Phyre^2

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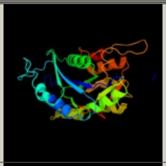
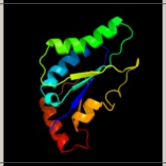
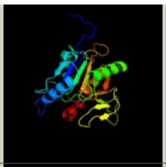
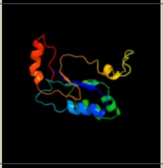
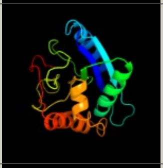
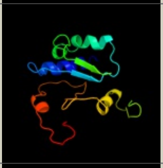
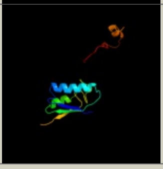
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2z86D_	Alignment		99.7	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**chondroitin synthase; **PDBTitle:** crystal structure of chondroitin polymerase from2 escherichia coli strain k4 (k4cp) complexed with udp-glcua3 and udp
2	c3f1yC_	Alignment		99.7	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
3	c1xhbA_	Alignment		99.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 1; **PDBTitle:** the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
4	c2ffuA_	Alignment		99.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 2; **PDBTitle:** crystal structure of human ppgalnact-2 complexed with udp2 and ea2
5	c3ckvA_	Alignment		99.6	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a mycobacterial protein
6	c2d7iA_	Alignment		99.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 10; **PDBTitle:** crsytal structure of pp-galnac-t10 with udp, galnac and mn2+
7	d1xhba2	Alignment		99.5	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
8	c3bcvA_	Alignment		99.5	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative glycosyltransferase protein; **PDBTitle:** crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
9	d1qg8a_	Alignment		99.4	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Spore coat polysaccharide biosynthesis protein SpsA
10	c1omxB_	Alignment		99.1	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**alpha-1,4-n-acetylhexosaminyltransferase extl2; **PDBTitle:** crystal structure of mouse alpha-1,4-n-2 acetylhexosaminyltransferase (extl2)
11	d1omza_	Alignment		99.1	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Exostosin

12	c2qgiA_	Alignment		98.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp synthase subunits region orf 6; **PDBTitle:** the udp complex structure of the sixth gene product of the f1-atpase2 operon of rhodobacter blasticus
13	d2bo4a1	Alignment		98.2	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**MGS-like
14	d1fo8a_	Alignment		96.8	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**N-acetylglucosaminyltransferase I
15	c2wvmA_	Alignment		96.3	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** h309a mutant of mannosyl-3-phosphoglycerate synthase from2 thermus thermophilus hb27 in complex with3 gdp-alpha-d-mannose and mg(ii)
16	c2zu8A_	Alignment		95.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
17	d1pzta_	Alignment		95.7	18	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**beta 1,4 galactosyltransferase (b4GalT1)
18	d1ga8a_	Alignment		89.1	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Galactosyltransferase LgtC
19	c1ga8A_	Alignment		89.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**galactosyl transferase lgtc; **PDBTitle:** crystal structure of galacosyltransferase lgtc in complex2 with donor and acceptor sugar analogs.
20	c3tztB_	Alignment		83.4	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase family 8; **PDBTitle:** the structure of a protein in glycosyl transferase family 8 from2 anaerococcus prevotii.
21	d1vh3a_	Alignment	not modelled	76.5	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
22	c3ednB_	Alignment	not modelled	70.4	24	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**phenazine biosynthesis protein, phzf family; **PDBTitle:** crystal structure of the bacillus anthracis phenazine2 biosynthesis protein, phzf family
23	c1u0kA_	Alignment	not modelled	67.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**gene product pa4716; **PDBTitle:** the structure of a predicted epimerase pa4716 from pseudomonas2 aeruginosa
24	c3lw6A_	Alignment	not modelled	65.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-4-galactosyltransferase 7; **PDBTitle:** crystal structure of drosophila beta1,4-galactosyltransferase-7
25	d1eyra_	Alignment	not modelled	58.4	19	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
26	d1i52a_	Alignment	not modelled	57.0	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
27	d1ll2a_	Alignment	not modelled	55.5	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Glycogenin
28	d1qy9a1	Alignment	not modelled	54.9	21	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like

29	d1w77a1	Alignment	not modelled	54.1	8	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
30	d1vgwa_	Alignment	not modelled	52.8	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
31	c1u1wA_	Alignment	not modelled	52.4	19	**PDB header:**isomerase, lyase **Chain:** A: **PDB Molecule:**phenazine biosynthesis protein phzf; **PDBTitle:** structure and function of phenazine-biosynthesis protein phzf from2 pseudomonas fluorescens 2-79
32	c1zcyA_	Alignment	not modelled	52.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogenin-1; **PDBTitle:** apo form of a mutant of glycogenin in which asp159 is replaced by ser
33	d1s7ja_	Alignment	not modelled	49.5	14	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
34	c1qy9B_	Alignment	not modelled	45.2	21	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ydde; **PDBTitle:** crystal structure of e. coli se-met protein ydde
35	d1a79a2	Alignment	not modelled	44.8	35	**Fold:**MutS N-terminal domain-like **Superfamily:**tRNA-intron endonuclease N-terminal domain-like **Family:**tRNA-intron endonuclease N-terminal domain-like
36	c2wawA_	Alignment	not modelled	36.4	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**moba relate protein; **PDBTitle:** crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
37	c2gkjA_	Alignment	not modelled	32.8	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**diaminopimelate epimerase; **PDBTitle:** crystal structure of diaminopimelate epimerase in complex2 with an irreversible inhibitor dl-azidap
38	c3okrA_	Alignment	not modelled	28.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
39	d1x4pa1	Alignment	not modelled	25.4	36	**Fold:**Surp module (SWAP domain) **Superfamily:**Surp module (SWAP domain) **Family:**Surp module (SWAP domain)
40	c1zctB_	Alignment	not modelled	23.9	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycogenin-1; **PDBTitle:** structure of glycogenin truncated at residue 270 in a2 complex with udp
41	c3d5nB_	Alignment	not modelled	21.1	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**q97w15_sulso; **PDBTitle:** crystal structure of the q97w15_sulso protein from2 sulfolobus solfataricus. nesg target ssr125.
42	c1ym5A_	Alignment	not modelled	18.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical 32.6 kda protein in dap2-slt2 **PDBTitle:** crystal structure of yhi9, the yeast member of the2 phenazine biosynthesis phzf enzyme superfamily.
43	d1xkpc1	Alignment	not modelled	16.8	36	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone
44	c2px7A_	Alignment	not modelled	16.1	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate **PDBTitle:** crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase from thermus thermophilus hb8
45	c2vshB_	Alignment	not modelled	16.0	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate **PDBTitle:** synthesis of cdp-activated ribitol for teichoic acid2 precursors in streptococcus pneumoniae
46	d1vyva2	Alignment	not modelled	14.7	39	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
47	d1k3ra2	Alignment	not modelled	14.6	12	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**Hypothetical protein MTH1 (MT0001), dimerisation domain
48	d1vyua2	Alignment	not modelled	14.4	39	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
49	d1uxoa_	Alignment	not modelled	13.7	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**YdeN-like
50	d1t0hb_	Alignment	not modelled	13.7	39	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
51	d1vpaa_	Alignment	not modelled	13.6	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
52	d1t3la2	Alignment	not modelled	13.4	39	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
53	c2rauA_	Alignment	not modelled	13.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative esterase; **PDBTitle:** crystal structure of a putative lipase (np_343859.1) from sulfolobus2 solfataricus at 1.85 a resolution
54	c1sneB_	Alignment	not modelled	13.3	53	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**tetrameric beta-beta-alpha mini-protein; **PDBTitle:** an oligomeric domain-swapped beta-beta-alpha mini-protein

55	c1sneA_	Alignment	not modelled	13.3	53	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**tetrameric beta-beta-alpha mini-protein; **PDBTitle:** an oligomeric domain-swapped beta-beta-alpha mini-protein
56	c1k3rA_	Alignment	not modelled	13.3	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein mt0001; **PDBTitle:** crystal structure of the methyltransferase with a knot from2 methanobacterium thermoautotrophicum
57	c3okrC_	Alignment	not modelled	13.1	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
58	c2o35A_	Alignment	not modelled	12.7	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein duf1244; **PDBTitle:** protein of unknown function (duf1244) from sinorhizobium meliloti
59	d2o35a1	Alignment	not modelled	12.7	21	**Fold:**SMc04008-like **Superfamily:**SMc04008-like **Family:**SMc04008-like
60	c2qkwA_	Alignment	not modelled	12.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**avirulence protein; **PDBTitle:** structural basis for activation of plant immunity by2 bacterial effector protein avrpto
61	d2qkwa1	Alignment	not modelled	12.7	12	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Avirulence protein AvrPto **Family:**Avirulence protein AvrPto
62	d1inla_	Alignment	not modelled	12.3	8	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Spermidine synthase
63	c1cn3F_	Alignment	not modelled	12.3	33	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**fragment of coat protein vp2; **PDBTitle:** interaction of polyomavirus internal protein vp2 with major2 capsid protein vp1 and implications for participation of3 vp2 in viral entry
64	c2zviB_	Alignment	not modelled	12.2	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-diketo-5-methylthiopentyl-1-phosphate **PDBTitle:** crystal structure of 2,3-diketo-5-methylthiopentyl-1-2 phosphate enolase from bacillus subtilis
65	c1okgA_	Alignment	not modelled	11.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible 3-mercaptopyruvate sulfurtransferase; **PDBTitle:** 3-mercaptopyruvate sulfurtransferase from leishmania major
66	c1qz7B_	Alignment	not modelled	11.5	43	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**axin; **PDBTitle:** beta-catenin binding domain of axin in complex with beta-2 catenin
67	d1pvma3	Alignment	not modelled	11.3	29	**Fold:**Rubredoxin-like **Superfamily:**Hypothetical protein Ta0289 C-terminal domain **Family:**Hypothetical protein Ta0289 C-terminal domain
68	c3fybA_	Alignment	not modelled	11.3	21	**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
69	c3rjoA_	Alignment	not modelled	11.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum aminopeptidase 1; **PDBTitle:** crystal structure of erap1 peptide binding domain
70	c3bwbA_	Alignment	not modelled	10.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**spermidine synthase; **PDBTitle:** crystal structure of the apo form of spermidine synthase from2 trypanosoma cruzi at 2.5 a resolution
71	c2vxhF_	Alignment	not modelled	10.9	14	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**chlorite dismutase; **PDBTitle:** the crystal structure of chlorite dismutase: a detox enzyme2 producing molecular oxygen
72	c2qjwA_	Alignment	not modelled	10.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein xcc1541; **PDBTitle:** crystal structure of a putative hydrolase of the alpha/beta2 superfamily (xcc1541) from xanthomonas campestris pv. campestris at3 1.35 a resolution
73	d1omha_	Alignment	not modelled	10.6	7	**Fold:**Origin of replication-binding domain, RBD-like **Superfamily:**Origin of replication-binding domain, RBD-like **Family:**Relaxase domain
74	c1vbkA_	Alignment	not modelled	10.3	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1313; **PDBTitle:** crystal structure of ph1313 from pyrococcus horikoshii ot3
75	c1jb0X_	Alignment	not modelled	10.3	26	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem i subunit psax; **PDBTitle:** crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
76	d1jb0x_	Alignment	not modelled	10.3	26	**Fold:**Single transmembrane helix **Superfamily:**Subunit PsaX of photosystem I reaction centre **Family:**Subunit PsaX of photosystem I reaction centre
77	d2qqra1	Alignment	not modelled	10.3	27	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
78	d1a2za_	Alignment	not modelled	10.2	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) **Family:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
79	d2pbla1	Alignment	not modelled	9.8	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases

						Family: Carboxylesterase
80	c2j0bA_	Alignment	not modelled	9.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-1,3-n-acetylglucosaminyltransferase manic fringe; **PDBTitle:** structure of the catalytic domain of mouse manic fringe in2 complex with udp and manganese
81	d1f2si_	Alignment	not modelled	9.7	36	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Plant inhibitors of proteinases and amylases **Family:**Plant inhibitors of proteinases and amylases
82	c1f2sI_	Alignment	not modelled	9.7	36	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** I: **PDB Molecule:**trypsin inhibitor a; **PDBTitle:** crystal structure of the complex formed between bovine beta-2 trypsin and mcti-a, a trypsin inhibitor of squash family3 at 1.8 a resolution
83	c3tqdA_	Alignment	not modelled	9.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** structure of the 3-deoxy-d-manno-octulosonate cytidylyltransferase2 (kdsb) from coxiella burnetii
84	c3nn4C_	Alignment	not modelled	9.6	11	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**chlorite dismutase; **PDBTitle:** structure of chlorite dismutase from candidatus nitrospira defluvii2 r173k mutant
85	c3orjA_	Alignment	not modelled	9.6	17	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sugar-binding protein; **PDBTitle:** crystal structure of a sugar-binding protein (bacova_04391) from2 bacteroides ovatus at 2.16 a resolution
86	c3k6gA_	Alignment	not modelled	9.6	23	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**telomeric repeat-binding factor 2-interacting protein 1; **PDBTitle:** crystal structure of rap1 and trf2 complex
87	d1uoya_	Alignment	not modelled	9.3	45	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Bubble protein **Family:**Bubble protein
88	d1t0tv_	Alignment	not modelled	9.3	21	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Chlorite dismutase-like
89	c3l3bA_	Alignment	not modelled	9.2	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**es1 family protein; **PDBTitle:** crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
90	c3dnmA_	Alignment	not modelled	9.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase/lipase; **PDBTitle:** crystal structure hormone-sensitive lipase from a2 metagenome library
91	d1c2ya_	Alignment	not modelled	9.1	21	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
92	c2jobA_	Alignment	not modelled	9.1	21	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**antilipopolysaccharide factor; **PDBTitle:** solution structure of an antilipopolysaccharide factor from2 shrimp and its possible lipid a binding site
93	c2otnB_	Alignment	not modelled	9.0	25	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**diaminopimelate epimerase; **PDBTitle:** crystal structure of the catalytically active form of diaminopimelate2 epimerase from bacillus anthracis
94	d1nxia_	Alignment	not modelled	9.0	42	**Fold:**Ferredoxin-like **Superfamily:**Hypothetical protein VC0424 **Family:**Hypothetical protein VC0424
95	c2qh5B_	Alignment	not modelled	9.0	5	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**mannose-6-phosphate isomerase; **PDBTitle:** crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
96	d1ecfa1	Alignment	not modelled	9.0	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
97	d1q0ra_	Alignment	not modelled	8.9	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Aclacinomycin methylesterase RdmC
98	c3pcqX_	Alignment	not modelled	8.9	26	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem i 4.8k protein; **PDBTitle:** femtosecond x-ray protein nanocrystallography
99	c3giuA_	Alignment	not modelled	8.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pyrrolidone-carboxylate peptidase; **PDBTitle:** 1.25 angstrom crystal structure of pyrrolidone-carboxylate peptidase2 (pcp) from staphylococcus aureus