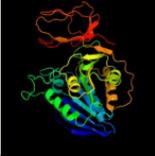
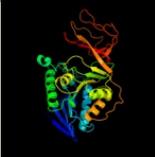
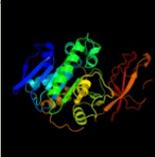
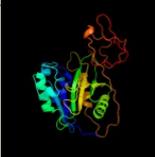


Phyre2

| | |
|---------------|-----------------------------|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P76215 |
| Date | Thu Jan 5 12:20:39 GMT 2012 |
| Unique Job ID | ff23e9677742543e |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | d2g9da1 |  Alignment |  | 100.0 | 34 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: AstE/AspA-like |
| 2 | d1yw6a1 |  Alignment |  | 100.0 | 97 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: AstE/AspA-like |
| 3 | d2bcoa1 |  Alignment |  | 100.0 | 32 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: AstE/AspA-like |
| 4 | d1yw4a1 |  Alignment |  | 100.0 | 38 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: AstE/AspA-like |
| 5 | d2gu2a1 |  Alignment |  | 100.0 | 17 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: AstE/AspA-like |
| 6 | c3nh8A |  Alignment |  | 100.0 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: aspartoacylase-2; PDBTitle: crystal structure of murine aminoacylase 3 in complex with n-acetyl-s-2 1,2-dichlorovinyl-l-cysteine |
| 7 | d2i3ca1 |  Alignment |  | 100.0 | 18 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: AstE/AspA-like |
| 8 | c3na6A |  Alignment |  | 100.0 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: succinylglutamate desuccinylase/aspartoacylase; PDBTitle: crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution |
| 9 | c3cdxB |  Alignment |  | 100.0 | 14 | PDB header: hydrolase Chain: B: PDB Molecule: succinylglutamatedesuccinylase/aspartoacylase; PDBTitle: crystal structure of 2 succinylglutamatedesuccinylase/aspartoacylase from 3 rhodobacter sphaeroides |
| 10 | c3fmcC |  Alignment |  | 100.0 | 21 | PDB header: hydrolase Chain: C: PDB Molecule: putative succinylglutamate desuccinylase / aspartoacylase; PDBTitle: crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution |
| 11 | c2qj8B |  Alignment |  | 100.0 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: mlr6093 protein; PDBTitle: crystal structure of an aspartoacylase family protein (mlr6093) from 2 mesorhizobium loti maff303099 at 2.00 a resolution |

| | | | | | | |
|----|-------------------------|-----------|---|-------|----|---|
| 12 | c2qvpC | Alignment |  | 100.0 | 19 | PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative metallopeptidase (sama_0725) from2 shewanella amazonensis sb2b at 2.00 a resolution |
| 13 | c3b2yB | Alignment |  | 99.9 | 21 | PDB header: hydrolase Chain: B: PDB Molecule: metallopeptidase containing co-catalytic metalloactive PDBTitle: crystal structure of a putative metallopeptidase (sden_2526) from2 shewanella denitrificans os217 at 1.74 a resolution |
| 14 | c3d4uA | Alignment |  | 99.5 | 17 | PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: carboxypeptidase b2; PDBTitle: bovine thrombin-activatable fibrinolysis inhibitor (tafia) in complex2 with tick-derived carboxypeptidase inhibitor. |
| 15 | dlz5ra1 | Alignment |  | 99.5 | 16 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Pancreatic carboxypeptidases |
| 16 | dlkwa1 | Alignment |  | 99.5 | 19 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Pancreatic carboxypeptidases |
| 17 | dlnsaa1 | Alignment |  | 99.5 | 20 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Pancreatic carboxypeptidases |
| 18 | dlobra | Alignment |  | 99.5 | 19 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Carboxypeptidase T |
| 19 | c3mn8A | Alignment |  | 99.4 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: lp15968p; PDBTitle: structure of drosophila melanogaster carboxypeptidase d isoform 1b2 short |
| 20 | dljqqa1 | Alignment |  | 99.4 | 21 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Pancreatic carboxypeptidases |
| 21 | dlh8la2 | Alignment | not modelled | 99.4 | 16 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Pancreatic carboxypeptidases |
| 22 | dlm4la | Alignment | not modelled | 99.4 | 21 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Pancreatic carboxypeptidases |
| 23 | d2bo9a1 | Alignment | not modelled | 99.4 | 26 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Pancreatic carboxypeptidases |
| 24 | c3l2nA | Alignment | not modelled | 99.4 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: peptidase m14, carboxypeptidase a; PDBTitle: crystal structure of putative carboxypeptidase a (yp_562911.1) from2 shewanella denitrificans os-217 at 2.39 a resolution |
| 25 | c1nsaA | Alignment | not modelled | 99.4 | 20 | PDB header: serine protease Chain: A: PDB Molecule: procarboxypeptidase b; PDBTitle: three-dimensional structure of porcine procarboxypeptidase2 b: a structural basis of its inactivity |
| 26 | dlayeal | Alignment | not modelled | 99.4 | 21 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Pancreatic carboxypeptidases |
| 27 | clh8lA | Alignment | not modelled | 99.4 | 18 | PDB header: carboxypeptidase Chain: A: PDB Molecule: carboxypeptidase gp180 residues 503-882; PDBTitle: duck carboxypeptidase d domain ii in complex with gemsa |
| 28 | d2c1ca1 | Alignment | not modelled | 99.4 | 20 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Pancreatic carboxypeptidases |
| | | | | | | PDB header: hydrolase |

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|----|-------------------------|-----------|--------------|------|----|---|
| 29 | c1uwvA | Alignment | not modelled | 99.3 | 22 | Chain: A: PDB Molecule: carboxypeptidase m; PDBTitle: crystal structure of human carboxypeptidase m |
| 30 | d1uwya2 | Alignment | not modelled | 99.3 | 20 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Pancreatic carboxypeptidases |
| 31 | c1jqgA | Alignment | not modelled | 99.3 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: carboxypeptidase a; PDBTitle: crystal structure of the carboxypeptidase a from2 helicoverpa armigera |
| 32 | c2boaB | Alignment | not modelled | 99.3 | 21 | PDB header: hydrolase Chain: B: PDB Molecule: carboxypeptidase a4; PDBTitle: human procarboxypeptidase a4. |
| 33 | c3k2kA | Alignment | not modelled | 99.3 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: putative carboxypeptidase; PDBTitle: crystal structure of putative carboxypeptidase (yp_103406.1) from2 burkholderia mallei atcc 23344 at 2.49 a resolution |
| 34 | c1ayeA | Alignment | not modelled | 99.3 | 21 | PDB header: serine protease Chain: A: PDB Molecule: procarboxypeptidase a2; PDBTitle: human procarboxypeptidase a2 |
| 35 | c3dgvB | Alignment | not modelled | 99.2 | 22 | PDB header: hydrolase Chain: B: PDB Molecule: carboxypeptidase b2; PDBTitle: crystal structure of thrombin activatable fibrinolysis inhibitor2 (tafi) |
| 36 | c2nsmA | Alignment | not modelled | 99.2 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: carboxypeptidase n catalytic chain; PDBTitle: crystal structure of the human carboxypeptidase n (kininase i)2 catalytic domain |
| 37 | d2q7sa1 | Alignment | not modelled | 96.3 | 15 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: FGase-like |
| 38 | c1cpbB | Alignment | not modelled | 96.0 | 21 | PDB header: hydrolase (c-terminal peptidase) Chain: B: PDB Molecule: carboxypeptidase b; PDBTitle: structure of carboxypeptidase b at 2.8 angstroms resolution |
| 39 | c1cpbA | Alignment | not modelled | 95.5 | 12 | PDB header: hydrolase (c-terminal peptidase) Chain: A: PDB Molecule: carboxypeptidase b; PDBTitle: structure of carboxypeptidase b at 2.8 angstroms resolution |
| 40 | d2odfa1 | Alignment | not modelled | 91.8 | 13 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: FGase-like |
| 41 | c1m6bA | Alignment | not modelled | 43.1 | 9 | PDB header: signaling protein, transferase Chain: A: PDB Molecule: receptor protein-tyrosine kinase erbb-3; PDBTitle: structure of the her3 (erbb3) extracellular domain |
| 42 | c1nqlA | Alignment | not modelled | 40.7 | 11 | PDB header: hormone/growth factor receptor Chain: A: PDB Molecule: epidermal growth factor receptor; PDBTitle: structure of the extracellular domain of human epidermal growth factor2 (egf) receptor in an inactive (low ph) complex with egf. |
| 43 | c3qayC | Alignment | not modelled | 38.3 | 11 | PDB header: lyase Chain: C: PDB Molecule: endolysin; PDBTitle: catalytic domain of cd271 endolysin targeting clostridia difficile |
| 44 | c3ltgA | Alignment | not modelled | 38.3 | 19 | PDB header: transferase/transferase regulator Chain: A: PDB Molecule: epidermal growth factor receptor; PDBTitle: crystal structure of the drosophila epidermal growth factor receptor2 ectodomain complexed with a low affinity spitz mutant |
| 45 | c3be1A | Alignment | not modelled | 31.6 | 8 | PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: dual specific bh1 fab in complex with the extracellular domain of2 her2/erbb-2 |
| 46 | c3i2tA | Alignment | not modelled | 30.0 | 19 | PDB header: transferase Chain: A: PDB Molecule: epidermal growth factor receptor, isoform a; PDBTitle: crystal structure of the unliganded drosophila epidermal growth factor2 receptor ectodomain |
| 47 | d1jwqa | Alignment | not modelled | 26.6 | 14 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: N-acetylmuramoyl-L-alanine amidase-like |
| 48 | c3p11A | Alignment | not modelled | 21.5 | 11 | PDB header: immune system Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-3; PDBTitle: anti-egfr/her3 fab dl11 in complex with domains i-iii of the her32 extracellular region |
| 49 | c2q5cA | Alignment | not modelled | 19.2 | 12 | PDB header: transcription Chain: A: PDB Molecule: ntrc family transcriptional regulator; PDBTitle: crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum |
| 50 | c1bdeA | Alignment | not modelled | 18.1 | 26 | PDB header: aids Chain: A: PDB Molecule: vpr protein; PDBTitle: helical structure of polypeptides from the c-terminal half2 of hiv-1 vpr, nmr, 20 structures |
| 51 | c1xovA | Alignment | not modelled | 18.0 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: ply protein; PDBTitle: the crystal structure of the listeria monocytogenes bacteriophage psa2 endolysin plympsa |
| 52 | d1xova2 | Alignment | not modelled | 17.7 | 15 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: N-acetylmuramoyl-L-alanine amidase-like |
| 53 | c2ahxB | Alignment | not modelled | 17.2 | 8 | PDB header: cell cycle,signaling protein Chain: B: PDB Molecule: receptor tyrosine-protein kinase erbb-4; PDBTitle: crystal structure of erbb4/her4 extracellular domain |
| 54 | c2hklB | Alignment | not modelled | 15.9 | 16 | PDB header: transferase Chain: B: PDB Molecule: l,d-transpeptidase; PDBTitle: crystal structure of enterococcus faecium l,d-2 |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | transpeptidase c442s mutant |
| 55 | c3czxA_ | Alignment | not modelled | 14.6 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: putative n-acetylmuramoyl-l-alanine amidase; PDBTitle: the crystal structure of the putative n-acetylmuramoyl-l-2 alanine amidase from neisseria meningitidis |
| 56 | c3lkxB_ | Alignment | not modelled | 13.3 | 13 | PDB header: chaperone Chain: B: PDB Molecule: nascent polypeptide-associated complex subunit alpha; PDBTitle: human nac dimerization domain |
| 57 | d1no7a_ | Alignment | not modelled | 10.9 | 23 | Fold: Major capsid protein VP5 Superfamily: Major capsid protein VP5 Family: Major capsid protein VP5 |
| 58 | c1no7A_ | Alignment | not modelled | 10.9 | 23 | PDB header: viral protein Chain: A: PDB Molecule: major capsid protein; PDBTitle: structure of the large protease resistant upper domain of 2 vp5, the major capsid protein of herpes simplex virus-1 |
| 59 | c1dsjA_ | Alignment | not modelled | 10.4 | 28 | PDB header: viral peptide Chain: A: PDB Molecule: vpr protein; PDBTitle: nmr solution structure of vpr50_75, 20 structures |
| 60 | d2ix0a3 | Alignment | not modelled | 8.0 | 26 | Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like |
| 61 | d2ihoA2 | Alignment | not modelled | 7.6 | 42 | Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: MOA C-terminal domain-like |
| 62 | c1moxB_ | Alignment | not modelled | 7.2 | 11 | PDB header: transferase/growth factor Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: crystal structure of human epidermal growth factor receptor (residues 2 1-501) in complex with tgf-alpha |
| 63 | d1g5ba_ | Alignment | not modelled | 6.5 | 22 | Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase |
| 64 | c1igrA_ | Alignment | not modelled | 6.5 | 28 | PDB header: hormone receptor Chain: A: PDB Molecule: insulin-like growth factor receptor 1; PDBTitle: type 1 insulin-like growth factor receptor (domains 1-3) |
| 65 | d2grea2 | Alignment | not modelled | 6.1 | 11 | Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases |
| 66 | c3pctA_ | Alignment | not modelled | 5.9 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: class c acid phosphatase; PDBTitle: structure of the class c acid phosphatase from pasteurilla multocida |
| 67 | c3et4A_ | Alignment | not modelled | 5.7 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: outer membrane protein p4, nadp phosphatase; PDBTitle: structure of recombinant haemophilus influenzae e(p4) acid phosphatase |