

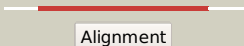



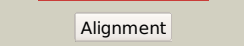





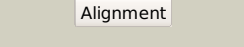

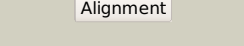

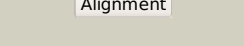

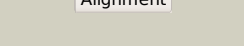

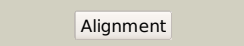




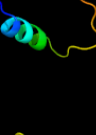



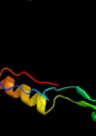
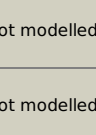


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1716 (- )_1943583_1944413
Date	Fri Aug 2 13:30:31 BST 2019
Unique Job ID	fd2e0aa6da1da3c2

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5nnaB_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> isatin hydrolase a; <b>PDBTitle:</b> isatin hydrolase a (iha) from labrenzia aggregata bound to benzyl2 benzoate
2	<a href="#">c4j0nA_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> isatin hydrolase b; <b>PDBTitle:</b> crystal structure of a manganese dependent isatin hydrolase
3	<a href="#">c5nmpF_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> isatin hydrolase; <b>PDBTitle:</b> isatin hydrolase a (iha) from ralstonia solanacearum
4	<a href="#">c4coaA_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> kynurenine formamidase; <b>PDBTitle:</b> crystal structure of kynurenine formamidase from bacillus2 anthracis complexed with 2-aminoacetophenone.
5	<a href="#">d1r61a_</a>	 Alignment		100.0	27	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Putative cyclase <b>Family:</b> Putative cyclase
6	<a href="#">c4cogB_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> kynurenine formamidase; <b>PDBTitle:</b> crystal structure of kynurenine formamidase from burkholderia2 cenocepacia
7	<a href="#">c4cobA_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> kynurenine formamidase; <b>PDBTitle:</b> crystal structure kynurenine formamidase from pseudomonas aeruginosa
8	<a href="#">d2b0aa1</a>	 Alignment		100.0	26	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Putative cyclase <b>Family:</b> Putative cyclase
9	<a href="#">c5ibzD_</a>	 Alignment		100.0	30	<b>PDB header:</b> lyase <b>Chain:</b> D; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a novel cyclase (pfam04199).
10	<a href="#">d2fvta1</a>	 Alignment		80.6	22	<b>Fold:</b> MTH938-like <b>Superfamily:</b> MTH938-like <b>Family:</b> MTH938-like
11	<a href="#">c2gm2A_</a>	 Alignment		57.1	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> nmr structure of xanthomonas campestris xcc1710: northeast2 structural genomics consortium target xcr35

12	<a href="#">d1zy9a2</a>	Alignment		46.5	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> YicI catalytic domain-like
13	<a href="#">c5ir2A</a>	Alignment		42.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulase; <b>PDBTitle:</b> crystal structure of novel cellulases from microbes associated with2 the gut ecosystem
14	<a href="#">c2k2eA</a>	Alignment		40.4	32	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein bp2786; <b>PDBTitle:</b> solution nmr structure of bordetella pertussis protein2 bp2786, a mth938-like domain. northeast structural3 genomics consortium target ber31
15	<a href="#">c3e4fB</a>	Alignment		39.3	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside n3-acetyltransferase; <b>PDBTitle:</b> crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
16	<a href="#">d2nyga1</a>	Alignment		38.1	13	<b>Fold:</b> TTHA0583/YokD-like <b>Superfamily:</b> TTHA0583/YokD-like <b>Family:</b> Aminoglycoside 3-N-acetyltransferase-like
17	<a href="#">c3smaD</a>	Alignment		37.9	23	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> frbf; <b>PDBTitle:</b> a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
18	<a href="#">c4ce0A</a>	Alignment		37.6	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-methyltransferase; <b>PDBTitle:</b> crystal structure of sah-bound spinosyn rhamnosyl 4'-o-2 methyltransferase spnh from saccharopolyspora spinosa
19	<a href="#">d2q4qa1</a>	Alignment		37.2	13	<b>Fold:</b> MTH938-like <b>Superfamily:</b> MTH938-like <b>Family:</b> MTH938-like
20	<a href="#">c4zgwB</a>	Alignment		36.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase; <b>PDBTitle:</b> short-chain dehydrogenase/reductase from serratia marcescens bccr2 10948
21	<a href="#">c6bc3A</a>	Alignment	not modelled	34.5	21	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> aac 3-vi protein; <b>PDBTitle:</b> cryo x-ray structure of sisomicin bound aac-via
22	<a href="#">d2fi9a1</a>	Alignment	not modelled	31.6	13	<b>Fold:</b> MTH938-like <b>Superfamily:</b> MTH938-like <b>Family:</b> MTH938-like
23	<a href="#">c5ht0B</a>	Alignment	not modelled	28.9	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoglycoside acetyltransferase hmb0005; <b>PDBTitle:</b> crystal structure of an antibiotic_nat family aminoglycoside2 acetyltransferase hmb0038 from an uncultured soil metagenomic sample3 in complex with coenzyme a
24	<a href="#">c6mb6A</a>	Alignment	not modelled	28.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aac(3)-iiib protein; <b>PDBTitle:</b> aac-iiib binary with coash
25	<a href="#">c3cvjB</a>	Alignment	not modelled	28.1	8	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphoheptose isomerase; <b>PDBTitle:</b> crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
26	<a href="#">c1zy9A</a>	Alignment	not modelled	28.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-galactosidase; <b>PDBTitle:</b> crystal structure of alpha-galactosidase (ec 3.2.1.22) (melibiase)2 (tm1192) from thermotoga maritima at 2.34 a resolution
27	<a href="#">d2gp4a1</a>	Alignment	not modelled	27.5	15	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> LeuD/IlvD-like <b>Family:</b> IlvD/EDD C-terminal domain-like
28	<a href="#">c2gp4B</a>	Alignment	not modelled	24.4	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphogluconate dehydratase; <b>PDBTitle:</b> structure of [fes]cluster-free apo form of 6-

						phosphogluconate2 dehydratase from shewanella oneidensis
29	<a href="#">c2pcnA</a>	Alignment	not modelled	23.1	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine:2-demethylmenaquinone <b>PDBTitle:</b> crystal structure of s-adenosylmethionine: 2-demethylmenaquinone2 methyltransferase (gk_1813) from geobacillus kaustophilus hta426
30	<a href="#">c2gp4A</a>	Alignment	not modelled	22.7	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydratase; <b>PDBTitle:</b> structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
31	<a href="#">c5ykjA</a>	Alignment	not modelled	22.6	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxiredoxin prx1, mitochondrial; <b>PDBTitle:</b> structural basis of the thiol resolving mechanism in yeast2 mitochondrial 1-cys peroxiredoxin via glutathione/thioredoxin systems
32	<a href="#">d2bgka1</a>	Alignment	not modelled	21.9	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
33	<a href="#">c3kw0D</a>	Alignment	not modelled	20.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cysteine peptidase; <b>PDBTitle:</b> crystal structure of cysteine peptidase (np_982244.1) from bacillus2 cereus atcc 10987 at 2.50 a resolution
34	<a href="#">c3c8oB</a>	Alignment	not modelled	20.2	21	<b>PDB header:</b> hydrolase regulator <b>Chain:</b> B: <b>PDB Molecule:</b> regulator of ribonuclease activity a; <b>PDBTitle:</b> the crystal structure of rraa from pao1
35	<a href="#">d1mpxa2</a>	Alignment	not modelled	19.9	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> PepX catalytic domain-like
36	<a href="#">c4pf1D</a>	Alignment	not modelled	18.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> peptidase s15/coce/nond; <b>PDBTitle:</b> crystal structure of aminopeptidase from marine sediment archaeon2 thaumarchaeota archaeon
37	<a href="#">c1wu8B</a>	Alignment	not modelled	18.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ph0463; <b>PDBTitle:</b> crystal structure of project ph0463 from pyrococcus horikoshii ot3
38	<a href="#">c2yvaB</a>	Alignment	not modelled	17.8	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dnaa initiator-associating protein diaa; <b>PDBTitle:</b> crystal structure of escherichia coli diaa
39	<a href="#">c2kz3A</a>	Alignment	not modelled	17.7	20	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein rad5113; <b>PDBTitle:</b> backbone 1h, 13c, and 15n chemical shift assignments for human rad51d2 from 1 to 83
40	<a href="#">c4xvzB</a>	Alignment	not modelled	17.2	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> mycinamicin iii 3''-o-methyltransferase; <b>PDBTitle:</b> mycf mycinamicin iii 3'-o-methyltransferase in complex with mg
41	<a href="#">d1rqpa2</a>	Alignment	not modelled	17.1	15	<b>Fold:</b> Bacterial fluorinating enzyme, N-terminal domain <b>Superfamily:</b> Bacterial fluorinating enzyme, N-terminal domain <b>Family:</b> Bacterial fluorinating enzyme, N-terminal domain
42	<a href="#">d2ot2a1</a>	Alignment	not modelled	16.8	33	<b>Fold:</b> OB-fold <b>Superfamily:</b> HupF/HypC-like <b>Family:</b> HupF/HypC-like
43	<a href="#">c2eq9C</a>	Alignment	not modelled	16.6	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate dehydrogenase complex, dihydrolipoamide <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
44	<a href="#">c3trjC</a>	Alignment	not modelled	16.4	25	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> structure of a phosphoheptose isomerase from francisella tularensis
45	<a href="#">c4gf5S</a>	Alignment	not modelled	16.4	19	<b>PDB header:</b> transferase <b>Chain:</b> S: <b>PDB Molecule:</b> cals11; <b>PDBTitle:</b> crystal structure of calicheamicin methyltransferase, cals11
46	<a href="#">c2eq8C</a>	Alignment	not modelled	16.1	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate dehydrogenase complex, dihydrolipoamide <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
47	<a href="#">c2q6oB</a>	Alignment	not modelled	16.0	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> sall-y70t with sam and cl
48	<a href="#">d1pjca2</a>	Alignment	not modelled	15.9	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> L-alanine dehydrogenase-like
49	<a href="#">d1q5xa</a>	Alignment	not modelled	15.2	18	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> RraA-like <b>Family:</b> RraA-like
50	<a href="#">c5jc8C</a>	Alignment	not modelled	15.2	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of a putative short-chain dehydrogenase/reductase2 from burkholderia xenovorans
51	<a href="#">c2d0iC</a>	Alignment	not modelled	15.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dehydrogenase; <b>PDBTitle:</b> crystal structure ph0520 protein from pyrococcus horikoshii ot3
52	<a href="#">c2zvbC</a>	Alignment	not modelled	14.7	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> crystal structure of uncharacterized conserved protein from thermotoga2 maritima
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp-dependent 2-hydroxyacid

53	<a href="#">c4xcvA_</a>	Alignment	not modelled	14.7	15	dehydrogenase; <b>PDBTitle:</b> probable 2-hydroxyacid dehydrogenase from rhizobium etli cfn 42 in2 complex with nadph
54	<a href="#">c1rqrA_</a>	Alignment	not modelled	14.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5'-fluoro-5'-deoxyadenosine synthase; <b>PDBTitle:</b> crystal structure and mechanism of a bacterial fluorinating enzyme,2 product complex
55	<a href="#">d2d59a1</a>	Alignment	not modelled	14.4	28	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
56	<a href="#">c6mn5A_</a>	Alignment	not modelled	14.4	14	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> aminoglycoside n(3)-acetyltransferase, aac(3)-iva; <b>PDBTitle:</b> crystal structure of aminoglycoside acetyltransferase aac(3)-iva,2 h154a mutant, in complex with gentamicin c1a
57	<a href="#">c4nx0G_</a>	Alignment	not modelled	14.3	25	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> abp, a gh27 beta-l-arabinopyranosidase; <b>PDBTitle:</b> crystal structure of abp-wt, a gh27-b-l-arabinopyranosidase from2 geobacillus stearothermophilus
58	<a href="#">d2z1ca1</a>	Alignment	not modelled	14.3	60	<b>Fold:</b> OB-fold <b>Superfamily:</b> HupF/HypC-like <b>Family:</b> HupF/HypC-like
59	<a href="#">c4g2nA_</a>	Alignment	not modelled	14.3	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-isomer specific 2-hydroxyacid dehydrogenase, nad-binding; <b>PDBTitle:</b> crystal structure of putative d-isomer specific 2-hydroxyacid2 dehydrogenase, nad-binding from polaromonas sp. js6 66
60	<a href="#">c3icrA_</a>	Alignment	not modelled	14.1	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme a-disulfide reductase; <b>PDBTitle:</b> crystal structure of oxidized bacillus anthracis coadr-rhd
61	<a href="#">c3d3rA_</a>	Alignment	not modelled	14.1	21	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase assembly chaperone hycp/hupf; <b>PDBTitle:</b> crystal structure of the hydrogenase assembly chaperone hycp/hupf2 family protein from shewanella oneidensis mr-1
62	<a href="#">c1mpxB_</a>	Alignment	not modelled	13.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-amino acid ester hydrolase; <b>PDBTitle:</b> alpha-amino acid ester hydrolase labeled with selenomethionine
63	<a href="#">d2cyja1</a>	Alignment	not modelled	13.8	19	<b>Fold:</b> MTH938-like <b>Superfamily:</b> MTH938-like <b>Family:</b> MTH938-like
64	<a href="#">d1tk9a_</a>	Alignment	not modelled	13.7	11	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
65	<a href="#">c2f4nA_</a>	Alignment	not modelled	13.7	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein mj1651; <b>PDBTitle:</b> crystal structure of protein mj1651 from methanococcus2 jannaschii dsm 2661, pfam duf62
66	<a href="#">c5fohA_</a>	Alignment	not modelled	13.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> polysaccharide monoxygenase; <b>PDBTitle:</b> crystal structure of the catalytic domain of nclpmo9a
67	<a href="#">c5oynB_</a>	Alignment	not modelled	13.6	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dehydratase, ilvd/edd family; <b>PDBTitle:</b> crystal structure of d-xylonate dehydratase in holo-form
68	<a href="#">c6ci9D_</a>	Alignment	not modelled	13.5	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-oxoacyl-[acyl-carrier-protein] reductase; <b>PDBTitle:</b> rmm microcompartment-associated aminopropanol dehydrogenase nadp +2 aminoacetone holo-structure
69	<a href="#">d1j3la_</a>	Alignment	not modelled	13.3	17	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> RraA-like <b>Family:</b> RraA-like
70	<a href="#">d2cyua1</a>	Alignment	not modelled	13.1	27	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
71	<a href="#">c5u9pB_</a>	Alignment	not modelled	13.1	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gluconate 5-dehydrogenase; <b>PDBTitle:</b> crystal structure of a gluconate 5-dehydrogenase from burkholderia2 cenocepacia j2315 in complex with nadp and tartrate
72	<a href="#">c3k4iC_</a>	Alignment	not modelled	12.9	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein pspto_3204 from2 pseudomonas syringae pv. tomato str. dc3000
73	<a href="#">c2wdzD_</a>	Alignment	not modelled	12.4	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of the short chain dehydrogenase2 galactitol-dehydrogenase (gatdh) of rhodobacter3 sphaeroides in complex with nad+ and 1,2-pentandiol
74	<a href="#">d1x94a_</a>	Alignment	not modelled	12.3	28	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
75	<a href="#">d1vi4a_</a>	Alignment	not modelled	12.0	19	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> RraA-like <b>Family:</b> RraA-like
76	<a href="#">c4pcvB_</a>	Alignment	not modelled	11.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bdca (yjgi); <b>PDBTitle:</b> the structure of bdca (yjgi) from e. coli
77	<a href="#">c4gh5B_</a>	Alignment	not modelled	11.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase sdr; <b>PDBTitle:</b> crystal structure of s-2-hydroxypropyl coenzyme m dehydrogenase (s-2 hpcdh)

78	<a href="#">c2cw5B_</a>	Alignment	not modelled	11.6	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> bacterial fluorinating enzyme homolog; <b>PDBTitle:</b> crystal structure of a conserved hypothetical protein from2 thermus thermophilus hb8
79	<a href="#">d3d3ra1</a>	Alignment	not modelled	11.5	21	<b>Fold:</b> OB-fold <b>Superfamily:</b> HupF/HypC-like <b>Family:</b> HupF/HypC-like
80	<a href="#">c2k4mA_</a>	Alignment	not modelled	11.4	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0146 protein mth_1000; <b>PDBTitle:</b> solution nmr structure of m. thermoautotrophicum protein mth_1000,2 northeast structural genomics consortium target tr8
81	<a href="#">c4nbrA_</a>	Alignment	not modelled	11.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 3-oxoacyl-(acyl-carrier protein) reductase; <b>PDBTitle:</b> crystal structure of 3-oxoacyl-[acyl-carrier protein] reductase from2 brucella melitensis atcc 23457
82	<a href="#">c6nrc_</a>	Alignment	not modelled	11.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-oxoacyl-acp reductase fabg; <b>PDBTitle:</b> putative short-chain dehydrogenase/reductase (sdr) from acinetobacter2 baumannii
83	<a href="#">c3r1iB_</a>	Alignment	not modelled	11.2	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain type dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of a short-chain type dehydrogenase/reductase from2 mycobacterium marinum
84	<a href="#">c3es4B_</a>	Alignment	not modelled	11.1	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein duf861 with a rmlc-like cupin fold; <b>PDBTitle:</b> crystal structure of protein of unknown function (duf861) with a rmlc-2 like cupin fold (17741406) from agrobacterium tumefaciens str. c583 (dupont) at 1.64 a resolution
85	<a href="#">d2jfga1</a>	Alignment	not modelled	10.8	30	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
86	<a href="#">c5tiiC_</a>	Alignment	not modelled	10.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-oxoacyl-acp reductase; <b>PDBTitle:</b> comprehensive analysis of a novel ketoreductase for pentangular2 polyphenol biosynthesis
87	<a href="#">c3rihB_</a>	Alignment	not modelled	10.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short chain dehydrogenase or reductase; <b>PDBTitle:</b> crystal structure of a putative short chain dehydrogenase or reductase2 from mycobacterium abscessus
88	<a href="#">c4fqsB_</a>	Alignment	not modelled	10.6	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable dehydrogenase protein; <b>PDBTitle:</b> crystal structure of a probable dehydrogenase protein
89	<a href="#">d2ocda1</a>	Alignment	not modelled	10.4	20	<b>Fold:</b> Glutaminase/Asparaginase <b>Superfamily:</b> Glutaminase/Asparaginase <b>Family:</b> Glutaminase/Asparaginase
90	<a href="#">c4z9yA_</a>	Alignment	not modelled	10.4	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-deoxy-d-gluconate 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of 2-keto-3-deoxy-d-gluconate dehydrogenase from2 pectobacterium carotovorum
91	<a href="#">c4b79B_</a>	Alignment	not modelled	10.4	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable short-chain dehydrogenase; <b>PDBTitle:</b> the aeropath project and pseudomonas aeruginosa high-throughput2 crystallographic studies for assessment of potential targets in3 early stage drug discovery.
92	<a href="#">c2wk1A_</a>	Alignment	not modelled	10.3	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> novp; <b>PDBTitle:</b> structure of the o-methyltransferase novp
93	<a href="#">c3awdD_</a>	Alignment	not modelled	10.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative polyol dehydrogenase; <b>PDBTitle:</b> crystal structure of gox2181
94	<a href="#">d2c42a4</a>	Alignment	not modelled	10.3	21	<b>Fold:</b> Pyruvate-ferredoxin oxidoreductase, PFOR, domain III <b>Superfamily:</b> Pyruvate-ferredoxin oxidoreductase, PFOR, domain III <b>Family:</b> Pyruvate-ferredoxin oxidoreductase, PFOR, domain III
95	<a href="#">c1nxjA_</a>	Alignment	not modelled	10.2	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable s-adenosylmethionine:2- <b>PDBTitle:</b> structure of rv3853 from mycobacterium tuberculosis
96	<a href="#">d1nxja_</a>	Alignment	not modelled	10.2	18	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> RraA-like <b>Family:</b> RraA-like
97	<a href="#">d2obba1</a>	Alignment	not modelled	10.2	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> BT0820-like
98	<a href="#">d1ygya1</a>	Alignment	not modelled	10.2	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
99	<a href="#">d1w85i_</a>	Alignment	not modelled	10.0	42	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex