Phyre2

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Description	P76402
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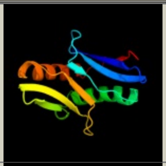
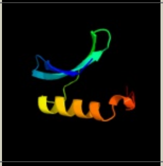
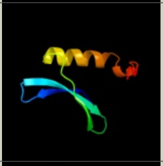
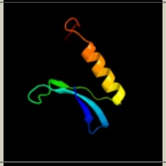
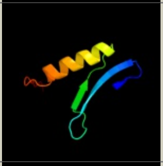
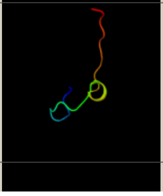
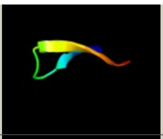
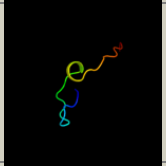
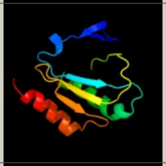
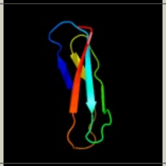
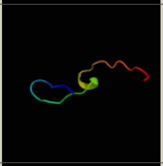
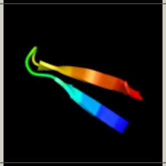
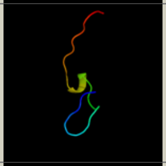
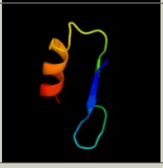
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k49A_	Alignment		100.0	65	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0339 protein so_3888; **PDBTitle:** solution nmr structure of upf0339 protein so3888 from shewanella2 oneidensis. northeast structural genomics consortium target sor190
2	c2k8eA_	Alignment		100.0	100	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0339 protein yegp; **PDBTitle:** solution nmr structure of protein of unknown function yegp from e.2 coli. ontario center for structural proteomics target ec0640_1_1233 northeast structural genomics consortium target et102.
3	d2k49a2	Alignment		99.8	71	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
4	d2k8ea1	Alignment		99.8	100	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
5	d2k7ia1	Alignment		99.8	28	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
6	c2k7iB_	Alignment		99.8	28	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**upf0339 protein atu0232; **PDBTitle:** solution nmr structure of protein atu0232 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att3. ontario center for structural proteomics target atc0223.
7	d3bida1	Alignment		99.7	28	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
8	d2k8ea2	Alignment		99.7	100	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
9	d2k49a1	Alignment		99.7	60	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
10	d1st9a_	Alignment		55.7	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
11	d1jkea_	Alignment		54.0	8	**Fold:**DTD-like **Superfamily:**DTD-like **Family:**DTD-like

12	c2qz7B_	Alignment		52.2	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein sco6318; **PDBTitle:** the crystal structure of a homologue of telluride resistance protein2 (terd), sco6318 from streptomyces coelicolor a3(2)
13	d1j7ga_	Alignment		51.5	12	**Fold:**DTD-like **Superfamily:**DTD-like **Family:**DTD-like
14	c2l5oA_	Alignment		42.6	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** solution structure of a putative thioredoxin from neisseria2 meningitidis
15	c3jqxA_	Alignment		39.5	20	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**colh protein; **PDBTitle:** crystal structure of clostridium histolyticum colh collagenase2 collagen binding domain 3 at 2.2 angstrom resolution in the presence3 of calcium and cademium
16	c3ko7E_	Alignment		38.8	20	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**d-tyrosyl-trna(tyr) deacylase; **PDBTitle:** dtd from plasmodium falciparum in complex with d-lysine
17	c2qngA_	Alignment		38.6	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sav2460; **PDBTitle:** crytal structure of unknown function protein sav2460
18	c2dboA_	Alignment		34.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d-tyrosyl-trna(tyr) deacylase; **PDBTitle:** crystal structure of d-tyr-trna(tyr) deacylase from aquifex aeolicus
19	d2fy6a1	Alignment		33.1	6	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
20	d2b5xa1	Alignment		26.9	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
21	d1h8la1	Alignment	not modelled	26.6	16	**Fold:**Prealbumin-like **Superfamily:**Carboxypeptidase regulatory domain-like **Family:**Carboxypeptidase regulatory domain
22	c2b1kA_	Alignment	not modelled	24.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbe; **PDBTitle:** crystal structure of e. coli ccmg protein
23	c3or5A_	Alignment	not modelled	24.1	6	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein, thioredoxin family **PDBTitle:** crystal structure of thiol:disulfide interchange protein, thioredoxin2 family protein from chlorobium tepidum tls
24	c3m86B_	Alignment	not modelled	23.2	14	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**amoebiasin-2; **PDBTitle:** crystal structure of the cysteine protease inhibitor, ehicp2, from2 entamoeba histolytica
25	c2f4nA_	Alignment	not modelled	23.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein mj1651; **PDBTitle:** crystal structure of protein mj1651 from methanococcus2 jannaschii dsm 2661, pfam duf62
26	c3cmiA_	Alignment	not modelled	22.8	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxiredoxin hyr1; **PDBTitle:** crystal structure of glutathione-dependent phospholipid peroxidase2 hyr1 from the yeast saccharomyces cerevisiae
27	c3m2oB_	Alignment	not modelled	22.3	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein; **PDBTitle:** crystal structure of a putative glyoxalase/bleomycin resistance2 protein from rhodopseudomonas palustris cga009
28	c2wgnB_	Alignment	not modelled	22.1	21	**PDB header:**hydrolase inhibitor **Chain:** B: **PDB Molecule:**inhibitor of cysteine peptidase compnd 3; **PDBTitle:** pseudomonas aeruginosa icp
						Fold: MalF N-terminal region-like

29	d2r6gf1	Alignment	not modelled	21.8	8	**Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
30	c2he3A_	Alignment	not modelled	21.2	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 2; **PDBTitle:** crystal structure of the selenocysteine to cysteine mutant of human2 glutathionine peroxidase 2 (gpx2)
31	c3gg4B_	Alignment	not modelled	20.9	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
32	d1knga_	Alignment	not modelled	19.9	6	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
33	c2kucA_	Alignment	not modelled	19.6	3	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative disulphide-isomerase; **PDBTitle:** solution structure of a putative disulphide-isomerase from bacteroides2 thetaiotaomicron
34	c3cxbA_	Alignment	not modelled	19.1	7	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein sifa; **PDBTitle:** crystal structure of sifa and skip
35	d1dfca3	Alignment	not modelled	18.8	16	**Fold:**beta-Trefoil **Superfamily:**Actin-crosslinking proteins **Family:**Fascin
36	d2hg7a1	Alignment	not modelled	18.8	22	**Fold:**gpW/XkdW-like **Superfamily:**XkdW-like **Family:**XkdW-like
37	c2hg7A_	Alignment	not modelled	18.8	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage-like element pbsx protein xkdw; **PDBTitle:** solution nmr structure of phage-like element pbsx protein2 xkdw, northeast structural genomics consortium target sr355
38	c3g73A_	Alignment	not modelled	18.7	26	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**forkhead box protein m1; **PDBTitle:** structure of the foxm1 dna binding
39	c2okvC_	Alignment	not modelled	18.5	8	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**probable d-tyrosyl-trna(tyr) deacylase 1; **PDBTitle:** c-myc dna unwinding element binding protein
40	c1dfcB_	Alignment	not modelled	18.2	11	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**fascin; **PDBTitle:** crystal structure of human fascin, an actin-crosslinking protein
41	d1k25a3	Alignment	not modelled	17.9	18	**Fold:**Penicillin binding protein dimerisation domain **Superfamily:**Penicillin binding protein dimerisation domain **Family:**Penicillin binding protein dimerisation domain
42	d2ch5a2	Alignment	not modelled	17.8	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
43	c3razA_	Alignment	not modelled	17.1	6	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-related protein; **PDBTitle:** the crystal structure of thioredoxin-related protein from neisseria2 meningitidis serogroup b
44	c3ibzA_	Alignment	not modelled	17.1	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative tellurium resistant like protein terd; **PDBTitle:** crystal structure of putative tellurium resistant like protein (terd)2 from streptomyces coelicolor a3(2)
45	c3erwG_	Alignment	not modelled	15.8	14	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**sporulation thiol-disulfide oxidoreductase a; **PDBTitle:** crystal structure of stoa from bacillus subtilis
46	d1ee8a2	Alignment	not modelled	15.2	32	**Fold:**N-terminal domain of MutM-like DNA repair proteins **Superfamily:**N-terminal domain of MutM-like DNA repair proteins **Family:**N-terminal domain of MutM-like DNA repair proteins
47	c2kxvA_	Alignment	not modelled	15.2	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**tellurite resistance protein; **PDBTitle:** nmr structure and calcium-binding properties of the tellurite2 resistance protein terd from klebsiella pneumoniae
48	d1fyhb1	Alignment	not modelled	14.8	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
49	c1x60A_	Alignment	not modelled	14.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sporulation-specific n-acetylmuramoyl-l-alanine **PDBTitle:** solution structure of the peptidoglycan binding domain of2 b. subtilis cell wall lytic enzyme cwlc
50	c2l57A_	Alignment	not modelled	14.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens
51	d1dfca4	Alignment	not modelled	14.4	26	**Fold:**beta-Trefoil **Superfamily:**Actin-crosslinking proteins **Family:**Fascin
52	d1z5ye1	Alignment	not modelled	14.2	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
53	c1k82D_	Alignment	not modelled	14.2	18	**PDB header:**hydrolase/dna **Chain:** D: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
54	c3eytA_	Alignment	not modelled	14.1	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein spoa0173; **PDBTitle:** crystal structure of thioredoxin-like superfamily protein spoa0173
						Fold:N-terminal domain of MutM-like DNA repair proteins

55	d1k3xa2	Alignment	not modelled	14.0	15	**Superfamily:**N-terminal domain of MutM-like DNA repair proteins **Family:**N-terminal domain of MutM-like DNA repair proteins
56	c3f9uA_	Alignment	not modelled	13.5	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported cytochrome c biogenesis-related protein; **PDBTitle:** crystal structure of c-terminal domain of putative exported cytochrome2 c biogenesis-related protein from bacteroides fragilis
57	d2f8aa1	Alignment	not modelled	13.4	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
58	c3nf5A_	Alignment	not modelled	13.4	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**nucleoporin nup116; **PDBTitle:** crystal structure of the c-terminal domain of nuclear pore complex2 component nup116 from candida glabrata
59	c2k3iA_	Alignment	not modelled	13.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yiis; **PDBTitle:** solution nmr structure of protein yiis from shigella2 flexneri. northeast structural genomics consortium target3 sfr90
60	d1y6kr1	Alignment	not modelled	12.7	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
61	c3kh7A_	Alignment	not modelled	12.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbe; **PDBTitle:** crystal structure of the periplasmic soluble domain of reduced ccmg2 from pseudomonas aeruginosa
62	c3ixrA_	Alignment	not modelled	12.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bacterioferritin comigratory protein; **PDBTitle:** crystal structure of xylella fastidiosa prxq c47s mutant
63	c3hz6A_	Alignment	not modelled	12.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulokinase; **PDBTitle:** crystal structure of xylulokinase from chromobacterium violaceum
64	d2je8a3	Alignment	not modelled	11.6	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
65	c2p5qA_	Alignment	not modelled	11.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 5; **PDBTitle:** crystal structure of the poplar glutathione peroxidase 5 in2 the reduced form
66	c3fcdB_	Alignment	not modelled	11.0	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**lyase; **PDBTitle:** crystal structure of a putative glyoxalase from an2 environmental bacteria
67	c2rp4C_	Alignment	not modelled	11.0	28	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcription factor p53; **PDBTitle:** solution structure of the oligomerization domain in dmp53
68	c3fn2A_	Alignment	not modelled	10.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative sensor histidine kinase domain; **PDBTitle:** crystal structure of a putative sensor histidine kinase domain from2 clostridium symbiosum atcc 14940
69	d1wp0a1	Alignment	not modelled	10.9	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
70	c2yugA_	Alignment	not modelled	10.7	25	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**protein frg1; **PDBTitle:** solution structure of mouse frg1 protein
71	d1mpya1	Alignment	not modelled	10.5	4	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
72	d1pyya3	Alignment	not modelled	10.3	19	**Fold:**Penicillin binding protein dimerisation domain **Superfamily:**Penicillin binding protein dimerisation domain **Family:**Penicillin binding protein dimerisation domain
73	c2gzvA_	Alignment	not modelled	10.2	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**prkca-binding protein; **PDBTitle:** the cystal structure of the pdz domain of human pick1 (casp target)
74	d1k82a2	Alignment	not modelled	9.7	18	**Fold:**N-terminal domain of MutM-like DNA repair proteins **Superfamily:**N-terminal domain of MutM-like DNA repair proteins **Family:**N-terminal domain of MutM-like DNA repair proteins
75	c2xpoB_	Alignment	not modelled	9.6	33	**PDB header:**transcription **Chain:** B: **PDB Molecule:**chromatin structure modulator; **PDBTitle:** crystal structure of a spt6-iws1(spn1) complex from2 encephalitozoon cuniculi, form ii
76	d1wzla1	Alignment	not modelled	9.6	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
77	c2b7kD_	Alignment	not modelled	9.6	18	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**sco1 protein; **PDBTitle:** crystal structure of yeast sco1
78	c2aivA_	Alignment	not modelled	9.6	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**fragment of nucleoporin nup116/nsp116; **PDBTitle:** multiple conformations in the ligand-binding site of the2 yeast nuclear pore targeting domain of nup116p
79	c3c12A_	Alignment	not modelled	9.4	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**flagellar protein; **PDBTitle:** crystal structure of flgd from xanthomonas campestris:2 insights into the hook capping essential for flagellar3 assembly
80	c2v1mA_	Alignment	not modelled	9.4	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase; **PDBTitle:** crystal structure of schistosoma mansoni glutathione2 peroxidase

81	d1rqpa2	Alignment	not modelled	9.1	21	**Fold:**Bacterial fluorinating enzyme, N-terminal domain **Superfamily:**Bacterial fluorinating enzyme, N-terminal domain **Family:**Bacterial fluorinating enzyme, N-terminal domain
82	d1aopa2	Alignment	not modelled	8.8	15	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
83	d1t6sa1	Alignment	not modelled	8.7	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ScpB/YpuH-like
84	c2p31B_	Alignment	not modelled	8.7	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutathione peroxidase 7; **PDBTitle:** crystal structure of human glutathione peroxidase 7
85	d1rwua_	Alignment	not modelled	8.7	16	**Fold:**Ferredoxin-like **Superfamily:**YbeD/HP0495-like **Family:**YbeD-like
86	c1rwuA_	Alignment	not modelled	8.7	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0250 protein ybed; **PDBTitle:** solution structure of conserved protein ybed from e. coli
87	c2kzrA_	Alignment	not modelled	8.6	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin thioesterase otu1; **PDBTitle:** solution nmr structure of ubiquitin thioesterase otu1 (ec 3.1.2.-)2 from mus musculus, northeast structural genomics consortium target3 mmt2a
88	d2ho2a1	Alignment	not modelled	8.6	16	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
89	c3dwvB_	Alignment	not modelled	8.5	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutathione peroxidase-like protein; **PDBTitle:** glutathione peroxidase-type tryparedoxin peroxidase,2 oxidized form
90	c2bsdC_	Alignment	not modelled	8.2	18	**PDB header:**receptor **Chain:** C: **PDB Molecule:**receptor binding protein; **PDBTitle:** structure of lactococcal bacteriophage p2 receptor binding2 protein
91	d1tocr1	Alignment	not modelled	8.2	18	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Soft tick anticoagulant proteins
92	d1ys7a1	Alignment	not modelled	8.1	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
93	c3gl3D_	Alignment	not modelled	7.9	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**putative thiol:disulfide interchange protein **PDBTitle:** crystal structure of a putative thiol:disulfide interchange2 protein dsbe from chlorobium tepidum
94	c3co7C_	Alignment	not modelled	7.9	15	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**forkhead box protein o1; **PDBTitle:** crystal structure of foxo1 dbd bound to dbe2 dna
95	c2cw5B_	Alignment	not modelled	7.7	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**bacterial fluorinating enzyme homolog; **PDBTitle:** crystal structure of a conserved hypothetical protein from2 thermus thermophilus hb8
96	d1r2za2	Alignment	not modelled	7.7	14	**Fold:**N-terminal domain of MutM-like DNA repair proteins **Superfamily:**N-terminal domain of MutM-like DNA repair proteins **Family:**N-terminal domain of MutM-like DNA repair proteins
97	d1m7xa1	Alignment	not modelled	7.7	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
98	c3g12A_	Alignment	not modelled	7.6	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative lactoylglutathione lyase; **PDBTitle:** crystal structure of a putative lactoylglutathione lyase2 from bdellovibrio bacteriovorus
99	c1w3gA_	Alignment	not modelled	7.5	24	**PDB header:**toxin/lectin **Chain:** A: **PDB Molecule:**hemolytic lectin from laetiporus sulphureus; **PDBTitle:** hemolytic lectin from the mushroom laetiporus sulphureus2 complexed with two n-acetyllactosamine molecules.