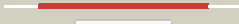



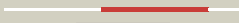
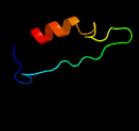





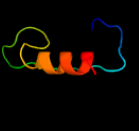

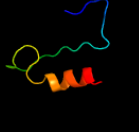


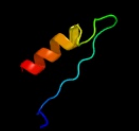


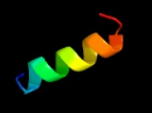
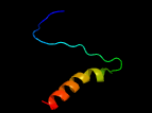



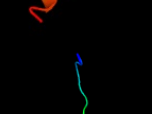
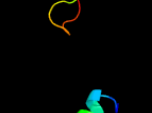
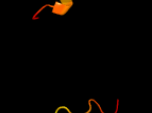
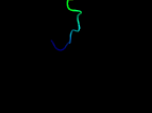


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3724A_(cut5a)_4169645_4169887
 Date Fri Aug 9 18:20:42 BST 2019
 Unique Job ID 05b3ea9bed201b2a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4psdA_	 Alignment		99.2	26	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate esterase family 5; PDBTitle: structure of trichoderma reesei cutinase native form.
2	c4oylC_	 Alignment		98.9	39	PDB header: hydrolase Chain: C: PDB Molecule: cutinase; PDBTitle: humicola insolens cutinase in complex with monoethylphosphate
3	c2czqB_	 Alignment		98.9	24	PDB header: hydrolase Chain: B: PDB Molecule: cutinase-like protein; PDBTitle: a novel cutinase-like protein from cryptococcus sp.
4	d1cexa_	 Alignment		98.8	26	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
5	c5x88A_	 Alignment		98.8	41	PDB header: hydrolase Chain: A: PDB Molecule: cutinase; PDBTitle: a crystal structure of cutinases from malbranchea cinnamomea
6	c3gbsA_	 Alignment		98.5	30	PDB header: hydrolase Chain: A: PDB Molecule: cutinase 1; PDBTitle: crystal structure of aspergillus oryzae cutinase
7	c3dd5F_	 Alignment		98.4	39	PDB header: hydrolase Chain: F: PDB Molecule: cutinase; PDBTitle: glomerella cingulata e600-cutinase complex
8	d1lqza_	 Alignment		98.2	32	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
9	d1g66a_	 Alignment		98.1	34	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
10	c3ajaA_	 Alignment		97.8	29	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of msmeg_6394
11	c3hc7A_	 Alignment		87.7	26	PDB header: cell adhesion Chain: A: PDB Molecule: gene 12 protein; PDBTitle: crystal structure of lysin b from mycobacteriophage d29

12	d2pv7a2	Alignment		18.7	56	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
13	d1jmsa4	Alignment		18.2	11	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: DNA polymerase beta-like
14	c3ingA_	Alignment		16.1	25	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of homoserine dehydrogenase (np_394635.1) from <i>Thermoplasma acidophilum</i> at 1.95 Å resolution
15	c3b20R_	Alignment		15.6	22	PDB header: oxidoreductase Chain: R: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase (nadp+); PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase2 complexed with nad from <i>Synechococcus elongatus</i> "
16	c1hdgO_	Alignment		15.2	22	PDB header: oxidoreductase (aldehyde(d)-nad(a)) Chain: O: PDB Molecule: holo-d-glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: the crystal structure of holo-glyceraldehyde-3-phosphate dehydrogenase2 from the hyperthermophilic bacterium <i>Thermotoga maritima</i> at 2.53 Å resolution
17	c5d5pC_	Alignment		15.1	35	PDB header: transferase Chain: C: PDB Molecule: hcgb; PDBTitle: hcgb from <i>Methanococcus marisaludis</i>
18	c2d2iO_	Alignment		14.5	22	PDB header: oxidoreductase Chain: O: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: crystal structure of nadp-dependent glyceraldehyde-3-phosphate dehydrogenase from <i>Synechococcus</i> sp. complexed3 with nadp+
19	c5e38D_	Alignment		13.6	36	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structural basis of mapping the spontaneous mutations with 5-2 fluorouracil in uracil phosphoribosyltransferase from <i>Mycobacterium tuberculosis</i>
20	c3docD_	Alignment		12.9	28	PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: crystal structure of trka glyceraldehyde-3-phosphate dehydrogenase2 from <i>Brucella melitensis</i>
21	d1i36a2	Alignment	not modelled	12.9	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
22	c1kdhA_	Alignment	not modelled	12.4	11	PDB header: transferase/dna Chain: A: PDB Molecule: terminal deoxynucleotidyltransferase short PDBTitle: binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna
23	d1qb7a_	Alignment	not modelled	12.1	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
24	c1cerC_	Alignment	not modelled	12.1	28	PDB header: oxidoreductase (aldehyde(d)-nad(a)) Chain: C: PDB Molecule: holo-d-glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: determinants of enzyme thermostability observed in the2 molecular structure of <i>Thermus aquaticus</i> d-glyceraldehyde-3-phosphate dehydrogenase at 2.5 Å resolution
25	c3brcA_	Alignment	not modelled	11.8	42	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein of unknown function; PDBTitle: crystal structure of a conserved protein of unknown function from <i>Methanobacterium thermoautotrophicum</i>
26	c1b7gO_	Alignment	not modelled	11.8	28	PDB header: oxidoreductase Chain: O: PDB Molecule: protein (glyceraldehyde 3-phosphate dehydrogenase); PDBTitle: glyceraldehyde 3-phosphate dehydrogenase
27	c2lepA_	Alignment	not modelled	11.5	36	PDB header: hydrolase Chain: A: PDB Molecule: rhomboid protease glgp 1; PDBTitle: solution structure of n-terminal cytosolic domain of rhomboid2 intramembrane protease from <i>Escherichia coli</i>
						PDB header: transport protein

28	c5nc8B_	Alignment	not modelled	11.4	28	Chain: B; PDB Molecule: potassium efflux system protein; PDBTitle: shewanella denitrificans kef ctd in amp bound form
29	d1ebfa1	Alignment	not modelled	11.1	44	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
30	c3cieC_	Alignment	not modelled	11.0	28	PDB header: oxidoreductase Chain: C; PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from cryptosporidium parvum
31	c2pv7B_	Alignment	not modelled	11.0	50	PDB header: isomerase, oxidoreductase Chain: B; PDB Molecule: ct-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) PDBTitle: crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
32	c2yjcC_	Alignment	not modelled	10.9	22	PDB header: oxidoreductase Chain: C; PDB Molecule: metalloreductase steap4; PDBTitle: rat steap4 oxidoreductase domain complexed with nadp
33	c2rafC_	Alignment	not modelled	10.8	22	PDB header: oxidoreductase Chain: C; PDB Molecule: putative dinucleotide-binding oxidoreductase; PDBTitle: crystal structure of putative dinucleotide-binding oxidoreductase2 (np_786167.1) from lactobacillus plantarum at 1.60 a resolution
34	c2yyvB_	Alignment	not modelled	10.4	38	PDB header: oxidoreductase Chain: B; PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase
35	c2i5pO_	Alignment	not modelled	10.3	22	PDB header: oxidoreductase Chain: O; PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase 1; PDBTitle: crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase isoform 1 from k. marxianus
36	c2f1kD_	Alignment	not modelled	10.3	33	PDB header: oxidoreductase Chain: D; PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis arogenate dehydrogenase
37	c4narA_	Alignment	not modelled	10.3	16	PDB header: isomerase Chain: A; PDB Molecule: putative uronate isomerase; PDBTitle: crystal structure of the q9wys3 protein from thermotoga maritima.2 northeast structural genomics consortium target vr152
38	c2g5cD_	Alignment	not modelled	10.2	44	PDB header: oxidoreductase Chain: D; PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from aquifex aeolicus
39	c1cf2Q_	Alignment	not modelled	9.8	33	PDB header: oxidoreductase Chain: Q; PDB Molecule: protein (glyceraldehyde-3-phosphate dehydrogenase); PDBTitle: three-dimensional structure of d-glyceraldehyde-3-phosphate2 dehydrogenase from the hyperthermophilic archaeon methanothermus3 fervidus
40	c3eywA_	Alignment	not modelled	9.7	29	PDB header: transport protein Chain: A; PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
41	c2pkrl_	Alignment	not modelled	9.7	25	PDB header: oxidoreductase Chain: I; PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase aor; PDBTitle: crystal structure of (a+cte)4 chimeric form of photosynthetic2 glyceraldehyde-3-phosphate dehydrogenase, complexed with nadp
42	c2ep7B_	Alignment	not modelled	9.6	28	PDB header: oxidoreductase Chain: B; PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: structural study of project id aq_1065 from aquifex aeolicus vf5
43	c1rm4O_	Alignment	not modelled	9.2	25	PDB header: oxidoreductase Chain: O; PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase a; PDBTitle: crystal structure of recombinant photosynthetic glyceraldehyde-3-2 phosphate dehydrogenase a4 isoform, complexed with nadp
44	c4qx6A_	Alignment	not modelled	9.2	22	PDB header: oxidoreductase Chain: A; PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 streptococcus agalactiae nem316 at 2.46 angstrom resolution
45	d2jfga1	Alignment	not modelled	9.2	32	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
46	c5t8xA_	Alignment	not modelled	9.0	22	PDB header: oxidoreductase Chain: A; PDB Molecule: prephenate dehydrogenase 1; PDBTitle: prephenate dehydrogenase from soybean
47	c4pg8B_	Alignment	not modelled	8.7	22	PDB header: oxidoreductase Chain: B; PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of s. aureus homoserine dehydrogenase at pH8.5
48	d2ahra2	Alignment	not modelled	8.2	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
49	c2b4rQ_	Alignment	not modelled	8.1	28	PDB header: oxidoreductase Chain: Q; PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 plasmodium falciparum at 2.25 angstrom

						resolution reveals intriguing3 extra electron density in the active site
50	c5ur0B_	Alignment	not modelled	7.6	28	PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystallographic structure of glyceraldehyde-3-phosphate dehydrogenase2 from naegleria gruberi
51	c2czcD_	Alignment	not modelled	7.5	25	PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 pyrococcus horikoshii ot3
52	c3c85A_	Alignment	not modelled	7.5	35	PDB header: transport protein Chain: A: PDB Molecule: putative glutathione-regulated potassium-efflux system PDBTitle: crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus
53	c4xb1B_	Alignment	not modelled	7.4	25	PDB header: oxidoreductase Chain: B: PDB Molecule: 319aa long hypothetical homoserine dehydrogenase; PDBTitle: hyperthermophilic archaeal homoserine dehydrogenase in complex with2 nadph
54	c5bseF_	Alignment	not modelled	7.4	17	PDB header: oxidoreductase Chain: F: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: crystal structure of medicago truncatula (delta)1-pyrroline-5-2 carboxylate reductase (mtp5cr)
55	d2g5ca2	Alignment	not modelled	7.2	44	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
56	c3c8mA_	Alignment	not modelled	7.2	31	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium
57	d1y60a_	Alignment	not modelled	7.1	14	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Formaldehyde-activating enzyme, FAE
58	c2izzE_	Alignment	not modelled	6.9	17	PDB header: oxidoreductase Chain: E: PDB Molecule: pyrroline-5-carboxylate reductase 1; PDBTitle: crystal structure of human pyrroline-5-carboxylate reductase
59	c4gjbB_	Alignment	not modelled	6.8	28	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase nad-binding; PDBTitle: crystal structure of nad-binding 6-phosphogluconate dehydrogenase from2 dyadobacter fermentans
60	d1bd3a_	Alignment	not modelled	6.7	40	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
61	d2hmva1	Alignment	not modelled	6.7	41	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
62	c3hq4R_	Alignment	not modelled	6.5	22	PDB header: oxidoreductase Chain: R: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase 1; PDBTitle: crystal structure of c151s mutant of glyceraldehyde-3-phosphate2 dehydrogenase 1 (gapdh1) complexed with nad from staphylococcus3 aureus mrsa252 at 2.2 angstrom resolution
63	c1ebuA_	Alignment	not modelled	6.5	44	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: homoserine dehydrogenase complex with nad analogue and l-2 homoserine
64	c1s7cA_	Alignment	not modelled	6.3	22	PDB header: structural genomics, oxidoreductase Chain: A: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase a; PDBTitle: crystal structure of mes buffer bound form of glyceraldehyde 3-2 phosphate dehydrogenase from escherichia coli
65	c2x5kO_	Alignment	not modelled	6.3	39	PDB header: oxidoreductase Chain: O: PDB Molecule: d-erythrose-4-phosphate dehydrogenase; PDBTitle: structure of an active site mutant of the d-erythrose-4-phosphate2 dehydrogenase from e. coli
66	d1i5ea_	Alignment	not modelled	6.2	40	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
67	c6ok4A_	Alignment	not modelled	6.1	31	PDB header: oxidoreductase Chain: A: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase (gapdh)2 from chlamydia trachomatis with bound nad
68	c4nqkD_	Alignment	not modelled	6.1	26	PDB header: hydrolase/apoptosis Chain: D: PDB Molecule: probable atp-dependent rna helicase ddx58; PDBTitle: structure of an ubiquitin complex
69	c5avoA_	Alignment	not modelled	5.9	38	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of the reduced form of homoserine dehydrogenase from2 sulfobolus tokodaii.
70	d1b7go1	Alignment	not modelled	5.9	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
71	c3ktdC_	Alignment	not modelled	5.8	28	PDB header: oxidoreductase Chain: C: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
72	d1v9sa1	Alignment	not modelled	5.8	40	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
						PDB header: oxidoreductase

73	c3triB_	Alignment	not modelled	5.7	28	Chain: B: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
74	c5b37A_	Alignment	not modelled	5.7	26	PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophan dehydrogenase; PDBTitle: crystal structure of l-tryptophan dehydrogenase from nostoc2 punctiforme
75	c2ehjA_	Alignment	not modelled	5.6	40	PDB header: transferase Chain: A: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of uracil phosphoribosyl transferase
76	d2zjr1_	Alignment	not modelled	5.5	35	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
77	c1ffvB_	Alignment	not modelled	5.5	33	PDB header: hydrolase Chain: B: PDB Molecule: cutl1, molybdoprotein of carbon monoxide PDBTitle: carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava
78	d1qp8a1_	Alignment	not modelled	5.5	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
79	c3graA_	Alignment	not modelled	5.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase 1; PDBTitle: crystal structure of human pyrroline-5-carboxylate reductase complexed2 with nadp
80	c2rcyB_	Alignment	not modelled	5.4	17	PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline carboxylate reductase; PDBTitle: crystal structure of plasmodium falciparum pyrroline carboxylate2 reductase (mal13p1.284) with nadp bound
81	c2ejwB_	Alignment	not modelled	5.4	29	PDB header: oxidoreductase Chain: B: PDB Molecule: homoserine dehydrogenase; PDBTitle: homoserine dehydrogenase from thermus thermophilus hb8
82	c3llvA_	Alignment	not modelled	5.3	28	PDB header: nad(p) binding protein Chain: A: PDB Molecule: exopolyphosphatase-related protein; PDBTitle: the crystal structure of the nad(p)-binding domain of an2 exopolyphosphatase-related protein from archaeoglobus fulgidus to3 1.7a
83	d1xtta1_	Alignment	not modelled	5.3	40	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
84	c2ahrB_	Alignment	not modelled	5.3	17	PDB header: oxidoreductase Chain: B: PDB Molecule: putative pyrroline carboxylate reductase; PDBTitle: crystal structures of 1-pyrroline-5-carboxylate reductase from human2 pathogen streptococcus pyogenes
85	c3pduF_	Alignment	not modelled	5.3	33	PDB header: oxidoreductase Chain: F: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase family protein; PDBTitle: crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter sulfurreducens in complex with nadp+
86	c6dzsD_	Alignment	not modelled	5.3	26	PDB header: oxidoreductase Chain: D: PDB Molecule: homoserine dehydrogenase; PDBTitle: mycobacterial homoserine dehydrogenase thra in complex with nadp
87	c5jyfB_	Alignment	not modelled	5.3	22	PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: structures of streptococcus agalactiae gbs gapdh in different2 enzymatic states
88	d1o5oa_	Alignment	not modelled	5.2	40	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
89	c3b1fA_	Alignment	not modelled	5.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 mutans
90	c4e21B_	Alignment	not modelled	5.2	39	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase (decarboxylating); PDBTitle: the crystal structure of 6-phosphogluconate dehydrogenase from2 geobacter metallireducens
91	d2gycm1_	Alignment	not modelled	5.1	35	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11