



















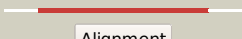



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2043c_(pncA)_2288689_2289249
Date	Mon Aug 5 13:25:15 BST 2019
Unique Job ID	61318c6543513151

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gbcA_	 Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: pyrazinamidase/nicotinamidas pncA; PDBTitle: determination of the crystal structure of the pyrazinamidase from <i>M.tuberculosis</i> : a structure-function analysis for prediction3 resistance to pyrazinamide
2	d1nbaa_	 Alignment		100.0	20	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
3	c2fq1A_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: isochorismatase; PDBTitle: crystal structure of the two-domain non-ribosomal peptide synthetase2 entb containing isochorismate lyase and aryl-carrier protein domains
4	c2h0rD_	 Alignment		100.0	29	PDB header: hydrolase Chain: D: PDB Molecule: nicotinamidase; PDBTitle: structure of the yeast nicotinamidase pnc1p
5	c3hu5B_	 Alignment		100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: isochorismatase family protein; PDBTitle: crystal structure of isochorismatase family protein from <i>desulfovibrio2 vulgaris</i> subsp. <i>vulgaris</i> str. hildenborough
6	d1im5a_	 Alignment		100.0	36	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
7	c3irvA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: cysteine hydrolase; PDBTitle: crystal structure of cysteine hydrolase pspph_2384 from <i>pseudomonas2 syringae</i> pv. <i>phaseolicola</i> 1448a
8	c3ot4F_	 Alignment		100.0	26	PDB header: hydrolase Chain: F: PDB Molecule: putative isochorismatase; PDBTitle: structure and catalytic mechanism of <i>bordetella bronchiseptica</i> nicf
9	c5gleA_	 Alignment		100.0	18	PDB header: lyase Chain: A: PDB Molecule: isochorismate lyase; PDBTitle: the structure of <i>vibrio anguillarum</i> 775 angb-icl
10	c3r2jC_	 Alignment		100.0	40	PDB header: hydrolase Chain: C: PDB Molecule: alpha/beta-hydrolase-like protein; PDBTitle: crystal structure of pnc1 from <i>I. infantum</i> in complex with nicotinate
11	d1nf9a_	 Alignment		100.0	18	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases

12	c3hb7G_	Alignment		100.0	25	PDB header: hydrolase Chain: G: PDB Molecule: isochorismatase hydrolase; PDBTitle: the crystal structure of an isochorismatase-like hydrolase from2 alkaliphilus metalliredigens to 2.3a
13	c5zn8B_	Alignment		100.0	26	PDB header: metal binding protein Chain: B: PDB Molecule: isochorismatase; PDBTitle: crystal structure of nicotinamidase pnca from bacillus subtilis
14	c5wxvL_	Alignment		100.0	19	PDB header: lyase Chain: L: PDB Molecule: isochorismate lyase; PDBTitle: the crystal structure of vabb-icl domain from vibrio anguillarum 775
15	d1j2ra_	Alignment		100.0	18	Fold: isochorismatase-like hydrolases Superfamily: isochorismatase-like hydrolases Family: isochorismatase-like hydrolases
16	c6azoC_	Alignment		100.0	24	PDB header: hydrolase Chain: C: PDB Molecule: putative amidase; PDBTitle: structural and biochemical characterization of a non-canonical biuret2 hydrolase (biuh) from the cyanuric acid catabolism pathway of3 rhizobium leguminasorum bv. viciae 3841
17	c3tb4A_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: vibriobactin-specific isochorismatase; PDBTitle: crystal structure of the isc domain of vibb
18	c3o93A_	Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: nicotinamidase; PDBTitle: high resolution crystal structures of streptococcus pneumoniae2 nicotinamidase with trapped intermediates provide insights into3 catalytic mechanism and inhibition by aldehydes
19	c3eefA_	Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: n-carbamoylsarcosine amidase related protein; PDBTitle: crystal structure of n-carbamoylsarcosine amidase from thermoplasma2 acidophilum
20	c2wtaA_	Alignment		100.0	37	PDB header: hydrolase Chain: A: PDB Molecule: nicotinamidase; PDBTitle: acinetobacter baumanii nicotinamidase pyrazinamidase
21	c3oqpA_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: putative isochorismatase; PDBTitle: crystal structure of a putative isochorismatase (bx_e_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
22	c3oqpB_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: putative isochorismatase; PDBTitle: crystal structure of a putative isochorismatase (bx_e_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
23	c3kl2K_	Alignment	not modelled	100.0	21	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: putative isochorismatase; PDBTitle: crystal structure of a putative isochorismatase from streptomyces2 avermitilis
24	c3mCWa_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of an a putative hydrolase of the isochorismatase2 family (cv_1320) from chromobacterium violaceum atcc 12472 at 1.06 a3 resolution
25	c4h17B_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase, isochorismatase family; PDBTitle: crystal structure of an isochorismatase (pp1826) from pseudomonas2 putida kt2440 at 1.60 a resolution
26	c2a67C_	Alignment	not modelled	100.0	19	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: isochorismatase family protein; PDBTitle: crystal structure of isochorismatase family protein
27	c3lqyA_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: putative isochorismatase hydrolase; PDBTitle: crystal structure of putative isochorismatase hydrolase from oleispira2 antarctica
						PDB header: hydrolase

28	c5ha8A	Alignment	not modelled	100.0	21	Chain: A: PDB Molecule: isochorismatase; PDBTitle: structure of a cysteine hydrolase
29	c1yzvA	Alignment	not modelled	100.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: hypothetical protein from trypanosoma cruzi
30	d1yaca	Alignment	not modelled	100.0	17	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
31	c2b34C	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: C: PDB Molecule: mar1 ribonuclease; PDBTitle: structure of mar1 ribonuclease from caenorhabditis elegans
32	d1x9ga	Alignment	not modelled	100.0	18	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
33	c5kinD	Alignment	not modelled	87.0	11	PDB header: lyase Chain: D: PDB Molecule: tryptophan synthase beta chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
34	c1ddzA	Alignment	not modelled	85.2	12	PDB header: lyase Chain: A: PDB Molecule: carbonic anhydrase; PDBTitle: x-ray structure of a beta-carbonic anhydrase from the red2 alga, porphyridium purpureum r-1
35	d1vp8a	Alignment	not modelled	82.1	26	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
36	d1xdpa3	Alignment	not modelled	74.5	24	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
37	d1pv8a	Alignment	not modelled	74.4	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
38	c1x1qA	Alignment	not modelled	73.2	17	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
39	c4negA	Alignment	not modelled	64.3	13	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: the crystal structure of tryptophan synthase subunit beta from2 bacillus anthracis str. 'ames ancestor'
40	d1cmwa2	Alignment	not modelled	59.6	16	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
41	c1xdoB	Alignment	not modelled	59.5	22	PDB header: transferase Chain: B: PDB Molecule: polyphosphate kinase; PDBTitle: crystal structure of escherichia coli polyphosphate kinase
42	d1onfa2	Alignment	not modelled	58.9	10	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
43	d1oi7a1	Alignment	not modelled	57.6	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
44	d1f2da	Alignment	not modelled	54.5	10	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
45	d1tfra2	Alignment	not modelled	54.2	7	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
46	d1ae1a	Alignment	not modelled	54.0	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
47	d2ae2a	Alignment	not modelled	52.2	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
48	c2ihnA	Alignment	not modelled	52.1	5	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
49	d1qopb	Alignment	not modelled	51.0	18	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
50	c5yvmA	Alignment	not modelled	50.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of the archaeal halo-thermophilic red sea brine pool2 alcohol dehydrogenase adh/d1 bound to nzq
51	c4qysA	Alignment	not modelled	49.1	11	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain 2; PDBTitle: trpb2 enzymes
52	d1v8za1	Alignment	not modelled	48.3	11	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
53	d1qwga	Alignment	not modelled	45.0	12	Fold: TIM beta/alpha-barrel Superfamily: (2r)-phospho-3-sulfolactate synthase ComA Family: (2r)-phospho-3-sulfolactate synthase ComA
54	c4igmA	Alignment	not modelled	44.1	10	PDB header: transferase Chain: A: PDB Molecule: cyclodextrin glucanotransferase;

54	c9jtmA	Alignment	not modelled	44.1	10	PDBTitle: crystal structure of gamma-cgtase from alkalophilic bacillus clarkii2 at 1.65 angstrom resolution PDB header: lyase
55	c2o2jA	Alignment	not modelled	43.1	23	Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: mycobacterium tuberculosis tryptophan synthase beta chain dimer2 (apoform)
56	c5yw2D	Alignment	not modelled	42.8	23	PDB header: transferase Chain: D: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 francisella tularensis.
57	d1ddza1	Alignment	not modelled	42.4	14	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
58	c6hpfA	Alignment	not modelled	40.7	19	PDB header: hydrolase Chain: A: PDB Molecule: endo-b-mannanase; PDBTitle: structure of inactive e165q mutant of fungal non-cbm carrying gh262 endo-b-mannanase from yunnania penicillata in complex with alpha-62-3 61-di-galactosyl-mannotriose
59	c5tchH	Alignment	not modelled	40.5	23	PDB header: lyase Chain: H: PDB Molecule: tryptophan synthase beta chain; PDBTitle: crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
60	d1a9xa3	Alignment	not modelled	39.5	17	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
61	c5yaaD	Alignment	not modelled	38.9	17	PDB header: hydrolase Chain: D: PDB Molecule: meiosis regulator and mrna stability factor 1; PDBTitle: crystal structure of marf1 nyn domain from mus musculus
62	c3zm8A	Alignment	not modelled	38.8	17	PDB header: hydrolase Chain: A: PDB Molecule: gh26 endo-beta-1,4-mannanase; PDBTitle: crystal structure of podospira anserina gh26-cbm352 beta-(1,4)-mannanase
63	c2wanA	Alignment	not modelled	38.7	11	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase; PDBTitle: pullulanase from bacillus acidopullulyticus
64	c5ybwA	Alignment	not modelled	38.3	23	PDB header: isomerase Chain: A: PDB Molecule: aspartate racemase; PDBTitle: crystal structure of pyridoxal 5'-phosphate-dependent aspartate2 racemase
65	c6ci9D	Alignment	not modelled	38.1	15	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: rmm microcompartment-associated aminopropanol dehydrogenase nadp +2 aminoacetone holo-structure
66	d1v7ca	Alignment	not modelled	38.0	13	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
67	c3toxG	Alignment	not modelled	37.9	19	PDB header: oxidoreductase Chain: G: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase in complex with2 nad(p) from sinorhizobium meliloti 1021
68	c2zsjB	Alignment	not modelled	37.1	18	PDB header: lyase Chain: B: PDB Molecule: threonine synthase; PDBTitle: crystal structure of threonine synthase from aquifex aeolicus vf5
69	c5iq2B	Alignment	not modelled	36.7	19	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of a short chain dehydrogenase/reductase sdr from2 burkholderia phymatum in complex with nad
70	c3zddA	Alignment	not modelled	35.9	21	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein xni; PDBTitle: structure of e. coli exoix in complex with the palindromic 5ov62 oligonucleotide and potassium
71	c6iaqA	Alignment	not modelled	35.4	10	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase n-terminus domain-containing PDBTitle: structure of amine dehydrogenase from mycobacterium smegmatis
72	c4yaiB	Alignment	not modelled	35.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: c alpha-dehydrogenase; PDBTitle: crystal structure of ligl in complex with nadh and gge from2 sphingobium sp. strain syk-6
73	c2dy0A	Alignment	not modelled	34.0	31	PDB header: transferase Chain: A: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of project jw0458 from escherichia coli
74	c2zatC	Alignment	not modelled	33.8	12	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase/reductase sdr family member 4; PDBTitle: crystal structure of a mammalian reductase
75	c1cmwA	Alignment	not modelled	33.6	21	PDB header: transferase Chain: A: PDB Molecule: protein (dna polymerase i); PDBTitle: crystal structure of taq dna-polymerase shows a new orientation for2 the structure-specific nuclease domain
76	d1xp8a1	Alignment	not modelled	33.2	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
77	d1j0aa	Alignment	not modelled	33.1	13	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
78	d2nu7a1	Alignment	not modelled	33.0	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain

79	d1nhpa2	Alignment	not modelled	32.7	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
80	c6hulB	Alignment	not modelled	31.7	14	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase beta chain 1; PDBTitle: sulfolobus solfataricus tryptophan synthase ab complex
81	c4urfB	Alignment	not modelled	30.8	17	PDB header: oxidoreductase Chain: B: PDB Molecule: cyclohexanol dehydrogenase; PDBTitle: molecular genetic and crystal structural analysis of 1-(4-2 hydroxyphenyl)-ethanol dehydrogenase from aromatoleum aromaticum ebn1
82	c3euaD	Alignment	not modelled	30.3	15	PDB header: isomerase Chain: D: PDB Molecule: putative fructose-aminoacid-6-phosphate deglycase; PDBTitle: crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution
83	c3imfA	Alignment	not modelled	29.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: 1.99 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor'
84	d1o2da	Alignment	not modelled	29.7	16	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
85	d1tyza	Alignment	not modelled	29.6	16	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
86	c6aioA	Alignment	not modelled	29.0	17	PDB header: flavoprotein Chain: A: PDB Molecule: pnpa; PDBTitle: crystal structure of p-nitrophenol 4-monooxygenase pnpa from2 pseudomonas putida dlI-e4
87	d1d7ya2	Alignment	not modelled	29.0	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
88	c4j2hA	Alignment	not modelled	28.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain alcohol dehydrogenase-related dehydrogenase; PDBTitle: crystal structure of a putative short-chain alcohol dehydrogenase from2 sinorhizobium meliloti 1021 (target nysgrc-011708)
89	c5idxB	Alignment	not modelled	28.1	25	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of an oxidoreductase from burkholderia vietnamiensis
90	d1o58a	Alignment	not modelled	28.0	18	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
91	c5u9pB	Alignment	not modelled	27.7	9	PDB header: oxidoreductase Chain: B: PDB Molecule: gluconate 5-dehydrogenase; PDBTitle: crystal structure of a gluconate 5-dehydrogenase from burkholderia2 cenocepacia j2315 in complex with nadp and tartrate
92	c5swcE	Alignment	not modelled	27.3	9	PDB header: lyase Chain: E: PDB Molecule: carbonic anhydrase; PDBTitle: the structure of the beta-carbonic anhydrase ccaa
93	c3fiuD	Alignment	not modelled	27.1	17	PDB header: ligase Chain: D: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nmN synthetase from francisella tularensis
94	c2zidA	Alignment	not modelled	27.0	12	PDB header: hydrolase Chain: A: PDB Molecule: dextran glucosidase; PDBTitle: crystal structure of dextran glucosidase e236q complex with2 isomaltotriose
95	c3bfjK	Alignment	not modelled	26.8	11	PDB header: oxidoreductase Chain: K: PDB Molecule: 1,3-propanediol oxidoreductase; PDBTitle: crystal structure analysis of 1,3-propanediol oxidoreductase
96	c3fkjA	Alignment	not modelled	26.5	18	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerases; PDBTitle: crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution
97	d1t57a	Alignment	not modelled	26.3	23	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
98	c4bmvH	Alignment	not modelled	26.0	20	PDB header: oxidoreductase Chain: H: PDB Molecule: short-chain dehydrogenase; PDBTitle: short-chain dehydrogenase from sphingobium yanoikuyae in2 complex with nadph
99	c3d3kD	Alignment	not modelled	25.2	9	PDB header: protein binding Chain: D: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
100	c3wtcB	Alignment	not modelled	24.7	23	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of gox2036
101	c4fn4A	Alignment	not modelled	24.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: short-chain nad(h)-dependent dehydrogenase/reductase from sulfolobus2 acidocaldarius
102	c3ak4C	Alignment	not modelled	24.6	12	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-dependent quinuclidinone reductase; PDBTitle: crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
103	d1uoka2	Alignment	not modelled	24.6	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain

104	c5wqnD_	Alignment	not modelled	24.5	17	PDB header: oxidoreductase Chain: D: PDB Molecule: probable dehydrogenase; PDBTitle: crystal structure of a carbonyl reductase from pseudomonas aeruginosa2 pao1 (condition ii)
105	d1v71a1	Alignment	not modelled	24.4	11	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
106	c5ff9C_	Alignment	not modelled	24.1	15	PDB header: oxidoreductase Chain: C: PDB Molecule: noroxomaritidine/norcroagsodine reductase; PDBTitle: noroxomaritidine/norcroagsodine reductase in complex with nadp+ and2 tyramine
107	d1xq1a_	Alignment	not modelled	24.0	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
108	c2d1fA_	Alignment	not modelled	23.9	16	PDB header: lyase Chain: A: PDB Molecule: threonine synthase; PDBTitle: structure of mycobacterium tuberculosis threonine synthase
109	d2hrca1	Alignment	not modelled	23.8	19	Fold: Chelatase-like Superfamily: Chelatase Family: Ferrochelatase
110	c3pzvB_	Alignment	not modelled	23.7	12	PDB header: hydrolase Chain: B: PDB Molecule: endoglucanase; PDBTitle: c2 crystal form of the endo-1,4-beta-glucanase from bacillus subtilis2 168
111	d1p5ja_	Alignment	not modelled	23.3	13	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
112	c1p5jA_	Alignment	not modelled	23.3	13	PDB header: lyase Chain: A: PDB Molecule: l-serine dehydratase; PDBTitle: crystal structure analysis of human serine dehydratase
113	c4iboA_	Alignment	not modelled	23.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: gluconate dehydrogenase; PDBTitle: crystal structure of a putative gluconate dehydrogenase from2 agrobacterium tumefaciens (target efi-506446)
114	c5jc8C_	Alignment	not modelled	22.6	20	PDB header: oxidoreductase Chain: C: PDB Molecule: putative short-chain dehydrogenase/reductase; PDBTitle: crystal structure of a putative short-chain dehydrogenase/reductase2 from burkholderia xenovorans
115	c6gwuB_	Alignment	not modelled	22.1	13	PDB header: lyase Chain: B: PDB Molecule: carbonic anhydrase; PDBTitle: carbonic anhydrase cancel103p from candida albicans
116	c5ak1A_	Alignment	not modelled	21.8	5	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate binding family 6; PDBTitle: the penta-modular cellulosomal arabinoxylanase ctxyl5a2 structure as revealed by x-ray crystallography
117	c3am1A_	Alignment	not modelled	21.4	8	PDB header: transferase Chain: A: PDB Molecule: os06g0726400 protein; PDBTitle: structure of the starch branching enzyme i (bei) from oryza sativa l
118	d1usua_	Alignment	not modelled	21.4	16	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Hsp90 middle domain
119	c5k9zB_	Alignment	not modelled	21.4	23	PDB header: oxidoreductase Chain: B: PDB Molecule: putative short-chain dehydrogenase/reductase; PDBTitle: crystal structure of putative short-chain dehydrogenase/reductase from2 burkholderia xenovorans lb400
120	c5zcrB_	Alignment	not modelled	21.3	13	PDB header: hydrolase Chain: B: PDB Molecule: maltooligosyl trehalose synthase; PDBTitle: dsm5389 glycosyltrehalose synthase