

## Report on PDB Structure 1ama

► [Genome Occurrence.](#)

Domain d1ama\_.

No additional domains.

Genome	Aful	Mjan	Mthe	Phor	Scer	Cele	Aaao	Syne	Ecol	Bsub	Mtub	Hinf	Hpyl	Mgen	Mpne	Bbur	Tpal	Ctra	Cpne	Rpro
<b>Fold</b>	18	16	15	18	32	40	19	23	36	43	33	15	9	2	2	3	5	8	10	5
<b>Superfamily</b>	18	16	15	18	32	40	19	23	36	43	33	15	9	2	2	3	5	8	10	5

► [Alignments.](#)

Domain d1ama\_.

No additional domains.

	# Pairs	untrimmed RMS	trimmed RMS	%sequence identity	structure p-value	sequence p-value
<b>Fold</b>	28	5.53	1.54	26.40	3.87e-23	6.42e-01
<b>Superfamily</b>	28	5.53	1.54	26.40	3.87e-23	6.42e-01
<b>Family</b>	6	2.00	0.43	48.66	1.57e-44	2.17e-68
<b>Fold only</b>	0	.	.	.	.	.
<b>Sfam only</b>	18	6.77	2.04	17.90	6.03e-23	1

► [Motions](#)

Protein	Motions	Database ID	Movies
	Aspartate Amino Transferase (AAT)	aat	

► [Function Classification](#)

Domain d1ama\_.

No additional domains.

	Augmented Flybase+ENZYME	GenProtEC	MIPS
d1ama_	E-2.6.1.1	3.1.04	01.01.01

► Core Structure does not exist for d1ama.

► [Rankings](#)

Domain d1ama\_.

No additional domains.

OCCURRENCES

Species	20	Aful	Mjan	Mthe	Phor	Scer	Cele	Aaao	Syne	Ecol	Bsub	Mtub	Hinf	Hpyl	Mgen	Mpne	Bbu
Number	352	18	16	15	18	32	40	19	23	36	43	33	15	9	2	2	3
Rank	14	11	7	7	7	14	38	8	10	8	5	14	9	9	21	25	25
%ile	96	92	94	94	93	93	84	95	95	96	97	93	95	94	78	75	80

ALIGNMENTS

	Aligned Pairs	Untrimmed RMS	Trimmed RMS	% Seq Identity	Structure P-Value	Sequence
FOLD	28	5.53	1.54	26.40	3.87e-23	6.42e-01