

























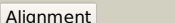

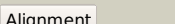
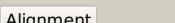
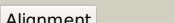

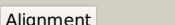
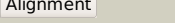
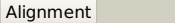
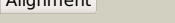
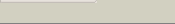




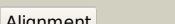
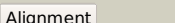
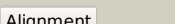

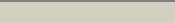


Phyre2


Email	mdejesus@rockefeller.edu
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Date	Wed Aug 7 12:50:29 BST 2019
Unique Job ID	b4913b37a3425e62

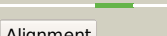

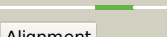
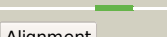
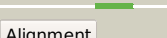

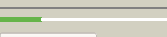



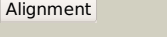

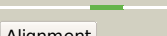
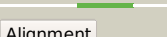



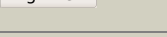
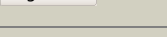
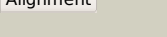
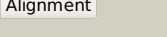
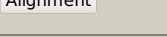
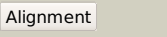
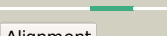
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4n7wA_	 Alignment		100.0	21	PDB header: transport protein Chain: A: PDB Molecule: transporter, sodium/bile acid symporter family; PDBTitle: crystal structure of the sodium bile acid symporter from yersinia2 frederiksenii
2	c3t38B_	 Alignment		100.0	40	PDB header: oxidoreductase Chain: B: PDB Molecule: arsenate reductase; PDBTitle: corynebacterium glutamicum thioredoxin-dependent arsenate reductase2 cg_arsc1'
3	d1jf8a_	 Alignment		100.0	34	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
4	c3rh0A_	 Alignment		100.0	34	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase; PDBTitle: corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
5	c2l18A_	 Alignment		100.0	37	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase; PDBTitle: an arsenate reductase in the phosphate binding state
6	d1p8aa_	 Alignment		100.0	22	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
7	d1y11a_	 Alignment		100.0	31	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
8	c2fekA_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight protein-tyrosine- PDBTitle: structure of a protein tyrosine phosphatase
9	c4lrqC_	 Alignment		100.0	24	PDB header: hydrolase Chain: C: PDB Molecule: phosphotyrosine protein phosphatase; PDBTitle: crystal structure of a low molecular weight phosphotyrosine2 phosphatase from vibrio choleraeo395
10	c4d74A_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine-phosphatase amsi; PDBTitle: 1.57 a crystal structure of erwinia amylovora tyrosine phosphatase2 amsi
11	c5z3mB_	 Alignment		100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: phosphotyrosine protein phosphatase; PDBTitle: crystal structure of low molecular weight phosphotyrosine phosphatase2 (vclmwptp-2) from vibrio choleraeo395

12	c2wmyH_	Alignment		100.0	17	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.
13	c4picA_	Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: arginine phosphatase ywle; PDBTitle: ywle arginine phosphatase from geobacillus stearothermophilus
14	d1dg9a_	Alignment		100.0	20	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
15	d5pnta_	Alignment		100.0	19	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
16	c2cwaA_	Alignment		100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight phosphotyrosine protein phosphatase; PDBTitle: crystal structure of tt1001 protein from thermus thermophilus hb8
17	c4egsB_	Alignment		100.0	31	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase rpib; PDBTitle: crystal structure analysis of low molecular weight protein tyrosine2 phosphatase from t. tengcongensis
18	d1j3a_	Alignment		100.0	34	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
19	c3jviA_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: protein tyrosine phosphatase; PDBTitle: product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica
20	c4etiA_	Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight protein-tyrosine-phosphatase ywle; PDBTitle: crystal structure of ywle from bacillus subtilis
21	d1d1qa_	Alignment	not modelled	100.0	18	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
22	c1zggA_	Alignment	not modelled	100.0	30	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
23	c1u2pA_	Alignment	not modelled	100.0	19	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
24	c4etmB_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: low molecular weight protein-tyrosine-phosphatase yfkj; PDBTitle: crystal structure of yfkj from bacillus subtilis
25	c5gotA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight phosphotyrosine phosphatase family PDBTitle: crystal structure of sp-ptp, low molecular weight protein tyrosine2 phosphatase from streptococcus pyogenes
26	c2qi4A_	Alignment	not modelled	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.
27	c3rofA_	Alignment	not modelled	100.0	22	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

28	c5o7bA	 Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: putative low molecular weight protein-tyrosine-phosphatase PDBTitle: crystal structure of the slr0328 tyrosine phosphatase wzb from2 synechocystis sp. pcc 6803
29	c4cz8A	 Alignment	not modelled	97.8	13	PDB header: membrane protein Chain: A: PDB Molecule: na+/h+ antiporter, putative; PDBTitle: structure of the sodium proton antiporter panhap from2 pyrococcus abyssii at ph 8.
30	c4bwzA	 Alignment	not modelled	97.5	10	PDB header: transport protein Chain: A: PDB Molecule: na(+)/h(+) antiporter; PDBTitle: crystal structure of the sodium proton antiporter, napa
31	c5bz3A	 Alignment	not modelled	97.5	10	PDB header: transport protein Chain: A: PDB Molecule: na(+)/h(+) antiporter; PDBTitle: crystal structure of sodium proton antiporter napa in outward-facing2 conformation.
32	c4czbB	 Alignment	not modelled	97.4	10	PDB header: membrane protein Chain: B: PDB Molecule: na(+)/h(+) antiporter 1; PDBTitle: structure of the sodium proton antiporter mjnhap1 from2 methanocaldococcus jannaschii at ph 8.
33	c5lm4A	 Alignment	not modelled	95.1	12	PDB header: transport protein Chain: A: PDB Molecule: excitatory amino acid transporter 1,neutral amino acid PDBTitle: structure of the thermostalilized eaat1 cryst-ii mutant in complex2 with l-asp and the allosteric inhibitor ucph101
34	c3fdfA	 Alignment	not modelled	93.4	26	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.
35	c4ky0B	 Alignment	not modelled	90.7	15	PDB header: transport protein, membrane protein Chain: B: PDB Molecule: proton/glutamate symporter, sdf family; PDBTitle: crystal structure of a substrate-free glutamate transporter homologue2 from thermococcus kodakarensis
36	c1zcdA	 Alignment	not modelled	90.4	19	PDB header: membrane protein Chain: A: PDB Molecule: na(+)/h(+) antiporter 1; PDBTitle: crystal structure of the na+/h+ antiporter nhaa
37	d2nwwa1	 Alignment	not modelled	90.2	15	Fold: Proton glutamate symport protein Superfamily: Proton glutamate symport protein Family: Proton glutamate symport protein
38	d1jzta	 Alignment	not modelled	88.9	13	Fold: YjeF N-terminal domain-like Superfamily: YjeF N-terminal domain-like Family: YjeF N-terminal domain-like
39	c1h6dL	 Alignment	not modelled	88.8	12	PDB header: protein translocation Chain: L: PDB Molecule: precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
40	c1ofgF	 Alignment	not modelled	88.4	12	PDB header: oxidoreductase Chain: F: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: glucose-fructose oxidoreductase
41	c1j6uA	 Alignment	not modelled	87.4	22	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-alanine ligase murc; PDBTitle: crystal structure of udp-n-acetylmuramate-alanine ligase murc (tm0231)2 from thermotoga maritima at 2.3 a resolution
42	c6cauA	 Alignment	not modelled	87.2	19	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: udp-n-acetylmuramate--alanine ligase from acinetobacter baumannii2 ab5075-uw with amppnp
43	d1v1va2	 Alignment	not modelled	86.1	19	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
44	c2f00A	 Alignment	not modelled	84.3	20	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: escherichia coli murc
45	d1j6ua1	 Alignment	not modelled	83.4	22	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
46	d1p3da1	 Alignment	not modelled	80.2	22	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
47	c3o2qB	 Alignment	not modelled	77.0	36	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
48	c3ceaA	 Alignment	not modelled	76.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: myo-inositol 2-dehydrogenase; PDBTitle: crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
49	d1u6ka1	 Alignment	not modelled	75.3	29	Fold: F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD) Superfamily: F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD) Family: F420-dependent methylenetetrahydromethanopterin dehydrogenase (MTD)
50	c2bibA	 Alignment	not modelled	74.6	17	PDB header: hydrolase Chain: A: PDB Molecule: teichoic acid phosphorylcholine esterase/ choline binding PDBTitle: crystal structure of the complete modular teichoic acid2 phosphorylcholine esterase pce (cbpe) from streptococcus pneumoniae
51	d1r8ka	 Alignment	not modelled	73.9	19	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: PdxA-like

52	c1tvmA	 Alignment	not modelled	73.4	22	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
53	c1vkrA	 Alignment	not modelled	73.0	26	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
54	d1vkra	 Alignment	not modelled	73.0	26	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellobiose specific IIB subunit
55	d1h6da1	 Alignment	not modelled	72.6	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
56	c5zbyA	 Alignment	not modelled	71.7	17	PDB header: hydrolase Chain: A: PDB Molecule: hydrogenase maturation protease hyci; PDBTitle: crystal structure of a [nife] hydrogenase maturation protease hyci2 from thermococcus kodakarensis kod1
57	d1duvg2	 Alignment	not modelled	71.2	17	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
58	c3dfzB	 Alignment	not modelled	71.2	18	PDB header: oxidoreductase Chain: B: PDB Molecule: precorrin-2 dehydrogenase; PDBTitle: sirc, precorrin-2 dehydrogenase
59	c4ehxA	 Alignment	not modelled	71.0	18	PDB header: transferase Chain: A: PDB Molecule: tetraacyldisaccharide 4'-kinase; PDBTitle: crystal structure of lpxk from aquifex aeolicus at 1.9 angstrom2 resolution
60	d1dxha2	 Alignment	not modelled	70.9	18	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
61	d1umdb2	 Alignment	not modelled	69.3	12	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
62	c4f67A	 Alignment	not modelled	69.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0176 protein lpg2838; PDBTitle: three dimensional structure of the double mutant of upf0176 protein2 lpg2838 from legionella pneumophila at the resolution 1.8a, northeast3 structural genomics consortium (nseg) target lgr82
63	c3dcjA	 Alignment	not modelled	67.8	16	PDB header: transferase Chain: A: PDB Molecule: probable 5'-phosphoribosylglycinamide formyltransferase PDBTitle: crystal structure of glycinamide formyltransferase (purn) from2 mycobacterium tuberculosis in complex with 5-methyl-5,6,7,8-3 tetrahydrofolic acid derivative
64	c3hn7A	 Alignment	not modelled	67.3	16	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
65	c2hi1A	 Alignment	not modelled	66.2	20	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.
66	c3c24A	 Alignment	not modelled	66.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase (yp_511008.1) from2 jannaschia sp. ccs1 at 1.62 a resolution
67	c3rbvA	 Alignment	not modelled	64.7	11	PDB header: sugar binding protein Chain: A: PDB Molecule: sugar 3-ketoreductase; PDBTitle: crystal structure of kjid10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
68	c3o2sB	 Alignment	not modelled	64.2	40	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
69	c3eagA	 Alignment	not modelled	64.1	14	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
70	c6norB	 Alignment	not modelled	63.6	16	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nad dependent dehydrogenase; PDBTitle: crystal structure of gend2 from gentamicin a biosynthesis in complex2 with nad
71	c4oqyA	 Alignment	not modelled	62.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: (s)-imine reductase; PDBTitle: streptomyces sp. gf3546 imine reductase
72	d1w85b2	Alignment	not modelled	61.0	16	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
73	c2eq8C	Alignment	not modelled	59.9	24	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
74	d2jfga1	Alignment	not modelled	58.8	16	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
75	c5vvaA	Alignment	not modelled	58.3	20	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-l-alanine ligase; PDBTitle: structure of murc from pseudomonas aeruginosa

76	c4iv5E_	 Alignment	not modelled	58.1	18	PDB header: transferase Chain: E: PDB Molecule: aspartate carbamoyltransferase, putative; PDBTitle: x-ray crystal structure of a putative aspartate carbamoyltransferase2 from trypanosoma cruzi
77	d1fmta2	 Alignment	not modelled	58.0	26	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
78	c2yvka_	 Alignment	not modelled	57.5	16	PDB header: isomerase Chain: A: PDB Molecule: methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
79	c3b1fa_	 Alignment	not modelled	56.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: putative prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 mutans
80	c4d3fb_	 Alignment	not modelled	55.7	18	PDB header: oxidoreductase Chain: B: PDB Molecule: imine reductase; PDBTitle: bcsired from bacillus cereus in complex with nadph
81	c4y7je_	 Alignment	not modelled	55.6	8	PDB header: membrane protein,transport protein Chain: E: PDB Molecule: large conductance mechanosensitive channel protein, PDBTitle: structure of an archaeal mechanosensitive channel in expanded state
82	c4z7fd_	 Alignment	not modelled	54.4	12	PDB header: transport protein Chain: D: PDB Molecule: folate ecf transporter; PDBTitle: crystal structure of folt bound with folic acid
83	c4bucA_	 Alignment	not modelled	53.9	15	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoylalanine--d-glutamate ligase; PDBTitle: crystal structure of murd ligase from thermotoga maritima in apo form
84	c2q62A_	 Alignment	not modelled	53.9	15	PDB header: flavoprotein Chain: A: PDB Molecule: arsh; PDBTitle: crystal structure of arsh from sinorhizobium meliloti
85	c2kyrA_	 Alignment	not modelled	53.9	18	PDB header: transferase Chain: A: PDB Molecule: fructose-like phosphotransferase enzyme iib component 1; PDBTitle: solution structure of enzyme iib subunit of pts system from2 escherichia coli k12. northeast structural genomics consortium target3 er315/ontario center for structural proteomics target ec0544
86	c1gqaA_	 Alignment	not modelled	53.0	23	PDB header: cell wall biosynthesis Chain: A: PDB Molecule: udp-n-acetylmuramate-l-alanine ligase; PDBTitle: murc - crystal structure of the apo-enzyme from haemophilus influenzae
87	c1e0cA_	 Alignment	not modelled	52.8	17	PDB header: sulfurtransferase Chain: A: PDB Molecule: sulfurtransferase; PDBTitle: sulfurtransferase from azotobacter vinelandii
88	c4o9uB_	 Alignment	not modelled	52.8	18	PDB header: membrane protein Chain: B: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
89	c2bp7F_	 Alignment	not modelled	52.6	20	PDB header: oxidoreductase Chain: F: PDB Molecule: 2-oxoisovalerate dehydrogenase beta subunit; PDBTitle: new crystal form of the pseudomonas putida branched-chain2 dehydrogenase (e1)
90	c2ph5A_	 Alignment	not modelled	52.2	13	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
91	c3triB_	 Alignment	not modelled	52.1	19	PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
92	c4ldrA_	 Alignment	not modelled	51.4	23	PDB header: isomerase, cell invasion Chain: A: PDB Molecule: methylthioribose-1-phosphate isomerase; PDBTitle: structure of the s283y mutant of mrdi
93	c4jqpa_	 Alignment	not modelled	50.9	26	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxythreonine-4-phosphate dehydrogenase; PDBTitle: x-ray crystal structure of a 4-hydroxythreonine-4-phosphate2 dehydrogenase from burkholderia phymatum
94	d1pqqa1	 Alignment	not modelled	50.6	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
95	c2eg4B_	 Alignment	not modelled	49.9	23	PDB header: transferase Chain: B: PDB Molecule: probable thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase
96	c3db2C_	 Alignment	not modelled	49.9	14	PDB header: oxidoreductase Chain: C: PDB Molecule: putative nadph-dependent oxidoreductase; PDBTitle: crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
97	d1qs0b2	 Alignment	not modelled	49.9	18	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
98	c2moiA_	 Alignment	not modelled	49.8	16	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the cytoplasmic rhodanese domain of the inner2 membrane protein ygap from escherichia coli
99	c1pitB_	 Alignment	not modelled	49.5	10	PDB header: transferase/oxidoreductase/lyase Chain: B: PDB Molecule: siroheme synthase; PDBTitle: the structure of the ser128ala point-mutant variant of

99	c1qjdB	Alignment	not modelled	49.5	19	cysg, the2 multifunctional methyltransferase/dehydrogenase/ferrochelatase for3 siroheme synthesis
100	c4ds3A	Alignment	not modelled	48.6	10	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 brucella melitensis
101	c4ew6A	Alignment	not modelled	47.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: d-galactose-1-dehydrogenase protein; PDBTitle: crystal structure of d-galactose-1-dehydrogenase protein from2 rhizobium etli
102	c1yx0B	Alignment	not modelled	47.7	23	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxythreonine-4-phosphate dehydrogenase 1; PDBTitle: crystal structure of pyridoxal phosphate biosynthetic protein pdxa2 pa0593
103	c2nqgA	Alignment	not modelled	46.3	25	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin biosynthesis protein moea; PDBTitle: moea r137q
104	d1ptma	Alignment	not modelled	45.8	19	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: PdxA-like
105	d1t2da1	Alignment	not modelled	45.5	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
106	c3dzba	Alignment	not modelled	44.5	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
107	c3gt0A	Alignment	not modelled	43.4	15	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
108	c3ilmD	Alignment	not modelled	43.2	11	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: alr3790 protein; PDBTitle: crystal structure of the alr3790 protein from anabaena sp. northeast2 structural genomics consortium target nsr437h
109	d1ryda1	Alignment	not modelled	42.9	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
110	c5ayvB	Alignment	not modelled	42.4	15	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of archaeal ketopantoate reductase complexed with2 coenzyme a and 2-oxopantoate
111	c1gpiA	Alignment	not modelled	42.4	21	PDB header: reductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: glutamyl-trna reductase from methanopyrus kandleri
112	c3wfdD	Alignment	not modelled	41.8	17	PDB header: oxidoreductase Chain: D: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: the complex structure of d-mandelate dehydrogenase with nadh
113	d1rhsa2	Alignment	not modelled	41.4	8	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
114	d1f37b	Alignment	not modelled	41.1	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioredoxin-like 2Fe-2S ferredoxin
115	c2i99A	Alignment	not modelled	41.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: mu-crystallin homolog; PDBTitle: crystal structure of human mu_crystallin at 2.6 angstrom
116	d2z06a1	Alignment	not modelled	40.4	14	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TTHA0625-like
117	c5gziB	Alignment	not modelled	39.9	17	PDB header: lyase Chain: B: PDB Molecule: lysine cyclodeaminase; PDBTitle: cyclodeaminase_pa
118	d2fug21	Alignment	not modelled	39.7	24	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: NQO2-like
119	c5gqsA	Alignment	not modelled	39.0	18	PDB header: transport protein Chain: A: PDB Molecule: pts galactitol transporter subunit iib; PDBTitle: nmr based solution structure of pts system, galactitol-specific iib2 component from methicillin resistant staphylococcus aureus
120	c3d1pA	Alignment	not modelled	38.6	11	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase yor285w; PDBTitle: atomic resolution structure of uncharacterized protein from2 saccharomyces cerevisiae