Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P76148
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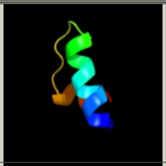
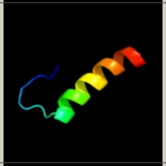
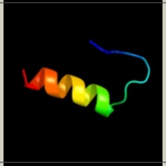
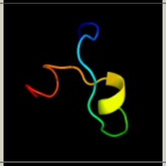
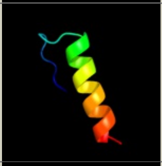
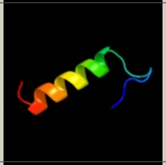
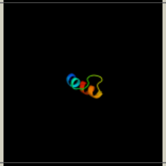
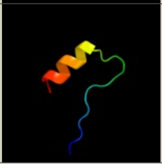
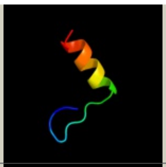
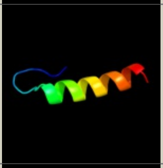
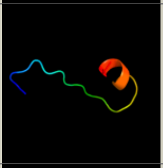
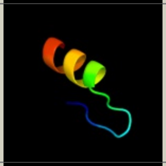
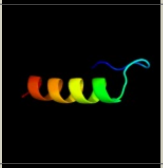
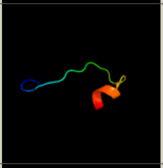
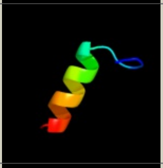
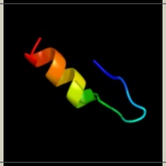
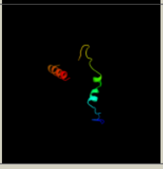
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fybA_	Alignment		80.6	50	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein of unknown function (duf1244); **PDBTitle:** crystal structure of a protein of unknown function (duf1244) from2 alcanivorax borkumensis
2	c2o35A_	Alignment		78.4	46	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein duf1244; **PDBTitle:** protein of unknown function (duf1244) from sinorhizobium meliloti
3	d2o35a1	Alignment		78.4	46	**Fold:**SMc04008-like **Superfamily:**SMc04008-like **Family:**SMc04008-like
4	c2ogeC_	Alignment		48.0	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**transaminase; **PDBTitle:** x-ray structure of s. venezuelae desv in its internal2 aldimine form
5	c3uwcA_	Alignment		46.8	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleotide-sugar aminotransferase; **PDBTitle:** structure of an aminotransferase (degt-dnrj-eryc1-strs family) from2 coxiella burnetii in complex with pmp
6	c3frkB_	Alignment		44.7	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**qdtb; **PDBTitle:** x-ray structure of qdtb from t. thermosaccharolyticum in2 complex with a plp:tdp-3-aminoquinovose aldimine
7	c3htkC_	Alignment		35.8	17	**PDB header:**recombination/replication/ligase **Chain:** C: **PDB Molecule:**e3 sumo-protein ligase mms21; **PDBTitle:** crystal structure of mms21 and smc5 complex
8	d1o69a_	Alignment		34.9	21	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
9	c3bcxA_	Alignment		34.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3- **PDBTitle:** e1 dehydrase
10	d1wpba_	Alignment		33.9	27	**Fold:**YfbU-like **Superfamily:**YfbU-like **Family:**YfbU-like
11	c3nysA_	Alignment		26.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase wbpe; **PDBTitle:** x-ray structure of the k185a mutant of wbpe (wlbe) from pseudomonas2 aeruginosa in complex with plp at 1.45 angstrom resolution

12	d1hj3a1	Alignment		26.5	29	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
13	c2po3B_	Alignment		25.9	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-dehydrase; **PDBTitle:** crystal structure analysis of desi in the presence of its2 tdp-sugar product
14	c2k6vA_	Alignment		25.8	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**putative cytochrome c oxidase assembly protein; **PDBTitle:** solution structures of apo sco1 protein from thermus2 thermophilus
15	c3ju7B_	Alignment		24.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative plp-dependent aminotransferase; **PDBTitle:** crystal structure of putative plp-dependent aminotransferase2 (np_978343.1) from bacillus cereus atcc 10987 at 2.19 a resolution
16	d2fnua1	Alignment		22.5	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
17	c2rliA_	Alignment		22.4	30	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**sco2 protein homolog, mitochondrial; **PDBTitle:** solution structure of cu(i) human sco2
18	c2kvcA_	Alignment		22.1	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
19	c2r0tA_	Alignment		20.5	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxamine 5-phosphate-dependent dehydrase; **PDBTitle:** crystal sructure of gdp-4-keto-6-deoxymannose-3-dehydratase2 with a trapped plp-glutamate geminal diamine
20	c1jiwP_	Alignment		20.5	35	**PDB header:**hydrolase/hyrolase inhibitor **Chain:** P: **PDB Molecule:**alkaline metalloproteinase; **PDBTitle:** crystal structure of the apr-aprin complex
21	c3gxqB_	Alignment	not modelled	18.0	25	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**putative regulator of transfer genes arta; **PDBTitle:** structure of arta and dna complex
22	d1riea_	Alignment	not modelled	18.0	25	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
23	c2kreA_	Alignment	not modelled	17.2	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin conjugation factor e4 b; **PDBTitle:** solution structure of e4b/ufd2a u-box domain
24	c2nvgA_	Alignment	not modelled	16.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit; **PDBTitle:** soluble domain of rieske iron sulfur protein.
25	c2k0mA_	Alignment	not modelled	14.9	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of the uncharacterized protein from2 rhodospirillum rubrum gene locus rru_a0810. northeast3 structural genomics target rrr43
26	d1wgma_	Alignment	not modelled	14.6	24	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
27	c2b7kD_	Alignment	not modelled	14.3	22	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**sco1 protein; **PDBTitle:** crystal structure of yeast sco1
28	d2k4xa1	Alignment	not modelled	14.2	61	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27a
						PDB header:hydrolase

29	c1vsy7_	Alignment	not modelled	13.0	13	**Chain:** 7: **PDB Molecule:**proteasome activator blm10; **PDBTitle:** proteasome activator complex
30	c2lkyA_	Alignment	not modelled	12.5	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of msmeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b
31	d1khda1	Alignment	not modelled	12.3	22	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
32	c2zxyA_	Alignment	not modelled	12.1	15	**PDB header:**oxygen binding, transport protein **Chain:** A: **PDB Molecule:**cytochrome c552; **PDBTitle:** crystal structure of cytochrome c555 from aquifex aeolicus
33	c2f42A_	Alignment	not modelled	12.0	20	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**stip1 homology and u-box containing protein 1; **PDBTitle:** dimerization and u-box domains of zebrafish c-terminal of hsp702 interacting protein
34	c2juhA_	Alignment	not modelled	11.7	17	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**telomere binding protein tbp1; **PDBTitle:** solution structure of dna binding domain of ngtrf1
35	c3n92A_	Alignment	not modelled	11.5	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-amylase, gh57 family; **PDBTitle:** crystal structure of tk1436, a gh57 branching enzyme from2 hyperthermophilic archaeon thermococcus kodakaraensis, in complex3 with glucose
36	c2ecyA_	Alignment	not modelled	11.4	38	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 3; **PDBTitle:** solution structure of the zinc finger, c3hc4 type (ring2 finger)" domain of tnf receptor-associated factor 3
37	d1h8ba_	Alignment	not modelled	11.2	23	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
38	c2i6hA_	Alignment	not modelled	11.1	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu0120; **PDBTitle:** structure of protein of unknown function atu0120 from agrobacterium2 tumefaciens
39	d2i6ha1	Alignment	not modelled	11.1	18	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Atu0120-like
40	c2d8tA_	Alignment	not modelled	10.7	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring finger protein 146; **PDBTitle:** solution structure of the ring domain of the human ring2 finger protein 146
41	c3jqoH_	Alignment	not modelled	10.6	11	**PDB header:**transport protein **Chain:** H: **PDB Molecule:**trao protein; **PDBTitle:** crystal structure of the outer membrane complex of a type iv2 secretion system
42	c2ofqA_	Alignment	not modelled	10.6	11	**PDB header:**protein transport/protein transport **Chain:** A: **PDB Molecule:**trao; **PDBTitle:** nmr solution structure of a complex between the virb9/virb72 interaction domains of the pkm101 type iv secretion system
43	c3ol4B_	Alignment	not modelled	10.3	24	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
44	d1w0ba_	Alignment	not modelled	10.2	19	**Fold:**Spectrin repeat-like **Superfamily:**Alpha-hemoglobin stabilizing protein AHSP **Family:**Alpha-hemoglobin stabilizing protein AHSP
45	d2e7ja1	Alignment	not modelled	10.2	21	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**SepSecS-like
46	c2cklA_	Alignment	not modelled	10.1	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polycomb group ring finger protein 4; **PDBTitle:** ring1b-bmi1 e3 catalytic domain structure
47	d1wp0a1	Alignment	not modelled	10.0	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
48	d2c2vv1	Alignment	not modelled	9.9	18	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
49	c3fl2A_	Alignment	not modelled	9.8	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase uhrf1; **PDBTitle:** crystal structure of the ring domain of the e3 ubiquitin-2 protein ligase uhrf1
50	d1z8ua1	Alignment	not modelled	9.8	19	**Fold:**Spectrin repeat-like **Superfamily:**Alpha-hemoglobin stabilizing protein AHSP **Family:**Alpha-hemoglobin stabilizing protein AHSP
51	c2cklB_	Alignment	not modelled	9.8	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**ubiquitin ligase protein ring2; **PDBTitle:** ring1b-bmi1 e3 catalytic domain structure
52	c2ecnA_	Alignment	not modelled	9.7	50	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring finger protein 141; **PDBTitle:** solution structure of the ring domain of the human ring2 finger protein 141
53	d1rmda2	Alignment	not modelled	9.5	38	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
						Fold: Cytochrome c

54	d1a56a_	Alignment	not modelled	9.5	19	**Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
55	d1t1ha_	Alignment	not modelled	9.5	38	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
56	c3dr4B_	Alignment	not modelled	9.5	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative perosamine synthetase; **PDBTitle:** gdp-perosamine synthase k186a mutant from caulobacter2 crescentus with bound sugar ligand
57	c2djbA_	Alignment	not modelled	9.4	30	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**polycomb group ring finger protein 6; **PDBTitle:** solution structure of the ring domain of the human polycomb2 group ring finger protein 6
58	c2kveA_	Alignment	not modelled	9.4	57	**PDB header:**hormone **Chain:** A: **PDB Molecule:**mesencephalic astrocyte-derived neurotrophic factor; **PDBTitle:** c-terminal domain of mesencephalic astrocyte-derived neurotrophic2 factor (manf)
59	c3bijC_	Alignment	not modelled	9.4	38	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein gsu0716; **PDBTitle:** crystal structure of protein gsu0716 from geobacter2 sulfurreducens. northeast structural genomics target gsr13
60	c2ecwA_	Alignment	not modelled	9.3	30	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tripartite motif-containing protein 30; **PDBTitle:** solution structure of the zinc finger, c3hc4 type (ring2 finger) domain tripartite motif protein 30
61	c2eciA_	Alignment	not modelled	9.2	30	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 6; **PDBTitle:** solution structure of the ring domain of the human tnf2 receptor-associated factor 6 protein
62	d2tpta1	Alignment	not modelled	9.1	33	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
63	d1ur6b_	Alignment	not modelled	8.8	38	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
64	d3cx5e1	Alignment	not modelled	8.6	35	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
65	c2ecjA_	Alignment	not modelled	8.6	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**tripartite motif-containing protein 39; **PDBTitle:** solution structure of the ring domain of the human2 tripartite motif-containing protein 39
66	c2w9vA_	Alignment	not modelled	8.5	63	**PDB header:**toxin **Chain:** A: **PDB Molecule:**short disintegrin jerdostatin; **PDBTitle:** solution structure of jerdostatin from trimeresurus2 jerdonii with end c-terminal residues n45g46 deleted
67	c2y43B_	Alignment	not modelled	8.2	30	**PDB header:**ligase **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase rad18; **PDBTitle:** rad18 ubiquitin ligase ring domain structure
68	c4a5bA_	Alignment	not modelled	8.1	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleoside-triphosphatase 2; **PDBTitle:** crystal structure of the c258s/c268s variant of toxoplasma gondii2 nucleoside triphosphate diphosphohydrolase 1 (ntpdase1)
69	d1jm7a_	Alignment	not modelled	8.0	38	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
70	d2elca1	Alignment	not modelled	7.9	24	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
71	d2b7ka1	Alignment	not modelled	7.8	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
72	c3ztgA_	Alignment	not modelled	7.7	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase rbbp6; **PDBTitle:** solution structure of the ring finger-like domain of2 retinoblastoma binding protein-6 (rbbp6)
73	c2y3aB_	Alignment	not modelled	7.7	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit beta; **PDBTitle:** crystal structure of p110beta in complex with icsh2 of p85beta and2 the drug gdc-0941
74	d1uoua1	Alignment	not modelled	7.6	37	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
75	c3l11A_	Alignment	not modelled	7.5	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase rnf168; **PDBTitle:** crystal structure of the ring domain of rnf168
76	d1ng7a_	Alignment	not modelled	7.4	56	**Fold:**Soluble domain of poliovirus core protein 3a **Superfamily:**Soluble domain of poliovirus core protein 3a **Family:**Soluble domain of poliovirus core protein 3a
77	d2cwqa1	Alignment	not modelled	7.3	19	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**TTHA0727-like
78	c2h0dB_	Alignment	not modelled	7.2	25	**PDB header:**metal binding protein/ligase **Chain:** B: **PDB Molecule:**ubiquitin ligase protein ring2; **PDBTitle:** structure of a bmi-1-ring1b polycomb group ubiquitin ligase complex
						PDB header:transferase

79	c3sqgG_	Alignment	not modelled	7.2	50	**Chain:** G: **PDB Molecule:**methyl coenzyme m reductase, alpha subunit; **PDBTitle:** crystal structure of a methyl-coenzyme m reductase purified from black2 sea mats
80	d1k78a1	Alignment	not modelled	7.1	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
81	c2yu4A_	Alignment	not modelled	7.1	0	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**e3 sumo-protein ligase nse2; **PDBTitle:** solution structure of the sp-ring domain in non-smc element2 2 homolog (mms21, s. cerevisiae)
82	d1v8ga1	Alignment	not modelled	6.9	24	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
83	c2csyA_	Alignment	not modelled	6.8	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**zinc finger protein 183-like 1; **PDBTitle:** solution structure of the ring domain of the zinc finger2 protein 183-like 1
84	c1tr6A_	Alignment	not modelled	6.7	80	**PDB header:**toxin **Chain:** A: **PDB Molecule:**omega-conotoxin gvia; **PDBTitle:** nmr solution structure of omega-conotoxin [k10]gvia, a cyclic cysteine2 knot peptide
85	c1omcA_	Alignment	not modelled	6.7	80	**PDB header:**presynaptic neurotoxin **Chain:** A: **PDB Molecule:**omega-conotoxin gvia; **PDBTitle:** solution structure of omega-conotoxin gvia using 2-d nmr2 spectroscopy and relaxation matrix analysis
86	c2ccoA_	Alignment	not modelled	6.7	80	**PDB header:**toxin **Chain:** A: **PDB Molecule:**omega-conotoxin gvia; **PDBTitle:** structure of the calcium channel blocker omega conotoxin2 gvia, nmr, 20 structures
87	d1omca_	Alignment	not modelled	6.7	80	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Conotoxin
88	c1ttlA_	Alignment	not modelled	6.7	80	**PDB header:**toxin **Chain:** A: **PDB Molecule:**omega-conotoxin gvia; **PDBTitle:** omega-conotoxin gvia, a n-type calcium channel blocker
89	c3tqcB_	Alignment	not modelled	6.7	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pantothenate kinase; **PDBTitle:** structure of the pantothenate kinase (coaa) from coxiella burnetii
90	d1vyxa_	Alignment	not modelled	6.6	50	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**Variant RING domain
91	d1st9a_	Alignment	not modelled	6.6	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
92	c3knvA_	Alignment	not modelled	6.5	50	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 2; **PDBTitle:** crystal structure of the ring and first zinc finger domains2 of traf2
93	d1c75a_	Alignment	not modelled	6.4	16	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
94	d2b5xa1	Alignment	not modelled	6.4	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
95	c1nhgD_	Alignment	not modelled	6.3	10	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** crystal structure analysis of plasmodium falciparum enoyl-2 acyl-carrier-protein reductase with triclosan
96	c3f6oB_	Alignment	not modelled	6.3	12	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**probable transcriptional regulator, arsr family **PDBTitle:** crystal structure of arsr family transcriptional regulator,2 rha00566
97	c2oixA_	Alignment	not modelled	6.3	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**xanthomonas outer protein d; **PDBTitle:** xanthomonas xopd c470a mutant
98	d1gp1a_	Alignment	not modelled	6.2	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
99	c3jvbA_	Alignment	not modelled	6.2	83	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**polyhedrin; **PDBTitle:** crystal structure of infectious baculovirus polyhedra