Supporting information

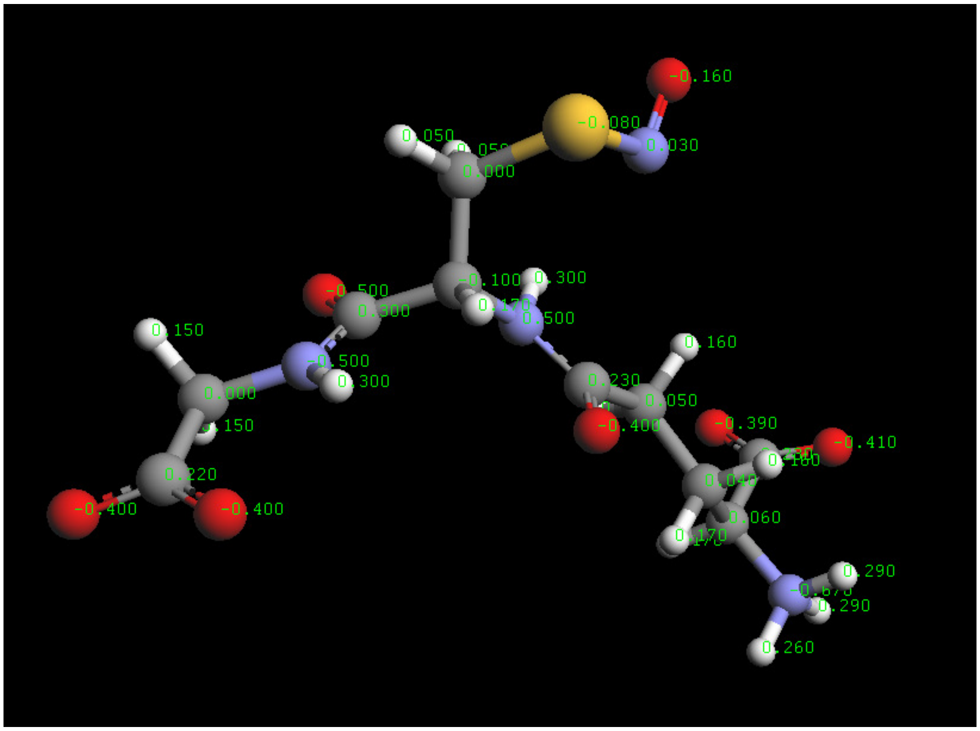


Figure S1: GSNO charge scheme. Structure and atomic charge distribution for GSNO employed in the docking calculations.

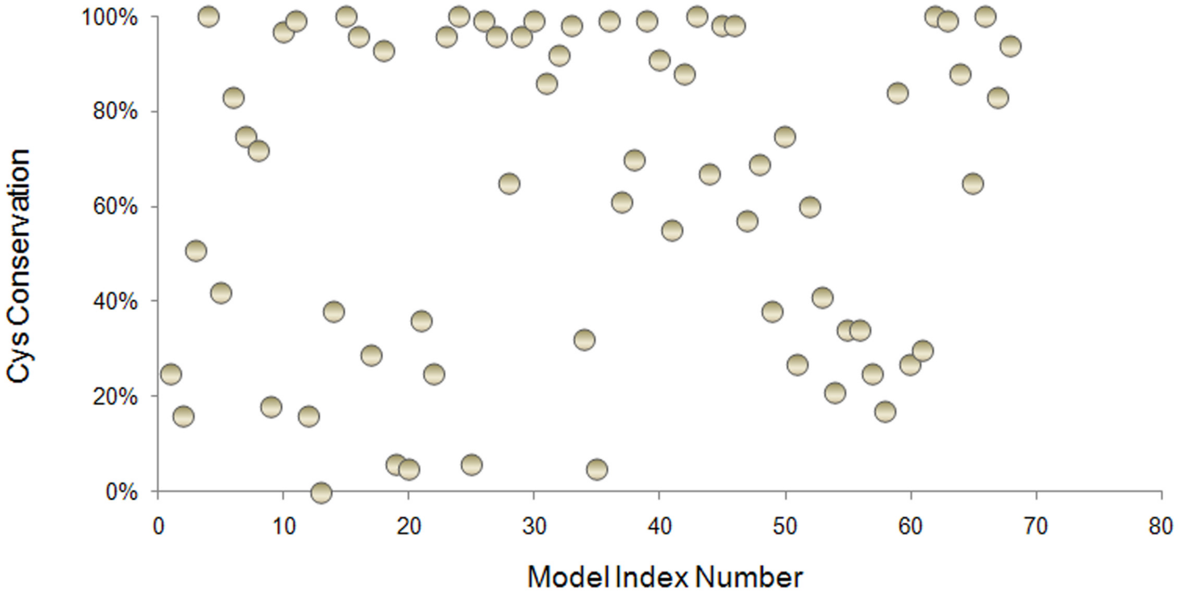
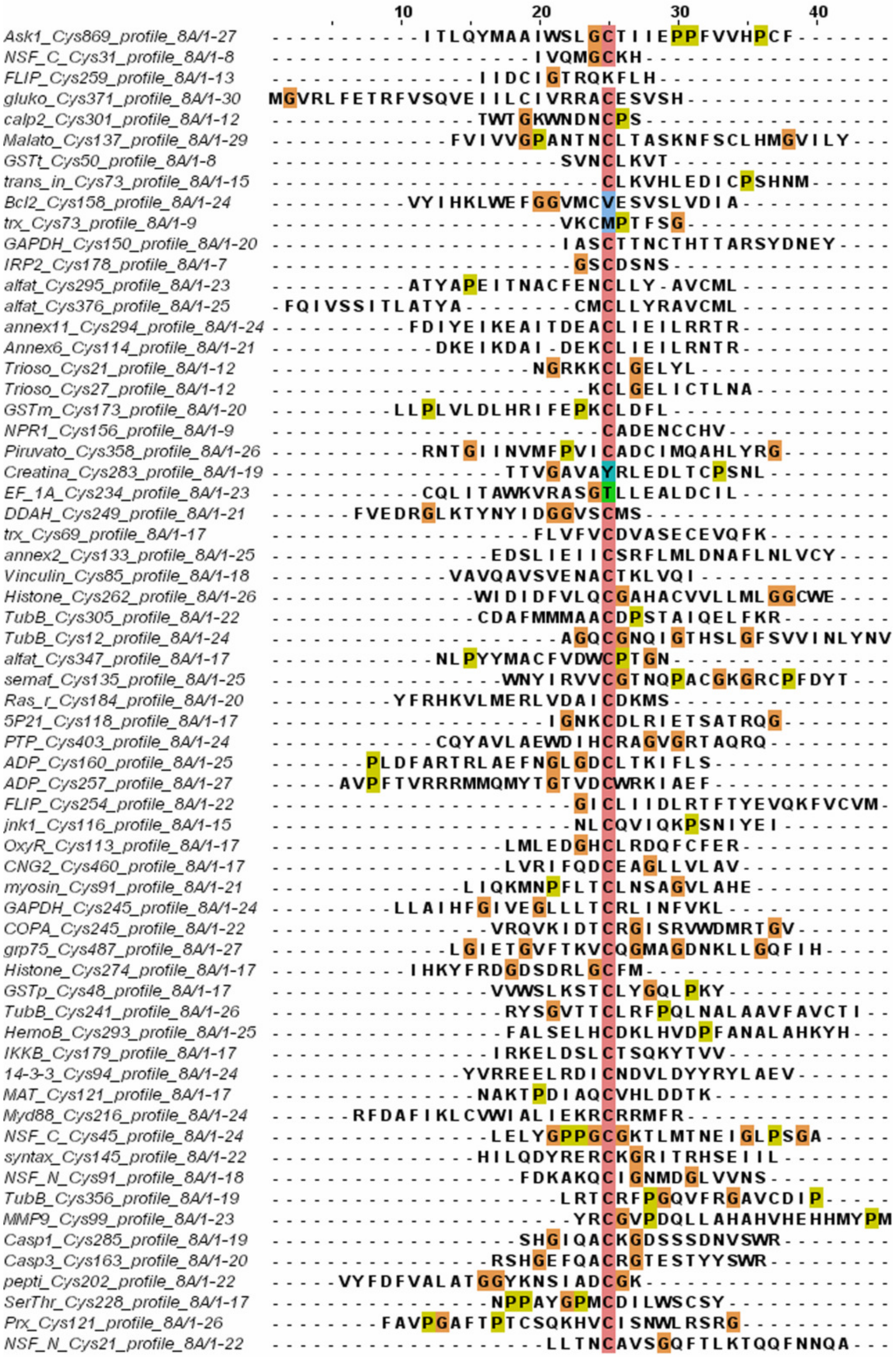


Figure S2: Cys conservation for each NO-Cys in the dataset. Proteins are shown in the same order as in the main text, and in the supplementary information, Table S1.



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Ask1_Cys869_profile_8A/1-27      -----------ITLQYMAAIWSLGCTIIEPPFVVHPCF-------
NSF_C_Cys31_profile_8A/1-8       -------------------IVQMGCKH------------------
FLIP_Cys259_profile_8A/1-13      ---------------IIDCIGTRQKFLH-----------------
gluko_Cys371_profile_8A/1-30     MGVRLFETRFVSQVEIILCIVRRACESVSH---------------
calp2_Cys301_profile_8A/1-12     ---------------TWTGKWNDNCPS------------------
Malato_Cys137_profile_8A/1-29    -------------FVIVVGPANTNCLTASKNFSCLHMGVILY---
GSTt_Cys50_profile_8A/1-8        ---------------------SVNCLKVT----------------
trans_in_Cys73_profile_8A/1-15   ------------------------CLKVHLEDICPSHNM------
Bcl2_Cys158_profile_8A/1-24      ----------VYIHKLWEFGGVMCVESVSLVDIA-----------
trx_Cys73_profile_8A/1-9         ---------------------VKCMPTFSG---------------
GAPDH_Cys150_profile_8A/1-20     ---------------------IASCTTNCTHTTARSYDNEY----
IRP2_Cys178_profile_8A/1-7       ----------------------GSCDSNS----------------
alfat_Cys295_profile_8A/1-23     ----------ATYAPEITNACFENCLLY-AVCML-----------
alfat_Cys376_profile_8A/1-25     -FQIVSSITLATYA--------CMCLLYRAVCML-----------
annex11_Cys294_profile_8A/1-24   ----------FDIYEIKEAITDEACLIEILRRTR-----------
Annex6_Cys114_profile_8A/1-21    ------------DKEIKDAI-DEKCLIEILRNTR-----------
Trioso_Cys21_profile_8A/1-12     -------------------NGRKKCLGELYL--------------
Trioso_Cys27_profile_8A/1-12     -----------------------KCLGELICTLNA----------
GSTm_Cys173_profile_8A/1-20      ---------LLPLVLDLHRIFEPKCLDFL----------------
NPR1_Cys156_profile_8A/1-9       ------------------------CADENCCHV------------
Piruvato_Cys358_profile_8A/1-26  -----------RNTGIINVMFPVICADCIMQAHLYRG--------
Creatina_Cys283_profile_8A/1-19  -----------------TTVGAVAYRLEDLTCPSNL---------
EF_1A_Cys234_profile_8A/1-23     -----------CQLITAWKVRASGTLLEALDCIL-----------
DDAH_Cys249_profile_8A/1-21      ------FVEDRGLKTYNYIDGGVSCMS------------------
trx_Cys69_profile_8A/1-17        -------------------FLVFVCDVASECEVQFK---------
annex2_Cys133_profile_8A/1-25    ----------------EDSLIEIICSRFLMLDNAFLNLVCY----
Vinculin_Cys85_profile_8A/1-18   -------------VAVQAVSVENACTKLVQI--------------
Histone_Cys262_profile_8A/1-26   ---------------WIDIDFVLQCGAHACVVLLMLGGCWE----
TubB_Cys305_profile_8A/1-22      ---------------CDAFMMMAACDPSTAIQELFKR--------
TubB_Cys12_profile_8A/1-24       ---------------------AGQCGNQIGTHSLGFSVVINLYNV
alfat_Cys347_profile_8A/1-17     ------------NLPYYMACFVDWCPTGN----------------
semaf_Cys135_profile_8A/1-25     -----------------WNYIRVVCGTNQPACGKGRCPFDYT---
Ras_r_Cys184_profile_8A/1-20     ---------YFRHKVLMERLVDAICDKMS----------------
5P21_Cys118_profile_8A/1-17      --------------------IGNKCDLRIETSATRQG--------
PTP_Cys403_profile_8A/1-24       ------------CQYAVLAEWDIHCRAGVGRTAQRQ---------
ADP_Cys160_profile_8A/1-25       -------PLDFARTRLAEFNGLGDCLTKIFLS-------------
ADP_Cys257_profile_8A/1-27       -----AVPFTVRRRMMQMYTGTVDCWRKIAEF-------------
FLIP_Cys254_profile_8A/1-22      ----------------------GICLIIDLRTFTYEVQKFVCVM-
jnk1_Cys116_profile_8A/1-15      ----------------------NLCQVIQKPSNIYEI--------
OxyR_Cys113_profile_8A/1-17      -----------------LMLEDGHCLRDQFCFER-----------
CNG2_Cys460_profile_8A/1-17      -----------------LVRIFQDCEAGLLVLAV-----------
myosin_Cys91_profile_8A/1-21     --------------LIQKMNPFLTCLNSAGVLAHE----------
GAPDH_Cys245_profile_8A/1-24     ---------LLAIHFGIVEGLLLTCRLINFVKL------------
COPA_Cys245_profile_8A/1-22      ----------------VRQVKIDTCRGISRVWDMRTGV-------
grp75_Cys487_profile_8A/1-27     -------------LGIETGVFTKVCQGMAGDNKLLGQFIH-----
Histone_Cys274_profile_8A/1-17   ----------IHKYFRDGDSDRLGCFM------------------
GSTp_Cys48_profile_8A/1-17       ----------------VVWSLKSTCLYGQLPKY------------
TubB_Cys241_profile_8A/1-26      -----------------RYSGVTTCLRFPQLNALAAVFAVCTI--
HemoB_Cys293_profile_8A/1-25     -----------------FALSELHCDKLHVDPFANALAHKYH---
IKKB_Cys179_profile_8A/1-17      ----------------IRKELDSLCTSQKYTVV------------
14-3-3_Cys94_profile_8A/1-24     --------------YVRREELRDICNDVLDYYRYLAEV-------
MAT_Cys121_profile_8A/1-17       ---------------NAKTPDIAQCVHLDDTK-------------
Myd88_Cys216_profile_8A/1-24     ------RFDAFIKLCVWIALIEKRCRRMFR---------------
NSF_C_Cys45_profile_8A/1-24      ----------------LELYGPPGCGKTLMTNEIGLPSGA-----
syntax_Cys145_profile_8A/1-22    ---------------HILQDYRERCKGRITRHSEIIL--------
NSF_N_Cys91_profile_8A/1-18      ------------------FDKAKQCIGNMDGLVVNS---------
TubB_Cys356_profile_8A/1-19      ---------------------LRTCRFPGQVFRGAVCDIP-----
MMP9_Cys99_profile_8A/1-23       ----------------------YRCGVPDQLLAHAHVHEHHMYPM
Casp1_Cys285_profile_8A/1-19     ------------------SHGIQACKGDSSSDNVSWR--------
Casp3_Cys163_profile_8A/1-20     ----------------RSHGEFQACRGTESTYYSWR---------
pepti_Cys202_profile_8A/1-22     -----VYFDFVALATGGYKNSIADCGK------------------
SerThr_Cys228_profile_8A/1-17    ----------------NPPAYGPMCDILWSCSY------------
Prx_Cys121_profile_8A/1-26       --------FAVPGAFTPTCSQKHVCISNWLRSRG-----------
NSF_N_Cys21_profile_8A/1-22      --------------------LLTNCAVSGQFTLKTQQFNNQA---
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Figure S3: Structural profile analysis of NO-Cys sites in the dataset. Overall, no common features were derived from the structural profile analysis.

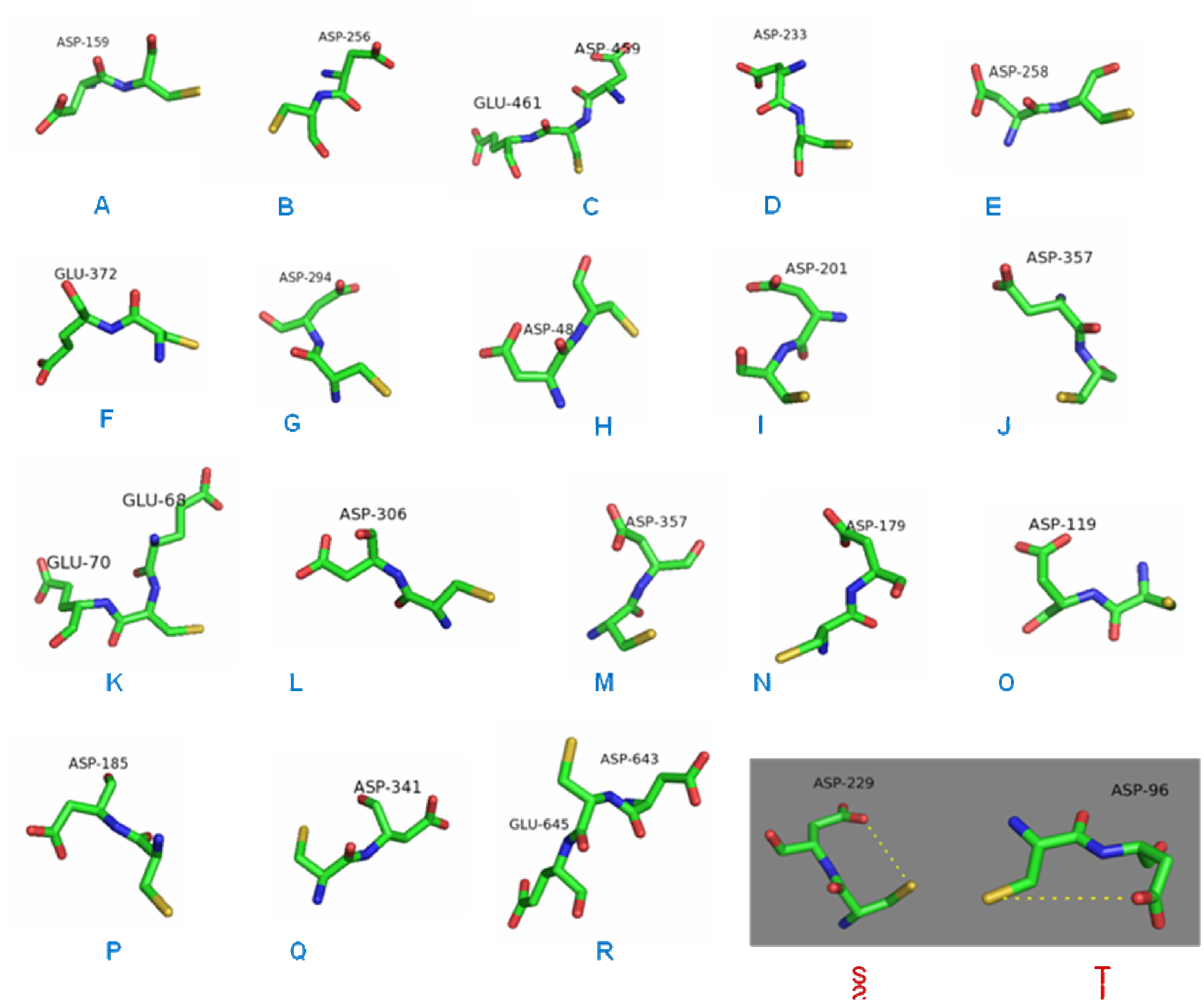

Figure S4: Relative positioning of negatively charged residues in vicinity of NO-Cys. All NO-Cys sites in our dataset with an acidic amino acid flanking Cys in the sequence were analyzed for the distance between charged groups and sulfur atoms. NO-Cys groups are indicated with a letter code (in brackets the name of the protein, complete or as abbreviated in main text): A=ADP/ATP translocase (Cys 160), B= ADP/ATP translocase (Cys 257), C= CNG2 (Cys 460), D=EF1A (Cys 234), E=FLIP (Cys 259), F=glukokinase (Cys 372), G=hemoglobin (Cys 293), H=Sodium/potassium-transporting ATPase (Cys 49), I=peptidylprolyl isomerase (Cys 202), J=pyruvate kinase (Cys 356), K=TRX1 (Cys 69), L=tubulin beta (Cys 305), M=tubulin beta (Cys 356), N=IRP2 (Cys 178), O=ras p21 (Cys 118), P= ras-related protein Rab-3B (Cys 186), Q=GRK2 (Cys 34), R=human DPR-1 (Cys 644), S=Ser/Thr protein phosphatase (Cys 228), T=dynamin (Cys 95). All but two have acidic residues pointing away with respect to the Cys functional group: two proteins (with NO-Cys numbering in brackets) are separately shown in the grey panel (panels S and T). This figure gives an immediate idea that whenever the acidic residue is flanking NO-Cys, in the three dimensional structure its distance and positioning of charged atoms are in the outward direction (i.e., going far from the sulfur atom).

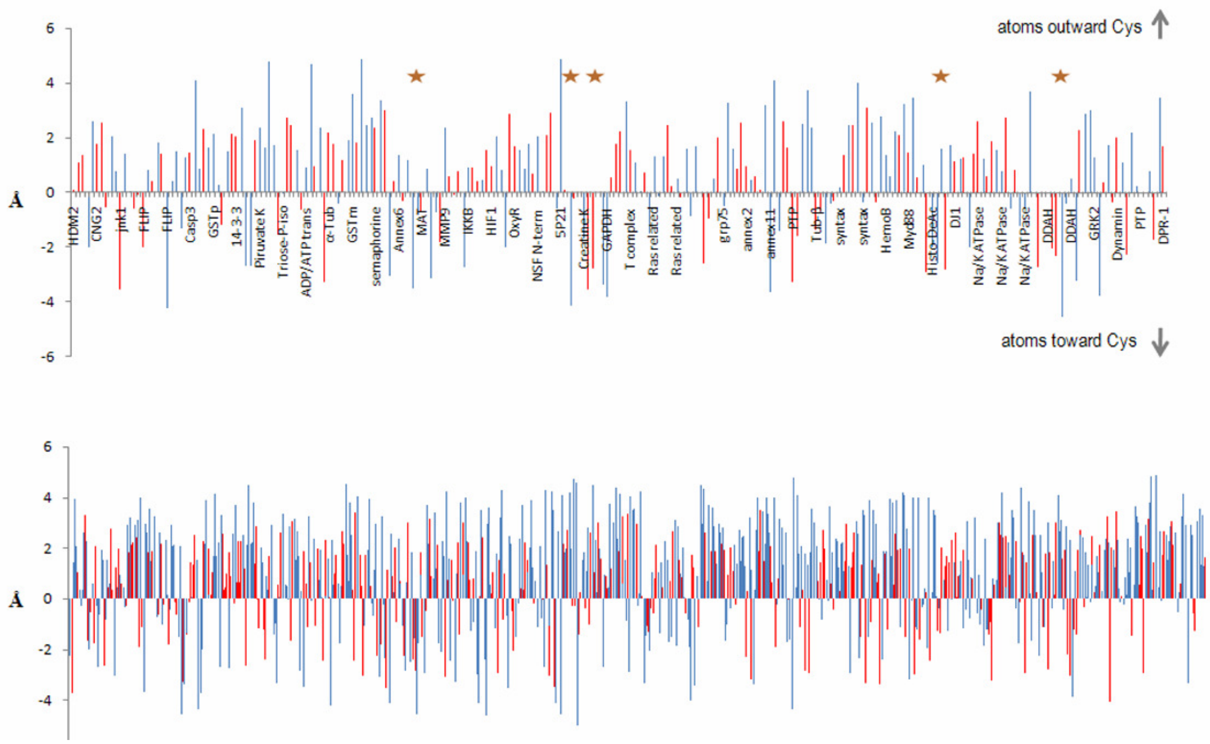

Figure S5: Orientation of charged functional groups relative to NO-Cys. Distribution of functional groups of basic (blue lines) and acidic (red lines) residues relative to the Cys sulfur atom, for both NO-Cys and a control set of non-modifiable Cys. Negative values (in Å, Y-axis) indicate that the charged atom points toward the Cys. In the X-axis, the corresponding proteins are indicated (for clarity, only for the NO-Cys set). A few proteins having NO-Cys with acidic and basic residues pointing toward the Cys are marked by a star. Details are given in the main text.

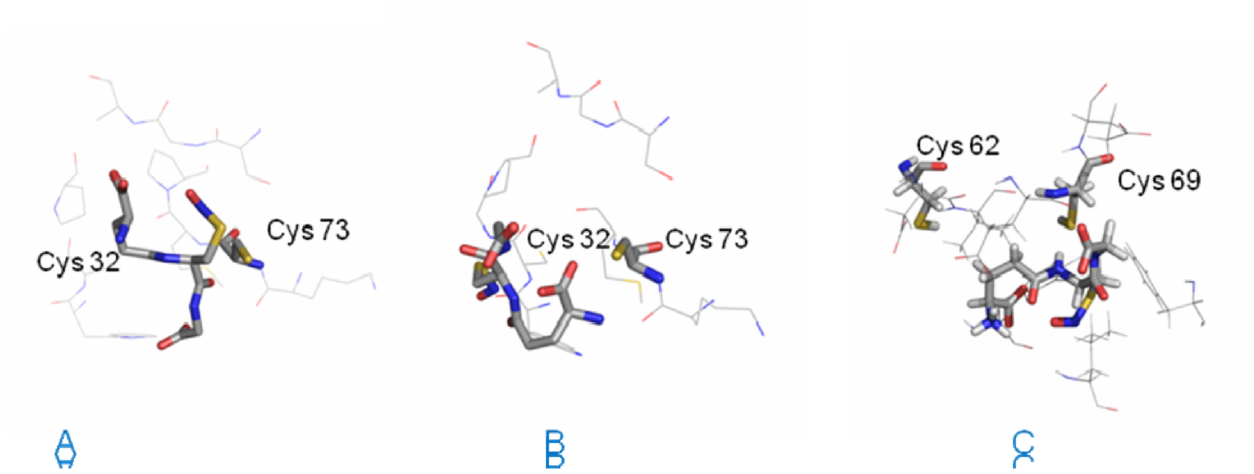

Figure S6: Docking GSNO to thioredoxin 1. (A) A model of GSNO (in stick representation) interacting with Cys 73 (in stick and labeled). This position is described in the main text and Table 2**.** GSNO favorably docks onto thioredoxin 1 in the region between Cys 73 and Cys 32 (the catalytic Cys). Two alternative models were found: one shown in (A), characterized by a S-S distance of 2.5 Å and interaction of -3.9 kcal/mol, and a non-reactive model (B) which shows GSNO oriented with its functional group toward Cys 32 (but at about 4 Å distance). (C) The best docking model of GSNO oriented toward Cys 69 and Cys 62 (both in stick and labeled). This model, even if characterized by a better energy score (-7 kcal/mol) than those in panels A and B, is not reactive. Thus, the Cys 69-Cys 62 region shows good affinity for GSNO, but in our calculations we did not find a consistent reactive model (especially, for Cys 62, which was always more distant than Cys 69 from GSNO).

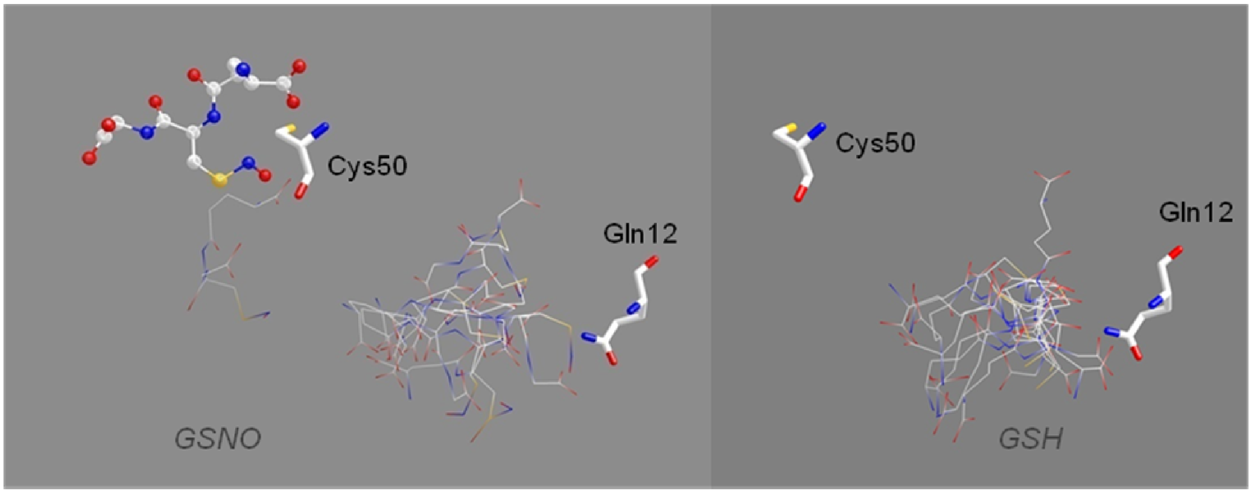

Figure S7: GSTt affinity for GSNO and GSH. Calculated docking reactivity of GSTt (in the dimer form) is shown for GSNO (left panel) and GSH (right). The modifiable Cys 50 and Gln 12 (taken as a reference for the natural binding site of GSH in this protein, Rossjohn et al, 1998) are shown in sticks. As can be seen from the figure, while GSH shows affinity for its natural binding site, GSNO has potential alternative models, bringing the substrate near Cys 50. However, as discussed in the text, among the first ranked docking positions only the cluster of models near Gln 12 is also found for GSNO. The reactive modes, proximal to Cys 50, are found at higher energy: for the model shown in balls and sticks, the associated energy value was -2.7 kcal/mol, but it was only ranked as the 32nd possible position.

Table S1. The dataset of NO-Cys containing proteins

Source	ID	Protein name	NO-Cys number	Hydr 6A	Hydr 13aa	pKa	6A q+/q-	8A q+/q-	SG(exp,1.2A)	Cys conservation	template (% id)	modeling coverage
Homo sapiens	P10599	Thioredoxin1	69	1.06	-0.25	9.5		**Y**	0	25%	2hsh (100%)	1-105
Homo sapiens	P10599	Thioredoxin1	73	-0.2	-0.06	8.4		**Y**	23	16%	2hsh (100%)	1-105
Mus musculus	O35099	cyclic nucleotide gated channel alpha 2	460	0.72	0.94	8.5	**Y**	**Y**	0.5	51%	1q3e (35%)	381-580
Mus musculus	O35099	Mitogen-activated protein kinase kinase kinase 5 (ASK1)	869	0.23	1.05	11.2		**Y**	0	100%	2clq (100%)	670-940
Homo sapiens	P45983	Mitogen-activated protein kinase (JNK1)	116	-0.26	0.53	9	**Y**	**Y**	45	42%	2h96 (99%)	7-364
Pseudomonas aeruginosa	Q02J31	Dimethylarginine dimethylaminohydrolase	273	0.027	1.56	7.8		**Y**	21.5	83%	2jaj (100%)	8 - 281
Homo sapiens	P10415	Apoptosis regulator Bcl-2	158	2.15	0.24	10.3	**Y**	**Y**	12.98	75%	2o2f (100%)	92-204
Homo sapiens	O15519-8	FADD-like apoptosis regulator isoform 1	254	0.24	1.57	11.5		**Y**	0	72%	3deh (23%)	244-477
Homo sapiens	O15519-8	FADD-like apoptosis regulator isoform 1	259	3	0.9	9		**Y**	37.65	18%	3deh (23%)	244-477
Homo sapiens	P42574	Caspase-3	163	-0.84	0.58	6.18		**Y**	19.3	97%	1cp3 (100%)	35-277
Homo sapiens	P29466	Caspase-1	285	-0.23	0.56	5.87		**Y**	22.36	99%	2h4y (100%)	119-298
Rattus norvegicus	Q07009	Calpain 2, large subunit	301	-1.7	-1.27	7.66		**Y**	26.7	16%	1kfu (93%)	2-700
Rattus norvegicus	P30713	Glutathione S-transferase theta 2	50	-0.38	0.077	8.22			42	0%	1ljr(78%)	1-244
Rattus norvegicus	P04906	Glutathione S-transferase P	48	-0.125	0.038	9.05			1.01	38%	1glqA (92%)	2-210
Rattus norvegicus	P63329	Serine/threonine protein phosphatase 2B	228	-0.12	0.06	13.1			4.8	100%	1AUI (99%)	2 to 381
Rattus norvegicus	P63102	14-3-3 protein	94	0.97	0.2	10.4		**Y**	0	96%	2c1j (99%)	2-210
Rattus norvegicus	P14152	Malate dehydrogenase, cytoplasmic	137	1.8	-0.7	11.9			0	29%	5MDH (95%)	2-334

Rattus norvegicus	P11980	Pyruvate kinase, isozymes M1/M2	358	1.8	0.8	12.9		**Y**	0	93%	2g50D (95%)	11 - 531
Rattus norvegicus	P48500	Triosephosphate isomerase	21	-1.53	-0.08	5.75	**Y**	**Y**	20	6%	1r2r (95%)	3 to 249
Rattus norvegicus	P48500	Triosephosphate isomerase	27	1.4	-0.05	7.51		**Y**	29.8	5%	1r2r (95%)	3 to 249
Rattus norvegicus	P46460	Vesicle-fusing ATPase C-terminal	250	0.025	0.23	9.1		**Y**	42	36%	3cf1 (33%)	220 - 465
Rattus norvegicus	P46460	Vesicle-fusing ATPase C-terminal	264	0.072	0.41	4.7		**Y**	0	25%	3cf1 (33%)	220 - 465
Rattus norvegicus	Q05962	ADP/ATP translocase	160	1.07	0.3	10.1		**Y**	0	96%	1okc (96%)	3 - 294
Rattus norvegicus	Q05962	ADP/ATP translocase	257	-0.5	-0.5	10.2		**Y**	0	100%	1okc (96%)	3 - 294
Rattus norvegicus	P06687	Sodium/potassium-transporting ATPase	49	2.4	-1.13	8.54		**Y**	1.4	6%	3b8e (87.5%)	16 - 1013
Rattus norvegicus	P06687	Sodium/potassium-transporting ATPase	364	2.4	-0.49	14.16		**Y**	0	99%	3b8e (87.5%)	16 - 1013
Rattus norvegicus	P06687	Sodium/potassium-transporting ATPase	695	2.6	0.76	10.6		**Y**	0.9	96%	3b8e (87.5%)	16 - 1013
Rattus norvegicus	Q6P9V9	Tubulin alpha	295	1.9	-0.35	11.2		**Y**	0	65%	1sa0 (100%)	2-437
Rattus norvegicus	Q6P9V9	Tubulin alpha	347	0.83	0.5	9.1		**Y**	22	96%	1sa0 (100%)	2-437
Rattus norvegicus	Q6P9V9	Tubulin alpha	376	2.2	0.06	12.25		**Y**	0	99%	1sa0 (100%)	2-437
Homo sapiens	P09488	Glutathione S-transferase Mu 1	173	0.1	-0.3	8.92	**Y**	**Y**	0.1	86%	1GTU (100%)	2-218
Homo sapiens	Q92854	Semaphorin 4D	135	-0.14	-1.46	11.45		**Y**	0	92%	1olz(100%)	22-678
Homo sapiens	P35557-2	Glucokinase	371	1.2	-0.43	12.24	**Y**	**Y**	0	98%	1v4s (99%)	16-465
Homo sapiens	P08133	Annexin-6	114	-0.18	0.76	10.8	**Y**	**Y**	2.6	32%	1m9i (100%)	10-673
Rattus norvegicus	P13444.2	S-adenosylmethionine synthetase isoform type-1	121	0.59	-0.32	7.45	**Y**	**Y**	22.8	5%	1qm4 (99%)	17 - 397
Homo sapiens	P14780	Matrix metalloproteinase 9 preproprotein	99	-1.05	-0.23	1	**Y**	**Y**	4.1	99%	1ck7.pdb (44%)	26 to 704
Homo sapiens	Q1HE21	Iron-responsive element	178	-0.55	-0.53	8.95		**Y**	41	61%	(2b3x) 56%	9-963

		binding protein 2										
Homo sapiens	O14920.1	Inhibitor of nuclear factor kappa-B kinase subunit beta	179	-6	0.48	7.6	**Y**	**Y**	5.2	70%	2acx (26%)	15 - 288
Arabidopsis thaliana	Q949U7.2	Peroxiredoxin-2E	121	-0.49	-0.39	1.9			1.5	99%	1tp9 (60%)	71-234
Escherichia coli	Q1R3U8	Oxidative stress transcriptional regulator (OxyR)	113	0.49	-0.49	8.9	**Y**	**Y**	0.4	91%	1i6a (99%)	1 to 212
Rattus norvegicus	P46459	Vesicle-fusing ATPase N-terminal	21	-0.52	0.06	9.35		**Y**	7.6	55%	1qcsA (91%)	1 - 201
Rattus norvegicus	P46459	Vesicle-fusing ATPase N-terminal	91	0.87	0.19	9.1		**Y**	9.88	88%	1qcsA (91%)	1 - 201
Homo sapiens	P01112	Ras p21 Protein	118	-2	0.43	8.72	**Y**	**Y**	10.3	67%	5p21 (100%)	1-166
Rattus norvegicus	P07335	Creatine kinase	283	0.29	0.71	8.15		**Y**	23.7	98%	1GOW (96%)	2 to 381
Rattus norvegicus	P04797	GAPDH	150	-1.1	0.85	5.35			19.5	98%	1u8f (94%)	2 to 333
Rattus norvegicus	P04797	GAPDH	245	1.63	0.13	10.15	**Y**	**Y**	0	57%	1u8f (94%)	2 to 333
Homo sapiens	P18206	Vinculin	85	1.72	0.29	8.72		**Y**	18.3	69%	1tr2 (88%)	1 to 1130
Homo sapiens	P40227	T-complex protein 1 subunit zeta	406	0.26	0.44	9.5		**Y**	0	75%	1q3r (38%)	19 to 524
Homo sapiens	P20337	Ras-related protein Rab-3B	184	0.65	-0.07	8.6		**Y**	9.4	27%	2gf9 (86%)	20 to 189
Homo sapiens	P23284	Peptidylprolyl isomerase B	202	0	0.61	9.15		**Y**	3.8	60%	1cyn (100%)	39 to 216
Homo sapiens	P35579	Myosin heavy chain 9	91	-0.62	0.33	10.3		**Y**	8.6	41%	2aka (48%)	8 to 782
Homo sapiens	P38646	Stress-70 protein	487	0.36	-0.7	10.75	**Y**	**Y**	1.9	21%	1yuw (55%)	52 to 597
Homo sapiens	P53621	COPA protein	245	-1.02	-1.3	10.8		**Y**	1.6	34%	2ovr (34%)	67 to 287
Homo sapiens	P07355	Annexin-2	133	1.77	-0.077	12.8		**Y**	0	34%	1w7b (100%)	21 to 339
Homo sapiens	P50995	Annexin-11	294	-0.05	1.17	9.3	**Y**	**Y**	4.4	25%	1ann (59%)	192 to 505
Homo sapiens	Q6IPS9	Elongation factor alpha 1	234	1.73	0.66	9.96		**Y**	12.7	17%	1f60 (81%)	2 to 443
Yersinia enterocolitica	P15273	Protein Tyrosine Phosphatase	215	-0.16	0.77	1.8		**Y**	2	84%	2cni (100%)	1 to 300

Homo sapiens	Q16623	Syntaxin 1A	145	9.38	-2.14	9.3	**Y**	**Y**	0.2	27%	3c98 (99%)	1-267
Homo sapiens	Q99836	Myeloid differentiation primary response protein MyD88	216	0.4	0.07	10.72		**Y**	0	30%	2js7(100%)	146-296
Homo sapiens	P68871.2	Hemoglobin subunit beta	293	-0.15	-0.32	6.8	**Y**	**Y**	0	100%	1dxt (100%)	1-147
Rattus norvegicus	P69897	Tubulin beta	12	-0.69	-0.25	11.25			12.4	99%	1sa0 (100%)	2-438
Rattus norvegicus	P69897	Tubulin beta	241	1.025	0.2	8.63		**Y**	17.6	88%	1sa0 (100%)	2-438
Rattus norvegicus	P69897	Tubulin beta	305	0.76	-1.1	10.73		**Y**	0	65%	1sa0 (100%)	2-438
Rattus norvegicus	P69897	Tubulin beta	356	0.24	-0.19	6.8		**Y**	6.05	100%	1sa0 (100%)	2-438
Homo sapiens	Q92769	Histone deacetylase 2	262	1.24	0.9	15		**Y**	0	83%	1t64 (41%)	13-374
Homo sapiens	Q92769	Histone deacetylase 2	274	0.82	-0.05	6	**Y**	**Y**	13	94%	1t64 (41%)	13-374
Homo sapiens	O88767	Parkinson disease protein 7 (DJ1)	46	1.04	-0.16	8.91		**Y**	0	28%	1ps4 (92%)	1 to 189
Homo sapiens	O88767	Parkinson disease protein 7 (DJ1)	53	1.6	0.02	9		**Y**	44	20%	1ps4 (92%)	1 to 189
Homo sapiens	P50570	Dynamin-2	607	0.933333	-0.73	15		**Y**	0.19	100%	2ys1 (100%)	516 to 621
Mus musculus	Q4FJR9	SG15 ubiquitin-like modifier	76	-1.76	0.86	9.05		**Y**	27.4	1%	1z2m (63%)	3 to 151
Homo sapiens	P25098	G-protein coupled receptor kinase 2 (GRK2)	340	0.55	-0.46	7.5		**Y**	20.6	53%	3cik (100%)	29 to 669
Homo sapiens	O00429	Dynamin-related protein 1	644	-1.31	-1.09	8.37		**Y**	30.44	100%	2j69(12.1%)	1 to 736

LEGEND:

Hydr 6A: average hydrophobicity (Kyte-Doolittle scale) of the 6 A region surrounding NO-Cys

Hydr 13 aa: average hydrophobicity (Kyte-Doolittle scale) of the primary sequence flanking the NO-Cys (6aa downstream and 6 aa upstream the Cys)

6A q+/q- = proteins presenting at least one positively charged (q+) AND one negatively charged (q-) amino acid in within 6A form NO-Cys sulfur atom: protein presenting the feature are labeled with "**Y**"

8A q+/q- = proteins presenting at least one q+ AND one q- within 8A form NO-Cys sulfur atom: protein presenting the feature are labeled with **"Y"**

SG (exp,1.2A) = sulfur atom exposure, calculated using a molecular probe of 1.2 A radius

Template (% id) = percentage of amino acid identity with the template used for the modeling session

Modeling coverage = coverage of the structural model in respect to the full length protein sequence (number indicates AA positions in respect to the full protein sequence)

Table S2. Exposed regions surrounding the NO-Cys sites

Protein name	NO-Cys number	Amino acids of the Exposed 8Å region (8A region)	8A region conservation	NO-Cys conservation
Thioredoxin1	69	PHE 11,LEU 15,CYS 62,ASP 64,VAL 65,ALA 66,SER 67,GLU 68,CYS 69,GLU 70,VAL 71,PHE 80,LYS 85	45%	25%
Thioredoxin1	73	GLU 70,VAL 71,LYS 72,CYS 73,MET 74,THR 76,PHE 89,SER 90,ASER 90,GLY 91	58%	16%
Cyclic nucleotide gated channel alpha 2	460	LEU 451, VAL 454, ARG 455, ILE 456, GLN 458, ASP 459, CYS 460, GLU 461, ALA 462, GLY 463, LEU 464, ALA 568, VAL 571	69%	51%
Mitogen-activated protein kinase kinase kinase 5 (ASK1)	869	THR 842,LEU 843,GLN 844,TYR 845,MET 846,ILE 872,GLU 873,PRO 879,PHE 881,VAL 899,HIS 900,PRO 901,PHE 919	75%	100%
Mitogen-activated protein kinase (JNK1)	116	ASN 114,CYS 116,GLN 117,VAL 118,ILE 119,GLN 120,LYS 153,PRO 154,SER 155,ASN 156,TYR 191,GLU 217,ILE 223	80%	42%
Dimethylarginine dimethylaminohydrolase	273	PHE 75,GLU 77,ASP 78,ARG 97,GLY 128,HIS 172,LYS 174,SER 175,VAL 267,ASP 268,AASP 268,LEU 270,THR 272,CYS 273,SER 275	32%	83%
Apoptosis regulator Bcl-2	158	TYR 18,HIS 20,LYS 22,LEU 23,TRP 30,GLU 152,PHE 153,VAL 156,VAL 159,GLU 160,VAL 162,SER 167,LEU 169,ASP 171,ALA 174	64%	75%
FADD-like apoptosis regulator isoform 1	254	GLY 252,LEU 255,ILE 257,ASP 258,LEU 267,ARG 268,THR 270,PHE 271,THR 272,TYR 276,GLU 277,VAL 278,GLN 279,LYS 280,VAL 309,CYS 310,VAL 311,MET 354	67%	72%
FADD-like apoptosis regulator isoform 1	259	ILE 257,ASP 258,CYS 259,ILE 260,GLY 261,ARG 268,GLN 279,LYS 280,PHE 281,LEU 282,HIS 283	53%	18%
Caspase-3	163	ARG 64,SER 120,HIS 121,GLY 122,GLU 123,PHE 128,GLN 161,CYS 163,ARG 164,GLY 165,THR 166,GLU 167,TYR 203,TYR 204,SER 205,TRP 206,ARG 207	65%	97%
Caspase-1	285	GLU 219,PHE 221,ALA 222,HIS 223,ARG 224,LYS 228,ASN 278,MET 279,ASN 281,THR 282,LYS 283,ASN 284,PRO 286,SER 287,LYS 289,ASP 290,LYS 293	60%	99%
Calpain 2, large subunit	301	THR 254,TRP 293,THR 294,GLY 295,LYS 296,ASN 298,ASP 299,ASN 300,CYS 301,PRO 302,SER 303	60%	16%
Glutathione S-transferase theta 2	50	THR 254,TRP 293,THR 294,GLY 295,LYS 296,ASN 298,ASP 299,ASN 300,CYS 301,PRO 302,SER 303	30%	0%
Glutathione S-transferase P	48	VAL 7,VAL 34,TRP 39,SER 43,LEU 44,LYS 45,SER 46,THR 47,CYS 48,LEU 49,TYR 50,GLY 51,GLN 52,LEU 53,PRO 54,LYS 55,TYR 64	50%	38%
Serine/threonine protein phosphatase 2B	228	ASN 150,PRO 221,PRO 222,ALA 223,TYR 224,GLY 225,PRO 226,MET 227,CYS 228,ASP 229,TRP 232,CYS 256,SER 257,TYR 258	90%	100%
14-3-3 protein	94	TYR 48,ARG 55,ARG 56,GLU 87,GLU 89,ARG 91,ASP 92,ILE 93,ASN 95,ASP 96,LEU 98,ASP 124,TYR 125,TYR 126,ARG 127,TYR 128,LEU 129,GLU 131,VAL 132	87%	96%
Malate dehydrogenase, cytoplasmic	137	VAL 129,GLY 130,THR 139,SER 141,LYS 149,ASN 151,SER 153,LEU 155,MET 269,VAL 271,ILE 272	56%	29%
Pyruvate kinase, isozymes M1/M2	358	ARG 43,ASN 44,GLY 46,ASN 70,MET 360,GLN 462,HIS 464,LEU 465,TYR 466,ARG 467,GLY 468	60%	93%
Triosephosphate isomerase	21	ASN 16,GLY 17,ARG 18,LYS 19,LYS 20,CYS 21,LEU 22,GLY 23,GLU 24,LEU 25,TYR 48,LEU 237	73%	6%
Triosephosphate isomerase	27	LYS 20,CYS 21,LEU 22,GLY 23,GLU 24,LEU 25,ILE 26,CYS 27,THR 28,ASN 30,ALA 31	66%	5%

Vesicle-fusing ATPase C-terminal	250	ILE 25,VAL 26,GLN 28,MET 29,GLY 30,CYS 31,LYS 32,HIS 33, GLU 143	65%	36%
Vesicle-fusing ATPase C-terminal	264	LEU 4,GLU 7,TYR 40,GLY 41,PRO 42,PRO 43,GLY 44,CYS 45,GLY 46,LYS 47,THR 48,LEU 50,MET 153,THR 154,ASN 155,GLU 175,ILE 176,GLY 177,LEU 178,PRO 179,SER 218,GLY 219,ALA 220	68%	25%
ADP/ATP translocase	160	PRO 133,LEU 134,ASP 135,ARG 138,ARG 140,LEU 141,GLU 153,PHE 154,ASN 155,GLY 156,LEU 157,GLY 158,ASP 159,LEU 161,THR 162,LYS 163,ILE 164,PHE 165,LEU 173	80%	96%
ADP/ATP translocase	257	PRO 230,PHE 231,ARG 235,ARG 236,MET 238,GLN 241,MET 250,TYR 251,THR 252,GLY 253,THR 254,VAL 255,ASP 256,TRP 258,ARG 259,LYS 260,ALA 262,GLU 265,PHE 270	81%	100%
Sodium/potassium-transporting ATPase	49	VAL 38,CYS 42,THR 47,ASP 48,CYS 49,VAL 50,GLN 51,GLY 52,ARG 245	70%	6%
Sodium/potassium-transporting ATPase	364	THR 362,ASP 366,LYS 688,ILE 691,VAL 692,CYS 695	80%	99%
Sodium/potassium-transporting ATPase	695	THR 362,GLU 693,CYS 695,GLN 696,ARG 697,GLN 698,GLY 699	78%	96%
Tubulin alpha	295	THR 271,ALA 273,PRO 274,GLU 290,ILE 291,ASN 293,ALA 294,CYS 295,PHE 296,GLU 297,ASN 300,MET 377	92%	65%
Tubulin alpha	347	ASN 258,LEU 259,PRO 261,TYR 262,TYR 312,ALA 314,CYS 315,PHE 343,VAL 344,ASP 345,TRP 346,CYS 347,PRO 348,THR 349,GLY 350,LYS 352	97%	96%
Tubulin alpha	376	LEU 269,THR 271,ALA 273,CYS 295,MET 377	91%	99%
Glutathione S-transferase Mu 1	173	LEU 127,LEU 130,PRO 131,ASP 164,ARG 167,ILE 168,PHE 169,GLU 170,PRO 171,LYS 172,CYS 173,LEU 174,ASP 175,PHE 177	54%	86%
Semaphorin 4D	135	TRP 66,TYR 90,ARG 92,ASN 108,GLN 111,PRO 112,ALA 113,LYS 132,GLY 133,ARG 134,PHE 137,ASP 138,TYR 143	63%	92%
Glucokinase	371	ARG 303,PHE 330,GLU 331,THR 332,ARG 333,PHE 334,SER 336,GLN 337,GLU 339,ILE 348,ILE 351,CYS 364,ILE 366,ARG 368,ARG 369,GLU 372,SER 373,HIS 416	41%	98%
Annexin-6	114	ASP 97,LYS 99,GLU 100,LYS 102,ASP 103,ALA 104,ILE 105,ASP 111,GLU 112,LYS 113,CYS 114,ILE 116,GLU 117,LEU 119,ARG 122,ASN 272,THR 273,ARG 276	54%	32%
S-adenosylmethionine synthetase isoform type-1	121	ASN 52,LYS 54,THR 73,PRO 116,ASP 117,ILE 118,ALA 119,GLN 120,CYS 121,VAL 122,HIS 123,LEU 124,ASP 125,THR 289,LYS 290	75%	5%
matrix metalloproteinase 9 preproprotein	99	TYR 52,ARG 98,CYS 99,GLY 100,VAL 101,PRO 102,ASP 103,GLN 108,LEU 187,LEU 188,ALA 189,HIS 190,ALA 191,HIS 203,VAL 398,HIS 401,GLU 402,HIS 405,HIS 411,MET 422	83%	99%
iron-responsive element binding protein 2	178	THR 173, ARG 175, GLY 176,SER 177,CYS 178,ASP 179,SER 180,ASN 186,SER 187	62%	61%
inhibitor of nuclear factor kappa-B kinase subunit beta	179	ILE 142,ARG 144,LYS 171,GLU 172,LEU 173,ASP 174,SER 177,LEU 178,CYS 179,THR 180,SER 181,GLN 197,LYS 198,TYR 199,THR 200,VAL 201	79%	70%
Peroxiredoxin-2E	121	PRO 114,ALA 116,PHE 117,THR 118,PRO 119,THR 120,CYS 121,SER 122,GLN 123,LYS 124,HIS 125,VAL 126,CYS 146,ASN 150,TRP 158,LEU 195,ARG 198,ARG 201,GLY 220	75%	99%
Oxidative stress transcriptional regulator (OxyR)	113	MET 107,LEU 108,GLU 109,ASP 110,GLY 111,HIS 112,CYS 113,LEU 114,ARG 115,ASP 116,GLN 117,PHE 121,PHE 123,GLU 129,ARG 134	47%	91%
Vesicle-fusing ATPase N-terminal	21	GLU 15, LEU 16,LEU 18,THR 19,CYS 21,SER 31,GLY 32,GLN 33,THR 48,LEU 49,LYS 50,THR 51,GLN	77%	55%

		124,ASN 126,ASN 127,GLN 128		
Vesicle-fusing ATPase N-terminal	91	PHE 85,ASP 86,LYS 87,ALA 88,LYS 89,GLN 90,CYS 91,GLY 93,ASN 127,MET 155,ASP 156,VAL 178,ASN 180,SER 181	75%	88%
Ras p21 Protein	118	ASN 116,LYS 117,CYS 118,ASP 119,LEU 120,ARG 123,ILE 142,GLU 143,ALA 146,THR 148,ARG 149,GLN 150,GLY 151	71%	67%
Creatine kinase	283	THR 59,THR 71,VAL 72,GLY 73,ALA 74,VAL 75,TYR 82,ARG 96,LEU 202,GLU 232,THR 282,CYS 283,SER 285,ASN 286	77%	98%
GAPDH	150	ILE 12,SER 149,CYS 150,THR 151,THR 175,HIS 177,THR 180,THR 209,ALA 211,ARG 232,SER 239,ASN 314,GLU 315,TYR 318	72%	98%
GAPDH	245	HIS 163,PHE 166,GLY 167,VAL 169,GLU 170,GLY 171,LEU 172,LEU 226,THR 244,ARG 246,ASN 304,PHE 305,VAL 306,LYS 307	89%	57%
Vinculin	85	VAL 44,ALA 45,GLN 48,ALA 49,VAL 51,SER 52,VAL 81,GLU 82,ASN 83,ALA 84,CYS 85,THR 86,LYS 87,VAL 89,GLN 90	91%	69%
T-complex protein 1 subunit zeta	406	GLU 135,GLU 136,VAL 137,LYS 138,VAL 139,SER 140,ARG 141,ASN 400,ASP 404,GLY 405,CYS 406,VAL 407,ASP 496,ASN 497,TYR 498,CYS 499,LYS 502	58%	75%
Ras-related protein Rab-3B	184	TYR 21,PHE 23,ARG 66,HIS 67,LYS 69,VAL 71,MET 96,GLU 177,ARG 178,LEU 179,ASP 181,ALA 182,ILE 183,CYS 184,ASP 185,LYS 186,MET 187,SER 188	47%	27%
peptidylprolyl isomerase B	202	TYR 47,ASP 49,VAL 77,ALA 78,THR 81,GLY 82,GLY 87,LYS 89,ASN 90,SER 91,ALA 200,ASP 201,CYS 202,GLY 203,LYS 204	62%	60%
Myosin heavy chain 9	91	LEU 31,ILE 72,GLN 73,LYS 74,MET 75,ASN 76,PRO 77,PHE 80,LEU 89,CYS 91,LEU 92,ASN 93,SER 96,ALA 765,GLY 766,VAL 767,LEU 768,ALA 769,HIS 770,GLU 773	75%	41%
Stress-70 protein	487	GLU 448,THR 449,GLY 452,VAL 453,PHE 454,THR 455,LYS 485,CYS 487,GLN 488,GLY 489,GLY 495,ASP 496,ASN 497,LYS 498,LEU 499,LEU 500,GLY 501,ILE 589	80%	21%
COPA protein	245	VAL 221,ARG 227,GLN 228,VAL 229,LYS 230,ILE 231,ASP 243,THR 244,CYS 245,ARG 246,GLY 247,SER 266, ARG 274,VAL 275,TRP 276,ASP 277,MET 278,ARG 281, VAL 284	57%	34%
Annexin-2	133	GLU 125,ASP 126,SER 127,ILE 132,CYS 133,SER 134,ARG 135,PHE 167,LEU 174,ASP 251,ASN 254,LEU 257,ASN 258,LEU 259,CYS 262,TYR 269	63%	34%
Annexin-11	294	PHE 276,ASP 277,ILE 278,TYR 279,GLU 280,LYS 282,GLU 283,ALA 284,ILE 285,THR 290,ASP 291,GLU 292,ALA 293,CYS 294,ILE 296,LEU 299,ARG 439,ARG 452,THR 453,ARG 456	53%	25%
Elongation factor alpha 1	234	GLN 147,LEU 148,ILE 149,THR 187,ALA 189,TRP 214,LYS 215,VAL 216,ARG 218,ALA 223,SER 224,GLY 225,THR 227,LEU 229,GLU 230,ASP 233,CYS 234,ILE 235,LEU 236	92%	17%
Protein Tyrosine Phosphatase	215	TYR 46,ASN 111,ASP 181,CYS 215,SER 216,ALA 217,ILE 219,GLY 220,ARG 221,GLN 262	61%	84%
Syntaxin 1A	145	GLN 138, ASP 140, TYR 141, ARG 142, GLU 143, ARG 144, LYS 146, GLY 147, ARG 148, THR 197, ARG 198, HIS 199, SER 200, GLU 201, ILE 202, ILE 203, LEU 205	60%	27%
Myeloid differentiation primary response protein MyD88	216	ARG 160,PHE 161,ASP 162,PHE 164,LYS 190,LEU 191,TRP 205,ILE 207,ALA 208,LEU 211,ILE 212,GLU 213,LYS 214,ARG 215,CYS 216,ARG 217,ARG 218,PHE 239,ARG 251	55%	30%
Hemoglobin subunit beta	293	ALA 286,LEU 288,GLU 290,LEU 291,HIS 292,CYS 293,ASP 294,LYS 295,LEU 296,HIS 297,VAL 298,ASP 299,PRO 300,ALA 340,LEU 341,ALA 342,HIS 343,LYS 344,TYR 345	76%	100%
Tubulin beta	12	GLY 10,GLN 11,CYS 12,GLN 15,ILE 16,SER 140,GLY 142,VAL 171,ASN 206,TYR 224,ASN 228,VAL 231	99%	99%

Tubulin beta	241	ALA 208,MET 301,ALA 303,ALA 304,CYS 305,ASP 306,PRO 307,GLN 385,GLU 386,ARG 390	99%	88%
Tubulin beta	305	ALA 208,MET 301,ALA 303,ALA 304,CYS 305,ASP 306,PRO 307,GLN 385,GLU 386,ARG 390	97%	65%
Tubulin beta	356	LEU 42,CYS 241,PHE 244,PRO 245,GLY 246,GLN 247,VAL 318,ARG 320,GLY 321,ALA 354,VAL 355,CYS 356,ASP 357,ILE 358,PRO 359	99%	100%
Histone deacetylase 2	262	TRP 136,ILE 174,ASP 177,PHE 242,HIS 282, ALA 283,CYS 285,VAL 286,VAL 289,LEU 296,MET 298,GLY 301,TRP 313,GLU 316	82%	83%
Histone deacetylase 2	274	ILE 178,HIS 179,LYS 201,TYR 205,PHE 206,ARG 230,ASP 231,GLY 232,ASP 265,SER 266,ASP 270,ARG 271,LEU 272,GLY 273,CYS 274,PHE 275,MET 351	91%	94%
Parkinson disease protein 7 (DJ1)	46	ALA 11,LYS 12,GLY 13,GLU 15,GLU 16,MET 17,THR 19,VAL 20,PRO 43,VAL 44,GLN 45,CYS 46,SER 47,ARG 48,ASP 49,VAL 50,VAL 51,ILE 52,CYS 53	44%	28%
Parkinson disease protein 7 (DJ1)	53	LYS 41,ASP 42,PRO 43,VAL 44,VAL 51,ILE 52,CYS 53,PRO 54,ASP 55	20%	50%
Dynamin-2	607	LEU 526,THR 527,HIS 584,CYS 607,ASP 608,SER 609,GLN 610,GLU 611,ASP 612,VAL 613,ASP 614,SER 615,TRP 616,LYS 617	100%	100%
SG15 ubiquitin-like modifier	76	PHE 41,GLN 42,ARG 44,VAL 73,GLN 74,ASN 75,CYS 76,SER 77,GLU 78,LEU 98	55%	1%
G-protein coupled receptor kinase 2 (GRK2)	340	ASN 238,MET 242,PHE 312,ARG 316,LEU 338,CYS 340,ASP 341,PHE 342,SER 343,LYS 345,LYS 346,PRO 347,HIS 348,VAL 351,TYR 368	78%	53%
Dynamin-related protein 1	644	LEU 460,HIS 461,ASP 462,ALA 463,ILE 464,GLN 641,ARG 642,ASP 643,CYS 644,GLU 645,VAL 646,ILE 647,GLU 648	100%	100%