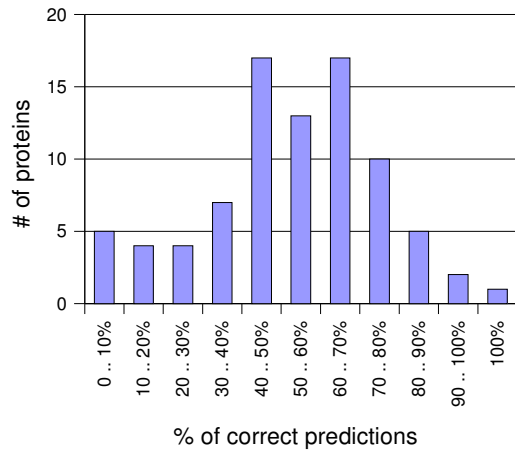
### Task 2.2: proteins



### Task 2.2: proteins



### Task 2.2: proteins



### Task 2.2: proteins

