



# SWISS-MODEL Homology Modelling Report

## Model Building Report

This document lists the results for the homology modelling project "A6NFH5" submitted to SWISS-MODEL workspace on March 7, 2017, 11:37 a.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 Berton; 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

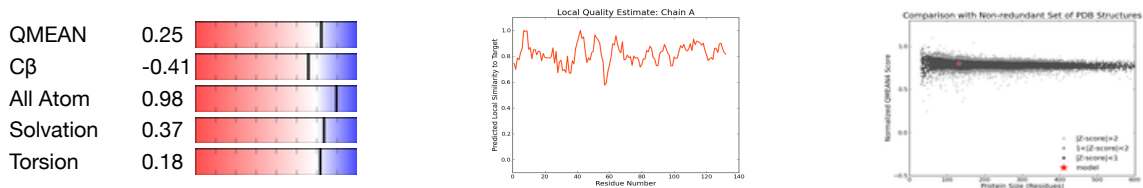
## Results

The SWISS-MODEL template library (SMTL version 2017-03-01, PDB release 2017-02-24) 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 478 templates were found (Table T2).

## Models

The following model was built (see Materials and Methods "Model Building"):

Model #01	File	Built with	Oligo-State	Ligands	GMQE	QMEAN
	PDB	ProMod3 Version 1.0.2.	MONOMER	None	0.80	0.25



Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
4a1h.1.A	65.91	monomer	HHblits	X-ray	2.20Å	0.49	1 - 132	0.94	MYELIN P2 PROTEIN
Ligand	Added to Model							Description	
CL	x - Not biologically relevant.							CHLORIDE ION	
GOL	x - Not biologically relevant.							GLYCEROL	
PLM	x - Binding site not conserved.							PALMITIC ACID	

Target

MIDQLQGTWKSISCENSEDYMKELGIGRASRKLGRLLAKPTVTISTDGDVITIKTKSIFKNNEISFKLGEEFEEITPGGHK

4a1h.1.A

MSNKLGTWKLVSSENFDDYMKALGVGLATRLKLNLAQPTVIISKSGDIITIRTESTFKNTEISFKLGQEFEEETADNRK

Target

TKSKVTLDKESLIQVQDWDGKETITRKLVDGKMVESTVNSVICRTRYEKVSSNSVSNS

4a1h.1.A

TKSIVTLQRGSLNQVQRWDGKETIKRKLVDGKMVAECKMKGVVCTRIYEKV-----

## Materials and Methods

### Template Search

Template search with Blast and HHblits has been performed against the SWISS-MODEL template library (SMTL, last update: 2017-03-01, last included PDB release: 2017-02-24).

The target sequence was searched with BLAST (Altschul et al., 1997) against the primary amino acid sequence contained in the SMTL. A total of 220 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 273 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.

MIDQLQGTWKSISCENSEDYMKELGIGRASRKLGRLLAKPTVTISTDGDVITIKTKSIFKNNEISFKLGEEFEEITPGGHKTKSKVTLDKESLIQVQDWDG  
KETITIRKLVDGKMMVESTVNSVICRTRYEKVSSNSVNS

### Table T2:

Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
4a1h.1.A	65.91	monomer	HHblits	X-ray	2.20Å	0.49	0.94	MYELIN P2 PROTEIN
2wut.1.A	65.91	monomer	HHblits	X-ray	1.85Å	0.48	0.94	MYELIN P2 PROTEIN
4a1y.1.A	65.15	monomer	HHblits	X-ray	1.20Å	0.48	0.94	MYELIN P2 PROTEIN
4a8z.1.A	65.15	homo-dimer	HHblits	X-ray	1.80Å	0.48	0.94	MYELIN P2 PROTEIN
4d6b.1.A	65.15	homo-dimer	HHblits	X-ray	2.12Å	0.48	0.94	MYELIN P2 PROTEIN
5bvq.1.A	61.36	monomer	HHblits	X-ray	2.10Å	0.48	0.94	fatty acid-binding protein
3nr3.1.A	66.15	monomer	HHblits	X-ray	1.95Å	0.49	0.93	PMP2 protein

Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
3nr3.1.A	66.15	monomer	BLAST	X-ray	1.95Å	0.49	0.93	PMP2 protein
5bvq.1.A	61.83	monomer	BLAST	X-ray	2.10Å	0.48	0.94	fatty acid-binding protein
1pmp.1.A	64.12	monomer	HHblits	X-ray	2.70Å	0.48	0.94	P2 MYELIN PROTEIN
1pmp.1.A	64.62	monomer	BLAST	X-ray	2.70Å	0.48	0.93	P2 MYELIN PROTEIN
1yiv.1.A	65.38	monomer	HHblits	X-ray	2.10Å	0.48	0.93	Myelin P2 protein
4a60.1.A	57.58	monomer	HHblits	X-ray	1.53Å	0.47	0.94	FATTY ACID-BINDING PROTEIN 9 TESTIS LIPID-BINDING PROTEIN, TLBP, TESTIS-TYPE FATTY ACID-BINDING PROTEIN, T-FABP
5hz9.1.A	51.13	monomer	HHblits	X-ray	2.30Å	0.45	0.95	Fatty acid-binding protein, heart
3wxq.1.A	51.13	monomer	HHblits	X-ray	1.60Å	0.45	0.95	Fatty acid-binding protein, heart
5b28.1.A	51.13	monomer	HHblits	X-ray	0.90Å	0.45	0.95	Fatty acid-binding protein, heart
3wbg.1.A	51.13	monomer	HHblits	X-ray	2.15Å	0.45	0.95	Fatty acid-binding protein, heart
3rsw.1.A	51.13	monomer	HHblits	X-ray	2.60Å	0.45	0.95	Fatty acid-binding protein, heart
5hz8.1.A	55.30	monomer	HHblits	X-ray	1.12Å	0.46	0.94	Fatty acid-binding protein, adipocyte
5b27.1.A	50.38	monomer	HHblits	X-ray	1.02Å	0.45	0.95	Fatty acid-binding protein, heart
5bvt.1.A	57.25	monomer	BLAST	X-ray	2.31Å	0.46	0.94	Epidermal fatty acid-binding protein
5ce4.1.A	51.52	monomer	HHblits	neutron diff.	0.98Å	0.46	0.94	Fatty acid-binding protein, heart
2hnx.1.A	55.30	monomer	HHblits	X-ray	1.50Å	0.46	0.94	Fatty acid-binding protein, adipocyte
5edb.1.A	55.30	monomer	HHblits	X-ray	1.18Å	0.46	0.94	Fatty acid-binding protein, adipocyte
5edc.1.A	55.30	monomer	HHblits	X-ray	1.29Å	0.46	0.94	Fatty acid-binding protein, adipocyte
3p6c.1.A	55.30	monomer	HHblits	X-ray	1.25Å	0.46	0.94	Fatty acid-binding protein, adipocyte
3q6l.1.A	55.30	monomer	HHblits	X-ray	1.40Å	0.46	0.94	Fatty acid-binding protein, adipocyte
3fr4.1.A	55.30	monomer	HHblits	X-ray	2.16Å	0.46	0.94	Fatty acid-binding protein, adipocyte
5hz8.1.A	55.73	monomer	BLAST	X-ray	1.12Å	0.46	0.94	Fatty acid-binding protein, adipocyte
5c0n.1.A	54.55	hetero- oligomer	HHblits	X-ray	3.00Å	0.45	0.94	Fatty acid-binding protein, adipocyte
5d8j.1.A	54.55	hetero- oligomer	HHblits	X-ray	3.00Å	0.45	0.94	Fatty acid-binding protein, adipocyte
2q9s.1.A	54.55	homo-dimer	HHblits	X-ray	2.30Å	0.45	0.94	Fatty acid-binding protein
5hz9.1.A	51.91	monomer	BLAST	X-ray	2.30Å	0.46	0.94	Fatty acid-binding protein, heart
5b28.1.A	51.91	monomer	BLAST	X-ray	0.90Å	0.46	0.94	Fatty acid-binding protein, heart
3wxq.1.A	51.91	monomer	BLAST	X-ray	1.60Å	0.46	0.94	Fatty acid-binding protein, heart
5ce4.1.A	51.91	monomer	BLAST	neutron diff.	0.98Å	0.46	0.94	Fatty acid-binding protein, heart
3rsw.1.A	51.91	monomer	BLAST	X-ray	2.60Å	0.46	0.94	Fatty acid-binding protein, heart
3wbg.1.A	51.91	monomer	BLAST	X-ray	2.15Å	0.46	0.94	Fatty acid-binding protein, heart
5bvt.1.A	55.30	monomer	HHblits	X-ray	2.31Å	0.45	0.94	Epidermal fatty acid-binding protein
5edc.1.A	55.73	monomer	BLAST	X-ray	1.29Å	0.46	0.94	Fatty acid-binding protein, adipocyte
3fr4.1.A	55.73	monomer	BLAST	X-ray	2.16Å	0.46	0.94	Fatty acid-binding protein, adipocyte
5edb.1.A	55.73	monomer	BLAST	X-ray	1.18Å	0.46	0.94	Fatty acid-binding protein, adipocyte
2hnx.1.A	55.73	monomer	BLAST	X-ray	1.50Å	0.46	0.94	Fatty acid-binding protein, adipocyte
3p6c.1.A	55.73	monomer	BLAST	X-ray	1.25Å	0.46	0.94	Fatty acid-binding protein, adipocyte
3q6l.1.A	55.73	monomer	BLAST	X-ray	1.40Å	0.46	0.94	Fatty acid-binding protein, adipocyte
5b27.1.A	51.15	monomer	BLAST	X-ray	1.02Å	0.45	0.94	Fatty acid-binding protein, heart
5c0n.1.A	54.96	hetero- oligomer	BLAST	X-ray	3.00Å	0.45	0.94	Fatty acid-binding protein, adipocyte
5d8j.1.A	54.96	hetero- oligomer	BLAST	X-ray	3.00Å	0.45	0.94	Fatty acid-binding protein, adipocyte
4azm.1.A	50.38	homo-dimer	HHblits	X-ray	2.75Å	0.44	0.95	FATTY ACID-BINDING PROTEIN, EPIDERMAL
2hmb.1.A	51.15	monomer	HHblits	X-ray	2.10Å	0.45	0.94	MUSCLE FATTY ACID BINDING PROTEIN

Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
1g5w.1.A	51.15	monomer	HHblits	NMR	NA	0.45	0.94	FATTY ACID-BINDING PROTEIN
5b29.1.A	51.15	monomer	HHblits	X-ray	1.28Å	0.45	0.94	Fatty acid-binding protein, heart
1bwy.1.A	51.15	monomer	HHblits	NMR	NA	0.45	0.94	PROTEIN (HEART FATTY ACID BINDING PROTEIN)
5b29.1.A	51.54	monomer	BLAST	X-ray	1.28Å	0.46	0.93	Fatty acid-binding protein, heart
2hmb.1.A	51.54	monomer	BLAST	X-ray	2.10Å	0.46	0.93	MUSCLE FATTY ACID BINDING PROTEIN
1g5w.1.A	51.54	monomer	BLAST	NMR	NA	0.46	0.93	FATTY ACID-BINDING PROTEIN
1bwy.1.A	51.54	monomer	BLAST	NMR	NA	0.46	0.93	PROTEIN (HEART FATTY ACID BINDING PROTEIN)
3fr5.1.A	55.38	monomer	HHblits	X-ray	2.20Å	0.46	0.93	Fatty acid-binding protein, adipocyte
1b56.1.A	50.76	monomer	HHblits	X-ray	2.05Å	0.44	0.94	FATTY ACID BINDING PROTEIN
1jjj.1.A	50.76	monomer	HHblits	NMR	NA	0.44	0.94	EPIDERMAL-TYPE FATTY ACID BINDING PROTEIN (E-FABP)
5hz5.1.A	50.76	monomer	HHblits	X-ray	1.40Å	0.44	0.94	Fatty acid-binding protein, epidermal
4lkt.1.A	50.76	monomer	HHblits	X-ray	2.57Å	0.44	0.94	Fatty acid-binding protein, epidermal
4lkp.1.A	50.76	monomer	HHblits	X-ray	1.67Å	0.44	0.94	Fatty acid-binding protein, epidermal
4lkt.3.A	50.76	monomer	HHblits	X-ray	2.57Å	0.44	0.94	Fatty acid-binding protein, epidermal
4azo.1.A	49.62	homo-dimer	HHblits	X-ray	2.33Å	0.44	0.95	FATTY ACID-BINDING PROTEIN, EPIDERMAL
4azr.1.A	50.76	homo-dimer	HHblits	X-ray	2.95Å	0.44	0.94	FATTY ACID-BINDING PROTEIN, EPIDERMAL
4azr.1.B	50.76	homo-dimer	HHblits	X-ray	2.95Å	0.44	0.94	FATTY ACID-BINDING PROTEIN, EPIDERMAL
3hk1.1.A	54.62	monomer	HHblits	X-ray	1.70Å	0.45	0.93	Fatty acid-binding protein, adipocyte
2ans.1.A	54.62	homo-dimer	HHblits	X-ray	2.50Å	0.45	0.93	ADIPOCYTE LIPID-BINDING PROTEIN
1alb.1.A	54.62	monomer	HHblits	X-ray	2.50Å	0.45	0.93	ADIPOCYTE LIPID-BINDING PROTEIN
1lic.1.A	54.62	homo-dimer	HHblits	X-ray	1.60Å	0.45	0.93	ADIPOCYTE LIPID-BINDING PROTEIN
4azp.1.A	48.87	monomer	HHblits	X-ray	2.10Å	0.44	0.95	FATTY ACID-BINDING PROTEIN, EPIDERMAL
1g7n.1.A	54.62	monomer	HHblits	X-ray	1.50Å	0.45	0.93	ADIPOCYTE LIPID-BINDING PROTEIN
3js1.1.A	53.44	homo-dimer	HHblits	X-ray	1.81Å	0.45	0.94	Adipocyte fatty acid-binding protein
3fr5.1.A	55.81	monomer	BLAST	X-ray	2.20Å	0.46	0.92	Fatty acid-binding protein, adipocyte
4lkt.1.A	51.15	monomer	BLAST	X-ray	2.57Å	0.45	0.94	Fatty acid-binding protein, epidermal
4lkp.1.A	51.15	monomer	BLAST	X-ray	1.67Å	0.45	0.94	Fatty acid-binding protein, epidermal
4lkt.3.A	51.15	monomer	BLAST	X-ray	2.57Å	0.45	0.94	Fatty acid-binding protein, epidermal
1b56.1.A	51.15	monomer	BLAST	X-ray	2.05Å	0.45	0.94	FATTY ACID BINDING PROTEIN
1jjj.1.A	51.15	monomer	BLAST	NMR	NA	0.45	0.94	EPIDERMAL-TYPE FATTY ACID BINDING PROTEIN (E-FABP)
5hz5.1.A	51.15	monomer	BLAST	X-ray	1.40Å	0.45	0.94	Fatty acid-binding protein, epidermal
4azm.1.A	51.15	homo-dimer	BLAST	X-ray	2.75Å	0.45	0.94	FATTY ACID-BINDING PROTEIN, EPIDERMAL
4azn.1.A	50.00	monomer	HHblits	X-ray	2.51Å	0.44	0.94	FATTY ACID-BINDING PROTEIN, EPIDERMAL
4azr.1.A	51.15	homo-dimer	BLAST	X-ray	2.95Å	0.45	0.94	FATTY ACID-BINDING PROTEIN, EPIDERMAL
4azr.1.B	51.15	homo-dimer	BLAST	X-ray	2.95Å	0.45	0.94	FATTY ACID-BINDING PROTEIN, EPIDERMAL
3hk1.1.A	55.04	monomer	BLAST	X-ray	1.70Å	0.46	0.92	Fatty acid-binding protein, adipocyte
2ans.1.A	55.04	homo-dimer	BLAST	X-ray	2.50Å	0.46	0.92	ADIPOCYTE LIPID-BINDING PROTEIN
1alb.1.A	55.04	monomer	BLAST	X-ray	2.50Å	0.46	0.92	ADIPOCYTE LIPID-BINDING PROTEIN
1lic.1.A	55.04	homo-dimer	BLAST	X-ray	1.60Å	0.46	0.92	ADIPOCYTE LIPID-BINDING PROTEIN
1g7n.1.A	55.04	monomer	BLAST	X-ray	1.50Å	0.46	0.92	ADIPOCYTE LIPID-BINDING PROTEIN
5hz6.1.A	55.04	monomer	HHblits	X-ray	1.14Å	0.45	0.92	Fatty acid-binding protein, adipocyte

Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
3js1.1.A	55.04	homo-dimer	BLAST	X-ray	1.81Å	0.45	0.92	Adipocyte fatty acid-binding protein
1acd.1.A	53.85	homo-dimer	HHblits	X-ray	2.70Å	0.45	0.93	ADIPOCYTE LIPID BINDING PROTEIN
4azo.1.A	50.38	homo-dimer	BLAST	X-ray	2.33Å	0.44	0.94	FATTY ACID-BINDING PROTEIN, EPIDERMAL
4azn.1.A	50.38	monomer	BLAST	X-ray	2.51Å	0.44	0.94	FATTY ACID-BINDING PROTEIN, EPIDERMAL
4azp.1.A	49.62	monomer	BLAST	X-ray	2.10Å	0.44	0.94	FATTY ACID-BINDING PROTEIN, EPIDERMAL
1acd.1.A	54.26	homo-dimer	BLAST	X-ray	2.70Å	0.45	0.92	ADIPOCYTE LIPID BINDING PROTEIN
1fdq.1.A	48.46	monomer	BLAST	X-ray	2.10Å	0.44	0.93	FATTY ACID-BINDING PROTEIN, BRAIN
1fdq.2.A	48.46	monomer	BLAST	X-ray	2.10Å	0.44	0.93	FATTY ACID-BINDING PROTEIN, BRAIN
1fe3.1.A	48.46	monomer	BLAST	X-ray	2.80Å	0.44	0.93	FATTY ACID-BINDING PROTEIN, BRAIN
1jjx.1.A	48.46	monomer	BLAST	NMR	NA	0.44	0.93	BRAIN-TYPE FATTY ACID BINDING PROTEIN
1fdq.1.A	48.46	monomer	HHblits	X-ray	2.10Å	0.44	0.93	FATTY ACID-BINDING PROTEIN, BRAIN
1fdq.2.A	48.46	monomer	HHblits	X-ray	2.10Å	0.44	0.93	FATTY ACID-BINDING PROTEIN, BRAIN
1fe3.1.A	48.46	monomer	HHblits	X-ray	2.80Å	0.44	0.93	FATTY ACID-BINDING PROTEIN, BRAIN
1jjx.1.A	48.46	monomer	HHblits	NMR	NA	0.44	0.93	BRAIN-TYPE FATTY ACID BINDING PROTEIN
5hz6.1.A	56.80	monomer	BLAST	X-ray	1.14Å	0.46	0.89	Fatty acid-binding protein, adipocyte
4i3b.2.A	40.60	monomer	HHblits	X-ray	1.20Å	0.41	0.95	Bilirubin-inducible fluorescent protein UnaG
4i3b.1.A	40.60	monomer	HHblits	X-ray	1.20Å	0.41	0.95	Bilirubin-inducible fluorescent protein UnaG
4i3d.1.A	40.60	monomer	HHblits	X-ray	2.30Å	0.41	0.95	Bilirubin-inducible fluorescent protein UnaG
4i3d.2.A	40.60	monomer	HHblits	X-ray	2.30Å	0.41	0.95	Bilirubin-inducible fluorescent protein UnaG
4i3d.3.A	40.60	monomer	HHblits	X-ray	2.30Å	0.41	0.95	Bilirubin-inducible fluorescent protein UnaG
4i3d.4.A	40.60	monomer	HHblits	X-ray	2.30Å	0.41	0.95	Bilirubin-inducible fluorescent protein UnaG
4i3c.1.A	40.60	monomer	HHblits	X-ray	2.00Å	0.41	0.95	Bilirubin-inducible fluorescent protein UnaG
4i3c.2.A	40.60	monomer	HHblits	X-ray	2.00Å	0.41	0.95	Bilirubin-inducible fluorescent protein UnaG
4i3c.1.A	40.60	monomer	BLAST	X-ray	2.00Å	0.41	0.95	Bilirubin-inducible fluorescent protein UnaG
4i3c.2.A	40.60	monomer	BLAST	X-ray	2.00Å	0.41	0.95	Bilirubin-inducible fluorescent protein UnaG
3ppt.1.A	41.54	monomer	HHblits	X-ray	1.28Å	0.41	0.93	Sodium-calcium exchanger
3pp6.1.A	40.77	monomer	HHblits	X-ray	1.90Å	0.40	0.93	Sodium-calcium exchanger
5hzq.1.A	38.17	monomer	HHblits	X-ray	1.75Å	0.40	0.94	Cellular retinoic acid-binding protein 2
5hzq.2.A	38.17	monomer	HHblits	X-ray	1.75Å	0.40	0.94	Cellular retinoic acid-binding protein 2
2poa.1.A	38.64	monomer	BLAST	NMR	NA	0.39	0.94	14 kDa fatty acid-binding protein
1vyg.1.A	38.64	monomer	BLAST	X-ray	2.40Å	0.39	0.94	FATTY ACID BINDING PROTEIN
1cbq.1.A	38.46	homo-trimer	HHblits	X-ray	2.20Å	0.40	0.93	CELLULAR RETINOIC ACID BINDING PROTEIN TYPE II
1cbs.1.A	38.46	monomer	HHblits	X-ray	1.80Å	0.40	0.93	CELLULAR RETINOIC ACID BINDING PROTEIN TYPE II
1blr.1.A	38.46	monomer	HHblits	NMR	NA	0.40	0.93	CELLULAR RETINOIC ACID BINDING PROTEIN-TYPE II
3cbs.1.A	38.46	monomer	HHblits	X-ray	2.00Å	0.40	0.93	PROTEIN (CRABP-II)
2fs6.1.A	38.46	monomer	HHblits	X-ray	1.35Å	0.40	0.93	Cellular retinoic acid-binding protein 2
2fs6.2.A	38.46	monomer	HHblits	X-ray	1.35Å	0.40	0.93	Cellular retinoic acid-binding protein 2

Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
2frs.1.A	38.46	monomer	HHblits	X-ray	1.51Å	0.40	0.93	Cellular retinoic acid-binding protein 2
2frs.2.A	38.46	monomer	HHblits	X-ray	1.51Å	0.40	0.93	Cellular retinoic acid-binding protein 2
3d96.1.A	36.92	monomer	HHblits	X-ray	1.71Å	0.39	0.93	Cellular retinoic acid-binding protein 2
3d96.2.A	36.92	monomer	HHblits	X-ray	1.71Å	0.39	0.93	Cellular retinoic acid-binding protein 2
2g79.1.A	36.92	monomer	HHblits	X-ray	1.69Å	0.39	0.93	Cellular retinoic acid-binding protein 2
3ppt.1.A	42.52	monomer	BLAST	X-ray	1.28Å	0.41	0.91	Sodium-calcium exchanger
1bm5.1.A	37.69	monomer	HHblits	NMR	NA	0.39	0.93	CELLULAR RETINOIC ACID BINDING PROTEIN-TYPE II
1xca.1.A	37.69	homo-dimer	HHblits	X-ray	2.30Å	0.39	0.93	CELLULAR RETINOIC ACID BINDING PROTEIN TYPE II
1xca.1.B	37.69	homo-dimer	HHblits	X-ray	2.30Å	0.39	0.93	CELLULAR RETINOIC ACID BINDING PROTEIN TYPE II
1o8v.1.A	34.09	monomer	BLAST	X-ray	1.60Å	0.38	0.94	FATTY ACID BINDING PROTEIN HOMOLOG
3pp6.1.A	41.73	monomer	BLAST	X-ray	1.90Å	0.41	0.91	Sodium-calcium exchanger
4qgv.2.A	36.92	monomer	HHblits	X-ray	1.73Å	0.39	0.93	Cellular retinoic acid-binding protein 2
4qgv.1.A	36.92	monomer	HHblits	X-ray	1.73Å	0.39	0.93	Cellular retinoic acid-binding protein 2
3cr6.1.A	36.92	monomer	HHblits	X-ray	1.22Å	0.39	0.93	Cellular retinoic acid-binding protein 2
3fen.1.A	36.92	monomer	HHblits	X-ray	1.56Å	0.39	0.93	Cellular retinoic acid-binding protein 2
3fen.2.A	36.92	monomer	HHblits	X-ray	1.56Å	0.39	0.93	Cellular retinoic acid-binding protein 2
3i17.1.A	37.98	homo-dimer	HHblits	X-ray	1.68Å	0.39	0.92	Cellular retinoic acid-binding protein 2
3i17.1.B	37.98	homo-dimer	HHblits	X-ray	1.68Å	0.39	0.92	Cellular retinoic acid-binding protein 2
1o8v.1.A	34.85	monomer	HHblits	X-ray	1.60Å	0.38	0.94	FATTY ACID BINDING PROTEIN HOMOLOG
4qgx.2.A	36.92	monomer	HHblits	X-ray	1.47Å	0.39	0.93	Cellular retinoic acid-binding protein 2
2g7b.1.A	36.92	monomer	HHblits	X-ray	1.18Å	0.39	0.93	Cellular retinoic acid-binding protein 2
3d97.1.A	36.92	monomer	HHblits	X-ray	1.50Å	0.39	0.93	Cellular retinoic acid-binding protein 2
3d97.2.A	36.92	monomer	HHblits	X-ray	1.50Å	0.39	0.93	Cellular retinoic acid-binding protein 2
4qgx.1.A	36.92	monomer	HHblits	X-ray	1.47Å	0.39	0.93	Cellular retinoic acid-binding protein 2
5hzq.1.A	39.84	monomer	BLAST	X-ray	1.75Å	0.40	0.91	Cellular retinoic acid-binding protein 2
5hzq.2.A	39.84	monomer	BLAST	X-ray	1.75Å	0.40	0.91	Cellular retinoic acid-binding protein 2
4qgw.1.A	36.92	monomer	HHblits	X-ray	1.77Å	0.39	0.93	Cellular retinoic acid-binding protein 2
4qgw.2.A	36.92	monomer	HHblits	X-ray	1.77Å	0.39	0.93	Cellular retinoic acid-binding protein 2
1vyg.1.A	37.12	monomer	HHblits	X-ray	2.40Å	0.37	0.94	FATTY ACID BINDING PROTEIN
3f9d.1.A	36.15	monomer	HHblits	X-ray	2.00Å	0.39	0.93	Cellular retinoic acid-binding protein 2
3f9d.2.A	36.15	monomer	HHblits	X-ray	2.00Å	0.39	0.93	Cellular retinoic acid-binding protein 2
3fel.1.A	36.15	monomer	HHblits	X-ray	1.85Å	0.39	0.93	Cellular retinoic acid-binding protein 2
3fel.2.A	36.15	monomer	HHblits	X-ray	1.85Å	0.39	0.93	Cellular retinoic acid-binding protein 2
3fa8.1.A	36.15	monomer	HHblits	X-ray	1.78Å	0.39	0.93	Cellular retinoic acid-binding protein 2
3fa8.2.A	36.15	monomer	HHblits	X-ray	1.78Å	0.39	0.93	Cellular retinoic acid-binding protein 2
3fa9.1.A	36.15	monomer	HHblits	X-ray	1.94Å	0.39	0.93	Cellular retinoic acid-binding protein 2
3fa9.2.A	36.15	monomer	HHblits	X-ray	1.94Å	0.39	0.93	Cellular retinoic acid-binding protein 2
4m7m.1.A	35.38	monomer	HHblits	X-ray	2.57Å	0.38	0.93	Cellular retinoic acid-binding protein 2
1cbr.1.A	37.69	homo-dimer	HHblits	X-ray	2.90Å	0.38	0.93	CELLULAR RETINOIC ACID BINDING PROTEIN TYPE I
1cbi.1.A	37.69	homo-dimer	HHblits	X-ray	2.70Å	0.38	0.93	CELLULAR RETINOIC ACID BINDING PROTEIN I
1cbi.1.B	37.69	homo-dimer	HHblits	X-ray	2.70Å	0.38	0.93	CELLULAR RETINOIC ACID BINDING PROTEIN I
2cbr.1.A	37.69	monomer	HHblits	X-ray	2.80Å	0.38	0.93	PROTEIN (CRABP-I)
3fa7.1.A	37.21	monomer	HHblits	X-ray	1.90Å	0.39	0.92	Cellular retinoic acid-binding protein 2
3fa7.2.A	37.21	monomer	HHblits	X-ray	1.90Å	0.39	0.92	Cellular retinoic acid-binding protein 2
4i9r.1.A	35.38	monomer	HHblits	X-ray	2.60Å	0.38	0.93	Cellular retinoic acid-binding protein 2

Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
2poa.1.A	36.64	monomer	HHblits	NMR	NA	0.38	0.94	14 kDa fatty acid-binding protein
3f8a.1.A	37.21	monomer	HHblits	X-ray	1.95Å	0.39	0.92	Cellular retinoic acid-binding protein 2
4yfp.1.A	34.62	monomer	HHblits	X-ray	1.95Å	0.38	0.93	Cellular retinoic acid-binding protein 2
3d95.1.A	35.66	monomer	HHblits	X-ray	1.20Å	0.39	0.92	Cellular retinoic acid-binding protein 2
3d95.2.A	35.66	monomer	HHblits	X-ray	1.20Å	0.39	0.92	Cellular retinoic acid-binding protein 2
3cwk.1.A	35.66	monomer	HHblits	X-ray	1.60Å	0.39	0.92	Cellular retinoic acid-binding protein 2
2flj.1.A	34.35	monomer	HHblits	NMR	NA	0.37	0.94	Fatty acid-binding protein
3fa6.1.A	35.66	monomer	HHblits	X-ray	1.54Å	0.39	0.92	Cellular retinoic acid-binding protein 2
3fa6.2.A	35.66	monomer	HHblits	X-ray	1.54Å	0.39	0.92	Cellular retinoic acid-binding protein 2
3fek.2.A	35.66	monomer	HHblits	X-ray	1.51Å	0.39	0.92	Cellular retinoic acid-binding protein 2
3fek.1.A	35.66	monomer	HHblits	X-ray	1.51Å	0.39	0.92	Cellular retinoic acid-binding protein 2
4ykm.1.A	34.62	monomer	HHblits	X-ray	1.58Å	0.38	0.93	Cellular retinoic acid-binding protein 2
4i9s.1.A	35.66	monomer	HHblits	X-ray	2.58Å	0.39	0.92	Cellular retinoic acid-binding protein 2
4yko.1.A	34.62	monomer	HHblits	X-ray	1.57Å	0.38	0.93	Cellular retinoic acid-binding protein 2
1opa.1.B	37.69	homo-dimer	BLAST	X-ray	1.90Å	0.38	0.93	CELLULAR RETINOL BINDING PROTEIN II
1eii.1.A	37.69	monomer	BLAST	NMR	NA	0.38	0.93	CELLULAR RETINOL-BINDING PROTEIN II
1opa.1.A	37.69	homo-dimer	BLAST	X-ray	1.90Å	0.38	0.93	CELLULAR RETINOL BINDING PROTEIN II
1b4m.1.A	37.69	monomer	BLAST	NMR	NA	0.38	0.93	CELLULAR RETINOL-BINDING PROTEIN II
1opb.2.A	37.69	monomer	BLAST	X-ray	1.90Å	0.38	0.93	CELLULAR RETINOL BINDING PROTEIN II
4m6s.1.A	35.66	monomer	HHblits	X-ray	2.47Å	0.38	0.92	Cellular retinoic acid-binding protein 2
4ybp.1.A	34.88	monomer	HHblits	X-ray	1.83Å	0.38	0.92	Cellular retinoic acid-binding protein 2
1lpj.1.A	35.11	monomer	HHblits	X-ray	2.00Å	0.37	0.94	Retinol-binding protein IV, cellular
5ljd.1.A	32.33	monomer	HHblits	X-ray	1.61Å	0.36	0.95	Retinol-binding protein 1
2flj.1.A	36.72	monomer	BLAST	NMR	NA	0.39	0.91	Fatty acid-binding protein
5lje.1.A	32.33	monomer	HHblits	X-ray	1.40Å	0.35	0.95	Retinol-binding protein 1
5ljb.1.A	32.33	monomer	HHblits	X-ray	1.26Å	0.35	0.95	Retinol-binding protein 1
1cbq.1.A	40.80	homo-trimer	BLAST	X-ray	2.20Å	0.40	0.89	CELLULAR RETINOIC ACID BINDING PROTEIN TYPE II
1cbs.1.A	40.80	monomer	BLAST	X-ray	1.80Å	0.40	0.89	CELLULAR RETINOIC ACID BINDING PROTEIN TYPE II
1blr.1.A	40.80	monomer	BLAST	NMR	NA	0.40	0.89	CELLULAR RETINOIC ACID BINDING PROTEIN-TYPE II
3cbs.1.A	40.80	monomer	BLAST	X-ray	2.00Å	0.40	0.89	PROTEIN (CRABP-II)
2fs6.1.A	40.80	monomer	BLAST	X-ray	1.35Å	0.40	0.89	Cellular retinoic acid-binding protein 2
2fs6.2.A	40.80	monomer	BLAST	X-ray	1.35Å	0.40	0.89	Cellular retinoic acid-binding protein 2
2frs.1.A	40.80	monomer	BLAST	X-ray	1.51Å	0.40	0.89	Cellular retinoic acid-binding protein 2
2frs.2.A	40.80	monomer	BLAST	X-ray	1.51Å	0.40	0.89	Cellular retinoic acid-binding protein 2
5ljc.1.A	32.33	monomer	HHblits	X-ray	1.43Å	0.35	0.95	Retinol-binding protein 1
1ftp.1.A	33.85	homo-dimer	HHblits	X-ray	2.20Å	0.37	0.93	MUSCLE FATTY ACID BINDING PROTEIN
1opa.1.B	33.33	homo-dimer	HHblits	X-ray	1.90Å	0.36	0.94	CELLULAR RETINOL BINDING PROTEIN II
1eii.1.A	33.33	monomer	HHblits	NMR	NA	0.36	0.94	CELLULAR RETINOL-BINDING PROTEIN II
1opa.1.A	33.33	homo-dimer	HHblits	X-ray	1.90Å	0.36	0.94	CELLULAR RETINOL BINDING PROTEIN II
1b4m.1.A	33.33	monomer	HHblits	NMR	NA	0.36	0.94	CELLULAR RETINOL-BINDING PROTEIN II

Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
1opb.2.A	33.33	monomer	HHblits	X-ray	1.90Å	0.36	0.94	CELLULAR RETINOL BINDING PROTEIN II
1bm5.1.A	40.00	monomer	BLAST	NMR	NA	0.40	0.89	CELLULAR RETINOIC ACID BINDING PROTEIN-TYPE II
1xca.1.A	40.00	homo-dimer	BLAST	X-ray	2.30Å	0.40	0.89	CELLULAR RETINOIC ACID BINDING PROTEIN TYPE II
1xca.1.B	40.00	homo-dimer	BLAST	X-ray	2.30Å	0.40	0.89	CELLULAR RETINOIC ACID BINDING PROTEIN TYPE II
3i17.1.A	40.00	homo-dimer	BLAST	X-ray	1.68Å	0.40	0.89	Cellular retinoic acid-binding protein 2
3i17.1.B	40.00	homo-dimer	BLAST	X-ray	1.68Å	0.40	0.89	Cellular retinoic acid-binding protein 2
3d96.1.A	39.20	monomer	BLAST	X-ray	1.71Å	0.40	0.89	Cellular retinoic acid-binding protein 2
3d96.2.A	39.20	monomer	BLAST	X-ray	1.71Å	0.40	0.89	Cellular retinoic acid-binding protein 2
2g79.1.A	39.20	monomer	BLAST	X-ray	1.69Å	0.40	0.89	Cellular retinoic acid-binding protein 2
1kgl.1.A	32.58	monomer	HHblits	NMR	NA	0.36	0.94	CELLULAR RETINOL-BINDING PROTEIN TYPE I
1jbh.1.A	32.58	monomer	HHblits	NMR	NA	0.36	0.94	CELLULAR RETINOL-BINDING PROTEIN TYPE I
4qgv.2.A	39.20	monomer	BLAST	X-ray	1.73Å	0.40	0.89	Cellular retinoic acid-binding protein 2
4qgv.1.A	39.20	monomer	BLAST	X-ray	1.73Å	0.40	0.89	Cellular retinoic acid-binding protein 2
3cr6.1.A	38.40	monomer	BLAST	X-ray	1.22Å	0.40	0.89	Cellular retinoic acid-binding protein 2
3fen.1.A	38.40	monomer	BLAST	X-ray	1.56Å	0.40	0.89	Cellular retinoic acid-binding protein 2
3fen.2.A	38.40	monomer	BLAST	X-ray	1.56Å	0.40	0.89	Cellular retinoic acid-binding protein 2
2a0a.1.A	30.00	monomer	HHblits	NMR	NA	0.37	0.93	Der f 13
4qgx.2.A	39.20	monomer	BLAST	X-ray	1.47Å	0.40	0.89	Cellular retinoic acid-binding protein 2
2g7b.1.A	39.20	monomer	BLAST	X-ray	1.18Å	0.40	0.89	Cellular retinoic acid-binding protein 2
3d97.1.A	39.20	monomer	BLAST	X-ray	1.50Å	0.40	0.89	Cellular retinoic acid-binding protein 2
3d97.2.A	39.20	monomer	BLAST	X-ray	1.50Å	0.40	0.89	Cellular retinoic acid-binding protein 2
4qgx.1.A	39.20	monomer	BLAST	X-ray	1.47Å	0.40	0.89	Cellular retinoic acid-binding protein 2
1lpj.1.A	36.72	monomer	BLAST	X-ray	2.00Å	0.38	0.91	Retinol-binding protein IV, cellular
1ggl.1.A	31.82	monomer	HHblits	X-ray	2.31Å	0.35	0.94	PROTEIN (CELLULAR RETINOL-BINDING PROTEIN III)
1ggl.2.A	31.82	monomer	HHblits	X-ray	2.31Å	0.35	0.94	PROTEIN (CELLULAR RETINOL-BINDING PROTEIN III)
4qgw.1.A	39.20	monomer	BLAST	X-ray	1.77Å	0.40	0.89	Cellular retinoic acid-binding protein 2
4qgw.2.A	39.20	monomer	BLAST	X-ray	1.77Å	0.40	0.89	Cellular retinoic acid-binding protein 2
3fa7.1.A	39.20	monomer	BLAST	X-ray	1.90Å	0.40	0.89	Cellular retinoic acid-binding protein 2
3fa7.2.A	39.20	monomer	BLAST	X-ray	1.90Å	0.40	0.89	Cellular retinoic acid-binding protein 2
3f9d.1.A	38.40	monomer	BLAST	X-ray	2.00Å	0.39	0.89	Cellular retinoic acid-binding protein 2
3f9d.2.A	38.40	monomer	BLAST	X-ray	2.00Å	0.39	0.89	Cellular retinoic acid-binding protein 2
3fel.1.A	38.40	monomer	BLAST	X-ray	1.85Å	0.39	0.89	Cellular retinoic acid-binding protein 2
3fel.2.A	38.40	monomer	BLAST	X-ray	1.85Å	0.39	0.89	Cellular retinoic acid-binding protein 2
3fa8.1.A	38.40	monomer	BLAST	X-ray	1.78Å	0.39	0.89	Cellular retinoic acid-binding protein 2
3fa8.2.A	38.40	monomer	BLAST	X-ray	1.78Å	0.39	0.89	Cellular retinoic acid-binding protein 2
3fa9.1.A	38.40	monomer	BLAST	X-ray	1.94Å	0.39	0.89	Cellular retinoic acid-binding protein 2
3fa9.2.A	38.40	monomer	BLAST	X-ray	1.94Å	0.39	0.89	Cellular retinoic acid-binding protein 2
3f8a.1.A	39.20	monomer	BLAST	X-ray	1.95Å	0.39	0.89	Cellular retinoic acid-binding protein 2
1cbr.1.A	40.00	homo-dimer	BLAST	X-ray	2.90Å	0.39	0.89	CELLULAR RETINOIC ACID BINDING PROTEIN TYPE I
1cbi.1.A	40.00	homo-dimer	BLAST	X-ray	2.70Å	0.39	0.89	CELLULAR RETINOIC ACID BINDING PROTEIN I
1cbi.1.B	40.00	homo-dimer	BLAST	X-ray	2.70Å	0.39	0.89	CELLULAR RETINOIC ACID BINDING PROTEIN I
2cbr.1.A	40.00	monomer	BLAST	X-ray	2.80Å	0.39	0.89	PROTEIN (CRABP-I)
3d95.1.A	37.60	monomer	BLAST	X-ray	1.20Å	0.39	0.89	Cellular retinoic acid-binding protein 2



Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
3d95.2.A	37.60	monomer	BLAST	X-ray	1.20Å	0.39	0.89	Cellular retinoic acid-binding protein 2
3cwk.1.A	37.60	monomer	BLAST	X-ray	1.60Å	0.39	0.89	Cellular retinoic acid-binding protein 2
1ggl.1.A	34.38	monomer	BLAST	X-ray	2.31Å	0.37	0.91	PROTEIN (CELLULAR RETINOL-BINDING PROTEIN III)
1ggl.2.A	34.38	monomer	BLAST	X-ray	2.31Å	0.37	0.91	PROTEIN (CELLULAR RETINOL-BINDING PROTEIN III)
3fa6.1.A	37.60	monomer	BLAST	X-ray	1.54Å	0.39	0.89	Cellular retinoic acid-binding protein 2
3fa6.2.A	37.60	monomer	BLAST	X-ray	1.54Å	0.39	0.89	Cellular retinoic acid-binding protein 2
3fek.2.A	37.60	monomer	BLAST	X-ray	1.51Å	0.39	0.89	Cellular retinoic acid-binding protein 2
3fek.1.A	37.60	monomer	BLAST	X-ray	1.51Å	0.39	0.89	Cellular retinoic acid-binding protein 2
4m7m.1.A	37.60	monomer	BLAST	X-ray	2.57Å	0.39	0.89	Cellular retinoic acid-binding protein 2
4i9s.1.A	37.60	monomer	BLAST	X-ray	2.58Å	0.39	0.89	Cellular retinoic acid-binding protein 2
4m6s.1.A	37.60	monomer	BLAST	X-ray	2.47Å	0.39	0.89	Cellular retinoic acid-binding protein 2
4i9r.1.A	37.60	monomer	BLAST	X-ray	2.60Å	0.39	0.89	Cellular retinoic acid-binding protein 2
5h8t.1.A	32.31	monomer	HHblits	X-ray	1.21Å	0.36	0.93	Retinol-binding protein 1
5h9a.1.A	32.31	monomer	HHblits	X-ray	1.38Å	0.36	0.93	Retinol-binding protein 1
5hbs.1.A	32.31	monomer	HHblits	X-ray	0.89Å	0.36	0.93	Retinol-binding protein 1
4ybp.1.A	36.80	monomer	BLAST	X-ray	1.83Å	0.39	0.89	Cellular retinoic acid-binding protein 2
2rct.1.A	33.08	monomer	HHblits	X-ray	1.20Å	0.36	0.93	Retinol-binding protein II, cellular
5faz.1.A	33.33	monomer	HHblits	X-ray	1.40Å	0.36	0.92	Retinol-binding protein 2
5faz.2.A	33.33	monomer	HHblits	X-ray	1.40Å	0.36	0.92	Retinol-binding protein 2
1mx7.1.A	33.33	monomer	BLAST	NMR	NA	0.36	0.92	CELLULAR RETINOL-BINDING PROTEIN I, APO
1mx8.1.A	33.33	monomer	BLAST	NMR	NA	0.36	0.92	CELLULAR RETINOL-BINDING PROTEIN I, HOLO
1crb.1.A	33.33	monomer	BLAST	X-ray	2.10Å	0.36	0.92	CELLULAR RETINOL BINDING PROTEIN
1kgl.1.A	33.33	monomer	BLAST	NMR	NA	0.36	0.92	CELLULAR RETINOL-BINDING PROTEIN TYPE I
1jbh.1.A	33.33	monomer	BLAST	NMR	NA	0.36	0.92	CELLULAR RETINOL-BINDING PROTEIN TYPE I
1kqx.1.A	31.30	monomer	HHblits	X-ray	1.70Å	0.35	0.94	Cellular retinol-binding protein
1kqw.1.A	31.30	monomer	HHblits	X-ray	1.38Å	0.35	0.94	Cellular retinol-binding protein
4yfp.1.A	36.80	monomer	BLAST	X-ray	1.95Å	0.39	0.89	Cellular retinoic acid-binding protein 2
4exz.1.A	33.33	monomer	HHblits	X-ray	1.61Å	0.36	0.92	Retinol-binding protein 2
4exz.2.A	33.33	monomer	HHblits	X-ray	1.61Å	0.36	0.92	Retinol-binding protein 2
4ruu.1.A	33.33	monomer	HHblits	X-ray	1.40Å	0.36	0.92	Retinol-binding protein 2
4ruu.2.A	33.33	monomer	HHblits	X-ray	1.40Å	0.36	0.92	Retinol-binding protein 2
5f58.1.A	33.33	monomer	HHblits	X-ray	1.54Å	0.36	0.92	Retinol-binding protein 2
5f58.2.A	33.33	monomer	HHblits	X-ray	1.54Å	0.36	0.92	Retinol-binding protein 2
1kqx.1.A	35.71	monomer	BLAST	X-ray	1.70Å	0.38	0.90	Cellular retinol-binding protein
1kqw.1.A	35.71	monomer	BLAST	X-ray	1.38Å	0.38	0.90	Cellular retinol-binding protein
4zj0.1.A	33.33	monomer	HHblits	X-ray	1.50Å	0.36	0.92	Retinol-binding protein 2
4zj0.2.A	33.33	monomer	HHblits	X-ray	1.50Å	0.36	0.92	Retinol-binding protein 2
4zr2.1.B	33.33	homo-dimer	HHblits	X-ray	1.80Å	0.36	0.92	Retinol-binding protein 2
4zr2.1.A	33.33	homo-dimer	HHblits	X-ray	1.80Å	0.36	0.92	Retinol-binding protein 2
2a0a.1.A	30.71	monomer	BLAST	NMR	NA	0.37	0.91	Der f 13
4zh6.1.A	33.33	homo-dimer	HHblits	X-ray	1.55Å	0.36	0.92	Retinol-binding protein 2
5dg4.3.A	33.33	monomer	HHblits	X-ray	1.50Å	0.36	0.92	Retinol-binding protein 2
5dg4.4.A	33.33	monomer	HHblits	X-ray	1.50Å	0.36	0.92	Retinol-binding protein 2
5f6b.1.A	32.56	monomer	HHblits	X-ray	1.31Å	0.36	0.92	Retinol-binding protein 2
5f6b.2.A	32.56	monomer	HHblits	X-ray	1.31Å	0.36	0.92	Retinol-binding protein 2

Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
1mx7.1.A	32.56	monomer	HHblits	NMR	NA	0.36	0.92	CELLULAR RETINOL-BINDING PROTEIN I, APO
1mx8.1.A	32.56	monomer	HHblits	NMR	NA	0.36	0.92	CELLULAR RETINOL-BINDING PROTEIN I, HOLO
1crb.1.A	32.56	monomer	HHblits	X-ray	2.10Å	0.36	0.92	CELLULAR RETINOL BINDING PROTEIN
5ffh.1.A	32.56	monomer	HHblits	X-ray	1.68Å	0.36	0.92	Retinol-binding protein 2
5fen.1.A	32.56	monomer	HHblits	X-ray	1.55Å	0.36	0.92	Retinol-binding protein 2
5fen.2.A	32.56	monomer	HHblits	X-ray	1.55Å	0.36	0.92	Retinol-binding protein 2
5ljd.1.A	33.86	monomer	BLAST	X-ray	1.61Å	0.37	0.91	Retinol-binding protein 1
4qzu.3.A	33.59	monomer	HHblits	X-ray	1.50Å	0.36	0.91	Retinol-binding protein 2
4qyn.2.A	33.59	monomer	HHblits	X-ray	1.19Å	0.36	0.91	Retinol-binding protein 2
4qzt.2.A	33.59	monomer	HHblits	X-ray	1.90Å	0.36	0.91	Retinol-binding protein 2
4qzu.4.A	33.59	monomer	HHblits	X-ray	1.50Å	0.36	0.91	Retinol-binding protein 2
4zh9.1.B	33.59	homo-dimer	HHblits	X-ray	2.66Å	0.36	0.91	Retinol-binding protein 2
5faz.1.A	37.10	monomer	BLAST	X-ray	1.40Å	0.38	0.89	Retinol-binding protein 2
5faz.2.A	37.10	monomer	BLAST	X-ray	1.40Å	0.38	0.89	Retinol-binding protein 2
5lje.1.A	33.86	monomer	BLAST	X-ray	1.40Å	0.37	0.91	Retinol-binding protein 1
5ljb.1.A	33.86	monomer	BLAST	X-ray	1.26Å	0.37	0.91	Retinol-binding protein 1
5h8t.1.A	33.86	monomer	BLAST	X-ray	1.21Å	0.37	0.91	Retinol-binding protein 1
5h9a.1.A	33.86	monomer	BLAST	X-ray	1.38Å	0.37	0.91	Retinol-binding protein 1
5hbs.1.A	33.86	monomer	BLAST	X-ray	0.89Å	0.37	0.91	Retinol-binding protein 1
4zgu.2.A	33.59	monomer	HHblits	X-ray	1.49Å	0.36	0.91	Retinol-binding protein 2
4zcb.1.B	33.59	homo-dimer	HHblits	X-ray	1.70Å	0.36	0.91	Retinol-binding protein 2
4zcb.1.A	33.59	homo-dimer	HHblits	X-ray	1.70Å	0.36	0.91	Retinol-binding protein 2
4zgu.1.A	33.59	monomer	HHblits	X-ray	1.49Å	0.36	0.91	Retinol-binding protein 2
4zgu.4.A	33.59	monomer	HHblits	X-ray	1.49Å	0.36	0.91	Retinol-binding protein 2
4efg.1.A	31.78	monomer	HHblits	X-ray	1.58Å	0.35	0.92	Retinol-binding protein 2
4eej.1.A	31.78	monomer	HHblits	X-ray	1.50Å	0.35	0.92	Retinol-binding protein 2
5f7g.1.A	32.81	monomer	HHblits	X-ray	1.48Å	0.36	0.91	Retinol-binding protein 2
4yko.1.A	36.59	monomer	BLAST	X-ray	1.57Å	0.39	0.88	Cellular retinoic acid-binding protein 2
5ljc.1.A	33.86	monomer	BLAST	X-ray	1.43Å	0.36	0.91	Retinol-binding protein 1
4ede.1.A	31.78	monomer	HHblits	X-ray	1.40Å	0.35	0.92	Retinol-binding protein 2
4ede.2.A	31.78	monomer	HHblits	X-ray	1.40Å	0.35	0.92	Retinol-binding protein 2
4ykm.1.A	37.40	monomer	BLAST	X-ray	1.58Å	0.39	0.88	Cellular retinoic acid-binding protein 2
4exz.1.A	37.10	monomer	BLAST	X-ray	1.61Å	0.38	0.89	Retinol-binding protein 2
4exz.2.A	37.10	monomer	BLAST	X-ray	1.61Å	0.38	0.89	Retinol-binding protein 2
4ruu.1.A	37.10	monomer	BLAST	X-ray	1.40Å	0.38	0.89	Retinol-binding protein 2
4ruu.2.A	37.10	monomer	BLAST	X-ray	1.40Å	0.38	0.89	Retinol-binding protein 2
5f58.1.A	37.10	monomer	BLAST	X-ray	1.54Å	0.38	0.89	Retinol-binding protein 2
5f58.2.A	37.10	monomer	BLAST	X-ray	1.54Å	0.38	0.89	Retinol-binding protein 2
5dpq.1.A	32.81	homo-dimer	HHblits	X-ray	1.78Å	0.36	0.91	Retinol-binding protein 2
5dpq.1.B	32.81	homo-dimer	HHblits	X-ray	1.78Å	0.36	0.91	Retinol-binding protein 2
1t8v.1.A	29.46	monomer	HHblits	NMR	NA	0.35	0.92	Fatty acid-binding protein, intestinal
4zj0.1.A	37.10	monomer	BLAST	X-ray	1.50Å	0.38	0.89	Retinol-binding protein 2
4zj0.2.A	37.10	monomer	BLAST	X-ray	1.50Å	0.38	0.89	Retinol-binding protein 2
4zr2.1.B	37.10	homo-dimer	BLAST	X-ray	1.80Å	0.38	0.89	Retinol-binding protein 2
4zr2.1.A	37.10	homo-dimer	BLAST	X-ray	1.80Å	0.38	0.89	Retinol-binding protein 2
4gkc.1.A	32.03	monomer	HHblits	X-ray	1.30Å	0.35	0.91	Retinol-binding protein 2
5fen.1.A	36.29	monomer	BLAST	X-ray	1.55Å	0.38	0.89	Retinol-binding protein 2
5fen.2.A	36.29	monomer	BLAST	X-ray	1.55Å	0.38	0.89	Retinol-binding protein 2
4qzu.3.A	36.29	monomer	BLAST	X-ray	1.50Å	0.38	0.89	Retinol-binding protein 2

Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
4qyn.2.A	36.29	monomer	BLAST	X-ray	1.19Å	0.38	0.89	Retinol-binding protein 2
4qzt.2.A	36.29	monomer	BLAST	X-ray	1.90Å	0.38	0.89	Retinol-binding protein 2
4qzu.4.A	36.29	monomer	BLAST	X-ray	1.50Å	0.38	0.89	Retinol-binding protein 2
4zh9.1.B	36.29	homo-dimer	BLAST	X-ray	2.66Å	0.38	0.89	Retinol-binding protein 2
2rct.1.A	36.29	monomer	BLAST	X-ray	1.20Å	0.38	0.89	Retinol-binding protein II, cellular
5f6b.1.A	36.29	monomer	BLAST	X-ray	1.31Å	0.38	0.89	Retinol-binding protein 2
5f6b.2.A	36.29	monomer	BLAST	X-ray	1.31Å	0.38	0.89	Retinol-binding protein 2
4zh6.1.A	36.29	homo-dimer	BLAST	X-ray	1.55Å	0.38	0.89	Retinol-binding protein 2
5dg4.3.A	36.29	monomer	BLAST	X-ray	1.50Å	0.38	0.89	Retinol-binding protein 2
5dg4.4.A	36.29	monomer	BLAST	X-ray	1.50Å	0.38	0.89	Retinol-binding protein 2
5ffh.1.A	36.29	monomer	BLAST	X-ray	1.68Å	0.38	0.89	Retinol-binding protein 2
5f7g.1.A	36.29	monomer	BLAST	X-ray	1.48Å	0.38	0.89	Retinol-binding protein 2
3akn.1.A	28.68	monomer	HHblits	X-ray	1.60Å	0.35	0.92	Fatty acid-binding protein, intestinal
1ael.1.A	28.68	monomer	HHblits	NMR	NA	0.35	0.92	FATTY ACID-BINDING PROTEIN
1ure.1.A	28.68	monomer	HHblits	NMR	NA	0.35	0.92	INTESTINAL FATTY ACID-BINDING PROTEIN
1ifb.1.A	28.68	monomer	HHblits	X-ray	1.96Å	0.35	0.92	INTESTINAL FATTY ACID BINDING PROTEIN
1ifc.1.A	28.68	monomer	HHblits	X-ray	1.19Å	0.35	0.92	INTESTINAL FATTY ACID BINDING PROTEIN
4zgu.2.A	36.29	monomer	BLAST	X-ray	1.49Å	0.38	0.89	Retinol-binding protein 2
4zcb.1.B	36.29	homo-dimer	BLAST	X-ray	1.70Å	0.38	0.89	Retinol-binding protein 2
4zcb.1.A	36.29	homo-dimer	BLAST	X-ray	1.70Å	0.38	0.89	Retinol-binding protein 2
4zgu.1.A	36.29	monomer	BLAST	X-ray	1.49Å	0.38	0.89	Retinol-binding protein 2
4zgu.4.A	36.29	monomer	BLAST	X-ray	1.49Å	0.38	0.89	Retinol-binding protein 2
5dpq.1.A	35.48	homo-dimer	BLAST	X-ray	1.78Å	0.38	0.89	Retinol-binding protein 2
5dpq.1.B	35.48	homo-dimer	BLAST	X-ray	1.78Å	0.38	0.89	Retinol-binding protein 2
1icn.1.A	27.91	monomer	HHblits	X-ray	1.74Å	0.34	0.92	INTESTINAL FATTY ACID BINDING PROTEIN
1dc9.1.A	28.68	monomer	HHblits	X-ray	2.10Å	0.34	0.92	INTESTINAL FATTY ACID BINDING PROTEIN
4gkc.1.A	35.48	monomer	BLAST	X-ray	1.30Å	0.37	0.89	Retinol-binding protein 2
4efg.1.A	35.48	monomer	BLAST	X-ray	1.58Å	0.37	0.89	Retinol-binding protein 2
4eej.1.A	35.48	monomer	BLAST	X-ray	1.50Å	0.37	0.89	Retinol-binding protein 2
4ede.1.A	35.48	monomer	BLAST	X-ray	1.40Å	0.37	0.89	Retinol-binding protein 2
4ede.2.A	35.48	monomer	BLAST	X-ray	1.40Å	0.37	0.89	Retinol-binding protein 2
2mo5.1.A	26.36	monomer	HHblits	NMR	NA	0.34	0.92	Fatty acid-binding protein, intestinal
1kzx.1.A	26.36	monomer	HHblits	NMR	NA	0.34	0.92	INTESTINAL FATTY ACID-BINDING PROTEIN (T54)
3akm.1.A	26.36	monomer	HHblits	X-ray	1.90Å	0.34	0.92	Fatty acid-binding protein, intestinal
1kzw.1.A	26.36	monomer	HHblits	NMR	NA	0.34	0.92	INTESTINAL FATTY ACID-BINDING PROTEIN (A54)
3ifb.1.A	26.36	monomer	HHblits	NMR	NA	0.34	0.92	INTESTINAL FATTY ACID BINDING PROTEIN
2mji.1.A	26.36	monomer	HHblits	NMR	NA	0.34	0.92	Fatty acid-binding protein, intestinal
1t8v.1.A	34.15	monomer	BLAST	NMR	NA	0.37	0.88	Fatty acid-binding protein, intestinal
3akm.1.A	27.56	monomer	BLAST	X-ray	1.90Å	0.35	0.91	Fatty acid-binding protein, intestinal
1kzw.1.A	27.56	monomer	BLAST	NMR	NA	0.35	0.91	INTESTINAL FATTY ACID-BINDING PROTEIN (A54)
3ifb.1.A	27.56	monomer	BLAST	NMR	NA	0.35	0.91	INTESTINAL FATTY ACID BINDING PROTEIN
2mji.1.A	27.56	monomer	BLAST	NMR	NA	0.35	0.91	Fatty acid-binding protein, intestinal
1kzx.1.A	27.56	monomer	BLAST	NMR	NA	0.35	0.91	INTESTINAL FATTY ACID-BINDING PROTEIN (T54)

Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
1icn.1.A	33.33	monomer	BLAST	X-ray	1.74Å	0.37	0.88	INTESTINAL FATTY ACID BINDING PROTEIN
1ifc.1.A	33.33	monomer	BLAST	X-ray	1.19Å	0.37	0.88	INTESTINAL FATTY ACID BINDING PROTEIN
3akn.1.A	33.33	monomer	BLAST	X-ray	1.60Å	0.37	0.88	Fatty acid-binding protein, intestinal
1ael.1.A	33.33	monomer	BLAST	NMR	NA	0.37	0.88	FATTY ACID-BINDING PROTEIN
1ure.1.A	33.33	monomer	BLAST	NMR	NA	0.37	0.88	INTESTINAL FATTY ACID-BINDING PROTEIN
1ifb.1.A	33.33	monomer	BLAST	X-ray	1.96Å	0.37	0.88	INTESTINAL FATTY ACID BINDING PROTEIN
1ftp.1.A	37.50	homo-dimer	BLAST	X-ray	2.20Å	0.39	0.86	MUSCLE FATTY ACID BINDING PROTEIN
1dc9.1.A	33.33	monomer	BLAST	X-ray	2.10Å	0.37	0.88	INTESTINAL FATTY ACID BINDING PROTEIN
5b0u.1.A	21.54	monomer	HHblits	X-ray	1.71Å	0.32	0.93	Oplophorus-luciferin 2-monooxygenase catalytic subunit
5b0u.2.A	21.54	monomer	HHblits	X-ray	1.71Å	0.32	0.93	Oplophorus-luciferin 2-monooxygenase catalytic subunit
5ibo.1.A	21.54	monomer	HHblits	X-ray	1.95Å	0.32	0.93	Oplophorus-luciferin 2-monooxygenase catalytic subunit
5ibo.2.A	21.54	monomer	HHblits	X-ray	1.95Å	0.32	0.93	Oplophorus-luciferin 2-monooxygenase catalytic subunit
2mo5.1.A	28.23	monomer	BLAST	NMR	NA	0.35	0.89	Fatty acid-binding protein, intestinal
2qo5.1.A	29.60	monomer	HHblits	X-ray	1.50Å	0.34	0.89	Liver-basic fatty acid binding protein
2qo6.1.A	29.60	monomer	HHblits	X-ray	1.90Å	0.34	0.89	Liver-basic fatty acid binding protein
2qo4.1.A	29.60	monomer	HHblits	X-ray	1.50Å	0.34	0.89	Liver-basic fatty acid binding protein
1mdc.1.A	22.48	monomer	HHblits	X-ray	1.75Å	0.31	0.92	INSECT FATTY ACID BINDING PROTEIN
1p6p.1.A	25.60	monomer	HHblits	X-ray	2.50Å	0.33	0.89	Fatty acid-binding protein, liver
2ft9.1.A	25.60	monomer	HHblits	X-ray	2.50Å	0.33	0.89	Fatty acid-binding protein 2, liver
2ftb.1.A	25.60	monomer	HHblits	X-ray	2.00Å	0.33	0.89	Fatty acid-binding protein 2, liver
1tw4.1.A	28.00	monomer	HHblits	X-ray	2.00Å	0.33	0.89	Fatty acid-binding protein
1zry.1.A	28.00	monomer	HHblits	NMR	NA	0.33	0.89	Fatty acid-binding protein, liver
1mvq.1.A	28.00	monomer	HHblits	NMR	NA	0.33	0.89	Liver basic Fatty Acid Binding Protein
1tvq.1.A	28.00	monomer	HHblits	X-ray	2.00Å	0.33	0.89	Fatty acid-binding protein
2k62.1.A	28.00	monomer	HHblits	NMR	NA	0.33	0.89	Liver fatty acid-binding protein
2jn3.1.A	28.00	monomer	HHblits	NMR	NA	0.33	0.89	Fatty acid-binding protein, liver
2lba.1.A	24.60	monomer	HHblits	NMR	NA	0.33	0.90	BABP protein
2lfo.1.A	28.00	monomer	HHblits	NMR	NA	0.33	0.89	Fatty acid-binding protein, liver
2n93.1.A	25.20	monomer	HHblits	NMR	NA	0.32	0.91	Fatty acid-binding protein
1eio.1.A	25.40	monomer	HHblits	NMR	NA	0.32	0.90	ILEAL LIPID BINDING PROTEIN
1eal.1.A	25.40	monomer	HHblits	NMR	NA	0.32	0.90	ILEAL LIPID BINDING PROTEIN
3em0.1.A	28.00	monomer	HHblits	X-ray	2.20Å	0.32	0.89	Ileal Bile Acid-Binding Protein
3em0.2.A	28.00	monomer	HHblits	X-ray	2.20Å	0.32	0.89	Ileal Bile Acid-Binding Protein
3elx.1.A	28.00	monomer	HHblits	X-ray	1.60Å	0.32	0.89	Ileal bile acid-binding protein
3elz.1.A	28.00	monomer	HHblits	X-ray	2.20Å	0.32	0.89	ileal Bile Acid-Binding Protein
3elz.3.A	28.00	monomer	HHblits	X-ray	2.20Å	0.32	0.89	ileal Bile Acid-Binding Protein
1o1v.1.A	23.81	monomer	HHblits	NMR	NA	0.31	0.90	Gastrotropin
1o1u.1.A	23.81	monomer	HHblits	NMR	NA	0.31	0.90	Gastrotropin
2mm3.1.A	23.81	monomer	HHblits	NMR	NA	0.31	0.90	Gastrotropin
5l8i.1.A	23.81	monomer	HHblits	X-ray	1.88Å	0.31	0.90	Gastrotropin
5l8i.2.A	23.81	monomer	HHblits	X-ray	1.88Å	0.31	0.90	Gastrotropin
5l8i.3.A	23.81	monomer	HHblits	X-ray	1.88Å	0.31	0.90	Gastrotropin
2f73.1.A	22.22	monomer	HHblits	X-ray	2.50Å	0.30	0.90	Fatty acid-binding protein, liver

Template	Seq Identity	Oligo-state	Found by	Method	Resolution	Seq Similarity	Coverage	Description
2f73.2.A	22.22	monomer	HHblits	X-ray	2.50Å	0.30	0.90	Fatty acid-binding protein, liver
2ju8.1.A	20.80	monomer	HHblits	NMR	NA	0.31	0.89	Fatty acid-binding protein, liver
2ju3.1.A	20.80	monomer	HHblits	NMR	NA	0.31	0.89	Fatty acid-binding protein, liver
2ju7.1.A	20.80	monomer	HHblits	NMR	NA	0.31	0.89	Fatty acid-binding protein, liver
1fo.1.A	20.80	monomer	HHblits	X-ray	2.30Å	0.31	0.89	LIVER FATTY ACID BINDING PROTEIN
3stm.1.A	22.40	monomer	HHblits	X-ray	2.22Å	0.31	0.89	Fatty acid-binding protein, liver
3stn.1.A	22.40	monomer	HHblits	X-ray	2.60Å	0.31	0.89	Fatty acid-binding protein, liver
2lkk.1.A	22.40	monomer	HHblits	NMR	NA	0.31	0.89	Fatty acid-binding protein, liver
2l67.1.A	22.40	monomer	HHblits	NMR	NA	0.31	0.89	Fatty acid-binding protein, liver
2l68.1.A	22.40	monomer	HHblits	NMR	NA	0.31	0.89	Fatty acid-binding protein, liver
2py1.1.A	22.40	monomer	HHblits	NMR	NA	0.31	0.89	Fatty acid-binding protein, liver
1a57.1.A	26.32	monomer	HHblits	NMR	NA	0.33	0.81	INTESTINAL FATTY ACID-BINDING PROTEIN
1sa8.1.A	25.96	monomer	HHblits	NMR	NA	0.34	0.74	Fatty acid-binding protein, intestinal
2qo5.1.A	32.26	monomer	BLAST	X-ray	1.50Å	0.35	0.66	Liver-basic fatty acid binding protein
2ft9.1.A	27.96	monomer	BLAST	X-ray	2.50Å	0.34	0.66	Fatty acid-binding protein 2, liver
2ftb.1.A	27.96	monomer	BLAST	X-ray	2.00Å	0.34	0.66	Fatty acid-binding protein 2, liver
2qo6.1.A	32.58	monomer	BLAST	X-ray	1.90Å	0.35	0.64	Liver-basic fatty acid binding protein
2qo4.1.A	32.58	monomer	BLAST	X-ray	1.50Å	0.35	0.64	Liver-basic fatty acid binding protein
2lfo.1.A	32.58	monomer	BLAST	NMR	NA	0.35	0.64	Fatty acid-binding protein, liver
1tw4.1.A	32.58	monomer	BLAST	X-ray	2.00Å	0.35	0.64	Fatty acid-binding protein
1zry.1.A	32.58	monomer	BLAST	NMR	NA	0.35	0.64	Fatty acid-binding protein, liver
1mvg.1.A	32.58	monomer	BLAST	NMR	NA	0.35	0.64	Liver basic Fatty Acid Binding Protein
1tvq.1.A	32.58	monomer	BLAST	X-ray	2.00Å	0.35	0.64	Fatty acid-binding protein
2k62.1.A	32.58	monomer	BLAST	NMR	NA	0.35	0.64	Liver fatty acid-binding protein
2jn3.1.A	32.58	monomer	BLAST	NMR	NA	0.35	0.64	Fatty acid-binding protein, liver
1x4r.1.A	10.64	monomer	HHblits	NMR	NA	0.28	0.34	Parp14 protein
3jah.20.A	27.91	monomer	HHblits	EM	NA	0.35	0.31	eL22
3jaj.14.A	27.91	monomer	HHblits	EM	NA	0.35	0.31	Ribosomal protein eL22
3j79.1.X	21.43	hetero-oligomer	HHblits	EM	NA	0.32	0.30	60S ribosomal protein eL22
4pww.1.A	22.50	homo-dimer	HHblits	X-ray	1.47Å	0.31	0.29	OR494
5kph.1.A	21.88	monomer	HHblits	NMR	NA	0.31	0.23	De novo Beta Sheet Design Protein OR485
2mo5.1.A	15.63	monomer	HHblits	NMR	NA	0.30	0.23	Fatty acid-binding protein, intestinal
1t8v.1.A	18.75	monomer	HHblits	NMR	NA	0.30	0.23	Fatty acid-binding protein, intestinal
3q6l.1.A	25.81	monomer	HHblits	X-ray	1.40Å	0.31	0.22	Fatty acid-binding protein, adipocyte
3akn.1.A	19.35	monomer	HHblits	X-ray	1.60Å	0.30	0.22	Fatty acid-binding protein, intestinal
1ael.1.A	19.35	monomer	HHblits	NMR	NA	0.30	0.22	FATTY ACID-BINDING PROTEIN
1ure.1.A	19.35	monomer	HHblits	NMR	NA	0.30	0.22	INTESTINAL FATTY ACID-BINDING PROTEIN
1ifb.1.A	19.35	monomer	HHblits	X-ray	1.96Å	0.30	0.22	INTESTINAL FATTY ACID BINDING PROTEIN
1kzx.1.A	16.13	monomer	HHblits	NMR	NA	0.30	0.22	INTESTINAL FATTY ACID-BINDING PROTEIN (T54)
5ji4.1.A	30.43	monomer	HHblits	NMR	NA	0.35	0.16	W37
4r80.1.A	25.00	monomer	HHblits	X-ray	2.45Å	0.35	0.14	OR486
4r80.2.A	25.00	monomer	HHblits	X-ray	2.45Å	0.35	0.14	OR486