Phyre2

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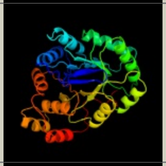
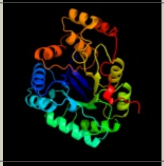
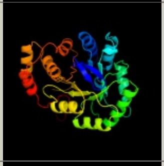
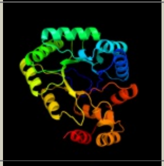
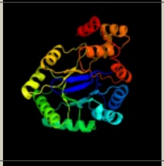
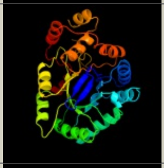
Unique Job ID	523bb0908edb3b62

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1mzra_	Alignment		100.0	100	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
2	c1vbjB_	Alignment		100.0	42	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**prostaglandin f synthase; **PDBTitle:** the crystal structure of prostaglandin f synthase from2 trypanosoma brucei
3	d1frba_	Alignment		100.0	41	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
4	c3f7jB_	Alignment		100.0	45	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**yvgn protein; **PDBTitle:** b.subtilis yvgn
5	d1hw6a_	Alignment		100.0	51	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
6	c3h7uA_	Alignment		100.0	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase; **PDBTitle:** crystal structure of the plant stress-response enzyme akr4c9
7	d1hqta_	Alignment		100.0	38	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
8	c2wztA_	Alignment		100.0	42	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase; **PDBTitle:** crystal structure of a mycobacterium aldo-keto reductase in2 its apo and liganded form
9	c3o0kB_	Alignment		100.0	51	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldo/keto reductase; **PDBTitle:** crystal structure of aldo/keto reductase from brucella melitensis
10	d1qwka_	Alignment		100.0	39	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
11	d1vp5a_	Alignment		100.0	45	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)

12	c3b3dA_	Alignment		100.0	46	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative morphine dehydrogenase; **PDBTitle:** b.subtilis ytbe
13	c2bgsA_	Alignment		100.0	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldose reductase; **PDBTitle:** holo aldose reductase from barley
14	d1q5ma_	Alignment		100.0	36	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
15	d1c9wa_	Alignment		100.0	40	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
16	d1ah4a_	Alignment		100.0	41	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
17	d1mi3a_	Alignment		100.0	40	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
18	d2alra_	Alignment		100.0	40	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
19	c3up8B_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative 2,5-diketo-d-gluconic acid reductase b; **PDBTitle:** crystal structure of a putative 2,5-diketo-d-gluconic acid reductase b
20	d1afsa_	Alignment		100.0	34	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
21	d1j96a_	Alignment	not modelled	100.0	38	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
22	d1us0a_	Alignment	not modelled	100.0	40	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
23	d1s1pa_	Alignment	not modelled	100.0	37	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
24	c1zgdB_	Alignment	not modelled	100.0	37	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**chalcone reductase; **PDBTitle:** chalcone reductase complexed with nadp+ at 1.7 angstrom2 resolution
25	c3h7rA_	Alignment	not modelled	100.0	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase; **PDBTitle:** crystal structure of the plant stress-response enzyme akr4c8
26	c3buvB_	Alignment	not modelled	100.0	35	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-oxo-5-beta-steroid 4-dehydrogenase; **PDBTitle:** crystal structure of human delta(4)-3-ketosteroid 5-beta-reductase in2 complex with nadp and hepes. resolution: 1.35 a.
27	d1ur3m_	Alignment	not modelled	100.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
28	d1lqaa_	Alignment	not modelled	100.0	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
29		Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase;

29	[illegible]	Alignment	not modelled	100.0	[illegible]	**PDBTitle:** structure of the glycerol dehydrogenase akr11b4 from gluconobacter2 oxydans
30	c3krbB_	Alignment	not modelled	100.0	37	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldose reductase; **PDBTitle:** structure of aldose reductase from giardia lamblia at 1.75a resolution
31	c3erpA_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of idp01002, a putative oxidoreductase from and essential2 gene of salmonella typhimurium
32	d1pz1a_	Alignment	not modelled	100.0	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
33	d1pyfa_	Alignment	not modelled	100.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
34	d3eaua1	Alignment	not modelled	100.0	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
35	c3lutA_	Alignment	not modelled	100.0	27	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**voltage-gated potassium channel subunit beta-2; **PDBTitle:** a structural model for the full-length shaker potassium channel kv1.2
36	c3n6qF_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**yghz aldo-keto reductase; **PDBTitle:** crystal structure of yghz from e. coli
37	c1ynpA_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** aldo-keto reductase akr11c1 from bacillus halodurans (apo form)
38	d1gvea_	Alignment	not modelled	100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
39	c2bp1C_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**aflatoxin b1 aldehyde reductase member 2; **PDBTitle:** structure of the aflatoxin aldehyde reductase in complex2 with nadph
40	c3ln3A_	Alignment	not modelled	100.0	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodiol dehydrogenase; **PDBTitle:** crystal structure of putative reductase (np_038806.2) from2 mus musculus at 1.18 a resolution
41	c3g8rA_	Alignment	not modelled	74.8	13	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**probable spore coat polysaccharide biosynthesis protein e; **PDBTitle:** crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
42	c2ftpA_	Alignment	not modelled	59.7	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
43	d1jpma1	Alignment	not modelled	58.7	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
44	d1x87a_	Alignment	not modelled	56.2	18	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
45	c3oa3A_	Alignment	not modelled	46.7	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aldolase; **PDBTitle:** crystal structure of a putative deoxyribose-phosphate aldolase from2 coccidioides immitis
46	c3k13A_	Alignment	not modelled	45.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydrofolate-homocysteine methyltransferase; **PDBTitle:** structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
47	c1vliA_	Alignment	not modelled	43.3	9	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**spore coat polysaccharide biosynthesis protein spse; **PDBTitle:** crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
48	d1o0ya_	Alignment	not modelled	40.7	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
49	c3eegB_	Alignment	not modelled	39.4	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
50	d1ub3a_	Alignment	not modelled	39.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
51	d1r0ma1	Alignment	not modelled	36.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
52	c1xuzA_	Alignment	not modelled	35.8	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
53	d1vlia2	Alignment	not modelled	35.5	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase

						Family: NeuB-like
54	d1sr9a2	Alignment	not modelled	34.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**HMGL-like
55	d1mzha_	Alignment	not modelled	34.2	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
56	c2yl8A_	Alignment	not modelled	32.8	13	**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
57	c3ngjC_	Alignment	not modelled	32.7	7	**PDB header:**lyase **Chain:** C: **PDB Molecule:**deoxyribose-phosphate aldolase; **PDBTitle:** crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
58	c3ewbX_	Alignment	not modelled	31.7	12	**PDB header:**transferase **Chain:** X: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of n-terminal domain of putative 2-2 isopropylmalate synthase from listeria monocytogenes
59	c2ph5A_	Alignment	not modelled	29.7	7	**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
60	c3ke8A_	Alignment	not modelled	29.7	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate **PDBTitle:** crystal structure of isph:hmbpp-complex
61	c2cw6B_	Alignment	not modelled	29.7	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hydroxymethylglutaryl-coa lyase, mitochondrial; **PDBTitle:** crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
62	c2it0A_	Alignment	not modelled	27.1	12	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**iron-dependent repressor ider; **PDBTitle:** crystal structure of a two-domain ider-dna complex crystal2 form ii
63	c2ylaA_	Alignment	not modelled	26.8	14	**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
64	c2qdeA_	Alignment	not modelled	26.7	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme family **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing family2 protein from azoarcus sp. ebn1
65	d2ijqa1	Alignment	not modelled	26.6	9	**Fold:**Hyaluronidase domain-like **Superfamily:**TTHA0068-like **Family:**TTHA0068-like
66	d1oi7a1	Alignment	not modelled	25.3	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
67	c3dnfB_	Alignment	not modelled	24.9	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate reductase; **PDBTitle:** structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
68	c3rpmA_	Alignment	not modelled	24.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetyl-hexosaminidase; **PDBTitle:** crystal structure of the first gh20 domain of a novel beta-n-acetyl-2 hexosaminidase strh from streptococcus pneumoniae r6
69	d1wlza1	Alignment	not modelled	24.4	4	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
70	c1wlzD_	Alignment	not modelled	24.4	4	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**cap-binding protein complex interacting protein **PDBTitle:** crystal structure of djbp fragment which was obtained by2 limited proteolysis
71	c2x4hA_	Alignment	not modelled	24.1	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hypothetical protein sso2273; **PDBTitle:** crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
72	d1vcva1	Alignment	not modelled	23.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
73	d1n7ka_	Alignment	not modelled	23.6	6	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
74	d1yhta1	Alignment	not modelled	23.4	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
75	c1u83A_	Alignment	not modelled	23.0	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphosulfolactate synthase; **PDBTitle:** psl synthase from bacillus subtilis
76	d1u83a_	Alignment	not modelled	23.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
77	c3ng3A_	Alignment	not modelled	22.7	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**deoxyribose-phosphate aldolase; **PDBTitle:** crystal structure of deoxyribose phosphate aldolase from mycobacterium2 avium 104 in a schiff base with an unknown aldehyde
						PDB header:transcription

78	c2k6xA_	Alignment	not modelled	22.0	4	**Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpod; **PDBTitle:** autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
79	c3lmzA_	Alignment	not modelled	21.8	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative sugar isomerase; **PDBTitle:** crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distasonis atcc 8503 at 1.44 a resolution
80	c2nqlB_	Alignment	not modelled	21.5	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**isomerase/lactonizing enzyme; **PDBTitle:** crystal structure of a member of the enolase superfamily from2 agrobacterium tumefaciens
81	c2eeeA_	Alignment	not modelled	21.0	32	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**uncharacterized protein c6orf130; **PDBTitle:** solution structure of the a1pp domain from human protein2 c6orf130
82	c3smaD_	Alignment	not modelled	20.8	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**frbf; **PDBTitle:** a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
83	d1p1xa_	Alignment	not modelled	19.9	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
84	d2zdra2	Alignment	not modelled	19.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
85	c2zyfA_	Alignment	not modelled	18.6	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homocitrate synthase; **PDBTitle:** crystal structure of homocitrate synthase from thermus thermophilus2 complexed with magnesuim ion and alpha-ketoglutarate
86	c3e4fB_	Alignment	not modelled	18.4	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminoglycoside n3-acetyltransferase; **PDBTitle:** crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
87	d1sjda1	Alignment	not modelled	17.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
88	d1g3wa2	Alignment	not modelled	17.2	10	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
89	c3ejfA_	Alignment	not modelled	17.2	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** crystal structure of ibv x-domain at ph 8.5
90	c1ydnA_	Alignment	not modelled	16.7	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
91	c3ik4A_	Alignment	not modelled	16.6	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing protein; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing protein2 from herpetosiphon aurantiacus
92	c3i6eA_	Alignment	not modelled	16.5	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**muconate cycloisomerase i; **PDBTitle:** crystal structure of muconate lactonizing enzyme from2 ruegeria pomeroyi.
93	d1sfla_	Alignment	not modelled	16.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
94	c1nvmG_	Alignment	not modelled	16.4	11	**PDB header:**lyase/oxidoreductase **Chain:** G: **PDB Molecule:**4-hydroxy-2-oxovalerate aldolase; **PDBTitle:** crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
95	c3l2iB_	Alignment	not modelled	15.3	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.85 angstrom crystal structure of the 3-dehydroquinate dehydratase2 (arod) from salmonella typhimurium lt2.
96	c3ivuB_	Alignment	not modelled	15.3	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
97	c3ktcB_	Alignment	not modelled	14.9	35	**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
98	c3ddmD_	Alignment	not modelled	14.8	10	**PDB header:**lyase **Chain:** D: **PDB Molecule:**putative mandelate racemase/muconate lactonizing **PDBTitle:** crystal structure of mandelate racemase/muconate2 lactonizing enzyme from bordetella bronchiseptica rb50
99	c2qgyA_	Alignment	not modelled	14.7	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**enolase from the environmental genome shotgun **PDBTitle:** crystal structure of an enolase from the environmental2 genome shotgun sequencing of the sargasso sea