

Broader and same Taxonomic Scope : Archeae, Eukaryotes, Prokaryotes (Bacteria)
PS00571 & PS01199

Segments in MDL output common to both families :

A	5680 2466	GRV	3 4	TNLT	1 1
E	3548 1272	KEC	2 1	KIKE	4 2
V	3303 1970	VKN	10 5	TIGK	2 1
I	2840 1606	QQV	5 1	VIAS	1 5
M	1238 517	YFK	3 4	EAGA	5 1
T	2768 1440	YLK	6 1	VSLP	4 1
Q	1797 845	RIL	9 2	AVKN	1 1
Y	1070 319	LPH	4 2	IVGM	1 1
F	1420 403	VNL	7 2	AKGE	1 3
N	1874 930	TVT	9 10	ALSS	3 1
R	2443 893	ENF	2 11	KAKE	3 1
C	577 103	QVR	5 2	ATAV	2 2
G	2928 795	KEN	6 2	RIAV	1 1
S	3597 1547	GKT	5 6	DATV	3 1
W	240 13	IGK	5 13	FDTV	1 5
K	2874 1987	GIDP	3 3	EEAIK	1 2
D	3035 1159	SVDV	3 1		
H	906 163	DVII	2 2		
L	4434 1849	EALK	8 2		
P	1745 466	EKVD	4 1		

Observation:

Some short segments of length upto 5 are seen common to both families when they span a broader taxonomic range

Same Taxonomic Scope

Eukaryotes (Viruses) : PS51527 & PS51528

G	492 498	GEDGCWYGMEIRP	8 8
V	802 807	RNPLSRNSTHEMY	4 4
A	738 748	AKGSRAIWYMWLG	4 4
W	90 91	FIKFAEGRRGAAE	4 4
C	79 84	MYADDTAGWDTRIT	9 8
Y	128 126	LMGLDKGWPIKMD	6 6
D	318 311	EWCCRCTLPLRY	4 4
E	385 396	GEAAAIFMTATPPG	4 4
F	193 196	MGMGTTYLALMATF	4 4
H	119 122	CVYNMMGKREKKLG	4 4
I	575 582	GEDGCWYGMEIRPL	5 4
S	558 560	DFVVTTDISEMGAN	4 4
K	539 529	RRLRTLVLAPTRVVL	4 4
P	205 217	CSPRTGLDFNEMVLL	4 4
M	301 311	IHEWCCRCTLPLR	4 4
L	754 762	EVDRSEAKEGLKRGE	4 4
Q	182 185	WPKSHTLWSNGVLES	4 4
R	511 518	RMAISGDDCVVKPLD	5 4

T	743 746	VKYEGETDAPCKIPFS	4 4
N	282 280	CDFTPWLAWHVAANV	4 4
RAWN	4 4	KFEKQLGQVMLLVLC	6 6
NMLKR	4 4	QRGLLGRSQVGVGVFQ	4 4
IPMVTQ	4 4	RFLEFEALGFLNEDHW	5 5
MNNQRKK	6 6	ISNGTGNIVSSVNMVS	4 4
RVPNYNL	6 6	EDDLHNEEKITQQMDP	4 4
KEKEENLV	4 4	DVFYTLMHEEPGSRAM	4 4
TPNPTIEN	4 4	LVRNPLSRNSTHEMYW	4 4
PEDIDCWC	4 4	FKDYLSMDRHDHLHWE	4 4
DWQQVPFCS	5 5	AGPVSQHNYPGYHTQ	7 7
EKEENMVKS	4 7	EAIEERVERIKSEYMT	4 4
LKPRWLDAR	4 4	LVVPCRDQDELVGRAR	4 4
SPGCGWSVRE	4 4	IKVLNPYMPSVIEKME	5 5
LVAHYAIIIGP	4 4	KRNLTIMDLHPGSGKTR	4 4
LRDISKIPGG	4 4	GKTVWFVPSIKAGNDIA	6 6
VWNRVWIEEN	5 5	GGAMYADDTAGWDTRIT	4 4
SRENSGGGVEG	4 4	PPEKCDTLLCDIGESSP	11 11
VPFCSHHFHFL	4 4	DWDFVVTDDISEMGANF	5 7
GYTKGGPGHEEP	4 4	CVYNMMGKREKKLGFEF	10 10
ERVILAGPMPVT	4 4	CLQRAGKKVIQLNRKSY	5 5
EPDDVDCWCNAT	4 4	SALTLEHFRKGSIGKM	5 4
SQLAKRFSKGLL	6 6	GEEVQVIAVEPGKNPKN	4 4
MAERDAPEAFLT	4 4	AVGLMFIVGGGLAELDI	6 6
TAIQQVRSIGN	4 4	EAKMLLDNINTPEGIIP	4 4
NLDIIGQRIENIK	4 4	TFVDLMRRGDLPVWLAY	4 4
YADDTAGWDTRIT	8 8	GEVKSCTWPETHTLWGD	7 8
AIDGEYRLRGEAR	4 4	VWNRVWITNNPHMQDKT	4 4
VEMMVLGLATLGV	4 4	MLSIINKRKKTSLCLMM	4 4
AANEMGLETTKKDLGIGH	4 4	SGVEGEGLHKLGYILRDISKIP	4 4
HYAIIIGPGLQAKATREAQKR	4 5	SVIVTVHTGDQHQVGNETTEHGT	4 4
VVQADMGCVINWKGKELKCG	4 4	EHLPTAWQVHRDWFNDLALPWKH	5 5
TKVELGEAAAFMTATPPGT	4 4	MRPMAFVGLLFRRLTSREVLLLT	4 4
LHFLNAMSKVRKDIQEWKPS	6 6	ERLKRMAISGDDCVVKPIDDRFA	8 8
GRTTWSIHGKGEWMTTEDML	5 5	VTQVLMMRTTWALCEALTATGP	6 6
WEEVPFCSHHFHFLVMKDGR	4 4	EIRPLKEKEENLVNSLVTAGHGQ	5 5
LDVSRVIDGRNTNIKPEEVDG	4 4	APSMTMRCIGISNRDFVEGVSGG	5 4
GSASSMVNGVVRLLTCPWDV	5 5	EDERFWDLVHRERELHKQGKCAT	4 4
CPLLVNTEPEDIDCWCNLT	5 4	LHQQGRCTCVYNMMGKREKKLS	5 5
PPEKCDTLLCDIGESSNPT	6 6	TCAKFKCVTKLEGKIVQYENLKY	4 4
LNDMGKVRKDIPQWEPKSGW	4 4	LVAHYAIIIGPGLQAKATREAQKR	4 4
NDWDFVVTDDISEMGANFKA	6 6	ATITPQAPTSEIQLTDYGALTLD	4 4
LEFEALGFLNEDHWFSRENS	5 5	VGLGLETRTETWMSSEGAWKQIQ	4 4
RDFVEGLSGATWVDVVLEHG	5 5	WCFVVRTSISRMMLGTLVLLASL	4 4
RNNQILEENMDVEIWTKEGE	4 5	FSRENSLSGVEGEGLHKLGYILR	6 6
NPTIEEGRTLRLVLMVEPW	4 5	RCPTQGEPYLKKEEQDQQYICRRD	5 4
GNEIVDVMCHATLTHRLMSP	6 6	NMCTLMAMDLGELCEDTITYKCP	4 4
LRTLILAPTRVAAEMEEAL	4 4	ELTGTRRVTTASAAQRRGRVGRQ	5 5
DIQPARSWGTYVLVLSLFTPY	4 4	MEITAEWLWRTLGRNKRPRCTR	4 4
MWLGARFLEFEALGFLNEDHW	7 7	QRKHGGMLVRNPLSRNSTHEMYW	4 4

IIGVEPGQLKLNWFKKGSSIG	4 4	ASAAQRRGRVGRNPQKENDQYIF	4 4
MAMTDTTPFGQQRVFKEKVD	5 9	SWASVKKDLISYGGGWRFGGSWN	4 4
RDMRLLSLAVSSAVPTSWVPQ	4 4	RMAVSGDDCVVRPIDDRFGLALS	4 4
WPKSHTLWSNGVLESEMIIPK	4 4	SLILPGIKAQQSKLAQRRVFHGVA	4 4
GPRSWYNRIPGYSEQVKGPWK	4 4	GVFHTMWHVTRGAVLMYQGKRLEP	4 4
EHEILNDSGETVKCRAPGGAK	4 4	VIDLGCGRGGWSYYCAGLKKVTEV	8 8
SALTALNDMGKIRKDIQQWEP	4 4	WVPTSRTTWSIAHHQWMTTEDML	4 4
YLEFEALGFLNEDHWASRENS	4 4	GEGVFKSIQHLTITEEIAVQNWLA	4 4
QGGVLRSMVVADNGELLSEGG	4 4	EKGGKAHRMALEELPDALETITLI	4 4

Observation:

Many longer segments are seen common to both families when they belong to same taxonomic group and their family names are very close like PS51527 & PS51528

Disjoint taxonomic scope :

i) Prokaryotes : PS51208

ii) Eukaryotes : PS51527

A	5070 748	G	5517 498
I	3512 582	K	3060 529
M	769 311	S	6550 560
Q	2502 185	W	485 91
Y	1657 126	D	3401 311
F	2161 196	H	1120 122
E	2809 396	L	4786 762
N	5288 280	P	1747 217
R	1751 518	T	5411 746
V	3758 807	PQP	5 1
C	386 84	NSGG	11 3

Observation:

Almost no significant length common segments are seen when the families are in different taxonomic range

Same Taxonomic Range:

Prokaryotes (Bacteria) : PS51208 and PS51305

V	3758 754	I	3512 628
A	5070 538	E	2809 761
W	485 51	K	3060 664
C	386 53	L	4786 705
Y	1657 164	M	769 144
D	3401 666	N	5288 460
F	2161 219	Q	2502 373
H	1120 175	R	1751 440
G	5517 467	S	6550 420
P	1747 299	T	5411 459

Observation:

Almost no significant length common segments are seen though the families are in same taxonomic range. This may be because the family names are not showing enough similarity unlike in an earlier case