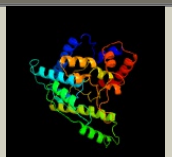
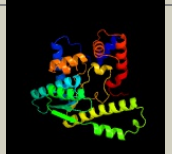
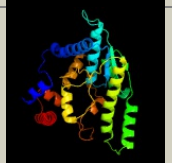
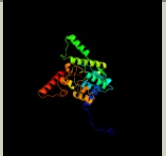
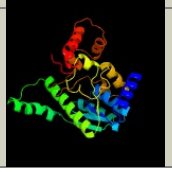
Phyre2

Email	arsen.orazbek@nu.edu.kz
Description	Student__
Date	Sat Oct 16 13:04:15 BST 2021
Unique Job ID	8d48c9655093e29c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1kqpa_	Alignment		100.0	46	**Fold:** Adenine nucleotide alpha hydrolase-like **Superfamily:** Adenine nucleotide alpha hydrolases-like **Family:** N-type ATP pyrophosphatases **PDB entry:** PDBe RCSB PDBj
2	c4xfdA_	Alignment		100.0	100	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of a nh(3)-dependent nad(+) synthetase from2 pseudomonas aeruginosa **PDB Entry:** PDBe RCSB PDBj
3	c3dpiA_	Alignment		100.0	54	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nad+ synthetase; **PDBTitle:** crystal structure of nad+ synthetase from burkholderia pseudomallei **PDB Entry:** PDBe RCSB PDBj
4	c4q16C_	Alignment		100.0	50	**PDB header:**ligase **Chain:** C: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nad+ synthetase from deinococcus radiodurans **PDB Entry:** PDBe RCSB PDBj
5	d1wxia1	Alignment		100.0	48	**Fold:** Adenine nucleotide alpha hydrolase-like **Superfamily:** Adenine nucleotide alpha hydrolases-like **Family:** N-type ATP pyrophosphatases **PDB entry:** PDBe RCSB PDBj
6	c5hujB_	Alignment		100.0	53	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of nade from streptococcus pyogenes **PDB Entry:** PDBe RCSB PDBj
7	c3q4gA_	Alignment		100.0	55	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nad synthetase from vibrio cholerae **PDB Entry:** PDBe RCSB PDBj
8	c6ofbA_	Alignment		100.0	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** crystal structure of human glutamine-dependent nad+ synthetase2 complexed with naad+, amp, pyrophosphate, and mg2+ **PDB Entry:** PDBe RCSB PDBj
9	c5khaA_	Alignment		100.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine-dependent nad+ synthetase; **PDBTitle:** structure of glutamine-dependent nad+ synthetase from acinetobacter2 baumannii in complex with adenosine diphosphate (adp) **PDB Entry:** PDBe RCSB PDBj
10	c4f4hA_	Alignment		100.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine dependent nad+ synthetase; **PDBTitle:** crystal structure of a glutamine dependent nad+ synthetase from2 burkholderia thailandensis **PDB Entry:** PDBe RCSB PDBj
11	c2e18B_	Alignment		100.0	35	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of project ph0182 from pyrococcus horikoshii ot3 **PDB Entry:** PDBe RCSB PDBj

12	c3fiuD_	Alignment		100.0	35	**PDB header:**ligase **Chain:** D: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nmn synthetase from francisella tularensis **PDB Entry:** PDBe RCSB PDBj
13	c3dlaD_	Alignment		100.0	26	**PDB header:**ligase **Chain:** D: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don **PDB Entry:** PDBe RCSB PDBj
14	c3n05B_	Alignment		100.0	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis **PDB Entry:** PDBe RCSB PDBj
15	c6kv3A_	Alignment		100.0	46	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of nad+ synthetase from staphylococcus aureus **PDB Entry:** PDBe RCSB PDBj
16	c3ilvA_	Alignment		100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** crystal structure of a glutamine-dependent nad(+) synthetase from2 cytophaga hutchinsonii **PDB Entry:** PDBe RCSB PDBj
17	d1xnga1	Alignment		100.0	31	**Fold:** Adenine nucleotide alpha hydrolase-like **Superfamily:** Adenine nucleotide alpha hydrolases-like **Family:** N-type ATP pyrophosphatases **PDB entry:** PDBe RCSB PDBj
18	c3p52B_	Alignment		100.0	28	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** nh3-dependent nad synthetase from campylobacter jejuni subsp. jejuni2 nctc 11168 in complex with the nitrate ion **PDB Entry:** PDBe RCSB PDBj
19	c2vxoB_	Alignment		100.0	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** human gmp synthetase in complex with xmp **PDB Entry:** PDBe RCSB PDBj
20	c1gpmD_	Alignment		100.0	20	**PDB header:**transferase (glutamine amidotransferase) **Chain:** D: **PDB Molecule:**gmp synthetase; **PDBTitle:** escherichia coli gmp synthetase complexed with amp and pyrophosphate **PDB Entry:** PDBe RCSB PDBj
21	c5tw7E_	Alignment	not modelled	100.0	23	**PDB header:**ligase **Chain:** E: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** crystal structure of a gmp synthase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae **PDB Entry:** PDBe RCSB PDBj
22	c3uowB_	Alignment	not modelled	100.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthetase; **PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum **PDB Entry:** PDBe RCSB PDBj
23	c3tqiB_	Alignment	not modelled	100.0	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** structure of the gmp synthase (guaa) from coxiella burnetii **PDB Entry:** PDBe RCSB PDBj
24	c7sbcA_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** crystal structure of a gmp synthase from acinetobacter baumannii2 ab5075-uw **PDB Entry:** PDBe RCSB PDBj
25	c2hmaA_	Alignment	not modelled	100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable trna (5-methylaminomethyl-2-thiouridylate)- **PDBTitle:** the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trmu from streptococcus pneumoniae **PDB Entry:** PDBe RCSB PDBj
26	c2ywcC_	Alignment	not modelled	100.0	21	**PDB header:**ligase **Chain:** C: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp **PDB Entry:** PDBe RCSB PDBj

27	c2dplA_	Alignment	not modelled	100.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing] subunit b; **PDBTitle:** crystal structure of the gmp synthase from pyrococcus horikoshii ot3 **PDB Entry:** PDBe RCSB PDBj
28	c2derA_	Alignment	not modelled	99.9	25	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna-specific 2-thiouridylase mnma; **PDBTitle:** cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state **PDB Entry:** PDBe RCSB PDBj
29	d1gpma1	Alignment	not modelled	99.9	18	**Fold:** Adenine nucleotide alpha hydrolase-like **Superfamily:** Adenine nucleotide alpha hydrolases-like **Family:** N-type ATP pyrophosphatases **PDB entry:** PDBe RCSB PDBj
30	c6jp9C_	Alignment	not modelled	99.9	22	**PDB header:**ligase **Chain:** C: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing] subunit b; **PDBTitle:** crsytal structure of a xmp complexed atppase subunit of m. jannaschii2 gmp synthetase **PDB Entry:** PDBe RCSB PDBj
31	c5udwB_	Alignment	not modelled	99.9	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lactate racemization operon protein lare; **PDBTitle:** lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with nickel **PDB Entry:** PDBe RCSB PDBj
32	c4kr7A_	Alignment	not modelled	99.8	19	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**probable trna sulfurtransferase; **PDBTitle:** crystal structure of a 4-thiouridine synthetase - rna complex with2 bound atp **PDB Entry:** PDBe RCSB PDBj
33	c2c5sA_	Alignment	not modelled	99.8	19	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**probable thiamine biosynthesis protein thii; **PDBTitle:** crystal structure of bacillus anthracis thii, a trna-modifying enzyme2 containing the predicted rna-binding thump domain **PDB Entry:** PDBe RCSB PDBj
34	c5udtD_	Alignment	not modelled	99.8	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**lactate racemization operon protein lare; **PDBTitle:** lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with amp **PDB Entry:** PDBe RCSB PDBj
35	d2c5sa1	Alignment	not modelled	99.8	19	**Fold:** Adenine nucleotide alpha hydrolase-like **Superfamily:** Adenine nucleotide alpha hydrolases-like **Family:** Thil-like **PDB entry:** PDBe RCSB PDBj
36	d1j20a1	Alignment	not modelled	99.7	16	**Fold:** Adenine nucleotide alpha hydrolase-like **Superfamily:** Adenine nucleotide alpha hydrolases-like **Family:** N-type ATP pyrophosphatases **PDB entry:** PDBe RCSB PDBj
37	d1wy5a1	Alignment	not modelled	99.7	15	**Fold:** Adenine nucleotide alpha hydrolase-like **Superfamily:** Adenine nucleotide alpha hydrolases-like **Family:** PP-loop ATPase **PDB entry:** PDBe RCSB PDBj
38	c3k32D_	Alignment	not modelled	99.7	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uncharacterized protein mj0690; **PDBTitle:** the crystal structure of predicted subunit of trna methyltransferase2 from methanocaldococcus jannaschii dsm **PDB Entry:** PDBe RCSB PDBj
39	d1vl2a1	Alignment	not modelled	99.6	16	**Fold:** Adenine nucleotide alpha hydrolase-like **Superfamily:** Adenine nucleotide alpha hydrolases-like **Family:** N-type ATP pyrophosphatases **PDB entry:** PDBe RCSB PDBj
40	c3bl5E_	Alignment	not modelled	99.6	20	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**queuosine biosynthesis protein quec; **PDBTitle:** crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis **PDB Entry:** PDBe RCSB PDBj
41	d1ni5a1	Alignment	not modelled	99.6	13	**Fold:** Adenine nucleotide alpha hydrolase-like **Superfamily:** Adenine nucleotide alpha hydrolases-like **Family:** PP-loop ATPase **PDB entry:** PDBe RCSB PDBj
42	c2e21A_	Alignment	not modelled	99.6	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils in a complex with ampppnp from aquifex2 aeolicus. **PDB Entry:** PDBe RCSB PDBj
43	d1k92a1	Alignment	not modelled	99.5	18	**Fold:** Adenine nucleotide alpha hydrolase-like **Superfamily:** Adenine nucleotide alpha hydrolases-like **Family:** N-type ATP pyrophosphatases **PDB entry:** PDBe RCSB PDBj
44	c6xnqA_	Alignment	not modelled	99.5	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of argininosuccinate synthase from legionella2 pneumophila philadelphia 1 **PDB Entry:** PDBe RCSB PDBj
45	c5ghaC_	Alignment	not modelled	99.5	17	**PDB header:**transferase/transport protein **Chain:** C: **PDB Molecule:**sulfur transferase ttua; **PDBTitle:** sulfur transferase ttua in complex with sulfur carrier ttub **PDB Entry:** PDBe RCSB PDBj
46	c3vrhA_	Alignment	not modelled	99.5	15	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph0300; **PDBTitle:** crystal structure of ph0300 **PDB Entry:** PDBe RCSB PDBj
47	d2pg3a1	Alignment	not modelled	99.5	19	**Fold:** Adenine nucleotide alpha hydrolase-like **Superfamily:** Adenine nucleotide alpha hydrolases-like **Family:** N-type ATP pyrophosphatases **PDB entry:** PDBe RCSB PDBj
48	c6scyA_	Alignment	not modelled	99.5	18	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**[4fe-4s]-dependent u34-arnt thiolase; **PDBTitle:** u34-trna thiolase ncsa from methanococcus maripaludis with its [4fe-2 4s] cluster

						PDB Entry: PDBe RCSB PDBj
49	c2nz2A_	Alignment	not modelled	99.5	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline **PDB Entry:** PDBe RCSB PDBj
50	c1kh2D_	Alignment	not modelled	99.5	16	**PDB header:**ligase **Chain:** D: **PDB Molecule:**argininosuccinate synthetase; **PDBTitle:** crystal structure of thermus thermophilus hb8 argininosuccinate2 synthetase in complex with atp **PDB Entry:** PDBe RCSB PDBj
51	c1k97A_	Alignment	not modelled	99.5	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline **PDB Entry:** PDBe RCSB PDBj
52	c4u7jB_	Alignment	not modelled	99.4	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of argininosuccinate synthase from mycobacterium2 thermoresistibile **PDB Entry:** PDBe RCSB PDBj
53	c3a2kB_	Alignment	not modelled	99.4	17	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils complexed with trna **PDB Entry:** PDBe RCSB PDBj
54	c1vl2C_	Alignment	not modelled	99.4	15	**PDB header:**ligase **Chain:** C: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution **PDB Entry:** PDBe RCSB PDBj
55	c1ni5A_	Alignment	not modelled	99.3	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative cell cycle protein mesj; **PDBTitle:** structure of the mesj pp-atpase from escherichia coli **PDB Entry:** PDBe RCSB PDBj
56	c4nzpA_	Alignment	not modelled	99.2	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** the crystal structure of argininosuccinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168 **PDB Entry:** PDBe RCSB PDBj
57	d1q15a1	Alignment	not modelled	99.2	14	**Fold:** Adenine nucleotide alpha hydrolase-like **Superfamily:** Adenine nucleotide alpha hydrolases-like **Family:** N-type ATP pyrophosphatases **PDB entry:** PDBe RCSB PDBj
58	d1sura_	Alignment	not modelled	99.2	8	**Fold:** Adenine nucleotide alpha hydrolase-like **Superfamily:** Adenine nucleotide alpha hydrolases-like **Family:** PAPS reductase-like **PDB entry:** PDBe RCSB PDBj
59	d1vbka1	Alignment	not modelled	99.1	13	**Fold:** Adenine nucleotide alpha hydrolase-like **Superfamily:** Adenine nucleotide alpha hydrolases-like **Family:** Thil-like **PDB entry:** PDBe RCSB PDBj
60	c7rgeA_	Alignment	not modelled	99.1	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3'-phosphoadenylylsulfate reductase; **PDBTitle:** crystal structure of phosphoadenylyl-sulfate (paps) reductase from2 candida auris, phosphate complex **PDB Entry:** PDBe RCSB PDBj
61	d1jgta1	Alignment	not modelled	99.1	17	**Fold:** Adenine nucleotide alpha hydrolase-like **Superfamily:** Adenine nucleotide alpha hydrolases-like **Family:** N-type ATP pyrophosphatases **PDB entry:** PDBe RCSB PDBj
62	d1zuna1	Alignment	not modelled	99.0	15	**Fold:** Adenine nucleotide alpha hydrolase-like **Superfamily:** Adenine nucleotide alpha hydrolases-like **Family:** PAPS reductase-like **PDB entry:** PDBe RCSB PDBj
63	c6vpuB_	Alignment	not modelled	99.0	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** 1.90 angstrom resolution crystal structure phosphoadenosine2 phosphosulfate reductase (cysh) from vibrio vulnificus **PDB Entry:** PDBe RCSB PDBj
64	c1zunA_	Alignment	not modelled	99.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfate adenylyltransferase subunit 2; **PDBTitle:** crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae **PDB Entry:** PDBe RCSB PDBj
65	d1ct9a1	Alignment	not modelled	98.9	14	**Fold:** Adenine nucleotide alpha hydrolase-like **Superfamily:** Adenine nucleotide alpha hydrolases-like **Family:** N-type ATP pyrophosphatases **PDB entry:** PDBe RCSB PDBj
66	c1q15A_	Alignment	not modelled	98.9	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cara; **PDBTitle:** carbapenam synthetase **PDB Entry:** PDBe RCSB PDBj
67	c2goyC_	Alignment	not modelled	98.9	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**adenosine phosphosulfate reductase; **PDBTitle:** crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps **PDB Entry:** PDBe RCSB PDBj
68	c1m1zB_	Alignment	not modelled	98.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactam synthetase; **PDBTitle:** beta-lactam synthetase apo enzyme **PDB Entry:** PDBe RCSB PDBj
69	c6gq3A_	Alignment	not modelled	98.9	17	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**asparagine synthetase [glutamine-hydrolyzing]; **PDBTitle:** human asparagine synthetase (asns) in complex with 6-diazo-5-oxo-l-2 norleucine (don) at 1.85 a resolution **PDB Entry:** PDBe RCSB PDBj
70	c2o8vA_	Alignment	not modelled	98.8	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** paps reductase in a covalent complex with thioredoxin

						c35a **PDB Entry:** PDBe RCSB PDBj
71	c1ct9D_	Alignment	not modelled	98.8	13	**PDB header:**ligase **Chain:** D: **PDB Molecule:**asparagine synthetase b; **PDBTitle:** crystal structure of asparagine synthetase b from2 escherichia coli **PDB Entry:** PDBe RCSB PDBj
72	c7lhrA_	Alignment	not modelled	98.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** crystal structure of adenosine-5'-phosphosulfate reductase from2 mycobacterium tuberculosis **PDB Entry:** PDBe RCSB PDBj
73	c4bwvB_	Alignment	not modelled	98.5	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**phosphoadenosine-phosphosulphate reductase; **PDBTitle:** structure of adenosine 5-prime-phosphosulfate reductase apr-b from2 physcomitrella patens **PDB Entry:** PDBe RCSB PDBj
74	d1ru8a_	Alignment	not modelled	98.5	17	**Fold:** Adenine nucleotide alpha hydrolase-like **Superfamily:** Adenine nucleotide alpha hydrolases-like **Family:** N-type ATP pyrophosphatases **PDB entry:** PDBe RCSB PDBj
75	c3g59A_	Alignment	not modelled	98.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fmn adenylyltransferase; **PDBTitle:** crystal structure of candida glabrata fmn adenylyltransferase in2 complex with atp **PDB Entry:** PDBe RCSB PDBj
76	c2wsiA_	Alignment	not modelled	98.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fad synthetase; **PDBTitle:** crystal structure of yeast fad synthetase (fad1) in complex2 with fad **PDB Entry:** PDBe RCSB PDBj
77	c2oq2B_	Alignment	not modelled	98.3	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** crystal structure of yeast paps reductase with pap, a product complex **PDB Entry:** PDBe RCSB PDBj
78	c1vbkA_	Alignment	not modelled	98.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1313; **PDBTitle:** crystal structure of ph1313 from pyrococcus horikoshii ot3 **PDB Entry:** PDBe RCSB PDBj
79	c5hyyA_	Alignment	not modelled	97.9	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nta1p; **PDBTitle:** crystal structure of n-terminal amidase **PDB Entry:** PDBe RCSB PDBj
80	d2d13a1	Alignment	not modelled	97.6	22	**Fold:** Adenine nucleotide alpha hydrolase-like **Superfamily:** Adenine nucleotide alpha hydrolases-like **Family:** N-type ATP pyrophosphatases **PDB entry:** PDBe RCSB PDBj
81	c3c8uA_	Alignment	not modelled	83.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructokinase; **PDBTitle:** crystal structure of putative fructose transport system kinase2 (yp_612366.1) from silicibacter sp. tm1040 at 1.95 a resolution **PDB Entry:** PDBe RCSB PDBj
82	d1rz3a_	Alignment	not modelled	77.1	21	**Fold:** P-loop containing nucleoside triphosphate hydrolases **Superfamily:** P-loop containing nucleoside triphosphate hydrolases **Family:** Phosphoribulokinase/pantothenate kinase **PDB entry:** PDBe RCSB PDBj
83	d1sq5a_	Alignment	not modelled	76.3	14	**Fold:** P-loop containing nucleoside triphosphate hydrolases **Superfamily:** P-loop containing nucleoside triphosphate hydrolases **Family:** Phosphoribulokinase/pantothenate kinase **PDB entry:** PDBe RCSB PDBj
84	c2gesA_	Alignment	not modelled	71.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase; **PDBTitle:** pantothenate kinase from mycobacterium tuberculosis (mtpank) in2 complex with a coenzyme a derivative, form-i (rt) **PDB Entry:** PDBe RCSB PDBj
85	d1t5la1	Alignment	not modelled	70.8	16	**Fold:** P-loop containing nucleoside triphosphate hydrolases **Superfamily:** P-loop containing nucleoside triphosphate hydrolases **Family:** Tandem AAA-ATPase domain **PDB entry:** PDBe RCSB PDBj
86	c4oqqA_	Alignment	not modelled	67.6	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**deoxyribonucleoside regulator; **PDBTitle:** structure of the effector-binding domain of deoxyribonucleoside2 regulator deor from bacillus subtilis **PDB Entry:** PDBe RCSB PDBj
87	c5b3fB_	Alignment	not modelled	64.6	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribulokinase/uridine kinase; **PDBTitle:** crystal structure of phosphoribulokinase from methanospirillum2 hungatei **PDB Entry:** PDBe RCSB PDBj
88	c2j0eA_	Alignment	not modelled	62.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** three dimensional structure and catalytic mechanism of 6-2 phosphogluconolactonase from trypanosoma brucei **PDB Entry:** PDBe RCSB PDBj
89	d1npya1	Alignment	not modelled	55.6	18	**Fold:** NAD(P)-binding Rossmann-fold domains **Superfamily:** NAD(P)-binding Rossmann-fold domains **Family:** Aminoacid dehydrogenase-like, C-terminal domain **PDB entry:** PDBe RCSB PDBj
90	c6nbgD_	Alignment	not modelled	49.0	10	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** 2.05 angstrom resolution crystal structure of hypothetical protein2 kp1_5497 from klebsiella pneumoniae. **PDB Entry:** PDBe RCSB PDBj
91	c6vyeB_	Alignment	not modelled	43.6	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** 6-phosphogluconolactonase from trypanosoma cruzi **PDB Entry:** PDBe RCSB PDBj

92	c6gveG_	Alignment	not modelled	41.5	11	**PDB header:**photosynthesis **Chain:** G: **PDB Molecule:**phosphoribulokinase; **PDBTitle:** gapdh-cp12-prk complex **PDB Entry:** PDBe RCSB PDBj
93	c3vewA_	Alignment	not modelled	41.2	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**o-carbamoyltransferase tobz; **PDBTitle:** crystal structure of the o-carbamoyltransferase tobz in complex with2 adp **PDB Entry:** PDBe RCSB PDBj
94	c2bkxB_	Alignment	not modelled	40.5	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** structure and kinetics of a monomeric glucosamine-6-2 phosphate deaminase: missing link of the nagb superfamily **PDB Entry:** PDBe RCSB PDBj
95	d2nx2a1	Alignment	not modelled	40.3	16	**Fold:** MCP/YpsA-like **Superfamily:** MCP/YpsA-like **Family:** YpsA-like **PDB entry:** PDBe RCSB PDBj
96	c3lwdA_	Alignment	not modelled	40.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of putative 6-phosphogluconolactonase (yp_574786.1)2 from chromohalobacter salexigens dsm 3043 at 1.88 a resolution **PDB Entry:** PDBe RCSB PDBj
97	d2eyqa4	Alignment	not modelled	38.8	18	**Fold:** P-loop containing nucleoside triphosphate hydrolases **Superfamily:** P-loop containing nucleoside triphosphate hydrolases **Family:** Tandem AAA-ATPase domain **PDB entry:** PDBe RCSB PDBj
98	d2aa4a1	Alignment	not modelled	38.8	11	**Fold:** Ribonuclease H-like motif **Superfamily:** Actin-like ATPase domain **Family:** ROK **PDB entry:** PDBe RCSB PDBj
99	d1vl1a_	Alignment	not modelled	38.7	14	**Fold:** NagB/RpiA/CoA transferase-like **Superfamily:** NagB/RpiA/CoA transferase-like **Family:** NagB-like **PDB entry:** PDBe RCSB PDBj
100	c3ch4B_	Alignment	not modelled	38.2	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphomevalonate kinase; **PDBTitle:** the crystal structure of human phosphomavelonate kinase at2 1.8 a resolution **PDB Entry:** PDBe RCSB PDBj
101	c4r9nA_	Alignment	not modelled	37.8	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lmo0547 protein; **PDBTitle:** deor family transcriptional regulator from listeria monocytogenes. **PDB Entry:** PDBe RCSB PDBj
102	d1qgpa_	Alignment	not modelled	37.0	25	**Fold:** DNA/RNA-binding 3-helical bundle **Superfamily:** "Winged helix" DNA-binding domain **Family:** Z-DNA binding domain **PDB entry:** PDBe RCSB PDBj
103	c6h7gB_	Alignment	not modelled	36.9	21	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**phosphoribulokinase, chloroplastic; **PDBTitle:** crystal structure of redox-sensitive phosphoribulokinase (prk) from2 the green algae chlamydomonas reinhardtii **PDB Entry:** PDBe RCSB PDBj
104	d1qbjc_	Alignment	not modelled	36.7	25	**Fold:** DNA/RNA-binding 3-helical bundle **Superfamily:** "Winged helix" DNA-binding domain **Family:** Z-DNA binding domain **PDB entry:** PDBe RCSB PDBj
105	c3n0vD_	Alignment	not modelled	36.7	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution **PDB Entry:** PDBe RCSB PDBj
106	c3o1lB_	Alignment	not modelled	36.2	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution **PDB Entry:** PDBe RCSB PDBj
107	c2i14B_	Alignment	not modelled	35.7	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide2 pyrophosphorylase from pyrococcus furiosus **PDB Entry:** PDBe RCSB PDBj
108	c3zeuE_	Alignment	not modelled	35.4	31	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**probable trna threonylcarbamoyladenosine biosynthesis **PDBTitle:** structure of a salmonella typhimurium ygjd-yeaz heterodimer bound to2 atpgammas **PDB Entry:** PDBe RCSB PDBj
109	c3nwpA_	Alignment	not modelled	35.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of a 6-phosphogluconolactonase (sbal_2240) from2 shewanella baltica os155 at 1.40 a resolution **PDB Entry:** PDBe RCSB PDBj
110	c3tqcB_	Alignment	not modelled	35.0	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pantothenate kinase; **PDBTitle:** structure of the pantothenate kinase (coaa) from coxiella burnetii **PDB Entry:** PDBe RCSB PDBj
111	c3vthA_	Alignment	not modelled	34.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hydrogenase maturation factor; **PDBTitle:** crystal structure of full-length hypf in the phosphate- and2 nucleotide-bound form **PDB Entry:** PDBe RCSB PDBj
112	c1smkD_	Alignment	not modelled	34.6	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**malate dehydrogenase, glyoxysomal; **PDBTitle:** mature and translocatable forms of glyoxysomal malate2 dehydrogenase have different activities and stabilities3 but similar crystal structures **PDB Entry:** PDBe RCSB PDBj
						PDB header:transferase

113	c1ytkA_	Alignment	not modelled	34.5	23	**Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase from thermoplasma **PDBTitle:** crystal structure of a nicotinate phosphoribosyltransferase from2 thermoplasma acidophilum with nicotinate mononucleotide **PDB Entry:** PDBe RCSB PDBj
114	d2gxba1	Alignment	not modelled	34.0	25	**Fold:** DNA/RNA-binding 3-helical bundle **Superfamily:** "Winged helix" DNA-binding domain **Family:** Z-DNA binding domain **PDB entry:** PDBe RCSB PDBj
115	c7cokB_	Alignment	not modelled	33.9	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**5-ketofructose reductase; **PDBTitle:** crystal structure of ligand-free form of 5-ketofructose reductase of2 gluconobacter sp. strain chm43 **PDB Entry:** PDBe RCSB PDBj
116	c3louB_	Alignment	not modelled	33.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution **PDB Entry:** PDBe RCSB PDBj
117	c1pbtA_	Alignment	not modelled	33.4	11	**PDB header:**hydrolase, oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** the crystal structure of tm1154, oxidoreductase, sol/devb2 family from thermotoga maritima **PDB Entry:** PDBe RCSB PDBj
118	c4adsF_	Alignment	not modelled	32.8	30	**PDB header:**transferase/transferase **Chain:** F: **PDB Molecule:**pyridoxine biosynthetic enzyme pdx1 homologue, putative; **PDBTitle:** crystal structure of plasmodial plp synthase complex **PDB Entry:** PDBe RCSB PDBj
119	c2zbtB_	Alignment	not modelled	32.8	32	**PDB header:**lyase **Chain:** B: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8 **PDB Entry:** PDBe RCSB PDBj
120	c3lhiA_	Alignment	not modelled	32.7	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative 6-phosphogluconolactonase; **PDBTitle:** crystal structure of putative 6-phosphogluconolactonase(yp_207848.1)2 from neisseria gonorrhoeae fa 1090 at 1.33 a resolution **PDB Entry:** PDBe RCSB PDBj