Phyre^{2}

Email	l.a.kelley@imperial.ac.uk
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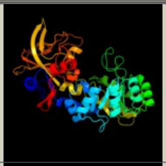
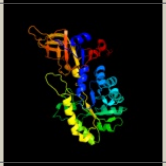
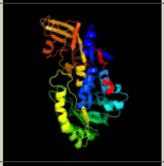
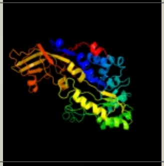
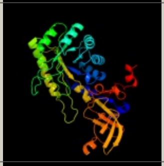
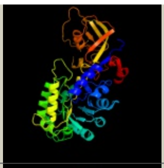
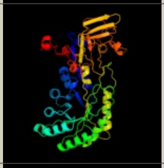
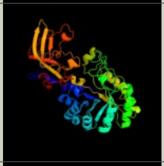
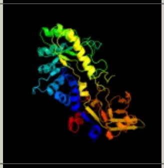
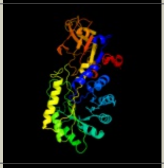
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1knwA_	Alignment		100.0	100	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of diaminopimelate decarboxylase
2	c1tufA_	Alignment		100.0	29	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of diaminopimelate decarboxylase from m.2 jannaschi
3	c2o0tB_	Alignment		100.0	27	**PDB header:**lyase **Chain:** B: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** the three dimensional structure of diaminopimelate decarboxylase from2 mycobacterium tuberculosis reveals a tetrameric enzyme organisation
4	c2on3A_	Alignment		100.0	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ornithine decarboxylase; **PDBTitle:** a structural insight into the inhibition of human and2 leishmania donovani ornithine decarboxylases by 3-aminooxy-3 1-aminopropane
5	c1d7kB_	Alignment		100.0	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**human ornithine decarboxylase; **PDBTitle:** crystal structure of human ornithine decarboxylase at 2.12 angstroms resolution
6	c2p3eA_	Alignment		100.0	33	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of aq1208 from aquifex aeolicus
7	c3n2bD_	Alignment		100.0	31	**PDB header:**lyase **Chain:** D: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** 1.8 angstrom resolution crystal structure of diaminopimelate2 decarboxylase (lysa) from vibrio cholerae.
8	c2qghA_	Alignment		100.0	35	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of diaminopimelate decarboxylase from helicobacter2 pylori complexed with l-lysine
9	c2j66A_	Alignment		100.0	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**btrk; **PDBTitle:** structural characterisation of btrk decarboxylase from2 butirosin biosynthesis
10	c2yxxA_	Alignment		100.0	34	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure analysis of diaminopimelate decarboxylate (lysa)
11	c3btnA_	Alignment		100.0	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**antizyme inhibitor 1; **PDBTitle:** crystal structure of antizyme inhibitor, an ornithine2 decarboxylase homologous protein

12	c3n29A_	Alignment		100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carboxynorspermidine decarboxylase; **PDBTitle:** crystal structure of carboxynorspermidine decarboxylase complexed with2 norspermidine from campylobacter jejuni
13	c2pljA_	Alignment		100.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**lysine/ornithine decarboxylase; **PDBTitle:** crystal structure of lysine/ornithine decarboxylase complexed with2 putrescine from vibrio vulnificus
14	c3mt1B_	Alignment		100.0	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative carboxynorspermidine decarboxylase protein; **PDBTitle:** crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti
15	c3nzpA_	Alignment		100.0	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**arginine decarboxylase; **PDBTitle:** crystal structure of the biosynthetic arginine decarboxylase spea from2 campylobacter jejuni, northeast structural genomics consortium target3 br53
16	c2nvaH_	Alignment		100.0	20	**PDB header:**lyase **Chain:** H: **PDB Molecule:**arginine decarboxylase, a207r protein; **PDBTitle:** the x-ray crystal structure of the paramecium bursaria2 chlorella virus arginine decarboxylase bound to agmatine
17	c3nzqB_	Alignment		100.0	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**biosynthetic arginine decarboxylase; **PDBTitle:** crystal structure of biosynthetic arginine decarboxylase adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
18	c3n2oA_	Alignment		100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**biosynthetic arginine decarboxylase; **PDBTitle:** x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
19	c1njjC_	Alignment		100.0	23	**PDB header:**lyase **Chain:** C: **PDB Molecule:**ornithine decarboxylase; **PDBTitle:** crystal structure determination of t. brucei ornithine2 decarboxylase bound to d-ornithine and to g418
20	d1knwa2	Alignment		100.0	100	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
21	d1d7ka2	Alignment	not modelled	100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
22	d1twia2	Alignment	not modelled	100.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
23	d1f3ta2	Alignment	not modelled	100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
24	d1hkva2	Alignment	not modelled	100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
25	d7odca2	Alignment	not modelled	100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
26	d1knwa1	Alignment	not modelled	100.0	93	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
27	d1hkva1	Alignment	not modelled	100.0	33	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
28	d1twia1	Alignment	not modelled	100.0	41	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
29	c3anuA_	Alignment	not modelled	100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**d-serine dehydratase; **PDBTitle:** crystal structure of d-serine dehydratase from chicken

						kidney
30	c1xfcB_	Alignment	not modelled	100.0	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** the 1.9 a crystal structure of alanine racemase from mycobacterium2 tuberculosis contains a conserved entryway into the active site
31	c3oo2B_	Alignment	not modelled	100.0	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase 1; **PDBTitle:** 2.37 angstrom resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col
32	c3llxA_	Alignment	not modelled	100.0	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**predicted amino acid aldolase or racemase; **PDBTitle:** crystal structure of an ala racemase-like protein (il1761) from2 idiomarina loihiensis at 1.50 a resolution
33	c3kw3B_	Alignment	not modelled	100.0	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from bartonella henselae with2 covalently bound pyridoxal phosphate
34	c3gwqB_	Alignment	not modelled	100.0	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-serine deaminase; **PDBTitle:** crystal structure of a putative d-serine deaminase (bxe_a4060) from2 burkholderia xenovorans lb400 at 2.00 a resolution
35	c1vftA_	Alignment	not modelled	100.0	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of l-cycloserine-bound form of alanine2 racemase from d-cycloserine-producing streptomyces3 lavendulae
36	c3oo2A_	Alignment	not modelled	100.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase 1; **PDBTitle:** 2.37 angstrom resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col
37	c2dy3B_	Alignment	not modelled	100.0	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from corynebacterium glutamicum
38	d7odca1	Alignment	not modelled	100.0	19	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
39	d1d7ka1	Alignment	not modelled	99.9	20	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
40	d1f3ta1	Alignment	not modelled	99.9	22	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
41	c1niuA_	Alignment	not modelled	99.9	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** alanine racemase with bound inhibitor derived from l-2 cycloserine
42	c3e6eC_	Alignment	not modelled	99.9	21	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from e.faecalis2 complex with cycloserine
43	c2odoC_	Alignment	not modelled	99.9	16	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of pseudomonas fluorescens alanine racemase
44	c3hurA_	Alignment	not modelled	99.9	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from oenococcus oeni
45	d2toda1	Alignment	not modelled	99.9	22	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
46	c3mubB_	Alignment	not modelled	99.9	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** the crystal structure of alanine racemase from streptococcus2 pneumoniae
47	c3co8B_	Alignment	not modelled	99.9	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from oenococcus oeni
48	c2rjgC_	Alignment	not modelled	99.9	19	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of biosynthetic alaine racemase from escherichia2 coli
49	d1njjb1	Alignment	not modelled	99.9	23	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
50	d1vfsa2	Alignment	not modelled	99.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
51	d1bd0a2	Alignment	not modelled	99.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
52	d1rcqa2	Alignment	not modelled	99.7	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
53	c2vd9A_	Alignment	not modelled	99.7	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** the crystal structure of alanine racemase from bacillus2 anthracis (ba0252) with bound l-ala-p
54	c1w8gA_	Alignment	not modelled	99.7	13	**PDB header:**plp-binding protein **Chain:** A: **PDB Molecule:**hypothetical upf0001 protein yggs; **PDBTitle:** crystal structure of e. coli k-12 yggs
						PDB header:structure genomics, unknown function

55	c3r79B_	Alignment	not modelled	99.6	13	**Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharactertized protein from agrobacterium2 tumefaciens
56	c3cpgA_	Alignment	not modelled	99.5	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an unknown protein from bifidobacterium2 adolescentis
57	d1ct5a_	Alignment	not modelled	99.2	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**"Hypothetical" protein ybl036c
58	d1bd0a1	Alignment	not modelled	97.6	17	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Alanine racemase
59	d1rcqa1	Alignment	not modelled	97.1	20	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Alanine racemase
60	d1vfsa1	Alignment	not modelled	96.7	25	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Alanine racemase
61	d1ur4a_	Alignment	not modelled	80.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
62	d1vc4a_	Alignment	not modelled	76.6	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
63	d1vhca_	Alignment	not modelled	70.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
64	d2tpsa_	Alignment	not modelled	67.1	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
65	d2q02a1	Alignment	not modelled	66.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
66	d1goxa_	Alignment	not modelled	66.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
67	c1ydoC_	Alignment	not modelled	63.9	20	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hmg-coa lyase; **PDBTitle:** crystal structure of the bacillis subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
68	c1vc3B_	Alignment	not modelled	62.7	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**l-aspartate-alpha-decarboxylase heavy chain; **PDBTitle:** crystal structure of l-aspartate-alpha-decarboxylase
69	d1wbha1	Alignment	not modelled	57.5	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
70	c2ylaA_	Alignment	not modelled	55.0	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
71	c3plxB_	Alignment	not modelled	54.9	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** the crystal structure of aspartate alpha-decarboxylase from2 campylobacter jejuni subsp. jejuni nctc 11168
72	d1a53a_	Alignment	not modelled	52.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
73	c2yl8A_	Alignment	not modelled	52.1	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
74	c3nm3D_	Alignment	not modelled	46.5	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**thiamine biosynthetic bifunctional enzyme; **PDBTitle:** the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosyhthesis of eukaryotes
75	c2hk1D_	Alignment	not modelled	45.5	10	**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
76	c2kytA_	Alignment	not modelled	42.8	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**group xvi phospholipase a2; **PDBTitle:** solution struture of the h-rev107 n-terminal domain
77	c3nsnA_	Alignment	not modelled	40.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylglucosaminidase; **PDBTitle:** crystal structure of insect beta-n-acetyl-d-hexosaminidase ofhex12 complexed with tmg-chitotriomycin
78	d2z1ca1	Alignment	not modelled	40.0	38	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
79	c2w5fB_	Alignment	not modelled	39.5	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endo-1,4-beta-xylanase y; **PDBTitle:** high resolution crystallographic structure of the2 clostridium thermocellum n-terminal endo-1,4-beta-d-3 xylanase 10b (xyn10b) cbm22-1-gh10 modules complexed with4 xylohexaose
80	d1saza1	Alignment	not modelled	39.0	38	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
81	c2ftpA	Alignment	not modelled	37.8	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase;

81	c2ftpA_	Alignment	not modelled	37.8	21	**PDBTitle:** crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
82	d1gz0f2	Alignment	not modelled	37.5	13	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**RNA 2'-O ribose methyltransferase substrate binding domain
83	d2csga1	Alignment	not modelled	37.4	15	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**YbiU-like
84	d1xfka_	Alignment	not modelled	37.1	16	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
85	c2eivH_	Alignment	not modelled	36.5	12	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**arginase; **PDBTitle:** crystal structure of the arginase from thermus thermophilus
86	d1uuma_	Alignment	not modelled	35.1	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
87	c1pyuD_	Alignment	not modelled	34.5	9	**PDB header:**lyase **Chain:** D: **PDB Molecule:**aspartate 1-decarboxylase alfa chain; **PDBTitle:** processed aspartate decarboxylase mutant with ser25 mutated to cys
88	c3cqkB_	Alignment	not modelled	34.4	11	**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
89	c3rcnA_	Alignment	not modelled	34.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** crystal structure of beta-n-acetylhexosaminidase from arthrobacter2 aurescens
90	c2dbiA_	Alignment	not modelled	33.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ybiu; **PDBTitle:** crystal structure of a hypothetical protein jw0805 from2 escherichia coli
91	c3bleA_	Alignment	not modelled	33.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citramalate synthase from leptospira interrogans; **PDBTitle:** crystal structure of the catalytic domain of licms in2 complexed with malonate
92	d1tz9a_	Alignment	not modelled	33.2	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**UxuA-like
93	c1pt1B_	Alignment	not modelled	32.5	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine
94	c3lmyA_	Alignment	not modelled	32.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-hexosaminidase subunit beta; **PDBTitle:** the crystal structure of beta-hexosaminidase b in complex with2 pyrimethamine
95	d2c0ha1	Alignment	not modelled	31.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
96	c2kksA_	Alignment	not modelled	31.7	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of protein dsy2949 from desulfitobacterium2 hafniense. northeast structural genomics consortium target dhr27
97	d3eeqa1	Alignment	not modelled	31.3	14	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like
98	c3navB_	Alignment	not modelled	30.8	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
99	c3ktcB_	Alignment	not modelled	30.8	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase; **PDBTitle:** crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
100	c3ju2A_	Alignment	not modelled	30.7	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein smc04130; **PDBTitle:** crystal structure of protein smc04130 from sinorhizobium meliloti 1021
101	d3by5a1	Alignment	not modelled	30.5	5	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like
102	c3by5A_	Alignment	not modelled	30.5	5	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cobalamin biosynthesis protein; **PDBTitle:** crystal structure of cobalamin biosynthesis protein chig from2 agrobacterium tumefaciens str. c58
103	d2ceva_	Alignment	not modelled	30.2	14	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
104	d1gz0a2	Alignment	not modelled	29.6	13	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**RNA 2'-O ribose methyltransferase substrate binding domain
105	d3bula2	Alignment	not modelled	29.4	14	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
106	d2ot2a1	Alignment	not modelled	29.0	17	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
						Fold: Ferredoxin-like

107	d1zj8a1	Alignment	not modelled	28.5	16	**Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
108	c1xrsB_	Alignment	not modelled	28.0	7	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**d-lysine 5,6-aminomutase beta subunit; **PDBTitle:** crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
109	c2ou4C_	Alignment	not modelled	27.3	7	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-tagatose 3-epimerase; **PDBTitle:** crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
110	d1xi3a_	Alignment	not modelled	27.2	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
111	c2yciX_	Alignment	not modelled	27.0	15	**PDB header:**transferase **Chain:** X: **PDB Molecule:**5-methyltetrahydrofolate corrinoid/iron sulfur protein **PDBTitle:** methyltransferase native
112	d1i60a_	Alignment	not modelled	26.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
113	c3ivuB_	Alignment	not modelled	26.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
114	c2a7nA_	Alignment	not modelled	26.5	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l(+)-mandelate dehydrogenase; **PDBTitle:** crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase
115	d1xria_	Alignment	not modelled	26.0	17	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
116	d1aopa2	Alignment	not modelled	25.9	10	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
117	d1ppya_	Alignment	not modelled	25.8	8	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Pyruvoyl dependent aspartate decarboxylase, ADC
118	d2w6ka1	Alignment	not modelled	25.3	18	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like
119	c2zdsB_	Alignment	not modelled	25.1	11	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of sco6571 from streptomyces coelicolor2 a3(2)
120	c2c3zA_	Alignment	not modelled	25.1	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus