

Reference sequence (1): Vitvi14g02865
Identities normalised by aligned length.
Colored by: identity

		cov	pid	241	[]	241
1	Vitvi14g02865	100.0%	100.0%			N
2	Vitvi14g01108	92.1%	75.6%			-
3	NA1	79.4%	72.4%			-
4	Vitvi14g01106	80.7%	73.8%			-
5	Vitvi14g01080	96.9%	84.6%			-
6	Vitvi14g01075	96.9%	89.6%			-
7	Vitvi14g01113	96.9%	90.0%			-
8	Vitvi14g01082	96.9%	90.5%			-
9	Vitvi14g04720	96.9%	92.3%			-
10	Vitvi14g01096	96.9%	91.9%			-
11	NA2	96.9%	91.9%			-
12	Vitvi14g04724	96.9%	91.9%			-
13	Vitvi14g01112	96.9%	91.9%			-
14	Vitvi14g02863	96.9%	91.4%			-

15	Vitvi14g02864	96.9%	91.4%	-
	consensus/100%			.
	consensus/90%			.
	consensus/80%			.
	consensus/70%			.

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Consensus pattern definitions

Consensus patterns are based on equivalence classes, that is, sets of residues that share some predefined property. These classes are not mutually exclusive and the consensus mechanism will choose the most specific class that summarizes a given column at the desired percent identity.

The default for protein alignments is called P1 and is defined by physicochemical property as follows:

```
[P1]
#Protein consensus: conserved physicochemical classes, derived from
#the Venn diagrams of: Taylor W. R. (1986). The classification of amino
#acid
#conservation. J. Theor. Biol. 119:205-218.
#description => symbol members
*      => .
A      => A      { A }
C      => C      { C }
D      => D      { D }
E      => E      { E }
F      => F      { F }
G      => G      { G }
H      => H      { H }
I      => I      { I }
K      => K      { K }
L      => L      { L }
M      => M      { M }
N      => N      { N }
P      => P      { P }
Q      => Q      { Q }
R      => R      { R }
S      => S      { S }
T      => T      { T }
V      => V      { V }
W      => W      { W }
Y      => Y      { Y }
alcohol => o      { S, T }
aliphatic=> l      { I, L, V }
aromatic=> a      { F, H, W, Y }
charged  => c      { D, E, H, K, R }
hydrophobic=> h      { A, C, F, G, H, I, K, L, M, R, T, V, W, Y }
negative  => -      { D, E }
polar     => p      { C, D, E, H, K, N, Q, R, S, T }
positive   => +      { H, K, R }
small     => s      { A, C, D, G, N, P, S, T, V }
tiny      => u      { A, G, S }
turnlike   => t      { A, C, D, E, G, H, K, N, Q, R, S, T }
```

Percent Identity Matrix - created by Clustal2.1

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	Protein lenght
1 Vitvi14g02865															228
2 Vitvi14g01108	79.52														210
3 NA1	88.4	97.24													181
4 Vitvi14g01106	88.59	95.65	100												184
5 Vitvi14g01080	89.59	83.81	93.37	93.48											234
6 Vitvi14g01075	89.59	85.24	93.92	93.48	94.12										221
7 Vitvi14g01113	90.05	83.33	92.27	92.39	94.12	95.93									221
8 Vitvi14g01082	90.5	84.76	93.92	94.02	95.48	97.29	98.64								221
9 Vitvi14g04720	92.31	85.24	95.03	95.11	96.83	97.29	96.83	98.19							221
10 Vitvi14g01096	91.86	85.24	95.03	95.11	96.38	96.83	97.29	98.64	99.55						221
11 NA2	91.86	84.76	94.48	94.57	96.38	97.74	97.29	98.64	99.55	99.1					221
12 Vitvi14g04724	91.86	84.76	94.48	94.57	96.38	97.74	97.29	98.64	99.55	99.1	100				221
13 Vitvi14g01112	91.86	84.76	94.48	94.57	96.38	97.74	97.29	98.64	99.55	99.1	100	100			221
14 Vitvi14g02863	91.4	84.76	94.48	94.57	95.93	97.29	97.74	99.1	99.1	99.55	99.55	99.55	99.55		221
15 Vitvi14g02864	91.4	84.76	94.48	94.57	95.93	97.29	97.74	99.1	99.1	99.55	99.55	99.55	99.55	100	221