Phyre2

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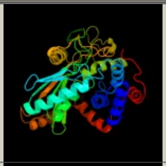
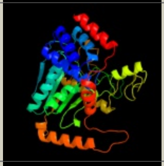
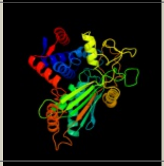
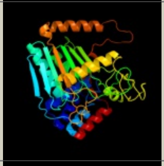
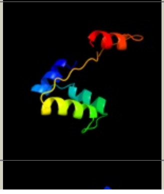
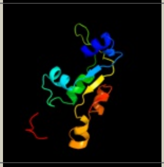
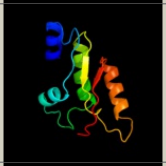
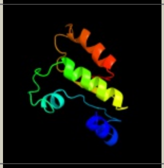
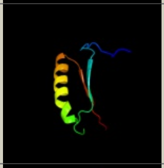
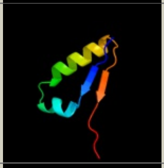
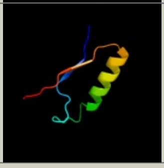
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xrha_	Alignment		100.0	96	**Fold:**L-sulfolactate dehydrogenase-like **Superfamily:**L-sulfolactate dehydrogenase-like **Family:**L-sulfolactate dehydrogenase-like
2	c1vbiA_	Alignment		100.0	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**type 2 malate/lactate dehydrogenase; **PDBTitle:** crystal structure of type 2 malate/lactate dehydrogenase from thermus2 thermophilus hb8
3	c1z2iA_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of agrobacterium tumefaciens malate2 dehydrogenase, new york structural genomics consortium
4	c3i0pA_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of malate dehydrogenase from entamoeba histolytica
5	c2g8yB_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate/l-lactate dehydrogenases; **PDBTitle:** the structure of a putative malate/lactate dehydrogenase from e. coli.
6	d1rfma_	Alignment		100.0	34	**Fold:**L-sulfolactate dehydrogenase-like **Superfamily:**L-sulfolactate dehydrogenase-like **Family:**L-sulfolactate dehydrogenase-like
7	c1wtjB_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ureidoglycolate dehydrogenase; **PDBTitle:** crystal structure of delta1-piperideine-2-carboxylate2 reductase from pseudomonas syringae pvar.tomato
8	d1nxua_	Alignment		100.0	22	**Fold:**L-sulfolactate dehydrogenase-like **Superfamily:**L-sulfolactate dehydrogenase-like **Family:**L-sulfolactate dehydrogenase-like
9	c3uoeB_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from sinorhizobium meliloti
10	c1v9nA_	Alignment		100.0	34	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structure of malate dehydrogenase from pyrococcus horikoshii ot3
11	d2ebfx2	Alignment		54.3	18	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**PMT domain-like

12	c3b8iF_	Alignment		50.4	13	**PDB header:**lyase **Chain:** F: **PDB Molecule:**pa4872 oxaloacetate decarboxylase; **PDBTitle:** crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
13	c2qiwA_	Alignment		46.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pep phosphonomutase; **PDBTitle:** crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
14	d1muma_	Alignment		45.7	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
15	c2ze3A_	Alignment		41.8	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dfa0005; **PDBTitle:** crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
16	c2hjpA_	Alignment		40.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonopyruvate hydrolase; **PDBTitle:** crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
17	c3irvA_	Alignment		40.2	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cysteine hydrolase; **PDBTitle:** crystal structure of cysteine hydrolase pspph_2384 from pseudomonas2 syringae pv. phaseolicola 1448a
18	c3ih1A_	Alignment		40.1	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
19	c3eefA_	Alignment		39.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-carbamoylsarcosine amidase related protein; **PDBTitle:** crystal structure of n-carbamoylsarcosine amidase from thermoplasma2 acidophilum
20	c3kl2K_	Alignment		35.9	16	**PDB header:**structural genomics, unknown function **Chain:** K: **PDB Molecule:**putative isochorismatase; **PDBTitle:** crystal structure of a putative isochorismatase from streptomyces2 avermitilis
21	c3eooL_	Alignment	not modelled	31.1	17	**PDB header:**lyase **Chain:** L: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
22	d1nf9a_	Alignment	not modelled	29.2	7	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
23	c3ot4F_	Alignment	not modelled	29.0	22	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**putative isochorismatase; **PDBTitle:** structure and catalytic mechanism of bordetella bronchiseptica nicf
24	c3fa4D_	Alignment	not modelled	27.4	18	**PDB header:**lyase **Chain:** D: **PDB Molecule:**2,3-dimethylmalate lyase; **PDBTitle:** crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
25	c2b34C_	Alignment	not modelled	27.3	10	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**mar1 ribonuclease; **PDBTitle:** structure of mar1 ribonuclease from caenorhabditis elegans
26	d1nbaa_	Alignment	not modelled	26.6	18	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
27	c1zlpA_	Alignment	not modelled	26.5	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**petal death protein; **PDBTitle:** petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
28	c1e0mA_	Alignment	not modelled	25.7	29	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**wwprototype; **PDBTitle:** prototype ww domain
29	c1yiuA_	Alignment	not modelled	25.1	36	**PDB header:**ligase **Chain:** A: **PDB Molecule:**itchy e3 ubiquitin protein ligase;

						PDBTitle: itch e3 ubiquitin ligase ww3 domain
30	c2uygF_	Alignment	not modelled	25.0	21	**PDB header:**lyase **Chain:** F: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystallographic structure of the typeii 3-dehydroquinase2 from thermus thermophilus
31	c3l4hA_	Alignment	not modelled	24.0	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase hecw1; **PDBTitle:** helical box domain and second ww domain of the human e3 ubiquitin-2 protein ligase hecw1
32	c3bzrA_	Alignment	not modelled	23.9	18	**PDB header:**membrane protein, protein transport **Chain:** A: **PDB Molecule:**escu; **PDBTitle:** crystal structure of escu c-terminal domain with n262d mutation, space2 group p 41 21 2
33	d3bzra1	Alignment	not modelled	23.9	18	**Fold:**EscU C-terminal domain-like **Superfamily:**EscU C-terminal domain-like **Family:**EscU C-terminal domain-like
34	d1vp8a_	Alignment	not modelled	23.1	13	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
35	c1bmxA_	Alignment	not modelled	22.8	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**human immunodeficiency virus type 1 capsid; **PDBTitle:** hiv-1 capsid protein major homology region peptide analog,2 nmr, 8 structures
36	c2ysbA_	Alignment	not modelled	22.7	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**salvador homolog 1 protein; **PDBTitle:** solution structure of the first ww domain from the mouse2 salvador homolog 1 protein (sav1)
37	c3t7yB_	Alignment	not modelled	22.4	20	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**yop proteins translocation protein u; **PDBTitle:** structure of an autocleavage-inactive mutant of the cytoplasmic domain2 of ct091, the yscu homologue of chlamydia trachomatis
38	d1bdga1	Alignment	not modelled	22.2	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
39	c1ymzA_	Alignment	not modelled	22.1	29	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cc45; **PDBTitle:** cc45, an artificial ww domain designed using statistical2 coupling analysis
40	c2ysdA_	Alignment	not modelled	21.6	33	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**membrane-associated guanylate kinase, ww and pdz **PDBTitle:** solution structure of the first ww domain from the human2 membrane-associated guanylate kinase, ww and pdz domain-3 containing protein 1. magi-1
41	c3hb7G_	Alignment	not modelled	21.1	7	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**isochorismatase hydrolase; **PDBTitle:** the crystal structure of an isochorismatase-like hydrolase from2 alkaliphilus metalliredigens to 2.3a
42	d1f8ab1	Alignment	not modelled	20.3	20	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
43	c2jlhA_	Alignment	not modelled	20.2	23	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**yop proteins translocation protein u; **PDBTitle:** crystal structure of the cytoplasmic domain of yersinia2 pestis yscu n263a mutant
44	c1wr7A_	Alignment	not modelled	19.8	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nedd4-2; **PDBTitle:** solution structure of the third ww domain of nedd4-2
45	d2csua3	Alignment	not modelled	19.8	11	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
46	d1yaca_	Alignment	not modelled	19.7	9	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
47	d1ujqa_	Alignment	not modelled	19.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
48	d1t57a_	Alignment	not modelled	19.4	16	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
49	c2hg2A_	Alignment	not modelled	19.4	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase a; **PDBTitle:** structure of lactaldehyde dehydrogenase
50	d1k9ra_	Alignment	not modelled	18.9	27	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
51	c2djyA_	Alignment	not modelled	18.9	21	**PDB header:**ligase/signaling protein **Chain:** A: **PDB Molecule:**smad ubiquitination regulatory factor 2; **PDBTitle:** solution structure of smurf2 ww3 domain-smad7 py peptide2 complex
52	c2lawA_	Alignment	not modelled	18.5	36	**PDB header:**signaling protein/transcription **Chain:** A: **PDB Molecule:**yorkie homolog; **PDBTitle:** structure of the second ww domain from human yap in complex with a2 human smad1 derived peptide
53	c3mcwA_	Alignment	not modelled	17.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of an a putative hydrolase of the isochorismatase2 family (cv_1320) from chromobacterium violaceum atcc 12472 at 1.06 a3 resolution
54	c1wmvA_	Alignment	not modelled	17.6	28	**PDB header:**oxidoreductase, apoptosis **Chain:** A: **PDB Molecule:**ww domain containing oxidoreductase; **PDBTitle:** solution structure of the second ww domain of wwox

55	c1wr4A_	Alignment	not modelled	17.5	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin-protein ligase nedd4-2; **PDBTitle:** solution structure of the second ww domain of nedd4-2
56	d1tk7a1	Alignment	not modelled	17.2	21	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
57	d1j2ra_	Alignment	not modelled	17.2	10	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
58	c3gveB_	Alignment	not modelled	17.0	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**yfkn protein; **PDBTitle:** crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis
59	d2cfua2	Alignment	not modelled	16.8	12	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Alkylsulfatase-like
60	c2kykA_	Alignment	not modelled	16.5	36	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase itchy homolog; **PDBTitle:** the sandwich region between two lmp2a py motif regulates the2 interaction between aip4ww2domain and py motif
61	d1a4sa_	Alignment	not modelled	16.1	19	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
62	c2jmfA_	Alignment	not modelled	16.0	20	**PDB header:**ligase/signaling protein **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase suppressor of deltex; **PDBTitle:** solution structure of the su(dx) ww4- notch py peptide2 complex
63	d2jmfa1	Alignment	not modelled	14.9	21	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
64	d1i5hw_	Alignment	not modelled	14.5	20	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
65	d3djba1	Alignment	not modelled	14.4	17	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
66	c2ez5W_	Alignment	not modelled	14.0	33	**PDB header:**signalling protein,ligase **Chain:** W: **PDB Molecule:**e3 ubiquitin-protein ligase nedd4; **PDBTitle:** solution structure of the dnedd4 ww3* domain- comm lpsy2 peptide complex
67	d3ci0k2	Alignment	not modelled	14.0	19	**Fold:**SAM domain-like **Superfamily:**GspK insert domain-like **Family:**GspK insert domain-like
68	c2fq1A_	Alignment	not modelled	13.9	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isochorismatase; **PDBTitle:** crystal structure of the two-domain non-ribosomal peptide synthetase2 entb containing isochorismate lyase and aryl-carrier protein domains
69	c2h0rD_	Alignment	not modelled	13.8	7	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nicotinamidase; **PDBTitle:** structure of the yeast nicotinamidase pnc1p
70	d1wjfa_	Alignment	not modelled	13.4	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**N-terminal Zn binding domain of HIV integrase **Family:**N-terminal Zn binding domain of HIV integrase
71	c2yshA_	Alignment	not modelled	13.4	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**growth-arrest-specific protein 7; **PDBTitle:** solution structure of the ww domain from the human growth-2 arrest-specific protein 7, gas-7
72	c2nu9E_	Alignment	not modelled	13.0	18	**PDB header:**ligase **Chain:** E: **PDB Molecule:**succinyl-coa synthetase beta chain; **PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
73	c3oqpA_	Alignment	not modelled	12.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative isochorismatase; **PDBTitle:** crystal structure of a putative isochorismatase (bxe_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
74	c2k29A_	Alignment	not modelled	12.7	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
75	d1sgma2	Alignment	not modelled	12.4	16	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
76	c3jz4C_	Alignment	not modelled	12.0	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**succinate-semialdehyde dehydrogenase [nadp+]; **PDBTitle:** crystal structure of e. coli nadp dependent enzyme
77	c2pmzF_	Alignment	not modelled	11.5	23	**PDB header:**translation, transferase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit f; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
78	c3ifgH_	Alignment	not modelled	11.3	19	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**succinate-semialdehyde dehydrogenase (nadp+); **PDBTitle:** crystal structure of succinate-semialdehyde dehydrogenase from2 burkholderia pseudomallei, part 1 of 2
79	c3k2wD_	Alignment	not modelled	11.2	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**betaine-aldehyde dehydrogenase; **PDBTitle:** crystal structure of betaine-aldehyde dehydrogenase from2 pseudoalteromonas atlantica t6c
80	d1lvaa3	Alignment	not modelled	11.2	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain

						Family:C-terminal fragment of elongation factor SelB
81	c2kxqA_	Alignment	not modelled	11.1	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase smurf2; **PDBTitle:** solution structure of smurf2 ww2 and ww3 bound to smad7 py motif2 containing peptide
82	c2d4eB_	Alignment	not modelled	11.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**5-carboxymethyl-2-hydroxymuconate semialdehyde **PDBTitle:** crystal structure of the hpcc from thermus thermophilus hb8
83	c2l4jA_	Alignment	not modelled	10.7	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**yes-associated protein 2 (yap2); **PDBTitle:** yap ww2
84	d1f61a_	Alignment	not modelled	10.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
85	c2ve5H_	Alignment	not modelled	10.3	18	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** crystallographic structure of betaine aldehyde2 dehydrogenase from pseudomonas aeruginosa
86	d1o5ha_	Alignment	not modelled	10.2	25	**Fold:**Methenyltetrahydrofolate cyclohydrolase-like **Superfamily:**Methenyltetrahydrofolate cyclohydrolase-like **Family:**Methenyltetrahydrofolate cyclohydrolase-like
87	c2ysgA_	Alignment	not modelled	10.1	29	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**syntaxin-binding protein 4; **PDBTitle:** solution structure of the ww domain from the human syntaxin-2 binding protein 4
88	c3iwkB_	Alignment	not modelled	10.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aminoaldehyde dehydrogenase; **PDBTitle:** crystal structure of aminoaldehyde dehydrogenase 1 from2 pisum sativum (psamadh1)
89	d2f21a1	Alignment	not modelled	9.9	23	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
90	c2lazA_	Alignment	not modelled	9.9	14	**PDB header:**signaling protein/transcription **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase smurf1; **PDBTitle:** structure of the first ww domain of human smurf1 in complex with a2 mono-phosphorylated human smad1 derived peptide
91	c2lb0A_	Alignment	not modelled	9.9	14	**PDB header:**signaling protein/transcription **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase smurf1; **PDBTitle:** structure of the first ww domain of human smurf1 in complex with a di-2 phosphorylated human smad1 derived peptide
92	c3hazA_	Alignment	not modelled	9.9	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**proline dehydrogenase; **PDBTitle:** crystal structure of bifunctional proline utilization a2 (puta) protein
93	c2a67C_	Alignment	not modelled	9.8	7	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**isochorismatase family protein; **PDBTitle:** crystal structure of isochorismatase family protein
94	d1wdja_	Alignment	not modelled	9.8	14	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hypothetical protein TT1808 (TTHA1514)
95	c3lqyA_	Alignment	not modelled	9.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative isochorismatase hydrolase; **PDBTitle:** crystal structure of putative isochorismatase hydrolase from2 oleispira antarctica
96	c2cfuA_	Alignment	not modelled	9.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sdsa1; **PDBTitle:** crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
97	c2dmvA_	Alignment	not modelled	9.5	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**itchy homolog e3 ubiquitin protein ligase; **PDBTitle:** solution structure of the second ww domain of itchy homolog2 e3 ubiquitin protein ligase (itch)
98	c2ysfA_	Alignment	not modelled	9.5	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase itchy homolog; **PDBTitle:** solution structure of the fourth ww domain from the human2 e3 ubiquitin-protein ligase itchy homolog, itch
99	c2w8qA_	Alignment	not modelled	9.4	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate-semialdehyde dehydrogenase, **PDBTitle:** the crystal structure of human ssadh in complex with ssa.