Phyre2

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Description	RVBD0743c_(-)_833889_834446
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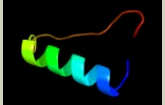
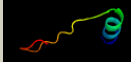
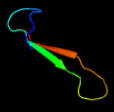
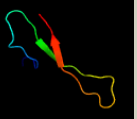
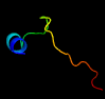
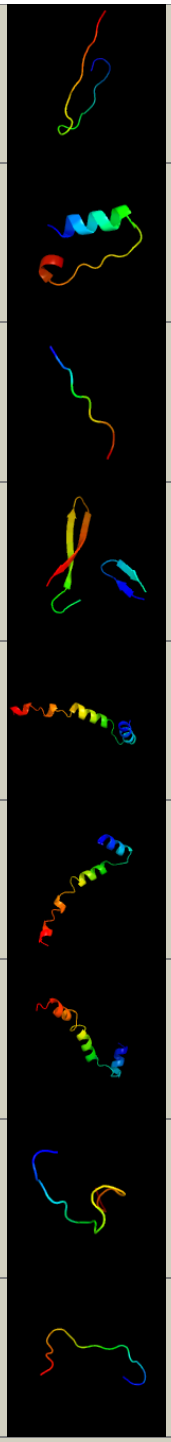
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4e8iA_	Alignment		86.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lincosamide resistance protein; **PDBTitle:** crystal structure of lincosamide antibiotic adenylyltransferase lina,2 apo
2	d1no5a_	Alignment		54.7	24	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
3	d1wota_	Alignment		54.2	37	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
4	c2mdwA_	Alignment		50.3	50	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein; **PDBTitle:** nmr structure of a strand-swapped dimer of the ww domain
5	c2ky8A_	Alignment		48.6	25	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**methyl-cpg-binding domain protein 2; **PDBTitle:** solution structure and dynamic analysis of chicken mbd2 methyl binding2 domain bound to a target methylated dna sequence
6	c3fm2A_	Alignment		44.1	32	**PDB header:**heme-binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein, distantly related to a heme **PDBTitle:** crystal structure of a putative heme-binding protein (ava_4353) from2 anabaena variabilis atcc 29413 at 1.80 a resolution
7	d1ig4a_	Alignment		39.4	22	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**Methyl-CpG-binding domain, MBD
8	d1ylqa1	Alignment		38.4	17	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
9	c2l9dA_	Alignment		36.3	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of the protein yp_546394.1, the first structural2 representative of the pfam family pf12112
10	d1ub1a_	Alignment		35.8	25	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**Methyl-CpG-binding domain, MBD
11	c3zvrA_	Alignment		33.7	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dynamin-1; **PDBTitle:** crystal structure of dynamin

12	d1tu1a_	Alignment		30.6	19	**Fold:**Mog1p/PsbP-like **Superfamily:**Mog1p/PsbP-like **Family:**PA0094-like
13	d2gc6a1	Alignment		27.8	17	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**Folylpolyglutamate synthetase, C-terminal domain
14	c3snhA_	Alignment		26.3	44	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**dynamin-1; **PDBTitle:** crystal structure of nucleotide-free human dynamin1
15	c5xmcA_	Alignment		25.3	32	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase itchy; **PDBTitle:** crystal structure of the auto-inhibited nedd4 family e3 ligase itch
16	d2qdya1	Alignment		23.0	27	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
17	d1v29a_	Alignment		22.9	27	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
18	c3qyhG_	Alignment		22.6	31	**PDB header:**lyase **Chain:** G: **PDB Molecule:**co-type nitrile hydratase alpha subunit; **PDBTitle:** crystal structure of co-type nitrile hydratase beta-h71l from2 pseudomonas putida.
19	c4l9cA_	Alignment		22.5	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**f-box only protein 7; **PDBTitle:** crystal structure of the fp domain of human f-box protein fbxo72 (native)
20	c2yscA_	Alignment		22.4	38	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**amyloid beta a4 precursor protein-binding family **PDBTitle:** solution structure of the ww domain from the human amyloid2 beta a4 precursor protein-binding family b member 3, apbb3
21	d1qk9a_	Alignment	not modelled	21.7	26	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**Methyl-CpG-binding domain, MBD
22	c3kepA_	Alignment	not modelled	21.0	11	**PDB header:**protein transport, rna binding protein **Chain:** A: **PDB Molecule:**nucleoporin nup145; **PDBTitle:** crystal structure of the autoproteolytic domain from the nuclear pore2 complex component nup145 from saccharomyces cerevisiae
23	c2kq0A_	Alignment	not modelled	20.4	56	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase nedd4; **PDBTitle:** human nedd4 3rd ww domain complex with ebola zaire virus matrix2 protein vp40 derived peptide ilptappeymea
24	c2z0bB_	Alignment	not modelled	20.0	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative glycerophosphodiester phosphodiesterase 5; **PDBTitle:** crystal structure of cbm20 domain of human putative2 glycerophosphodiester phosphodiesterase 5 (kiaa1434)
25	c4yntA_	Alignment	not modelled	19.3	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucose oxidase, putative; **PDBTitle:** crystal structure of aspergillus flavus fad glucose dehydrogenase
26	c1ju2A_	Alignment	not modelled	18.9	30	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxynitrile lyase; **PDBTitle:** crystal structure of the hydroxynitrile lyase from almond
27	c1naaB_	Alignment	not modelled	18.2	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cellobiose dehydrogenase; **PDBTitle:** cellobiose dehydrogenase flavoprotein fragment in complex with2 cellobionolactam
28	c2lazA_	Alignment	not modelled	18.2	44	**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
29	c2lb0A_	Alignment	not modelled	18.2	44	**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
30	c1gpeA_	Alignment	not modelled	18.1	20	**PDB header:**oxidoreductase(flavoprotein) **Chain:** A: **PDB Molecule:**protein (glucose oxidase); **PDBTitle:** glucose oxidase from penicillium amagasakiense
31	c6ql4B_	Alignment	not modelled	17.9	56	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**putative mitochondrial dynamin protein; **PDBTitle:** crystal structure of nucleotide-free mgm1
32	c3vxvA_	Alignment	not modelled	17.6	19	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**methyl-cpg-binding domain protein 4; **PDBTitle:** crystal structure of methyl cpg binding domain of mbd4 in complex with2 the 5mcg/tg sequence
33	d1kdga1	Alignment	not modelled	17.6	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
34	d1ugpa_	Alignment	not modelled	17.5	27	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
35	d1cgta2	Alignment	not modelled	17.0	12	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**Starch-binding domain
36	c5nccB_	Alignment	not modelled	16.9	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**fatty acid photodecarboxylase; **PDBTitle:** structure of fatty acid photodecarboxylase in complex with fad and2 palmitic acid
37	d1cf3a1	Alignment	not modelled	16.8	30	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
38	d2itka1	Alignment	not modelled	16.8	44	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
39	c3q9tB_	Alignment	not modelled	16.6	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**choline dehydrogenase and related flavoproteins; **PDBTitle:** crystal structure analysis of formate oxidase
40	c1wr4A_	Alignment	not modelled	16.6	38	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin-protein ligase nedd4-2; **PDBTitle:** solution structure of the second ww domain of nedd4-2
41	c3fimB_	Alignment	not modelled	16.6	44	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aryl-alcohol oxidase; **PDBTitle:** crystal structure of aryl-alcohol-oxidase from pleurotus eryingii
42	c5aa6F_	Alignment	not modelled	16.6	38	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**vanadium-dependent bromoperoxidase 2; **PDBTitle:** homohexameric structure of the second vanadate-dependent2 bromoperoxidase (anii) from ascophyllum nodosum
43	d1k9ra_	Alignment	not modelled	16.3	36	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
44	c4h7uA_	Alignment	not modelled	16.2	44	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyranose dehydrogenase; **PDBTitle:** crystal structure of pyranose dehydrogenase from agaricus meleagris,2 wildtype
45	c2n8tA_	Alignment	not modelled	16.0	31	**PDB header:**ligase/peptide **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase nedd4; **PDBTitle:** solution structure of the rnedd4 ww2 domain-cx43ct peptide complex by2 nmr
46	c4qi4A_	Alignment	not modelled	15.7	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cellobiose dehydrogenase; **PDBTitle:** dehydrogenase domain of myriococcum thermophilum cellobiose2 dehydrogenase, mtdh
47	c2jmfA_	Alignment	not modelled	15.4	38	**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
48	c4fm4C_	Alignment	not modelled	15.4	18	**PDB header:**lyase **Chain:** C: **PDB Molecule:**nitrile hydratase alpha subunit; **PDBTitle:** wild type fe-type nitrile hydratase from comamonas testosteroni ni1
49	d2f21a1	Alignment	not modelled	15.3	56	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
50	c3pz8A_	Alignment	not modelled	15.3	44	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**segment polarity protein dishevelled homolog dvl-1; **PDBTitle:** crystal structure of dvl1-dix(y17d) mutant
51	d1pina1	Alignment	not modelled	15.3	56	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
52	c1cf3A_	Alignment	not modelled	14.9	30	**PDB header:**oxidoreductase(flavoprotein) **Chain:** A: **PDB Molecule:**protein (glucose oxidase); **PDBTitle:** glucose oxidase from apergillus niger
53	c3qw4B_	Alignment	not modelled	14.8	19	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**ump synthase; **PDBTitle:** structure of leishmania donovani ump synthase
54	c6h3gC_	Alignment	not modelled	14.5	50	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**alcohol oxidase; **PDBTitle:** alcohol oxidase from phanerochaete chrysosporium

55	d1cyga2	Alignment	not modelled	14.5	25	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**Starch-binding domain
56	c2yshA_	Alignment	not modelled	14.4	29	**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
57	c4whjA_	Alignment	not modelled	14.3	44	**PDB header:**antiviral protein, hydrolase **Chain:** A: **PDB Molecule:**interferon-induced gtp-binding protein mx2; **PDBTitle:** myxovirus resistance protein 2 (mxb)
58	c5hsaG_	Alignment	not modelled	14.3	42	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**alcohol oxidase 1; **PDBTitle:** alcohol oxidase aox1 from pichia pastoris
59	c4n0iB_	Alignment	not modelled	14.2	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit b, **PDBTitle:** crystal structure of s. cerevisiae mitochondrial gatfab in complex2 with glutamine
60	c2jbvA_	Alignment	not modelled	14.1	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**choline oxidase; **PDBTitle:** crystal structure of choline oxidase reveals insights into the2 catalytic mechanism
61	c3ip4B_	Alignment	not modelled	13.9	30	**PDB header:**ligase **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** the high resolution structure of gatcab
62	c2ebuA_	Alignment	not modelled	13.9	28	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication factor c subunit 1; **PDBTitle:** solution structure of the brct domain from human2 replication factor c large subunit 1
63	d1f8ab1	Alignment	not modelled	13.8	43	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
64	c2reeB_	Alignment	not modelled	13.7	18	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**cura; **PDBTitle:** crystal structure of the loading gnatl domain of cura from lyngbya2 majuscula
65	d2f5va1	Alignment	not modelled	13.6	44	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
66	d1prtb1	Alignment	not modelled	13.6	29	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
67	c1e0mA_	Alignment	not modelled	13.4	44	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**wwprototype; **PDBTitle:** prototype ww domain
68	d1i8gb_	Alignment	not modelled	13.4	56	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
69	d1cxla2	Alignment	not modelled	13.4	47	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**Starch-binding domain
70	c3t37A_	Alignment	not modelled	13.2	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** crystal structure of pyridoxine 4-oxidase from mesorbium loti
71	d1cw0a_	Alignment	not modelled	13.1	18	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Very short patch repair (VSR) endonuclease
72	d2f2ab2	Alignment	not modelled	13.0	30	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**GatB/GatE catalytic domain-like
73	c4udpA_	Alignment	not modelled	13.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucose-methanol-choline oxidoreductase; **PDBTitle:** crystal structure of 5-hydroxymethylfurfural oxidase (hmfo) in the2 oxidized state
74	d1ju2a1	Alignment	not modelled	12.8	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
75	c2l4jA_	Alignment	not modelled	12.8	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**yes-associated protein 2 (yap2); **PDBTitle:** yap ww2
76	d2jmfa1	Alignment	not modelled	12.7	63	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
77	d1y7pa1	Alignment	not modelled	12.6	28	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**AF1403 C-terminal domain-like
78	c1coyA_	Alignment	not modelled	12.6	50	**PDB header:**oxidoreductase(oxygen receptor) **Chain:** A: **PDB Molecule:**cholesterol oxidase; **PDBTitle:** crystal structure of cholesterol oxidase complexed with a steroid2 substrate. implications for fad dependent alcohol oxidases
79	d1gpea1	Alignment	not modelled	12.5	20	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
80	c3al0B_	Alignment	not modelled	12.3	36	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
81	c2vsgA_	Alignment	not modelled	12.3	36	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**syntaxin-binding protein 4;

81	c2ysgA_	Alignment	not modelled	12.3	36	**PDBTitle:** solution structure of the ww domain from the human syntaxin-2 binding protein 4
82	c2g5iB_	Alignment	not modelled	12.2	30	**PDB header:**ligase **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase **PDBTitle:** structure of trna-dependent amidotransferase gatcab2 complexed with adp-alf4
83	c1s3bB_	Alignment	not modelled	12.2	40	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**amine oxidase [flavin-containing] b; **PDBTitle:** crystal structure of maob in complex with n-methyl-n-2 propargyl-1(r)-aminoindan
84	c1yw5A_	Alignment	not modelled	12.2	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl prolyl cis/trans isomerase; **PDBTitle:** peptidyl-prolyl isomerase ess1 from candida albicans
85	c2dmvA_	Alignment	not modelled	12.2	38	**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)
86	d1tk7a2	Alignment	not modelled	12.1	56	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
87	c1ymzA_	Alignment	not modelled	11.9	56	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cc45; **PDBTitle:** cc45, an artificial ww domain designed using statistical2 coupling analysis
88	d1d7ya3	Alignment	not modelled	11.8	19	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
89	c2ysfA_	Alignment	not modelled	11.8	56	**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
90	c2ez5W_	Alignment	not modelled	11.7	23	**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
91	c4p4sA_	Alignment	not modelled	11.6	44	**PDB header:**antiviral protein/hydrolase **Chain:** A: **PDB Molecule:**interferon-induced gtp-binding protein mx1; **PDBTitle:** gmppcp-bound stalkless-mxa
92	c5b3zB_	Alignment	not modelled	11.4	50	**PDB header:**isomerase,sugar binding protein **Chain:** B: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase nima-interacting 1, **PDBTitle:** crystal structure of hpin1 ww domain (5-39) fused with maltose-binding2 protein
93	d1qhoa2	Alignment	not modelled	11.4	20	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**Starch-binding domain
94	d1tk7a1	Alignment	not modelled	11.3	31	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
95	c1wr7A_	Alignment	not modelled	11.3	56	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nedd4-2; **PDBTitle:** solution structure of the third ww domain of nedd4-2
96	d3bmva2	Alignment	not modelled	11.3	33	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**Starch-binding domain
97	c2gewA_	Alignment	not modelled	11.1	40	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cholesterol oxidase; **PDBTitle:** atomic resolution structure of cholesterol oxidase @ ph 9.02 (streptomyces sp. sa-coo)
98	d1nmva1	Alignment	not modelled	11.1	43	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
99	c1dxlC_	Alignment	not modelled	11.0	27	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** dihydrolipoamide dehydrogenase of glycine decarboxylase2 from pisum sativum