Phyre^2

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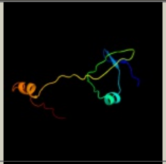
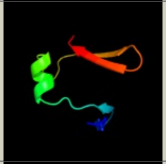
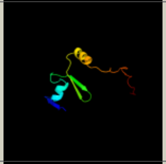
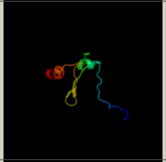
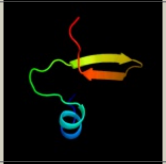
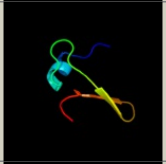
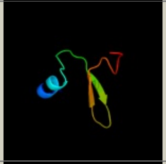
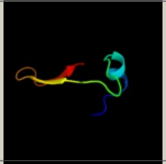
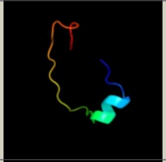
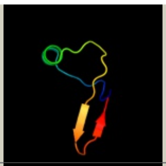
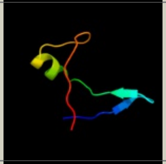
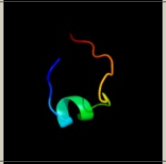
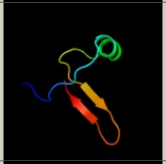
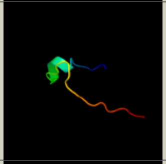
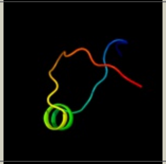
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ub4c_	Alignment		100.0	100	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/PemI addiction antidote
2	d1mvfd_	Alignment		99.7	100	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/PemI addiction antidote
3	c3zvkG_	Alignment		99.0	16	**PDB header:**antitoxin/toxin/dna **Chain:** G: **PDB Molecule:**antitoxin of toxin-antitoxin system vapb; **PDBTitle:** crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
4	c3tndF_	Alignment		98.4	29	**PDB header:**translation, toxin **Chain:** F: **PDB Molecule:**antitoxin vapb; **PDBTitle:** crystal structure of shigella flexneri vapbc toxin-antitoxin complex
5	d1yfba1	Alignment		97.0	28	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**AbrB N-terminal domain-like
6	d2fy9a1	Alignment		96.9	22	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**AbrB N-terminal domain-like
7	c2w1tB_	Alignment		96.5	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of b. subtilis spovt
8	c2l66B_	Alignment		96.2	24	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, abrb family; **PDBTitle:** the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
9	c2ro5B_	Alignment		95.7	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** rdc-refined solution structure of the n-terminal dna2 recognition domain of the bacillus subtilis transition-3 state regulator spovt
10	c3o27B_	Alignment		94.2	27	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the crystal structure of c68 from the hybrid virus-plasmid pssvx
11	c2glwA_	Alignment		93.3	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**92aa long hypothetical protein; **PDBTitle:** the solution structure of phs018 from pyrococcus horikoshii

12	c2pjhB_	Alignment		85.2	24	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** strctural model of the p97 n domain- npl4 ubd complex
13	d2d9ra1	Alignment		85.1	17	**Fold:**Double-split beta-barrel **Superfamily:**AF2212/PG0164-like **Family:**PG0164-like
14	c1cz5A_	Alignment		81.9	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**vcp-like atpase; **PDBTitle:** nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
15	d1cz5a1	Alignment		78.9	32	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
16	d2iv2x1	Alignment		69.1	16	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
17	d2jioa1	Alignment		63.7	13	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
18	d2vbua1	Alignment		62.0	28	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**CTP-dependent riboflavin kinase-like
19	d1e32a1	Alignment		62.0	22	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
20	d1h0ha1	Alignment		61.5	23	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
21	c1wlfA_	Alignment	not modelled	60.2	24	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**peroxisome biogenesis factor 1; **PDBTitle:** structure of the n-terminal domain of pex1 aaa-atpase:2 characterization of a putative adaptor-binding domain
22	d1vlfm1	Alignment	not modelled	57.8	16	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
23	d1g8ka1	Alignment	not modelled	57.5	13	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
24	c2iv2X_	Alignment	not modelled	57.4	16	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**formate dehydrogenase h; **PDBTitle:** reinterpretation of reduced form of formate dehydrogenase h2 from e. coli
25	d1ogya1	Alignment	not modelled	55.0	16	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
26	d1kqfa1	Alignment	not modelled	54.1	30	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
27	d1eu1a1	Alignment	not modelled	54.0	13	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
28	d1zq1a1	Alignment	not modelled	52.4	22	**Fold:**Sm-like fold **Superfamily:**GatD N-terminal domain-like **Family:**GatD N-terminal domain-like
						PDB header:oxidoreductase

29	c2ki8A_	Alignment	not modelled	52.1	26	**Chain:** A: **PDB Molecule:**tungsten formylmethanofuran dehydrogenase, **PDBTitle:** solution nmr structure of tungsten formylmethanofuran2 dehydrogenase subunit d from archaeoglobus fulgidus,3 northeast structural genomics consortium target att7
30	d1dmra1	Alignment	not modelled	52.0	13	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
31	d1tmoa1	Alignment	not modelled	51.8	23	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
32	d1y5ia1	Alignment	not modelled	45.1	18	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
33	c2v45A_	Alignment	not modelled	44.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic nitrate reductase; **PDBTitle:** a new catalytic mechanism of periplasmic nitrate reductase2 from desulfovibrio desulfuricans atcc 27774 from3 crystallographic and epr data and based on detailed4 analysis of the sixth ligand
34	c1g8jC_	Alignment	not modelled	42.6	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**arsenite oxidase; **PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
35	c3cf1C_	Alignment	not modelled	40.3	24	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97/vcp in complex with adp/adp.alfx
36	c1h9mB_	Alignment	not modelled	39.8	11	**PDB header:**binding protein **Chain:** B: **PDB Molecule:**molybdenum-binding-protein; **PDBTitle:** two crystal structures of the cytoplasmic molybdate-binding2 protein modg suggest a novel cooperative binding mechanism3 and provide insights into ligand-binding specificity.4 peg-grown form with molybdate bound
37	d3d31a1	Alignment	not modelled	38.0	12	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
38	c1vlfQ_	Alignment	not modelled	36.6	16	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**pyrogallol hydroxytransferase large subunit; **PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici complexed3 with inhibitor 1,2,4,5-tetrahydroxy-benzene
39	c2nyaF_	Alignment	not modelled	34.3	26	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**periplasmic nitrate reductase; **PDBTitle:** crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli
40	c2e7zA_	Alignment	not modelled	33.3	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**acetylene hydratase ahy; **PDBTitle:** acetylene hydratase from pelobacter acetylenicus
41	c1kqgA_	Alignment	not modelled	32.3	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, major subunit; **PDBTitle:** formate dehydrogenase n from e. coli
42	c2dxbR_	Alignment	not modelled	32.2	28	**PDB header:**hydrolase **Chain:** R: **PDB Molecule:**thiocyanate hydrolase subunit gamma; **PDBTitle:** recombinant thiocyanate hydrolase comprising partially-modified cobalt2 centers
43	c1tmoA_	Alignment	not modelled	31.4	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**trimethylamine n-oxide reductase; **PDBTitle:** trimethylamine n-oxide reductase from shewanella massilia
44	c3hu2C_	Alignment	not modelled	30.0	24	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97 n-d1 r86a mutant in complex with atpgs
45	c1eu1A_	Alignment	not modelled	29.5	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dimethyl sulfoxide reductase; **PDBTitle:** the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments.
46	d1ylea1	Alignment	not modelled	29.5	19	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**AstA-like
47	c1h5nC_	Alignment	not modelled	29.5	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dmso reductase; **PDBTitle:** dmso reductase modified by the presence of dms and air
48	d1v29a_	Alignment	not modelled	28.7	29	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
49	c1ogyA_	Alignment	not modelled	27.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic nitrate reductase; **PDBTitle:** crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides
50	c2k5hA_	Alignment	not modelled	27.9	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of protein encoded by mth693 from2 methanobacterium thermoautotrophicum: northeast structural3 genomics consortium target tt824a
51	d2d6fa1	Alignment	not modelled	27.7	11	**Fold:**Sm-like fold **Superfamily:**GatD N-terminal domain-like **Family:**GatD N-terminal domain-like
52	c1s3sA_	Alignment	not modelled	27.3	24	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**transitional endoplasmic reticulum atpase (ter **PDBTitle:** crystal structure of aaa atpase p97/vcp nd1 in complex

						with2 p47 c
53	c1h0hA_	Alignment	not modelled	27.2	21	**PDB header:**dehydrogenase **Chain:** A: **PDB Molecule:**formate dehydrogenase (large subunit); **PDBTitle:** tungsten containing formate dehydrogenase from2 desulfovibrio gigas
54	c1y5iA_	Alignment	not modelled	24.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**respiratory nitrate reductase 1 alpha chain; **PDBTitle:** the crystal structure of the narghi mutant nari-k86a
55	d1wlfa2	Alignment	not modelled	24.3	18	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
56	c2he4A_	Alignment	not modelled	23.8	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**na(+)/h(+) exchange regulatory cofactor nhe-rf2; **PDBTitle:** the crystal structure of the second pdz domain of human2 nherf-2 (slc9a3r2) interacting with a mode 1 pdz binding3 motif
57	c3qyhG_	Alignment	not modelled	22.9	20	**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.
58	d2i6va1	Alignment	not modelled	22.6	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
59	d1h9ma1	Alignment	not modelled	21.6	17	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
60	c3qglD_	Alignment	not modelled	21.6	10	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**sorting nexin-27; **PDBTitle:** crystal structure of pdz domain of sorting nexin 27 (snx27) in complex2 with the eseskv peptide corresponding to the c-terminal tail of girk3
61	c2fugC_	Alignment	not modelled	21.3	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-quinone oxidoreductase chain 3; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
62	d1fr3a_	Alignment	not modelled	20.5	16	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**Molybdate/tungstate binding protein MOP
63	c2qt7B_	Alignment	not modelled	20.2	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**receptor-type tyrosine-protein phosphatase-like **PDBTitle:** crystallographic structure of the mature ectodomain of the2 human receptor-type protein-tyrosine phosphatase ia-2 at3 1.30 angstroms
64	d1h9ma2	Alignment	not modelled	20.2	11	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
65	d2qdya1	Alignment	not modelled	19.7	21	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
66	d2i4sa1	Alignment	not modelled	19.0	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
67	c2ivfA_	Alignment	not modelled	18.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ethylbenzene dehydrogenase alpha-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
68	c3idwA_	Alignment	not modelled	18.5	27	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**actin cytoskeleton-regulatory complex protein sla1; **PDBTitle:** crystal structure of sla1 homology domain 2
69	c3d31B_	Alignment	not modelled	16.8	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**sulfate/molybdate abc transporter, atp-binding **PDBTitle:** modbc from methanosarcina acetivorans
70	d1iz6a2	Alignment	not modelled	15.9	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
71	d1guta_	Alignment	not modelled	15.6	17	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**Molybdate/tungstate binding protein MOP
72	c1uheA_	Alignment	not modelled	14.8	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aspartate 1-decarboxylase alpha chain; **PDBTitle:** crystal structure of aspartate decarboxylase, isoaspargine complex
73	d1h9ra1	Alignment	not modelled	14.4	31	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
74	c3mhxB_	Alignment	not modelled	14.4	17	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**putative ferrous iron transport protein a; **PDBTitle:** crystal structure of stenotrophomonas maltophilia feoa complexed with2 zinc: a unique procaryotic sh3 domain protein possibly acting as a3 bacterial ferrous iron transport activating factor
75	c2k5lA_	Alignment	not modelled	14.3	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**feoa; **PDBTitle:** solution nmr structure of protein feoa from clostridium2 thermocellum, northeast structural genomics consortium3 target cmr17
76	c2vpyE_	Alignment	not modelled	14.0	26	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**thiosulfate reductase; **PDBTitle:** polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
						Fold:OB-fold

77	d1a62a2	Alignment	not modelled	14.0	15	**Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
78	d1yela1	Alignment	not modelled	13.4	17	**Fold:**DNA-binding pseudobarrel domain **Superfamily:**DNA-binding pseudobarrel domain **Family:**B3 DNA binding domain
79	c2bkdN_	Alignment	not modelled	13.2	33	**PDB header:**nuclear protein **Chain:** N: **PDB Molecule:**fragile x mental retardation 1 protein; **PDBTitle:** structure of the n-terminal domain of fragile x mental2 retardation protein
80	c2jxoA_	Alignment	not modelled	13.1	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ezrin-radixin-moesin-binding phosphoprotein 50; **PDBTitle:** structure of the second pdz domain of nherf-1
81	c2jilA_	Alignment	not modelled	12.8	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glutamate receptor interacting protein-1; **PDBTitle:** crystal structure of 2nd pdz domain of glutamate receptor2 interacting protein-1 (grip1)
82	d1qw1a1	Alignment	not modelled	12.5	23	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
83	d1x5qa1	Alignment	not modelled	12.4	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
84	c3plxB_	Alignment	not modelled	12.0	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** the crystal structure of aspartate alpha-decarboxylase from2 campylobacter jejuni subsp. jejuni nctc 11168
85	c3pjyB_	Alignment	not modelled	11.8	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**hypothetical signal peptide protein; **PDBTitle:** crystal structure of a putative transcription regulator (r01717) from2 sinorhizobium meliloti 1021 at 1.55 a resolution
86	d1udxa3	Alignment	not modelled	11.8	25	**Fold:**Obg GTP-binding protein C-terminal domain **Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain
87	c1vc3B_	Alignment	not modelled	11.3	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**l-aspartate-alpha-decarboxylase heavy chain; **PDBTitle:** crystal structure of l-aspartate-alpha-decarboxylase
88	d2byga1	Alignment	not modelled	11.3	25	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
89	c1zeqX_	Alignment	not modelled	11.0	12	**PDB header:**metal binding protein **Chain:** X: **PDB Molecule:**cation efflux system protein cusf; **PDBTitle:** 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
90	d1zoka1	Alignment	not modelled	10.9	29	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
91	c2kl0A_	Alignment	not modelled	10.9	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thiamin biosynthesis this; **PDBTitle:** solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
92	c1zc1A_	Alignment	not modelled	10.9	21	**PDB header:**protein turnover **Chain:** A: **PDB Molecule:**ubiquitin fusion degradation protein 1; **PDBTitle:** ufd1 exhibits the aaa-atpase fold with two distinct2 ubiquitin interaction sites
93	d1d5ga_	Alignment	not modelled	10.9	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
94	c2c45F_	Alignment	not modelled	10.9	32	**PDB header:**lyase **Chain:** F: **PDB Molecule:**aspartate 1-decarboxylase precursor; **PDBTitle:** native precursor of pyruvoyl dependent aspartate2 decarboxylase
95	c1qw1A_	Alignment	not modelled	10.8	23	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** solution structure of the c-terminal domain of dtxr2 residues 110-226
96	d1qvpa_	Alignment	not modelled	10.7	21	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
97	c1pt1B_	Alignment	not modelled	10.0	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine
98	d2gkpa1	Alignment	not modelled	10.0	42	**Fold:**NMB0488-like **Superfamily:**NMB0488-like **Family:**NMB0488-like
99	c3ougA_	Alignment	not modelled	9.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** crystal structure of cleaved l-aspartate-alpha-decarboxylase from2 francisella tularensis