

**Table S6. Predicted yeast thiol oxidoreductases**

	sequence id	template (%id homology modeling template)	Best Cys	Active Site Similarity Score	Cys Reactivity score	Combined score	Predicted by the Sec/Cys method	Protein (associated gene name)
1)	>gi 6320881	1fva (36%)	24	3.5	2	5.5	YES	MsrA (Mxr1)
2)	>gi 6321648	2fa4 (100%)	33	3.5	2	5.5	YES	Thioredoxin (Trx2)
3)	>gi 6323505	1rp4 (100%)	352	3.25	2	5.25	YES	Ero1-p (Ero1)
4)	>gi 6323072	2i9h (100%)	32	3.5	1.5	5	YES	Thioredoxin (Trx1)
5)	>gi 6320720	2jac (67%)	60	3	1.75	4.75	YES	Glutaredoxin (Grx2)
6)	>gi 6324862	2dml (42%)	61	3.5	1.25	4.75	YES	PDI related protein A (Mpd1)
7)	>gi 6322826	2p5q (43%)	36	2.5	2	4.5	YES	Glutathione peroxidase (Gpx1)
8)	>gi 6319925	2fa4 (43%)	57	3.5	1	4.5	YES	Thioredoxin (Trx3)
9)	>gi 6319806	2b5e (100%)	406	3.5	0.75	4.25	YES	PDI_A family (Pdi1)
10)	>gi 6320492	1wjk (43%)	33	3.25	1	4.25	YES	Unknown/glutaredoxin like protein (YDR286C)
11)	>gi 6319816	3cez (39%)	157	2	2	4	YES	SeiR/MsrB (YCL033C)
12)	>gi 6324484	2djj (38%)	56	3	1.25	4.25	YES	Protein Disulfide Isomerase (Mpd2)
13)	>gi 6322186	2b5e (35%)	60	3	1	4	YES	Thioredoxin-like (Eps1)
14)	>gi 6323396	2ht9 (30%)	24	2	2	4	YES	Glutaredoxin (Grx8)
15)	>gi 6319814	2jac (98%)	26	3	1	4	YES	Glutaredoxin (Grx1)
16)	>gi 6323613	1qmv (66%)	47	2.75	1	3.75	YES	2cys peroxiredoxin (Tsa1)
17)	>gi 6320661	1qmv (60%)	48	3.5	0.25	3.75	YES	Peroxiredoxin (Tsa2)
18)	>gi 6320726	2b5e (42%)	61	3.5	0.25	3.75	YES	PDI-A family (Eug1)
19)	>gi 6320560	1vdc (62%)	142	2	1.5	3.5	YES	Thioredoxin reductase (Trr1)
20)	>gi 6325330	1dlq (99%)	13	2	1.5	3.5	<b>NO</b>	phosphotyrosine phosphatase (Ltp1)
21)	>gi 6320303	1wik (60%)	72	2.5	1	3.5	YES	Glutaredoxin (Grx3)
22)	>gi 6321022	2j23 (36%)	36	2.5	1	3.5	YES	Monothiol Glutaredoxin (Grx4)
23)	>gi 6681846	1oqc (47%)	129	1.5	2	3.5	YES	Erv-1 (Erv1)
24)	>gi 6320193	2e7p (38%)	135	3.5	0	3.5	YES	Glutaredoxin (Grx6)
25)	>gi 6325296	1jr8 (100%)	120	1.5	2	3.5	YES	Erv-2 (Erv2)
26)	>gi 6322409	2i5p (76%)	149	1.5	2	3.5	<b>NO</b>	Glyceraldehyde-3-phosphate dehydrogenase 1 (Tdh1)
27)	>gi 14318558	1ezv (100%)	122	1.25	2	3.25	<b>NO</b>	ubiquinol-cytochrome c oxidoreductase subunit 6 (Qcr6)
28)	>gi 6321898	1tde (51%)	165	1.25	2	3.25	YES	mitochondrial thioredoxin reductase (Trr2)
29)	>gi 6321631	2i5p (78%)	149	1.25	2	3.25	<b>NO</b>	Glyceraldehyde-3-phosphate dehydrogenase 3 (Tdh3)
30)	>gi 6325166	2hqm (100%)	61	1	2	3	YES	Glutathione reductase (Glr1)
31)	>gi 14318501	1v59 (100%)	65	1	2	3	YES	Dihydrolipoamide dehydrogenase (Lpd1)
32)	>gi 6322228	2p5q (50%)	36	3	0	3	YES	Glutathione peroxidase (Hyr1)
33)	>gi 6320661	1qmv (62%)	47	3	0	3	YES	Peroxiredoxin (TSA2)
34)	>gi 6322180	2a4v (98%)	106	3	0	3	YES	alkyl hydroperoxide reductase /AhpC (Dot5)
35)	>gi 6322155	1izn (50%)	62	1	2	3	<b>NO</b>	capping-addition of actin subunits (Cap2)

<b>36)</b>	>gi 6324268	1ixk (36%)	477	1	2	3	<b>NO</b>	nucleolar function in rapid growth (Nop2)
<b>37)</b>	>gi 6322921	1wc9 (58%)	79	1	2	3	<b>NO</b>	targeting and/or fusion of ER-to-Golgi transport vesicles (Bet3)
<b>38)</b>	>gi 6319721	2p5w (51%)	37	3	0	3	YES	Glutathione peroxidase paralogue (Gpx2p)
<b>39)</b>	>gi 6319407	1prx (49%)	90	2.5	0.25	2.75	YES	Mitochondrial peroxiredoxin (Prx1)
<b>40)</b>	>gi 6323138	1tp9 (40%)	61	2.5	0.25	2.75	YES	AhpD (Ahp1)
<b>41)</b>	>gi 6321388	2it2 (28%)	53	1.75	1	2.75	<b>NO</b>	uncharacterized protein (Tyw3)
<b>42)</b>	>gi 93117370	1sfe (48%)	168	0.75	2	2.75	YES	6-O-methylguanine-DNA methylase (Mgt1)