

PROTEIN	E MJ(2661)	E Mtl	E Ma(N-3)	E Mm(C5)	E Mm(S2)	E Mv(SB)	E Mm(C6)	E Mvo(A3)	E Mm(C7)	E Mvo(PS)
Geninfo ID	15668966	2833439	150401449	134046577	45357690	150399877	159905212	163799431	150403049	2833442
total #aa	299	299	299	299	299	299	299	299	299	299
N-term Domain	1 - 254	1 - 254	1 - 254	1 - 254	1 - 254	1 - 254	1 - 254	1 - 254	1 - 254	1 - 254
C-term Domain	255 - 299	255 - 299	255 - 299	255 - 299	255 - 299	255 - 299	255 - 299	255 - 299	255 - 299	255 - 299

SEQUENCE SIMILARITIES

E MJ(2661)	100	88.8	88.7	85.7	85.7	85.9	85.7	88.7	85	87
E Mtl	88.8	100	93.4	90.9	90.8	91.1	90.8	91.1	90.1	91.5
E Ma(N-3)	88.7	93.4	100	90.4	90.1	90.9	90.1	90.8	89.5	90.5
E Mm(C5)	85.7	90.9	90.4	100	97.3	95.8	98.2	92.7	96.6	91.8
E Mm(S2)	85.7	90.8	90.1	97.3	100	97	98.3	93.1	97.6	92.4
E Mv(SB)	85.9	91.1	90.9	95.8	97	100	96.8	92.4	96	91.4
E Mm(C6)	85.7	90.8	90.1	98.2	98.3	96.8	100	93.3	98.2	92.1
E Mvo (A3)	88.7	91.1	90.8	92.7	93.1	92.4	93.3	100	91.1	95.6
E Mm(C7)	85	90.1	89.5	96.6	97.6	96	98.2	91.1	100	91.3
E Mvo(PS)	87	91.5	90.5	91.8	92.4	91.4	92.1	95.6	91.3	100
E Mth(w)	82.1	80.1	79.1	80.1	79.8	80.2	80.1	80.6	79.7	80.9
E Mth(dH)	82.6	80.8	79.8	79.7	79.7	79.7	79.7	80.6	79.3	81.1
E Mtm	82.7	80.8	79.1	79.5	79.7	79.9	79.5	80.3	79.1	80.8
E Ml(Z)	81.6	80.8	79.1	78.4	78.8	78.4	78.5	79.1	78.7	80.1
E Ms(ATCC)	82.3	80.4	80.7	81.3	81.3	81.5	81.5	82	81.5	81.9
E Mk(AV19)	79.5	78.6	78.1	76.6	76.6	76.1	76.7	77.1	76.4	78.1
P2 Mj(2661)	60.5	60.1	60.1	60.7	60.8	59	60.7	61.1	58.9	59.6
P Ma(N-3)	59.6	59.6	59.4	58.6	58.5	58.9	58.6	58.7	58.9	58.9
P Mv(SB)	60.1	60.9	59.2	59.1	58.9	59.7	58.9	59.5	59.7	59.1
P1 Mj(2661)	60.2	60.2	59.5	59.3	59.3	59.8	59.5	59.2	59.5	59.6
P1 Mth(dH)	59.1	58.9	59.1	58.5	58.8	59.4	58.8	58.7	58.9	59.5
P2 Mth(dH)	59.7	61.8	60.1	59.2	59.3	60	59.4	61.1	59.3	61.8
P1 Mtm	59.7	60	60.1	58.9	58.9	59.4	59	58.7	59	60.8
P2 Mtm	59.6	61.6	60.8	59	59.2	59.6	59.3	60.6	59.2	61.4
P Mm(C7)	60.1	60.1	59.5	58.9	58.8	58.8	58.9	58.9	58.9	58.9
P Mm(C6)	60.1	60.1	59.5	58.8	58.7	58.8	58.9	58.9	58.9	58.9
P Mm(S2)	60.1	60.7	59.2	58.8	58.7	59.2	58.8	58.7	58.8	58.7
P Mm(C5)	59.8	59.8	59.2	58.7	58.5	58.5	58.8	58.7	58.8	58.7
P1 Mk(AV19)	57.4	58.6	58	56.6	56.9	57.5	56.6	58	56.6	58
P2 Mk(AV19)	59.3	58.5	58.6	58.2	58.3	58.8	58.5	58.6	58.8	58.8
Pd Ma(N-3)	52.8	54.5	55.3	53.8	52.1	53.2	52.1	54.8	52.1	55.2
Pd Mj(2661)	53.6	54.5	53.8	55.1	52.1	53.1	53.7	54.1	54.7	54.5
Pd Mm(C7)	55.7	53.5	56.1	53.1	53.5	53.4	53.4	54.8	53.4	56.6

PROTEIN	E Mth(dH)	E Mtm	E MI(Z)	E Ms(ATCC)	E Mk(AV19)	P2 Mj(2661)	P Ma(N-3)	P Mv(SB)	P1 Mj(2661)
Geninfo ID	15679153	2828203	124486556	148642632	20093453	15668897	150401123	150399766	15669529
total #aa	304	301	298	295	310	250	250	250	261
N-term Domain	1 - 259	1 - 256	1 - 253	1 - 250	1 - 265	1 - 205	1 - 205	1 - 205	1 - 216
C-term Domain	260 - 304	257 - 301	254 - 298	251 - 295	266 - 310	206 - 250	206 - 250	206 - 250	217 - 261

SEQUENCE SIMILARITIES

E MJ(2661)	82.6	82.7	81.6	82.3	79.5	60.5	59.6	60.1	60.2
E MI	80.8	80.8	80.8	80.4	78.6	60.1	59.6	60.9	60.2
E Ma(N-3)	79.8	79.1	79.1	80.7	78.1	60.1	59.4	59.2	59.5
E Mm(C5)	79.7	79.5	78.4	81.3	76.6	60.7	58.6	59.1	59.3
E Mm(S2)	79.7	79.7	78.8	81.3	76.6	60.8	58.5	58.9	59.3
E Mv(SB)	79.7	79.9	78.4	81.5	76.1	59	58.9	59.7	59.8
E Mm(C6)	79.7	79.5	78.5	81.5	76.7	60.7	58.6	58.9	59.5
E Mvo (A3)	80.6	80.3	79.1	82	77.1	61.1	58.7	59.5	59.2
E Mm(C7)	79.3	79.1	78.7	81.5	76.4	58.9	58.9	59.7	59.5
E Mvo(PS)	81.1	80.8	80.1	81.9	78.1	59.6	58.9	59.1	59.6
E Mth(w)	98.5	97.7	87.7	85.8	78.1	59.5	59	59.1	58.9
E Mth(dH)	100	98.4	87.4	85.8	77.5	59.8	59	59.5	59.2
E Mtm	98.4	100	86.1	85.3	77.8	59.9	58.6	59.2	59
E MI(Z)	87.4	86.1	100	83.1	76.2	61.1	58.3	59.5	60.1
E Ms(ATCC)	85.8	85.3	83.1	100	79.8	59.2	58.8	58.8	59.3
E Mk(AV19)	77.5	77.8	76.2	79.8	100	60.7	59.8	59.7	58.6
P2 Mj(2661)	59.8	59.9	61.1	59.2	60.7	100	78.6	77.8	82.1
P Ma(N-3)	59	58.6	58.3	58.8	59.8	78.6	100	87.4	85.9
P Mv(SB)	59.5	59.2	59.5	58.8	59.7	77.8	87.4	100	85.5
P1 Mj(2661)	59.2	59	60.1	59.3	58.6	82.1	85.9	85.5	100
P1 Mth(dH)	59.9	58.3	59.6	58.9	59.5	76	81.3	81.2	81.6
P2 Mth(dH)	59.2	59	61.1	59.3	59.2	78.6	83.1	83.4	84.6
P1 Mtm	60.3	59	58.5	59.5	60.3	76.2	80.3	81.2	81.5
P2 Mtm	59.2	59.2	60.1	59.2	59.6	77.1	82.2	82.7	83.7
P Mm(C7)	59.7	59.5	59.2	59.1	61.3	77.4	87.1	92.1	86.2
P Mm(C6)	59.7	59.5	58.9	58.8	60.1	76.9	88.1	93.1	86.1
P Mm(S2)	60.1	59.1	59.7	58.9	60.9	77.1	87.7	93.1	85.6
P Mm(C5)	59.7	59.5	58.9	58.6	61.1	76.8	87.7	92.5	85.5
P1 Mk(AV19)	60.7	60.8	58.6	58.5	58.1	66.2	66.8	65.6	68.1
P2 Mk(AV19)	59.4	59.3	59.3	57.9	60.2	65.6	66.8	64.1	67.7
Pd Ma(N-3)	53	53.1	54.2	53.9	52.4	57.1	58.7	58.5	57.6
Pd Mj(2661)	53.6	53.3	53.9	53.9	53.6	55.3	56.1	56.3	55.9
Pd Mm(C7)	51.6	53.1	55.1	53.3	56	56.7	56.9	55.1	57.5

PROTEIN	P1 Mth(dH)	P2 Mth(dH)	P1 Mtm	P2 Mtm	P Mm(C7)	P Mm(C6)	P Mm(S2)	P Mm(C5)	P1 Mk(AV19)
Geninfo ID	15678532	15679509	7573569	7573567	150402915	159905340	45359279	134046716	20094558
total #aa	256	253	253	253	250	250	250	250	228
N-term Domain	1 - 211	1 - 208	1 - 208	1 - 208	1 - 205	1 - 205	1 - 205	1 - 205	1 - 184
C-term Domain	212 - 256	209 - 253	209 - 253	209 - 253	206 - 250	206 - 250	206 - 250	206 - 250	185 - 228

SEQUENCE SIMILARITIES

E MJ(2661)	59.1	59.7	59.7	59.6	60.1	60.1	60.1	59.8	57.4
E Mtl	58.9	61.8	60	61.6	60.1	60.1	60.7	59.8	58.6
E Ma(N-3)	59.1	60.1	60.1	60.8	59.5	59.5	59.2	59.2	58
E Mm(C5)	58.5	59.2	58.9	59	58.9	58.8	58.8	58.7	56.6
E Mm(S2)	58.8	59.3	58.9	59.2	58.8	58.7	58.7	58.5	56.9
E Mv(SB)	59.4	60	59.4	59.6	58.8	58.8	59.2	58.5	57.5
E Mm(C6)	58.8	59.4	59	59.3	58.9	58.9	58.8	58.8	56.6
E Mvo (A3)	58.7	61.1	58.7	60.6	58.9	58.9	58.7	58.7	58
E Mm(C7)	58.9	59.3	59	59.2	58.9	58.9	58.8	58.8	56.6
E Mvo(PS)	59.5	61.8	60.8	61.4	58.9	58.9	58.7	58.7	58
E Mth(w)	58.4	59	59.2	59	59.2	59.2	59.7	59.2	60.8
E Mth(dH)	59.9	59.2	60.3	59.2	59.7	59.7	60.1	59.7	60.7
E Mtm	58.3	59	59	59.2	59.5	59.5	59.1	59.5	60.8
E MI(Z)	59.6	61.1	58.5	60.1	59.2	58.9	59.7	58.9	58.6
E Ms(ATCC)	58.9	59.3	59.5	59.2	59.1	58.8	58.9	58.6	58.5
E Mk(AV19)	59.5	59.2	60.3	59.6	61.3	60.1	60.9	61.1	58.1
P2 Mj(2661)	76	78.6	76.2	77.1	77.4	76.9	77.1	76.8	66.2
P Ma(N-3)	81.3	83.1	80.3	82.2	87.1	88.1	87.7	87.7	66.8
P Mv(SB)	81.2	83.4	81.2	82.7	92.1	93.1	93.1	92.5	65.6
P1 Mj(2661)	81.6	84.6	81.5	83.7	86.2	86.1	85.6	85.5	68.1
P1 Mth(dH)	100	88.8	94.6	88.5	83.4	83.6	82.1	83.7	65.4
P2 Mth(dH)	88.8	100	89.2	97.7	83.4	83.6	82.1	83.7	65.4
P1 Mtm	94.6	89.2	100	88.8	81.7	81.5	81.4	81.1	66.7
P2 Mtm	88.5	97.7	88.8	100	82.1	82.1	82.6	83.1	66
P Mm(C7)	83.4	83.4	81.7	82.1	100	98.5	97.4	98.2	66.4
P Mm(C6)	83.6	83.6	81.5	82.1	98.5	100	96.8	97.9	66.4
P Mm(S2)	82.1	82.1	81.4	82.6	97.4	96.8	100	95.9	65.7
P Mm(C5)	83.7	83.7	81.1	83.1	98.2	97.9	95.9	100	65.9
P1 Mk(AV19)	65.4	65.4	66.7	66	66.4	66.4	65.7	65.9	100
P2 Mk(AV19)	66.1	66.5	66.8	66.7	65.7	65.9	65.1	65.4	67.3
Pd Ma(N-3)	55.8	55.8	55.7	56.5	58.2	58.4	58.1	57.5	55.8
Pd Mj(2661)	56.3	56.3	57.1	55.1	55.9	55.6	54.1	56.5	56.4
Pd Mm(C7)	55.1	55.1	55.5	54.9	56.7	57.3	56.9	57	58

PROTEIN	P2 Mk(AV19)	Pd Ma(N-3)	Pd Mj(2661)	Pd Mm(C7)
Geninfo ID	20094801	150401448	15668793	150402684
total #aa	248	342	346	344
N-term Domain	1 - 204	1 - 297	1 - 301	1 - 299
C-term Domain	205 - 248	297 - 342	302 - 346	300 - 344

SEQUENCE SIMILARITIES

E MJ(2661)	59.3	52.8	53.6	55.7
E Mtl	58.5	54.5	54.5	53.5
E Ma(N-3)	58.6	55.3	53.8	56.1
E Mm(C5)	58.2	53.8	55.1	53.1
E Mm(S2)	58.3	52.1	52.1	53.5
E Mv(SB)	58.8	53.2	53.1	53.4
E Mm(C6)	58.5	52.1	53.7	53.4
E Mvo (A3)	58.6	54.8	54.1	54.8
E Mm(C7)	58.8	52.1	54.7	53.4
E Mvo(PS)	58.8	55.2	54.5	56.6
E Mth(w)	59.6	52.8	53.5	51.6
E Mth(dH)	59.4	53	53.6	51.6
E Mtm	59.3	53.1	53.3	53.1
E Ml(Z)	59.3	54.2	53.9	55.1
E Ms(ATCC)	57.9	53.9	53.9	53.3
E Mk(AV19)	60.2	52.4	53.6	56
P2 Mj(2661)	65.6	57.1	55.3	56.7
P Ma(N-3)	66.8	58.7	56.1	56.9
P Mv(SB)	64.1	58.5	56.3	55.1
P1 Mj(2661)	67.7	57.6	55.9	57.5
P1 Mth(dH)	66.1	55.8	56.3	55.1
P2 Mth(dH)	66.5	55.8	56.3	55.1
P1 Mtm	66.8	55.7	57.1	55.5
P2 Mtm	66.7	56.5	55.1	54.9
P Mm(C7)	65.7	58.2	55.9	56.7
P Mm(C6)	65.9	58.4	55.6	57.3
P Mm(S2)	65.1	58.1	54.1	56.9
P Mm(C5)	65.4	57.5	56.5	57
P1 Mk(AV19)	67.3	55.8	56.4	58
P2 Mk(AV19)	100	53.7	56.8	52.9
Pd Ma(N-3)	53.7	100	80.9	81.3
Pd Mj(2661)	56.8	80.9	100	81.8
Pd Mm(C7)	52.9	81.3	81.8	100

Genes:

E = H₂-forming 4(H)MPT dehydrogenase
P = H₂-forming 4(H)MPT dehydrogenase paralog
Pd = Prephenate dehydrogenase

Organisms:

MJ(2661) = Methanocaldococcus jannaschii strain 2661
Mtl = Methanococcus thermolithotrophicus
Ma (N-3) = Methanococcus aeolicus Nankai-3
Mm(C5) = Methanococcus maripaludis strain C5
Mm(S2) = Methanococcus maripaludis strain S2
Mv(SB) = Methanococcus vanniellii strain SB
Mm(C6) = Methanococcus maripaludis strain C6
Mvo (PS) = Methanococcus voltae strain PS
Mvo (A3) = Methanococcus voltae strain A3
Mm(C7) = Methanococcus maripaludis strain C7
Mth(w) = Methanothermobacter thermautotrophicus strain Winter
Mth(dH) = Methanothermobacter thermautotrophicus strain delta H
Mtm = Methanothermobacter marburgensis
MI(Z) = Methanocorpusculum labreanum strain Z
Ms(ATCC) = Methanobrevibacter smithii ATCC 35061
Mk(AV19) = Methanopyrus kandleri AV19

References:

MJ(2661) = [16]
Mtl = [17]
Ma (N-3) = Copeland, A, *et al.*: **Complete sequence of Methanococcus aeolicus Nankai-3. US DOE Joint Genome Institute** (unpublished).
Mm(C5) = Copeland, A, *et al.*: **Complete sequence of chromosome of Methanococcus maripaludis C5. US DOE Joint Genome Institute** (unpublished).
Mm(S2) = [18]
Mv(SB) = Copeland, A, *et al.*: **Complete sequence of Methanococcus vanniellii SB. US DOE Joint Genome Institute** (unpublished).
Mm(C6) = Copeland, A, *et al.*: **Complete sequence of Methanococcus maripaludis C6. US DOE Joint Genome Institute** (unpublished).
Mvo (PS) = Hartmann G, Thauer RK: **Hmd genomic sequence. Direct Submission to NCBI databases** 1996.
Mvo (A3) = Copeland, A, *et al.*: **Sequencing of the draft genome and assembly of Methanococcus voltae A3. US DOE Joint Genome Institute (JGI-PGF)** (unpublished).
Mm(C7) = Copeland, A, *et al.*: **Complete sequence of Methanococcus maripaludis C7. US DOE Joint Genome Institute** (unpublished).
Mth(w) = [19]
Mth(dH) = [20]
Mtm = [21]
MI(Z) = Copeland, A, *et al.*: **Complete sequence of Methanocorpusculum labreanum Z. US DOE Joint Genome Institute** (unpublished).
Ms(ATCC) = [22]
Mk(AV19) = [23]