























# Phyre2

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Description	RVBD3262_(fbiB)_3641532_3642878
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2phna1</a>	 Alignment		100.0	37	<b>Fold:</b> CofE-like <b>Superfamily:</b> CofE-like <b>Family:</b> CofE-like
2	<a href="#">c4xomB_</a>	 Alignment		100.0	100	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> coenzyme f420:l-glutamate ligase; <b>PDBTitle:</b> coenzyme f420:l-glutamate ligase (fbib) from mycobacterium2 tuberculosis (c-terminal domain).
3	<a href="#">c5heiE_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> nfra2; <b>PDBTitle:</b> structure of b. megaterium nfra2
4	<a href="#">c5hdjA_</a>	 Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nfra1; <b>PDBTitle:</b> structure of b. megaterium nfra1
5	<a href="#">c3n2sD_</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nadh-dependent nitro/flavin reductase; <b>PDBTitle:</b> structure of nfra1 nitroreductase from b. subtilis
6	<a href="#">c2islB_</a>	 Alignment		100.0	20	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> blub; <b>PDBTitle:</b> blub bound to reduced flavin (fmnh2) and molecular oxygen.2 (clear crystal form)
7	<a href="#">d1zcha1</a>	 Alignment		100.0	17	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
8	<a href="#">c3eofB_</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of putative oxidoreductase (yp_213212.1) from2 bacteroides fragilis nctc 9343 at 1.99 a resolution
9	<a href="#">d1f5va_</a>	 Alignment		100.0	20	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
10	<a href="#">d2ifaa1</a>	 Alignment		100.0	14	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
11	<a href="#">d1bkja_</a>	 Alignment		100.0	20	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase

12	<a href="#">c4eo3A_</a>	Alignment		100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bacterioferritin comigratory protein/nadh dehydrogenase; <b>PDBTitle:</b> peroxiredoxin nitroreductase fusion enzyme
13	<a href="#">c5ko8B_</a>	Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of haliscomenobacter hydrossis iodotyrosine2 deiodinase (iyd) bound to fmn and mono-iodotyrosine (i-tyr)
14	<a href="#">c3eo8A_</a>	Alignment		100.0	21	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> blub-like flavoprotein; <b>PDBTitle:</b> crystal structure of blub-like flavoprotein (yp_001089088.1) from2 clostridium difficile 630 at 1.74 a resolution
15	<a href="#">c2wqfA_</a>	Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> copper induced nitroreductase d; <b>PDBTitle:</b> crystal structure of the nitroreductase cind from2 lactococcus lactis in complex with fmn
16	<a href="#">d1ywqa1</a>	Alignment		100.0	18	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
17	<a href="#">c2wzvB_</a>	Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nfnb protein; <b>PDBTitle:</b> crystal structure of the fmn-dependent nitroreductase nfnb2 from mycobacterium smegmatis
18	<a href="#">c3k6hB_</a>	Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitroreductase family protein; <b>PDBTitle:</b> crystal structure of a nitroreductase family protein from2 agrobacterium tumefaciens str. c58
19	<a href="#">c3gh8A_</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> iodotyrosine dehalogenase 1; <b>PDBTitle:</b> crystal structure of mus musculus iodotyrosine deiodinase (iyd) bound2 to fmn and di-iodotyrosine (dit)
20	<a href="#">c3gfaB_</a>	Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nitroreductase; <b>PDBTitle:</b> crystal structure of a putative nitroreductase in complex with fmn2 (cd3205) from clostridium difficile 630 at 1.35 a resolution
21	<a href="#">c3gr3B_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of a nitroreductase-like family protein (pnba,2 bh06130) from bartonella henselae str. houston-1 at 1.45 a resolution
22	<a href="#">c2hayD_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative nad(p)h-flavin oxidoreductase; <b>PDBTitle:</b> the crystal structure of the putative nad(p)h-flavin oxidoreductase2 from streptococcus pyogenes m1 gas
23	<a href="#">c2i7hE_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> nitroreductase-like family protein; <b>PDBTitle:</b> crystal structure of the nitroreductase-like family protein from2 bacillus cereus
24	<a href="#">c3ek3A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of nitroreductase with bound fmn (yp_211706.1) from2 bacteroides fragilis nctc 9343 at 1.70 a resolution
25	<a href="#">c3ge6B_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of a putative nitroreductase in complex with fmn2 (exig_2970) from exiguobacterium sibiricum 255-15 at 1.85 a3 resolution
26	<a href="#">d1vfra_</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
27	<a href="#">c3gagB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadh dehydrogenase, nadph nitroreductase; <b>PDBTitle:</b> crystal structure of a nitroreductase-like protein (smu.346) from2 streptococcus mutans at 1.70 a resolution

28	<a href="#">d2b67a1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
29	<a href="#">d1noxa</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
30	<a href="#">c3pxvD</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of a nitroreductase with bound fmn (dhaf_2018) from2 desulfitobacterium hafniense dcb-2 at 2.30 a resolution
31	<a href="#">c3to0A</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> iodotyrosine deiodinase 1; <b>PDBTitle:</b> crystal structure of mus musculus iodotyrosine deiodinase (iyd) c217a,2 c239a bound to fmn
32	<a href="#">c3of4A</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of a fmn/fad- and nad(p)h-dependent nitroreductase2 (fnfb, il2077) from idiomarina loihiensis l2tr at 1.90 a resolution
33	<a href="#">c4glyB</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enone reductase cla-er; <b>PDBTitle:</b> crystal structure of cla-er, a novel enone reductase catalyzing a key2 step of a gut-bacterial fatty acid saturation metabolism,3 biohydrogenation
34	<a href="#">c3gbhC</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nad(p)h-flavin oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative nad(p)h:fmn oxidoreductase (se1966)2 from staphylococcus epidermidis atcc 12228 at 2.00 a resolution
35	<a href="#">c6czpH</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> oxygen-insensitive nad(p)h nitroreductase; <b>PDBTitle:</b> 2.2 angstrom resolution crystal structure oxygen-insensitive nad(p)h-2 dependent nitroreductase nfsb from vibrio vulnificus in complex with3 fmn
36	<a href="#">d1ykia1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
37	<a href="#">c3bemA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nad(p)h nitroreductase ydfn; <b>PDBTitle:</b> crystal structure of putative nitroreductase ydfn (2632848) from2 bacillus subtilis at 1.65 a resolution
38	<a href="#">d2frea1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
39	<a href="#">c3kwkA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nadh dehydrogenase/nad(p)h nitroreductase; <b>PDBTitle:</b> crystal structure of putative nadh dehydrogenase/nad(p)h2 nitroreductase (np_809094.1) from bacteroides thetaiotaomicron vpi-3 5482 at 1.54 a resolution
40	<a href="#">c3m5kA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nadh dehydrogenase/nad(p)h nitroreductase; <b>PDBTitle:</b> crystal structure of putative nadh dehydrogenase/nad(p)h2 nitroreductase (bdi_1728) from parabacteroides distasonis atcc 85033 at 1.86 a resolution
41	<a href="#">d1kqba</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
42	<a href="#">c4dn2A</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of putative nitroreductase from geobacter2 metallireducens gs-15
43	<a href="#">c3e10B</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadh oxidase; <b>PDBTitle:</b> crystal structure of putative nadh oxidase (np_348178.1) from2 clostridium acetobutylicum at 1.40 a resolution
44	<a href="#">c3ge5A</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nad(p)h:fmn oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative nad(p)h:fmn oxidoreductase (pg0310)2 from porphyromonas gingivalis w83 at 1.70 a resolution
45	<a href="#">c3e39A</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nitroreductase; <b>PDBTitle:</b> crystal structure of a putative nitroreductase in complex with fmn2 (dde_0787) from desulfovibrio desulfuricans subsp. at 1.70 a3 resolution
46	<a href="#">c3koqC</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nitroreductase family protein; <b>PDBTitle:</b> crystal structure of a nitroreductase family protein (cd3355) from2 clostridium difficile 630 at 1.58 a resolution
47	<a href="#">c2r01A</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitroreductase family protein; <b>PDBTitle:</b> crystal structure of a putative fmn-dependent nitroreductase (ct0345)2 from chlorobium tepidum t1s at 1.15 a resolution
48	<a href="#">c3qdID</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxygen-insensitive nadph nitroreductase; <b>PDBTitle:</b> crystal structure of rdxa from helicobacter pylori
49	<a href="#">c5j62B</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative reductase; <b>PDBTitle:</b> fmn-dependent nitroreductase (cdr20291_0684) from clostridium2 difficile r20291
50	<a href="#">c5j6cA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative reductase; <b>PDBTitle:</b> fmn-dependent nitroreductase (cdr20291_0767) from clostridium2 difficile r20291
						<b>PDB header:</b> oxidoreductase

51	<a href="#">c3g14B_</a>	Alignment	not modelled	100.0	15	<b>Chain:</b> B: <b>PDB Molecule:</b> nitroreductase family protein; <b>PDBTitle:</b> crystal structure of nitroreductase family protein (yp_877874.1) from2 clostridium novyi nt at 1.75 a resolution
52	<a href="#">c2h0uA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph-flavin oxidoreductase; <b>PDBTitle:</b> crystal structure of nad(p)-h-flavin oxidoreductase from helicobacter2 pylori
53	<a href="#">c4urpB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid repression mutant protein 2; <b>PDBTitle:</b> the crystal structure of nitroreductase from saccharomyces2 cerevisiae
54	<a href="#">c3bm2B_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> protein ydja; <b>PDBTitle:</b> crystal structure of a minimal nitroreductase ydja from escherichia2 coli k12 with and without fmn cofactor
55	<a href="#">c3hj9A_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative nitroreductase (reut_a1228) from2 ralstonia eutropha jmp134 at 2.00 a resolution
56	<a href="#">c3hoiA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fmn-dependent nitroreductase bf3017; <b>PDBTitle:</b> crystal structure of fmn-dependent nitroreductase bf3017 from2 bacteroides fragilis nctc 9343 (yp_212631.1) from bacteroides3 fragilis nctc 9343 at 1.55 a resolution
57	<a href="#">c5lq4B_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cyagox; <b>PDBTitle:</b> the structure of thcox, the first oxidase protein from the cyanobactin2 pathways
58	<a href="#">c3eo7A_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> putative nitroreductase; <b>PDBTitle:</b> crystal structure of a putative nitroreductase (ava_2154) from2 anabaena variabilis atcc 29413 at 1.80 a resolution
59	<a href="#">d1vkwA_</a>	Alignment	not modelled	99.8	25	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> Putative nitroreductase TM1586
60	<a href="#">c2ymvA_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acg nitroreductase; <b>PDBTitle:</b> structure of reduced m smegmatis 5246, a homologue of m.2 tuberculosis acg
61	<a href="#">c6gosC_</a>	Alignment	not modelled	99.5	11	<b>PDB header:</b> antibiotic/inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> microcin b17-processing protein mbc; <b>PDBTitle:</b> e. coli microcin synthetase mcbbcd complex with pro-mccb17 bound
62	<a href="#">c4ir1A_</a>	Alignment	not modelled	59.6	11	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iv; <b>PDBTitle:</b> polymerase-dna complex
63	<a href="#">c2j89A_</a>	Alignment	not modelled	49.6	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine sulfoxide reductase a; <b>PDBTitle:</b> functional and structural aspects of poplar cytosolic and2 plastidial type a methionine sulfoxide reductases
64	<a href="#">c4db4A_</a>	Alignment	not modelled	44.5	37	<b>PDB header:</b> rna-binding protein/dna,rna <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase mss116, mitochondrial; <b>PDBTitle:</b> mss116p dead-box helicase domain 2 bound to a chimaeric rna-dna duplex
65	<a href="#">d1oeyj_</a>	Alignment	not modelled	44.2	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> CAD & PB1 domains <b>Family:</b> PB1 domain
66	<a href="#">d1srsa_</a>	Alignment	not modelled	43.3	13	<b>Fold:</b> SRF-like <b>Superfamily:</b> SRF-like <b>Family:</b> SRF-like
67	<a href="#">d1mnma_</a>	Alignment	not modelled	41.6	13	<b>Fold:</b> SRF-like <b>Superfamily:</b> SRF-like <b>Family:</b> SRF-like
68	<a href="#">d2oc6a1</a>	Alignment	not modelled	40.6	18	<b>Fold:</b> Secretion chaperone-like <b>Superfamily:</b> YdhG-like <b>Family:</b> YdhG-like
69	<a href="#">c2bvtB_</a>	Alignment	not modelled	36.8	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-1,4-mannanase; <b>PDBTitle:</b> the structure of a modular endo-beta-1,4-mannanase from cellulomonas2 fimi explains the product specificity of glycoside hydrolase family3 26 mannanases.
70	<a href="#">d1egwa_</a>	Alignment	not modelled	36.4	17	<b>Fold:</b> SRF-like <b>Superfamily:</b> SRF-like <b>Family:</b> SRF-like
71	<a href="#">c2z0mA_</a>	Alignment	not modelled	33.9	28	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> 337aa long hypothetical atp-dependent rna <b>PDBTitle:</b> crystal structure of hypothetical atp-dependent rna2 helicase from sulfolobus tokodaii
72	<a href="#">d2i8da1</a>	Alignment	not modelled	33.9	16	<b>Fold:</b> Secretion chaperone-like <b>Superfamily:</b> YdhG-like <b>Family:</b> YdhG-like
73	<a href="#">d2hiya1</a>	Alignment	not modelled	32.7	4	<b>Fold:</b> SP0830-like <b>Superfamily:</b> SP0830-like <b>Family:</b> SP0830-like
74	<a href="#">c3pilA_</a>	Alignment	not modelled	32.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peptide methionine sulfoxide reductase; <b>PDBTitle:</b> crystal structure of mxr1 from saccharomyces cerevisiae in reduced2 form
75	<a href="#">c3exsB_</a>	Alignment	not modelled	30.7	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> rrmpd (hexulose-6-phosphate synthase); <b>PDBTitle:</b> crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p
76	<a href="#">c3gyxl_</a>	Alignment	not modelled	29.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J: <b>PDB Molecule:</b> adenylsulfate reductase; <b>PDBTitle:</b> crystal structure of adenylsulfate reductase from2

						desulfovibrio gigas
77	<a href="#">c4dcia_</a>	Alignment	not modelled	27.5	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of unknown function protein from synechococcus sp.2 wh 8102
78	<a href="#">c3bqha_</a>	Alignment	not modelled	27.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peptide methionine sulfoxide reductase msra/msrb; <b>PDBTitle:</b> structure of the central domain (msra) of neisseria meningitidis pilb2 (oxidized form)
79	<a href="#">d1f52a1</a>	Alignment	not modelled	26.9	37	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Glutamine synthetase, N-terminal domain <b>Family:</b> Glutamine synthetase, N-terminal domain
80	<a href="#">d1n6ja_</a>	Alignment	not modelled	26.9	17	<b>Fold:</b> SRF-like <b>Superfamily:</b> SRF-like <b>Family:</b> SRF-like
81	<a href="#">c4anra_</a>	Alignment	not modelled	26.3	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> soluble lytic transglycosylase b; <b>PDBTitle:</b> crystal structure of soluble lytic transglycosylase sltb12 from pseudomonas aeruginosa
82	<a href="#">d1hi9a_</a>	Alignment	not modelled	25.7	16	<b>Fold:</b> Dipeptide transport protein <b>Superfamily:</b> Dipeptide transport protein <b>Family:</b> Dipeptide transport protein
83	<a href="#">c2ds2B_</a>	Alignment	not modelled	25.5	10	<b>PDB header:</b> plant protein <b>Chain:</b> B: <b>PDB Molecule:</b> sweet protein mabinlin-2 chain b; <b>PDBTitle:</b> crystal structure of mabinlin ii
84	<a href="#">c3dmdA_</a>	Alignment	not modelled	24.8	25	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle receptor; <b>PDBTitle:</b> structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
85	<a href="#">c4ljya_</a>	Alignment	not modelled	24.3	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pre-mrna-processing atp-dependent rna helicase prp5; <b>PDBTitle:</b> crystal structure of rna splicing effector prp5 in complex with adp
86	<a href="#">c1zu4A_</a>	Alignment	not modelled	24.1	12	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> ftsyl; <b>PDBTitle:</b> crystal structure of ftsyl from mycoplasma mycoides-space2 group p21212
87	<a href="#">c6c48E_</a>	Alignment	not modelled	23.7	22	<b>PDB header:</b> cell cycle/dna binding <b>Chain:</b> E: <b>PDB Molecule:</b> protein lin-52 homolog; <b>PDBTitle:</b> crystal structure of b-myb-lin9-lin52 complex
88	<a href="#">c1pnbB_</a>	Alignment	not modelled	23.4	14	<b>PDB header:</b> seed storage protein <b>Chain:</b> B: <b>PDB Molecule:</b> napin bnib; <b>PDBTitle:</b> structure of napin bnib, nmr, 10 structures
89	<a href="#">d1j8yf2</a>	Alignment	not modelled	23.3	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
90	<a href="#">c6nr2A_</a>	Alignment	not modelled	21.9	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily m <b>PDBTitle:</b> cryo-em structure of the trpm8 ion channel in complex with the menthol2 analog ws-12 and pi(4,5)p2
91	<a href="#">c6nr2D_</a>	Alignment	not modelled	21.9	17	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily m <b>PDBTitle:</b> cryo-em structure of the trpm8 ion channel in complex with the menthol2 analog ws-12 and pi(4,5)p2
92	<a href="#">c6nr2B_</a>	Alignment	not modelled	21.9	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily m <b>PDBTitle:</b> cryo-em structure of the trpm8 ion channel in complex with the menthol2 analog ws-12 and pi(4,5)p2
93	<a href="#">c6nr2C_</a>	Alignment	not modelled	21.9	17	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily m <b>PDBTitle:</b> cryo-em structure of the trpm8 ion channel in complex with the menthol2 analog ws-12 and pi(4,5)p2
94	<a href="#">c2kl4A_</a>	Alignment	not modelled	21.3	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bh2032 protein; <b>PDBTitle:</b> nmr structure of the protein nb7804a
95	<a href="#">c4euvA_</a>	Alignment	not modelled	21.1	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> peld; <b>PDBTitle:</b> crystal structure of peld 158-ct from pseudomonas aeruginosa pao1, in2 complex with c-di-gmp, form 1
96	<a href="#">c3o8oC_</a>	Alignment	not modelled	20.4	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 6-phosphofructokinase subunit alpha; <b>PDBTitle:</b> structure of phosphofructokinase from saccharomyces cerevisiae
97	<a href="#">c5ibzD_</a>	Alignment	not modelled	20.1	33	<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).
98	<a href="#">d1hyoa2</a>	Alignment	not modelled	19.6	34	<b>Fold:</b> FAH <b>Superfamily:</b> FAH <b>Family:</b> FAH
99	<a href="#">d2v94a1</a>	Alignment	not modelled	19.4	12	<b>Fold:</b> Ribosomal proteins S24e, L23 and L15e <b>Superfamily:</b> Ribosomal proteins S24e, L23 and L15e <b>Family:</b> Ribosomal protein S24e