

## Supplementary File S1– Sequence identity and peptide sequences of spherule-surface proteins.

### CSP5N2\_COCP7 (100%), 26,142.0 Da

Sod\_Cu domain-containing protein OS=Coccidioides posadasii (strain C735) OX=222929 GN=CPC735\_033580 PE=4 SV=1  
10 exclusive unique peptides, 20 exclusive unique spectra, 36 total spectra, 49/248 amino acids (20% coverage)

M H A K S L L A F T	S L L S A G F A A A	Q T G R <b>L G D A D V</b>	<b>T V G N S P A V V Y</b>	E A E L L D K N N T
N F R G T V L V S G	S S D G V G V I Y N	V N F T G F P P F G	G P F L Y H V H D Q	P V P E N G D C L G
T L A H L D P Y E R	<b>G E M P K C D P S R</b>	<b>P Q T C Q V G D L S</b>	<b>G K F G D I E G V N</b>	G S F S F Q Q Y H
D P Y S S V T Y G L	G S F V G N R S I V	V H F A N T T R I N	<b>C G N F T L K E I R</b>	P G S R G L P C N G
R F C P N S P S G S	M S V P V P T T T S	P P T F E G D A A K	V S V M S A T G V L	A A L I G L L W

**Peptide sequences:** (R)LGDADVTVGNSPA(V); (R)LGDADVTVGNSPAVY(E);

(R)LGDADVTVGNSPAVYEA(E); (R)GEMPKCDPSRPQTQVQGDLSGK(F); (K)CDPSRPQT(C);

(K)CDPSRPQT(C); (K)CDPSRPQTQ(V); (K)CDPSRPQTQVQGDLSGK(F);

(C)DPSRPQTQVQGDLSGK(F); (R)INCQNTLKEIR(E);

### Cu<sup>2+</sup>/Zn<sup>2+</sup> superoxide dismutase

NCBI Sequence ID ABB36775.1 (248 aa)

1 mhaksllaft sllsagfaaa qtgrlgdad tvgnspavvy eaelldknnt nfrgtvlvsg  
61 ssdvgvgviyn vnftgfppfg gpflyhvhdq pvpengdclg tlahldpyer gempkcdpsr  
121 pqtcqvgdls gkfgdiegvn gsfsfqqqyh dpyssvtygl gsfvgnrsiv vhfantrin  
181 cgnftlkeir pgsgrlpcng rfcpnspsgs msdpvpsttts pptfegdaak vsymsatgvl  
241 aaligllw

### CSP1H6\_COCP7 (100%), 26,378.8 Da

Uncharacterized protein OS=Coccidioides posadasii (strain C735) OX=222929 GN=CPC735\_056990 PE=4 SV=1  
5 exclusive unique peptides, 6 exclusive unique spectra, 6 total spectra, 42/231 amino acids (18% coverage)

M H L A S I L T C L	L A A T V S V S A S	P G S E R T Q K R P	S L A V P R C P R K	<b>A T A S F D K S V P</b>
E M K A F P N T Q V	D L C W E P T A F Q	F T F K <b>A F D E T N</b>	<b>F Y F D P K H R T N</b>	D D I W K Y E V M E
A F I Y H G T N D P	Q T Y F E F E V S P	N N V T Y Q T F V Y	N P S K V R K E G A	P F D H F F V S D P
A A D G F T S I T T	L D R <b>K A Q T W V S</b>	<b>E V K I P L A L F N</b>	<b>V D R P R L S R W R</b>	M N F F R T V T S P
A T Y P N Q E L G A	W N S P D V A S F H	V T P F F G D V I L	V	

**Peptide sequences:** (R)KATASF(S); (K)AFDETNYFDPK(H); (R)KAQTWVSEVK(I);  
(K)AQTWVSEVK(I); (K)IPLALFNVDPR(L)

### DOMON-like type 9 carbohydrate-binding module

NCBI Sequence ID AEB21190.1 (231 aa)

1 mhlasiltcl laatvsas pgsertqkrp slavprcprk atasfdksvp emkafpntqv  
61 dlcweptafq ftfkafdetn fyfdpkhrtn ddiwkyevme afiyhgtnp qtyfefevsp  
121 nnvtyqtfvy npskvrkega pfhdffvsdp aadgftsitt ldrkaqtwvs evkiplalfn  
181 vdrprlsrwr mnffrtvtsp atypnqelga wnsdpvasfh vtpffgdvil v

### CSP9L1\_COCP7 (100%), 43,558.2 Da

Aspartyl proteinase OS=Coccidioides posadasii (strain C735) OX=222929 GN=CPC735\_005950 PE=3 SV=1  
3 exclusive unique peptides, 3 exclusive unique spectra, 3 total spectra, 43/399 amino acids (11% coverage)

M R N S I L L A A T	V L L G C T S A K V	H K L K L K K L P L	T E Q L E Y G D I E	T H V R A L G Q K Y
F G S L P S S Q Q Q	T V L S D E Y S T T	G G H N V L V D N F	L N A Q Y F S E I S	I G N P P Q N F K V
V L D T G S S N L W	V P S S E C G S I A	C Y L H N K <b>Y D S S</b>	<b>A S S T Y K K N G T</b>	E F A I R Y G S G S
<b>L S G F V S Q D T L</b>	<b>R I G D L T I E G Q</b>	D F A E A T N E P G	L A F A F G R <b>F D G</b>	<b>I L G L G Y D T I S</b>
<b>V N K I V P P F Y N</b>	M I N E G L I D E P	V F G F Y L G D T N	K E G D D S Y A T F	G G V D S S L F S G
E M I K I P L R R K	A Y W E V D F D A I	A F G N E R A E L E	D T G I I L D T G T	S L I A L P S T L A
E L L N R E I G A K	K S W N G Q Y T V D	C N K R P S L P D L	T F T L S G H N F T	I G P Y D L E V
Q G S C I S S F M G	M D F P E P V G P L	A I L G D A F L R R	F Y T M Y D L G N N	L V G L A K A G N

**Peptide sequences:** (K)YDSSASSTYKK(N); (R)YGSGSLSGFVSQDTLR(I); (R)FDGILGLGYDTISVNK(I)

## Aspartyl proteinase

NCBI Sequence ID QVM08509.1 (399 aa)

1 mrnsillaat vllgctsakov hklklkkpl teqleygdie thvralgqky fgsipssqqq  
61 tvlsdeystt gghnvlvdnf lnaqyfseis ignppqnfkv vldtgssnlw vpssecgsia  
121 cylhnkydss asstykkngt efairygsgs lsgfvsqdtl rigdltiegq dfaeatnepg  
181 lafafgrfdg ilglgydtis vnkivppfyn mineglidep vfgfylgdtm kegddsyatf  
241 ggvdsslifsg emikiplrrk aywevdfdai afgneraele dtgiildtgt slialpstla  
301 ellnreigak kswngqytvd cnkrpslpdl tftlsghnft igpydyilev qgscissfmq  
361 mdfpepgpl ailgdaflrr fytmydlgnv lvglakagn

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CSPAFO\_COCOP7 (100%), 56,919.7 Da

alpha-1,2-Mannosidase OS=Coccidioides posadasii (strain C735) OX=222929 GN=CPC735\_008870 PE=3 SV=1  
2 exclusive unique peptides, 2 exclusive unique spectra, 2 total spectra, 28/519 amino acids (5% coverage)

M K G S P V L A V C	A A A L T L I P S V	V A L P M I D K D L	P S S I S Q S S D K	T S Q E R A E A V K
D A F R F A W E G Y	L E H A F P N D E L	H P V S N T P G N S	R N G W G A S A V D	A L S T A I I M D M
P D V V E K I L D H	I S N I D Y S Q T D	T M C S L F E T T I	R Y L G G M I S A Y	D L L K G P G S H L
V S D P A K V D V L	L A Q S L K L A D V	L K F A F D T K T G	I P A N E L N I T D	K S T D G S T T N G
L A T T G T L V L E	W T R L S D I T G D	P E Y G R L A Q K G	E S Y L L N P Q P S	S S E P F P G L V G
R T I D I E T G L F	R D D Y V S W G G G	S D S F Y E Y L I K	M Y V Y D K G R F G	K Y K D R W V T A A
E S T I E H L K S S	P S T R K D L T F V	A T Y S G G R L G L	N S G H L T C F D G	G N F L L G G Q I L
N R D D F T K F G L	E L V E G C Y A T Y	A A T A T K I G P E	G F G W D A T K V P	E A Q A E F Y K E A
G F Y I T T S Y Y N	L R P E V I E S I Y	Y A Y R M T K D P K	Y Q E W A W D A F V	A I N A T T R T S T
G F T A I G D V N T	P D G G R K Y D N Q	E S F L F A E V M K	Y S Y L I H S P E A	D W Q V A G P G G T
N A Y V F N T E A H	P V K V F S R G C			

Peptide sequences: (R)TSTGFTAIGDVNTPDGGR(K); (Y)VFNTEAHPVK(V)

## Mannosyl-oligosaccharide alpha-1,2-mannosidase

NCBI Sequence ID E9CXX8.1 (519 aa)

1 mkgspvlavc aaaltlipsv valpmidkdl pssisqssdk tsqeraeavk aafrfawegy  
61 lehafpndel hpsntpgns rngwgasavd alstaiimdm pdvvekildh isnidysqtd  
121 tmcslfetti rylggmisay dkkpgpgshl vsdpakvdv laqslkladv lkfafdtktg  
181 ipanelnitz kstdgsttng lattgtlvle wtrlsditgd peygrlaqkg esyllnpqps  
241 ssepfpvg lg rtidietglf rddyvswggg sdsfyeylik myvydkgrfg kykdrwvtaa  
301 estiehlkss pstrkdltfv atyssgrlgl nsghltcfdg gnflggqil nrddftkfgl  
361 elvegcyaty aatatkigpe gfgwdatkvp eaqaefykea gfyittsyn lrpeviesiy  
421 yayrmtkdpk yqewawdafv ainattrst gftaigdvnt pdggrkydnq esflfaevmk  
481 ysylhspea dwqvagpggt nayvnateah pkvvsrgc