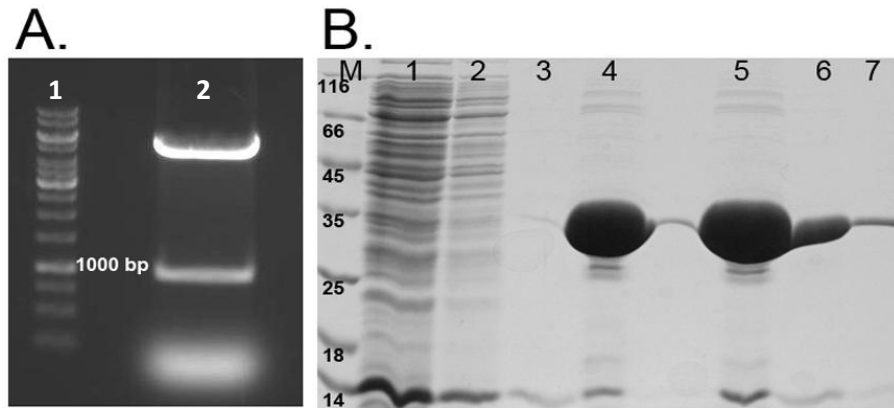


Supplementary data

Supplementary figure 1



Cloning of LdOASS gene and affinity purification of the protein. (A) DNA ladder was run in lane 1. Double digest of pET21c containing LdOASS construct with NdeI and NotI was run in lane 2. The fallout corresponds to 976 base pairs. (B) Lane M: molecular weight markers (kDa), lane 1 : flow through, lane 2 : wash, lanes 3-7: Ni-NTA purified fractions

Supplementary figure 2.

```

LdoOASS      --MAAPFDKSKNVAQSIDQLIGQTFALYLNKLN-----TKAKVVLKMECENPMASVKDR 53
EhoOASS      MEQISISSPRKRIYHNILETIGGTFPLVELHGVTEHPRIKKGTRILVKLEYFNPMSVKDR 60
TmoOASS      -----MMERLIGSTPIVRLDSID-----SRIFLKLEKNNPGGSVKDR 37
MtbOASS      -----MSIAEDITQLIGRTPLVRLRRVTDG----AVADIVAKLEFFNPANSVKDR 46
AtoOASS      -----MASRIAKDVTELI GNTPLVYLNNVAEG----CVGRVAAKLEMMEPCSSVKDR 48
StoOASS      -----SKIYEDNSLTIGHTPLVRLNLRIG-----NGRILAKVESRNPFSFSVKCR 43
HioOASS      -----MAIYADNSYSIGNTFLVRLKHFH-----NGNVVVKIEGRNPSYSVKCR 44
                ** ** : * . : * : * : * ** *

LdoOASS      LGFAIYDKAEKEGKLI PGKSI VVESSSGNTGVSLAHLGAIRGYKVIITMPESMSLERRCL 113
EhoOASS      VGFNIVYQAIKDGRLKPGM-EIESTSGNTGIALCQAGAVFGYRVNIAMPSTMSVERQMI 119
TmoOASS      PALFMILDAEKRGLLKNG---IVEPTSGNMGIAIAMI GAKRGHRVILTMPETMSVERRKV 94
MtbOASS      IGVAMLQAAEQAGLIKPD T-IILEPTSGNTGIALAMVCAARGYRCVLTMPETMSLERRML 105
AtoOASS      IGFSMISDAEKKGLIKPGESVLEIPTSNTGVGLAFTAAAKGYKLIITMPASMSTERRII 108
StoOASS      IGANMIWDAEKRGVLPKGV-ELVEPTNGNTGIALAYVAAARGYKLTITMPETMSLERKRL 102
HioOASS      IGANMVWQAEKDGTLTKGK-EIVDATSGNTGIALAYVAAARGYKLTITMPETMSLERRRL 103
                . : * : * : . : : : . ** * : : . * * : : : ** : ** * : :

LdoOASS      LRIFGAEVILTPAALGMKGAVAMAKKIVAANPN-AVLADQFATKYNALIHEETTGP EIW E 172
EhoOASS      MKAFGAELILTEGKKGMPGAIEEVNKMIKENPGKYFVANQFGNPDNTAAHHTAN-EIWE 178
TmoOASS      LKMLGAELVLTPEGLMKGAVEKALEISRETG--AHMLNQFENPNVNYSHQFTTGP EILK 152
MtbOASS      LRAYGAELILTPGADGMSGAIKAEELAKTDQR-YFVPOQFENPANPAIHRVTTAEVVR 164
AtoOASS      LLAFGVELVLTDPAKGMKGAIAKAEIILAKTPNGY-MLQQFENPANPKIHETTGP EIW K 167
StoOASS      LKALGANLVLTGAKGMKGAIQKAEIIVASDPQYLLQLQFNSNPANPEIHEKTTGP EIW E 162
HioOASS      LCGLGVNLVLTGAKGMKGAIAKAEIIVASDPSRYVMLKQFENPANPQIHRETTGP EIW K 163
                : * : : : ** ** * : . : : : : . ** . * * * : * : .

LdoOASS      QTNHNVD CFIAGVGTGGTTLTGVARALK-KMGS-HARIVAVEPTESPVLSGG-----KPG 224
EhoOASS      DTDGEVDIVVSAVGTSGTIVIGVAEKLKEKKKG--IKIIAVEPEESAVLEGK-----AKG 230
TmoOASS      QMDYQIDAFVAGVGTGGTISGVGRVLRKGGFFGN-GVKIVAVEPAKSPVLSGG-----QPG 205
MtbOASS      DTDGKVDIVVAGVGTGGTITGVAQVIKERKES--ARFVAVEPAASPVLSGG-----QKG 216
AtoOASS      GTGGKIDGFVSGIGTGGTITGAGKYLKEQNAN--VKLYGVEPVESAILSGG-----KPG 219
StoOASS      DTDGQVDVVISGVGTGGTITGVTRYIKGKTKGKTDLITVAVEPTDSPVIAQALAGEEIKPG 222
HioOASS      DTDGKVDVVVAGVGTGGTITGSRKIDLFCK-QITSVAVEPVESPVISQTLAGEEVKPG 222
                . : : * . : : : ** * : : * . : * : . ** * * : : *

LdoOASS      PHKIQQIGIGGFVPPVLDLRSIIDEVLCVAGDDAIE TALKL TRSDGVFCGFSGGANVYAAALK 284
EhoOASS      PHGIQQIGAGFIPDIYKKEFVDEIPIKTDQAWKMARAVVKYDGMCGMSSGAAI LAGLK 290
TmoOASS      KHAIQQIGAGFVPKILD RSVIDEVITVEDEEAYEMARYLAKKEGLLVGISSGANVAAALK 265
MtbOASS      PHPIQQIGAGFVPPVLDQLDVEIITVGNEDALNVARRLAREEGLLVGISSGAATVAALQ 276
AtoOASS      PHKIQQIGAGFIPSVLNVDLIDEVYQVSSDESIDMARQLALKEGLLVGISSGAAAAAIK 279
StoOASS      PHKIQQIGAGFIPGNLDLKLIDKVVGITNEEAISTARRLMEEEGILAGISSGA AVAAALK 282
HioOASS      PHKIQQIGAGFIPKLNLDLSIIDRVETVDSDTALATARRLM AEEGILAGISSGA AVAAADR 282
                * ***** * : * . : : : * : : : * : : * : * : * * . :

LdoOASS      IAERPMEGKTIVTVIPSFGERYLSTTLYRSVRDEVSSLP----- 324
EhoOASS      EAKEPNEGKTIVII VPSCGERYLSTDLYKIKDEGTKIQILDSLLNE 337
TmoOASS      VAQKLGPDAR-VVTVPADHAERYLSIL----- 291
MtbOASS      VARRPENAGKLIVVLPDFGERYLSTPLFADVAD----- 310
AtoOASS      LAQRPENAGKLFVAIFPSFGERYLSTVLFDATRKEAEAMTFEA---- 322
StoOASS      LQEDESFTNKNIVVILPSSGERYLSTALFADLFTEKELQQ----- 322
HioOASS      LAKLPEFADKLIVVILPSSASERYLSTALFEGIEG----- 316
                . : * : * . *****

```

Amino acid alignment of OASS from *L. donovani* with those of *E. histolytica* (Eh), *T. maritima* (Tm), *A. thaliana* (At), *M. tuberculosis* (Mtb), *S. typhimurium* (St) and *H. influenza* (Hi). Sequences highlighted in green indicate the consensus amino acid residues of the pyridoxal phosphate-binding motif and active site lining amino acids known to be important for binding the co-factor, PLP and substrates. The lysines important for sulfhydrylase activity are highlighted in orange. The red boxes indicate $\beta 8$ - $\beta 9$ loop at the entrance of the active site. The positively charged residues involved in binding with SAT are highlighted in blue. The sequence highlighted in pink corresponds to the N-terminal variable loop from where maximum structural differences start.

Supplementary figure 3

<i>Arabidopsis thaliana</i>	-DYVI	471.1Å ²
<i>Mycobacterium tuberculosis</i>	-DFSI	449.0Å ²
<i>Hemophilus influenzae</i>	-NLNI	452.3Å ²
<i>Escherichia coli</i>	-DYII	488.0Å ²
<i>Entamoeba histolytica</i>	-SPSI	381.9Å ²
<i>Leishmania donovani</i>	-GSGI	328.0Å ²
<i>Brucella abortus</i>	-GDGI	341.9Å ²
Designed peptides	}	DWSI 480.8Å ²
		DYSI 453.1Å ²

C-terminal ends of SATs from various organisms and their corresponding surface area
The last two peptides were designed and showed strong binding with LdOASS

Supplementary table 1

S.NO:	PEPTIDES	GLIDE_SCORE	GOLD_SCORE	CVDW
1	DWSI	-12.61	86.33	-68.1
2	DYSI	-12.23	80.8	-64.2
3	DFSI	-11.62	94.76	-63.7
4	DTTI	-10.96	73.41	-66.5
5	DPTI	-10.9	75.15	-62

Ranking of peptides mimicking C-terminal sequence of SAT on the basis of different binding energies and interactions with LdOASS structure

Supplementary table 2

Peptide	% inhibition
1) DPTI	45.7±3
2) DTTI	37.3±2
3) DFSI	48.8±2
4) DYSI	52.9±2
5) DWSI	54.6±1
6) LERDGSGI(derived from LdSAT)	48.8±4

Inhibition of EhOASS with peptides mimicking the SAT C-terminal sequences.

Supplementary table 3

Interactions with DWSI								Interactions with DGSGI									
Protein atom				Ligand atom				distance	Protein atom				Ligand atom				distance
LLP A	51	NZ	<>	2407	CG2	ILE	4	3.93	LLP A	51	NZ	<>	2406	OXT	ILE	5	3.69
SER A	78	O	<>	2409	O	ILE	4	4.37	SER A	78	O	<>	2405	O	ILE	5	4.66
SER A	79	OG	<>	2409	O	ILE	4	2.69	SER A	79	OG	<>	2405	O	ILE	5	2.79
SER A	80	OG	<>	2399	OG	SER	3	3.08	SER A	80	OG	<>	2394	N	GLY	4	3.04
GLY A	81	C	<>	2410	OXT	ILE	4	3.55	GLY A	81	C	<>	2406	OXT	ILE	5	3.56
ASN A	82	N	<>	2410	OXT	ILE	4	3.17	ASN A	82	N	<>	2406	OXT	ILE	5	3.10
THR A	83	N	<>	2410	OXT	ILE	4	2.95	THR A	83	N	<>	2406	OXT	ILE	5	2.86
GLY A	84	N	<>	2410	OXT	ILE	4	4.78	GLY A	84	N	<>	2406	OXT	ILE	5	4.88
ARG A	110	NH2	<>	2399	OG	SER	3	3.04	MET A	106	CE	<>	2385	CA	GLY	2	4.40
LEU A	128	O	<>	2379	OD2	ASP	1	4.98	MET A	130	CG	<>	2390	CB	SER	3	3.16
GLY A	129	CA	<>	2379	OD2	ASP	1	3.38	GLN A	152	NE2	<>	2405	O	ILE	5	2.99
MET A	130	N	<>	2379	OD2	ASP	1	2.94	PHE A	153	CZ	<>	2403	CG2	ILE	5	3.92
LYS A	131	N	<>	2379	OD2	ASP	1	4.69	GLY A	186	CA	<>	2402	CD1	ILE	5	3.99
VAL A	134	CG2	<>	2393	CZ2	TRP	2	4.37	THR A	187	CG2	<>	2403	CG2	ILE	5	4.06
GLN A	152	NE2	<>	2409	O	ILE	4	2.97	GLY A	224	O	<>	2381	OD2	ASP	1	4.03
PHE A	153	CZ	<>	2391	CZ3	TRP	2	3.78	PRO A	225	CA	<>	2381	OD2	ASP	1	3.14
GLY A	186	CA	<>	2406	CD1	ILE	4	3.83	HIS A	226	N	<>	2381	OD2	ASP	1	2.93
THR A	187	CG2	<>	2407	CG2	ILE	4	4.10	LYS A	227	O	<>	2383	O	ASP	1	4.52
PRO A	225	CB	<>	2374	N	ASP	1	4.74	ILE A	228	O	<>	2376	N	ASP	1	4.43
HIS A	226	NE2	<>	2384	CB	TRP	2	4.45	GLN A	229	CG	<>	2397	O	GLY	4	3.70
GLN A	229	C	<>	2401	O	SER	3	3.82	GLY A	230	N	<>	2397	O	GLY	4	3.14
GLY A	230	N	<>	2401	O	SER	3	2.75	ILE A	231	O	<>	2402	CD1	ILE	5	3.90
ILE A	231	C	<>	2406	CD1	ILE	4	4.03	GLY A	232	C	<>	2402	CD1	ILE	5	4.34
GLY A	232	O	<>	2384	CB	TRP	2	3.47	PRO A	233	CA	<>	2402	CD1	ILE	5	3.84
PRO A	233	O	<>	2387	NE1	TRP	2	3.19									
GLY A	234	N	<>	2386	CD1	TRP	2	4.89									
PHE A	235	CE2	<>	2393	CZ2	TRP	2	4.36									

List of contacts generated through GetNeares for interaction between the peptides DWSI and DGSGI.