BIOZENTRUM Universität Basel The Center for Molecular Life Sciences

SWISS-MODEL Homology Modelling Report

Model Building Report

This document lists the results for the homology modelling project "TPH2_GG" submitted to SWISS-MODEL workspace on Oct. 20, 2017, 10:14 p.m..The submitted primary amino acid sequence is given in Table T1.

If you use any results in your research, please cite the relevant publications:

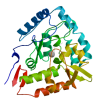
Marco Biasini; Stefan Bienert; Andrew Waterhouse; Konstantin Arnold; Gabriel Studer; Tobias Schmidt; Florian Kiefer; Tiziano Gallo Cassarino; Martino Bertoni; Lorenza Bordoli; Torsten Schwede. (2014). SWISS-MODEL: modelling protein tertiary and quaternary structure using evolutionary information. Nucleic Acids Research (1 July 2014) 42 (W1): W252-W258; doi: 10.1093/nar/gku340.
Arnold, K., Bordoli, L., Kopp, J. and Schwede, T. (2006) The SWISS-MODEL workspace: a web-based environment for protein structure homology modelling. Bioinformatics, 22, 195-201.
Benkert, P., Biasini, M. and Schwede, T. (2011) Toward the estimation of the absolute quality of individual protein structure models. Bioinformatics, 27, 343-350

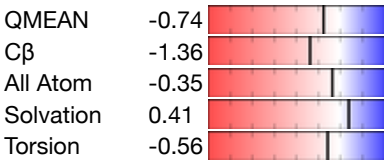
Results

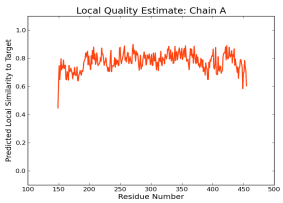
The SWISS-MODEL template library (SMTL version 2017-10-11, PDB release 2017-10-06) was searched with Blast (Altschul et al., 1997) and HHBlits (Remmert, et al., 2011) for evolutionary related structures matching the target sequence in Table T1. For details on the template search, see Materials and Methods. Overall 277 templates were found (Table T2).

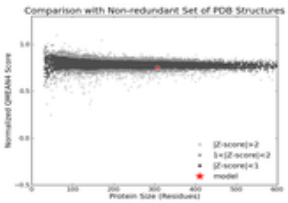
Models

The following models were built (see Materials and Methods "Model Building"):

Model #02	File	Built with	Oligo-State	Ligands	GMQE	QMEAN
	PDB	ProMod3 Version 1.1.0.	MONOMER	1 x FE: FE (III) ION; 1 x IMD: IMIDAZOLE; 1 x TRP: TRYPTOPHAN;	0.64	-0.74







Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
3e2t.1.A	83.71	monomer	BLAST	X-ray	1.90Å	0.57	149 - 455	0.64	Tryptophan 5-hydroxylase 1

Ligand	Added to Model	Description
FE	✓	FE (III) ION
IMD	✓	IMIDAZOLE
TRP	✓	TRYPTOPHAN
PGE	✕ - Not biologically relevant.	TRIETHYLENE GLYCOL
PGE	✕ - Not biologically relevant.	TRIETHYLENE GLYCOL
SO4	✕ - Not biologically relevant.	SULFATE ION

```
Target    MQPAMMMFSSKYWARRGFSLDSALPEERPGGLTINRSSSGKNEDKKGNKGNGKGESVSEGGKTAVVFSLKNEVGGLVKAL
3e2t.1.A  ------------------------------------------------------------------------------

Target    RLFQEKHVSMVHIESRKSKRRNSEVEIFVDCDCSKKEFNELIQLLKFQTNIVSLNPPENIWTDEEDLDCVPWFPRKISEL
3e2t.1.A  ------------------------------------------------------------DMENIPWYPKKISDL

Target    DKCSQRVLMYGSELDADHPGFKDNVYRQRRKYFVDVAMSYKYGQPIPRVEYTAEEIKTWGVVFRELSKLYPTHACREYLK
3e2t.1.A  DKCANRVLMYGSDLDADHPGFKDNVYRKRRKYFADLAMNYKHGDPIPEIEFTEEEIKTWGTVYRELNKLYPTHACREYLK

Target    NFPLLTKYCGYREDNVPQLEDVSIFLKERSGFTVRPVAGYLSPRDFLAGLAYRVFHCTQYVRHGSDPLYTPEPDTCHELL
3e2t.1.A  NLPLLTKYCGYREDNIPQLEDVSRFLKERTGFTIRPVAGYLSPRDFLAGLAFRVFHCTQYVRHSSDPLYTPEPDTCHELL

Target    GHVPLLADPKFAQFSQEIGLASLGASDEDVQKLATCYFFTIEFGLCKQEGQLRAYGAGLLSSIGELKHALSDKAKVKTFD
3e2t.1.A  GHVPLLAEPSFAQFSQEIGLASLGASDEAVQKLATCYFFTVEFGLCKQEGQLRVYGAGLLSSISELKHSLSGSAKVKPFD

Target    PKTTCLQECLITTFQEAYFVSESFEEAKEKMRDFAKSINRPFSVYFNPYTQSIEILKDTRSIENVVQDLRSDLNTVCDAL
```

```
3e2t.1.A  PKVTCKQECLITTFQEVYFVSESFEEAKEKMREFAKTIKRPFGVKYNPYTQSVQILKD----------------------

Target    SKMNRYLGI
3e2t.1.A  ---------
```

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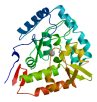
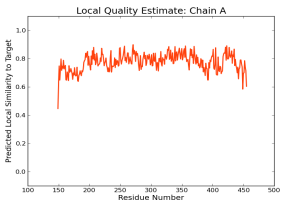
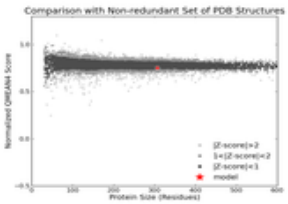
	PDB	ProMod3 Version 1.1.0.	MONOMER	1 x FE: FE (III) ION; 1 x IMD: IMIDAZOLE; 1 x TRP: TRYPTOPHAN;	0.64	-0.74

QMEAN	-0.74
Cβ	-1.36
All Atom	-0.35
Solvation	0.41
Torsion	-0.56





Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
3e2t.1.A	83.71	monomer	BLAST	X-ray	1.90Å	0.57	149 - 455	0.64	Tryptophan 5-hydroxylase 1

Ligand	Added to Model	Description
FE	✓	FE (III) ION
IMD	✓	IMIDAZOLE
TRP	✓	TRYPTOPHAN
PGE	✕ - Not biologically relevant.	TRIETHYLENE GLYCOL
PGE	✕ - Not biologically relevant.	TRIETHYLENE GLYCOL
SO4	✕ - Not biologically relevant.	SULFATE ION

```
Target    MQPAMMMFSSKYWARRGFSLDSALPEERPGGLTINRSSSGKNEDKKGNKGNGKGESVSEGGKTAVVFSLKNEVGGLVKAL
3e2t.1.A  --------------------------------------------------------------------------------

Target    RLFQEKHVSMVHIESRKSKRRNSEVEIFVDCDCSKKEFNELIQLLKFQTNIVSLNPPENIWTDEEDLDCVPWFPRKISEL
3e2t.1.A  ------------------------------------------------------------DMENIPWYPKKISDL

Target    DKCSQRVLMYGSELDADHPGFKDNVYRQRRKYFVDVAMSYKYGQPIPRVEYTAEEIKTWGVVFRELSKLYPTHACREYLK
3e2t.1.A  DKCANRVLMYGSDLDADHPGFKDNVYRKRRKYFADLAMNYKHGDPIPEIEFTEEEIKTWGTVYRELNKLYPTHACREYLK

Target    NFPLLTKYCGYREDNVPQLEDVSIFLKERSGFTVRPVAGYLSPRDFLAGLAYRVFHCTQYVRHGSDPLYTPEPDTCHELL
3e2t.1.A  NLPLLTKYCGYREDNIPQLEDVSRFLKERTGFTIRPVAGYLSPRDFLAGLAFRVFHCTQYVRHSSDPLYTPEPDTCHELL

Target    GHVPLLADPKFAQFSQEIGLASLGASDEDVQKLATCYFFTIEFGLCKQEGQLRAYGAGLLSSIGELKHALSDKAKVKTFD
3e2t.1.A  GHVPLLAEPSFAQFSQEIGLASLGASDEAVQKLATCYFFTVEFGLCKQEGQLRVYGAGLLSSISELKHSLSGSAKVKPFD

Target    PKTTCLQECLITTFQEAYFVSESFEEAKEKMRDFAKSINRPFSVYFNPYTQSIEILKDTRSIENVVQDLRSDLNTVCDAL
3e2t.1.A  PKVTCKQECLITTFQEVYFVSESFEEAKEKMREFAKTIKRPFGVKYNPYTQSVQILKD----------------------

Target    SKMNRYLGI
3e2t.1.A  ---------
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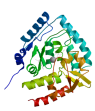
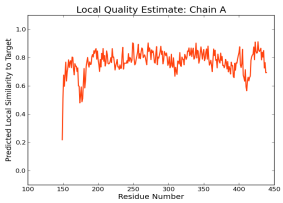
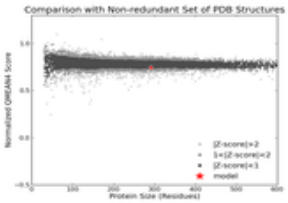
Model #03	File	Built with	Oligo-State	Ligands	GMQE	QMEAN
	PDB	ProMod3 Version 1.1.0.	MONOMER	1 x 6Z4: (3~{S})-8-[2-azanyl-6-[(1~{R})-1-(4-chloranyl-2-phenyl-phenyl)-2,2,2-tris(fluoranyl)ethoxy]pyrimidin-4-yl]-2,8-diazaspiro[4.5]decane-3-carboxylic acid; 1 x FE: FE (III) ION;	0.59	-0.82

QMEAN	-0.82
Cβ	-0.92
All Atom	-0.48

Solvation	0.57
Torsion	-0.76





Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
5l01.1.A	73.33	monomer	HHblits	X-ray	1.90Å	0.53	149 - 439	0.89	Tryptophan 5-hydroxylase 1

Ligand	Added to Model	Description
6Z4	✓	(3~{S})-8-[2-azanyl-6-[(1~{R})-1-(4-chloranyl-2-phenyl-phenyl)-2,2,2-tris(fluoranyl)ethoxy]pyrimidin-4-yl]-2,8-diazaspiro[4.5]decane-3-carboxylic acid
FE	✓	FE (III) ION

```
Target    MQPAMMMFSSKYWARRGFSLDSALPEERPGGLTINRSSSGKNEDKKGNKGNGKGESVSEGGKTAVVFSLKNEVGGLVKAL
5l01.1.A  ----------------------------------------------------KDHSLERGRASLIFSLKNEVGGLIKAL

Target    RLFQEKHVSMVHIESRKSKRRNSEVEIFVDCDCSKKEFNELIQLLKFQTNIVSLNPPENIWTDEEDLDCVPWFPRKISEL
5l01.1.A  KIFQEKHVNLLHIESRKSKRRNSEFEIFVDCDINREQLNDIFHLLKSHTNVLSVNLPDNFTLKEDGMETVPWFPKKISDL

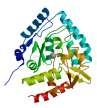
Target    DKCSQRVLMYGSELDADHPGFKDNVYRQRRKYFVDVAMSYKYGQPIPRVEYTAEEIKTWGVVFRELSKLYPTHACREYLK
5l01.1.A  DHCANRVLMYGSELDADHPGFKDNVYRKRRKYFADLAMNYKHGDPIPKVEFTEEEIKTWGTVFQELNKLYPTHACREYLK

Target    NFPLLTKYCGYREDNVPQLEDVSIFLKERSGFTVRPVAGYLSPRDFLAGLAYRVFHCTQYVRHGSDPLYTPEPDTCHELL
5l01.1.A  NLPLLSKYCGYREDNIPQLEDVSNFLKERTGFSIRPVAGYLSPRDFLSGLAFRVFHCTQYVRHSSDPFYTPEPDTCHELL

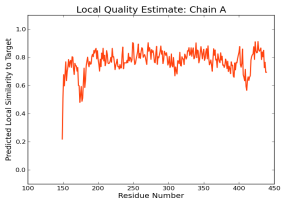
Target    GHVPLLADPKFAQFSQEIGLASLGASDEDVQKLATCYFFTIEFGLCKQEGQLRAYGAGLLSSIGELKHALSDKAKVKTFD
5l01.1.A  GHVPLLAEPSFAQFSQEIGLASLGASEEAVQKLATCYFFTVEFGLCKQDGQLRVFGAGLLSSISELKHALSGHAKVKPFD

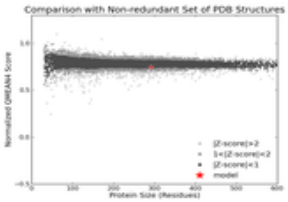
Target    PKTTCLQECLITTFQEAYFVSESFEEAKEKMRDFAKSINRPFSVYFNPYTQSIEILKDTRSIENVVQDLRSDLNTVCDAL
5l01.1.A  PKITCKQECLITTFQDVYFVSESFEDAKEKMREFTKTIKRPFGVKYNPYTRSIQILKDTKSITSAMNELQHDLDVVSDAL

Target    SKMNRYLGI
5l01.1.A  AKVSRKPS-
```

Model #01	File	Built with	Oligo-State	Ligands	GMQE	QMEAN
	PDB	ProMod3 Version 1.1.0.	MONOMER	1 x 6Z4: (3~{S})-8-[2-azanyl-6-[(1~{R})-1-(4-chloranyl-2-phenyl-phenyl)-2,2,2-tris(fluoranyl)ethoxy]pyrimidin-4-yl]-2,8-diazaspiro[4.5]decane-3-carboxylic acid; 1 x FE: FE (III) ION;	0.59	-0.82

QMEAN	-0.82
Cβ	-0.92
All Atom	-0.48
Solvation	0.57
Torsion	-0.76





Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
5l01.1.A	73.33	monomer	HHblits	X-ray	1.90Å	0.53	149 - 439	0.89	Tryptophan 5-hydroxylase 1

Ligand	Added to Model	Description
6Z4	✓	(3~{S})-8-[2-azanyl-6-[(1~{R})-1-(4-chloranyl-2-phenyl-phenyl)-2,2,2-tris(fluoranyl)ethoxy]pyrimidin-4-yl]-2,8-diazaspiro[4.5]decane-3-carboxylic acid
FE	✓	FE (III) ION

Ligand	Added to Model	Description

```
Target    MQPAMMMFSSKYWARRGFSLDSALPEERPGGLTINRSSSGKNEDKKGNKGNGKGESVSEGGKTAVVFSLKNEVGGLVKAL
5l01.1.A  ----------------------------------------------------KDHSLERGRASLIFSLKNEVGGLIKAL

Target    RLFQEKHVSMVHIESRKSKRRNSEVEIFVDCDCSKKEFNELIQLLKFQTNIVSLNPPENIWTDEEDLDCVPWFPRKISEL
5l01.1.A  KIFQEKHVNLLHIESRKSKRRNSEFEIFVDCDINREQLNDIFHLLKSHTNVLSVNLPDNFTLKEDGMETVPWFPKKISDL

Target    DKCSQRVLMYGSELDADHPGFKDNVYRQRRKYFVDVAMSYKYGQPIPRVEYTAEEIKTWGVVFRELSKLYPTHACREYLK
5l01.1.A  DHCANRVLMYGSELDADHPGFKDNVYRKRRKYFADLAMNYKHGDPIPKVEFTEEEIKTWGTVFQELNKLYPTHACREYLK

Target    NFPLLTKYCGYREDNVPQLEDVSIFLKERSGFTVRPVAGYLSPRDFLAGLAYRVFHCTQYVRHGSDPLYTPEPDTCHELL
5l01.1.A  NLPLLSKYCGYREDNIPQLEDVSNFLKERTGFSIRPVAGYLSPRDFLSGLAFRVFHCTQYVRHSSDPFYTPEPDTCHELL

Target    GHVPLLADPKFAQFSQEIGLASLGASDEDVQKLATCYFFTIEFGLCKQEGQLRAYGAGLLSSIGELKHALSDKAKVKTFD
5l01.1.A  GHVPLLAEPSFAQFSQEIGLASLGASEEAVQKLATCYFFTVEFGLCKQDGQLRVFGAGLLSSISELKHALSGHAKVKPFD

Target    PKTTCLQECLITTFQEAYFVSESFEEAKEKMRDFAKSINRPFSVYFNPYTQSIEILKDTRSIENVVQDLRSDLNTVCDAL
5l01.1.A  PKITCKQECLITTFQDVYFVSESFEDAKEKMREFTKTIKRPFGVKYNPYTRSIQILKDTKSITSAMNELQHDLDVVSDAL

Target    SKMNRYLGI
5l01.1.A  AKVSRKPS-
```

Materials and Methods

Template Search

Template search with Blast and HHBlits has been performed against the SWISS-MODEL template library (SMTL, last update: 2017-10-11, last included PDB release: 2017-10-06).

The target sequence was searched with BLAST (Altschul et al., 1997) against the primary amino acid sequence contained in the SMTL. A total of 49 templates were found.

An initial HHblits profile has been built using the procedure outlined in (Remmert, et al., 2011), followed by 1 iteration of HHblits against NR20. The obtained profile has then be searched against all profiles of the SMTL. A total of 232 templates were found.

Template Selection

For each identified template, the template's quality has been predicted from features of the target-template alignment. The templates with the highest quality have then been selected for model building.

Model Building

Models are built based on the target-template alignment using ProMod3. Coordinates which are conserved between the target and the template are copied from the template to the model. Insertions and deletions are remodelled using a fragment library. Side chains are then rebuilt. Finally, the geometry of the resulting model is regularized by using a force field. In case loop modelling with ProMod3 fails, an alternative model is built with PROMOD-II (Guex, et al., 1997).

Model Quality Estimation

The global and per-residue model quality has been assessed using the QMEAN scoring function (Benkert, et al., 2011) . For improved performance, weights of the individual QMEAN terms have been trained specifically for SWISS-MODEL.

Ligand Modelling

Ligands present in the template structure are transferred by homology to the model when the following criteria are met (Gallo - Casserino, to be published): (a) The ligands are annotated as biologically relevant in the template library, (b) the ligand is in contact with the model, (c) the ligand is not clashing with the protein, (d) the residues in contact with the ligand are conserved between the target and the template. If any of these four criteria is not satisfied, a certain ligand will not be included in the model. The model summary includes information on why and which ligand has not been included.

Oligomeric State Conservation

Homo-oligomeric structure of the target protein is predicted based on the analysis of pairwise interfaces of the identified template structures. For each relevant interface between polypeptide chains (interfaces with more than 10 residue-residue interactions), the QscoreOligomer (Mariani et al., 2011) is predicted from features such as similarity to target and frequency of observing this interface in the identified templates (Kiefer, Bertoni, Biasini, to be published). The prediction is performed with a random forest regressor using these features as input parameters to predict the probability of conservation for each interface. The QscoreOligomer of the whole complex is then calculated as the weight-averaged QscoreOligomer of the interfaces. The oligomeric state of the target is predicted to be the same as in the template when QscoreOligomer is predicted to be higher or equal to 0.5.

References

Altschul, S.F., Madden, T.L., Schaffer, A.A., Zhang, J., Zhang, Z., Miller, W. and Lipman, D.J. (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res, 25, 3389-3402.
Remmert, M., Biegert, A., Hauser, A. and Soding, J. (2012) HHblits: lightning-fast iterative protein sequence searching by HMM-HMM alignment. Nat Methods, 9, 173-175.
Guex, N. and Peitsch, M.C. (1997) SWISS-MODEL and the Swiss-PdbViewer: an environment for comparative protein modeling. Electrophoresis, 18, 2714-2723.
Sali, A. and Blundell, T.L. (1993) Comparative protein modelling by satisfaction of spatial restraints. J Mol Biol, 234, 779-815.
Benkert, P., Biasini, M. and Schwede, T. (2011) Toward the estimation of the absolute quality of individual protein structure models. Bioinformatics, 27, 343-350.
Mariani, V., Kiefer, F., Schmidt, T., Haas, J. and Schwede, T. (2011) Assessment of template based protein structure predictions in CASP9. Proteins, 79 Suppl 10, 37-58.

Table T1:

Primary amino acid sequence for which templates were searched and models were built.

```
MQPAMMMFSSKYWARRGFSLDSALPEERPGGLTINRSSSGKNEDKKGNKGNGKGESVSEGGKTAVVFSLKNEVGGLVKALRLFQEKHVSMVHIESRKSKR
RNSEVEIFVDCDCSKKEFNELIQLLKFQTNIVSLNPPENIWTDEEDLDCVPWFPRKISELDKCSQRVLMYGSELDADHPGFKDNVYRQRRKYFVDVAMSY
KYGQPIPRVEYTAEEIKTWGVVFRELSKLYPTHACREYLKNFPLLTKYCGYREDNVPQLEDVSIFLKERSGFTVRPVAGYLSPRDFLAGLAYRVFHCTQY
VRHGSDPLYTPEPDTCHELLGHVPLLADPKFAQFSQEIGLASLGASDEDVQKLATCYFFTIEFGLCKQEGQLRAYGAGLLSSIGELKHALSDKAKVKTFD
PKTTCLQECLITTFQEAYFVSESFEEAKEKMRDFAKSINRPFSVYFNPYTQSIEILKDTRSIENVVQDLRSDLNTVCDALSKMNRYLGI
```

Table T2:

Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
5l01.1.A	73.33	monomer	HHblits	X-ray	1.90Å	0.53	0.89	Tryptophan 5-hydroxylase 1
5l01.1.A	74.71	monomer	BLAST	X-ray	1.90Å	0.54	0.87	Tryptophan 5-hydroxylase 1
5den.1.B	53.79	homo-tetramer	HHblits	X-ray	2.90Å	0.45	0.92	Phenylalanine-4-hydroxylase
5den.1.A	53.79	homo-tetramer	HHblits	X-ray	2.90Å	0.45	0.92	Phenylalanine-4-hydroxylase
5fgj.1.A	53.79	homo-tetramer	HHblits	X-ray	3.60Å	0.45	0.92	Phenylalanine-4-hydroxylase
5fgj.1.B	53.79	homo-tetramer	HHblits	X-ray	3.60Å	0.45	0.92	Phenylalanine-4-hydroxylase
5egq.1.A	53.57	homo-tetramer	HHblits	X-ray	2.50Å	0.45	0.92	Phenylalanine-4-hydroxylase
5egq.1.B	53.57	homo-tetramer	HHblits	X-ray	2.50Å	0.45	0.92	Phenylalanine-4-hydroxylase
5egq.1.C	53.57	homo-tetramer	HHblits	X-ray	2.50Å	0.45	0.92	Phenylalanine-4-hydroxylase
5egq.1.D	53.57	homo-tetramer	HHblits	X-ray	2.50Å	0.45	0.92	Phenylalanine-4-hydroxylase
5den.1.B	57.01	homo-tetramer	BLAST	X-ray	2.90Å	0.47	0.86	Phenylalanine-4-hydroxylase
5den.1.A	57.01	homo-tetramer	BLAST	X-ray	2.90Å	0.47	0.86	Phenylalanine-4-hydroxylase
5fgj.1.A	57.01	homo-tetramer	BLAST	X-ray	3.60Å	0.47	0.86	Phenylalanine-4-hydroxylase
5fgj.1.B	57.01	homo-tetramer	BLAST	X-ray	3.60Å	0.47	0.86	Phenylalanine-4-hydroxylase
5egq.1.A	56.77	homo-tetramer	BLAST	X-ray	2.50Å	0.47	0.86	Phenylalanine-4-hydroxylase
5egq.1.B	56.77	homo-tetramer	BLAST	X-ray	2.50Å	0.47	0.86	Phenylalanine-4-hydroxylase
5egq.1.C	56.77	homo-tetramer	BLAST	X-ray	2.50Å	0.47	0.86	Phenylalanine-4-hydroxylase
5egq.1.D	56.77	homo-tetramer	BLAST	X-ray	2.50Å	0.47	0.86	Phenylalanine-4-hydroxylase
2phm.1.A	55.53	homo-dimer	HHblits	X-ray	2.60Å	0.46	0.87	PROTEIN (PHENYLALANINE-4-HYDROXYLASE)
4v06.1.A	96.21	monomer	BLAST	X-ray	2.63Å	0.60	0.70	TRYPTOPHAN 5-HYDROXYLASE 2
4v06.1.A	96.19	monomer	HHblits	X-ray	2.63Å	0.60	0.70	TRYPTOPHAN 5-HYDROXYLASE 2
2phm.1.A	59.05	homo-dimer	BLAST	X-ray	2.60Å	0.47	0.81	PROTEIN (PHENYLALANINE-4-HYDROXYLASE)
5jk5.1.B	53.67	homo-dimer	HHblits	X-ray	2.07Å	0.46	0.81	Phenylalanine-4-hydroxylase

Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
5jk5.1.A	53.67	homo-dimer	HHblits	X-ray	2.07Å	0.46	0.81	Phenylalanine-4-hydroxylase
5jk8.1.A	53.67	homo-dimer	HHblits	X-ray	2.39Å	0.46	0.81	Phenylalanine-4-hydroxylase
5jk5.1.B	53.44	homo-dimer	BLAST	X-ray	2.07Å	0.46	0.80	Phenylalanine-4-hydroxylase
5jk5.1.A	53.44	homo-dimer	BLAST	X-ray	2.07Å	0.46	0.80	Phenylalanine-4-hydroxylase
5jk8.1.A	53.44	homo-dimer	BLAST	X-ray	2.39Å	0.46	0.80	Phenylalanine-4-hydroxylase
3e2t.1.A	83.71	monomer	BLAST	X-ray	1.90Å	0.57	0.64	Tryptophan 5-hydroxylase 1
3e2t.1.A	83.65	monomer	HHblits	X-ray	1.90Å	0.57	0.64	Tryptophan 5-hydroxylase 1
1toh.1.A	61.72	homo-tetramer	HHblits	X-ray	2.30Å	0.49	0.69	TYROSINE HYDROXYLASE
2toh.1.A	61.42	homo-tetramer	HHblits	X-ray	2.30Å	0.49	0.69	TYROSINE 3-MONOOXYGENASE
2pah.1.A	62.39	homo-tetramer	HHblits	X-ray	3.10Å	0.49	0.69	PROTEIN (PHENYLALANINE HYDROXYLASE)
2pah.1.B	62.39	homo-tetramer	HHblits	X-ray	3.10Å	0.49	0.69	PROTEIN (PHENYLALANINE HYDROXYLASE)
2pah.1.A	62.57	homo-tetramer	BLAST	X-ray	3.10Å	0.49	0.68	PROTEIN (PHENYLALANINE HYDROXYLASE)
2pah.1.B	62.57	homo-tetramer	BLAST	X-ray	3.10Å	0.49	0.68	PROTEIN (PHENYLALANINE HYDROXYLASE)
2xsn.1.A	60.00	homo-tetramer	HHblits	X-ray	2.68Å	0.48	0.69	TYROSINE 3-MONOOXYGENASE
1mlw.1.A	82.06	monomer	BLAST	X-ray	1.71Å	0.57	0.62	Tryptophan 5-monooxygenase
5j6d.1.A	81.73	monomer	BLAST	X-ray	1.90Å	0.57	0.62	Tryptophan 5-hydroxylase 1
1mlw.1.A	82.33	monomer	HHblits	X-ray	1.71Å	0.57	0.61	Tryptophan 5-monooxygenase
5j6d.1.A	82.00	monomer	HHblits	X-ray	1.90Å	0.57	0.61	Tryptophan 5-hydroxylase 1
5tpg.1.A	82.27	monomer	HHblits	X-ray	1.50Å	0.57	0.61	Tryptophan 5-hydroxylase 1
5tpg.1.A	82.55	monomer	BLAST	X-ray	1.50Å	0.57	0.61	Tryptophan 5-hydroxylase 1
1mmk.1.A	63.58	homo-dimer	HHblits	X-ray	2.00Å	0.49	0.66	Phenylalanine-4-hydroxylase
1lrm.1.A	63.58	homo-dimer	HHblits	X-ray	2.10Å	0.49	0.66	Phenylalanine-4-hydroxylase
4anp.1.A	63.78	monomer	HHblits	X-ray	2.11Å	0.49	0.66	PHENYLALANINE-4-HYDROXYLASE
3hfb.1.A	83.45	monomer	HHblits	X-ray	1.92Å	0.57	0.59	Tryptophan 5-hydroxylase 1
3hfb.1.A	83.74	monomer	BLAST	X-ray	1.92Å	0.57	0.59	Tryptophan 5-hydroxylase 1
1mmk.1.A	65.71	homo-dimer	BLAST	X-ray	2.00Å	0.50	0.64	Phenylalanine-4-hydroxylase
1lrm.1.A	65.71	homo-dimer	BLAST	X-ray	2.10Å	0.50	0.64	Phenylalanine-4-hydroxylase
4anp.1.A	65.71	monomer	BLAST	X-ray	2.11Å	0.50	0.64	PHENYLALANINE-4-HYDROXYLASE
1pah.1.A	65.91	monomer	HHblits	X-ray	2.00Å	0.50	0.63	PHENYLALANINE HYDROXYLASE
1tdw.1.A	65.58	monomer	HHblits	X-ray	2.10Å	0.50	0.63	Phenylalanine-4-hydroxylase
1dmw.1.A	66.12	monomer	HHblits	X-ray	2.00Å	0.50	0.63	PHENYLALANINE HYDROXYLASE
1pah.1.A	66.12	monomer	BLAST	X-ray	2.00Å	0.50	0.63	PHENYLALANINE HYDROXYLASE
1tdw.1.A	65.80	monomer	BLAST	X-ray	2.10Å	0.50	0.63	Phenylalanine-4-hydroxylase
4q3w.1.A	30.83	monomer	HHblits	X-ray	1.40Å	0.34	0.52	Phenylalanine-4-hydroxylase
4etl.1.A	30.43	monomer	HHblits	X-ray	1.49Å	0.34	0.52	Phenylalanine-4-hydroxylase
3tcy.1.A	30.43	monomer	HHblits	X-ray	1.55Å	0.34	0.52	Phenylalanine-4-hydroxylase
3tk2.1.A	30.04	monomer	HHblits	X-ray	1.35Å	0.34	0.52	Phenylalanine-4-hydroxylase
1ltu.1.A	30.43	monomer	HHblits	X-ray	1.74Å	0.34	0.52	PHENYLALANINE-4-HYDROXYLASE
4jpy.1.A	30.43	monomer	HHblits	X-ray	2.13Å	0.34	0.52	Phenylalanine-4-hydroxylase
4q3z.1.A	30.43	monomer	HHblits	X-ray	1.35Å	0.34	0.52	Phenylalanine-4-hydroxylase
4q3x.1.A	30.43	monomer	HHblits	X-ray	1.35Å	0.34	0.52	Phenylalanine-4-hydroxylase
4q3y.1.A	30.43	monomer	HHblits	X-ray	1.40Å	0.34	0.52	Phenylalanine-4-hydroxylase

Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
4jpx.1.A	30.04	monomer	HHblits	X-ray	1.55Å	0.34	0.52	Phenylalanine-4-hydroxylase
4esm.1.A	30.43	monomer	HHblits	X-ray	1.35Å	0.34	0.52	Phenylalanine-4-hydroxylase
4bpt.1.A	35.15	monomer	HHblits	X-ray	2.50Å	0.37	0.49	PHENYLALANINE-4-HYDROXYLASE (PAH) (PHE-4-MONOOXYGENASE)
4bpt.1.A	35.96	monomer	BLAST	X-ray	2.50Å	0.38	0.47	PHENYLALANINE-4-HYDROXYLASE (PAH) (PHE-4-MONOOXYGENASE)
2v28.1.A	31.03	homo-dimer	HHblits	X-ray	1.95Å	0.35	0.47	PHENYLALANINE-4-HYDROXYLASE
2v28.1.B	31.03	homo-dimer	HHblits	X-ray	1.95Å	0.35	0.47	PHENYLALANINE-4-HYDROXYLASE
2v27.1.A	31.03	homo-dimer	HHblits	X-ray	1.50Å	0.35	0.47	PHENYLALANINE HYDROXYLASE
2v27.1.B	31.03	homo-dimer	HHblits	X-ray	1.50Å	0.35	0.47	PHENYLALANINE HYDROXYLASE
4q3w.1.A	36.36	monomer	BLAST	X-ray	1.40Å	0.37	0.45	Phenylalanine-4-hydroxylase
1ltu.1.A	35.91	monomer	BLAST	X-ray	1.74Å	0.37	0.45	PHENYLALANINE-4-HYDROXYLASE
4jpy.1.A	35.91	monomer	BLAST	X-ray	2.13Å	0.37	0.45	Phenylalanine-4-hydroxylase
3tcy.1.A	35.91	monomer	BLAST	X-ray	1.55Å	0.37	0.45	Phenylalanine-4-hydroxylase
4etl.1.A	35.91	monomer	BLAST	X-ray	1.49Å	0.37	0.45	Phenylalanine-4-hydroxylase
3tk2.1.A	35.45	monomer	BLAST	X-ray	1.35Å	0.37	0.45	Phenylalanine-4-hydroxylase
4q3z.1.A	35.91	monomer	BLAST	X-ray	1.35Å	0.37	0.45	Phenylalanine-4-hydroxylase
4q3x.1.A	35.91	monomer	BLAST	X-ray	1.35Å	0.37	0.45	Phenylalanine-4-hydroxylase
4q3y.1.A	35.91	monomer	BLAST	X-ray	1.40Å	0.37	0.45	Phenylalanine-4-hydroxylase
4jpx.1.A	35.45	monomer	BLAST	X-ray	1.55Å	0.37	0.45	Phenylalanine-4-hydroxylase
4esm.1.A	35.91	monomer	BLAST	X-ray	1.35Å	0.37	0.45	Phenylalanine-4-hydroxylase
2v28.1.A	34.72	homo-dimer	BLAST	X-ray	1.95Å	0.37	0.39	PHENYLALANINE-4-HYDROXYLASE
2v28.1.B	34.72	homo-dimer	BLAST	X-ray	1.95Å	0.37	0.39	PHENYLALANINE-4-HYDROXYLASE
2v27.1.A	34.72	homo-dimer	BLAST	X-ray	1.50Å	0.37	0.39	PHENYLALANINE HYDROXYLASE
2v27.1.B	34.72	homo-dimer	BLAST	X-ray	1.50Å	0.37	0.39	PHENYLALANINE HYDROXYLASE
3tvi.1.A	21.62	homo-dimer	HHblits	X-ray	3.00Å	0.30	0.23	Aspartokinase
3tvi.1.B	21.62	homo-dimer	HHblits	X-ray	3.00Å	0.30	0.23	Aspartokinase
3tvi.2.A	21.62	homo-dimer	HHblits	X-ray	3.00Å	0.30	0.23	Aspartokinase
3tvi.2.B	21.62	homo-dimer	HHblits	X-ray	3.00Å	0.30	0.23	Aspartokinase
3tvi.3.A	21.62	homo-dimer	HHblits	X-ray	3.00Å	0.30	0.23	Aspartokinase
3tvi.3.B	21.62	homo-dimer	HHblits	X-ray	3.00Å	0.30	0.23	Aspartokinase
3tvi.4.B	21.62	homo-dimer	HHblits	X-ray	3.00Å	0.30	0.23	Aspartokinase
3tvi.5.A	21.62	homo-dimer	HHblits	X-ray	3.00Å	0.30	0.23	Aspartokinase
3tvi.5.B	21.62	homo-dimer	HHblits	X-ray	3.00Å	0.30	0.23	Aspartokinase
3tvi.6.A	21.62	homo-dimer	HHblits	X-ray	3.00Å	0.30	0.23	Aspartokinase
3tvi.6.B	21.62	homo-dimer	HHblits	X-ray	3.00Å	0.30	0.23	Aspartokinase
3mwb.1.A	17.86	homo-tetramer	HHblits	X-ray	2.00Å	0.28	0.23	Prephenate dehydratase
3mwb.1.B	17.86	homo-tetramer	HHblits	X-ray	2.00Å	0.28	0.23	Prephenate dehydratase

Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
3luy.1.A	15.96	homo-dimer	HHblits	X-ray	2.00Å	0.28	0.19	Probable chorismate mutase
5fii.1.B	37.33	homo-dimer	HHblits	X-ray	1.80Å	0.39	0.15	PHENYLALANINE-4-HYDROXYLASE
5fii.1.A	37.33	homo-dimer	HHblits	X-ray	1.80Å	0.39	0.15	PHENYLALANINE-4-HYDROXYLASE
5fii.2.B	37.33	homo-dimer	HHblits	X-ray	1.80Å	0.39	0.15	PHENYLALANINE-4-HYDROXYLASE
2qmx.1.A	26.92	homo-dimer	HHblits	X-ray	2.30Å	0.33	0.16	Prephenate dehydratase
2qmx.1.B	26.92	homo-dimer	HHblits	X-ray	2.30Å	0.33	0.16	Prephenate dehydratase
2mda.1.A	19.23	homo-dimer	HHblits	NMR	NA	0.31	0.16	Tyrosine 3-monooxygenase
5fii.1.B	43.28	homo-dimer	BLAST	X-ray	1.80Å	0.41	0.14	PHENYLALANINE-4-HYDROXYLASE
5fii.1.A	43.28	homo-dimer	BLAST	X-ray	1.80Å	0.41	0.14	PHENYLALANINE-4-HYDROXYLASE
5fii.2.B	43.28	homo-dimer	BLAST	X-ray	1.80Å	0.41	0.14	PHENYLALANINE-4-HYDROXYLASE
4lub.1.A	23.68	homo-dimer	HHblits	X-ray	2.10Å	0.30	0.16	Putative prephenate dehydratase
4lub.1.B	23.68	homo-dimer	HHblits	X-ray	2.10Å	0.30	0.16	Putative prephenate dehydratase
2qmw.1.A	20.00	homo-tetramer	HHblits	X-ray	2.30Å	0.30	0.15	Prephenate dehydratase
2qmw.1.B	20.00	homo-tetramer	HHblits	X-ray	2.30Å	0.30	0.15	Prephenate dehydratase
1tdj.1.A	20.55	homo-dimer	HHblits	X-ray	2.80Å	0.29	0.15	BIOSYNTHETIC THREONINE DEAMINASE
2fgc.1.A	13.70	homo-dimer	HHblits	X-ray	2.30Å	0.28	0.15	acetolactate synthase, small subunit
2lvw.1.A	9.59	homo-dimer	HHblits	NMR	NA	0.27	0.15	Acetolactate synthase isozyme 1 small subunit
5kps.1.A	11.11	hetero-oligomer	HHblits	EM	NA	0.28	0.15	GTP pyrophosphokinase
5kpv.1.w	11.11	hetero-oligomer	HHblits	EM	NA	0.28	0.15	GTP pyrophosphokinase
5kpw.1.w	11.11	hetero-oligomer	HHblits	EM	NA	0.28	0.15	GTP pyrophosphokinase
5kpx.1.w	11.11	hetero-oligomer	HHblits	EM	NA	0.28	0.15	GTP pyrophosphokinase
5iqr.1.w	9.72	hetero-oligomer	HHblits	EM	3.00Å	0.28	0.15	GTP pyrophosphokinase
2pc6.1.A	12.50	homo-dimer	HHblits	X-ray	2.50Å	0.28	0.15	Probable acetolactate synthase isozyme III (Small subunit)
2pc6.1.B	12.50	homo-dimer	HHblits	X-ray	2.50Å	0.28	0.15	Probable acetolactate synthase isozyme III (Small subunit)
2pc6.2.B	12.50	homo-dimer	HHblits	X-ray	2.50Å	0.28	0.15	Probable acetolactate synthase isozyme III (Small subunit)
5l3p.1.t	11.27	hetero-oligomer	HHblits	EM	NA	0.28	0.15	GTP pyrophosphokinase,GTP pyrophosphokinase,GTP pyrophosphokinase
2f1f.1.A	12.86	homo-dimer	HHblits	X-ray	1.75Å	0.28	0.14	Acetolactate synthase isozyme III small subunit
2f1f.1.B	12.86	homo-dimer	HHblits	X-ray	1.75Å	0.28	0.14	Acetolactate synthase isozyme III small subunit
1y7p.2.A	13.24	homo-dimer	HHblits	X-ray	1.90Å	0.29	0.14	Hypothetical protein AF1403
1y7p.1.B	13.24	homo-dimer	HHblits	X-ray	1.90Å	0.29	0.14	Hypothetical protein AF1403
1y7p.1.A	13.24	homo-dimer	HHblits	X-ray	1.90Å	0.29	0.14	Hypothetical protein AF1403

Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
5it4.1.A	8.45	homo-dimer	HHblits	X-ray	2.10Å	0.24	0.15	Phosphoserine phosphatase
5t41.1.A	8.57	monomer	HHblits	X-ray	3.15Å	0.24	0.14	Phosphoserine phosphatase
5uyy.1.B	7.35	homo-dimer	HHblits	X-ray	2.60Å	0.26	0.14	Prephenate dehydrogenase
5uyy.1.A	7.35	homo-dimer	HHblits	X-ray	2.60Å	0.26	0.14	Prephenate dehydrogenase
5uyy.2.A	7.35	homo-dimer	HHblits	X-ray	2.60Å	0.26	0.14	Prephenate dehydrogenase
1sc6.1.A	13.85	homo-tetramer	HHblits	X-ray	2.09Å	0.28	0.13	D-3-phosphoglycerate dehydrogenase
1sc6.1.B	13.85	homo-tetramer	HHblits	X-ray	2.09Å	0.28	0.13	D-3-phosphoglycerate dehydrogenase
1sc6.1.C	13.85	homo-tetramer	HHblits	X-ray	2.09Å	0.28	0.13	D-3-phosphoglycerate dehydrogenase
1sc6.1.D	13.85	homo-tetramer	HHblits	X-ray	2.09Å	0.28	0.13	D-3-phosphoglycerate dehydrogenase
2p9g.1.A	14.06	homo-tetramer	HHblits	X-ray	2.80Å	0.29	0.13	D-3-phosphoglycerate dehydrogenase
2p9g.1.B	14.06	homo-tetramer	HHblits	X-ray	2.80Å	0.29	0.13	D-3-phosphoglycerate dehydrogenase
1psd.1.A	14.06	homo-tetramer	HHblits	X-ray	2.75Å	0.28	0.13	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (PHOSPHOGLYCERATE DEHYDROGENASE)
1psd.1.B	14.06	homo-tetramer	HHblits	X-ray	2.75Å	0.28	0.13	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (PHOSPHOGLYCERATE DEHYDROGENASE)
2f06.1.A	22.58	homo-tetramer	HHblits	X-ray	2.10Å	0.31	0.13	conserved hypothetical protein
2f06.1.B	22.58	homo-tetramer	HHblits	X-ray	2.10Å	0.31	0.13	conserved hypothetical protein
3nrb.1.A	15.63	homo-tetramer	HHblits	X-ray	2.05Å	0.28	0.13	Formyltetrahydrofolate deformylase
3p96.1.A	10.94	homo-dimer	HHblits	X-ray	2.05Å	0.28	0.13	Phosphoserine phosphatase SerB
1zpv.1.A	10.61	homo-trimer	HHblits	X-ray	1.90Å	0.25	0.13	ACT domain protein
1zpv.1.B	10.61	homo-trimer	HHblits	X-ray	1.90Å	0.25	0.13	ACT domain protein
5jjb.1.A	10.94	homo-dimer	HHblits	X-ray	2.31Å	0.28	0.13	Phosphoserine phosphatase
1yba.1.A	14.29	homo-tetramer	HHblits	X-ray	2.24Å	0.29	0.13	D-3-phosphoglycerate dehydrogenase
1yba.1.C	14.29	homo-tetramer	HHblits	X-ray	2.24Å	0.29	0.13	D-3-phosphoglycerate dehydrogenase
1yba.1.D	14.29	homo-tetramer	HHblits	X-ray	2.24Å	0.29	0.13	D-3-phosphoglycerate dehydrogenase
2p9c.1.A	14.29	homo-tetramer	HHblits	X-ray	2.46Å	0.28	0.13	D-3-phosphoglycerate dehydrogenase
2p9e.1.B	14.29	homo-tetramer	HHblits	X-ray	2.60Å	0.28	0.13	D-3-phosphoglycerate dehydrogenase
2p9e.1.C	14.29	homo-tetramer	HHblits	X-ray	2.60Å	0.28	0.13	D-3-phosphoglycerate dehydrogenase
2p9e.1.D	14.29	homo-tetramer	HHblits	X-ray	2.60Å	0.28	0.13	D-3-phosphoglycerate dehydrogenase
2p9e.1.A	14.29	homo-tetramer	HHblits	X-ray	2.60Å	0.28	0.13	D-3-phosphoglycerate dehydrogenase
2p9c.1.B	14.29	homo-tetramer	HHblits	X-ray	2.46Å	0.28	0.13	D-3-phosphoglycerate dehydrogenase
5it0.1.A	9.09	homo-dimer	HHblits	X-ray	1.97Å	0.24	0.13	Phosphoserine phosphatase

Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
3n0v.1.A	10.77	homo-tetramer	HHblits	X-ray	2.25Å	0.25	0.13	Formyltetrahydrofolate deformylase
5it4.1.A	9.52	homo-dimer	HHblits	X-ray	2.10Å	0.27	0.13	Phosphoserine phosphatase
3mtj.1.A	11.11	homo-tetramer	HHblits	X-ray	2.15Å	0.27	0.13	Homoserine dehydrogenase
3p96.1.A	9.23	homo-dimer	HHblits	X-ray	2.05Å	0.24	0.13	Phosphoserine phosphatase SerB
3k5p.1.A	12.90	homo-tetramer	HHblits	X-ray	2.15Å	0.28	0.13	D-3-phosphoglycerate dehydrogenase
2ko1.1.A	7.69	homo-dimer	HHblits	NMR	NA	0.24	0.13	GTP pyrophosphokinase
2ko1.1.B	7.69	homo-dimer	HHblits	NMR	NA	0.24	0.13	GTP pyrophosphokinase
3ibw.1.A	7.69	homo-dimer	HHblits	X-ray	1.93Å	0.24	0.13	GTP pyrophosphokinase
3ibw.1.B	7.69	homo-dimer	HHblits	X-ray	1.93Å	0.24	0.13	GTP pyrophosphokinase
5t41.1.A	7.94	monomer	HHblits	X-ray	3.15Å	0.26	0.13	Phosphoserine phosphatase
3obi.1.A	7.81	homo-tetramer	HHblits	X-ray	1.95Å	0.25	0.13	Formyltetrahydrofolate deformylase
3o1l.1.A	7.81	homo-dimer	HHblits	X-ray	2.20Å	0.25	0.13	Formyltetrahydrofolate deformylase
5it0.1.A	9.68	homo-dimer	HHblits	X-ray	1.97Å	0.27	0.13	Phosphoserine phosphatase
5is2.1.A	9.68	homo-dimer	HHblits	X-ray	1.88Å	0.27	0.13	Phosphoserine phosphatase
5v0s.1.A	8.06	homo-dimer	HHblits	X-ray	2.01Å	0.27	0.13	Prephenate dehydrogenase
2jhe.1.A	13.11	homo-dimer	HHblits	X-ray	2.30Å	0.27	0.12	TRANSCRIPTION REGULATOR TYRR
2jhe.1.B	13.11	homo-dimer	HHblits	X-ray	2.30Å	0.27	0.12	TRANSCRIPTION REGULATOR TYRR
2jhe.2.A	13.11	homo-dimer	HHblits	X-ray	2.30Å	0.27	0.12	TRANSCRIPTION REGULATOR TYRR
2jhe.2.B	13.11	homo-dimer	HHblits	X-ray	2.30Å	0.27	0.12	TRANSCRIPTION REGULATOR TYRR
2re1.1.A	18.97	homo-dimer	HHblits	X-ray	2.75Å	0.31	0.12	Aspartokinase, alpha and beta subunits
2re1.1.B	18.97	homo-dimer	HHblits	X-ray	2.75Å	0.31	0.12	Aspartokinase, alpha and beta subunits
2zho.1.B	8.20	homo-dimer	HHblits	X-ray	2.98Å	0.26	0.12	Aspartokinase
2zho.1.A	8.20	homo-dimer	HHblits	X-ray	2.98Å	0.26	0.12	Aspartokinase
2zho.2.B	8.20	homo-dimer	HHblits	X-ray	2.98Å	0.26	0.12	Aspartokinase
2zho.3.A	8.20	homo-dimer	HHblits	X-ray	2.98Å	0.26	0.12	Aspartokinase
2zho.3.B	8.20	homo-dimer	HHblits	X-ray	2.98Å	0.26	0.12	Aspartokinase
2dt9.1.A	8.20	homo-dimer	HHblits	X-ray	2.15Å	0.26	0.12	Aspartokinase
2dt9.1.B	8.20	homo-dimer	HHblits	X-ray	2.15Å	0.26	0.12	Aspartokinase
3aaw.1.B	13.79	hetero-oligomer	HHblits	X-ray	2.50Å	0.30	0.12	Aspartokinase LysC beta subunit
3ab2.1.B	13.79	hetero-oligomer	HHblits	X-ray	2.59Å	0.30	0.12	Aspartokinase
2dtj.1.A	13.79	homo-dimer	HHblits	X-ray	1.58Å	0.30	0.12	Aspartokinase

Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
2dtj.1.B	13.79	homo-dimer	HHblits	X-ray	1.58Å	0.30	0.12	Aspartokinase
1ygy.1.A	11.48	homo-tetramer	HHblits	X-ray	2.30Å	0.26	0.12	D-3-phosphoglycerate dehydrogenase
1ygy.1.B	11.48	homo-tetramer	HHblits	X-ray	2.30Å	0.26	0.12	D-3-phosphoglycerate dehydrogenase
3ddn.1.A	11.48	homo-tetramer	HHblits	X-ray	2.40Å	0.26	0.12	D-3-phosphoglycerate dehydrogenase
3ddn.1.B	11.48	homo-tetramer	HHblits	X-ray	2.40Å	0.26	0.12	D-3-phosphoglycerate dehydrogenase
5jjb.1.A	7.94	homo-dimer	HHblits	X-ray	2.31Å	0.24	0.13	Phosphoserine phosphatase
5is2.1.A	7.94	homo-dimer	HHblits	X-ray	1.88Å	0.23	0.13	Phosphoserine phosphatase
3s1t.1.A	11.86	hetero-oligomer	HHblits	X-ray	1.63Å	0.28	0.12	Aspartokinase
3ab4.3.C	10.17	hetero-oligomer	HHblits	X-ray	2.47Å	0.28	0.12	Aspartokinase
3ab4.1.C	10.17	hetero-oligomer	HHblits	X-ray	2.47Å	0.28	0.12	Aspartokinase
3ab4.2.A	10.17	hetero-oligomer	HHblits	X-ray	2.47Å	0.28	0.12	Aspartokinase
3ab4.2.C	10.17	hetero-oligomer	HHblits	X-ray	2.47Å	0.28	0.12	Aspartokinase
3ab4.3.A	10.17	hetero-oligomer	HHblits	X-ray	2.47Å	0.28	0.12	Aspartokinase
3ab4.1.A	10.17	hetero-oligomer	HHblits	X-ray	2.47Å	0.28	0.12	Aspartokinase
3ab4.4.C	10.17	hetero-oligomer	HHblits	X-ray	2.47Å	0.28	0.12	Aspartokinase
4go5.1.A	15.25	homo-dimer	HHblits	X-ray	2.60Å	0.28	0.12	Aspartokinase
4go7.1.A	15.25	homo-dimer	HHblits	X-ray	2.00Å	0.28	0.12	Aspartokinase
2zho.1.B	13.56	homo-dimer	HHblits	X-ray	2.98Å	0.28	0.12	Aspartokinase
2zho.1.A	13.56	homo-dimer	HHblits	X-ray	2.98Å	0.28	0.12	Aspartokinase
2zho.2.B	13.56	homo-dimer	HHblits	X-ray	2.98Å	0.28	0.12	Aspartokinase
2zho.3.A	13.56	homo-dimer	HHblits	X-ray	2.98Å	0.28	0.12	Aspartokinase
2zho.3.B	13.56	homo-dimer	HHblits	X-ray	2.98Å	0.28	0.12	Aspartokinase
2dt9.1.A	13.56	homo-dimer	HHblits	X-ray	2.15Å	0.28	0.12	Aspartokinase
2dt9.1.B	13.56	homo-dimer	HHblits	X-ray	2.15Å	0.28	0.12	Aspartokinase
3l76.1.A	11.67	homo-dimer	HHblits	X-ray	2.54Å	0.26	0.12	Aspartokinase
3l76.1.B	11.67	homo-dimer	HHblits	X-ray	2.54Å	0.26	0.12	Aspartokinase
1tdj.1.A	11.67	homo-dimer	HHblits	X-ray	2.80Å	0.26	0.12	BIOSYNTHETIC THREONINE DEAMINASE
3ab2.1.C	12.07	hetero-oligomer	HHblits	X-ray	2.59Å	0.29	0.12	Aspartokinase
3aaw.1.C	12.07	hetero-oligomer	HHblits	X-ray	2.50Å	0.29	0.12	Aspartokinase
3ab2.1.A	12.07	hetero-oligomer	HHblits	X-ray	2.59Å	0.29	0.12	Aspartokinase
3aaw.1.A	12.07	hetero-oligomer	HHblits	X-ray	2.50Å	0.29	0.12	Aspartokinase

Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
3ab2.3.A	12.07	hetero-oligomer	HHblits	X-ray	2.59Å	0.29	0.12	Aspartokinase
3ab2.4.C	12.07	hetero-oligomer	HHblits	X-ray	2.59Å	0.29	0.12	Aspartokinase
2nyi.1.A	8.33	homo-dimer	HHblits	X-ray	1.80Å	0.25	0.12	unknown protein
2nyi.1.B	8.33	homo-dimer	HHblits	X-ray	1.80Å	0.25	0.12	unknown protein
4go5.1.A	10.34	homo-dimer	HHblits	X-ray	2.60Å	0.28	0.12	Aspartokinase
4go7.1.A	10.34	homo-dimer	HHblits	X-ray	2.00Å	0.28	0.12	Aspartokinase
3s1t.1.A	13.79	hetero-oligomer	HHblits	X-ray	1.63Å	0.27	0.12	Aspartokinase
3aaw.1.B	10.53	hetero-oligomer	HHblits	X-ray	2.50Å	0.28	0.12	Aspartokinase LysC beta subunit
3ab2.1.B	10.53	hetero-oligomer	HHblits	X-ray	2.59Å	0.28	0.12	Aspartokinase
2dtj.1.A	10.53	homo-dimer	HHblits	X-ray	1.58Å	0.28	0.12	Aspartokinase
2dtj.1.B	10.53	homo-dimer	HHblits	X-ray	1.58Å	0.28	0.12	Aspartokinase
2re1.1.A	10.34	homo-dimer	HHblits	X-ray	2.75Å	0.26	0.12	Aspartokinase, alpha and beta subunits
2re1.1.B	10.34	homo-dimer	HHblits	X-ray	2.75Å	0.26	0.12	Aspartokinase, alpha and beta subunits
3ab4.1.B	8.77	hetero-oligomer	HHblits	X-ray	2.47Å	0.27	0.12	Aspartokinase
3ab4.1.D	8.77	hetero-oligomer	HHblits	X-ray	2.47Å	0.27	0.12	Aspartokinase
3ab4.2.D	8.77	hetero-oligomer	HHblits	X-ray	2.47Å	0.27	0.12	Aspartokinase
3ab4.3.B	8.77	hetero-oligomer	HHblits	X-ray	2.47Å	0.27	0.12	Aspartokinase
3ab4.3.D	8.77	hetero-oligomer	HHblits	X-ray	2.47Å	0.27	0.12	Aspartokinase
3ab4.4.D	8.77	hetero-oligomer	HHblits	X-ray	2.47Å	0.27	0.12	Aspartokinase
3l76.1.A	12.07	homo-dimer	HHblits	X-ray	2.54Å	0.26	0.12	Aspartokinase
3l76.1.B	12.07	homo-dimer	HHblits	X-ray	2.54Å	0.26	0.12	Aspartokinase
3ab4.1.B	12.00	hetero-oligomer	HHblits	X-ray	2.47Å	0.29	0.10	Aspartokinase
3ab4.1.D	12.00	hetero-oligomer	HHblits	X-ray	2.47Å	0.29	0.10	Aspartokinase
3ab4.2.D	12.00	hetero-oligomer	HHblits	X-ray	2.47Å	0.29	0.10	Aspartokinase
3ab4.3.B	12.00	hetero-oligomer	HHblits	X-ray	2.47Å	0.29	0.10	Aspartokinase
3ab4.3.D	12.00	hetero-oligomer	HHblits	X-ray	2.47Å	0.29	0.10	Aspartokinase
3ab4.4.D	12.00	hetero-oligomer	HHblits	X-ray	2.47Å	0.29	0.10	Aspartokinase
2ktr.1.B	5.88	hetero-oligomer	HHblits	NMR	NA	0.27	0.10	Sequestosome-1
2nyi.1.A	7.69	homo-dimer	HHblits	X-ray	1.80Å	0.25	0.11	unknown protein
2nyi.1.B	7.69	homo-dimer	HHblits	X-ray	1.80Å	0.25	0.11	unknown protein
4mjs.2.B	3.92	hetero-oligomer	HHblits	X-ray	2.50Å	0.26	0.10	Sequestosome-1

Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
4mjs.1.B	3.92	hetero-oligomer	HHblits	X-ray	2.50Å	0.26	0.10	Sequestosome-1
4mjs.3.B	3.92	hetero-oligomer	HHblits	X-ray	2.50Å	0.26	0.10	Sequestosome-1
4mjs.4.B	3.92	hetero-oligomer	HHblits	X-ray	2.50Å	0.26	0.10	Sequestosome-1
4mjs.5.B	3.92	hetero-oligomer	HHblits	X-ray	2.50Å	0.26	0.10	Sequestosome-1
4mjs.8.B	3.92	hetero-oligomer	HHblits	X-ray	2.50Å	0.26	0.10	Sequestosome-1
4mjs.10.B	3.92	hetero-oligomer	HHblits	X-ray	2.50Å	0.26	0.10	Sequestosome-1
4mjs.11.B	3.92	hetero-oligomer	HHblits	X-ray	2.50Å	0.26	0.10	Sequestosome-1
4mjs.12.B	3.92	hetero-oligomer	HHblits	X-ray	2.50Å	0.26	0.10	Sequestosome-1
4uf9.1.A	3.92	homo-60-mer	HHblits	EM	10.30Å	0.26	0.10	SEQUESTOSOME-1
4uf8.1.A	3.92	homo-tetramer	HHblits	EM	10.90Å	0.26	0.10	SEQUESTOSOME-1
2kkc.1.A	4.00	monomer	HHblits	NMR	NA	0.26	0.10	Sequestosome-1
3lou.1.A	8.33	homo-tetramer	HHblits	X-ray	1.90Å	0.25	0.10	Formyltetrahydrofolate deformylase
3lou.1.B	8.33	homo-tetramer	HHblits	X-ray	1.90Å	0.25	0.10	Formyltetrahydrofolate deformylase
1u8s.1.A	13.89	homo-dimer	HHblits	X-ray	2.45Å	0.31	0.07	glycine cleavage system transcriptional repressor, putative
1u8s.1.B	13.89	homo-dimer	HHblits	X-ray	2.45Å	0.31	0.07	glycine cleavage system transcriptional repressor, putative
2f06.1.A	11.76	homo-tetramer	HHblits	X-ray	2.10Å	0.30	0.07	conserved hypothetical protein
2f06.1.B	11.76	homo-tetramer	HHblits	X-ray	2.10Å	0.30	0.07	conserved hypothetical protein
1u8s.1.A	8.57	homo-dimer	HHblits	X-ray	2.45Å	0.26	0.07	glycine cleavage system transcriptional repressor, putative
1u8s.1.B	8.57	homo-dimer	HHblits	X-ray	2.45Å	0.26	0.07	glycine cleavage system transcriptional repressor, putative
3w7b.1.A	3.23	homo-tetramer	HHblits	X-ray	2.71Å	0.26	0.06	Formyltetrahydrofolate deformylase
3lw6.1.A	10.71	monomer	HHblits	X-ray	1.81Å	0.26	0.06	Beta-4-galactosyltransferase 7
4lw3.1.A	10.71	monomer	HHblits	X-ray	2.00Å	0.26	0.06	Beta-4-galactosyltransferase 7