

**Online Supporting Information S4.** Detailed results predicted by various predictors<sup>a</sup> on the 14 independent proteins in Online Supporting Information S3.

Protein code	Observed SNO site	Predicted SNO site <sup>b</sup>		
		GPS-SNO <sup>c</sup>	iSNO-PseAAC <sup>d</sup>	iSNO-AAPair
P61982	112	97; <b>112</b> ;194	194	<b>112</b>
P23528	147	139	39;80; <b>147</b>	39;139; <b>147</b>
P13804	53	<b>53</b> ;159	<b>53</b> ;109;159;194	<b>53</b> ;60;68;155
O35295	250	None	<b>250</b>	285
Q9DC70	164	None	194	164; <b>194</b>
P19338	543	None	<b>543</b>	<b>543</b>
Q9NPA8	40	None	<b>40</b> ;50	<b>40</b> ;50
Q9R0P5	23	<b>23</b>	<b>23</b> ;39;46	12; <b>23</b> ;147
P48444	441	9	389; <b>441</b> ;444	286;479
Q8VDG5	308	None	<b>308</b>	<b>308</b>
O09110	29	120	<b>29</b> ;120	207;227
O75390	211	103;202; <b>221</b> ;479;58 5;928;1105;2038	101; <b>211</b> ;359	18;101; <b>211</b>
P56965	222;274	<b>274</b>	84; <b>274</b>	<b>222</b> ;274
Q9QZX7	113	2;6; <b>113</b> ;309	46; <b>113</b> ;128;217	<b>113</b> ;217

<sup>a</sup> The results for the method proposed in [1] and that in [2] were not listed because the former had no web-server and latter's web-server did not work.

<sup>b</sup> The number colored with red means the SNO site of correct prediction.

<sup>c</sup> The method proposed in [3] where the threshold parameter was set at "medium" to get its highest overall accuracy.

<sup>d</sup> The method proposed in [4].

## REFERENCES

1. Li BQ, Hu LL, Niu S, Cai YD, Chou KC (2012) Predict and analyze S-nitrosylation modification sites with the mRMR and IFS approaches. *J Proteomics* 75: 1654-1665.
2. Li YX, Shao YH, Jing L, Deng NY (2011) An efficient support vector machine approach for identifying protein S-nitrosylation sites. *Protein Pept Lett* 18: 573-587.
3. Xue Y, Liu Z, Gao X, Jin C, Wen L, et al. (2010) GPS-SNO: computational prediction of protein S-nitrosylation sites with a modified GPS algorithm. *PLoS One* 5: e11290.
4. Xu Y, Ding J, Wu LY, Chou KC (2013) iSNO-PseAAC: Predict cysteine S-nitrosylation sites in proteins by incorporating position specific amino acid propensity into pseudo amino acid composition *PLoS ONE* 8: e55844.