

Efficacy of a novel bacteriophage in controlling *Escherichia coli* associated with swine farm environments and its potential for biofilm disruption

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Supplementary TableS1. Bacterial lytic activity and efficiency of plating (EOP) of *Escherichia* phage vECPW9

Strain	Phage vECPW9	
	Lytic Activity	EOP
MDR <i>E. coli</i> PPW001	+	High (0.88)
MDR <i>E. coli</i> PPW002	-	-
MDR <i>E. coli</i> PPW003	+	Moderate (0.1)
MDR <i>E. coli</i> PPW004	-	-
MDR <i>E. coli</i> PPW005	+	High (0.75)
MDR <i>E. coli</i> PPW006	-	-
MDR <i>E. coli</i> PPW007	+	High (Host = 1)
MDR <i>E. coli</i> PPW008	-	-
MDR <i>E. coli</i> PPW009	+	High (0.58)
MDR <i>E. coli</i> PPW010	+	High (0.67)
MDR <i>E. coli</i> PPW011	-	-
MDR <i>E. coli</i> PPW012	-	-
MDR <i>E. coli</i> PPW013	-	-
MDR <i>E. coli</i> PPW014	+	Moderate (0.13)
MDR <i>E. coli</i> PPW015	-	-
MDR <i>E. coli</i> PPW016	-	-
MDR <i>E. coli</i> PPW017	-	-
MDR <i>E. coli</i> PPW018	-	-
MDR <i>E. coli</i> PPW019	+	High (0.53)
MDR <i>E. coli</i> PPW020	-	-

Results were recorded as positive (+) for lysis observed on the bacterial lawn, or negative (-) for the absence of lysis on the bacterial lawn. The efficacy of plating (EOP) values were categorized into 4 groups: high production (EOP $\geq$ 0.5), moderate production ($0.1 \leq$ EOP < 0.5), low production ($0.001 <$ EOP < 0.1), and no production (a ratio $\leq$ 0.001). All experiments were conducted independently in triplicate, with each experiment involving duplicate plaque assays, and the entire process was repeated twice.

Supplementary Table S2. Functional annotation of open reading frames (ORFs) in phage vECPW9. ORFs were annotated using PhageScope, and the predicted amino acid sequences of each coding sequence were further analyzed by BLASTp for putative functional identification.

CDSs	Start Point	End Point	Strand	Nucleotide length (bp)	Amino acid sequence	Amino acid length	PhageScope analysis results	Results of BLASTp analysis								
							Protein Product	Protein Product	Organism	Score	Total Score	Query Cover	E value	Percent identity	Accession Length	Accession
contig1_1	2	283	+	282	LQCFDDIPLFVRLIYVKEEDLRMVCKLNSILAYADKQGISFEEAKAEKEAIALCRAKKDKAWLKKRKIEPSTVAKRRKQIVKILLQEIES	93	nucleic acid binding	HNH endonuclease	Escherichia phage vB_EcoM-Ro121c4YLVW	183	183	100%	9.00E-65	100	184	YP_009984946.1
contig1_2	320	928	+	609	MQIVQDWDLVVALPDVAWLEWLNKISGLGVKIDITFTKNADYDLTNYFPGFREFEENINPYGFLDNP HLYDTMGFVPGMPDFLKYVSRKGSNLLIASVTKGGHLSKKHKHVLRLTDTIDFSKSGSNGFFATKE KYLLPCDIAIDRADNLLYPFDEVKVIYFNTPYKDNHLEELKKKPNVVTGLEQWLTCLDVFNTLN NFKN	202	deoxyribonucleotide catabolic process	hypothetical protein JR326_gp177	Escherichia phage ukendt	412	412	100	6.00E-145	99.01	202	YP_009986833.1
contig1_3	938	1936	+	999	MTKQISASIIAHSITEDGKEIVTFELEYPRIIHSELMTHRLFSRNAASSRAIPVKTLIEMVRNQPARPYR FGANQPGMQDKGVDDHALIDAGYTAQEWDLAALSAAFAEEFSLAGYHKQVANRLLEPFQRIK TFLTATEYENFWLRRDDKADPTIEALAKEMHKEYEGSTPEVLKPGQWHTPYVDHFYDTIGTEGD DHFVGGYYVQDESGEVVLTLEEAKAISASCAQVSYYRRLNATKDKALDIYGRLLTGRKVHASP FEHQATPMQETYEQYGENCFEDLFINAPWDFNSWEPGITHVDRNGKFWSGNFKGWIQHRQLLTNH TKW	332	flavin adenine dinucleotide binding	hypothetical protein JR327_gp251	Escherichia phage Mt1B1_P17	699	699	100	0.00E+00	100	332	YP_009987112.1
contig1_4	2035	2445	+	411	MSLYNTTTWATVSMSTVMSTPIWKLESNKHNGNPIHEKQNAVIRASLVMLGMAEDSHYSVERN V NIRSNNDRKRVVFANTTLTFPVSPNCGFKRIYQENDIFHFGDEEFTGWGASHIKMDDFGNSYDPAK ADDTNQ	136	hypothetical protein	hypothetical protein G377_gp157	Escherichia phage phAPEC8	285	285	100	8.00E-97	99.26	136	YP_007348480.1
contig1_5	2454	2696	+	243	MTDNKYEGCEIEVYFDETVGCNVTVILDTSKRLSPKRQEADRRAKAGKGFDDITHFEGFLYANGLFN EMKFGYDVDVLNMH	80	hypothetical protein	hypothetical protein HOV53_gp094	Escherichia phage vB_EcoM_Schickermoser	176	176	100	2.00E-55	100	84	YP_009823760.1
contig1_6	2713	4959	+	2247	MIRFVTKSNGKTEEFNPEKLRKWSEFAAGKLNWSEIELEAVKRCYDGVSTRDLHKAMIAACIDKKT QAYSMDAGRLLGMIVKQAHGGYHSIPSLNTFYHDMVERGHWAKMDYTDEEKEIGKIVKHKNK LTYGYSVLRQMVDKYLIRDAVNDVHESPFQFLIGIAMKVMIEQPKERRIEDIKKLYTVYVSDKLINL PPSYLTTLRTPIKGSASCCLFRADDTAESLAIANYLAHEYLTNNAGIGVNLQTRATGGQVKNRNIHG GLLPYLKWMEDSVGASKQASRGGSATVTFTILEPFDLIRLKNPPTPIDKRVDKLDYSIVVNSRFL RRAAKNEDWMLVSCDDAPELYEALYKSEEFDAVYDKVSRRRIKKFKVARDLLEIIVQRAETGR IYMFADNVNHNHTPFLDVTYQSNLCQEIFLPTKAFHNMPDLFTGENTEDQELALCFLSSIVAGRVLP EYEDVAYYTVLTIDNVETMDYFPKHNEITAKARRSIGVGITNLAHYLASNFVNSDAYAKKLMLH ELAERHYFLWAKASRLRAKEKGNAEWIDKTKWPQGWLPIDITYAKTVDSIGNFDLKMDEWGLRAEI IEQGGIRNSVLAIAIPNESSLSVNTTNSLYPVRDITIMYKQSQKGSVLFVDPYEKLMMFYQSAWDT PAKDLAEMYGIFTKFTDQGISCDSWLDYSKLVGGRLSVKEEMKFILNFARLGGKSLYYLNSRTKSA DSLAQEDNLESCEGCGCSM	748	ribonucleotide reductase, barrel domain	NrdA-like aerobic NDP reductase large subunit	Escherichia phage ESCO13	1559	1559	100	0	99.73	748	YP_009786557.1
contig1_7	4968	5600	+	633	MLKGKRAVTVTTERGEIPLVDVERRLFVDGKPDPSYKAWKNMFERAYKMEQARPGYTGVTVCD EWFMSNFDMDWYQENFVANFVLDKDLVLGENTTVYCPAYCRFPYAVYVNTLLSYSKRTERKSLLG V TVRKSDGKISSKSSGHKGHLGYFATEEEAHFALWKDKAKSIRETADRYKEEHFYPEVYNTLVNK ADFYWHLAETKTVFRG	210	sequence-specific DNA binding transcription factor activity	HNH endonuclease	Escherichia phage EF1-1	439	439	100	4.00E-155	100	210	XPO96260.1
contig1_8	5644	6729	+	1086	MAAINHNEVYKTGKYPVFLGEQLGIFDSVNVYTEMHKLKYLKQAQWDENEVNLQDTRKDFV ACSKNNYDVMIKNLSFQWENDSLAKSIITLFSPLSNNEACAMMMKQSEMEVLHALTYSEIIRQCTP DPIEVNQMIMNDIFNRMGIIADIMGQLEAGHKYALGLIENDELRLILKGMVALIGLEIGIQIFSSF SATFAMAEQQLFVGACKLIQKIMLDLHVKMDYAVIDALMHDPIWRKIYEDNIEELTLILDVTVEQ EEQWCYDLFSEGRFIVGLNAELSKQWVYFNAAPIYRRLKMKAKFKAPKHSPLAWMEKWLNPDLIQ SAAQEIQLTNYKLSANKDLSDEELDF	361	ribonucleotide reductase, small chain	ribonucleotide reductase of class Ia (aerobic), beta subunit	Escherichia phage AV126	746	746	100	0	99.72	362	WPK38304.1
contig1_9	6729	6938	+	210	MILRCVGIIDTFKDVFDKGASYEASEMKNGFCDFVFGKRLKKNGDPWLGVMSCGHIIVNGVAKFEI KEE	69	hypothetical protein	hypothetical protein G377_gp162	Escherichia phage phAPEC8	141	141	100	6.00E-42	100	69	YP_007348475.1
contig1_10	6938	7090	+	153	MAEKLIFPCVCGGTQMEVEIMVTFPCLNCHGEGRVVVFEKEGLEVEDGE	50	unknown	hypothetical protein G377_gp163	Escherichia phage phAPEC8	74.7	74.7	70	6.00E-16	100	48	YP_007348474.1
contig1_11	7080	7244	+	165	MESEKEYVRIPRELTDHIAEIAIFEARCCGGIAYDIYIEAIIKAAQEEEMKNGY	54	represses a number of genes involved in the response to DNA damage (SOS response), including recA and LexA. In the presence of single-stranded DNA, RecA interacts with LexA causing an autocatalytic cleavage which disrupts the DNA-binding part of LexA, leading to derepression of the SOS regulon and eventually DNA repair	hypothetical protein	Escherichia phage vB_EcoM_DE16	106	106	98	2.00E-28	100	54	WAX24688.1
contig1_12	7234	7560	+	327	MGIDIEWRLMQGAPFNKWEVVGEDPRIEEFFDGFNFWFLQEGLDLSRISPFYDADESYCIYGIYLE GGEGSVAVDLEQVNNENAKEAYAELEKYNIKTETIISQHVW	108	hypothetical protein	hypothetical protein ECO340P1_00193	Escherichia phage ECO340P1	221	221	100	4.00E-72	100	108	WAX14452.1
contig1_13	7570	8136	+	567	MKVVEKTIEGAVIKPDDYKDDRGFFLETYNEQKYEDIIGKQTFVQDNMSKSNFGVLRGMHFOTN NPQGGKLVRCVSGEVLDFAVDLRKDSPTYGAWDGVVLRARHHTQFWLPPGLAHGFIVLSMDAIFEY KCTTPYDPSSEQSLRWDDPDIGIDWGFDMIFDEGFKPILSTKDAMAKSFQQLRSEGV	188	dTDP-4-dehydrorhamnose 3,5-epimerase activity	dTDP-4-dehydrorhamnose 3,5-epimerase	Escherichia phage ESCO5	394	394	100	4.00E-138	100	188	YP_009787075.1
contig1_14	8130	8972	+	843	MLTYLVLGNGQLGQALRKVVPSNVSLIYPKERVDTITFEAVRNAIVEDYVDGVINCAAYTAVDK AEHDFATALAVNAYGPANIAAVCSKLIKIDFVHISTDYIFNYSHPFEDTTPNPINNYGYTKELGEKM VRGVNPNAIIRTASVYSEFGNNFLKTMLSRYNDGQRDHFIVADQFSCTPYAPDLAEIFAIVLKTGW SRSVKYTYHAGSHFISWAEFAEKILQMPPEPVKISAVSASTYNAPARPVKSQLVTSHYLTKSIDLK GIEQSLAVLLNKER	280	dTDP-4-dehydrorhamnose reductase activity	nucleotide-sugar epimerase	Escherichia phage anhybsys	581	581	100%	0	99.64%	280	YP_009985534.1

contig1_15	8972	9232	+	261	MEFVIFGKPNCFCEMSKQLLTMNRNKQFEYLSLDQDYDLESMTKTVVDLTVGVPRTFPQILSEVNG EVTYVGGFTELRDLMAQIAE	86	protein disulfide oxidoreductase activity	putative glutaredoxin 1	Escherichia phage ESCO5	176	176	100	4.00E-55	98.84	86	YP_009787073.1
contig1_16	9238	9387	+	150	MKSQKQKRKIFSRALANELKSNIKKTKPKRETSPEHLFLNELDHVGVDDE	49	hypothetical protein	hypothetical protein G377_gp171	Escherichia phage phAPEC8	100	100	100	3.00E-26	100	49	YP_007348466.1
contig1_17	9395	9895	+	501	MAKVNVDEEDMLRVDEGLKLTVYQDHLGYWTVGIGHLLTKIKDKAKAIQILDNLLGRKCTNGVITEK EARQIFADDVAKVKRDIKNSITLSPIYDKVSDTRKLGINMVFQLGLKGAEGFQNSLTLSNAYYTQ AGKNMRKSRWYSQTPNRAERVIKVLTSGTLDAYN	166	defense response to bacterium	endolysin	Escherichia phage iGC_PHA_EC001	337	337	100	5.00E-117	100	166	WMI32602.1
contig1_18	10000	10691	+	692	MGNKTTAAKFQQRKLANSAKIESRYAAKAVGNDYDLRDFMEPGDQNKVQSMIWNDLTVVNAP AGTGKTSVALWKALQMLRSGDFRKLFLFKNPTEVGGDQIGFLSGDKTDKLAAHYESTKRIFQEQMT ANKLENDIGSGKIELNIPNYLLGATLDNTVIIDEAQLMSTETLKLILIERAGINTHVILGDRQVITYAIK KRSNGLHQLELLYPENEEGVREPIVDFIGYVELTDDNKRGRLSKLITEVFI	252	PhoH-like protein	PhoH-like phosphate starvation- inducible	Escherichia phage ESCO13	517	517	100	0.00E+00	100	269	YP_009786543.1
contig1_19	10727	11227	+	501	MGVATIAIGRSGIDECYQTLGKPNFQRQICVNIHIEKIALTENMTLRDKLEMFKCWCLGEDWLLN HFQELSDSKESLFDCHIGIAGSDPSLLHITHEEAKLLFLSNLNFNKALLVRDCSDDLNNPLATSDQIFVD KETLRAIEYICKYVNGGKAVLKTLEEEE	166	hypothetical protein	hypothetical protein ESCO37_00175	Escherichia phage vB_EcoM_ESCO37	338	338	100	7.00E-117	99.4	166	UPW38775.1
contig1_20	11227	11919	+	693	MTTHATKNKILSDGKVTFGGRVDSINFKKVKRIGDYLVGGAGRLTSVLSFFQWFEQNLQCEAARD AVPGLMIHSDPKDEDEEFIALVHPDGRIFLHEGNNPTRYAVIDEYYAVGSGSDFALAALDAGATP EQAMEVAKKRDAFSGGETFIEEQDEIEELTDDDLNFSEKELINLLKFGNPYGEIEPRNVAGNEADTE EKSVAEENLTKSKSENINLVNADFEEAT	230	peptidase HslV family	hypothetical protein	Escherichia phage BI-EHEC	320	320	69	1.00E-95	100	159	UGV23951.1
contig1_21	11965	12399	+	435	MLQVPAPKFVEGAHISYRQTCRKARNCLDGLVAKTYTVEKKRWFQGDVVEYNIFGEHKLNHDTP ENMLIEFLRDKDISPMDYQLLKFYDSSLAIDKFVEDILSRKTDKNTYPLEADQIGLLNEISSFKELDNI TKEEILDGIRL	144	hypothetical protein	hypothetical protein JR321_gp184	Escherichia phage anhsbysj	296	296	100	8.00E-101	99.31	144	YP_009985527.1
contig1_22	12383	12892	+	510	MALDYDRPTSDYYPTPQKAINSLFSVIDFKNLKEEGWVFAEPCRGAEAIYRHFPEGSEYCELEEGK DYFSHEWENRPDIITNPPFKLAMEFLEKSLKEADVCIYLLRGLFLESKKRREFHQKNPPTNLIVLSER PSFVAGGDTKATAYAWYVYDPKNRLGSLQPFFV	169	methyltransferase activity	hypothetical protein ECO340P2_00207	Escherichia phage ECO340P2	351	351	100	8.00E-112	99.41	169	WAX14739.1
contig1_23	12905	13141	+	237	MGKLMITVAIDFDEVDESINLSLSTDYDGEDMNIEAATLFFKKIAIEVYAHEAANQAVDYGGIVR ALVHSTEGDNWED	78	unknown	hypothetical protein JR324_gp052	Escherichia phage niezany	154	154	100	9.00E-47	98.72	78	YP_009986172.1
contig1_24	13141	13344	+	204	MAYNYCYIAHEKKKGDGTGNVYAESESHAKEIGAILLSRWGTGNNYSAEDMFAEVDSSIQEDNITT T	67	hypothetical protein	hypothetical protein	Escherichia phage vB_EcoM_DE16	137	137	100	2.00E-40	98.51	67	WAX24673.1
contig1_25	13390	13584	+	195	MQSGEELLEKQFSTRQQALSYMVFLSNLDVNEILLRREGNFWSVKYHATRSVYILEEAESFLVE	64	unknown	hypothetical protein JR325_gp226	Escherichia phage tuntematon	128	128	100	9.00E-37	98.44	64	YP_009986599.1
contig1_26	13599	14171	+	573	MRSTFTGKINAGLIFTAVSILSKFKVNVLPVCVDFDHVFDPSNPTRCIVRSNVENPTENLFYVTKPS QSLNQVEAKLIPNGKYYSFLPCKSVEVENSTFANNLVSFVFFVSQDEIDEMVATVRSLYDSLGV VYSQQVCENNAKCAVDIINGICVCRVESFWLHDITYTVTAEVISEPRFSHAVSLII	190	histidyl tRNA synthetase	histidyl tRNA synthetase	Escherichia phage phAPEC8	387	387	100	2.00E-135	100	190	YP_007348456.1
contig1_27	14182	14511	+	330	MEITTEQALIDGRKILEKYLGIEHKTPGYLGWRIVEAVDFLPRNSKNVEMRSLFLVKVDGDTFPFK DAAEHIEKVEEKAYAEAFDLVLEQIEGKVNIFIFLDFEEDK	109	hypothetical protein	hypothetical protein G377_gp182	Escherichia phage phAPEC8	219	219	100	2.00E-71	100	109	YP_007348455.1
contig1_28	14508	15251	+	744	MIHKEITVKSDDQLFIIGDLHGVCNLYEKGKAKLGRDTPDVVSLGDLTRGQKQFRCVLEFTRKH NRYAIRGNHEDMMIKMGLEGRSYECWQYQNGGYTVFFEECGEGGATLAAAMTDEDLPVVLIVNYR GMKLAIFHGGVPSLEYLPTVDIPEYISKMTKTQENRFAEALMWDRMDVCAKEGMKLPVVMGV DYVFHGHSYVKTPIINANRVYMDTGSVFNNNLTFAYFDMDDGLGQFYSTLEED	247	hydrolase activity	NinI-like serine-threonine phosphatase	Escherichia phage vB_EcoM-Ro121c4YLWV	355	355	68	3.00E-122	100	169	YP_009984973.1
contig1_29	15251	15559	+	309	MYKITIISVSGNIRKEVILETDVNLVREIVLKEDNLQA VESDAPNLMVDQEYSELRRIFEEIQKKTQ PTKIFPGPYDPSNPSSPWIMRNTEPYTFPEITC	102	unknown	hypothetical protein ESCO25_00029	Escherichia phage vB_EcoM_ESCO25	206	206	100	1.00E-66	99.02	102	UPW38042.1
contig1_30	15567	16148	+	582	MAELFYTVGVSIRDISEEEWALMVGIGKWLNLGFKLRSGKAEGSDSAFETGVQSEENPTNKEIYVP WENFKNGQIPGDVIVLAKPDTMNYAISVQWIKDVHPAYEKLKQGARLKHQRNVHQVGLGRDENP APSCFLACANTDKHGDAKGGTATAWKIAKANNVPCLNIRGKTKQEYDFLRPLVMRAITSDS	193	DNA mediated transformation	DprA-like DNA recombination- mediator protein	Escherichia phage vB_Ec-G1	403	403	100	1.00E-141	99.48	193	XKC19724.1
contig1_31	16138	16650	+	513	MIPKRRKRGQRNLAEILDYNMVNDVTKEILPVVEDILQRLGRFCSDRVHFMVTHKSDSALNFYPL DYTLNNTEMKDINKYLMGYKDITETVGLGAEILANDILRNINKALDRSPAGVVSVFAVPDMVKYE STIPNKAYAFLLRRDVRGNVLEMESNYKIEEVLWQSSDQ	170	hypothetical protein	hypothetical protein JR319_gp206	Escherichia phage vB_EcoM-Ro121c4YLWV	309	309	88	1.00E-105	100	149	YP_009984976.1
contig1_32	16629	16919	+	291	MAEFGSVTSFESNFVTAWEAWDEMGVGELFYFNVTLRPEYAYLVEPGTVQIGMYLSQDGVVQFE FYSNTTDNEFTYRAFHVNMSLGEEKFYDDQV	96	hypothetical protein	hypothetical protein HOR21_gp067	Escherichia phage ESCO13	197	197	100	3.00E-63	100	96	YP_009786529.1
contig1_33	16903	17100	+	198	MTTKFKTVEEA VKAA YEALAEAEQLADETGKGRFSP EYGMGGYVDPEDENENTGTNWHPPSSLSC	65	unknown	hypothetical protein	Escherichia phage BI-EHEC	136	136	100	6.00E-40	100	69	UGV23932.1
contig1_34	17112	17387	+	276	MGIEDIKGYKAHTDDKIGKVNAIKDAEERLGLIFKALEEYCEAYHGSFGDTEKELDLAYERIDQIR CAIKHLKEASMWACRSVFQPEEKY	91	hypothetical protein	hypothetical protein JR326_gp144	Escherichia phage ukendt	186	186	100	3.00E-59	100	91	YP_009986800.1
contig1_35	17387	17605	+	219	MSDRNVVEELTEKAQAIMALVDLTKEAEDAGFLSLENDIAICFEDWQSSSCYGE GDDGFVNSQG VWHSSSC	72	hypothetical protein	hypothetical protein MEKHABCG_00044	Escherichia phage vB_EcoM_UP17	145	145	100	2.00E-43	98.61	72	CAA7332612.1
contig1_36	17615	17887	+	273	MESEGELLIKKKVKEMEQAQRKFRKEIEELCEQFQEQA WIGDYNGETYYPTGTAAADHYIDFICED YGVLEDENGLTTRGVWISSSMC	90	hypothetical protein	hypothetical protein JR319_gp202	Escherichia phage vB_EcoM-Ro121c4YLWV	161	161	83	3.00E-49	100	75	YP_009984980.1
contig1_37	17978	18919	+	942	MVLIGSRALQIHAMDMDKDLRPRVCLDYLCTEQEWELSKMFSQEEFVELVERKGNKGHVHKMIA GAHLEYDIASQGDSTALISYCEDSDVRRITYAGHVVA PLDVLVLLKMSHRFKKDSHPHFKTMKDI HFMRS LGAKIPENLKS IYELREKETTYTSHPLNVKSKDFPKGDEVPPVYVDHDSIHEAIAVMDAPA YKSYMYKDGSEVMTSKEKFFAQPKHVRLLGVYEEACV LALERSQIPFGGEIGGPTPKQSFIMALSKV CTITSGWFREYAWENFYVVIKLYENMGENDYVERFKANQHVVKPFEGGY	313	hypothetical protein	phage protein (ACLAME 1471)	Escherichia phage phAPEC8_ev052	653	653	100	0	99.68	313	VUF54267.1
contig1_38	18921	19316	+	396	MCGYLSSEYFKVTHEDLEKARLKLTAIEEYSNTVDHRLKTTKVSVPCLWLRLHKIMSQHDHVVREM HGWCWFHDVALHFGYITEEHRFCETYRIPTLHDLWKAANEIFLTESDWRKVMACLEWRGNE	131	unknown	hypothetical protein EcG1_003	Escherichia phage vB_Ec-G1	271	271	100	2.00E-91	99.24	131	XKC19716.1
contig1_39	19309	19992	+	684	MSKTVLSMFDGSGIMVLRVYAEAGHKCFVNADEGDHGKYEVREHNPNTYVNAWIDSTFNPEDH GPKRPDIIFGPPCTMLAGSGSKHERSTEELDEALANIRVVEALGNKYNVPWMIENPVGKLSLWRK PDFYFDPYEGGYLFEEGSFHPKMPTRDGYTKKTCIWHNGNFVQPVKKPVDHIGCFWGWKSLG GASAKTKQLRSLTARGFARAVFLSNNLLDKEK	227	methyltransferase activity	DNA methyltransferase	Escherichia phage phAPEC8	477	477	100	1.00E-169	100	227	YP_007348443.1

contig1_40	20000	20645	+	646	MSNSKPVVAYQVDRNDGEGSVVIFSTHGLEARRKGAYRLECEFEDCTSHRVKQFDQYADKGFVPI KALLEDGWVVVYAFDYSRLEESASCASIEIYDDYYDTLYLPEWLVFSPDERSVWKTWEEEMERHAY SINEALDRKAWFIEAVKAAYPQSFCDFTGGPGYITHTASFPEGSGRYKGNVYWDWENKQPSAQ DFRCYVCQGDQALDKYLQSLV	217	hypothetical protein	hypothetical protein ESCO37_00196	Escherichia phage vB_EcoM_ESCO37	452	452	100	3.00E-160	100	217	UPW38754.1
contig1_41	20704	21189	+	486	MFQVNVNVHNSYSDCETCGYNSSNVVRISGDLGEASFGEASCSGMDAEWNDAHWLVSKLKE KEKPPPTLLDRSLVEDAGKAYADYAYADGKYLEDKANHLLVYVEAESAYDNYSMSNLRLE AEFDIYFEVEFSEDITYEYNSYDPFEEEECCQE	161	hypothetical protein	hypothetical protein	Escherichia phage dw-ec	325	3225	100	5.00E-112	99.38	161	UJQ43776.1
contig1_42	21174	21989	+	816	MPRRVIFVSGAGLSADSGIRTFRTDSDGRALWEEYDLEEVCDIGAFAQGYRVRTSPDLPVVGGVD ENGMDLYAKTHEFYNKRRELKVDQOPNAHHQIAKWFKEYPNQIVNLTTNVDDLERAGVDRDS VIHVHIGLPEVYVRMHDPGDKYTLVDIGYNSINDDYNWVKPNVVFGEAAPLYADMAHLFDTLT MQDILVVVVGCSNQVINFNWELFPALSMGTMKVVVNGPVNYEETLLYEDRGVVFYREKAATAFSN EGFIKMVEDHLNK	271	NAD+ binding	Sir2 (NAD-dependent deacetylase)	Escherichia phage anhysbys	562	562	100	0	99.63	271	YP_009985506.1
contig1_43	22033	22305	+	273	MTEIRDYLLAHYVYFANATQKGEGNLYLATGHGTGVRKSNIDNALAQVAAGLEDKLQTPVVV VMQNISYLASCTETEFNASETQSNEE	90	hypothetical protein	hypothetical protein	Escherichia phage dw-ec	176	176	94	3.00E-55	100	85	UJQ43772.1
contig1_44	22375	22605	-	231	MLNKIEGCMAFLVDPNPFPMVKVHVHGEYLVGYDEWDCSINSEMHYQPTILKTQDMARITVEDELI JELYERALHK	76	hypothetical protein	hypothetical protein JR319_gp194	Escherichia phage vB_EcoM-Ro121c4YLWV	143	143	100	2.00E-42	100	67	YP_009984988.1
contig1_45	22697	22978	-	282	MELVQELYNALGAKGKDWPEHALIAIRDSDEGEKFSSVSKHEIVETKLGIYMRGTCLFNTRMVEA PVIEDGTDKCPHTVKSEYKFFYAKA	93	hypothetical protein	hypothetical protein	Escherichia phage PNJ1809-36	192	192	99%	2.00E-61	97.85%	93	QP112901.1
contig1_46	22991	23164	-	174	MTKRTDFKCMHCGKSGFDHQARTFCNPRKGRGNFKGFNPAHVYSPDYDKPEEEKFVI	57	hypothetical protein	hypothetical protein LJIJOHLM_00247	Escherichia phage KKP 3954	117	117	100	9.00E-33	98.28	58	WLW41529.1
contig1_47	23217	23318	-	102	MVSFIVGVVVGYLINKYQDVITAKVKDILDSSK	33	unknown	hypothetical protein G377_gp265	Escherichia phage phAPEC8	63.9	63.9	100	4.00E-12	100	33	YP_007348435.1
contig1_48	23328	23936	-	609	MEEKIWDGKDPLEVGHVVRVKKSTTGPGFSGLYHIPEEQGHVTILARDKQNGATPVWIVRWYDKD LNLCSLPIMAHLLAEPCEALFVSAFQKATGLTLDAKDVQKAFDIQEDNDTTSNDELVEVTLSSA DIREIDNCDFPITFKMSQDKMQSSGSCF GIPRWFFDSIKNSTGSDYDQDDVLWLKNREIVLSPLK	202	unknown	hypothetical protein ECO340P1_00229	Escherichia phage ECO340P1	418	418	100	2.00E-147	100	202	WAX14488.1
contig1_49	23945	24208	-	264	MSHSPFFCFVDLENESLIVDSEGYFTYWESEHETISVVKIEMQTNPSLVHVKYGIKAVFVTKTEYTK ERSTLYHNIIEVHYFKDVI	87	hypothetical protein	hypothetical protein HOR21_gp050	Escherichia phage ESCO13	177	177	100	1.00E-55	98.85	87	YP_009786512.1
contig1_50	24205	24372	-	168	MMQVGDVVCLKGANKQMTVIESYGESCKVTWFDENGELQHAIFDQKALRKVEEKE	55	unknown	hypothetical protein ETECTG_CDS0096	Escherichia phage ETEC-TG	113	113	100	4.00E-31	100	54	WPK30611.1
contig1_51	24369	24818	-	450	MSQNAKEKEVITVIRQMEGAENNAFVTKILLNIFEDVILNPNHGKDYQYDVMGGALEINKNTFAE YEQHMLPEEDQDYLILSGLSAQENFYHVLNMAAYADELAVSLERIQMVRDVMNEQIEVEDLVA EPLAEIRAAIEKQKGTQS	149	unknown	hypothetical protein JR323_gp184	Escherichia phage nepoznato	301	301	100	1.00E-102	99.33	149	YP_009985947.1
contig1_52	24802	24999	-	198	MAKMLEIDNVVITITSIPCPMPPCYCGGAGYVMAADVGGIYECNCKTGTGYIESEKHVEPKR	65	DNA ligase	DNA ligase	Escherichia phage ESCO13	135	135	100	2.00E-39	100	65	YP_009786509.1
contig1_53	25002	25220	-	219	MTKMYAAVDKLDGSDSVFILNKMGLVLYARTSQNIEHQVEAAQILEQITPPYLYSNVERFDNALG LTLIAEW	72	unknown	hypothetical protein MEKHABCG_00026	Escherichia phage vB_EcoM_UP17	148	148	100	2.00E-44	98.61	72	CAA7332594.1
contig1_54	25234	25449	-	216	MSSNFLYKAKDSRDGENHWWLITGDGVILPWDGETKVQILEKVKGVSNFISHDITTFKAFAMNPS LVAEW	71	unknown	hypothetical protein G377_gp207	Escherichia phage phAPEC8	147	147	100	4.00E-44	98.59	71	YP_007348428.1
contig1_55	25810	26019	-	210	MLKAFAYVSTVGFFYWHVVGCVLGSVVVMGEWLTYNVFEWDVVCRSLLIWTAIVCWITVSLT LDLY	69	unknown	hypothetical protein HOV53_gp042	Escherichia phage vB_EcoM_Schickermoser	133	133	100	9.00E-39	100	69	YP_009823708.1
contig1_56	26013	26432	-	420	MLGKIKAFFKRVIEGSPTEGALGRSLTGEPLAIIISIRHGGYSIRQTPLGIEGSMLSWTISQVGDNRLA AIALLRGEYDYCLSASCKKHLIEHIRDRVEREGGYFFETKRNQEGTLDFTKVYWDNHRQTVEQLLE ERC	139	hypothetical protein	hypothetical protein JR327_gp199	Escherichia phage Mt1B1_P17	288	288	100	7.00E-98	100	139	YP_009987164.1
contig1_57	26450	26584	-	135	MSKKLFNIRENRDGSFVVNEFNVSVGTFITKRQAEQVRDTLNK	44	unknown	hypothetical protein	Escherichia phage dw-ec	89.7	89.7	100	5.00E-22	100	55	UJQ43751.1
contig1_58	26577	26780	-	204	MNGVKNYHRWLESYLKKCELGVPGYTYDTEILDEMEWFKEPRELLANILMAWDGTAQSIIEGGR NE	67	unknown	hypothetical protein HOR21_gp041	Escherichia phage ESCO13	141	141	100	6.00E-42	100	67	YP_009786503.1
contig1_59	26767	27105	-	339	MYTTEYILNFFKGWLKWAQAPVGDVFPWDSRQGLCRLEDWLITTYNSETKKSTSNRLKM LFEEDGLDPIYPFGESFHNGLFLGTQHYDKDRVDVWKEKVAQYEWG	112	unknown	hypothetical protein G377_gp211	Escherichia phage phAPEC8	236	236	100	3.00E-78	100	112	YP_007348422.1
contig1_60	27157	27768	-	612	MIQCTHIQITWRDELYHLGQFTVGETYPIKHNPNIANFDRMVLVEDDLGQTYSLDLKYPFSGYD WIVTFDEAENKTMNEKNWYRCELPVVGKGVIFVPDLERSYSDSSYSPVKEGTEVEIAHRTS HGNDVAVVFWDDGGAACAGGFVAGNFPELPDPLKEAILGVSFGLSYTSAQEIVELINGLTVPNEI FKQIK	203	unknown	hypothetical protein JR321_gp145	Escherichia phage anhysbys	424	424	100	2.00E-149	100	203	YP_009985488.1
contig1_61	27773	28045	-	273	MDRQTLKTMADATNSPYFEKVSKLVAQAAEEGYYNINIHNPSLILEMPSDKKIQESICEGIVSYWRE RGCGANMALDSANIVRYINISWG	90	unknown	hypothetical protein G377_gp213	Escherichia phage phAPEC	189	189	100	2.00E-60	100	90	YP_007348420.1
contig1_62	28045	28410	-	366	MTIDLKCKRILLDFYNNWLEHLRFPRESGYADVGLCRGLRMYISDEFRAEHSLAYSVYGMQLASF ENAGLDTTFPNTAKSFQECKEKRCMFNEKRVQWVKDRVKQLEQELDFFYDEAE	121	unknown	hypothetical protein	Escherichia phage dw-ec	254	254	100	7.00E-85	100	127	UJQ43744.1
contig1_63	28388	28810	-	423	MKQENESIDHLMLSALFAGWDVFFENLFNSATDGSDFMRQFKRRTRVEDYTFYSGLIEKGYEDTNT TLTKVLDMVMSVIDAIDESLPLDNCNTKVYVYKIAARYVANSCLLSTQIAVNNLANLFDEGETFY DNRFEV	140	unknown	hypothetical protein JR327_gp192	Escherichia phage Mt1B1_P17	287	287	100	1.00E-97	100	140	YP_009987171.1
contig1_64	28819	29490	-	672	MKKFVYVSRLSKQKKGEAQYGMESQENDIRYFLDSVPDAEIVGQFSEYYSKGDKWKQRKELVKA VEMCKATGATLLVAKVDRLGRNNAVSATLLEMIDVKIAIMPDADKMVIQLLSVLAEQEVRGIAIRI KGLAVAKSGVLLGSANPKTAAARRKGKMEYNSVKADAFATFRERLEILRDLNTPYKTIAEK NSKKIATARGGKWDAKTVSRLCARLNIK	223	recombinase activity	hypothetical protein HOV53_gp034	Escherichia phage vB_EcoM_Schickermoser	257	257	100	2.00E-84	100	128	YP_009823700.1
contig1_65	29561	29773	-	213	MAKHYPHPDPKNKAVILRQWQRVCRCKPINSPHNVKDYDLGTFVEYTYIDKNKRKHVEEYCL RVEWL	70	hypothetical protein	hypothetical protein JR327_gp190	Escherichia phage Mt1B1_P17	149	149	100	4.00E-45	100	70	YP_009987173.1
contig1_66	30000	30097	-	98	MQAVVNEAIMNLSFLLAGLGGVLIGLALIWCIIRRLIGYRQKGVSCEFVSYNFTTAYSNEVGSNGAQA FLTPYPTVEDIRNLEVELMGLGDNYTSLVIQNIIFRLKQES	107	unknown	hypothetical protein JR327_gp189	Escherichia phage Mt1B1_P17	218	218	100%	1.00E-79	100.00%	107	YP_009987174.1

contig1_67	30108	30407	-	300	MQVEDLIHLNKAKEKGAIKDWKRETSDELSHCCREFYIEGIANDHYTIEWYNLMLTKHGSFEVWF DDIDVNGFHGPKIAMQLSYRREVVAHLGLHN	99	unknown	hypothetical protein G377_gp217	Escherichia phage phAPEC8	208	208	100	1.00E-67	100	99	YP_007348414.1
contig1_68	30418	30972	-	555	MKKFICTRSTNSDLVGKVIKELGFHANGKKYILLKDSFNGEYPRCTFFNYNTPFAEGDAWDWAE LHPFCEDGQTEEQEESTGSLRDKLRNKAQANSHFTMVDVAVLLEIEDCAEQGFEKYFEPSSFGLC NNPSSVEQISEQKRGANVVA TILRAKGLDVTLATAEHISIFGIKHIVISWN	184	unknown	hypothetical protein G377_gp218	Escherichia phage phAPEC9	384	384	100	1.00E-134	99.46	184	YP_007348413.1
contig1_69	31027	31347	-	321	MSEELLTFYRTYLAWLEAGAPEGEPFTRCTGLCTNLVDFYDMGESERYEPLVDEMHEQFYLGKLV VLFPNSNFGKYTLEAEKSRCHLNVDVNVWVKERVAAEIMG	106	hypothetical protein	hypothetical protein JR327_gp186	Escherichia phage Mt1B1_P17	219	219	100	1.00E-71	98.11	106	YP_009987177.1
contig1_70	31344	31556	-	213	MWIVRLKYDGKFPWEKDYCACDSSAAHAKAAGQAVVDMYNNTFPDEMAGVMTSMFTYYSFEV YYHEGEWK	70	unknown	hypothetical protein G377_gp220	Escherichia phage phAPEC8	145	145	100	2.00E-43	97.14	72	YP_007348411.1
contig1_71	31559	31786	-	228	MSDYNWYLEAVCOFYDSIVLRDPICQELSRASALAINVKVHDWVANLEKELEFLETTRVFHKV FPEWFEMEE	75	unknown	hypothetical protein JR327_gp184	Escherichia phage Mt1B1_P17	154	154	100	6.00E-47	98.67	75	YP_009987179.1
contig1_72	31786	32112	-	327	MKTSTGLMEFYKIYLAWIDVGAPDGKPFRRDCLCANLFDYVHADGYNLLITLSDSEMHSQFYFK GLSQELPFENYDAYVLESDAEVCNLNVDRINWVRDRIAEDE	108	hypothetical protein	hypothetical protein JR327_gp183	Escherichia phage Mt1B1_P18	226	226	100	2.00E-74	99.07	108	YP_009987180.1
contig1_73	32078	32350	-	273	MNKDRFLSLVAEAPFDVLGVRLWKDRNYGLDVQTYSLWLVEHSLDSELCMGRDSRSLCLKFRSL ERANKQEKLTRWLNENKHRVDGVL	90	unknown	hypothetical protein HOR27_gp025	Escherichia phage ESCO5	184	184	100	3.00E-58	100	90	YP_009787016.1
contig1_74	32413	32610	-	198	MEEKLERIHELAMSIGYDDCFLQTIGETQDDYDSWVKELEELKTSLIADFAEADKADRYNYLCR	65	unknown	hypothetical protein	Escherichia phage dw-ec	131	131	100	4.00E-38	100	66	UJQ43721.1
contig1_75	32610	32972	-	363	MSKDFVEFVKDEETGLGTGFCIEETFKREQEKAILMHRYDHALEQWKNAEQCKKNLYAENRKLQ DQMELLAISRLSLA VEDGFKNPDPGFPVSDIEHDLYLARGAYFYVQKRPVEGEK	120	unknown	hypothetical protein	Escherichia phage dw-ec	252	252	100	1.00E-83	100	160	UJQ43720.1
contig1_76	32974	33237	-	264	MKETLPAAYRLNDRIEWTDVSCFYPEIVQYWRAKGCGVVVNPICGVPDEDCLYLNGKWHYSYCR WPFEWCKEDLPEGWEYPKANRR	87	unknown	hypothetical protein JR327_gp180	Escherichia phage Mt1B1_P17	182	182	100	2.00E-57	100	87	YP_009987183.1
contig1_77	33242	33688	-	447	MTKVRRHYAVNCNDAWRLCPDDPTGTFVRYEDYKELSDAVIALLTDIRSRYPGQDTCPHIKLLAC LVGEKEVKDGKFRVEYQGETLDVPEFVNVIATDSGDGRYGYSHKPEIPDWIPARISVSTGDYIFL GVGSSKDWRFSLTEV	148	hypothetical protein	hypothetical protein ECO340P1_00257	Escherichia phage ECO340P1	308	308	100	2.00E-105	100	148	WAX14516.1
contig1_78	33699	34097	-	399	MKKIIVGFLLLIASLGTANASQVYECVSDVVVKNLKGGEIVSGPKMASVINKDNSFILKNSGGAL MSGILOHTGKEKSGDGSAMYGSQQIGITTEVVMRTEYRDTLAWFLKNDKTTITNVLTEADCTQ R	132	unknown	hypothetical protein ECO340P1_00258	Escherichia phage ECO340P1	271	271	100	3.00E-91	100	132	WAX14517.1
contig1_79	34194	34400	-	207	MSCFTKAVSICKKQYESDYGIFNIPVDHTEYCSCGGRMKKTVIYADNGDELVPVMVCKACHSVKT LKA	68	unknown	hypothetical protein JR321_gp126	Escherichia phage anhsys	142	142	100	3.00E-42	100	68	YP_009985469.1
contig1_80	34403	34624	-	222	MKIRVCDVLGYVGFEVNIQIPFVVEAHLVSDDMTTFVTIEEMSKVEGWFEEDVWEGCDYVFFS DEVNVLSE	73	unknown	hypothetical protein HOR21_gp018	Escherichia phage ESCO13	146	146	100	7.00E-44	100	73	YP_009786480.1
contig1_81	34626	34814	-	189	MVIEIKLEYAGAVALIAQTLGAKIEEVYINAWSEVIDPMDNIANRLLVAECERTNIIYKGA	62	unknown	hypothetical protein JR327_gp175	Escherichia phage Mt1B1_P17	123	123	100	7.00E-35	100	62	YP_009987188.1
contig1_82	34829	35029	-	201	MPIVFSFLVIMVVLFAAWLWDFDPAQAQQRATDWKEQCVILKHHERNAEKFLDLECDRLVRYKQ DK	66	unknown	hypothetical protein G377_gp232	Escherichia phage phAPEC8	137	137	100	3.00E-40	100	66	YP_007348399.1
contig1_83	35020	35334	-	315	MSEELKEFYQAYHNWLAGAPDNNPFWHDKGLCSCLYLWTGGYDDLNYEMQMQRAGLSEEP PFDDGDWFKYDFAQRNGLLHLNAAARIKWKDHATQEDYVQCQ	104	hypothetical protein	hypothetical protein EcG1_233	Escherichia phage vB_Eco-G1	218	218	100	4.00E-71	100	104	XKC19946.1
contig1_84	35335	35511	-	177	MATFQQLKDVSRVLRKIREADAAVRNALTPAEREDLEEVEKTAENAFAYVSLTYTGG	58	unknown	hypothetical protein JR319_gp156	Escherichia phage vB_EcoM-Rol21e4YLVW	117	117	100	1.00E-32	100	58	YP_009985026.1
contig1_85	35527	35886	-	360	MSGFEFRKVKDISLFEQDVVRINGRLKFKHQLMYPSTTRNVMFVQFVFAASDYTPYSAETEVYFEG YVDRPLAKEMWDKYHINITDSRGVFWNYPSEGVAFDSCDRDLAEELAEWRDIN	119	unknown	hypothetical protein JR327_gp171	Escherichia phage Mt1B1_P17	251	251	100	1.00E-83	100	119	YP_009987192.1
contig1_86	35896	36087	-	192	MKIRLEKGDITETRKEITEPEERSTILVDGVLYCCSVKYSYKEDQYGDPEIWFVGDVY	63	unknown	hypothetical protein ESCO25_00257	Escherichia phage vB_EcoM_ESCO25	127	127	100	1.00E-36	98.41	63	UPW38260.1
contig1_87	36068	36286	-	219	MKTSIRVKHDPNSSYPYADVERHEGDYTIKRVPTDTGTFNFDVIALDDQGVNDLNVALLALKEG RYENQTN	72	unknown	hypothetical protein JR327_gp169	Escherichia phage Mt1B1_P17	147	147	100	3.00E-44	98.61	72	YP_009987194.1
contig1_88	36283	36756	-	474	MAGLKLLEMLTKQEFVPEHGETYIAFLISDFYGDLEYVELECEPHYQMDAETGYCLGTSVAVYNGDN GIPFHTPMRYEAKNRKLLTEEEKETYKYHEEEDQRFWWEKTFWFLSDRRNLQIHPEELDSEMSIGIMK KKDFMHQVREANKFRVAIKEENKT	157	unknown	hypothetical protein ECO340P1_00266	Escherichia phage ECO340P1	236	236	100	9.00E-78	100	112	WAX14525.1
contig1_89	36769	37002	-	234	MKGKMKMKNQVPSAYTLWLARALHQTIKDPKPKMSGKKFMSKGKTTGFTFRMSVKMKRLGY KPNYARYPSEYNWFD	77	unknown	hypothetical protein	Escherichia phage BI-EHEC	159	159	100	8.00E-49	10	78	UGV23840.1
contig1_90	37002	37301	-	300	MNLTEQLRRIAKEASFNPVEEVIETCFEAERAGNSSRNTFSPDGLDNSPTHPGEIYNQVKWMDEA VAILRERGLVVYKEMDLNGAYEWITIDWSEVK	99	hypothetical protein	hypothetical protein HOV53_gp010	Escherichia phage vB_EcoM_Schickmooser	207	207	100	2.00E-67	100	99	YP_009823676.1
contig1_91	37329	37766	-	438	MFKNVAVYCFKSKAACEAFSMISDENFKMAALIEGSCFRVEDVSESGVCSLTLLDSGDIEAGQYP FRSWEILLARGERNNFMCVSAGEVVKETKDVSVYNSEFISYSEYQHLEGIVGHLISLIDIECDLPESLK EELKALDLL	145	unknown	hypothetical protein G377_gp238	Escherichia phage phAPEC8	293	293	100	1.00E-99	99.31	145	YP_007348393.1
contig1_92	37779	38234	-	456	MFKEGHVYRFQDEDYMRLYSTFDNSIASIENGFEEVLSTDANGNLSIVIGRDGVITASDGDRIYI NSAHIDYFVGGIRGRGKPEEPVDTTKEWYVVMDDTDCISGFESYEALKEAAEHKMANPTEE VEVYKRLVATIGVSFV	151	unknown	hypothetical protein JR327_gp162	Escherichia phage Mt1B1_P17	308	308	100	2.00E-105	99.34	151	YP_009987201.1
contig1_93	38240	38695	-	456	MFKVGTGYFKFSVADQGDMAHTDKANIAVCQAGNEVFVKVMNTDDKYGHVLEFYINGTLYTAG VTPGFSNVTYLIDNEEFKYFEVKEETMGKAEPQWHVIVVIGSECVDVCSSEFKAASEVATKAKKDY SKTVEIYARVAVANATITIDKE	151	unknown	hypothetical protein JR327_gp161	Escherichia phage Mt1B1_P17	310	310	100	3.00E-106	100	151	YP_009987202.1
contig1_94	38688	38882	-	195	MNKGTTVYLVTKNTPGWSQCSTVPYKICATLELAQRAEAEDAMQYSYGEIPTFLEQEGAHHV	64	unknown	hypothetical protein ECO340P1_00273	Escherichia phage ECO340P1	136	136	100	4.00E-40	100	64	WAX14532.1
contig1_95	38875	39336	-	462	MRQFTILAAVYQCVHDYVSHTGLLEVTSKIEGNMGTVCVQHTLSNVFKVFTVVAADYNRVDV RFLDHNFRNALDNIEDYLPVKPLSFPPSRANNVVTNLNERNVAMHKVRQLKMLMEMQEEIEKEL KEDFGMLPKDALKWYDELGGESYE	153	hypothetical protein	hypothetical protein HOR21_gp006	Escherichia phage ESCO13	317	317	100	8.00E-109	100	153	YP_009786468.1
contig1_96	39333	39572	-	240	MILPVDNIEAMNVLDTIFYFNHYSETWMTNTQTLEKQALIKCDRYLQRAEEDNITLASARRVSI FNKMLALWGGRK	79	unknown	hypothetical protein	Escherichia phage vB_EcoM_EP57	48.1	48.1	100	1.00E-04	95.45	79	WPK29159.1
contig1_97	39569	39790	-	222	MKNLKTVMFLTDPTRVQALAKASRVAVEFQNFKPSVVTGSETCVIDFNEYFRGNPVGRYFIKLN KDAEQVQ	73	unknown	hypothetical protein MEKHABCG_00272	Escherichia phage vB_EcoM_UP17	143	143	100	1.00E-42	97.14	73	CAA7332829.1
contig1_98	40000	40203	-	204	MTNSIPLSAATLRFYKAWIANYPAMNRTTSLGCGCLVDYVNFVGETTREETRRWRDSDLLRLKY EMRKQFTCAGLDYNLPFNADCMYDLSECLNACHTNTLRQVWKDRIEDANNACIE	122	hypothetical protein	hypothetical protein JR327_gp155	Escherichia phage Mt1B1_P17	254	254	100%	2.00E-93	100.00%	122	YP_009987208.1

contig1_99	40193	40537	-	345	MQESKNVPLSSLRLMKFYKAWFAGEVEGHTTSGLCICLIKYVEGTYPDELLPRLQEQEMKSQFIGAGLDYNNFPNEGGEYEEYTFEHKKLICHNKHRIQWVLDRIQDYEGEKNDK	114	hypothetical protein	hypothetical protein HOR21_gp001	Escherichia phage ESCO13	238	238	100	8.00E-79	99.12	114	YP_009786463.1
contig1_100	42159	42578	-	420	MNIXSNPAYSFDNAPCHGSAAGFEIDGKLIVNVVDGEEVAVYPVNDVKSRLQCRMDVTA YQLDPPIRVVALVLEEIKAMHHSNKFIGDAQDNMNVCRHVVNEALKECGFKDLMIKRDEKFRFRNDLANRYSIYEAL	139	unknown	hypothetical protein G377_gp246	Escherichia phage phAPEC8	287	287	100	2.00E-97	100	139	YP_007348385.1
contig1_101	42718	43086	-	369	MSKSAIKALKAQEVIA TSTTGAKVNLVGYLTDETIRKNWRNADLLACLLINSVANAFQCAETASLEENLFDNMDQAIETYIQSNLDSWNSKTWPDNLRDITDQLIRLAVMVERDYNVYNS TK	122	unknown	hypothetical protein ECO340P2_00002	Escherichia phage ECO340P2	248	248	100	2.00E-82	100	122	WAX14544.1
contig1_102	43165	43398	-	234	MIEQIKSTKPNVNGNVSHFIGNERKGTPTAAVTVQPNQDGYWFTVYGSYSGFRSAHDKILQVVKPTGKNITAEKFYKK	77	hypothetical protein	hypothetical protein HOR27_gp134	Escherichia phage ESCO5	161	161	100	2.00E-49	100	77	YP_009787254.1
contig1_103	43788	44072	-	285	MKKMIAVVALVVGINTPVMANDLPESITLTDINAIRGVNRYRLCLAAKTFQDGTTEYYGFEGIRCGELARDLKEDPDLEAIPMTVNGKAYVSR	94	unknown	hypothetical protein ECO340P1_00283	Escherichia phage ECO340P1	187	187	100	1.00E-59	95.74	94	WAX14542.1
contig1_104	44128	44364	-	237	MSIATVNLNAVKTAESSGLHVELIDQPGDGLLVQVYPPKVGDDYYWCYSDFTEQVDTKAITAFILKAJEENNPHYNNIQ	78	hypothetical protein	hypothetical protein LJJOHLM_00003	Escherichia phage KKP_3954	164	164	100	1.00E-50	100	78	WLW41295.1
contig1_105	44409	44708	-	300	METIAIVTVKLVVGDV FALMVPNSSKLGAYEVM DHKNESFGDGCTMAVKS LKDGIIQRANWHKGNQVGLISANFLPEEQ TLDQLSGGKTLAELLETAI	99	unknown	hypothetical protein HOR21_gp139	Escherichia phage ESCO13	203	203	100	1.00E-65	100	99	YP_009786737.1
contig1_106	44790	45176	-	387	MKTEHIEIINGYKEAFIFAESARDHEGNFIDNDDYDFSPSADERIAQDVTAFINANLAAISEAMSDGATANQIGNDLHFTRNGHGVGFWDREIYTTNTANRLTNAAKFMPNVSAIYIGEDNLIYE	128	hypothetical protein	hypothetical protein HOR27_gp138	Escherichia phage ESCO5	261	261	100	2.00E-87	100	128	YP_009787249.1
contig1_107	45173	45388	-	216	MITNKTKGTEFLRGLQV GKPEIWHCTKSAHNEMKDF TATLQRVKISITQKKALLVENEIPQTIIIVERTA	71	hypothetical protein	hypothetical protein G377_gp253	Escherichia phage phAPEC8	145	145	100	2.00E-43	100	71	YP_007348378.1
contig1_108	45587	45724	-	138	MKTFNASTIGYIITVQAVDLVAAANKIKKMIPTGSEFSVWEVK	45	unknown	hypothetical protein JR319_gp135	Escherichia phage vB_EcoM-Ro121c4YLVW	91.3	91.3	100	1.00E-22	100	48	YP_009985047.1
contig1_109	45769	46023	-	255	MTAGKQRSKVYVHIGRRNGPPLITEEKQIMPTMFYVSRKGHNIFWSEDLNEAMTFARDRVAIGGVNITVTDENGIEYYNGDNEE	84	unknown	hypothetical protein JR327_gp011	Escherichia phage Mt1B1_P17	117	117	100	8.00E-33	100	56	YP_009986936.1
contig1_110	46025	46360	-	336	MYLVGRQWCRSQEERKIMKITKSLTNYAARRGLCLTVENLKGEDFLCFWELENDCEWMFSYSICEDYQGLCLTWRNGIYLP EEEKELPGTIMTERQLKEVIDFVGQNIKK	111	hypothetical protein	hypothetical protein ECO340P1_00006	Escherichia phage ECO340P1	194	194	100	4.00E-62	100	94	WAX14275.1
contig1_111	46508	46669	-	162	MKTTDIIKEIALAAGVIEEIVIALNLTENDLRNYEASVKSAGAVLYVDPANK	53	unknown	hypothetical protein ECO340P1_00007	Escherichia phage ECO340P1	103	103	100	2.00E-27	100	53	WAX14276.1
contig1_112	46680	46799	-	120	MSKYTVEYTVENPAVSEGKMTFAISIIAFVVTLSIIL	39	membrane protein	membrane protein	Escherichia phage anhybsys	76.3	76.3	100	6.00E-17	100	39	YP_009985440.1
contig1_113	46898	47182	-	285	MSKANTVLMFSLINDLAYLSNMTQEGNTLTAFTNKLDRVHISLKTVSKGFYSLAYHWITDDETSQDYSAPFPESMAREHIAAVVNDGLFTE	94	hypothetical protein	hypothetical protein ECO340P1_00009	Escherichia phage ECO340P1	211	211	100	1.00E-68	100	104	WAX14278.1
contig1_114	47254	47460	-	207	MITAKQEKIHDVAAVA AAIIGSY YDTRFSPAMHEVAASAVSGVLFYVGKRYLSPMINKLTPWKNKG	68	unknown	hypothetical protein JR323_gp134	Escherichia phage nepoznato]	139	139	100	7.00E-41	100	68	YP_009985997.1
contig1_115	47546	47731	-	186	MTLNEKLTAYNATLKIAVRYRDEYGFIAQQVILGFSDDGLIYVDAHNNKVKPNVISIKYL	61	unknown	hypothetical protein HOR21_gp151	Escherichia phage ESCO13	124	124	100	2.00E-35	98.36	61	YP_009786725.1
contig1_116	47787	47933	-	147	MNTSNRAEKIQSSKIRKAWNEEVIRKGDKNKTKRGKSDKYNWMDLED	48	unknown	hypothetical protein G377_gp145	Escherichia phage phAPEC8	94.4	94.4	100	8.00E-24	97.92	48	YP_007348637.1
contig1_117	48013	48366	-	354	MKAQNAIKYILAAIDFNDYGITTEKEKIAELMRFNSEYWYPDNQSRFNYSIVKALASWLQGLPSDINIAFEYWEIDRLTWSGYIKENSSDDKIQRERENWLYIAGVILACS YE	117	hypothetical protein	hypothetical protein HOR21_gp153	Escherichia phage ESCO13	238	238	100	6.00E-79	100	117	YP_009786723.1
contig1_118	48445	48666	-	222	MITFAIYAVVASQVYINDITFTEDKAAAGDITAVYNECKAVERMLAPCMLMSERQDGITVFTNIETGYQMVVTK	73	unknown	hypothetical protein ECO340P1_00014	Escherichia phage ECO340P1	149	149	100	4.00E-45	100	73	WAX14283.1
contig1_119	48740	48958	-	219	MAIRKIKVVCISTGGAFVVGQKYNAVLMGVDWKVKGLDGYEYGTTCGLRGRIGYVSFDNKEKFVFDVTMSK	72	unknown	hypothetical protein JR327_gp023	Escherichia phage Mt1B1_P17	145	145	100	1.00E-43	100	72	YP_009986948.1
contig1_120	49037	49204	-	168	MITFATREAAARNVARKVNAANL GATLAPVKDESQWIFPLGRHADKLGTL SLKK	55	hypothetical protein	hypothetical protein G377_gp148	Escherichia phage phAPEC8	111	111	100	1.00E-30	100	55	YP_007348634.1
contig1_121	49297	49512	-	216	MANIRTLKNASQVLSFDSDEYFNK DITGVKNLKDVKDVIIGIRSLRGDYYGKNQVYKLNQSYDFTLIIS	71	hypothetical protein	hypothetical protein HOR21_gp156	Escherichia phage ESCO13	141	141	100	6.00E-42	100	71	YP_009786720.1
contig1_122	49603	49830	-	228	MAINIVRVSGTVGSSQVIAVVTNKKINDVCEILNKWAIANFGEYTSVEYIESYQVPTISLTDNLVDRLLCLDELI	75	hypothetical protein	MAG: hypothetical protein M1M20_gp125	Dompiswa phage TSP7_1	148	148	100	1.00E-44	97.33	75	YP_010356294.1
contig1_123	50000	50160	-	161	MAKSKMYNGHKNKTHWNVSLWINNDESILYRLAQDFINANARNRDAARDMMLFLEQTGDQKTPDGFKYSTTAIRAAMVGM	79	hypothetical protein	hypothetical protein Eco3D2_00001	Escherichia phage vB_EcoA_3D2	164	164	100%	6.00E-60	98.73%	79	YCB25301.1
contig1_124	50250	50615	-	366	MAININVSAYATLANTAKIELSSIEAVHISARRWFQOSYGNITYFSMLVDVEIGGKLIEVVNVFPQYGYGDHFDTVALEEFSKVINMEGKEFSRGAYLSRFCRDNGITVYSHASDVKRKKDL	121	hypothetical protein	hypothetical protein JR319_gp120	Escherichia phage vB_EcoM-Ro121c4YLVW	250	250	100	2.00E-83	99.17	121	YP_009985062.1
contig1_125	50713	50892	-	180	MAIIAKTEHIGLSILLA YEETLKMYVVTVGDYVREYIDLAFCFYIRQVKNKAYNDYR	59	unknown	hypothetical protein HOR21_gp160	Escherichia phage ESCO13	115	115	100	4.00E-32	98.31	59	YP_009786716.1
contig1_126	50976	51338	-	363	MSKQINTIMFNLVSFRDEMKNLPRETVDIHVSAYRALIDMLPLKRQDHAANMMLNAMLKKMIQTDLTLAYEYQGRLYATYNKAVPGLGST EELHGLNDQNTWDSMRVMVWAESGKIYE	120	hypothetical protein	hypothetical protein	Escherichia phage vB_EcoM_EP57	249	249	100%	3.00E-83	99.17%	139	WAX14290.1
contig1_127	51476	51634	+	159	MRALIVPTVKLFSLLIIVSLLHNFTMSGTIAALRGKYYASGDDMSKRTIFVF	52	unknown	hypothetical protein ECO340P1_00021	Escherichia phage ECO340P1	251	251	100	9.00E-84	100	120	WAX14290.1
contig1_128	51608	52165	-	558	MGREYVIQSVWKHEADDPRIIPDHIDESTGYSGEQIGNRLARSNGNVKARYVRPGWLANGNADLSSAEDASDGAKDNPLYKIDPAFRVLDEYPSKIAALDQALESKRITWTAYNMAKNVLDGKLQIAERKLAKIAAIAQEEDEETEEEEEY EIIPLLVCDAFPDYQPT EEEKRIALENFENSL	185	hypothetical protein	hypothetical protein ECO340P1_00022	Escherichia phage ECO340P1	378	378	100	5.00E-132	100	185	WAX14291.1
contig1_129	52167	52424	-	258	MYFIKILKGHVIAFKDNAFYRLAKYALIHPHYVYIRGRDEINFDQTCENIEIRKVGVRDYRTSFYCKDSASLKFVCQLLKKGG	85	unknown	hypothetical protein G377_gp268	Escherichia phage phAPEC8	177	177	100	1.00E-55	100	85	YP_007348628.1
contig1_130	52501	52830	-	330	MYHIGRRNGPAAHNRHIIMASYSATMIVAGTGKPMSSGGGSFANINIDGRSLDAAITVARETFPKKECKFNKQDYLGAIEKTA RFVDYKSPKMVDTLTKAQDVAFLL	109	hypothetical protein	hypothetical protein Eco1D1_00146	Escherichia phage vB_EcoA_ID1	223	223	100%	2.00E-73	98.17%	109	YCB25171.1
contig1_131	52863	53060	-	198	MATLHIVAKAGQINVIVNGFTEFSHPQDDHETVLSFIDS LLEMGVITEDQHATCKCRNVQIAGIE	65	unknown	hypothetical protein G377_gp008	Escherichia phage phAPEC8	134	134	100	2.00E-39	100	65	YP_007348626.1
contig1_132	53082	53195	+	114	MMFFVGGRWIMEILTFARPALRPVVVYCRCAAPPSTR	37	unknown	hypothetical protein	Escherichia phage vB_EcoM_DE16	69.3	69.3	89%	2.00E-14	96.97%	42	WAX24842.1
contig1_133	53192	53425	+	234	MNTTLPGEERQPLFQSFLFSCLLYIKERIAIIFLRPQPGRTTKKGRHHDKYYITPYALIGLARRHGAPGSKRNLKLG	77	unknown	hypothetical protein HOT48_199	Klebsiella phage ZCKP1	156	156	100%	8.00E-48	97.40%	77	YP_009803492.1

contig1_134	53492	53833	-	342	MSRAPVSPRHVIRITDPARKASDYFIFFLYKYIAPSLPAINLPTSAPGLMAPPLRRGVALLPLYVKQYKPPDPWACQDYFLFSCQDRTPNQKYSISRAPGGILLSPPPLQAYR	113	unknown	hypothetical protein G377_gp099	Escherichia phage phAPEC8	215	215	100%	5.00E-70	94.69%	113	YP_007348625.1
contig1_135	54406	54948	-	543	MRITDDYVFFSHKDFVSNWYIAPFTETEPGYNQTFNCVEQYMMWRKALLFNDHNTAQAILTHSLRKDEKIQAYYKRMGRAVSDFDNNVWEENRERIVMRGLCLXYQNPDLYADLHLYQYKTFVEASPYDKYVYIGMGMYEPGLNPATWKGQNLGKYHNKLEILFPDKIPQRRYL	180	domain of unknown function (DUF1768)	hypothetical protein JR325_gp050	Escherichia phage tuntematon	380	380	100	2.00E-133	99.44	180	YP_009986426.1
contig1_136	54935	55159	-	225	MATGGWINKGETMARLADNPVFPVLDLYDELTYVVERYNYNEDLENTNKLVLVLMKAYQQGQR EILSEMKNNANN	74	unknown	hypothetical protein Eco1D1_00141	Escherichia phage vB_EcoA_1D1	150	150	100%	1.00E-45	98.65%	74	YCB25166.1
contig1_137	55137	55502	-	366	MLVDVQIMRNERMDFFEAVEKHLRWDEYFVAPGCGPVEHLAEDDDVYMIIRQVYQTDQCEETPE LILFECKDLAKYFDYGGKEGHNSLRYNKRLILDYMRNNKHKLIDADAVYGYWWM	121	unknown	hypothetical protein	Escherichia phage MircacidM_Esher1	252	252	100	4.00E-84	99.17	121	XKC20763.1
contig1_138	55496	56698	-	1203	MAKTLEQYIGECKPIAEAKGYEIIIGIVEPFGVHTKMINFPCPNHGEWRTSTFANFRKGSGCPRCKN EKARQDNSKNLDYYLSECKPIAEAKGKILGINGEFIVHTKMINLCPHEGEWRTLTfHNLKGGSGC PKCGNKRSRNSKILPDDQHIQDFINTQKFKKEGTIFTKTDKKRGDSLWCVECPACSHDEYVQAGVC DGKFYVAGNDLKQGGKIPRCATNCHYTEAQITYRVKKAVERKGYIWWGVWGKPSVRLGKFYGYC KKHGVQIGRASGLLNHGTGCPQCANQTQQCCYINHHIDEQGILCALKFGIANNSDRRIKKQNSRNVFTMKQVQVWHFPTVKQCKDAEKRCKRVLHTEAVSKYAMPDGYTETVELSCMASIQNIYKLYGGT LQEETC	400	endonuclease	endonuclease	Escherichia phage vB_EcoM-Ro121c4YLVW	832	832	100	0	99.75	400	YP_009985073.1
contig1_139	56779	57918	-	1140	MKYTIFGDVAVVNKEYGVEANKLPAGVWVNCDPHGNSLVYRGESFSLPNTLYGETKDRAAHVYKTFARRSKEGKNTGVLLTGKSGSKTMLAKLSMSLMSSTEGLGIPITLVTPQYTDAGLFEMSKITDR AVVLFDEFDFKYAKKEDQEAALLTLDDGTGSGNKLTYLTKNSGYISEYFVNRPSRIYYSFNYDKLSSETMLDYLDKNLVNKKHVDNFQRLWDVSTELSFVIGIVLEELNFYPKMTFKCELEMMGISLGNDAK WNVASIVANGKTLKVNWINNWHDFTPTKFLSGACSLNIYQLSKLDDEVEAMETNSYVILDEGGDP HIDLCATADGLTCDLIEGGKILVMSTPGNLTFRVLEVPYQRTSTTLGVSF	379	ATPase family associated with various cellular activities (AAA)	hypothetical protein	Escherichia phage vB_EcoM_EP57	772	772	100	0	100	501	WPK29215.1
contig1_140	57918	58274	-	357	MKKLILATLLATVSFTTYAQKFVAVKTDIGKDVITGNKKEYITPGNGVLEECQDVEAYTGKEDNTE RHFYSHIATCKNEIVAIIKQYKADAPGGEYLLVKNIKSEKTAFTVIIKGETF	118	unknown	hypothetical protein JR321_gp073	Escherichia phage anhybsys	233	233	100	5.00E-77	99.15	118	YP_009985416.1
contig1_141	58286	58450	-	165	MILNFIINLCLTLGLLCAIVSPLVGEYCESELMAFIVLGAAIANMFIAICMLWE	54	unknown	hypothetical protein	Escherichia phage PNJ1809-36	103	103	100	3.00E-27	100	54	QPI12810.1
contig1_142	58460	58624	-	165	MISLESIAFKKGYTAGFKFGMKNVNPYCPMTHKKFEFEWENGFSKGYQAKGWL	54	unknown	hypothetical protein ECO340P1_00033	Escherichia phage ECO340P1	113	113	100	4.00E-31	100	54	WAX14302.1
contig1_143	58638	58889	-	252	MLSVKPKMISEDQKDFIYKCGRIWREYTKGNEVVVTEHQBIESDLFGDYLQVIKLGIDRGLVQVLT LSQVEAEHLDKHIVEF	83	hypothetical protein	hypothetical protein HOT48_gp189	Klebsiella phage ZCKP1	168	168	100	5.00E-52	100	83	YP_009803482.1
contig1_144	58889	59227	-	339	MFSKEMREVIATLVVDHGVEVERHWKDEPPFFDLASRAKSHMYLLEDDDKDFILRMRYDREFRIPLDTPDDVVLWLAEHFAFNALHGRSFGNERWDITCKRHNIPEYGS	112	hypothetical protein	hypothetical protein ASO2A_252	Escherichia phage vB_EcoM_AS02A	232	232	100	2.00E-76	99.11	112	UAW58361.1
contig1_145	59238	59414	-	177	MSEFFTMAFLGIYLIISAVGLIMSLIEEMGIKWNCVFGIALMLTPVWIYCKSVELIG	58	unknown	hypothetical protein G377_gp020	Escherichia phage phAPEC8	114	114	100	3.00E-31	100	58	YP_007348614.1
contig1_146	59417	59773	-	357	MKIVHDEIQEESDMLDLDALGKVIYAGIKAFREKANNSTVFMPTKLMRVLYPNRSPAPYDDEEE TGRREWLNILEKMEFAIDSGNPEIYVYAEQQRKARLEGRLEFASFYFDNLWS	118	hypothetical protein	hypothetical protein LJJOHLM_00044	Escherichia phage KKP_3954	243	243	100	1.00E-80	99.15	118	WLW41336.1
contig1_147	60000	60057	-	58	MYYSQNEVANIKA VGDGLVSPNYHWDNTDLVEVTHVHGVEGIVLYTLGGGVVGEEMERYTTTKK LVSSYRMFLHQGSEETAFLLKLKLDADREKAR	95	hypothetical protein	hypothetical protein JR327_gp049	Escherichia phage Mt1B1_P17	195	195	100	2.00E-62	100	95	YP_009986974.1
contig1_148	60095	60586	-	492	MAYPDYIDERAMGFFRNFLVGRSHGDNSSYKTSWDSQC GAKATKTKLMPGRPLCAYCGNEALA LOPGIEGHGYTIKGYTCVCKGAMDEADWVKEKAEMEERHKREAYEMEKRMPVPDLQVKKNIVA KMMKEVQKAETEDLNRALENLRNFKEKELEIEMW	163	hypothetical protein	hypothetical protein JR327_gp050	Escherichia phage Mt1B1_P17	342	342	100	2.00E-118	100	163	YP_009986975.1
contig1_149	60599	60889	-	291	MNITLATKNISETINGFOGIVALHGNNEKWLASFEDRQHNILDAPIKVMHIVGESKVLTSRSSKEQI TNELVKLLDNVLNMFDPNAPIDTKRVL	96	hypothetical protein	hypothetical protein HOR21_gp181	Escherichia phage ESCO13	194	194	100	4.00E-62	100	96	YP_009786695.1
contig1_150	61007	61432	+	426	MQNMTWTEAKAMQNGKRVKHEYFCSDSEWFEMQYGVILDEHGYNMSNWFGEAWQEEGWSVI EKEDSKEEGLVSNVEREMRETQIPALDFVYLEELVAASFVAGNLWKTVPVSRLENQNNPSARNHKLY KGNHNKLLKKRKK	141	hypothetical protein	hypothetical protein JR327_gp052	Escherichia phage Mt1B1_P17	289	289	100	4.00E-98	98.58	141	YP_009986977.1
contig1_151	61484	62470	+	987	MINEEQFVKVPMWILKISQVNGHKFTDSKANLYCYLRGDFRAFPSYAKIGDVGFTTPRAAEERVKK LLEMGLIKDARPSSNLYRVLDIPKGESSLDPDSEKFEAIVKAVQEQPLMEWKNFKK WYSPSGNE YTATLPAVEIYSYIAGFNEQGQECYATQKTLANIGMVSDBRQVRNINMFVDMGVLSEARHGQTSI YKTLPLPETEMNVKKQKRVEIKPIY TENQSDWCFYIQLVSPFYTC LKAGITVINDRRIKEQSKNSMFK HYLLDSFSGDYATIFSLEKEVKGFNRSLCLCKEWLPDGYTETYNLEDYESIKNFVSEKLIKE	328	endonuclease	hypothetical protein JR327_gp053	Escherichia phage Mt1B1_P17	682	682	100	0	100	328	YP_009986978.1
contig1_152	62473	62622	+	150	MIYKNKFTGCLRKFIDKGYVSLDNGVTWENGTSLEQILALPYEEV	49	hypothetical protein	hypothetical protein JR327_gp054	Escherichia phage Mt1B1_P17	103	103	100	2.00E-27	100	49	YP_009986979.1
contig1_153	62623	62946	+	324	MSNSLFSVSIAPRVNIRCFVTLPGVTHITLEYDPRSRDNPITGKIDCAYGDFVMDHQTLLCCVQRL QAGSLYIFKTVFQEIQAQAVESGMETLNMVIEAANOKEVL	107	hypothetical protein	hypothetical protein ECML183-2_000195	Escherichia phage ECML-183-2	224	224	100	2.00E-73	99.07	107	WCD43507.1
contig1_154	62943	63200	+	258	MTLYHVTTTEGDEGRTTKDLGYVEADSPHAIKYLSHGKYYATYEYTIYKVEVSPQVATPMAELK HLKAKVRGIVSDYKGEVK	85	unknown	hypothetical protein JR327_gp056	Escherichia phage Mt1B1_P17	171	171	100	5.00E-53	100	85	YP_009986981.1
contig1_155	63197	63409	+	213	MSGWIKVSGTEDVPIGEVLWIMANGKKGFCVKNKTRNGTIAVINGHFYFDLAPVIAHYHALPTYEEI NNG	70	hypothetical protein	hypothetical protein JR319_gp094	Escherichia phage vB_EcoM-Ro121c4YLVW	104	104	100	2.00E-27	100	49	YP_009985088.1
contig1_156	63402	63719	+	318	MANKEPHVYALVKHLNKNERNRIADYRKFKRSSLNRYMPHAAFDATTRAFRAKIAEMDNLLKL ARLSHIAHSKVTGVTHFFDFDTKALYAPEAGEQLIYLLTKK	105	hypothetical protein	hypothetical protein JR327_gp058	Escherichia phage Mt1B1_P17	214	214	100	7.00E-70	100	105	YP_009803472.1
contig1_157	63896	64093	+	198	MLVSELPDSNGNQITIDWFGPTGTLDTLAEWSGDIYGGVLSLSTEQMIILRDFLISLDLGENK	65	unknown	hypothetical protein	Escherichia phage AV125	130	130	100	3.00E-37	98.46	78	WPK37890.1
contig1_158	64090	64359	+	270	MSKTSIEFIEKSPVKLYRLSEIEPMSVFFYYDSEVSEQERDYLATDTGAVCLTGSRAGEYIVTSRF NEADYCWAKVETKIVINITNH	89	unknown	hypothetical protein ECO340P1_00048	Escherichia phage ECO340P1	184	184	100	2.00E-58	100	89	WAX14317.1
contig1_159	64442	64639	+	198	MATKKQKMKCLTLTELQASNCVTVGKIYSTVLDDKNNSTFFKDDNGNPQVGIYPSCAFETWEK V	65	unknown	hypothetical protein ECO340P2_00053	Escherichia phage ECO340P2	135	135	100	7.00E-40	98.46	65	WAX14595.1
contig1_160	64683	64856	+	174	MGDKQSNIRYALYGRMGADCEWMLLSQRIPSYEAKLEKRDYYKQTWFRVICKHYLEA	57	unknown	hypothetical protein HOR27_gp172	Escherichia phage ESCO5	120	120	100	6.00E-34	98.25	57	YP_009787213.1
contig1_161	64856	65164	+	309	MSTLSLATVTHQYEEAVKDSENPSTLVFEDRTGLKWESGDELYFWYPQGCTSNNSLYSYELEYP APVDEDDNYIMYYVNNCGGETFNVVSFKALKSDEEM	102	hypothetical protein	hypothetical protein JR327_gp063	Escherichia phage Mt1B1_P17	211	211	100	8.00E-69	100	102	YP_009986988.1

contig1_162	65164	65469	+	306	MRHNTTSLAVAAHMLYNDSVKNELSPVSLAFYLIDRDWMFSGEDEIYVYNSRGFIESFELEHRAP TAEDDRFIMFCVKDGYGEVYDVVFEKRNQKTEEEF	101	hypothetical protein	hypothetical protein ECO340P1_00052	Escherichia phage ECO340P1	211	211	100	9.00E-69	100	101	WAX14321.1
contig1_163	65470	65832	+	363	MKRLLCVLIMITTNATAARDGFKIGVEGSOQFTWYGGAEVQYVDDKKYCNCKFDRIDRGVDNWG DAYKATGFYCTKDLITVTKPEQDNRKVLFIIVNPAKFEERKAYYYDMFIEYKKEEK	120	hypothetical protein	hypothetical protein ECO340P1_00053	Escherichia phage ECO340P1	246	246	100	8.00E-82	100	120	WAX14322.1
contig1_164	65829	66191	+	363	MRETIVDVVINGQRYVVPVVEKAEPDALDVVFEDDGLGTVYREYFRLLSTLWEEEDSFGKRPF NSCWQFDLIGLIDAGYLEGKYYRDEDEGGIEDTDYDREEADKLQGLIARMCLG	120	hypothetical protein	hypothetical protein G377_gp036	Escherichia phage phAPEC8	241	241	100	8.00E-80	100	120	YP_007348598.1
contig1_165	66193	66561	+	369	MKVNLNFYHLGKTIPEGAVYIGRAMPHELMKASKFANPFKLKDDPEPRGSITQRYKEWLWEQRCGKI TLEDLLELEGKDLVCFCSPPQCHGDVLVAAVTWARKEWDKRHPYTVDNYYWIEENF	122	hydroxymethylglutaryl-CoA reductase (NADPH) activity	ribonucleotide reductase NrdA-like	Escherichia phage Mt1B1_P17	258	258	100	2.00E-86	100	122	YP_009986992.1
contig1_166	66501	66917	+	417	MGQKASYLCRQLDLGGFEFLKNIIDVDVFGITALQDKQATLYYHKKEDKAYIYILGAEKFGVGD MALNVEGDLPLPEQLKLVFRFTRDVKLDGVIAILQEDHYMYMVFVTPAFSGLNGEEALNDVILKIGN ALNDVN	138	hypothetical protein	hypothetical protein	Escherichia phage vB_EcoM_EP57	261	261	100%	2.00E-96	95.65%	136	WPK29238.1
contig1_167	66932	67441	+	510	MFFDANSFLSVTAGQSAVNAEFEEREEDWNHNYDPSNLNWCSDLVGNLSRDNALRAYYSVYTV DNLYQYYVFRSLIVNLNLAGRLKNNKAFTLGHYIPFRKGGVHFPCNWIQTRKENSAGDTPMPRFK DKWITWEKQMGYINAHLPNLEKPYASRAKEMMRIVKSFY	169	hypothetical protein	hypothetical protein ETECTG_CDS0273	Escherichia phage ETEC-TG	355	355	100	3.00E-123	99.41	169	WPK30788.1
contig1_168	67456	69048	+	1593	MSTQLSFTPTTEQYAIESGYKENRFVTJQAKSGSGKTSITLYMLANGTNDLSILYAFNKSMAEEARRK MPPNVMCRTLHISICYQRLPQNLRHKLSRPEGQYVNVAGTGEIAKKFKIQNLIDKNGKVLITRAMI GLMVKQTLKAYEFSDDDEHIGHKHFVKVHMSDLKRRKNINQKLINEVVKYAKQLWRERIDPKSETI MTHDTYVKLFELSKEDLYDIIFGDEFQDVNPAFLSILNRKASAKRIVVVGDEFOSIYQFRGSQNM MKQATATYGIELPLTTCFRFGPKVADIANAILSDRSPLKHPLVKGQYDVTVGSFHSDDVDYSKPYTIF RKNLTILLEAMDRIANGEEIINVDTKDFISMVDSVNLALRRGDLKVKHETVLPYTSWEEFVECAES DPDARLLNIVVSGKANNIAYTLRMRHNSPTAKVTLTTHAKSKGLEWQVIVANDFPSNYDKKGE WVGLEESERNLLYVAHTRICKLQWNRTVQEILDMHRLGKSTAPVSEEDKLIAALARKINQREDR*	530	ATP-dependent DNA helicase activity	hypothetical protein ECO340P1_00058	Escherichia phage ECO340P1	1109	1109	100	0	100	530	WAX14327.1
contig1_169	69049	69300	+	252	MAGYHITDIKKQPYGSIEKIEVEELFDAVEQDCKIMQLVELSDIIGAVEGVLEQFPDMTLQDLJI MSSITKRAFTGGRS	83	hypothetical protein	hypothetical protein JR327_gp071	Escherichia phage Mt1B1_P17	169	169	100	2.00E-52	100	83	YP_009986996.1
contig1_170	69297	69851	+	555	MNVAVIAQAADYYGRFAEMLEVPPYLVADILAATLPEGKEDRPLHGPNGKFYVASAEQSLQMEK DGFEEFSDHPYMALTPCYRTEELDDVHENIFLKEIEFYPGASIKIEYAETMRYYFWTYKQVQTQIE TDIGLDVEDMYGLELGSFGMRTPSQGHPHYLATGIAEPRAISAIKRGGLL	184	histidyl tRNA synthetase	histidyl tRNA synthetase	Escherichia phage Mt1B1_P17	379	379	100	1.00E-132	100	184	YP_009986997.1
contig1_171	70000	71194	+	1195	MNVYTHQDLVTAANNRGLFDRCLKAIEIAYGWTKETDPKLTGOYALLHGCTNFPYICHTVGTNE FSGEPTVGDNLEFRFTGDAAMLDLILKTKMLKIEDVYDTNSLSEEEIGEMITTFNNTTGKSFWTKSDA SRLKRVDPALPEDGKKYRKVIFYDKMAGLDALHLECGSLVPPVYREHEFAVEVEAQFKDMFYTK HYRVKVEDVEQKETFEPEDEPTIYIPNTGIQPCEDFVQVRYKNGVLVECKANHFWEKDYDSEWQIE EYFVLPRTAKYQAHIGGRPCDGPVNLFRNGDQGGKLAETFYWHSISGDSGSDIVGYIKLNPSPRY RKRRQKPPVGGKSVVRVLYTTOQTYTFKNVVDVQVTEERVYIQDREVTGEEKSVTTEENKLV AIVFEESKVENGKAYTVRDSFLRNIDGTWDYNGHDGTAVKNGKIMGRQFLSKR	448	ribonucleotide reductase	hypothetical protein ECO340P1_00061	Escherichia phage ECO340P1	933	933	100%	0	99.78%	448	WAX14330.1
contig1_172	71295	73121	+	1827	MKDLYQDVFSFLDRITSETYTRENANKPSHLVNTHRDLAIGLSKHMAMTOQLPKNLSEWHTEGFGH IHDLDYLLSPNLCCLVNYQDMLENGFKIGAAQIEKPKSIGVATTVLTQIIQAVASSQYGGOTCAHI DEGLKQYVEKSYNKFNNLSKNYRGPNTEDELEKRAMEVVDSLVYDAMQTLTYOVNTLMSVNGQS PFTILSLGLDTSVFGRMITKNYLYKVIHTGGLGKDRVTPVFPKVVFFLKDGYNMKPGDPNPDYDLKLA MECCAEERYPDISFVPLNMEVETGSSDGKVTSMGCRSFLSHYATEQGEKYDGRFNLGVSINPLIAA EARSKGESFTDLNKNHMEIAYDAHMLRVNRIRHTKASENPILFMEGALARLANDEHGVLFEGGYA SISIGYVGLAEALEILYPEEKDKKELGKNILQHMKDVCVAFKERSNLAFSLYGTPAESLCYKFATAL NEKYPLGVERDYLTNSFHQPVLVITNPFKWDYEAGFAQISNGGNISYVETPNLKNLLEALETILD YAYEHYFYGINQPVQDQCFKCGFHGEFKATAKGFECPCDGNHEETISVVRVRSYGSLAPNSRPYN KGMQEQVLQREKHL	608	ribonucleoside-triphosphate reductase activity	anaerobic ribonucleoside- triphosphate reductase	Escherichia phage ECO340P1	1272	1272	100	0	100	608	WAX14331.1
contig1_173	73118	73588	+	471	MNFAGYEPVDLINGEGYRCSLWVSGCSHGCRGCFNQKAWSYSYGKPFTHENVEVQKLDLSRPFV KGLTILGGEPLDPQNIYNVNKLNIEKVRDVGSSKDIMVYTGTYTFEVPLYIKNLVDIIVDGKYEINNP TTKPFRRGSDNQRLWKTASGWQSD	156	4 iron, 4 sulfur cluster binding	anaerobic ribonucleotide reductase small subunit	Escherichia phage phAPEC8	326	326	100	3.00E-112	100	156	YP_007348589.1
contig1_174	73602	73793	+	192	MVTYFAGVRDVGTAGELLKNSDRDVKDILATLVILQKRELLSDRDVAKLLDIGGDELQRLPF	63	hypothetical protein	hypothetical protein	Escherichia phage vB_EcoM_EP57	122	122	100	2.00E-34	98.41	63	WPK29246.1
contig1_175	73809	74414	+	606	MQHSVVVNMPNSGDKSFGVPAKKVWKAHFHLTLSNVSSEELMKAAKIIGAKCTTIDLHRDTSQR DRMLTKYQSDLDITLMLQCVEKLEAGNFNVRYKLERMFKHVACVLFMDLSKENYGEVHIKTA SDPEVETNFRISSNAEEIDYRFYNARLYSAEDKLRFNEAYDMLLSQIKQIGYHIEQVYVDSNLNL DAWWA	201	unknown	hypothetical protein	Escherichia phage PNJ1809-36	422	422	100	8.00E-149	99.5	201	QPI12776.1
contig1_176	74416	75072	+	657	MTIKHISFDVWNTLITANSNYADMRAWTIKYGDTVEARAAAYKKIKKELDNAALQGKAECAA AWERLGSELGITPWKSAKLRFCEQWFLKFPHPHVAVDLPMLYLLYSGRYDLSIKSNTNFISGDILRR ACKFDSWNCFEFTFSDALLCKPDPFRFARTLTVSIIPLLGHEVLHVGDSEEDYDGKCVDLGFNFC IKNPNDLLEKLKRGIVNA	218	hydrolase	hydrolase	Escherichia phage phAPEC8	455	455	100	2.00E-161	100	218	YP_007348586.1
contig1_177	75065	75892	+	828	MRNQTIQFANKFDDLETATFDIQDYSKLFGFSNQAAARRMGKELALQFFAQVAMKHIGEQFVIISP YNHVHNAATMMTDHFINYFNMLSQYDQGRSAELDIHRRKVSYINDYGLDKASKKKLIDGDTFY CNKEFWGDKKLVFIDDVNITGTHEDKLIHLEIDENQVKNVYFLYAKYEGNQADTEAKLNFNYNIT PEAFVKMINERDAQCLVRPIKYLGMQNHEDFKIILSQLPHYVVEQLFFGCLGEGYNRISKYAEINF FLDRYTKQHIL	275	PRTase ComF-like	hypothetical protein JR327_gp080	Escherichia phage Mt1B1_P17	572	572	100	0	100	275	YP_009987005.1
contig1_178	75906	76379	+	474	MLKMKTCGNLIDAAKAGEVTVIAHCCNCMCMNMGAGIAPOIKQAFPPYAAADLDRAGDQSKLGSF SLGVDPDEQDPLVYNLYGQYRYGYNAKGRQLDYYDALYDALIAMANDLLLRDQKCKIGLPMIGAG YAGGNWAIQVMEIETLVKTGHDVTIYKL	157	cysteine-type peptidase activity	phosphatase	Escherichia phage niezmany	318	318	100	3.00E-109	98.73	157	YP_009986295.1
contig1_179	76392	76613	+	222	MGVFAGIVAVVSFFVIAFMLSLIPAWLLLLAYNYVAEVMGHADITVPVFTWTVCVSFLAVLRGIF SSHSTK	73	hypothetical protein	hypothetical protein HOR27_gp190	Escherichia phage ESCO5	142	142	100	3.00E-42	98.63	73	YP_009787195.1

contig1_180	76693	77667	+	975	MQLGFEPIIDVVVLVGLALSIGIDFFGHKENKEIGIKSALLWSVFWIALALGYAFIWEHGEKEFAAL FLSGVYLEKSLVDNLMVFMFAIFASFGIKSTHLQHKILLWGIAIGAFVFGIFVAAGTALFNLHWSVQ VLFGLIIVAWSAVAIIKGGDEEDIDYSKHHAVRLVGKVLPHVHNALDGEKFTITKNGIKYATPALLCV FVIELTDIVFSDFSVPVAVIGVTOEPLVSVYSSAMLMVGLRALFVLSVAVKYLVHLEKAVAVVLVF VGAKLMYHPFGETLHAKWSFLPHDISPNVSLMIVLGTALGVIASFIPEKEEAASV	324	Integral membrane protein TerC family	membrane protein	Escherichia phage phAPEC8	643	643	100	0	100	324	YP_007348582.1
contig1_181	77710	78060	+	351	MNNFDEIQELIWDLSGDVDYVLDYLSKVYPGVSVMIVTKDPINLPNNVACCGSGSGEVEPVSRWE LTKAVSKRNGEVLNIDIEQIWTSPAAKWNDPNGWDLFWFDNETDDEVFLK	116	unknown	hypothetical protein JR321_gp035	Escherichia phage anhysbys	235	235	100	1.00E-77	100	116	YP_009985378.1
contig1_182	78057	78302	+	246	MKYLLVVFENICF AIGLFVIFVLT SVINGSKVS L YRDGEQLVCFSGD FKHRCINSQNEESKEYKTSP DFNWLYLFNSLRG	81	unknown	hypothetical protein HOR21_gp212	Escherichia phage ESCO13	167	167	100	9.00E-52	100	81	YP_009786664.1
contig1_183	78244	78681	+	438	MKKLALILIGICFLTACEDETNPAAQQYQQPQQYAAQQSGSDGDTTIINNGGSSSSGVGEFATGMLLGH MMSGGSRNSGDYNDNRITINKHYNTPKPKTNFYGPKPKQEIKEYEKPQRTFTINSSYTRKSYNSP LSKKSSSRSKRR	145	hypothetical protein	hypothetical protein	Escherichia phage vB_EcoM_EP57	299	299	100	9.00E-102	100	170	WPK29255.1
contig1_184	78696	79289	+	594	MTISIRTSITGVKSLPNALQITRALRDTFS AVDEHKMLDNLSNWPYFHYFKNEDDEFIDAVSYGYDF GKEVSPPEEFVATVPNGLPTRSKRKKGPKNKKRATNKATITFTDGTQYTIKDFEEVSYTAGGSLSFY TIKKQNYTFSHVSNMIEMLVEDIESVAVLGMHKSFLITNISDFSASLSGPDFEATTTYFAFKV	197	unknown	hypothetical protein ECML183- 2_000218	Escherichia phage ECML-183-2	405	405	100	2.00E-142	100	197	WCD43530.1
contig1_185	79293	79883	+	591	MHTERDLQLLWWEVMQEKEDFPVYYNMLREAGYKACVRNKNVNSFGWCNRYRDKIVVNVNHL HKNSTRDMIVDTMKHEIAHAIDGCMGKFSRHGAHWQLKLAELGANPKATSKPELNEYKYVILVLV VDRFA TRCVRGYNRKPNNRMPGKQPNNWLKSDKEGTEGLWLYKWDDWVKVAKYEGVSPYIR DAEEENEE	196	SprT homologues.	hypothetical protein WPEC1_CDS220	Escherichia phage WPEC1	411	411	99%	4.00E-144	99.49%	264	XUY43087.1
contig1_186	80000	80992	+	993	MTPSFLKAAATGGQKKPEMSVFAATDASKSVFASPLVDASPVYAAPQEVVPLPSMTROEIEIG AEAGTTLRLSNAEVLKHORSNQGDQMSERLTALIKQAKQLDPNSIKQSGITLIKVKVMGMKEDLF GFDNVNNRIEELVKNLQMDIRKEEDSLVYLEKLHQAIQGYAASLNDRMQLLTATYKEEQALAAAL PEDAVQVQVIRDTLDLEIRIADLKLRLLCVQMGRPVQGMQKVSASLMRSARNIVNNVPAYASA NFSMYIESLRQMKAAETQNNVLDEFNLAIKLGSDLATQNIQIEAAALANRQVLDIETLRHDQENLVK MLEETNRINTEARAARVDYINEVQSLDEGMVAAVKRGGLGK	370	Toxic anion resistance protein (TelA)	tellurite resistance	Escherichia phage phAPEC8	752	752	100%	0	100.00%	370	YP_007348577.1
contig1_187	80989	81186	+	198	MRIRIYIIDDIGVRYDDEKRFAPMGGIYPPSVLA VCRDCYIYEGCRNFRKFELLADIDFNEEEE	65	unknown	hypothetical protein HOR27_gp198	Escherichia phage ESCO5	131	131	100	4.00E-38	100	65	YP_009787187.1
contig1_188	81186	81359	+	174	MKILRVNIETAWCGCNEVVDIEEDMSQEDIEDLAHETFDQDYNCGFHLEEEEDV	57	hypothetical protein	hypothetical protein G377_gp059	Escherichia phage phAPEC8	115	115	100	4.00E-32	100	57	YP_007348575.1
contig1_189	81352	81750	+	399	MYNPTIGILLKLTVDPTLFTKLASGEVYEVMKDGDGWCYLGCYFLCDAEEIESIVTKGYEYPGRF VETTKQPDITLTRQELTIHEDAFIDGWNQDNDWGGPEAFLEHKA YGEFCETTVALDNLKEGL	132	unknown	hypothetical protein JR327_gp091	Escherichia phage Mt1B1_P17	271	271	100	1.00E-91	100	132	YP_009987016.1
contig1_190	81750	82319	+	570	MGCFSFLCKESGKAALSTSFDDGSPCYLFLKLDGKVIEMHGNYSYGRVFSKKQDAHGNRESFKW TIPWSDVCDLMFSVNRGDGIAMLAEHFTGEAPTERSEDDPNQGWGDGEEEEEDYFYSTENIFK RVDNYPYHKVHNVL TETEDDKMEI EDDPLVTLPISELQKTKEAYDLGFGIGRGGMRV	189	hypothetical protein	hypothetical protein ECO340P1_00080	Escherichia phage ECO340P1	390	390	ECO	1.00E-136	100	189	WAX14349.1
contig1_191	82312	82590	+	279	MFRFNIEEKSQDPIAFEDLDVGATFMYDYDAYEDAGLDTRYRNLVFIKNSNSAICINGSLAQRGYT HCIPPDNTNMVEDLEVNTITLKKKE	92	hypothetical protein	hypothetical protein HOR21_gp221	Escherichia phage ESCO13	193	193	100	6.00E-62	100	92	YP_009786655.1
contig1_192	82592	83386	+	795	MSEKISLKKRQENLAFSLKKNKLNNEGKIVLRVACALDISGMHGLYSSGVVSDFVGKLLPFGMLF DDNQIDIMWAFNTSQELTPATADVDDYVVGKCMRNVRIGGGTNYAPVMADIYDEYFGTVTKYI TTKQVYQEEAPKKGFFNRLLGKTETVSVEREKVVAVSEPGADVTPGVVFFQTDGENDGDPASVRRLI EENKNKPIYWF MVGVGNEKFGLKELANAYDNVGFIGIKDLDTDSLEYDKLLEEFGEWVVKVG AKK	264	vWA found in TerF C terminus	hypothetical protein HOR21_gp222	Escherichia phage ESCO13	540	540	100	0.00E+00	100	264	YP_009786654.1
contig1_193	83383	83631	+	249	MIDELASQVIENYWRERAFIMRSKEYFIGTVRMEDIVSRVEIHWDPDYEEWVDKENENAILRIYK PEITLGGRSVKLRN	82	unknown	hypothetical protein HOV53_gp225	Escherichia phage vB_EcoM_Schickermoser	165	165	100	6.00E-51	98.78	82	YP_009823856.1
contig1_194	83612	83881	+	270	MLNFEIDEQKVNKRCLTIKDLVDGDTFVYENAFDENGDLSEIIVLYKVDGDGENDYS AVELNHHAQ LVSQNTSKLLEVELTVTGTLK	89	hypothetical protein	hypothetical protein	Escherichia phage SKA64	176	176	100	5.00E-55	98.88	89	UKM17319.1
contig1_195	83897	84499	+	603	MTDKISLKKGSSEKISLKKVAPALKELRLEFSWKS DSKLDLDVSA LVCRHNAAGNPEMLSARHLVC YANKFDPERSTFAGDDVRDGTGSGMEQIDITLAKISPDAAQIAFVL TIDDDTLGKRFHGHASEGMLKIF DSERNVEILD FDLAPEVAGNTICHVASLVRDGEWKLKAYGVGKAGLDICDVMAFGGKKEWY ECP	200	response to stress	hypothetical protein	Escherichia phage AV126	409	409	100	1.00E-143	99.5	200	WPK38128.1
contig1_196	84599	85120	+	522	MUIKNFVTVALLSLTAFTTPVVAKEAAANVKTAKVHHKCTKYNDKILACAIYAEGRGLGKKG MNA VGNVNVINRRNDTYFPNTVRGVLFQKGQFSYAKTFNVTEKDKWQEA KIAERLLYLEKHFPPEL RSVLDTYK GALYFKKRNIRTNWERDMRLVYRDKVHGFYLPKGS	173	Cell Wall Hydrolase	hypothetical protein ECO340P1_00086	Escherichia phage ECO340P1	357	357	100	3.00E-124	100	173	WAX14355.1
contig1_197	85122	85406	+	285	MQEDNTVVVASYLVVGLTEEDVYVYTRKHLEAYATLFMEDEKDVDKYSIDMINDSIYPCMLVKVD AVLWERFARTHDAVECSAVMSQNNILGEIH	94	hypothetical protein	hypothetical protein	Escherichia phage vB_EcoM_EP57	195	195	100	2.00E-62	100	104	WPK29269.1
contig1_198	85406	85636	+	231	MGEVIEVNRITKQKVQKYVVIKNICVVCFTNVIYDSRRGENENEPYIEISKNGQCICKNCAVAIKE VYVNEWADWQ	76	hypothetical protein	hypothetical protein ETECTG_CDS0243	Escherichia phage ETEC-TG	152	152	100	5.00E-46	100	92	WPK30758.1
contig1_199	85614	85805	+	192	MKT.LGTNETGEISLQEVNTDNKLIKLRDVARDHLEQSFKEYMEARDRVIIQIQEMIKRGIVADS	63	hypothetical protein	Phi92_gp167	Escherichia phage phi92	74.7	74.7	90	1.00E-15	58.06	64	YP_009012499.1
contig1_200	85822	86385	+	564	MIYYITPYLTGNIGKAINAIAVLPPDDSWVCLRDITMTFLPDQPSMLEELVMSNPPFDVIGATCNR LGSYGQLFSGINDDPDILNHEIYAKIAREYHKVSVEEVPFGTLAGFLLFRKSLWNIEPFEESKIQF DLFSRPTLHEKGKRLGLMRGMYLFHIYRLGQTNPQRSIHLLHCHDHSKTI	187	transferase activity	glycosyltransferase	Escherichia phage ukendt	390	390	100	7.00E-137	99.47	187	YP_009986919.1
contig1_201	86394	87077	+	684	MENIKIGVGVITVGRPLKDYLVTDPRADRFRVNDPDRKGVAYARNELMHQFYEEGYDYWFIFDD DCYPVMEGWETYFVGQAVSGWDFGMPYFKDKVVVSGSKEVILWELAMCQFAMYSRAVVEK MGYFRPYTHGYGFEAEWGHRLQAAAGLNHGIQATPCPLRIMAYIHPDDVFGNPMMPFANLTKEEK EAAIGINWEEYKASLEDIKNGKIRISYEEALAHVK	227	glycosyltransferase	hypothetical protein ECO340P1_00091	Escherichia phage ECO340P1	473	473	100	3.00E-168	100	227	WAX14360.1

contig1_202	87067	88014	+	948	MSNKKWSKLIDAKPHSGCDYHRIVMPFNNNNFQPKKDIVVFNRIHSGAEYVLSLKROGVKV V VLDLDDFYQNLPEHYLASLYESNTHAIVAMVKLADVIVITTEYLA YKIRHLNRNVVIRNALPFDSDG QFTLSNDRSSGTPVVWAGGASHEPDLRLVNSNTFDDLELTIAGYEASQSITGQEWIKIRRNLPNAKYK AAVCKDLNMYMSVYESHAIAIAPLVNDNFNNCKSNLKLKLEAGAKGIPICSKVLPYFNPVDARAVAY AENKAWEHYEIVKLLRNPNYREDRGLFLAEHVRTHYNLADANELRRQVIESL	315	glycosyltransferase	hypothetical protein ECO340P1_00092	Escherichia phage ECO340P1	651	651	100	0	100	315	WAX14361.1
contig1_203	88022	88966	+	945	MGOIILDNRNGINYSVCDHRVVLPYSRQFSSQPKYNYVFNQVPTKGKEGFLALKNLGFKMVMVD LDDSLVIPKGHMLEGIFESGIREHLKWFLEHSDLVTTTTALQVELSQYNNDNVHIHPNGLPYDEGQFV LTRDRYSKTPLVWAGSETHKQDLAILPDFGKDLTICGFRDRSEVLSRSEWSVIRENVAPTCVYEGVR PYANYMESYDGHQISLAPLIDNVFNNAKSNLKILEAGAKGPLICSSPRENYHTQEFKDLFFAETPSE WKDITEYLLSAPDVCEMKGALALAKYVRTHYHIDVLENERRLLFEEL	314	glycosyltransferase	glycosyltransferase	Escherichia phage Mt1B1_P17	655	655	100	0	100	314	YP_009987030.1
contig1_204	88966	89244	+	279	MINTFDFEYTTNRNGKALVVEVDY YEEPNPLSRESWDYHGGLLIDGIRFYEGETEVFEKDLNVTV AEIAFQFRKHMEELEAEYMMETNEPF	92	hypothetical protein	hypothetical protein G377_gp075	Escherichia phage phAPEC8	188	188	100	6.00E-60	98.91	92	YP_007348559.1
contig1_205	90000	91035	+	1036	MSHIITKYGFVDVLSKEGHTGCPRCMKNGKDRSRNLMVYGLDSNGEHKGAKCFACEYTIPSEVW LRENGEVLEEEIIVGSEFNKQIHRKIVQETSTNPRGYRGIKEKVSSFYGVRYEYRQEGDQMVVESC LYPTTGKELVGFKRRHHPKDFSKPIGQVKGKVDLFGQIRFADRSHTVVTGGHEHDALAA YQMLSEN LDNKYELPAVVSOGTTGETSMYKQVQAQYPPFEKFKKIVCMNDKAKAGNEAFENIVKVLPRNKVYR MQMDLKDANQYLEEGRADKDFVKAFSARLYTPAGVYASNVLYEAALECLSEKMITLPPFMRVAA NMLGGGLVEEITVILAKTSIGKTLMVNEITKHIIVAHPEHTLGLSLEATYKKYSRNLSSFLHPIHLR KTPEEKQILEENKEKILDFYEREDGSPRFYVCDRDGADVSEIKEVLEMIHYFGVTILVIDPYSDLLS GMDVQAQLELATWLKRIMKEYAITIIVISHVKKSANGGNEHLTEDDAMGSSFLAKGAGITLALERD KAAEDPVERNTTHCFILKNREFSETGPAGQFYDIRTATLHDKEQYFNNPANLPTDSNY	592	DNA helicase activity	DNA primase/helicase	Escherichia phage vB_EcoM-Ro121c4YLVW	1180	1180	100	0	100	567	YP_009984869.1
contig1_206	91128	91559	+	432	MRMTIDLNAKVKAAGALGAGVIKHQALAFIAPHMIVEDHPEEFAVKVVENNVSVIEHLPTGRSY RVVSSSGFRFDVSPSFTKGAGRSKYGILSYKYIDKVAADVAFCRVSEKGVDFIHKNTKNMVISDD GKVDLTIEFANN	143	unknown	hypothetical protein JR319_gp033	Escherichia phage vB_EcoM-Ro121c4YLVW	289	289	100	3.00E-98	99.3	143	YP_009984870.1
contig1_207	91569	92363	+	795	MSKLNLTLDQYYTNPAYAGFLCDKIKEIFGEEANYVEPSAGEGAFSSCFKNITSDPIDPKFEDCIEADF LAQSVESVGSVTA FVGNPPFGKNASLAIKFFNHCAEMLDNEGIGCFLPRTQKIFFAHKLNPMHHL LYEEECPGKGSFILHGEFWDVPCVQVQWIKRNEKSPVVLGENRLFVLGNSKDYDIAVRRAGASAGK VLSEEDSLSEASTYFLKALTSDLKTRIEAYPLLKAEASKTAGVRSLSLKEQWVLENIRKEE	264	methyltransferase activity	putative DNA N6-adenine methyltransferase	Escherichia phage vB_EcoM_ESCO37	545	545	100	0.00E+00	99.62	264	WP_229504230.1
contig1_208	92363	94960	+	2598	MSKFTWDEIANGLLNNDTIDYLASPYRLKDTFQMHCIVLENHETGEIVAFHDGPKYIFDGRPYEESD GRKYTYVLKEYVAQDYTHFOLKDFDPFINHEGYFKDKPEYL VEMAVAHNGINYDWLATKLEYGLD YSVYKNTWGNKVKKLDSLSKVLNPDRIKIEGSGHSLAALSRLKAGGDVKKIDFRKEIPEEDRFKTF AADMLYYCYDKNKANTSYNYLMEEWGDDYDKWEGPPELEQVADIITRQEHGRGAFNMKQAEEN LAFDLAEMERLRLLEPILPPKPA TKGYLKA FIPPKLQIKKNLEPTNHHMNF AKKHDGHLEERDGDW WLVMLGKEWKLPA ADEPLCDPNIPATLNDTTHIKNWLVLGFWPSEYKDKDLTLKSGTKIKKSE EELQKGIRAYVEQTLSSNFQCDRCDHLECTPETLERKQIERIAKGGRLGVLNTPCFTKGQKEKICP NLQALGEKFPYATQIVYEYLYTKHRRNSILGGGADWEDEEDQEYDKGFLAAVRADGRIPTPAATCD AATSRMKHRSVANIPRVTSLFGWEMRNLFGEVVPKYFQIGYDFDLSLEAKIESHYCWRYEPPEHYC NALLLEKPNVDHTMMAKRITETIGRKFERSPAKSVKYGITYGAQADKVAKTIGSDKFTGQLVDFDAF WEA AFPLARLKERLNDFWKTGQYVLGIDGRKVPTRS AHAILNSLFGSGGVICAKRAMVIYDDM IEEGLSVDFPKDDWKNKDFVQQMIA YHDEAQLEVSRLNLFVKWFSPESLGWKKVDDPEEQKKID KECLAKV EEWKHNKEKETGQIWANIHESPKGGWFTAYSRAGELAAALVTKAGEFYNLNVQLTAG YDVGNWSWASCH	865	DNA polymerase family A	DNA polymerase I	Escherichia phage phAPEC8	1803	1803	100	0	100	865	YP_007348555.1
contig1_209	95009	95200	+	192	MHYDLDCLGMPYLPDEFEGEEEREWDGDIRCWSGCKDMSYEQHMHNDGFCIHICYNEIDLEED	63	unknown	hypothetical protein HOR21_gp239	Escherichia phage ESCO13	130	130	100	2.00E-37	100	63	YP_009786637.1
contig1_210	95200	95367	+	168	MGNIGIMICYKIVRIVGDEITTRYFMIESQADEVYNDWLEKGGYDFVSKETFRLEV	55	unknown	hypothetical protein HOR27_gp221	Escherichia phage ESCO5	113	113	100	3.00E-31	100	55	YP_009787164.1
contig1_211	95378	95596	+	219	MRKLVSFNVLSILVDEQNEDVIKGLANKIAGGMMTEAEVWEECARLYEEGVIEVLGDEINMDDVVKV TVERIND	72	unknown	hypothetical protein JR325_gp124	Escherichia phage tuntematon	140	140	100	2.00E-41	98.61	72	YP_009986500.1
contig1_212	95589	96182	+	594	MTSKSQINIAKEILTVLKIADPNSVLAGGAVRDWRILDIAGRDLDFYTSLPAHRTTEEQIGLIASALM GTNIRKLNGKEASDNYEGVTGLKHVFEFERDQCLNLMIMEPSVMTTFLENFDSLICQAAFDGKDC YYSKDFETTLETIGICFLHKDVRREDAKHVIKIATRFYPYLRFKVEKVVRPPQVQDTRLEEDDIPW	197	transferase activity	hypothetical protein	Escherichia phage vB_EcoM_EP57	196	196	47	2.00E-61	100	92	WPK29286.1
contig1_213	96228	96620	+	393	MTERSKIAVETVYGNYSLSLTLVEKNVVLGDNIFYQILVIQGGNKKLTARVETSEIETTITVTKFESIL QDITRNVIDEEGKAATIKLGGFPVQIVHFPNGEIGVGIGKGKYLEQDDMERLSFCAKLM	130	hypothetical protein	hypothetical protein	Escherichia phage EF1-I	262	262	100	6.00E-88	99.23	130	XPO96336.1
contig1_214	96637	97524	+	888	MSVINTEIDRRKGTVTYATGIVDYVKLDKFAEPKTFHWEKGTITVSHRASLVLEKGAKPDEKGV WISLDIELKEGYENLQVKEGDNWITEKGVVEYSIDIRVDNKGKGTYYNTKSRITVLSIDGVOKS NKSNGNKSNDAPKOSYKKRDTVGLGTGHA VNGALELIRNGVKGDAFDIAGVQVSATVTLTKVSI AESRGVDINDYDLGASVGHAILNACKDHTIKTVSVEDLIDSAKRVLALSDKVA AAIIRGSAEQPKKE EKKVEVKKPEQPPEPTSPNQEEPMDFDDDDIF	295	hypothetical protein	hypothetical protein JR324_gp212	Escherichia phage niezmany	595	595	100	0	100	310	YP_009986332.1

contig1_215	100000	100263	-	264	MFPIPIFTIMTSTGVVPLPAGIVKKVITLTDYPDNAAGNSNSSLAILLNDGRFLTQGANLFGIEADGTRSA RFNNFHLASTVVADVFTADRCFVIKTNSGGWQYSGLTAGLVGSIAAGGTDACVTTWTSFSPSVITGI SLANLKEVKGQYNNLTWLMNSGVLYSGSQNTVSGSLGASTTNEVSTPRQITSSAVFADAGYNQCSY VNNVGTLRVCGASKGLAGNNNTTAFVFNATISATETVYVKDYINTVSQITVVGDTSGGTGTVNYL YVRSNTETTYTKLDTFAAGFSTWKFPNRRHSFFVGINNLSWAIGKNYTANLGLGYDSASGDPLOVG KPVKPEGVGSWDINKLTSVHTLNMIDITNLQGVQGTFFVYNGDMYYSGIWKDGKASYLFNSGLNY NKFTPIASSVITGDILATGLTDDSLGICIVGGTKQLTHSVSPEGGKLFENIKYTSSAPANMTISSTGLMTF HAEGGFDAGMTALNAEGTTLSDTSGGYASTLSVYTPSLSAMDVGTITQTMVAEITPTGAASLPGMV VEYFSNDPTVATVDPVTGVITAVADGGCRIGCRATYQGVVTAEDSSYLTVNAVIVMDYDLTQETI PADVKVNRNRYARASGDILVTESSAPVAPLEYVGTTPQGRRVVAANRTHIFINNLTITASPWLK TNLTVTASTINSPVGTANTYKLTPTSTSGQHILSAVNTASDITAGKHWAASVFLKPDGITKVKLLKT SGDEINEGTYDLVAGTFTGADANIIDMNGWYRVILHKVTVAKQASITYEIALNASGSDTFAGDGT AGLIAWVPQLEMGMTPNPVWAGTFVCSYARDTTSAVTFTIPKNGHTGVDIYHTDGTQREVFTG TATTWMLTFTAASADWGSKFITGLKYD	891	N-acetylmuramoyl-L-alanine amidase activity	hypothetical protein ECO340P1_00105	Escherichia phage ECO340P1	1794	1794	100	0	99.78	891	WAX14374.1
contig1_216	100305	102329	-	2025	MNLTRPNSAIADLVEATYRKRRSFEAGFTLRNSREVLLAAEGNYYQWKGTFFPKVVPANSTPATG GISSLAWQNVGTADDIAINAKFTAQQQIDDLSETIPEAGKSAYQIALDNGFVGTAEQWLASLKG TGAQLNIKGSLASTSELPSTGNVAGDGYIVGDVIYAWDGSVWKLISLGPPEGKSAYEVLWADGNT GSVYDFLTSIKGDKGDVGTGPQGPVANGFDYRGDLPSNTLPQPNSENVQAYSINGNLVY SNGTAVWVMGNIVGPQGPQGEAGDKGDLGDTGDDEGKSAYQSWLDAGNEGTEVDFIASLKGPKG DKGDQGERGPGQELGPQGPVAGTSGGLEIGVLNSEALEPPTGEVGDYAKINNDLYVWVQDATEW MNVGSLGTSITAKGHVPNSEALPVYNNYGDAYLTEDTSNLYIYTYDQDINSASFVDMGSIKGD GEKGDKGDKGDPTNGTNGTDGTNGKDKGAQWFAVATNPVAGDGVINDYAFNTTTGAVFKKTD STWTLIGTLPISPEAPQDGLTYGRSDGNWIEISGSDPTAITPTKVTA GFMELETTTANSASWTPSGT SNMYVVTVDALTVGAWPGVTGSTKPKAFSAMIYLIQDTHGHTVTLDA SYGALNDTEIATTANAV TILQLTYPGVGNIVDMVVVTR	674	tail fiber protein	tail spike protein	Escherichia phage ECO340P1	1337	1337	100%	0	99.85%	674	WAX14375.1
contig1_217	102392	105445	-	3054	MATFPTYPATSLAQVLDLVIFSSNQLHDVINGSATSIETESGLIPTLRKALVDNFFKSPLDWAQGT NETVFNQLRYFQNGVLSGYYYAPNALTNPIMPQGTGPVGDNNWVLWGLKTEQLATEVTPWVYSG ATGYETVISPYYIFDSAIVTINGVIQVLGEAFRIEDSKILSEPLGHDPATGLPNKLFAYIGKIVASADT DPNLNENRLVLETKTEELTESMDKVPLQTIARKYGLLDEVAAYATAGQSLTGKALYDPVAQSSYTL PPNITGTLTSLVSGVMYSGGSVDLSALAVERGQFVHLPTSGNNVTLTAKNQTIGRGAGRYRWA GSLPKSILASDTLETSGGLGPNAWVLTNTEGLLTPRGGTYNDLFDVVYVSEFANNNTTYTPEAAFQ AALLAAKSSSKILDAYGCDMTFTTSSFDIQTILRGVFRGQDVRVQNAVTGTTFRSRNMY WGGAVRMFCDLWDGAPRAGQVGSVLFQGNPISGTFEIDNCTFKNGLYGILQGGTGEVPTRGVFNR LTFMDMQGDIAELNVINKHYDDGCVIENIYLSNIDGTNAPILSNWGGIGVAGKGPYGYGIPDDQY CKNITIRNVFAKRCRQIVHVEVGRNISIEIHGDPDQTVSVGTGLATGA VVMYGSKDFIDGVYGE KTDGSTLASNIRMIYLEWGTNAVLDDEGNPVVPAQGRPSNPCFNYSVRNIHTKGRVFAGSAGPG YENRVSFENIRCAALQLFGIASWLSMSNITCNIFDCVGPESGPGTFYDGFRRKESVLEMVNVCY PDGKTMVTRGPQWSCRYSDIHRVNCNVEANMYTNIAGGIGAIVGTGKYVYLEPNPSRNDGMH PFTGKEFDKGMIVKADNTFFLVTTSAGAYIPDIPAFGIRATQAGDTFLTQNLTPNGTATNASWLYHY PLSAGTRIRIPGAGVGGADLDTVITRAPYQDNDDTWNPKIDIAADPIVTPTSAGVRIKTIPNDSSNV VGNTAVIRPTPVVDVPTT	1017	colanic acid degradation	hypothetical protein ECO340P1_00107	Escherichia phage ECO340P1	2084	2084	100	0	100	1017	WAX14376.1
contig1_218	105449	105784	-	336	MEFQEAWGLAKDAIIPLIGVIWFFFKQKMDKFGSDLEEMEEKSRELEKKLVFVESTYATKAELTQM LNQINSLTMANNNTLEQKIEKIMDLKNA TIQMMLDDIVKRTQNKG	111	lipoprotein	hypothetical protein	Escherichia phage vB_EcoM_EP57	164	164	75	4.00E-50	100	83	WPK29294.1
contig1_219	105794	106339	-	546	MIFTNFKKYIPEDPELKEVAEANILFLRCQGYDWDYLRSTEFNNDKMKVVFDDQNRIVFWNTDP TLLCPEDLSIAQVDFNIDTFEDIRNKVLDLETLTKDKKEYSREELMTQASAKIRSLQETAVALITPLQY AKDLEMATEDELAYLKNLQVYVVKLNRVPLQKDYPPAIDWPTLFTE	181	Caudovirales tail fibre assembly protein	tail fiber assembly protein	Escherichia phage phAPEC8	366	366	100	2.00E-127	100	181	YP_007348544.1
contig1_220	106340	107401	-	1062	MAKPIYYPDWATQTVTLPGTLTNKIRPKETIRTVGMDYGOIMTCEEMNWILNIGLWIRYLVDDF LPTLPTNYLPLVGTKITMAGDATGEATWNGNKEVTLISIQVQDNHNLHSANITDATSSTVTPNVLV KRDAGGAIYGGDVYVNGTSTTDPATLFFKNFAGQTNGEISAEYQSGGQLYIYRRNPSTGVSAGVR LYDAGYVLIDNPRNSGQDTSNGNALVRLDYLSNRLTSLQNTLTNTVQNNLNNVNSLNSSRN NVESNHQSQITNNYVANGTFVRDIRYTSQGVYYPGNEVSWTYICSSGYVLSGHIYQETGRSSAD NIGGVYFKRLQRNVNGNWYDIGG	353	tail fiber protein	hypothetical protein ECO340P1_00110	Escherichia phage ECO340P1	714	714	100	0	100	353	WAX14379.1
contig1_221	107411	108040	-	630	MAVSVDHVTWASINEDVKNLLIEDFKSSPNIVKLLYIVSSEKQKIDQAMIYLAHRLISTA GKYL DILGEEMGIERNSSDDEEYRTILKIRAYRVAASGTGRGDIIDIFARFTGTERELNTYVGLNKTFDVFY NLCLQSDQALEQLLSVPIISSYRLGAKAGAFGSSYYATKPPHGGIGGLSLYMESTGDEGTMRCT LLKQID	209	baseplate protein	baseplate protein	Escherichia phage ESCO5	429	429	100	2.00E-151	99.52	209	YP_009787153.1
contig1_222	108043	109530	-	1488	MDEYGLTDAGFVIPTFDDVLNNYMTAVKNTFGADAATSSEDTVIGQLFRHAYTDYTLWEGMQGVY NTQTLDGAEGIYLDIEFSKRGFYRAGAAASTGYAVYKSNNAAWTYELGTDIYFNSDSMDMNYVS TPTMLNAKIAAYQISRANATATGPNNTIFYAQASVDDGGLNSKTLAPGSSFTIDLETFIKANLTEADR SLVFSDSGNLSIGFTSLTSDTPVGLVTPIKFYASVPVGTGKWEIIPVAAEKGYNPVGVESITGISSTFT GYLDSNGFYSFSPGRDVEDTAEFRSRFNDNVEANAGTRAAYKALLTDGVTKVKIYDNPILHD QEHAPAMTFQTIYVGGSAEEIANVIYKTPINTLTHGTTNTITVTDEGGQEIRFSPGASAMYSVKLV YQTVNGTTLSGTEKQNIVEALQNLQAYFELGSSSVTNDQIKGVYIYAAALAFGRLLTSRVYVKLNTEDD SKYTENNIVPAYNVPSFDLDNISYEYGV	495	Baseplate J-like protein	baseplate wedge subunit	Escherichia phage vB_EcoM_Schickermoser	1000	1000	100	0	100	495	YP_009823827.1
contig1_223	109530	109793	-	264	MAKEKNFGKKFIRGMFCTYPNGVSSSTKVWNAVGMVSMTGMFILGIEKEIPEWGMGVAVFMIT PSRLMKNLIDLWRGSQSTKEDD	87	membrane protein	hypothetical protein	Escherichia phage vB_EcoM_EP57	71.2	71.2	100	4.00E-14	100	33	WPK29299.1

contig1_224	110130	111740	-	1611	MSTITITNLPETSKVNGSDYLVLDQPKTVKSTVSNFLTDGTGVVLTQLKDISGATKYPELQMSRWR DEGDVRGWGAGEEGFNAAMSELSANGGGTLFVNEDILFSLPMHKENVTVRWNAVAKVKSGLT AEYAYIMDGGADTPYSSSHHFTKANKNYCNLFVAEDYTTGISAKGVCVRHCYGWTYEGGAII GFNNMGFEYETNNYEGKASKFTMVVANTRLDNSVGFESNSTDSWSELSPPVGYSIGLKFNKSANVV DKAHPWGNVTDNVRVGMGMKNVGVITENAGFSTYSNIIITDTPVRKNTNNAAPSRNNGGVGVICDA WDCVLDGLVLP SRHDTVAKSTLPMITTTQSRSTIKDFQVSGEQYVTDIWSIFENNSGIARNHISGYGY AEKMRMTGTFGPNSGAVLASADGVTMSQTLTSGIWTNLSFSIATTTVAIIPSATGDIVNIAPIVYG IKSGFGGTVRGGLYAFYYATANSAKQLYDVSLVVSDNTAKFLLTFIDGTTRYAHWTDVSDGSAR AISISGTINIV	536	Catalytic beta propeller domain of bacteriophage endosialidase	hypothetical protein ECO340P1_00114	Escherichia phage ECO340P1	1097	1097	100	0	100	536	WAX14383.1
contig1_225	111749	113902	-	2154	MKQAIFTVTRDKRVNASSFNYYTVDGTAVAGRDYIAKSGTLVPDDADSAITVVEVFERPKNSIDL NFSLQVSGISQNNMMVETTINCITTIQENTTPITWTTKDVKMFSPMYWTIDSQATESCSIVSHGDSFT ARFVNRTITAGLAGVIWSTVDKYDHKGVGYPHTDLSSEKLWFKMEISQNMPPGKKEPLVPTLTVTL LDKSVHYVSLGFYASDISEDGKTATIKLDFGNIFSGPNNDIPLDMSAVDNIFSLITARYEIEIIVPIA SQEAWFTFTLLEPTSGYSMMKVSNNLVQPEHDIRMCTSYDDMYNLTTPERVINYNTYALGYRGMINH NGMSHYYEFSWNGTSWALNRSVFLNPATEAWLNSFHISIANENGYTIMNSLSFELMSTVCPVEWVQ HDWNDALAAATGYEPPSYVLSPTIDEGMEYLQNVINKIASIQANNIPVVIQIEGPWWYNTASKMP CITYDYTKLAFNTETGLFAQDAGTIDNYKTGTPFDEYVAFLSRKLGLRVTKFATDTRATYPGAIVTL LPFLPSIIGNGLMEKVNFPSDYYIPEAFDFYCSEYDWLLEGKMMKAFDAITIPHEKLGFEYSIDHYL AGFVPDAITLAPLYGFDPESNYRTYLWKMIIGNIVLNANKFNGLTQYIWAYPQIMHDSITVNSQSQ VFYMGNVPLNVYLQDITLKQVNVETIASITGITLTKSGEDLVTTQKFYI	717	Cabx-beta domain	non-contractile tail sheath	Escherichia phage ECO340P1	1488	1488	100	0	100	717	WAX14384.1
contig1_226	113911	116787	-	2877	MSRVKHNIDNTFQIEGLVQFLERNTGLTIDPTVQHYIINPQNVLANNRHFINTWAQEQPNGDATT EGQSVLITGFAYAYLATGDKKYLESAEKYWAQYIDHFFGGQPIPDPAKYRPNWIINGKEPRLAHY PLTDDGYPTHGGFGKSMMTWINGRTIUPKGAPHWGEYLDKAWFAFNGNLGWSNVNATVYATNPD GSTNWKEYGDQWDVEIIDLGRKVDWDGNILSTGHSAEYGTVQLKNASVNGDYKFNYATCNP VEHGGYLLKRNEMWHRPNVNPVELGYQDNASDAETWCDANYLMYQITGERKYWLCWQSSLL LCQDYSNIDMFDFRRTTAAIPTDGTGISYDYSYPTAIPKYSRDELGYTVIRODVAQTTLEQQAV WFRYVDQNSAKLRIEFQGVDDAGEVLFPRPELELSKTKSETDVTYRRCGLPLGAANMTKMDIPLSSFM RTEPPGGGVYIIAEPRIVDWGSNTVIQYKYATGIAGTNSDQIVSANMDSGGGTIGFWLTPTKTANL KSTIRYSYADFNITITDSAGRWWMAMLEKTNASAWTKALSPADFKLSTWQPNHDDTETKPSINL TAVDQINIALDSEPAINGLTGAIDFYCVNDIPSLYSAAAGDDYTMFRVTVSSENPTYAKLGDCTILD YKLDLSLNTYPGIIPFSNISDPNTALYDGRGIPYPGYQYPSLYCFKGRDIDWVRMNSIDFLYDSQM WYFNKFAFVMPGPMQAQYVWDRWDAAHYGNKNEFTMYHWNKAWDGYEARAFFACHTVY ELKQGAEVPEKLLTVCKNWINYLKWFQDNNEGRTPTTIFYPNGEVAAAPVDDFTSHMSALFMAGCA IMGMAGYDSEIPNIKIVADRCFELIQENYIVLGNPHVMNGCWSAAPRPDSNGVFFGFHAGELLRG FGLYALYKKLPNQNALPVLDDSSNIPALVLTMANISVDVTE	958	catalytic activity	hypothetical protein ECO340P1_00116	Escherichia phage ECO340P1	1998	1998	100	0	100	958	WAX14385.1
contig1_227	116787	117260	-	474	MADLTTIKISDLTQTTSVSDTDFVTDQAGITKTKSLKVLSSGAGVTRNRLNARGTVTSTLALDISSA EYFSATLSSATCTISFTNIPVATNAVLFNLALRQSGGANKVWVPSVKWSFGRPPVLYSRQGATDT FEFISYDNGATWTGSLVLAVI	157	N-acetylmuramoyl-L-alanine amidase activity	tail fiber protein	Escherichia phage nieznany	311	311	100	2.00E-106	100	157	YP_009986349.1
contig1_228	117260	117886	-	627	MGIPFDLKLGNNDLIMDDGDLVLTTRTEIAAAQTGILNTYRGWFLNTNFGVPYLPQEIHVARKK DIVDRIFLAEAKNVYIDTINSYKSAYDMDQRYYSMTVMVTVGADTVTSIFNTQPSFEIYPEAGED NAAIICEAYSIIVENSRLRYFINFVGLPRDPTSTWNNWSTESAVERIMVNEKGDALATNNDPFGITA MTGVVEE	208	baseplate wedge subunit	hypothetical protein JR321_gp249	Escherichia phage anhybsys	425	425	100	6.00E-150	100	208	YP_009985601.1
contig1_229	117888	118622	-	735	MDALNFVTAMRGLMTEQLAEVHTALPVRVTGVNYGAKTVTLESIVKNTRSSDEIDYPTFEDVPFM VNGGDTGRISFPIKSGDLGTVIFSERDPSNALQTSGETSSSTFMQPCGLYPICFIPKIATGTDTEAVD SEKVVISNNKNTYASFDPGTGNISJWNSQGMKIDITTSGITITDGTGTLDLKGGNLTFFKGGVADINGLK IDQNLMTDNGNIGFHTHTHTRNQSQSSAESLKPTGA	244	baseplate spike	baseplate spike	Escherichia phage anhybsys	496	496	100	1.00E-176	100	244	YP_009985600.1
contig1_230	118622	119632	-	1011	MAEREYTKAPAPNLNRAYKLLIGSATNTIQKRTKNSAFKSTVDLDTKLGTTEKSSSNLYLLQDHQIT FSIKKDNNDPNQAEIVVYNLSDDTVYINRGIRNLAVALAVGYEGEELVMVFKGTIQVWVSDTF DSVDRKTTLHCLDGGINIAEARTSRYPKGTIKIRVVTDLVKDLGTTEGNIHVNDNQTLSSATAMC GNTSHYLEHICKSIDHNVISIQDGSVYVTPRSQMSSARSAYISPETGLIGSPPEFHNDIKPTKKVTKSS KKAKKPTDGVKFKCQMGAILPEKTIWLKSRDYDGPFKVVSVSHNGDKEGKEWVTEVECVSSEI MTKEK	336	baseplate hub	baseplate hub	Escherichia phage ESCO5	696	696	100	0	99.7	336	YP_009787144.1
contig1_231	120000	120055	-	56	MTTYSKTRTSTNTGYSAVYLEDHSTYFAWYLYKTEEYPDQTYTVTLDGVDYDIRLRWNTRDESQ CQIGLSGDDPSISFKVTNGLDLLKPYKLYLESVPDQGLYIVDVKINGRPGYTTTGRDKRFVLVYIDN KPNQA	137	virion structural protein	MAG: virion structural protein	Dompiswa phage TSP7_1	280	280	100%	4.00E-103	99.27%	137	YP_010356189.1
contig1_232	120058	120759	-	702	MAAMTPQQSVRAVYKAEQEINSTENKNTSASTVKGDNGFCILASVYNSSSDQYIQNFKAITFDSVP EVGVITREADVTSFPVESGSDVSDHYQIKNNRFLKSGIITETPIRLMRDQLYSAGVNGARISQAEIYLD QIFESRQPIVLLTEHRTFENVILKGSYDYKSEFAMQFDFLEFEQIRLVSKATTNAIAVKTAPNKSSTGG DYKQGVASNGPKSDITVRTAEANTPTNNGG	233	tail fiber protein	tail fiber protein	Escherichia phage phAPEC8	479	479	100	3.00E-170	99.57	233	YP_007348531.1
contig1_233	120886	122874	-	1989	MLEINASKISNVVTFKVDKNSLKEAKDAVLVSQKFANKMQPTMNMTKFRQQMKIEIERELKKAQT QSQKPMRAPTPAGAGAPVGGSGRPRTPKTPQGREEEKARKAAEREAKAAARREDLGNLRQNFN YRARAFSKASPGAMQEARDVMGKAVEQYKKGEITLQRMNQALAHQLDALRRSHREKNAIEDEV RGRRRIRRELEAEAKMRIRMRNRELRIERNRKLRLAQQRDRDRRYGOLKEGAAGLNPRMIASSLI GAGLFAGGSVVGNTLMTNRIKLVSRAENQVQNAAILAMTAWGEQNGVDSANIIKSIDNIKD VRELRGNTVLASKWNEKEGKWGGDNGINDIMNLFGWNPQLKPLQDPLAFIQAITYNEGERRG MNSAQIGRLLENLGDLLMYHQRMFSKNGEGYNEVLKMLQRTGATLTQEQIDASKETRFATVQL VGQGMQNHLEGFVKALPKDDSWLDNVKVLQDQAKDLGEELGKTTVQLGGFAKELGDFGFSFTN WLKETFPDFTGDNTDPNKSMAQKAYEATQSGDSNPVADWLYNLTGIDTQDGRMWRGEQTRTRA FGFGNPLEDLRESAYTPNVSLARNQPVVENTYAIPLDLKIVTSPSSEFGNILDGRIQNSGNSIFQRLSL STLGGQSNTGG	662	tail length tape measure protein	tail length tape measure protein	Escherichia phage Mt1B1_P17	1353	1353	100	0	100	662	YP_009987060.1

contig1_234	123161	123643	-	483	MSQEQDNTIQKYARPEEVVEIPLDGNRSVTFRIMKWSPSKVFDRIPELGSVLVVPMTMYSTATMSA DEDLESRIAMALIQLFAGLEEKNLTFLRLKILDEVYTDQDGYNV AENFDELMAHPELVLDLTAKVLE VNYGPFFKRFGFKLTQLQAMTSLAAN	160	tail assembly chaperone	tail assembly chaperone	Escherichia phage EF1-1	328	328	100	4.00E-113	99.38	160	XPO96314.1
contig1_235	123689	124168	-	480	MDKMLTGVMAYDPSQVILSLGGWEPWGAADTKIIVAKSDNIINPYAGTDGDVSLASRNRLGLT MSLQRTSPANEVLATYAQTMYSTRQVAFSVYLEDPRGYISTIGWIQSQPEDTIGEMITENQWVIGL KDALSLRNEVGVGLSTLNSISALTIO	159	protein of unknown function (DUF3277)	virion structural protein	Escherichia phage Mt1B1_P17	322	322	100	7.00E-111	100	159	YP_009987063.1
contig1_236	124215	125588	-	1374	MATFREKVATVTLLYGATSIRETFQDIPLLTGQNVTEAIIQYSSSDALLEAGYGLNDPAYIMAVK LFNGLFPDPQVMVYGKREVTNFTLTPIVEDSATYTTIKNGTKKKEFKFIADDTATAQEIVVGLTEMIN ADLYYGPFLTVPANNGAAMTFTPVEGKFGSIDSTGFTQETVYANATEDIAALHIDIDSSWFWTLSDSH ETEDVLALAAWVEENDKYVFFSSSEPGIKTKAEDNVLERLNDLGYNNTCFALWMTDADSVFEAA VVGAICSRQPLGTLTHGKTLVGVIEKLDQTSENNIVQQNGNIYRKEHGTFLFYRDGLMVSGFFVDY VVHALWFKARTEESLFTLFKQQSMLGGGVSRATSNGLALIRQAVLANPIQVIGILNGSIANEVVTSSET GLRVDLKPVIYIPSRADMTDAQINARLVDMKIEYVYAGFFHYVKVQVNVLTNRNAN	457	protein of unknown function (DUF3283)	tail sheath	Escherichia phage ESCO5	940	940	100	0	99.78	457	YP_009787138.1
contig1_237	125623	126282	-	660	MEQKEETLANIYQQIEAYENAIVLNIGGFLQELVGLPVYVMDKPFIKPDPYPLALRIITSSDSGGWSY RSSIQNDMYSYEMDNTYIEIELVAYRGRPTTLMSYVLAALRGAEFLKYKHLYSKGLGFLGASNIAQA NTIVDGDKTELARAMVMTFNTRMSIEDIATPIEAINMHIRSFRSDYNNDPIPLDLILNRVYAITLVPGE YSSVYNQNGSLFNNPTE	219	hypothetical protein	hypothetical protein JR319_gp064	Escherichia phage vB_EcoM-Ro121c4YLVW	433	433	100	6.00E-153	99.53	219	YP_009984901.1
contig1_238	126254	126694	-	441	MYTKKEIQVLLDQFTLLDTEYQRRRVYKEAVGSVIANLESSVEYEPFTIEAASLPISGKTLNAPL EGYRSKAQYSFWTKTEMKGLQQGTEQLSDQLIDGKWYSVSYLKDWTRTSLFVHHHCVAIILDDQN NSWSYGTGEGNGF	146	minor head protein	MAG: minor head protein	Dompiswa phage TSP7_1	304	304	100%	2.00E-112	100.00%	146	YP_010356182.1
contig1_239	126716	127204	-	489	MESEILPGDDTDWETIIKKMMDLEQVQIEAGFLTNRKHPSDLTIPAAIAIQQYGNETNNIPARPFITD GAVISQNNIAKKMKQFVANYLLNNVGLAVFEPIARASREGIAQAIAMQRYRPLSPVTIKIRQDKGN YSNHILJDTAHMINAIETIKTKSKSK	162	tail completion or Neck1 protein	tail completion or Neck1 protein	Escherichia phage anhsbys	333	333	100	4.00E-115	100	162	YP_009985590.1
contig1_240	127204	127752	-	549	MLNAVELAPLIRILVYNPSQEVLPDAMLIQIITWIDIIGNEKDCKCAVLWNSLISVLEYLWNNDVLN NSTQTGGAMSRRKMGVEVEVFKPNNGQVYTKSPWEDIYHNYLNGLMVIPGCTAGRGATSKVLI GGVDAREIDRVNSDPNSVNLGNVASVDNRNTRNVNLRNYGPVSFYRRDK	182	hypothetical protein	hypothetical protein G377_gp112	Escherichia phage phAPEC8	370	370	100	5.00E-129	99.45	182	YP_007348522.1
contig1_241	127762	128106	-	345	MSNPELKRKYFSYHEMIRDFESLPLIDADKTLVSAPPMSFYLKDGRIALGGNFHFLTRLRETEGILVH PFASEEHMGYLYSVSYEDYAPVKIKEEVLKVEAVDTPAKKRSLRKK	114	hypothetical protein	hypothetical protein HOR27_gp252	Escherichia phage ESCO5	233	233	100%	5.00E-85	100.00%	131	YP_009787133.1
contig1_242	128191	129192	-	1002	MPAVIDLQVVDSPMIELQDSPDTLIASLNLFSVDYHSTTAIEIGKEKAEDALISARERGGERNFLSM KNPELKAFRIPFPFLDKNIKAQDISQSRFSAAMAGINDSLRTDAEVVNRYSQILRVDVAKTKEKIFAE AVMGRAYNGVGGGAANSAYNWYTEWGATQKSAVDFASTTVSPAATIEKEARAYIIDTKQDGSTA TRIVALCSREFFASLVNSPFRQAYQYFGQTPNLLRDLRSGNMDVQVFEWNGVTYIEDIHGNIPAGE AYVLPMGIEGMFQAHYAPADTPELANAQARELYTFMISQHRTIQLQSEFSLAVNTRPELVKLTATA	333	phage major capsid protein E	putative major head protein	Escherichia phage anhsbys	691	691	100	0	100	333	YP_009985587.1
contig1_243	129214	129612	-	399	MAKGITLNSNRQEFHGLVLGGVFSSDLGHCVRVENVLTKATMKIGSILKADNTEAAKAEADA VLWIDTALFGIDDVAVGDTFTAVVGVGRDLTLNRFAVYKYDGSGLVDDAGVALETHDLKLT TS	132	head decoration	hypothetical protein LJJOHLM_00144	Escherichia phage KKP 3954	177	177	100	1.00E-54	100	91	WLW41436.1
contig1_244	130000	130747	-	748	MANTYLTNVDFSGKATEESLGAHIAYTDFDQGAASGYNTPLLFKSDGSPDITFEKLEALTKMGED VTELRSYIQQVMDRISEKREKFEAGWDWVYVIDADFDANVAIFCSDNMGMSFGKVDGLNVE VEEVAKPVVRVTDYQVVDGDMISIDFFEDVLDLALSNLVKSSLKQSQVQVDYLVKAHAKANTNS VDAEANPAGDKSANTTGINKGETPLENINKKEFLKSAEFQELMKAQIAEAVEKAAADARAAAELEA QEKIAKAEQAEELRKAQARIEEYTTVKSYSFVEEDKVEALVKYLVNDNKDIAETIVKAFEKARA EVDVAKKEFGTERGVDVINTQPVAKSSSELISQKAAELKKAQKQ	371	hypothetical protein	hypothetical protein JR326_gp261	Escherichia phage ukendt	744	744	100%	0	99.73%	371	YP_009986874.1
contig1_245	130750	131229	-	480	MELNKDITLWELFKTFAGKETSESQDSDPSQKPEITLVKQNKFDEEKMQVIEVLYCPPEEDDLHGER MSDLERKMDVDFNENITNISGNLGHMKNTDKFSPIKAWVNEVDCYIGDELVVEGTPLVKIQFNDP ELYQARKDGVGLKGLSIGAMGVKVKKD	159	Pfam:Peptidase_S78_2	hypothetical protein IBKAFEPJ_00147	Acinetobacter phage vB_AbaM_ ABPW7	327	327	100	1.00E-112	100	159	UZN23962.1
contig1_246	131323	132888	-	1566	MSTGKRTYTKKSEYWDKAANKAALSPTKEAEKEKTLTLLSPEIGTIGLSIKAFTNFMOPYETRFPE CIRTFKEMGEDPDVATALDATYIFVDRAFFDFKIKYNNVNSAKSRKAAKFIDYMLRNMQAQPROYV RSLLTYYKQYGAFAEKVYELDEDPKSPYFGYWRLTKLAERPDQTLHMAQPTYSADGRSILSVNQ ITNTMLAPGNTTLETGIKEIPFSKVLFGVSNITENNPLGVSPLLAYRSWREKSLQEEFVIGVSKDLG GMPVLKVPSPDILNRASLDPAAGDEAQSRLVLOANIANLHSGEQAYMVLPSDVVEGTVMROYDLVF QGVGDGTQKQFDTQALIKORKLDIYNRFGAGVILMGDGDAGSFALSDNKOITLLSHFIERDVIDVEA INSOLIPQTLRLNINFLSDEDMPKFVSGEMGDPDIEVNAKAIQQLVASGAIPLTPEVINEFLEKIGFEY RIPDDIVANKEKFEFMDNYPDKTSRSGDGLATAGTGSDTVSALDPSAQNLSN	521	portal protein	portal protein	Escherichia phage ESCO13	1072	1072	100	0	100	521	YP_009786600.1
contig1_247	132990	135065	-	2076	MAKKKAAGSLAGVDIEVKAQPGKQTLAMDLMPVMIYGGAAGCVSAETEYLTGDWRQISEYSG EDIYQYNPNKRLLELVTPYFVEYDLNGDNLRYRITNGVGLFQELSMEHRFVYFKKKKKKKHFEILVG DLIALQIQIGKPLQGYVENPFGKRVPFNIPGKKSTYLKIHVEISTDDKKYCFETPSSYIVFRGDHCFV TGNSGKSRLLLLALKYAYKDPLFGGILFRKNTTAHRKPGGLFTEAKRLYLPLQPHVKESTMDIIE ATGGGTLKFDHLENDNVTAETNHQGTQYSMVGFDELTHFTQYEMLYLLGRMRSESETSFMLCTCN PDADSVWLVNWLPLYLDEGGYPREDMCGKQKYFIHNVDEPVFADTPEELKEKYPENCFCMENPNTGE TVDIEPTFTFVIGGTIFDNPILRLPNYLAQLKSQTAIKRAQLDGCWFARIQKESFFQREWLHKISY KDVPNNLKLMRAWDKAVSVPTETRYRDPDYTSVMGKGDDQGNIFYGDYDYDAVDEKSKIFGRF RRLPGERDNLINQCKIDGPEVTVVLPKDPSGAGTIEYTESAKKLILEGFVVKPDAMPGNKKKLQRF MPFSSACQNGFVYIVEDSPFNVELTHFYKELESFNGERSTATIKDDIPDAASCFNTLSKENTFKAV AIPPTTNAPTGYSRMNSGFHQPSYVRKR	691	Terminase-like family	terminase large subunit	Escherichia phage anhsbys	1442	1442	100	0	100	691	YP_009985582.1
contig1_248	135075	135359	-	285	MMTGCSSTKVSPVLIDECKAVAIKVKGPSDLMDKVSTPPVPTKQIAKGVSRSVNNQTQN NALGQDRRKVLGLQTYIKTLQEKGIHAE	94	Rz-like spanin	hypothetical protein JR324_gp250	Escherichia phage nicznany	190	190	100	1.00E-60	100	94	YP_009986370.1
contig1_249	135310	135702	-	393	MNLKTKTIVLSVLIVLILAGMFAYNKIRESGYKDGVAAYQTQVYQAAQAKAKQDFDVLQKRADE ERALLNTQINNLSKNNAQLKADLEKKQKTINEDTTNYAKTNSGSMSCFAPNDDGLFIINKSFSSSY	130	Rz-like spanin	Rz-like spanin	Escherichia phage phAPEC8	256	256	100	6.00E-89	100	130	YP_007348513.1

contig1_250	135753	135923	-	171	MRFNVVKNDFNRSSYHKDKKNDYTRAWNLEELIYDDREDVGRDPSGGSTDGSEEDS	56	hypothetical protein	hypothetical protein JR327_gp152	Escherichia phage Mt1B1_P17	113	113	100	3.00E-31	98.21	56	YP_009987077.1
contig1_251	136064	136360	-	297	MPKLRKRGGRPTAEMQQIYAMDAAQASVKELFAEHYLEAMRYIVELVNDKDAAPLRFQAQAAIK EQVEEWLEEHYEAMEETPAVQNTDDVPKKIVI	98	hypothetical protein	Phi92_gp115	Escherichia phage phi92	112	112	100	2.00E-29	69.39	96	YP_009012447.1
contig1_252	138739	138987	-	249	MSLLEKHVFEDGNGNAVFLFHPEKYTSENNGTISVITDKVKVIDFLALMREMDLEINTFNAEALVV ALLEKKDSSEEAIEYA	82	hypothetical protein	AG: hypothetical protein MIM20_gp	Dompiswa phage TSP7_1	166	166	100%	2.00E-60	100.00%	104	YP_010356438.1
contig1_253	138996	139247	-	252	MPITPHLGFGYGMQNSFYFRACRNRHLTNHSRRDKNGVIKESDLSICTGLAFDDSPERVYQHQC IDVLVSNLVEDEQLTD	83	unknown	hypothetical protein G377_gp124	Escherichia phage phAPEC8	166	166	100	5.00E-51	100	104	YP_010356438.1
contig1_254	139285	139470	-	186	MISENPCKWHHVPIKDCMSCNPRSINIYASDDDNVLDDDEGWEDLDWTGYETKKDKKIIPS	61	hypothetical protein	hypothetical protein HOR27_gp130	Escherichia phage ESCO5]	116	116	100	4.00E-32	100	56	YP_009787120.1
contig1_255	140000	140275	+	276	MRFTRQEVVVLDEAMTMIVFYEDIFCAAHYLNDIQIEWQQAFLDKSNHLDFGEYLEWDGAKE VKIVGLNHDQIVDMQCKLCHYQFSKNVKLERQLEVVKDDSTN	107	hypothetical protein	hypothetical protein HOR27_gp129	Escherichia phage ESCO5	221	221	100%	7.00E-81	100.00%	107	YP_009787119.1
contig1_256	140259	140375	+	117	MIALISENPVLTITVLIFAMCVVHDILVSYFDNKGKKK	38	unknown	hypothetical protein JR327_gp280	Escherichia phage Mt1B1_P17	78.6	78.6	100	9.00E-18	100	38	YP_009987083.1
contig1_257	140372	140566	+	195	MKDVIQMVFRVTLDDGIHVVKGTQNYTEAKYFLEWIDTLTKQDVSYSRVTLTGDHTPIMEYVKK	64	hypothetical protein	hypothetical protein	Escherichia phage vB_EcoM_EP57	56.6	56.6	100	1.00E-07	100	138	WPK29350.1
contig1_258	140563	140802	+	240	MSNPYITGVTVSCVAKGGLYTVVEFPKPAIGISKVFDPPVIYEDLRTGQRQYWRVFNDFLRMEVVS GENTEEVIAKAKERY	79	hypothetical protein	DNA ligase	Escherichia phage vB_EcoM_EP57	158	158	100	7.00E-46	100	267	WPK29351.1
contig1_259	140756	141109	+	354	MAKTPKKLSKPKNVTKPKNEVLKVAKSPKKDKDFTEAFVDTPIEKIEEALQRLLEEADPMAE PLTADQIYVWGIWTLQLPEAKRRGMTSVPTCAKEAAVVLGLYKESKKRSKKK	117	hypothetical protein	hypothetical protein JR319_gp260	Escherichia phage vB_EcoM-Ro121c4YLVW	114	114	100	2.00E-30	100	54	YP_009984922.1
contig1_260	141106	141387	+	282	MIKTLFKCVKATDNEWYSGLFTAGKKYELNGTGKFSLVNDEGTQMVFAESSVYGIFEVVQE GSPMILEYHGNTKPYTAIDVINNKRNAK	93	hypothetical protein	hypothetical protein ECO340P1_00159	Escherichia phage ECO340P1	192	192	100	1.00E-61	100	93	WAX14418.1
contig1_261	141384	141566	+	183	MILLYSGKAKYMQGVKRVEVTKTVTGKSFIVYYFLVNGKEYAVAKTLVDKGKTWKVEAL	60	hypothetical protein	hypothetical protein G377_gp131	Escherichia phage phAPEC8	117	117	100	9.00E-33	100	60	YP_007348501.1
contig1_262	141563	141769	+	207	MIPVAGVVVLATLNGNVTVETKTFKAPEDCYNSLTVPRDEDDKAIEYQCFYIEGKPVFEVVKV EEK	68	unknown	hypothetical protein JR326_gp200	Escherichia phage ukendt	140	140	100	1.00E-41	100	68	YP_009986856.1
contig1_263	141766	142236	+	471	MKIKVTKAYDDNPKFISLNKSYGIENGDEFEVIDLFEDHGIVKAPITEQAIIILRTEAVEVSGDEPQY DSPYMTIEWIVAVDVGGMVSVLKAPNLHPGFTENGKTALDYGLPEDVENTPPGMRYWCSFHEKD WESGLVDDWHFEVSSFLIMPA	156	hypothetical protein	hypothetical protein JR326_gp199	Escherichia phage ukendt	322	322	100	1.00E-110	100	156	YP_009986855.1
contig1_264	142247	142591	+	345	MKVWIDDMRNPADYGGQEDAIWFKTSQEAAMFLNDPAKLYRRVTEWSEFDNGLGMESDQGDYDVF LHLEELAFGKPCFGSPFTVHTSNPAAGDKFMLAKESMQRYGIKMIRVHY	114	hypothetical protein	hypothetical protein ECO340P1_00163	Escherichia phage ECO340P1	242	242	100	1.00E-80	100	114	WAX14422.1
contig1_265	142601	142744	+	144	MHHSVWSEQEDEGYFIYREEEDWPDTSNDLLLPDTSFFEDNLREED	47	hypothetical protein	hypothetical protein HOR21_gp119	Escherichia phage ESCO13	95.9	95.9	100	2.00E-24	100	47	YP_009786581.1
contig1_266	142751	143107	+	357	MSGIENNICYQPLTWMGEGHYAQRVIVCAANKYILNNGEELIIPCVRHANPVLVLAQLNLKEAGVI NKTLCTPDNQGFIDQYYNWSRADAYIIAENADQIDHERNGHDEHSEGLY	118	hypothetical protein	hypothetical protein ECO340P2_00170	Escherichia phage ECO340P2	246	246	100	9.00E-82	99.15	118	WAX14702.1
contig1_267	143107	143658	+	552	MFITSDLHFMHKRIEFAPEYRPWEDMDHMTALIEAWNKCATTSGVKMWHLGDFCFGTEEDTRK IASRLQGDITYCVGNHDYSKHREVLAEYGEVVYVDEYVKQLFFVLVSHYPMA5WNKQGRG5IML HGSHSGSPDEAYGKMLDVGWDAHGKILHFDIISMMSKRDIVTDHKKIHKGE	183	hydrolase activity	phosphoesterase	Escherichia phage nepoznato	380	380	100	6.00E-133	98.91	183	YP_009985879.1
contig1_268	143660	144592	+	933	MAKFNCDLVEKGLVHKKTYKEGEYSGLSVLKVKYKNVFWDNLWSIDSRLLCEGRGIVVDAADDNVV IWPFKIFNRFENGDTLPADEFVDVVRKVNNGFMASVGVYKGLIVSTTGSLESDFASIAKNHIVSEC DDIEHFHKWTESAKATLFEICDPSDPIHVEEPGAYLIGARIONPDGTSFMLPEGALDGLIASVTIKFR PEVHPMVKFSDDVYEMSKHCKHEGFVVRFTNYPFNLLLKISPHYLTKKFLMRGGDKKWDLIWDN PKNAKQMVDEEYVALLIEWIRNFTKIQWAALNQERREKIEENFFGG	310	RNA ligase	hypothetical protein ECO340P1_00167	Escherichia phage ECO340P1	644	644	100	0	100	310	WAX14426.1
contig1_269	144593	144997	+	405	MKQLJILRGVSGAGKSTVAEIISEGYWPICEADQYHYTESGVYDWKPVNGKAHAHQWCGIVRDAM ASNLNKIIVSNTSTTEKELKPYLALAEKFGYQVISLVVENRHNDSIHEVPQYIRDQOEKRLRGSLKL Q	134	ATPase	ATPase	Escherichia phage ukendt	278	278	100	6.00E-94	99.25	134	YP_009986849.1
contig1_270	145007	145333	+	327	MQIYTDDRKYETILDEDTGRITVLRHGEWRDETGDNVILSLIHIEQMRDDYAEHYENEANKVKF ENELKEESEMVYVYKKEISRLLEEIDALQEIIYELNNELNA	108	hol-like chemotaxis	hypothetical protein MNOOCJFK_00108	Escherichia phage vB_EcoM_01	209	209	100	8.00E-68	99.07	108	WVW37508.1
contig1_271	145343	145534	+	192	MKKDIVVVGWLTCPGNSDITVNTGDKNYLIFYGDKITCNTCGRVGIHETDDCCAFESWDEEE	63	hypothetical protein	hypothetical protein	Escherichia phage phiWec188	125	125	100	6.00E-36	96.83	63	YP_009803357.1
contig1_272	145531	145752	+	222	MSTAFYVRSGDEFLATFDDGDLMDYEDMLDYAKRQGSTSIDYMLATSTILLDADLDEVNCRLK ISVFKWED	73	unknown	hypothetical protein	Escherichia phage PNJ1809-36	146	146	100	7.00E-44	100	73	QP112958.1
contig1_273	145752	146867	+	1116	MQQNTQTLYGKDSKGLKQWTVTYDGAVVTVAHGRVGGKITEKSYTAEAKNIGRSNETTPEEQA ELEAFAKWTKQLKNGYYKTKEEAENHVSPTPMKCQDYKYPERVVPFGYAQYKLNGLRSMINM KGECLSKAGEVYNLPHPHWGIPNFISEVGHPLDGEVFAAGLVLSLQQNSAWKKHNAINTPLLYN YVYDIPVPLPEKRVLDVLAALKA VVEDYGLDELICVHTYEIENQEQDAFYEKALLEKAEGVVY RNAHGVYEFDKRSYDVIKRKPRLTLEVKVNSKSDKNGDGLVTGEMENGVYVFLMRKDAHETI NRYKAENASTLNQFVEIEYEFSDEGIPTKPVGVRIKREMPGWPEAE	371	DNA ligase (ATP) activity	ATP-dependent DNA ligase	Escherichia phage Mt1B1_P17	769	769	100	0	100	371	YP_009987099.1
contig1_274	146877	147071	+	195	MFLAILVFSVLSFCMNASESFPKNSKRTVCIADSCMSGVGYAVVSCFLAYHCAKYALEAFL	64	unknown	hypothetical protein JR321_gp213	Escherichia phage anhsysys	129	129	100	4.00E-37	100	64	YP_009985556.1
contig1_275	147068	147250	+	183	MHLATILMMLIAIAIVILASFPADKWYFNIPRMLVFGFAGIYMGETVNNISNFIYESYFK	60	hypothetical protein	hypothetical protein	Escherichia phage BI-EHEC	118	118	100	1.00E-32	100	86	UGV23997.1
contig1_276	147260	147985	+	726	MIENFFDKDKDFTEFFKNAAKHVIDWNAKARGGEQPEFTQELFMSQIGFVREELKEYETAAKVNDH VELDAAADIFVVS5LYTMFFGEEHTMNFLDYAVGDVFTPTVYTFDFALEQTFTEPVQMALMAA GIMRMSRDTLIRSKYPEKKVIKVLKSNDSKYPTKQQLLTKWKTSDIDSIAQECALIEERNANRPE GAYTGVHAYVNEKQKVYVFFDDKGKIMKPSFTVKPNIAIINK	241	protein disulfide oxidoreductase activity	hypothetical protein	Escherichia phage vB_EcoM_EP57	488	488	100	6.00E-174	100	237	WPK29354.1
contig1_277	148042	148920	+	879	MFVKSFKSALPMVVGDDASVASLNSITDIPLEFVTAEGSQSHTIGLVRFEDDSKFVKFSDLELLNV GOSVKKVDDKKVKRILNERLEMRQDMESGKEFVVKVEVVKAMKEDIEFALLPETEPEDFNYYV VLDKTTNLLVVLNGSKVAEITSLRSVLGTTPSVGFSVHEAIVKSGFELLENHEADRITLGNVYK MESEGVVVWSKESLYESKAVELKEDGKDVVAIGLEYDGVVDFVVDKEFKLSKLRFPKYADEEG SIEASVLCCFNEIRGLMEDLTATILK	292	Putative exonuclease, RdgC	hypothetical protein NWUPM118_103	Escherichia phage vB_EcoM_118_SA_NWU	578	578	100	0	99.66	292	WIL79405.1

contig1_278	148993	149202	+	210	MKKILTVVLLAFSFTVAAGQITLLSDSEVNGNTKYCYYSNANQDEVIAIPKSRQCPYTKTFSTEDDDE	69	hypothetical protein	hypothetical protein HOR27_gp105	Escherichia phage ESCO5	142	142	100	4.00E-42	98.55	69	YP_009787095.1
contig1_279	150000	150333	+	334	MPVEYKSERLDIKPLQSETKDYLVFHNQDVTVEADDELEKYGFQGYKDYKRTGKFSYIVVSI DKDSLHTPSILFNFYKEDGVFKNPDIILIDESIGDIWVDKGKKKEVKGWGSYWLAYQMLMGDKTD SIRPYQDFDIKFGDITCFNLLSACKTQAEOLFQTVKDTYYSWFPDGVNFTSWDGEEVHMTTDEWIETI FQLVYMKRWDNDDTTFESMLQSYISQQEAE	229	exonuclease activity	putative exonuclease	Escherichia phage ESCO13	473	473	100	1.00E-165	100	372	YP_009786567.1
contig1_280	150330	151289	+	960	MSRLTEEQKADILSMSAEGMSSRNIAAIVLGSPTRKSTVNDFLARFGASKQEPVKKKQPVIKIIDVET APEIAYTFRRFKAFISPDQVIRRGYLLSYSSADLYTGEVEGKNLSSYPFLDIDHTDDWELCQDLWNLL NEADVVAHNGYKFDRAYINQRFAYHDMAPPSNYVVVDTLKAAKKQFALPSNSLKEMGAYFET ESEKLDNEGFLWKACCEGDRDAFERMQIYNDGDVVSRLDLYMKILPWIPQHPNLSAAYYPDEKVR CSRCGSDHVVHTGKQYHTAVSSFDIIRCESCGGLSRSRANTRSKDKRAATIIGI	319	nucleic acid binding	putative exonuclease	Escherichia phage vB_EcoM-Ro1211w	642	642	100	0	100	305	AXA27916.1
contig1_281	151376	151603	+	228	MSITLTGNEIFELFEMLGLNYTIEKDPDLLDVEITIQEDTAIYNDGDVYQGRVAYYTDYPEEGAVG IQEENYV	75	unknown	hypothetical protein HOT48_gp055	Klebsiella phage ZCKP1	148	148	100	2.00E-44	100	75	YP_009803348.1
contig1_282	151596	151997	+	402	MSNAFDNQVDGDHYTKMAMQPIELAYLVGGTPCFCKLAKYATRIKGERQINLDKAHICIELERTLM QNNTYMVRENYPMSMTNAAKHDQAMLLIDFFTCDPLIRVALKHMVNSSYVDAIEAIKQLKERISGE QY	133	hypothetical protein	hypothetical protein G377_gp152	Escherichia phage phAPEC8	281	281	100	3.00E-95	99.25	133	YP_007348485.1
contig1_283	151942	152175	+	234	MLKLLNNLRNVLVASNTKQYGAGEVYKIFNRKGDKLLLTIPETMCKAGLDRLLFFKHNIIPPGE YTAKKVSNIQR	77	hypothetical protein	hypothetical protein	Escherichia phage dw-ec	133	133	100	8.00E-39	98.44	77	UJQ43839.1
contig1_284	152186	152455	+	270	MWGEGTPWKTQAEFYTYLRGCFRKAWMRHPNKKIKVINARRFKVDRVDKDGVMIDKKTGKPKQ VWNCECEICGHRGGMKDFQVDHIHAAK	90	nucleic acid binding	HNH endonuclease	Klebsiella phage ZCKP1	196	196	100%	1.00E-69	100.00%	184	YP_009803345.1

Supplementary TableS3. Antibiotic resistance profile of MDR *Escherichia coli*

Bacterial isolates	Antibiotics															
	Aminoglycosides		Carbapenems			Cephalosporins				Fluoroquinolones		Penicillins			Other	
	Amikacin	Gentamicin	Imipenem	Meropenem	Ertapenem	Cefazolin	Cefuroxime	Cefuroxime Axetil	Cefepime	Ceftriaxone	Ciprofloxacin	Ampicillin	Amoxicillin/Clavulanic Acid	Piperacillin/Tazobactam	Tetracycline	Trimethoprim/Sulfamethoxazole
MDR <i>E. coli</i> PPW001	S	S	S	S	S	R	R	R	S	R	S	R	S	S	R	S
MDR <i>E. coli</i> PPW002	S	S	S	S	S	R	R	R	S	R	S	R	S	S	R	S
MDR <i>E. coli</i> PPW003	S	S	S	S	S	R	R	R	S	R	S	R	S	S	R	S
MDR <i>E. coli</i> PPW004	S	S	S	S	S	R	R	R	S	R	S	R	S	S	R	S
MDR <i>E. coli</i> PPW005	S	S	S	S	S	R	R	R	S	R	S	R	S	S	R	S
MDR <i>E. coli</i> PPW006	S	S	S	S	S	R	R	R	S	R	S	R	S	S	R	S
MDR <i>E. coli</i> PPW007	S	R	S	S	S	R	R	R	S	R	S	R	S	S	R	R
MDR <i>E. coli</i> PPW008	S	S	S	S	S	R	R	R	S	R	S	R	S	S	R	R
MDR <i>E. coli</i> PPW009	S	R	S	S	S	R	R	R	S	R	S	R	S	S	R	R
MDR <i>E. coli</i> PPW010	S	R	S	S	S	R	R	R	I	R	S	R	S	S	R	R
MDR <i>E. coli</i> PPW011	S	S	S	S	S	R	R	R	R	R	R	R	S	S	R	R
MDR <i>E. coli</i> PPW012	S	S	S	S	S	R	R	R	R	R	R	R	S	S	R	R
MDR <i>E. coli</i> PPW013	S	R	S	S	S	R	R	R	S	R	S	R	S	S	R	S
MDR <i>E. coli</i> PPW014	S	S	S	S	S	R	R	R	R	R	R	R	S	S	R	R
MDR <i>E. coli</i> PPW015	S	S	S	S	S	R	R	R	S	R	S	R	S	S	R	S
MDR <i>E. coli</i> PPW016	S	R	S	S	S	R	R	R	S	R	S	R	S	S	R	S
MDR <i>E. coli</i> PPW017	S	S	S	S	S	R	R	R	S	R	R	R	R	S	R	S
MDR <i>E. coli</i> PPW018	S	R	S	S	S	R	R	R	S	R	S	R	S	S	R	S
MDR <i>E. coli</i> PPW019	S	S	S	S	S	R	R	R	S	R	S	R	S	S	R	R
MDR <i>E. coli</i> PPW020	S	S	S	S	S	R	R	R	S	R	S	R	S	S	R	S