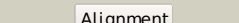
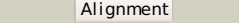
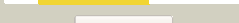
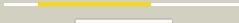
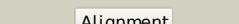
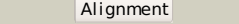
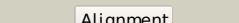
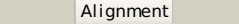
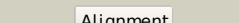
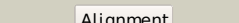
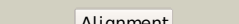
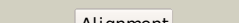
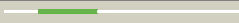


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fekA_	 Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight protein-tyrosine- PDBTitle: structure of a protein tyrosine phosphatase
2	c2wmyH_	 Alignment		100.0	54	PDB header: hydrolase Chain: H: PDB Molecule: putative acid phosphatase wzb; PDBTitle: crystal structure of the tyrosine phosphatase wzb from2 escherichia coli k30 in complex with sulphate.
3	d1dg9a_	 Alignment		100.0	30	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
4	c2gi4A_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: possible phosphotyrosine protein phosphatase; PDBTitle: solution structure of the low molecular weight protein2 tyrosine phosphatase from campylobacter jejuni.
5	c3jviA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: protein tyrosine phosphatase; PDBTitle: product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica
6	c2cwaA_	 Alignment		100.0	37	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight phosphotyrosine protein phosphatase; PDBTitle: crystal structure of tt1001 protein from thermus thermophilus hb8
7	c3rofA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight protein-tyrosine-phosphatase ptpa; PDBTitle: crystal structure of the s. aureus protein tyrosine phosphatase ptpa
8	d5pnta_	 Alignment		100.0	30	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
9	d1p8aa_	 Alignment		100.0	22	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
10	c1zgga_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: putative low molecular weight protein-tyrosine- PDBTitle: solution structure of a low molecular weight protein2 tyrosine phosphatase from bacillus subtilis
11	c1u2pA_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight protein-tyrosine- PDBTitle: crystal structure of mycobacterium tuberculosis low2 molecular protein tyrosine phosphatase (mptpa) at 1.9a3 resolution

12	d1d1qa_	Alignment		100.0	28	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
13	c2l18A_	Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase; PDBTitle: an arsenate reductase in the phosphate binding state
14	d1jf8a_	Alignment		100.0	23	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
15	d1jl3a_	Alignment		100.0	22	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
16	d1y11a_	Alignment		100.0	27	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
17	c3rh0A_	Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase; PDBTitle: corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
18	c3t38B_	Alignment		100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: arsenate reductase; PDBTitle: corynebacterium glutamicum thioredoxin-dependent arsenate reductase2 cg_arsc1'
19	c3fdfA_	Alignment		97.5	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: fr253; PDBTitle: crystal structure of the serine phosphatase of rna2 polymerase ii ctd (ssu72 superfamily) from drosophila3 melanogaster. orthorhombic crystal form. northeast4 structural genomics consortium target fr253.
20	c3o2qB_	Alignment		96.9	31	PDB header: hydrolase Chain: B: PDB Molecule: rna polymerase ii subunit a c-terminal domain phosphatase PDBTitle: crystal structure of the human symplekin-ssu72-ctd phosphopeptide2 complex
21	c3o2sB_	Alignment	not modelled	96.6	32	PDB header: hydrolase Chain: B: PDB Molecule: rna polymerase ii subunit a c-terminal domain phosphatase PDBTitle: crystal structure of the human symplekin-ssu72 complex
22	c2f00A_	Alignment	not modelled	93.3	17	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: escherichia coli murc
23	d1gpja2	Alignment	not modelled	91.8	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
24	c1j6uA_	Alignment	not modelled	89.0	15	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-alanine ligase murc; PDBTitle: crystal structure of udp-n-acetylmuramate-alanine ligase2 murc (tm0231) from thermotoga maritima at 2.3 a resolution
25	d1p3da1	Alignment	not modelled	87.8	20	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
26	c1gpjA_	Alignment	not modelled	86.7	16	PDB header: reductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: glutamyl-trna reductase from methanopyrus kandleri
27	d1j6ua1	Alignment	not modelled	83.9	14	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
28	c1gqqA_	Alignment	not modelled	82.6	20	PDB header: cell wall biosynthesis Chain: A: PDB Molecule: udp-n-acetylmuramate-l-alanine ligase; PDBTitle: murc - crystal structure of the apo-enzyme from haemophilus2 influenzae PDB header: hydrolase

29	c2bibA	 Alignment	not modelled	81.6	9	Chain: A: PDB Molecule: teichoic acid phosphorylcholine esterase/ choline binding PDBTitle: crystal structure of the complete modular teichoic acid2 phosphorylcholine esterase pce (cbpe) from streptococcus3 pneumoniae
30	c3eagA	 Alignment	not modelled	76.0	12	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso- PDBTitle: the crystal structure of udp-n-acetylmuramate:l-alanyl-gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from neisseria3 meningitides
31	c2eq8C	 Alignment	not modelled	72.3	21	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
32	c3czcA	 Alignment	not modelled	71.9	14	PDB header: transferase Chain: A: PDB Molecule: rmpb; PDBTitle: the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
33	d1vlva2	 Alignment	not modelled	71.3	8	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
34	d1u6ka1	 Alignment	not modelled	71.3	25	Fold: F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD) Superfamily: F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD) Family: F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD)
35	d1vkra	 Alignment	not modelled	71.2	21	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellobiose specific IIB subunit
36	c1vkrA	 Alignment	not modelled	71.2	21	PDB header: transferase Chain: A: PDB Molecule: mannitol-specific pts system enzyme iiabc components; PDBTitle: structure of iib domain of the mannitol-specific permease enzyme ii
37	c3ktdC	 Alignment	not modelled	71.0	13	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
38	d1pjqa1	 Alignment	not modelled	70.1	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
39	c3kcgA	 Alignment	not modelled	69.5	15	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 anaplasma phagocytophilum
40	c3oj0A	 Alignment	not modelled	64.5	22	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: crystal structure of glutamyl-trna reductase from thermoplasma2 volcanium (nucleotide binding domain)
41	c3hn7A	 Alignment	not modelled	63.8	13	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-l-alanine ligase; PDBTitle: crystal structure of a murein peptide ligase mpl (psyc_0032) from2 psychrobacter arcticus 273-4 at 1.65 a resolution
42	c2ph5A	 Alignment	not modelled	60.3	9	PDB header: transferase Chain: A: PDB Molecule: homospermidine synthase; PDBTitle: crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
43	c1e0cA	 Alignment	not modelled	57.3	16	PDB header: sulfurtransferase Chain: A: PDB Molecule: sulfurtransferase; PDBTitle: sulfurtransferase from azotobacter vinelandii
44	c1wv9B	 Alignment	not modelled	56.3	28	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: rhodanese homolog tt1651; PDBTitle: crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
45	d2czca2	 Alignment	not modelled	56.2	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
46	c3d1pA	 Alignment	not modelled	55.9	14	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase yor285w; PDBTitle: atomic resolution structure of uncharacterized protein from2 saccharomyces cerevisiae
47	c2k0zA	 Alignment	not modelled	55.7	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein hp1203; PDBTitle: solution nmr structure of protein hp1203 from helicobacter pylori2 26695. northeast structural genomics consortium (nesg) target3 pt1/ontario center for structural proteomics target hp1203
48	d1w4ha1	 Alignment	not modelled	55.0	16	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
49	d1yt8a4	 Alignment	not modelled	54.8	12	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
50	d1bala	 Alignment	not modelled	54.8	19	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid

					dehydrogenase complex
51	d2z06a1	Alignment	not modelled	54.6	18 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TTHA0625-like
52	d2fug21	Alignment	not modelled	54.5	29 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: NQO2-like
53	c3fojA	Alignment	not modelled	53.9	14 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of ssp1007 from staphylococcus2 saprophyticus subsp. saprophyticus. northeast structural3 genomics target syr101a.
54	d1w85i	Alignment	not modelled	53.7	13 Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
55	c2i99A	Alignment	not modelled	53.3	15 PDB header: oxidoreductase Chain: A: PDB Molecule: mu-crystallin homolog; PDBTitle: crystal structure of human mu_crystallin at 2.6 angstrom
56	c1tvmA	Alignment	not modelled	53.3	24 PDB header: transferase Chain: A: PDB Molecule: pts system, galactitol-specific iib component; PDBTitle: nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system
57	c3c1oA	Alignment	not modelled	52.4	8 PDB header: oxidoreductase Chain: A: PDB Molecule: eugenol synthase; PDBTitle: the multiple phenylpropene synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages
58	c2eq9C	Alignment	not modelled	51.7	25 PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
59	d1wraa1	Alignment	not modelled	49.7	9 Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Pce catalytic domain-like
60	c3dfzB	Alignment	not modelled	49.6	16 PDB header: oxidoreductase Chain: B: PDB Molecule: precorrin-2 dehydrogenase; PDBTitle: sirc, precorrin-2 dehydrogenase
61	d1cmca	Alignment	not modelled	49.5	15 Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Met repressor, MetJ (MetR)
62	c2auvA	Alignment	not modelled	49.0	21 PDB header: oxidoreductase Chain: A: PDB Molecule: potential nad-reducing hydrogenase subunit; PDBTitle: solution structure of hndac : a thioredoxin-like [2fe-2s]2 ferredoxin involved in the nadp-reducing hydrogenase3 complex
63	c2eq7C	Alignment	not modelled	48.2	19 PDB header: oxidoreductase Chain: C: PDB Molecule: 2-oxoglutarate dehydrogenase e2 component; PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
64	d2cyua1	Alignment	not modelled	48.2	19 Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
65	c3tqrA	Alignment	not modelled	48.0	15 PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
66	c3emeA	Alignment	not modelled	46.9	19 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: rhodanese-like domain protein; PDBTitle: crystal structure of rhodanese-like domain protein from2 staphylococcus aureus
67	c1zwvA	Alignment	not modelled	46.3	22 PDB header: transferase Chain: A: PDB Molecule: lipoamide acyltransferase component of branched- PDBTitle: solution structure of the subunit binding domain (hbsbd) of2 the human mitochondrial branched-chain alpha-ketoacid3 dehydrogenase
68	c1w3dA	Alignment	not modelled	46.2	13 PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase PDBTitle: nmr structure of the peripheral-subunit binding domain of2 bacillus stearothermophilus e2p
69	c2jrlA	Alignment	not modelled	45.3	19 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: solution structure of the berylliofluoride-activated ntrc4 receiver2 domain dimer
70	c3i2vA	Alignment	not modelled	44.9	29 PDB header: transferase Chain: A: PDB Molecule: adenyllyltransferase and sulfurtransferase mocs3; PDBTitle: crystal structure of human mocs3 rhodanese-like domain
71	d1t71a	Alignment	not modelled	43.6	17 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DR1281-like
72	c1w4kA	Alignment	not modelled	43.2	19 PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase e2; PDBTitle: peripheral-subunit binding domains from mesophilic,2 thermophilic, and hyperthermophilic bacteria fold by3 ultrafast, apparently two-state transitions
					PDB header: structural genomics, unknown function

73	c3ilmD_	Alignment	not modelled	42.5	24	Chain: D: PDB Molecule: alr3790 protein; PDBTitle: crystal structure of the alr3790 protein from anabaena sp. northeast2 structural genomics consortium target nsr437h
74	c2e85B_	Alignment	not modelled	42.5	23	PDB header: hydrolase Chain: B: PDB Molecule: hydrogenase 3 maturation protease; PDBTitle: crystal structure of the hydrogenase 3 maturation protease
75	d1f0ya2	Alignment	not modelled	42.1	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
76	c2cooA_	Alignment	not modelled	41.6	25	PDB header: transferase Chain: A: PDB Molecule: lipoamide acyltransferase component of branched- PDBTitle: solution structure of the e3_binding domain of2 dihydrolipoamide branched chaintransacylase
77	d1rrma_	Alignment	not modelled	41.0	7	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
78	d1w85b2	Alignment	not modelled	41.0	11	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
79	d1f37b_	Alignment	not modelled	40.8	22	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioredoxin-like 2Fe-2S ferredoxin
80	c2rgwD_	Alignment	not modelled	40.5	10	PDB header: transferase Chain: D: PDB Molecule: aspartate carbamoyltransferase; PDBTitle: catalytic subunit of m. jannaschii aspartate2 transcarbamoylase
81	c3k96B_	Alignment	not modelled	38.7	9	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p)+]; PDBTitle: 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii
82	c3g5jA_	Alignment	not modelled	38.6	24	PDB header: nucleotide binding protein Chain: A: PDB Molecule: putative atp/gtp binding protein; PDBTitle: crystal structure of n-terminal domain of putative atp/gtp binding2 protein from clostridium difficile 630
83	c2weuD_	Alignment	not modelled	36.9	20	PDB header: antifungal protein Chain: D: PDB Molecule: tryptophan 5-halogenase; PDBTitle: crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
84	c3dv0l_	Alignment	not modelled	36.6	18	PDB header: oxidoreductase/transferase Chain: I: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase PDBTitle: snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
85	d1jzta_	Alignment	not modelled	36.4	9	Fold: YjeF N-terminal domain-like Superfamily: YjeF N-terminal domain-like Family: YjeF N-terminal domain-like
86	d1okga2	Alignment	not modelled	35.4	9	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
87	c3gt0A_	Alignment	not modelled	35.2	9	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: crystal structure of pyrroline 5-carboxylate reductase from bacillus2 cereus. northeast structural genomics consortium target bcr38b
88	c3luyA_	Alignment	not modelled	34.6	11	PDB header: isomerase Chain: A: PDB Molecule: probable chorismate mutase; PDBTitle: putative chorismate mutase from bifidobacterium adolescentis
89	c3dcjA_	Alignment	not modelled	34.5	18	PDB header: transferase Chain: A: PDB Molecule: probable 5'-phosphoribosylglycinamide PDBTitle: crystal structure of glycinamide formyltransferase (purn)2 from mycobacterium tuberculosis in complex with 5-methyl-5,3 6,7,8-tetrahydrofolic acid derivative
90	d1cfza_	Alignment	not modelled	32.7	37	Fold: Phosphorylase/hydrolase-like Superfamily: HybD-like Family: Hydrogenase maturing endopeptidase HybD
91	d1urha1	Alignment	not modelled	32.6	21	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
92	c3l6dB_	Alignment	not modelled	32.3	11	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
93	d1e0ca1	Alignment	not modelled	32.2	16	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
94	c2hi1A_	Alignment	not modelled	32.2	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 4-hydroxythreonine-4-phosphate dehydrogenase 2; PDBTitle: the structure of a putative 4-hydroxythreonine-4-phosphate2 dehydrogenase from salmonella typhimurium.
95	c3bfjK_	Alignment	not modelled	31.5	12	PDB header: oxidoreductase Chain: K: PDB Molecule: 1,3-propanediol oxidoreductase; PDBTitle: crystal structure analysis of 1,3-propanediol oxidoreductase
96	c3nbmA_	Alignment	not modelled	31.5	20	PDB header: transferase Chain: A: PDB Molecule: pts system, lactose-specific iibc components; PDBTitle: the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
97	d1iiba_	Alignment	not modelled	30.7	11	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like

					Family: PTS system, Lactose/Cellobiose specific IIB subunit
98	c3ippA_	Alignment	not modelled	29.7	11 PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase ynje; PDBTitle: crystal structure of sulfur-free ynje
99	d1e6ca_	Alignment	not modelled	29.0	15 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Shikimate kinase (AroK)
100	c2jtaA_	Alignment	not modelled	28.6	19 PDB header: transferase Chain: A: PDB Molecule: phage shock protein e; PDBTitle: rhodanese from e.coli
101	d1umdb2	Alignment	not modelled	28.2	13 Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
102	d2jfga1	Alignment	not modelled	28.2	12 Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
103	d1ekxa2	Alignment	not modelled	28.0	13 Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
104	d2bw0a2	Alignment	not modelled	27.8	12 Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
105	c1s3iA_	Alignment	not modelled	26.5	12 PDB header: hydrolase, oxidoreductase Chain: A: PDB Molecule: 10-formyltetrahydrofolate dehydrogenase; PDBTitle: crystal structure of the n terminal hydrolase domain of 10-2 formyltetrahydrofolate dehydrogenase
106	d1meoa_	Alignment	not modelled	26.1	10 Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
107	c3gk5A_	Alignment	not modelled	26.0	19 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized rhodanese-related protein PDBTitle: crystal structure of rhodanese-related protein (tvg0868615)2 from thermoplasma volcanium, northeast structural genomics3 consortium target tvr109a
108	c1ulza_	Alignment	not modelled	25.6	29 PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase n-terminal domain; PDBTitle: crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
109	d1dxha2	Alignment	not modelled	25.6	15 Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
110	d1t70a_	Alignment	not modelled	25.3	20 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DR1281-like
111	d1duvg2	Alignment	not modelled	25.2	11 Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
112	c3nhza_	Alignment	not modelled	24.9	27 PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
113	c3nhvE_	Alignment	not modelled	24.9	13 PDB header: structural genomics, unknown function Chain: E: PDB Molecule: bh2092 protein; PDBTitle: crystal structure of bh2092 protein from bacillus halodurans,2 northeast structural genomics consortium target bhr228f
114	c3aaxB_	Alignment	not modelled	24.7	16 PDB header: transferase Chain: B: PDB Molecule: putative thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
115	d1uara2	Alignment	not modelled	24.3	16 Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
116	c3cm0A_	Alignment	not modelled	24.1	21 PDB header: transferase Chain: A: PDB Molecule: adenylate kinase; PDBTitle: crystal structure of adenylate kinase from thermus2 thermophilus hb8
117	c3klbA_	Alignment	not modelled	23.7	30 PDB header: flavoprotein Chain: A: PDB Molecule: putative flavoprotein; PDBTitle: crystal structure of putative flavoprotein in complex with frn2 (yp_213683.1) from bacteroides fragilis nctc 9343 at 1.75 a3 resolution
118	d1rhsa1	Alignment	not modelled	23.6	13 Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
119	d2qmwa2	Alignment	not modelled	22.9	13 Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
120	c2dumD_	Alignment	not modelled	22.3	16 PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein ph0823; PDBTitle: crystal structure of hypothetical protein, ph0823