Phyre^2

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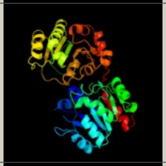
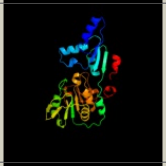
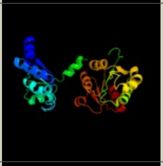
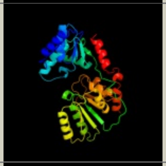
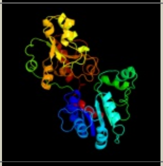
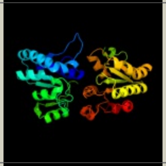
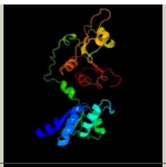
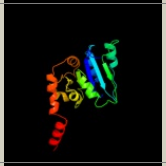
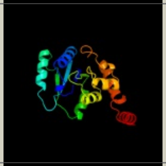
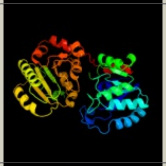
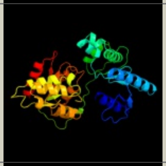
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gejA_	Alignment		98.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol mannosyltransferase (pima); **PDBTitle:** crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man
2	c3ot5D_	Alignment		97.5	12	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
3	c2x0dA_	Alignment		96.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**wsaf; **PDBTitle:** apo structure of wsaf
4	d1v4va_	Alignment		96.8	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
5	c2xmpB_	Alignment		96.5	14	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**trehalose-synthase tret; **PDBTitle:** crystal structure of trehalose synthase tret mutant e326a2 from p.horishiki in complex with udp
6	c2vsnB_	Alignment		96.5	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**xcogt; **PDBTitle:** structure and topological arrangement of an o-glcnac2 transferase homolog: insight into molecular control of3 intracellular glycosylation
7	c3c4vB_	Alignment		96.0	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**predicted glycosyltransferases; **PDBTitle:** structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.
8	c3oy2A_	Alignment		96.0	10	**PDB header:**viral protein,transferase **Chain:** A: **PDB Molecule:**glycosyltransferase b736l; **PDBTitle:** crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
9	c2jjmH_	Alignment		95.9	13	**PDB header:**transferase **Chain:** H: **PDB Molecule:**glycosyl transferase, group 1 family protein; **PDBTitle:** crystal structure of a family gt4 glycosyltransferase from2 bacillus anthracis orf ba1558.
10	d1f6da_	Alignment		95.7	13	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
11	c2x6rA_	Alignment		95.6	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**trehalose-synthase tret; **PDBTitle:** crystal structure of trehalose synthase tret from p.2 horikoshi produced by soaking in trehalose

12	d1o6ca_	Alignment		95.4	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
13	c1uquB_	Alignment		95.2	14	**PDB header:**synthase **Chain:** B: **PDB Molecule:**alpha, alpha-trehalose-phosphate synthase; **PDBTitle:** trehalose-6-phosphate from e. coli bound with udp-glucose.
14	c3pe3D_	Alignment		95.2	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine--peptide n- **PDBTitle:** structure of human o-glcnac transferase and its complex with a peptide2 substrate
15	c2r60A_	Alignment		94.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
16	c3okaA_	Alignment		92.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gdp-mannose-dependent alpha-(1-6)-phosphatidylinositol **PDBTitle:** crystal structure of corynebacterium glutamicum pimb' in complex with2 gdp-man (triclinic crystal form)
17	c3dzcA_	Alignment		91.9	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.35 angstrom resolution structure of wecb (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
18	c2xcuC_	Alignment		87.5	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**3-deoxy-d-manno-2-octulosonic acid transferase; **PDBTitle:** membrane-embedded monofunctional glycosyltransferase waaa of aquifex2 aeolicus, comlex with cmp
19	d2iw1a1	Alignment		85.7	11	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
20	d2f9fa1	Alignment		83.7	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
21	d2bfwa1	Alignment	not modelled	76.2	10	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
22	d1duvg2	Alignment	not modelled	69.1	20	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
23	d1uqta_	Alignment	not modelled	66.3	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Trehalose-6-phosphate synthase, OtsA
24	d2bisa1	Alignment	not modelled	64.8	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
25	d1pswa_	Alignment	not modelled	60.5	13	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**ADP-heptose LPS heptosyltransferase II
26	c3oneA_	Alignment	not modelled	55.1	9	**PDB header:**hydrolase/hydrolase substrate **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
27	c2w37A_	Alignment	not modelled	53.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, catabolic; **PDBTitle:** crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
28	c1v8bA_	Alignment	not modelled	49.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of a hydrolase
						PDB header:transferase

29	c3tovB_	Alignment	not modelled	48.5	17	**Chain:** B: **PDB Molecule:**glycosyl transferase family 9; **PDBTitle:** the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008
30	d1qs0b1	Alignment	not modelled	43.7	16	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
31	d1dxha2	Alignment	not modelled	38.8	14	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
32	d1vlva2	Alignment	not modelled	38.0	16	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
33	c3dhyC_	Alignment	not modelled	36.4	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
34	c2h1fB_	Alignment	not modelled	33.1	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipopolysaccharide heptosyltransferase-1; **PDBTitle:** e. coli heptosyltransferase waac with adp
35	d1li4a2	Alignment	not modelled	32.9	13	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**S-adenosylhomocystein hydrolase
36	d1pvva2	Alignment	not modelled	27.9	24	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
37	c1d4fD_	Alignment	not modelled	27.5	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-adenosylhomocysteine hydrolase; **PDBTitle:** crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
38	c3r1fO_	Alignment	not modelled	27.5	26	**PDB header:**transcription **Chain:** O: **PDB Molecule:**esx-1 secretion-associated regulator espr; **PDBTitle:** crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
39	c1ortD_	Alignment	not modelled	27.3	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine transcarbamoylase; **PDBTitle:** ornithine transcarbamoylase from pseudomonas aeruginosa
40	c3updA_	Alignment	not modelled	26.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** 2.9 angstrom crystal structure of ornithine carbamoyltransferase2 (argf) from vibrio vulnificus
41	d1iyjb5	Alignment	not modelled	22.6	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
42	d1xmba1	Alignment	not modelled	22.3	8	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
43	c2otcA_	Alignment	not modelled	22.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine transcarbamoylase complexed with n-2 (phosphonacetyl)-l-ornithine
44	d2bfdb1	Alignment	not modelled	21.9	14	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
45	c1olsB_	Alignment	not modelled	20.7	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-oxoisovalerate dehydrogenase beta subunit; **PDBTitle:** roles of his291-alpha and his146-beta' in the reductive2 acylation reaction catalyzed by human branched-chain3 alpha-ketoacid dehydrogenase
46	c3en0A_	Alignment	not modelled	18.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyanophycinase; **PDBTitle:** the structure of cyanophycinase
47	c3rhzB_	Alignment	not modelled	17.8	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nucleotide sugar synthetase-like protein; **PDBTitle:** structure and functional analysis of a new subfamily of2 glycosyltransferases required for glycosylation of serine-rich3 streptococcal adhesions
48	c3cseA_	Alignment	not modelled	15.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrofolate reductase; **PDBTitle:** candida glabrata dihydrofolate reductase complexed with2 nadph and 2,4-diamino-5-(3-(2,5-dimethoxyphenyl)prop-1-3 ynyl)-6-ethylpyrimidine (ucp120b)
49	c1vlvA_	Alignment	not modelled	15.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
50	c2kzkA_	Alignment	not modelled	15.2	37	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**uncharacterized protein yol083w; **PDBTitle:** solution structure of alpha-mannosidase binding domain of atg34
51	c1jb9A_	Alignment	not modelled	15.1	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin-nadp reductase; **PDBTitle:** crystal structure of the ferredoxin:nadp+ reductase from maize root at2 1.7 angstroms
52	c3q3hA_	Alignment	not modelled	14.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hmw1c-like glycosyltransferase; **PDBTitle:** crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
53	d1x6va1	Alignment	not modelled	14.5	20	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain

54	d1otha2	Alignment	not modelled	14.3	20	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
55	c2qzsA_	Alignment	not modelled	14.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogen synthase; **PDBTitle:** crystal structure of wild-type e.coli gs in complex with adp2 and glucose(wtgsb)
56	d1rzua_	Alignment	not modelled	14.1	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
57	c2kzbA_	Alignment	not modelled	14.0	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**autophagy-related protein 19; **PDBTitle:** solution structure of alpha-mannosidase binding domain of atg19
58	d2nx2a1	Alignment	not modelled	13.4	14	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**YpsA-like
59	c2jzcA_	Alignment	not modelled	13.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine transferase subunit **PDBTitle:** nmr solution structure of alg13: the sugar donor subunit of2 a yeast n-acetylglucosamine transferase. northeast3 structural genomics consortium target yg1
60	c3jrnA_	Alignment	not modelled	13.0	16	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**at1g72930 protein; **PDBTitle:** crystal structure of tir domain from arabidopsis thaliana
61	d1u9ya1	Alignment	not modelled	12.9	8	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
62	c3d64A_	Alignment	not modelled	12.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
63	d1pj3a1	Alignment	not modelled	12.2	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
64	c1dkrB_	Alignment	not modelled	12.1	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase; **PDBTitle:** crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
65	d2f62a1	Alignment	not modelled	12.0	11	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**N-deoxyribosyltransferase
66	d1jhda1	Alignment	not modelled	11.9	7	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
67	d1wdds_	Alignment	not modelled	11.3	33	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
68	d1s2da_	Alignment	not modelled	11.1	15	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**N-deoxyribosyltransferase
69	d2v6ai1	Alignment	not modelled	11.1	33	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
70	c3c7cB_	Alignment	not modelled	11.1	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**octopine dehydrogenase; **PDBTitle:** a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine)
71	c3q98A_	Alignment	not modelled	10.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcarbamylase; **PDBTitle:** structure of ygew encoded protein from e. coli
72	c2z5bB_	Alignment	not modelled	10.6	21	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**uncharacterized protein ylr021w; **PDBTitle:** crystal structure of a novel chaperone complex for yeast2 20s proteasome assembly
73	d1miua5	Alignment	not modelled	10.5	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
74	d1g8fa1	Alignment	not modelled	10.5	21	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
75	c3q6nF_	Alignment	not modelled	10.4	16	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**heat shock protein hsp 90-alpha; **PDBTitle:** crystal structure of human mc-hsp90 in p21 space group
76	d1uzdc1	Alignment	not modelled	10.3	33	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
77	c2dgdD_	Alignment	not modelled	10.3	10	**PDB header:**lyase **Chain:** D: **PDB Molecule:**223aa long hypothetical arylmalonate decarboxylase; **PDBTitle:** crystal structure of st0656, a function unknown protein from2 sulfolobus tokodaii
78	d1v47a1	Alignment	not modelled	10.3	10	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
79	d8ruci_	Alignment	not modelled	10.3	33	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit

80	d1ej7s_	Alignment	not modelled	10.2	33	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
81	d1gk8i_	Alignment	not modelled	9.8	33	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
82	d2pmra1	Alignment	not modelled	9.7	25	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**AF1782-like **Family:**AF1782-like
83	c2r5wA_	Alignment	not modelled	9.0	13	**PDB header:**hydrolase, transferase **Chain:** A: **PDB Molecule:**nicotinamide-nucleotide adenylyltransferase; **PDBTitle:** crystal structure of a bifunctional nmn2 adenylyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
84	d2e74g1	Alignment	not modelled	8.8	44	**Fold:**Single transmembrane helix **Superfamily:**PetG subunit of the cytochrome b6f complex **Family:**PetG subunit of the cytochrome b6f complex
85	c1ml4A_	Alignment	not modelled	8.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate transcarbamoylase; **PDBTitle:** the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
86	d1m8pa1	Alignment	not modelled	8.6	17	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
87	c1zh8B_	Alignment	not modelled	8.6	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
88	c3nv9A_	Alignment	not modelled	8.4	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malic enzyme; **PDBTitle:** crystal structure of entamoeba histolytica malic enzyme
89	d1f8ya_	Alignment	not modelled	8.3	15	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**N-deoxyribosyltransferase
90	c3oziB_	Alignment	not modelled	8.1	21	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**l6tr; **PDBTitle:** crystal structure of the tir domain from the flax disease resistance2 protein l6
91	c1zcoA_	Alignment	not modelled	8.1	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphoheptonate aldolase; **PDBTitle:** crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase
92	c3mtqA_	Alignment	not modelled	7.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative phosphoenolpyruvate-dependent sugar **PDBTitle:** crystal structure of a putative phosphoenolpyruvate-dependent sugar2 phosphotransferase system (pts) permease (kpn_04802) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.70 a resolution
93	d1ir1s_	Alignment	not modelled	7.6	33	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
94	c1qr6A_	Alignment	not modelled	7.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malic enzyme 2; **PDBTitle:** human mitochondrial nad(p)-dependent malic enzyme
95	c3hftA_	Alignment	not modelled	7.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**wbms, polysaccharide deacetylase involved in o-antigen **PDBTitle:** crystal structure of a putative polysaccharide deacetylase involved in2 o-antigen biosynthesis (wbms, bb0128) from bordetella bronchiseptica3 at 1.90 a resolution
96	c3clbA_	Alignment	not modelled	7.3	21	**PDB header:**oxidoreductase, transferase **Chain:** A: **PDB Molecule:**dhfr-ts; **PDBTitle:** structure of bifunctional tcdhfr-ts in complex with tmq
97	c2z5cA_	Alignment	not modelled	7.3	19	**PDB header:**chaperone/hydrolase **Chain:** A: **PDB Molecule:**protein ypl144w; **PDBTitle:** crystal structure of a novel chaperone complex for yeast2 20s proteasome assembly
98	d1gq2a1	Alignment	not modelled	7.2	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
99	c1a1sA_	Alignment	not modelled	7.2	24	**PDB header:**transcarbamylase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine carbamoyltransferase from pyrococcus furiosus