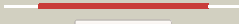



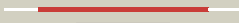



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0574c_(- )_667255_668397
Date	Fri Jul 26 01:50:13 BST 2019
Unique Job ID	f41fa8ca24bf1ba4

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1t70a_</a>	 Alignment		100.0	17	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> DR1281-like
2	<a href="#">d1t71a_</a>	 Alignment		100.0	18	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> DR1281-like
3	<a href="#">c4b2oB_</a>	 Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ymdb phosphodiesterase; <b>PDBTitle:</b> crystal structure of bacillus subtilis ymdb, a global2 regulator of late adaptive responses.
4	<a href="#">d2z06a1</a>	 Alignment		99.9	26	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> TTHA0625-like
5	<a href="#">d1usha2</a>	 Alignment		99.8	15	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
6	<a href="#">d2z1aa2</a>	 Alignment		99.8	18	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
7	<a href="#">c3jyfB_</a>	 Alignment		99.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 2',3'-cyclic nucleotide 2'-phosphodiesterase/3'- <b>PDBTitle:</b> the crystal structure of a 2,3-cyclic nucleotide 2-2 phosphodiesterase/3-nucleotidase bifunctional periplasmic precursor3 protein from klebsiella pneumoniae subsp. pneumoniae mgh 78578
8	<a href="#">c3ivdA_</a>	 Alignment		99.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotidase; <b>PDBTitle:</b> putative 5'-nucleotidase (c4898) from escherichia coli in complex with2 uridine
9	<a href="#">c1oidA_</a>	 Alignment		99.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein usha; <b>PDBTitle:</b> 5'-nucleotidase (e. coli) with an engineered disulfide2 bridge (s228c, p513c)
10	<a href="#">c3gveB_</a>	 Alignment		99.7	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> yfkn protein; <b>PDBTitle:</b> crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis
11	<a href="#">c3qfkA_</a>	 Alignment		99.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> 2.05 angstrom crystal structure of putative 5'-nucleotidase from2 staphylococcus aureus in complex with alpha-ketoglutarate

12	<a href="#">c2z1aA_</a>	Alignment		99.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 5'-nucleotidase; <b>PDBTitle:</b> crystal structure of 5'-nucleotidase precursor from thermus2 thermophilus hb8
13	<a href="#">c2wdfA_</a>	Alignment		99.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfur oxidation protein soxb; <b>PDBTitle:</b> termus thermophilus sulfate thiohydrolase soxb
14	<a href="#">c3zu0A_</a>	Alignment		99.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nad nucleotidase; <b>PDBTitle:</b> structure of haemophilus influenzae nad nucleotidase (nadm)
15	<a href="#">c4h1sB_</a>	Alignment		99.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 5'-nucleotidase; <b>PDBTitle:</b> crystal structure of a truncated soluble form of human cd73 with ecto-2 5'-nucleotidase activity
16	<a href="#">c5h7wB_</a>	Alignment		99.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> venom 5'-nucleotidase; <b>PDBTitle:</b> crystal structure of 5'-nucleotidase from venom of naja atra
17	<a href="#">c3c9fB_</a>	Alignment		99.2	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 5'-nucleotidase; <b>PDBTitle:</b> crystal structure of 5'-nucleotidase from candida albicans sc5314
18	<a href="#">d3c9fa2</a>	Alignment		99.2	12	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
19	<a href="#">c2q8uA_</a>	Alignment		97.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exonuclease, putative; <b>PDBTitle:</b> crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at 2.20 a resolution
20	<a href="#">c3qg5D_</a>	Alignment		97.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> mre11; <b>PDBTitle:</b> the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
21	<a href="#">c4ltyD_</a>	Alignment	not modelled	97.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> exonuclease subunit sbcd; <b>PDBTitle:</b> crystal structure of e.coli sbcd at 1.8 a resolution
22	<a href="#">c4ykeA_</a>	Alignment	not modelled	97.2	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mre11; <b>PDBTitle:</b> crystal structure of eukaryotic mre11 catalytic domain from chaetomium2 thermophilum
23	<a href="#">d1ii7a_</a>	Alignment	not modelled	96.9	14	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> DNA double-strand break repair nuclease
24	<a href="#">c3av0A_</a>	Alignment	not modelled	96.8	16	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna double-strand break repair protein mre11; <b>PDBTitle:</b> crystal structure of mre11-rad50 bound to atp s
25	<a href="#">c3tl1C_</a>	Alignment	not modelled	96.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> double-strand break repair protein mre11a; <b>PDBTitle:</b> crystal structure of human mre11: understanding tumorigenic mutations
26	<a href="#">c4fbkB_</a>	Alignment	not modelled	96.5	20	<b>PDB header:</b> hydrolase, protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> dna repair and telomere maintenance protein nbs1,dna repair <b>PDBTitle:</b> crystal structure of a covalently fused nbs1-mre11 complex with one2 manganese ion per active site
27	<a href="#">c3auzA_</a>	Alignment	not modelled	96.1	16	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna double-strand break repair protein mre11; <b>PDBTitle:</b> crystal structure of mre11 with manganese
28	<a href="#">c2ejcA_</a>	Alignment	not modelled	95.7	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pantoate--beta-alanine ligase; <b>PDBTitle:</b> crystal structure of pantoate--beta-alanine ligase (panc)2

						from thermotoga maritima
29	<a href="#">c2xmoB_</a>	Alignment	not modelled	95.6	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lmo2642 protein; <b>PDBTitle:</b> the crystal structure of lmo2642
30	<a href="#">c4fcxB_</a>	Alignment	not modelled	95.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dna repair protein rad32; <b>PDBTitle:</b> s.pombe mre11 apoenzym
31	<a href="#">c3tghA_</a>	Alignment	not modelled	95.0	21	<b>PDB header:</b> cell invasion <b>Chain:</b> A: <b>PDB Molecule:</b> glideosome-associated protein 50; <b>PDBTitle:</b> gap50 the anchor in the inner membrane complex of plasmodium
32	<a href="#">c3qfNA_</a>	Alignment	not modelled	94.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
33	<a href="#">d1v8fa_</a>	Alignment	not modelled	94.5	23	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
34	<a href="#">c3n8hA_</a>	Alignment	not modelled	94.4	12	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> crystal structure of pantoate-beta-alanine ligase from francisella2 tularensis
35	<a href="#">c3l23A_</a>	Alignment	not modelled	94.3	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> sugar phosphate isomerase/epimerase; <b>PDBTitle:</b> crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution
36	<a href="#">d1ihoA_</a>	Alignment	not modelled	94.1	18	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
37	<a href="#">c1xzwB_</a>	Alignment	not modelled	94.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> purple acid phosphatase; <b>PDBTitle:</b> sweet potato purple acid phosphatase/phosphate complex
38	<a href="#">c3zk4A_</a>	Alignment	not modelled	93.9	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> diphosphonucleotide phosphatase 1; <b>PDBTitle:</b> structure of purple acid phosphatase ppd1 isolated from2 yellow lupin (lupinus luteus) seeds
39	<a href="#">d2qfra2</a>	Alignment	not modelled	93.9	16	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> Purple acid phosphatase-like
40	<a href="#">c2hk1D_</a>	Alignment	not modelled	93.8	15	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> d-psicose 3-epimerase; <b>PDBTitle:</b> crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose
41	<a href="#">c1kbpB_</a>	Alignment	not modelled	93.6	13	<b>PDB header:</b> hydrolase (phosphoric monoester) <b>Chain:</b> B: <b>PDB Molecule:</b> purple acid phosphatase; <b>PDBTitle:</b> kidney bean purple acid phosphatase
42	<a href="#">c3ib7A_</a>	Alignment	not modelled	93.4	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> icc protein; <b>PDBTitle:</b> crystal structure of full length rv0805
43	<a href="#">c3ag5A_</a>	Alignment	not modelled	93.0	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> crystal structure of pantothenate synthetase from staphylococcus2 aureus
44	<a href="#">c3uk2B_</a>	Alignment	not modelled	92.5	9	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> the structure of pantothenate synthetase from burkholderia2 thailandensis
45	<a href="#">d1xwa2</a>	Alignment	not modelled	91.8	15	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> Purple acid phosphatase-like
46	<a href="#">c2ou4C_</a>	Alignment	not modelled	91.2	9	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> d-tagatose 3-epimerase; <b>PDBTitle:</b> crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
47	<a href="#">d1uf3a_</a>	Alignment	not modelled	91.0	13	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> TT1561-like
48	<a href="#">d1rpxa_</a>	Alignment	not modelled	90.4	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
49	<a href="#">c3innB_</a>	Alignment	not modelled	90.0	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> crystal structure of pantoate-beta-alanine-ligase in complex2 with atp at low occupancy at 2.1 a resolution
50	<a href="#">d2a84a1</a>	Alignment	not modelled	90.0	26	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
51	<a href="#">c3mxtA_</a>	Alignment	not modelled	89.7	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> crystal structure of pantoate-beta-alanine ligase from campylobacter2 jejuni
52	<a href="#">d2yvta1</a>	Alignment	not modelled	89.3	9	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> TT1561-like
53	<a href="#">d1gqna_</a>	Alignment	not modelled	89.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
54	<a href="#">c5y0tD_</a>	Alignment	not modelled	88.2	20	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> thermotoga maritima tmcal; <b>PDBTitle:</b> crystal structure of thermotoga maritima tmcal bound

						with alpha-thio2 atp(form ii)
55	<a href="#">c5y0nB_</a>	Alignment	not modelled	87.9	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> upf0348 protein b4417_3650; <b>PDBTitle:</b> crystal structure of bacillus subtilis tmcal bound with atp (semet2 derivative)
56	<a href="#">c3rmjB_</a>	Alignment	not modelled	87.7	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
57	<a href="#">c3vniC_</a>	Alignment	not modelled	85.4	13	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> xylose isomerase domain protein tim barrel; <b>PDBTitle:</b> crystal structures of d-psicose 3-epimerase from clostridium2 cellulolyticum h10 and its complex with ketohexose sugars
58	<a href="#">c2yr1B_</a>	Alignment	not modelled	85.3	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-dehydroquinatase dehydratase; <b>PDBTitle:</b> crystal structure of 3-dehydroquinatase dehydratase from geobacillus2 kaustophilus hta426
59	<a href="#">c3guzB_</a>	Alignment	not modelled	84.6	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> structural and substrate-binding studies of pantothenate2 synthenate (ps)provide insights into homotropic inhibition3 by pantoate in ps's
60	<a href="#">c5kwvA_</a>	Alignment	not modelled	84.6	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> crystal structure of a pantoate-beta-alanine ligase from neisseria2 gonorrhoeae with bound amppnp
61	<a href="#">c4utwB_</a>	Alignment	not modelled	84.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative n-acetylmannosamine-6-phosphate 2-epimerase; <b>PDBTitle:</b> structural characterisation of nane, mannac6p c2 epimerase,2 from clostridium perfringens
62	<a href="#">d1sfla_</a>	Alignment	not modelled	83.9	9	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
63	<a href="#">c5xceB_</a>	Alignment	not modelled	83.7	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 29; <b>PDBTitle:</b> crystal structure of wild type vps29 from entamoeba histolytica
64	<a href="#">c3l2iB_</a>	Alignment	not modelled	83.6	23	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-dehydroquinatase dehydratase; <b>PDBTitle:</b> 1.85 angstrom crystal structure of the 3-dehydroquinatase dehydratase2 (arod) from salmonella typhimurium lt2.
65	<a href="#">c3dx5A_</a>	Alignment	not modelled	83.6	6	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein asbf; <b>PDBTitle:</b> crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
66	<a href="#">c4madA_</a>	Alignment	not modelled	83.2	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of beta-galactosidase c (bgac) from bacillus2 circulans atcc 31382
67	<a href="#">c4ovxA_</a>	Alignment	not modelled	82.3	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> xylose isomerase domain protein tim barrel; <b>PDBTitle:</b> crystal structure of xylose isomerase domain protein from planctomyces2 limnophilus dsm 3776
68	<a href="#">c3wqoB_</a>	Alignment	not modelled	82.1	5	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein mj1311; <b>PDBTitle:</b> crystal structure of d-tagatose 3-epimerase-like protein
69	<a href="#">d1z2wa1</a>	Alignment	not modelled	82.0	15	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> YfcE-like
70	<a href="#">c3ewbX_</a>	Alignment	not modelled	81.7	9	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of n-terminal domain of putative 2-isopropylmalate2 synthase from listeria monocytogenes
71	<a href="#">c5tenH_</a>	Alignment	not modelled	81.2	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> structure of 4-hydroxy-tetrahydrodipicolinate reductase from vibrio2 vulnificus with 2,5 furan dicarboxylic and nadh with intact3 polyhistidine tag
72	<a href="#">c4ph6A_</a>	Alignment	not modelled	80.7	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinatase dehydratase; <b>PDBTitle:</b> structure of 3-dehydroquinatase dehydratase from enterococcus faecalis
73	<a href="#">c5n2pA_</a>	Alignment	not modelled	80.4	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> sulfolobus solfataricus tryptophan synthase a
74	<a href="#">c3js3C_</a>	Alignment	not modelled	79.6	16	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-dehydroquinatase dehydratase; <b>PDBTitle:</b> crystal structure of type i 3-dehydroquinatase dehydratase (arod) from2 clostridium difficile with covalent reaction intermediate
75	<a href="#">c3gmiA_</a>	Alignment	not modelled	79.1	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0348 protein mj0951; <b>PDBTitle:</b> crystal structure of a protein of unknown function from2 methanocaldococcus jannaschii
76	<a href="#">d3ck2a1</a>	Alignment	not modelled	77.9	11	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> YfcE-like
77	<a href="#">c5hmqE_</a>	Alignment	not modelled	77.6	16	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> 4-hydroxyphenylpyruvate dioxygenase; <b>PDBTitle:</b> xylose isomerase-like tim barrel/4-hydroxyphenylpyruvate dioxygenase2 fusion protein
78	<a href="#">c2nydB_</a>	Alignment	not modelled	76.5	11	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> upf0135 protein sa1388; <b>PDBTitle:</b> crystal structure of staphylococcus aureus hypothetical

						protein sa1388
79	<a href="#">c2gx8B_</a>	Alignment	not modelled	76.4	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> nif3-related protein; <b>PDBTitle:</b> the crystal structure of bacillus cereus protein related to nif3
80	<a href="#">d2gx8a1</a>	Alignment	not modelled	76.2	15	<b>Fold:</b> NIF3 (NGG1p interacting factor 3)-like <b>Superfamily:</b> NIF3 (NGG1p interacting factor 3)-like <b>Family:</b> NIF3 (NGG1p interacting factor 3)-like
81	<a href="#">c5b4bB_</a>	Alignment	not modelled	74.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-2,3-diacylglucosamine hydrolase; <b>PDBTitle:</b> crystal structure of lpxh with lipid x in spacegroup c2
82	<a href="#">d2fywa1</a>	Alignment	not modelled	74.2	22	<b>Fold:</b> NIF3 (NGG1p interacting factor 3)-like <b>Superfamily:</b> NIF3 (NGG1p interacting factor 3)-like <b>Family:</b> NIF3 (NGG1p interacting factor 3)-like
83	<a href="#">c5w8mD_</a>	Alignment	not modelled	73.9	12	<b>PDB header:</b> endocytosis <b>Chain:</b> D: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 29; <b>PDBTitle:</b> crystal structure of chaetomium thermophilum vps29
84	<a href="#">d2a22a1</a>	Alignment	not modelled	73.7	15	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> YfcE-like
85	<a href="#">c5ks8D_</a>	Alignment	not modelled	73.2	17	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate carboxylase subunit beta; <b>PDBTitle:</b> crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
86	<a href="#">c2dwaA_</a>	Alignment	not modelled	73.2	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis
87	<a href="#">c3khjE_</a>	Alignment	not modelled	72.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> inosine-5-monophosphate dehydrogenase; <b>PDBTitle:</b> c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
88	<a href="#">d1i60a_</a>	Alignment	not modelled	71.4	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> loll-like
89	<a href="#">c4iwmD_</a>	Alignment	not modelled	71.2	19	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> upf0135 protein mj0927; <b>PDBTitle:</b> crystal structure of the conserved hypothetical protein mj0927 from2 methanocaldococcus jannaschii (in p21 form)
90	<a href="#">d1h1ya_</a>	Alignment	not modelled	71.0	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
91	<a href="#">c3l9cA_</a>	Alignment	not modelled	70.8	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinate dehydratase; <b>PDBTitle:</b> the crystal structure of smu.777 from streptococcus mutans ua159
92	<a href="#">d1qhwa_</a>	Alignment	not modelled	68.5	12	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> Purple acid phosphatase-like
93	<a href="#">c1qhwA_</a>	Alignment	not modelled	68.5	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (purple acid phosphatase); <b>PDBTitle:</b> purple acid phosphatase from rat bone
94	<a href="#">c2y8kA_</a>	Alignment	not modelled	68.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate binding family 6; <b>PDBTitle:</b> structure of ctgh5-cbm6, an arabinoxylan-specific xylanase.
95	<a href="#">c5tnvA_</a>	Alignment	not modelled	67.8	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ap endonuclease, family protein 2; <b>PDBTitle:</b> crystal structure of a xylose isomerase-like tim barrel protein from2 mycobacterium smegmatis in complex with magnesium
96	<a href="#">d1nmpa_</a>	Alignment	not modelled	67.6	19	<b>Fold:</b> NIF3 (NGG1p interacting factor 3)-like <b>Superfamily:</b> NIF3 (NGG1p interacting factor 3)-like <b>Family:</b> NIF3 (NGG1p interacting factor 3)-like
97	<a href="#">c5zfsA_</a>	Alignment	not modelled	67.5	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> d-allulose-3-epimerase; <b>PDBTitle:</b> crystal structure of arthrobacter globiformis m30 sugar epimerase2 which can produce d-allulose from d-fructose
98	<a href="#">d2q02a1</a>	Alignment	not modelled	67.4	9	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> loll-like
99	<a href="#">d3d03a1</a>	Alignment	not modelled	66.8	10	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> GpdQ-like
100	<a href="#">c5wlyA_</a>	Alignment	not modelled	66.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-2,3-diacylglucosamine hydrolase; <b>PDBTitle:</b> e. coli lpxh- 8 mutations
101	<a href="#">c3thdD_</a>	Alignment	not modelled	66.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of human beta-galactosidase in complex with 1-2 deoxygalactonojirimycin
102	<a href="#">d1w0ma_</a>	Alignment	not modelled	66.1	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
103	<a href="#">c2bmbA_</a>	Alignment	not modelled	65.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> folic acid synthesis protein fol1; <b>PDBTitle:</b> x-ray structure of the bifunctional 6-hydroxymethyl-7,8-2 dihydroxypterin pyrophosphokinase dihydropterate synthase from3 saccharomyces cerevisiae
104	<a href="#">c5k8kA_</a>	Alignment	not modelled	65.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-2,3-diacylglucosamine hydrolase; <b>PDBTitle:</b> structure of the haemophilus influenzae lpxh-lipid x complex



105	<a href="#">c2kknA_</a>	Alignment	not modelled	65.1	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of themotoga maritima protein tm1076:2 northeast structural genomics consortium target vt57
106	<a href="#">c3rxyA_</a>	Alignment	not modelled	64.9	40	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> nif3 protein; <b>PDBTitle:</b> crystal structure of nif3 superfamily protein from sphaerobacter2 thermophilus
107	<a href="#">c2o7qA_</a>	Alignment	not modelled	64.9	22	<b>PDB header:</b> oxidoreductase,transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional 3-dehydroquinatase dehydratase/shikimate <b>PDBTitle:</b> crystal structure of the a. thaliana dhq-dehydroshikimate-sdh-2 shikimate-nadp(h)
108	<a href="#">d1b4ub_</a>	Alignment	not modelled	64.8	13	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> LigB-like <b>Family:</b> LigB-like
109	<a href="#">c5ks8F_</a>	Alignment	not modelled	64.3	17	<b>PDB header:</b> ligase <b>Chain:</b> F: <b>PDB Molecule:</b> pyruvate carboxylase subunit beta; <b>PDBTitle:</b> crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
110	<a href="#">c3vylB_</a>	Alignment	not modelled	64.0	11	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> l-ribose 3-epimerase; <b>PDBTitle:</b> structure of l-ribose 3-epimerase
111	<a href="#">d1hg3a_</a>	Alignment	not modelled	63.1	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
112	<a href="#">c5ijwA_</a>	Alignment	not modelled	62.9	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> glutamate racemase (muri) from mycobacterium smegmatis with bound d-2 glutamate, 1.8 angstrom resolution, x-ray diffraction
113	<a href="#">c2yybA_</a>	Alignment	not modelled	62.2	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ttha1606; <b>PDBTitle:</b> crystal structure of ttha1606 from thermus thermophilus hb8
114	<a href="#">c6mp2B_</a>	Alignment	not modelled	62.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> blman5b; <b>PDBTitle:</b> crystal structure of blman5b solved by siras
115	<a href="#">d1nvma2</a>	Alignment	not modelled	62.1	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> HMGL-like
116	<a href="#">c1nvmG_</a>	Alignment	not modelled	62.1	11	<b>PDB header:</b> lyase/oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> 4-hydroxy-2-oxovalerate aldolase; <b>PDBTitle:</b> crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
117	<a href="#">c2ocza_</a>	Alignment	not modelled	61.2	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinatase dehydratase; <b>PDBTitle:</b> the structure of a putative 3-dehydroquinatase dehydratase from2 streptococcus pyogenes.
118	<a href="#">c2nx9B_</a>	Alignment	not modelled	61.2	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> oxaloacetate decarboxylase 2, subunit alpha; <b>PDBTitle:</b> crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
119	<a href="#">c3ijpA_</a>	Alignment	not modelled	60.4	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate reductase from bartonella2 henselae at 2.0a resolution
120	<a href="#">c2gzmb_</a>	Alignment	not modelled	59.9	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of the glutamate racemase from bacillus anthracis