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Description	P76535
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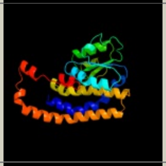
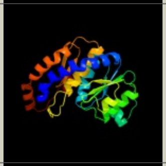
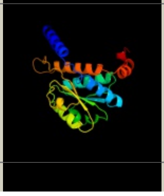
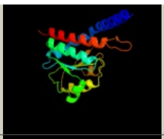
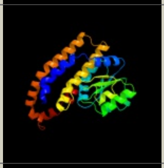
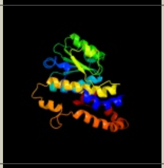
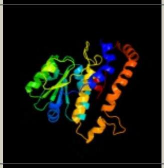
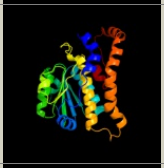
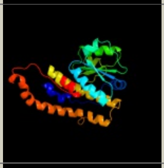
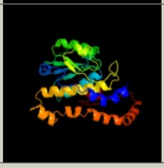
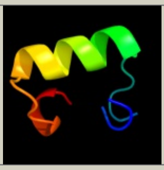
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1nriA_	Alignment		100.0	58	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hi0754; **PDBTitle:** crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
2	d1nria_	Alignment		100.0	58	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
3	c3cvjB_	Alignment		99.9	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoheptose isomerase; **PDBTitle:** crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
4	d1tk9a_	Alignment		99.9	17	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
5	c2amlB_	Alignment		99.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of lmo0035 protein (46906266) from listeria2 monocytogenes 4b f2365 at 1.50 a resolution
6	c2yvaB_	Alignment		99.9	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dnaa initiator-associating protein diaa; **PDBTitle:** crystal structure of escherichia coli diaa
7	c3g68A_	Alignment		99.9	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution
8	c2x3yA_	Alignment		99.9	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** crystal structure of gmha from burkholderia pseudomallei
9	d1x92a_	Alignment		99.9	15	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
10	c3fj1A_	Alignment		99.9	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerase; **PDBTitle:** crystal structure of putative phosphosugar isomerase (yp_167080.1)2 from silicibacter pomeroyi dss-3 at 1.75 a resolution
11	c3etnD_	Alignment		99.9	17	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative phosphosugar isomerase involved in capsule **PDBTitle:** crystal structure of putative phosphosugar isomerase involved in2 capsule formation (yp_209877.1) from bacteroides fragilis nctc 93433 at 1.70 a resolution

12	c2xhzC_	Alignment		99.9	18	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**arabinose 5-phosphate isomerase; **PDBTitle:** probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
13	c3knzA_	Alignment		99.9	18	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative sugar binding protein; **PDBTitle:** crystal structure of putative sugar binding protein (np_459565.1) from2 salmonella typhimurium lt2 at 2.50 a resolution
14	c3hbaA_	Alignment		99.9	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (sden_2705)2 from shewanella denitrificans os217 at 2.00 a resolution
15	c3fxaA_	Alignment		99.9	14	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
16	c2puwA_	Alignment		99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isomerase domain of glutamine-fructose-6-phosphate **PDBTitle:** the crystal structure of isomerase domain of glucosamine-6-phosphate2 synthase from candida albicans
17	c2zj3A_	Alignment		99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine--fructose-6-phosphate **PDBTitle:** isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
18	d1moqa_	Alignment		99.9	20	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
19	c3tbfA_	Alignment		99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine--fructose-6-phosphate aminotransferase **PDBTitle:** c-terminal domain of glucosamine-fructose-6-phosphate aminotransferase2 from francisella tularensis.
20	c1jxaA_	Alignment		99.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine 6-phosphate synthase; **PDBTitle:** glucosamine 6-phosphate synthase with glucose 6-phosphate
21	c3i0zB_	Alignment	not modelled	99.9	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of putative putative tagatose-6-phosphate2 ketose/aldose isomerase (np_344614.1) from streptococcus pneumoniae3 tigr4 at 1.70 a resolution
22	c3trjC_	Alignment	not modelled	99.9	16	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** structure of a phosphoheptose isomerase from francisella tularensis
23	c3odpA_	Alignment	not modelled	99.9	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of a putative tagatose-6-phosphate ketose/aldose2 isomerase (nt01cx_0292) from clostridium novyi nt at 2.35 a3 resolution
24	d1x94a_	Alignment	not modelled	99.9	18	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
25	c2a3nA_	Alignment	not modelled	99.9	17	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative glucosamine-fructose-6-phosphate aminotransferase; **PDBTitle:** crystal structure of a putative glucosamine-fructose-6-phosphate2 aminotransferase (stm4540.s) from salmonella typhimurium lt2 at 1.353 a resolution
26	c3euaD_	Alignment	not modelled	99.9	14	**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
27	d1j5xa_	Alignment	not modelled	99.8	14	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain

28	c3fkjA_	Alignment	not modelled	99.8	12	**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
29	d1vima_	Alignment	not modelled	99.8	18	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
30	d1m3sa_	Alignment	not modelled	99.8	17	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
31	c3c3jA_	Alignment	not modelled	99.8	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of tagatose-6-phosphate ketose/aldose isomerase from2 escherichia coli
32	c3shoA_	Alignment	not modelled	99.8	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, rpir family; **PDBTitle:** crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
33	c2decA_	Alignment	not modelled	99.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**325aa long hypothetical protein; **PDBTitle:** crystal structure of the ph0510 protein from pyrococcus horikoshii ot3
34	d1jeoa_	Alignment	not modelled	99.7	16	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
35	d1x9ia_	Alignment	not modelled	99.7	17	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
36	c3ff1B_	Alignment	not modelled	97.9	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** structure of glucose 6-phosphate isomerase from staphylococcus aureus
37	c2q8nB_	Alignment	not modelled	97.8	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of glucose-6-phosphate isomerase (ec2 5.3.1.9) (tm1385) from thermotoga maritima at 1.82 a3 resolution
38	d1c7qa_	Alignment	not modelled	97.6	17	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
39	c1zzgB_	Alignment	not modelled	97.5	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of hypothetical protein tt0462 from thermus2 thermophilus hb8
40	c3jx9B_	Alignment	not modelled	97.4	10	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoheptose isomerase; **PDBTitle:** crystal structure of putative phosphoheptose isomerase2 (yp_001815198.1) from exiguobacterium sp. 255-15 at 1.95 a resolution
41	c3ljkA_	Alignment	not modelled	97.3	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** glucose-6-phosphate isomerase from francisella tularensis.
42	d1gzda_	Alignment	not modelled	97.2	21	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
43	d1q50a_	Alignment	not modelled	97.2	17	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
44	c1t10A_	Alignment	not modelled	97.1	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** phosphoglucose isomerase from leishmania mexicana in complex with2 substrate d-fructose-6-phosphate
45	c2wu8A_	Alignment	not modelled	97.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv
46	d1iata_	Alignment	not modelled	96.9	19	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
47	c3hjbA_	Alignment	not modelled	96.9	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.
48	c2zkqb_	Alignment	not modelled	96.9	14	**PDB header:**ribosomal protein/rna **Chain:** B: **PDB Molecule:**rna expansion segment es3; **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
49	d1hm5a_	Alignment	not modelled	96.7	17	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
50	c3ujhB_	Alignment	not modelled	96.6	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of substrate-bound glucose-6-phosphate isomerase2 from toxoplasma gondii
51	d2gy9b1	Alignment	not modelled	96.6	19	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
52	c2o2cB_	Alignment	not modelled	96.6	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase, glycosomal; **PDBTitle:** crystal structure of phosphoglucose isomerase from t. brucei2 containing glucose-6-phosphate in the active site
						PDB header:isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase;

53	c3pr3B_	Alignment	not modelled	96.5	24	**PDBTitle:** crystal structure of plasmodium falciparum glucose-6-phosphate2 isomerase (pf14_0341) in complex with fructose-6-phosphate
54	c3bchA_	Alignment	not modelled	96.5	15	**PDB header:**cell adhesion, ribosomal protein **Chain:** A: **PDB Molecule:**40s ribosomal protein sa; **PDBTitle:** crystal structure of the human laminin receptor precursor
55	d1u0fa_	Alignment	not modelled	96.3	13	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
56	c2xznB_	Alignment	not modelled	96.3	11	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**rps0e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
57	c3iz6A_	Alignment	not modelled	96.3	11	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein sa (s2p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
58	c3nbuC_	Alignment	not modelled	96.1	12	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of pgi glucosephosphate isomerase
59	d2uubb1	Alignment	not modelled	95.8	14	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
60	c3izbA_	Alignment	not modelled	95.5	11	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein rps0 (s2p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
61	c1s1hB_	Alignment	not modelled	95.1	11	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**40s ribosomal protein s0-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
62	c3bbnB_	Alignment	not modelled	94.3	21	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**ribosomal protein s2; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
63	c2ivfA_	Alignment	not modelled	91.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ethylbenzene dehydrogenase alpha-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
64	d1vi6a_	Alignment	not modelled	90.5	15	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
65	c1y5iA_	Alignment	not modelled	88.2	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**respiratory nitrate reductase 1 alpha chain; **PDBTitle:** the crystal structure of the narghi mutant nari-k86a
66	d2iv2x2	Alignment	not modelled	87.6	11	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
67	c2vpyE_	Alignment	not modelled	87.1	17	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**thiosulfate reductase; **PDBTitle:** polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
68	d1y5ia2	Alignment	not modelled	85.9	11	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
69	c1tr8A_	Alignment		85.1	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**conserved protein (mth177); **PDBTitle:** crystal structure of archaeal nascent polypeptide-associated complex2 (aenac)
70	d2jfga1	Alignment	not modelled	83.5	21	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
71	d1p3da1	Alignment	not modelled	82.4	15	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
72	d1j6ua1	Alignment	not modelled	81.3	13	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
73	c2r0tA_	Alignment	not modelled	76.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxamine 5-phosphate-dependent dehydrase; **PDBTitle:** crystal sructure of gdp-4-keto-6-deoxymannose-3-dehydratase2 with a trapped plp-glutamate geminal diamine
74	c2dg2D_	Alignment	not modelled	76.4	13	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**apolipoprotein a-i binding protein; **PDBTitle:** crystal structure of mouse apolipoprotein a-i binding2 protein
75	c3on5B_	Alignment	not modelled	75.9	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bh1974 protein; **PDBTitle:** crystal structure of a xanthine dehydrogenase (bh1974) from bacillus2 halodurans at 2.80 a resolution
76	d1efva2	Alignment	not modelled	75.8	12	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit

77	d1ma3a_	Alignment	not modelled	75.4	10	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
78	c2e7zA_	Alignment	not modelled	75.0	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**acetylene hydratase ahy; **PDBTitle:** acetylene hydratase from pelobacter acetylenicus
79	c3jwpA_	Alignment	not modelled	74.2	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein sir2 homologue; **PDBTitle:** crystal structure of plasmodium falciparum sir2a (pf13_0152) in2 complex with amp
80	d1yc5a1	Alignment	not modelled	74.0	10	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
81	d1m2ka_	Alignment	not modelled	72.6	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
82	c3pkiF_	Alignment	not modelled	72.6	13	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
83	c3d3kD_	Alignment	not modelled	71.8	17	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
84	d2jioa2	Alignment	not modelled	70.4	10	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
85	c2iv2X_	Alignment	not modelled	69.8	11	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**formate dehydrogenase h; **PDBTitle:** reinterpretation of reduced form of formate dehydrogenase h2 from e. coli
86	c3k35D_	Alignment	not modelled	68.3	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
87	d1ovma2	Alignment	not modelled	66.8	18	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
88	c3nysA_	Alignment	not modelled	66.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase wbpe; **PDBTitle:** x-ray structure of the k185a mutant of wbpe (wlbe) from pseudomonas2 aeruginosa in complex with plp at 1.45 angstrom resolution
89	d2b4ya1	Alignment	not modelled	65.6	8	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
90	d3clsd2	Alignment	not modelled	65.5	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
91	c1efpC_	Alignment	not modelled	64.7	14	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**protein (electron transfer flavoprotein); **PDBTitle:** electron transfer flavoprotein (etf) from paracoccus2 denitrificans
92	d1a9xa4	Alignment	not modelled	63.3	24	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
93	d1pjqa1	Alignment	not modelled	62.9	6	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
94	d1vega_	Alignment	not modelled	62.7	22	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
95	c3e6gA_	Alignment	not modelled	61.9	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cystathionine gamma-lyase-like protein; **PDBTitle:** crystal structure of xometc, a cystathionine c-lyase-like2 protein from xanthomonas oryzae pv.oryzae
96	d1dmra2	Alignment	not modelled	59.7	18	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
97	c2z2uA_	Alignment	not modelled	59.3	32	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**upf0026 protein mj0257; **PDBTitle:** crystal structure of archaeal tyw1
98	d1xjca_	Alignment	not modelled	58.6	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
99	d1huua_	Alignment	not modelled	58.6	12	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
100	c3c85A_	Alignment	not modelled	58.5	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative glutathione-regulated potassium-efflux system **PDBTitle:** crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus
101	c3uagA_	Alignment	not modelled	58.1	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**protein (udp-n-acetylmuramoyl-l-alanine:d- **PDBTitle:** udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase
102	d2ji7a1	Alignment	not modelled	57.8	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
						Fold:IHF-like DNA-binding proteins

103	d1p71a_	Alignment	not modelled	57.7	24	**Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
104	c2v45A_	Alignment	not modelled	57.7	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic nitrate reductase; **PDBTitle:** a new catalytic mechanism of periplasmic nitrate reductase2 from desulfovibrio desulfuricans atcc 27774 from3 crystallographic and epr data and based on detailed4 analysis of the sixth ligand
105	d1gc0a_	Alignment	not modelled	57.5	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
106	d1mdoa_	Alignment	not modelled	57.4	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
107	c1ogyA_	Alignment	not modelled	57.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic nitrate reductase; **PDBTitle:** crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides
108	d1kjqa2	Alignment	not modelled	56.5	13	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
109	d1efpa2	Alignment	not modelled	56.3	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
110	d1zpda2	Alignment	not modelled	56.1	15	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
111	d2o97b1	Alignment	not modelled	55.3	21	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
112	d1wj7a1	Alignment		55.2	22	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
113	d1pvda2	Alignment	not modelled	54.5	14	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
114	d1ozha2	Alignment	not modelled	54.3	17	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
115	d1b8za_	Alignment	not modelled	53.9	16	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
116	c2ph5A_	Alignment	not modelled	52.7	14	**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
117	d2djia2	Alignment	not modelled	52.2	16	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
118	d1h0ha2	Alignment	not modelled	51.7	14	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
119	c3ke8A_	Alignment	not modelled	50.7	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate **PDBTitle:** crystal structure of isph:hmbpp-complex
120	c2np2B_	Alignment	not modelled	50.4	15	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**hbb; **PDBTitle:** hbb-dna complex