Phyre2

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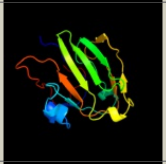
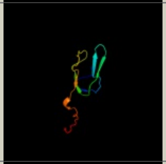
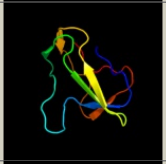
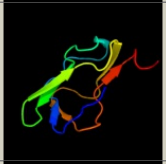
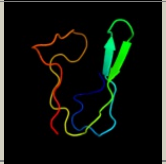
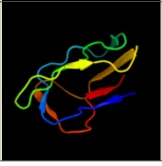
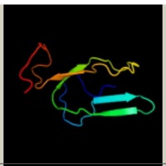
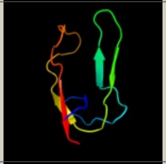
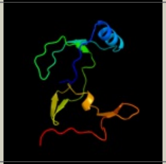
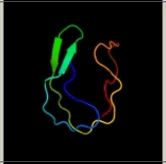
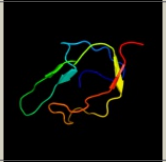
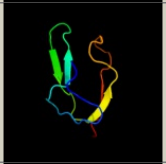
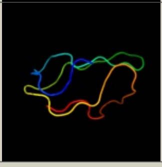
Description	P0A8K1
Date	Thu Jan 5 11:08:01 GMT 2012
Unique Job ID	6b9d16282375025e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2gpra_	Alignment		97.4	17	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
2	d1gpra_	Alignment		96.7	17	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
3	d2f3ga_	Alignment		96.6	16	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
4	d1glaf_	Alignment		96.4	13	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
5	c2dncA_	Alignment		89.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase protein x component; **PDBTitle:** solution structure of rsgi ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase
6	c2ejmA_	Alignment		88.8	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methylcrotonoyl-coa carboxylase subunit alpha; **PDBTitle:** solution structure of ruh-072, an apo-biotnyl domain form2 human acetyl coenzyme a carboxylase
7	c2dn8A_	Alignment		88.7	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** solution structure of rsgi ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase
8	d1bdoa_	Alignment		88.4	12	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
9	c2b8gA_	Alignment		88.2	13	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**biotin/lipoyl attachment protein; **PDBTitle:** solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure)
10	d1laba_	Alignment		87.1	11	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
11	c2ejgD_	Alignment		87.0	10	**PDB header:**ligase **Chain:** D: **PDB Molecule:**149aa long hypothetical methylmalonyl-coa decarboxylase **PDBTitle:** crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3

12	d1y8ob1	Alignment		85.9	13	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
13	d1dcza_	Alignment		85.9	11	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
14	d1ghja_	Alignment		85.1	12	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
15	c2dneA_	Alignment		84.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** solution structure of rsgi ruh-058, a lipoyl domain of2 human 2-oxoacid dehydrogenase
16	c2qikA_	Alignment		83.5	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0131 protein ykqa; **PDBTitle:** crystal structure of ykqa from bacillus subtilis. northeast2 structural genomics target sr631
17	c2l5tA_	Alignment		81.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase; **PDBTitle:** solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
18	d1qjoa_	Alignment		81.7	7	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
19	d1iyua_	Alignment		81.5	7	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
20	d1gjxa_	Alignment		81.3	9	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
21	c2kccA_	Alignment	not modelled	78.9	8	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
22	d1k8ma_	Alignment	not modelled	77.8	10	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
23	c2q8iB_	Alignment	not modelled	75.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase component of **PDBTitle:** pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
24	d1pmra_	Alignment	not modelled	75.4	7	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
25	d1o78a_	Alignment	not modelled	73.1	9	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
26	c1urzC_	Alignment	not modelled	59.5	34	**PDB header:**virus/viral protein **Chain:** C: **PDB Molecule:**envelope protein; **PDBTitle:** low ph induced, membrane fusion conformation of the2 envelope protein of tick-borne encephalitis virus
27	c3cdxB_	Alignment	not modelled	50.4	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**succinylglutamatedesuccinylase/aspartoacylase; **PDBTitle:** crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
28	d1z66a1	Alignment	not modelled	45.9	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains

						Family: Class II viral fusion proteins C-terminal domain
29	c2jqmA_	Alignment	not modelled	40.9	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**envelope protein e; **PDBTitle:** yellow fever envelope protein domain iii nmr structure2 (s288-k398)
30	c3na6A_	Alignment	not modelled	39.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinylglutamate desuccinylase/aspartoacylase; **PDBTitle:** crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
31	c1vdzA_	Alignment	not modelled	39.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**a-type atpase subunit a; **PDBTitle:** crystal structure of a-type atpase catalytic subunit a from2 pyrococcus horikoshii ot3
32	c2hsiB_	Alignment	not modelled	38.5	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative peptidase m23; **PDBTitle:** crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium
33	c2h0pA_	Alignment	not modelled	38.4	28	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein; **PDBTitle:** nmr structure of the dengue-4 virus envelope protein domain2 iii
34	c2qj8B_	Alignment	not modelled	37.5	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mlr6093 protein; **PDBTitle:** crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
35	d1svba1	Alignment	not modelled	36.9	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
36	d1pjwa_	Alignment	not modelled	30.2	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
37	d1xpma2	Alignment	not modelled	30.2	40	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
38	c2ka7A_	Alignment	not modelled	29.7	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** nmr solution structure of tm0212 at 40 c
39	d1qwya_	Alignment	not modelled	29.6	20	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Peptidoglycan hydrolase LytM
40	c3mxuA_	Alignment	not modelled	29.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of glycine cleavage system protein h from bartonella2 henselae
41	c3lazB_	Alignment	not modelled	28.5	5	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-galactarate dehydratase; **PDBTitle:** the crystal structure of the n-terminal domain of d-2 galactarate dehydratase from escherichia coli cft073
42	c2aujD_	Alignment	not modelled	28.4	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of thermus aquaticus rna polymerase beta'-subunit2 insert
43	c1otcB_	Alignment	not modelled	26.9	35	**PDB header:**protein/dna **Chain:** B: **PDB Molecule:**protein (telomere-binding protein beta subunit); **PDBTitle:** the o. nova telomere end binding protein complexed with2 single strand dna
44	c2i0qB_	Alignment	not modelled	26.5	35	**PDB header:**structural protein/dna **Chain:** B: **PDB Molecule:**telomere-binding protein beta subunit; **PDBTitle:** crystal structure of a telomere single-strand dna-protein2 complex from o. nova with full-length alpha and beta3 telomere proteins
45	d1jb7b_	Alignment	not modelled	26.5	35	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
46	d1ok8a1	Alignment	not modelled	26.0	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
47	c3egpA_	Alignment	not modelled	25.3	25	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope protein; **PDBTitle:** crystal structure analysis of dengue-1 envelope protein2 domain iii
48	c2jkuA_	Alignment	not modelled	24.7	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**propionyl-coa carboxylase alpha chain, **PDBTitle:** crystal structure of the n-terminal region of the biotin2 acceptor domain of human propionyl-coa carboxylase
49	c2aukA_	Alignment	not modelled	24.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of e. coli rna polymerase beta' g/g' insert
50	c2b44A_	Alignment	not modelled	23.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycyl-glycine endopeptidase lytm; **PDBTitle:** truncated s. aureus lytm, p 32 2 1 crystal form
51	c3it5B_	Alignment	not modelled	22.4	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protease lasa; **PDBTitle:** crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
52	c3iftA_	Alignment	not modelled	21.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of glycine cleavage system protein h from2 mycobacterium tuberculosis, using x-rays from the compact light3 source.
53	c2edgA	Alignment	not modelled	20.7	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glycine cleavage system h protein;

53	c2edgA_	Alignment	not modelled	20.7	18	**PDBTitle:** solution structure of the gcv_h domain from mouse glycine
54	c2r9qD_	Alignment	not modelled	19.9	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**2'-deoxycytidine 5'-triphosphate deaminase; **PDBTitle:** crystal structure of 2'-deoxycytidine 5'-triphosphate deaminase from2 agrobacterium tumefaciens
55	d1wqla2	Alignment	not modelled	19.5	24	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Ring hydroxylating alpha subunit catalytic domain
56	d1r0va2	Alignment	not modelled	19.3	11	**Fold:**Restriction endonuclease-like **Superfamily:**tRNA-intron endonuclease catalytic domain-like **Family:**tRNA-intron endonuclease catalytic domain-like
57	c2k33A_	Alignment	not modelled	19.0	24	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**acra; **PDBTitle:** solution structure of an n-glycosylated protein using in2 vitro glycosylation
58	d2b1xa2	Alignment	not modelled	18.2	21	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Ring hydroxylating alpha subunit catalytic domain
59	d1onla_	Alignment	not modelled	18.0	34	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
60	c2gu1A_	Alignment	not modelled	16.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
61	c3fmcC_	Alignment	not modelled	15.9	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative succinylglutamate desuccinylase / aspartoacylase; **PDBTitle:** crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution
62	d2q07a1	Alignment	not modelled	15.6	21	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
63	d1ulia2	Alignment	not modelled	14.8	24	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Ring hydroxylating alpha subunit catalytic domain
64	d2bmoa2	Alignment	not modelled	14.7	16	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Ring hydroxylating alpha subunit catalytic domain
65	d1o7na2	Alignment	not modelled	14.5	16	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Ring hydroxylating alpha subunit catalytic domain
66	c3c6dB_	Alignment	not modelled	13.7	31	**PDB header:**virus **Chain:** B: **PDB Molecule:**polyprotein; **PDBTitle:** the pseudo-atomic structure of dengue immature virus
67	d2f5tx2	Alignment	not modelled	13.6	21	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**TrmB middle domain-like
68	c3lehA_	Alignment	not modelled	13.5	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative hydroxymethylglutaryl-coa synthase; **PDBTitle:** the crystal structure of smu.943c from streptococcus mutans ua159
69	c2f9aA_	Alignment	not modelled	12.9	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-hydroxy-3-methylglutaryl coenzyme a synthase 1; **PDBTitle:** hmg-coa synthase from brassica juncea in complex with f-244
70	d1miua3	Alignment	not modelled	12.5	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
71	c2lc0A_	Alignment	not modelled	12.4	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**putative uncharacterized protein tb39.8; **PDBTitle:** rv0020c_nter structure
72	d1s6na_	Alignment	not modelled	12.3	32	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
73	c3k3sG_	Alignment	not modelled	12.3	15	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**altronate hydrolase; **PDBTitle:** crystal structure of altronate hydrolase (fragment 1-84) from shigella2 flexneri.
74	c3csqC_	Alignment	not modelled	12.3	40	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**morphogenesis protein 1; **PDBTitle:** crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
75	c3uajA_	Alignment	not modelled	12.2	21	**PDB header:**viral protein/immune system **Chain:** A: **PDB Molecule:**envelope protein; **PDBTitle:** crystal structure of the envelope glycoprotein ectodomain from dengue2 virus serotype 4 in complex with the fab fragment of the chimpanzee3 monoclonal antibody 5h2
76	c3c64A_	Alignment	not modelled	12.0	25	**PDB header:**cd36-binding protein,cell adhesion **Chain:** A: **PDB Molecule:**pfemp1 variant 2 of strain mc; **PDBTitle:** the mc179 portion of the cysteine-rich interdomain region2 (cidr) of a plasmodium falciparum erythrocyte membrane3 protein-1 (pfemp1)
77	c2f1mA_	Alignment	not modelled	11.9	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein a; **PDBTitle:** conformational flexibility in the multidrug efflux system protein acra
78	c1x9eB_	Alignment	not modelled	11.5	35	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hmg-coa synthase;

78	c1x9eB_	Alignment	not modelled	11.5	33	**PDBTitle:** crystal structure of hmg-coa synthase from enterococcus2 faecalis
79	d2nqwa1	Alignment	not modelled	11.5	11	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
80	c1txtB_	Alignment	not modelled	11.5	40	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-hydroxy-3-methylglutaryl-coa synthase; **PDBTitle:** staphylococcus aureus 3-hydroxy-3-methylglutaryl-coa2 synthase
81	c2wusR_	Alignment	not modelled	11.3	18	**PDB header:**structural protein **Chain:** R: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** bacterial actin mreb assembles in complex with cell shape2 protein rodz
82	c3nyyA_	Alignment	not modelled	10.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycyl-glycine endopeptidase lytm; **PDBTitle:** crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus atcc 29149 at 1.60 a3 resolution
83	c2f5tX_	Alignment	not modelled	10.5	21	**PDB header:**transcription **Chain:** X: **PDB Molecule:**archaeal transcriptional regulator trmb; **PDBTitle:** crystal structure of the sugar binding domain of the archaeal2 transcriptional regulator trmb
84	d1ztxe1	Alignment	not modelled	10.5	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
85	c2p8uB_	Alignment	not modelled	10.0	43	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hydroxymethylglutaryl-coa synthase, cytoplasmic; **PDBTitle:** crystal structure of human 3-hydroxy-3-methylglutaryl coa synthase i
86	c3d4rE_	Alignment	not modelled	9.9	18	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**domain of unknown function from the pfam-b_34464 family; **PDBTitle:** crystal structure of a duf2118 family protein (mmp0046) from2 methanococcus maripaludis at 2.20 a resolution
87	c1orhA_	Alignment	not modelled	9.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arginine n-methyltransferase 1; **PDBTitle:** structure of the predominant protein arginine methyltransferase prmt1
88	c3e9uA_	Alignment	not modelled	9.1	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**na/ca exchange protein; **PDBTitle:** crystal structure of calx cbd2 domain
89	d2gtaa1	Alignment	not modelled	9.0	13	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
90	c3ddcB_	Alignment	not modelled	8.9	11	**PDB header:**hydrolase/apoptosis **Chain:** B: **PDB Molecule:**ras association domain-containing family protein 5; **PDBTitle:** crystal structure of nore1a in complex with ras
91	c3n6rK_	Alignment	not modelled	8.8	16	**PDB header:**ligase **Chain:** K: **PDB Molecule:**propionyl-coa carboxylase, alpha subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
92	d1iyjb3	Alignment	not modelled	8.6	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
93	c3fymA_	Alignment	not modelled	8.3	5	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the 1a structure of ymfm, a putative dna-binding membrane2 protein from staphylococcus aureus
94	c3llbA_	Alignment	not modelled	8.2	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of the protein pa3983 with unknown2 function from pseudomonas aeruginosa pao1
95	c1t5eB_	Alignment	not modelled	8.1	21	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**multidrug resistance protein mexa; **PDBTitle:** the structure of mexa
96	d1y7ma2	Alignment	not modelled	7.7	13	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
97	d3brda3	Alignment	not modelled	7.6	13	**Fold:**beta-Trefoil **Superfamily:**DNA-binding protein LAG-1 (CSL) **Family:**DNA-binding protein LAG-1 (CSL)
98	d2a9da1	Alignment	not modelled	7.4	28	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Molybdenum-containing oxidoreductases-like dimerisation domain
99	d2fx0a2	Alignment	not modelled	7.4	33	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain