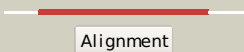

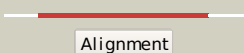

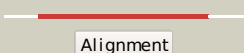

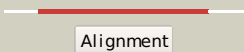

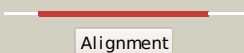

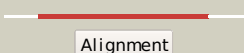

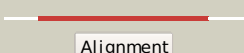

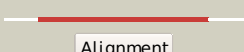

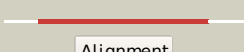

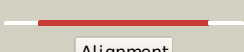

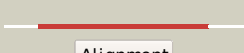

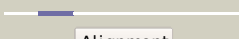

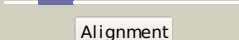
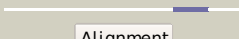
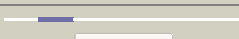
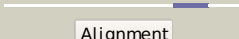


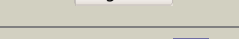

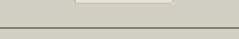

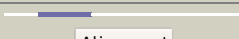
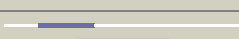


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sdoB_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrilotriacetate monooxygenase; PDBTitle: structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
2	c1tvIA_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: protein ytnj; PDBTitle: structure of ytnj from bacillus subtilis
3	d1tvIA_	 Alignment		100.0	21	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
4	c3raoB_	 Alignment		100.0	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative luciferase-like monooxygenase; PDBTitle: crystal structure of the luciferase-like monooxygenase from bacillus2 cereus atcc 10987.
5	c3b9nB_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: alkane monooxygenase; PDBTitle: crystal structure of long-chain alkane monooxygenase (lada)
6	d1nqka_	 Alignment		100.0	21	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
7	c2wgkA_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 3,6-diketocamphane 1,6 monooxygenase; PDBTitle: type ii baeyer-villiger monooxygenase oxygenating2 constituent of 3,6-diketocamphane 1,6 monooxygenase from3 pseudomonas putida
8	d1luca_	 Alignment		100.0	11	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
9	d1lucb_	 Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
10	c1z69D_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: D: PDB Molecule: coenzyme f420-dependent n(5),n(10)- PDBTitle: crystal structure of methylenetetrahydromethanopterin2 reductase (mer) in complex with coenzyme f420
11	d1ezwa_	 Alignment		100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases

12	c2i7gA_	Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: monooxygenase; PDBTitle: crystal structure of monooxygenase from agrobacterium tumefaciens
13	c3c8nB_	Alignment		100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: probable f420-dependent glucose-6-phosphate dehydrogenase PDBTitle: crystal structure of apo-fgd1 from mycobacterium tuberculosis
14	d1f07a_	Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
15	d1rhca_	Alignment		100.0	19	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
16	c2b81D_	Alignment		100.0	17	PDB header: oxidoreductase Chain: D: PDB Molecule: luciferase-like monooxygenase; PDBTitle: crystal structure of the luciferase-like monooxygenase from bacillus cereus
17	d1nfpa_	Alignment		99.9	14	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (LuxF, FP390)
18	d1fvpa_	Alignment		99.5	14	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (LuxF, FP390)
19	c1zlpA_	Alignment		83.4	8	PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
20	c3b8iF_	Alignment		82.5	19	PDB header: lyase Chain: F: PDB Molecule: pa4872 oxaloacetate decarboxylase; PDBTitle: crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
21	c3fa4D_	Alignment	not modelled	82.1	11	PDB header: lyase Chain: D: PDB Molecule: 2,3-dimethylmalate lyase; PDBTitle: crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
22	c3eool_	Alignment	not modelled	81.9	14	PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
23	c2ze3A_	Alignment	not modelled	81.1	19	PDB header: isomerase Chain: A: PDB Molecule: dfa0005; PDBTitle: crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
24	c3lyeA_	Alignment	not modelled	81.1	16	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
25	d1ujqa_	Alignment	not modelled	80.7	14	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
26	d1muma_	Alignment	not modelled	80.3	14	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
27	c2qiwa_	Alignment	not modelled	79.4	11	PDB header: transferase Chain: A: PDB Molecule: pep phosphonomutase; PDBTitle: crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
28	c3qy6A_	Alignment	not modelled	78.3	8	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase ywqe; PDBTitle: crystal structures of ywqe from bacillus subtilis and cpsb

						from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases
29	c3ih1A	Alignment	not modelled	77.7	8	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
30	c2x7vA	Alignment	not modelled	68.2	28	PDB header: hydrolase Chain: A: PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
31	d1s2wa	Alignment	not modelled	49.4	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
32	c2wjEA	Alignment	not modelled	49.2	16	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase cpsb; PDBTitle: crystal structure of the tyrosine phosphatase cps4b from2 streptococcus pneumoniae tigr4.
33	d1hl9a2	Alignment	not modelled	43.8	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Putative alpha-L-fucosidase, catalytic domain
34	c2hjpA	Alignment	not modelled	42.7	17	PDB header: hydrolase Chain: A: PDB Molecule: phosphonopyruvate hydrolase; PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
35	c3ez4B	Alignment	not modelled	36.8	13	PDB header: transferase Chain: B: PDB Molecule: 3-methyl-2-oxobutanoate hydroxymethyltransferase; PDBTitle: crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei
36	d1jpdX1	Alignment	not modelled	35.1	15	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
37	c3kwsB	Alignment	not modelled	34.2	9	PDB header: isomerase Chain: B: PDB Molecule: putative sugar isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distasonis atcc 8503 at 1.68 a resolution
38	d1r3sa	Alignment	not modelled	29.6	13	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Uroporphyrinogen decarboxylase, UROD
39	c1jpkA	Alignment	not modelled	28.6	13	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: gly156asp mutant of human urod, human uroporphyrinogen iii2 decarboxylase
40	d2noca1	Alignment	not modelled	26.5	29	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
41	c1gshA	Alignment	not modelled	26.3	16	PDB header: glutathione biosynthesis ligase Chain: A: PDB Molecule: glutathione biosynthetic ligase; PDBTitle: structure of escherichia coli glutathione synthetase at ph 7.5
42	d2d69a1	Alignment	not modelled	26.2	16	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
43	c3e02A	Alignment	not modelled	26.2	25	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849; PDBTitle: crystal structure of a duf849 family protein (bx_e_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
44	c2hk1D	Alignment	not modelled	25.8	22	PDB header: isomerase Chain: D: PDB Molecule: d-psicose 3-epimerase; PDBTitle: crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose
45	d1xp3a1	Alignment	not modelled	25.3	23	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Endonuclease IV
46	c2r8wB	Alignment	not modelled	24.8	17	PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
47	d1j93a	Alignment	not modelled	24.7	19	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Uroporphyrinogen decarboxylase, UROD
48	c3gzaB	Alignment	not modelled	24.0	20	PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-l-fucosidase; PDBTitle: crystal structure of putative alpha-l-fucosidase (np_812709.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.60 a resolution
49	c3bh1A	Alignment	not modelled	22.4	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0371 protein dip2346; PDBTitle: crystal structure of protein dip2346 from corynebacterium diphtheriae
50	d1xkya1	Alignment	not modelled	21.9	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
51	c1hl8B	Alignment	not modelled	21.7	26	PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-l-fucosidase; PDBTitle: crystal structure of thermotoga maritima alpha-fucosidase
52	c3bi8A	Alignment	not modelled	20.8	17	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from clostridium2 botulinum
53	c2wvsD	Alignment	not modelled	20.6	19	PDB header: hydrolase Chain: D: PDB Molecule: alpha-l-fucosidase; PDBTitle: crystal structure of an alpha-l-fucosidase gh29 trapped2 covalent intermediate from bacteroides thetaiotaomicron in3 complex with 2-fluoro-fucosyl fluoride using an e288q4 mutant

54	c3pueA	 Alignment	not modelled	20.0	14	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
55	c3e38A	 Alignment	not modelled	19.4	16	PDB header: hydrolase Chain: A: PDB Molecule: two-domain protein containing predicted php-like metal- PDBTitle: crystal structure of a two-domain protein containing predicted php-2 like metal-dependent phosphoesterase (bv_u_3505) from bacteroides3 vulgatus atcc 8482 at 2.20 a resolution
56	c2nuxB	 Alignment	not modelled	18.1	8	PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate PDBTitle: 2-keto-3-deoxygluconate aldolase from sulfolobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
57	d2a6na1	 Alignment	not modelled	17.1	7	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
58	c1m7xC	 Alignment	not modelled	16.8	27	PDB header: transferase Chain: C: PDB Molecule: 1,4-alpha-glucan branching enzyme; PDBTitle: the x-ray crystallographic structure of branching enzyme
59	c3lerA	 Alignment	not modelled	16.1	14	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
60	c3k1dA	 Alignment	not modelled	16.0	31	PDB header: transferase Chain: A: PDB Molecule: 1,4-alpha-glucan-branching enzyme; PDBTitle: crystal structure of glycogen branching enzyme synonym: 1,4-alpha-d-2 glucan:1,4-alpha-d-glucan 6-glucosyl-transferase from mycobacterium3 tuberculosis h37rv
61	d1oyaa	 Alignment	not modelled	15.2	4	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
62	c2r94B	 Alignment	not modelled	15.1	16	PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxy-(6-phospho-)gluconate aldolase; PDBTitle: crystal structure of kd(p)ga from t.tenax
63	d1gxha	 Alignment	not modelled	15.0	27	Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins
64	d8ruca1	 Alignment	not modelled	14.0	10	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
65	c2ejaB	 Alignment	not modelled	13.9	10	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
66	d1z41a1	 Alignment	not modelled	13.5	21	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
67	c3gg2B	 Alignment	not modelled	13.4	9	PDB header: oxidoreductase Chain: B: PDB Molecule: sugar dehydrogenase, udp-glucose/gdp-mannose PDBTitle: crystal structure of udp-glucose 6-dehydrogenase from2 porphyromonas gingivalis bound to product udp-glucuronate
68	c2hmcA	 Alignment	not modelled	13.3	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
69	d1m6ya2	 Alignment	not modelled	13.2	11	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: MraW-like putative methyltransferases
70	c3dcpB	 Alignment	not modelled	12.9	24	PDB header: hydrolase Chain: B: PDB Molecule: histidinol-phosphatase; PDBTitle: crystal structure of the putative histidinol phosphatase2 hisk from listeria monocytogenes. northeast structural3 genomics consortium target lmr141.
71	c2infB	 Alignment	not modelled	12.8	10	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 bacillus subtilis
72	c3na8A	 Alignment	not modelled	12.4	16	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
73	c1rcxH	 Alignment	not modelled	12.0	10	PDB header: lyase (carbon-carbon) Chain: H: PDB Molecule: ribulose biphosphate carboxylase/oxygenase; PDBTitle: non-activated spinach rubisco in complex with its substrate2 ribulose-1,5-biphosphate
74	d1mzha	 Alignment	not modelled	12.0	6	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
75	c2vwtA	 Alignment	not modelled	11.8	12	PDB header: lyase Chain: A: PDB Molecule: yfau, 2-keto-3-deoxy sugar aldolase; PDBTitle: crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
76	d1vcva1	 Alignment	not modelled	11.6	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
77	c1bf2A	 Alignment	not modelled	11.3	16	PDB header: hydrolase Chain: A: PDB Molecule: isoamylase; PDBTitle: structure of pseudomonas isoamylase
		 Alignment				Fold: TIM beta/alpha-barrel

78	d1vyra_	Alignment	not modelled	11.2	14	Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
79	c3c6cA_	Alignment	not modelled	11.1	20	PDB header: hydrolase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
80	d1jpma1	Alignment	not modelled	11.0	21	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
81	d1m3ua_	Alignment	not modelled	10.8	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
82	c2l69A_	Alignment	not modelled	10.7	12	PDB header: de novo protein Chain: A: PDB Molecule: rossmann 2x3 fold protein; PDBTitle: solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or28
83	c2gq8A_	Alignment	not modelled	10.6	12	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, fmn-binding; PDBTitle: structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone
84	d2jnaa1	Alignment	not modelled	10.4	20	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
85	d1w3ia_	Alignment	not modelled	10.2	4	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
86	d1gsaa1	Alignment	not modelled	10.1	12	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Prokaryotic glutathione synthetase, N-terminal domain
87	d1q45a_	Alignment	not modelled	9.9	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
88	c2uwqA_	Alignment	not modelled	9.8	5	PDB header: apoptosis Chain: A: PDB Molecule: apoptosis-stimulating of p53 protein 2; PDBTitle: solution structure of aspp2 n-terminus
89	c3eypB_	Alignment	not modelled	9.8	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative alpha-l-fucosidase; PDBTitle: crystal structure of putative alpha-l-fucosidase from bacteroides2 thetaiotaomicron
90	d1m53a2	Alignment	not modelled	9.7	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
91	d1vjia_	Alignment	not modelled	9.7	12	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
92	c3l5aA_	Alignment	not modelled	9.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh/flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus
93	c3gkaB_	Alignment	not modelled	9.5	11	PDB header: oxidoreductase Chain: B: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
94	c1jd7A_	Alignment	not modelled	9.4	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplantis alpha-amylase
95	d1vhxa_	Alignment	not modelled	9.4	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
96	d1gwja_	Alignment	not modelled	9.3	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
97	c3cqkB_	Alignment	not modelled	9.2	23	PDB header: isomerase Chain: B: PDB Molecule: l-ribulose-5-phosphate 3-epimerase ulae; PDBTitle: crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
98	d1icpa_	Alignment	not modelled	9.1	12	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
99	c3gr7A_	Alignment	not modelled	9.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal2 crystal form