Phyre^2

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Description	P0A722
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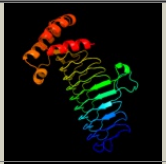
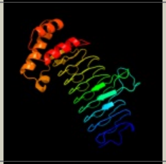
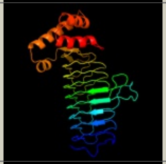
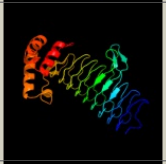
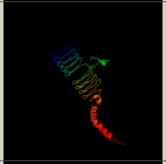
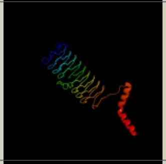
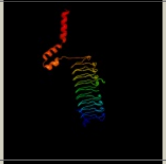
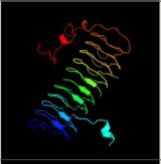
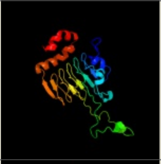
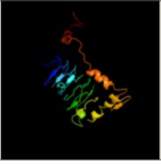
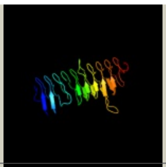
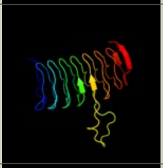
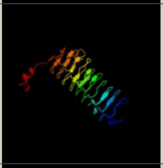
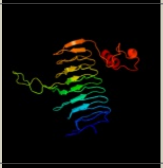
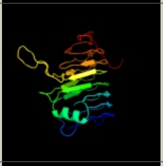
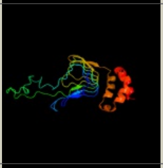
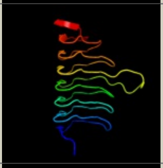
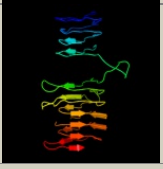
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2jf2a1	Alignment		100.0	100	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**UDP N-acetylglucosamine acyltransferase
2	c3i3aC_	Alignment		100.0	41	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n- **PDBTitle:** structural basis for the sugar nucleotide and acyl chain2 selectivity of leptospira interrogans lpxa
3	d1j2za_	Alignment		100.0	40	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**UDP N-acetylglucosamine acyltransferase
4	c3r0sA_	Alignment		100.0	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o- **PDBTitle:** udp-n-acetylglucosamine acyltransferase from campylobacter jejuni
5	c2iu9C_	Alignment		100.0	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine **PDBTitle:** chlamydia trachomatis lpxd with 100mm udpglcnac (complex ii)
6	c3pmoA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine n-acyltransferase; **PDBTitle:** the structure of lpxd from pseudomonas aeruginosa at 1.3 a resolution
7	c3eh0C_	Alignment		100.0	24	**PDB header:**transferase **Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine n- **PDBTitle:** crystal structure of lpxd from escherichia coli
8	c3fsbB_	Alignment		100.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**qdtc; **PDBTitle:** crystal structure of qdtc, the dtdp-3-amino-3,6-dideoxy-d-2 glucose n-acetyl transferase from thermoanaerobacterium3 thermosaccharolyticum in complex with coa and dtdp-3-amino-4 quinovose
9	d1g97a1	Alignment		100.0	19	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
10	d1mr7a_	Alignment		100.0	18	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
11	c3c8vA_	Alignment		100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** crystal structure of putative acetyltransferase (yp_390128.1) from2 desulfovibrio desulfuricans g20 at 2.28 a resolution

12	d2oi6a1	Alignment		100.0	14	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
13	c3mqhD_	Alignment		100.0	29	**PDB header:**transferase **Chain:** D: **PDB Molecule:**lipopolysaccharides biosynthesis acetyltransferase; **PDBTitle:** crystal structure of the 3-n-acetyl transferase wlbb from bordetella2 petrii in complex with coa and udp-3-amino-2-acetamido-2,3-dideoxy3 glucuronic acid
14	c1hm8A_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine-1-phosphate uridyltransferase; **PDBTitle:** crystal structure of s.pneumoniae n-acetylglucosamine-1-phosphate2 uridyltransferase, glmu, bound to acetyl coenzyme a
15	c3jqyB_	Alignment		99.9	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polysialic acid o-acetyltransferase; **PDBTitle:** crystal strucutre of the polysia specific acetyltransferase neuo
16	c2wlgA_	Alignment		99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polysialic acid o-acetyltransferase; **PDBTitle:** crystallographic analysis of the polysialic acid o-2 acetyltransferase oatwy
17	d1xata_	Alignment		99.9	21	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
18	c3cj8B_	Alignment		99.9	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2,3,4,5-tetrahydropyridine-2-carboxylate n- **PDBTitle:** crystal structure of 2,3,4,5-tetrahydropyridine-2-carboxylate n-2 succinyltransferase from enterococcus faecalis v583
19	c2v0hA_	Alignment		99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** characterization of substrate binding and catalysis of the2 potential antibacterial target n-acetylglucosamine-1-3 phosphate uridyltransferase (glmu)
20	d2f9ca1	Alignment		99.9	15	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**YdcK-like
21	c3eevC_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**chloramphenicol acetyltransferase; **PDBTitle:** crystal structure of chloramphenicol acetyltransferase vca0300 from2 vibrio cholerae o1 biovar eltor
22	c2oi6A_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4
23	d3bswa1	Alignment	not modelled	99.9	26	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**PglD-like
24	c3ectA_	Alignment	not modelled	99.9	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexapeptide-repeat containing-acetyltransferase; **PDBTitle:** crystal structure of the hexapeptide-repeat containing-2 acetyltransferase vca0836 from vibrio cholerae
25	c3fttA_	Alignment	not modelled	99.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase sacol2570; **PDBTitle:** crystal structure of the galactoside o-acetyltransferase2 from staphylococcus aureus
26	d1krra_	Alignment	not modelled	99.9	22	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
27	c3srtB_	Alignment	not modelled	99.9	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**maltose o-acetyltransferase; **PDBTitle:** the crystal structure of a maltose o-acetyltransferase from2 clostridium difficile 630
28	c2ic7A_	Alignment	not modelled	99.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**maltose transacetylase; **PDBTitle:** crystal structure of maltose transacetylase from2 geobacillus kaustophilus

29	c3r3rA_	Alignment	not modelled	99.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ferripyochelin binding protein; **PDBTitle:** structure of the yrda ferripyochelin binding protein from salmonella2 enterica
30	d1qrea_	Alignment	not modelled	99.9	13	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**gamma-carbonic anhydrase-like
31	c1qreA_	Alignment	not modelled	99.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** a closer look at the active site of gamma-carbonic anhydrases: high2 resolution crystallographic studies of the carbonic anhydrase from3 methanosarcina thermophila
32	d1xhda_	Alignment	not modelled	99.9	21	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**gamma-carbonic anhydrase-like
33	d1ocxa_	Alignment	not modelled	99.9	30	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
34	d1v3wa_	Alignment	not modelled	99.9	20	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**gamma-carbonic anhydrase-like
35	c3eg4A_	Alignment	not modelled	99.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- **PDBTitle:** crystal structure of 2,3,4,5-tetrahydropyridine-2-2 carboxylate n-succinyltransferase from brucella melitensis3 biovar abortus 2308
36	c3r1wA_	Alignment	not modelled	99.9	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** crystal structure of a carbonic anhydrase from a crude oil degrading2 psychrophilic library
37	d1t3da_	Alignment	not modelled	99.9	31	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Serine acetyltransferase
38	c1t3dB_	Alignment	not modelled	99.9	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** crystal structure of serine acetyltransferase from e.coli at 2.2a
39	d1ssqa_	Alignment	not modelled	99.9	29	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Serine acetyltransferase
40	c3ixcA_	Alignment	not modelled	99.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexapeptide transferase family protein; **PDBTitle:** crystal structure of hexapeptide transferase family protein from2 anaplasma phagocytophilum
41	c3mc4A_	Alignment	not modelled	99.9	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ww/rsp5/wwp domain:bacterial transferase **PDBTitle:** crystal structure of ww/rsp5/wwp domain: bacterial2 transferase hexapeptide repeat: serine o-acetyltransferase3 from brucella melitensis
42	d3tdta_	Alignment	not modelled	99.8	24	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Tetrahydrodipicolinate-N-succinlytransferase, THDP-succinlytransferase, DapD
43	c2ggqA_	Alignment	not modelled	99.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**401aa long hypothetical glucose-1-phosphate **PDBTitle:** complex of hypothetical glucose-1-phosphate thymidylyltransferase from2 sulfolobus tokodaii
44	c3q1xA_	Alignment	not modelled	99.8	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** crystal structure of entamoeba histolytica serine acetyltransferase 12 in complex with l-serine
45	c3f1xA_	Alignment	not modelled	99.8	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** three dimensional structure of the serine acetyltransferase from2 bacteroides vulgatus, northeast structural genomics consortium target3 bvr62.
46	c3kwdA_	Alignment	not modelled	99.7	18	**PDB header:**lyase, protein binding, photosynthesis **Chain:** A: **PDB Molecule:**carbon dioxide concentrating mechanism protein; **PDBTitle:** inactive truncation of the beta-carboxysomal gamma-carbonic anhydrase,2 ccmm, form 1
47	c3fsyC_	Alignment	not modelled	99.6	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**tetrahydrodipicolinate n-succinyltransferase; **PDBTitle:** structure of tetrahydrodipicolinate n-succinyltransferase2 (rv1201c;dapd) in complex with succinyl-coa from mycobacterium3 tuberculosis
48	c3d98A_	Alignment	not modelled	99.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
49	c2qkxA_	Alignment	not modelled	99.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** n-acetyl glucosamine 1-phosphate uridyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
50	d1yp2a1	Alignment	not modelled	99.3	16	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
51	c2rijA_	Alignment	not modelled	99.2	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative 2,3,4,5-tetrahydropyridine-2-carboxylate n- **PDBTitle:** crystal structure of a putative 2,3,4,5-tetrahydropyridine-2-2 carboxylate n-succinyltransferase (cj1605c, dapd) from campylobacter3 jejuni at 1.90 a resolution

52	c1yp3C_	Alignment	not modelled	99.1	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glucose-1-phosphate adenylyltransferase small **PDBTitle:** crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
53	d1fxja1	Alignment	not modelled	99.0	18	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
54	c1fwyA_	Alignment	not modelled	98.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of n-acetylglucosamine 1-phosphate2 uridyltransferase bound to udp-glcnac
55	c3brkX_	Alignment	not modelled	98.4	14	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glucose-1-phosphate adenylyltransferase; **PDBTitle:** crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
56	d1hbga_	Alignment	not modelled	39.0	18	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
57	d1jl6a_	Alignment	not modelled	38.5	16	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
58	c3nepX_	Alignment	not modelled	32.9	6	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** 1.55a resolution structure of malate dehydrogenase from salinibacter2 ruber
59	d1jl7a_	Alignment	not modelled	31.9	18	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
60	d1x9fb_	Alignment	not modelled	30.0	12	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
61	c3evrA_	Alignment	not modelled	28.8	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**myosin light chain kinase, green fluorescent **PDBTitle:** crystal structure of calcium bound monomeric gcamp2
62	d2qmma1	Alignment	not modelled	28.7	26	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF1056-like
63	d1itha_	Alignment	not modelled	24.5	21	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
64	d1ez4a2	Alignment	not modelled	21.8	11	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
65	c1mldA_	Alignment	not modelled	21.6	18	**PDB header:**oxidoreductase(nad(a)-choh(d)) **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** refined structure of mitochondrial malate dehydrogenase2 from porcine heart and the consensus structure for3 dicarboxylic acid oxidoreductases
66	c2da4A_	Alignment	not modelled	21.4	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dkfzp686k21156; **PDBTitle:** solution structure of the homeobox domain of the2 hypothetical protein, dkfzp686k21156
67	c1yhuX_	Alignment	not modelled	20.7	9	**PDB header:**oxygen storage/transport **Chain:** X: **PDB Molecule:**hemoglobin b2 chain; **PDBTitle:** crystal structure of riftia pachyptila c1 hemoglobin reveals novel2 assembly of 24 subunits.
68	c1yhuJ_	Alignment	not modelled	18.6	12	**PDB header:**oxygen storage/transport **Chain:** J: **PDB Molecule:**giant hemoglobins b chain; **PDBTitle:** crystal structure of riftia pachyptila c1 hemoglobin reveals novel2 assembly of 24 subunits.
69	c2jmlA_	Alignment	not modelled	18.3	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna binding domain/transcriptional regulator; **PDBTitle:** solution structure of the n-terminal domain of cara repressor
70	c1ez4B_	Alignment	not modelled	17.3	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lactate dehydrogenase; **PDBTitle:** crystal structure of non-allosteric l-lactate dehydrogenase2 from lactobacillus pentosus at 2.3 angstrom resolution
71	c1yhuA_	Alignment	not modelled	17.1	7	**PDB header:**oxygen storage/transport **Chain:** A: **PDB Molecule:**hemoglobin a1 chain; **PDBTitle:** crystal structure of riftia pachyptila c1 hemoglobin reveals novel2 assembly of 24 subunits.
72	c3n0lA_	Alignment	not modelled	17.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
73	d1y9ia_	Alignment	not modelled	17.0	20	**Fold:**YutG-like **Superfamily:**YutG-like **Family:**YutG-like
74	c3g2bA_	Alignment	not modelled	16.9	12	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**coenzyme pqq synthesis protein d; **PDBTitle:** crystal structure of pqqd from xanthomonas campestris
75	d1wh5a_	Alignment	not modelled	16.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
76	c1k5hB_	Alignment	not modelled	15.6	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose-5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose-5-phosphate reductoisomerase

77	d1hyha2	Alignment	not modelled	15.2	8	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
78	c3au9A_	Alignment	not modelled	14.9	18	**PDB header:**isomerase/isomerase inhibitor **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of the quaternary complex-1 of an isomerase
79	d2a1ja1	Alignment	not modelled	14.9	17	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
80	c2eghA_	Alignment	not modelled	14.5	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
81	c2jcyA_	Alignment	not modelled	14.5	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** x-ray structure of mutant 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase, dxr, rv2870c, from mycobacterium3 tuberculosis
82	c3itcA_	Alignment	not modelled	14.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**renal dipeptidase; **PDBTitle:** crystal structure of sco3058 with bound citrate and glycerol
83	d1itua_	Alignment	not modelled	14.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Renal dipeptidase
84	c1r0lD_	Alignment	not modelled	14.1	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose 5-phosphate reductoisomerase from2 zymomonas mobilis in complex with nadph
85	d1lhta_	Alignment	not modelled	14.0	14	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
86	c1tlqA_	Alignment	not modelled	13.9	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ypjq; **PDBTitle:** crystal structure of protein ypjq from bacillus subtilis, pfam duf64
87	d1tlqa_	Alignment	not modelled	13.9	17	**Fold:**YutG-like **Superfamily:**YutG-like **Family:**YutG-like
88	c2d2mB_	Alignment	not modelled	13.9	9	**PDB header:**oxygen storage/transport **Chain:** B: **PDB Molecule:**giant hemoglobin, a2(a5) globin chain; **PDBTitle:** structure of an extracellular giant hemoglobin of the2 gutless beard worm oligobrachia mashikoi
89	c2hjrK_	Alignment	not modelled	13.3	9	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of cryptosporidium parvum malate2 dehydrogenase
90	d2v1fa1	Alignment	not modelled	13.2	14	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
91	d3bzka3	Alignment	not modelled	13.0	9	**Fold:**Tex N-terminal region-like **Superfamily:**Tex N-terminal region-like **Family:**Tex N-terminal region-like
92	d2c1xa1	Alignment	not modelled	12.6	7	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
93	c1x3kA_	Alignment	not modelled	12.4	17	**PDB header:**oxygen storage/transport **Chain:** A: **PDB Molecule:**hemoglobin component v; **PDBTitle:** crystal structure of a hemoglobin component (ta-v) from2 tokunagayusurika akamusi
94	c2zs0A_	Alignment	not modelled	12.2	12	**PDB header:**oxygen storage, oxygen transport **Chain:** A: **PDB Molecule:**extracellular giant hemoglobin major globin subunit a1; **PDBTitle:** structural basis for the heterotropic and homotropic interactions of2 invertebrate giant hemoglobin
95	c2ld7A_	Alignment	not modelled	12.0	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**histone deacetylase complex subunit sap30; **PDBTitle:** solution structure of the msin3a pah3-sap30 sid complex
96	d1x9fd_	Alignment	not modelled	12.0	9	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
97	d2pv7a1	Alignment	not modelled	11.7	16	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**TyrA dimerization domain-like
98	c3a14B_	Alignment	not modelled	11.7	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of dxr from thermotoga maritima, in complex with2 nadph
99	c2d4aC_	Alignment	not modelled	11.4	10	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structure of the malate dehydrogenase from aeropyrum pernix