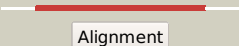



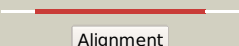





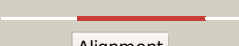




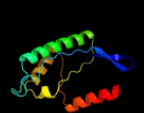

















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0496 (- )_586397_587383
Date	Fri Jul 26 01:50:04 BST 2019
Unique Job ID	3d7f543527904b6a

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2floA_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> exopolyphosphatase; <b>PDBTitle:</b> crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
2	<a href="#">c3cerD_</a>	 Alignment		100.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D; <b>PDB Molecule:</b> possible exopolyphosphatase-like protein; <b>PDBTitle:</b> crystal structure of the exopolyphosphatase-like protein q8g5j2.2 northeast structural genomics consortium target blr13
3	<a href="#">c3mdqA_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> exopolyphosphatase; <b>PDBTitle:</b> crystal structure of an exopolyphosphatase (chu_0316) from cytophaga2 hutchinsonii atcc 33406 at 1.50 a resolution
4	<a href="#">c3hi0B_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> putative exopolyphosphatase; <b>PDBTitle:</b> crystal structure of putative exopolyphosphatase (17739545) from2 agrobacterium tumefaciens str. c58 (dupont) at 2.30 a resolution
5	<a href="#">c1t6dB_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> exopolyphosphatase; <b>PDBTitle:</b> miras phasing of the aquifex aeolicus ppx/gppa phosphatase: crystal2 structure of the type ii variant
6	<a href="#">d1t6ca2</a>	 Alignment		100.0	24	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Ppx/GppA phosphatase
7	<a href="#">d1u6za3</a>	 Alignment		100.0	22	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Ppx/GppA phosphatase
8	<a href="#">d1t6ca1</a>	 Alignment		100.0	23	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Ppx/GppA phosphatase
9	<a href="#">d1u6za2</a>	 Alignment		100.0	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Ppx/GppA phosphatase
10	<a href="#">c3aapA_</a>	 Alignment		99.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> ectonucleoside triphosphate diphosphohydrolase i; <b>PDBTitle:</b> crystal structure of lp1ntpdase from legionella pneumophila
11	<a href="#">c5u7xF_</a>	 Alignment		99.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> nod factor binding lectin-nucleotide phosphohydrolase; <b>PDBTitle:</b> crystal structure of a nucleoside triphosphate diphosphohydrolase2 (ntpdase) from the legume vigna unguiculata subsp. cylindrica3 (dolichos biflorus) in complex with phosphate and manganese

12	<a href="#">c5u7wA_</a>	Alignment		99.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> apyrase; <b>PDBTitle:</b> crystal structure of a nucleoside triphosphate diphosphohydrolase2 (ntpdase) from the legume trifolium repens in complex with adenine3 and phosphate
13	<a href="#">c3zx2A_</a>	Alignment		99.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> ectonucleoside triphosphate diphosphohydrolase 1; <b>PDBTitle:</b> ntpdase1 in complex with decavanadate
14	<a href="#">c3cj9A_</a>	Alignment		99.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> ectonucleoside triphosphate diphosphohydrolase 2; <b>PDBTitle:</b> structure of rattus norvegicus ntpdase2 in complex with2 calcium, amp and phosphate
15	<a href="#">c3agrB_</a>	Alignment		98.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> nucleoside triphosphate hydrolase; <b>PDBTitle:</b> crystal structure of nucleoside triphosphate hydrolases from neospora2 caninum
16	<a href="#">c3h1qB_</a>	Alignment		98.7	15	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> ethanolamine utilization protein eutj; <b>PDBTitle:</b> crystal structure of ethanolamine utilization protein eutj from2 carboxydothemus hydrogenoformans
17	<a href="#">c4a5bA_</a>	Alignment		98.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> nucleoside-triphosphatase 2; <b>PDBTitle:</b> crystal structure of the c258s/c268s variant of toxoplasma gondii2 nucleoside triphosphate diphosphohydrolase 1 (ntpdase1)
18	<a href="#">c5eoxB_</a>	Alignment		98.2	13	<b>PDB header:</b> peptide binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> type 4 fimbrial biogenesis protein pilm; <b>PDBTitle:</b> pseudomonas aeruginosa pilm bound to adp
19	<a href="#">c1e4gT_</a>	Alignment		98.1	10	<b>PDB header:</b> bacterial cell division <b>Chain:</b> T; <b>PDB Molecule:</b> cell division protein ftsa; <b>PDBTitle:</b> ftsa (atp-bound form) from thermotoga maritima
20	<a href="#">c4czeA_</a>	Alignment		98.0	16	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> rod shape-determining protein mreB; <b>PDBTitle:</b> c. crescentus mreB, double filament, empty
21	<a href="#">c2ychA_</a>	Alignment	not modelled	98.0	17	<b>PDB header:</b> cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> competence protein pilm; <b>PDBTitle:</b> pilm-piln type iv pilus biogenesis complex
22	<a href="#">c3wqtB_</a>	Alignment	not modelled	98.0	11	<b>PDB header:</b> structural genomics <b>Chain:</b> B; <b>PDB Molecule:</b> cell division protein ftsa; <b>PDBTitle:</b> staphylococcus aureus ftsa complexed with amppnp
23	<a href="#">c3js6A_</a>	Alignment	not modelled	97.9	12	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized parm protein; <b>PDBTitle:</b> crystal structure of apo psk41 parm protein
24	<a href="#">c4apwH_</a>	Alignment	not modelled	97.8	12	<b>PDB header:</b> structural protein <b>Chain:</b> H; <b>PDB Molecule:</b> alp12; <b>PDBTitle:</b> alp12 filament structure
25	<a href="#">c2d0oA_</a>	Alignment	not modelled	97.7	16	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> diol dehydratase-reactivating factor large <b>PDBTitle:</b> strcuture of diol dehydratase-reactivating factor complexed2 with adp and mg2+
26	<a href="#">c1mwmA_</a>	Alignment	not modelled	97.7	14	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> parm; <b>PDBTitle:</b> parm from plasmid r1 adp form
27	<a href="#">d1e4ft2</a>	Alignment	not modelled	97.5	9	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
28	<a href="#">c5tkyA_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation
29	<a href="#">c5mb9B_</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> chaperone <b>Chain:</b> B; <b>PDB Molecule:</b> putative heat shock protein; <b>PDBTitle:</b> crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair

30	<a href="#">d2zgya2</a>	Alignment	not modelled	97.4	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
31	<a href="#">c2fsnB</a>	Alignment	not modelled	97.3	16	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ta0583; <b>PDBTitle:</b> crystal structure of ta0583, an archaeal actin homolog, complex with2 adp
32	<a href="#">d1jcea2</a>	Alignment	not modelled	97.1	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
33	<a href="#">c5obuA</a>	Alignment	not modelled	97.1	18	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone protein dnak; <b>PDBTitle:</b> mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.
34	<a href="#">c4xe7A</a>	Alignment	not modelled	97.1	11	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> bacillus thuringiensis parm in apo form
35	<a href="#">d2fsja1</a>	Alignment	not modelled	97.1	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Ta0583-like
36	<a href="#">c3d2fC</a>	Alignment	not modelled	96.8	12	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> heat shock protein homolog sse1; <b>PDBTitle:</b> crystal structure of a complex of sse1p and hsp70
37	<a href="#">c3dwIB</a>	Alignment	not modelled	96.8	10	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> actin-related protein 3; <b>PDBTitle:</b> crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
38	<a href="#">c6gfaA</a>	Alignment	not modelled	96.8	13	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein 105 kda; <b>PDBTitle:</b> structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed
39	<a href="#">c1jcgA</a>	Alignment	not modelled	96.8	12	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> rod shape-determining protein mreB; <b>PDBTitle:</b> mreB from thermotoga maritima, amppnp
40	<a href="#">c2v7yA</a>	Alignment	not modelled	96.7	16	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone protein dnak; <b>PDBTitle:</b> crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state
41	<a href="#">c4gniA</a>	Alignment	not modelled	96.7	13	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> putative heat shock protein; <b>PDBTitle:</b> structure of the ssz1 atpase bound to atp and magnesium
42	<a href="#">c5jygA</a>	Alignment	not modelled	96.7	14	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> actin-like atpase; <b>PDBTitle:</b> cryo-em structure of the mamk filament at 6.5 a
43	<a href="#">c3c7nB</a>	Alignment	not modelled	96.6	16	<b>PDB header:</b> chaperone/chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> heat shock cognate; <b>PDBTitle:</b> structure of the hsp110:hsc70 nucleotide exchange complex
44	<a href="#">c4j8fA</a>	Alignment	not modelled	96.6	18	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock 70 kda protein 1a/1b, hsc70-interacting protein; <b>PDBTitle:</b> crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip
45	<a href="#">c6izrK</a>	Alignment	not modelled	96.5	8	<b>PDB header:</b> protein fibril <b>Chain:</b> K: <b>PDB Molecule:</b> putative plasmid segregation protein parm; <b>PDBTitle:</b> whole structure of a 15-stranded parm filament from clostridium2 botulinum
46	<a href="#">c2khoA</a>	Alignment	not modelled	96.2	15	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein 70; <b>PDBTitle:</b> nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate
47	<a href="#">c5e84B</a>	Alignment	not modelled	96.1	14	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> 78 kda glucose-regulated protein; <b>PDBTitle:</b> atp-bound state of bip
48	<a href="#">c4xhpA</a>	Alignment	not modelled	96.1	18	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> parm hybrid fusion protein; <b>PDBTitle:</b> bacillus thuringiensis parm hybrid protein with adp, containing two2 parm mutants
49	<a href="#">c1dkgD</a>	Alignment	not modelled	95.9	16	<b>PDB header:</b> complex (hsp24/hsp70) <b>Chain:</b> D: <b>PDB Molecule:</b> molecular chaperone dnak; <b>PDBTitle:</b> crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak
50	<a href="#">c4pl7B</a>	Alignment	not modelled	95.8	15	<b>PDB header:</b> structural protein, contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> actin,thymosin beta-4; <b>PDBTitle:</b> structure of komagataella pastoris actin-thymosin beta4 hybrid
51	<a href="#">c1o1f4</a>	Alignment	not modelled	95.6	14	<b>PDB header:</b> contractile protein <b>Chain:</b> 4: <b>PDB Molecule:</b> skeletal muscle actin; <b>PDBTitle:</b> molecular models of averaged rigor crossbridges from tomograms of2 insect flight muscle
52	<a href="#">c5afuB</a>	Alignment	not modelled	95.3	13	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> dyndactin; <b>PDBTitle:</b> cryo-em structure of dynein tail-dyndactin-bicd2n complex
53	<a href="#">c3uleB</a>	Alignment	not modelled	95.0	17	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> actin-related protein 2; <b>PDBTitle:</b> structure of bos taurus arp2/3 complex with bound inhibitor ck-869 and2 atp
54	<a href="#">c4jd2B</a>	Alignment	not modelled	95.0	9	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> actin-related protein 2; <b>PDBTitle:</b> crystal structure of bos taurus arp2/3 complex binding with mus2 musculus gmf
55	<a href="#">d1dkgd2</a>	Alignment	not modelled	95.0	23	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70

56	<a href="#">c2v7zA</a>	Alignment	not modelled	94.8	12	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock cognate 71 kda protein; <b>PDBTitle:</b> crystal structure of the 70-kda heat shock cognate protein2 from rattus norvegicus in post-atp hydrolysis state
57	<a href="#">c3qb0C</a>	Alignment	not modelled	94.3	15	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> actin-related protein 4; <b>PDBTitle:</b> crystal structure of actin-related protein arp4 from s. cerevisiae2 complexed with atp
58	<a href="#">c2p9IA</a>	Alignment	not modelled	94.3	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> actin-like protein 3; <b>PDBTitle:</b> crystal structure of bovine arp2/3 complex
59	<a href="#">d1bupa2</a>	Alignment	not modelled	94.2	28	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
60	<a href="#">c6etxH</a>	Alignment	not modelled	94.2	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> actin-related protein 5; <b>PDBTitle:</b> cryo-em structure of the human ino80 complex bound to nucleosome
61	<a href="#">d2e8aa2</a>	Alignment	not modelled	94.0	32	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
62	<a href="#">c6bqwH</a>	Alignment	not modelled	93.8	11	<b>PDB header:</b> cytosolic protein <b>Chain:</b> H: <b>PDB Molecule:</b> bacterial actin alfa; <b>PDBTitle:</b> alfa filament bound to amppnp
63	<a href="#">c4kboA</a>	Alignment	not modelled	93.3	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> stress-70 protein, mitochondrial; <b>PDBTitle:</b> crystal structure of the human mortalin (grp75) atpase domain in the2 apo form
64	<a href="#">c3iucC</a>	Alignment	not modelled	92.9	17	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> heat shock 70kda protein 5 (glucose-regulated <b>PDBTitle:</b> crystal structure of the human 70kda heat shock protein 52 (bip/grp78) atpase domain in complex with adp
65	<a href="#">d1nm1a2</a>	Alignment	not modelled	92.7	21	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
66	<a href="#">c6gejR</a>	Alignment	not modelled	92.1	13	<b>PDB header:</b> nuclear protein <b>Chain:</b> R: <b>PDB Molecule:</b> actin-like protein arp6; <b>PDBTitle:</b> chromatin remodeller-nucleosome complex at 3.6 a resolution.
67	<a href="#">d2hf3a2</a>	Alignment	not modelled	91.9	21	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
68	<a href="#">c4fo0A</a>	Alignment	not modelled	91.8	21	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> actin-related protein 8; <b>PDBTitle:</b> human actin-related protein arp8 in its atp-bound state
69	<a href="#">c6fhsJ</a>	Alignment	not modelled	91.6	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> J: <b>PDB Molecule:</b> arp5; <b>PDBTitle:</b> cryoem structure of ino80core
70	<a href="#">c2p9kB</a>	Alignment	not modelled	91.4	17	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> actin-like protein 2; <b>PDBTitle:</b> crystal structure of bovine arp2/3 complex co-crystallized with atp2 and crosslinked with glutaraldehyde
71	<a href="#">d2fxua2</a>	Alignment	not modelled	91.4	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
72	<a href="#">c4i6mA</a>	Alignment	not modelled	91.4	13	<b>PDB header:</b> transcription/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> actin-related protein 7; <b>PDBTitle:</b> structure of arp7-arp9-snf2(hsa)-rtt102 subcomplex of swi/snf2 chromatin remodeler.
73	<a href="#">c4i6mB</a>	Alignment	not modelled	91.2	15	<b>PDB header:</b> transcription/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> actin-like protein arp9; <b>PDBTitle:</b> structure of arp7-arp9-snf2(hsa)-rtt102 subcomplex of swi/snf2 chromatin remodeler.
74	<a href="#">c5aftJ</a>	Alignment	not modelled	91.0	21	<b>PDB header:</b> motor protein <b>Chain:</b> J: <b>PDB Molecule:</b> actin related protein 11; <b>PDBTitle:</b> cryoem structure of dynactin complex at 4.0 angstrom2 resolution
75	<a href="#">c1hpmA</a>	Alignment	not modelled	91.0	14	<b>PDB header:</b> hydrolase (acting on acid anhydrides) <b>Chain:</b> A: <b>PDB Molecule:</b> 44k atpase fragment (n-terminal) of 7o kd heat- <b>PDBTitle:</b> how potassium affects the activity of the molecular2 chaperone hsc70. ii. potassium binds specifically in the3 atpase active site
76	<a href="#">c1nbwA</a>	Alignment	not modelled	90.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol dehydratase reactivase alpha subunit; <b>PDBTitle:</b> glycerol dehydratase reactivase
77	<a href="#">d1k8kb1</a>	Alignment	not modelled	90.7	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
78	<a href="#">c4cj7B</a>	Alignment	not modelled	90.3	14	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> actin/actin family protein; <b>PDBTitle:</b> structure of crenactin, an archeal actin-like protein
79	<a href="#">d1yaga2</a>	Alignment	not modelled	90.2	22	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
80	<a href="#">c3bfjK</a>	Alignment	not modelled	89.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> 1,3-propanediol oxidoreductase; <b>PDBTitle:</b> crystal structure analysis of 1,3-propanediol oxidoreductase
81	<a href="#">c6fmJL</a>	Alignment	not modelled	88.7	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> J: <b>PDB Molecule:</b> actin related protein 5; <b>PDBTitle:</b> cryoem structure ino80core nucleosome complex

82	<a href="#">d1k8ka2</a>	Alignment	not modelled	87.3	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
83	<a href="#">c4rtfD</a>	Alignment	not modelled	87.2	14	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> chaperone protein dnak; <b>PDBTitle:</b> crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv
84	<a href="#">c4fr2A</a>	Alignment	not modelled	87.0	18	<b>PDB header:</b> oxidoreductase, metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> 1,3-propanediol dehydrogenase; <b>PDBTitle:</b> alcohol dehydrogenase from oenococcus oeni
85	<a href="#">c5j9wb</a>	Alignment	not modelled	85.8	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetophenone carboxylase gamma subunit; <b>PDBTitle:</b> crystal structure of the apc core complex
86	<a href="#">c4am6A</a>	Alignment	not modelled	83.8	19	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> actin-like protein arp8; <b>PDBTitle:</b> c-terminal domain of actin-related protein arp8 from s. cerevisiae
87	<a href="#">c5yvmA</a>	Alignment	not modelled	83.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of the archaeal halo-thermophilic red sea brine pool2 alcohol dehydrogenase adh/d1 bound to nzq
88	<a href="#">c3ox4D</a>	Alignment	not modelled	81.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> alcohol dehydrogenase 2; <b>PDBTitle:</b> structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
89	<a href="#">c1ta9A</a>	Alignment	not modelled	80.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol dehydrogenase; <b>PDBTitle:</b> crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
90	<a href="#">c3ce9A</a>	Alignment	not modelled	79.8	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol dehydrogenase; <b>PDBTitle:</b> crystal structure of glycerol dehydrogenase (np_348253.1) from2 clostridium acetobutylicum at 2.37 a resolution
91	<a href="#">c5m45K</a>	Alignment	not modelled	79.6	28	<b>PDB header:</b> ligase <b>Chain:</b> K: <b>PDB Molecule:</b> acetone carboxylase beta subunit; <b>PDBTitle:</b> structure of acetone carboxylase purified from xanthobacter2 autotrophicus
92	<a href="#">c3cetA</a>	Alignment	not modelled	77.3	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved archaeal protein; <b>PDBTitle:</b> crystal structure of the pantheonate kinase-like protein q6m145 at the2 resolution 1.8 a. northeast structural genomics consortium target3 mrr63
93	<a href="#">d1saza1</a>	Alignment	not modelled	74.8	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
94	<a href="#">c2dpnB</a>	Alignment	not modelled	73.3	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of the glycerol kinase from thermus2 thermophilus hb8
95	<a href="#">c5hvnA</a>	Alignment	not modelled	73.2	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinate synthase; <b>PDBTitle:</b> 3.0 angstrom crystal structure of 3-dehydroquinate synthase (arob)2 from francisella tularensis in complex with nad.
96	<a href="#">d1rrma</a>	Alignment	not modelled	73.1	13	<b>Fold:</b> Dehydroquinate synthase-like <b>Superfamily:</b> Dehydroquinate synthase-like <b>Family:</b> Iron-containing alcohol dehydrogenase
97	<a href="#">c3g25B</a>	Alignment	not modelled	71.3	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol.
98	<a href="#">d1o2da</a>	Alignment	not modelled	70.4	13	<b>Fold:</b> Dehydroquinate synthase-like <b>Superfamily:</b> Dehydroquinate synthase-like <b>Family:</b> Iron-containing alcohol dehydrogenase
99	<a href="#">c3flcX</a>	Alignment	not modelled	67.7	7	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of the his-tagged h232r mutant of glycerol kinase2 from enterococcus casseliflavus with glycerol
100	<a href="#">c6c76A</a>	Alignment	not modelled	66.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> structure of iron containing alcohol dehydrogenase from thermococcus2 thioreducens in an orthorhombic crystal form
101	<a href="#">c4mcaB</a>	Alignment	not modelled	64.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol dehydrogenase; <b>PDBTitle:</b> crystal structure of glycerol dehydrogenase from serratia to 1.9a
102	<a href="#">c5ya2A</a>	Alignment	not modelled	64.8	15	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> autoinducer-2 kinase; <b>PDBTitle:</b> crystal structure of lsrk-hpr complex with adp
103	<a href="#">d1zc6a1</a>	Alignment	not modelled	64.4	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
104	<a href="#">c5j9wB</a>	Alignment	not modelled	63.9	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> acetophenone carboxylase gamma subunit; <b>PDBTitle:</b> crystal structure of the apc core complex
105	<a href="#">c2d4wA</a>	Alignment	not modelled	62.1	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
106	<a href="#">d2p3ra1</a>	Alignment	not modelled	60.8	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
107	<a href="#">d2d0oa3</a>	Alignment	not modelled	60.4	29	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ATPase domain of dehydratase reactivase alpha subunit
						<b>Fold:</b> Dehydroquinate synthase-like

108	<a href="#">d1jq5a_</a>	Alignment	not modelled	59.9	14	<b>Superfamily:</b> Dehydroquinase synthase-like <b>Family:</b> Iron-containing alcohol dehydrogenase
109	<a href="#">c6jkdD_</a>	Alignment	not modelled	59.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> methanol dehydrogenase; <b>PDBTitle:</b> crystal structure of sulfoacetaldehyde reductase from bifidobacterium2 kashiwanohense in complex with nad+
110	<a href="#">c3zokB_</a>	Alignment	not modelled	59.4	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-dehydroquinase synthase; <b>PDBTitle:</b> structure of 3-dehydroquinase synthase from actinidia chinensis in2 complex with nad
111	<a href="#">d2i1qa1</a>	Alignment	not modelled	58.1	27	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Rad51 N-terminal domain-like <b>Family:</b> DNA repair protein Rad51, N-terminal domain
112	<a href="#">d1nbwa3</a>	Alignment	not modelled	58.1	30	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ATPase domain of dehydratase reactivase alpha subunit
113	<a href="#">d1szpa1</a>	Alignment	not modelled	56.5	20	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Rad51 N-terminal domain-like <b>Family:</b> DNA repair protein Rad51, N-terminal domain
114	<a href="#">d1kq3a_</a>	Alignment	not modelled	55.2	17	<b>Fold:</b> Dehydroquinase synthase-like <b>Superfamily:</b> Dehydroquinase synthase-like <b>Family:</b> Iron-containing alcohol dehydrogenase
115	<a href="#">c3ezwD_</a>	Alignment	not modelled	54.6	13	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of a hyperactive escherichia coli glycerol kinase2 mutant gly230 --> asp obtained using microfluidic crystallization3 devices
116	<a href="#">c3okfA_</a>	Alignment	not modelled	54.5	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinase synthase; <b>PDBTitle:</b> 2.5 angstrom resolution crystal structure of 3-dehydroquinase synthase2 (arob) from vibrio cholerae
117	<a href="#">c3hl0B_</a>	Alignment	not modelled	54.2	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> maleylacetate reductase; <b>PDBTitle:</b> crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
118	<a href="#">c3cqyA_</a>	Alignment	not modelled	53.8	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> anhydro-n-acetylmuramic acid kinase; <b>PDBTitle:</b> crystal structure of a functionally unknown protein (so_1313) from2 shewanella oneidensis mr-1
119	<a href="#">d1szpb1</a>	Alignment	not modelled	52.1	20	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Rad51 N-terminal domain-like <b>Family:</b> DNA repair protein Rad51, N-terminal domain
120	<a href="#">c1xupO_</a>	Alignment	not modelled	49.9	7	<b>PDB header:</b> transferase <b>Chain:</b> O: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> enterococcus casseliflavus glycerol kinase complexed with glycerol