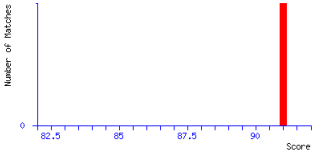


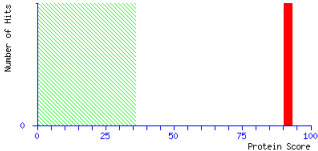
User : Lily-mascot
E-mail : l.r.adair@pgr.reading.ac.uk
Search title : K_pneumoniae_VIM1_9470_Da
MS data file : K_pneumoniae_VIM1_9470_Da.mgf
Databases : 1: contaminants 20160129 (247 sequences; 128,130 residues)
2: Trembl_22_05_2024 22_05_2024_2024_02 (248,234,451 sequences; 87,367,689,973 residues)
Taxonomy : 1: (none)
2: Bacteria (Eubacteria) (158,221,737 sequences)
Timestamp : 21 Jul 2025 at 11:54:48 GMT

▼Search parameters
Type of search : MS/MS Ion Search
Enzyme : NoCleave
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein mass : Unrestricted
Peptide mass tolerance : ± 20 ppm
Fragment mass tolerance : ± 0.2 Da
Max missed cleavages : 0
Instrument type : MALDI-QIT-TOF
Number of queries : 1

▼Score distribution



Peptide score distribution. Ions score is $-10 \log(P)$, where P is the probability that the observed match is a random event. There is 1 peptide match above identity threshold and 1 match above homology threshold for 1 queries. On average, individual ions scores > 36 (beyond green shading) indicate identity or extensive homology ($p < 0.05$).



[Deprecated] Protein score distribution. Score distribution for family members in the first 50 proteins. Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein families.

▼Legend

Peptide columns and rows

Dupes	...	Expect	Rank	U	1	2	Peptide	
		0.037	▶	1			GAYLSLR	significant
		9	▶	1			GFLFVEGGR	top ranking
		6.4e-05	▶	1			GSSIFGLAPGK	significant and top ranking
		1.3e-06	▶	1	■		SSGTSYPDVLYK	peptide is found in all proteins in family member 1
		6.2e-07	▶	1	■		VCNYVSWIK	peptide is found in some but not all proteins in family member 2
		6.4e-05	▶	1	U		GSSIFGLAPGK	unique
▶	2	5.7e-05	▶	1			LNTLETEEWFFK	peptide has two duplicates
		0.18	▶	1			LNTLETEEWFFK	duplicate peptide

Right-facing triangle (▶) in the Dupes or Rank column indicates content that can be expanded by clicking on it. Down-facing triangle (▼) indicates the content is expanded and can be collapsed. For more details about particular columns, see [results format help](#).

Protein quantitation ratios

	Score	...	114/113	115/113
CFAH_HUMAN	37559		0.962	1.129
FHR2_HUMAN	1330		0.859	1.128

When quantitation method is Reporter (e.g. iTRAQ) or Multiplex (e.g. iPTL), protein ratios are displayed when a family is expanded. Ratios in *italic* indicate that the peptide log-ratios do not appear to come from a normal distribution. **Bold** indicates that if you can assume peptide ratios are normally distributed, the protein ratio is significantly different from 1.0 (at significance level 0.05).

Note that lack of bold or italic can also mean that significance or normality testing has not been performed (for example, if protein ratio type does not support it).

Protein Family Summary

Significance threshold p< Max. number of families
Target FDR (overrides sig. threshold) (not set) ▼ FDR type
Display non-sig. matches ☐ Min. number of sig. unique sequences
Dendrograms cut at
Preferred taxonomy

▼Sensitivity and FDR (reversed protein sequences)

	Target	Decoy	FDR
Protein family members	1	0	0.00% Not enough decoy protein hits for a meaningful FDR calculation.
Sequences above homology	1	0	0.00% Not enough decoy matches above significance threshold for a meaningful FDR calculation.

Decoy results are available in [the decoy report](#).

Protein family 1 (out of 1)

10 per page 1

▼1	2::A0A08616S5_KLEPN			92	DNA-binding protein HU-alpha OS=Klebsiella pneumoniae OX=573 GN=hupA PE=3 SV=1
1.1	2::A0A08616S5_KLEP	Score	Mass	Matches	Sequences
		92	9471	1 (1)	1 (1)
	DNA-binding protein HU-alpha OS=Klebsiella pneumoniae OX=573 GN=hupA PE=3 SV=1				
	▼47 same sets of 2::A0A08616S5_KLEPN				
	2::A0A087FL90_KLEV	92	9471	1 (1)	1 (1)
	DNA-binding protein HU-alpha OS=Klebsiella varicola OX=244366 GN=hupA PE=3 SV=1				
	2::A0A094Z8D9_KLEA	92	9471	1 (1)	1 (1)
	DNA-binding protein HU-alpha OS=Klebsiella aerogenes OX=548 GN=hupA PE=3 SV=1				
	2::A0A0D5WX15_9EN	92	9471	1 (1)	1 (1)
	DNA-binding protein HU-alpha OS=Klebsiella michiganensis OX=1134687 GN=hupA PE=3 SV=1				
	2::A0A0E1CLK0_KLEP	92	9471	1 (1)	1 (1)
	DNA-binding protein HU-alpha OS=Klebsiella pneumoniae 30660/NIST258_1 OX=1420012 GN=KPN01_05215 PE=3 SV=1				
	2::A0A0H3FPC6_KLEF	92	9471	1 (1)	1 (1)
	DNA-binding protein HU-alpha OS=Klebsiella aerogenes (strain ATCC 13048 / DSM 30053 / CCUG 1429 / JCM 1235 / KCTC 2190 / NBRC 13534 / NCIMB 10102 / NCTC 10006 / CDC 819-56) OX=1028307 GN=EAE_08210 PE=3 SV=1				
	2::A0A0H3GLR9_KLEI	92	9471	1 (1)	1 (1)
	DNA-binding protein HU-alpha OS=Klebsiella pneumoniae subsp. pneumoniae (strain HS11286) OX=1125630 GN=KPHS_02190 PE=3 SV=1				
	2::A0A1C1E1B3_9ENT	92	9471	1 (1)	1 (1)
	DNA-binding protein HU-alpha OS=Klebsiella quasipneumoniae OX=1463165 GN=hupA PE=3 SV=1				
	2::A0A1F2M4C4_9EN	92	9471	1 (1)	1 (1)
	DNA-binding protein HU-alpha OS=Klebsiella sp. HMSC16C06 OX=1581110 GN=HMPREF3142_11150 PE=3 SV=1				
	2::A0A1X7M486_9EN	92	9471	1 (1)	1 (1)
	DNA-binding protein HU-alpha OS=Cedecea sp. NFIX57 OX=1566286 GN=SAMN03159353_104127 PE=3 SV=1				
	2::A0A223UHP4_9EN	92	9471	1 (1)	1 (1)
	DNA-binding protein HU-alpha OS=Klebsiella quasivariicola OX=2026240 GN=hupA PE=3 SV=1				
	2::A0A291E476_9ENT	92	9471	1 (1)	1 (1)
	DNA-binding protein HU-alpha OS=Cedecea neteri OX=158822 GN=hupA PE=3 SV=1				

	Score	Mass	Matches	Sequences
2::A0A2P8VEF7_9ENI	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Sicobacter turicensis OX=357233 GN=C7G83_19460 PE=3 SV=1				
2::A0A259UBK4_CRO	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Cronobacter sakazakii OX=28141 GN=hupA PE=3 SV=1				
2::A0A2T7AQJ6_9ENI	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Cronobacter mytjensii OX=413501 GN=AUN14_15325 PE=3 SV=1				
2::A0A2T7BSA5_9ENI	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Cronobacter turicensis OX=413502 GN=BS411_10565 PE=3 SV=1				
2::A0A2W0U2V0_KLE	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Klebsiella pneumoniae subsp. pneumoniae OX=72407 GN=hupA PE=3 SV=1				
2::A0A376DYE1_9ENI	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Cronobacter universalis NCTC 9529 OX=1074000 GN=hupA PE=3 SV=1				
2::A0A377YXW0_KLE	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Klebsiella pneumoniae subsp. ozaenae OX=574 GN=hupA PE=3 SV=1				
2::A0A3Q9U9E9_9ENI	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Klebsiella sp. LY OX=2015795 GN=CE636_16405 PE=3 SV=1				
2::A0A3S4MHA5_9EN	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Cedecea lapagel OX=158823 GN=hupA PE=3 SV=1				
2::A0A4P8YFQ2_9ENI	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Jejubacter calystegiae OX=2579935 GN=hupA PE=3 SV=1				
2::A0A4R3ZHY6_9ENI	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Raoultella sp. B1G0138 OX=248515 GN=EDF73_12034 PE=3 SV=1				
2::A0A6B8MMU0_KLE	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Klebsiella oxytoca OX=571 GN=hupA PE=3 SV=1				
2::A0A6H1FMK6_9EN	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Cedecea sp. FDAARGOS_727 OX=2545798 GN=hupA PE=3 SV=1				
2::A0A7H0MJB2_9ENI	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Kosakonia sp. SMBL-WEM22 OX=2725560 GN=hupA PE=3 SV=1				
2::A0A7U2ZR01_9ENI	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Klebsiella africana OX=2489010 GN=hupA PE=3 SV=1				
2::A0A806XRQ6_9ENI	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=[Enterobacter] lignolyticus OX=1334193 GN=A0703_01140 PE=3 SV=1				
2::A0A807L905_9ENI	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Kosakonia cowanii JCM 10956 = DSM 18146 OX=1300165 GN=BW195_00665 PE=3 SV=1				
2::A0A844CG21_9ENI	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Enterobacteriaceae bacterium RIT693 OX=2666197 GN=hupA PE=3 SV=1				
2::A0A850FBL2_9ENI	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Enterobacteriaceae bacterium BIT-123 OX=2742797 GN=hupA PE=3 SV=1				
2::A0A9P1KIT4_9ENI	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Klebsiella quasipneumoniae subsp. quasipneumoniae OX=1667327 GN=hupA PE=3 SV=1				
2::A0A9Q2DMC0_9ENI	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Klebsiella sp. Kos OX=2758579 GN=hupA PE=3 SV=1				
2::A0A9Q4T8Q3_9ENI	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Cronobacter dublinensis OX=413497 GN=EH13_21645 PE=3 SV=1				
2::A0A9W5J5W1_9EN	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Enterobacter sp. Ag1 OX=1202448 GN=A936_17526 PE=3 SV=1				
2::A0AA90GVY2_9ENI	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Kosakonia sp. HypNH10 OX=2980101 GN=hupA PE=4 SV=1				
2::W1DNP4_KLEPN	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Klebsiella pneumoniae IS43 OX=1432552 PE=3 SV=1				
2::E3G343_ENTLS	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Enterobacter lignolyticus (strain SCF1) OX=701347 GN=Entcl_4159 PE=3 SV=1				
2::S3J8I5_9ENTR	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Cedecea davisae DSM 4568 OX=566551 GN=HMPREF0201_00033 PE=3 SV=1				
2::B5XYD8_KLEP3	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Klebsiella pneumoniae (strain 342) OX=507522 GN=hupA PE=3 SV=1				
2::VSU491_9ENTR	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Cronobacter malonicus OX=413503 GN=C3E80_19780 PE=3 SV=1				
2::A6TGG7_KLEPZ	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578) OX=272620 GN=hupA PE=3 SV=1				
2::A7M187_CROSB	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Cronobacter sakazakii (strain ATCC BAA-894) OX=290339 GN=ESA_03673 PE=3 SV=1				
2::K7ZYZ6_9ENTR	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Cronobacter condimenti 1330 OX=1073999 GN=BN137_723 PE=3 SV=1				
2::K8CI34_CROSK	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Cronobacter sakazakii 701 OX=1208663 GN=BN129_3674 PE=3 SV=1				
2::K8DFI3_CROSK	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Cronobacter sakazakii 696 OX=1208664 GN=BN128_3575 PE=3 SV=1				
2::WRVDD5_KLEPN	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Klebsiella pneumoniae 30684/NIST258_2 OX=1420013 GN=KPNJ2_00441 PE=3 SV=1				
2::C9XT66_CROTZ	92	9471	1 (1)	1 (1)
DNA-binding protein HU-alpha OS=Cronobacter turicensis (strain DSM 18703 / CCUG 55852 / LMG 23827 / z3032) OX=693216 GN=hupA PE=3 SV=1				

▼ 1 peptide matches (1 non-duplicate, 0 duplicate)

Query	Dupes	Observed	Mr (expt)	Mr (calc)	ppm	M	Score	Expect	Rank	U	Peptide
1		9472.2678	9471.2605	9471.1467	12.0	0	92	1.5e-07	1	U	-, MNKTQLIDVIADKADLSKAQAKAALESTLAAITESLKEGDVQLVGFQTFVNHRAERTGRNPQTGREIKIAAANVPAPVSGKALKDAVK, -

Protein View: A0A08616S5_KLEPN

DNA-binding protein HU-alpha OS=Klebsiella pneumoniae OX=573 GN=hupA PE=3 SV=1

Detailed information about this protein hit is shown below. (help)

Database: Trembl_22_05_2024
Score: 92
Monoisotopic mass (M1): 9471
Calculated pI: 9.57
Taxonomy: Klebsiella pneumoniae

Sequence similarity is available as an NCBI BLAST search of A0A08616S5_KLEPN against nr.

Search parameters

MS data file: K_pneumoniae_YIM1_9470_Da.mgf
Enzyme: NoCleave: cuts C-term side of J unless next residue is ABCDEFGHIKLMNOPQRSTUVWXYZ.
Variable modifications: Oxidation (M)

Protein sequence coverage: 100%

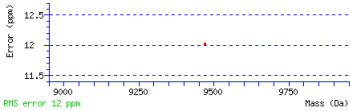
Matched peptides shown in bold red.

1 MNKTQLIDVI ADKADLSKAQ AKAALESTLA AITESLKEGD AVQLVGFOTF
51 KVNHRAERTG RNPQTGKEIK TAAANVPAPV SGKALKDAVK

Unformatted sequence string: 90 residues (for pasting into other applications).

Sort by residue number increasing mass decreasing mass
Show matched peptides only predicted peptides also

Table with 12 columns: Query, Start, End, Observed, Mr(expt), Mr(calc), ppm, M, Score, Expect, Rank, U, Peptide. Row 1: 1, 1, 90, 9472.2678, 9471.2605, 9471.1467, 12.0, 0, 92, 1.5e-07, 1, U, -MNKTQLIDVIADKADLSKAQAKAALESTLAAITESLKEGDVAVQLVGFOTFKVNHRAERTGRNPQTGKEIKTAAANVPAPVSGKALKDAVK.-



ID A0A08616S5_KLEPN Unreviewed; 90 AA.
AC A0A08616S5; A0A0J2G3Y5; A0A4V0HJ07;
DT 29-OCT-2014, integrated into UniProtKB/TrEMBL.
DT 29-OCT-2014, sequence version 1.
DT 18-JUN-2025, entry version 87.
DE RecName: Full=DNA-binding protein HU-alpha (ECO:0000256|ARBA:ARBA00039360);
DE AltName: Full=HU-2 (ECO:0000256|ARBA:ARBA00041400);
DE AltName: Full=NS2 (ECO:0000256|ARBA:ARBA00031534, ECO:0000256|ARBA:ARBA00032034);
GN Name=hupA (ECO:0000313|EMBL:SKN34013.1);
GN ORFNames=B5196_09065 (ECO:0000313|EMBL:OVF74521.1), B6168_29260
GN (ECO:0000313|EMBL:PLE24172.1), BANRA_01515
GN (ECO:0000313|EMBL:VCV74244.1), BL124_00009465
GN (ECO:0000313|EMBL:ROG99069.1), CP554_24130
GN (ECO:0000313|EMBL:FVU60120.1), DM078_26290
GN (ECO:0000313|EMBL:RBZ17003.1), DW286_26715
GN (ECO:0000313|EMBL:ROT85044.1), E1814_24765
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GN (ECO:0000313|EMBL:QOU51607.1), GJJ18_24480
GN (ECO:0000313|EMBL:MRL38561.1), GNP00_27100
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GN (ECO:0000313|EMBL:QOQ71395.1), KPZ09_48950
GN (ECO:0000313|EMBL:GKM35159.1), L545_27305
GN (ECO:0000313|EMBL:KI101143.1), NCTC11679_05415
GN (ECO:0000313|EMBL:STV73210.1), NCTC13443_00932
GN (ECO:0000313|EMBL:STT00646.1), NCTC13465_05240
GN (ECO:0000313|EMBL:SQK49040.1), NCTC13635_03237
GN (ECO:0000313|EMBL:YEB02921.1), NCTC204_01561
GN (ECO:0000313|EMBL:STU80583.1), NCTC5047_03254
GN (ECO:0000313|EMBL:STT82298.1), NCTC5051_05049
GN (ECO:0000313|EMBL:STU53965.1), NCTC5052_03601
GN (ECO:0000313|EMBL:STT95126.1), NCTC5053_04523
GN (ECO:0000313|EMBL:STV39518.1), NCTC8849_00314
GN (ECO:0000313|EMBL:STT51806.1), NCTC9128_04120
GN (ECO:0000313|EMBL:SQCL6162.1), NCTC9140_01026
GN (ECO:0000313|EMBL:ST879353.1), NCTC9617_07031
GN (ECO:0000313|EMBL:STX08004.1), NCTC9637_06272
GN (ECO:0000313|EMBL:STT51247.1), NCTC9645_02196
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GN (ECO:0000313|EMBL:VGDA1728.1), SAMEA2273558_05217
GN (ECO:0000313|EMBL:SBH49495.1), SAMEA3499874_05052
GN (ECO:0000313|EMBL:SGKI9142.1), SAMEA3499901_05070
GN (ECO:0000313|EMBL:SKN34013.1), SAMEA3515122_05101
GN (ECO:0000313|EMBL:SYH37655.1), SAMEA3538828_04903
GN (ECO:0000313|EMBL:SVK47761.1), SAMEA3649591_05013
GN (ECO:0000313|EMBL:SVN66957.1), SAMEA3649713_05427
GN (ECO:0000313|EMBL:SVS29667.1), SAMEA3720909_05004
GN (ECO:0000313|EMBL:SWF77219.1), SAMEA3729652_04860
GN (ECO:0000313|EMBL:SWT2158.1), SAMEA4364603_05179
GN (ECO:0000313|EMBL:SKG60927.1), SAMEA4873632_05184
GN (ECO:0000313|EMBL:VGL17218.1);
OS Klebsiella pneumoniae.
OC Bacteria; Pseudomonadati; Pseudomonadota; Gammaproteobacteria;
OC Enterobacterales; Enterobacteriaceae; Klebsiella/Raoultella group;
OC Klebsiella; Klebsiella pneumoniae complex.
OX NCBI_TaxID=573 (ECO:0000313|EMBL:SKN34013.1, ECO:0000313|Proteomes:UP000259975);
RN [1] (ECO:0000313|EMBL:KI101143.1, ECO:0000313|Proteomes:UP000031820)
RF NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=UMNturkey9 (ECO:0000313|EMBL:KI101143.1,
ECO:0000313|Proteomes:UP000031820);
RA Lang K., Dorn K., Danzeisen J., Johnson T.;
RT "Plasmid movement, recombination, and chromosomal integration amongst
RT multidrug resistant commensal Escherichia coli clones within a single
RT commercial turkey flock.";
RL Submitted (OCT-2014) to the EMBL/GenBank/DBJ databases.
RW [2] (ECO:0000313|EMBL:PLE24172.1, ECO:0000313|Proteomes:UP000234439)
RF NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=COL-Kpn30 (ECO:0000313|EMBL:PLE24172.1,
ECO:0000313|Proteomes:UP000234439);
RX PubMed=2902188; DOI=10.93/infdis/j1x524;
RA Rojas L.J., Weinstock G.M., De La Cadena E., Diaz L., Rios R., Hanson B.M.,
RA Brown J.S., Vats P., Phillips D.S., Nguyen H., Hujer K.M., Correa A.,
RA Adams M.D., Perez F., Sodergren E., Narechania A., Planet P.J.,
RA Villegas M.V., Bonomo R.V., Arias C.A.;
RT "An Analysis of the Epidemic of Klebsiella pneumoniae Carbapenemase-
RT Producing K. pneumoniae: Convergence of Two Evolutionary Mechanisms Creates
RT the Perfect Storm.";
RL J. Infect. Dis. 217:82-92 (2017).
RN [3] (ECO:0000313|EMBL:OVF74521.1, ECO:0000313|Proteomes:UP000196447)
RF NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=39383 (ECO:0000313|EMBL:OVF74521.1,
ECO:0000313|Proteomes:UP000196447);
RA Fouts D., Stalin M.J., Chen L., Wright M., Sutton G., Nguyen K.,
RA Vanduin D., Rojas L., Hujer A., Hujer K., Bonomo R., Kreiswirth B.,
RA Adams M.;
RL Submitted (MAR-2017) to the EMBL/GenBank/DBJ databases.
RN [4] (ECO:0000313|EMBL:FVU60120.1, ECO:0000313|Proteomes:UP000245817)
RF NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=H51664TA (ECO:0000313|EMBL:FVU60120.1,
ECO:0000313|Proteomes:UP000245817);
RA Founou L., Founou R.C., Allam M., Ismail A., Essack S.Y.;
RT "Molecular Epidemiology of Livestock-Associated Methicillin Resistant
RT Staphylococcus aureus (LA-MRSA) and Extended-Spectrum Beta-Lactamase
RT (ESBL)-Producing Enterobacteriaceae in Pigs and Exposed Workers in Cameroon
RT and South Africa.";
RL Submitted (SEP-2017) to the EMBL/GenBank/DBJ databases.
RN [5] (ECO:0000313|Proteomes:UP000250675, ECO:0000313|Proteomes:UP000251088)
RF NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NCTC11679 (ECO:0000313|EMBL:STV73210.1,
ECO:0000313|Proteomes:UP000255239), NCTC13443
RC (ECO:0000313|EMBL:STT00646.1, ECO:0000313|Proteomes:UP000255518),
RC NCTC13465 (ECO:0000313|EMBL:SQK49040.1,
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RC NCTC5047 (ECO:0000313|EMBL:STT82298.1,
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RC NCTC8849 [ECO:0000313|EMBL:STT51806.1,
RC [ECO:0000313|Proteomes:UP000254799], NCTC9128
RC [ECO:0000313|EMBL:SQ16162.1, ECO:0000313|Proteomes:UP000251088],
RC NCTC9140 [ECO:0000313|EMBL:STS79353.1,
RC [ECO:0000313|Proteomes:UP000254938], NCTC9617
RC [ECO:0000313|EMBL:STX8004.1, ECO:0000313|Proteomes:UP000255167],
RC NCTC9637 [ECO:0000313|EMBL:STT51247.1,
RC [ECO:0000313|Proteomes:UP000255099], and NCTC9645
RC [ECO:0000313|EMBL:SQZ1359.1, ECO:0000313|Proteomes:UP000250675];
RG Pathogen Informatics;
RA Doyle S.;
RL Submitted (JUN-2018) to the EMBL/GenBank/DBJ databases.
RN [6] [ECO:0000313|EMBL:RDT85044.1]
RP NUCLEOTIDE SEQUENCE
RC STRAIN-K293 [ECO:0000313|EMBL:RDT85044.1];
RA He F.;
RT "Draft genome sequence of Klebsiella pneumoniae K293.";
RL Submitted (JUL-2018) to the EMBL/GenBank/DBJ databases.
RN [7] [ECO:0000313|EMBL:RBZ17003.1]
RP NUCLEOTIDE SEQUENCE
RC STRAIN-BC_5001 [ECO:0000313|EMBL:RBZ17003.1];
RA Martins R.C., Perdigao-Neto L.V., Costa S.F., Levin A.S.S.;
RL Submitted (JUL-2018) to the EMBL/GenBank/DBJ databases.
RN [8] [ECO:0000313|EMBL:RBZ17003.1]
RP NUCLEOTIDE SEQUENCE
RC STRAIN-BC_5001 [ECO:0000313|EMBL:RBZ17003.1];
RA Martins R.C.R., Perdigao-Neto L.V., Costa S.F., Levin A.S.S.;
RT "Klebsiella pneumoniae genome sequencing and assembly.";
RL Submitted (AUG-2018) to the EMBL/GenBank/DBJ databases.
RN [9] [ECO:0000313|Proteomes:UP000257587, ECO:0000313|Proteomes:UP000258253]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN-430807D6470422 [ECO:0000313|EMBL:SRK60927.1,
RC [ECO:0000313|Proteomes:UP000252603], 5012STDY312589
RC [ECO:0000313|EMBL:VGD41728.1, ECO:0000313|Proteomes:UP000294876],
RC 5012STDY7626430 [ECO:0000313|EMBL:VGL17218.1,
RC [ECO:0000313|Proteomes:UP000376235], EUSCAPE_AT002
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RC EUSCAPE_AT029 [ECO:0000313|EMBL:SXN34013.1,
RC [ECO:0000313|Proteomes:UP000259975], EUSCAPE_GRP03
RC [ECO:0000313|EMBL:SVN66957.1, ECO:0000313|Proteomes:UP000258905],
RC EUSCAPE_GRI14 [ECO:0000313|EMBL:SVS29667.1,
RC [ECO:0000313|Proteomes:UP000259497], EUSCAPE_HU047
RC [ECO:0000313|EMBL:SYR47761.1, ECO:0000313|Proteomes:UP000258253),
RC EUSCAPE_IT093 [ECO:0000313|EMBL:SYH37655.1,
RC [ECO:0000313|Proteomes:UP000259673], EUSCAPE_TRL25
RC [ECO:0000313|EMBL:SWT22158.1, ECO:0000313|Proteomes:UP000258798),
RC EUSCAPE_UK014 [ECO:0000313|EMBL:SWF77219.1,
RC [ECO:0000313|Proteomes:UP000259364], K480
RC [ECO:0000313|EMBL:SBH9495.1], K480
RC [ECO:0000313|Proteomes:UP000077826], and NCTC13635
RC [ECO:0000313|EMBL:VEB02921.1, ECO:0000313|Proteomes:UP000282433];
RG Pathogen Informatics;
RL Submitted (AUG-2018) to the EMBL/GenBank/DBJ databases.
RN [10] [ECO:0000313|EMBL:ROG99069.1, ECO:0000313|Proteomes:UP000283322]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN-CR0165 [ECO:0000313|EMBL:ROG99069.1,
RC [ECO:0000313|Proteomes:UP000283322];
RA Vanduin D., Fouts D., Wright M., Sutton G., Nguyen K., Kreiswirth B.,
RA Chen L., Rojas L., Hujer A., Hujer K., Bonomo R., Adams M.;
RL Submitted (OCT-2018) to the EMBL/GenBank/DBJ databases.
RN [11] [ECO:0000313|EMBL:RRF07461.1]
RP NUCLEOTIDE SEQUENCE
RC STRAIN-KLPN_104 [ECO:0000313|EMBL:RRF07461.1];
RA Fan Y., Timp W., Bergman Y., Tamma P., Sinner P.;
RL Submitted (OCT-2018) to the EMBL/GenBank/DBJ databases.
RN [12] [ECO:0000313|EMBL:VCV74244.1, ECO:0000313|Proteomes:UP000269921]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN-Kpneu006 [ECO:0000313|EMBL:VCV74244.1];
RA Noll B N.;
RL Submitted (OCT-2018) to the EMBL/GenBank/DBJ databases.
RN [13] [ECO:0000313|EMBL:RRF07461.1, ECO:0000313|Proteomes:UP000275975]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN-KLPN_104 [ECO:0000313|EMBL:RRF07461.1,
RC [ECO:0000313|Proteomes:UP000275975];
RX PubMed-30373801;
RA Tamma P.D., Fan Y., Bergman Y., Pettea G., Kazmi A., Lewis S.,
RA Carroll K.C., Timp W., Bergman Y., Tamma P., Sinner P.J.;
RT "Applying Rapid Whole Genome Sequencing to Predict Phenotypic Antimicrobial
Susceptibility Testing Results Among Carbapenem-Resistant Klebsiella
pneumoniae Clinical Isolates.";
RL Antimicrob. Agents Chemother. 0:0-0 (2019).
RN [14] [ECO:0000313|EMBL:TDJ93081.1, ECO:0000313|Proteomes:UP000294951]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN-RJ1071 [ECO:0000313|EMBL:TDJ93081.1,
RC [ECO:0000313|Proteomes:UP000294951];
RA Wang S.;
RT "Multidrug-Resistant Klebsiella pneumoniae Clinical Bloodstream Isolates in
Shanghai, China.";
RL Submitted (MAR-2019) to the EMBL/GenBank/DBJ databases.
RN [15] [ECO:0000313|EMBL:MSS34360.1, ECO:0000313|Proteomes:UP000468995]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN-EN5275 [ECO:0000313|EMBL:MSS34360.1,
RC [ECO:0000313|Proteomes:UP000468995];
RA Mukherjee S., Naha S., Bhadury P., Basu S.;
RT "Genome sequence of OXA-232-producing Klebsiella pneumoniae ST23 from
septicemic neonate.";
RL Submitted (JUL-2019) to the EMBL/GenBank/DBJ databases.
RN [16] [ECO:0000313|EMBL:TYL73673.1, ECO:0000313|Proteomes:UP000322977]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN-OCO-494 [ECO:0000313|EMBL:TYL73673.1,
RC [ECO:0000313|Proteomes:UP000322977];
RA Morales-Leon F., Caro C., Opazo-Capurro A., Lincopan N.,
RA Dominguez-Yevenes M., Lima C., Bello-Toledo H., Gonzalez-Rocha G.;
RT "Phenotypic and genetic characterization of extended-spectrum b-lactamase-
producing hypercolonious Klebsiella pneumoniae from Chile.";
RL Submitted (AUG-2019) to the EMBL/GenBank/DBJ databases.
RN [17] [ECO:0000313|EMBL:MUA43494.1, ECO:0000313|Proteomes:UP000485085]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN-WP_38044 [ECO:0000313|EMBL:MUA43494.1,
RC [ECO:0000313|Proteomes:UP000485085];
RA Zhou K.;
RT "Emergence of a novel subclone of carbapenem-resistant Klebsiella
pneumoniae ST11 with enhanced virulence and transmissibility: a molecular
epidemiological, clinical, genomic study.";
RL Submitted (NOV-2019) to the EMBL/GenBank/DBJ databases.
RN [18] [ECO:0000313|EMBL:MRJ99543.1, ECO:0000313|Proteomes:UP000441029]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN-CriePir115 [ECO:0000313|EMBL:MRL38561.1), and CriePir226
RC [ECO:0000313|EMBL:MRJ99543.1, ECO:0000313|Proteomes:UP000441029];
RA Shelenkov A., Mikhaylova Y., Yanushevich Y., Samoilov A., Petrova L.,
RA Fomina V., Gusarov V., Zamyatin M., Shagin D.;
RT "Molecular typing, antibiotic resistance determination and virulence
profiling for 36 multidrug-resistant clinical Klebsiella pneumoniae
isolates using second- and third-generation sequencing.";
RL Submitted (NOV-2019) to the EMBL/GenBank/DBJ databases.
RN [19] [ECO:0000313|EMBL:QOU51607.1, ECO:0000313|Proteomes:UP000439817]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN-CriePir120 [ECO:0000313|EMBL:QOU51607.1,
RC [ECO:0000313|Proteomes:UP000439817];
RX PubMed-32429555;
RA Shelenkov A., Mikhaylova Y., Yanushevich Y., Samoilov A., Petrova L.,
RA Fomina V., Gusarov V., Zamyatin M., Shagin D., Akimkin V.;
RT "Molecular Typing, Characterization of Antimicrobial Resistance, Virulence
Profiling and Analysis of Whole-Genome Sequence of Clinical Klebsiella
pneumoniae Isolates.";
RL Antibiotics 9:8261-8261 (2020).
RN [20] [ECO:0000313|EMBL:NGN75773.1, ECO:0000313|Proteomes:UP000479475]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN-2429 [ECO:0000313|EMBL:NGN75773.1,
RC [ECO:0000313|Proteomes:UP000479475];
RA Starkova E., Sulyan O.S., Likholetova D.V., Ageevets V.A., Lazareva I.V.,
RA Sopova J.V., Sidorenko S.V.;
RT "Klebsiella pneumoniae genome sequencing and assembly.";
RL Submitted (FEB-2020) to the EMBL/GenBank/DBJ databases.
RN [21] [ECO:0000313|EMBL:MED3707804.1]
RP NUCLEOTIDE SEQUENCE
RC STRAIN-NK1593 [ECO:0000313|EMBL:MED3707804.1];
RA Gomez-Simmonds A., Annavaajala M.K., Uhlemann A.-C.;
RT "Clinical and genomic characterization of carbapenemase-producing
Enterobacteriales causing secondary infections during the COVID-19 crisis at
a New York City hospital.";
RL Submitted (JUL-2020) to the EMBL/GenBank/DBJ databases.
RN [22] [ECO:0000313|EMBL:GHR55159.1]
RP NUCLEOTIDE SEQUENCE
RC STRAIN-Zam_UTH_09 [ECO:0000313|EMBL:GHR55159.1];
RA Shava M., Furuota T., Simbotwe M., Mulenga E., Mubanga M., Mulenga G.,
RA Kalle C., Zorzipt, Hang'ombe B., Higashi H.;
RT "Genome Sequence of ESBL Producing Zambian Clinical Strains.";
RL Submitted (OCT-2020) to the EMBL/GenBank/DBJ databases.
RN [23] [ECO:0000313|EMBL:QQL33423.1, ECO:0000313|Proteomes:UP000532829]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN-WCKFP090374 [ECO:0000313|EMBL:QQL33423.1,
RC [ECO:0000313|Proteomes:UP000532829];
RA Wei L., Wen H., Liu L., Feng T., Zong Z.;
RT "The complete genome of Klebsiella pneumoniae strain 090374.";
RL Submitted (DEC-2020) to the EMBL/GenBank/DBJ databases.
RN [24] [ECO:0000313|EMBL:QQZ71395.1, ECO:0000313|Proteomes:UP000595568]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN-59493 [ECO:0000313|EMBL:QQZ71395.1,
RC [ECO:0000313|Proteomes:UP000595568];
RA Chen L., Kreiswirth B.;
RT "Genome sequencing of apramycin resistant K. pneumoniae.";
RL Submitted (JAN-2021) to the EMBL/GenBank/DBJ databases.
RN [25] [ECO:0000313|EMBL:MDP0970564.1]

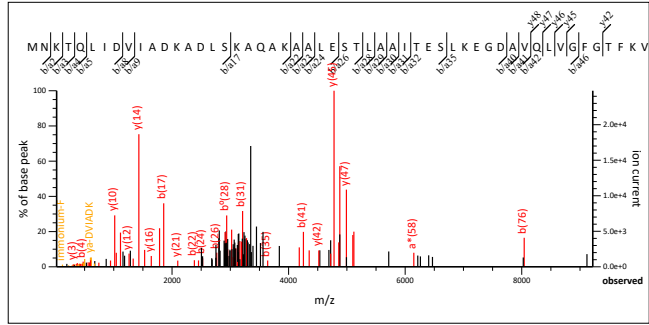
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RC STRAIN-KP219 [ECO:0000313]EMBL:MDP0970564.1);
RA Peng Z.;
RL Submitted (JUL-2023) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: Histone-like DNA-binding protein which is capable of wrapping
CC DNA to stabilize it, and thus to prevent its denaturation under extreme
CC environmental conditions. (ECO:0000256[ARBA:ARBA00003819]).
CC !- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC (ECO:0000256[ARBA:ARBA0001870]).
CC !- SIMILARITY: Belongs to the bacterial histone-like protein family.
CC (ECO:0000256[ARBA:ARBA00010529], ECO:0000256[RuleBase:RU003939]).
CC -----
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DR EMBL: BNFF01000001; GHK55159.1; -; Genomic DNA.
DR EMBL: JRRF01000004; K101143.1; -; Genomic DNA.
DR EMBL: JAXTE010000001; MBD3707804.1; -; Genomic DNA.
DR EMBL: JAUUIA010000035; MDP0970564.1; -; Genomic DNA.
DR EMBL: WUVJ010000032; MNJ99543.1; -; Genomic DNA.
DR EMBL: WUWF010000037; MRJ38561.1; -; Genomic DNA.
DR EMBL: VYIN010000037; MSS34360.1; -; Genomic DNA.
DR EMBL: WNF0010000061; MUA43494.1; -; Genomic DNA.
DR EMBL: JAAKYD010000039; NGN75773.1; -; Genomic DNA.
DR EMBL: NGBR010000044; OVF74521.1; -; Genomic DNA.
DR EMBL: NCMJ010000227; PIE24172.1; -; Genomic DNA.
DR EMBL: PCFF010000046; PVU60120.1; -; Genomic DNA.
DR EMBL: CP063008; QOU51607.1; -; Genomic DNA.
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DR EMBL: CP068602; QQT71395.1; -; Genomic DNA.
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DR EMBL: MFTG010000047; RCG99069.1; -; Genomic DNA.
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DR EMBL: UASO010000004; SQC21359.1; -; Genomic DNA.
DR EMBL: UAWQ010000019; SQC49040.1; -; Genomic DNA.
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DR EMBL: UGKQ010000007; STS79353.1; -; Genomic DNA.
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DR EMBL: UGLB010000003; STT51247.1; -; Genomic DNA.
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DR EMBL: UGMD010000002; STU80583.1; -; Genomic DNA.
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DR EMBL: UIXM010000034; SVS29667.1; -; Genomic DNA.
DR EMBL: UJHM010000034; SWT77219.1; -; Genomic DNA.
DR EMBL: UJRG010000026; SWT22158.1; -; Genomic DNA.
DR EMBL: UKAW010000027; SXG19142.1; -; Genomic DNA.
DR EMBL: URG010000003; SXN34013.1; -; Genomic DNA.
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DR EMBL: ULCI010000029; SYR47761.1; -; Genomic DNA.
DR EMBL: SMTN010000042; TDJ93081.1; -; Genomic DNA.
DR EMBL: VSSY010000032; TYL73673.1; -; Genomic DNA.
DR EMBL: UNVH010000001; VCV74244.1; -; Genomic DNA.
DR EMBL: LR134162; VEB02921.1; -; Genomic DNA.
DR EMBL: CAAGWG010000032; VGD41728.1; -; Genomic DNA.
DR EMBL: CAHCCC010000019; VGL17218.1; -; Genomic DNA.
RefSeq: WP_002848342.1; WP_MYAM01000044.1.
GeneID: 93309822; -.
DR KEGG: kpb:PH42_18270; -.
DR KEGG: kpne:KU54_025510; -.
DR KEGG: kpnu:1196_25350; -.
DR KEGG: kpx:PMK1_01865; -.
DR OMA: ISQEKQC; -.
DR Proteomes: UP000031820; Unassembled WGS sequence.
DR Proteomes: UP000077826; Unassembled WGS sequence.
DR Proteomes: UP000196447; Unassembled WGS sequence.
DR Proteomes: UP000234439; Unassembled WGS sequence.
DR Proteomes: UP000245817; Unassembled WGS sequence.
DR Proteomes: UP000250575; Unassembled WGS sequence.
DR Proteomes: UP000251088; Unassembled WGS sequence.
DR Proteomes: UP000251721; Unassembled WGS sequence.
DR Proteomes: UP000252603; Unassembled WGS sequence.
DR Proteomes: UP000253559; Unassembled WGS sequence.
DR Proteomes: UP000254103; Unassembled WGS sequence.
DR Proteomes: UP000254141; Unassembled WGS sequence.
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DR Proteomes: UP000254387; Unassembled WGS sequence.
DR Proteomes: UP000254657; Unassembled WGS sequence.
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DR Proteomes: UP000255192; Unassembled WGS sequence.
DR Proteomes: UP000255239; Unassembled WGS sequence.
DR Proteomes: UP000255518; Unassembled WGS sequence.
DR Proteomes: UP000257587; Unassembled WGS sequence.
DR Proteomes: UP000258253; Unassembled WGS sequence.
DR Proteomes: UP000258673; Unassembled WGS sequence.
DR Proteomes: UP000258798; Unassembled WGS sequence.
DR Proteomes: UP000258905; Unassembled WGS sequence.
DR Proteomes: UP000259364; Unassembled WGS sequence.
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DR Proteomes: UP000259975; Unassembled WGS sequence.
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DR Proteomes: UP000275975; Unassembled WGS sequence.
DR Proteomes: UP000282433; Chromosome.
DR Proteomes: UP000283322; Unassembled WGS sequence.
DR Proteomes: UP000294876; Unassembled WGS sequence.
DR Proteomes: UP000294951; Unassembled WGS sequence.
DR Proteomes: UP000322977; Unassembled WGS sequence.
DR Proteomes: UP000376235; Unassembled WGS sequence.
DR Proteomes: UP000439817; Chromosome.
DR Proteomes: UP000441029; Unassembled WGS sequence.
DR Proteomes: UP000468995; Unassembled WGS sequence.
DR Proteomes: UP000479475; Unassembled WGS sequence.
DR Proteomes: UP000485085; Unassembled WGS sequence.
DR Proteomes: UP000532829; Chromosome.
DR Proteomes: UP000595568; Chromosome.
DR Proteomes: UP000655094; Unassembled WGS sequence.
DR Proteomes: UP000657739; Unassembled WGS sequence.
DR Proteomes: UP001244490; Unassembled WGS sequence.
DR GO: GO:0005829; Cytoplasm; IEA:TreeGrafter.
DR GO: GO:0003677; P:DNA binding; IEA:UniProtKB-KW.
DR GO: GO:0030527; P:structural constituent of chromatin; IEA:InterPro.
DR GO: GO:0030261; P:chromosome condensation; IEA:UniProtKB-KW.
DR CDD: cdd3831; HU; 1.
DR FunFam: 4.10.520.10.FF:000001; DNA-binding protein HU; 1.
DR Gene3D: 4.10.520.10; IHF-like DNA-binding proteins; 1.
DR InterPro: IPR000119; Hist_DNA-bd.
DR InterPro: IPR020816; Histone-like DNA-bd_CS.
DR InterPro: IPR010992; IHF-like DNA-bd_dom_sf.
DR NCBIfam: NF008023; PRK10753.1; 1.
DR PANTHER: PTHR33175; DNA-BINDING PROTEIN HU; 1.
DR PANTHER: PTHR33175:SF12; DNA-BINDING PROTEIN HU-ALPHA; 1.
DR Pfam: PF00216; Bac DNA binding; 1.
DR PRINTS: PR01727; DNABINDINGHU.
DR SMART: SM00411; BHL; 1.
DR SUPFAM: SSF47729; IHF-like DNA-binding proteins; 1.
DR PROSITE: PS00045; HISTONE_LIKE; 1.
PE 3; Inferred from homology;
KW DNA condensation (ECO:0000256[ARBA:ARBA00023067]);
KW DNA-binding (ECO:0000256[ARBA:ARBA00023125], ECO:0000313[EMBL:SNX34013.1]).
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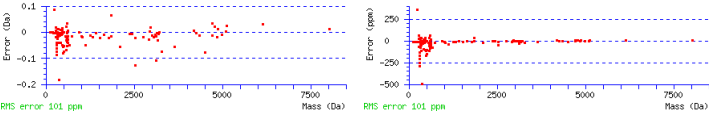
Peptide View

MS/MS Fragmentation of **MNKTQLDIVADKADLSKAQAKALESTLAAIITLESKEGDVQLVGFGTKYNHRAERTGRNPQTGKEIKIAAANVPFVSGKALKDAVK**
Found in **A0A086I6S5_KLEPN** in **Trembl_22_05_2024**, DNA-binding protein HU-alpha OS=Klebsiella pneumoniae OX=573 GN=hupA PE=3 SV=1

Match to Query 1: 9471.260524 from(9472.267800,1+) intensity(337307.9494) index(0)
Title: Reading Top-Down experiment
Data file K_pneumoniae_VIM1_9470_Da.mgf



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NHRAE	580.2950	608.2899	HR	266.1724	294.1673	HRA	337.2095	365.2044
HRAE	466.2521	494.2470	HRAER	622.3532	650.3481	RA	200.1506	228.1455
RAE	329.1932	357.1881	RAER	485.2943	513.2892	RAERT	586.3420	614.3369
RAERTG	643.3634	671.3583	AE	173.0921	201.0870	AER	329.1932	357.1881
AERT	430.2409	458.2358	AERTG	487.2623	515.2572	AERTGR	643.3634	671.3583
ER	258.1561	286.1510	ERT	359.2037	387.1987	ERTG	416.2252	444.2201
ERTGR	572.3263	600.3212	ERTGRN	686.3692		RT	230.1612	258.1561
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RTGRNP	654.3794	682.3743	TG	131.0815	159.0764	TGR	287.1826	315.1775
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GR	186.1349	214.1299	GRN	300.1779	328.1728	GRNP	397.2306	425.2255
GRNPQ	525.2892	553.2841	GRNPQT	626.3369	654.3318	GRNPQTG	683.3583	
RN	243.1564	271.1513	RNP	340.2092	368.2041	RNPQ	468.2677	496.2627
RNPQT	569.3154	597.3103	RNPQTG	626.3369	654.3318	NP	184.1081	212.1030
NPQ	312.1666	340.1615	NPQT	413.2143	441.2092	NPQTG	470.2358	498.2307
NPQTGK	598.3307	626.3257	PQ	198.1237	226.1186	PQT	299.1714	327.1663
PQTG	356.1928	384.1878	PQTGK	484.2878	512.2827	PQTGKE	613.3304	641.3253
QT	202.1186	230.1135	QTG	259.1401	287.1350	QTGK	387.2350	415.2300
QTGKE	516.2776	544.2726	QTGKEI	629.3617	657.3566	TGK	259.1765	287.1714
TGKE	388.2191	416.2140	TGKEI	501.3031	529.2980	TGKEIK	629.3981	657.3930
GK	158.1288	186.1237	GKE	287.1714	315.1663	GKEI	400.2554	428.2504
GKEIK	528.3504	556.3453	GKEIKI	641.4345	669.4294	KEI	343.2340	371.2289
KEIK	471.3289	499.3239	KEIKI	584.4130	612.4079	KEIKIA	655.4501	683.4450
EI	215.1390	243.1339	EIK	343.2340	371.2289	EIKI	456.3180	484.3130
EIKIA	527.3552	555.3501	EIKIAA	598.3923	626.3872	EIKIAAA	669.4294	697.4243
IK	214.1914	242.1863	IKI	327.2755	355.2704	IKIA	398.3126	426.3075
IKIAA	469.3497	497.3446	IKIAAA	540.3868	568.3817	IKIAAAN	654.4297	682.4246
KI	214.1914	242.1863	KIA	285.2285	313.2234	KIAA	356.2656	384.2605
KIAAA	427.3027	455.2976	KIAAAN	541.3457	569.3406	KIAAANV	640.4141	668.4090
IAA	228.1707	256.1656	IAAA	299.2078	327.2027	IAAAN	413.2507	441.2456
IAAANV	512.3191	540.3140	IAAANVP	609.3719	637.3668	IAAANVPA	680.4090	
AAA	186.1237	214.1186	AAAN	300.1666	328.1615	AAANV	399.2350	427.2300
AAANVP	496.2878	524.2827	AAANVPA	567.3249	595.3198	AAN	229.1295	257.1244
AANV	328.1979	356.1928	AANVP	425.2507	453.2456	AANVPA	496.2878	524.2827
AANVPAF	643.3562	671.3511	AN	158.0924	186.0873	ANV	257.1608	285.1557
ANVP	354.2136	382.2085	ANVPA	425.2507	453.2456	ANVPAF	572.3191	600.3140
ANVPAFV	671.3875	699.3824	NV	186.1237	214.1186	NVP	283.1765	311.1714
NVPA	354.2136	382.2085	NVPAF	501.2820	529.2769	NVPAFV	600.3504	628.3453
NVPAFVS	687.3824		VP	169.1335	197.1285	VPA	240.1707	268.1656
VPAF	387.2391	415.2340	VPAFV	486.3075	514.3024	VPAFVS	573.3395	601.3344
VPAFVSG	630.3610	658.3559	PA	141.1022	169.0972	PAF	288.1707	316.1656
PAFV	387.2391	415.2340	PAFVS	474.2711	502.2660	PAFVSG	531.2926	559.2875
PAFVSGK	659.3875	687.3824	AF	191.1179	219.1128	AFV	290.1863	318.1812
AFVS	377.2183	405.2132	AFVSG	434.2398	462.2347	AFVSGK	562.3348	590.3297
AFVSGKA	633.3719	661.3668	FV	219.1492	247.1441	FVS	306.1812	334.1761
FVSG	363.2027	391.1976	FVSGK	491.2976	519.2926	FVSGKA	562.3348	590.3297
FVSGKAL	675.4188		VS	159.1128	187.1077	VSG	216.1343	244.1292
VSGK	344.2292	372.2241	VSGKA	415.2663	443.2613	VSGKAL	528.3504	556.3453
VSGKALK	656.4454	684.4403	SG	117.0659	145.0608	SGK	245.1608	273.1557
SGKA	316.1979	344.1928	SGKAL	429.2820	457.2769	SGKALK	557.3770	585.3719
SGKALKD	672.4039		GKA	229.1659	257.1608	GKAL	342.2500	370.2449
GKALK	470.3449	498.3398	GKALKD	585.3719	613.3668	GKALKDA	656.4090	684.4039
KAL	285.2285	313.2234	KALK	413.3235	441.3184	KALKD	528.3504	556.3453
KALKDA	599.3875	627.3824	KALKDAV	698.4559		ALK	285.2285	313.2234
ALKD	400.2554	428.2504	ALKDA	471.2926	499.2875	ALKDAV	570.3610	598.3559
LKD	329.2183	357.2132	LKDA	400.2554	428.2504	LKDAV	499.3239	527.3188
KD	216.1343	244.1292	KDA	287.1714	315.1663	KDAV	386.2398	414.2347



NCBI BLAST search of [MNKTLIDVIADKADLSKAOAKAALESTLAAITESLKEGDVAVLVGFGTFKYNHRAERTGRNPOTGKEIKIAAANVPAFVSGKALKDAVK](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
91.5	9471.1467	0.1138	MNKTLIDVIADKADLSKAOAKAALESTLAAITESLKEGDVAVLVGFGTFKYNHRAERTGRNPOTGKEIKIAAANVPAFVSGKALKDAVK
67.0	9471.1103	0.1502	MNKTLIDVIADKADLSKAOAKAALESTLAAITESLKEGDVAVLVGFGTFKYNHRAERTGRNPOTGKEIKIAAANVPAFVSGKALKDAVK
62.2	9471.1467	0.1138	MNKTLIDVIADKADLSKTOAKAALEATLAAITESLKDGDVAVLVGFGTFKYNHRAERTGRNPOTGKEIKIAAANVPAFVSGKALKDAVK
53.9	9471.1467	0.1138	MNKTLIDAIAEKADLSKVOAKAALESTLAAITDALKEGDVAVLVGFGTFKYNHRAERTGRNPOTGKEIKIAAANVPAFVSGKALKDAVK
0.6	9471.1579	0.1026	NKNDLVAAVAADTDLSKTDAAKAVDSVILMVTALKKGDEVRLVGFGTFEATKREASEGRNPRTGKEIKIAASKOPKFRAGKGLKDAIN
0.3	9471.1192	0.1413	MLNFIWFIVGVFGLIARWVVPGENHMGFLTMTTVVGIVGSIJGLIGYLFKRPPPGSKFHHTAGFLMSIVGAHILMLLLRYFNPO

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