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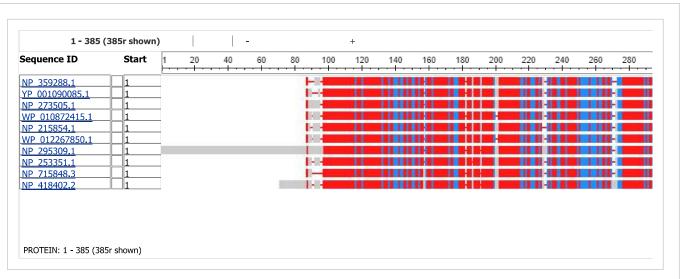
COBALT Constraint-based Multiple Alignment Tool

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Multiple Alignment Results - BAB42246:glutamate racemase [Staphylococcus... - Cobalt RID 2F85TRR3211 (10 seqs)

Graphical Overview



Descriptions

✓ Select All Re-align Alignment parameters

Accession	Description	Links
✓ NP 359288.1	glutamate racemase [Streptococcus pneumoniae R6]	Related Information
✓ YP_001090085.1	glutamate racemase [Clostridioides difficile 630]	Related Information
✓ NP 273505.1	glutamate racemase [Neisseria meningitidis MC58]	Related Information
✓ WP_010872415.1	MULTISPECIES: glutamate racemase [Synechocystis]	Related Information
✓ NP 215854.1	glutamate racemase [Mycobacterium tuberculosis H37Rv]	Related Information
✓ WP_012267850.1	MULTISPECIES: glutamate racemase [Microcystis]	Related Information
✓ NP 295309.1	glutamate racemase [Deinococcus radiodurans R1]	Related Information
✓ NP 253351.1	glutamate racemase [Pseudomonas aeruginosa PAO1]	Related Information
✓ NP_715848.3	glutamate racemase Murl [Shewanella oneidensis MR-1]	Related Information
✓ NP_418402.2	glutamate racemase [Escherichia coli str. K-12 substr. MG1655]	Related Information

Alignments

✓ Select All Re-align Mouse over the sequence identifer for sequence title View Format: Compact ▼ Conservation Setting: 2 Bits ▼

```
✓ NP 359288

                        M----DNR--PIGFLDSGVGGLTVVRELMRQLPHEEIVYIGDSARAPYGPRPAEQIREYTWQLVNFLLTK-DVKMI

✓ YP 001090085

                        MNN----K--PIGVFDSGLGGLTVLKEIMKILPNEDIIYFGDTARIPYGSRSKETIIKYTFQAINFLKTK-GVKAI
              1

✓ NP 273505

                        MENIGROR--PIGVFDSGIGGLTNVRALMERLPMENIIYFGDTARVPYGTKSKATIENFSMQIVDFLLEH-DVKAM 73
               1

<u>WP_010872415</u> 1

                        MRE-PQRS--RIGVFDSGVGGLTVLRELYRQLPKESILYFGDTARLPYGKRSPQVILQYVREILTWMAAE-EVKMV 72
✓ NP 215854
                1
                        MN--SPLA--PVGVFDSGVGGLTVARAIIDOLPDEDIVYVGDTGNGPYGPLTIPEIRAHALAIGDDLVGR-GVKAL 71

✓ WP 012267850 1

                        MRE-SQLS--PIGVFDSGVGGLTVLRELYRQLPQESILYFADTARLPYGTRSKGEIIEFVLEILTWMSER-RVKMV 72
✓ NP 295309
                     [87]ASDpAPRSa1PIGVFDSGAGGLSVLAELQRALPQEDVLYLADTAHVPYGARSDEDIRDLTARAVAELVRR-GVKAV 162
               1

✓ NP 253351

               1
                        MAV--ESA--AVGVFDSGVGGLSVLREIRARLPSESLLYVADNAHVPYGEKSAEYIRERCERIGDFLLEQ-GAKAL 71
✓ NP 715848
               1
                        MSQ-----PILVFDSGIGGLSVLAEIRKRLPHHDYCYVFDNARLPYGELEEQELVSGCVALISQLVERTHACIV
                    [16]PSE--PRP--TVLVFDSGVGGLSVYDEIRHLLPDLHYIYAFDNVAFPYGEKSEAFIVERVVAIVTAVQERvPLALA 88

✓ NP 418402

               1
✓ NP 359288
                    VIACNTATAVVWEEIKAQL-DIPVLGVILPGASAAIKSSQGKIGVIGTPMTVQSDIYRQKIHDLD--PDLQVESLACPK 146
               70

✓ YP 001090085 70

                    VIACNTATARSLKEAQEKY-DIPIIGVIEAGARTAVSSTKNKIVGIIGTEGTISSKAYNLEISKID--ESIEIVNKACPL 146

✓ NP 273505

               74
                    VIACNTIAAVAGQKIRQKTgNMPVLDVISAGAKAALATTRNNKIGIIATNTTVNSNAYARAIHRNN--PDTLVRTQAAPL 151
☑ <u>WP 010872415</u> 73
                    IMACNTSSALALETVQQEF-NMPILGVILPGARAAVR--QGRRIGVISTPATAASNAYRHAIHEIT--PDALVWQMACPE 147

✓ NP 215854

                    VIACNSASSACLRDARERY-OVPVVEVILPAVRRAVAATRNGRIGVIGTRATITSHAYODAFAAA---RDTEITAVACPR 147
               72

<u>WP</u> <u>012267850</u> 73

                    IMACNTSSALALEEVQAEFkDLPILGVILPGAKTAVQ--KGKRIGVISTPATAKSNAYKQAIQEID--PTAQVWQIPCPE 148

✓ NP 295309

               163 VVACNTASAFSLTHLRERF-ELPIIGLV-PAVKPAVAATKSGVVGVLATPGTLRGTLLADVIRQWAepAGVRVMQAVSTE

✓ NP 253351

               72
                    VLACNTATAAAAAELRERYPQVP-LVAMEPAVKPAAAATRNGRVGVLATTGTLKSARFAALLDRFA--SDVQVFTQPCPG
✓ NP 715848
                    VVACNTASTVVLPALRAKL-HIPVVGVV-PAIKPAALLSKSKRIGLLATPGTVKRHYTHELISOFA--DDCHVELFGCSE
               70
✓ NP 418402
               89
                    VVACNTASTVSLPALREKF-DFPVVGVV-PAIKPAARLTANGIVGLLATRGTVKRSYTHELIARFA--NECOIEMLGSAE 164
№ NP 359288
               147 FAPLVESGALSTSVTKKVVYETLRPLV---GKVDSLILGCTHYPLLRPIIQNVMGPKVQLIDSGAECVRDISVLLNYFEI 223

☑ YP 001090085 147 FVPIVEEGWANTEVAKLTAKIYLQELK--EKNIDSLVLGCTHYPILKRTIGEEVGEHIKLVNPAKETAKDLKKILEVQNI

✓ NP 273505
               152 LVPLVEEGWLEHEVTRLTVCEYLKPLL--ADGIDTLVLGCTHFPLLKPLIGREAG-NVALVDSAITTAEETARVLAQEGL
✓ NP 215854
               148
                    FVDFVERGVTSGRQVLGLAQGYLEPLQ--RAEVDTLVLGCTHYPLLSGLIQLAMGENVTLVSSAEETAKEVVRVLTEIDL

<u>WP_012267850</u> 149

                    FVPLIEANRIFDPYTTQVAREYLQPLL--AENIDTLVYGCTHYRHLSPVLRRLLPSSVRLVDPAASVVRAAEKELELLGL

✓ NP 295309

                    LVPLVEAGKADSPEARVVLRDVLEPLA--EAGADQLVLGCTHYPFLAGSIRAEFGDTFALVDSGAAVARHTRNVLSRGGL
               241
✓ NP_253351
               149
                    LVERIEAGDLYGPOTRALLERLLAPIL -- EOGCDTLILGCTHYPFVKPLLAELIPAEMAVIDTGAAVAROLERVLSARAL 226

✓ NP 715848

               146
                    LVMMAEHKIATGQLGIARLTQILSPVV--DANLDVLVLGCTHFPMLRDELQQVLGLGVTLLDSGAAIAKRVDTLLAHGKN 223
✓ NP 418402
                    MVELAEAKLHGEDVSLDALKRILRPWLrmKEPPDTVVLGCTHFPLLQEELLQVLPEGTRLVDSGAAIARRTAWLLEHEAP 244

✓ NP 359288

                    NRGRDAgPLHHRFYTTASSQSFAQIGEEWLEKE--I-HVEHVEL-----
                224
                                                                            264

✓ YP 001090085 225 INNTEI-HGTYQYYVSDIPEKFSDIAREFLKKK--IdKIQKVEIQKY----

                                                                            268
✓ NP 273505
                229 LNTDNN-NPDYRFYVSDIPLKFRTIGERFLGRT--MeQIEMVSLG-----
                                                                            270
✓ <u>WP 010872415</u> 226
                    RNSEM--SIATRFTVSGCPQQFAELSHQWLGFT--P-MVEKISLPCLSSIC[ 8] 279

✓ NP 215854

                226
                    LRPHDApPATRIFEATGDPEAFTKLAARFLG---P-VLGGVQPVHPSRIH

✓ WP 012267850 227

                    KNPET--PLPTNFAVSGDPDTFARLSRQWLGFS--P-RVEKVYLQCRVKTL[11] 283

✓ NP 295309

               319 LRGGDR-TGEVSYLTTSDPAHLRALLMTLRPGG-----ADGASLPDPPSPR[ 6] 369

✓ NP 253351

               227 LASGQA--ATPRFWTSALPEEMERILP-ILWGS--PeSVGKLVV------
✓ NP 715848
               224 ISHNSE-----YERNGSLMRAFYTKAeiTeGLATTLADCGFSTL[11] 273
✓ NP 418402
               245 DAKSADaNIAFCMAMTPGAEQLLPVLQRYGFET-----LEKLAVLG-----
                                                                            285
```