Phyre2

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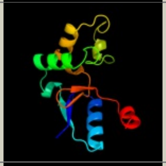
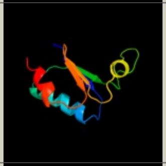
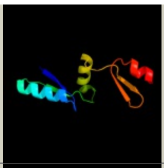
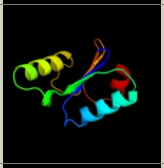
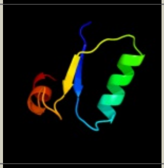
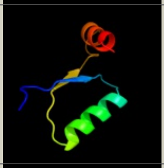
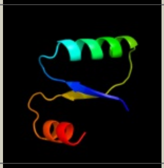
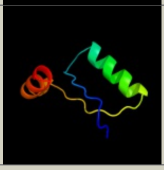
Description	P76569
Date	Thu Jan 5 12:24:41 GMT 2012
Unique Job ID	cfa11ccfc7c3a7c0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3f0iA_	Alignment		100.0	59	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** arsenate reductase from vibrio cholerae.
2	c3rdwB_	Alignment		100.0	68	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative arsenate reductase; **PDBTitle:** putative arsenate reductase from yersinia pestis
3	d1j9ba_	Alignment		100.0	39	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
4	d1rw1a_	Alignment		100.0	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
5	d1z3ea1	Alignment		100.0	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
6	c3l78A_	Alignment		100.0	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein spx; **PDBTitle:** the crystal structure of smu.1142c from streptococcus mutans ua159
7	c2kokA_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** solution structure of an arsenate reductase (arsc) related protein2 from brucella melitensis. seattle structural genomics center for3 infectious disease target braba.00007.a.
8	c3gkxB_	Alignment		100.0	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative arsc family related protein; **PDBTitle:** crystal structure of putative arsc family related protein from2 bacteroides fragilis
9	c3fz4A_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative arsenate reductase; **PDBTitle:** the crystal structure of a possible arsenate reductase from2 streptococcus mutans ua159
10	d1h75a_	Alignment		99.0	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
11	c3nznA_	Alignment		98.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** the crystal structure of the glutaredoxin from methanosarcina mazei2 go1

12	d1r7ha_	Alignment		98.8	31	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
13	c3ic4A_	Alignment		98.8	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin (grx-1); **PDBTitle:** the crystal structure of the glutaredoxin(grx-1) from archaeoglobus2 fulgidus
14	c3lgcA_	Alignment		98.4	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**glutaredoxin 1; **PDBTitle:** crystal structure of glutaredoxin 1 from francisella2 tularensis
15	d1nm3a1	Alignment		98.2	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
16	c1nm3B_	Alignment		98.1	22	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**protein hi0572; **PDBTitle:** crystal structure of heamophilus influenza hybrid-prx5
17	c2khpA_	Alignment		98.1	27	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from brucella melitensis
18	d1fova_	Alignment		98.0	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
19	c2klxA_	Alignment		97.9	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from bartonella henselae str.2 houston
20	d1t1va_	Alignment		97.8	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**SH3BGR (SH3-binding, glutamic acid-rich protein-like)
21	c2ht9A_	Alignment	not modelled	97.7	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-2; **PDBTitle:** the structure of dimeric human glutaredoxin 2
22	c3fzaA_	Alignment	not modelled	97.7	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** crystal structure of poplar glutaredoxin s12 in complex with2 glutathione and beta-mercaptoethanol
23	d1abaa_	Alignment	not modelled	97.6	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
24	c2e7pC_	Alignment	not modelled	97.6	18	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**glutaredoxin; **PDBTitle:** crystal structure of the holo form of glutaredoxin c1 from populus2 tremula x tremuloides
25	c3h8qB_	Alignment	not modelled	97.5	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin reductase 3; **PDBTitle:** crystal structure of glutaredoxin domain of human thioredoxin2 reductase 3
26	d1egoa_	Alignment	not modelled	97.3	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
27	d1wika_	Alignment	not modelled	97.1	28	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
28	d1z9ha2	Alignment	not modelled	97.1	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
						Fold: Thioredoxin fold

29	d1ktea_	Alignment	not modelled	97.0	21	**Superfamily:**Thioredoxin-like **Family:**Thioltransferase
30	d1eema2	Alignment	not modelled	96.9	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
31	c1oktA_	Alignment	not modelled	96.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** x-ray structure of glutathione s-transferase from the2 malarial parasite plasmodium falciparum
32	d1jhba_	Alignment	not modelled	96.9	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
33	c2vo4A_	Alignment	not modelled	96.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2,4-d inducible glutathione s-transferase; **PDBTitle:** glutathione transferase from glycine max
34	c1ykaA_	Alignment	not modelled	96.8	23	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**monothiol glutaredoxin ydhd; **PDBTitle:** solution structure of grx4, a monothiol glutaredoxin from2 e. coli.
35	c2hzfA_	Alignment	not modelled	96.6	16	**PDB header:**electron transport, oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** crystal structures of a poxviral glutaredoxin in the oxidized and2 reduced states show redox-correlated structural changes
36	c1oyjC_	Alignment	not modelled	96.6	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** crystal structure solution of rice gst1 (osgstu1) in complex with2 glutathione.
37	c2ct6A_	Alignment	not modelled	96.6	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sh3 domain-binding glutamic acid-rich-like **PDBTitle:** solution structure of the sh3 domain-binding glutamic acid-2 rich-like protein 2
38	d1oyja2	Alignment	not modelled	96.5	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
39	c1eemA_	Alignment	not modelled	96.5	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione-s-transferase; **PDBTitle:** glutathione transferase from homo sapiens
40	d1gwca2	Alignment	not modelled	96.4	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
41	c1z9hB_	Alignment	not modelled	96.3	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**membrane-associated prostaglandin e synthase-2; **PDBTitle:** microsomal prostaglandin e synthase type-2
42	c1k0dB_	Alignment	not modelled	96.2	9	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**ure2 protein; **PDBTitle:** ure2p in complex with glutathione
43	d1k0da2	Alignment	not modelled	96.2	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
44	c1ljrB_	Alignment	not modelled	96.2	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** glutathione transferase (hgst t2-2) from human
45	d1v58a1	Alignment	not modelled	96.2	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
46	c2jl4A_	Alignment	not modelled	96.2	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**maleylpyruvate isomerase; **PDBTitle:** holo structure of maleyl pyruvate isomerase, a bacterial2 glutathione-s-transferase in zeta class
47	d1okta2	Alignment	not modelled	96.2	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
48	d1ljra2	Alignment	not modelled	96.2	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
49	c1yy7A_	Alignment	not modelled	96.2	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stringent starvation protein a; **PDBTitle:** crystal structure of stringent starvation protein a (sspa),2 an rna polymerase-associated transcription factor
50	c3lg6B_	Alignment	not modelled	96.2	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative glutathione transferase; **PDBTitle:** crystal structure of putative glutathione transferase from2 coccidioides immitis
51	c3rbtD_	Alignment	not modelled	96.1	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutathione transferase o1; **PDBTitle:** crystal structure of glutathione s-transferase omega 3 from the2 silkworm bombyx mori
52	d1gnwa2	Alignment	not modelled	96.1	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
53	c1g7oA_	Alignment	not modelled	96.1	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin 2; **PDBTitle:** nmr solution structure of reduced e. coli glutaredoxin 2
54	d1k0dd2	Alignment	not modelled	96.0	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
55	c3cbuB_	Alignment	not modelled	96.0	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable gst-related protein; **PDBTitle:** crystal structure of a putative glutathione s-transferase

						(reut_a1011)2 from ralstonia eutropha jmp134 at 2.05 a resolution
56	c1gwcC_	Alignment	not modelled	96.0	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glutathione s-transferase tsi-1; **PDBTitle:** the structure of a tau class glutathione s-transferase from2 wheat, active in herbicide detoxification
57	c1v57A_	Alignment	not modelled	96.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbg; **PDBTitle:** crystal structure of the disulfide bond isomerase dsbg
58	c3l4nA_	Alignment	not modelled	95.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-6; **PDBTitle:** crystal structure of yeast monothiol glutaredoxin grx6
59	c3bbyA_	Alignment	not modelled	95.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized gst-like protein yfcf; **PDBTitle:** crystal structure of glutathione s-transferase (np_416804.1) from2 escherichia coli k12 at 1.85 a resolution
60	d1g7oa2	Alignment	not modelled	95.9	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
61	d1jlva2	Alignment	not modelled	95.8	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
62	d1ttza_	Alignment	not modelled	95.8	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
63	d1v2aa2	Alignment	not modelled	95.8	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
64	c3ipzA_	Alignment	not modelled	95.7	26	**PDB header:**electron transport, oxidoreductase **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-s14, chloroplastic; **PDBTitle:** crystal structure of arabidopsis monothiol glutaredoxin atgrxcp
65	d1e6ba2	Alignment	not modelled	95.7	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
66	c2jacA_	Alignment	not modelled	95.7	22	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** glutaredoxin grx1p c30s mutant from yeast
67	c3lykA_	Alignment	not modelled	95.6	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**stringent starvation protein a homolog; **PDBTitle:** structure of stringent starvation protein a homolog from2 haemophilus influenzae
68	c2c3nB_	Alignment	not modelled	95.6	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase theta 1; **PDBTitle:** human glutathione-s-transferase t1-1, apo form
69	c2wulB_	Alignment	not modelled	95.6	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin related protein 5; **PDBTitle:** crystal structure of the human glutaredoxin 5 with bound2 glutathione in an fes cluster
70	c1e6bA_	Alignment	not modelled	95.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** crystal structure of a zeta class glutathione s-transferase2 from arabidopsis thaliana
71	c3m3mA_	Alignment	not modelled	95.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** crystal structure of glutathione s-transferase from pseudomonas2 fluorescens [pf-5]
72	c3nivD_	Alignment	not modelled	95.5	14	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** the crystal structure of glutathione s-transferase from legionella2 pneumophila
73	c3lypA_	Alignment	not modelled	95.5	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stringent starvation protein a; **PDBTitle:** structure of stringent starvation protein a homolog from pseudomonas2 fluorescens
74	d1pn9a2	Alignment	not modelled	95.5	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
75	c3lxzD_	Alignment	not modelled	95.5	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutathione s-transferase family protein; **PDBTitle:** structure of probable glutathione s-transferase(pp0183) from2 pseudomonas putida
76	d1jlwa2	Alignment	not modelled	95.5	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
77	c3fy7B_	Alignment	not modelled	95.4	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**chloride intracellular channel protein 3; **PDBTitle:** crystal structure of homo sapiens clic3
78	d1aw9a2	Alignment	not modelled	95.4	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
79	c3d5jB_	Alignment	not modelled	95.4	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin-2, mitochondrial; **PDBTitle:** structure of yeast grx2-c30s mutant with glutathionyl mixed2 disulfide
80	c1v2aD_	Alignment	not modelled	95.3	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutathione transferase gst1-6; **PDBTitle:** glutathione s-transferase 1-6 from anopheles dirus species b
81	c3m8nA_	Alignment	not modelled	95.3	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible glutathione s-transferase; **PDBTitle:** crystal structure of a possible gutathione s-tranferase from2 rhodopseudomonas palustris
						Fold: Thioredoxin fold

82	d1axda2	Alignment	not modelled	95.3	23	**Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
83	c3c1sA_	Alignment	not modelled	95.3	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** crystal structure of grx1 in glutathionylated form
84	c3ay8A_	Alignment	not modelled	95.2	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** glutathione s-transferase unclassified 2 from bombyx mori
85	c3touB_	Alignment	not modelled	95.2	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase protein; **PDBTitle:** crystal structure of glutathione transferase (target efi-501058) from2 ralstonia solanacearum gmi1000 with gsh bound
86	c2imiA_	Alignment	not modelled	95.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**epsilon-class glutathione s-transferase; **PDBTitle:** structures of an insect epsilon-class glutathione s-2 transferase from the malaria vector anopheles gambiae:3 evidence for high ddt-detoxifying activity
87	c1jlvA_	Alignment	not modelled	95.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione transferase gst1-3; **PDBTitle:** anopheles dirus species b glutathione s-transferases 1-3
88	c2r4vA_	Alignment	not modelled	95.0	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**chloride intracellular channel protein 2; **PDBTitle:** structure of human clic2, crystal form a
89	d1r5aa2	Alignment	not modelled	95.0	28	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
90	c3gv1A_	Alignment	not modelled	95.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**disulfide interchange protein; **PDBTitle:** crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
91	c1gnwA_	Alignment	not modelled	94.9	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** structure of glutathione s-transferase
92	c1u6tA_	Alignment	not modelled	94.9	19	**PDB header:**protein binding, signaling protein **Chain:** A: **PDB Molecule:**sh3 domain-binding glutamic acid-rich-like **PDBTitle:** crystal structure of the human sh3 binding glutamic-rich2 protein like
93	c1k0nB_	Alignment	not modelled	94.9	24	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**chloride intracellular channel protein 1; **PDBTitle:** chloride intracellular channel 1 (clic1) complexed with glutathione
94	c3f6fA_	Alignment	not modelled	94.8	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cg18548-pa (ip02196p) (ip02193p); **PDBTitle:** crystal structure of glutathione transferase dmgstd10 from2 drosophila melanogaster
95	c1jlwA_	Alignment	not modelled	94.8	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione transferase gst1-4; **PDBTitle:** anopheles dirus species b glutathione s-transferases 1-4
96	d1fw1a2	Alignment	not modelled	94.7	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
97	c1r5aA_	Alignment	not modelled	94.7	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione transferase; **PDBTitle:** glutathione s-transferase
98	d1wjka_	Alignment	not modelled	94.7	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
99	c3ic8D_	Alignment	not modelled	94.7	13	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized gst-like proteinprotein; **PDBTitle:** the crystal structure of a gst-like protein from pseudomonas syringae2 to 2.4a
100	c1byeA_	Alignment	not modelled	94.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (glutathione s-transferase); **PDBTitle:** glutathione s-transferase i from mais in complex with2 atrazine glutathione conjugate
101	c2cz2A_	Alignment	not modelled	94.4	25	**PDB header:**isomerase, transferase **Chain:** A: **PDB Molecule:**maleylacetoacetate isomerase; **PDBTitle:** crystal structure of glutathione transferase zeta 1-12 (maleylacetoacetate isomerase) from mus musculus (form-1 crystal)
102	c3gx0A_	Alignment	not modelled	94.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gst-like protein yfcg; **PDBTitle:** crystal structure of gsh-dependent disulfide bond2 oxidoreductase
103	c1aw9A_	Alignment	not modelled	94.4	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase iii; **PDBTitle:** structure of glutathione s-transferase iii in apo form
104	c1jzdA_	Alignment	not modelled	94.2	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** dsbc-dsbdalpha complex
105	c3gx8A_	Alignment	not modelled	94.1	23	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-5, mitochondrial; **PDBTitle:** structural and biochemical characterization of yeast2 monothiol glutaredoxin grx5
106	d1k0ma2	Alignment	not modelled	93.8	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
107	c2aheA_	Alignment	not modelled	93.5	18	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**chloride intracellular channel protein 4; **PDBTitle:** crystal structure of a soluble form of clic4. intercellular2 chloride ion channel
108	c2x64A_	Alignment	not modelled	93.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione-s-transferase;

						PDBTitle: glutathione-s-transferase from xylella fastidiosa
109	d1iloa_	Alignment	not modelled	93.4	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
110	c3m0fA_	Alignment	not modelled	93.3	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein gst_n; **PDBTitle:** crystal structure of glutathione s transferase in complex2 with glutathione from pseudomonas fluorescens
111	c3ergA_	Alignment	not modelled	93.3	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase 2; **PDBTitle:** crystal structure of gtt2 from saccharomyces cerevisiae in complex2 with glutathione sulfnate
112	c2fgxA_	Alignment	not modelled	93.3	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** solution nmr structure of protein ne2328 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net3.
113	c1zl9A_	Alignment	not modelled	93.3	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase 5; **PDBTitle:** crystal structure of a major nematode c.elegans specific gst (ce01613)
114	c1yq1A_	Alignment	not modelled	93.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** structural genomics of caenorhabditis elegans: glutathione2 s-transferase
115	d1n2aa2	Alignment	not modelled	93.1	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
116	d1pd212	Alignment	not modelled	93.1	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
117	d1t3ba1	Alignment	not modelled	93.1	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
118	c1t3bA_	Alignment	not modelled	93.1	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** x-ray structure of dsbc from haemophilus influenzae
119	c2ws2B_	Alignment	not modelled	92.8	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** the 2 angstrom structure of a nu-class gst from haemonchus contortus
120	d1tu7a2	Alignment	not modelled	92.5	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain