Supplementary Materials

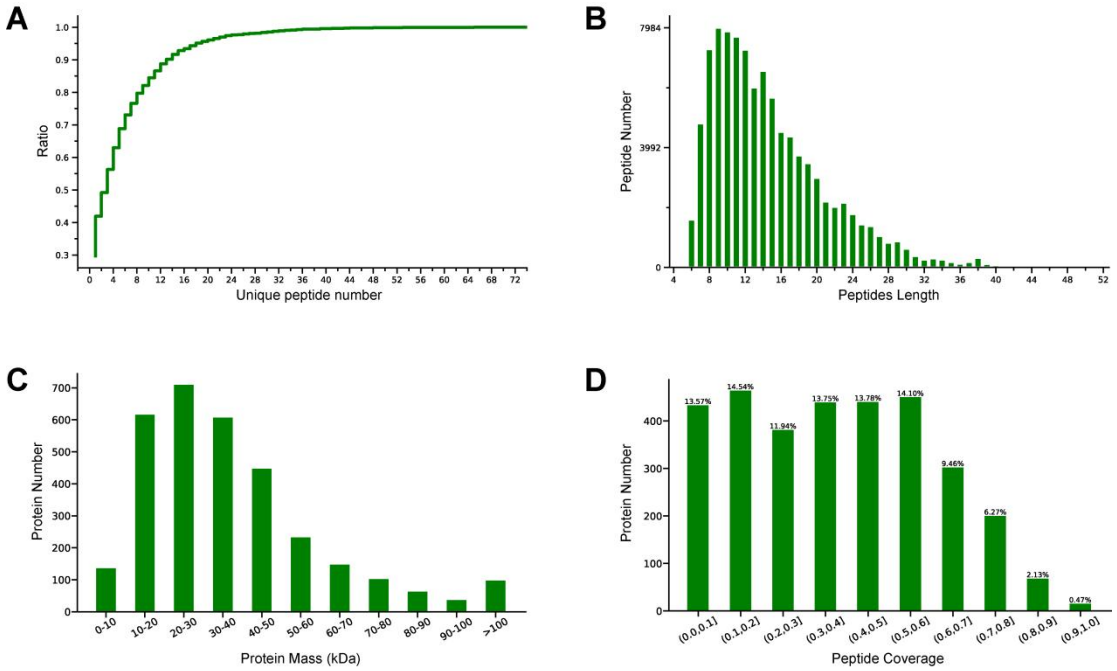

Figure S1. Profiles of the whole-cell-lysate proteins identified in the MDR, XDR, and DS strains. (A) Quantitative distribution of unique peptides identified for individual proteins. (B) Length distribution of the identified peptides. (C) Distribution of molecular mass among all identified proteins. (D) Proportional distribution of the amino acid sequence of each identified protein covered by peptides.

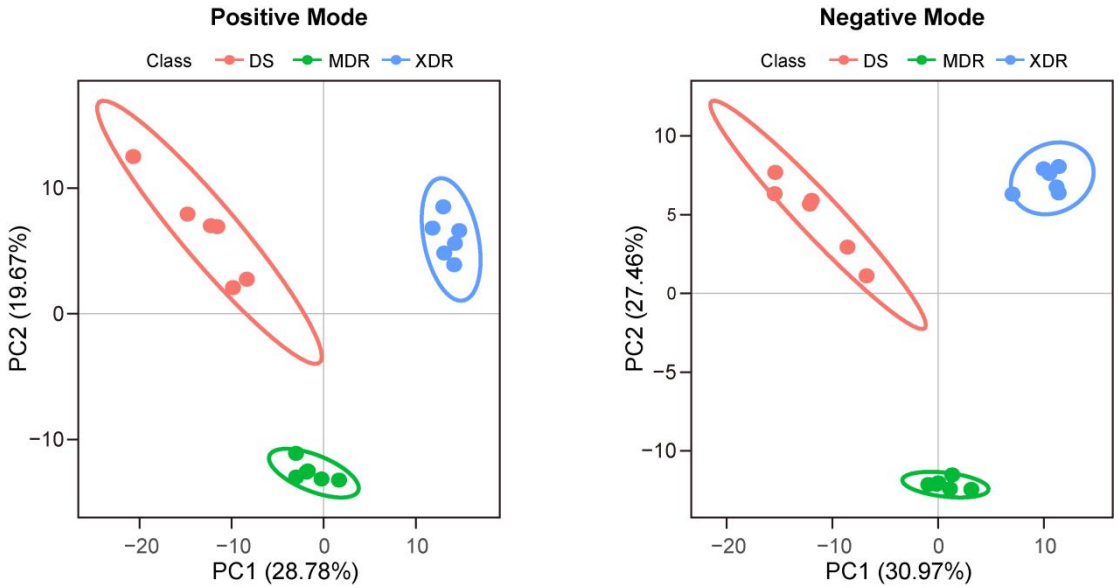

Figure S2. PCA of total metabolic data of the MDR, XDR, and DS strains under the positive (left) and negative (right) ion modes.

Table S1: TMT labeling information of the DS, MDR and XDR strains.

Strains	**Sample ID**	**TMT isotope**
DS	DS-1	127N
	DS-2	128N
	DS-3	129N
MDR	MDR-1	130N
	MDR-2	131N
	MDR-3	132N
XDR	XDR-1	133N
	XDR-2	134N
	XDR-3	135N

Table S2: DEPs in MDR vs. DS strains.

Protein ID	Description	Protein Coverage (%)	Peptides	PSMs	Unique Peptide Number	Mass [kDa]	Protein Seqence	FC MDR/DS	*P*-value MDR/DS	Regulate
A0A009G507	Glycosyltransferase subfamily 4-like, N-terminal domain	48	12	21	11	42.9	MQNKKIVLIGTTGSSFYGFRADLIRSLVANGHQVYAFTSEYTENCLDKIKALGAEPITYQLSRGG LNPFADIASTYQLIRKIKKIKPDIVFSYFAKPVIYGTLAASFAKVPHIIGMLEGLGYTFTAQPEGQSS KTKLIRNIQVLLYRLAFPRLDDMIFLNPDDEKDLIHTYTLPVKKVHILGGIGLDLKEYSYSVAPVS PVSFLFIGRLLKEKGIFEFIDAIRIVKHKYPNTKFTILGGLDTQNMGALSKSQLDELIAEGLFEYPG HVSNVKDWIANSSVFVLPSYREGVPRSTQEAMAIGRPVITTDVPGCRETVINDVNGFIVPCWDA KALAEKMCFFIESPSQINLMGLESMKMAHQKFDAEKVNNRLFEIMGLNSSYEKIG
A0A009G8E9	Tyrosine-protein kinase wzc-like, C-terminal domain	45	27	88	18	82.0	MSQTSKTEDTIDLKELFFSLIAQWKLIVLCILISLVCALIYLRVTPNTYSVDALVQVEDTKSAASA ALLGELSKMVDQKSPAQAEIEVLTSRMVLGQVINNLNLDITIKNHDDTFFNRLLSQDKQNIDYKK DAVTFSNKDSYFSIQQLQIPSYYLDKPLLLSFKDQRHFTFSYKDKVIFSGQLNSNNLVTAREGQW KVRINSTHAPSVEQQFTISKLALPTAVQKLGSTYGVAERGKQTGVISLNYQGTDKEHITEVLNNI LAVYHSQNIERRTLESKQTLDFLDKQLPDLKQQLEESERKFNQFREKYNTVDVTQEAELYLKQNI ALETTKTELKQKQAELAAKYTNDHPLMAEINAQLAAVNKKSAELSDTLKRLPEVQRQYLQLYR DVKVNTELYTSLLNSYQQLKIAKAGEIGNVRIIDTAVEPVNPIKPKTLIVLVLTIFIGGFIGILIALLR NMLRTGVKDSTQIENDLNLPVYATVPRSPIQETRMNILKKKKSIPILAVKSSDDIAIESLRSIRTAIH FALTTAKNNIIMIAGPSPEVGKSFISTNLATIFAQSNKRVLLIDADMRRGYMHKYFDVDVKPGLS ELLSGQADLSQVLHKTQVANLDVITRGKSPTNPSEMLSSTQFKDLLEKFQTQYDHIIIDTPPVLAV TDGIIISQYTGVNLIVARYAKSHMKELELTINRFEQAGVKVNGFILNDIQRSSGGGYGYNYAYAY KAQKED
A0A009G8K1	UDP-N-acetyl-D-mannosamine/glucosamine dehydrogenase	53	19	40	11	47.7	MFNLEQLHIAIIGLGYVGLPLAVEFGKKVPVIGFDIHQKRIDELNNGQDHTLEVSKEEIQQAVKLR YTSSLEDLKDCNFFIVTVPTPIDDFKQPDLTPLIKASTSIGQALKKGDVVVYESTVYPGATEEVCIP VLEKISGLNFNQDFFAGYSPERINPGDKLHRVTNILKITSGSTPEVADYVDEVYNLIIEAGTHKAPS IKVAEAAKVIENTQRDVNIALINELALIFNKLNIDTEDVLKAAGTKWNFLPFRPGLVGGHCIGVD PYYLTHKAQSIGLHPEIILAARRLNDRMGEYVATQLIKEMVKQRIQVVGARILVMGLSFKENCPD IRNTKIVDFIKALKEYDLDLDIYDPWVDENEVQHEYGLAPIKKLGNGLYDAIVIAVAHNQFKTM RAQEFQALGKEKYVLYDLKYILDKTESDLRL
A0A009GVM1	Thiolase	83	21	98	1	40.8	MTDIVIVNGARTAMGGFQGSLSGLTAPELGAVTIKEAIARAGLQPTDVEEVIMGCVLPAGLKQG PARQAMRKAGLPDSTGAVTINKLCGSGMKAVMQAADMIKAGSAEIVVAGGMESMTNAPYVLP KARAGYRMGHGEIKDHMFFDGLEDAETGRLMGSFAQDMANTRGYTREQMDDFAIRSLKRAQT AITEGYFKDEIVPVTVSTRKGDVIVDQDEQPLNAKIDKIPSLKPAFAKDGTITAANASSISDGASAL VLTSSEVAAQRGLQPLAKIIATASNSQHPSEFTIAPVGAIEKVLKKAGWNAQDVDLWEINEAFAM VTMCPIDDFKLDPEKVNIHGGACALGHPVGSTGSRIILTLIHALKRTGGKKGVAALCIGGGEATA VAIEIL
A0A009H3M3	Protein-tyrosine phosphatase, low molecular weight	40	5	12	2	16.5	MQINNILVVCVGNICRSPMAEYLLKRQFPHLHIESAGISGLIGHNADEKAQLCMQRLGINMQAHI AQKLDAEHIKRADLILVMSHNQQKHIEQTWPFAKGKTFRLGHWQNKNVPDPYQHDQTIFDETC ELIQKCLDDWKNYI
A0A009HXJ2	Aminomethyltransferase folate-binding domain protein	42	8	28	1	26.7	MSLLAFSSYALNGVDAQKFLQGQVTVDTERLAENETRYTAICDLKGRIHFGLWLKKNNAESFDII VTQDQAEEFAKHIKKYGAFSKMTLSEQGAVFPKVVNGHTEFSSTETDISEWQKQAIMTGQAWIA QATEHEFQPQELRLHQREGVNYDKGCYLGQEIVARLWFKAKPKHWLHLVQGTGDAPAPATQL HNDVEVVNSTQTTDGYIALVVAKPAALQELGLQVLDLPEALSGDVARPQ
A0A009PBA1	ER-bound oxygenase mpaB/mpaB'/Rubber oxygenase catalytic domain-containing protein	7	3	4	1	47.3	MISPTRLASFNDMQDSNFFTQFLNICCEKPVQPSYTEYVSLQHALYEGDIEMDKVIDWVMQNPK DHRIIFEKILFQGRDELSEPIPTELENFFNYIEQKPDWLDQQQIDEAVKFTHRLGINNGFILRDLSL MAGYLYPGFNQPLILTGALKKEAGTRLAETTKWWVDITEPHGLSRLSAGFTSTIYVRFIHALVRR QLKKSDRWDNEVWGIPLNQFDLAMTNLAFSSVVLLGIRALGIWPTKQEAKSFLHFWRYVGWL MGIEEKWLIQSEPEGWRLLYWMQFAHPRSDHSSIELGSSLSKEPLERKYLHLRSLQQKLAYRQH LELTQFFIGKKRMKLLGLPQQSASWFAYYLIVRNLLLYNGAKLSPKVEKFLSKSGRNIQKLGLTL YQNQGKAKTLASMHHNSGI
A0A009QKJ4	Polyprenyl synthetase family protein	61	13	51	1	35.5	MVIDFKQDILAPVATDFAAMDHLINEGISSKVGLVMSVSKHVVEAGGKRMRPIMCLLAARACGL DNMQNAQRLAAIIEMLHTATLVHDDVVDESGLRRGRPTANATWNNQTAVLVGDFLIARAFDLL VDLNNMTLLKDFSTGTCEIAEGEVLQLQSQHQPDTTEETYLKIIHGKTSRLFELATEGAAILAGQE AYREPLRLFAGHFGNAFQIIDDILDYTSDAEILGKNIGDDLMEGKPTLPLISALAHSTGEEHAIIRR SIATGGVDQLPKVIEIVQKSGALDYCQRRAQEETEAALQALSILPDTPYRQALINLTRLALHRIQ

A0A009T164	DUF4393 domain-containing protein	30	6	9	6	27.2	MTEKDNNLNASFLDHRVATYKAIAGLIPGFGSILSEVVGAIIPDQRMDRLVKYIKILDTKVQKINS DLLEIAKQNELAIDLIEEGFVQASRSLSNERREYIANVVANGISDEEKNYADSKYILKLLGELNDQ EVIWLRFFLHPTFDGDEEFRQQHQNVIEPIATYIGADENILEKKDIQESYKSHLERLGLIRSNYRID KNTGLPKFNHQGVPEVSYRFVTPLGKMMLKKIGLIDSANT	3.4554463	0.0019882	up
A0A062I638	Endoribonuclease L-PSP family protein	24	2	2	1	14.7	MRTAIFPQDRHALYEQHGYSAAIQSKDLLFVSGQVGSLEDGSPVPDFEKQVIQAFKNLAETLKA AGCTFDDIIDVTTFHTDPERQFKSIMKVKNQIFTQKPYPNWTAVGVTWLAGFDFEIKVIARIPHN N	2.9206882	0.015092862	up
A0A062IDU6	Glycerol-3-phosphate dehydrogenase	40	17	27	1	57.4	MKVQPNDYSKIYDLAVIGGGINGVGIANDAAGRGLSVFLCEKDDLASHTSSASSKLIHGGLRYLE HKEFRLVREALAEREVLLAKAPHIIKPMRFIMPHRPHLRPAWLIRAGLFFYDHLGKREKLLGSNLI YFKEDSPLKPAITRGFEYSDCTVDDARLVVLNALQAKEKGAKVVTRTSCVKAYRQQELWHLEL QSRAEFYQIRAKAIVNAAGPWVEEIISKNLGLSSPYQIRLIQGSHIVVPKLYDCHKAFIMQNEDRRI VFAIPYLEKYTLIGTTDQEYTGDPQKVEITDVEIDYLLTVTNSHFKKQLTRADIVSQYSGVRALC DDESDNPSAITRDYTLALQAEDKTTPLLSVFGGKITTYRKLAEAALEHLAPFFNDMAEEWTADE ALPGAENWTTLEDLINQIKTRVSGISDSLANRWAHAYGTRVWNMLKERNAIEQLGQHFGHDLF ECEVRYLCEYEWAHTAEDILWRRSKLGLAFDEKQVKVLEAYLAERRLKDDAA	6.3592133	0.004022169	up
A0A062IH37	Efflux transporter, outer membrane factor (OMF) lipo, NodT family protein	75	25	134	1	52.8	MQKVWSISGRSIAVSALALALAACQSMRGPEPVVKTDIPQSYAYNSASGTSIAEQGYKQFFADPR LLEVIDLALANNRDLRTATLNIERAQQQYQITQNNQLPTIGASGSAIRQVSQSRDPNNPYSTYQV GLGVTAYELDFWGRVRSLKDAALDSYLATQSARDSTQISLISQVAQAWLNYSFATANLRLAEQT LKAQLDSYNLNKKRFDVGIDSEVPLRQAQISVETARNDVANYKTQIAQAQNLLNLLVGQPVPQN LLPTQPVKRIAQQNVFTAGLPSDLLNNRPDVKAAEYNLSAAGANIGAAKARLFPTISLTGSAGYA STDLSDLFKSGGFVWSVGPSLDLPIFDWGTRRANVKISETDQKIALSDYEKSVQSAFREVNDALA TRANIGERLTAQQRLVEATNRNYTLSNARFRAGIDSYLTVLDAQRSSYAAEQGLLLLQQANLNN QIELYKTLGGGLKANTSDTVVHQPSTAELKKQ	4.7510868	0.014454606	up
A0A062IRH0	Valine--tRNA ligase	53	42	188	1	108.5	MTDAQTAQNIATTYDPTEIEKKWYKTWEEQGYFKPSGHGESFCIMIPPPNVTGSLHMGHGFNN AIMDALTRYNRMMGKNTLWQPGTDHAGIATQMVVERQLGLQGITRHDLGREKFIEKVWEWKE QSGGTITKQIRRLGSSVDWSRERFTMDEGLSNAVKEVFVRLHEDGLIYRGKRLVNWDPKLQTAL SDLEVESKEEKGSLWHFKYFFEDKSVKTQDGKDYLVVATTRPETLLGDTAVAVHPEDERYAHL VGKNIVLPITGRLIPIVADDYVEKDFGTGCVKITPAHDFNDYELGKRNSLPIINIFNKNAEVLGEFE YIAKAGEQISKTITAPADYAGLERFEARKKLVAQAEAEGWLDQIQPYDLKAPRGDRSGVIIEPLL TDQWYVKIAPLAEPAIEAVQDGRIKFVPEQYSNMYMAWMRDIQDWCISRQLWWGHRIPAWYD ADGNIYVGRSEEEVRAKNNIAADIELKQDEDVLDTWFSSALWTFSTLGWPEQTPELKTFHPTDV LVTGFDIIFFWVARMIMMTMHFMKNEDGSSQIPFKTVYVHGLVRDGEGQKMSKSKGNVLDPLD LIDGIDLESLVAKRTTGLMNPKDAAKIEKSTRKEFPDGINAYGTDAVRFTFCALANTGRDIKFDL KRVEGYRNFCNKIWNATRFVLMNVEGQTVGTDARPDLWELPEQWIISRLQKAEAAVHQAFATY RLDLAAQAIYDFIWNEYCDWYVELTKPVLNDAEVSEERKAEVRRVLLAVMEASLRLAHPLMPY LTEEIWQTLAPMLGQGGPTIMTAQYPIPEQAKINEQAEADMQWLQGLIGAVRNIRGEMGLGNA RLLPVLLQNISNAEREQITRIEALFKALAKVESIEFLGKDQEPPLSSSSVVGHASVFVPMKGLIDPK AELARLQKDLDKIQKQHDQIANKLANEGFVSKAPAAVVEGEKAKLAEFAAQLDKVKANMEQIA AL
A0A062IS18	Porin B	50	15	78	1	46.8	MKTHKSLMVSCLSVLSITLFVQHAQAAAAFDPNGSWMLGDWNGQRTALQAQGYDFSFGYTGE YAGILDSKQTSTHGSAYTGQLALGSHLDLGKILGWQDTEAQITLTYRDGQSLSEHSPALAGHQSS VQEVWGREQTWRLTDLWIKKKFLDQKLDVKVGRFGEGEDFNSFDCDFQNLALCGSQVGNWV GDQWYNWPVSQWAMRVKYNLQPDLYTQVGVYEYNPENLERGKGFNLSTDGSHGAIIPAEVV WSPKLGVQSMPGEYRLGYYYSTADAKEIADSTKTSHKQGVWVTAKQKLFQPADQTDRGLTGF VNLTFHDSDTNKVDNMQNIGLVYKGLLNQRPQDELALGVARIHINDDWSDVQAKEYDTEYNTE LYYGIHATNWLTIRPNVQYVRHVGALKNGDNTWVGGIKFSTAF	2.4314241	0.001234418	up
A0A097I5C2	FnlC	40	10	44	2	42.8	MKKLKLMTVVGTRPEIIRLSRVMAACDEYFDHVIVHTGQNYDYELNEIFFTDLGIRKPDHFLNA AGATGAETIGNVIIAVDKILDEVKPEALLVLGDTNSCMAVLPAKRRKIPTFHMEAGNRCFDMRV PEEINRRIVDHTADINLTYSTIARDYLLAEGLPADLVIKSGSPMFEVLHHYKAKIEASDVLERLNL KEHEYFIVSAHREENINSDQNFLDLVEMLNAVAEKYKYPVIVSTHPRTRKRIEELNVEFHPLIQLL KPLGFSDYNKLQLSAKAALSDSGTINEESSILNFPALNLRQAHERPEGMEEAAVMMVGLKAERIL QGLAILEGQTRGEDRLLRLVEDYSMPNVSEKVVRIIMSYTDYVNRVIWKQF	0.2078959	0.014078591	down

A0A0E1FL10	Glucose-6-phosphate isomerase	26	13	20	9	62.9	MSKSIEQFPKDLSSPLIQLKSSVEKNSKLHIKELFALEPERFQNYSVKFDQLFFDYSKQRITKNILE QLVALANNKQLTQWINRLFSQDKINCTEQREAMHWALRLPSEYSKFPELAKQVHIQLQRMYTL VEKIHAGQYRGATGEVIQDVVNIGVGGSDLGPHMVTHALADFKVKTAKPLNVHFVSTMDGSQL SDLLHQLRPETTLFIISSKSFGTIDTLSNAQTVRQWLEKALGKHDRVVKSHFIGVSTKAEKMTEW GIAPDNQLLLWDWVGGRYSLWSCIGFPIALTIGIDGFQQLLAGAHAVDEHFQNTSFERNIPVLMA LLGIWNNNFLNIQTHAVLPYDGRLKYFAAYLQQLEMESNGKSVQRDGQKVELDTCPIVWGEVG PNAQHAFYQLLHQGTQAVSCDFIAPVQRYNADHFTYVENAEALIEQHHLALSNCLAQSRLLAFG NEALDAAELKNLPIYKQYEGNQPSSTLLLDELNPYNLGMLIALYEHKVFVQSVIWNINPFDQWG VEKGKQIADQLLPILNGVQNDFSKLDASTRGLIKILLGKVDG	0.2436056	0.000153685	down
A0A0E1PN17	Uncharacterized protein	21	9	23	1	43.5	MRYKNTIVRITVDMSFVPQIKIPATYMRGGTSKGVFFKLDDLPEKAQVAGQARDQLLLRVIGSP DPYGKQIDGMGGATSSTSKTVILAKSTQPDHDVDYLFGQVSIDQAFVDWSGNCGNLTAAVGSF AISNGLVDADRIPENGLCTVRIWQKNIQKTIIAHVPIINGQVQETGDFELDGVTFPAAEVQIEFLDP ADDGEEGGDMFPTGNVVDQLDVPEIGSFQATFINAGIPTIFLNAEDLGYEGTELQDHINGDAAAL ARFEKIRAYGAVQMGLIKDISEAAARQHTPKIAFVSKPKNYTASSGKNVSENDADLLVRALSMG KLHHAMMGTAAVAIGTAAAIPGTLVNLAAGGGEREAVRFGHPSGTLRVGAQAELTNGQWVVK KAIMSRSARVLMEGWVRVPGDSF	0.4011239	0.000110633	down
A0A0E1PNX1	Outer membrane protein transport protein (OMPP1/FadL/TodX)	61	17	118	15	54.2	MKFKERLKMKLKHLSTAMILATLPATGVFAAALDRSGQSMSAFFQPGNYFEAGISVLDPDVAG KEAGSSATRRDIGDMANDYYFPSAALKLQINDQFSFGLLYDQPFGADAEYSGNNVFVSNPGSDTI LSQKALGDLASSSIQKLVQASGSAFTPALIEVTKVTGGDPTKPTQTEILGALQQVAAGGNTTVGA GLTALQKTQAAINAANNYLGTGGTKVKVDTQNLSFVFGYQPTKNFNFYAGPVLQTVKGNVSLR GQAYSLYNGYDANIKETTGAGWLAGAAYQIPEIALRASVTYRSEIDHKVNIDENLSILNFPGLTS VLAGLDVPASKLQAINSSGKTTITTPQSVNLDFQTGIMADTVAFANVRWVNWKDFSIQPYKFGK VSEAVGGLVGRPNGFNLVEYSDDQWSVNAGVGRKLNDKWAGNVSVGWDSGAGNPVTTLGPT EGYWNVGLGVQYSPTPQTFIAGGVKYFWLGDAKAQTGAQAGSDEYVADFSDNNAIAYGLKLG YKF	0.3490728	0.021088184	down
A0A0E1PQH3	DcaP outer membrane protein	51	20	102	10	47.4	MMDLFLNRKSFVVKSLAITVTALMMSGANAATSDKEEIRKLRQEVEALKALVQEQRQVQQQQ QQVQQQQQQVQLAEVKAQPQPVAAPVSPLAGFKSKAGADVNLYGFVRGDANYIIEGADNDFGD VSKSDGKTHDKLRATAKTTRLGLDFNTPVGDDKVGGKIEVDFAGSTTDSNGSLRIRHAYLTYNN WLFGQTTSNFLANHAPEMIDFSTNIGGGTKRVPQVRYNYKLGPTTQLFVSAEKGDSTTSVTGDSI KYSLPALTAKITQGYAEGRGSASARVLVENYKSQLADDDKTGWGVAVGTDFKVSDPLKLFADA SYVVGDNSYLYGSNSPYAVDGNSIEQNEFVAVQVGGTYKILPNLRSTLAYGAQFSDDGTDYARL NASANEKVQQAWINFIYTPVKPIDLGVEYVNGKRDTFDGKSYKDNRVGLMAKYSF	0.2056725	0.033611545	down
A0A0E1PVE2	Alanine racemase	30	10	34	3	40.5	MPRPITAVIHRQALQNNLAVVRKAMPNSKVFAVVKANAYGHGIERVYEAFKAADGFALLDIEE AKRIRALGWTGPILLLEGVFSPQDLFDCVQYQLSFTIHSEAQIEWVEQHPYPAQFDVFLKMNSGM NRLGFKPQHYVQAWERLNNLANVAKITHMMHFSDADGDRFGQQGIDYQITAFEEIVKDLPGER SVSNSAAILRYQDQLKSDYVRSGIMLYGSSPDYPTHSIADWGLQPTMSLRSEIISVQHLEPNESVG YGSNFVAEQPMTIGIVACGYADGYQRISPTGTPVLVDSVRTRTVGRVSMDMLAVDLTGIESAKV GSEVVLWGQSSTGVILPIDDVAVSSGTVGYELMCAVTARVQFINQV	0.4001897	0.001655058	down
A0A0E1PVE6	Nucleotidyltransferase superfamily	33	6	15	1	30.2	MSDFIQLEYLQEKLQQLLAESLFAIYLYGSAVDGGLGPESDLDVLVVVTQPLTSALREQLAQELL KISQPVGELQRPLEVTILLKDEIQSGNYPLSYEMQFGEWLREELKEGGTLSSQKDPDISILLRKARF HHAVLFGPALDQWAPEISDQELWQAMSDTYPEIVAHWDEDADERNQILALCRIYFSLVMKDIAS KDNAARWVKSQLPPEQKFVLQRLIQEYRGEIGKQNWQEEHYALQPIVNFLSSKIEEQFEQKRNLI	0.2788376	0.000837326	down
A0A0F6SYM7	beta-lactamase	75	19	427	1	30.9	MNKYFTCYVVASLFLSGCTVQHNLINETPSQIVQGHNQVIHQYFDEKNTSGVLVIQTDKKINLY GNALSRANTEYVPASTFKMLNALIGLENQKTDINEIFKWKGEKRSFTAWEKDMTLGEAMKLSA VPVYQELARRIGLDLMQKEVKRIGFGNAEIGQQVDNFWLVGPLKVTPIQEVEFVSQLAHTQLPFS EKVQANVKNMLLLEESNGYKIFGKTGWAMDIKPQVGWLTGWVEQPDGKIVAVALNMEMRSE MPASIRNELLMKSLKQLNII	0.3504038	0.029209816	down
A0A0G4QU89	NAD(P)H quinone oxidoreductase, PIG3 family protein	51	14	50	1	35.9	MNLPTTMKIVEITVPGGPEVLKLQDSNVPVPQADEVLIEVKAAGINRPDVLQRMGLYPMPKGVT QIPGLEVAGVVVAVGEQVQQFKVGDKVCALTNGGGYAEYCAVTATQVLPIPENLSFTQAAAIPE TFFTVWANLFDIGRLKKDETALIHGGASGIGTTALAICHALGIKTFATVGSEDKVEALSDLTTAIN YKTQDFEQEILNHTQEQGVDVILDIVGGSYFQKNLNLLKRDGRLVIIGFMGGRIAKEFDLQKLILK RATITGSTMRARNSQEKAQIAQSLHEHVWPLLAQGKCLPQIYKTYAFSDVQSAHACMEQGDHIG KIVLEMNA	2.2629758	0.000559363	up

A0A0H4UME6	Outer membrane protein transport protein (OMPP1/FadL/TodX)	57	14	74	11	46.5	MKLKHLSTAMILATLPATGVFAAALDRSGQSMSAFFQPGNYFEAGISVLDPDVSGKDTSGNATGDMANDYYFPSAALKLQLTDKFSFGLLYDQPFGSDSEYSGKNNFVANPNDRLLPSPASPTLGQAGLGNTITGGTSVEVDTQNLALVFGFQPTVNWNIYGGGVYQTIKGNVHLRGSAYSLYNGYDADIKETGGAGWLAGVAYQIPEIALKASLTYRSEIDHDVNIKENIPIVNLVAANPALLFGALGITDPATQAAIGKQLASLQSDGKTTITTPQSVNLDFQTGIMANTVAFANVRWVNWKDFAVQPYKFGIVSKAAGQLLPQLGKPNGFNLVDYSDDQWSVTAGVGRKLNDKWAGNVSVGWDSGAGNPVTTLGPTEGYWNVGLGVQYSPTPQTFIAGGVKYFWLGDADAVTGAHSAAGTFDDNNAIAYGLKLGYKF	6.7126771	0.004824438	up
A0A125S0J9	Dihydropteroate synthase	80	15	70	2	30.3	MSYLFLSCTEIIIEAPMNKSLIIFGIVNITSDSFSDGGRYLAPDAAIAQARKLMAEGADVIDLGPASSNPDAAPVSSDTEIARIAPVLDALKADGIPVSLDSYQPATQAYALSRGVAYLNDIRGFPDAAFYPQLAKSSAKLVVMHSVQDGQADRREAPAGDIMDHIAAFFDARIAALTGAGIKRNRLVLDPGMGFFLGAAPETSLSVLARFDELRLRFDLPVLLSVSRKSFLRALTGRGPGDVGAATLAAELAAAAGGADFIRTHEPRPLRDGLAVLAALKETARIR	2.6269742	0.000331783	up
A0A1B1LW15	histidine kinase	12	1	1	1	15.6	SHGDLSARAYDNRIHSAEMSELLYNFNDMAQKLEVSVKNAQVWNAAIAHELRTPITILQGRLQGIIDGVFKPDEVLFKSLLNQVEGLSHLVEDLRTLSLVENQQLRLNYELFDLKAVVEKVLKAFEDRLDQAKLVPE	0.2990488	0.000392103	down
A0A1E3M652	Isocitrate dehydrogenase [NADP]	69	23	138	2	45.6	MGYQKIVVPADGDKITVKADLSLNVPNHPIIPFIEGDGIGVDITPTMKKVVDAAILKAYGGKRSIEWMEVYCGEKANKIYGTYMPEETFEALREFVVSIKGPLTTPVGGGIRSLNVALRQELDLYVCVRPVRWFQGVPSPVQHPELTDMVIFRENSEDIYAGIEWKADSEEAKKVIKFLQEEMGVTKIRFPEGCGIGIKPVSKEGTQRLVRKAIQFAIDNDKPSVTLVHKGNIMKYTEGAFKEWGYELALDRFGGELIDGGPWVKIKNPKNGKDIIIKDVIADAFLQQILMRPADYSVIATLNLNGDYISDALAAEVGGIGIAPGANIGGAIAVYEATHGTAPKYAGQDKVNPGSIILSAEMMLRDMGWIEAADLIIKGISGAIAAKTVTYDFERLMPGATLLRCSEFGDAIIQHMED	8.6604865	0.039514455	up
A0A1E3MB56	Neutral zinc metallopeptidase	57	10	28	2	33.0	MRWKGRRVSTNVEDRRGGGGVRAGGISIIGLVVAFVAWKFFGVDPQQAYQATQQVTASQQSNATAPESLTAEQKEASDFIRTILADTEDTWTPIFKQLGKTYTPPKLVLFSGMIQSGCGTAQSAMGPFYCPADQKVYIDTEFFKDMREQMGISGEQNQTELSRQDQAGDFAQAYVVAHEVGHHVQTLLGISSQVQQARAQVSQREGNQLSVRQELQADCLAGIWANHNQQRTQFLEQGDVEEAMDAAQKIGDDYLQKRATGQVVPDSFTHGSSEQRMHWFQVGLKTGDISQCDTFNNSI	9.7628866	0.003294874	up
A0A1E3MBC2	Geranylgeranyl diphosphate synthase	61	13	54	1	35.6	MVIDFKQDILAPVATDFAAMDHLINEGISSKVGLVMSVSKHVVEAGGKRMRPIMCLLAARACDLDNMQNAQRLAAIIEMLHTATLVHDDVVDESGLRRGRPTANATWNNQTAVLVGDFLIARAFDLLVDLNNMTLLKDFSTGTCEIAEGEVLQLQSQHQPDTTEETYLKIIHGKTSRLFELATEGAAILAGQEAYREPLRLFAGHFGNAFQIIDDILDYTSDAETLGKNIGDDLMEGKPTLPLISALAHSTGEEHAIIRRSIATGGVDQLPKVIEIVQKSGALDYCQRRAQEETEAALQALSILPDTPYRQALINLTRLALHRIQ	5.7546712	9.66E-07	up
A0A1E3MBE0	DUF3298 domain-containing protein	45	7	24	1	29.6	MQLYDKKIIFILPMLAAMVAVSGCQPKSTAKDEQLASSASVKEQKQAEVPVIQAKVVPVKLPKPKVCLEDGCTEYDFQTVQTNQKWINDYFTNRIKKADPNAFANLADKPVEVPEGEPSSSQSAIYVRYLGQNYNLATFAFQTYSYSAGAAHGMSHQEFVNFDLLNKKHITVEELIKPDVEKQLVDALFDANTNWLQEHNISREKLQLSDNFYYGANGIVFVYPIYELASYAEGMSELTLPYFEAAKYIKPEYLPS	4.0746296	0.017079326	up
A0A1S2FL61	D-amino acid dehydrogenase	73	21	145	1	46.5	MRVIVLGSGVIGVASAYYLARQGAEVTVLDRQSGPAEETSFGNAGQISPGYSTPWAAPGIPFKAVKWMFQHHAPLAINLDGSMWQLQWMAQMLKNCNPQSYAVNKERMMRVAEYSRDCLRELRKDTGIHYENRAKGTLQLFRKEAQMEAVQRDISVLEECGVSYELLNGNELGRVEPALANAQDKLVGGLHLPNDETGDCYLFTNALAQIAKELGVNFQFNQNVEKLIVEGDEIKGVQVNGKVLTADRYVLAFGSYSRDFLKPLDLQLPVYPVKGYSLTIPIVDPAFAPQSTVLDETYKIAITRFDQRIRVGGMAELSGFNLGLNEDRRATLQMVTQDLFPGGDMEQASFWTGLRPMTPDSTPIIGATRFKNLFLNTGHGTLGWTMACGSGKLISDIVLNHKTDISTDGLSIQRYSHAHAA	0.1655451	0.016840737	down
A0A1S2GAH7	Valine--tRNA ligase	53	41	173	1	108.6	MTDAQTAQNIATTYDPTEIEKKWYKTWEEQGYFKPSGHGESFCIMIPPPNVTGSLHMGHGFNNAIMDALTRYNRMMGKNTLWQPGTDHAGIATQMVVERQLGLQGITRHDLGREKFIEKVWEWKEQSGGTITKQIRRLGSSVDWSRERFTMDEGLSNAVKEVFVRLHEDGLIYRGKRLVNWDPKLQTALSDLEVESKEEKGSLWHFKYFFEDKSVKTQDGKDYLVVATTRPETLLGDTAVAVHPEDERYAHLVGKNIVLPITGRLIPIVADDYVEKDFGTGCVKITPAHDFNDYELGKRNSLPIINIFNKNAEVLGEFEYIATAGEQISKTITAPADYAGLERFEARKKLVAQAEAEGWLDQIQPYDLKAPRGDRSGVIIEPLLTDQWYVKIVPLAEPAIEAVQDGRIKFVPEQYSNMYMAWMRDIQDWCISRQLWWGHRIPAWYDANGNIYVGRSEEEVRAKNNIAADVELKQDEDVLDTWFSSALWTFSTLGWPEQTPELKTFHPTDVLVTGFDIIFFWVARMIMMTMHFMKNEDGSSQIPFKTVYVHGLVRDGEGQKMSKSKGNVLDPLDLIDGIDLESLVAKRTTGLMNPKDAAKIEKSTRKEFPEGINAYGTDAVRFTFCALANTGRDIKFDLKRVEGYRNFCNKIWNATRFVLMNVEGQTVGQEARPDLWELPEQWIISRLQKAEAAVHQAFATYRLDLAAQAIYDFIWNEYCDWYVELTKPVLNDAEVSEERKAEVRRVLLAVMEASLRLAHPLMPYLTEEIWQTLAPMLGQGGPTIMTAQYPIPEQAKINEQAEADMQWLQGLIGAVRNIRGEMGLGNARLLPVLLQNISDAEREQITRIEALFKALAKVESIEFLGKDQEPPLSSSSVVGHASVFVPMKGLIDPKAELGRLQKDLDKIQKQHDQIANKLANEGFVSKAPAAVVEGEKAKLAEFAAQLDKVKANMEQIAAL			

A0A1S8V5S4	Long-chain fatty acid transport protein	13	6	27	1	53.2	MKLKHLSTAMILATLPATGVFAAALDRSGQSMSAFLQPNNYFEAGISVLDPDVAGKEAGVSATR RDISDMGNDYYFPNAALKLQLTDKFSFGLLYDQPFGADAEYSGQNVFVSDPSNTILAPAALDAIR TSTIDTTFNNLTADQRVGAALQAQGVNLSTPEGKAQFAATLTAYNSNPATKAAIDAGVKQGVA AKVDAGIKQINGLLGTGNTKVKVDTQNLSFVFGFQPTQNWNIYAGGVYQTVKGNVSLRGQAYS IYNGYDADIKETGGAGWLAGVAYQIPEIALKASLTYRSEIDHDVNIREKIPTLPALSLLGQDAAA AAIANSSADTTITTPQSVNFDFQTGIMANTVAFANVRWVNWKDFSIQPYKFGQLSKVVGPLADP RRPNGFNLVEYSDDQWSVNAGVGRKLNDKWAGNVSVGWDSGAGNPVTTLGPTEGYWNVGL GVQYSPTPQTFIAGGVKYFWLGDAKAQTGAQAGSDQYVADFSDNDAIAYGLKLGYKF	0.3513625	0.001805428	down
A0A1T0DRB8	TetR family transcriptional regulator	21	4	8	1	24.2	MTNRHETDLVNEDTLKKKRGRPKCFDEQQVLEKAMLLFWEHGYEATSISDLTHALEITAPSLYS AFGDKAGLFYKSIDYYLAHEACPIETIFLEAKTAKIAFELYLYDNVKRLVQPNKPAGCMLVVAA MNCSDATQEVQQNLLDKRIKTKEKLLKRLEQGVEQGDLPTNAPLQEMTDFYATVIQGLTIQARD GANTEQLHKVVEHAMKAWTLF	2.9054455	0.000158422	up
A0A241ZE65	5-oxoprolinase subunit A	43	7	22	7	26.9	MFVDLNSDLGESFGSWKMGNDDQILPVVTSANIACGFHAGDPLGILKTVRKAVELGVTIGAHVS YPDLVGFGRRNMDLSRDELIADVLYQISALDGLAKVAGSKVQYVKPHGALYNTIAHDQAQAAA VIDAIKMYNPELVLVALAGSNLVEQARAAGLKVVSEAFADRAYNSDGSLVSRRLEGAVLHDSGF VASRVVSMLKNGGVESIDGVFTPIQADTICLHGDTDGALEMSAAIKAELVKNNIEIRPFVNKA	2.0656034	0.044210776	up
A0A241ZJ54	DcaP-like protein	61	23	121	13	48.1	MDLFLNRKSFVVKSLAITVTALMMSGANAATSDKEEIRKLRQEVEALKALVQEQRQVQQQQQQ VQQQQQVQLAEVKAQPQPVAAPVSPLAGFKSKAGADVNLYGFVRGDANYIIEGADNDFGKVA ESKGEATDKIRATAKTTRLGLDFTAPVNDAKVGGKLEVDFAGSTTDSNGSLRVRHAYVTYNNW LFGQTTSNFLANHAPEMIDFSTNIGGGTTRVPQVRYNYKLGPTTQLFVAAEKGDSTGLTGTKDK DNNWVNDSIKYSLPVLTAKITQGYADGKGSASARALVENYKSKAGGDNQTGWGVAVGTDFKV SDPLKLFADASYVVGNSNYLYGSNKAYTVVDGDIEQNKFVAVQVGGTYKILPNLRSTLAYGAQ FADDGTDYATAYKDGNEKVQQAWINFIYTPVKPIDLGVEYVNGKRDTFDGKSYKDNRVGLMA KYSF	5.6146577	0.029855992	up
A0A2U9QFX2	FnlC	47	11	52	3	42.1	MTVVGTRPEIIRLSRVMAACDEYFDHILVHTGQNYDYELNEIFFTDLGIRKPDHFLNAAGATGAE TIGNVIIAVDKILEEVQPEALLVLGDTNSCMAVLPAKRRKIPTFHMEAGNRCFDMRVPEEINRRIV DHTADINLTYSTIARDYLLAEGLPADLVIKTGSPMFEVLHHYKAKIEASDVLERLNLKEHEYFIVS AHREENINSDQNFLDLVEMLNAVADKYKYPVIVSTHPRTRKRIEELNVEFHPLIQLLKPLGFSDY NKLQLSAKAALSDSGTINEESSILNFPALNLRQAHERPEGMEEAAVMMVGLKAERILQGLAILEG QTRGENRLLRLVEDYSMPNVSEKVVRIIMSYTDYVNRVIWKQF	0.213308	0.009596458	down
A0A380V1V9	Outer membrane efflux protein	75	25	137	1	52.8	MQKVWSISGHSIAVSALALALAACQSMRGPEPVVKTDIPQSYAYNSASGTSIAEQGYKQFFADP RLLEVIDLALANNRDLRTATLNIERAQQQYQITQNNQLPTIGASGSAIRQVSQSRDPNNPYSTYQ VGLGVTAYELDFWGRVRSLKDAALDSYLATQSARDSTQISLISQVAQAWLNYSFATANLRLAEQ TLKAQLDSYNLNKKRFDVGIDSEVPLRQAQISVETARNDVANYKTQIAQAQNLLNLLVGQPVPQ NLLPTQPVKRIAQQNVFTAGLPSDLLNNRPDVKAAEYNLSAAGANIGAAKARLFPTISLTGSAGY ASTDLSDLFKSGGFVWSVGPSLDLPIFDWGTRRANVKISETDQKIALSDYEKSVQSAFREVNDAL ATRANIGERLTAQQRLVEATNRNYTLSNARFRAGIDSYLTVLDAQRSSYAAEQGLLLLQQANLN NQIELYKTLGGGLKANTSDTVVHQPSSAELKKQ	0.3613512	0.007524025	down
A0A385ER43	Int	20	5	9	5	35.8	MLDREILLKKWLDEYLLANKSNETIYTLKNSLNLFFEYTNLALEEIEASDIRTFIAYRAQNGVGVS TLKKNISAIRTFFHYLTKEKLINFNPAEDIKIKKSSKVLPKFHEVTVINEVLDSNKNLEFERPSSTVI FKRDLALIEIAYSCGLRLEEIHSLQIENVEVKRKQVRVTGKGNKTRIIPLGSKAIEAYLEWLPLREE IMNKDTNQKHNYVFVTTTGAQLSRVQINKRIKNAFKLAGYPIQSNPHMLRHSFATHLINNSVGIR EIQEMLGHSNLNTTQIYTDLDHTSMTNVYMDTHPRAVKNTEGEN	2.9185192	0.026565133	up
A0A385EU35	Biotin carboxylase	43	20	61	3	62.0	MNTEKLLIANRGEIAVRIIHACRDMGIASVALYADDDINSMHVELADEAWGLAGATASETYLNI PAIIEVAKKSKATMVHPGYGFLSERAEFAQAVIDAGLKWVGPSPSAIEKLGDKIEARKIAASVGA PLVQGTQDPLNNAEEALEFAKQYGLPIAIKAAFGGGGRGLKVAWKLEEVKELYESAVREAKAA FGRGECFVEQYLDKPRHVEAQVIADQHGNIVVLGTRDCSLQRRNQKLVEEAPAPFISDEIYQQIL SSAKNICQAANYVGAGTVEYLLSRDGKLSFLEVNTRLQVEHPVTEETSKVDLVVEQIRVAQGEV LSIKETPKAQGHAIEFRINAEDPARGFIPAFGVLSLFEAPFGHGVRVDTGVRTGSLVSSHFDSLMA KLIVSGPTREVAIARAKRALKQFKIEGVASVLDFHRAVLNEPGFTDEFNVHTRWIENDFKQELKP TKRGIPNHQQPMLLSYIEIDGKLHRLGLPAGMFAQGPATAVQAQIAEPEVSAEHLLAPINGVISA WKVENGEQVTEGQVVAIMEAMKMEVQVLAHRSGVIQIGAEKGTTCHAETVIASIH	2.2215249	0.02693144	up
A0A3F3MQT9	Adenosine 5'-phosphosulfate reductase	63	12	38	1	28.5	MRPSLLPGTPMTVIPTIDIVDALAAEYAAKSPREILELALSQQGEIAISFSGAEDVVLIDIASRLGKP FRVFSLDTGRLHPETYQFIETVRKHYNINIEICFPDAEAVQSMVNEKGLFSFFKDGHQECCGIRKV QPLRKKLATLDGWITGQRKDQSPGTRTEIPVLQADAGFSGPGKQLIKYNPLANWSSADVWSYIR MMEIPYNPLHERGFVSIGCEPCTRPVLPNQHEREGRWWWEEATQKECGLHAGNLKK	5.0298294	0.025259277	up

A0A3S0N6T4	Cro/C1-type helix-turn-helix domain	26	5	10	5	24.3	MTIGARLKEERERLGYTQPVFAELAGTTKKSQIDYEKDLTQPKAGYLAAIAEVGADIGYIVTGN KSPKLQNSDFAYEFDLVNVYDVSVSAGDGAVCLGETEPASRLAFRKDWLARHGLYAKDLVIVY AKGDSMEPTIHDKEPLLINTIDKELTDGFIYVVRNHENFWVKRVQRQFNELLLLSDNEKYLPMK LDLNESTDVEIIGRWIPPSRGTFY	4.4910334	0.000474458	up
A0A411VGD7	DNA-directed RNA polymerase beta subunit, bacterial-type	71	74	609	2	151.8	MAYSYTEKKRIRKNFGKLPQVMDAPYLLSIQVDSYRTFLQDGKSPKNREDIGLQAAFRSVFPIES YSGNAALEFVEYSLGKPEFDVRECILRGSTYAAPMRVKIRLIIKDRETKSIKDVREQEVYMGEIPL MTENGTFVINGTERVIVSQLHRSPGVFFDHDKGKTHSSGKVLYSARIIPYRGSWLDFEFDAKDLV YVRIDRRRKLLATVVLRALGYNNEQILNLFYEKVPVYLDMGSYQIDLVPERLRGEMAQFDITDN EGKVIVEQGKRINARHVRQMEAAGLTKLSVPDEYLYERITAEDITLRDGEVIAANTLLSHEVMV KLAEGGVKQFNILFTNDIDRGSFVADTLRADLTRDREEALVEIYKVMRPGEPPTKEAAENLFNNL FFSSERYDLSPVGRMKFNRRLGRPYEVGTDQKSREVEGILSHEDIIDVLRTLVEIRNGKGEVDDID HLGNRRVRSVGEMTENQFRVGLVRVERAVKERLSQAETDNLSPQDLINAKPVAAAIKEFFGSSQ LSQFMDQNNPLSEITHKRRVSAFGPGGLTRERAGFEVRDVHQTHYGRVCPIETPEGPNIGLINSLS VYAKANDFGFLETPYRKVVDGRVTDDVEYLSAIEEVGTVIAQADSAVDKDGNLTEEFVSVRHQ GEFVRMPPEKVTHMDVSAQQVVSVAASLIPFLEHDDANRALMGSNMQRQAVPTLRADKPLVG TGMEANVARDSGVCVIANRGGVIEYVDASRIVIRVNEDEMVAGEAGVDIYNLIKYTRSNQNTCI NQNVIVNLGDKVARGDILADGPSTDMGELALGQNMRVAFMTWNGYNYEDSILLSERVLQEDRL TSIHIQELSCVARDTKLGAEEITADIPNVGEAALSKLDESGIVYIGAEVTAGDILVGKVTPKGETQ LTPEEKLLRAIFGEKAADVKDSSLRVPSGTKGTVIDVQVFTRDGLEKDDRALAIEKAQLDSYRKD LKEEYKIFEEAARERVIRLLKGQESNGGGSTKRGDKLSEDLLSGLELVDLLEIQPADEAIAERLTQI QVFLKEKSAEIDEKFAEKKRKLATGDELTTGVLKVVKVYLAVKRRIQPGDKMAGRHGNKGVVS NILPVEDMPHDANGVPVDIVLNPLGVPSRMNVGQILETHLGMAAKGLGDKIEKMLKEQRTVLE LREFLDKIYNKVGGEQEDLDSLTDEEILALAGNLRAGVPLATPVFDGAEESQIKDLLELADISRTG QTVLFDGRTGEQFDRPVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRF GEMEVWALEAYGAAYTLQEMLTVKSDDVEGRTRIYKNIVDGNHYMDPGMPESFNVLTKEIRSL GINIELKNGD	2.8761778	0.007471461	up
A0A481WVU6	Pgt1	4	2	2	2	71.5	MAKLDTLQNKVVWVTGASSGLGKALAGEFALQGAQVILTSRRFEELEEVRVGLLHPDQHLSVV ADITNQEQVQEAYEQILKAKGRIDWLINNAGLSQRALIQDTTMATERAIMEVDYFSQVALTKTV LPTMLKQKSGRVVFVSSVAGLLGTQYRASYSAAKAAIHMWANSLRAEVADQGVEVSVIFPGFV KTNVSFNALNGAGQTQGHQDEAIENGLEADVFAEQSVKALMQGQEYIVVGGTKEKLGVMVSR MSPKLLYKMIRKTKVK	2.8761778	0.007471461	up
A0A4Q4H7V6	2-methyl-aconitate isomerase PrpF	20	9	21	1	42.0	MVFLRQQLLFIFIAFLSTCVGIYVAWDMNLTWHKFYTYLISEKAIFSILFNYAVIQLFFIILGRKYT ALCLSQLFVIFLNFINKKKQQYLFSNLSPEDIFLLPEAMKATPWHLQLIFFILIIFFLIILLIAVRKESK ATFHTYVPNIIIFGLISSGLIYLNFIRNPTGACFSENKPMICASLQEFPNTRNDWIGDYRKIQDYGFV TFYVSKVLDNVTSVLLPSRKVSEQDIQQILQQHHFVQPLEKNEKEYPNIIIVMEESFWDSHHLESG LPKDLLSFVHQNQVSNLLSPSFGGGTANVEFEVLTSLNTTFFPNELLYVSKLKKPIYALPYYLKSI GYQTVAMHNNYSYYYNRNKVYPELGFEKFISLENMIAQKDRSNIFNQGGWATDDLIFDSIKSTL KENEQQPKFIYAITVENHPMYNDDRFGKQNYKFNKELSDTEKQKLSTYTAGTVRANQKLKELA EYLKTVDRPTILVAFGDHLPNLQEVYESYGFFKDDPERTSLKNYQTPFVVWSNYKLDKKPLKQP YIAASFVAPKLLKLAGLPLSDYYQFVDDVSSCYSAIHQKFINENPTCNFDKKVLLKGYENLNKDV LDGHNHTYKIMQNNKEEMEQ	2.6178254	0.000403858	up
A0A505ZPT1	Glucose-6-phosphate isomerase	35	13	26	9	62.6	MSKSIEKFPKELVSPIAQLHSLVEKNSKLHIKELFAAEQDRFQNYSVKFDQLVFDYSKHRITKSVL EQLFALAKTKQLTHWIERLFSQDKVNCTEQRAAMHWALRLPSEYSKFPELTKQVHTQLQRMYA LVEKIHAGQYRGATGEVIQDVVNIGVGGSDLGPQMVTHALCDFKVKTAKPLNVHFVSTMDGSQ LSDLLHQLRPETTLFIISSKSFGTIDTLSNAQTVRQWLEKALGKHERVVKSHFIGVSTKADKMTE WGIAPENQLLLWEWVGGRYSLWSCIGLPIALSVGIDGFQQLLAGAHAVDEHFQNTSFEQNIPVL MALLGVWNNNFLNIQTHAVLPYDGRLKYFAAYLQQLEMESNGKSVQRDGQKVELDTCPIVWG EVGPNAQHAFYQLLHQGTQAVTCDFIAPIKRYNADHFTYVENAEALVEQHHLALSNCLAQSRLL AFGNEALDSAELKNLPIYKQYEGNQPSSTLLLKELNPYSLGMLIALYEHKVFVQSVIWNINPFDQ WGVEKGKQIADQLLPILNGAQNDLSTLDASTRGLIKILLGKVDG	2.9586195	0.002161753	up

A0A5K1MHI6	Uncharacterised protein family, zinc metallopeptidase putative	57	9	27	1	33.0	MRWRDRRVSTNVEDRRGGGGVRAGGISIIGLVVAFVAWKFFGVDPQQAYQATQQVTASQQSN ATAPESLTAEQKEASDFVGTVLADTEDTWTPIFKQLGKTYTPPKLVLFSGMIQSGCGTAQSAMG PFYCPADQKVYIDTEFFKDMREQMGISGEQNQTELSRQDQAGDFAQAYVVAHEVGHHVQTLLG ISSQVQQARAQVSQREGNQLSVRQELQADCLAGIWANHNQQRTQFLEQGDVEEAMDAAQKIGD DYLQKRATGQVVLDSFTHGSSEQRMHWFQVGLKTGDISQCDTFNNSI	0.1788883	0.000985786	down
A0A5K1MJI7	Outer membrane protein Omp38	46	17	358	2	38.5	MKLSRIALATMLVAAPLAAANAGVTVTPLLLGYTFQDSQHNNGGKDGNLTNAPELQDDLFVGA ALGIELTPWLGFEAEYNQVKGDVDGASAGAEYKQKQINGNFYVTSDLITKNYDSKIKPYVLLGA GHYKYDFDGVNRGTRGNSEEGTLGNAGVGAFWRLNDALSLRTEARATYNADEEFWNYTALAG LNVVLGGHLKPAAPVVEVAPVEPTPVAPQPQELTEDLNMELRVFFDTNKSNIKDQYKPEIAKVA EKLSEYPNATARIEGHTDNTGPRKLNERLSLARANSVKSALVNEYNVDASRLSTQGFAWDQPIA DNKTKEGRAMNRRVFATITGSRTVVVQPGQEAATPAAAQ	5.8857718	4.39E-07	up
A0A5K1MJT9	Flavoprotein-like superfamily	53	5	9	1	20.1	MSNSNIAVVYFSGYGHTKVVAETFANEINAQLIQIDQEGNITDQDWETLNNAKGIVFGAPTYMG TAPWQFKKFADATSKVWFTRGWQDKVFAGFTNSASLNGDKQVTLIQLQTLASQHGGIWVSLGL LPANTKDATREDVNNLGGSVGLLVQSPSDASVDEVPTGDLETAKVYAKRVQAIVNKIYG	4.1133094	0.006925691	up
A0A5P1UJC1	EvpB family type VI secretion protein	33	13	23	13	55.3	MNNTQSAAMPLVENEEVNLLDSIVEQSRIARNEEEHSRAKSLIGELAKEVMAGTITVSENMTLSI DKRIAEIDALISKQLSQIMHNEQFQKIESTWRGLYYFCQETPSNPLIKIRMLNTTKKELVKDFQGA TDFDQSTLFKKIYEEEYGSFGGAPYSALIGDFEFDRTPSDMYLLEQISHVSAAAHAPFISAASPSIL GLESFTDIDRPRDVSKIFETAEYVQWRSFRDSEDSRYVALTLPHVLGRLPYHPKEGTATEGFNFIE DVSGENHNEYLWMNAAYAFGTRLTNAFDMHGWCAAIRGVEGGGLVEGLPVHTFKTQDGEVV FKCPTEIAITDRREKELSDLGFIPLVHCKNTDYAAFFGAQSTQKPKKYDNDTANANSALSSQIQYI MAVSRIAHYLKAMMRDKVGSFASAGNVEAFLNEWLSQYVLLDDGASQEAKAQYPLREASVKV VEDPAQPGHYKSVVFLRPHFQLDELSVSLRLVTELPQSSN	2.4499686	0.023928486	up
A0A5P3MF62	Glycosyltransferase subfamily 4-like, N-terminal domain	8	2	2	1	43.6	MSSKICIIGTTADSITGFRSDLIKQLIVYGYEVFAFTCEYNDKQLVEISALGAKPVTYKMSRGGLN PFSDIKALFNLKSEIEKIKPDLVLSYFTKPVVYGSLASKFSKVPKIIGMIEGLGTPFTEHSNGQSLKV KFIKFFQITLYRLVFPFIDKIIFLNKDDPQDLIYKNKIKHKNNSVNILGPIGLNLNDYPYMKWQESS TISFIFVARLIAEKGIFEFVEAAKIVKQKYKDVRFIVIGGLDTENPFGLSRTQLDDLIASGLIEYPGF VTDVAKRIQDSAVFVLPSYYREGVPRSTQEAMAIGRPVITTDVPGCRETVENGVNGFLVPKWDP EALAEKMCYFIENPEQVNIMGLKSYEIAQEKFDAEKVNAKLIDIMGLKDLNEKTS	3.7225275	0.02816838	up
A0A5P6FNN8	Bifunctional protein PutA	64	57	370	1	138.7	MAEIDMNTMDTFHQMDKSHQGYITEFNDKSEFEQRINTAWRRAEPEAVEELLQAAAVSDDLDH KIYDLAFNLAHNLRERKTSSGKAGIVQGLLQEFSLSSQEGVALMCLAEALLRIPDTATRDLLIRDK INQGNWKEHVGQSSLMFVNAAAWGLMLTGKLMETPKQTSLSSVLTGLLARSGRGIIRKAVDVA MRMMGEQFVTGETIEEAVDHAKVLEDKGFRYSYDMLGEAALTDHDAERYFNDYTQAIHAIGK ASNGKGVYDGPGISIKLSALHPRYQRAQIERVHKELYGKVFELARLAKQYNIGLNIDAEESERLEI SLELLERLCFEPELANWKGIGFVIQAYQKRCFFVVDYIIDLAKRSQKRLMIRLVKGAYWDSEIKK AQIEGMDDYPVFTRKVHTDLSYIACAKKLLAAPEFIYPQFATHNAQTLATIYHLADPSKYYAGQ YEFQCLHGMGEPLYEQVVGPREQNKLGVPCRIYAPVGNHETLLAYLVRRLLENGANTSFVNRIA DKTLKVEDLIQSPIYDIRNAAKLEGSVGLKHPSIPLPLDMYGTLRKNSKGYDLANDTPLAALDST AQELRNRIWQSHPLLANADSLEQGHSVAITNPAQNDEIVGYVQEADLKHVEIALTAAEQTQSEW SNTPKDQRAQYLKHAADLMESRIQELMVLLCRESGKTYANAIAEVREAVDFLRYYATQVENLP ANTVIQPLGTVLCISPWNFPLAIFSGQIAAALVSGNCVIAKPAEQTPLIAAQAVQILWEAGIPHGA VQLLPGRGETVGAQLSQDSRINGIMFTGSTEVAKILQKTVAKRLSENGQSIPLIAETGGQNAMIV DSSALTEQVVLDVVSSAFDSAGQRCSALRILCVQEDSAATVIKMLKGAMQQLIVGNPAILKTDIG PVIDDEAKQTIDQHIQKMKSKGYPVHQLMFGATSQTELDKGTFVVPTAIELPNLDDLQREVFGP VLHIITYKYGELEQLISRINAKGYGLTMGLHTRIDETIQTVIQHAEVGNLYINRNIVGAVVGVQPF GGEGLSGTGPKAGGPLYMYRLMQHCSNKVLATPFAVKNEQTIFEGFNREVYQSLQNWAKQHLP QANREIEPFGVGKFYELQGPTGESNQYIILPRHRVLSIADTEQDQLHQLLAIFAVGSQAAVMPNSP LLAKHKQTLPKDVLDAITTIKNITTDDFDAVLHHGNREEIFSLQQEIASRSGAIVGITHVEPNESIP LERLVIERAISVNTAAAGGNASLMTMSE
A0A654L2G6	Uncharacterized protein	16	1	4	1	14.8	MGWEIPIFHFRVNGEPRVLAYLKPHASEAYTEELSYVYDLVNDELNEYFNDDEFTYNSNELRLF YLQRPAEAFILWHPDQVHNQEQIQFVYGVGIPNANRLTTIDIPEIPESFPHIFWDKTEDQ	3.9262415	0.000390981	up
A0A654L2Q2	Uncharacterized protein	12	2	2	2	33.4	MAGQIVLKSQNAIDNLADLPDINYYINRVKADGGVIYNMNALLDVFAFIYSKNITDSEVFSAINP AWGVKYDPATGNISKLYSLFDPAGDLNAFGGSLPIKLQNDLGVPSAYLGGSQNTYLKAAGTVSG VETIGYATAAVIPQLSNYGAGAGTNFPLGLLWSREAHDAADPVGSVTPYVAASWYVGRPDTSNI TLSQWTEYFSVFSSTGSAGSNALTGYENAKPLSAFADTGGLRVYKNGLQVLFDSTVTQTPIHKD KLELLIGATVTGTGAPATTYFLGHFIENWVLVNTASEKMIEISKRINDKYYAVIPH	2.3409555	2.46E-05	up

A0A654L3J1	Carbohydrate porin	51	15	80	1	46.0	MVSCLSVLSITLFVQHAQAAAAFDPNGSWMLGDWNGQRTALQAQGYDFSFGYTGEYAGILDSKEQTSTHGSAYTGQLALGSHLDLGKILGWQDTEAQITLTYRDGQSLSEHSPALAGHQSSVQEVWGREQTWRLTDLWIKKKFLDQKLDVKVGRFGEGEDFNSFDCDFQNLALCGSQVGNWVGDQWYNWPVSQWAMRVKYNLQPDLYTQVGVYEYNPENLERGKGFNLSTDGSHGAIIPAEVVWSPKLGVQSMPGEYRLGYYYSTADAKEIADSTKTSHKQGVWVTAKQKLFQPADQTDRGLTGFVNLTFHDSDTNKVDNMQNIGLVYKGLLNQRPQDELALGVARIHINDDWNDVQAKEYDTEYNTELYYGIHATNWLTIRPNVQYVRHVGALKNGDNTWVGGIKFSTAF
A0A654L9F1	Lipoprotein	49	8	11	8	20.5	MKNLITIAGFLLLAGCSTQKQPQSEPPYVKQNYSESDPAAKLSVSQFAGVVKSIYPAYQISHSNDGSEVKFLPNDVKADTKFMPNNNWYSIKIIKEPNTENWKGLIVEVFNKGSFGESKAVAAKDCQKIFGNIDNRVPAVLYDLENRLNQSPNASISNRQYGYTFHLDASHYNQGYPVTCMVSN
A0A6B9KPL0	Gtr89	60	14	37	14	30.8	MISLITATYNREKLLKKLYESLCVQTVKKFEWIVIDDGSIDKTDELINSFKLDNIIDITYLKKTNGGKHTAMNIGVEIAKYAYVFFIDSDDFLPNDSIEKIINYIDKVSAREDYSEISGVCGLIADFQGNLIGTKYSENLCCSYIDYRYKYHIKGDKAEIFKREVLLEYKFPVIEKEKFCPEALVWNRISDKYKMYFFNEVIYYREYLEGGLSDRSVEIRKKAPISTLLYYKELYLNKNLNWYYRIRAYINYMRFKFIS
A0A6B9KQE9	Gtr93	19	7	9	7	41.4	MRILYVITGLGGGGAEKVVCDLADEMCSRGHIVKIAYLKGEIVVFPKNKEIELVYLGLESILNALSFFRNYRDLIISFTPDVVHSHMVHANIFTRISRKFYSIPKLICTAHSSNEGSKFRMLAYNFTHNLADLTTNVSLEASRNFEIRKGVPKGGIRTIYNGIDLSKFIKSPLNKDKIKNNLGIENGIPIFIAVGRFHEAKDYPNLINAFRIFKTKIIHNSQDNNLPILLIVGDGELKSEVELLIESFNLKDNIKLLGRRNDIPDLLNIADYFILSSKYEGLPTVIMEAMACETFVISTNCSGVEEIMNDTGIMVPICDSEALAEGLIKAYNLSPKEIELNNLSARRRIEKIFSLEKSIETWLEIYES
A0A6F8TC76	Oxidoreductase	60	7	21	2	17.5	MLNTALPVLYKDGTIADNTYQIIAEDGVIPRGDVVLTTAQLDQLANIQGKKALYVTVNDSPEDHTFPLSELDAIFIEFAGFGDGRGYSFAALLRRQGFQGELRATGDVFKDVLNYLKRSGFDSFVIKEGKDVQEAAAGLQDFTHPYQASTAVPKASYQTGA
A0A6H3SGL6	RNA-binding protein Hfq	39	6	64	1	19.0	MSKGQTLQDPFLNSLRKERIPVSIFLVNGIKLQGHIESFDQYVVLLKNTVSQMVYKHAISTVVPARNPRPAGAQGAGFPAQGGSQGGFGGQGAGFGNTTFNLQTIYDVFSHDLASSTTNLEGILNIADEYVLETEEGLLPLISSHSINLKNHVLSLEFSPKALTSLLSGRSLVNPKAA
A0A6H3SV37	Glutathione peroxidase	83	12	98	1	20.2	MTQSVYHIPVKAISGETVDLDQYKGKVLLIVNTASKCGLTPQYEGLEKLYQAKKDQGLEILGFPANNFKEQEPGSDEEIQQFCSLNYDVHFPLFSKISVAGEDKHPLYQVLTTAQPERIGEGPFRERLEGLGIPTNPAPEVLWNFEKFLINKNGEVVARFAPNLTADDEQIVKAVEAELAK
A0A6H3T3L2	Tetrahydrofolate dehydrogenase/cyclohydrolase	73	14	69	2	29.7	MALVLDGRALAKQIEENLLVRVEALKAKTGRTPILATILVGDDGASATYVRMKGNACRRVGMDSLKIELLQETTTEQLLAEIEKLNANPDVHGILLQHPVPAQIDERACFDAISLAKDVDGVTCLGFGRMAMGEAAYGSATPAGIMTILKENNIEIAGKHAVVVGRSAILGKPMAMMLLQANATVTICHSRTQNLPELVKQADIIVGAVGKAELIQKDWIKQGAVVVDAGFHPRDGGGVGDIQLQGIEEIASAYTPVPGGVGPMTITTLIRQTVEAAEKALG
A0A6H3UE57	Winged helix DNA-binding domain superfamily	16	4	8	4	36.1	MKKDLVVKDNALINASYNLDLAEQRLILLAILEARESNTPSDRDLTIHAESYINHFNVHRNTAYKVLKDACKNLFERRFSYQKLTAKGNLENVMSRWVQRVSYVENEALVRIRFSDDVAPLITNLEKHFTSYELEQVSSLTSAYAIRLYELLIAWRSTGKVSMLETKELRSRLGVSDTEHQRMESFKRRVLEPAIQQINDHTDIKAEYEQHKRGRSIVGFSFSFKQKSKPKTINHERDPSTVDMFCNLSDSQINTYSSILSKVHSISDLAGNKDYQAFAIWIANILRDPTSVREETAKRIFKALRTETDFKG
A0A6I4HT95	Uncharacterized protein	46	5	9	5	16.5	MKNIYILIFIGALIACSDKGTDKNQHNSNHKLDVVQTETNKSQSVVGENQENTDKMVKTKEADQVAQFSCSNPNITQWYGFNENIAEPKCEVVKNFQLTAYKCDISKNAFGASKDAILLENQDKRIFVYSTSKDCNEMLEVRNANAP	0.3126067	0.026249203	down
A0A7S8F867	phosphomannomutase	46	19	57	2	51.0	MTTLTCFKAYDIRGKLGTELNEEIAYKIGRAYGQIYKPKTVVVGCDIRLSSEALKQATIRGLNDAGVNVLDLGMTGTEEVYFAAFHLDVQGGIEVTASHNPMDYNGMKLVRENARPISADTGLKEIQAIAETNNFEEVSQKGTTQSYNILPEFVDHLLTYIEPTKIRPLKLVVNAGNGAAGHVIDAIEEKFKALNVPVEFIKIHHEADGTFPNGIPNPILIENRDSTRNAVLEHKADMGIAWDGDFDRCFLFDEKGQFIEGYYIVGLLAQAFLIKQSGEKIVHDPRLVWNTFDIVDEYKGVAVQSKSGHAFIKDVMREHNAVYGGEMSAHHYFRDFAYCDSGMIPWLLTVALLSETGQSLSTLVENMITKFPCSGEINFKVADTQITIQKIFDFYAAQNPEIDRTDGVSLDFGAWRFNVRASNTEPLLRLNIESRADRQAQPMQYYVDELTSLIQS	7.6025923	0.000544816	up
A0A7S8ZW19	Replication initiation protein	15	3	5	3	36.3	MKKELVVKDNALINASYNLDLSEQRLILLAILEARQSNTPNDKDLTIHAESYINHFNVHRNTAYKVLKDACKSLFDRRFSYQKLTQKGNIENVISRWVQRISYVENEALVRIKFSDDVVPLITNLEKHFTSYELEQVSSLTSVYAIRLYELLIAWRSTGKVTMVELEELRLKLGIEPNEYKRMGQFKEKVLHLAIDQINKYTDIKAEYEQHKRGRSIIGFSFKFKQKQQPKKLDSKRDPNTPDFFIRMTDAQRHLFGNKLAHDARVQSEYSHLIGTGSYEDFAKLLADMLAEEQHFKMFYPLLVEHGYKA	2.866637	0.001459985	up

A0A7U3Y2S3	Uncharacterized protein	60	6	21	1	17.4	MLNTALPVLYKDGTIADNTYQIIAEDGVIPQGDVVLTTAQLDQLANTQGKKALYVTVNDSPEDHTFPLSELDAIFIEFAGFGDGRGYSFAALLRRQGFQGELRATGDVFKDVLNYLKRSGFDSFVIKEGKDVQEAAAGLQDFTHPYQASTAVPKASYQTGA	0.2595185	0.012055299	down
A0A7U4BQ44	Uncharacterized protein	71	4	23	3	8.7	MNSKFSVDQSNKISLKAVLEDLGDQMFEANKCPDTHPVYDQLRERLRKDRQLLDALDAQDENANTEERSRSLDIN	2.1256345	1.52E-05	up
A0A7X5C6N3	Uncharacterized protein	57	3	9	1	7.4	MDNSKLPINQIIARINDAAKHGEALVLTAEEVKILSKDIGDKVFIPVLTNEQVVQLVKEGKLGQKIK	2.5141939	0.022932107	up
A0A7Z1WNT5	Metallo-beta-lactamase superfamily lactonases	49	12	52	1	35.4	MKKLFVALGLIMGSLHISYAEPASAQQVPGYYHHQFGNYRITSLLDGTIYLDPKLFKNLSPAEKTKILTKYAAVNEKGIQTSVNAFLVDDGKSLTLVDSGAASCFGPQLGSIAKNLELAGYQLANVKTVLLTHLHPDHVCGIAQNGKAVFPNATIYAHEREADYWLNPANEKTVPEDKKENYLGTVKNVKAALAPYQAKKAFKTFKDGDVIQGFEVINTQGHTPGHHSFRLKSKGQQIVFVGDIVHSHSLQFDAPKTGVDFDVNSEQAINTRLKMFAEISNKQQWVAAPHLPFPGIGHVYKVSAEQYQWIPLYFNNSLDK	2.6041452	0.042582489	up
A0A829K710	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	81	29	148	1	53.7	MAEAQKLKLIDGWEVVIGIEIHTQLATNSKIFSGSSTEFGQDPNTQASLVDLAMPGVLPVLNEKVVELAIRFGLGIDAYIDQASVFARKNYFYPDSPKGYQISQMDNPIVGLGHIDIQLEDGTTKRIGVTRAHLEEDAGKSVHDQFEGMSGIDLNRAGTPLLEIVSEPDMRSVEEAVAYIKAIHTLVRWLGISDGNMAEGSFRADCNVSLRRPGQPFGTRCELKNLNSFRFIEQAINVEIERQMEILEWGGEIDQETRLFDPNKMETRSMRSKEEANDYRYFPDPDLLPVIIPDEQIEAIKATMPELPAARRARFIADFGVTEYDAHVLTLSREMADFYEAVVAAAGGAKQGKIAANWVMGEFSGALNKAGLELTDSPVSAEQLGGMIARIIDNTISGKIAKQVFGFMWESEGKSADDIIAEKGLKQETDTGAIEAIIKEVLAANEKMVEEYKSGKEKAFNGLVGQVMKASKGKANPAQVNELMKKLIG	0.4560349	0.000884237	down
A0A829RFQ7	Alanine racemase	30	9	33	2	40.5	MPRPITAVIHRQALQNNLAVVRKAMPNSKVFAVVKANAYGHGIERVYEAFKAADGFALLDLDEAKRIRALGWTGPILLLEGIFSPQDLFDCVQYQLSFTIHSEAQIEWVEQHPYPAQFDVFLKMNSGMNRLGFKPQHYVQAWERLNNLANVAKITHMMHFSDADGDRFGQQGIDYQITAFEEVVKDLPGERSVSNSAAILRYQDQLKSDYVRSGIMLYGSSPDYPTHSIADWGLQPTMSLRSEIISVQHLEPNESVGYGSNFVAEQPMTIGIVACGYADGYQRISPTGTPVLVDSVRTRTVGRVSMDMLAVDLTGIESAKVGSEVVLWGQSSTGVVLPIDDVAVSSGTVGYELMCAVTARVQFINQV	5.6266962	0.020238648	up
A0A837Q8N8	Type VI secretion system, RhsGE-associated Vgr family subset	2	2	4	1	122.6	MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALKQFIGCQVAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKSVRDISEILFKEWQEKSPLFASSITLDTSGLTKDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVDESQLFIADPNASIQPQVLRLIDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQRWQADALQQEEGSGSVQGTQKHSEHYDNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQIEQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNDHPELDQHDSADKEFLILSKHYYNQNNLPKELQQQLERLLPQGKLKAAQLDSQNPEQRHFAELNVVRRNIKAVPEYNPLEHRPAAHPQRARVVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLTPWAGAGYGARFLPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGFNQLRFDDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAIRAGSGLLVSTHKQDQAQGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLDMLENIQTFLEVLKQEDPKKAAEFQSAVMLLASPKSIAVSSNEDIHLSANGQLTQSAGDSINISTQKNIVSHASQKISLFAAQEGARLFAGQGKVEIQAQGDGLDVIARKGVQITSIEDTVYITSPTEINLTANGSQVKLNGSGIFPVTGGKLEVKAGQHLFMGGGKVDVKVPKLKELNITKKYSNKLDVYEIFPTNKFTDLTMSVKGSDGVVEEHKIDKYGRSPRISDAEPKELEVLVGGDVWNYFIKNIGGTKDDPFYFKFLDYVGKPIVGMECYLLDNSLNIVKKEVTDGNGEVEFVYTDEYLPIMGVMKFDDNTVKPICYVNHHNCREYIFISPKVKANLALLEEGQKGEYLRAGYRVKEGESLQNIADKYSITTDEIISLNTGMENIDVNTKLVEGAYIKLPNYINREEWKNG	0.4041687	0.009226782	down
A0A8I0F482	D-amino acid dehydrogenase	72	21	150	1	47.2	MREGMEMRVIVLGSGVIGVASAYYLARQGAEVTVLDRQSGPAEETSFGNAGQISPGYSTPWAAPGIPFKAVKWMFQHHAPLAINLDGSMWQLQWMAQMLKNCNPQSYAVNKERMMRVAEYSRDCLRELRKDTGIHYENRAKGTLQLFRKEAQMEAVQRDISVLEECGVSYELLNANELGRVEPALANAQDKLVGGLHLPNDETGDCYLFTNALAQIAKELGVNFQFNQNVEKLIVEGDQIKGVQVNGKVLTADRYVLAFGSYSRDFLKPLDLQLPVYPVKGYSLTIPIVDPAFAPQSTVLDETYKIAITRFDQRIRVGGMAELSGFNLGLNEDRRATLQMVTQDLFPGGDMEQASFWTGLRPMTPDSTPIIGATRFKNLFLNTGHGTLGWTMACGSGKLISDIVLNHKTDISTDGLSIQRYSHAHAA	0.2780168	0.017199038	down
A0A9P2P5S8	MmcQ/YjbR family DNA-binding protein	29	3	3	1	14.4	MNGVQLHQLAIEAARNLPFSEQTHPFGPEYEVFKILEKMFMLTVEVSGVKMINVKCDPYKSQEYQELYPFIIPGYHMNKKHWISIKPHKNLTSDFLRDLIRDSYDLVVKKLPLKDQKRLNNQ	3.7316764	0.00041903	up

A0A9P2QG90	Aspartate/other aminotransferase	68	17	115	1	44.9	MFQHIPPYAGDPILSLMEQFNADTRSEKVNLSIGLYYNEDSIVPQLETIIEAQKRIEPKNGKTKLYL PMEGFKPYREAIQALLFGANSPAVKAGRAVTIQTLGGSGALKVGADFLKTYFPSSDVWVSQPTW DNHVAIFNGAGIKTHFYPYFDAETRGVDFDGMLSTLKTLPEQSIVLLHPCCHNPTGADLNPAQW DQVIAVLKDRNLIPFLDIAYQGFGDGMEEDAYAIRALDQAGLNFIVSNSFSKIFSLYGERVGGLTF VCDDAEAAQCTFGQLKATVRRIYSSPPTTGAWLVDEVLNDAELNQQWQGEVKEMRERIIKMRS ILKDELTKALPDRDFSYLVNQKGMFSYTGLTAEQVDILREEYAIYLVRSGRICVAGLNMNNVYT VAKAMAEVLAKSVEAA	3.7415104	0.00511352	up
A0A9P2UCI4	Uncharacterized protein	32	4	7	3	17.9	MPQYLFLAETIYKKMKNEKLFSKDVLENMYILMKVIRKEIKGTEYKLKYNFIDFNEVLSKSKND CKVKIDVSLIPSYNLREEYILWLAGFIQKITEGGPKPPPPIKEYIPEFINLESELDFLTLNLEKNQNN GEEIVNYFNSKHYKATFKK	2.1691094	0.000570068	up
A0A9P2UE60	Acetate-CoA ligase	41	17	31	1	72.2	MNEIYPVPEEFKKTARTVEADYFKRYQHSIENPDEFWAEQAKIVDWIKPFTQVKNTSFDKDNFKI EWFADGELNVSANCLDRHLKEHPHKPAIIWEGDHPSRHKIVSYKELHDEVCRFANVLKKYGIGK GDRVVLYMPMVTEAAIAMLACARIGAVHCVVFGGFSPDSLASRIEDSQAKLVITADSSLRAGKL LPLKENVDLALALPGTECVENVIVVYRNANPIEMKPGRDLWYHLIIMEVDANCPPEPMKAEDPL FILYTSGSTGKPKGVLHTTGGYLVYVASTFKEVFDLKQDDVYWCTADVGWITGHSYLIYGPLA NGTTTLMFEGVPQYPTWARLGHVVDKHKVSILYTAPTAIRAMMREGDSYVRESNRSSLRLLGS VGEPINPEAWNWYYNVVGEGRCPIVDTWWQTETGGILIAPLPGATALKPGSATRPLFGIQPAIVD GEGNELEGAAEGNLVIKDSWPGQMRTIWGDPDRFIEAYFSTFKNTYFTGDGARRDEDGYYWIT GRVDDVLNVSGHRLGTAEIESALVSHEAVAEAAVVGMPHDIKGQGICTFVTLQAGVPESEELRK ELISWVRKVLGPVASPDALHWAPALPKTRSGKIMRRILRKIAANELDSLGDTSTLAEPAVVDQLI TTVYPDRQK	4.5325444	0.019459766	up
A0A9P2UFA0	RutC-like superfamily	86	7	50	2	13.1	MSNSDIQKINTNEVMSAVTVFNKVVYLSGQVPKNTEQDVAGQTREILATIEELLALANTDKSRL LSAQLYLKNLSDFSTVNAIWVDWLKGCVAPSRATIQADLVNPDWLIEIAVTAAQK	0.4951441	0.004996274	down
A0A9P2XJK2	DNA gyrase subunit B	61	40	149	3	92.1	MSSESQSASQTEQTNEKAYDSSSIKVLRGLDAVRKRPGMYIGDTDDGTGLHHMVFEVVDNAIDE ALAGHCDEIIVTIHEDESVSVSDNGRGIPTDIHPEEGVSAAEVILTILHAGGKFDDNSYKVSGGLH GVGVSVVNALSSKLHLTIYRAGQIHEQEYHHGDPQYPLRVIGETDNTGTTVRFWPSAETFSQTIF NVEILARRLRELSFLNAGVRIVLRDERINLEHVYDYEGGLSEFVKYINEGKNHLNEIFHFTADADN GIAVEVALQWNDSYQENVRCFTNNIPQKDGGTHLAGFRAALTRGLNQYLENENILKKEKVNVT GDDAREGLTAIISVKVPDPKFSSQTKEKLVSSEVKPAVEQAMNKEFSAYLLENPQAAKSIAGKIID AARARDAARKAREMTRRKSALDIAGLPGKLADCQEKDPALSELYLVEGDSAGGSAKQGRNRK MQAILPLKGKILNVERARFDKMISSQDVGTLITALGCGIGREEYNPDKLRYHKIIIMTDADVDGS HIRTLLLTFFFRQMPELVERGHIYIAQPPLYKLKKGKQEQYIKDNDALETYLISNAIDELALHISAD APAITGEALAKVIQDYQVSQKSLQRLTLRYPASLLDALLEVDAFKADQNHDQAYVQQWADQVR EAVQRLQPSLRPEITLETFERENAQGEKSAHYWPRVTVYVHNLPHAYLLDAGLLNSAEYARLLK NSKSWFKLIEDGAYLQKGDRRIQVANFHQVWQHILQDSRRGMMIQRYKGLGEMNAEQLWETT MDPENRNMLQVTIDDAIEADRMFSCLMGDDVEPRRAFIEENALNADIDA	2.0927906	0.014651926	up
A0A9Q1N8I6	Uncharacterized protein	66	5	10	5	12.7	MNFQTILSSFKNQSTGTDAFKNLKSACEHHLKHSSDLNEKAVIYLIYGFARSYVILYEGEAVTTEF AQASKEMLVNYMNRLNEALRTQDNHIILNTLNQVSNDYMQGSRIF	2.2548089	0.005192214	up
A0A9Q1RYZ7	Octanoyltransferase	29	5	8	1	24.9	MSLDKPTLIIRQWNDLQDYQSKFESMKNLTNQRDENTADELWLLQHHEVLTQGQAGKPEHILIP SNIPVVQTDRGGQVTWHGPGQLVAYFMFDLNRLKWNVRTLVSFAEQFMIDVLKKYNIEAYAKP DAPGVYVDGRKIGSLGFKIRRGRSYHGLALNLDCALTGFQTINPCGYAGLEMVRIQDLVTPYPLF EQLCQDFIEYIKGTGYFNDPEVKIE	0.4660374	6.33E-05	down
A0A9Q1RZT3	2-methylisocitrate dehydratase AcnD, Fe/S-dependent	59	35	98	5	86.6	MNTKYRKPLAGTQLEYYDVRQAVEDIQPGAYEKLPYTSKVLAEQLVRRADAENLTAYLTQLIE RRQDLDFPWYPARVVCHDILGQTALVDLAGLRDAIAEKGGDPSKVNPVVPTQLIVDHSLAVEYG GADPDAFAKNRAVEDRRNEDRFHFIEWTKTAFKNVDVIPAGNGIMHQINLEKMSPVIQARDGV AFPDTCVGTDSHTPHTDALGVISVGVGGLEAENVMLGRASWMRLPDIIGVELVGQRQAGITATD IVLALTEFLRKERVVGAYLEFFGEGADSMSVGDRATISNMTPEYGATAAMFYIDQNTIDYLRLT GREDAQVALVEQYAKEIGLWASEMTKAEYPRVLRFDLSTVTRNIAGPSNPHARVSTSDLKEKGI AGVVENRSDGLMPDGAIIIAAITSCTNTSNPRNTVAAGLLARKANELGLVRKPWVKSSFAPGSKA AALYLEEAGVLKDLEKLGFGIVAYACTTCNGMSGALDPAIQQEIIDRDLYATAVLSGNRNFDGRI HPYAKQAFLASPPLVVAYAIAGTIRFDIEKDALGYDKEGNPIYLKDIWPSDAEIDALVKQAVKPE QFRKVYIPMFDLGEVEQAKSPLYDWRPQSTYIRRPPYWEGALAAPRTLANMRPLAILGDNITTD HLSPSNAILMDSAAGEYLHKMGVPEEDFNSYATHRGDHLTAQRATFANPKLYNEMVRRSDGTI KQGSKARVEPEGEVMRMWEAIETYMNRKQPLIIIAGADYGQGSSRDWAAKGVRLAGVEAIVAE GFERIHRTNLVGMGVLPLEFK	2.5504691	0.046897123	up

A0A9Q1S3Z9	Isocitrate dehydrogenase NADP-dependent, dimeric, prokaryotic	69	23	150	1	45.6	MGYQKIVVPADGDKITVKADLSLNVQNHPIIPFIEGDGIGVDITPAMKKVVDAAILKAYGGKRSIEWMEVYCGEKANKIYGTYMPEETFEALREFVVSIKGPLTTPVGGGIRSLNVALRQELDLYVCVRPVRWFQGVPSPVQHPELTDMVIFRENSEDIYAGIEWKADSEEAKKVIKFLQEEMGVTKIRFPEGCGIGIKPVSKEGTQRLVRKAIQFAIDNDKPSVTLVHKGNIMKYTEGAFKEWGYELALDRFGGELIDGGPWVKIKNPKNGKDIIIKDVIADAFLQQILMRPADYSVIATLNLNGDYISDALAAEVGGIGIAPGANIGGAIAVYEATHGTAPKYAGQDKVNPGSIILSAEMMLRDMGWTEAADLIIKGISGAIAAKTVTYDFERLMPGATLLRCSEFGDAIIQHMED	4.9176527	0.026406369	up
A0A9Q1ZY45	Methylated DNA-protein cysteine methyltransferase, DNA binding domain	27	3	4	3	12.9	MSTFMDSILTTQYELHRQILEVIALIPYGKVATYGQVARMAGLPKHARLVGYVLKHLEADHQVPWYRVINSQGKISLSKFNEKGENIQQLKLEAEGIYLLNGKVNLKEFAWQP	0.4716612	0.043913993	down
A0A9Q4SJB7	Bacterial solute-binding protein 3	56	14	31	1	31.7	MTTLTFQNVKHILAASLLSLGLVACDKGTQSTEKSADTTQTTSSIEQIKKNGVVRIGVFSDKPPFGYLDAQGKNQGFDVEIAKHVAKDLLGDEIKVEFVLTEAANRVEYLKANKVDIIFANFTVTPERKEVVDFAKPYLKVALGVVSPKSHPITDVAQLKDKTLLVNKGTTADSFFTKTHPEIKLQKYEQNTETFDALKDGRGVALAHDNLLVLAWAKENPNYTVGITNLGEQDLIAPAVKKGDKELLDWLNQDLEKLAKEGVIHQAYEKTLKPVYGDTINPKDLLVE	6.4986295	0.000369088	up
A0A9Q4SK06	Flavoprotein-like superfamily	23	14	19	1	96.5	MFKKFLFQIHWFLGISAGLILSIMGVTGAIYSYDQQILKWVNTDSYVVQVQSSPKLTPAQLYQHFTTIQPEIKINSITIAKDPTASSVVNIEKEGERRGYNMMVNPYTAQVLPEVQGRKLLLLIQQIHRNLTAGEFGKQITGACALMLIYFVLSGLYLRWPKKHSARQWLAVKPKLKGRNFIWDLHAVVGTWVIVFYLLFACTGLYWSYDWWRSGMFKVLGVEQPKMQGHSGSGRNKDQLPKIQLDNAQLITALNQTWSGFNNQIGRDYSTLTVNLPKKDDGKIELSFVDATPQHERARNQAVYNYKTANIEKMELYEDKKLNQKIMSSMLPVHRGSFFGPVYQFVAMLASLAMPLFFVTGWMLYLKRRKQKKLTQAARQSLAGHYIDQNAKPWLITYATQTGVAEQLAWSTATSLQEAHQPVQVKSVQQLTEADLQQHEQILFVISTYGTGEAPDLASNFAKKLLKTNLELQHVKYAVLALGSKEYPDTYCSFGHTVDEWLKNNGAKALFDIIEVDNANPADIQNWNQALVKATKLDLHAVNIEKVFDNWTLQQRDLLNPNSLGQPAYNIELTASHEAVWQAGDIAEIQPGNSPERINKFLQHHHHILKNAVVDSLQVSIEKALWNKDLTGEIEPFANLDHLLEQLPTLPTREYSIASIPSQQVLRLVVRQQYDESGDLGLGSGWLTQHTEINQNVALRIRTNESFHLIDDNRPIICIGNGTGIAGLMSLLHTRTRHNYTENWLIFGERQRAHDFFYASTIEAWQTMGMLKRLDLAFSRDQEQRVYYVQDIIRQNAAELINWIERGAVLYVCGSIDGMASGVDQALIHILGEEQVDELRQOGRYRRDVY	7.7372727	7.40E-05	up
A0A9Q7I520	Uncharacterized protein	45	4	11	4	8.9	MASTAAERKAKQRQEMLKKGFTRKDLWLSKESLEVIEKFKSEHKLSSNDEAINLLLKTIVVIEKFKSEHKFNTIDE	2.1172617	0.001905203	up
B0VRV5	TonB-dependent receptor protein	31	16	25	7	78.7	MSLLRLDRLHYCILMSMGCISSPLVWAEDLNSDVAKLPTLHVEATRTDTGYLQTPASVFRIEAPQVDSSSQVNLTEVVKGIPSLQIRNRENYAQDLQLSMRGFGARSTFGVRGIRLYVDGIPATMPDGQGQTSNIDLSSLDHVEVLTGPFSSLYGNSSGGTILTSTKEGQGKDSIELSYSGGSHDKSRAGLVLQGGAKGANEPSYIISSSYFDTDGYREHSGAEKVLNNAKLSWNLDDGSKINWVTNYVKINADDPGGLTRADWQNNPKQVVQNVLDYNARKEIEQTQTGLTWSKPINDQHELYAMTYMGQRQVTQYQSIPDTVQKNPNTPYQAGGVIDFKRNYYGADFRWTGKELLPNTTLSIGVALDAMKEDRQGYQNFNDTGDKGVKGALRRDEDNTLWNIDPYVQASWQFLPTWRLDTGVRYSNVHYKSKDYYIVGLNGDNSGKTSYEEVLPSVALSWQITPEVLAYASYAKGFETPTFTEMAYPAQGGASTLDLKPSTSDTYETGLKSQNQLGDFTLAVFQTKTKNDIVSAESFGGRSTFRNADKTLREGVEFAWNKKLWRDLIAIASYTYLDATFDSTVPAAGKISEIPEGNAIPGIAKNQAYVSLAWQPSHGLYGGVDVQYMDKVYVNDTNSDAAPSYSVTSANVGYAWVMGDWKVNSFARVDNLFDRNYAGSVIVNDSTQPVGRYFEPADGRNWSAGLRVIKOF	3.7724832	0.002244576	up
N0A436	L-lactate permease	13	6	10	1	62.3	MFKILRYKNSPRHFKEMTMLNMWQQLYDPLNNIWLSSAVALIPIIFFFLALAVFRLKGSIAGTGTVIIALLIALFFYQMPGQMAFASIIYGFFYGLWPISWIIIGAVFLYKISVKTGQFEVIRSSILSITEDQRLQMLLVGFAFGTFLEGAAGFGAPVAITAALLVGLGFKPLYAAGLCLIVNTAPVAFGAMGIPIIVAGGPELPDITAAIASLVSLTLLFRVWKPKHIFRFEPEAGQTLAQQPTTVQRYSIGKIAKAWSPFAILTVGVMVTIWSVKPFKALFAKDGALEHWIFKLEVPYLHKLVEKMPPIVSEMKPYEAIYKFDWFSATGTAIFIAAIITVIFLKMKASEAVTTFGETLNELKTPIYSIGMVLAFAFIANYSGLSATLALALSHTGHAFTFFSPFLGWLGVFLTGSDTSSNALFSALQATTAQQIGIPEVLLVAANTSGGVTGKMISPQSIAIACAAVGLVGKESDLFRFTVKHSIIFTVFVGIIITVQAYLVPWMIP	0.1862711	0.048143237	down
N9JQM5	Nitroreductase domain-containing protein	56	13	26	2	26.4	MNLEQVRLVDEAITSRHSVRAFLSTPIEPEIIKDILRVASRAPSGTNTQPWKVYVVTGYKRDEMVERVCAAQIEVSKNPELAEQYKETFAYYPEKWVSPFIDRRRENGWGLYGLLDIKKGEKEKMAAQQLRNFKLFDAPVGIFFTVNKAMGIGSKMDIAMMIQNVMVAAKARGLDTCPQAAWNHFHPLVLDILGAADDEELVCAIALGHADPEHIVNTFITPREPVENFAVFLD	9.1143973	0.001574766	up

N9JQN7	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	81	29	147	1	53.7	MAEAQKLKLIDGWEVVIGIEIHTQLATNSKIFSGSSTEFGQDPNTQASLVDLAMPGVLPVLNEKV VELAIRFGLGIDAYIDQASVFARKNYFYPDSPKGYQISQMDNPIVGLGHIDIQLEDGTTKRIGVTR AHLEEDAGKSVHDQFEGMSGIDLNRAGTPLLEIVSEPDMRSVEEAVAYIKAIHTLVRWLGISDGN MAEGSFRADCNVSLRRPGQPFGTRCELKNLNSFRFIEQAINVEIERQMEILEWGGEIDQETRLFDP NKMETRSMRSKEEANDYRYFPDPDLLPVIIPDEQIEAIKATMPELPAARRARFIADFGVTEYDAH VLTLSREMADFYEAVVAAAGGAKQGKIAANWVMGEFSGALNKAGLELTDSPVSAEQLGGMIA RIVDNTISGKIAKQVFGFMWESEGKSADDIIAEKGLKQETDTGAIEAIIKEVLAANEKMVEEYKS GKEKAFNGLVGQVMKASKGKANPAQVNELMKKLIG	3.2201135	6.15E-05	up
N9KZS5	Acetyl-CoA C-acetyltransferase	83	21	102	1	40.8	MTDIVIVNGARTAMGGFQGSLSGLTAPELGAVTIKEAIARAGLQPTDVEEVIMGCVLPAGLKQG PARQAMRKAGLPDSTGAVTINKLCGSGMKAVMQAADMIKAGSAEIVVAGGMESMTNAPYVLP KARAGYRMGHGEIKDHMFFDGLEDAETGRLMGSFAQDMANTRGYTREQMDDFAIRSLKRAQT AITEGYFKDEIVPVTVSTRKGDVIVDQDEQPLNAKIDKIPSLKPAFAKDGTITAANASSISDGASAL VLTSSEVAAQRGLQSLAKIIATASNSQHPSEFTIAPVGAIEKVLKKAGWNAQDVDLWEINEAFAM VTMCPIDDFKLDPEKVNIHGGACALGHPVGSTGSRIILTLIHALKRTGGKKGVAALCIGGGEATA ———	4.6551086	9.37E-06	up
S3TD50	Fumarylacetoacetase-like, C-terminal domain superfamily	3	1	2	1	42.7	MNFTLNSQNSLPDDATQGCLIGRAWIPSQISGPSPIILRGNQVFDISEKFHTISELLESADPLKALSE IEGRPVGSIDELFANTVAEPDTNKAYFLAPIDLQVIKAAGVTFAASMLERVIEEQAGGDAQKAQSI REVVQGVIGDNLKTIEPGSEKALQLKEYLIEQKMWSQYLEVGIGTDAEIFTKAPVLAAVGTGQNI GIHPKSEWNNPEPEVVLVANSQGKILGATLGNDVNLRDFEGRSALLLSKAKDNNASCAIGPFIRL FDHTFTLNDIRTCDVELQIQGTDNFVLNGVSSMSQISRDPEDLIQQTLNENHQYPDGFVLFLGTLF APTQDREQAGAGFTHKVGDVVRIHSPKLGTLYNTVMTSDKATPWNFGINALMRNLKQRELL	2.6185843	0.015338542	up
V5RCJ8	UTP--glucose-1-phosphate uridylyltransferase	24	7	23	1	31.9	MIKKAILPVAGLGSRFLPASKSIPKEMVTVVDRPAIEYVVHEAIKAGIEQIILVTHSSKSSIENYFDR NFELETILEEKKKFDLLAEIRQIIPAYVSVVSIRQPQPLGLGHAVLCAKSVVGQDDFAVLLPDVLV KDNSSQNDLARMISRYNKNRAAQIMVESVPDHLVDQYGIVDVAKSPNIGESVAVQGIVEKPAVG TAPSNLSVVGRYILPAKIMQLLEKTPKGAGNEIQLTDAIALLQQIETVEAYRMQGQTFDCGSKLG YLKAVLHYGVEHPKLGNDFKQLIQELKL	3.1981094	0.000413844	up

Table S3: DEPs in XDR vs. DS strains.

Protein ID	Description	Protein Coverage (%)	Peptides	PSMs	Unique Peptide Number	Mass [kDa]	Protein Seqence	FC XDR/DS	*P*-value XDR/DS	Regulate
A0A009GAT0	Short-chain dehydrogenase/reductase SDR	23	4	7	4	27.0	MKIQGKHFVITGGGSGLGAATAEYLVKQGASVTLVDMNVEAGEQQAKQLGPKADFVKLDVTDEVAAEQFFKDVLVKHSHLHGLVNCAGIGPSAKVVGREGVHDLGLFAKTLNINVTGTFNMLRFAADAMSKNTVEAGEEDRGVIVNTASVAAFDGQIGQAAYSASKGAIVAMTLPIARELARHAIRIMTIAPGIMETPMLKGMPQNVQDALGQMVPYPSRLGKPEEFARLVAHIAENSYLNGEVIRLDGAIRM	2.0835149	0.002310928	up
A0A009GKU9	UDP-glucose 6-dehydrogenase, bacterial type	40	12	27	1	47.2	MKIALFGTTLYAGVMAALLAEYGNQIYWCTSVTCEENISILSYQDQEVNHYLNKQRKAGFLKESPFSEIPLDIEVYLFCFSPTQIELALKTVEKLSERPIVHPRLMINGSTFGLHGTDQLKQHLPKDEWVYFPDVIQEGNAINSVLNVKHVIVGVESSYAQDTMQELLRPFFRFSYQYLFMPILDAEFTKLSISGMLATRISYMNDLAMVAEKLGIDIANVKHGIAADTRIGAAYLSAGVGFGGENFSHDILTLSSTVSGTGAKSRLLEQVWAINEQQKEILFRKLWNYYHCDLSGKTVAIWGASFKENTSSTHNSPIHILLAALWAQGVKVRLHDPQALDEIATTYGDREDLVLCADQYEAAQGAHALCLVTAWKQYWSPDFKQLQQLMQHPLILDGRNIYDPAYVKSKGFAYEGVGRL	3.5105708	2.43E-05	up
A0A009GY40	Flavoprotein pyridine nucleotide cytochrome reductase	69	17	57	17	39.8	MSQFVPLKVKSITPQTDEAICIAFDVVPEQQEQFQFQPGQHLTIRHLTEAGEIRRCYSICSYAGKEDISIAVKKIDQGQFSNWANDHLKVGDVLEVMPPQGVFFQKAAKMGGQNYLGVAAGSGITPILSIIKQVLFEQPEANFTLLYGNRSWKQTMFAEQIMDLKDQFKERFQLINIFSREFNDSELMNGRIDAEKLKQLFDYEVLETNFDHVFACGPDEMMNAVENTLPNFGIAKERIHTERFHTGQARKRSVEADANRKEEKVNIILDGRELIVSVAQDDESILDAALRAGADLPYACKGGVCATCRCKVLSGEVDMFLNYSLEEDEVEKGYVLSCQTLPKGSNVRLSFDE	3.8748642	0.011906512	up
A0A009HBN0	AMP-binding enzyme, C-terminal domain superfamily	27	10	12	10	63.4	MQQERLSYASGPSTQPLLGMTIGEQFDQACQQYAEKEAIVSFHQNRRLTYKALQDEVNAFACSLLKLGLKKGDRLAIWSPNCVEWTITQFAAFKAGIILVNLNTAYKSHELEYVLNKVSCKGLIIASQFKTTDYQELLTKIAPELTTCTDKVLSSERLPHLKFVIKIDDQQHTGIYRFSDLLTTPTSEQLEQLKQLARQLQFDETINIQFTSGTTGNPKGTMLTHHNILNNGYFVGEGIRLTPQDKVCISVPLFHCFGMVMGNLACVTHGATMVYPSAVFNPLETLKAIHQERCTAAYGVPTMFIATLEHEQFNDFDLSSLRTGIMAGSPCPREIMQRVIDRMHMSEITICYGMTETSPVSVQSSVNDSIDKRVSTVGHVHPHVEIKIVDLEGQIVPQGTLGELCVRGYSVMAGYWGEEEKTREVIDAAGWMHTGDIAEMDQDGFIKIKGRIKDVVIRGGENLFPKEIEDFLYTHPDVSDVQVIGLPDAKYGEELCACIILHEHHQVDEDSIRQFCKEHISHNKVPRYVRFFNEFPMTASGKAQKFKLQEIMRAELNLMGNVFD	2.0331583	0.011389836	up
A0A009QD14	Enoyl-CoA hydratase/isomerase family protein	43	6	16	6	27.9	MQELIKASTAADGVLLLTLNRPEKRNALNNATLQCLCELLEEAEHNAQVKAVVLTGNAQCFAAGADLSELAAMDAVSLQLDIRPKLWQKIDAFSKPLISAVNGYALGAGFELVLHSDMVICGENARFALPEIGLGMLPGAGGTQRLARLVGQQLTMRWAMTGEMISAKQAEQHGICSQVVPTELTVEYAVQLAAKIAKQAPLAIRVIKQSIKSIHETTLSQGLKFERQNFVWLAATKDRNEGINAFFEKRKPVFRGE	3.5824164	0.001466599	up
A0A009S9H1	DMT family protein	11	1	2	1	13.4	MSPTVLAFVLLIISNCFMTLAWYGHLKFLHHAPFWQAILFGWAIALLEYSFMIPATRLLSDQGWTLGEMKITQEVVTLIVFVPFMVLLFKQPFKLDYVWAMLCLFGCVYFVFRSQ	2.1481773	2.08E-05	up
A0A062IHP7	Ribosome hibernation promoting factor	54	5	14	5	12.8	MQITIRGHHLAITPAIEENIKAKFNQLTKHLDQVNSMQIKLTKDHQIDKRSNKGSSNHVAEAIVRLPGIELFAQATADDMYTSIKKLTEKLKKQLLKYRKMQCTYSQVAVSI	2.0372474	0.000109003	up
A0A090B7C1	NirD/YgiW/YdeI family stress tolerance protein	6	1	1	1	12.8	MKMLKVILMTAGMATAGVVVANTPVNQAAIAPATVTTVKQALASKDNTPVKLHGQVVKSLGDEKYQFRDKSGSITIDVDDELWQGRAVSANTNVTLIGEVDIDYKPLKRVEIDVDQVQF	3.6694291	0.007846562	up
A0A090B850	FinQ	35	13	30	13	44.5	MASLNSEFQIPLKVVTTRLNHMKINLPQLVKKIEKRAIENLKRRKDKKEQIDLLITWDDWIYAALDADHERIHGSADPHPLPPTFKNNMVSGVYEKALKNVMGHFGVKATVPAWAANIKVGEHIPKELLDRLPVTTGELVTLGNWMLTKNIYRFEDIVINELIKTGFNGVIPNHILNLPDLCVYIQTDNAKGLTFENRQVVGVLFCVTELCGDRLLVSTMYLDDGMPRTIAIMLNEDQDIEASLTNFVDQFQQDYDPETMASDLKERLKIQKKLINLVLWFSQSKPEVTPLTPDATNKPVQFVEVKKEKRLFEAGKYKTFKIGSETARKLTKLYEEIEVAKAEGKVSGREPHLRKSHWHLYWYGKKGRYERYDFLLIPVTIVGGVSKD	3.7584108	0.017189116	up
A0A097I5C2	FnlC	40	10	44	2	42.8	MKKLKLMTVVGTRPEIIRLSRVMAACDEYFDHVIVHTGQNYDYELNEIFFTDLGIRKPDHFLNAAGATGAETIGNVIIAVDKILDEVKPEALLVLGDTNSCMAVLPAKRRKIPTFHMEAGNRCFDMRVPEEINRRIVDHTADINLTYSTIARDYLLAEGLPADLVIKSGSPMFEVLHHYKAKIEASDVLERLNLKEHEYFIVSAHREENINSDQNFLDLVEMLNAVAEKYKYPVIVSTHPRTRKRIEELNVEFHPLIQLLKPLGFSDYNKLQLSAKAALSDSGTINEESSILNFPALNLRQAHERPEGMEEAAVMMVGLKAERILQGLAILEGQTRGEDRLLRLVEDYSMPNVSEKVVRIIMSYTDYVNRVIWKQF	0.1666574	0.013408089	down

A0A0E1FIC9	Carbohydrate deacetylase YdjC-like	8	2	2	2	30.2	MAKVCYCADDFAMNAEISDAIIQLIEQGALQATSCMTQSDLWETAAAKLKPFSDRVDIGLHLNL THAFASGNLVFPLPMLIVRAWSASLNRELITQCIEEQWDLFVSVLGKQPDFIDGHQHIHQFPFIRDI LLQLLKEKKFTGWIRNLQQPINPPPYRFKTRMLSALGSNSLAKACQTYHFNQNGQFAGIYDFKLT NYGQLNQYWLANAKDHLLIMCHPALAQSKDQDPIQHARIQEYQYFSSDQFQLDCQQYGIQLTR LGAMQ	2.8036745	0.000572588	up
A0A0E1FL10	Glucose-6-phosphate isomerase	26	13	20	9	62.9	MSKSIEQFPKDLSSPLIQLKSSVEKNSKLHIKELFALEPERFQNYSVKFDQLFFDYSKQRITKNILE QLVALANNKQLTQWINRLFSQDKINCTEQREAMHWALRLPSEYSKFPELAKQVHIQLQRMYTL VEKIHAGQYRGATGEVIQDVVNIGVGGSDLGPHMVTHALADFKVKTAKPLNVHFVSTMDGSQL SDLLHQLRPETTLFIISSKSFGTIDTLSNAQTVRQWLEKALGKHDRVVKSHFIGVSTKAEKMTEW GIAPDNQLLLWDWVGGRYSLWSCIGFPIALTIGIDGFQQLLAGAHAVDEHFQNTSFERNIPVLMA LLGIWNNNFLNIQTHAVLPYDGRLKYFAAYLQQLEMESNGKSVQRDGQKVELDTCPIVWGEVG PNAQHAFYQLLHQGTQAVSCDFIAPVQRYNADHFTYVENAEALIEQHHLALSNCLAQSRLLAFG NEALDAAELKNLPIYKQYEGNQPSSTLLLDELNPYNLGMLIALYEHKVFVQSVIWNINPFDQWG VEKGKQIADQLLPILNGVQNDFSKLDASTRGLIKILLGKVDG	0.2123071	0.004067271	down
A0A0E1PTG5	Outer membrane efflux protein	51	22	51	19	51.5	MENTMSKSTIVSRGLILSTLSIALVACVNMQAPQPAITSHIPQNFSQNHSGKMIAEKSYKEFISDPK LLQVIEISLNNNRDLRTATLNIERVQQEYQITKNSQLPTIGVTGNAVRQVSPSINPNNPVSTFQVG LGMTAYELDFWGRVQNLKDAALNNYLATQSAKEAVQIGLISNITQVWLNYAFAQANLNLAEQT LKAQVDAYNLNKKRFDVGIDSEVPLKQAQISVETARNDVATYKTQIQQAKNLLDLLAGHPVPQ NLLPDHAIQNITFEKNFAAGLPSDLLNHRPDLKAAEYELRVAGANIGAAKARMFPTISLTGSTGY ASSELKDLFKTGNFAWSIGPNIDLPIFDWGTRKTNIKIAETDQKIALAKYEKAIQSAFREVNDALA THAHIGERLDAQRRLVSATAATYKLSMARYKAGVDSYFTVLDAQRSAYAAQQGLLALEQIKLN NQIEIYKVLGGGISKV	2.2015614	0.005500687	up
A0A0E1PV91	Lipoprotein	49	10	18	10	27.8	MHQTNKRSAIALLFIVYSKCCSFATIPYFYIFYAYSTYLLQLVLFVVMKKVLQGAFFPFVIFASGM LLLGCDQTQDHAKEQESVQTNDQISDQADDSQQEITATQNKTELKNGNVFYIVRDAANLQLKA GDYIEKLKDTQLDVEQAIQDKDQHELKTTVTTLKAQLEGLNQALLGLDIRSQEVENIRQSLLQA NQQALSMPLLNGKLEQINFDQIEKQLNTIQMDMVKLAAMIMAGDEKSDSKTDS	2.8707707	0.001192664	up
A0A0E3KX17	Thiol:disulfide interchange protein	45	7	11	7	26.6	MKKFLLTFAVAISSYSIAYADVAEDIKSNIQKNYPATTVTQVNKTPLTGIYEVVMGRNVAYTDK DGRYFIFGNLFDMKTQTDLTTTPTSSNKVEVGFPNADRLKDAIKTVKGNGKRKLVVFSDPDCPY CQQLERNLQSIDNVTIYTFLYPLESIHPTAKTTAVSIWCSKNPGKAFQDYMIENIKPSSKNCAHPID RNIEFASSMNIQGTPSLIFEDGSMVPGAVGVSELERLLNSSQKSK	0.4990737	0.03425805	down
A0A0J1ACY0	Gp49-like PF05973 family protein	17	2	2	2	13.7	MAWDVETTELFDSWLAEQDENAQDKILASLLVLSELGPNLGRPHVDTIKESKYPNMKEIRVQVK GHPIRGFFAFDPERKAIVLCAGDKKGLNEKAFYKEMIKIADEQYEQYLRDNYGDK	0.3100382	0.014124653	down
A0A0Q1HCL9	L-alanine-DL-glutamate epimerase	52	12	20	4	40.2	MYRTIETILVDIPTIRPHQLSVTTMRTQTLVLVKITTTDGIVGWGEATTIGGLNYGEESPESVKAN IDTYFAPLLTSVKDLNVAQTLKLIRKNINGNRFAKCAIQTALLDIQAKRLGVPLSEVLGGRLRNSL PVLWTLASGDTEKDIAEARKMIELKRHNTFKLKIGARPLQQDVDHVIAIKKALGADVSVRVDVN RAWSELECIHGIQQLQDGGIDLIEQPCAIQNTEALARLTHRFDVAIMADEALTGPDSAYRIAKNH GADVFAVKIEQSGGLIEACEVGKIAGLAGIDLYGGTMLEGPVGSIASAHVFATFETLAFGTELFGP LLLTEEILKEPLRYENFELHLPTAPGLGIEIDEDKIEKLRR	2.0594246	0.000305644	up
A0A125S0J9	Dihydropteroate synthase	80	15	70	2	30.3	MSYLFLSCTEIIIEAPMNKSLIIFGIVNITSDSFSDGGRYLAPDAAIAQARKLMAEGADVIDLGPASS NPDAAPVSSDTEIARIAPVLDALKADGIPVSLDSYQPATQAYALSRGVAYLNDIRGFPDAAFYPQ LAKSSAKLVVMHSVQDGQADRREAPAGDIMDHIAAFFDARIAALTGAGIKRNRLVLDPGMGFFL GAAPETSLSVLARFDELRLRFDLPVLLSVSRKSFLRALTGRGPGDVGAATLAAELAAAAGGADFI RTHEPRPLRDGLAVLAALKETARIR	7.3373026	0.009361366	up
A0A126W935	Nicotinate-nucleotide pyrophosphorylase	44	9	22	1	30.5	MSIPQSLLEQSIQINIQQALQEDIGDGDITAMLTPEDEQATATIISREDMVLAGQPWVVNALISAYD NTVQVTWLKHEGDRVAANEAFLKLAGSARSLLTVERPALNFIQTLSAVATKTAEYVQHLEGLN TKLLDTRKTLPGLRIAQKYAVTVGGGKNHRLGLFDAFLIKENHIMAAGGIAQAIAKAHQIAPGKP VEVEVETWDELNQALEAGADIVMLDNFSQQQMIDAVKHVAGRCKLEASGNITIENLREVATTG VDYISMGVLTKDVKAVDLSMRFNA	7.1278649	0.001170788	up
A0A158LWX7	Thiosulphate/Sulfate-binding protein	46	13	28	13	37.1	MRFSQLKVGVIAALLSVSSFAAQEFLNVSYDPTRELYTDFNKQFGTYWKQRTGQDIEFKQSHGG SGKQARAVIDGLNADVVTLALAADIDEIAEKAKLLPTDWQKKLPQNSTPYTSTIVFLVRKGNPK QIKDWGDLIKPGVEIITPNPKTSGGARWNYLAAWAWAKHQVGGNDAKAQEFVRQIYKHTKVL DSGARGATTTFAERGIGDVLLAWENEAHLAIREQPGKFEIVTPSLSILAEPPVAIVEKNAAKKGNL TIAKGYLNYLYSPAGQEIAARNFYRPRNAAVLKKYSNVFKPLKLVTIDKEFGGWTKVQKQHFD NGGVFDQIVKINSAEK	3.0946621	0.046670866	up

A0A158LX87	Phosphoethanolamine transferase	14	6	26	1	60.2	MFNLIIAIWLGAILNIGFYHQVHTLTPYFGVKAILFLAATLIILVATYYAVLQILNWKWTAKIFAILLIFIGGFSSYFVNTLGVIISPDQIQNMVQTDVSEVTDLISLRFVLWTVFFVILPIFLITQVKFKQEKVSRLLLKKVFSLVASFAVVGVLLFTYYVDFAAIFREHRDLKGMISPQNSISSLMSYYHKKAPKKNLPLVIYGQDAHQVQRVQKNLPKLMILVVGETARAESFSLNGYAKNTNPELSKQDIFNFSQVSSCGTATAVSVPCMFSGMPRADYDEQLASHREGLLDIAKRAGYQVTWIDNNSGCKGACDRVEQYQIPEDLKQKWCKDGECLDDILIDSLKQYLASIPKDDKRPRLVVLHQMGSHGPAYYKRAPEGYQPFKPTCDTNAIQGCSPAELINSYDNTIVYTDHVLSQMINTLKEVSNYQTGFWYLSDHGESTGEHGMYLHGSPYSIAPSQQTHIPMIMWFSDGWKQNNLAQVNCLNQQTKQKLSQDNLFPSLLSMLDVKTQVINPQLDMLHSCANVN	10.622329	3.50E-06	up
A0A1E3M2G1	Phenylacetic acid degradation bifunctional protein PaaZ	53	28	106	2	76.7	MLEQAHLEGTSTDTDFQQSGLQLPHLASYVYGTWHSSDEELRTVYHAITGESIYAVSSHGIDMKRVVQYAKQIGSELANWTFHQRANALKQIAQHLLERKEDFYKLAYATGATRKDAWIDIEGGIQTLFAYSSLVRRELNDEKIITEDSWIQLSKNGTFGAKHILSPKAGVAVHINAFNFPIWGMLEKIAPTLLAGVPCIVKPATDGAQLTQAVVKAIEETHVLPKGSLQLICGQTYDLLEQLGPQDCVTFTGSAYTGQKLRNHPHLNKYSIPFSMEADSVNSAILSPDANEETVDLFVREVFREMTTKAGQKCTAIRRAFVPENLLATVQEKLTAKLAKVVVGDPQKEETTMGALASIKQKHDVAEKVAELSKDAKIVFGGNDSFTFNADHPEKGAFFAPTLLVCEQPLQATNVHTTEAFGPVCTLMPYQNIEELADLVSRGEGSLVASVVKNNDENIEQIIQKIAPWHGRVHVLDAESAKESTGHGSPLPHLVHGGPGRAGGGEELGGIRAVKHYMQRTAIQGSPNSLTQITHSWTAGSKVNEDRVHPFKKSFDELVIGERLLTARRTVTEADIVNFACLSGDYFYAHTDKIAAAESFFGERVAHGYFIVSAAAGLFVDAAQGPVIANYGMDNLRFVEPVKIGDSIQVELTCKQKTPKPQKDPSQPAHGVVVWDIKVKNQRGELVATYDILTLVAREA	2.1042205	0.000119866	up
A0A1E3M9X9	MFS transporter	10	4	5	4	49.2	MMNALERRSTFALSSIFALRMLGLFMIIPVFSVVGQSYQYATPALIGLAVGVYGLSQAILQIPFSLLADRFSRKPLVVFGLLLFAIGGAIAGLSDTIYGVIIGRAIAGAGAVSAVVMALLADVTREEQRTKAMAAMGMSIGLSFVVAFSLGPWLTSLVGISGLFFVTTIMGLIAIAMLLLVPKVTRHHRNYQQGYMAQLKQVIQMGDLNRLHVSVFALHLLLTAMFIYVPSQLIEFAHIPLASHGLVYLPLLVISLFFAFPSIIIAEKYRKMRGIFLTAITGIIAGLLLLIFGYQSKYVLLAGLGIFFIAFNVMEALLPSWLSKSAPIQSKATAMGVNASSQFLGAFFGGTLGGQLLMLHNTAIGWSVLAGIAIIWLLISFGLAQPRYLSSIVLPLPQVQQVNEWTTQLLAIRGIEEVVVMPDQQVAYIKVDKQSLDDASRRDLTQLFGKEVAI	2.1273575	6.07E-05	up
A0A2U8NGD1	Wza	33	11	28	1	41.3	MHKGSRVKYCQFFSVLALSLSAASCAVTSGLQTYDIPSEGVYKTDLGTTVNVVKISQETLPAIQPAQIDYQRDYASLFKNQQTIYRLSPGDVLSIQLWAYPEITPPVNNISNEQSIQANGYPIDQSGYIQFPLVGRYKAAGKTLAQVNRELHNQLARFLKNPDIVVRVLSYEGQRFSVQGSVLKGGQFYLSDQPISIYAALGLAGGVSDKGDNTYIQLIRNGRTYNLNTIDLERAGYSLHKLLVQPNDTIYVSTRENQKIYVMGESGKNQALPMRDQGMTLSDALGESLGLNPLSASASRIYVLRTNPNDRTTELYHLNLMSIGDFGLANQFRMRSNDIVYVDATGLTRWQRVVNQIIPFSSALYNIDRLGQ	6.0208426	0.009272748	up
A0A2U9QFX2	FnlC	47	11	52	3	42.1	MTVVGTRPEIIRLSRVMAACDEYFDHILVHTGQNYDYELNEIFFTDLGIRKPDHFLNAAGATGAETIGNVIIAVDKILEEVQPEALLVLGDTNSCMAVLPAKRRKIPTFHMEAGNRCFDMRVPEEINRRIVDHTADINLTYSTIARDYLLAEGLPADLVIKTGSPMFEVLHHYKAKIEASDVLERLNLKEHEYFIVSAHREENINSDQNFLDLVEMLNAVADKYKYPVIVSTHPRTRKRIEELNVEFHPLIQLLKPLGFSDYNKLQLSAKAALSDSGTINEESSILNFPALNLRQAHERPEGMEEAAVMMVGLKAERILQGLAILEGQTRGENRLLRLVEDYSMPNVSEKVVRIIMSYTDYVNRVIWKQF	0.232939	0.009243759	down
A0A333V6L2	Thioesterase family protein	30	6	10	6	29.9	MNAYYQLLNRTIGPQGEVIAHYCSTVHAQGAWNPHEQHMAPASGVIAVELEQFSPRQDMRIGRISFDIFGLIAFGEFTIKTHVIRAGKTIELIEAELQAQGKTCIVARAWRMCTQDSSEIAGLEDQPIHHPDTFTEWSGMKRWPGGFIQTLVTKTNDQHRAGKGIVWLNNDKEMVEGQSTTDFAHLIGMVDAANGIVPRQEGEFTWGFPNLDLQIHMHRYPQGKWLGLETVQQYGSDGIGLTSAVLHDVYGPFGRSEQILTLRKMTK	2.1827376	0.001638443	up
A0A335J3M4	Thiolase	60	17	57	1	43.1	MEDVLICDFIRTPIGRYAGALSAVRADDLAALPIKYLKDKHPNLPWNTVDEVFLGCANQAGEDNRNVARMATLLAGLPDTVPAMTVNRLCASGLDAVGLAARSIKAGEAQFVLAGGVESMSRAPFVQAKLTEAFSRTPEIYDTTIGWRFVNKQLKAQYGTDSMPETAENVAEKYQISREDQDAFALRSQQKTAAAQQNGFFNDEILPVEITDRKKNVVVVNRDEHPRETTLEALAKLKAPFKKEGGSVTAGNASGVNDGAACVLITNREFADTHGLKPLARVIGIASAGVEPKYMGIGPVPAVQKILKQTGLTLDQMDVIELNEAFAAQSLACMRELGLKDDDERVNPNGGAIALGHPLGMSGTRLVITATRELKKRGGRYALCTMCVGVGQGVALILENLN	5.6399191	3.46E-05	up
A0A385EQQ7	SnoaL-like domain-containing protein	64	5	10	1	14.2	MSLSQKEIAVRFLELAAAGEVDEAYGNYTAPNFKHHNPYYAGDKISLKEGMRESAIETPNKVLEVQHVIEDGALVAVHSKLEMQMNNKLTILAVVHICRFENEKIAEFWDIGQIQPDPLVNENGMF	2.0106519	0.02521531	up
A0A385ET64	Uncharacterized protein	64	2	10	2	6.6	MKLAKTLLATTLALTAASTFAASKHDQAHNTAGEEKVVVSTQEQANTANAASDAVGSASEAAPATR	2.4323265	0.021655299	up

A0A385EUA0	1,2-epoxyphenylacetyl-CoA isomerase	58	12	47	3	28.9	MDYQNIIAEEKNGVGYLTFNRPKALNSFNVDMHREVAEVLSQWTKNPDVRCVVISGEGRGFCAGQDLGDRVVDPNAEAPDLGYSIETYYNPLIKTIVNMPKPVICAVNGVAAGAGANIALACDLVIAAKSANFVQAFCRLGLVPDSAGTWFLPRAVGHARAMGLTLLGDKLPAETAKEWGMIWDVVEDAELKTKVTELAERLAKQPTFGLSLIKKAIHQSSNNTFDEQMLLERDLQRIAGRSEDYREGVQAFMNKREPNFKGR	4.6632177	2.86E-05	up
A0A385EUT6	3-hydroxyadipyl-CoA dehydrogenase	38	17	35	17	57.1	MTDLDLSRARIAVIGSGTMGIGIAQLAIVNGHTTVLYDLDAQKAQQAVQGLGQTFKKLVEKSKLTEQQADEALARLTVVNQIEALRDADLVIEAVVEKKEVKQSLFKQLAEICSAQTIFASNTSSISVTAISAGITHPERVVGLHFFNPAPVMKLVEIVQGLKTPNSLCLALKNLMLNWKKIPVLTKSTPGFIVNRIARPFYAEGFRALQEQVTSYDQLDYALKQCGGFAMGPCELTDLIGQDVNFSVTQSVYQEFFYEPRYRPSLVQKELVDAGAWGRKSKQGFYTYNEKNQYQTFQPQAVVAKPVDAHIQLKGTWSQLPAFLTRLGLKSGSASDDNILQIDDIDLRLSQGESANIHYLSRKVVLMDWHHDFEQAEALVLSHNELCETNDLAKVEAYFAQFGMSVMWIKDHPALLTLRTIALLINEACEASLHGVASLEDIDNAMKYGVNYPKGPYQWLTQMGGAYVLQTLNNLYALYGEEKYRASIYLKQYVAKTQNIATQYSRDMTEFA	4.6983635	2.48E-05	up
A0A385F0B4	Phosphatidylglycerophosphatase A	5	1	1	1	19.2	MDTNTLHKPPIHFKDMSWFNRCIVFCGVGFGSGLAPKAPGTFGSAFALLFVPIWLSLGFTLSLIAILIMSVVGIYICGQTAKILDVHDDGRIVWDEFAGQSITFLPLLYLQQINWIWVITGFILFRIFDVWKPWPIRVIDRQVHGGFGIMLDDIIAGVWAALCTLIIIHLS	2.3384263	0.025399419	up
A0A385F1H2	Uncharacterized protein	30	2	3	2	12.1	MHSKIIGLTVIMGIISSMAFAEPAIQPGETLESLSKARITTNVNTQAATPTAQTSDATTEVKVEDIDPIIEEKTEETVKAAIQPAPQATAEAVVTPIASSQLNVSVDDIDVAHPTE	3.5949194	0.031256102	up
A0A3R9RP79	Uncharacterized protein	62	4	6	4	10.9	PVSNSGYWTGQFDRLVGTLILESDGTGVICQDHLGTARVMSVKLLNDRLYSQDGTYWKISNFTPTSLELNYALGGGYKMIRDNGLKFASPACKDKLNTK	2.0059312	0.000802109	up
A0A3S0KUX5	Domain of unknown function DUF306, Meta/HslJ	60	16	115	1	41.1	MKIKYLILALLPFSLMACQTVSNTQAPIVSEQQQNLATTLSEYAWTYQNVKASKPLILNFNADGKLAINTGCNGQGGTWKVEGNQLVTSPLASTMMACQDDLMKQEQLSNSIFSEAKLPIEISNNNGQAILSVTDKAGQKHIFQGEKATHTQALTDYSWSYQPENTKKPIVLNFTNDRLSIDTGCNRQGTTWKVENNTIVTTDVMSTMMACEPALMKQEQFSSSLFQKRAIPFELNTTNVDQPTLTVTDAQGQKYTFTGKMTPEAKYQSEGKTVFLEVAPETKSCTGVAPQTCLQVREVKYDDKGVKTYADKNWSLYYGQIEGFEHNPNQRVILRVKRFEVKNPAADQSSQADVLDMVVEQELVKKPKK	0.4813625	0.001105413	down
A0A411MUY4	Patatin-like phospholipase domai	41	18	36	6	57.7	MFEKIRSDMNPHQAYRIKKLQRQLDMAESYEEWKSFALKLDEETGAQEWKFDNSSPYFDAELISYRYTLLKRYRQQHRTLDLIYLLKEGLTYDIANIGHPMLFAATHVGTKKLIEDYIEEVSQSLAYIASSECITFQRKKKIEFFENCEKAYGQPALMFSGGATLGLFHTGVCKALIEQDLMPKVLSGSSAGAIMTGMLGISASEDIQNLLNGEQFFSDAFHFRKLRELIKGNGGIADVHYLKKFLIENLGDLTFEEAFKKSGLNINVAVAPYDATENPRIMNAIMTPNVLVWSAVLASCAVPVLFPPVRLTSKRYDGEHTPYMANTKWVDGSVRSDFPQERMARLYNLNYTIASQVNPHVVPFMQDDARRFRKDVLSWPERILRRQGKVLSMGLMDFTRQRLGAISPVRRLLDHGYGVVGQRYYGDVNIIAKYSLKHYAYTLQNPRPHLFKRLQREGERATWPKISSIETHARIGKTIQHCLEVLRFEEKKQQPESYYAEA	2.3507761	9.44E-05	up
A0A429MK36	catechol 1,2-dioxygenase	64	13	34	13	33.2	RQQIDALVKQMNVDTAKGEVDARVQQIVVRLLGDLFQAIEDLDIQPSEVWKGLEYFTDAGQANELGLLAAGLGLEHYLDLRADEADAKAGITGGTPRTIEGPLYVAGAPESVGFARMDDGTETGKIDTLIIEGTVTDTDGNIIENAKVEVWHANSLGNYSFFDKSQSDFNLRRTIFTDADGKYVALTTMPVGYGCPPEGTTQALLNKLGRHGNRPSHVHYFVSAPGYRKLTTQFNIEGDEYLWDDFAFATRDGLVATAVDVTDPAEIQRRGLDHAFKHITFNIELVKEAAAAPSTEVERRRASA	2.6308623	0.014646065	up
A0A4P8VDY7	Universal stress protein A family	47	10	15	7	31.2	MSKIIACIDGSLVTNTVCDYAAWFSDKLNSPIKLLHVIDKPKAKAPQDLSGAIGLGSRETLLKELVELEERKGKIELEHGQILLREAKNYLVEKFSIDAQSFQRHGSVLETIMGMEDDIRVLVMGKHGNETEHDSSKIGTHIENVVRALHKPVLITSAPFSPPKSFLIAFDGSQTARKCVERIASSPLLKGLAVHLVYVGNPNSEMQNQLSWAKEQLESQGFNITSNTLDGEVDKAIINYAEQHQIDLIVVGAYGHSKIRQFFIGSTTTKVITSANKPVLLLR	2.745513	0.004392489	up
A0A4Q4GN90	Uncharacterized protein	36	5	12	5	16.1	MMQPIHTHSTLQYIHISVPEILLSNIEIKNSWQDYNQEWSYRLDPPHASHPFQRDLYIIKSKNIETEDIKKLLDNIVVKNSKNKDDLKNIVEAETVIKEILDLSNYIPIENWLNDTGNRSIVESMIDKNKVKLLDII	0.3730088	9.96E-06	down
A0A4Q4H670	Enoyl-CoA hydratase/isomerase	40	8	17	8	28.9	MSYQFLQLEQQGQVAYIWLNRPELHNAFNTTVIEELHACFKQINTRDDIRVVVLAGRGKSFSAGADLNWMKQAGQASSAENEADALKLAQMLDALATLKQPTIARVHGIAFGGGMGLASACDICIASTDAKFATSEVRLGLAPSTISPYVIRAIGARQASRYFLTAERISAREAKQIGLAHEVADAEDLDKKVQEIVDALLLGGPHAQAASKQLIQMVSNQTMSNDLLQQTAHHIAQVRQGSEAKEGLSAFLNKQQPAWVSNSNNNN	2.2411993	0.004437908	up
A0A505MKS4	1,2-phenylacetyl-CoA epoxidase subunit A	29	7	16	1	35.5	MENNYQKFEQNIANEITIEAKDQMPDAYRKTLIRQIGQHGHSEIVGMLPEGNWITRAPTLKRKAVLLAKVQDEAGHGLYLYSAAETLGADRDDMMEKLIDGKMKYSSIFNYPTLTWADVAAIGWLVDGAAIVNQVALCRTSYGPYARAMVRICKEESFHQRQGFEAMMALAGGTPEQKQMAQDAVNRYWWPALMMFGPSDEHSPNSAQSMAWKIKRFSNDELRQKFVDNTVPQILQLGLEVPDPDLKLNEETGHYEFGEIDWHEFNEVIAGRGPCNHERIEARRKAWENGKWVRDAAVVYAKKQQLEANKVA	2.7650739	0.042392874	up

A0A505ZPT1	Glucose-6-phosphate isomerase	35	13	26	9	62.6	MSKSIEKFPKELVSPIAQLHSLVEKNSKLHIKELFAAEQDRFQNYSVKFDQLVFDYSKHRITKSVLEQLFALAKTKQLTHWIERLFSQDKVNCTEQRAAMHWALRLPSEYSKFPELTKQVHTQLQRMYALVEKIHAGQYRGATGEVIQDVVNIGVGGSDLGPQMVTHALCDFKVKTAKPLNVHFVSTMDGSQLSDLLHQLRPETTLFIISSKSFGTIDTLSNAQTVRQWLEKALGKHERVVKSHFIGVSTKADKMTEWGIAPENQLLLWEWVGGRYSLWSCIGLPIALSVGIDGFQQLLAGAHAVDEHFQNTSFEQNIPVLMALLGVWNNNFLNIQTHAVLPYDGRLKYFAAYLQQLEMESNGKSVQRDGQKVELDTCPIVWGEVGPNAQHAFYQLLHQGTQAVTCDFIAPIKRYNADHFTYVENAEALVEQHHLALSNCLAQSRLLAFGNEALDSAELKNLPIYKQYEGNQPSSTLLLKELNPYSLGMLIALYEHKVFVQSVIWNINPFDQWGVEKGKQIADQLLPILNGAQNDLSTLDASTRGLIKILLGKVDG	2.950822	0.00369683	up
A0A517D2C4	Two-component system response regulator PmrA	37	5	28	5	25.5	MTKILMIEDDFMIAESTITLLQYHQFEVEWVNNGLDGLAQLAKTKFDLILLDLGLPMMDGMQVLKQIRQRAATPVLIISARDQLQNRVDGLNLGADDYLIKPYEFDELLARIHALLRRSGVEAQLASQDQLLESGDLVLNVEQHIATFKGQRIDLSNREWAILIPLMTHPNKIFSKANLEDKLYDFDSDVTSNTIEVYVHHLRAKLGKDFILTIRGLGYRLGQS	6.3911739	6.10E-05	up
A0A5K6CRD2	(R)-benzylsuccinyl-CoA dehydrogenase	59	19	43	19	45.9	MFELSKKAQDFAERTKKFIQEEIEPVEAKFWEEVHELNPDGNWKKWQWPELLETLKSKAKQAGLWNMFLPDEKLGAGLSVQEYAHIAELTGRSLLAPTVFNCNAPDTGNMEVLWRYGSEQQKQQWLEPLLDGKIRSVFCMTEPDVASSDATNMQATALIDGNEIVLNGKKWWSSGLGDPNAKVIIFMAHTPDETKDRHHQHSMVLVPIDTAGVEIQRMLPVFGDYDAPHGHGEVHFNNVRVPIENFIGGAGQGFEIAQGRLGPGRIHHCMRCIGAAEKALELMIDRGMSRTAFGKEILKLGGNLERVADARVAIDQARLLTLYAAYKMDTLGNMAALTEISAIKVVAPSVLEKVVDMAIQLHGGAGVSRDTPLTGFFAQARSLRLADGPDEVHKGMIAKLELAKRGYFGRHKKV	2.4459057	0.003548222	up
A0A5N0FZ32	Glutamine amidotransferase type 2 domain	52	53	149	1	162.9	MHMPSPNTVAPAQGLYQPDEFKDNCGFGLIAHMKGESSHHLVETAIHSLSCMTHRGGIAADGKTGDGCGLLLAMPKQFFRDEAKKLSDITLSEIFAVGTVFLNIDPALAQHSKNILTKEIESEGLRVLAWRIVPTNNDALGEIALQSLPAFEQVIVNCPMGVTEVEFNRKLFLARRRAEQQLKNDPLFYVTTLCSTVISYKGLMMPAAIAEFYTDLADERLKSHIVVFHQRFSTNTLPRWPLAQPFRYLAHNGEINTITANRNRWALARTPKFENPLLPGLTELNPIVNRTGSDSSSLDNMLEILVGGGMDLFRALRMLVPPAWQNVETLDADLRAFYEFNSKHMEAWDGPAGLVIQDGRHAICMLDRNGLRPARWVITKNDYITLASEIGVWGYEPEDVVSKGRVGPGQILVVDTLTGKVLDTKDVSNHLKNMRPYREWLRDHAIRLNANPELEEQLVDKGLTGDALKAAQKMFMVTFEERDQLLRPIAESGQEAVGSMGDDTPMAVLSRQVRHVTDYFRQQFAQVTNPPIDPLRESIVMSLETCLGREQNVFEQGPEHADRIIISSPVLSNSKMQQIRSIERAGYEAVDIDLNYAETEGLQAAITRICEESAQAVRDGKTLIVLTDKNIRQGYLPANAALATGAVHHHLIKTGLRTDANIMVETGFARDPHQFAVLLGFGATAIYPYLAYDVINDLIAKGELLGDPIHAQANFRKGIEKGLLKVLSKMGISTVASYRGGQLFEAVGLSSEVVDQCFLGVPSRIQGATFVDLENDQKKLAATAWSNRKPIDQGGLLKFVFGKEYHAFNPDVINSLHKAVRSGKYEDFKEYAELVNNRPIATIRDLFKLKTTNPIPVEQVESVEAILPRFDSAGMSLGALSPEAHEAIAIAMNTIGGRSNSGEGGEDPARYGTIRNSKIKQIASGRFGVTPAYLTSAEVLQIKVAQGAKPGEGGQLPGGKVNGLIARLRYSVPGVTLISPPPHHDIYSIEDLSQLIFDLKQVNPKAMVSVKLVSEPGVGTIAAGVAKAYADFITISGYDGGTAASPLSSIHHAGSPWELGLSEAHQALRVNDLRGKVRVQTDGGLKTGLDVIKAAILGAESFGFGSTPMIALGCKYLRICHLNNCATGVATQQDHLRQEHYIGEPQMLINFFHFIAEETREWLAALGVASLKDLIGRVDLLEVLPGETEKHAHLDLSALLTSHPAAEGKAQYCEVEGNAPFDKGVLAERMVEEMLPAIESSAGGQFNFNVVNCDRSIGARVSGEIARRYGNLGMEAHPVVMNLTGTAGQSLGVWNAGGLHIRLEGDANDYVGKGMAGGRISIFPPKGSPFQTQNTAIIGNTCLYGATGGKLFAAGTAGERFAVRNSGAFAVIEGAGDHCCEYMTGGVVTVLGKVGHNFGAGMTGGFAYVLDLDNDFVDYYNHELIDLTRISTESMEDHKEFLLRIIDEHIKETGSAWAYKIRNEFDFYSRKFWLVKPKAANLQSLLKTTQADPQ	2.9123303	0.00043383	up
A0A6B2QRH5	Phosphoethanolamine--lipid A transferase PmrC	23	11	47	1	62.2	MLNFFSTLRNKQISLFMFNLIIAIWLGAILNIGFYHQVHTLTPYFGVKAILFLAATLIILVATYYAVLQILNWKWTAKIFAILLIFIGGFSSYFVNTLGVIISPDQIQNMVQTDVSEVTDLISLRFVLWTIFFVILPIFLITQVKFKQEKVSRLLLKKVFSLVASLAVVGVLLFTYYVDFAAIFREHRDLKGMISPQNSISSLMSYYHKKAPKKNLPLVIYGQDAHQVQQVQKNLPKLMILVVGETARAESFSLNGYAKNTNPELSKQDIFNFSQVSSCGTATAVSVPCMFSGMPRVDYDEQLASHREGLLDIAKRAGYQVTWIDNNSGCKGACDRVEQYQIPENLKKKWCKDGECYDDILIDSLKQYLSTIAKDDDRPRLIVLHQVGSHGPAYYKRAPEAYQPFKPTCDTNAIQGCSQTELLNSYDNTIVYTDHVLSQMINTLKEISKYQTGLWYLSDHGESTGEHGLYLHGSPYAIAPSQQTHVPMIMWFSESWKQHNLAQVNCLSQQTKQKLSQDNLFPSLLSLLDVTTQVINPQLDMLHSCAHVN	5.6355987	1.86E-05	up
A0A6F8TCX5	serine-type D-Ala-D-Ala carboxypeptidase	74	19	110	1	37.9	MDYETGQILASKNENEKLAPASMTKMMTSYIIEQKLLKGELTENEQVRMNESAWCKGSSSESCMYVPLNGTATVLEMLRGIIIQSGNDASKAMAEHIAGNEGTFAHMMNQEAKRIGMTNTQFINSTGMPAEGHYSTAKDMAVLAQHIIKDSSKYYPIYSEKEFTFNGIKQGNRNALLYTDPSVDGLKTGHTDEAGYCLTTSSKRGPMRLISVIFGTPSMSERADQTRALLAWGFANFETANVQPANQVLAKAKVWFGKENEVQVGLAENFNVTMPKGKADGIKTQLVVQPNLNAPLQKGQVVGKLVASLDGKVIAEKPLVALKPVEEAGFFARLIDHIKQFFSNLF	3.029423	0.015825741	up

A0A6H3EK80	Pyruvate flavodoxin/ferredoxin oxidoreductase, pyrimidine binding domain	52	46	90	46	127.9	MNIATKVTPNIIATKDVSLEDKYVSDNGTAFMTGIQALVRLPLAQTRRDAINGYHTAGFISGYRG SPIGNYDNFLWQVEGLLKSHNVVFQPGVNEDLAATAIWGTQQANLSGQGKYDGVSSWWYGKG PGVDRSGDVLRHANLAGTSERGGVVALFGDDHSCKSSTVPHQSEHVMIGCGIPIFYPTSVQQILD FGVHAIAVSRFSGLWTSMKLVSEIVETSASVHVDLDRVTPVIPEDVNFPEGGVNIRWPDHGIQQE ERLYKYRLPAVLAYARANKINTVTWPCENARIGIAASGKGYLDTIEALRILGIEDETAQQLGLRV YQVGLIWPLEPQGIREFAKGLEELIVIEEKRPILETQIKDELYSLPDDQRPRVIGKATDGKGEWSTS IEEAPLIGHYEYQPEPIAKMLAARFLKLDIPESLKVQIQGRIDLLLKAEQESKRVIDLAERKPYFCS GCPHNSSTVVPEGSRALGGIGCHYIAVSLDRGTETFSQMGGEGVSWVGASPFTNEKHIFANLGD GTYFHSGYLAIRQSIAAKTNITYKILYNDAVAMTGGQHVDGHLSVAQLTRQLDAEGIKKQVIVT DEIKLLNEEDGIAPGVEIRHRNELDAVQRELREISGVTALIYVQTCASEKRRRRKRDAYPDPAERL FINTDICEGCGDCSKKSNCLSIEPVETALGTKRQINQSSCNKDFTCAEGFCPSFVTVHTRDMKRPA KFEGISAGWPTSPIIPQLYDVPSRIMVGGIGGTGVVTIGALLGMAAHLEGKATRVMDMAGLAQK GGTVYSYVQLAASDEQISSTKIPAGQCELLIGADAVVAGSGAALSRLKEDALVIVNEDSTPTSEFI KSRDWYAPITDLIDRLRGRVRQGQLVSLPAARIATLLLGDSIYTNQLLLGMAWQSGRIPLLRESIE KAIRLNGTAVEKNIEAFRVGCHLASDPTLAARLLAAMPKTKTPQTLAELVEDRSARLTDYWNEA YAAKYRTLVELAAKKLPEELTGTIATQLYRVMAYKDEYEVARLLTGKSFKESIETQFGKGLRLT YHLAPPALLGGLKNVRKRAFGYWMRFPMMMLARLQWLRETFLDPFARQEERQHEQAWRDRYI AFVEALVEAPDNHNLAVAEQIAKLPAEVRGYGHIKMKAMDAAKQRWDELTPTLLKVRN	2.837405	0.017862637	up
A0A6H3T0T0	Trimeric LpxA-like superfamily	18	15	23	2	147.9	MNQFVTNTKNVIRGKYHPEFLQNEVLSDIFAHTAQTLPDKTALIEADKTLSYGELYQQALIMAQ HLALKGVKPGHIVGLWLPRGIELLKAQLAICLSGAAWLPFDMDTPADRIAVCLEDAEAVGMITT DEWYEHLAEVPQTKWTNTELQKTLSESVSLAKTTPDQPAYIIYTSGSTGKPKGIVITQKNICHFLR SENSILGIQEQDKVYQGFSVAFDMSFEEIWLSYLVGATLWIAPKSLVSDPERLCQTLKQEQITVLH AVPTLLALFPEDVPNLRIINLGGEMCPDSLVDRWALPHHQMFNTYGPTETTVSASLELLERGKPV TIGKPLPNYGMLVINSERELLEQGETGELCIFGPSVAQGYLGRPDLTADKFIENPWAMSVEEELL YRTGDLAKIDEFGQVHCLGRADDQVKIRGFRVELGEIEAALCDIDGIGTAAVILRPEDGIDQLIAFI APEIDAKQAIEIKELRHNLSQRLPPYMVPNRFEIIEEVPRLLSGKIDRKALKARPLTSVVDRSESDQ PQNPAEEILFEILNRLFPNMPIKLDSDFFDDLGGHSLLAAVLISNLREHAEYSHLTIQNLYQARRVG AIAALMLEQPEPTLFDSQIGQDNPRNQTYKWLCGIAQLVTIPVLISINILQWLAPFFTYHYFTGGT RDSIPYAIALSLLVYVSVIMSSFVLSITVKRLLMLGIGAGRYPLWGLTYFRWWLADRISNISPVYL LSGSTLLNLYLKALGAKIGHDVTISSVHIRMPSLLTIEDGVSIGSQVNLENAKVEHGHLVLGSIHL KQDSYVGSYAVLEENTVLEKQAHVNALTSIEYDTVVPEGEIWDGTPAQKIGHIDEQAKLPGRPK LSFIRKIAEYGYYGVSALIIACLFFIPIFPSFLLVDWLDVNVFNINPNNHLQIALYYFILAIPASAMM MMITAVISSGLRKIALPRLETGTYAVHGSTYYRKWFAAQILETSLQTLHGLFATIYAPTWFRMLG AKVGKNTEISTATGVIPEMLTLGEESFIADAVMLGDEEIKGGWMSLKATKIGNRSFVGNSAYIAD GTVLPDNVLIGVQSKTPDNREMYDGQTWFGSPALLLPAREAAEKYPDHLTFKPSIKRRLMRGFI EGLRIVLPAALAIGVGYMIVLDVIDVINNYNIETGLVALTLAGLLYGVGCFLIVALLKWILIGRYQ PRSAPMWTMFVWLSEGITSLYESVAIPNFLNYLRGTPMLPFFLRILGVRIGKDVYMDTADITEFD CVSIGDRAEFNSFSGPQTHLFEDRIMKIGQVNVGNDVVVNARSIILYNANVNNHAVLGPLTLVM KGENIPAKSAWIGSPAVPWVHK	2.792456	0.000221419	up
A0A6H3T2F1	HTH-type transcriptional regulator with aminotransferase domain	4	2	3	1	54.0	MTFQYQVLANQLAHRIYQDELKPHQKLISLRDFARQHGISLSTAKSCYELLEARGLIYVKPKSGY FVVARTPSSPIPDSPDFLSLPRHVSNLELHNQIQEAALQSHLVPLGSIQLTPHFIPVEGLRRSIQRAL KNCQPQDFLYCNKQGHEQLRKALSDHWREDGIYIAPEDIFITNGCMPALSLVIQKLTEVGDSILIP TPTYNGHLQLLASLKRQIVEIPADHRGIDLERLESLMQQGLAKVCLMTANYQNPLGYCFSNTEK QKIVELAAKYQCFIIEDDIFGECGYSSERPLPIRYWDREGYVIWCGSVSKSLSSAYRVGWFCLTTK LEHLKLELLVSNIGVNTPLQLGLADFIYSRAYREHLEQLRPNLMRQVEEYRSCILRAFEGIPIALSQ PEGGYALWIQLPKSVDSLALYYTAQAQGITVVPGHVFGEDERYRHFIRLNAGHELTADVRQAIM SLADWSRQQMQTVS	2.1373708	0.02105281	up
A0A6I4HS79	Aminotransferase	70	30	213	1	59.7	MGKVDYSKYAKLSPFELKDNLIELAQSKTDRIMLNAGRGNPNFLATIPRRAFFQLGLFSATESEFS FSYMPEGLGGFPRTVGLQSRFDNFILENRDKPGVVFLGKAVSYVRDQLGLDPDLFLLEMVEGILG CNYPVPDRMLRVSETIIKEYVLREMGVQGMQKRDLDLFAVEGGTAAMAYIFNSLKENKIIKNGD RIAIGSPIFTPYLEIPKLNDYQLEEVLIEADPKLGWQYPESELRKLEDPSIKAFFLVNPSNPPSVKMS DEGLAILADIVKKRPDLIILTDDVYGTFADNFKSLFAICPDNTILVYSFSKYFGATGWRLGVIALSN NNVLDKQIANLSKKEKKELEDRYSSLTTDPASIKFIDRLVADSRNVALNHTAGLSTPQQVQMVLF ALFNMMDSRQSYKKAVKSVVRERDAALYRQLGVDVPTDPNAVDYYTLVNLENTSRTLYGDEF ADWVMKNKNPTELLFRVADETGVVLLPGSGFGVQHPSARASLANLNEYQYAAIGESLRRFADE AYAEYTKTKKIK	0.2942293	0.003361679	down

A0A7U3Y047	Uncharacterized protein	33	12	17	6	60.7	MELKRVNQDFYVAGQITANDIVKIADQGIKTLICNRPDGEGADQPNVIEIEEAAQRHGLNVIYQP VISGKISDQQVTEFKQLYQNAQKPVLAYCRSGMRAISLWALAEVAPQDAALLVESGNKLGFNLK GLVPRILKRDHEPATIPCYSVVIVGAGAAGISVASSLLCREPHLDIVIIDPADTHYYQPGWTMVGG GIFKPQVTARSMTSVIPSKVKWMKAAVAGFDPEHNQVILEGCQPIQYKALVVCPGLKLNWHGIE GLVETLGKNGVTSNYRYDLAPYTWELVQQLNSGKAIFTQPPMPIKCAGAPQKAMYLSADYWL	0.4212515	0.005422655	down
A0A7U4BKB8	Atypical kinase ADCK	51	17	61	17	48.8	KQGKLKDISIHFYNTGAVLFGVKEYVPALMQYVEKYGTELHFNHQLVKVDGPAKKAWFKVVN DENAALVETDFDMLHVVPPQQAPDFIRASTLTDEAGWVSVNPQTLQHTQHANIFALGDVMNAP NAKTAAAARTQAPIVAVNVIAQLKGEKNFCEYNGYGSCPLTVERGKIVLAEFGYGGKLLPSFPK WVIDGQKPSRLAWLLKERILPPIYWQGMLKGREWMVKPEQG	MAKNASSPGKRFMKLAGMTASIATKTVSNSIRNLTADEEQKLAAKTKLFQDIGLQIADTLGEMK GAVMKVGQIASQYKDIFPPEVAKAISKLQRQAPAMPFAAIQQQVERELGKPLNVAFKSFEQEPFA AASIGQVHKAVLPSGEQVVVKVQYPGVDEACESDLKQVRLALRLMGVLKIDKKLQDQLFAEIQ	2.4948709	8.43E-06	up
A0A7U4BQ44	Uncharacterized protein	71	4	23	3	8.7	DSLSAELNYEIEAQNLEVFKTFHSKLDDKIIIPTVYKDYSSRRILTLSLEQGDSIETASSWPIEIRNTI GRRLIRALGQEMFFLKRFHCDPHPGNFAFRQDGSVIIYDYGSVKTLSNEIVYSFKRLVNAARHEDI DLIETELLELHSLAEKGKFPSDLYKLWIEVLLRPLTTTYDFAENSSHHDGMLLVKKSLKYWDVF KPSPDTLMVNRTISGHYWNLIHLKVHDNLNDLFEELVPPSN	MNSKFSVDQSNKISLKAVLEDLGDQMFEANKCPDTHPVYDQLRERLRKDRQLLDALDAQDENA NTEERSRSLDIN	4.9091896	0.043382292	up
A0A7U4DEJ2	Acid shock protein	37	4	10	4	13.9	MKMTAKIALFSAAIVTMGSLAACQSTTQPPKPEHGMMQDGPRDGHHHRMKHREFTPEQKAAW EQHRAERKARFEQIQKACEGKAVGQTVNVQVGDKTLEGTCNLRFEPKRPQPPVNAPAPVASQAA K	2.2344161	0.001327044	up
A0A7U4F8B0	Ribosomal RNA aminoglycoside-resistance methyltransferase, Gram-negative bacteria	45	10	33	10	30.1	MDKNDVVKKILESKKYENLDSDIVEKVVSISEKKYKLKEVENYSKKKLHQIWGSYYSAYPNWD KLLKKYNQGQLSIEDLLKIHSSTNERVATLNDFYTYVFGNIKHVSSILDFGCGFNPLALYQWNEN EKIIYHAYDIDRAEIAFLSSIIGKLKTTIKYRFLNKESDVYKGTYDVVFLLKMLPVLKQQDVNILDF LQLFHTQNFVISFPIKSLSGKEKGMEENYQLWFESFTKGWIKILDSKVIGNELVYITSGFQK	2.0225283	0.012510744	up
A0A7U5XU67	Peptidyl-prolyl cis-trans isomerase	70	12	49	1	25.2	MKKISLVIAASTMSLSVFAATPITNKSPAKDQFSYSYGYLMGRNNTDALTDLNLDIFYQGLQEGA QNKTARLTDEEMAKAINDYKKTLEAKQLVEFQKQGQQNAQAGAAFLAENAKKSGVITTKSGL QYQVLKEGTGKTPKATSRVKVNYEGRLLDGTVFDSSIARNHPVDFQLNQVIAGWTEGLQTMKE GGKTRFFIPANLAYGEVGAGDTIGPNSTLIFDIELLQVLPK	4.3474903	4.95E-05	up
A0A7U5XUN1	Uncharacterized protein	67	5	11	5	9.7	MSVIDRAVEKNANLSYVALKVIECFKDAGLDLNYIDDKISEFSDLSNYAALHQALRILDDKNINR LADKLGVSISDLETTLFVLNKI	0.4389467	0.02882993	down
A0A7Z1WKR3	FAD/NAD(P)-binding domain superfamily	21	8	13	1	45.4	MSEVLDVVIVGGGLVGGLTALLLAQGGVQPTVLDAAPVLDVEKTLSVMNPRVLALSQATIHLL KTVNVWDDLARQMPYTGMQVWNLNGYGEINFGHESVQRPMPEQALGSMVEPSVLNVAIQQK MLEQLTDYRTQVRVTRIEQGVGCWHLQLADGTTLKTKLLIGADGANSFVREQAFIDLDVLDYK QAAISCAIKTSKPHHYVARQIFLPTGPLAYLPMASLEESENGYWQSIVWTLPDDYADEYSALSDA EFMQLLTRESQHMLGEVLDVRSRAQFPLKARAAKQYVKDGLALIGDAAHVIHPLAGQGVNIGC LDAAVLCDALLHDLGRGVWAHEQTLMRYEHRRKGQNDAMMHSMSAIGWLESSELFPLIWARN VGLKQVEQISFLKERFMQQANGLRALQNTQYSR	2.7927749	0.0363443	up
A0A7Z2CM08	Uncharacterized protein	6	1	1	1	28.7	MILDDYLGHAANSKKLAQIAIKERRFDDAWKHLNHQKDYYLKHASRMGFSKTETLVIDSSPHE DMANVLRLEGKHKNALSSISYTYKAAYTANRPIITLEKKLEAYYNRAYKKQPFKKFLSLLKALP NSDYISVRDLVEIYFPLSPNDDEVAPKERNLSEQEIKKVNDNFLKQRSTARSKEHIGIPPPLSNKPV KAVKPSYPEPKYPTKVIEPQNDNNLILGYPASEWIIGLMVGVALLIGLIWLLSVSVR	2.4253152	0.003240562	up
A0A828SQM8	Muconolactone Delta-isomerase	23	2	2	2	10.5	MDVHIPLDMPADKANEIKAVEKAYSQDLQRQGKWRHIWRITGQYSNISIFDVESNEELHNILQG LPLYPYMDIEVMALNRHPSSVRDDDS	2.4350006	0.020024063	up
A0A828STC4	Phenylacetate-CoA oxygenase, PaaJ subunit	52	6	13	6	18.6	MQMIRHCIDQCWDVLQTVSDPEIPVLSVVDLGMIRGVEINDQQEIIVRLTPTYSGCPATDMLKAQ IVEAFTAEALTPVKVMVDLSEAWTTDWMSEAGKKKLQVYGIAPPEGLAHQCGTHVHLTNGVE CPRCKSRHTRLLTEFSSTACKALYKCQDCLEPFDYFKCI	4.5638832	1.46E-06	up
A0A829K6I4	DAHP synthase, class 1	7	2	2	2	38.8	MNALNNLLTQSNTKETPVSLPVQLKAKYPLVQTFARQIAEHRQIIQNILAGKDQRLMVITGPCSI HDPVAVLEYADRLQKLQEKVKDQIFIVMRAYIEKPRTTVGWKGFMYDPNLDGSSNLQLGLEKS RELYLQIIEKGLPIASEILSPMATGYFDDLLAWGAIGARTSESQIHREISSHMPYSIGFKNGTDGSIQ IALDAIQSAQNEHQFLGMNQQGLPSVIQSSGNPLPHLILRGANHGPNYDLASIQAIREKHKQNLPA LVIDCSHGNSGKDPLRQPEVLQQIVAERLKTQVKGVMIESHLVDGNQKISCEMTYGQSVTDGCL GWDKTEQLLLNVAKQLKASELAHSA	0.4931359	0.008049031	down

A0A829KCA3	Condensation domain	1	1	1	1	112.3	MQLVIIFICLYDAETRLICQPSYRSMCELTSMQAACWFGRSGNATLGGVAAHLYAEFDGQFIDLQ KLHLALQRLYKEHPILRLSLSADGIANIMSEKTQQILEVDNFSKLNDHQIEQMLMQKREQWTHQ KLDLSQGQTARFSISVLKDNIFRFHVDTDMIAIDPSSFLNLMEDLSLFYEDPEISFSRPPNFFDWYQ KIRTDPDLKKLNQRDRLWWKQRLPHISPAPSLPFIHQEFKTAKSDRLSTWLSPEERKALQQLARE QRITVTNLILGLFAYTLGHTTKDHSFRLNIPTFWREPVLKNVEGTIGDFANLVILDVDMNKTTTL AAFCKQIANQMLELLEHSHYPGVNVLRDLSRYHGSAQIAPVVFTAALDLENDNLLSERVRRVFG SMNWVISQGPQVALDAQVAHVDDGILVNWDIRLDALPKEWITNLFESFIHLLKNLAAHPEQLNT QIISPAQNTSSDRTSQKPLNALQQAYLLGRTQALPLGGVAMQEFRQYHGTMDIVLLRQRLTEMV RRHDSLRTYIDKNRLVQYVSDQVSVNLKEIDLTTWEPEHASHHIESYKNSYTHELFDLNQSPWNI TVFLLKNNLLTIFVRFDALILDGRSIASLMLELFDGQQHDIQTQIEKNEVENSLSVYQADMAYWE RKFSKLSAIPALPWKTPLQHLPTSRYQRNSLVIEKDQFKQLSKIGAKHSLFKNSVIMALILEVLSH WNTEKSLCVAVPTLPLYAGPFSNSSTFIAVEWKALDQFAEQANRLQTEVLEGLQHLSFSGVDLA RLLFEKVGTAPVLPIVITNGLSWPVLSESHPIQQLDGLTQTPQVAIDIRFSTRNDGALIFDIDYAQE AFPPNMIDDFLDALQLAIKQIIGSEIFSFDLSNFFSELQNKRPYFKNNESDHSSIPLENNAKQQNQL LDIYLEVIGHTPNKEVDNSTHFTHLGLRPHHLKAVSKRINETYAIQLSPVQLIQCRNIADVEKLLT AH	2.4822485	0.005282474	up
A0A836LYR7	Ankyrin repeat family protein	8	1	2	1	19.1	MHKSNIIRQNQENNILIRNAIKKHELITVKKIFSEFPGLLSIDTPFGSWLHVAASSGALEIVKYLITE GLSPNKKGGTFGGNSLNTAVSNGHIDIVEYLLLLNVEMDTTEPERNPLFGAIMKGSLPIVEKLISH DIDYKISYTGDYMNNMDAESFALERGEIEIANYLNSLK	5.7643192	0.024189459	up
A0A837Q8N8	Type VI secretion system, RhsGE-associated Vgr family subset	2	2	4	1	122.6	MQMSVSSILERLGLVSQNRAVHIQFSNQSLNQQVFLQRIEGEHTLNQGSVAELLCLSTNAHIALK QFIGCQVAVDQVTDTGQFFRTTGIITEASQGQSDGSLTIYNLTLKDPTALWHKRRNSRVFMNKS VRDISEILFKEWQEKSPLFASSITLDTSGLTKDYDVRPFVMQSNESDYDFLTRLWRSEGINWLVD ESQLFIADPNASIQPQVLRLIDDNQNYQALERRSIRYQRSSATEQFDTITQVKAERRLQPTSVHVQ RWQADALQQEEGSGSVQGTQKHSEHYDNASLNLEDAWHVSPAWMQDLNGEDQATASGNSQI EQLNQHINAYHHLSSKQFTVAGNVRDAQVGYWFELNDHPELDQHDSADKEFLILSKHYYNQNN LPKELQQQLERLLPQGKLKAAQLDSQNPEQRHFAELNVVRRNIKAVPEYNPLEHRPAAHPQRAR VVGLEGESIHVDQWGRIKVRFLFTRADDHSHDGGAGSNDNDTDSAWVDVLTPWAGAGYGARF LPRVGEIVVIDFFDGNIDRPFVVGRIHEAERHPTQFDQKGQLPDTKKLSGIRSEEVDGKGFNQLRF DDTTGQISAQLQSSHAASQLNLGNLSHPKDKAESDGRGEGFELRTDQWGAIRAGSGLLVSTHKQ DQAQGVHLDASEAKQQIEGGLNNAKALSEVAKNQQTDPLDMLENIQTFLEVLKQEDPKKAAEF QSAVMLLASPKSIAVSSNEDIHLSANGQLTQSAGDSINISTQKNIVSHASQKISLFAAQEGARLFA GQGKVEIQAQGDGLDVIARKGVQITSIEDTVYITSPTEINLTANGSQVKLNGSGIFPVTGGKLEVK AGQHLFMGGGKVDVKVPKLKELNITKKYSNKLDVYEIFPTNKFTDLTMSVKGSDGVVEEHKID KYGRSPRISDAEPKELEVLVGGDVWNYFIKNIGGTKDDPFYFKFLDYVGKPIVGMECYLLDNSL NIVKKEVTDGNGEVEFVYTDEYLPIMGVMKFDDNTVKPICYVNHHNCREYIFISPKVKANLALL EEGQKGEYLRAGYRVKEGESLQNIADKYSITTDEIISLNTGMENIDVNTKLVEGAYIKLPNYINRE EWKNG	0.2476975	0.003227445	down
A0A8E4GYA6	Beta-lactamase	72	16	58	1	27.5	HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRVDAGQE QLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHN MGDHVTRLDRWEPELNEAIPNDERDTTMPAAMATTLRKLLTGELLTLASRQQLIDWMEADKV AGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRILVIYTTGNQATMHERNR	2.2819141	0.009981889	up
A0A9P2P3T1	TIGR01244 family phosphatase	18	7	9	1	60.6	MELKRVNQDFYVAGQITADDIVKIADQGIKTLICNRPDGEGADQPNVIEIEEAAQRHSLKVIYQP VTSGKISDGQVTEFKQLYQNAQKPVLAYCRSGMRAISLWALAEVAPQDVALLVESGNKLGFNL KGLVPRILKRDHEPATIPCYSVVIVGAGAAGISVASSLLCREPHLDIVIIDPADTHYYQPGWTMVG GGIFKPQVTARSMASVIPSKVKWMKAAVAGFDPQHNQIILEGCQPIQYKALVVCPGLKLNWHGI EGLVETLGKNGVTSNYRYDLAPYTWELVQELNGGKAIFTQPPMPIKCAGAPQKAMYLSADYW LKQGKLKDISIHFYNTGAVLFGVKEYVPALMQYVEKYGSELHFNHQLVKVDGPAKKAWFKVV NDENAALVETDFDMLHVVPPQQAPDFIRASTLTDEAGWVSVNPQTLQHTQHANIFALGDVMNA PNAKTAAAARAQAPIVAVNVIAQLKGEQNFCEYNGYGSCPLTVERGKIVLAEFGYGGKLLPSFP KWVIDGQKPSRLAWLLKEQILPPIYWQGMLKGREWMVKPERG	0.4814324	0.004751295	down

A0A9P2UE60	Acetate-CoA ligase	41	17	31	1	72.2	MNEIYPVPEEFKKTARTVEADYFKRYQHSIENPDEFWAEQAKIVDWIKPFTQVKNTSFDKDNFKIEWFADGELNVSANCLDRHLKEHPHKPAIIWEGDHPSRHKIVSYKELHDEVCRFANVLKKYGIGKGDRVVLYMPMVTEAAIAMLACARIGAVHCVVFGGFSPDSLASRIEDSQAKLVITADSSLRAGKLLPLKENVDLALALPGTECVENVIVVYRNANPIEMKPGRDLWYHLIIMEVDANCPPEPMKAEDPLFILYTSGSTGKPKGVLHTTGGYLVYVASTFKEVFDLKQDDVYWCTADVGWITGHSYLIYGPLANGTTTLMFEGVPQYPTWARLGHVVDKHKVSILYTAPTAIRAMMREGDSYVRESNRSSLRLLGSVGEPINPEAWNWYYNVVGEGRCPIVDTWWQTETGGILIAPLPGATALKPGSATRPLFGIQPAIVDGEGNELEGAAEGNLVIKDSWPGQMRTIWGDPDRFIEAYFSTFKNTYFTGDGARRDEDGYYWITGRVDDVLNVSGHRLGTAEIESALVSHEAVAEAAVVGMPHDIKGQGICTFVTLQAGVPESEELRKELISWVRKVLGPVASPDALHWAPALPKTRSGKIMRRILRKIAANELDSLGDTSTLAEPAVVDQLITTVYPDROK	6.6664201	0.006090192	up
A0A9P2UEN7	1,2-phenylacetyl-CoA epoxidase, subunit C	55	13	31	13	28.8	MNHSVLSKFLLHIGDSQLVLSQRLAEWCGHAPELEIDIALANIGLDLLGQARNFLTLAGQYDEAKRDEDQLAYFRTEREFLNLLLCEQPNGDFAQTIVRQWLMDHYHLHLFTALAQSSLPELSALAVKSLKEVKYHIRFSTSWMERLSLSTDEAHQRVQDGLDNLWRFTAELFELSADEKALVAEGVIPDFSNEKEQWNQTIADELKRFELNVAVNGAYRRGAKQGLHTEHLGYLLAEMQCIQRTYPGMTW	4.1423264	0.00939901	up
A0A9P2XHD2	Phosphotransferase enzyme family protein	56	16	38	16	43.3	MSVIDVGGEVREGEELDIGAVENWLKNQGVELVGPAVVTQYTGGASNWTYRLKYENTDLILRRPPKGTKAKSAHDMAREYMVQKNLAPYYPVLPKMVALCQDESVIGCDFYVMERIEGIIPRAKLPPELGFNEDDVHELCVNVIDKLIELHQVPYENTPLAELGKGTGYCRRQVEGWDKRYEKVRTINVPSFKYVRKWLNDNIPQDSTTCIIHNDWRFDNVILDPEHPTEVIGVLDWEMATLGDPLMDLGSALAYWVEPTDNMIFRSTRRQPTHLKGMFSRKEVVDYYLQKTGLEPQNWTFYEVFGVFRLAVIAQQIYYRYYHKQTRNPAFKDFWIVIHALHIRALKLIAQQKLQESEFAQQSLQKIQGILRR	2.3901882	9.91E-05	up
A0A9P2XJK2	DNA gyrase subunit B	61	40	149	3	92.1	MSSESQSASQTEQTNEKAYDSSSIKVLRGLDAVRKRPGMYIGDTDDGTGLHHMVFEVVDNAIDEALAGHCDEIIVTIHEDESVSVSDNGRGIPTDIHPEEGVSAAEVILTILHAGGKFDDNSYKVSGGLHGVGVSVVNALSSKLHLTIYRAGQIHEQEYHHGDPQYPLRVIGETDNTGTTVRFWPSAETFSQTIFNVEILARRLRELSFLNAGVRIVLRDERINLEHVYDYEGGLSEFVKYINEGKNHLNEIFHFTADADNGIAVEVALQWNDSYQENVRCFTNNIPQKDGGTHLAGFRAALTRGLNQYLENENILKKEKVNVTGDDAREGLTAIISVKVPDPKFSSQTKEKLVSSEVKPAVEQAMNKEFSAYLLENPQAAKSIAGKIIDAARARDAARKAREMTRRKSALDIAGLPGKLADCQEKDPALSELYLVEGDSAGGSAKQGRNRKMQAILPLKGKILNVERARFDKMISSQDVGTLITALGCGIGREEYNPDKLRYHKIIIMTDADVDGSHIRTLLLTFFFRQMPELVERGHIYIAQPPLYKLKKGKQEQYIKDNDALETYLISNAIDELALHISADAPAITGEALAKVIQDYQVSQKSLQRLTLRYPASLLDALLEVDAFKADQNHDQAYVQQWADQVREAVQRLQPSLRPEITLETFERENAQGEKSAHYWPRVTVYVHNLPHAYLLDAGLLNSAEYARLLKNSKSWFKLIEDGAYLQKGDRRIQVANFHQVWQHILQDSRRGMMIQRYKGLGEMNAEQLWETTMDPENRNMLQVTIDDAIEADRMFSCLMGDDVEPRRAFIEENALNADIDA	2.311472	0.006567827	up
A0A9P2XK89	Bacterial transferase hexapeptide family protein	30	4	9	4	20.9	MKKKLRKLIYFILPCIRLFLNLFFKRKYLEGRFFSKSLSGYVWAVRSIWVKNILRLSKPTPFPTALTCSISNPYNIHFHPDDLNNFQSPGTYFQNFSAHIYIGKGSYIAPNVGIITSNHDLADLESHTEGKDVVIGDKCWIGMNSVILPGVVLGNGTIVAAGAVVTKSFKQGNIVIAGVPAKIIKEIK	2.3572579	2.78E-06	up
A0A9P3CXB6	Dolichyl-phosphate-mannose-mannosyltransferase family protein	13	5	10	5	63.3	MQQWLRSSKFLLIFLPIWLFVLSWIRPLSVPDEGRYGDISRTMFESGDWLTPRIDGLPFMHKPPLLHWLSSMFMELFGVHVWVLRLVPVLAGTLMLVGLFLFVKKHISESVAQLTVIILATNLLFFGSSQYINHDLLLASWITISVLCFVDFTISAQKSILFLGYIAGAAAFLSKGLIGILIPGMILLPWLIYTKQWKKIPSLLNPLAILLFLLIVSPWLYLVQSKYPQFLHYFFIDQQFNRFSSKEFNNKQPWCFYLIILFVSFLPWLFASRFTSIKTIFKDYKSCSLLALFVWWFVSVTVFFSIPPSKLAGYILPAVPPLAIFFALVMNKVLESSNKTRLQTWGIPVFTILVGIGVSATPHFIRAHQPFFQNQAIFIYLIGALLIVLPLVLVGLYKKQKLKYLTYIFISLIVLCSAVPFAVRILDTKNNVGQTDFAEYIAPSTKIVFYNYYFYDVPFLLKLKQPVYIVNQWDTVHSDSASLEIKDGLLFEPQLKKYLWSEQQLQDALMQKQDLIVISQPHNFATKDPSVKTLHYRNYDVFIFHPSK	3.9504132	1.66E-07	up
A0A9P3CXM7	Nucleotide sugar dehydrogenase family protein	64	20	77	16	47.1	MQLADLRIAIIGLGYVGLPLAVEFGKKGPVIGFDINQNRIDELKSGKDHTLEVSPEELQKAEQLSFSANLDDLKTSNFFIVTVPTPVDQVNRPDLTPLKKASETVGQALKKGDIVVYESTVYPGATEEVCIPILEKVSGLKFNQDFFAGYSPERINPGDKVNTLTKIKKITSGSTPEVANTVDAVYASIITAGTHKASSIKVAEAAKVIENTQRDLNIALVNELSVIFDRIGIDTLDVLEAAGSKWNFLPFRPGLVGGHCIGVDPYYLTHKAEEVGYHPQVILAGRRINDNMARYVARNTIKLMLQNGIDVPRSKVGVLGVTFKENCPDIRNSKVADLIKELEFWGAQVVVADPWADAEEVKHEYGVELGTVNAQNPVDSLIVAVGHSEFRSLSASELRSYVKAEKPVLADVKSLFDRTQMSDVGFTVFRL	5.9515789	0.000445966	up
A0A9P3CY71	Bacterial transferase hexapeptide family protein	41	5	7	5	21.9	MPCYSIDGVIPVVSPDAFVHPTAVLIGDVIIEAGVYVGPFASLRADFGRIHIKQNANIQDSCTVHGFPQSVTLVEEMGHIGHGTTLHGCRIGKNVLVGMNSVILDYAEIGENTIIGANSLVKTKDIIPANVLAMGSPAKVARDLSEQEKKWKTRGTQEYIELAQRCLNSMQEVQPLTSELDDRLTYKDFSSSNYQIKQDSV	2.397699	0.002278304	up

A0A9Q1N7W9	Uncharacterized protein	55	10	18	10	23.8	MNNEYFKLYTDSQFLSPYAFTVFVGLHEKQIPFEIAAIDLGQQGQFETSFVEKSLTAKVPVLEHN DFALSESSAILEYLEELYPDTAIYPKDIQARARARQIQAWLRSDLVALRTERPTDVIFIQPKSTPLS EEGKKAAEKLFFVAEKLLASDAEFLFGSWSIVDAELALMLQRLIQNGDAVSERLKNYALQQWQ RPSVQKWLALRHK	2.7425208	0.015721617	up
A0A9Q1NA93	Uncharacterized protein	77	14	44	1	29.0	MNISDNTPQGQLSSQQFYRQYSANALLPELDWQSIFPHSKLSEAHIKALNTIYQCAVPLALNVFH DLNFDVFAPAAYHPQGLGLFDKLAQQEENFLKVLTAESENLDHETRHQIWSMLLRGGAVLVFK AWLGHVKLGENQLDMTQFDELSDLLFIKTPPHQLAERLHVDEKAKLDHIFLMYGNDIFLDRFNS LETAALFVDLGVYDAAFLSLRDDCVAEYLKSKGYVTQEQIDDLQCALNPLYCDSLTPKQDCLA	2.2016594	0.024916312	up
A0A9Q1RV14	Poly-beta-1,6 N-acetyl-D-glucosamine synthase PgaC/IcaA	4	2	4	1	44.7	MIGAIIFYWKERKAPPYDQPAPLESYPKVAVLIPCFNEGDNAEETITHALKLDYPHFEVIAINDGS SDNTGEVLDRLAEQHEKLRVVHLAQNQGKAMGLQAGSLMTDAEFLIGIDGDALLDPHAAKWM VRHFLQNPTVAAVTGNPRIRTRSTLLGRIQVGEFSSIVGMIKRAQRTFGRLFTVSGVITAFRKSAV HQVDYWSPNMLTEDIDITWKLQRAGWDIRFEPNALVWILMPETLNGLWKQRLRWAMGGAQV LIKNIDVFTKPKLNFLWPLMFELCLTLVWSYLMLAMALLWLVHFILPVPALAVVSSPFLPYGSGI LLGATCLIQFALSKWMDSRYEPHLGKNYFWMIWYPLVFWLITISATIVAFPKVLRRGDEKRARW VSPDRGIRG	2.4326443	0.039103683	up
A0A9Q1S0P9	Phenylacetyl-CoA epoxidase, subunit B	45	4	12	4	11.3	MEDKNNWSLYEVFVRSKQGLSHRHVGSLRAPDDEIALQHARDVYTRRNEGISIWVVRSELIKSS QPDEKAEFFDPSLDKVYRHPTFYHIPDGIEHM	3.8485288	0.000984997	up
A0A9Q1W4V0	Poly-beta-1,6-N-acetyl-D-glucosamine N-deacetylase PgaB	54	27	96	27	75.7	MITRFASPLLNLTLGLALAGLSGMVLANPPKIDASTLTVIGYHEITDTKNALIPQYAVTTQQFTEH VDWLQKNGFHFITVDQLIRAHQGKAALPTKPVLLTVDDGYQSFYQNAYPVIKAKKIPVVLAVV GSWLEPKAGQKVDFSGEEIPRDKILSWGELKEMQDSGFVEIASHSYHLHRGITGNPQGNSEPAAT TRFYDVKTKTYENDSQYQARIYNDLKKNNQLLKEHGIRSPRIMVWPYGRYNMQTVQIAKKLG MPITITLDDGADHAKQSLQNMSRILVEGGMSTNDLAQEIKNRELNLTDNNRPQKIMHIDLDYIYD PDPQQQERNLGHLLDRINAMGVNTVYLQAFSDPDANGSADMVYFPNRHIPMRADLFNRVAWQI QTRTPVSRIYAWMPLLAWELPKTDPVSKDLVVTEQAKAGEHLNMGYIRLSPFSPEARQTIREIYQ DLAKSASFNGILFHDDVTLSDYEDASPDALKAYAKQGLPTDLAKIRENDQDLQKWTAYKTKYL DDFAMQLVEDVRQYEPFLLTARNLYAQVALKPYAENWYSQSLEESLRRYDFTAIMAMPYMEQ VDNADQFYKDMIDRVKKYPNGIKKTVFELQATNWRNNEKVPSTEMAATIHSLYQQGAMHVAY YPDDPIKDHPDVNVMHKAFAEKSSRLVP	3.6960134	0.002657392	up
A0A9Q2E0D7	Trimeric LpxA-like superfamily	35	4	13	4	20.5	MSFYQHETAIVDNGAQIGEDSRVWHFVHVCGGAKIGKGVSLGQNVFVGNRVVIGDHCKVQNN VSVYDNVTLEEGVFCGPSMVFTNVYNPRSLIERKDQYRDTLVKKGATLGANCTIVCGVTIGAYA FVGAGAVVNKDVPAYALMVGVPAKQIGWMSEFGEQLDLPLQGQAQAICSHTGAVYQLHGTTL TKQG	4.1537782	0.000199345	up
A0A9Q4SH60	Metallo-beta-lactamase	29	4	6	4	26.0	MFFKQFFEKESSTYTYMLGCEETREAVLIDPVASDIEIYAKELEQHQFTLIYTLDTHVHADHITAA NLLRERFHCKSVLHRNSEVSCGDILITDGCMLKVGDLSIEARYTPGHTNACTSYLVGNMIFTGDA LLIDGCGRTDFQQGNAGTLYDSIHKQLFSLPDETIVYPGHDYKGRLSSTIGYERLNNSRLGQNRS REDFIKLMNNLNLPYPKQIDKALPANQACGSISQL	0.4674651	0.003166142	down
A0A9Q4XE51	Bacterial sugar transferase	47	7	10	6	23.4	MKRLVDIVISLIALTVLSPIFLIVAYKVRKNLGSPIFFYQERPGKDGKLFKMIKFRSMKDAFDAQG NPLPDEARITPFGQKLRSTSLDEMPQLINVLKGDMSVVGPRPMLKDFVALYSPEQARRLEVRPG MTGLAQVSGRNELDYEERFKCDVWYVDNHNVWVDFKIMFKTVKVMLRREGINAPGHVGPSLF KGNDTQENVDSSVK	2.8668673	0.000856601	up
A0A9Q6DAC3	Domain of unknown function DUF306, Meta/HslJ	65	17	164	2	40.7	MKIKYLILALLPFSLMACQTVSNTQAPIVSEQQQNLATTLSEYTWTYQNVKASKPLILNFNADGK LAINTGCNGQGGTWKVEGNQLITSPLASTMMACQDDLMKQEQLSNSIFSEAKLPIEISNNNGLVI LSVTDKAGQKHIFQGEKATNTQALTDYSWSYQPENTKKPIVLNFTNDRLSIDTGCNRQGTTWK VENNTIVTTDVMSTMMACEPALMKQEQFSSSLFQKRAIPFELNTTNVDQPTLTVTDAQGQKYTF TGKMTPEAKYQSEGKTVFLEVAPETKSCTGVAPQTCLQVREVKYDDKGVKTYADKNWSLYYG QIEGFEHNPNQRVILRVKRFEVKNPAADQSSQADVLDMVVEQELVK	0.3685637	0.00855052	down

A0A9Q6DWC7	ANL, N-terminal domain	18	14	19	1	148.0	MNQFVTNTKNVIRGKYHPEFLQNEVLADIFAHTAQTLPDKTALIEADKTLSYGELYQQALIMAQ HLALKGVKPGHIVGLWLPRGIELLKAQLAICLSGAAWLPFDMDTPADRIAVCLEDAEAVGMITT DEWYEHLAEVPQTKWTNTELQKPLSESVSLAKTTPDQPAYIIYTSGSTGKLKGIVITQKNICHFLR SENSILGIQEQDKVYQGFSVAFDMSFEEIWLSYLVGATLWIAPKSLVSDPERLCQTLKQEQITVLH AVPTLLALFPEDVPNLRIINLGGEMCPDSLVDRWALPHHQMFNTYGPTETTVSASLELLERGKPV TIGKPLPNYGMLVINSERELLEQGETGELCIFGPSVAQGYLGRPDLTADKFIENPWAMSVEEELL YRTGDLAKIDEFGQVHCLGRADDQVKIRGFRVELGEIEAALCDIDGIGTAAVILRPEDGIDQLIAFI APEIDAKQAIEIKELRHNLSQRLPPYMVPNRFEIIEEVPRLLSGKIDRKALKARPLTSVVDRSESDQ PQNPAEEILFEILNRLFPNMPIKLDSDFFDDLGGHSLLAAVLISNLREHAEYSHLTIQNLYQARRVG AIAALMLEQPEPTLFDSQIGQDNPRNQTYKWLCGIAQLVTIPVLISINILQWLAPFFTYHYFTGGT RDSIPYAIALSLLVYVSVIMSSFVLSITVKRLLMLGIGAGRYPLWGLTYFRWWLADRISNISPVYL 3.635188 1.10E-05 up
							LSGSTLLNLYLKALGAKIGHDVTISSVHIRMPSLLTIEDGVSIGSQVNLENAKVEHGHLVLGSIHL KQDSYVGSYAVLEENTVLEKQAHVNALTSIEYDTVVPEGEIWDGTPAQKIGHIDEQAKLPERPK LSFIRKIAEYGYYGVSALIIACLFFIPIFPSFLLVDWLDVNVFNINPNNHLQIALYYFILAIPASAMM MMITAVISSGLRKIALPRLEIGTYAVHGSTYYRKWFAAQILETSLQTLHGLFATIYAPTWFRMLG AKVGKNTEISTATGVIPEMLTLGEESFIADAVMLGDEEIKGGWMSLKATKIGNRSFVGNSAYIAD GTVLPDNVLIGVQSKTPDNREMYDGQTWFGSPALLLPAREAAEKYPDHLTFKPSIKRRLMRGFI EGLRIVLPAALAIGVGYMIVLDVIDVINNYNIETGLVALTLAGLLYGVGCFLIVALLKWILIGRYQ PRSAPMWTMFVWLSEGITSLYESVAIPNFLNYLRGTPMLPFFLRILGVRIGKDVYMDTADITEFD CVSIGDRAEFNSFSGPQTHLFEDRIMKIGQVNVGNDVVVNTRSIILYNANVSNHAVLGPLTLVMK GENIPAKSAWIGSPAVPWVHK			
A0A9Q7DS60	Aldehyde dehydrogenase domain	56	29	123	3	74.2	MPHLASYVYGTWHSSDEELRTVYHAITGEAIYAVSSHGVDMKRVVQYAKQNGSELANWTFHQ RANALKQIAQHLLERKEDFYKLAYATGATRKDAWIDIEGGIQTLFAYSSLVRRELNDEKIITEDS WIQLSKNGTFGAKHILSPKAGVAVHINAFNFPIWGMLEKIAPTLLAGVPCIVKPATDGAQLTQAV VKAIEETHVLPKGALQLICGQTYDLLEQLGPQDCVTFTGSAYTGQKLRNHPHLNKYSIPFSMEAD SVNSAILSPEANEETVDLFVREVFREMTTKAGQKCTAIRRAFVPENLLATVQEKLTAKLAKVVV GDPQKEETTMGALASIKQKHDVAEKVAELSKDAKIVFGGNDSFTFNADHPEKGAFFAPTLLVCE QPLQATNVHTTEAFGPVCTLMPYQNIEELADLVSRGEGSLVASVVKNNDENIEQIIQKIAPWHGR VHVLDAESAKESTGHGSPLPHLVHGGPGRAGGGEELGGIRAVKHYMQRTAIQGSPNSLTQITHS WTAGSKVNEDRVHPFKKSFDELVIGERLLTARRTVTEADIVNFACLSGDYFYAHTDKIAAAESFF GERVAHGYFIVSAAAGLFVDAAQGPVIANYGMDNLRFVEPVKIGDSIQVELTCKQKTPKPQKDA SQPAHGVVVWDIKVKNQRGELVATYDILTLVAREA			
A0A9Q7I520	Uncharacterized protein	45	4	11	4	8.9	MASTAAERKAKQRQEMLKKGFTRKDLWLSKESLEVIEKFKSEHKLSSNDEAINLLLKTIVVIEKF KSEHKFNTIDE	3.4312351	0.008868339	up
A0A9Q7ZZR4	Domain of unknown function DUF4468 with TBP-like fold	51	9	22	8	19.4	MKKILLAGFLGLGLAGCATTPQQPSEPVKFEKVYQIDGLKQGQIYDGARQWFATAFRSANAVIQ YEDKTTGSIIGKGNMPYRCSGFADCMTVTAGDRVDFTVRVDTKDGKMKVSYDNLTHYKPAQV ISGVRYNETNRPITEDYPSAKIIMDELNKSSDQMAEKIKTQQKINADW	4.9651379	9.75E-06	up
B0V8Q7	SLC26A/SulP transporter	6	3	5	3	79.9	MVVFMPALELKNRFHVNDLLSGVVVFLVALPLCLGIALASGAPIISGIIAGIVGGIIVGLLSGSHISV SGPAAGLTAVILVQLDQLGGNYAAFLLCIVFAGILQILFGVFKLGFFANFIPNNVILGLLAAIGAILI VTQLPYLFGLTDFSWKEVWTATPDTFIQKFDAGAALIGLLSLFLILAWDSSPLKKLALPSALIAVV LAAVFNFVLISIGSSWAVQSNNLIQLPNILQAPEEVLVFPDFSYLAEPLIYTGAITLAIVASLETLLN LEAADKLDPQKRSSPPNRELWAQGAGNIVSGLIGGMPVTSVIVRSSVNANTGARSKCSTIIHGVL LLLAILFFVPLMNMIPLSALAAILIVTGFKLTHPKLFKQLYQKGWRQFLPFIITLVAILLTDLLTGIL VGLFTSSAFILYGNFNKGVRVYKEKHLHGIVTRIELPSQVTFLNRSALISALEHIHKDQQLIIDATQ CDSIDPDIYQVIQDYQNETAVKRQVDLKLIGFKQHYEEVDDAVLDIYISTRDLQRKLSPQQVITLL KEGNERFVKNERLQRDIYRQIRVTADEGQHPIAAVLGCMDSRAPTEMIFDVGIGDLFSLRIAGNIA GQKVLGSLEFACQAKGSKVILVLGHTDCGAVTSACQLRLQQKQISDVKEMPHIQYVLGPLMHS VESVYDIMQPRELNKTFVNQVTAMNVHYNIQYIINNSTVLKDLLDRGEIAIVGAIYDVKTGHVEF LDA	2.3762185	0.003365344	up

B0VNB8	Acetyl-coenzyme A synthetase	37	17	30	1	72.1	MNEIYPVPEEFKKTARTVEADYFKRYQHSIENPDEFWAEQAKIVDWIKPFTQVKNTSFDKDNFKI EWFADGELNVSANCLDRHLKEHPHKPAIIWEGDHPSRHKIVSYKELHDEVCRFANVLKKYGIGK GDRVVLYMPMVTEAAIAMLACARIGAVHCVVFGGFSPDSLASRIEDSQAKLVITADSSLRAGKL LPLKENVDLALALPGTECVENVIVVYRNANPIEMKLGRDLWYHLIIMEVDANCPPEPMKAEDPL FILYTSGSTGKPKGVLHTTGGYLVYVASTFKEVFDLKQDDVYWCTADVGWITGHSYLIYGPLA NGTTTLMFEGVPQYPTWARLGHVVDKHKVSILYTAPTAIRAMMREGDSYVRESNRSSLRLLGS VGEPINPEAWNWYYNVVGEGRCPIVDTWWQTETGGILIAPLPGATALKPGSATRPLFGIQPAIVD GEGNELEGAAEGNLVIKDSWPGQMRTIWGDPDRFIEAYFSTFKNTYFTGDGARRDEDGYCWIT GRVDDVLNVSGHRLGTAEIESALVSHEAVAEAAVVGMPHDIKGQGICTFVTLQAGVPESEELRK ELISWVRKVLGPVASPDALHWAPALPKTRSGKIMRRILRKIAANELDSLGDTSTLAEPAVVDQLI ATVYPDRQK	2.1841252	0.0030777	up
B0VNR0	Arc-like DNA binding domain-containing protein	27	3	5	3	11.7	MSKNGGHLTVQYNLRWSEELRDKIADEAKKNTRSMNQEIIARLEHSFRSESASKPFLSFDKDTSH LVIGDAEERKRLAQIAAKAVFDALGQSLDQDDDEKKAP	2.0431226	5.62E-05	up
D0C6V6	Muconate cycloisomerase 1	44	9	14	1	40.2	MYRTIETILVDIPTIRPHQLSVTTMRTQTLVLVKITTTDGIVGWGEATTIGGLNYGEESPESVKAN IDTYFAPLLASVKDLNVAQTLKLIRKNINGNRFAKCAIQTALLDIQAKRLSVPLSEVLGGRLRDSL PVLWTLASGDTEKDIAEARKMIELKRHNTFKLKIGSRPLQHDVDHVIAIKKALGADVSVRVDVN RAWSELECIHGIQQLQDGGIDLIEQPCAIQNTEALARLTQRFDVAIMADEALTGPDSAYRIAKNH GADVFAVKIEQSGGLIEACEVGKIAGLAGIDLYGGTMLEGPVGSIASAHVFATFETLAFGTELFGP LLLTEEILKEPLRYENFELHLPTAPGLGIEIDEDKIEKLRR	2.7581104	0.000125252	up
G1CBP8	histidine kinase PmrB	32	10	23	10	50.7	MHYSLKKRLIWGTSIFSVILGCILIFSAYKVALQEVDEILDTQMKYLAERTAEHPLKTVSSKFDFH KTYHEEDLFIDIWAYKDQAHLSHHLHLLVPPVEQAGFYSHKTAQGIVRTYVLPLKDYQIQVSQQ ERVREAFAWELAGSMFIPYLIILPFAIFALAAIIRRGLKPIDDFKNELKERDSEELTPIEVHDYPQEL LPTIDEMNRLFERISKAQNEQKQFIADAAHELRTPVIALNLQTKILLSQFPEHESLQNLSKGLARIQ HLVTQLLALAKQDVTLSMVEPTGYFQLNDVALNCVEQLVNLAMQKEIDLGFVRNEPIEMHSIEP TVHSIIFNLIDNAIKYTPHQGVINISVYTDPDHYACIQIEDSGAGIDPENYDKVLKRFYRVHHHLE VGSGLGLSIVDRATQRLGGTLTLDKSLELGGLSVLVKLPKVLHLHETRA	3.8550336	5.55E-07	up
H6UQA3	Transposition protein C	55	13	31	13	35.0	MEKYEHLAEHVLEIMQLSDSERIETLFTDRWIGYKKAITIMNTLTDILNRPRKLRPECLLIVGDSN MGKTTIIHEFARQYYTKTVSDADMDLLSVTKPVLPILAPAKANVKELYINILNHFFVPFRASDPEA KLRNQAVHLMRKYETKMLIIDEIHNCLTGSAKLLPEVMNTLKNLSNELSLNIVGVGTREAITILH TDPQYASRFDVVNLPKWELNQDFLRLLVSYVRLLPLKKQSNLASKEIATLIFEVSGGNLGDLNRL LVECAKEAILQGDEEITYDIVHKFKWLKPTEGLRNIRNINLSLS	2.4517581	0.021356976	up
H6VX66	Zeta toxin	63	25	228	25	56.3	MTQKNELDTKYAVIVAGGNGAGKSTLIDNVIIPKFNSLNLDINFINADVWQLQHFGHFDNTNPT HAREAQKWAEAERQKHLDEGRSFIAETVFSHPSKVDLIKEAKSKGFYVVLYHIHLENSDIALDRI KDRVRKGGHDVDEDKVKARYERVLPLVAEATQYADLTFVLDNSVRDRPHQQVFKLEYGKITAI DNNVPDWAIKAYEKQLTDYLGLDQATKISNTNEDLTMSNTKEKLGFEYNARLLANDIQPQHRE TVVANYRKNFVEHVANSAAVAGNSHKLDDVASLINGTTVGGHSVKDQRQVLNLIDASNELVN MVRNGNFALNKSTYLKVNGIVADRESIEAGVLRGEGVEQSFTPDVGIRHFRTHRPMKTEEDAPA LNKFMQEGFDHINSLKNPLEKGIATFLYGSLNQFTFEGEKRTAHLMMNGVLMSAGLDAISIPAD KAIDFRQKMVRFYESKNADEVMEFLADLHPALNNTKKLDAEKEKKSENDFGRSFQ	3.8847758	0.020245792	up
N0A436	L-lactate permease	13	6	10	1	62.3	MFKILRYKNSPRHFKEMTMLNMWQQLYDPLNNIWLSSAVALIPIIFFFLALAVFRLKGSIAGTGT VIIALLIALFFYQMPGQMAFASIIYGFFYGLWPISWIIIGAVFLYKISVKTGQFEVIRSSILSITEDQRL QMLLVGFAFGTFLEGAAGFGAPVAITAALLVGLGFKPLYAAGLCLIVNTAPVAFGAMGIPIIVAG QVSGVDTMEISQMVGRQLPFLTIIVLFWIMAIMDGWRGVKETWPAVLVGGGAFAIAQYLTSNFI GPELPDITAAIASLVSLTLLFRVWKPKHIFRFEPEAGQTLAQQPTTVQRYSIGKIAKAWSPFAILTV MVTIWSVKPFKALFAKDGALEHWIFKLEVPYLHKLVEKMPPIVSEMKPYEAIYKFDWFSATGTA IFIAAIITVIFLKMKASEAVTTFGETLNELKTPIYSIGMVLAFAFIANYSGLSATLALALSHTGHAFT FFSPFLGWLGVFLTGSDTSSNALFSALQATTAQQIGIPEVLLVAANTSGGVTGKMISPQSIAIACA AVGLVGKESDLFRFTVKHSIIFTVFVGIIITVQAYLVPWMIP	0.1798631	0.047128004	down
Q4A208	Putative outer membrane protein	92	16	63	16	25.6	YQAEVGGSYNYLDPDNGSSVSKFGVDGTYYFNPVQTRNAPLAEAAFLNRASNVNAHVNYGDN SGTKDTQYGVGVEYFVPNSDFYLSGDVGRNEREIDNTNIDSKVTTYAAEVGYLPAPGLLLALGV KGYDEKDGKDGADPTVRAKYVTQVGQHDVNLEAYGAFGDLDEYKVRGDYYIDKTLSLGVDY YNNDLTDKDEFGINAKKFLNQQVSVEGRVGFGDNDNTYGVRAAYRF	0.4239015	0.000421047	down
S3TFV1	Glycosyltransferase	9	2	2	2	36.5	MNIKPFLSCVVPAYNEAENLKTFIPALANSLKQQNLSYEIIVVDDGSKDDTIPILQTMIEDYPLVV LELSRNFGKEAALSAGLDHVTGEVALLIDADFQHPFEAIPTMINLWKNGYDMVYGIRNRTTESW LKRVLTQAYYRILNLSSPIDIPESAGDFRLLDARVVEAIKQLPEKNRYMKGLYAWVGFKSIGINFS EQERQHGRSSFNLKSLFNLAMSGLTGFSDLPLRVCIYLGAILALGAMSYGVWIIIKTLIEGISIPGW ATLAAGMTLLGGIQLLFIGILGEYIGRIYAEVKNRPKYIISTEHSRTKQEHSIAHQENTFSSF	3.2927298	0.001053475	up

V5RCU9	Glycosyltransferase	12	4	7	4	42.3	MKILHAAYMKDASSGIVNQMYWEQEAAKELGISWKSILFVQNPNGFHNNEIVTVCNDIMGGEL KKWFKAKKSYYSWLEGIMQEYDVLIIRHSLCDPFEPFFIRKMIKPVYIMHHTFEIDELYSYNYGV KTKIKSLMEIYFGKKSISYSKGIVAVTKEIFLYENSRVNGKFKKEIVYPNGIISQHDIILDDRNDNIP EIVFIASYFNGWHGLDLLLHNLSSINDDFILHIVGDVSVEDELLAKKDSRVILHGHLNNIEISQLMS KMWIGLASFGLFRKGMKEACTLKVREYLNYGLPIYSGHKDIFPEEFEYYKFGEPKFVDILSFAHL MRKVSKSDVKQAAIKFIDKKILLKELYEQLLEEKS	5.2220253	5.68E-08	up
V5REA9	DgaA	34	9	37	9	35.8	MKKFALIGAAGYIAPRHLKAIKETGNTLAVAMDVNDSVGIMDSHFPEAEFFTEFEEFEAYVEDQ KLKGEKLDYVAICSPNYLHAPHMKYALKNGIDVICEKPLVLNSEDLNMLAEYEKQYGAKVNSIL QLRLHPSIIALRDKVQAAPADKVFDVDLTYLTSRGKWYLKSWKGVDNKSGGVATNIGVHFYD MLHFIFGKIVKNEVHYRDEKTASGYLEYERARVRWFLSIDANNLPENAVQGEKLTYRSITIENEE LEFSGGFTDLHTQSYQRVLEGKGYGVEENRAAIETVEVIRVSPIIENPENPHPLLAKVKKA	3.9525062	2.91E-06	up
V5REF7	Wza	42	13	40	1	40.5	MKYCQFFSVLALSLSAASCAVTSGLQTYDIPSEGVYKTDLGTTVNVVKISQETLPAIQPAQIDYQ RDYASLFKTQQSIYRLSPGDVLSIQLWAYPEITPPVNSISNEQSVQANGYPIDQTGYIQFPLVGRY KAAGKTLAQVNRELHSQLARFLKNPDVVVRVVSYEGQRFSVQGSVTKGGQFYLSDQPVSIYTA LGMAGGVTTTGDNTYIQLIRNGRTYNLNTIDLEKAGYSLHKLLVQPNDTIYVSTRENQKIYVMG ESGKNQALPMRDQGMTLTDALGESLGINPLSGSASRIYVVRTNPNDRTTEIYHLNLMSIGDFGLA NQFRLRSNDVVYVDATGLTRWQRIVNQIIPFSNALYNIDRLGQ	10.146481	0.032607011	up
X2F9Q9	Amylovoran biosynthesis protein AmsE	7	2	4	2	31.9	MFSVLSSIYHKEQPEHFNTCMESIWDNQTLKPTEIVLIEDGPLTPELDQVIAQWQKKLGDVLRVT KLEKNVGTGKAKNIGLQECNYDIVSIVDTDDIYVPERFEKQIKFLQQNPEISIVGGQIFEFIEDIGNP VGMRKVPLSNVELRNYAKKQSPFNNMTITYRKSHILEVGGYQHHLWMEDYNLFLRVIAKGYKI ENLPDVLVYARIDNGMHGRRKGLQYIKSEKQLLDLKKQLKLQNPLYANMLFLVRSAFRLLPAN LLGTIYNTFLRKDIKK	2.2516504	0.001826913	up
X2FEM8	Aminotransferase DegT	50	13	55	13	39.3	MIDFIDLKAQQNRIKDKIDAGIQNVLTHGQYILGPEVIELEEKLASYVGAKHCITCANGTDALQIA QMAFGIGPDDEVITPGFTYIATAETVALLGAKPVYVDVNPKTYNLDVEKLEAAITPRTKAIIPVSL YGQCADFDAINAIAKKYSIPVIEDAAQSFGATYKGRKSCNLSTVACTSFFPSKPLGCYGDGGAIFT NDDELAKVIRQIARHGQDKRYHHIRVGVNSRLDTLQAAILLPKLEILDDEMQARQRVAEVYNRL FDEVGIHTTPYIEAHNTSAWAQYTIQVDNRAEVQEKLKAQGIPTAVHYPIPLNKQPAVADSDIHL PIGDAIAEKVMSLPMHPYLAIDDQLKIVKAFG	5.1735465	0.003466715	up
X2FEM9	Glycosyl transferase	40	8	14	8	39.0	MKILFLINSLKSKSGSERVAVELANKMAAIGSYNITLLNRESIKENAAYSIADNVEVIALSGSLFEF YKKLKKQISSNNYDVVVVHNMGKLSLLCAFVPNIKKLVVLEHVSFISRPKKIQILSKFLYRNIDQ VVTLTQNDKEQFDKFHSNVIVIPNFSPFSIASQPRNNNKQIVTIGRLTDQKNYIHLLQAWKKIYQS IPDWQLNIYGEGEQEEILQDYIKQQSLKNVSLKGSTSNVKEVYEQSSFFVMSSKYEGLPMVLIEA QSFGLPIVSYNCPYGPSDVIRDSKNGFLVEDQNVDELAAAVLKVALSPQLLEQFSQSSLLNAKKY QPEQILKIWIEKVLEG	4.7465335	0.001542928	up

Table S4: DEPs in XDR vs. MDR strains.

Protein ID	Description	Protein Coverage (%)	Peptides	PSMs	Unique Peptide Number	Mass [kDa]	Protein Seqence	FC XDR/MDR	*P*-value XDR/MDR	Regulate
A0A009G507	Glycosyltransferase subfamily 4-like, N-terminal domain	48	12	21	11	42.9	MQNKKIVLIGTTGSSFYGFRADLIRSLVANGHQVYAFTSEYTENCLDKIKALGAEPITYQLSRGG LNPFADIASTYQLIRKIKKIKPDIVFSYFAKPVIYGTLAASFAKVPHIIGMLEGLGYTFTAQPEGQSS KTKLIRNIQVLLYRLAFPRLDDMIFLNPDDEKDLIHTYTLPVKKVHILGGIGLDLKEYSYSVAPVS PVSFLFIGRLLKEKGIFEFIDAIRIVKHKYPNTKFTILGGLDTQNMGALSKSQLDELIAEGLFEYPG HVSNVKDWIANSSVFVLPSYREGVPRSTQEAMAIGRPVITTDVPGCRETVINDVNGFIVPCWDA KALAEKMCFFIESPSQINLMGLESMKMAHQKFDAEKVNNRLFEIMGLNSSYEKIG
A0A009G8E9	Tyrosine-protein kinase wzc-like, C-terminal domain	45	27	88	18	82.0	MSQTSKTEDTIDLKELFFSLIAQWKLIVLCILISLVCALIYLRVTPNTYSVDALVQVEDTKSAASA ALLGELSKMVDQKSPAQAEIEVLTSRMVLGQVINNLNLDITIKNHDDTFFNRLLSQDKQNIDYKK DAVTFSNKDSYFSIQQLQIPSYYLDKPLLLSFKDQRHFTFSYKDKVIFSGQLNSNNLVTAREGQW KVRINSTHAPSVEQQFTISKLALPTAVQKLGSTYGVAERGKQTGVISLNYQGTDKEHITEVLNNI LAVYHSQNIERRTLESKQTLDFLDKQLPDLKQQLEESERKFNQFREKYNTVDVTQEAELYLKQNI ALETTKTELKQKQAELAAKYTNDHPLMAEINAQLAAVNKKSAELSDTLKRLPEVQRQYLQLYR DVKVNTELYTSLLNSYQQLKIAKAGEIGNVRIIDTAVEPVNPIKPKTLIVLVLTIFIGGFIGILIALLR NMLRTGVKDSTQIENDLNLPVYATVPRSPIQETRMNILKKKKSIPILAVKSSDDIAIESLRSIRTAIH FALTTAKNNIIMIAGPSPEVGKSFISTNLATIFAQSNKRVLLIDADMRRGYMHKYFDVDVKPGLS ELLSGQADLSQVLHKTQVANLDVITRGKSPTNPSEMLSSTQFKDLLEKFQTQYDHIIIDTPPVLAV TDGIIISQYTGVNLIVARYAKSHMKELELTINRFEQAGVKVNGFILNDIQRSSGGGYGYNYAYAY KAQKED
A0A009G8K1	UDP-N-acetyl-D-mannosamine/glucosamine dehydrogenase	53	19	40	11	47.7	MFNLEQLHIAIIGLGYVGLPLAVEFGKKVPVIGFDIHQKRIDELNNGQDHTLEVSKEEIQQAVKLR YTSSLEDLKDCNFFIVTVPTPIDDFKQPDLTPLIKASTSIGQALKKGDVVVYESTVYPGATEEVCIP VLEKISGLNFNQDFFAGYSPERINPGDKLHRVTNILKITSGSTPEVADYVDEVYNLIIEAGTHKAPS IKVAEAAKVIENTQRDVNIALINELALIFNKLNIDTEDVLKAAGTKWNFLPFRPGLVGGHCIGVD PYYLTHKAQSIGLHPEIILAARRLNDRMGEYVATQLIKEMVKQRIQVVGARILVMGLSFKENCPD IRNTKIVDFIKALKEYDLDLDIYDPWVDENEVQHEYGLAPIKKLGNGLYDAIVIAVAHNQFKTM RAQEFQALGKEKYVLYDLKYILDKTESDLRL
A0A009GAT0	Short-chain dehydrogenase/reductase SDR	23	4	7	4	27.0	MKIQGKHFVITGGGSGLGAATAEYLVKQGASVTLVDMNVEAGEQQAKQLGPKADFVKLDVTD EVAAEQFFKDVLVKHSHLHGLVNCAGIGPSAKVVGREGVHDLGLFAKTLNINVTGTFNMLRFA ADAMSKNTVEAGEEDRGVIVNTASVAAFDGQIGQAAYSASKGAIVAMTLPIARELARHAIRIMTI APGIMETPMLKGMPQNVQDALGQMVPYPSRLGKPEEFARLVAHIAENSYLNGEVIRLDGAIRM AAK
A0A009GKU9	UDP-glucose 6-dehydrogenase, bacterial type	40	12	27	1	47.2	MKIALFGTTLYAGVMAALLAEYGNQIYWCTSVTCEENISILSYQDQEVNHYLNKQRKAGFLKES PFSEIPLDIEVYLFCFSPTQIELALKTVEKLSERPIVHPRLMINGSTFGLHGTDQLKQHLPKDEWVY FPDVIQEGNAINSVLNVKHVIVGVESSYAQDTMQELLRPFFRFSYQYLFMPILDAEFTKLSISGML ATRISYMNDLAMVAEKLGIDIANVKHGIAADTRIGAAYLSAGVGFGGENFSHDILTLSSTVSGTG AKSRLLEQVWAINEQQKEILFRKLWNYYHCDLSGKTVAIWGASFKENTSSTHNSPIHILLAALW AQGVKVRLHDPQALDEIATTYGDREDLVLCADQYEAAQGAHALCLVTAWKQYWSPDFKQLQ QLMQHPLILDGRNIYDPAYVKSKGFAYEGVGRL
A0A009GU27	Protein of unknown function DUF4760	29	6	10	6	20.6	MAQVQDPTFWGGNIAFWIQTLVFFISALIAIYTLRRNEAQAKKRATVDLVLSETQDMYFRDIKEK FGKYKKQGMNFTKLACEELADNPEENDVIMTILNHYEFIASGIFEKALDEEIYKRMKKGILVRD WKTLEPYVMELRRKENRKAIYAETQRLAEKWEKDKGPSSKFWKR
A0A009GVM1	Thiolase	83	21	98	1	40.8	MTDIVIVNGARTAMGGFQGSLSGLTAPELGAVTIKEAIARAGLQPTDVEEVIMGCVLPAGLKQG PARQAMRKAGLPDSTGAVTINKLCGSGMKAVMQAADMIKAGSAEIVVAGGMESMTNAPYVLP KARAGYRMGHGEIKDHMFFDGLEDAETGRLMGSFAQDMANTRGYTREQMDDFAIRSLKRAQT AITEGYFKDEIVPVTVSTRKGDVIVDQDEQPLNAKIDKIPSLKPAFAKDGTITAANASSISDGASAL VLTSSEVAAQRGLQPLAKIIATASNSQHPSEFTIAPVGAIEKVLKKAGWNAQDVDLWEINEAFAM VTMCPIDDFKLDPEKVNIHGGACALGHPVGSTGSRIILTLIHALKRTGGKKGVAALCIGGGEATA VAIEIL

A0A009GY40	Flavoprotein pyridine nucleotide cytochrome reductase	69	17	57	17	39.8	MSQFVPLKVKSITPQTDEAICIAFDVVPEQQEQFQFQPGQHLTIRHLTEAGEIRRCYSICSYAGKE DISIAVKKIDQGQFSNWANDHLKVGDVLEVMPPQGVFFQKAAKMGGQNYLGVAAGSGITPILSI IKQVLFEQPEANFTLLYGNRSWKQTMFAEQIMDLKDQFKERFQLINIFSREFNDSELMNGRIDAE KLKQLFDYEVLETNFDHVFACGPDEMMNAVENTLPNFGIAKERIHTERFHTGQARKRSVEADA NRKEEKVNIILDGRELIVSVAQDDESILDAALRAGADLPYACKGGVCATCRCKVLSGEVDMFLN YSLEEDEVEKGYVLSCQTLPKGSNVRLSFDE	2.8491423	0.002352016	up
A0A009H3M3	Protein-tyrosine phosphatase, low molecular weight	40	5	12	2	16.5	MQINNILVVCVGNICRSPMAEYLLKRQFPHLHIESAGISGLIGHNADEKAQLCMQRLGINMQAHI AQKLDAEHIKRADLILVMSHNQQKHIEQTWPFAKGKTFRLGHWQNKNVPDPYQHDQTIFDETC ELIQKCLDDWKNYI	0.1581607	5.88E-05	down
A0A009HXJ2	Aminomethyltransferase folate-binding domain protein	42	8	28	1	26.7	MSLLAFSSYALNGVDAQKFLQGQVTVDTERLAENETRYTAICDLKGRIHFGLWLKKNNAESFDII VTQDQAEEFAKHIKKYGAFSKMTLSEQGAVFPKVVNGHTEFSSTETDISEWQKQAIMTGQAWIA QATEHEFQPQELRLHQREGVNYDKGCYLGQEIVARLWFKAKPKHWLHLVQGTGDAPAPATQL HNDVEVVNSTQTTDGYIALVVAKPAALQELGLQVLDLPEALSGDVARPQ	0.3332263	0.00064365	down
A0A009PBA1	ER-bound oxygenase mpaB/mpaB'/Rubber oxygenase catalytic domain-containing protein	7	3	4	1	47.3	MISPTRLASFNDMQDSNFFTQFLNICCEKPVQPSYTEYVSLQHALYEGDIEMDKVIDWVMQNPK DHRIIFEKILFQGRDELSEPIPTELENFFNYIEQKPDWLDQQQIDEAVKFTHRLGINNGFILRDLSL MAGYLYPGFNQPLILTGALKKEAGTRLAETTKWWVDITEPHGLSRLSAGFTSTIYVRFIHALVRR QLKKSDRWDNEVWGIPLNQFDLAMTNLAFSSVVLLGIRALGIWPTKQEAKSFLHFWRYVGWL MGIEEKWLIQSEPEGWRLLYWMQFAHPRSDHSSIELGSSLSKEPLERKYLHLRSLQQKLAYRQH LELTQFFIGKKRMKLLGLPQQSASWFAYYLIVRNLLLYNGAKLSPKVEKFLSKSGRNIQKLGLTL YQNQGKAKTLASMHHNSGI	0.1232098	0.021701975	down
A0A009PWD1	Short chain dehydrogenase family protein	62	13	26	2	27.7	MAKTILITGASSGLGAGMAHEFAAKGYNLAICARRLDRLETLKTELENQYGIKVIAKSLDVTNY DQVFEVFRAFKQEFGYLDRIIVNAGVGNGRRIGKGNFEINRATAETNFISALAQCEAAIEIFRAQN AGHLVVMSSMSAMRGLPKHLSTYAASKAAVAHLAEGIRAELLDTPIKVSTIFPGYIRTEMNEGA KHLPFEVDAKTGCKALVKAIEKQPVKAYVPQWPWLPMSIAMKVLPLRLVNKLGLCTRQK	2.2289624	0.005116918	up
A0A009QD14	Enoyl-CoA hydratase/isomerase family protein	43	6	16	6	27.9	MQELIKASTAADGVLLLTLNRPEKRNALNNATLQCLCELLEEAEHNAQVKAVVLTGNAQCFAA GADLSELAAMDAVSLQLDIRPKLWQKIDAFSKPLISAVNGYALGAGFELVLHSDMVICGENARF ALPEIGLGMLPGAGGTQRLARLVGQQLTMRWAMTGEMISAKQAEQHGICSQVVPTELTVEYAV QLAAKIAKQAPLAIRVIKQSIKSIHETTLSQGLKFERQNFVWLAATKDRNEGINAFFEKRKPVFRG E	2.6323829	0.000836971	up
A0A009QHT0	DUF3298 domain-containing protein	28	7	14	1	32.5	MNLSKKTIIALVVAAIALILAICVFVWKKPQSSSSSQENSASTQDHPVEKAEVLPYLNLTETKANY AVPFCEKKNCIDVDIQTIKTQDAWLNSWIEKNQTKVIQAQINLKKDLSLQQAINAYVKKSDEWQ DKYSKNRAYELHIRTRIASQRNQYVLLQLALDSKQEEVTIKDRYYFFVADRKLHKNLTLLDVLK KDQQPTVHQIVQTAYQDWLKKQTADVKKQAPKTLYWGQADWFFDGEGVGLHYQANQITKDA PQLDIYLTTEQTKKILQPQVYEQMF	0.4880952	0.02361419	down
A0A009QKJ4	Polyprenyl synthetase family protein	61	13	51	1	35.5	MVIDFKQDILAPVATDFAAMDHLINEGISSKVGLVMSVSKHVVEAGGKRMRPIMCLLAARACGL DNMQNAQRLAAIIEMLHTATLVHDDVVDESGLRRGRPTANATWNNQTAVLVGDFLIARAFDLL VDLNNMTLLKDFSTGTCEIAEGEVLQLQSQHQPDTTEETYLKIIHGKTSRLFELATEGAAILAGQE AYREPLRLFAGHFGNAFQIIDDILDYTSDAEILGKNIGDDLMEGKPTLPLISALAHSTGEEHAIIRR SIATGGVDQLPKVIEIVQKSGALDYCQRRAQEETEAALQALSILPDTPYRQALINLTRLALHRIQ	6.4177215	2.03E-05	up
A0A009T164	DUF4393 domain-containing protein	30	6	9	6	27.2	MTEKDNNLNASFLDHRVATYKAIAGLIPGFGSILSEVVGAIIPDQRMDRLVKYIKILDTKVQKINS DLLEIAKQNELAIDLIEEGFVQASRSLSNERREYIANVVANGISDEEKNYADSKYILKLLGELNDQ EVIWLRFFLHPTFDGDEEFRQQHQNVIEPIATYIGADENILEKKDIQESYKSHLERLGLIRSNYRID KNTGLPKFNHQGVPEVSYRFVTPLGKMMLKKIGLIDSANT	0.1894989	6.26E-05	down
A0A059ZG34	BolA family transcriptional regulator	46	3	9	3	11.3	MSLEQQLIERLQTLAPSYLEVINESAGHGGYFPGKESHFKVIVVSEEFNGLRLVQRHQKVYALAS DLMNPGQIHALAIHAYLPSEWQGQAPASPECAHAPKS	2.0066563	3.29E-05	up
A0A062I638	Endoribonuclease L-PSP family protein	24	2	2	1	14.7	MRTAIFPQDRHALYEQHGYSAAIQSKDLLFVSGQVGSLEDGSPVPDFEKQVIQAFKNLAETLKA AGCTFDDIIDVTTFHTDPERQFKSIMKVKNQIFTQKPYPNWTAVGVTWLAGFDFEIKVIARIPHN N	0.3251437	0.043644326	down
A0A062IBU4	Activator of Hsp90 ATPase homologue 1/2-like C-terminal domain-containing protein	32	4	10	4	16.6	MTTGTVKLHRVFKAPAERVYRAFLDPDALVKWMAPHGFTAKVHSFDAKVGGLYKMSFTNFST GSTHSFGGTYVELVPNELIRYNDQFDDTNLPGTMQVTITLKTVLVGTEIHITQEGIPEVIPVEACY LGWQESLSLLKLLVEADIPDQ	2.2967846	0.033664917	up

A0A062IDU6	Glycerol-3-phosphate dehydrogenase	40	17	27	1	57.4	MKVQPNDYSKIYDLAVIGGGINGVGIANDAAGRGLSVFLCEKDDLASHTSSASSKLIHGGLRYLE HKEFRLVREALAEREVLLAKAPHIIKPMRFIMPHRPHLRPAWLIRAGLFFYDHLGKREKLLGSNLI YFKEDSPLKPAITRGFEYSDCTVDDARLVVLNALQAKEKGAKVVTRTSCVKAYRQQELWHLEL QSRAEFYQIRAKAIVNAAGPWVEEIISKNLGLSSPYQIRLIQGSHIVVPKLYDCHKAFIMQNEDRRI VFAIPYLEKYTLIGTTDQEYTGDPQKVEITDVEIDYLLTVTNSHFKKQLTRADIVSQYSGVRALC DDESDNPSAITRDYTLALQAEDKTTPLLSVFGGKITTYRKLAEAALEHLAPFFNDMAEEWTADE ALPGAENWTTLEDLINQIKTRVSGISDSLANRWAHAYGTRVWNMLKERNAIEQLGQHFGHDLF ECEVRYLCEYEWAHTAEDILWRRSKLGLAFDEKQVKVLEAYLAERRLKDDAA	0.1180205	0.023806631	down
A0A062IH37	Efflux transporter, outer membrane factor (OMF) lipo, NodT family protein	75	25	134	1	52.8	MQKVWSISGRSIAVSALALALAACQSMRGPEPVVKTDIPQSYAYNSASGTSIAEQGYKQFFADPR LLEVIDLALANNRDLRTATLNIERAQQQYQITQNNQLPTIGASGSAIRQVSQSRDPNNPYSTYQV GLGVTAYELDFWGRVRSLKDAALDSYLATQSARDSTQISLISQVAQAWLNYSFATANLRLAEQT LKAQLDSYNLNKKRFDVGIDSEVPLRQAQISVETARNDVANYKTQIAQAQNLLNLLVGQPVPQN LLPTQPVKRIAQQNVFTAGLPSDLLNNRPDVKAAEYNLSAAGANIGAAKARLFPTISLTGSAGYA STDLSDLFKSGGFVWSVGPSLDLPIFDWGTRRANVKISETDQKIALSDYEKSVQSAFREVNDALA TRANIGERLTAQQRLVEATNRNYTLSNARFRAGIDSYLTVLDAQRSSYAAEQGLLLLQQANLNN QIELYKTLGGGLKANTSDTVVHQPSTAELKKQ	0.1836444	0.049188659	down
A0A062IH60	Nitroreductase family protein	56	13	28	2	26.4	MNLEQVRLVDEAITSRHSVRAFLSTPIEPEVIKDILRVASRAPSGTNTQPWKVYVVTGHKRDEM VERVCAAQIEVSKNPELAEQYKETFAYYPEKWVSPFIDRRRENGWGLYGLLDIKKGEKEKMAA QQLRNFKLFDAPVGIFFTVNKAMGIGSKMDIAMMIQNVMVAAKARGLDTCPQAAWNHFHSLV LDILGAADDEELVCAIALGHADPEHIVNTFITPREPVENFAVFLD	3.3480194	1.11E-07	up
A0A062IMZ0	Apolipoprotein A1/A4/E domain protein	36	10	62	4	18.3	MTTENKLDELKAKAADAKVQGEKALDDLKENVKEKQTAGKEAVADKVDELKTKAADAKVQG EKALEDLKENVKEKQAAAKEAVEDKASDLKGKLDDAQHSLQDKFDHLRTEAAHKLDDAKAKA AELKEEAATKFDELKTQATAKFDELKKTATEKLNKLKNHDSAE	2.578007	0.00291249	up
A0A062IRH0	Valine--tRNA ligase	53	42	188	1	108.5	MTDAQTAQNIATTYDPTEIEKKWYKTWEEQGYFKPSGHGESFCIMIPPPNVTGSLHMGHGFNN AIMDALTRYNRMMGKNTLWQPGTDHAGIATQMVVERQLGLQGITRHDLGREKFIEKVWEWKE QSGGTITKQIRRLGSSVDWSRERFTMDEGLSNAVKEVFVRLHEDGLIYRGKRLVNWDPKLQTAL SDLEVESKEEKGSLWHFKYFFEDKSVKTQDGKDYLVVATTRPETLLGDTAVAVHPEDERYAHL VGKNIVLPITGRLIPIVADDYVEKDFGTGCVKITPAHDFNDYELGKRNSLPIINIFNKNAEVLGEFE YIAKAGEQISKTITAPADYAGLERFEARKKLVAQAEAEGWLDQIQPYDLKAPRGDRSGVIIEPLL TDQWYVKIAPLAEPAIEAVQDGRIKFVPEQYSNMYMAWMRDIQDWCISRQLWWGHRIPAWYD ADGNIYVGRSEEEVRAKNNIAADIELKQDEDVLDTWFSSALWTFSTLGWPEQTPELKTFHPTDV LVTGFDIIFFWVARMIMMTMHFMKNEDGSSQIPFKTVYVHGLVRDGEGQKMSKSKGNVLDPLD LIDGIDLESLVAKRTTGLMNPKDAAKIEKSTRKEFPDGINAYGTDAVRFTFCALANTGRDIKFDL KRVEGYRNFCNKIWNATRFVLMNVEGQTVGTDARPDLWELPEQWIISRLQKAEAAVHQAFATY RLDLAAQAIYDFIWNEYCDWYVELTKPVLNDAEVSEERKAEVRRVLLAVMEASLRLAHPLMPY LTEEIWQTLAPMLGQGGPTIMTAQYPIPEQAKINEQAEADMQWLQGLIGAVRNIRGEMGLGNA RLLPVLLQNISNAEREQITRIEALFKALAKVESIEFLGKDQEPPLSSSSVVGHASVFVPMKGLIDPK AELARLQKDLDKIQKQHDQIANKLANEGFVSKAPAAVVEGEKAKLAEFAAQLDKVKANMEQIA AL
A0A062IS18	Porin B	50	15	78	1	46.8	MKTHKSLMVSCLSVLSITLFVQHAQAAAAFDPNGSWMLGDWNGQRTALQAQGYDFSFGYTGE YAGILDSKQTSTHGSAYTGQLALGSHLDLGKILGWQDTEAQITLTYRDGQSLSEHSPALAGHQSS VQEVWGREQTWRLTDLWIKKKFLDQKLDVKVGRFGEGEDFNSFDCDFQNLALCGSQVGNWV GDQWYNWPVSQWAMRVKYNLQPDLYTQVGVYEYNPENLERGKGFNLSTDGSHGAIIPAEVV WSPKLGVQSMPGEYRLGYYYSTADAKEIADSTKTSHKQGVWVTAKQKLFQPADQTDRGLTGF VNLTFHDSDTNKVDNMQNIGLVYKGLLNQRPQDELALGVARIHINDDWSDVQAKEYDTEYNTE LYYGIHATNWLTIRPNVQYVRHVGALKNGDNTWVGGIKFSTAF	0.3870759	0.011842212	down
A0A076G2N9	HTH cro/C1-type domain-containing protein	35	4	11	4	11.0	MAKLNDIISKRSPESQQRIKKMANQMLLDINLSNLREELKISQAEIAKNLGVSQAAISKREKLGKD LKISSLKEYVEAMGGKVRLDVELPNGKHVAISI	0.314573	0.005842773	down
A0A076G2Y6	Uncharacterized protein	55	6	14	6	20.5	MSSYSIQIGQVKGLYDVFLETCVPKNSPQYPELQKIGDDFLNKVVMEDPDYHNSQVFTILSQVAV PEIQNRLKRLESKAKNKDFEKNYFDWNYIERGVVQERKDFINAIHLKQIYEKTKKLYEAQNGEE LTSSIYADLLNANPQNLRRMLTHKREIDTRLLEEAKKCLEKLSTK	0.3594811	1.59E-05	down
A0A076G3Q9	Transcriptional regulator	20	1	1	1	10.6	MKTKEIIQMPLKLISSSKKDDVYENIEALVLSIKKDGFLLPISVRMNPDKTGEFIVNLGENRFRAA LALGLNTIPVYIEEAPKISIDFLFTSPE	0.4544614	0.005268512	down
A0A090B7C1	NirD/YgiW/YdeI family stress tolerance protein	6	1	1	1	12.8	MKMLKVILMTAGMATAGVVVANTPVNQAAIAPATVTTVKQALASKDNTPVKLHGQVVKSLG DEKYQFRDKSGSITIDVDDELWQGRAVSANTNVTLIGEVDIDYKPLKRVEIDVDQVQF	3.7488241	0.001545261	up

A0A090BAM3	Anthranilate 1,2-dioxygenase large subunit	52	17	45	17	53.9	MTSSNLKQWNDFIDGCIDFRPNDGVFRIARDMFTEPELFDLEMEFIFEKVWIYACHESEIPNNHDFLTVQIGRQPIIVSRDGKGELHAMVNACEHRGATLTRVAKGNQSTFTCPFHAWCYKSDGRLVKVKAPSEYCEDFDKSSRGLKQGRIASYRGFVFVSLDTQATDSLEDFLGDAKLFLDLMVNQSPTGELEVLQGKSSYTFAGNWKLQNENGLDGYHVSTVHYNYVSTVQHRQQVNASKGAELDTLDYSKLGAGDSETDDGWFSFKNGHSVLFSDMPNPTVRPGYSTVMPYMVEKYGEKYAEWAMHRLRNLNLYPSLFFMDQISSQLRIVRPVAWNKTEVISQCIGVKGETTEARRNRIRQFEDFFNVSGLGTPDDLVEFREQQKGFQARLERWSDISRGCQSWEYGATKNSQDLGIQPVITGREFTHEGLYVNQHGHWQRLMLDGLNKKALKMQDITFENNAVMDEV	2.68764	0.003791067	up
A0A097I5H7	protein-tyrosine-phosphatase	67	7	15	3	16.3	MQIKNILVVCIGNICRSPMAEYLLKQQYPQLNIESAGISGLIGHQADEKAQLCMQRLGIDMQPHIARKLNAELIKKADLILVMSSNQQKHIEQTWPFAKGKTFRLGHWQNKNVPDPYQHEQAVFDETCQLIQQCVADWKLYI	3.7803763	5.19E-06	up
A0A0D5YE03	Helix-turn-helix domain-containing protein	42	9	13	6	28.5	MSTLQERMSLAIKHYESVTGKRFKNTELARFAGVSRANVGLWVNGPTQELEGSNLVKAAEFLGVSKDWLAGQGNKMIATQLDGGGAQLNVLDIEAFKQKYNIPDSEDAVKFVQTSDKPFPIQKRYVPVKAYSKMGMDGYFTDMGYDGNAGDGYVPTHSAGPRAYGIKGTGDSMFPAIRNGWYVVCDPDAELVPNEFVQVCLKDGRCTIKEFVGINGGVLSLLSVNGGERFFFEMDEVESITAITDIVPPSQHRQEHPYSH	3.9187661	1.31E-05	up
A0A0D8EQN4	Isoleucine--tRNA ligase	50	37	161	1	106.3	MSDKQTTENAVDYKATLNLPDTQFAMKANLAVREVKWLEEWYTDNIYQQIRASRIGKKKYILHDGPPYANGTIHLGHAVNKVLKDIIVKSRTLAGFDAPYVPGWDCHGLPIELKVEEKVGKVGEKVDAATFRKHCREYALKQIDLQRTDFKRLGILGDWDNPYLTMNYKQEADIVRALGLIQKNGHIQPGLKPVNWCMDCGSALAEAEVEYEDKKSDAIDVGFGVVDLKDLSARVNVEVQDPTDIVIWTTTPWTLPANQAVALHAEIEYQLVQVTTERGKQNFILAKDLVASAIERYKLENPVVLADFTGSALENLTLQHPLLTDRQVPVILGEHVIATSGTGAVHTAPGHGADDYKVGLQYNLKVENPVGGNGVYLPTAPIFAGEHIYKANPKIIEALGAVGRLWAHQPIKHSYPHCWRHKTPIIFRATPQWFISMDQKGLRDGALNAIENDIEFVPNWGKNRIESMIEGRPDWCISRQRTWGVPIPFFVHKDTNELHPRTPELIEEVAKLIEKEGIDAWFNRDAKDFIGEDAEQYNAVRDTLDVWFDSGTTHYAVLEQRDELESPADLYLEGSDQHRGWFQSSLLTSMAIHNRAPYKALLTHGFTVDENGRKLSKSLGNYIPLEEIIKHLGADGLRLYVASSDYRYEIAASKEIFSRVSDSYRRIRNTLRFLLANLNGFKPSTDALAVDDLIALDQYILQRANEVQQTIIAAYEEMNFHVVCSALTSFCINDLGGFYLDIIKDRQYTTKADSQARRSAQTALYHIVQAFVRWMSPILSFTAQEAWPLIPEQTEKYVFTAEWYDLPVSSKANLLSEADWQTLISVKSAVNKQIEAARNAKLVGSNLSAKVELWANESLQTVLNQLADELRFVLITSQVVVHPFAEQGEATEMEGLRVQVSAAEGEKCARCWHVLPDVNTHVDHPGLCGRCIVNVTGRGEVRKYA	2.0613764	0.012674424	up
A0A0E1FIC9	Carbohydrate deacetylase YdjC-like	8	2	2	2	30.2	MAKVCYCADDFAMNAEISDAIIQLIEQGALQATSCMTQSDLWETAAAKLKPFSDRVDIGLHLNLTHAFASGNLVFPLPMLIVRAWSASLNRELITQCIEEQWDLFVSVLGKQPDFIDGHQHIHQFPFIRDILLQLLKEKKFTGWIRNLQQPINPPPYRFKTRMLSALGSNSLAKACQTYHFNQNGQFAGIYDFKLTNYGQLNQYWLANAKDHLLIMCHPALAQSKDQDPIQHARIQEYQYFSSDQFQLDCQQYGIQLTR	2.6972978	0.007859562	up
A0A0E1PN17	Uncharacterized protein	21	9	23	1	43.5	MRYKNTIVRITVDMSFVPQIKIPATYMRGGTSKGVFFKLDDLPEKAQVAGQARDQLLLRVIGSPDPYGKQIDGMGGATSSTSKTVILAKSTQPDHDVDYLFGQVSIDQAFVDWSGNCGNLTAAVGSFAISNGLVDADRIPENGLCTVRIWQKNIQKTIIAHVPIINGQVQETGDFELDGVTFPAAEVQIEFLDPADDGEEGGDMFPTGNVVDQLDVPEIGSFQATFINAGIPTIFLNAEDLGYEGTELQDHINGDAAALARFEKIRAYGAVQMGLIKDISEAAARQHTPKIAFVSKPKNYTASSGKNVSENDADLLVRALSMGKLHHAMMGTAAVAIGTAAAIPGTLVNLAAGGGEREAVRFGHPSGTLRVGAQAELTNGQWVVKKAIMSRSARVLMEGWVRVPGDSF	2.6494059	6.38E-06	up
A0A0E1PNX1	Outer membrane protein transport protein (OMPP1/FadL/TodX)	61	17	118	15	54.2	MKFKERLKMKLKHLSTAMILATLPATGVFAAALDRSGQSMSAFFQPGNYFEAGISVLDPDVAGKEAGSSATRRDIGDMANDYYFPSAALKLQINDQFSFGLLYDQPFGADAEYSGNNVFVSNPGSDTILSQKALGDLASSSIQKLVQASGSAFTPALIEVTKVTGGDPTKPTQTEILGALQQVAAGGNTTVGAGLTALQKTQAAINAANNYLGTGGTKVKVDTQNLSFVFGYQPTKNFNFYAGPVLQTVKGNVSLRGQAYSLYNGYDANIKETTGAGWLAGAAYQIPEIALRASVTYRSEIDHKVNIDENLSILNFPGLTSVLAGLDVPASKLQAINSSGKTTITTPQSVNLDFQTGIMADTVAFANVRWVNWKDFSIQPYKFGKVSEAVGGLVGRPNGFNLVEYSDDQWSVNAGVGRKLNDKWAGNVSVGWDSGAGNPVTTLGPTEGYWNVGLGVQYSPTPQTFIAGGVKYFWLGDAKAQTGAQAGSDEYVADFSDNNAIAYGLKLGYKF	2.6923462	0.004076788	up
A0A0E1PP65	Metallo-beta-lactamase	49	12	49	1	35.3	MKKLFVALGLIMGSLHISYAEPASAQQVPGYYHHQFGNYRITSLLDGTIYLDPKLFKNLSPAEKTKILTKYAAVNEKGIQTSVNAFLVDDGKSLTLVDSGAASCFGPQLGSIAKNLELASYQLANVKTVLLTHLHPDHVCGIAQNGKAVFPNATIYAHEREADYWLNPANEKTVPADKKENYLGTVKNVKAALAPYQAKKAFKTFKDGDVIQGFEVINTHGHTPGHHSFRLKSKGQQIVFVGDIVHSHSLQFDAPKTGVDFDVNSEQAINTRLKMFAEISNKQQWVAAPHLPFPGIGHVYKVSAEQYQWIPLYFNNSLDK	2.8704422	1.13E-05	up

A0A0E1PQH3	DcaP outer membrane protein	51	20	102	10	47.4	MMDLFLNRKSFVVKSLAITVTALMMSGANAATSDKEEIRKLRQEVEALKALVQEQRQVQQQQ QQVQQQQQVQLAEVKAQPQPVAAPVSPLAGFKSKAGADVNLYGFVRGDANYIIEGADNDFGD VSKSDGKTHDKLRATAKTTRLGLDFNTPVGDDKVGGKIEVDFAGSTTDSNGSLRIRHAYLTYNN WLFGQTTSNFLANHAPEMIDFSTNIGGGTKRVPQVRYNYKLGPTTQLFVSAEKGDSTTSVTGDSI KYSLPALTAKITQGYAEGRGSASARVLVENYKSQLADDDKTGWGVAVGTDFKVSDPLKLFADA SYVVGDNSYLYGSNSPYAVDGNSIEQNEFVAVQVGGTYKILPNLRSTLAYGAQFSDDGTDYARL NASANEKVQQAWINFIYTPVKPIDLGVEYVNGKRDTFDGKSYKDNRVGLMAKYSF	2.1884338	9.40E-05	up
A0A0E1PSU4	Protein of unknown function DUF3800	3	1	1	1	27.7	MRTFIYLDESGDLGWNMEKPYQKGGSSRMLTLAAICLPENKVKYVQRIVRALYEKRKRPLKNE LKSVDLNLKDKEIFVKLTAKLIKDHPDIQLRSITANKEFVNARFKNDPNAFYNYMVKLLLLGTIC KHKYVDFMPDRRSERVSLKWNMGEYLKQMVLECGIENQIVNQSCNIMPMDSSKCLELQFIDFY	2.3705251	0.000181544	up
A0A0E1PV91	Lipoprotein	49	10	18	10	27.8	MHQTNKRSAIALLFIVYSKCCSFATIPYFYIFYAYSTYLLQLVLFVVMKKVLQGAFFPFVIFASGM LLLGCDQTQDHAKEQESVQTNDQISDQADDSQQEITATQNKTELKNGNVFYIVRDAANLQLKA GDYIEKLKDTQLDVEQAIQDKDQHELKTTVTTLKAQLEGLNQALLGLDIRSQEVENIRQSLLQA NQQALSMPLLNGKLEQINFDQIEKQLNTIQMDMVKLAAMIMAGDEKSDSKTDS	3.2286971	0.000341739	up
A0A0E1PVE2	Alanine racemase	30	10	34	3	40.5	MPRPITAVIHRQALQNNLAVVRKAMPNSKVFAVVKANAYGHGIERVYEAFKAADGFALLDIEE AKRIRALGWTGPILLLEGVFSPQDLFDCVQYQLSFTIHSEAQIEWVEQHPYPAQFDVFLKMNSGM NRLGFKPQHYVQAWERLNNLANVAKITHMMHFSDADGDRFGQQGIDYQITAFEEIVKDLPGER SVSNSAAILRYQDQLKSDYVRSGIMLYGSSPDYPTHSIADWGLQPTMSLRSEIISVQHLEPNESVG YGSNFVAEQPMTIGIVACGYADGYQRISPTGTPVLVDSVRTRTVGRVSMDMLAVDLTGIESAKV GSEVVLWGQSSTGVILPIDDVAVSSGTVGYELMCAVTARVQFINQV	3.76797	0.032456329	up
A0A0E1PVE6	Nucleotidyltransferase superfamily	33	6	15	1	30.2	MSDFIQLEYLQEKLQQLLAESLFAIYLYGSAVDGGLGPESDLDVLVVVTQPLTSALREQLAQELL KISQPVGELQRPLEVTILLKDEIQSGNYPLSYEMQFGEWLREELKEGGTLSSQKDPDISILLRKARF HHAVLFGPALDQWAPEISDQELWQAMSDTYPEIVAHWDEDADERNQILALCRIYFSLVMKDIAS KDNAARWVKSQLPPEQKFVLQRLIQEYRGEIGKQNWQEEHYALQPIVNFLSSKIEEQFEQKRNLI	3.8252272	2.07E-06	up
A0A0E1PVF3	DNA-binding HTH domain, TetR-type	7	1	2	1	22.7	MERSFLLGMCMRTKEFETDEIAEAAMQVFWRRGYAATSVQDLVDGTGLSRSSLYSTFQNKQGL YQKALLRYELLTTLNNVKLLSGSGSAKALIRQLLMRVVEDELNDSEHKGCLVANACLELAGHD EEVSQFVVSNLQKLQHALESLLIKAQQSGEIASTQNPRALASFFLNTMQGLRVLGKGSPHEQRKQ CLMDVVEVALNVL	3.1422764	6.75E-06	up
A0A0F6SYM7	beta-lactamase	75	19	427	1	30.9	MNKYFTCYVVASLFLSGCTVQHNLINETPSQIVQGHNQVIHQYFDEKNTSGVLVIQTDKKINLY GNALSRANTEYVPASTFKMLNALIGLENQKTDINEIFKWKGEKRSFTAWEKDMTLGEAMKLSA VPVYQELARRIGLDLMQKEVKRIGFGNAEIGQQVDNFWLVGPLKVTPIQEVEFVSQLAHTQLPFS EKVQANVKNMLLLEESNGYKIFGKTGWAMDIKPQVGWLTGWVEQPDGKIVAVALNMEMRSE MPASIRNELLMKSLKQLNII	2.0267156	0.003245112	up
A0A0G4QU89	NAD(P)H quinone oxidoreductase, PIG3 family protein	51	14	50	1	35.9	MNLPTTMKIVEITVPGGPEVLKLQDSNVPVPQADEVLIEVKAAGINRPDVLQRMGLYPMPKGVT QIPGLEVAGVVVAVGEQVQQFKVGDKVCALTNGGGYAEYCAVTATQVLPIPENLSFTQAAAIPE TFFTVWANLFDIGRLKKDETALIHGGASGIGTTALAICHALGIKTFATVGSEDKVEALSDLTTAIN YKTQDFEQEILNHTQEQGVDVILDIVGGSYFQKNLNLLKRDGRLVIIGFMGGRIAKEFDLQKLILK RATITGSTMRARNSQEKAQIAQSLHEHVWPLLAQGKCLPQIYKTYAFSDVQSAHACMEQGDHIG KIVLEMNA	0.4274178	1.15E-05	down
A0A0H4UME6	Outer membrane protein transport protein (OMPP1/FadL/TodX)	57	14	74	11	46.5	MKLKHLSTAMILATLPATGVFAAALDRSGQSMSAFFQPGNYFEAGISVLDPDVSGKDTSGNATG DMANDYYFPSAALKLQLTDKFSFGLLYDQPFGSDSEYSGKNNFVANPNDRLLPSPASPTLGQAG LGNTITGGTSVEVDTQNLALVFGFQPTVNWNIYGGGVYQTIKGNVHLRGSAYSLYNGYDADIK ETGGAGWLAGVAYQIPEIALKASLTYRSEIDHDVNIKENIPIVNLVAANPALLFGALGITDPATQA AIGKQLASLQSDGKTTITTPQSVNLDFQTGIMANTVAFANVRWVNWKDFAVQPYKFGIVSKAA GQLLPQLGKPNGFNLVDYSDDQWSVTAGVGRKLNDKWAGNVSVGWDSGAGNPVTTLGPTEG YWNVGLGVQYSPTPQTFIAGGVKYFWLGDADAVTGAHSAAGTFDDNNAIAYGLKLGYKF	0.1798398	0.005364409	down
A0A0J1ACY0	Gp49-like PF05973 family protein	17	2	2	2	13.7	MAWDVETTELFDSWLAEQDENAQDKILASLLVLSELGPNLGRPHVDTIKESKYPNMKEIRVQVK GHPIRGFFAFDPERKAIVLCAGDKKGLNEKAFYKEMIKIADEQYEQYLRDNYGDK	0.2723999	2.51E-05	down
A0A0J1DET4	Endoribonuclease L-PSP	68	4	15	1	12.9	MTVKRLHVTSRYCEVAISGNLVHLAGQLADDTSVDITAQTQQTLDNIDRLLAEAGTDKSHILSV MIFLKDIDKDYAAMNAVWDAWISKEHPPARTCVESKLYAPDVLVEMTVVAVLP	0.2163971	0.000149491	down
A0A0Q1HCL9	L-alanine-DL-glutamate epimerase	52	12	20	4	40.2	MYRTIETILVDIPTIRPHQLSVTTMRTQTLVLVKITTTDGIVGWGEATTIGGLNYGEESPESVKAN IDTYFAPLLTSVKDLNVAQTLKLIRKNINGNRFAKCAIQTALLDIQAKRLGVPLSEVLGGRLRNSL PVLWTLASGDTEKDIAEARKMIELKRHNTFKLKIGARPLQQDVDHVIAIKKALGADVSVRVDVN RAWSELECIHGIQQLQDGGIDLIEQPCAIQNTEALARLTHRFDVAIMADEALTGPDSAYRIAKNH GADVFAVKIEQSGGLIEACEVGKIAGLAGIDLYGGTMLEGPVGSIASAHVFATFETLAFGTELFGP LLLTEEILKEPLRYENFELHLPTAPGLGIEIDEDKIEKLRR	2.2352126	0.000249856	up

A0A125S0J9	Dihydropteroate synthase	80	15	70	2	30.3	MSYLFLSCTEIIIEAPMNKSLIIFGIVNITSDSFSDGGRYLAPDAAIAQARKLMAEGADVIDLGPASSNPDAAPVSSDTEIARIAPVLDALKADGIPVSLDSYQPATQAYALSRGVAYLNDIRGFPDAAFYPQLAKSSAKLVVMHSVQDGQADRREAPAGDIMDHIAAFFDARIAALTGAGIKRNRLVLDPGMGFFLGAAPETSLSVLARFDELRLRFDLPVLLSVSRKSFLRALTGRGPGDVGAATLAAELAAAAGGADFIRTHEPRPLRDGLAVLAALKETARIR	2.7930623	0.002038154	up
A0A126W935	Nicotinate-nucleotide pyrophosphorylase	44	9	22	1	30.5	MSIPQSLLEQSIQINIQQALQEDIGDGDITAMLTPEDEQATATIISREDMVLAGQPWVVNALISAYDNTVQVTWLKHEGDRVAANEAFLKLAGSARSLLTVERPALNFIQTLSAVATKTAEYVQHLEGLNTKLLDTRKTLPGLRIAQKYAVTVGGGKNHRLGLFDAFLIKENHIMAAGGIAQAIAKAHQIAPGKPVEVEVETWDELNQALEAGADIVMLDNFSQQQMIDAVKHVAGRCKLEASGNITIENLREVATTGVDYISMGVLTKDVKAVDLSMRFNA	6.980508	2.28E-05	up
A0A158LX87	Phosphoethanolamine transferase	14	6	26	1	60.2	MFNLIIAIWLGAILNIGFYHQVHTLTPYFGVKAILFLAATLIILVATYYAVLQILNWKWTAKIFAILLIFIGGFSSYFVNTLGVIISPDQIQNMVQTDVSEVTDLISLRFVLWTVFFVILPIFLITQVKFKQEKVSRLLLKKVFSLVASFAVVGVLLFTYYVDFAAIFREHRDLKGMISPQNSISSLMSYYHKKAPKKNLPLVIYGQDAHQVQRVQKNLPKLMILVVGETARAESFSLNGYAKNTNPELSKQDIFNFSQVSSCGTATAVSVPCMFSGMPRADYDEQLASHREGLLDIAKRAGYQVTWIDNNSGCKGACDRVEQYQIPEDLKQKWCKDGECLDDILIDSLKQYLASIPKDDKRPRLVVLHQMGSHGPAYYKRAPEGYQPFKPTCDTNAIQGCSPAELINSYDNTIVYTDHVLSQMINTLKEVSNYQTGFWYLSDHGESTGEHGMYLHGSPYSIAPSQQTHIPMIMWFSDGWKQNNLAQVNCLNQQTKQKLSQDNLFPSLLSMLDVKTQVINPQLDMLHSCANVN	6.2421835	4.38E-06	up
A0A1B1LW15	histidine kinase	12	1	1	1	15.6	SHGDLSARAYDNRIHSAEMSELLYNFNDMAQKLEVSVKNAQVWNAAIAHELRTPITILQGRLQGIIDGVFKPDEVLFKSLLNQVEGLSHLVEDLRTLSLVENQQLRLNYELFDLKAVVEKVLKAFEDRLDQAKLVPE	3.5245971	0.000805269	up
A0A1E3M437	Uncharacterized protein	86	7	42	2	13.1	MSNSDIQKINTNEVMSAVTVFNKVVYLSGQVPKNTEQDVAGQTREILATIDELLALANTDKSRLLSAQLYLKNLSDFSTVNAIWVDWLKGCVAPSRATIQADLVNPNWLIEIAVTAAQK	0.0892574	0.019920098	down
A0A1E3M652	Isocitrate dehydrogenase [NADP]	69	23	138	2	45.6	MGYQKIVVPADGDKITVKADLSLNVPNHPIIPFIEGDGIGVDITPTMKKVVDAAILKAYGGKRSIEWMEVYCGEKANKIYGTYMPEETFEALREFVVSIKGPLTTPVGGGIRSLNVALRQELDLYVCVRPVRWFQGVPSPVQHPELTDMVIFRENSEDIYAGIEWKADSEEAKKVIKFLQEEMGVTKIRFPEGCGIGIKPVSKEGTQRLVRKAIQFAIDNDKPSVTLVHKGNIMKYTEGAFKEWGYELALDRFGGELIDGGPWVKIKNPKNGKDIIIKDVIADAFLQQILMRPADYSVIATLNLNGDYISDALAAEVGGIGIAPGANIGGAIAVYEATHGTAPKYAGQDKVNPGSIILSAEMMLRDMGWIEAADLIIKGISGAIAAKTVTYDFERLMPGATLLRCSEFGDAIIQHMED	0.1316173	0.040924774	down
A0A1E3MB56	Neutral zinc metallopeptidase	57	10	28	2	33.0	MRWKGRRVSTNVEDRRGGGGVRAGGISIIGLVVAFVAWKFFGVDPQQAYQATQQVTASQQSNATAPESLTAEQKEASDFIRTILADTEDTWTPIFKQLGKTYTPPKLVLFSGMIQSGCGTAQSAMGPFYCPADQKVYIDTEFFKDMREQMGISGEQNQTELSRQDQAGDFAQAYVVAHEVGHHVQTLLGISSQVQQARAQVSQREGNQLSVRQELQADCLAGIWANHNQQRTQFLEQGDVEEAMDAAQKIGDDYLQKRATGQVVPDSFTHGSSEQRMHWFQVGLKTGDISQCDTFNNSI	0.1230412	0.003748649	down
A0A1E3MBC2	Geranylgeranyl diphosphate synthase	61	13	54	1	35.6	MVIDFKQDILAPVATDFAAMDHLINEGISSKVGLVMSVSKHVVEAGGKRMRPIMCLLAARACDLDNMQNAQRLAAIIEMLHTATLVHDDVVDESGLRRGRPTANATWNNQTAVLVGDFLIARAFDLLVDLNNMTLLKDFSTGTCEIAEGEVLQLQSQHQPDTTEETYLKIIHGKTSRLFELATEGAAILAGQEAYREPLRLFAGHFGNAFQIIDDILDYTSDAETLGKNIGDDLMEGKPTLPLISALAHSTGEEHAIIRRSIATGGVDQLPKVIEIVQKSGALDYCQRRAQEETEAALQALSILPDTPYRQALINLTRLALHRIQ	0.156712	2.81E-07	down
A0A1E3MBE0	DUF3298 domain-containing protein	45	7	24	1	29.6	MQLYDKKIIFILPMLAAMVAVSGCQPKSTAKDEQLASSASVKEQKQAEVPVIQAKVVPVKLPKPKVCLEDGCTEYDFQTVQTNQKWINDYFTNRIKKADPNAFANLADKPVEVPEGEPSSSQSAIYVRYLGQNYNLATFAFQTYSYSAGAAHGMSHQEFVNFDLLNKKHITVEELIKPDVEKQLVDALFDANTNWLQEHNISREKLQLSDNFYYGANGIVFVYPIYELASYAEGMSELTLPYFEAAKYIKPEYLPS	0.2533594	0.017616394	down
A0A1S2G0B0	ParB/RepB/Spo0J family partition protein	59	22	61	22	47.0	MSSLLGDLNAVDSSLTSANLNANNNSDRTILKLPLNRVKLDPQNVRLEYDQDYVKELANTILRDGLLQPISVRADSDNPGEYIINMGHYRYLAHKHLNLDTIEATIDNKLGSRRVKMSENLFRKDMSLLEVATNLKLMLEEGVAENPKYSYDDLANEINKSKTWVSRRLQLLESDDYLKSLMANKMVNDAETGTIIKNLLAEYPEEVKALVADHEGAISSKLARVWSKELKGEIITSSTSEVTQSSLELQNSPKAGEKNEDSKVDNTQELITETKETLQQPAKVQESVENTEAVKDEKSFTTTTQKQTKEIVKQANEKAFSELETAYFNGILESYVSILDLTESEDEDLVSVACGFLRSFNDENTANLFSWKSLIQYPVLVNELATILDSMAQLHVFVPSSNVEDSRMQVILNQQDLI	0.2403727	3.13E-07	down

A0A1S2GAH7	Valine--tRNA ligase	53	41	173	1	108.6	MTDAQTAQNIATTYDPTEIEKKWYKTWEEQGYFKPSGHGESFCIMIPPPNVTGSLHMGHGFNN AIMDALTRYNRMMGKNTLWQPGTDHAGIATQMVVERQLGLQGITRHDLGREKFIEKVWEWKE QSGGTITKQIRRLGSSVDWSRERFTMDEGLSNAVKEVFVRLHEDGLIYRGKRLVNWDPKLQTAL SDLEVESKEEKGSLWHFKYFFEDKSVKTQDGKDYLVVATTRPETLLGDTAVAVHPEDERYAHL VGKNIVLPITGRLIPIVADDYVEKDFGTGCVKITPAHDFNDYELGKRNSLPIINIFNKNAEVLGEFE YIATAGEQISKTITAPADYAGLERFEARKKLVAQAEAEGWLDQIQPYDLKAPRGDRSGVIIEPLLT DQWYVKIVPLAEPAIEAVQDGRIKFVPEQYSNMYMAWMRDIQDWCISRQLWWGHRIPAWYDA NGNIYVGRSEEEVRAKNNIAADVELKQDEDVLDTWFSSALWTFSTLGWPEQTPELKTFHPTDVL VTGFDIIFFWVARMIMMTMHFMKNEDGSSQIPFKTVYVHGLVRDGEGQKMSKSKGNVLDPLDL IDGIDLESLVAKRTTGLMNPKDAAKIEKSTRKEFPEGINAYGTDAVRFTFCALANTGRDIKFDLK RVEGYRNFCNKIWNATRFVLMNVEGQTVGQEARPDLWELPEQWIISRLQKAEAAVHQAFATYR LDLAAQAIYDFIWNEYCDWYVELTKPVLNDAEVSEERKAEVRRVLLAVMEASLRLAHPLMPYL TEEIWQTLAPMLGQGGPTIMTAQYPIPEQAKINEQAEADMQWLQGLIGAVRNIRGEMGLGNAR LLPVLLQNISDAEREQITRIEALFKALAKVESIEFLGKDQEPPLSSSSVVGHASVFVPMKGLIDPKA ELGRLQKDLDKIQKQHDQIANKLANEGFVSKAPAAVVEGEKAKLAEFAAQLDKVKANMEQIAA L	0.2828602	9.28E-07	down
A0A1S8V5S4	Long-chain fatty acid transport protein	13	6	27	1	53.2	MKLKHLSTAMILATLPATGVFAAALDRSGQSMSAFLQPNNYFEAGISVLDPDVAGKEAGVSATR RDISDMGNDYYFPNAALKLQLTDKFSFGLLYDQPFGADAEYSGQNVFVSDPSNTILAPAALDAIR TSTIDTTFNNLTADQRVGAALQAQGVNLSTPEGKAQFAATLTAYNSNPATKAAIDAGVKQGVA AKVDAGIKQINGLLGTGNTKVKVDTQNLSFVFGFQPTQNWNIYAGGVYQTVKGNVSLRGQAYS IYNGYDADIKETGGAGWLAGVAYQIPEIALKASLTYRSEIDHDVNIREKIPTLPALSLLGQDAAA AAIANSSADTTITTPQSVNFDFQTGIMANTVAFANVRWVNWKDFSIQPYKFGQLSKVVGPLADP RRPNGFNLVEYSDDQWSVNAGVGRKLNDKWAGNVSVGWDSGAGNPVTTLGPTEGYWNVGL GVQYSPTPQTFIAGGVKYFWLGDAKAQTGAQAGSDQYVADFSDNDAIAYGLKLGYKF	2.3582364	0.000166821	up
A0A1T0DRB8	TetR family transcriptional regulator	21	4	8	1	24.2	MTNRHETDLVNEDTLKKKRGRPKCFDEQQVLEKAMLLFWEHGYEATSISDLTHALEITAPSLYS AFGDKAGLFYKSIDYYLAHEACPIETIFLEAKTAKIAFELYLYDNVKRLVQPNKPAGCMLVVAA MNCSDATQEVQQNLLDKRIKTKEKLLKRLEQGVEQGDLPTNAPLQEMTDFYATVIQGLTIQARD GANTEQLHKVVEHAMKAWTLF	0.3913784	0.000669201	down
A0A241ZEM6	Cysteine synthase	55	13	79	2	35.1	MSTDPQFPTPNNLGIAVYSNNAEAIGNTPLVRINRLIKTGATVLAKVESRNPAFSVKCRIGAALIA DAEKRGVLKEGMHIVEPTSGNTGIALAFVAAAKGYSITLTMPASMSLERRKVLKALGANLVLTE PAKGMKGAVDEAVRLATEQPEVYFLPQQFENPANPQIHVDTTGPEIWQATGGQVDILVAGVGT GGTITGISRYFEQVQNKPLYSVAVEPAESPIITQTKKGENITPAPHKIQGIGANFIPKNLDLDLVDE VLPVSSEEAIQWARNCATQEGILVGISSGAALAAAAKIAERPENAGKTIVVILPDSGERYLSSVLF			
A0A241ZJ54	DcaP-like protein	61	23	121	13	48.1	MDLFLNRKSFVVKSLAITVTALMMSGANAATSDKEEIRKLRQEVEALKALVQEQRQVQQQQQQ VQQQQQVQLAEVKAQPQPVAAPVSPLAGFKSKAGADVNLYGFVRGDANYIIEGADNDFGKVA ESKGEATDKIRATAKTTRLGLDFTAPVNDAKVGGKLEVDFAGSTTDSNGSLRVRHAYVTYNNW LFGQTTSNFLANHAPEMIDFSTNIGGGTTRVPQVRYNYKLGPTTQLFVAAEKGDSTGLTGTKDK DNNWVNDSIKYSLPVLTAKITQGYADGKGSASARALVENYKSKAGGDNQTGWGVAVGTDFKV SDPLKLFADASYVVGNSNYLYGSNKAYTVVDGDIEQNKFVAVQVGGTYKILPNLRSTLAYGAQ FADDGTDYATAYKDGNEKVQQAWINFIYTPVKPIDLGVEYVNGKRDTFDGKSYKDNRVGLMA KYSF	0.2023531	0.03135368	down
A0A2I8CT67	Isocitrate dehydrogenase NADP-dependent, dimeric, prokaryotic	66	22	137	1	45.6	MGYQKIVVPADGDKITVKADLSLDVPNHPIIPFIEGDGIGVDITPAMKKVVDAAILKAYGGKRSIE WMEVYCGEKANKIYGTYMPEETFEALREFVVSIKGPLTTPVGGGIRSLNVALRQELDLYVCVRP VRWFQGVPSPVQHPELTDMVIFRENSEDIYAGIEWKADSEEAKKVIKFLQEEMGVTKIRFPEGCG IGIKPVSKEGTQRLVRKAIQFAIDNDKPSVTLVHKGNIMKYTEGAFKEWGYELALDRFGGELIDG GPWVKIKNPKNGKDIIIKDVIADAFLQQILMRPADYSVIATLNLNGDYISDALAAEVGGIGIAPGA NIGGAIAVYEATHGTAPKYAGQDKVNPGSIILSAEMMLRDMGWTEAANLIIKGISGAIAAKTVT YDFERLMPGATLLRCSEFGDAIIQHMED	3.9574347	1.77E-05	up
A0A2U8NGD1	Wza	33	11	28	1	41.3	MHKGSRVKYCQFFSVLALSLSAASCAVTSGLQTYDIPSEGVYKTDLGTTVNVVKISQETLPAIQP AQIDYQRDYASLFKNQQTIYRLSPGDVLSIQLWAYPEITPPVNNISNEQSIQANGYPIDQSGYIQFP LVGRYKAAGKTLAQVNRELHNQLARFLKNPDIVVRVLSYEGQRFSVQGSVLKGGQFYLSDQPIS IYAALGLAGGVSDKGDNTYIQLIRNGRTYNLNTIDLERAGYSLHKLLVQPNDTIYVSTRENQKIY VMGESGKNQALPMRDQGMTLSDALGESLGLNPLSASASRIYVLRTNPNDRTTELYHLNLMSIGD FGLANQFRMRSNDIVYVDATGLTRWQRVVNQIIPFSSALYNIDRLGQ	4.4095486	0.001035596	up

A0A335J3M4	Thiolase	60	17	57	1	43.1	MEDVLICDFIRTPIGRYAGALSAVRADDLAALPIKYLKDKHPNLPWNTVDEVFLGCANQAGEDNRNVARMATLLAGLPDTVPAMTVNRLCASGLDAVGLAARSIKAGEAQFVLAGGVESMSRAPFVQAKLTEAFSRTPEIYDTTIGWRFVNKQLKAQYGTDSMPETAENVAEKYQISREDQDAFALRSQQKTAAAQQNGFFNDEILPVEITDRKKNVVVVNRDEHPRETTLEALAKLKAPFKKEGGSVTAGNASGVNDGAACVLITNREFADTHGLKPLARVIGIASAGVEPKYMGIGPVPAVQKILKQTGLTLDQMDVIELNEAFAAQSLACMRELGLKDDDERVNPNGGAIALGHPLGMSGTRLVITATRELKKRGGRYALCTMCVGVGQGVALILENLN	3.0438897	0.000583786	up
A0A380V1V9	Outer membrane efflux protein	75	25	137	1	52.8	MQKVWSISGHSIAVSALALALAACQSMRGPEPVVKTDIPQSYAYNSASGTSIAEQGYKQFFADPRLLEVIDLALANNRDLRTATLNIERAQQQYQITQNNQLPTIGASGSAIRQVSQSRDPNNPYSTYQVGLGVTAYELDFWGRVRSLKDAALDSYLATQSARDSTQISLISQVAQAWLNYSFATANLRLAEQTLKAQLDSYNLNKKRFDVGIDSEVPLRQAQISVETARNDVANYKTQIAQAQNLLNLLVGQPVPQNLLPTQPVKRIAQQNVFTAGLPSDLLNNRPDVKAAEYNLSAAGANIGAAKARLFPTISLTGSAGYASTDLSDLFKSGGFVWSVGPSLDLPIFDWGTRRANVKISETDQKIALSDYEKSVQSAFREVNDALATRANIGERLTAQQRLVEATNRNYTLSNARFRAGIDSYLTVLDAQRSSYAAEQGLLLLQQANLNNQIELYKTLGGGLKANTSDTVVHQPSSAELKKQ	4.0364465	0.000145908	up
A0A385EQQ7	SnoaL-like domain-containing protein	64	5	10	1	14.2	MSLSQKEIAVRFLELAAAGEVDEAYGNYTAPNFKHHNPYYAGDKISLKEGMRESAIETPNKVLEVQHVIEDGALVAVHSKLEMQMNNKLTILAVVHICRFENEKIAEFWDIGQIQPDPLVNENGMF	4.4729858	0.00268032	up
A0A385ET64	Uncharacterized protein	64	2	10	2	6.6	MKLAKTLLATTLALTAASTFAASKHDQAHNTAGEEKVVVSTQEQANTANAASDAVGSASEAAPATR	5.3994648	0.002729004	up
A0A385EUA0	1,2-epoxyphenylacetyl-CoA isomerase	58	12	47	3	28.9	MDYQNIIAEEKNGVGYLTFNRPKALNSFNVDMHREVAEVLSQWTKNPDVRCVVISGEGRGFCAGQDLGDRVVDPNAEAPDLGYSIETYYNPLIKTIVNMPKPVICAVNGVAAGAGANIALACDLVIAAKSANFVQAFCRLGLVPDSAGTWFLPRAVGHARAMGLTLLGDKLPAETAKEWGMIWDVVEDAELKTKVTELAERLAKQPTFGLSLIKKAIHQSSNNTFDEQMLLERDLQRIAGRSEDYREGVQAFMNKREPNFKGR	2.935053	0.000658446	up
A0A385EUT6	3-hydroxyadipyl-CoA dehydrogenase	38	17	35	17	57.1	MTDLDLSRARIAVIGSGTMGIGIAQLAIVNGHTTVLYDLDAQKAQQAVQGLGQTFKKLVEKSKLTEQQADEALARLTVVNQIEALRDADLVIEAVVEKKEVKQSLFKQLAEICSAQTIFASNTSSISVTAISAGITHPERVVGLHFFNPAPVMKLVEIVQGLKTPNSLCLALKNLMLNWKKIPVLTKSTPGFIVNRIARPFYAEGFRALQEQVTSYDQLDYALKQCGGFAMGPCELTDLIGQDVNFSVTQSVYQEFFYEPRYRPSLVQKELVDAGAWGRKSKQGFYTYNEKNQYQTFQPQAVVAKPVDAHIQLKGTWSQLPAFLTRLGLKSGSASDDNILQIDDIDLRLSQGESANIHYLSRKVVLMDWHHDFEQAEALVLSHNELCETNDLAKVEAYFAQFGMSVMWIKDHPALLTLRTIALLINEACEASLHGVASLEDIDNAMKYGVNYPKGPYQWLTQMGGAYVLQTLNNLYALYGEEKYRASIYLKQYVAKTQNIATQYSRDMTEFA	2.5755996	0.002153939	up
A0A385F163	Ion channel protein Tsx	28	6	10	1	27.7	MQLKQLAATCALLSATAMVQAKPIWQDFSVTGLYGENYEVVDDKETTITLEYAAKVKYADVFFFMDRMRGEDDYKSTYFELSPRLSLGEVSGKKLTYGPIKDVLISTTWESNTQNGNNFDNFLYGFAVDLDIPYFQYANLNFYRANNEKTDDDYQMTFVYGIPFKIASEDFLVDGFLDWSTAEDDHASELNWTTQWKWNVGKHISPDTRLYLGIEHSVWNNKFGIKGADENNVSALVKYHF	0.345583	0.006040995	down
A0A385F1H2	Uncharacterized protein	30	2	3	2	12.1	MHSKIIGLTVIMGIISSMAFAEPAIQPGETLESLSKARITTNVNTQAATPTAQTSDATTEVKVEDIDPIIEEKTEETVKAAIQPAPQATAEAVVTPIASSQLNVSVDDIDVAHPTE	3.0333718	0.033480176	up
A0A3F3MQT9	Adenosine 5'-phosphosulfate reductase	63	12	38	1	28.5	MRPSLLPGTPMTVIPTIDIVDALAAEYAAKSPREILELALSQQGEIAISFSGAEDVVLIDIASRLGKPFRVFSLDTGRLHPETYQFIETVRKHYNINIEICFPDAEAVQSMVNEKGLFSFFKDGHQECCGIRKVQPLRKKLATLDGWITGQRKDQSPGTRTEIPVLQADAGFSGPGKQLIKYNPLANWSSADVWSYIRMMEIPYNPLHERGFVSIGCEPCTRPVLPNQHEREGRWWWEEATQKECGLHAGNLKK	0.1998814	0.025160069	down
A0A3S0N6T4	Cro/C1-type helix-turn-helix domain	26	5	10	5	24.3	MTIGARLKEERERLGYTQPVFAELAGTTKKSQIDYEKDLTQPKAGYLAAIAEVGADIGYIVTGNKSPKLQNSDFAYEFDLVNVYDVSVSAGDGAVCLGETEPASRLAFRKDWLARHGLYAKDLVIVYAKGDSMEPTIHDKEPLLINTIDKELTDGFIYVVRNHENFWVKRVQRQFNELLLLSDNEKYLPMKLDLNESTDVEIIGRWIPPSRGTFY	0.2194652	0.000307458	down
A0A410J6J6	Resolvase	28	5	8	5	24.1	MNNVARIYMRVSTEKQDLERQDKVINDARNAGYYIAAVYREKASGITPDRPELNRMIHDLQAGEVVIAERIDRISRLPLPEAEKLIVAIKEKGAKLSIPGVIDLSEFSKDASGISKIVLDQVQDMLLKIALQMAHEDYLLIKKRREEGIELRKNKGLYNGRKADKKLHDKIVELRKQNISISKTALIANCSVSLVKLVWKRYSESNSSQALK	0.4093049	0.04215265	down

A0A411MUY4	Patatin-like phospholipase domai	41	18	36	6	57.7	MFEKIRSDMNPHQAYRIKKLQRQLDMAESYEEWKSFALKLDEETGAQEWKFDNSSPYFDAELIS YRYTLLKRYRQQHRTLDLIYLLKEGLTYDIANIGHPMLFAATHVGTKKLIEDYIEEVSQSLAYIAS SECITFQRKKKIEFFENCEKAYGQPALMFSGGATLGLFHTGVCKALIEQDLMPKVLSGSSAGAIM TGMLGISASEDIQNLLNGEQFFSDAFHFRKLRELIKGNGGIADVHYLKKFLIENLGDLTFEEAFKK SGLNINVAVAPYDATENPRIMNAIMTPNVLVWSAVLASCAVPVLFPPVRLTSKRYDGEHTPYMA NTKWVDGSVRSDFPQERMARLYNLNYTIASQVNPHVVPFMQDDARRFRKDVLSWPERILRRQG KVLSMGLMDFTRQRLGAISPVRRLLDHGYGVVGQRYYGDVNIIAKYSLKHYAYTLQNPRPHLF KRLQREGERATWPKISSIETHARIGKTIQHCLEVLRFEEKKQQPESYYAEA	2.2976708	9.41E-05	up
A0A411VGD7	DNA-directed RNA polymerase beta subunit, bacterial-type	71	74	609	2	151.8	MAYSYTEKKRIRKNFGKLPQVMDAPYLLSIQVDSYRTFLQDGKSPKNREDIGLQAAFRSVFPIES YSGNAALEFVEYSLGKPEFDVRECILRGSTYAAPMRVKIRLIIKDRETKSIKDVREQEVYMGEIPL MTENGTFVINGTERVIVSQLHRSPGVFFDHDKGKTHSSGKVLYSARIIPYRGSWLDFEFDAKDLV YVRIDRRRKLLATVVLRALGYNNEQILNLFYEKVPVYLDMGSYQIDLVPERLRGEMAQFDITDN EGKVIVEQGKRINARHVRQMEAAGLTKLSVPDEYLYERITAEDITLRDGEVIAANTLLSHEVMV KLAEGGVKQFNILFTNDIDRGSFVADTLRADLTRDREEALVEIYKVMRPGEPPTKEAAENLFNNL FFSSERYDLSPVGRMKFNRRLGRPYEVGTDQKSREVEGILSHEDIIDVLRTLVEIRNGKGEVDDID HLGNRRVRSVGEMTENQFRVGLVRVERAVKERLSQAETDNLSPQDLINAKPVAAAIKEFFGSSQ LSQFMDQNNPLSEITHKRRVSAFGPGGLTRERAGFEVRDVHQTHYGRVCPIETPEGPNIGLINSLS VYAKANDFGFLETPYRKVVDGRVTDDVEYLSAIEEVGTVIAQADSAVDKDGNLTEEFVSVRHQ GEFVRMPPEKVTHMDVSAQQVVSVAASLIPFLEHDDANRALMGSNMQRQAVPTLRADKPLVG TGMEANVARDSGVCVIANRGGVIEYVDASRIVIRVNEDEMVAGEAGVDIYNLIKYTRSNQNTCI NQNVIVNLGDKVARGDILADGPSTDMGELALGQNMRVAFMTWNGYNYEDSILLSERVLQEDRL TSIHIQELSCVARDTKLGAEEITADIPNVGEAALSKLDESGIVYIGAEVTAGDILVGKVTPKGETQ LTPEEKLLRAIFGEKAADVKDSSLRVPSGTKGTVIDVQVFTRDGLEKDDRALAIEKAQLDSYRKD LKEEYKIFEEAARERVIRLLKGQESNGGGSTKRGDKLSEDLLSGLELVDLLEIQPADEAIAERLTQI QVFLKEKSAEIDEKFAEKKRKLATGDELTTGVLKVVKVYLAVKRRIQPGDKMAGRHGNKGVVS NILPVEDMPHDANGVPVDIVLNPLGVPSRMNVGQILETHLGMAAKGLGDKIEKMLKEQRTVLE LREFLDKIYNKVGGEQEDLDSLTDEEILALAGNLRAGVPLATPVFDGAEESQIKDLLELADISRTG QTVLFDGRTGEQFDRPVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRF GEMEVWALEAYGAAYTLQEMLTVKSDDVEGRTRIYKNIVDGNHYMDPGMPESFNVLTKEIRSL GINIELKNGD	0.2497468	0.003300984	down
A0A429LHC2	SDR family NAD(P)-dependent oxidoreductase	63	12	30	4	29.2	MAKLDTLQNKVVWVTGASSGLGKALAGEFALQGAQVILTSRRFEELEEVRVGLLHPDQHLSVV ADITNQEQVQEAYEQILKAKGRIDWLINNAGLSQRALIQDTTMATERAIMEVDYFSQVALTKTV LPTMLKQKSGRVVFVSSVAGLLGTQYRASYSAAKAAIHMWANSLRAEVADQGVEVSVIFPGFV KTNVSFNALNGAGQTQGHQDEAIENGLEADVFAEQSVKALMQGQEYIVVGGTKEKLGVMVSR MSPKLLYKMIRKTKVK	0.3580605	0.000396847	down
A0A429MK36	catechol 1,2-dioxygenase	64	13	34	13	33.2	RQQIDALVKQMNVDTAKGEVDARVQQIVVRLLGDLFQAIEDLDIQPSEVWKGLEYFTDAGQAN ELGLLAAGLGLEHYLDLRADEADAKAGITGGTPRTIEGPLYVAGAPESVGFARMDDGTETGKID TLIIEGTVTDTDGNIIENAKVEVWHANSLGNYSFFDKSQSDFNLRRTIFTDADGKYVALTTMPVG YGCPPEGTTQALLNKLGRHGNRPSHVHYFVSAPGYRKLTTQFNIEGDEYLWDDFAFATRDGLV ATAVDVTDPAEIQRRGLDHAFKHITFNIELVKEAAAAPSTEVERRRASA	2.6515409	0.01798234	up
A0A481WVU6	Pgt1	4	2	2	2	71.5	MVFLRQQLLFIFIAFLSTCVGIYVAWDMNLTWHKFYTYLISEKAIFSILFNYAVIQLFFIILGRKYT ALCLSQLFVIFLNFINKKKQQYLFSNLSPEDIFLLPEAMKATPWHLQLIFFILIIFFLIILLIAVRKESK ATFHTYVPNIIIFGLISSGLIYLNFIRNPTGACFSENKPMICASLQEFPNTRNDWIGDYRKIQDYGFV TFYVSKVLDNVTSVLLPSRKVSEQDIQQILQQHHFVQPLEKNEKEYPNIIIVMEESFWDSHHLESG LPKDLLSFVHQNQVSNLLSPSFGGGTANVEFEVLTSLNTTFFPNELLYVSKLKKPIYALPYYLKSI GYQTVAMHNNYSYYYNRNKVYPELGFEKFISLENMIAQKDRSNIFNQGGWATDDLIFDSIKSTL KENEQQPKFIYAITVENHPMYNDDRFGKQNYKFNKELSDTEKQKLSTYTAGTVRANQKLKELA EYLKTVDRPTILVAFGDHLPNLQEVYESYGFFKDDPERTSLKNYQTPFVVWSNYKLDKKPLKQP YIAASFVAPKLLKLAGLPLSDYYQFVDDVSSCYSAIHQKFINENPTCNFDKKVLLKGYENLNKDV LDGHNHTYKIMQNNKEEMEQ	0.3462259	0.000362193	down
A0A481WW07	Wza	53	15	35	4	41.2	MHKGSRVKYCQFFSVLALSLSAASCAVTSGLQTYDIPSEGVYKTDLGTTVNVVKISQETLSAIQP AQIDYQRDYASLFKTQQSIYRLSPGDILSIQLWAYPEITPPVNGISSEQSIQANGYPIDQSGYIQFPL VGRYKAAGKTLAQVNRELHNQLARFLKNPDVIVRVLSYEGQRFSVQGSVTKGGQFYLSDQPVSI YTALGMAGGVTTTGDNTYIQLIRNGRTYNLNTIDLEKAGYSLHKLLVQPNDTIYVSTRENQKIY VMGESGKNQALPMRDQGMTLTDALGESLGINPLSGSSSRIYVVRTNPNDRTTEIYHLNLMSIGDF GLANQFRLRSNDIVYIDATGLTRWQRVVNQIIPFSNALYNIDRLGQ	2.7377637	0.003436815	up

A0A4P8VDY7	Universal stress protein A family	47	10	15	7	31.2	MSKIIACIDGSLVTNTVCDYAAWFSDKLNSPIKLLHVIDKPKAKAPQDLSGAIGLGSRETLLKELVELEERKGKIELEHGQILLREAKNYLVEKFSIDAQSFQRHGSVLETIMGMEDDIRVLVMGKHGNETEHDSSKIGTHIENVVRALHKPVLITSAPFSPPKSFLIAFDGSQTARKCVERIASSPLLKGLAVHLVYVGNPNSEMQNQLSWAKEQLESQGFNITSNTLDGEVDKAIINYAEQHQIDLIVVGAYGHSKIRQFFIGSTTTKVITSANKPVLLLR	2.5441704	0.002200668	up
A0A4Q4H7V6	2-methyl-aconitate isomerase PrpF	20	9	21	1	42.0	MSFVPQIKIPATYMRGGTSKGVFFKLDDLPEKAQVAGQARDQLLLRVIGSPDPYGKQIDGMGGATSSTSKTVILAKSTQPNHDVDYLFGQVSIDQPFVDWSGNCGNLTAAVGSFAISNGLVDADRIPENGLCTVRIWQKNIQKTIIAHVPITNGQVQETGDFELDGVTFPAAEVQIEFLDPADDGEEGGDMFPTGNVVDQLDVPEIGSFQATFINAGIPTIFLNAEDLGYEGTELQDHINGDAAALARFEKIRAYGAVQMGLIKDISEAAARQHTPKIAFVSKPKNYTASSGKNVSEKDVDLLVRALSMGKLHHAMMGTAAVAIGTAAAVPGTLVNLAAGGGEREAVRFGHPSGTLRVGAQAELTNGQWVVKKAIMSRSARVLMEGWVRIPGDSF	0.208348	0.010811004	down
A0A4V5MUT8	Isocitrate dehydrogenase [NADP]	69	23	160	2	45.6	MGYQKIVVPADGDKITVKADLSLNVPNHPIIPFIEGDGIGVDITPAMKKVVDAAILKAYGGKRSIEWMEVYCGEKANKIYGTYMPEETFEALREFVVSIKGPLTTPVGGGIRSLNVALRQELDLYVCVRPVRWFQGVPSPVQHPELTDMVIFRENSEDIYAGIEWKADSEEAKKVIKFLQEEMGVTKIRFPEGCGIGIKPVSKEGTQRLVRKAIQFAIDNDKPSVTLVHKGNIMKYTEGAFKEWGYELALDRFGGELIDGGPWVKIKNPKNGKDIIIKDVIADAFLQQILMRPADYSVIATLNLNGDYISDALAAEVGGIGIAPGANIGGAIAVYEATHGTAPKYAGQDKVNPGSIILSAEMMLRDMGWTEAADLIIKGISGAIAAKTVAYDFERLMPGATLLRCSEFGDAIIQHMED	2.988667	1.14E-05	up
A0A517D2C4	Two-component system response regulator PmrA	37	5	28	5	25.5	MTKILMIEDDFMIAESTITLLQYHQFEVEWVNNGLDGLAQLAKTKFDLILLDLGLPMMDGMQVLKQIRQRAATPVLIISARDQLQNRVDGLNLGADDYLIKPYEFDELLARIHALLRRSGVEAQLASQDQLLESGDLVLNVEQHIATFKGQRIDLSNREWAILIPLMTHPNKIFSKANLEDKLYDFDSDVTSNTIEVYVHHLRAKLGKDFILTIRGLGYRLGQS	4.236701	0.003257215	up
A0A5K1MHI6	Uncharacterised protein family, zinc metallopeptidase putative	57	9	27	1	33.0	MRWRDRRVSTNVEDRRGGGGVRAGGISIIGLVVAFVAWKFFGVDPQQAYQATQQVTASQQSNATAPESLTAEQKEASDFVGTVLADTEDTWTPIFKQLGKTYTPPKLVLFSGMIQSGCGTAQSAMGPFYCPADQKVYIDTEFFKDMREQMGISGEQNQTELSRQDQAGDFAQAYVVAHEVGHHVQTLLGISSQVQQARAQVSQREGNQLSVRQELQADCLAGIWANHNQQRTQFLEQGDVEEAMDAAQKIGDDYLQKRATGQVVLDSFTHGSSEQRMHWFQVGLKTGDISQCDTFNNSI	5.5364372	4.05E-06	up
A0A5K1MJI7	Outer membrane protein Omp38	46	17	358	2	38.5	MKLSRIALATMLVAAPLAAANAGVTVTPLLLGYTFQDSQHNNGGKDGNLTNAPELQDDLFVGAALGIELTPWLGFEAEYNQVKGDVDGASAGAEYKQKQINGNFYVTSDLITKNYDSKIKPYVLLGAGHYKYDFDGVNRGTRGNSEEGTLGNAGVGAFWRLNDALSLRTEARATYNADEEFWNYTALAGLNVVLGGHLKPAAPVVEVAPVEPTPVAPQPQELTEDLNMELRVFFDTNKSNIKDQYKPEIAKVAEKLSEYPNATARIEGHTDNTGPRKLNERLSLARANSVKSALVNEYNVDASRLSTQGFAWDQPIADNKTKEGRAMNRRVFATITGSRTVVVQPGQEAATPAAAQ	0.1738403	2.90E-07	down
A0A5K1MJT9	Flavoprotein-like superfamily	53	5	9	1	20.1	MSNSNIAVVYFSGYGHTKVVAETFANEINAQLIQIDQEGNITDQDWETLNNAKGIVFGAPTYMGTAPWQFKKFADATSKVWFTRGWQDKVFAGFTNSASLNGDKQVTLIQLQTLASQHGGIWVSLGLLPANTKDATREDVNNLGGSVGLLVQSPSDASVDEVPTGDLETAKVYAKRVQAIVNKIYG	0.2540446	0.033508444	down
A0A5K6CRD2	(R)-benzylsuccinyl-CoA dehydrogenase	59	19	43	19	45.9	MFELSKKAQDFAERTKKFIQEEIEPVEAKFWEEVHELNPDGNWKKWQWPELLETLKSKAKQAGLWNMFLPDEKLGAGLSVQEYAHIAELTGRSLLAPTVFNCNAPDTGNMEVLWRYGSEQQKQQWLEPLLDGKIRSVFCMTEPDVASSDATNMQATALIDGNEIVLNGKKWWSSGLGDPNAKVIIFMAHTPDETKDRHHQHSMVLVPIDTAGVEIQRMLPVFGDYDAPHGHGEVHFNNVRVPIENFIGGAGQGFEIAQGRLGPGRIHHCMRCIGAAEKALELMIDRGMSRTAFGKEILKLGGNLERVADARVAIDQAARLLTLYAAYKMDTLGNMAALTEISAIKVVAPSVLEKVVDMAIQLHGGAGVSRDTPLTGFFAQARSLRLADGPDEVHKGMIAKLELAKRGYFGRHKKV	2.8119316	1.42E-05	up
A0A5P1UPF1	1,2-phenylacetyl-CoA epoxidase subunit A	31	7	16	1	35.6	MENNYQKFEQNIANEITIEAKDQMPDAYRKTLIRQIGQHGHSEIVGMLPEGNWITRAPTLKRKAVLLAKVQDEAGHGLYLYSAAETLGADRDDMMEKLINGKMKYSSIFNYPTLTWADVAAIGWLVDGAAIVNQVALCRTSYGPYARAMVRICKEESFHQRQGFEAMMALANGTPEQKQMAQDAVNRFWWPALMMFGPSDKHSPNSAQSMAWKIKRFSNDELRQKFVDNTVPQVLQLGLEVPDPDLKFNEETGHYEFGEIDWHEFNEVIAGRGPCNHERIEARRKAWENGKWVRDAAVVYAKKQQLEANKVA	3.5942695	0.046054207	up

A0A646MCI5	Phage capsid protein	18	4	7	1	33.3	MTTTVNSDMIIYNQLAQTAYLERLQDNLNVFNQASNGAIVYRNEIIEGDFNKEAFYKVGGSIKHRDVNSIAKVVPEKIGSGESVGVKVPYKYGPYASTEEAFKRRARTPEEFAMILGYDLADALVAGRLQYSLASLKAAISSNPDMVAKGSIAVDGRKALTRGMRKFGDKFGRISLWVMNSDTYFDIVDDAITKQIYGESEIVIYGGLPGTLGKPVLVTDAVGDDDAFGLQMGAVTVTESQVPGFRAYDINDEENLGIGMRAEGAFNLDILGYSWDTSKGENPDLTLLGSSANWKKHATSNKMTAG	3.0290224	0.001153574	up
A0A654KV19	Aminotransferase	68	17	114	1	44.9	MFQHIPPYAGDPILSLMEQFNADTRSEKVNLSIGLYYNEDSIVPQLETIIEAQKRIEPKNGKTKLYLPMEGFKPYREAIQALLFGVNSPAVKAGRAVTIQTLGGSGALKVGADFLKTYFPNSDVWVSQPTWDNHVAIFNGAGIKTHFYPYFDAETRGVDFDGMLSTLKTLPEQSIVLLHPCCHNPTGADLNPAQWDQVIAVLKDRNLIPFLDIAYQGFGDGMEEDAYAIRALDQAGLNFIVSNSFSKIFSLYGERVGGLTFVCDDAEAAQCTFGQLKATVRRIYSSPPTTGAWLVDEVLNDAELNQQWQGEVKEMRERIIKMRSILKDELTKALPDRDFSYLVNQKGMFSYTGLTAEQVDILREEYAIYLVRSGRICVAGLNMNNVYTVAKAMAEVLAKSVEAA	9.1141835	1.02E-05	up
A0A654KWM6	Small-conductance mechanosensitive channel	17	8	55	8	59.1	MNEFFNGPRGAQFDAMYYWDQFHPILAAIVILLVGWIIALLVAAGVKKLLQKVNTNAKLSSATGRTPNIEGLISKVVFWFILILAVVAALNVLNISGVSGPFSNMVNQVLVYIPNIIAAVVVGFIGWIVARLVRAGVTNVLSRTQLDDKLSSEVGVGGISQNIGEILYWLVLLLFLPIVLSILGLTGLLIPVQNMVNDAVAFLPNIFIAGVIVFVGYILAKIVRGIVEGLINSLGVQSQAEKIGLFKNSNVGKFLGSFVFAIIIITTLIVAFEALGIETISQPATAMLNEILQAIPNIIAAGLILLVAYIVSRFVGRLVAELIAGTGVDEIPAKLDVQRFLGQTKVSNAVGWLIVFFTMLFAVSEAADRLGFDQISGLIAMFIHFGANILLGAVILVIGFWLANVVANVVQRGEYNSSRWLGSLVRVLIIGLVLALGLRAMGIADSIVNLAFGLTLGAVAVAFALAFGLGGRQPAERLLSDLLDKAKKEASQPNPLYQPPTNNKTTGSSTTVSTPSTTTTAPSTTVSSDAKPADSAQVNPSQPPVNKPFGSTGENDEI	2.0611001	0.008026215	up
A0A654L2G6	Uncharacterized protein	16	1	4	1	14.8	MGWEIPIFHFRVNGEPRVLAYLKPHASEAYTEELSYVYDLVNDELNEYFNDDEFTYNSNELRLFYLQRPAEAFILWHPDQVHNQEQIQFVYGVGIPNANRLTTIDIPEIPESFPHIFWDKTEDQ	0.2491475	0.00720467	down
A0A654L2Q2	Uncharacterized protein	12	2	2	2	33.4	MAGQIVLKSQNAIDNLADLPDINYYINRVKADGGVIYNMNALLDVFAFIYSKNITDSEVFSAINPAWGVKYDPATGNISKLYSLFDPAGDLNAFGGSLPIKLQNDLGVPSAYLGGSQNTYLKAAGTVSGVETIGYATAAVIPQLSNYGAGAGTNFPLGLLWSREAHDAADPVGSVTPYVAASWYVGRPDTSNITLSQWTEYFSVFSSTGSAGSNALTGYENAKPLSAFADTGGLRVYKNGLQVLFDSTVTQTPIHKDKLELLIGATVTGTGAPATTYFLGHFIENWVLVNTASEKMIEISKRINDKYYAVIPH	0.4055468	2.95E-05	down
A0A654L9F1	Lipoprotein	49	8	11	8	20.5	MKNLITIAGFLLLAGCSTQKQPQSEPPYVKQNYSESDPAAKLSVSQFAGVVKSIYPAYQISHSNDGSEVKFLPNDVKADTKFMPNNNWYSIKIIKEPNTENWKGLIVEVFNKGSFGESKAVAAKDCQKIFGNIDNRVPAVLYDLENRLNQSPNASISNRQYGYTFHLDASHYNQGYPVTCMVSN	0.20581	0.004263857	down
A0A6B2QRH5	Phosphoethanolamine--lipid A transferase PmrC	23	11	47	1	62.2	MLNFFSTLRNKQISLFMFNLIIAIWLGAILNIGFYHQVHTLTPYFGVKAILFLAATLIILVATYYAVLQILNWKWTAKIFAILLIFIGGFSSYFVNTLGVIISPDQIQNMVQTDVSEVTDLISLRFVLWTIFFVILPIFLITQVKFKQEKVSRLLLKKVFSLVASLAVVGVLLFTYYVDFAAIFREHRDLKGMISPQNSISSLMSYYHKKAPKKNLPLVIYGQDAHQVQQVQKNLPKLMILVVGETARAESFSLNGYAKNTNPELSKQDIFNFSQVSSCGTATAVSVPCMFSGMPRVDYDEQLASHREGLLDIAKRAGYQVTWIDNNSGCKGACDRVEQYQIPENLKKKWCKDGECYDDILIDSLKQYLSTIAKDDDRPRLIVLHQVGSHGPAYYKRAPEAYQPFKPTCDTNAIQGCSQTELLNSYDNTIVYTDHVLSQMINTLKEISKYQTGLWYLSDHGESTGEHGLYLHGSPYAIAPSQQTHVPMIMWFSESWKQHNLAQVNCLSQQTKQKLSQDNLFPSLLSLLDVTTQVINPQLDMLHSCAHVN	5.5380995	7.34E-06	up
A0A6B9KPL0	Gtr89	60	14	37	14	30.8	MISLITATYNREKLLKKLYESLCVQTVKKFEWIVIDDGSIDKTDELINSFKLDNIIDITYLKKTNGGKHTAMNIGVEIAKYAYVFFIDSDDFLPNDSIEKIINYIDKVSAREDYSEISGVCGLIADFQGNLIGTKYSENLCCSYIDYRYKYHIKGDKAEIFKREVLLEYKFPVIEKEKFCPEALVWNRISDKYKMYFFNEVIYYREYLEGGLSDRSVEIRKKAPISTLLYYKELYLNKNLNWYYRIRAYINYMRFKFIS	0.1938871	0.015338432	down
A0A6B9KQE9	Gtr93	19	7	9	7	41.4	MRILYVITGLGGGGAEKVVCDLADEMCSRGHIVKIAYLKGEIVVFPKNKEIELVYLGLESILNALSFFRNYRDLIISFTPDVVHSHMVHANIFTRISRKFYSIPKLICTAHSSNEGSKFRMLAYNFTHNLADLTTNVSLEASRNFEIRKGVPKGGIRTIYNGIDLSKFIKSPLNKDKIKNNLGIENGIPIFIAVGRFHEAKDYPNLINAFRIFKTKIIHNSQDNNLPILLIVGDGELKSEVELLIESFNLKDNIKLLGRRNDIPDLLNIADYFILSSKYEGLPTVIMEAMACETFVISTNCSGVEEIMNDTGIMVPICDSEALAEGLIKAYNLSPKEIELNNLSARRRIEKIFSLEKSIETWLEIYES	0.2374266	0.021794684	down
A0A6B9KZP3	UDP-glucose 4-epimerase	45	14	57	2	37.2	MAKILVTGGAGYIGSHTCVELLEAGHEVIVFDNLSNSSKESLNRVQEITQKSLTFVEGDIRNSGELDQVFQEHAIDAVIHFAGLKAVGESQEKPLIYFDNNIAGSIQLVKSMEKAGVYTLVFSSSATVYDEANTSPLNEDMPTGMPSNNYGYTKLIVEQLLQKLSVADSKWSIALLRYFNPVGAHKSGRIGEDPQGIPNNLMPYVTQVAVGRREKLSIYGNDYDTVDGTGVRDYIHVVDLASAHLCALNNRLQAQGCRAWNIGTGNGSSVLQVKNTFEQVNSIPVAFEFAPRRAGDVATSFADNARAVAELGWKPQYGLEDMLKDSWNWQKHNPTGYKR	0.3080406	0.018931692	down

A0A6F8TC76	Oxidoreductase	60	7	21	2	17.5	MLNTALPVLYKDGTIADNTYQIIAEDGVIPRGDVVLTTAQLDQLANIQGKKALYVTVNDSPEDHTFPLSELDAIFIEFAGFGDGRGYSFAALLRRQGFQGELRATGDVFKDVLNYLKRSGFDSFVIKEGKDVQEAAAGLQDFTHPYQASTAVPKASYQTGA	0.19412	0.028246243	down
A0A6F8TGE6	Uncharacterized protein	17	1	3	1	5.2	MKLLALVSMGVAASYWYKTIKDSKPTLLKPNFDEIVKNFVIAEFKV	3.3954011	0.006753311	up
A0A6H2UPY5	Sel1-like repeat	52	12	16	1	29.6	MKRLLIASLIAISSSSIFAADTTTSAAKNDVFKQAEQLYAAKNYPAAFQEVQRLAQTGNAQAIYNLGYMTQMGQGTAKDNAKALKYYEDASNKGYAQASYTLAQIYETGELGVAKDSNKFSQYIQKAAAQGSDDATVKIATILFAQKKPQSHQIALQKLAPLIRKGNYPAIQVKALYDISQGVENKNPLMKRQGIEALQTIAQKGYAPASMALATMMANGNIIPQNLPQAKQIFTELAKQNVPNARESLASVEKIIAEKNKQAAAAPTQPAPKK	0.4314752	0.045043046	down
A0A6H3SV37	Glutathione peroxidase	83	12	98	1	20.2	MTQSVYHIPVKAISGETVDLDQYKGKVLLIVNTASKCGLTPQYEGLEKLYQAKKDQGLEILGFPANNFKEQEPGSDEEIQQFCSLNYDVHFPLFSKISVAGEDKHPLYQVLTTAQPERIGEGPFRERLEGLGIPTNPAPEVLWNFEKFLINKNGEVVARFAPNLTADDEQIVKAVEAELAK	0.2243731	0.008896651	down
A0A6H3T2F1	HTH-type transcriptional regulator with aminotransferase domain	4	2	3	1	54.0	MTFQYQVLANQLAHRIYQDELKPHQKLISLRDFARQHGISLSTAKSCYELLEARGLIYVKPKSGYFVVARTPSSPIPDSPDFLSLPRHVSNLELHNQIQEAALQSHLVPLGSIQLTPHFIPVEGLRRSIQRALKNCQPQDFLYCNKQGHEQLRKALSDHWREDGIYIAPEDIFITNGCMPALSLVIQKLTEVGDSILIPTPTYNGHLQLLASLKRQIVEIPADHRGIDLERLESLMQQGLAKVCLMTANYQNPLGYCFSNTEKQKIVELAAKYQCFIIEDDIFGECGYSSERPLPIRYWDREGYVIWCGSVSKSLSSAYRVGWFCLTTKLEHLKLELLVSNIGVNTPLQLGLADFIYSRAYREHLEQLRPNLMRQVEEYRSCILRAFEGIPIALSQPEGGYALWIQLPKSVDSLALYYTAQAQGITVVPGHVFGEDERYRHFIRLNAGHELTADVRQAIMSLADWSRQQMQTVS	2.1376865	0.02369312	up
A0A6H3T3L2	Tetrahydrofolate dehydrogenase/cyclohydrolase	73	14	69	2	29.7	MALVLDGRALAKQIEENLLVRVEALKAKTGRTPILATILVGDDGASATYVRMKGNACRRVGMDSLKIELLQETTTEQLLAEIEKLNANPDVHGILLQHPVPAQIDERACFDAISLAKDVDGVTCLGFGRMAMGEAAYGSATPAGIMTILKENNIEIAGKHAVVVGRSAILGKPMAMMLLQANATVTICHSRTQNLPELVKQADIIVGAVGKAELIQKDWIKQGAVVVDAGFHPRDGGGVGDIQLQGIEEIASAYTPVPGGVGPMTITTLIRQTVEAAEKALG	0.4573897	3.31E-05	down
A0A6H3T9J1	Phosphoadenosine phosphosulphate/adenosine 5'-phosphosulphate reductase	73	13	42	1	27.5	MTVIPTIDIVDALAAEYAAKSPREILDLALSQQGEIAISFSGAEDVVLIDMASRLGKPFRVFSLDTGRLHPETYQFIETVRKHYNINIEICFPDAEAVQSMVNEKGLFSFFKDGHQECCGIRKVQPLRKKLATLDGWITGQRKDQSPGTRTEIPVVQADAGFSGPGKQLIKYNPLANWSSADVWSYIRMMEIPYNPLHERGFVSIGCEPCTRPVLPNQHEREGRWWWEEATQKECGLHAGNLKK	2.7158473	0.000172013	up
A0A6H3TEL8	Lipoprotein	17	2	5	2	11.7	MKKLSTILTAGVLAMLSVSAFACPKGTQLQGGTGPNHKGGKCVAVHGKATAQKAKKEATKTKQEVKKDLTMQKHDAMTSATHAQHESHQMTHQMKQGAVKTANTAKAATKP	2.0935425	0.021494633	up
A0A6H3UE57	Winged helix DNA-binding domain superfamily	16	4	8	4	36.1	MKKDLVVKDNALINASYNLDLAEQRLILLAILEARESNTPSDRDLTIHAESYINHFNVHRNTAYKVLKDACKNLFERRFSYQKLTAKGNLENVMSRWVQRVSYVENEALVRIRFSDDVAPLITNLEKHFTSYELEQVSSLTSAYAIRLYELLIAWRSTGKVSMLETKELRSRLGVSDTEHQRMESFKRRVLEPAIQQINDHTDIKAEYEQHKRGRSIVGFSFSFKQKSKPKTINHERDPSTVDMFCNLSDSQINTYSSILSKVHSISDLAGNKDYQAFAIWIANILRDPTSVREETAKRIFKALRTETDFKG	0.1887928	0.003349216	down
A0A6I4HS79	Aminotransferase	70	30	213	1	59.7	MGKVDYSKYAKLSPFELKDNLIELAQSKTDRIMLNAGRGNPNFLATIPRRAFFQLGLFSATESEFSFSYMPEGLGGFPRTVGLQSRFDNFILENRDKPGVVFLGKAVSYVRDQLGLDPDLFLLEMVEGILGCNYPVPDRMLRVSETIIKEYVLREMGVQGMQKRDLDLFAVEGGTAAMAYIFNSLKENKIIKNGDRIAIGSPIFTPYLEIPKLNDYQLEEVLIEADPKLGWQYPESELRKLEDPSIKAFFLVNPSNPPSVKMSDEGLAILADIVKKRPDLIILTDDVYGTFADNFKSLFAICPDNTILVYSFSKYFGATGWRLGVIALSNNNVLDKQIANLSKKEKKELEDRYSSLTTDPASIKFIDRLVADSRNVALNHTAGLSTPQQVQMVLFALFNMMDSRQSYKKAVKSVVRERDAALYRQLGVDVPTDPNAVDYYTLVNLENTSRTLYGDEFADWVMKNKNPTELLFRVADETGVVLLPGSGFGVQHPSARASLANLNEYQYAAIGESLRRFADEAYAEYTKTKKIK	0.4772167	0.04313485	down
A0A6I4HT95	Uncharacterized protein	46	5	9	5	16.5	MKNIYILIFIGALIACSDKGTDKNQHNSNHKLDVVQTETNKSQSVVGENQENTDKMVKTKEADQVAQFSCSNPNITQWYGFNENIAEPKCEVVKNFQLTAYKCDISKNAFGASKDAILLENQDKRIFVYSTSKDCNEMLEVRNANAP	2.0568558	3.91E-06	up
A0A7L9DUK6	Protein of unkown function DUF2303	42	8	16	1	30.0	MSEKIEIEKFLGLAKPVIPLERGQLVALHHDYSVIAAEKFMDARFRPHGEFTTPTFNDFKDFVVAEGGKDTPIFVNQNDMKAIAVLNFHGEGQTQGHCDYLASLCLESTVVWKKLNQLKDHKLDQRNFAVFIEDWAQVLNAFDENNNAIDIKDALVAVRNMQIEASTTSNAEVENTRQVQSEMAQIAASAKKGVLPAYFTIQDSAYLGLAEREIKLRLIVNSTGSTPQFAIQIVKEELLRNEIIEDFKEEVIALLPENP	0.4585165	0.004436792	down

A0A7L9DVL0	FAD/NAD(P)-binding domain superfamily	62	23	81	23	48.6	MDIAIIGSGMAGLAAARILKDAGHTITIFEALPGRGMDSHSIEFDGGIIDAPLRVMNPHLWKNTLS LAAHLGIKTFPVRTYMSCSWLFEDRTETWLTTSRSRIGNFPIINNRKGIQQYGWRLVKGMLQLKT AIHQFFKSKNQDITLAEFINQNDIEEVFWHGVVMPVLYTICTCNPKTIGDWPAKNLLEFLRHLTD GDMLLRMKGGTPAFVDSLIKGIDIHSGSAIKKVELQGEKVLVENEKGDQGTFDRVIVATPTSKLE EFLNPEQFAEDMNLLKQFRFEQGDLVIHTDATVMPPRRKDWSVLSYMMDRKFTRQQFTVWMN AVEPSLVGKNPVFQTWRPVVDIDPKKVISKVTLTRAVVDSQTIALNKELQQRHLQPNRKVFYCG SWSCDGLPILESAVTSAMHIAEILGAPLPFVGLKPKVEVAPELGY	0.4645246	1.50E-05	down
A0A7M3FN66	DNA-binding protein H-NS-like, C-terminal domain	61	6	33	5	12.2	MSQISELSIEELKDLQLEAAKLIEIKKEQAIEDAYLKIISIAESVGYSVEDLLKVGAANSKKKARKS VKPRYRSKANEQDTWTGRGKQPRWLVAEIEKGAKLEDLRIN	0.2489345	0.012158484	down
A0A7M3FNP5	Uncharacterized protein	13	1	1	1	8.9	MSNVDPQLEHVDPAHPAAPDAYMRVLNCKSNYVNILAGWFLKDGKKKFYIADVRGNEVEAGF NRLDWLTEFDTIYKGK	0.4801587	0.004361998	down
A0A7S8F867	phosphomannomutase	46	19	57	2	51.0	MTTLTCFKAYDIRGKLGTELNEEIAYKIGRAYGQIYKPKTVVVGCDIRLSSEALKQATIRGLNDA GVNVLDLGMTGTEEVYFAAFHLDVQGGIEVTASHNPMDYNGMKLVRENARPISADTGLKEIQA LAETNNFEEVSQKGTTQSYNILPEFVDHLLTYIEPTKIRPLKLVVNAGNGAAGHVIDAIEEKFKAL NVPVEFIKIHHEADGTFPNGIPNPILIENRDSTRNAVLEHKADMGIAWDGDFDRCFLFDEKGQFIE GYYIVGLLAQAFLIKQSGEKIVHDPRLVWNTFDIVDEYKGVAVQSKSGHAFIKDVMREHNAVY GGEMSAHHYFRDFAYCDSGMIPWLLTVALLSETGQSLSTLVENMITKFPCSGEINFKVADTQITI QKIFDFYAAQNPEIDRTDGVSLDFGAWRFNVRASNTEPLLRLNIESRADRQAQPMQYYVDELTS			
A0A7S8WB40	Histidine phosphatase family protein	28	6	14	6	26.7	MTTIYLVRHGQASFGKSNYDELSENGEAQATLLGQYFKKILKEQPYVVAGTMQRHEQTAQLAL KECFPDAVIHHNNLWNEFNHQQVFARYETRFEQPELLKADVAKEHNPRAYLAKIFEGAIERWTD GDFHHEYDESWPHFKERVETALQQLCDELAKTKPRYAVVFTSGGVISVAIGKLLELSPNRTFAL NWAITNTSLTTLRLVGNEAQVLSLNEHHFIKAEHPDLLTWI	2.0659071	0.008108107	up
A0A7S8ZW13	Uncharacterized protein	46	4	12	4	12.5	MNNVAQTNDESVKAENDAVNTNSNETKAKDESGNIEDYLSPKGKKLAQRKEQMKRELELLDE QIAQEVEQAKLKVKDDLFKLLDRNKLLEISPKVWKKHMDDIKKILLG	0.2143468	0.006317437	down
A0A7S8ZW19	Replication initiation protein	15	3	5	3	36.3	MKKELVVKDNALINASYNLDLSEQRLILLAILEARQSNTPNDKDLTIHAESYINHFNVHRNTAYK VLKDACKSLFDRRFSYQKLTQKGNIENVISRWVQRISYVENEALVRIKFSDDVVPLITNLEKHFTS YELEQVSSLTSVYAIRLYELLIAWRSTGKVTMVELEELRLKLGIEPNEYKRMGQFKEKVLHLAID QINKYTDIKAEYEQHKRGRSIIGFSFKFKQKQQPKKLDSKRDPNTPDFFIRMTDAQRHLFGNKLA HDARVQSEYSHLIGTGSYEDFAKLLADMLAEEQHFKMFYPLLVEHGYKA	0.2735039	0.008604104	down
A0A7U3Y2S3	Uncharacterized protein	60	6	21	1	17.4	MLNTALPVLYKDGTIADNTYQIIAEDGVIPQGDVVLTTAQLDQLANTQGKKALYVTVNDSPED HTFPLSELDAIFIEFAGFGDGRGYSFAALLRRQGFQGELRATGDVFKDVLNYLKRSGFDSFVIKEG KDVQEAAAGLQDFTHPYQASTAVPKASYQTGA	4.2133224	2.62E-05	up
A0A7U4BKB8	Atypical kinase ADCK	51	17	61	17	48.8	MAKNASSPGKRFMKLAGMTASIATKTVSNSIRNLTADEEQKLAAKTKLFQDIGLQIADTLGEMK GAVMKVGQIASQYKDIFPPEVAKAISKLQRQAPAMPFAAIQQQVERELGKPLNVAFKSFEQEPFA AASIGQVHKAVLPSGEQVVVKVQYPGVDEACESDLKQVRLALRLMGVLKIDKKLQDQLFAEIQ DSLSAELNYEIEAQNLEVFKTFHSKLDDKIIIPTVYKDYSSRRILTLSLEQGDSIETASSWPIEIRNTI GRRLIRALGQEMFFLKRFHCDPHPGNFAFRQDGSVIIYDYGSVKTLSNEIVYSFKRLVNAARHEDI DLIETELLELHSLAEKGKFPSDLYKLWIEVLLRPLTTTYDFAENSSHHDGMLLVKKSLKYWDVF KPSPDTLMVNRTISGHYWNLIHLKVHDNLNDLFEELVPPSN	2.2208355	1.98E-05	up
A0A7U4BNK2	Coenzyme A transferase family I	52	6	12	6	22.9	MSYQKLSRDQIAQLVAQDIPDGAYVNLGIGLPTKIASYLPADKDVFLHSENGLLAFGPPPAAGEE DPELINAGKEFVTMLEGGSFFHHGDSFAMMRGGHLDIAVLGAFQVAANGDLANWHTGAPDAIP AVGGAMDLAVGAKKVFIITDHITKQGEPKIVAELTYPVTGKHCVDRIYTDLCVIDVTKDGLKVI EKVEGLSFDELQALTGATLIDATQG	2.2802428	0.003326181	up
A0A7U5XU67	Peptidyl-prolyl cis-trans isomerase	70	12	49	1	25.2	MKKISLVIAASTMSLSVFAATPITNKSPAKDQFSYSYGYLMGRNNTDALTDLNLDIFYQGLQEGA QNKTARLTDEEMAKAINDYKKTLEAKQLVEFQKQGQQNAQAGAAFLAENAKKSGVITTKSGL QYQVLKEGTGKTPKATSRVKVNYEGRLLDGTVFDSSIARNHPVDFQLNQVIAGWTEGLQTMKE GGKTRFFIPANLAYGEVGAGDTIGPNSTLIFDIELLQVLPK	4.2490566	4.17E-06	up
A0A7U5XUJ7	Uncharacterized protein	6	1	1	1	13.0	MIVSVTQDSREFNINILKAKRNNEAPFKYWLENVLKRGDILPRGKFFKGKTAGKPIWVTDEFWM HREDDIFTSNFIVPPARYGLSIFSEGEAEHFMLVGTTRRGRNYESDD	0.3641985	0.046013867	down
A0A7U5XUN1	Uncharacterized protein	67	5	11	5	9.7	MSVIDRAVEKNANLSYVALKVIECFKDAGLDLNYIDDKISEFSDLSNYAALHQALRILDDKNINR LADKLGVSISDLETTLFVLNKI	0.2732505	0.001142735	down
A0A7U7KGU4	Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily protein	58	6	52	1	16.7	MQLNHYLNFQGQAEQAFNFYKSVFGGEFAMLSRYSDMPPHDGVTLSEAQKNLVLHVSLPINEY TVLMASDVIDQFCTPNSVFTQGNNHYIAINLEKDEQEKAKQLFDALSVNGKIEMPLEKTFWGAL YGAFTDQFGVKWMINCQLDT	2.059774	0.000375682	up

A0A7Z1WNT5	Metallo-beta-lactamase superfamily lactonases	49	12	52	1	35.4	MKKLFVALGLIMGSLHISYAEPASAQQVPGYYHHQFGNYRITSLLDGTIYLDPKLFKNLSPAEKT KILTKYAAVNEKGIQTSVNAFLVDDGKSLTLVDSGAASCFGPQLGSIAKNLELAGYQLANVKTV LLTHLHPDHVCGIAQNGKAVFPNATIYAHEREADYWLNPANEKTVPEDKKENYLGTVKNVKA ALAPYQAKKAFKTFKDGDVIQGFEVINTQGHTPGHHSFRLKSKGQQIVFVGDIVHSHSLQFDAPK TGVDFDVNSEQAINTRLKMFAEISNKQQWVAAPHLPFPGIGHVYKVSAEQYQWIPLYFNNSLDK	0.2293999	0.014144021	down
A0A7Z1WQ98	Lipoprotein	27	3	8	3	17.7	MKKIFLTALATVGLQACTTPYQEMGASGGVEATIIDDNVFQVRASVNGYTHKSIANQYALRKA AEVSKSLGCSYFSAINNTSQSYNQNISKVDSGLMTTPNGVYYVSSAGTQYKLIKPSRNNTYVCFN QKPNTVLPGLIYNVKYVLGSPMPTGKFKVPNSWR	0.486477	0.012632773	down
A0A7Z2CM08	Uncharacterized protein	6	1	1	1	28.7	MILDDYLGHAANSKKLAQIAIKERRFDDAWKHLNHQKDYYLKHASRMGFSKTETLVIDSSPHE DMANVLRLEGKHKNALSSISYTYKAAYTANRPIITLEKKLEAYYNRAYKKQPFKKFLSLLKALP NSDYISVRDLVEIYFPLSPNDDEVAPKERNLSEQEIKKVNDNFLKQRSTARSKEHIGIPPPLSNKPV KAVKPSYPEPKYPTKVIEPQNDNNLILGYPASEWIIGLMVGVALLIGLIWLLSVSVR	2.2301003	0.003279783	up
A0A828SQM8	Muconolactone Delta-isomerase	23	2	2	2	10.5	MDVHIPLDMPADKANEIKAVEKAYSQDLQRQGKWRHIWRITGQYSNISIFDVESNEELHNILQG LPLYPYMDIEVMALNRHPSSVRDDDS	2.8101852	0.015432534	up
A0A828STC4	Phenylacetate-CoA oxygenase, PaaJ subunit	52	6	13	6	18.6	MQMIRHCIDQCWDVLQTVSDPEIPVLSVVDLGMIRGVEINDQQEIIVRLTPTYSGCPATDMLKAQ IVEAFTAEALTPVKVMVDLSEAWTTDWMSEAGKKKLQVYGIAPPEGLAHQCGTHVHLTNGVE CPRCKSRHTRLLTEFSSTACKALYKCQDCLEPFDYFKCI	2.6145793	0.001895603	up
A0A829K710	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	81	29	148	1	53.7	MAEAQKLKLIDGWEVVIGIEIHTQLATNSKIFSGSSTEFGQDPNTQASLVDLAMPGVLPVLNEKV VELAIRFGLGIDAYIDQASVFARKNYFYPDSPKGYQISQMDNPIVGLGHIDIQLEDGTTKRIGVTR AHLEEDAGKSVHDQFEGMSGIDLNRAGTPLLEIVSEPDMRSVEEAVAYIKAIHTLVRWLGISDGN MAEGSFRADCNVSLRRPGQPFGTRCELKNLNSFRFIEQAINVEIERQMEILEWGGEIDQETRLFDP NKMETRSMRSKEEANDYRYFPDPDLLPVIIPDEQIEAIKATMPELPAARRARFIADFGVTEYDAH VLTLSREMADFYEAVVAAAGGAKQGKIAANWVMGEFSGALNKAGLELTDSPVSAEQLGGMIA RIIDNTISGKIAKQVFGFMWESEGKSADDIIAEKGLKQETDTGAIEAIIKEVLAANEKMVEEYKSG KEKAFNGLVGQVMKASKGKANPAQVNELMKKLIG	2.2866118	7.24E-05	up
A0A829RFQ7	Alanine racemase	30	9	33	2	40.5	MPRPITAVIHRQALQNNLAVVRKAMPNSKVFAVVKANAYGHGIERVYEAFKAADGFALLDLDE AKRIRALGWTGPILLLEGIFSPQDLFDCVQYQLSFTIHSEAQIEWVEQHPYPAQFDVFLKMNSGM NRLGFKPQHYVQAWERLNNLANVAKITHMMHFSDADGDRFGQQGIDYQITAFEEVVKDLPGER SVSNSAAILRYQDQLKSDYVRSGIMLYGSSPDYPTHSIADWGLQPTMSLRSEIISVQHLEPNESVG YGSNFVAEQPMTIGIVACGYADGYQRISPTGTPVLVDSVRTRTVGRVSMDMLAVDLTGIESAKV GSEVVLWGQSSTGVVLPIDDVAVSSGTVGYELMCAVTARVQFINQV	0.1911852	0.020850693	down
A0A829RK63	DNA modification/repair radical SAM protein, putative	3	1	1	1	48.1	MSDRIREKLQILADAAKYDVSCSSSGSDRKNKNKGLGDASHSGICHSYTEDGRCVSLLKILFSNV CIFDCAYCVSRRSNDVQRAAFTVQEVVDLTINFYRRNYIEGLFLSSGIFKSADHTMERMLQVVKK LRLEENFNGYIHLKTIPGASPELIHEAGLYADRMSINLEMPTEIGLKTFAPEKSHQEVQKDLGLVR DRLIQLKDERQIIKHVPKYVPAGQTTQMVVGAHQESDQDVLFIADKHYKEFKLKRVYFSGYIPIN TENNYLPAVGSAPPLLRENRLYQSDWLMRFYGFEVNEIVNEKHPNLDLDVDPKLSWALRHPEQ FPVDLNRADYQMILRVPGIGVKSAKKIVQARRFGKIHIDLLKKLGVAYQRAKFFIRCEDSPKFQK ELSSSFIRQQILTQGSSKYVQQLSPQLSLGF	0.4368904	0.000202092	down
A0A836LYR7	Ankyrin repeat family protein	8	1	2	1	19.1	MHKSNIIRQNQENNILIRNAIKKHELITVKKIFSEFPGLLSIDTPFGSWLHVAASSGALEIVKYLITE GLSPNKKGGTFGGNSLNTAVSNGHIDIVEYLLLLNVEMDTTEPERNPLFGAIMKGSLPIVEKLISH DIDYKISYTGDYMNNMDAESFALERGEIEIANYLNSLK	2.2474831	0.020436713	up
A0A836M1S1	Flavodoxin family protein	23	14	19	1	96.5	MFKKFLFQIHWFLGISAGLILSIMGVTGAIYSYDQQILKWVNTDSYVVQAQSSPKLTPAQLYQHF TTIQPEIKINSITIAKDPTASSVVNIEKEGERRGYNMMVNPYTAQVLPEVQGRKLLLLIQQIHRNLT AGEFGKQITGACALMLIYFVLSGLYLRWPKKHSARQWLAVKPKLKGRNFIWDLHAVVGTWVIV FYLLFACTGLYWSYDWWRSGMFKVLGVEQPKMQGHSGSGRNKDQLPKIQLDNAQLITALNQT WSGFNNQIGRDYSTLTVNLPKKDDGKIELSFVDATPQHERARNQAVYNYKTANIEKMELYEDK KLNQKIMSSMLPVHRGSFFGPVYQFVAMLASLAMPLFFVTGWMLYLKRRKQKKLTQAARQSL AGHYIDQNAKPWLITYATQTGVAEQLAWSTATSLQEAHQPVQVKSVQQLTEADLQQHEQILFVI STYGTGEAPDLASNFAKKLLKTNLELQHVKYAVLALGSKEYPDTYCSFGHTVDEWLKNNGAKA FFDIIEVDNANPADIQNWNQALVKATKLDLHAVNIEKVFDNWTLQQRDLLNPNSLGQPAYNIEL TASHEAVWQAGDIAEIQPGNSPERINKFLQHHHILKNAVVDSLQVSIEKALWNKDLTGEIEPFAN LDHLLEQLPTLPTREYSIASIPSQQVLRLVVRQQHDESGDLGLGSGWLTQHTEINQNVALRIRTNE SFHLIDDNRPIICIGNGTGIAGLMSLLHTRTRHNYTENWLIFGERQRAHDFFYASTIEAWQTMGM LKRLDLAFSRDQEQRVYYVQDIIRQNAAELINWIERGAVLYVCGSIDGMASGVDQALIHILGEEQV DELRQQGRYRRDVY	3.2989324	0.004111448	up
A0A836YML5	Bacterial regulatory s, tetR family protein	25	4	8	1	20.1	MLLFWEHGYEATSISDLTHALEITAPSLYSAFGDKAGLFYKSIDYYLAHEACPIETIFLEAKTAKIA FELYLYDNVKRLVQPNKPAGCMLVVAAMNCSDATQEVQQNLLDKRIKTKEKLLKRLEQGVEQ GDLPINAPLQEMTDFYATVIQGLTIQARDGASTEQLHKVVEHAMKAWTLF	2.8458333	8.91E-05	up

A0A8B4MT53	Octanoyltransferase	29	5	9	1	24.9	MSLDKPTLIIRQWNDLQDYQSKFESMKNLTNQRDENTADELWLLQHHEVLTQGQAGKPEHILIP SNIPVVQTDRGGQVTWHGPGQLVAYFLFDLNRLKWNVRTLVSFAEQFMIDVLKKYNIEAYAKP DAPGVYVDGRKIGSLGFKIRRGRSYHGLALNLDCALTGFQTINPCGYAGLEMVRIQDLVTPYPSF EQLCQDFIEYIKATGYFNDPEVKIE	0.4552976	1.91E-05	down
A0A8E4GYA6	Beta-lactamase	72	16	58	1	27.5	HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRVDAGQE QLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHN MGDHVTRLDRWEPELNEAIPNDERDTTMPAAMATTLRKLLTGELLTLASRQQLIDWMEADKV AGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRILVIYTTGNQATMHERNR	2.0706876	0.006659573	up
A0A8I0F482	D-amino acid dehydrogenase	72	21	150	1	47.2	MREGMEMRVIVLGSGVIGVASAYYLARQGAEVTVLDRQSGPAEETSFGNAGQISPGYSTPWAA PGIPFKAVKWMFQHHAPLAINLDGSMWQLQWMAQMLKNCNPQSYAVNKERMMRVAEYSRD CLRELRKDTGIHYENRAKGTLQLFRKEAQMEAVQRDISVLEECGVSYELLNANELGRVEPALAN AQDKLVGGLHLPNDETGDCYLFTNALAQIAKELGVNFQFNQNVEKLIVEGDQIKGVQVNGKVL TADRYVLAFGSYSRDFLKPLDLQLPVYPVKGYSLTIPIVDPAFAPQSTVLDETYKIAITRFDQRIRV GGMAELSGFNLGLNEDRRATLQMVTQDLFPGGDMEQASFWTGLRPMTPDSTPIIGATRFKNLFL NTGHGTLGWTMACGSGKLISDIVLNHKTDISTDGLSIQRYSHAHAA	5.7351811	0.03622829	up
A0A9P2P5S8	MmcQ/YjbR family DNA-binding protein	29	3	3	1	14.4	MNGVQLHQLAIEAARNLPFSEQTHPFGPEYEVFKILEKMFMLTVEVSGVKMINVKCDPYKSQEY QELYPFIIPGYHMNKKHWISIKPHKNLTSDFLRDLIRDSYDLVVKKLPLKDQKRLNNQ	0.3191363	5.20E-05	down
A0A9P2QE53	DUF937 domain-containing protein	7	1	3	1	19.9	MTNLSNIVEVLAKQALGGNQQASGQGGLGGILGSVLGQMGGNTSSGAQGGLGGVLGSVLGQV TGNNNTPQASGGVQSLLIAVVPLILGWVQQQGGLQAALEKLKGAGLGSQVQSWVDPNQSNSEV PTQQLQSLFNPADIEQVAQQAQAPKEQVYGAIASVLPQVIDSLTPQGESTDHQEANQDIQNVMN LVSGFLK	2.0520231	0.015381726	up
A0A9P2QG90	Aspartate/other aminotransferase	68	17	115	1	44.9	MFQHIPPYAGDPILSLMEQFNADTRSEKVNLSIGLYYNEDSIVPQLETIIEAQKRIEPKNGKTKLYL PMEGFKPYREAIQALLFGANSPAVKAGRAVTIQTLGGSGALKVGADFLKTYFPSSDVWVSQPTW DNHVAIFNGAGIKTHFYPYFDAETRGVDFDGMLSTLKTLPEQSIVLLHPCCHNPTGADLNPAQW DQVIAVLKDRNLIPFLDIAYQGFGDGMEEDAYAIRALDQAGLNFIVSNSFSKIFSLYGERVGGLTF VCDDAEAAQCTFGQLKATVRRIYSSPPTTGAWLVDEVLNDAELNQQWQGEVKEMRERIIKMRS ILKDELTKALPDRDFSYLVNQKGMFSYTGLTAEQVDILREEYAIYLVRSGRICVAGLNMNNVYT VAKAMAEVLAKSVEAA	0.1451973	1.11E-05	down
A0A9P2U9F4	Phosphoadenosine phosphosulphate reductase	16	3	3	3	32.8	MTEHHVLGLSGGKDSAALAIYMRQNFPELKIRYFFTDTGKELPEVYEFLAKLEGFLGQKIEYING DRDFDFWLRQYNNFLPSAQTRWCTRQLKLTPFKKWIKPWLDQGDKVYSYVAIRADEDHRQGL VSQHKNLEVKLPFREHGIDKPGVYDLLESSGIGLPAYYEWRSRSGCTFCFFQQKIEWARLKERHP KAFEDAKAYEKTAIDSGSPFTWTRGESLSDLEKPERLAQIYKDYELRKQRAMHRKPVNPLRPQRI DTIDIDDLYLEDEGAGACLVCHK	0.4968609	0.035099758	down
A0A9P2UEN7	1,2-phenylacetyl-CoA epoxidase, subunit C	55	13	31	13	28.8	MNHSVLSKFLLHIGDSQLVLSQRLAEWCGHAPELEIDIALANIGLDLLGQARNFLTLAGQYDEAK RDEDQLAYFRTEREFLNLLLCEQPNGDFAQTIVRQWLMDHYHLHLFTALAQSSLPELSALAVKS LKEVKYHIRFSTSWMERLSLSTDEAHQRVQDGLDNLWRFTAELFELSADEKALVAEGVIPDFSN EKEQWNQTIADELKRFELNVAVNGAYRRGAKQGLHTEHLGYLLAEMQCIQRTYPGMTW	2.8856875	0.00192446	up
A0A9P2UFA0	RutC-like superfamily	86	7	50	2	13.1	MSNSDIQKINTNEVMSAVTVFNKVVYLSGQVPKNTEQDVAGQTREILATIEELLALANTDKSRL LSAQLYLKNLSDFSTVNAIWVDWLKGCVAPSRATIQADLVNPDWLIEIAVTAAQK	3.4774875	0.00065741	up
A0A9P2UFT2	Diacylglycerol kinase, catalytic domain	42	7	10	2	34.4	MKPLSIIYNEKSGFHASKHEDVYEQLMTVFTEYGFEIQVFELNENTLFDDLINNVIHRHSQNENT GVVVAAGGDGTLNAVATKLKNTSIPMGILPLGTFNYVAKVLEIPLDLLEAAEVIATGKPRSVHV AVINDHIYLNNASLGLYPLFIKKRELYNKYLGRLPLHAYTSALDVLLRENKSMKLSITVDGKKYP VKAPLIFFGNNQLQLCDMKLRIAECAAQGRVAGVVITKSDKLSLLNMLWQWVQGKVEDAQDV YSFCADHVIVDCAKKTKLTVALDGEIIEMKPPLNFTVEKNALNIMVPNVTTSV	2.8084037	0.003572572	up
A0A9P2UGQ7	Endoribonuclease	68	4	17	1	12.9	MTVKRLHVTSRYCEVAISGNLVHLAGQLADDTSVDITAQTQQTLDNIDRLLAEAGTDKSHILSV MIFLKDIDKDYAAMNTVWDAWISKEHPPARTCVESKLYAPDVLVEMTVVAVLP	2.9405966	8.61E-06	up
A0A9P2X8Z1	Uncharacterized protein	43	8	17	8	27.8	MGTSTSSKGPNGKTPLVPSWANEGGGAISCGIDNTLGEFRGYLGKAANKPSGPSGTNLRKAIGH YAKNATGGKKVAPKRYQKLIAAGGGLFDLFQNIQAGKDHLNLKIADLNGQPIDIVIDQIIENLLV VDGDSERIRASLNQSLAECLDGMDDFDFTQISSDMIIDLMLNYTEQYLFQQIILDSRAAFDKADTP ENIASLEQDLHSLIKSSVDKHMSAQLKNRENTLTRSEIEHIQMKALEDIWGEWEDYLND	0.4833703	0.042906604	down
A0A9P2XHD2	Phosphotransferase enzyme family protein	56	16	38	16	43.3	MSVIDVGGEVREGEELDIGAVENWLKNQGVELVGPAVVTQYTGGASNWTYRLKYENTDLILRR PPKGTKAKSAHDMAREYMVQKNLAPYYPVLPKMVALCQDESVIGCDFYVMERIEGIIPRAKLPP ELGFNEDDVHELCVNVIDKLIELHQVPYENTPLAELGKGTGYCRRQVEGWDKRYEKVRTINVPS FKYVRKWLNDNIPQDSTTCIIHNDWRFDNVILDPEHPTEVIGVLDWEMATLGDPLMDLGSALAY WVEPTDNMIFRSTRRQPTHLKGMFSRKEVVDYYLQKTGLEPQNWTFYEVFGVFRLAVIAQQIY YRYYHKQTRNPAFKDFWIVIHALHIRALKLIAQQKLQESEFAQQSLQKIQGILRR	3.2336421	8.78E-05	up

A0A9P2XJZ6	UDP-glucose 6-dehydrogenase	40	12	27	1	47.2	MKIAVFGTTLHAGVMAALLAEYGNQIYWCTSVTCEENISILSYQDQEVNHYLNKQRKAGFLKESPFSEIPLDIEVYLFCFSPTQIELALKTVEKLSERPIVHPRLMINGSTFGLHGTNQLKQHLPKDEWVYFPDVIQEGNAINSVLNVKHVIVGVESSYAQDTMQELLRPFFRFSYQYLFMPILDAEFTKLSISGMLATRISYMNDLAMVAEKLGIDIANVKHGIAADTRIGAAYLSAGVGFGGENFSHDILTLSSTVSGTGAKSRLLEQVWAINEQQKEILFRKLWNYYHCDLSGKTVAIWGASFKENTSSTHNSPIHILLAALWAQGVKVRLHDPQALDEIETTYGDREDLVLCADQYEAAQGAHALCLVTAWKQYWSPDFKQLQQVMQHPLILDGRNIYDPAYVKAKGFAYEGVGRL	0.4080428	0.000410168	down
A0A9P2XK89	Bacterial transferase hexapeptide family protein	30	4	9	4	20.9	MKKKLRKLIYFILPCIRLFLNLFFKRKYLEGRFFSKSLSGYVWAVRSIWVKNILRLSKPTPFPTALTCSISNPYNIHFHPDDLNNFQSPGTYFQNFSAHIYIGKGSYIAPNVGIITSNHDLADLESHTEGKDVVIGDKCWIGMNSVILPGVVLGNGTIVAAGAVVTKSFKQGNIVIAGVPAKIIKEIK	2.3719896	6.61E-06	up
A0A9P3CXB6	Dolichyl-phosphate-mannose-mannosyltransferase family protein	13	5	10	5	63.3	MQQWLRSSKFLLIFLPIWLFVLSWIRPLSVPDEGRYGDISRTMFESGDWLTPRIDGLPFMHKPPLLHWLSSMFMELFGVHVWVLRLVPVLAGTLMLVGLFLFVKKHISESVAQLTVIILATNLLFFGSSQYINHDLLLASWITISVLCFVDFTISAQKSILFLGYIAGAAAFLSKGLIGILIPGMILLPWLIYTKQWKKIPSLLNPLAILLFLLIVSPWLYLVQSKYPQFLHYFFIDQQFNRFSSKEFNNKQPWCFYLIILFVSFLPWLFASRFTSIKTIFKDYKSCSLLALFVWWFVSVTVFFSIPPSKLAGYILPAVPPLAIFFALVMNKVLESSNKTRLQTWGIPVFTILVGIGVSATPHFIRAHQPFFQNQAIFIYLIGALLIVLPLVLVGLYKKQKLKYLTYIFISLIVLCSAVPFAVRILDTKNNVGQTDFAEYIAPSTKIVFYNYYFYDVPFLLKLKQPVYIVNQWDTVHSDSASLEIKDGLLFEPQLKKYLWSEQQLQDALMQKQDLIVISQPHNFATKDPSVKTLHYRNYDVFIFHPSK	3.6057037	5.58E-08	up
A0A9P3CXM7	Nucleotide sugar dehydrogenase family protein	64	20	77	16	47.1	MQLADLRIAIIGLGYVGLPLAVEFGKKGPVIGFDINQNRIDELKSGKDHTLEVSPEELQKAEQLSFSANLDDLKTSNFFIVTVPTPVDQVNRPDLTPLKKASETVGQALKKGDIVVYESTVYPGATEEVCIPILEKVSGLKFNQDFFAGYSPERINPGDKVNTLTKIKKITSGSTPEVANTVDAVYASIITAGTHKASSIKVAEAAKVIENTQRDLNIALVNELSVIFDRIGIDTLDVLEAAGSKWNFLPFRPGLVGGHCIGVDPYYLTHKAEEVGYHPQVILAGRRINDNMARYVARNTIKLMLQNGIDVPRSKVGVLGVTFKENCPDIRNSKVADLIKELEFWGAQVVVADPWADAEEVKHEYGVELGTVNAQNPVDSLIVAVGHSEFRSLSASELRSYVKAEKPVLADVKSLFDRTQMSDVGFTVFRL	5.1588481	3.78E-06	up
A0A9Q1N7W9	Uncharacterized protein	55	10	18	10	23.8	MNNEYFKLYTDSQFLSPYAFTVFVGLHEKQIPFEIAAIDLGQQGQFETSFVEKSLTAKVPVLEHNDFALSESSAILEYLEELYPDTAIYPKDIQARARARQIQAWLRSDLVALRTERPTDVIFIQPKSTPLSEEGKKAAEKLFFVAEKLLASDAEFLFGSWSIVDAELALMLQRLIQNGDAVSERLKNYALQQWQRPSVQKWLALRHK	2.3960197	0.003082826	up
A0A9Q1NIM9	Ring-hydroxylating dioxygenase beta subunit	39	7	14	7	19.1	MSQELHFAVSQFLYKKAELCDAYDWDAYLELYDEDSEYHIPQWIDDHNYVQDPNQGLSYIYYADRTGLEDRVFRIRTGKAASATPLPRTLHSINNIRVKTLEDGLIEAKVAWQTLYNRQGLEGCFYGHATYLLRQTADGFRIRRQHSILLNDKIDSVLDFYHV	2.1510864	0.002562947	up
A0A9Q1NNH7	Beta-ketoadipyl CoA thiolase	62	18	55	2	43.1	MEDVLICDFIRTPIGRYAGALSAVRADDLAALPIKYLKDKHPNLPWNTVDEVFLGCANQAGEDNRNVARMATLLAGLPDTVPAMTVNRLCASGLDAVGLAARSIKAGEAQFVLAGGVESMSRAPFVQAKPTEAFSRTPEIYDTTIGWRFVNKQLKAQYGTDSMPETAENVAEKYQISREDQDAFALRSQQKTAAAQQNGFFNDEILPVEITDRKKNVVVNRDEHPRETTLEALAKLKAPFKKEGGSVTAGNASGVNDGAACVLITNREFADTHGLKPLARVIGIASAGVEPKYMGIGPVPAVQKILKQTGLTLDQMDVIELNEAFAAQSLACMRELGLKDDDERVNTNGGAIALGHPLGMSGTRLVITATRELKKRGGRYALCTMCVGVGQGVALILENLN	2.5920738	0.01150206	up
A0A9Q1RYZ7	Octanoyltransferase	29	5	8	1	24.9	MSLDKPTLIIRQWNDLQDYQSKFESMKNLTNQRDENTADELWLLQHHEVLTQGQAGKPEHILIPSNIPVVQTDRGGQVTWHGPGQLVAYFMFDLNRLKWNVRTLVSFAEQFMIDVLKKYNIEAYAKPDAPGVYVDGRKIGSLGFKIRRGRSYHGLALNLDCALTGFQTINPCGYAGLEMVRIQDLVTPYPLFEQLCQDFIEYIKGTGYFNDPEVKIE	2.6587972	1.35E-05	up
A0A9Q1RZT3	2-methylisocitrate dehydratase AcnD, Fe/S-dependent	59	35	98	5	86.6	MNTKYRKPLAGTQLEYYDVRQAVEDIQPGAYEKLPYTSKVLAEQLVRRADAENLTAYLTQLIERRQDLDFPWYPARVVCHDILGQTALVDLAGLRDAIAEKGGDPSKVNPVVPTQLIVDHSLAVEYGGADPDAFAKNRAVEDRRNEDRFHFIEWTKTAFKNVDVIPAGNGIMHQINLEKMSPVIQARDGVAFPDTCVGTDSHTPHTDALGVISVGVGGLEAENVMLGRASWMRLPDIIGVELVGQRQAGITATDIVLALTEFLRKERVVGAYLEFFGEGADSMSVGDRATISNMTPEYGATAAMFYIDQNTIDYLRLTGREDAQVALVEQYAKEIGLWASEMTKAEYPRVLRFDLSTVTRNIAGPSNPHARVSTSDLKEKGIAGVVENRSDGLMPDGAIIIAAITSCTNTSNPRNTVAAGLLARKANELGLVRKPWVKSSFAPGSKAAALYLEEAGVLKDLEKLGFGIVAYACTTCNGMSGALDPAIQQEIIDRDLYATAVLSGNRNFDGRIHPYAKQAFLASPPLVVAYAIAGTIRFDIEKDALGYDKEGNPIYLKDIWPSDAEIDALVKQAVKPEQFRKVYIPMFDLGEVEQAKSPLYDWRPQSTYIRRPPYWEGALAAPRTLANMRPLAILGDNITTDHLSPSNAILMDSAAGEYLHKMGVPEEDFNSYATHRGDHLTAQRATFANPKLYNEMVRRSDGTIKQGSKARVEPEGEVMRMWEAIETYMNRKQPLIIIAGADYGQGSSRDWAAKGVRLAGVEAIVAEGFERIHRTNLVGMGVLPLEFK

A0A9Q1S0P9	Phenylacetyl-CoA epoxidase, subunit B	45	4	12	4	11.3	MEDKNNWSLYEVFVRSKQGLSHRHVGSLRAPDDEIALQHARDVYTRRNEGISIWVVRSELIKSSQPDEKAEFFDPSLDKVYRHPTFYHIPDGIEHM	3.0360604	0.001948252	up
A0A9Q1S3Z9	Isocitrate dehydrogenase NADP-dependent, dimeric, prokaryotic	69	23	150	1	45.6	MGYQKIVVPADGDKITVKADLSLNVQNHPIIPFIEGDGIGVDITPAMKKVVDAAILKAYGGKRSIEWMEVYCGEKANKIYGTYMPEETFEALREFVVSIKGPLTTPVGGGIRSLNVALRQELDLYVCVRPVRWFQGVPSPVQHPELTDMVIFRENSEDIYAGIEWKADSEEAKKVIKFLQEEMGVTKIRFPEGCGIGIKPVSKEGTQRLVRKAIQFAIDNDKPSVTLVHKGNIMKYTEGAFKEWGYELALDRFGGELIDGGPWVKIKNPKNGKDIIIKDVIADAFLQQILMRPADYSVIATLNLNGDYISDALAAEVGGIGIAPGANIGGAIAVYEATHGTAPKYAGQDKVNPGSIILSAEMMLRDMGWTEAADLIIKGISGAIAAKTVTYDFERLMPGATLLRCSEFGDAIIQHMED	0.2551807	0.029880242	down
A0A9Q1W4V0	Poly-beta-1,6-N-acetyl-D-glucosamine N-deacetylase PgaB	54	27	96	27	75.7	MITRFASPLLNLTLGLALAGLSGMVLANPPKIDASTLTVIGYHEITDTKNALIPQYAVTTQQFTEHVDWLQKNGFHFITVDQLIRAHQGKAALPTKPVLLTVDDGYQSFYQNAYPVIKAKKIPVVLAVVGSWLEPKAGQKVDFSGEEIPRDKILSWGELKEMQDSGFVEIASHSYHLHRGITGNPQGNSEPAATTRFYDVKTKTYENDSQYQARIYNDLKKNNQLLKEHGIRSPRIMVWPYGRYNMQTVQIAKKLGMPITITLDDGADHAKQSLQNMSRILVEGGMSTNDLAQEIKNRELNLTDNNRPQKIMHIDLDYIYDPDPQQQERNLGHLLDRINAMGVNTVYLQAFSDPDANGSADMVYFPNRHIPMRADLFNRVAWQIQTRTPVSRIYAWMPLLAWELPKTDPVSKDLVVTEQAKAGEHLNMGYIRLSPFSPEARQTIREIYQDLAKSASFNGILFHDDVTLSDYEDASPDALKAYAKQGLPTDLAKIRENDQDLQKWTAYKTKYLDDFAMQLVEDVRQYEPFLLTARNLYAQVALKPYAENWYSQSLEESLRRYDFTAIMAMPYMEQVDNADQFYKDMIDRVKKYPNGIKKTVFELQATNWRNNEKVPSTEMAATIHSLYQQGAMHVAYYPDDPIKDHPDVNVMHKAFAEKSSRLVP	2.5761532	0.00016328	up
A0A9Q1ZY45	Methylated DNA-protein cysteine methyltransferase, DNA binding domain	27	3	4	3	12.9	MSTFMDSILTTQYELHRQILEVIALIPYGKVATYGQVARMAGLPKHARLVGYVLKHLEADHQVPWYRVINSQGKISLSKFNEKGENIQQLKLEAEGIYLLNGKVNLKEFAWQP	2.5693831	1.24E-05	up
A0A9Q2E0D7	Trimeric LpxA-like superfamily	35	4	13	4	20.5	MSFYQHETAIVDNGAQIGEDSRVWHFVHVCGGAKIGKGVSLGQNVFVGNRVVIGDHCKVQNNVSVYDNVTLEEGVFCGPSMVFTNVYNPRSLIERKDQYRDTLVKKGATLGANCTIVCGVTIGAYAFVGAGAVVNKDVPAYALMVGVPAKQIGWMSEFGEQLDLPLQGQAQAICSHTGAVYQLHGTTL	3.1447773	0.000646353	up
A0A9Q2I4G4	NAD(P)H dehydrogenase (quinone)	3	1	1	1	26.6	MNILIVHAHPEPLSFTTSLKTTAQQTFKKLGHQVEISDLYAMQFNPVASKEDFLELNQPDYFNYALEQRNATKQQLLSPDIQAEIDKVNRADLVILNFPLYWTSVPAILKGWIDRVFVSGLFYGGKRFYNHGGMAGKKAMLCLTLGGRTHMFGENSIHGPIEHYLSPIQRGTLAYTGFEVLPPFIAYHVAYISQEARETILEDYVTYLTHLDQLEPLKFPKLEEFDEKLYPL	2.0277427	0.001498574	up
A0A9Q4SJB7	Bacterial solute-binding protein 3	56	14	31	1	31.7	MTTLTFQNVKHILAASLLSLGLVACDKGTQSTEKSADTTQTTSSIEQIKKNGVVRIGVFSDKPPFGYLDAQGKNQGFDVEIAKHVAKDLLGDEIKVEFVLTEAANRVEYLKANKVDIIFANFTVTPERKEVVDFAKPYLKVALGVVSPKSHPITDVAQLKDKTLLVNKGTTADSFFTKTHPEIKLQKYEQNTETFDALKDGRGVALAHDNLLVLAWAKENPNYTVGITNLGEQDLIAPAVKKGDKELLDWLNQDLEKLAKEGVIHQAYEKTLKPVYGDTINPKDLLVE	0.1650206	0.007138888	down
A0A9Q4SK06	Flavoprotein-like superfamily	23	14	19	1	96.5	MFKKFLFQIHWFLGISAGLILSIMGVTGAIYSYDQQILKWVNTDSYVVQVQSSPKLTPAQLYQHFTTIQPEIKINSITIAKDPTASSVVNIEKEGERRGYNMMVNPYTAQVLPEVQGRKLLLLIQQIHRNLTAGEFGKQITGACALMLIYFVLSGLYLRWPKKHSARQWLAVKPKLKGRNFIWDLHAVVGTWVIVFYLLFACTGLYWSYDWWRSGMFKVLGVEQPKMQGHSGSGRNKDQLPKIQLDNAQLITALNQTWSGFNNQIGRDYSTLTVNLPKKDDGKIELSFVDATPQHERARNQAVYNYKTANIEKMELYEDKKLNQKIMSSMLPVHRGSFFGPVYQFVAMLASLAMPLFFVTGWMLYLKRRKQKKLTQAARQSLAGHYIDQNAKPWLITYATQTGVAEQLAWSTATSLQEAHQPVQVKSVQQLTEADLQQHEQILFVISTYGTGEAPDLASNFAKKLLKTNLELQHVKYAVLALGSKEYPDTYCSFGHTVDEWLKNNGAKALFDIIEVDNANPADIQNWNQALVKATKLDLHAVNIEKVFDNWTLQQRDLLNPNSLGQPAYNIELTASHEAVWQAGDIAEIQPGNSPERINKFLQHHHILKNAVVDSLQVSIEKALWNKDLTGEIEPFANLDHLLEQLPTLPTREYSIASIPSQQVLRLVVRQQYDESGDLGLGSGWLTQHTEINQNVALRIRTNESFHLIDDNRPIICIGNGTGIAGLMSLLHTRTRHNYTENWLIFGERQRAHDFFYASTIEAWQTMGMLKRLDLAFSRDQEQRVYVQDIIRQNAAELINWIERGAVLYVCGSIDGMASGVDQALIHILGEEQVDELRQQGRYRRDVY	0.2100811	0.000107539	down
A0A9Q4XE51	Bacterial sugar transferase	47	7	10	6	23.4	MKRLVDIVISLIALTVLSPIFLIVAYKVRKNLGSPIFFYQERPGKDGKLFKMIKFRSMKDAFDAQGNPLPDEARITPFGQKLRSTSLDEMPQLINVLKGDMSVVGPRPMLKDFVALYSPEQARRLEVRPGMTGLAQVSGRNELDYEERFKCDVWYVDNHNVWVDFKIMFKTVKVMLRREGINAPGHVGPSLFKGNDTQENVDSSVK	3.104304	0.00913383	up

A0A9Q6DWC7	ANL, N-terminal domain	18	14	19	1	148.0	MNQFVTNTKNVIRGKYHPEFLQNEVLADIFAHTAQTLPDKTALIEADKTLSYGELYQQALIMAQ HLALKGVKPGHIVGLWLPRGIELLKAQLAICLSGAAWLPFDMDTPADRIAVCLEDAEAVGMITT DEWYEHLAEVPQTKWTNTELQKPLSESVSLAKTTPDQPAYIIYTSGSTGKLKGIVITQKNICHFLR SENSILGIQEQDKVYQGFSVAFDMSFEEIWLSYLVGATLWIAPKSLVSDPERLCQTLKQEQITVLH AVPTLLALFPEDVPNLRIINLGGEMCPDSLVDRWALPHHQMFNTYGPTETTVSASLELLERGKPV TIGKPLPNYGMLVINSERELLEQGETGELCIFGPSVAQGYLGRPDLTADKFIENPWAMSVEEELL YRTGDLAKIDEFGQVHCLGRADDQVKIRGFRVELGEIEAALCDIDGIGTAAVILRPEDGIDQLIAFI APEIDAKQAIEIKELRHNLSQRLPPYMVPNRFEIIEEVPRLLSGKIDRKALKARPLTSVVDRSESDQ PQNPAEEILFEILNRLFPNMPIKLDSDFFDDLGGHSLLAAVLISNLREHAEYSHLTIQNLYQARRVG AIAALMLEQPEPTLFDSQIGQDNPRNQTYKWLCGIAQLVTIPVLISINILQWLAPFFTYHYFTGGT RDSIPYAIALSLLVYVSVIMSSFVLSITVKRLLMLGIGAGRYPLWGLTYFRWWLADRISNISPVYL LSGSTLLNLYLKALGAKIGHDVTISSVHIRMPSLLTIEDGVSIGSQVNLENAKVEHGHLVLGSIHL KQDSYVGSYAVLEENTVLEKQAHVNALTSIEYDTVVPEGEIWDGTPAQKIGHIDEQAKLPERPK LSFIRKIAEYGYYGVSALIIACLFFIPIFPSFLLVDWLDVNVFNINPNNHLQIALYYFILAIPASAMM MMITAVISSGLRKIALPRLEIGTYAVHGSTYYRKWFAAQILETSLQTLHGLFATIYAPTWFRMLG AKVGKNTEISTATGVIPEMLTLGEESFIADAVMLGDEEIKGGWMSLKATKIGNRSFVGNSAYIAD GTVLPDNVLIGVQSKTPDNREMYDGQTWFGSPALLLPAREAAEKYPDHLTFKPSIKRRLMRGFI EGLRIVLPAALAIGVGYMIVLDVIDVINNYNIETGLVALTLAGLLYGVGCFLIVALLKWILIGRYQ PRSAPMWTMFVWLSEGITSLYESVAIPNFLNYLRGTPMLPFFLRILGVRIGKDVYMDTADITEFD CVSIGDRAEFNSFSGPQTHLFEDRIMKIGQVNVGNDVVVNTRSIILYNANVSNHAVLGPLTLVMK GENIPAKSAWIGSPAVPWVHK	2.0800207	0.000444415	up
A0A9Q7DS60	Aldehyde dehydrogenase domain	56	29	123	3	74.2	MPHLASYVYGTWHSSDEELRTVYHAITGEAIYAVSSHGVDMKRVVQYAKQNGSELANWTFHQ RANALKQIAQHLLERKEDFYKLAYATGATRKDAWIDIEGGIQTLFAYSSLVRRELNDEKIITEDS WIQLSKNGTFGAKHILSPKAGVAVHINAFNFPIWGMLEKIAPTLLAGVPCIVKPATDGAQLTQAV VKAIEETHVLPKGALQLICGQTYDLLEQLGPQDCVTFTGSAYTGQKLRNHPHLNKYSIPFSMEAD SVNSAILSPEANEETVDLFVREVFREMTTKAGQKCTAIRRAFVPENLLATVQEKLTAKLAKVVV GDPQKEETTMGALASIKQKHDVAEKVAELSKDAKIVFGGNDSFTFNADHPEKGAFFAPTLLVCE QPLQATNVHTTEAFGPVCTLMPYQNIEELADLVSRGEGSLVASVVKNNDENIEQIIQKIAPWHGR VHVLDAESAKESTGHGSPLPHLVHGGPGRAGGGEELGGIRAVKHYMQRTAIQGSPNSLTQITHS WTAGSKVNEDRVHPFKKSFDELVIGERLLTARRTVTEADIVNFACLSGDYFYAHTDKIAAAESFF GERVAHGYFIVSAAAGLFVDAAQGPVIANYGMDNLRFVEPVKIGDSIQVELTCKQKTPKPQKDA SQPAHGVVVWDIKVKNQRGELVATYDILTLVAREA	2.3672363	0.003203587	up
A0A9Q7GEX3	Uncharacterized protein	4	1	1	1	18.3	LFTTYSPIWLVVWFTSIYQIINITIKIDDLISKKLNNRQYIKTSLNSILIFFKKLSSALQKSLQLPDDIE PWSKKIPTPVKKFGIYIESSIWFIASLTTTTYFILIALLTILTKKLLTIPDFLTIFGISAILVVCSRFLYV EGRRCLLKAKNYNKINI	0.4286605	0.041248887	down
A0A9Q7ZZR4	Domain of unknown function DUF4468 with TBP-like fold	51	9	22	8	19.4	MKKILLAGFLGLGLAGCATTPQQPSEPVKFEKVYQIDGLKQGQIYDGARQWFATAFRSANAVIQ YEDKTTGSIIGKGNMPYRCSGFADCMTVTAGDRVDFTVRVDTKDGKMKVSYDNLTHYKPAQV ISGVRYNETNRPITEDYPSAKIIMDELNKSSDQMAEKIKTQQKINADW	4.7346021	1.13E-05	up
A0A9Q8MVK5	ATP-binding cassette sub-family D	12	5	9	5	46.3	MFKSFFPSPRYFFISAVIWIALNMVLWYTGGDHWGQYLGFPQGYADAEVPIGVSRFWSPAFLWF YLWFLVSTALFASFWKIISNNPWQRWSIWGSAFILFNIWFSVQVSVAINAWYVPFWDLIQQMLSS GGGDLSALYSETLVFLYIAMVAVTLAVINAFFTSHYVFRWRTAMNEYYTEHWEKLRHIEGASQ RVQEDTMRFATILEDLGVELVKAVITLIAFLPILFQLSKHVPVLPIVGELEHSLVWAAIVWSIFGTV LLMVVGIKLPGLQFNNQKVEAAYRKELVYGEDHADRAKPATLRELFSNVRKNYFRLYFHYAYF NMTAIWYGQLDILYNLVVLFPSIAAGKLTLGLIQQIANVFGRVRESFQYLITSWKTIIELLSIYKRL KAFESILHK	2.4858844	4.06E-05	up
B0V8Q7	SLC26A/SulP transporter	6	3	5	3	79.9	MVVFMPALELKNRFHVNDLLSGVVVFLVALPLCLGIALASGAPIISGIIAGIVGGIIVGLLSGSHISV SGPAAGLTAVILVQLDQLGGNYAAFLLCIVFAGILQILFGVFKLGFFANFIPNNVILGLLAAIGAILI VTQLPYLFGLTDFSWKEVWTATPDTFIQKFDAGAALIGLLSLFLILAWDSSPLKKLALPSALIAVV LAAVFNFVLISIGSSWAVQSNNLIQLPNILQAPEEVLVFPDFSYLAEPLIYTGAITLAIVASLETLLN LEAADKLDPQKRSSPPNRELWAQGAGNIVSGLIGGMPVTSVIVRSSVNANTGARSKCSTIIHGVL LLLAILFFVPLMNMIPLSALAAILIVTGFKLTHPKLFKQLYQKGWRQFLPFIITLVAILLTDLLTGIL VGLFTSSAFILYGNFNKGVRVYKEKHLHGIVTRIELPSQVTFLNRSALISALEHIHKDQQLIIDATQ CDSIDPDIYQVIQDYQNETAVKRQVDLKLIGFKQHYEEVDDAVLDIYISTRDLQRKLSPQQVITLL KEGNERFVKNERLQRDIYRQIRVTADEGQHPIAAVLGCMDSRAPTEMIFDVGIGDLFSLRIAGNIA GQKVLGSLEFACQAKGSKVILVLGHTDCGAVTSACQLRLQQKQISDVKEMPHIQYVLGPLMHS VESVYDIMQPRELNKTFVNQVTAMNVHYNIQYIINNSTVLKDLLDRGEIAIVGAIYDVKTGHVEF LDA	2.4862206	0.003102158	up

B0VNR0	Arc-like DNA binding domain-containing protein	27	3	5	3	11.7	MSKNGGHLTVQYNLRWSEELRDKIADEAKKNTRSMNQEIIARLEHSFRSESASKPFLSFDKDTSHLVIGDAEERKRLAQIAAKAVFDALGQSLDQDDDEKKAP	3.1586265	1.78E-05	up
B0VQQ0	NAD(P)-binding domain-containing protein	3	1	3	1	30.9	MHILFIGYGKTSQRVAKQLFEKGHQITTISRSEKTDPYGTHLVQDIFTLDLSEIAPVDVVYILLSPDDSTVEGYQHTYVDSIEPIRQALKSHPVKRLIVVSSTRVYGENSGETIDDHSEIHPNDAQGHILHNMELLWQKYFPSQCVIVRPTGIYGASIDCLKRMAEHTQTYPNIHYSNRIHIDDLARFLAFLADFEKPHKSYLVANNAPVPLHEVLLWFQSQLDLPLLTLDSAHVSGKKIYAKHLFETGFQLEHPICFNDYLLCLNAHGTN	2.0556358	0.000501151	up
B0VR23	Regulatory protein RecX	42	2	3	2	8.7	MSFWQKLFLADQQHNEHKNQTACVENDCSCKTNEQLLSALAQATDEDVIKGIKKVLISRGYSRKELNELTQKTSIH	0.4503444	0.000636543	down
B0VRV5	TonB-dependent receptor protein	31	16	25	7	78.7	MSLLRLDRLHYCILMSMGCISSPLVWAEDLNSDVAKLPTLHVEATRTDTGYLQTPASVFRIEAPQVDSSSQVNLTEVVKGIPSLQIRNRENYAQDLQLSMRGFGARSTFGVRGIRLYVDGIPATMPDGQGQTSNIDLSSLDHVEVLTGPFSSLYGNSSGGTILTSTKEGQGKDSIELSYSGGSHDKSRAGLVLQGGAKGANEPSYIISSSYFDTDGYREHSGAEKVLNNAKLSWNLDDGSKINWVTNYVKINADDPGGLTRADWQNNPKQVVQNVLDYNARKEIEQTQTGLTWSKPINDQHELYAMTYMGQRQVTQYQSIPDTVQKNPNTPYQAGGVIDFKRNYYGADFRWTGKELLPNTTLSIGVALDAMKEDRQGYQNFNDTGDKGVKGALRRDEDNTLWNIDPYVQASWQFLPTWRLDTGVRYSNVHYKSKDYYIVGLNGDNSGKTSYEEVLPSVALSWQITPEVLAYASYAKGFETPTFTEMAYPAQGGASTLDLKPSTSDTYETGLKSQNQLGDFTLAVFQTKTKNDIVSAESFGGRSTFRNADKTLREGVEFAWNKKLWRDLIAIASYTYLDATFDSTVPAAGKISEIPEGNAIPGIAKNQAYVSLAWQPSHGLYGGVDVQYMDKVYVNDTNSDAAPSYSVTSANVGYAWVMGDWKVNSFARVDNLFDRNYAGSVIVNDSTQPVGRYFEPADGRNWSAGLRVIKQF	0.3119711	0.002570096	down
C7FEK7	Acetyltransferase (GNAT) family protein	43	5	8	5	20.3	MNYSLDSNFRLIDCNEAEHAVAILEILNDAIVNSTALYDYVPRSLDSMKTWFSVKRENGFPVIGVVDELGKLLGFASWGTFRAFPAYKYTVEHSIYIHHEHRGCGLSKVLMQALIQRAQQAQLHVLIGCIDATNQASIGLHEKMGFTHAGTFKQVGFKFGQWLDAAFYQLILNTPFEPVDG	2.1628808	0.009292239	up
D0C6V6	Muconate cycloisomerase 1	44	9	14	1	40.2	MYRTIETILVDIPTIRPHQLSVTTMRTQTLVLVKITTTDGIVGWGEATTIGGLNYGEESPESVKANIDTYFAPLLASVKDLNVAQTLKLIRKNINGNRFAKCAIQTALLDIQAKRLSVPLSEVLGGRLRDSLPVLWTLASGDTEKDIAEARKMIELKRHNTFKLKIGSRPLQHDVDHVIAIKKALGADVSVRVDVNRAWSELECIHGIQQLQDGGIDLIEQPCAIQNTEALARLTQRFDVAIMADEALTGPDSAYRIAKNHGADVFAVKIEQSGGLIEACEVGKIAGLAGIDLYGGTMLEGPVGSIASAHVFATFETLAFGTELFGPLLLTEEILKEPLRYENFELHLPTAPGLGIEIDEDKIEKLRR	3.0748731	6.46E-05	up
D0CDQ9	DUF3298 domain-containing protein	43	7	24	1	30.9	MYSGRSEFTGINMQLYDKKTIFILPMLAAMVAVSGCQPKSTAKDEQPASSASVKEQKQAEVPVIQAKVVPVKLPKPKVCLEDGCTEYDFQTVQTNQKWINDYFTNRIKKADPNAFANLADKPVEVPEGEPSSSQSAIYVRYLGQNYNLATFAFQTYSYSAGAAHGMSHQEFVNFDLLNKKHITVEELIKPDVEKQLVDALFDANTNWLQEHNISREKLQLSDNFYYGANGIVFVYPIYELASYAEGMSELTLPYFEAAKYIKPEYLPSVPNYNL	16.16189	1.21E-05	up
G1CBP8	histidine kinase PmrB	32	10	23	10	50.7	MHYSLKKRLIWGTSIFSVILGCILIFSAYKVALQEVDEILDTQMKYLAERTAEHPLKTVSSKFDFHKTYHEEDLFIDIWAYKDQAHLSHHLHLLVPPVEQAGFYSHKTAQGIVRTYVLPLKDYQIQVSQQERVREAFAWELAGSMFIPYLIILPFAIFALAAIIRRGLKPIDDFKNELKERDSEELTPIEVHDYPQELLPTIDEMNRLFERISKAQNEQKQFIADAAHELRTPVIALNLQTKILLSQFPEHESLQNLSKGLARIQHLVTQLLALAKQDVTLSMVEPTGYFQLNDVALNCVEQLVNLAMQKEIDLGFVRNEPIEMHSIEPTVHSIIFNLIDNAIKYTPHQGVINISVYTDPDHYACIQIEDSGAGIDPENYDKVLKRFYRVHHHLEVGSGLGLSIVDRATQRLGGTLTLDKSLELGGLSVLVKLPKVLHLHETRA	2.9264585	1.58E-06	up
H6VX66	Zeta toxin	63	25	228	25	56.3	MTQKNELDTKYAVIVAGGNGAGKSTLIDNVIIPKFNSLNLDINFINADVWQLQHFGHFDNTNPTHAREAQKWAEAERQKHLDEGRSFIAETVFSHPSKVDLIKEAKSKGFYVVLYHIHLENSDIALDRIKDRVRKGGHDVDEDKVKARYERVLPLVAEATQYADLTFVLDNSVRDRPHQQVFKLEYGKITAIDNNVPDWAIKAYEKQLTDYLGLDQATKISNTNEDLTMSNTKEKLGFEYNARLLANDIQPQHRETVVANYRKNFVEHVANSAAVAGNSHKLDDVASLINGTTVGGHSVKDQRQVLNLIDASNELVNMVRNGNFALNKSTYLKVNGIVADRESIEAGVLRGEGVEQSFTPDVGIRHFRTHRPMKTEEDAPALNKFMQEGFDHINSLKNPLEKGIATFLYGSLNQFTFEGEKRTAHLMMNGVLMSAGLDAISIPADKAIDFRQKMVRFYESKNADEVMEFLADLHPALNNTKKLDAEKEKKSENDFGRSFQ	2.0732884	0.009928293	up
N9JQM5	Nitroreductase domain-containing protein	56	13	26	2	26.4	MNLEQVRLVDEAITSRHSVRAFLSTPIEPEIIKDILRVASRAPSGTNTQPWKVYVVTGYKRDEMVERVCAAQIEVSKNPELAEQYKETFAYYPEKWVSPFIDRRRENGWGLYGLLDIKKGEKEKMAAQQLRNFKLFDAPVGIFFTVNKAMGIGSKMDIAMMIQNVMVAAKARGLDTCPQAAWNHFHPLVLDILGAADDEELVCAIALGHADPEHIVNTFITPREPVENFAVFLD	0.1053083	0.00149368	down

N9JQN7	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	81	29	147	1	53.7	MAEAQKLKLIDGWEVVIGIEIHTQLATNSKIFSGSSTEFGQDPNTQASLVDLAMPGVLPVLNEKV VELAIRFGLGIDAYIDQASVFARKNYFYPDSPKGYQISQMDNPIVGLGHIDIQLEDGTTKRIGVTR AHLEEDAGKSVHDQFEGMSGIDLNRAGTPLLEIVSEPDMRSVEEAVAYIKAIHTLVRWLGISDGN MAEGSFRADCNVSLRRPGQPFGTRCELKNLNSFRFIEQAINVEIERQMEILEWGGEIDQETRLFDP NKMETRSMRSKEEANDYRYFPDPDLLPVIIPDEQIEAIKATMPELPAARRARFIADFGVTEYDAH VLTLSREMADFYEAVVAAAGGAKQGKIAANWVMGEFSGALNKAGLELTDSPVSAEQLGGMIA RIVDNTISGKIAKQVFGFMWESEGKSADDIIAEKGLKQETDTGAIEAIIKEVLAANEKMVEEYKS GKEKAFNGLVGQVMKASKGKANPAQVNELMKKLIG	0.4831422	0.000167798	down
N9KZS5	Acetyl-CoA C-acetyltransferase	83	21	102	1	40.8	MTDIVIVNGARTAMGGFQGSLSGLTAPELGAVTIKEAIARAGLQPTDVEEVIMGCVLPAGLKQG PARQAMRKAGLPDSTGAVTINKLCGSGMKAVMQAADMIKAGSAEIVVAGGMESMTNAPYVLP KARAGYRMGHGEIKDHMFFDGLEDAETGRLMGSFAQDMANTRGYTREQMDDFAIRSLKRAQT AITEGYFKDEIVPVTVSTRKGDVIVDQDEQPLNAKIDKIPSLKPAFAKDGTITAANASSISDGASAL VLTSSEVAAQRGLQSLAKIIATASNSQHPSEFTIAPVGAIEKVLKKAGWNAQDVDLWEINEAFAM VTMCPIDDFKLDPEKVNIHGGACALGHPVGSTGSRIILTLIHALKRTGGKKGVAALCIGGGEATA			
Q0ZAQ7	Outer membrane protein A	58	11	210	2	26.3	TFQDSQHNNGGKDGNLTNSPELQDDLFVGAALGIELTPWLGFEAEYNQVKGDVDGASAGAEYK QKQINGNFYVTSDLITKNYDSKIKPYVLLGAGHYKYDFDGVNRGTRGTSEEGTLGNAGVGAFW RLNDALSLRTEARATYNADEEFWNYTALAGLNVVLGGHLKPAAPVVEVAPVEPTPVAPQPQEL TEDLNMELRVFFDTNKSNIKDQYKPEIAKVAEKLSEYPNATARIEGHTDNTG	2.2769934	3.87E-05	up
S3TFV1	Glycosyltransferase	9	2	2	2	36.5	MNIKPFLSCVVPAYNEAENLKTFIPALANSLKQQNLSYEIIVVDDGSKDDTIPILQTMIEDYPLVV LELSRNFGKEAALSAGLDHVTGEVALLIDADFQHPFEAIPTMINLWKNGYDMVYGIRNRTTESW LKRVLTQAYYRILNLSSPIDIPESAGDFRLLDARVVEAIKQLPEKNRYMKGLYAWVGFKSIGINFS EQERQHGRSSFNLKSLFNLAMSGLTGFSDLPLRVCIYLGAILALGAMSYGVWIIIKTLIEGISIPGW ATLAAGMTLLGGIQLLFIGILGEYIGRIYAEVKNRPKYIISTEHSRTKQEHSIAHQENTFSSF	3.1230809	0.01314211	up
U5QBG8	ATPase	63	14	30	14	29.1	MKKIVITNEKGGIGKTSVAVHLAHYCYERGMRVLFVDMDKQGNSGFSLSKVAVEIKDTHSLFA DIQNFETLDKYFVLFKGNKSLKSLFDPTEQEFKLDKVEEYQRNFKSNIAKANEFFDICIFDTPPTD GPFQRLPLLVSEFALSPFLLDKYSILGLRGIIDTTQEIKEVNPKIQFLGLLPNMVSANSVTQKTTLN ELQKQLSHLMLDKTAFIPNRSAIADASEQQVPVWKIDKTSAKDVGRKIKKINQLVLEKMGV	0.2671509	9.27E-06	down
V5RC11	Peptidyl-prolyl cis-trans isomerase	74	11	66	1	26.0	MSKALPIAVAVVLGGAALVPVYYATQHPTTEVGRKADKNASPIQKISYVLGYEVAQQTPPQLDT KAFVQGIHDARNKQPSAYTQEDLKAAVAAYEKELQQKMQHQDKPEQSGTATDSADAQFLAEN KTKAGVKTTASGLQYIITKEGTGKQPTAQSIVKVHYEGRLINGQVFDSSYKRGQPVEFPLNQVIP GWTEGLQLMKEGGKATFFIPSNLAYGPQELPGIPANSTLIFDVELISVK	2.6710075	0.001612486	up
V5RCJ8	UTP--glucose-1-phosphate uridylyltransferase	24	7	23	1	31.9	MIKKAILPVAGLGSRFLPASKSIPKEMVTVVDRPAIEYVVHEAIKAGIEQIILVTHSSKSSIENYFDR NFELETILEEKKKFDLLAEIRQIIPAYVSVVSIRQPQPLGLGHAVLCAKSVVGQDDFAVLLPDVLV KDNSSQNDLARMISRYNKNRAAQIMVESVPDHLVDQYGIVDVAKSPNIGESVAVQGIVEKPAVG TAPSNLSVVGRYILPAKIMQLLEKTPKGAGNEIQLTDAIALLQQIETVEAYRMQGQTFDCGSKLG YLKAVLHYGVEHPKLGNDFKQLIQELKL	0.2763977	0.000346486	down
V5RCU9	Glycosyltransferase	12	4	7	4	42.3	MKILHAAYMKDASSGIVNQMYWEQEAAKELGISWKSILFVQNPNGFHNNEIVTVCNDIMGGEL KKWFKAKKSYYSWLEGIMQEYDVLIIRHSLCDPFEPFFIRKMIKPVYIMHHTFEIDELYSYNYGV KTKIKSLMEIYFGKKSISYSKGIVAVTKEIFLYENSRVNGKFKKEIVYPNGIISQHDIILDDRNDNIP EIVFIASYFNGWHGLDLLLHNLSSINDDFILHIVGDVSVEDELLAKKDSRVILHGHLNNIEISQLMS KMWIGLASFGLFRKGMKEACTLKVREYLNYGLPIYSGHKDIFPEEFEYYKFGEPKFVDILSFAHL MRKVSKSDVKQAAIKFIDKKILLKELYEQLLEEKS	4.9436775	8.60E-07	up
V5REA9	DgaA	34	9	37	9	35.8	MKKFALIGAAGYIAPRHLKAIKETGNTLAVAMDVNDSVGIMDSHFPEAEFFTEFEEFEAYVEDQ KLKGEKLDYVAICSPNYLHAPHMKYALKNGIDVICEKPLVLNSEDLNMLAEYEKQYGAKVNSIL QLRLHPSIIALRDKVQAAPADKVFDVDLTYLTSRGKWYLKSWKGVDNKSGGVATNIGVHFYD MLHFIFGKIVKNEVHYRDEKTASGYLEYERARVRWFLSIDANNLPENAVQGEKLTYRSITIENEE LEFSGGFTDLHTQSYQRVLEGKGYGVEENRAAIETVEVIRVSPIIENPENPHPLLAKVKKA	3.8906298	6.64E-06	up
V5REF7	Wza	42	13	40	1	40.5	MKYCQFFSVLALSLSAASCAVTSGLQTYDIPSEGVYKTDLGTTVNVVKISQETLPAIQPAQIDYQ RDYASLFKTQQSIYRLSPGDVLSIQLWAYPEITPPVNSISNEQSVQANGYPIDQTGYIQFPLVGRY KAAGKTLAQVNRELHSQLARFLKNPDVVVRVVSYEGQRFSVQGSVTKGGQFYLSDQPVSIYTA LGMAGGVTTTGDNTYIQLIRNGRTYNLNTIDLEKAGYSLHKLLVQPNDTIYVSTRENQKIYVMG ESGKNQALPMRDQGMTLTDALGESLGINPLSGSASRIYVVRTNPNDRTTEIYHLNLMSIGDFGLA NQFRLRSNDVVYVDATGLTRWQRIVNQIIPFSNALYNIDRLGQ	7.8474743	0.033811446	up
V5VBV2	Type II toxin-antitoxin system HicA family toxin	51	2	9	2	7.5	MKKVVKAKNLIAFRIWLEKLGYSVKNLADGKGFTFSFKKEYGLVTCDLAGNALAMQLGEEFED HLKA	2.6198339	0.011942211	up

X2FEM8	Aminotransferase DegT	50	13	55	13	39.3	MIDFIDLKAQQNRIKDKIDAGIQNVLTHGQYILGPEVIELEEKLASYVGAKHCITCANGTDALQIA QMAFGIGPDDEVITPGFTYIATAETVALLGAKPVYVDVNPKTYNLDVEKLEAAITPRTKAIIPVSL YGQCADFDAINAIAKKYSIPVIEDAAQSFGATYKGRKSCNLSTVACTSFFPSKPLGCYGDGGAIFT NDDELAKVIRQIARHGQDKRYHHIRVGVNSRLDTLQAAILLPKLEILDDEMQARQRVAEVYNRL FDEVGIHTTPYIEAHNTSAWAQYTIQVDNRAEVQEKLKAQGIPTAVHYPIPLNKQPAVADSDIHL PIGDAIAEKVMSLPMHPYLAIDDQLKIVKAFG	4.8302018	0.000102458	up
X2FEM9	Glycosyl transferase	40	8	14	8	39.0	MKILFLINSLKSKSGSERVAVELANKMAAIGSYNITLLNRESIKENAAYSIADNVEVIALSGSLFEF YKKLKKQISSNNYDVVVVHNMGKLSLLCAFVPNIKKLVVLEHVSFISRPKKIQILSKFLYRNIDQ VVTLTQNDKEQFDKFHSNVIVIPNFSPFSIASQPRNNNKQIVTIGRLTDQKNYIHLLQAWKKIYQS IPDWQLNIYGEGEQEEILQDYIKQQSLKNVSLKGSTSNVKEVYEQSSFFVMSSKYEGLPMVLIEA QSFGLPIVSYNCPYGPSDVIRDSKNGFLVEDQNVDELAAAVLKVALSPQLLEQFSQSSLLNAKKY QPEQILKIWIEKVLEG	4.3031901	2.88E-05	up
X2FIS4	Uncharacterized protein	59	6	17	6	14.2	MVDETRYIPVKVLRQGNIYYLNCEAFDIVEKSSNLLHCIEQMKNRIIEKVVALHHAGEKLPVFDL YKSLKSGGILLEIPSSCFDDTLERVTLTLPKSVITGIDAVSPNRSAKFTQLAKEFIDGDNK	0.1910772	3.30E-05	down
X2FIW9	Peptidyl-prolyl cis-trans isomerase	81	12	76	1	26.4	MEPFMSKALPIAVAVVLGGAALVPVYYATQHPTTEVGRKADKNASPIQKISYVLGYEVAQQTPP ELDTKAFVQGIHDARNKQPSAYTQEDLKAAVAAYEKELQQKMQHQDKPEQAGTAADSADTQF LAENKTKAGVKTTASGLQYIITKEGTGKQPTAQSIVKVHYEGRLINGQVFDSSYKRGQPVEFPLN QVIPGWTEGLQLMKEGGKATFFIPSNLAYGPQELPGIPANSTLIFDVELISVK			

Table S5: Clustering analysis of DEPs across *A. baumannii* resistance phenotypes.

Cluster	Number of Proteins	Members of Proteins
1	73	A0A0D8EQN4; A0A6H3EK80; A0A9P3CXM7; A0A9Q1NNH7; A0A8E4GYA6; A0A7U4BKB8; A0A009GY40; A0A5K6CRD2; A0A7U5XU67; X2FEM8; A0A411MUY4; A0A6B2QRH5; A0A9P2UFA0; A0A9P2XHD2; V5REF7; A0A517D2C4; A0A429MK36; A0A0Q1HCL9; A0A126W935; A0A9P2UEN7; A0A009QD14; A0A2U8NGD1; A0A009PWD1; A0A654KWM6; A0A009GKU9; D0C6V6; A0A0E1PV91; A0A4P8VDY7; V5REA9; G1CBP8; A0A158LX87; A0A062IH60; A0A097I5H7; A0A4Q4H670; X2FEM9; A0A9P2UFT2; A0A062IMZ0; A0A9Q1N7W9; A0A7U4BNK2; A0A9Q7ZZR4; V5VBV2; A0A9Q2E0D7; A0A7S8WB40; A0A062IHP7; A0A9Q4XE51; A0A385EQQ7; A0A9Q1S0P9; A0A9P3CXB6; A0A646MCI5; A0A7U4DEJ2; A0A009GAT0; A0A9P2XK89; C7FEK7; A0A385ET64; V5RCU9; A0A9Q8MVK5; A0A385F1H2; B0V8Q7; A0A062IBU4; A0A6H3TEL8; B0VNR0; A0A009S9H1; A0A6F8TGE6; S3TFV1; X2F9Q9; A0A9P2QE53; B0VQQ0; A0A828SQM8; A0A6H3T2F1; A0A0E1FIC9; A0A0E1PSU4; A0A090B7C1; A0A7Z2CM08
2	25	A0A7L9DVL0; A0A241ZEM6; A0A1S2G0B0; U5QBG8; A0A1E3M437; A0A076G2Y6; A0A7L9DUK6; A0A7M3FN66; X2FIS4; A0A9P2X8Z1; A0A009QHT0; A0A7U5XUN1; A0A0E3KX17; A0A7S8ZW13; A0A385F163; A0A410J6J6; A0A7Z1WQ98; A0A076G2N9; A0A9P2U9F4; B0VR23; A0A0J1ACY0; A0A076G3Q9; A0A7M3FNP5; A0A7U5XUJ7; A0A9Q7GEX3
3	68	A0A411VGD7; A0A5P6FNN8; A0A062IRH0; N9JQN7; A0A1S2GAH7; A0A062IH37; A0A9Q1RZT3; A0A9P2QG90; N9KZS5; A0A241ZJ54; A0A9Q1S3Z9; A0A1E3M652; A0A009G8E9; A0A0H4UME6; A0A5K1MJI7; A0A6H3T3L2; A0A1E3MBC2; A0A062IS18; A0A6H3SV37; A0A385EU35; A0A7S8F867; A0A7Z1WNT5; A0A6B9KZP3; A0A0G4QU89; A0A009G8K1; A0A429LHC2; A0A9Q4SJB7; B0VRV5; A0A1E3MB56; A0A3F3MQT9; A0A829RFQ7; A0A1E3MBE0; A0A009HXJ2; A0A062IDU6; A0A6B9KPL0; A0A241ZE65; A0A9P2XJZ6; A0A009G507; A0A5P1UJC1; A0A9Q4SK06; V5RCJ8; A0A6F8TC76; N9JQM5; A0A6H2UPY5; A0A9Q1N8I6; A0A4Q4H7V6; A0A0J1DET4; A0A5K1MJT9; A0A654L9F1; A0A009H3M3; A0A8B4MT53; A0A7X5C6N3; A0A3S0N6T4; A0A009T164; A0A6B9KQE9; A0A6H3UE57; A0A1T0DRB8; A0A9P2UCI4; A0A7S8ZW19; A0A654L2Q2; A0A9P2P5S8; A0A654L2G6; A0A009PBA1; A0A481WVU6; A0A062I638; A0A5P3MF62; S3TD50; A0A829RK63
4	38	A0A829K710; A0A0E1PNX1; A0A380V1V9; A0A8I0F482; A0A1S2FL61; A0A4V5MUT8; A0A654KV19; A0A0F6SYM7; A0A009GVM1; A0A2I8CT67; X2FIW9; A0A654L3J1; A0A009QKJ4; A0A090BAM3; V5RC11; Q0ZAQ7; A0A481WW07; A0A6H3T9J1; A0A5K1MHI6; A0A0E1PVE2; A0A7U7KGU4; D0CDQ9; A0A836M1S1; A0A7U3Y2S3; A0A0E1PN17; A0A0D5YE03; A0A0E1PVE6; A0A1S8V5S4; A0A9P2UGQ7; A0A059ZG34; A0A9Q1RYZ7; A0A009GU27; A0A9Q1NIM9; A0A836YML5; A0A0E1PVF3; A0A9Q1ZY45; A0A1B1LW15; A0A9Q2I4G4
5	17	A0A9Q6DAC3; A0A6I4HS79; A0A3S0KUX5; A0A0E1PQH3; A0A2U9QFX2; Q4A208; A0A0E1PP65; A0A097I5C2; A0A7U3Y047; A0A0E1FL10; N0A436; A0A9P2P3T1; A0A4Q4GN90; A0A9Q4SH60; A0A6I4HT95; A0A829K6I4; A0A837Q8N8
6	39	A0A5N0FZ32; A0A9P2XJK2; H6VX66; A0A9Q7DS60; A0A9Q1W4V0; A0A6F8TCX5; A0A1E3M2G1; A0A125S0J9; A0A335J3M4; A0A0E1PTG5; A0A9Q1NA93; A0A9P2UE60; A0A385EUT6; A0A505ZPT1; B0VNB8; H6UQA3; A0A6H3T0T0; A0A385EUA0; A0A9Q6DWC7; A0A7U4F8B0; A0A090B850; A0A158LWX7; A0A6H3SGL6; A0A009HBN0; A0A828STC4; A0A5P1UPF1; A0A7U4BQ44; A0A7Z1WKR3; A0A505MKS4; A0A9P3CY71; A0A385ER43; A0A333V6L2; A0A3R9RP79; A0A9Q7I520; A0A1E3M9X9; A0A9Q1RV14; A0A385F0B4; A0A836LYR7; A0A829KCA3

Table S6: DEMs in MDR vs. DS strains.

Compound ID	Name	Formula	Molecular Weight	RT [min]	m/z	mzCloud Results	mzVault Results	MassList Results	KEGG ID	ClassyFire functional classification	FC MDR/DS	*P*-value MDR/DS	VIP	Regulate
Com_1000_neg	N-Acetylaspartic acid	C6 H9 N O5	175.04762	1.869	174.04035	Full match	Full match	Full match	cpd:C01042	Organic acids and derivatives	2.7017374	0.00018019	1.2633	up
Com_10085_pos	Metyrosine	C10 H13 N O3	195.08933	1.195	196.0966	No results	No results	Full match	cpd:C07921	--	0.18102589	0.04209877	1.181034	down
Com_1027_pos	N-(2-hydroxyphenyl)acetamide	C8 H9 N O2	173.04354	1.464	174.05084	Invalid mass	No results	No results	--	--	4.07040747	0.00145322	1.574182	up
Com_1037_neg	Guanosine	C10 H13 N5 O5	283.09192	3.682	282.08463	Full match	Full match	Full match	cpd:C00387	Nucleosides, nucleotides, and analogues	6.44587455	5.0929E-05	1.259118	up
Com_1037_pos	1,5-dimethyl-N-(4-morpholinobenzyl)-1H-pyrazole-3-carboxamide	C17 H22 N4 O2	628.34787	4.985	315.18121	Invalid mass	No results	No results	--	--	0.436118	8.8642E-06	1.002827	down
Com_10469_neg	N-Acetyl-L-phenylalanine	C11 H13 N O3	225.09982	5.571	224.0927	Invalid mass	Invalid mass	No results	cpd:C03519	Organic acids and derivatives	2.70719891	0.00087648	1.737554	up
Com_10641_pos	P-Aminohippuric Acid	C9 H10 N2 O3	194.06887	4.966	406.17123	No results	No results	Full match	cpd:D06890	Benzenoids	4.91621845	4.9284E-06	1.687851	up
Com_1082_pos	L-cysteine	C3 H7 N O2 S	121.01977	1.32	122.02705	No results	No results	Full match	cpd:C00097	Organic acids and derivatives	0.4626108	0.01269198	1.171775	down
Com_10905_pos	Tauroursodeoxycholic acid	C26 H45 N O6 S	499.29842	5.324	500.30569	No results	No results	Full match	cpd:C16868	Lipids and lipid-like molecules	0.49242589	0.00099953	1.057743	down
Com_10929_neg	L-Cysteinesulfinic acid	C3 H7 N O4 S	153.00903	1.361	152.00175	No results	No results	Full match	cpd:C00606	Organic acids and derivatives	4.75999502	3.5127E-05	1.791118	up
Com_11_pos	LPE 18:1	C23 H46 N O7 P	479.30051	9.346	480.30781	No results	Full match	Full match	--	Lipids and lipid-like molecules	0.08117273	0.00810178	1.105241	down
Com_11030_pos	Methyl EudesMate	C11 H14 O5	226.08386	4.997	227.09114	No results	No results	Full match	--	Benzenoids	3.08879099	0.00165568	1.521316	up
Com_1134_neg	N-Acetyl-DL-tryptophan	C13 H14 N2 O3	246.10066	5.521	245.0932	Full match	Full match	Full match	--	Organic acids and derivatives	2.42119703	0.00012065	1.454222	up
Com_1141_pos	DL-Lysine	C6 H14 N2 O2	146.10533	1.14	147.11256	Full match	Full match	Full match	cpd:C16440	Organic acids and derivatives	0.07874939	0.00069914	1.708858	down
Com_1151_pos	Oleoyl ethanolamide	C20 H39 N O2	307.28682	9.347	308.2941	Invalid mass	No results	No results	cpd:C20792	Organic nitrogen compounds	0.0712691	0.01313724	1.373087	down
Com_1177_pos	Guanine	C5 H5 N5 O	151.04927	1.617	152.05655	No results	No results	Full match	cpd:C00242	Organoheterocyclic compounds	0.2918236	5.5225E-05	1.545317	down
Com_119_neg	2-Hydroxyvaleric acid	C5 H10 O3	118.0622	5.255	117.05492	Invalid mass	Invalid mass	No results	--	Lipids and lipid-like molecules	59.4231004	5.2389E-14	1.818733	up
Com_1217_neg	Pantothenic acid	C9 H17 N O5	219.1106	5.015	218.10331	Full match	Full match	Full match	cpd:C00864	Organic oxygen compounds	2.46400285	1.0196E-06	1.847551	up
Com_12308_neg	IDP	C10 H14 N4 O11 P2	428.01449	3.688	427.00721	No results	No results	Full match	cpd:C00104	Nucleosides, nucleotides, and analogues	9.67838626	0.00084531	1.686685	up
Com_1245_pos	Acetylcysteine	C5 H9 N O3 S	163.02992	1.5	146.02663	No results	No results	Full match	cpd:C06809	Organic acids and derivatives	7.0552721	1.3004E-06	1.817203	up
Com_1258_pos	Phe-Pro	C14 H18 N2 O3	262.13112	5.648	263.1384	No results	No results	Full match	--	Organic acids and derivatives	0.28558596	6.282E-06	1.268481	down
Com_1286_neg	Uridine 5'-diphosphate	C9 H14 N2 O12 P2	404.00291	1.337	402.99564	Full match	No results	Full match	cpd:C00015	Nucleosides, nucleotides, and analogues	0.31529829	0.00621701	1.558024	down
Com_1296_neg	Hippuric acid	C9 H9 N O3	179.05789	5.927	178.05059	No results	No results	Full match	cpd:C01586	Benzenoids	2.61094054	5.8346E-05	1.61676	up
Com_13_neg	17-AAG	C31 H43 N3 O8	567.29161	5.562	566.28431	Invalid mass	No results	No results	--	--	0.23759903	4.8774E-08	1.8416	down
Com_13022_neg	Biopterin	C9 H11 N5 O3	237.08502	1.431	236.07774	No results	No results	Full match	cpd:C06313	Organoheterocyclic compounds	0.18477632	0.01614326	1.466351	down
Com_1334_neg	2'-Deoxyinosine	C10 H12 N4 O4	252.08587	4.055	251.07859	Full match	Full match	Full match	cpd:C05512	Nucleosides, nucleotides, and analogues	3.84470071	0.00123083	1.732261	up
Com_1344_neg	4-Hydroxy-L-Glutamic	C5 H9 N O5	163.04881	5.043	162.04153	No results	No results	Full match	cpd:C03079	Organic acids and derivatives	2.36905799	6.1131E-06	1.554088	up
Com_13462_neg	dCMP	C9 H14 N3 O7 P	307.05824	3.686	306.05096	No results	No results	Full match	cpd:C00239	Nucleosides, nucleotides, and analogues	22.7799459	7.8799E-06	1.782052	up
Com_138_neg	Fumaric acid	C4 H4 O4	116.01017	2.364	115.00288	No results	Invalid mass	No results	cpd:C00122	Organic acids and derivatives	2.31385629	0.00122185	1.630001	up
Com_1409_pos	DL-Arginine	C6 H14 N4 O2	174.11148	1.209	175.11874	Full match	Full match	Full match	cpd:C02385	Organic acids and derivatives	0.18017219	0.01119575	1.374111	down
Com_1445_pos	Guanosine monophosphate	C10 H14 N5 O8 P	363.0575	1.591	364.06478	No results	No results	Full match	cpd:C00144	Nucleosides, nucleotides, and analogues	0.063104	2.4446E-06	1.781664	down
Com_1494_neg	LPG 17:1	C23 H45 O9 P	496.28111	9.11	495.27383	No results	Full match	No results	--	Lipids and lipid-like molecules	0.14616402	0.017246	1.413575	down
Com_153_pos	Tyramine	C8 H11 N O	137.08408	5.404	120.08081	No results	No results	Full match	cpd:C00483	Benzenoids	0.2203383	6.3426E-05	1.643533	down
Com_155_neg	Mycophenolic acid	C17 H20 O6	320.12368	5.598	319.1164	Invalid mass	No results	No results	cpd:C20380	Organoheterocyclic compounds	450.817901	2.3269E-11	1.771228	up
Com_1563_pos	2,6-Dihydroxypurine	C5 H4 N4 O2	152.03335	4.751	153.04062	No results	No results	Full match	cpd:C00385	Organoheterocyclic compounds	35.2401791	5.0142E-06	1.707512	up
Com_1574_pos	LPE 14:0	C19 H40 N O7 P	425.25379	8.172	426.26104	No results	Full match	Full match	--	Lipids and lipid-like molecules	4.2406332	9.8198E-07	1.32501	up
Com_159_pos	N-Acetylmethionine	C7 H13 N O3 S	191.06144	5.236	214.05068	No results	Full match	Full match	cpd:C02712	Organic acids and derivatives	6.82676997	1.1343E-05	1.808867	up
Com_1591_neg	Asp-glu	C9 H14 N2 O7	262.0793	5.165	261.07202	No results	No results	Full match	--	Organic acids and derivatives	0.12298857	1.4826E-05	1.908689	down
Com_1592_neg	LPG 16:0	C22 H45 O9 P	484.28041	9.397	483.27313	No results	Full match	No results	--	Lipids and lipid-like molecules	0.08312874	0.03117309	1.24168	down
Com_16_neg	N-Acetyl-L-methionine	C7 H13 N O3 S	191.06125	5.238	190.05395	Full match	Full match	Full match	cpd:C02712	Organic acids and derivatives	5.55333882	3.0887E-07	1.910275	up
Com_165_neg	trans-Cinnamic acid	C9 H8 O2	148.05177	5.603	147.0445	Full match	Full match	No results	cpd:C00423	Phenylpropanoids and polyketides	13.0982605	1.215E-07	1.67998	up
Com_1697_neg	2-Methylbutyroylcarnitine	C12 H23 N O4	245.16283	6.152	244.15556	No results	No results	Full match	--	Lipids and lipid-like molecules	12.9264666	1.5832E-07	1.513087	up
Com_1700_neg	N-Acetylvaline	C7 H13 N O3	159.08905	5.278	158.08177	No results	No results	Full match	--	Organic acids and derivatives	5.88824584	6.9596E-14	1.917242	up

Com_1708_neg	Guanosine monophosphate (GMP)	C10 H14 N5 O8 P	363.05875	1.52	362.05148	Full match	Full match	Full match	cpd:C00144	Nucleosides, nucleotides, and analogues	0.11335922	1.8736E-05	1.678151	down
Com_1720_pos	PC O-18:1	C26 H52 N O7 P	521.34787	9.431	522.35513	No results	Full match	Full match	--	--	0.09274921	0.00151917	1.469708	down
Com_1750_pos	5,7-dimethyl-2-phenylpyrazolo[1,5-a]pyrimidine	C14 H13 N3	245.09008	6.256	246.09718	Invalid mass	No results	No results	--	--	25.3971857	3.3792E-06	1.936016	up
Com_1787_pos	Enrofloxacin	C19 H22 F N3 O3	381.14639	6.255	382.1537	Invalid mass	No results	No results	--	Organoheterocyclic compounds	7.27574889	5.969E-13	1.018002	up
Com_1796_pos	LPE 17:1	C22 H44 N O7 P	465.28514	8.991	466.29242	No results	Full match	No results	--	Lipids and lipid-like molecules	4.74967273	0.00431946	1.476093	up
Com_1803_pos	1-allyl-4,5-diphenyl-2-(2-thienyl)-1H-imidazole	C22 H18 N2 S	342.12208	5.4	343.12936	Invalid mass	No results	No results	--	--	11.8510005	4.9173E-07	1.899645	up
Com_181_neg	Sucrose	C12 H22 O11	342.11685	1.356	387.11507	Full match	Full match	Full match	cpd:C00089	Organic oxygen compounds	0.32614841	0.03473197	1.073141	down
Com_1811_neg	Uric acid	C5 H4 N4 O3	168.02788	1.825	167.0206	Full match	Full match	Full match	cpd:C00366	Organoheterocyclic compounds	0.17440441	0.00039684	1.642116	down
Com_1818_pos	(4-amino-1,2,5-oxadiazol-3-yl)(morpholino)methanone	C7 H11 N5 O3	213.08601	1.264	214.09329	Full match	No results	No results	--	--	2.28565989	3.0512E-06	1.259566	up
Com_1832_pos	PC O-16:0	C24 H50 N O7 P	495.3319	9.187	496.33916	No results	Full match	Full match	--	--	0.13267224	0.00056886	1.330491	down
Com_184_pos	Methyl indole-3-acetate	C11 H11 N O2	189.07869	5.131	190.08596	Full match	Full match	Full match	cpd:C20635	Organoheterocyclic compounds	2.04736569	0.00013273	1.312348	up
Com_188_neg	N-Acetyl-D-tryptophan	C13 H14 N2 O3	246.10091	5.128	291.09912	No results	No results	Full match	cpd:C03137	Organic acids and derivatives	0.20305848	1.6078E-07	1.894656	down
Com_19_neg	LPG 18:1	C24 H47 O9 P	510.29631	9.734	509.28903	No results	Full match	Full match	--	Lipids and lipid-like molecules	0.04822284	0.02529343	1.138425	down
Com_1952_pos	5-Methoxyindole-3-Carbaldehyde	C10 H9 N O2	175.06321	4.769	176.07048	No results	No results	Full match	--	Organoheterocyclic compounds	2.28487838	6.2138E-06	1.328402	up
Com_2088_pos	Cytidine 5'-monophosphate (hydrate)	C9 H14 N3 O8 P	323.0515	1.399	324.05877	Full match	Full match	Full match	cpd:C00055	Nucleosides, nucleotides, and analogues	0.06488796	0.00176449	1.494039	down
Com_21_neg	Coenzyme A	C21 H36 N7 O16 P3 S	767.11602	4.946	382.55068	Full match	Full match	No results	cpd:C00010	Nucleosides, nucleotides, and analogues	0.30156334	1.3646E-05	1.734433	down
Com_210_pos	Methyl nicotinate	C7 H7 N O2	137.04763	5.474	138.0549	No results	No results	Full match	--	Organoheterocyclic compounds	2.99965419	0.00022749	1.784024	up
Com_212_neg	Phenylacetaldehyde	C8 H8 O	120.0569	5.602	119.04941	Invalid mass	No results	No results	cpd:C00601	Benzenoids	10.6847439	4.1223E-09	1.699575	up
Com_2126_neg	Lysope 18:1	C23 H46 N O7 P	479.30205	9.754	478.29477	No results	No results	Full match	--	Lipids and lipid-like molecules	0.13105801	0.03173843	1.112639	down
Com_2184_pos	Epigallocatechin	C15 H14 O7	612.15163	2.382	307.08309	No results	Invalid mass	No match	cpd:C12136	Phenylpropanoids and polyketides	5.75723435	0.00335584	1.661577	up
Com_221_neg	2-{1-[2-(1-benzothiophen-5-ylamino)-2-oxoethyl]cyclohexyl}acetic acid	C18 H21 N O3 S	331.12057	5.178	330.11329	Invalid mass	No results	No results	--	--	0.12191098	9.7274E-07	1.880874	down
Com_2224_pos	Gibberellic acid	C19 H22 O6	368.11908	5.131	369.12672	Invalid mass	No results	No results	cpd:C01699	Lipids and lipid-like molecules	0.49824426	0.00014477	1.520144	down
Com_2240_pos	ethyl 2-amino-8H-indeno[2,1-b]thiophene-3-carboxylate	C14 H13 N O2 S	259.06645	5.212	260.07373	Full match	No results	No results	--	--	12.3077715	4.9784E-06	1.810583	up
Com_2394_pos	4-(3,4-dihydro-2H-1,5-benzodioxepin-7-ylamino)-4-oxobutanoic acid	C13 H15 N O5	287.07662	5.523	288.08389	Invalid mass	No results	No results	--	--	3.98562476	8.4549E-06	1.742397	up
Com_2397_neg	1-Methyluric acid	C6 H6 N4 O3	182.04373	1.467	181.03645	No results	No results	Full match	cpd:C16359	Organoheterocyclic compounds	3.19645062	0.00548268	1.154972	up
Com_2453_pos	6-(7-methyloctyl)-1H,3H,4H,6H-furo[3,4-c]furan-1-one	C15 H24 O3	252.17016	6.76	253.17742	Invalid mass	No results	No results	--	--	3.31145874	0.00121949	1.575497	up
Com_2481_neg	L-Homocystine	C8 H16 N2 O4 S2	268.05382	5.638	267.04655	No results	No results	Full match	cpd:C01817	Organic acids and derivatives	11.1293548	8.0738E-08	1.849811	up
Com_252_pos	Paracetamol	C8 H9 N O2	151.06322	4.719	152.07049	Full match	Full match	Full match	cpd:C06804	Benzenoids	0.11147751	0.00514082	1.573577	down
Com_2549_neg	12-Hydroxydodecanoic	C12 H24 O3	216.17248	6.457	215.16521	Full match	No results	No results	cpd:C08317	Organic acids and derivatives	2.79625425	0.00020998	1.694439	up
Com_2559_pos	(1R,2R)-trans-N-Boc-1,2-cyclohexanediamine	C11 H22 N2 O2	214.16797	5.739	215.17525	No results	No results	Full match	--	Organic nitrogen compounds	4.71521369	3.9235E-05	1.144641	up
Com_2563_neg	LPC 18:1	C26 H52 N O7 P	567.35479	9.42	566.34751	No results	Invalid mass	No results	cpd:C04230	Lipids and lipid-like molecules	0.10118219	0.00053312	1.300642	down
Com_2639_neg	Butyryl-coenzyme A	C25 H42 N7 O17 P3 S	838.15329	4.689	418.06928	Invalid mass	No results	No results	cpd:C00136	Lipids and lipid-like molecules	7.6738276	0.01619724	1.40187	up

Com_2642_neg	Guanosine 5'-diphosphate	C10 H15 N5 O11 P2	443.0253	1.479	442.01803	Full match	No results	Full match	cpd:C00035	Nucleosides, nucleotides, and analogues	0.06272352	2.8601E-06	1.6703	down
Com_2708_neg	LPG 18:2	C24 H45 O9 P	508.28087	8.966	507.2736	No results	Full match	No results	--	Lipids and lipid-like molecules	0.11545642	0.02059332	1.303228	down
Com_2737_neg	LPC 16:0	C24 H50 N O7 P	541.33908	9.193	540.3318	No results	Invalid mass	No results	cpd:C04230	Lipids and lipid-like molecules	0.11370581	0.00020927	1.219122	down
Com_281_neg	Xanthosine	C10 H12 N4 O6	284.07586	4.751	283.06859	Full match	Full match	Full match	cpd:C01762	Nucleosides, nucleotides, and analogues	61.1629439	1.8933E-06	1.821532	up
Com_2821_pos	N-(4-fluorophenyl)-N'-(2-piperidinophenyl)urea	C18 H20 F N3 O	335.14538	5.329	336.15266	Invalid mass	No results	No results	--	--	0.23466633	6.5505E-05	1.505748	down
Com_284_neg	2-Hydroxy-4-methylthiobutanoic acid	C5 H10 O3 S	150.03448	5.202	149.02721	Full match	No results	No results	--	Lipids and lipid-like molecules	148.634395	1.3265E-11	1.722851	up
Com_285_pos	2-Phenylglycine	C8 H9 N O2	151.06321	5.523	152.07048	No results	No results	Full match	--	Organic acids and derivatives	0.25631741	0.01278733	1.453605	down
Com_29_neg	3'-Dephosphocoenzyme A	C21 H35 N7 O13 P2 S	687.15058	4.887	686.14331	Full match	No results	Full match	cpd:C00882	Nucleosides, nucleotides, and analogues	0.49193307	0.00237658	1.37989	down
Com_292_pos	Proline-hydroxyproline	C10 H16 N2 O4	228.1108	5.163	229.11808	No results	Full match	No results	--	Organic acids and derivatives	0.1831852	0.00012738	1.848648	down
Com_299_neg	Pimelic acid	C7 H12 O4	160.07301	5.387	159.06574	Full match	Full match	Full match	cpd:C02656	Lipids and lipid-like molecules	2.31008623	0.01210935	1.233683	up
Com_3_neg	2-Hydroxycaproic acid	C6 H12 O3	132.07784	5.592	131.07055	Invalid mass	Invalid mass	No results	--	Lipids and lipid-like molecules	67.4388415	3.4226E-13	1.797508	up
Com_3056_pos	Virginiamycin	C28 H35 N3 O7	507.23154	5.143	508.23882	Invalid mass	No results	No results	cpd:C11299	Phenylpropanoids and polyketides	3.38351195	0.00038066	1.600258	up
Com_3169_neg	6-Hydroxymelatonin	C13 H16 N2 O3	248.11623	5.142	247.10896	No results	No results	Full match	cpd:C05643	Organoheterocyclic compounds	0.25359591	0.00027213	1.761626	down
Com_3179_pos	6,6-dimethyl-4-piperidino-5,6-dihydro-2H-thiine-2-thione	C12 H19 N S2	241.09256	5.009	242.09984	Invalid mass	No results	No results	--	--	3.44595298	5.9629E-05	1.785211	up
Com_318_neg	Boc-beta-cyano-L-alanine	C9 H14 N2 O4	214.0957	5.327	427.18413	No results	No results	Full match	--	Organic acids and derivatives	0.35411934	5.3054E-07	1.597375	down
Com_3191_neg	Cytosine	C4 H5 N3 O	111.04274	1.456	156.04096	No results	No results	Full match	cpd:C00380	Organoheterocyclic compounds	4.42732083	5.2964E-06	1.613634	up
Com_3280_pos	N(6)-OH-Me-Adenosine	C11 H15 N5 O5	297.1071	3.954	298.11438	Full match	No results	Full match	--	Nucleosides, nucleotides, and analogues	0.34871036	0.00063443	1.022112	down
Com_3305_pos	Uridine 5'-monophosphate	C9 H13 N2 O9 P	324.03542	1.422	325.04267	No results	Full match	Full match	cpd:C00105	Nucleosides, nucleotides, and analogues	0.10429492	0.00063381	1.634257	down
Com_333_pos	Inosine	C10 H12 N4 O5	268.08053	3.68	269.08784	Full match	Full match	Full match	cpd:C00294	Nucleosides, nucleotides, and analogues	22.8915382	5.5327E-08	1.205227	up
Com_3363_pos	L-Cysteine-glutathione gisulfide	C13 H22 N4 O8 S2	426.08761	1.381	214.05108	No results	No results	Full match	--	--	6.02722299	4.2542E-05	1.795157	up
Com_3402_pos	1-(3-phenylpropanoyl)-4-piperidinecarboxylic acid	C15 H19 N O3	598.18792	4.756	300.10123	Invalid mass	No results	No results	--	--	24.3484279	1.8548E-08	1.701832	up
Com_35_neg	DL-4-Hydroxyphenyllactic acid	C9 H10 O4	182.05753	5.158	181.05026	Full match	No results	Full match	--	Phenylpropanoids and polyketides	3.24425158	7.2325E-06	1.285061	up
Com_357_neg	Uridine monophosphate	C9 H13 N2 O9 P	324.03636	1.457	323.02909	Full match	Full match	Full match	cpd:C00105	Nucleosides, nucleotides, and analogues	0.13932465	0.00035854	1.692266	down
Com_3591_neg	Prostaglandin G2	C20 H32 O6	368.22014	5.853	367.21286	No results	No results	Full match	cpd:C05956	Lipids and lipid-like molecules	0.27979703	0.00650976	1.351326	down
Com_3684_neg	Alloxan	C4 H4 N2 O5	160.01143	1.384	159.00422	No results	No results	Full match	--	Organoheterocyclic compounds	3.10826121	3.2913E-10	1.399929	up
Com_3902_pos	D-Fructose 6-phosphate	C6 H13 O9 P	260.02863	5.491	261.03592	No results	No results	Full match	cpd:C00085	--	4.1700823	3.7979E-05	1.451929	up
Com_397_neg	Syringic acid	C9 H10 O5	198.05249	4.951	179.03464	No results	No results	Full match	cpd:C10833	Benzenoids	0.40169896	0.002882	1.339661	down
Com_4002_neg	LPG 14:0	C20 H41 O9 P	456.24958	8.211	455.2423	No results	Full match	No results	--	Lipids and lipid-like molecules	3.11762799	0.00426698	1.33373	up
Com_41_neg	LPG 16:1	C22 H43 O9 P	482.26507	8.52	481.25779	No results	Full match	No results	--	Lipids and lipid-like molecules	0.34239171	0.00933248	1.440478	down
Com_414_neg	Glycerophospho-N-palmitoyl ethanolamine	C21 H44 N O7 P	453.28625	9.32	452.27897	Full match	Full match	Full match	--	Lipids and lipid-like molecules	0.21459094	0.02272326	1.171484	down
Com_4157_pos	gamma-	C10 H18 N2 O5 S	278.09357	4.882	279.10085	No results	Full match	No results	--	Organic acids and derivatives	5.45763943	0.00071376	1.60797	up
Com_4234_neg	L-arginine	C6 H14 N4 O2	174.11132	1.229	173.10403	No results	No results	Full match	cpd:C00062	Organic acids and derivatives	0.30012	0.0153999	1.293639	down
Com_4270_pos	8-Isoprostaglandin F1β	C20 H36 O5	373.28242	6.501	374.2897	Invalid mass	No results	No results	--	Lipids and lipid-like molecules	2.56979539	0.00436374	1.290135	up
Com_4355_pos	Deoxyadenosine	C10 H13 N5 O3	251.10149	5.023	252.10866	No results	No results	Full match	cpd:C00559	Nucleosides, nucleotides, and analogues	0.3240599	0.01188112	1.423333	down
Com_4447_pos	2-[4-(tert-butyl)-2-chlorophenoxy]-3-nitropyridine	C15 H15 Cl N2 O3	306.08076	1.366	307.08804	Invalid mass	No results	No results	--	--	5.32783158	4.1736E-06	1.236497	up
Com_4458_pos	3-methyl-5-oxo-5-(4-toluidino)pentanoic acid	C13 H17 N O3	235.12047	5.755	258.10976	Full match	No results	No results	--	--	0.48252557	0.01745243	1.410369	down
Com_45_pos	Pyridoxal	C8 H9 N O3	167.0581	4.842	168.06538	Full match	No results	No results	cpd:C00250	Organoheterocyclic compounds	5.04095136	3.566E-07	1.605029	up
Com_4532_neg	Lauric acid ethyl ester	C14 H28 O2	228.2088	8.167	227.20152	Full match	No results	Full match	--	Lipids and lipid-like molecules	3.72240046	1.1879E-06	1.33766	up
Com_4669_pos	11β-Hydroxyandrosterone	C19 H30 O3	323.2431	7.065	324.25038	Invalid mass	No results	No results	cpd:C14606	Lipids and lipid-like molecules	2.25618017	0.00012604	1.442432	up

Com_4786_pos	13,14-Dihydro prostaglandin E1	C20 H36 O5	338.24308	7.596	339.25036	Invalid mass	No results	No results	--	Lipids and lipid-like molecules	2.29582279	0.00026676	1.637639	up
Com_4909_neg	2-deoxyglucose-6-phosphate	C6 H13 O8 P	244.03543	1.266	289.03369	No results	No results	Full match	--	Organic acids and derivatives	0.23453408	0.01175167	1.082018	down
Com_496_pos	4-Pyridoxic acid	C8 H9 N O4	183.05308	4.784	184.06036	No results	No results	Full match	cpd:C00847	Organoheterocyclic compounds	6.84888367	2.4989E-05	1.936808	up
Com_4976_pos	ethyl 2-(benzylamino)-1,3-thiazole-5-carboxylate	C13 H14 N2 O2 S	262.07397	5.609	263.0814	Invalid mass	No results	No results	--	--	2.21700643	0.0004911	1.2196	up
Com_50_neg	17(S)-HpDHA	C22 H32 O4	396.20128	5.41	395.19398	Invalid mass	No results	No results	--	Lipids and lipid-like molecules	0.48696489	0.00194978	1.358106	down
Com_500_pos	Lysopg 18:1	C24 H47 O9 P	510.29557	9.74	533.28482	No results	No results	Full match	--	Lipids and lipid-like molecules	0.04033645	0.03862517	1.234085	down
Com_5002_neg	Pseudouridine	C9 H12 N2 O6	244.0696	2.027	243.06232	Full match	No results	Full match	cpd:C02067	Nucleosides, nucleotides, and analogues	0.33130795	1.4497E-07	1.281442	down
Com_502_pos	3-(4-nitrophenyl)[1,2,3]triazolo[1,5-a]quinazolin-5-amine	C15 H10 N6 O2	306.08233	5.988	307.08961	Invalid mass	No results	No results	--	--	3.19105784	0.00397406	1.543503	up
Com_5028_neg	Guanosine-3',5'-cyclic monophosphate	C10 H12 N5 O7 P	345.0479	2.439	344.04062	No results	Full match	Full match	cpd:C00942	Nucleosides, nucleotides, and analogues	0.22508547	0.00423945	1.413752	down
Com_5036_neg	Tyrosylalanine	C12 H16 N2 O4	252.11124	5.021	251.10394	Full match	No results	No results	--	Organic acids and derivatives	11.5051941	2.4715E-11	1.88723	up
Com_5076_neg	Propionyl-L-carnitine	C10 H19 N O4	217.13137	5.797	216.12409	No results	No results	Full match	cpd:C03017	Lipids and lipid-like molecules	2.8411467	3.7101E-06	1.731324	up
Com_5099_neg	CDP	C9 H15 N3 O11 P2	403.01887	1.316	402.0116	No results	No results	Full match	cpd:C00112	Nucleosides, nucleotides, and analogues	0.06858776	4.687E-05	1.762394	down
Com_5106_pos	2'-O-Methyladenosine	C11 H15 N5 O4	264.08522	4.891	282.11941	Invalid mass	Invalid mass	No results	--	Nucleosides, nucleotides, and analogues	8.84060829	1.3609E-06	1.651484	up
Com_5124_neg	Oxidized glutathione	C20 H32 N6 O12 S2	612.15367	2.335	611.1464	Full match	Full match	Full match	cpd:C00127	Organic acids and derivatives	4.25506359	1.6356E-05	1.839694	up
Com_5181_pos	Adipamide	C6 H12 N2 O2	144.08957	1.468	145.09683	No results	No results	Full match	--	Lipids and lipid-like molecules	9.04122627	1.9491E-10	1.734836	up
Com_520_pos	8-Hydroxyquinoline	C9 H7 N O	145.05262	5.777	146.05992	Full match	Full match	No results	cpd:C19434	Organoheterocyclic compounds	0.42793253	0.00832983	1.013947	down
Com_5287_neg	Methyldopa	C10 H13 N O4	211.08429	5.418	210.07697	No results	No results	Full match	cpd:C07194	Phenylpropanoids and polyketides	2.32838508	0.01809427	1.333459	up
Com_53_neg	N-Acetyl-D-alloisoleucine	C8 H15 N O3	173.1047	5.56	172.09742	Full match	Full match	Full match	--	Organic acids and derivatives	2.06084461	0.00017213	1.52712	up
Com_5311_pos	2-Thio-acetyl MAGE	C21 H42 O3 S	356.27785	6.606	357.28513	Invalid mass	No results	No results	--	Organic acids and derivatives	3.93232209	9.9779E-06	1.703281	up
Com_5458_neg	N-Acetyl-L-aspartic acid	C6 H9 N O5	175.04749	4.991	174.04022	No results	No results	Full match	cpd:C01042	Organic acids and derivatives	5.19747416	6.1297E-07	1.912016	up
Com_5464_pos	Azetidine-2-carboxylic acid	C4 H7 N O2	101.04798	5.23	102.05525	No results	No results	Full match	cpd:C08267	Organic acids and derivatives	5.45021496	8.8018E-07	1.81718	up
Com_5478_pos	GNK	C12 H23 N5 O5	634.34238	5.017	318.17847	Invalid mass	No results	No results	--	--	0.17920319	5.6024E-06	1.70991	down
Com_5514_pos	Dl-3-Hydroxy-kynurenine	C10 H12 N2 O4	224.07936	5.46	225.08664	No results	No results	Full match	--	Organic oxygen compounds	0.45236894	0.00423996	1.47846	down
Com_5665_pos	2,3,4-Trihydroxybenzoic	C7 H6 O5	170.02136	5.196	171.02863	No results	No results	Full match	--	Phenylpropanoids and polyketides	6.19798232	8.5112E-06	1.677538	up
Com_6095_pos	3-(4-pyridylmethylidene)chroman-4-one	C15 H11 N O2	237.08218	6	238.08949	Invalid mass	No results	No results	--	--	7.96749132	9.6314E-06	1.775071	up
Com_6115_neg	Levodopa	C9 H11 N O4	197.06869	4.805	242.06696	No results	No results	Full match	cpd:C00355	--	3.89231493	0.00022955	1.564869	up
Com_613_pos	N-(1-methyl-3-phenyl-1H-pyrazol-5-yl)-N'-(2-thienyl)urea	C15 H14 N4 O S	298.09269	5.486	299.09997	Invalid mass	No results	No results	--	--	0.27758314	1.5622E-07	1.951297	down
Com_6184_neg	Sedoheptulose 7-phosphate	C7 H15 O10 P	290.04079	1.288	289.03357	No results	No results	Full match	cpd:C05382	Organic oxygen compounds	0.22709977	0.00430744	1.180068	down
Com_6187_pos	6-anilino-1,3-dimethyl-1,2,3,4-tetrahydropyrimidine-2,4-dione	C12 H13 N3 O2	231.10397	4.022	232.11124	Invalid mass	No results	No results	--	--	14.7029574	1.5922E-05	1.664334	up
Com_6274_pos	Eicosapentaenoic acid	C20 H30 O2	308.23443	7.994	309.24171	Invalid mass	No results	No results	cpd:C06428	Lipids and lipid-like molecules	0.47860893	0.02011077	1.295828	down
Com_630_pos	LPE 16:0	C21 H44 N O7 P	453.28512	9.107	454.29236	No results	Full match	Full match	--	Lipids and lipid-like molecules	0.12903896	0.0094382	1.261987	down
Com_631_neg	5-Hydroxytryptophan	C11 H12 N2 O3	220.08466	4.977	219.07739	Full match	Full match	Full match	cpd:C01017	Organoheterocyclic compounds	2.21206171	0.00017009	1.669008	up
Com_6356_pos	5-hydroxy-6,7-dimethoxy-2-phenyl-4H-chromen-4-one	C17 H14 O5	336.04019	6.469	337.04747	Invalid mass	No results	No results	--	--	0.32188981	0.00861773	1.13964	down
Com_636_neg	2-Deoxyuridine	C9 H12 N2 O5	228.0746	2.009	227.06733	No results	No results	Full match	cpd:C00526	Nucleosides, nucleotides, and analogues	0.32435648	1.2091E-05	1.198222	down
Com_6385_pos	N-(2-hydroxy-2-phenylethyl)-N'-(2-thienyl)urea	C13 H14 N2 O2 S	262.07709	5.481	263.08437	Full match	No results	No results	--	--	0.13390173	0.00041204	1.720973	down

Com_652_neg	LPE 18:2	C23 H44 N O7 P	477.28629	9.059	476.27901	No results	Full match	Full match	--	Lipids and lipid-like molecules	0.15657962	0.01947591	1.154209	down
Com_6620_pos	(±)9-HpODE	C18 H32 O4	336.22738	6.818	354.26114	Invalid mass	No results	No results	--	--	2.51695037	0.01816371	1.169392	up
Com_677_neg	Cytidine-5'-monophosphate	C9 H14 N3 O8 P	323.0524	1.434	322.04512	No results	Full match	Full match	cpd:C00055	Nucleosides, nucleotides, and analogues	0.10438774	0.00188491	1.490727	down
Com_69_pos	5'-S-Methyl-5'-thioadenosine	C11 H15 N5 O3 S	297.08939	5.126	298.09667	Full match	Full match	Full match	cpd:C00170	Nucleosides, nucleotides, and analogues	0.23375606	1.4968E-06	1.734922	down
Com_711_neg	Xanthine	C5 H4 N4 O2	152.03288	2.173	151.0256	Full match	No results	Full match	cpd:C00385	Organoheterocyclic compounds	0.38598895	0.00533274	1.316867	down
Com_7128_neg	Phe-Phe	C18 H20 N2 O3	312.14787	6.157	311.14059	No results	No results	Full match	--	Organic acids and derivatives	0.17721541	1.4995E-05	1.567007	down
Com_7289_pos	(2E)-6-hydroxy-2-methyl-6-(4-methylphenyl)hept-2-enoic acid	C15 H20 O3	270.11849	6.235	271.12576	Invalid mass	No results	No results	--	--	3.10780491	7.4947E-05	1.460005	up
Com_73_neg	3,5-	C8 H9 N O4	183.05284	5.249	182.04556	Full match	No results	Full match	--	Organic acids and derivatives	3.01553567	0.00085732	1.612966	up
Com_7326_neg	LPE 20:5	C25 H42 N O7 P	499.27085	8.215	498.26358	No results	Full match	No results	--	Lipids and lipid-like molecules	0.2627919	5.3224E-05	1.556069	down
Com_7478_pos	2-OHE1-6-N3Ade	C23 H25 N5 O3	419.20378	4.976	420.21106	Invalid mass	No results	No results	--	--	0.24620427	2.7147E-07	1.649056	down
Com_7529_pos	L-Cystine	C6 H12 N2 O4 S2	240.02364	1.218	241.03092	Full match	Full match	Full match	cpd:C00491	Organic acids and derivatives	2.7638504	0.00554362	1.508138	up
Com_7643_neg	Fmoc-L-Isoleucine	C21 H23 N O4	353.16397	6.304	352.1567	No results	No results	Full match	--	Organic acids and derivatives	3.69637353	0.00081288	1.200609	up
Com_7662_pos	JNJ-1661010	C19 H19 N5 O S	365.13202	4.599	366.13929	No results	No results	Full match	--	Organoheterocyclic compounds	9.13921848	4.8954E-10	1.547427	up
Com_775_pos	D-(+)-Maltose	C12 H22 O11	364.09778	1.324	365.10506	Invalid mass	No results	No results	cpd:C01971	Organic oxygen compounds	0.25133243	0.03741849	1.184524	down
Com_7813_pos	3-(5,7-dimethoxy-4-oxo-4H-chromen-2-yl)propanoic acid	C14 H14 O6	261.05277	5.807	279.08686	Invalid mass	No results	No results	--	--	3.49455037	0.0003801	1.422867	up
Com_7826_pos	LPC 16:1-SN1	C24 H48 N O7 P	493.31659	8.716	494.32388	No results	Full match	Full match	--	--	0.35010084	0.00058953	1.184838	down
Com_7973_pos	1-(4-chlorophenyl)-4-hydroxy-6-isopropyl-3-phenylpyridin-2(1H)-one	C20 H18 Cl N O2	339.10045	6.109	340.10773	Invalid mass	No results	No results	--	--	0.29292007	0.00034588	1.414449	down
Com_8047_pos	ATP	C10 H16 N5 O13 P3	506.99597	4.783	508.00325	No results	No results	Full match	cpd:C00002	Nucleosides, nucleotides, and analogues	0.45292387	2.9054E-05	1.66018	down
Com_8122_neg	LysoPE 18:0	C23 H48 N O7 P	481.31799	9.185	480.31071	No results	No results	Full match	--	Lipids and lipid-like molecules	0.11536045	0.00173674	1.624922	down
Com_8209_pos	Vitamin B2	C17 H20 N4 O6	376.1382	4.9	377.14548	No results	No results	Full match	cpd:C00255	Organoheterocyclic compounds	3.40953228	3.1E-06	1.553349	up
Com_826_pos	NMK	C15 H29 N5 O5 S	746.35043	5.218	374.18249	Invalid mass	No results	No results	--	--	2.01115448	0.01350442	1.028573	up
Com_83_neg	Gallic acid	C7 H6 O5	124.01545	0.454	169.01366	Invalid mass	Invalid mass	No results	cpd:C01424	Benzenoids	0.16200684	0.0427166	1.097544	down
Com_8310_neg	Deoxycytidine	C9 H13 N3 O4	227.09039	3.359	226.08307	No results	No results	Full match	cpd:C00881	Nucleosides, nucleotides, and analogues	0.1866019	0.00116187	1.129094	down
Com_848_neg	o-Toluic Acid	C8 H8 O2	136.05199	5.157	135.04444	No results	No results	Full match	cpd:C07215	--	3.54907264	2.5867E-06	1.487272	up
Com_85_pos	Hypoxanthine	C5 H4 N4 O	136.03843	3.678	137.04571	Full match	Full match	Full match	cpd:C00262	Organoheterocyclic compounds	20.572297	1.783E-08	1.339864	up
Com_853_neg	Riboflavin	C17 H20 N4 O6	376.13905	5.287	375.13152	Full match	Full match	Full match	cpd:C00255	Organoheterocyclic compounds	4.92811271	9.3934E-07	1.870874	up
Com_8621_pos	Proscillaridin A	C30 H42 O8	530.29522	6.33	531.3025	Invalid mass	No results	No results	--	Lipids and lipid-like molecules	6.02750521	1.0607E-08	1.706805	up
Com_8957_neg	LPC 14:0	C22 H46 N O7 P	513.30753	8.211	512.30025	No results	Invalid mass	No results	cpd:C04230	Lipids and lipid-like molecules	0.24130776	5.3133E-07	1.201013	down
Com_9_neg	3-Phenyllactic acid	C9 H10 O3	166.06238	5.599	165.0551	Full match	Full match	Full match	cpd:C01479	Phenylpropanoids and polyketides	14.2549543	1.3897E-07	1.668337	up
Com_9089_neg	LPE 20:4	C25 H44 N O7 P	501.28674	8.704	500.27946	No results	Full match	No results	--	Lipids and lipid-like molecules	0.19256297	0.04092099	1.26068	down
Com_9125_pos	Deoxyinosine	C10 H12 N4 O4	252.0855	4.021	275.07481	No results	No results	Full match	cpd:C05512	Nucleosides, nucleotides, and analogues	8.74129394	6.1979E-09	1.820265	up
Com_9270_neg	5-Methylcytidine	C10 H15 N3 O5	211.09585	1.872	256.09419	No results	Invalid mass	No results	--	Nucleosides, nucleotides, and analogues	0.14551288	1.1866E-05	1.747062	down
Com_9307_neg	LPG 16:2	C22 H41 O9 P	480.24989	8.208	479.24261	No results	Full match	No results	--	Lipids and lipid-like molecules	0.35285657	0.00711701	1.481996	down
Com_937_pos	Valylproline	C10 H18 N2 O3	214.13154	5.213	215.13882	Full match	No results	No results	--	Organic acids and derivatives	0.32504023	6.1799E-05	1.544039	down
Com_9375_neg	Cystine	C6 H12 N2 O4 S2	240.02394	1.252	239.01666	No results	No results	Full match	cpd:C01420	Organic acids and derivatives	3.31853643	0.00617313	1.507369	up
Com_976_neg	Prostaglandin A2	C20 H30 O4	370.18568	5.385	369.1784	Invalid mass	No results	No results	cpd:C05953	Lipids and lipid-like molecules	0.27169875	5.0956E-07	1.749922	down
Com_9973_pos	beta-Nicotinamide adenine dinucleotide phosphate	C21 H28 N7 O17 P3	743.07407	1.393	372.54431	No results	No results	Full match	cpd:C00006	Nucleosides, nucleotides, and analogues	0.19562194	0.0002509	1.576589	down

Table S7: DEMs in XDR vs. DS strains.

Compound ID	Name	Formula	Molecular Weight	RT [min]	m/z	mzCloud Results	mzVault Results	MassList Results	KEGG ID	ClassyFire functional classification	FC XDR/DS	*P*-value XDR/DS	VIP	Regulate
Com_3465_pos	Vatalanib dihydrochloride	C20 H15 Cl N4	324.11761	5.633	347.1068	Invalid mass	No results	No results	--	--	21.2008979	3.8723E-11	1.805415	up
Com_3402_pos	1-(3-phenylpropanoyl)-4-piperidinecarboxylic acid	C15 H19 N O3	598.18792	4.756	300.10123	Invalid mass	No results	No results	--	--	30.9387387	6.3383E-11	1.65652	up
Com_3886_neg	2-Hydroxyestradiol	C18 H24 O3	288.16888	5.511	287.1616	Invalid mass	No results	No results	cpd:C05301	Lipids and lipid-like molecules	0.16447102	3.3355E-10	1.508374	down
Com_8957_neg	LPC 14:0	C22 H46 N O7 P	513.30753	8.211	512.30025	No results	Invalid mass	No results	cpd:C04230	Lipids and lipid-like molecules	0.08740985	1.1168E-09	1.836046	down
Com_4269_pos	Stanozolol	C21 H32 N2 O	328.24687	6.108	329.25415	Invalid mass	No results	No results	cpd:C07311	Lipids and lipid-like molecules	0.09893767	1.6674E-09	1.463412	down
Com_1249_pos	LPE 14:1	C19 H38 N O7 P	423.23826	7.633	424.24548	No results	Full match	No results	--	Lipids and lipid-like molecules	0.22534396	2.458E-09	1.758186	down
Com_993_neg	1-Methylguanosine	C11 H15 N5 O5	297.1076	3.708	296.10032	No results	No results	Full match	cpd:C04545	Nucleosides, nucleotides, and analogues	4.64607784	3.4837E-09	1.607284	up
Com_562_pos	3-((5-Phenyloxazol-2-yl)amino)benzonitrile	C16 H11 N3 O	261.08989	5.916	262.09717	Full match	No results	No results	--	Organoheterocyclic compounds	0.19710376	5.2335E-09	1.740996	down
Com_4900_neg	LPE 18:4	C23 H40 N O7 P	473.25482	7.961	472.24754	No results	Full match	No results	--	Lipids and lipid-like molecules	6.27522194	1.3363E-08	1.156152	up
Com_1037_pos	1,5-dimethyl-N-(4-morpholinobenzyl)-1H-pyrazole-3-carboxamide	C17 H22 N4 O2	628.34787	4.985	315.18121	Invalid mass	No results	No results	--	--	0.19304366	1.3678E-08	1.820439	down
Com_3874_pos	2-acetamido-3-(4-methoxyphenyl)propanoic acid	C12 H15 N O4	237.10013	5.126	238.10732	Full match	No results	Full match	--	--	2.65463882	1.551E-08	1.738027	up
Com_208_neg	Pantetheine	C11 H22 N2 O4 S	278.13032	5.27	277.12299	No results	No results	Full match	cpd:C00831	Organic acids and derivatives	5.75198788	1.6542E-08	1.772333	up
Com_6128_pos	LysoPE 18:2	C23 H44 N O7 P	477.28537	7.481	478.29264	No results	No results	Full match	--	--	0.16201795	1.8013E-08	1.721252	down
Com_2170_neg	LPE 18:3	C23 H42 N O7 P	475.27059	8.221	474.26332	No results	Full match	No results	--	Lipids and lipid-like molecules	0.08833778	2.3622E-08	1.74166	down
Com_1944_pos	5-Hydroxytryptophol	C10 H11 N O2	177.07893	5.484	178.08623	No results	No results	Full match	--	Organoheterocyclic compounds	3.07642003	3.3547E-08	1.555927	up
Com_4063_neg	Estrone	C18 H22 O2	540.32908	5.477	539.32177	Invalid mass	No results	No results	cpd:C00468	Lipids and lipid-like molecules	0.14035383	5.5582E-08	1.430078	down
Com_1000_neg	N-Acetylaspartic acid	C6 H9 N O5	175.04762	1.869	174.04035	Full match	Full match	Full match	--	Organic acids and derivatives	4.48886684	7.7914E-08	1.763868	up
Com_10905_pos	Tauroursodeoxycholic acid	C26 H45 N O6 S	499.29842	5.324	500.30569	No results	No results	Full match	cpd:C16868	Lipids and lipid-like molecules	0.25450623	8.5331E-08	1.768041	down
Com_1556_pos	4-ethoxy-7,9-dimethylpyrido[3',2':4,5]thieno[3,2-d]pyrimidine	C13 H13 N3 O S	259.08178	5.624	260.08906	Invalid mass	No results	No results	--	--	0.22567544	8.7122E-08	1.725478	down
Com_190_pos	gamma-Glutamylleucine	C11 H20 N2 O5	260.1371	5.304	261.1444	No results	Full match	Full match	--	Organic acids and derivatives	3.45079763	9.3456E-08	1.817079	up
Com_1685_pos	PC O-16:1	C24 H48 N O7 P	493.31644	8.478	494.32372	No results	Full match	Full match	--	--	0.04777148	1.2491E-07	1.821225	down
Com_1348_pos	Obscurolide A1	C15 H17 N O5	323.13799	5.049	324.14519	Invalid mass	No results	No results	--	Benzenoids	0.33396043	2.3644E-07	1.604479	down
Com_1818_pos	(4-amino-1,2,5-oxadiazol-3-yl)(morpholino)methanone	C7 H11 N5 O3	213.08601	1.264	214.09329	Full match	No results	No results	--	--	3.6958145	2.6548E-07	1.772203	up
Com_5478_pos	GNK	C12 H23 N5 O5	634.34238	5.017	318.17847	Invalid mass	No results	No results	--	--	0.16512167	3.0418E-07	1.623692	down
Com_2791_pos	PE 9:0_9:0	C23 H46 N O8 P	495.29606	7.705	496.30328	No results	Full match	No results	--	--	0.13533074	5.4533E-07	1.673713	down
Com_1424_neg	LPC 16:1	C24 H48 N O7 P	539.32316	8.471	538.31589	No results	Invalid mass	No results	cpd:C04230	Lipids and lipid-like molecules	0.06911985	5.4683E-07	1.822748	down
Com_3684_neg	Alloxan	C4 H4 N2 O5	160.01143	1.384	159.00422	No results	No results	Full match	--	Organoheterocyclic compounds	5.01469771	7.0271E-07	1.779697	up
Com_315_neg	N-lactoyl-phenylalanine	C12 H15 N O4	237.10021	5.62	236.09293	No results	No results	Full match	--	Organic acids and derivatives	0.23332311	1.0397E-06	1.728871	down
Com_6163_pos	6-(Dimethylamino)purine	C7 H9 N5	163.08578	5.16	164.09266	No results	No results	Full match	--	Organoheterocyclic compounds	0.26146143	1.1068E-06	1.1173	down
Com_1282_pos	Gly-Phe	C11 H14 N2 O3	222.10015	5.17	223.10749	No results	No results	Full match	--	Organic acids and derivatives	0.46851041	1.2246E-06	1.744491	down
Com_1049_neg	Esculin	C15 H16 O9	340.08592	5.114	339.07866	Invalid mass	No results	No results	cpd:C09264	Phenylpropanoids and polyketides	5.0794853	1.4866E-06	1.72246	up
Com_1353_pos	Physostigmine	C15 H21 N3 O2	275.16312	4.987	276.17037	Full match	No results	No results	cpd:C06535	Organoheterocyclic compounds	0.3886898	1.9544E-06	1.59015	down
Com_5849_neg	(+/-)12(13)-DiHOME	C18 H34 O4	296.2354	7.254	295.22812	Invalid mass	No results	No match	cpd:C14829	Lipids and lipid-like molecules	0.10883509	2.0205E-06	1.636124	down
Com_5772_pos	7,8-Dihydrofolate	C19 H21 N7 O6	443.15703	5.755	444.16431	No results	No results	Full match	cpd:C00415	--	7.22692687	2.0632E-06	1.624647	up
Com_2642_neg	Guanosine 5'-diphosphate (GDP)	C10 H15 N5 O11 P2	443.0253	1.479	442.01803	Full match	No results	Full match	cpd:C00035	Nucleosides, nucleotides, and analogues	0.04907788	2.5509E-06	1.586937	down
Com_78_pos	2'-Deoxyadenosine	C10 H13 N5 O3	251.10162	3.707	252.1089	Full match	Full match	Full match	cpd:C00559	Nucleosides, nucleotides, and analogues	2.98284496	2.582E-06	1.744922	up

Com_571_pos	Acetylcarnitine	C9 H17 N O4	203.11575	5.622	226.10483	No results	No results	Full match	cpd:C02571	Lipids and lipid-like molecules	0.29953272	2.6563E-06	1.573558	down
Com_205_pos	2-(1,3-dimethyl-1H-pyrazol-5-yl)-1H-isoindole-1,3(2H)-dione	C13 H11 N3 O2	241.0849	5.474	242.09217	Full match	No results	No results	--	--	0.08866853	2.9291E-06	1.615541	down
Com_9961_neg	myricetin 3-O-beta-D-galactopyranoside	C21 H20 O13	480.08997	2.146	479.08269	Full match	No results	No results	--	--	0.14547628	3.1107E-06	1.807449	down
Com_1773_pos	2-[(3S)-1-(Benzylsulfonyl)-3-pyrrolidinyl]-1-methyl-1H-benzimidazole	C19 H21 N3 O2 S	377.11998	5.001	378.12726	Invalid mass	No results	No results	--	Organoheterocyclic compounds	2.4938584	3.4025E-06	1.171656	up
Com_16_neg	N-Acetyl-L-methionine	C7 H13 N O3 S	191.06125	5.238	190.05395	Full match	Full match	Full match	cpd:C02712	Organic acids and derivatives	3.61559521	3.8588E-06	1.281069	up
Com_1445_pos	Guanosine monophosphate	C10 H14 N5 O8 P	363.0575	1.591	364.06478	No results	No results	Full match	cpd:C00144	Nucleosides, nucleotides, and analogues	0.08627341	4.0151E-06	1.450262	down
Com_285_neg	5-(tert-butyl)-2-methyl-N-(5-methyl-3-isoxazolyl)-3-furamide	C14 H18 N2 O3	262.13205	5.23	261.12477	Full match	No results	Full match	--	--	0.17665421	4.203E-06	1.781714	down
Com_3168_pos	Oxohongdenafil	C25 H32 N6 O4	458.27272	5.336	459.28067	Invalid mass	No results	No results	--	Organic oxygen compounds	0.22061381	4.3112E-06	1.561	down
Com_4669_pos	11β-Hydroxyandrosterone	C19 H30 O3	323.2431	7.065	324.25038	Invalid mass	No results	No results	cpd:C14606	Lipids and lipid-like molecules	2.89030532	4.5467E-06	1.67111	up
Com_1134_neg	N-Acetyl-DL-tryptophan	C13 H14 N2 O3	246.10066	5.521	245.0932	Full match	Full match	Full match	--	Organic acids and derivatives	3.13063958	4.7838E-06	1.672463	up
Com_5464_pos	Azetidine-2-carboxylic acid	C4 H7 N O2	101.04798	5.23	102.05525	No results	No results	Full match	cpd:C08267	Organic acids and derivatives	4.46017501	4.8823E-06	1.419863	up
Com_2286_pos	4-phenyl-6-(2-thienyl)-2,3,4,5-tetrahydropyridazin-3-one	C14 H12 N2 O S	256.07069	5.177	257.07796	Invalid mass	No results	No results	--	--	5.05925145	5.0862E-06	1.72306	up
Com_2287_pos	(3R)-8-hydroxy-3-(4-hydroxyphenyl)-3,4-dihydro-1H-2-benzopyran-1-one	C15 H12 O4	128.03542	5.181	257.078	Invalid mass	No results	No results	--	--	5.05925145	5.0862E-06	1.723909	up
Com_1673_pos	Melatonin	C13 H16 N2 O2	232.12105	5.053	233.12836	Full match	No results	Full match	cpd:C01598	Organoheterocyclic compounds	0.10224504	5.7171E-06	1.764178	down
Com_3486_neg	16α-Hydroxyestrone	C18 H22 O3	304.16372	5.443	303.15645	Invalid mass	No results	No results	cpd:C05300	Lipids and lipid-like molecules	0.226773	7.196E-06	1.6942	down
Com_6484_neg	11-Dehydro-thromboxane	C20 H32 O6	404.19692	6.502	403.18964	Invalid mass	No results	No results	cpd:C05964	Lipids and lipid-like molecules	3.08191804	7.2407E-06	1.693314	up
Com_3158_neg	LPG 14:1	C20 H39 O9 P	454.23382	7.623	453.22654	No results	Full match	No results	--	Lipids and lipid-like molecules	0.34132555	8.5294E-06	1.474827	down
Com_7128_neg	Phe-Phe	C18 H20 N2 O3	312.14787	6.157	311.14059	No results	No results	Full match	--	Organic acids and derivatives	0.12158553	8.6921E-06	1.649749	down
Com_1374_neg	4-Methyl-2-Oxopentanoic Acid	C6 H10 O3	130.06239	5.196	175.0607	No results	No results	Full match	--	--	3.33858522	8.7066E-06	1.751658	up
Com_4731_pos	PE 18:0	C23 H46 N O8 P	517.27809	7.697	518.28535	No results	Invalid mass	No results	cpd:C00350	Lipids and lipid-like molecules	0.16284975	9.2131E-06	1.573068	down
Com_4346_pos	Desthiobiotin	C10 H18 N2 O3	214.13148	3.746	215.13875	Full match	No results	No results	cpd:C01909	Organoheterocyclic compounds	0.17752328	9.6068E-06	1.601002	down
Com_1258_pos	Phe-Pro	C14 H18 N2 O3	262.13112	5.648	263.1384	No results	No results	Full match	--	Organic acids and derivatives	0.16155083	1.0002E-05	1.733197	down
Com_159_pos	N-Acetylmethionine	C7 H13 N O3 S	191.06144	5.236	214.05068	No results	Full match	Full match	cpd:C02712	Organic acids and derivatives	5.45676162	1.1843E-05	1.403443	up
Com_138_pos	Asp-Phe methyl ester	C14 H18 N2 O5	294.12133	5.311	295.1286	No results	No results	Full match	--	--	2.21999348	1.3997E-05	1.683686	up
Com_1703_pos	UDP	C9 H14 N2 O12 P2	404.0019	4.715	405.0091	No results	No results	Full match	cpd:C00015	Nucleosides, nucleotides, and analogues	3.39702747	1.4604E-05	1.744452	up
Com_130_neg	3-[(methoxycarbonyl) amino]-2,2,3-trimethylbutanoic acid	C9 H17 N O4	203.11558	5.622	202.1083	Full match	No results	Full match	--	--	0.36947864	1.4645E-05	1.574236	down
Com_1166_neg	Biotin	C10 H16 N2 O3 S	244.08833	5.323	243.08105	Full match	Full match	Full match	cpd:C00120	Organoheterocyclic compounds	2.03850789	1.559E-05	1.635052	up
Com_3191_neg	Cytosine	C4 H5 N3 O	111.04274	1.456	156.04096	No results	No results	Full match	cpd:C00380	Organoheterocyclic compounds	4.8243383	1.685E-05	1.531888	up
Com_2737_neg	LPC 16:0	C24 H50 N O7 P	541.33908	9.193	540.3318	No results	Invalid mass	No results	cpd:C04230	Lipids and lipid-like molecules	0.03326642	1.8976E-05	1.750094	down
Com_6810_pos	6-styryl-3-phenyl-2,5-dihydro-1,2,4-triazin-5-one	C17 H13 N3 O	275.10555	7.731	276.11284	Full match	No results	No results	--	--	3.1936772	1.917E-05	1.364578	up
Com_3179_pos	6,6-dimethyl-4-piperidino-5,6-dihydro-2H-thiine-2-thione	C12 H19 N S2	241.09256	5.009	242.09984	Invalid mass	No results	No results	--	--	3.03738193	2.0377E-05	1.438856	up

Com_1993_neg	2-[(3S)-1-(Cyclohexylmethyl)-3-pyrrolidinyl]-5-fluoro-1H-benzimidazole	C18 H24 F N3	301.20057	5.34	300.19329	Invalid mass	No results	No results	--	Organoheterocyclic compounds	0.07195943	2.0593E-05	1.600562	down
Com_2394_pos	4-(3,4-dihydro-2H-1,5-benzodioxepin-7-ylamino)-4-oxobutanoic acid	C13 H15 N O5	287.07662	5.523	288.08389	Invalid mass	No results	No results	--	--	3.8745332	2.2865E-05	1.486711	up
Com_4929_neg	LPE 10:0	C15 H32 N O7 P	369.19205	6.565	368.18476	No results	Full match	No results	cpd:C04230	Lipids and lipid-like molecules	0.16666274	2.7164E-05	1.666296	down
Com_3292_pos	1-(4-hydroxyphenyl) propane-1,2-diol	C9 H12 O3	190.0586	1.347	191.06587	Invalid mass	No results	No match	--	--	14.7694627	2.7542E-05	1.645455	up
Com_4547_pos	5-[4-(tert-butyl)phenyl]-1,3,4-oxadiazole-2-thiol	C12 H14 N2 O S	234.07956	5.727	257.06907	Invalid mass	No results	No results	--	--	2.35498949	2.9205E-05	1.555256	up
Com_1238_neg	Dl-Indole-3-lactic acid	C11 H11 N O3	205.07356	5.882	204.06628	No results	No results	Full match	--	Organoheterocyclic compounds	0.28347092	3.0445E-05	1.320537	down
Com_1803_pos	1-allyl-4,5-diphenyl-2-(2-thienyl)-1H-imidazole	C22 H18 N2 S	342.12208	5.4	343.12936	Invalid mass	No results	No results	--	--	6.3107666	3.0512E-05	1.312366	up
Com_7190_neg	8-Aminooctanoic acid	C8 H17 N O2	159.12545	5.618	158.11819	No results	No results	Full match	--	Organic acids and derivatives	0.26882702	3.081E-05	1.610041	down
Com_1708_neg	Guanosine monophosphate	C10 H14 N5 O8 P	363.05875	1.52	362.05148	Full match	Full match	Full match	cpd:C00144	Nucleosides, nucleotides, and analogues	0.13562059	3.3669E-05	1.483244	down
Com_7352_neg	Glu-Glu	C10 H16 N2 O7	276.09627	1.446	275.08899	No results	No results	Full match	cpd:C01425	Organic acids and derivatives	3.57850712	3.4556E-05	1.534331	up
Com_1217_neg	Pantothenic acid	C9 H17 N O5	219.1106	5.015	218.10331	Full match	Full match	Full match	cpd:C00864	Organic oxygen compounds	2.04564255	3.9295E-05	1.304703	up
Com_5124_neg	L-Glutathione oxidized	C20 H32 N6 O12 S2	612.15367	2.335	611.1464	Full match	Full match	Full match	cpd:C00127	Organic acids and derivatives	2.92997955	4.3855E-05	1.233481	up
Com_2180_pos	5-Methyluridine	C10 H14 N2 O6	258.085	4.842	259.09221	No results	No results	Full match	--	Nucleosides, nucleotides, and analogues	3.3751319	6.2169E-05	1.62481	up
Com_1238_pos	EPH	C16 H23 N5 O6	381.1663	5.428	382.17357	Full match	No results	No results	--	--	0.0991221	6.8501E-05	1.605689	down
Com_1756_neg	D-Xylonic Acid	C5 H10 O6	166.04737	5.175	377.09293	No results	No results	Full match	--	Organic oxygen compounds	0.08361452	6.9953E-05	1.541806	down
Com_5099_neg	CDP	C9 H15 N3 O11 P2	403.01887	1.316	402.0116	No results	No results	Full match	cpd:C00112	Nucleosides, nucleotides, and analogues	0.11231742	7.4359E-05	1.362888	down
Com_404_neg	2-Deoxyribose 5-phosphate	C5 H11 O7 P	214.02416	1.381	213.01688	Full match	Full match	Full match	--	Organic oxygen compounds	2.19198478	7.9336E-05	1.656839	up
Com_153_pos	Tyramine	C8 H11 N O	137.08408	5.404	120.08081	No results	No results	Full match	cpd:C00483	Benzenoids	0.23472109	8.6184E-05	1.410392	down
Com_3764_pos	N-acetyl-L-ornithine	C7 H14 N2 O3	174.10089	5.467	366.23589	No results	No results	Full match	cpd:C00437	Organic acids and derivatives	0.12077924	9.2962E-05	1.719375	down
Com_1296_neg	Hippuric acid	C9 H9 N O3	179.05789	5.927	178.05059	No results	No results	Full match	cpd:C01586	Benzenoids	2.52801242	9.5561E-05	1.409447	up
Com_228_neg	Cysteinylglycine	C5 H10 N2 O3 S	178.04086	5.225	177.03358	Full match	No results	Full match	--	Organic acids and derivatives	0.0519155	9.8899E-05	1.658331	down
Com_845_pos	JWH 250 N-pentanoic acid	C22 H23 N O4	365.15825	4.875	366.16553	Invalid mass	No results	No results	--	Organoheterocyclic compounds	0.20688106	9.9821E-05	1.624121	down
Com_7826_pos	LPC 16:1-SN1	C24 H48 N O7 P	493.31659	8.716	494.32388	No results	Full match	Full match	--	--	0.18198223	0.0001022	1.707855	down
Com_4789_neg	Feruloyl Putrescine	C14 H20 N2 O3	264.14769	5.304	263.14046	No results	No results	Full match	cpd:C10497	Phenylpropanoids and polyketides	0.23722564	0.00011648	1.484596	down
Com_3041_neg	D-Erythrose 4-phosphate	C4 H9 O7 P	200.00827	1.289	199.001	No results	No results	Full match	cpd:C00279	--	2.55932697	0.00011873	1.575672	up
Com_9258_pos	4-acetyl-4-(ethoxycarbonyl)heptanedi	C12 H18 O7	296.08746	7.747	297.09469	Invalid mass	No results	No results	--	--	2.94811658	0.00011949	1.15817	up
Com_956_pos	N-(p-Coumaroyl) serotonin	C19 H18 N2 O3	322.12827	5.703	323.13554	Invalid mass	No results	No results	--	Organoheterocyclic compounds	2.21023936	0.0001225	1.644048	up
Com_777_pos	gamma-Glutamyltyrosine	C14 H18 N2 O6	293.0897	4.937	311.12353	No results	Invalid mass	No results	--	Organic acids and derivatives	2.09667019	0.0001235	1.624843	up
Com_973_pos	TQH	C15 H24 N6 O6	384.16905	5.961	385.17633	Invalid mass	No results	No results	--	--	4.6551448	0.00013059	1.371664	up
Com_543_pos	indoline-2-carboxylic acid	C9 H9 N O2	163.06324	5.3	164.07055	Full match	No results	Full match	--	--	3.72497417	0.00014719	1.227944	up
Com_9878_pos	Metanephrine	C10 H15 N O3	197.10504	5.229	198.1124	No results	No results	Full match	cpd:C05588	Benzenoids	2.82091847	0.00014904	1.557811	up
Com_1177_pos	Guanine	C5 H5 N5 O	151.04927	1.617	152.05655	No results	No results	Full match	cpd:C00242	Organoheterocyclic compounds	0.28867332	0.00016539	1.443287	down
Com_2907_pos	GPK	C13 H24 N4 O4	600.36274	5.381	301.18864	Invalid mass	No results	No results	--	--	0.22761538	0.0001684	1.681188	down
Com_4550_neg	6-phospho-D-glucono-1,5-lactone	C6 H11 O9 P	258.01324	5.076	257.00597	No results	No results	Full match	cpd:C01236	--	0.46674022	0.00017399	1.394361	down
Com_6115_neg	Levodopa	C9 H11 N O4	197.06869	4.805	242.06696	No results	No results	Full match	cpd:C00355	--	3.55025732	0.00017586	1.350327	up
Com_6551_pos	MAG (18:3)	C21 H36 O4	352.26078	7.269	353.26806	No results	No results	Full match	--	Lipids and lipid-like molecules	0.14913429	0.00018338	1.611141	down
Com_4051_neg	N2-Methylguanosine	C11 H15 N5 O5	297.10734	4.819	296.10006	Full match	Full match	Full match	--	Nucleosides, nucleotides, and analogues	0.36937747	0.00020561	1.095185	down
Com_164_pos	Cuminaldehyde	C10 H12 O	148.08873	5.701	149.096	Full match	No results	No results	cpd:C06577	Lipids and lipid-like molecules	2.04163676	0.00021816	1.596563	up
Com_6184_neg	s7p	C7 H15 O10 P	290.04079	1.288	289.03357	No results	No results	Full match	cpd:C05382	Organic oxygen compounds	0.11403829	0.00022519	1.508268	down
Com_94_pos	APK	C14 H26 N4 O4	356.20564	5.223	357.21293	Invalid mass	No results	No results	--	--	0.07306097	0.00022701	1.73451	down

Com_1952_pos	5-Methoxyindole-3-Carbaldehyde	C10 H9 N O2	175.06321	4.769	176.07048	No results	No results	Full match	--	Organoheterocyclic compounds	3.18693407	0.00023089	1.609666	up
Com_3197_neg	Cholic acid	C24 H40 O5	408.28828	7.151	407.28096	Full match	Full match	Full match	cpd:C00695	Lipids and lipid-like molecules	2.87445457	0.00023583	1.617735	up
Com_2563_neg	LPC 18:1	C26 H52 N O7 P	567.35479	9.42	566.34751	No results	Invalid mass	No results	cpd:C04230	Lipids and lipid-like molecules	0.03591135	0.00024639	1.663698	down
Com_826_pos	NMK	C15 H29 N5 O5 S	746.35043	5.218	374.18249	Invalid mass	No results	No results	--	--	2.90139617	0.00026335	1.479877	up
Com_1832_pos	PC O-16:0	C24 H50 N O7 P	495.3319	9.187	496.33916	No results	Full match	Full match	--	--	0.05593676	0.00026564	1.633336	down
Com_9973_pos	beta-Nicotinamide adenine dinucleotide phosphate	C21 H28 N7 O17 P3	743.07407	1.393	372.54431	No results	No results	Full match	cpd:C00006	Nucleosides, nucleotides, and analogues	0.20979018	0.000322	1.39625	down
Com_1449_pos	1-[(3S)-3-(1,3-Benzoxazol-2-yl)-1-pyrrolidinyl]-3-methoxy-1-propanone	C15 H18 N2 O3	274.13471	5.294	275.142	Invalid mass	No results	No results	--	Organoheterocyclic compounds	2.37028282	0.00033457	1.479871	up
Com_10929_neg	L-Cysteinesulfinic acid	C3 H7 N O4 S	153.00903	1.361	152.00175	No results	No results	Full match	cpd:C00606	Organic acids and derivatives	3.2675709	0.0003362	1.267528	up
Com_82_pos	Isoquinoline	C9 H7 N	129.0578	5.864	130.06507	Full match	No results	No results	cpd:C06323	Organoheterocyclic compounds	3.00366417	0.00036712	1.145822	up
Com_2397_neg	1-Methyluric acid	C6 H6 N4 O3	182.04373	1.467	181.03645	No results	No results	Full match	cpd:C16359	Organoheterocyclic compounds	6.71596717	0.00037624	1.605481	up
Com_4157_pos	gamma-	C10 H18 N2 O5 S	278.09357	4.882	279.10085	No results	Full match	No results	--	Organic acids and derivatives	5.70865488	0.00038852	1.435447	up
Com_491_neg	Roquefortine C	C22 H23 N5 O2	389.18045	5.188	388.17317	Invalid mass	No results	No results	--	Organoheterocyclic compounds	0.40439678	0.00047734	1.596654	down
Com_7417_pos	Deoxyribose 5-Phosphate	C5 H11 O7 P	214.02398	1.368	237.01321	No results	No results	Full match	--	--	3.30890052	0.00048252	1.444573	up
Com_496_pos	4-Pyridoxic acid	C8 H9 N O4	183.05308	4.784	184.06036	No results	No results	Full match	cpd:C00847	Organoheterocyclic compounds	3.2726606	0.00051726	1.100376	up
Com_909_neg	Leu-Pro	C11 H20 N2 O3	228.14708	5.151	227.13981	No results	No results	Full match	--	Organic acids and derivatives	0.21439864	0.00062283	1.413812	down
Com_6145_pos	2-{[(4-phenyl-1H-pyrazol-5-yl)amino]methylene}-1H-indene-1,3(2H)-dione	C19 H13 N3 O2	315.10007	6.294	316.10756	Full match	No results	No results	--	--	4.42727382	0.00065866	1.584471	up
Com_2887_neg	LPE 16:2	C21 H40 N O7 P	449.25505	8.345	448.24777	No results	Full match	No results	--	Lipids and lipid-like molecules	0.37829169	0.00066213	1.601428	down
Com_206_neg	Prostaglandin E3	C20 H30 O5	386.18642	6.88	431.1846	Invalid mass	No results	No results	cpd:C06439	Lipids and lipid-like molecules	2.43086882	0.00068562	1.604354	up
Com_240_pos	L-5-Hydroxytryptophan	C11 H12 N2 O3	203.05801	3.947	221.09184	Invalid mass	No results	No results	cpd:C00643	Organoheterocyclic compounds	2.4444218	0.00071118	1.538852	up
Com_34_neg	2-Hydroxy-1-(4-methoxyphenyl)propyl hexopyranoside	C16 H24 O8	344.14747	5.698	343.1402	Full match	No results	No results	--	--	2.40441545	0.00071465	1.624123	up
Com_4909_neg	2-deoxyglucose-6-phosphate	C6 H13 O8 P	244.03543	1.266	289.03369	No results	No results	Full match	--	Organic acids and derivatives	0.10604663	0.0007195	1.499342	down
Com_1027_pos	N-(2-hydroxyphenyl) acetamide	C8 H9 N O2	173.04354	1.464	174.05084	Invalid mass	No results	No results	--	--	4.4580118	0.00080103	1.486741	up
Com_11_pos	LPE 18:1	C23 H46 N O7 P	479.30051	9.346	480.30781	No results	Full match	Full match	--	Lipids and lipid-like molecules	0.02298234	0.00082701	1.650453	down
Com_3377_pos	R-1 Methanandamide	C23 H40 N O5 P	882.52264	4.991	442.26859	Invalid mass	No results	No results	--	Organic acids and derivatives	0.14906603	0.00088298	1.527628	down
Com_3363_pos	L-Cysteine-glutathione	C13 H22 N4 O8 S2	426.08761	1.381	214.05108	No results	No results	Full match	--	--	3.98979055	0.00091171	1.1705	up
Com_9839_neg	dCDP	C9 H15 N3 O10 P2	387.02492	1.852	386.01764	No results	No results	Full match	cpd:C00705	Organic oxygen compounds	2.02833672	0.00102937	1.435539	up
Com_711_neg	Xanthine	C5 H4 N4 O2	152.03288	2.173	151.0256	Full match	No results	Full match	cpd:C00385	Organoheterocyclic compounds	0.31544287	0.00107063	1.496831	down
Com_593_neg	1,5-Anhydro-D-glucitol	C6 H12 O5	164.068	5.711	163.06073	Full match	Full match	Full match	cpd:C07326	Organic oxygen compounds	2.1960835	0.00111728	1.615816	up
Com_594_neg	Dulcitol	C6 H14 O6	182.07863	5.715	163.06079	No results	No results	Full match	cpd:C01697	Organic oxygen compounds	2.1960835	0.00111728	1.615816	up
Com_4431_neg	2-(3,4-dimethoxyphenyl)-N-(4-morpholinophenyl) acetamide	C20 H24 N2 O4	356.17571	6.88	355.16843	Invalid mass	No results	No results	--	--	2.40288309	0.00115001	1.5746	up
Com_4976_pos	ethyl 2-(benzylamino)-1,3-thiazole-5-carboxylate	C13 H14 N2 O2 S	262.07397	5.609	263.0814	Invalid mass	No results	No results	--	--	3.30172061	0.00115101	1.495578	up
Com_1765_pos	1-Phenyl-3-methyl-5-pyrazolone	C10 H10 N2 O	174.07922	3.948	175.08648	Full match	Full match	No results	--	--	2.46898122	0.00119469	1.508806	up
Com_5181_pos	Adipamide	C6 H12 N2 O2	144.08957	1.468	145.09683	No results	No results	Full match	--	Lipids and lipid-like molecules	9.17814517	0.00121274	1.397382	up
Com_1720_pos	PC O-18:1	C26 H52 N O7 P	521.34787	9.431	522.35513	No results	Full match	Full match	--	--	0.06321167	0.00121964	1.54402	down
Com_3674_pos	7-(1H-pyrrol-1-yl)-5H-chromeno[2,3-b]pyridin-5-one	C16 H10 N2 O2	262.07398	6.331	263.08126	Full match	No results	No results	--	--	2.05765012	0.00129339	1.388391	up

Com_730_pos	Vitexin	C21 H20 O10	216.05347	5.185	455.09617	Invalid mass	No results	No results	cpd:C01460	Phenylpropanoids and polyketides	2.21074313	0.00148095	1.447985	up
Com_7360_pos	10-Nitrolinoleate	C18 H31 N O4	307.21193	7.529	308.21921	Invalid mass	No results	No results	cpd:C13800	Lipids and lipid-like molecules	3.04466439	0.00170402	1.519729	up
Com_5188_pos	N-butyl-N'-[5-(tert-butyl)-1,3,4-thiadiazol-2-yl]urea	C11 H20 N4 O S	278.11349	5.591	279.12045	Invalid mass	No results	No results	--	--	2.09230789	0.00180376	1.239252	up
Com_357_neg	Uridine monophosphate	C9 H13 N2 O9 P	324.03636	1.457	323.02909	Full match	Full match	Full match	cpd:C00105	Nucleosides, nucleotides, and analogues	0.21370108	0.00188895	1.184235	down
Com_8122_neg	LysoPE 18:0	C23 H48 N O7 P	481.31799	9.185	480.31071	No results	No results	Full match	--	Lipids and lipid-like molecules	0.11844779	0.00190371	1.449295	down
Com_1344_neg	4-Hydroxy-L-Glutamic	C5 H9 N O5	163.04881	5.043	162.04153	No results	No results	Full match	cpd:C03079	Organic acids and derivatives	2.40166707	0.00194336	1.353056	up
Com_677_neg	Cytidine-5'-monophosphate	C9 H14 N3 O8 P	323.0524	1.434	322.04512	No results	Full match	Full match	cpd:C00055	Nucleosides, nucleotides, and analogues	0.10929551	0.00204249	1.327709	down
Com_2088_pos	Cytidine 5'-monophosphate (hydrate)	C9 H14 N3 O8 P	323.0515	1.399	324.05877	Full match	Full match	Full match	cpd:C00055	Nucleosides, nucleotides, and analogues	0.06670999	0.00217539	1.302144	down
Com_73_neg	3,5-	C8 H9 N O4	183.05284	5.249	182.04556	Full match	No results	Full match	--	Organic acids and derivatives	2.36832451	0.00221331	1.138227	up
Com_1972_neg	LPE 8:0	C13 H28 N O7 P	341.16082	6.011	340.15354	No results	Full match	No results	--	Lipids and lipid-like molecules	0.48996595	0.0022685	1.165286	down
Com_8594_neg	Morphine-3-glucuronide	C23 H27 N O9	461.16877	6.446	460.16149	Full match	No results	No results	cpd:C16643	Alkaloids and derivatives	0.35220207	0.00239029	1.483808	down
Com_138_neg	Fumaric acid	C4 H4 O4	116.01017	2.364	115.00288	No results	Invalid mass	No results	cpd:C00122	Organic acids and derivatives	2.17833062	0.00252213	1.283108	up
Com_4447_pos	2-[4-(tert-butyl)-2-chlorophenoxy]-3-nitropyridine	C15 H15 Cl N2 O3	306.08076	1.366	307.08804	Invalid mass	No results	No results	--	--	14.1968452	0.00261307	1.563319	up
Com_3305_pos	Uridine 5'-monophosphate	C9 H13 N2 O9 P	324.03542	1.422	325.04267	No results	Full match	Full match	cpd:C00105	Nucleosides, nucleotides, and analogues	0.16134126	0.00272515	1.180921	down
Com_9142_neg	Glycoursodeoxycholic acid	C26 H43 N O5	449.31492	7.128	448.30764	Full match	No results	Full match	--	Lipids and lipid-like molecules	4.29199771	0.00275555	1.341225	up
Com_2749_pos	Radicinin	C12 H12 O5	236.07045	5.72	473.14819	Invalid mass	No results	No results	--	Organic oxygen compounds	3.16157606	0.00278434	1.232181	up
Com_53_neg	N-Acetyl-D-alloisoleucine	C8 H15 N O3	173.1047	5.56	172.09742	Full match	Full match	Full match	--	Organic acids and derivatives	2.07692768	0.0029209	1.297916	up
Com_4281_pos	2-{[(4,5-dimethoxy-2-nitrophenethyl)imino]methyl}phenol	C17 H18 N2 O5	330.1218	6.898	331.12908	Full match	No results	No results	--	--	2.46954374	0.00309212	1.500325	up
Com_3591_neg	Prostaglandin G2	C20 H32 O6	368.22014	5.853	367.21286	No results	No results	Full match	cpd:C05956	Lipids and lipid-like molecules	0.26486531	0.00322345	1.199121	down
Com_4841_pos	2-phenyl-2,4,6,7-tetrahydrothiino[4,3-c]pyrazol-3-ol	C12 H12 N2 O S	232.06809	5.75	233.0758	Full match	No results	No results	--	--	2.15157378	0.00327041	1.381451	up
Com_14668_neg	Nicotinuric Acid	C8 H8 N2 O3	180.0531	10.247	179.04582	No results	No results	Full match	cpd:C05380	Organic acids and derivatives	2.21974929	0.00348275	1.033273	up
Com_184_pos	Methyl indole-3-acetate	C11 H11 N O2	189.07869	5.131	190.08596	Full match	Full match	Full match	cpd:C20635	Organoheterocyclic compounds	2.58729808	0.00373648	1.462961	up
Com_95_neg	Perillic acid	C10 H14 O2	166.09891	6.151	165.09162	Full match	No results	Full match	cpd:C11924	Lipids and lipid-like molecules	0.20716575	0.00375058	1.118692	down
Com_2946_neg	3-(1-pyrrolidinyl)-5-(trifluoromethyl)pyridine-2-carbothioamide	C11 H12 F3 N3 S	278.10913	6.698	277.10186	Invalid mass	No results	No results	--	--	0.20394933	0.00394829	1.499422	down
Com_12510_neg	8,15-Dihete	C20 H32 O4	336.23058	6.632	335.22331	No results	No results	Full match	--	--	0.38809279	0.00413518	1.08282	down
Com_8274_pos	6-phenyl-1,2,3,4-tetrahydro-2,5-	C16 H14 N2 O	232.09981	6.216	233.10708	Invalid mass	No results	No results	--	--	2.26580906	0.00422351	1.349932	up
Com_5028_neg	Guanosine-3',5'-cyclic monophosphate	C10 H12 N5 O7 P	345.0479	2.439	344.04062	No results	Full match	Full match	cpd:C00942	Nucleosides, nucleotides, and analogues	0.22786393	0.00443759	1.183266	down
Com_630_pos	LPE 16:0	C21 H44 N O7 P	453.28512	9.107	454.29236	No results	Full match	Full match	--	Lipids and lipid-like molecules	0.09649968	0.00463734	1.249134	down
Com_659_pos	Kanosamine	C6 H13 N O5	179.08059	4.841	180.08786	Invalid mass	No results	No results	cpd:C12212	Organic oxygen compounds	9.28622579	0.00473564	1.326366	up
Com_2739_pos	EPK	C16 H28 N4 O6	372.20045	5.307	373.20772	Full match	No results	No results	--	--	0.09196003	0.00476041	1.332525	down
Com_7643_neg	Fmoc-L-Isoleucine	C21 H23 N O4	353.16397	6.304	352.1567	No results	No results	Full match	--	Organic acids and derivatives	6.33697439	0.00521279	1.434141	up
Com_6599_neg	Glycocholic acid	C26 H43 N O6	465.30971	6.655	464.30243	Full match	No results	Full match	cpd:C01921	Lipids and lipid-like molecules	3.648299	0.00524548	1.330487	up
Com_502_pos	3-(4-nitrophenyl)[1,2,3]triazolo[1,5-a]quinazolin-5-amine	C15 H10 N6 O2	306.08233	5.988	307.08961	Invalid mass	No results	No results	--	--	3.03573738	0.0054293	1.358659	up
Com_652_neg	LPE 18:2	C23 H44 N O7 P	477.28629	9.059	476.27901	No results	Full match	Full match	--	Lipids and lipid-like molecules	0.08681814	0.00549636	1.403278	down
Com_19_neg	LPG 18:1	C24 H47 O9 P	510.29631	9.734	509.28903	No results	Full match	Full match	--	Lipids and lipid-like molecules	0.01985627	0.00596528	1.481316	down
Com_5269_pos	Pyridoxamine	C8 H12 N2 O2	168.08995	5.94	207.05315	No results	No results	Full match	cpd:C00534	Organoheterocyclic compounds	2.57997964	0.0064355	1.02803	up
Com_9307_neg	LPG 16:2	C22 H41 O9 P	480.24989	8.208	479.24261	No results	Full match	No results	--	Lipids and lipid-like molecules	0.37057203	0.00687889	1.294349	down

Com_9375_neg	Cystine	C6 H12 N2 O4 S2	240.02394	1.252	239.01666	No results	No results	Full match	cpd:C01420	Organic acids and derivatives	3.12183846	0.00715345	1.264181	up
Com_2126_neg	Lysope 18:1	C23 H46 N O7 P	479.30205	9.754	478.29477	No results	No results	Full match	--	Lipids and lipid-like molecules	0.0734734	0.00739252	1.435946	down
Com_1151_pos	Oleoyl ethanolamide	C20 H39 N O2	307.28682	9.347	308.2941	Invalid mass	No results	No results	cpd:C20792	Organic nitrogen compounds	0.05628138	0.00842634	1.391984	down
Com_2184_pos	Epigallocatechin	C15 H14 O7	612.15163	2.382	307.08309	No results	Invalid mass	No match	cpd:C12136	Phenylpropanoids and polyketides	4.02835457	0.00852208	1.219451	up
Com_259_pos	1H-indol-3-yl(pyridin-2-yl)methanol	C14 H12 N2 O	246.07907	5.582	247.08634	Invalid mass	No results	No results	--	--	2.22288446	0.00886183	1.365043	up
Com_4204_neg	LPE 13:0	C18 H38 N O7 P	411.2392	7.565	410.23192	No results	Full match	Full match	--	Lipids and lipid-like molecules	2.76391785	0.0089686	1.247192	up
Com_8441_pos	Stearoyl Ethanolamide	C20 H41 N O2	327.3131	7.082	328.32037	Full match	No results	No results	--	Organic nitrogen compounds	2.57645022	0.00898503	1.333689	up
Com_7529_pos	L-Cystine	C6 H12 N2 O4 S2	240.02364	1.218	241.03092	Full match	Full match	Full match	cpd:C00491	Organic acids and derivatives	2.50021007	0.0093063	1.179362	up
Com_3163_pos	Asp-Phe	C13 H16 N2 O5	280.10473	5.435	263.10138	No results	No results	Full match	--	Organic acids and derivatives	0.43415879	0.01197657	1.344832	down
Com_397_neg	Syringic acid	C9 H10 O5	198.05249	4.951	179.03464	No results	No results	Full match	cpd:C10833	Benzenoids	0.45364264	0.01227217	1.171745	down
Com_9324_pos	RMH	C17 H30 N8 O4 S	482.21327	5.955	465.2099	Invalid mass	No results	No results	--	--	3.2554784	0.01386934	1.185122	up
Com_57_neg	Indole-3-lactic acid	C11 H11 N O3	205.07374	5.536	204.06646	Full match	Full match	Full match	cpd:C02043	Organoheterocyclic compounds	0.22863047	0.0159924	1.072153	down
Com_299_neg	Pimelic acid	C7 H12 O4	160.07301	5.387	159.06574	Full match	Full match	Full match	cpd:C02656	Lipids and lipid-like molecules	2.79996245	0.01642731	1.20647	up
Com_439_pos	Indole-3-propionic acid	C11 H11 N O2	189.07785	5.155	190.08513	No results	Invalid mass	No results	--	Organoheterocyclic compounds	2.16320727	0.01701736	1.273199	up
Com_9603_neg	LPG O-13:1	C19 H39 O8 P	426.23918	7.077	425.2319	No results	Full match	No results	--	--	4.41366533	0.01764389	1.268396	up
Com_11335_neg	Prostaglandin B2	C20 H30 O4	334.21284	7.057	333.20597	No results	No results	Full match	cpd:C05954	Lipids and lipid-like molecules	2.3050742	0.01834798	1.158599	up
Com_2708_neg	LPG 18:2	C24 H45 O9 P	508.28087	8.966	507.2736	No results	Full match	No results	--	Lipids and lipid-like molecules	0.09782554	0.01884808	1.220949	down
Com_13022_neg	Biopterin	C9 H11 N5 O3	237.08502	1.431	236.07774	No results	No results	Full match	cpd:C06313	Organoheterocyclic compounds	0.20145396	0.02029819	1.235795	down
Com_1769_neg	Royal jelly acid	C10 H18 O3	186.12575	5.669	231.12396	No results	No results	Full match	--	Organic acids and derivatives	3.77385113	0.02071738	1.101698	up
Com_9009_pos	S-(Methyl)Glutathione	C11 H19 N3 O6 S	321.09935	2.412	322.10662	No results	No results	Full match	--	Organic acids and derivatives	2.04109836	0.02090532	1.196271	up
Com_1326_neg	Adenosine diphosphate	C15 H23 N5 O14 P2	559.07302	1.425	558.06571	Full match	No results	Full match	cpd:C00301	Nucleosides, nucleotides, and analogues	2.49928452	0.02233471	1.08623	up
Com_7711_pos	L-Methionine Methyl Ester	C6 H13 N O2 S	163.0665	2.094	164.07377	No results	No results	Full match	--	--	6.59253111	0.02293794	1.169866	up
Com_6210_neg	Elaidic acid	C18 H34 O2	282.25606	10.286	281.24878	Full match	No results	No results	cpd:C01712	Lipids and lipid-like molecules	0.30294083	0.02650063	1.231615	down
Com_6457_pos	N1-cyclooctyl-4-hydroxy-1-piperidinecarbothioamide	C14 H26 N2 O S	292.15694	6.101	293.16421	Invalid mass	No results	No results	--	--	4.4945157	0.02686286	1.069863	up
Com_500_pos	Lysopg 18:1	C24 H47 O9 P	510.29557	9.74	533.28482	No results	No results	Full match	--	Lipids and lipid-like molecules	0.03256733	0.02805345	1.22331	down
Com_3578_neg	LPE 18:0	C23 H48 N O7 P	481.31785	10.22	480.31057	No results	Full match	Full match	--	Lipids and lipid-like molecules	0.07398494	0.03325163	1.199306	down
Com_4673_pos	LPC 16:0-SN1	C24 H50 N O7 P	495.33188	9.425	496.33915	No results	Full match	Full match	--	--	0.25918159	0.03492747	1.19356	down
Com_700_pos	Tritylalcohol	C24 H29 N3 O	357.22011	5.991	358.22739	Invalid mass	No results	No results	--	Benzenoids	3.35128565	0.03493231	1.139374	up
Com_982_pos	N1-[6-(2-fluorophenoxy)-3-pyridyl]-2-	C15 H13 F N2 O2	272.09458	5.937	273.1018	Invalid mass	No results	No results	--	--	2.51925237	0.04106935	1.147309	up
Com_822_neg	Oleoyl-L-α-	C21 H41 O7 P	436.25958	10.099	435.2523	Full match	Full match	No results	--	Lipids and lipid-like molecules	0.02391071	0.04316279	1.171293	down
Com_9089_neg	LPE 20:4	C25 H44 N O7 P	501.28674	8.704	500.27946	No results	Full match	No results	--	Lipids and lipid-like molecules	0.19823519	0.04441938	1.112752	down
Com_4470_pos	Artemisin	C15 H22 O5	282.14397	6.017	283.15123	Invalid mass	No results	No results	cpd:C09538	Lipids and lipid-like molecules	2.07610779	0.04553945	1.085053	up
Com_4270_pos	8-Isoprostaglandin F1β	C20 H36 O5	373.28242	6.501	374.2897	Invalid mass	No results	No results	--	Lipids and lipid-like molecules	2.68217733	0.04744619	1.000216	up

Table S8: DEMs in XDR vs. MDR strains.

Compound ID	Name	Formula	Molecular Weight	RT [min]	m/z	mzCloud Results	mzVault Results	MassList Results	KEGG ID	ClassyFire functional classification	FC XDR/MDR	*P*-value XDR/MDR	VIP	Regulate
Com_1787_pos	Enrofloxacin	C19 H22 F N3 O3	381.14639	6.255	382.1537	Invalid mass	No results	No results	--	Organoheterocyclic compounds	0.01813495	5.2836E-16	2.01951	down
Com_3_neg	2-Hydroxycaproic acid	C6 H12 O3	132.07784	5.592	131.07055	Invalid mass	Invalid mass	No results	--	Lipids and lipid-like molecules	0.01611625	5.5479E-13	1.72836	down
Com_205_pos	2-(1,3-dimethyl-1H-pyrazol-5-yl)-1H-isoindole-1,3(2H)-dione	C13 H11 N3 O2	241.0849	5.474	242.09217	Full match	No results	No results	--	--	0.09784852	9.9133E-13	1.70495	down
Com_2481_neg	L-Homocystine	C8 H16 N2 O4 S2	268.05382	5.638	267.04655	No results	No results	Full match	cpd:C01817	Organic acids and derivatives	0.11168941	9.9674E-13	1.64672	down
Com_212_neg	Phenylacetaldehyde	C8 H8 O	120.0569	5.602	119.04941	Invalid mass	No results	No results	cpd:C00601	Benzenoids	0.07725626	8.3479E-12	1.79887	down
Com_5036_neg	Tyrosylalanine	C12 H16 N2 O4	252.11124	5.021	251.10394	Full match	No results	No results	--	Organic acids and derivatives	0.12119203	8.5109E-11	1.60507	down
Com_6163_pos	6-(Dimethylamino)purine	C7 H9 N5	163.08578	5.16	164.09266	No results	No results	Full match	--	Organoheterocyclic compounds	0.11504954	9.3636E-11	1.97935	down
Com_119_neg	2-Hydroxyvaleric acid	C5 H10 O3	118.0622	5.255	117.05492	Invalid mass	Invalid mass	No results	--	Lipids and lipid-like molecules	0.02056054	2.2077E-10	1.70342	down
Com_155_neg	Mycophenolic acid	C17 H20 O6	320.12368	5.598	319.1164	Invalid mass	No results	No results	cpd:C20380	Organoheterocyclic compounds	0.002108	3.6167E-10	1.75558	down
Com_848_neg	o-Toluic Acid	C8 H8 O2	136.05199	5.157	135.04444	No results	No results	Full match	cpd:C07215	--	0.19220074	5.9613E-10	1.88164	down
Com_4063_neg	Estrone	C18 H22 O2	540.32908	5.477	539.32177	Invalid mass	No results	No results	cpd:C00468	Lipids and lipid-like molecules	0.09816108	9.3659E-10	1.85046	down
Com_2287_pos	(3R)-8-hydroxy-3-(4-hydroxyphenyl)-3,4-dihydro-1H-2-benzopyran-1-one	C15 H12 O4	128.03542	5.181	257.078	Invalid mass	No results	No results	--	--	3.58952048	1.6851E-09	1.45947	up
Com_2286_pos	4-phenyl-6-(2-thienyl)-2,3,4,5-tetrahydropyridazin-3-one	C14 H12 N2 O S	256.07069	5.177	257.07796	Invalid mass	No results	No results	--	--	3.59634912	1.8962E-09	1.46109	up
Com_3886_neg	2-Hydroxyestradiol	C18 H24 O3	288.16888	5.511	287.1616	Invalid mass	No results	No results	cpd:C05301	Lipids and lipid-like molecules	0.13438836	2.2276E-09	1.82577	down
Com_281_neg	Xanthosine	C10 H12 N4 O6	284.07586	4.751	283.06859	Full match	Full match	Full match	cpd:C01762	Nucleosides, nucleotides, and analogues	0.02084134	2.5449E-09	1.65279	down
Com_4269_pos	Stanozolol	C21 H32 N2 O	328.24687	6.108	329.25415	Invalid mass	No results	No results	cpd:C07311	Lipids and lipid-like molecules	0.06879534	3.7387E-09	1.85018	down
Com_5002_neg	Pseudouridine	C9 H12 N2 O6	244.0696	2.027	243.06232	Full match	No results	Full match	cpd:C02067	Nucleosides, nucleotides, and analogues	5.55761512	4.5952E-09	1.95523	up
Com_6128_pos	LysoPE 18:2	C23 H44 N O7 P	477.28537	7.481	478.29264	No results	No results	Full match	--	--	0.22887014	6.6151E-09	1.5212	down
Com_743_neg	Gamma-Glu-Leu	C11 H20 N2 O5	260.13743	5.445	259.13015	No results	No results	Full match	--	Organic acids and derivatives	0.43205883	6.9946E-09	1.8704	down
Com_1697_neg	2-Methylbutyroylcarnitine	C12 H23 N O4	245.16283	6.152	244.15556	No results	No results	Full match	--	Lipids and lipid-like molecules	0.03727195	8.1402E-09	1.89294	down
Com_543_pos	indoline-2-carboxylic acid	C9 H9 N O2	163.06324	5.3	164.07055	Full match	No results	Full match	--	--	6.71902998	8.3372E-09	1.86614	up
Com_284_neg	2-Hydroxy-4-methylthiobutanoic acid	C5 H10 O3 S	150.03448	5.202	149.02721	Full match	No results	No results	--	Lipids and lipid-like molecules	0.00484736	8.5319E-09	1.79438	down
Com_9_neg	3-Phenyllactic acid	C9 H10 O3	166.06238	5.599	165.0551	Full match	Full match	Full match	cpd:C01479	Phenylpropanoids and polyketides	0.05281641	1.7661E-08	1.81013	down
Com_7662_pos	JNJ-1661010	C19 H19 N5 O S	365.13202	4.599	366.13929	No results	No results	Full match	--	Organoheterocyclic compounds	0.06227275	1.9328E-08	1.89937	down
Com_562_pos	3-((5-Phenyloxazol-2-yl)amino)benzonitrile	C16 H11 N3 O	261.08989	5.916	262.09717	Full match	No results	No results	--	Organoheterocyclic compounds	0.28156104	2.1333E-08	1.48422	down
Com_5106_pos	2'-O-Methyladenosine	C11 H15 N5 O4	264.08522	4.891	282.11941	Invalid mass	Invalid mass	No results	--	Nucleosides, nucleotides, and analogues	0.08651871	2.1429E-08	1.82763	down
Com_8621_pos	Proscillaridin	C30 H42 O8	530.29522	6.33	531.3025	Invalid mass	No results	No results	--	Lipids and lipid-like molecules	0.14552106	3.2341E-08	1.79863	down
Com_208_neg	Pantetheine	C11 H22 N2 O4 S	278.13032	5.27	277.12299	No results	No results	Full match	cpd:C00831	Organic acids and derivatives	3.43766947	5.8563E-08	1.35874	up
Com_7478_pos	2-OHE1-6-N3Ade	C23 H25 N5 O3	419.20378	4.976	420.21106	Invalid mass	No results	No results	--	--	4.55989588	6.2814E-08	1.76861	up
Com_2170_neg	LPE 18:3	C23 H42 N O7 P	475.27059	8.221	474.26332	No results	Full match	No results	--	Lipids and lipid-like molecules	0.15997617	7.6816E-08	1.43449	down
Com_614_pos	2-[2-(2-pyridyloxy)ethoxy] pyridine	C12 H12 N2 O2	198.07917	5.515	199.08645	Invalid mass	No results	No results	--	--	0.45387797	8.9112E-08	1.90382	down
Com_613_pos	N-(1-methyl-3-phenyl-1H-pyrazol-5-yl)-N'-(2-thienyl) urea	C15 H14 N4 O S	298.09269	5.486	299.09997	Invalid mass	No results	No results	--	--	2.61426781	9.772E-08	1.43407	up
Com_4532_neg	Lauric acid ethyl ester	C14 H28 O2	228.2088	8.167	227.20152	Full match	No results	Full match	--	Lipids and lipid-like molecules	0.14843458	1.1218E-07	1.91324	down
Com_6551_pos	MAG (18:3)	C21 H36 O4	352.26078	7.269	353.26806	No results	No results	Full match	--	Lipids and lipid-like molecules	0.19210664	1.2979E-07	1.57904	down
Com_165_neg	trans-Cinnamic acid	C9 H8 O2	148.05177	5.603	147.0445	Full match	Full match	No results	cpd:C00423	Phenylpropanoids and polyketides	0.06121641	1.3765E-07	1.79558	down

Com_318_neg	Boc-beta-cyano-L-alanine	C9 H14 N2 O4	214.0957	5.327	427.18413	No results	No results	Full match	--	Organic acids and derivatives	3.26523051	1.6245E-07	1.78827	up
Com_1773_pos	2-[(3S)-1-(Benzylsulfonyl)-3-pyrrolidinyl]-1-methyl-1H-benzimidazole	C19 H21 N3 O2 S	377.11998	5.001	378.12726	Invalid mass	No results	No results	--	Organoheterocyclic compounds	4.02218441	1.7534E-07	1.94075	up
Com_188_neg	N-Acetyl-D-tryptophan	C13 H14 N2 O3	246.10091	5.128	291.09912	No results	No results	Full match	cpd:C03137	Organic acids and derivatives	3.70043301	2.0311E-07	1.52308	up
Com_69_pos	5'-S-Methyl-5'-thioadenosine	C11 H15 N5 O3 S	297.08939	5.126	298.09667	Full match	Full match	Full match	cpd:C00170	Nucleosides, nucleotides, and analogues	4.46109181	2.2032E-07	1.72666	up
Com_1685_pos	PC O-16:1	C24 H48 N O7 P	493.31644	8.478	494.32372	No results	Full match	Full match	--	--	0.15335158	2.3297E-07	1.22011	down
Com_1700_neg	N-Acetylvaline	C7 H13 N O3	159.08905	5.278	158.08177	No results	No results	Full match	--	Organic acids and derivatives	0.2354735	2.8766E-07	1.54495	down
Com_976_neg	Prostaglandin A2	C20 H30 O4	370.18568	5.385	369.1784	Invalid mass	No results	No results	cpd:C05953	Lipids and lipid-like molecules	3.64484071	3.1912E-07	1.70167	up
Com_1796_pos	LPE 17:1	C22 H44 N O7 P	465.28514	8.991	466.29242	No results	Full match	No results	--	Lipids and lipid-like molecules	0.0992861	3.9261E-07	1.55853	down
Com_2043_neg	Glutathione	C10 H17 N3 O6 S	307.08426	5.533	306.07699	No results	No results	Full match	cpd:C00051	Organic acids and derivatives	0.39403439	4.0735E-07	1.94144	down
Com_1424_neg	LPC 16:1	C24 H48 N O7 P	539.32316	8.471	538.31589	No results	Invalid mass	No results	cpd:C04230	Lipids and lipid-like molecules	0.19915286	4.0902E-07	1.19363	down
Com_35_neg	DL-4-Hydroxyphenyllactic acid	C9 H10 O4	182.05753	5.158	181.05026	Full match	No results	Full match	--	Phenylpropanoids and polyketides	0.16433436	4.8371E-07	1.93227	down
Com_1334_neg	2'-Deoxyinosine	C10 H12 N4 O4	252.08587	4.055	251.07859	Full match	Full match	Full match	cpd:C05512	Nucleosides, nucleotides, and analogues	0.33053217	5.6245E-07	1.29614	down
Com_1348_pos	Obscurolide A1	C15 H17 N O5	323.13799	5.049	324.14519	Invalid mass	No results	No results	--	Benzenoids	0.35770559	6.3404E-07	1.65033	down
Com_2819_pos	Capric acid	C10 H20 O2	172.14601	5.855	195.13514	No results	No results	Full match	cpd:C01571	Lipids and lipid-like molecules	0.12548467	6.4956E-07	1.98016	down
Com_10641_pos	P-Aminohippuric Acid	C9 H10 N2 O3	194.06887	4.966	406.17123	No results	No results	Full match	--	Benzenoids	0.18059347	7.2204E-07	1.78305	down
Com_5665_pos	2,3,4-Trihydroxybenzoic acid	C7 H6 O5	170.02136	5.196	171.02863	No results	No results	Full match	--	Phenylpropanoids and polyketides	0.13835082	7.3435E-07	1.78978	down
Com_206_neg	Prostaglandin E3	C20 H30 O5	386.18642	6.88	431.1846	Invalid mass	No results	No results	cpd:C06439	Lipids and lipid-like molecules	2.02430156	7.7242E-07	1.32727	up
Com_13_neg	17-AAG	C31 H43 N3 O8	567.29161	5.562	566.28431	Invalid mass	No results	No results	--	--	3.4180999	9.3295E-07	1.54083	up
Com_1574_pos	LPE 14:0	C19 H40 N O7 P	425.25379	8.172	426.26104	No results	Full match	Full match	--	Lipids and lipid-like molecules	0.11665739	1.2012E-06	1.93118	down
Com_5311_pos	2-Thio-acetyl MAGE	C21 H42 O3 S	356.27785	6.606	357.28513	Invalid mass	No results	No results	--	Organic acids and derivatives	0.26495347	1.2808E-06	1.60537	down
Com_3902_pos	D-Fructose 6-phosphate	C6 H13 O9 P	260.02863	5.491	261.03592	No results	No results	Full match	cpd:C00085	--	0.162317	1.2859E-06	1.78104	down
Com_1353_pos	Physostigmine	C15 H21 N3 O2	275.16312	4.987	276.17037	Full match	No results	No results	cpd:C06535	Organoheterocyclic compounds	0.41533641	1.2978E-06	1.6296	down
Com_5621_pos	p-Mentha-1,3,8-triene	C10 H14	134.10929	5.785	135.1166	No results	No results	Full match	--	Lipids and lipid-like molecules	0.38111432	1.4258E-06	1.87631	down
Com_4900_neg	LPE 18:4	C23 H40 N O7 P	473.25482	7.961	472.24754	No results	Full match	No results	--	Lipids and lipid-like molecules	16.0069497	1.8097E-06	1.94282	up
Com_7352_neg	Glu-Glu	C10 H16 N2 O7	276.09627	1.446	275.08899	No results	No results	Full match	cpd:C01425	Organic acids and derivatives	3.62578431	1.954E-06	1.62228	up
Com_1037_neg	Guanosine	C10 H13 N5 O5	283.09192	3.682	282.08463	Full match	Full match	Full match	cpd:C00387	Nucleosides, nucleotides, and analogues	0.05766831	1.9828E-06	1.91384	down
Com_2791_pos	PE 9:0_9:0	C23 H46 N O8 P	495.29606	7.705	496.30328	No results	Full match	No results	--	--	0.1988358	2.3056E-06	1.49073	down
Com_1556_pos	4-ethoxy-7,9-dimethylpyrido[3',2':4,5]thieno[3,2-d]pyrimidine	C13 H13 N3 O S	259.08178	5.624	260.08906	Invalid mass	No results	No results	--	--	0.31999697	2.6088E-06	1.45543	down
Com_1915_pos	N6-Isopentenyladenosine	C15 H21 N5 O4	335.15882	5.736	336.16609	No results	Full match	No results	cpd:C16427	Nucleosides, nucleotides, and analogues	0.29215541	2.8317E-06	1.87742	down
Com_4346_pos	Desthiobiotin	C10 H18 N2 O3	214.13148	3.746	215.13875	Full match	No results	No results	cpd:C01909	Organoheterocyclic compounds	0.22932447	3.2423E-06	1.52276	down
Com_2821_pos	N-(4-fluorophenyl)-N'-(2-piperidinophenyl)urea	C18 H20 F N3 O	335.14538	5.329	336.15266	Invalid mass	No results	No results	--	--	5.41508383	3.5477E-06	1.77221	up
Com_221_neg	2-{1-[2-(1-benzothiophen-5-ylamino)-2-oxoethyl]cyclohexyl}acetic acid	C18 H21 N O3 S	331.12057	5.178	330.11329	Invalid mass	No results	No results	--	--	5.58299657	3.7992E-06	1.5156	up
Com_1563_pos	2,6-Dihydroxypurine	C5 H4 N4 O2	152.03335	4.751	153.04062	No results	No results	Full match	cpd:C00385	Organoheterocyclic compounds	0.02498322	4.1235E-06	1.74282	down
Com_9270_neg	5-Methylcytidine	C10 H15 N3 O5	211.09585	1.872	256.09419	No results	Invalid mass	No results	--	Nucleosides, nucleotides, and analogues	5.63017214	4.2946E-06	1.55615	up
Com_3280_pos	N(6)-OH-Me-Adenosine	C11 H15 N5 O5	297.1071	3.954	298.11438	Full match	No results	Full match	--	Nucleosides, nucleotides, and analogues	7.58103923	4.8417E-06	1.88504	up
Com_12510_neg	8,15-Dihete	C20 H32 O4	336.23058	6.632	335.22331	No results	No results	Full match	--	--	0.24634997	5.1492E-06	1.81387	down
Com_4051_neg	N2-Methylguanosine	C11 H15 N5 O5	297.10734	4.819	296.10006	Full match	Full match	Full match	--	Nucleosides, nucleotides, and analogues	0.20116617	5.228E-06	1.88014	down
Com_50_neg	17(S)-HpDHA	C22 H32 O4	396.20128	5.41	395.19398	Invalid mass	No results	No results	--	Lipids and lipid-like molecules	2.39144946	7.2299E-06	1.6802	up
Com_3168_pos	Oxohongdenafil	C25 H32 N6 O4	458.27272	5.336	459.28067	Invalid mass	No results	No results	--	Organic oxygen compounds	0.23886034	7.2823E-06	1.61633	down
Com_2749_pos	Radicinin	C12 H12 O5	236.07045	5.72	473.14819	Invalid mass	No results	No results	--	Organic oxygen compounds	4.76342935	7.9854E-06	1.67071	up
Com_1238_neg	Dl-Indole-3-lactic acid	C11 H11 N O3	205.07356	5.882	204.06628	No results	No results	Full match	--	Organoheterocyclic compounds	0.19801359	8.5668E-06	1.84023	down

Com_7326_neg	LPE 20:5	C25 H42 N O7 P	499.27085	8.215	498.26358	No results	Full match	No results	--	Lipids and lipid-like molecules	4.20823938	8.7369E-06	1.68172	up
Com_636_neg	2-Deoxyuridine	C9 H12 N2 O5	228.0746	2.009	227.06733	No results	No results	Full match	cpd:C00526	Nucleosides, nucleotides, and analogues	6.44444881	9.1547E-06	1.93345	up
Com_6187_pos	6-anilino-1,3-dimethyl-1,2,3,4-tetrahydropyrimidine-2,4-dione	C12 H13 N3 O2	231.10397	4.022	232.11124	Invalid mass	No results	No results	--	--	0.05206626	9.2763E-06	1.80054	down
Com_5849_neg	(+/-)12(13)-DiHOME	C18 H34 O4	296.2354	7.254	295.22812	Invalid mass	No results	No match	cpd:C14829	Lipids and lipid-like molecules	0.13987538	1.3677E-05	1.593	down
Com_8893_pos	HMH	C17 H25 N7 O4 S	445.15318	5.806	446.16045	Invalid mass	No results	No results	--	--	0.39582373	1.3939E-05	1.73013	down
Com_571_pos	Acetylcarnitine	C9 H17 N O4	203.11575	5.622	226.10483	No results	No results	Full match	cpd:C02571	Lipids and lipid-like molecules	0.32078989	1.3965E-05	1.63494	down
Com_8209_pos	Vitamin B2	C17 H20 N4 O6	376.1382	4.9	377.14548	No results	No results	Full match	cpd:C00255	Organoheterocyclic compounds	0.25877718	1.4163E-05	1.72385	down
Com_5772_pos	7,8-Dihydrofolate	C19 H21 N7 O6	443.15703	5.755	444.16431	No results	No results	Full match	cpd:C00415	--	6.48855289	1.456E-05	1.66401	up
Com_4550_neg	6-phospho-D-glucono-1,5-lactone	C6 H11 O9 P	258.01324	5.076	257.00597	No results	No results	Full match	cpd:C01236	--	0.45323711	1.5454E-05	1.60316	down
Com_6810_pos	6-styryl-3-phenyl-2,5-dihydro-1,2,4-triazin-5-one	C17 H13 N3 O	275.10555	7.731	276.11284	Full match	No results	No results	--	--	3.82790764	1.7639E-05	1.73344	up
Com_6484_neg	11-Dehydro thromboxane B2	C20 H32 O6	404.19692	6.502	403.18964	Invalid mass	No results	No results	cpd:C05964	Lipids and lipid-like molecules	2.2957898	1.7665E-05	1.3305	up
Com_993_neg	1-Methylguanosine	C11 H15 N5 O5	297.1076	3.708	296.10032	No results	No results	Full match	cpd:C04545	Nucleosides, nucleotides, and analogues	4.01959663	1.7827E-05	1.62243	up
Com_3056_pos	Virginiamycin	C28 H35 N3 O7	507.23154	5.143	508.23882	Invalid mass	No results	No results	cpd:C11299	Phenylpropanoids and polyketides	0.29366044	1.8065E-05	1.54938	down
Com_7360_pos	10-Nitrolinoleate	C18 H31 N O4	307.21193	7.529	308.21921	Invalid mass	No results	No results	cpd:C13800	Lipids and lipid-like molecules	2.43307122	1.9249E-05	1.24331	up
Com_2240_pos	ethyl 2-amino-8H-indeno[2,1-b]thiophene-3-carboxylate	C14 H13 N O2 S	259.06645	5.212	260.07373	Full match	No results	No results	--	--	0.1247327	1.9963E-05	1.55746	down
Com_9961_neg	myricetin 3-O-beta-D-galactopyranoside	C21 H20 O13	480.08997	2.146	479.08269	Full match	No results	No results	--	--	0.31626494	2.0159E-05	1.1706	down
Com_82_pos	Isoquinoline	C9 H7 N	129.0578	5.864	130.06507	Full match	No results	No results	cpd:C06323	Organoheterocyclic compounds	4.90225504	2.1166E-05	1.79968	up
Com_13462_neg	dCMP	C9 H14 N3 O7 P	307.05824	3.686	306.05096	No results	No results	Full match	cpd:C00239	Nucleosides, nucleotides, and analogues	0.04876032	2.1937E-05	1.68735	down
Com_4731_pos	PE 18:0	C23 H46 N O8 P	517.27809	7.697	518.28535	No results	Invalid mass	No results	cpd:C00350	Lipids and lipid-like molecules	0.19384444	2.2764E-05	1.56539	down
Com_2687_pos	Mitragynine	C23 H30 N2 O4	398.2278	5.246	399.23508	Invalid mass	No results	No results	cpd:C09226	Alkaloids and derivatives	2.91246975	2.7472E-05	1.85333	up
Com_1993_neg	2-[(3S)-1-(Cyclohexylmethyl)-3-pyrrolidinyl]-5-fluoro-1H-benzimidazole	C18 H24 F N3	301.20057	5.34	300.19329	Invalid mass	No results	No results	--	Organoheterocyclic compounds	0.08335125	2.764E-05	1.64725	down
Com_8047_pos	ATP	C10 H16 N5 O13 P3	506.99597	4.783	508.00325	No results	No results	Full match	cpd:C00002	Nucleosides, nucleotides, and analogues	2.1414112	3.5475E-05	1.57537	up
Com_5076_neg	Propionyl-L-carnitine	C10 H19 N O4	217.13137	5.797	216.12409	No results	No results	Full match	--	Lipids and lipid-like molecules	0.39002881	3.8215E-05	1.5374	down
Com_85_pos	Hypoxanthine	C5 H4 N4 O	136.03843	3.678	137.04571	Full match	Full match	Full match	cpd:C00262	Organoheterocyclic compounds	0.01772402	4.0005E-05	1.90553	down
Com_285_neg	5-(tert-butyl)-2-methyl-N-(5-methyl-3-isoxazolyl)-3-furamide	C14 H18 N2 O3	262.13205	5.23	261.12477	Full match	No results	Full match	--	--	0.31603192	4.1957E-05	1.29769	down
Com_8258_neg	S-Lactoyglutathione	C13 H21 N3 O8 S	379.10492	4.807	378.09764	No results	No results	Full match	cpd:C03451	Organic acids and derivatives	2.28021771	4.2658E-05	1.75453	up
Com_2224_pos	Gibberellic acid	C19 H22 O6	368.11908	5.131	369.12672	Invalid mass	No results	No results	cpd:C01699	Lipids and lipid-like molecules	2.24786659	4.4971E-05	1.71378	up
Com_4118_neg	2-(acetylamino)-4-(methylthio)butanoic acid	C7 H13 N O3 S	209.06838	5.167	208.06109	Invalid mass	Invalid mass	No results	--	--	0.47055664	4.8267E-05	1.86348	down
Com_970_neg	2-(1-naphthyl)-N-(6-quinoxalinyl)acetamide	C20 H15 N3 O	313.12186	5.6	312.11458	Full match	No results	No results	--	--	0.2742953	4.9397E-05	1.86199	down
Com_1330_pos	Noroxycodone-d3	C17 H16 [2]H3 N O4	304.14925	5.172	305.15653	Full match	No results	No results	--	--	0.48308946	5.0641E-05	1.91557	down
Com_6356_pos	5-hydroxy-6,7-dimethoxy-2-phenyl-4H-chromen-4-one	C17 H14 O5	336.04019	6.469	337.04747	Invalid mass	No results	No results	--	--	4.39834422	5.6167E-05	1.6508	up
Com_1750_pos	5,7-dimethyl-2-phenylpyrazolo[1,5-a]pyrimidine	C14 H13 N3	245.09008	6.256	246.09718	Invalid mass	No results	No results	--	--	0.12448862	5.6204E-05	1.29879	down

Com_7289_pos	(2E)-6-hydroxy-2-methyl-6-(4-methylphenyl)hept-2-enoic acid	C15 H20 O3	270.11849	6.235	271.12576	Invalid mass	No results	No results	--	--	0.27736087	5.6843E-05	1.65968	down
Com_7973_pos	1-(4-chlorophenyl)-4-hydroxy-6-isopropyl-3-phenylpyridin-2(1H)-one	C20 H18 Cl N O2	339.10045	6.109	340.10773	Invalid mass	No results	No results	--	--	5.15293243	6.16E-05	1.82924	up
Com_315_neg	N-lactoyl-phenylalanine	C12 H15 N O4	237.10021	5.62	236.09293	No results	No results	Full match	--	Organic acids and derivatives	0.3593795	6.1912E-05	1.34611	down
Com_1049_neg	Esculin	C15 H16 O9	340.08592	5.114	339.07866	Invalid mass	No results	No results	cpd:C09264	Phenylpropanoids and polyketides	3.24049748	6.4981E-05	1.32665	up
Com_1449_pos	1-[(3S)-3-(1,3-Benzoxazol-2-yl)-1-pyrrolidinyl]-3-methoxy-1-propanone	C15 H18 N2 O3	274.13471	5.294	275.142	Invalid mass	No results	No results	--	Organoheterocyclic compounds	2.17684106	6.5557E-05	1.4187	up
Com_1523_neg	Mestranol	C21 H26 O2	310.18174	8.222	309.17447	No results	Invalid mass	No results	cpd:C07618	Lipids and lipid-like molecules	2.11847621	6.5799E-05	1.5134	up
Com_3158_neg	LPG 14:1	C20 H39 O9 P	454.23382	7.623	453.22654	No results	Full match	No results	--	Lipids and lipid-like molecules	0.33632672	6.5998E-05	1.60054	down
Com_600_pos	Meperidine-d4	C15 H17 [2]H4 N O2	251.18564	6.281	252.19292	Invalid mass	No results	No results	--	--	0.30637162	6.6732E-05	1.31577	down
Com_3486_neg	16α-Hydroxyestrone	C18 H22 O3	304.16372	5.443	303.15645	Invalid mass	No results	No results	cpd:C05300	Lipids and lipid-like molecules	0.31983863	7.0668E-05	1.42918	down
Com_1591_neg	Asp-glu	C9 H14 N2 O7	262.0793	5.165	261.07202	No results	No results	Full match	--	Organic acids and derivatives	4.6367508	7.2559E-05	1.38356	up
Com_973_pos	TQH	C15 H24 N6 O6	384.16905	5.961	385.17633	Invalid mass	No results	No results	--	--	6.01123809	7.3869E-05	1.744	up
Com_9258_pos	4-acetyl-4-(ethoxycarbonyl)	C12 H18 O7	296.08746	7.747	297.09469	Invalid mass	No results	No results	--	--	4.57516223	8.0023E-05	1.79208	up
Com_937_pos	Valylproline	C10 H18 N2 O3	214.13154	5.213	215.13882	Full match	No results	No results	--	Organic acids and derivatives	3.7293967	8.0995E-05	1.78659	up
Com_4789_neg	Feruloyl Putrescine	C14 H20 N2 O3	264.14769	5.304	263.14046	No results	No results	Full match	cpd:C10497	Phenylpropanoids and polyketides	0.21929122	8.4596E-05	1.69917	down
Com_1944_pos	5-Hydroxytryptophol	C10 H11 N O2	177.07893	5.484	178.08623	No results	No results	Full match	--	Organoheterocyclic compounds	2.8638789	8.7439E-05	1.62737	up
Com_130_neg	3-[(methoxycarbonyl) amino]-2,2,3-trimethylbutanoic acid	C9 H17 N O4	203.11558	5.622	202.1083	Full match	No results	Full match	--	--	0.40826892	9.6872E-05	1.56491	down
Com_1141_pos	DL-Lysine	C6 H14 N2 O2	146.10533	1.14	147.11256	Full match	Full match	Full match	cpd:C16440	Organic acids and derivatives	6.04118038	9.9282E-05	1.24994	up
Com_8310_neg	Deoxycytidine	C9 H13 N3 O4	227.09039	3.359	226.08307	No results	No results	Full match	cpd:C00881	Nucleosides, nucleotides, and analogues	15.4229488	0.0001114	1.86405	up
Com_4547_pos	5-[4-(tert-butyl)phenyl]-1,3,4-oxadiazole-2-thiol	C12 H14 N2 O S	234.07956	5.727	257.06907	Invalid mass	No results	No results	--	--	2.22589209	0.00011378	1.56633	up
Com_333_pos	Inosine	C10 H12 N4 O5	268.08053	3.68	269.08784	Full match	Full match	Full match	cpd:C00294	Nucleosides, nucleotides, and analogues	0.01270456	0.00012175	1.90711	down
Com_1238_pos	EPH	C16 H23 N5 O6	381.1663	5.428	382.17357	Full match	No results	No results	--	--	0.11808429	0.00013204	1.62588	down
Com_3292_pos	1-(4-hydroxyphenyl) propane-1,2-diol	C9 H12 O3	190.0586	1.347	191.06587	Invalid mass	No results	No match	--	--	7.40264912	0.00013324	1.37318	up
Com_1756_neg	D-Xylonic Acid	C5 H10 O6	166.04737	5.175	377.09293	No results	No results	Full match	--	Organic oxygen compounds	0.08703201	0.00013991	1.66523	down
Com_2180_pos	5-Methyluridine	C10 H14 N2 O6	258.085	4.842	259.09221	No results	No results	Full match	--	Nucleosides, nucleotides, and analogues	2.82411705	0.00016202	1.50141	up
Com_7813_pos	3-(5,7-dimethoxy-4-oxo-4H-chromen-2-yl)propanoic acid	C14 H14 O6	261.05277	5.807	279.08686	Invalid mass	No results	No results	--	--	0.2338851	0.00016454	1.59333	down
Com_335_pos	6-Methylquinoline	C10 H9 N	161.08399	5.321	144.0807	Invalid mass	No results	No results	--	Organoheterocyclic compounds	0.4550803	0.00020213	1.71056	down
Com_1374_neg	4-Methyl-2-Oxopentanoic Acid	C6 H10 O3	130.06239	5.196	175.0607	No results	No results	Full match	--	--	2.25306367	0.00021136	1.27003	up
Com_1578_neg	Azelaic acid	C9 H16 O4	188.10461	5.417	187.09734	Full match	No results	Full match	cpd:C08261	Lipids and lipid-like molecules	0.23105413	0.00023162	1.90363	down
Com_3764_pos	N-acetyl-L-ornithine	C7 H14 N2 O3	174.10089	5.467	366.23589	No results	No results	Full match	cpd:C00437	Organic acids and derivatives	0.2240987	0.00025543	1.32667	down
Com_520_pos	8-Hydroxyquinoline	C9 H7 N O	145.05262	5.777	146.05992	Full match	Full match	No results	cpd:C19434	Organoheterocyclic compounds	4.73680357	0.00025743	1.74335	up
Com_1245_pos	Acetylcysteine	C5 H9 N O3 S	163.02992	1.5	146.02663	No results	No results	Full match	cpd:C06809	Organic acids and derivatives	0.24615672	0.00028328	1.32588	down
Com_2501_neg	3-Hydroxydecanoic acid	C10 H20 O3	142.13542	6.773	187.13364	Invalid mass	Invalid mass	No results	--	Organic acids and derivatives	0.44846984	0.00029033	1.66566	down
Com_2502_neg	10-Hydroxydecanoic acid	C10 H20 O3	188.14098	6.778	187.13362	No results	No results	Full match	cpd:C02774	Organic acids and derivatives	0.44846984	0.00029033	1.66566	down
Com_228_neg	Cysteinylglycine	C5 H10 N2 O3 S	178.04086	5.225	177.03358	Full match	No results	Full match	--	Organic acids and derivatives	0.08619222	0.00031519	1.52287	down
Com_7190_neg	8-Aminooctanoic acid	C8 H17 N O2	159.12545	5.618	158.11819	No results	No results	Full match	--	Organic acids and derivatives	0.33573068	0.00034612	1.489	down
Com_2559_pos	(1R,2R)-trans-N-Boc-1,2-cyclohexanediamine	C11 H22 N2 O2	214.16797	5.739	215.17525	No results	No results	Full match	--	Organic nitrogen compounds	0.09299612	0.00038738	1.8508	down
Com_3169_neg	6-Hydroxymelatonin	C13 H16 N2 O3	248.11623	5.142	247.10896	No results	No results	Full match	cpd:C05643	Organoheterocyclic compounds	3.16010156	0.00042968	1.44598	up

Com_176_pos	DL-Norvaline	C5 H11 N O2	117.07901	1.3	118.08629	No results	No results	Full match	--	Organic acids and derivatives	4.65803528	0.00046211	1.57025	up
Com_2814_neg	Prostaglandin F3α	C20 H32 O5	398.23407	8.57	397.2268	Invalid mass	No results	No results	cpd:C06476	Lipids and lipid-like molecules	2.3382522	0.00051806	1.48939	up
Com_1971_neg	Thromoboxane B1	C20 H36 O6	408.22819	8.898	407.22091	Invalid mass	No match	No results	--	Lipids and lipid-like molecules	5.75753925	0.00059881	1.292	up
Com_4929_neg	LPE 10:0	C15 H32 N O7 P	369.19205	6.565	368.18476	No results	Full match	No results	cpd:C04230	Lipids and lipid-like molecules	0.27853661	0.00063079	1.34662	down
Com_3465_pos	Vatalanib dihydrochloride	C20 H15 Cl N4	324.11761	5.633	347.1068	Invalid mass	No results	No results	--	--	4.18798733	0.00065444	1.01521	up
Com_11030_pos	Methyl EudesMate	C11 H14 O5	226.08386	4.997	227.09114	No results	No results	Full match	--	Benzenoids	0.28907638	0.0006672	1.66685	down
Com_2500_neg	2-(1-{2-[(3-furylmethyl) amino]-2-oxoethyl} cyclohexyl)acetic acid	C15 H21 N O4	279.14744	5.731	278.14016	Full match	No results	No results	--	--	0.49048545	0.00073001	1.63178	down
Com_909_neg	Leu-Pro	C11 H20 N2 O3	228.14708	5.151	227.13981	No results	No results	Full match	--	Organic acids and derivatives	0.19678395	0.00074784	1.64268	down
Com_1249_pos	LPE 14:1	C19 H38 N O7 P	423.23826	7.633	424.24548	No results	Full match	No results	--	Lipids and lipid-like molecules	0.39386053	0.00075009	1.14797	down
Com_292_pos	Proline-hydroxyproline	C10 H16 N2 O4	228.1108	5.163	229.11808	No results	Full match	No results	--	Organic acids and derivatives	3.45417233	0.00093267	1.36874	up
Com_3641_neg	LPA 12:0	C15 H31 O7 P	354.18121	7.575	353.17393	No results	Full match	No results	cpd:C00681	Lipids and lipid-like molecules	22.2629971	0.00098799	1.71931	up
Com_4127_neg	Rutarin	C20 H24 O10	470.14787	5.079	469.1406	Invalid mass	No results	No results	cpd:C09309	Phenylpropanoids and polyketides	2.40512819	0.00104349	1.74082	up
Com_12308_neg	IDP	C10 H14 N4 O11 P2	428.01449	3.688	427.00721	No results	No results	Full match	cpd:C00104	Nucleosides, nucleotides, and analogues	0.11415571	0.00116325	1.5761	down
Com_845_pos	JWH 250 N-pentanoic acid metabolite	C22 H23 N O4	365.15825	4.875	366.16553	Invalid mass	No results	No results	--	Organoheterocyclic compounds	0.32109139	0.00119564	1.33663	down
Com_1651_neg	Pentadecanoic Acid	C15 H30 O2	288.23048	7.095	287.2232	Invalid mass	No results	No results	cpd:C16537	Lipids and lipid-like molecules	0.4473743	0.00120356	1.67102	down
Com_958_pos	Methionine sulfoxide	C5 H11 N O3 S	165.04575	1.945	148.04245	No results	No results	Full match	cpd:C02989	Organic acids and derivatives	2.89649302	0.00133211	1.21643	up
Com_4002_neg	LPG 14:0	C20 H41 O9 P	456.24958	8.211	455.2423	No results	Full match	No results	--	Lipids and lipid-like molecules	0.2293166	0.00136212	1.56094	down
Com_181_neg	Sucrose	C12 H22 O11	342.11685	1.356	387.11507	Full match	Full match	Full match	cpd:C00089	Organic oxygen compounds	3.61810423	0.00157016	1.32591	up
Com_1082_pos	L-cysteine	C3 H7 N O2 S	121.01977	1.32	122.02705	No results	No results	Full match	cpd:C00097	Organic acids and derivatives	2.72079196	0.00187034	1.50027	up
Com_161_neg	Porphobilinogen	C10 H14 N2 O4	226.09528	4.923	225.08801	Full match	No results	Full match	cpd:C00931	Organic nitrogen compounds	0.41934663	0.00236629	1.68464	down
Com_2453_pos	6-(7-methyloctyl)-1H,3H,4H,6H-furo[3,4-c] furan-1-one	C15 H24 O3	252.17016	6.76	253.17742	Invalid mass	No results	No results	--	--	0.35157781	0.00282607	1.34729	down
Com_1824_pos	α-Lactose	C12 H22 O11	359.14233	1.312	360.14961	Invalid mass	Invalid mass	No results	cpd:C00243	Organic oxygen compounds	4.28981011	0.00289157	1.13175	up
Com_1081_pos	D-Cysteine	C3 H7 N O2 S	103.99324	1.334	122.02706	Invalid mass	Invalid mass	No results	cpd:C00793	Organic acids and derivatives	2.79224689	0.00295679	1.4126	up
Com_775_pos	D-(+)-Maltose	C12 H22 O11	364.09778	1.324	365.10506	Invalid mass	No results	No results	cpd:C01971	Organic oxygen compounds	3.15569973	0.00298162	1.12993	up
Com_9125_pos	Deoxyinosine	C10 H12 N4 O4	252.0855	4.021	275.07481	No results	No results	Full match	cpd:C05512	Nucleosides, nucleotides, and analogues	0.25389869	0.00298798	1.28579	down
Com_10469_neg	N-Acetyl-L-phenylalanine	C11 H13 N O3	225.09982	5.571	224.0927	Invalid mass	Invalid mass	No results	cpd:C03519	Organic acids and derivatives	0.46220857	0.00356417	1.30343	down
Com_57_neg	Indole-3-lactic acid	C11 H11 N O3	205.07374	5.536	204.06646	Full match	Full match	Full match	cpd:C02043	Organoheterocyclic compounds	0.10501777	0.00365724	1.67504	down
Com_5307_pos	Kinetin	C10 H9 N5 O	215.08068	4.886	469.12496	No results	No results	Full match	cpd:C08272	Organoheterocyclic compounds	0.26819646	0.0041962	1.46115	down
Com_8594_neg	Morphine-3-glucuronide	C23 H27 N O9	461.16877	6.446	460.16149	Full match	No results	No results	cpd:C16643	Alkaloids and derivatives	0.4212662	0.00469579	1.31964	down
Com_9900_neg	LPA 14:0	C17 H35 O7 P	382.21216	8.621	381.20489	No results	Full match	No results	cpd:C00681	Lipids and lipid-like molecules	3.24268168	0.00479534	1.10094	up
Com_1811_neg	Uric acid	C5 H4 N4 O3	168.02788	1.825	167.0206	Full match	Full match	Full match	cpd:C00366	Organoheterocyclic compounds	3.55286789	0.00492578	1.14185	up
Com_1972_neg	LPE 8:0	C13 H28 N O7 P	341.16082	6.011	340.15354	No results	Full match	No results	--	Lipids and lipid-like molecules	0.45632275	0.00494887	1.34429	down
Com_4204_neg	LPE 13:0	C18 H38 N O7 P	411.2392	7.565	410.23192	No results	Full match	Full match	--	Lipids and lipid-like molecules	3.07063829	0.00570138	1.50683	up
Com_1769_neg	Royal jelly acid	C10 H18 O3	186.12575	5.669	231.12396	No results	No results	Full match	--	Organic acids and derivatives	4.04381804	0.00609882	1.14288	up
Com_6145_pos	2-{[(4-phenyl-1H-pyrazol-5-yl)amino]methylene} -1H-indene-1,3(2H)-dione	C19 H13 N3 O2	315.10007	6.294	316.10756	Full match	No results	No results	--	--	2.65918867	0.00750483	1.09562	up
Com_83_neg	Gallic acid	C7 H6 O5	124.01545	0.454	169.01366	Invalid mass	Invalid mass	No results	cpd:C01424	Benzenoids	5.18161427	0.00764051	1.39304	up
Com_7417_pos	Deoxyribose 5-Phosphate	C5 H11 O7 P	214.02398	1.368	237.01321	No results	No results	Full match	--	--	2.20210379	0.00850005	1.06277	up
Com_4804_pos	UR-144 N-(2-hydroxypentyl) metabolite	C21 H29 N O2	155.09448	5.341	173.12836	Invalid mass	No results	No results	--	Organoheterocyclic compounds	2.01061766	0.00930809	1.03375	up
Com_6095_pos	3-(4-pyridylmethylidene) chroman-4-one	C15 H11 N O2	237.08218	6	238.08949	Invalid mass	No results	No results	--	--	0.33547631	0.00954698	1.06252	down
Com_14668_neg	Nicotinuric Acid	C8 H8 N2 O3	180.0531	10.247	179.04582	No results	No results	Full match	cpd:C05380	Organic acids and derivatives	2.41711872	0.01164131	1.33701	up
Com_3377_pos	R-1 Methanandamide phosphate	C23 H40 N O5 P	882.52264	4.991	442.26859	Invalid mass	No results	No results	--	Organic acids and derivatives	0.34007988	0.01226055	1.03644	down
Com_9324_pos	HMR	C17 H30 N8 O4 S	482.21327	5.955	465.2099	Invalid mass	No results	No results	--	--	3.23766853	0.01545004	1.24251	up

Com_659_pos	3-Amino-3-deoxy-D-	C6 H13 N O5	179.08059	4.841	180.08786	Invalid mass	No results	No results	cpd:C12212	Organic oxygen compounds	5.68801122	0.01624991	1.16383	up
Com_95_neg	Perillic acid	C10 H14 O2	166.09891	6.151	165.09162	Full match	No results	Full match	cpd:C11924	Lipids and lipid-like molecules	0.10994493	0.01667212	1.26061	down
Com_9603_neg	LPG O-13:1	C19 H39 O8 P	426.23918	7.077	425.2319	No results	Full match	No results	--	--	4.27574624	0.02011391	1.33892	up
Com_3772_pos	Delta-Tridecalactone	C13 H24 O2	212.17735	6.358	235.16655	No results	No results	Full match	--	Organoheterocyclic compounds	0.45461939	0.02211146	1.36179	down
Com_5269_pos	Pyridoxamine	C8 H12 N2 O2	168.08995	5.94	207.05315	No results	No results	Full match	cpd:C00534	Organoheterocyclic compounds	2.47970679	0.02232011	1.27256	up
Com_5287_neg	Methyldopa	C10 H13 N O4	211.08429	5.418	210.07697	No results	No results	Full match	cpd:C07194	Phenylpropanoids and polyketides	0.48763928	0.03599247	1.1178	down
Com_2639_neg	Butyryl-coenzyme A	C25 H42 N7 O17 P3 S	838.15329	4.689	418.06928	Invalid mass	No results	No results	cpd:C00136	Lipids and lipid-like molecules	0.16230081	0.03612033	1.11277	down