



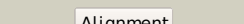

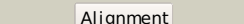
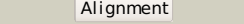


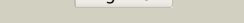












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2dlA_	 Alignment		100.0	100	PDB header: ligase(peptidoglycan synthesis) Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: vancomycin resistance: structure of d-alanine:d-alanine2 ligase at 2.3 angstroms resolution
2	c2i80B_	 Alignment		100.0	35	PDB header: ligase Chain: B: PDB Molecule: d-alanine-d-alanine ligase; PDBTitle: allosteric inhibition of staphylococcus aureus d-alanine:d-alanine2 ligase revealed by crystallographic studies
3	c1ehiB_	 Alignment		100.0	31	PDB header: ligase Chain: B: PDB Molecule: d-alanine:d-lactate ligase; PDBTitle: d-alanine:d-lactate ligase (lmdl2) of vancomycin-resistant2 leuconostoc mesenteroides
4	c3i12A_	 Alignment		100.0	35	PDB header: ligase Chain: A: PDB Molecule: d-alanine-d-alanine ligase a; PDBTitle: the crystal structure of the d-alanyl-alanine synthetase a from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
5	c1e4eB_	 Alignment		100.0	34	PDB header: ligase Chain: B: PDB Molecule: vancomycin/teicoplanin a-type resistance protein vana; PDBTitle: d-alanyl-d-lacate ligase
6	c3tgtB_	 Alignment		100.0	29	PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: structure of the d-alanine-d-alanine ligase from coxiella burnetii
7	c3e5nA_	 Alignment		100.0	38	PDB header: ligase Chain: A: PDB Molecule: d-alanine-d-alanine ligase a; PDBTitle: crystal strucutre of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331
8	c3se7A_	 Alignment		100.0	36	PDB header: ligase Chain: A: PDB Molecule: vana; PDBTitle: ancient vana
9	c3r23B_	 Alignment		100.0	34	PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis
10	c3lwbA_	 Alignment		100.0	34	PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of apo d-alanine:d-alanine ligase (ddl) from2 mycobacterium tuberculosis
11	c2zdgA_	 Alignment		100.0	41	PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine:d-alanine ligase with atp2 and d-alanine:d-alanine from thermus thermophilus hb8

12	c2pvpB_	Alignment		100.0	29	PDB header: ligase Chain: B: PDB Molecule: d-alanine-d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
13	c3k3pA_	Alignment		100.0	32	PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of the apo form of d-alanine:d-alanine ligase (ddl)2 from streptococcus mutans
14	c1m6vE_	Alignment		100.0	19	PDB header: ligase Chain: E: PDB Molecule: carbamoyl phosphate synthetase large chain; PDBTitle: crystal structure of the g359f (small subunit) point mutant of 2 carbamoyl phosphate synthetase
15	c1ulzA_	Alignment		100.0	21	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase n-terminal domain; PDBTitle: crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
16	c3g8cB_	Alignment		100.0	22	PDB header: ligase Chain: B: PDB Molecule: biotin carboxylase; PDBTitle: crystal stucture of biotin carboxylase in complex with2 biotin, bicarbonate, adp and mg ion
17	c2dzdB_	Alignment		100.0	21	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of the biotin carboxylase domain of 2 pyruvate carboxylase
18	c3ouzA_	Alignment		100.0	23	PDB header: ligase Chain: A: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
19	c3bg5C_	Alignment		100.0	18	PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate2 carboxylase
20	c1kjjA_	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase 2; PDBTitle: crystal structure of glyciniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
21	c2xd4A_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: nucleotide-bound structures of bacillus subtilis glyciniamide2 ribonucleotide synthetase
22	d1iowa2	Alignment	not modelled	100.0	100	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
23	c2hjwA_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: crystal structure of the bc domain of acc2
24	c2vpqA_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp
25	c2yyaB_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of gar synthetase from aquifex aeolicus
26	c1w96B_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: B: PDB Molecule: acetyl-coenzyme a carboxylase; PDBTitle: crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with soraphen a
27	c3lp8A_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
28	c3gidB_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: the biotin carboxylase (bc) domain of human acetyl-coa2 carboxylase 2 (acc2) in complex with soraphen a

51	d1w96a3	Alignment	not modelled	100.0	20	Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
52	c3ln6A_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae
53	d1a9xa5	Alignment	not modelled	100.0	16	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
54	cli7nA_	Alignment	not modelled	100.0	16	PDB header: neuropeptide Chain: A: PDB Molecule: synapsin ii; PDBTitle: crystal structure analysis of the c domain of synapsin ii2 from rat brain
55	d1vkza3	Alignment	not modelled	100.0	14	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
56	c1pk8D_	Alignment	not modelled	100.0	16	PDB header: membrane protein Chain: D: PDB Molecule: rat synapsin i; PDBTitle: crystal structure of rat synapsin i c domain complexed to2 ca.atp
57	d2r7ka2	Alignment	not modelled	100.0	17	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
58	c2qb5B_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: inositol-tetrakisphosphate 1-kinase; PDBTitle: crystal structure of human inositol 1,3,4-trisphosphate 5/6-kinase2 (itpk1) in complex with adp and mn2+
59	c2p0aA_	Alignment	not modelled	100.0	16	PDB header: neuropeptide Chain: A: PDB Molecule: synapsin-3; PDBTitle: the crystal structure of human synapsin iii (syn3) in complex with2 amppnp
60	d2r85a2	Alignment	not modelled	99.9	15	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
61	d2j9ga3	Alignment	not modelled	99.9	20	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
62	d1ulza3	Alignment	not modelled	99.9	20	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
63	d3etja3	Alignment	not modelled	99.9	21	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
64	d1a9xa6	Alignment	not modelled	99.9	18	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
65	c3ln7A_	Alignment	not modelled	99.9	23	PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 pasteurella multocida
66	d1kjqaz	Alignment	not modelled	99.9	15	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
67	d1gsoa3	Alignment	not modelled	99.9	15	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
68	d1pk8a2	Alignment	not modelled	99.9	17	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Synapsin C-terminal domain
69	d1uc8a2	Alignment	not modelled	99.9	18	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Lysine biosynthesis enzyme LysX ATP-binding domain
70	c3t9aA_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: inositol pyrophosphate kinase; PDBTitle: crystal structure of the catalytic domain of human diphosphoinositol2 pentakisphosphate kinase 2 (ppip5k2) in complex with amppnp at ph 7.0
71	c1gshA_	Alignment	not modelled	99.9	13	PDB header: glutathione biosynthesis ligase Chain: A: PDB Molecule: glutathione biosynthetic ligase; PDBTitle: structure of escherichia coli glutathione synthetase at ph 7.5
72	d1i7na2	Alignment	not modelled	99.9	17	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Synapsin C-terminal domain
73	c2qf7A_	Alignment	not modelled	99.9	25	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
74	d1iowa1	Alignment	not modelled	99.8	100	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain
75	d1gsaa2	Alignment	not modelled	99.6	11	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
76	d1ehia1	Alignment	not modelled	99.5	33	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain
77	d1e4ea1	Alignment	not modelled	99.5	35	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain

						Family: D-Alanine ligase N-terminal domain
78	c2r7mA	Alignment	not modelled	99.4	19	PDB header: ligase Chain: A: PDB Molecule: 5-formaminoimidazole-4-carboxamide-1-(beta)-d- PDBTitle: crystal structure of faicar synthetase (purp) from m.2 jannaschii complexed with amp
79	c2cqyA	Alignment	not modelled	99.3	30	PDB header: ligase Chain: A: PDB Molecule: propionyl-coa carboxylase alpha chain, PDBTitle: solution structure of b domain from human propionyl-coa2 carboxylase alpha subunit
80	c2pbzC	Alignment	not modelled	99.0	18	PDB header: ligase Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of an imp biosynthesis protein purp from2 thermococcus kodakaraensis
81	c2nu9E	Alignment	not modelled	98.9	18	PDB header: ligase Chain: E: PDB Molecule: succinyl-coa synthetase beta chain; PDBTitle: c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
82	c1wr2A	Alignment	not modelled	98.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1789; PDBTitle: crystal structure of ph1788 from pyrococcus horikoshii ot3
83	d1eucb2	Alignment	not modelled	98.9	17	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Succinyl-CoA synthetase, beta-chain, N-terminal domain
84	c1eucB	Alignment	not modelled	98.8	15	PDB header: ligase Chain: B: PDB Molecule: succinyl-coa synthetase, beta chain; PDBTitle: crystal structure of dephosphorylated pig heart, gtp-2 specific succinyl-coa synthetase
85	c3tinA	Alignment	not modelled	98.8	19	PDB header: ligase Chain: A: PDB Molecule: ttl protein; PDBTitle: tubulin tyrosine ligase
86	d1a9xa4	Alignment	not modelled	98.7	26	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
87	d2nu7b2	Alignment	not modelled	98.7	17	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Succinyl-CoA synthetase, beta-chain, N-terminal domain
88	d2pbza2	Alignment	not modelled	98.6	19	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
89	d1a9xa3	Alignment	not modelled	98.3	28	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
90	d1kjqaz	Alignment	not modelled	97.8	21	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
91	d1ulza2	Alignment	not modelled	97.8	20	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
92	c3mwdA	Alignment	not modelled	97.6	15	PDB header: transferase Chain: A: PDB Molecule: atp-citrate synthase; PDBTitle: truncated human atp-citrate lyase with citrate bound
93	d2j9ga2	Alignment	not modelled	97.6	26	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
94	d1gsoa2	Alignment	not modelled	97.2	14	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
95	c3ktdC	Alignment	not modelled	96.1	18	PDB header: oxidoreductase Chain: C: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
96	d1f0ya2	Alignment	not modelled	95.8	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
97	c3sc6F	Alignment	not modelled	95.6	17	PDB header: oxidoreductase Chain: F: PDB Molecule: ddtp-4-dehydrorhamnose reductase; PDBTitle: 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfd) from bacillus anthracis str. ames in complex with3 nadp
98	d1w96a2	Alignment	not modelled	95.6	20	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
99	d1e5qa1	Alignment	not modelled	95.4	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
100	d1uc8a1	Alignment	not modelled	95.4	13	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Lysine biosynthesis enzyme LysX, N-terminal domain
101	c3d8xB	Alignment	not modelled	95.3	11	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of saccharomyces cerevisiae nadph dependent2 thioredoxin reductase 1
102	d2jfga1	Alignment	not modelled	95.2	11	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
103	c2qx7A	Alignment	not modelled	95.0	21	PDB header: plant protein Chain: A: PDB Molecule: eugenol synthase 1; PDBTitle: structure of eugenol synthase from ocimum basilicum

104	c3k96B_	Alignment	not modelled	94.9	26	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p)+]; PDBTitle: 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii
105	c3l6dB_	Alignment	not modelled	94.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
106	d2hmva1	Alignment	not modelled	94.4	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
107	c3nhzA_	Alignment	not modelled	94.4	18	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
108	d1vkza2	Alignment	not modelled	94.2	15	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
109	d1lssa_	Alignment	not modelled	94.1	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
110	c1m75B_	Alignment	not modelled	94.1	23	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: crystal structure of the n208s mutant of l-3-hydroxyacyl-2 coa dehydrogenase in complex with nad and acetoacetyl-coa
111	c3eywA_	Alignment	not modelled	94.1	17	PDB header: transport protein Chain: A: PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
112	c3l4bG_	Alignment	not modelled	94.0	6	PDB header: transport protein Chain: G: PDB Molecule: trka k+ channel protien tm1088b; PDBTitle: crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
113	c2gr2A_	Alignment	not modelled	93.9	26	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin reductase; PDBTitle: crystal structure of ferredoxin reductase, bpha4 (oxidized form)
114	d1k0ia1	Alignment	not modelled	93.7	34	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
115	c3llvA_	Alignment	not modelled	93.6	22	PDB header: nad(p) binding protein Chain: A: PDB Molecule: exopolyphosphatase-related protein; PDBTitle: the crystal structure of the nad(p)-binding domain of an2 exopolyphosphatase-related protein from archaeoglobus fulgidus to3 1.7a
116	d1mvoa_	Alignment	not modelled	93.6	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
117	c3i3lA_	Alignment	not modelled	93.5	29	PDB header: hydrolase Chain: A: PDB Molecule: alkylhalidase cmls; PDBTitle: crystal structure of cmls, a flavin-dependent halogenase
118	c1phhA_	Alignment	not modelled	93.5	26	PDB header: oxidoreductase Chain: A: PDB Molecule: p-hydroxybenzoate hydroxylase; PDBTitle: crystal structure of p-hydroxybenzoate hydroxylase complexed with its2 reaction product 3,4-dihydroxybenzoate
119	d1pfka_	Alignment	not modelled	93.1	24	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
120	c2weuD_	Alignment	not modelled	92.9	27	PDB header: antifungal protein Chain: D: PDB Molecule: tryptophan 5-halogenase; PDBTitle: crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan