



STRUCTURAL BIOLOGY
COMMUNICATIONS

Volume 71 (2015)

Supporting information for article:

Crystallographic analysis of the N-terminal domain of *Middle East respiratory syndrome coronavirus* nucleocapsid protein

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Detailed Protein Report

Project Info

Name: ZBA LCMS 2015

Date:

January 9, 2015

Sample Info & Protocols

Name: 150312

Date: March 16, 2015

Search Result Info

Search Result

HCT_bacteria_NCBI_Mascot_2015-03-16 11:33:37 /ZBA LCMS 2015/150312/7713_C3_01_29121.D Mascot, 2.4.1 NCBIInr, NCBIInr_20150224.fasta 17/551

Protein 1: ectoine synthase [Sphingopyxis alaskensis]

Accession: gi|499862486

Database: NCBIInr

Seq. Coverage [%]: 78.80 %

Score:

MW [kDa]:

pI:

No. of Peptides:

564.94

15.10

5.14

14

Modification(s): Oxidation

10	20	30	40	50	60	70	80	90	100	110	120
MIVRNLGDIR	KTRDRNVRSDG	WASARMLLRD	DGMGFSFHV	TLFAGSELRM	HYQNHLEAVL	VLKGTGTIED	LATGEVHALR	PGVMYALDDH	DRHIVRPETD	ILTACVFNPF	VTGREVHDES
130	140										
GAYPADPELA	REPVAAD										

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
93	1	408.2000	-98.78	2	12.1	35.4	1	5-11	R.NLGDIRK.T	
130	1	609.7000	-167.83	2	13.6	48.9	1	15-25	R.NVRSDGWASAR.M	
126	1	425.2000	9.13	2	13.3	64.6	0	18-25	R.SDGWASAR.M	
478	1	891.4000	-50.73	3	26.0	51.5	1	26-49	R.MLLKDDGMGFSFHVTTTFAGSEL.R.M	
512	1	896.7000	-85.70	3	27.4	42.1	1	26-49	R.MLLKDDGMGFSFHVTTTFAGSEL.R.M	Oxidation: 8
505	1	902.4000	323.14	3	27.0	67.5	1	26-49	R.MLLKDDGMGFSFHVTTTFAGSEL.R.M	Oxidation: 1, 8
507	1	730.0000	442.17	3	27.0	64.5	0	30-49	K.DDGMGFSFHVTTTFAGSEL.R.M	
473	1	735.0000	-12.24	3	25.9	39.7	0	30-49	K.DDGMGFSFHVTTTFAGSEL.R.M	Oxidation: 4
313	2	847.9000	-66.01	2	19.5	66.9	0	50-63	R.MHYQNHLEAVLVK.G	
297	1	855.9000	-62.42	2	18.9	53.9	0	50-63	R.MHYQNHLEAVLVK.G	Oxidation: 1
359	1	580.6000	-61.32	3	21.2	38.6	0	64-80	K.GTGTIEDLATGEVHALR.P	
204	1	702.7000	-162.57	2	15.8	82.4	0	81-92	R.PGVMYALDDHDR.H	Oxidation: 4
211	1	928.3000	-136.24	2	16.1	73.9	0	115-131	R.EVHDESGAYPADPELAR.E	
271	1	813.3000	-92.29	3	17.9	22.3	1	115-137	R.EVHDESGAYPADPELAREPVAAD.-	

Protein 2: ferritin [Escherichia coli]

Accession: gi|446191906

Database: NCBIInr

Seq. Coverage [%]: 13.50 %

Score:

MW [kDa]:

pI:

No. of Peptides:

112.72

20.00

4.62

3

10	20	30	40	50	60	70	80	90	100	110	120
MWSTIMLKPE	MIEKLNQMN	LELYSSLLYQ	QMSAWCSYHT	FEGAAFLRR	HAQEEMTHMQ	RLFDYLDTDG	NLPRINTVES	PFAEYSSIDE	LFQETVKHEQ	LITQKINELA	HAAMTNDQYP
130	140	150	160	170	180						
TFNFLQWYVS	EQHEREKLFK	SIIDKLSLAG	KSGEGLYFID	KELSTLDTQN							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
71	1	389.2000	46.37	4	11.0	38.2	1	50-61	R.RHAQEEMTHMQR.L	
77	1	466.5000	-85.33	3	11.4	48.4	0	51-61	R.HAQEEMTHMQR.L	
329	1	382.2000	-94.32	3	20.1	26.2	1	141-151	K.SIIDKLSLAG.S	

ProteinScape 3.0

Printed:

March 16, 2015

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