



Compendium of overhangs

There are **136** overhangs in this report.

Please see the Appendix on the last page for an explanation of details.



AAAC

GTTT

GC content: **25 %**.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

K[PRQLH]

[PEGRSA*IKTQVL]N

[EQK*][T]

V[FWSCY*L]

[PEGWRSA*KTQMVL]F

[SGCR][LF]



AACA

TGTT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

N[RSIKTNM]

[PEGRSA*IKTQVL]T

[EQK*][HQ]

C[FWSCY*L]

[PGFSRACYIDTNVLH]V

[MVL][LF]



AACC

GGTT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

N[PRQLH]

[PEGRSA*IKTQVL]T

[EQK*][P]

G[FWSCY*L]

[PEGWRSA*KTQMVL]V

[RGW][LF]



AACT

AGTT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

N[FWSCY*L]

[PEGRSA*IKTQVL]T

[EQK*][L]

S[FWSCY*L]

[PEGRSA*IKTQVL]V

[EQK*][LF]



AAGT

ACTT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

K[FWSCY*L]

[PEGRSA*IKTQVL]S

[EQK*][V]

T[FWSCY*L]

[PEGRSA*IKTQVL]L

[HDYN][LF]



AATA

TATT

GC content: 0 %.

Can form the following amino acids in 6 translation frames:

N[RSIKTNM]

[PEGRSA*IKTQVL]I

[EQK*][Y*]

Y[FWSCY*L]

[PGFSRACYIDTNVLH]I

[IVL][LF]



AATC

GATT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

N[PRQLH]

[PEGRSA*IKTQVL]I

[EQK*][S]

D[FWSCY*L]

[PEGWRSA*KTQMVL]I

[RG*][LF]



AATT

AATT

GC content: 0 %.

The overhang is palindromic, cannot be used for DNA assembly.

Can form the following amino acids in 6 translation frames:

N[FWSCY*L]

[PEGRSA*IKTQVL]I

[EQK*][LF]

N[FWSCY*L]

[PEGRSA*IKTQVL]I

[EQK*][LF]



ACAA

TTGT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

T[RSIKTNM]

[PEGRSA*IKTQVL]Q

[HDYN][KN]

L[FWSCY*L]

[PGFSRACYIDTNVLH]C

[IVFL][V]



ACAG

CTGT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

T[GEADV]

[PEGRSA*IKTQVL]Q

[HDYN][RS]

L[FWSCY*L]

[PGFSRACYIDTNVLH]C

[SPAT][V]



ACCA

TGGT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

T[RSIKTNM]

[PEGRSA*IKTQVL]P

[HDYN][HQ]

W[FWSCY*L]

[PGFSRACYIDTNVLH]G

[MVL][V]



ACCG

CGGT

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

T[GEADV]

[PEGRSA*IKTQVL]P

[HDYN][R]

R[FWSCY*L]

[PGFSRACYIDTNVLH]G

[SPAT][V]



ACGA

TCGT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

T[RSIKTNM]

[PEGRSA*IKTQVL]R

[HDYN][ED]

S[FWSCY*L]

[PGFSRACYIDTNVLH]R

[IVFL][V]



ACGC

GCGT

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

T[PRQLH]

[PEGRSA*IKTQVL]R

[HDYN][A]

A[FWSCY*L]

[PEGWRSA*KTQMVL]R

[SGCR][V]



ACGT

ACGT

GC content: 50 %.

The overhang is palindromic, cannot be used for DNA assembly.

Can form the following amino acids in 6 translation frames:

T[FWSCY*L]

[PEGRSA*IKTQVL]R

[HDYN][V]

T[FWSCY*L]

[PEGRSA*IKTQVL]R

[HDYN][V]



ACTA

TAGT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

T[RSIKTNM]

[PEGRSA*IKTQVL]L

[HDYN][Y*]

*[FWSCY*L]

[PGFSRACYIDTNVLH]S

[IVL][V]



ACTG

CAGT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

T[GEADV]

[PEGRSA*IKTQVL]L

[HDYN][WC*]

Q[FWSCY*L]

[PGFSRACYIDTNVLH]S

[SPAT][V]



AGCC

GGCT

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

S[PRQLH]

[PEGRSA*IKTQVL]A

[EQK*][P]

G[FWSCY*L]

[PEGWRSA*KTQMVL]A

[RGW][L]



AGCG

CGCT

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

S[GEADV]

[PEGRSA*IKTQVL]A

[EQK*][R]

R[FWSCY*L]

[PGFSRACYIDTNVLH]A

[SPAT][L]



AGCT

AGCT

GC content: **50 %**.

The overhang is palindromic, cannot be used for DNA assembly.

Can form the following amino acids in 6 translation frames:

S[FWSCY*L]

[PEGRSA*IKTQVL]A

[EQK*][L]

S[FWSCY*L]

[PEGRSA*IKTQVL]A

[EQK*][L]



AGGA

TCCT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

R[RSIKTNM]

[PEGRSA*IKTQVL]G

[EQK*][ED]

S[FWSCY*L]

[PGFSRACYIDTNVLH]P

[IVFL][L]



AGGG

CCCT

GC content: **75 %**.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

R[GEADV]

[PEGRSA*IKTQVL]G

[EQK*][G]

P[FWSCY*L]

[PGFSRACYIDTNVLH]P

[SPAT][L]



ACCT

AGGT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

T[FWSCY*L]

[PEGRSA*IKTQVL]P

[HDYN][L]

R[FWSCY*L]

[PEGRSA*IKTQVL]G

[EQK*][V]



AGTA

TACT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

S[RSIKTNM]

[PEGRSA*IKTQVL]V

[EQK*][Y*]

Y[FWSCY*L]

[PGFSRACYIDTNVLH]T

[IVL][L]



AGTG

CACT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

S[GEADV]

[PEGRSA*IKTQVL]V

[EQK*][WC*]

H[FWSCY*L]

[PGFSRACYIDTNVLH]T

[SPAT][L]



ATAT

ATAT

GC content: 0 %.

The overhang is palindromic, cannot be used for DNA assembly.

Can form the following amino acids in 6 translation frames:

I[FWSCY*L]

[PEGRSA*IKTQVL]Y

[HDYN][MI]

I[FWSCY*L]

[PEGRSA*IKTQVL]Y

[HDYN][MI]



ATCC

GGAT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

I[PRQLH]

[PEGRSA*IKTQVL]S

[HDYN][P]

G[FWSCY*L]

[PEGWRSA*KTQMVL]D

[RGW][MI]



ATCG

CGAT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

I[GEADV]

[PEGRSA*IKTQVL]S

[HDYN][R]

R[FWSCY*L]

[PGFSRACYIDTNVLH]D

[SPAT][MI]



AGAT

ATCT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

R[FWSCY*L]

[PEGRSA*IKTQVL]D

[EQK*][MI]

I[FWSCY*L]

[PEGRSA*IKTQVL]S

[HDYN][L]



ATGA

TCAT

GC content: **25 %**.

The overhang contains the start codon ATG.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

M[RSIKTNM]

[PEGRSA*IKTQVL]*

[HDYN][ED]

S[FWSCY*L]

[PGFSRACYIDTNVLH]H

[IVFL][MI]



ACAT

ATGT

GC content: **25 %**.

The overhang contains the start codon ATG.

Can form the following amino acids in 6 translation frames:

T[FWSCY*L]

[PEGRSA*IKTQVL]H

[HDYN][MI]

M[FWSCY*L]

[PEGRSA*IKTQVL]C

[HDYN][V]



ATTA

TAAT

GC content: 0 %.

Can form the following amino acids in 6 translation frames:

I[RSIKTNM]

[PEGRSA*IKTQVL]L

[HDYN][Y*]

*[FWSCY*L]

[PGFSRACYIDTNVLH]N

[IVL][MI]



ATTC

GAAT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

I[PRQLH]

[PEGRSA*IKTQVL]F

[HDYN][S]

E[FWSCY*L]

[PEGWRSA*KTQMVL]N

[RG*][MI]



AAAT

ATTT

GC content: 0 %.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

K[FWSCY*L]

[PEGRSA*IKTQVL]N

[EQK*][MI]

I[FWSCY*L]

[PEGRSA*IKTQVL]F

[HDYN][LF]



CAAA

TTTG

GC content: **25 %**.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

Q[RSIKTNM]

[PGFSRACYIDTNVLH]K

[SPAT][KN]

F[GEADV]

[PGFSRACYIDTNVLH]L

[IVFL][WC*]



CAAC

GTTG

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

Q[PRQLH]

[PGFSRACYIDTNVLH]N

[SPAT][T]

V[GEADV]

[PEGWRSA*KTQMVL]L

[SGCR][WC*]



ATTG

CAAT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

I[GEADV]

[PEGRSA*IKTQVL]L

[HDYN][WC*]

Q[FWSCY*L]

[PGFSRACYIDTNVLH]N

[SPAT][MI]



CACA

TGTG

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

H[RSIKTNM]

[PGFSRACYIDTNVLH]T

[SPAT][HQ]

C[GEADV]

[PGFSRACYIDTNVLH]V

[MVL][WC*]



CACC

GGTG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

H[PRQLH]

[PGFSRACYIDTNVLH]T

[SPAT][P]

G[GEADV]

[PEGWRSA*KTQMVL]V

[RGW][WC*]



CACG

CGTG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

H[GEADV]

[PGFSRACYIDTNVLH]T

[SPAT][R]

R[GEADV]

[PGFSRACYIDTNVLH]V

[SPAT][WC*]



CAGA

TCTG

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

Q[RSIKTNM]

[PGFSRACYIDTNVLH]R

[SPAT][ED]

S[GEADV]

[PGFSRACYIDTNVLH]L

[IVFL][WC*]



CATC

GATG

GC content: **50 %**.

The overhang contains the start codon ATG.

Can form the following amino acids in 6 translation frames:

H[PRQLH]

[PGFSRACYIDTNVLH]I

[SPAT][S]

D[GEADV]

[PEGWRSA*KTQMVL]M

[RG*][WC*]



CATG

CATG

GC content: **50 %**.

The overhang is palindromic, cannot be used for DNA assembly.

The overhang contains the start codon ATG.

Can form the following amino acids in 6 translation frames:

H[GEADV]

[PGFSRACYIDTNVLH]M

[SPAT][WC*]

H[GEADV]

[PGFSRACYIDTNVLH]M

[SPAT][WC*]



AATG

CATT

GC content: **25 %**.

The overhang contains the start codon ATG.

Can form the following amino acids in 6 translation frames:

N[GEADV]

[PEGRSA*IKTQVL]M

[EQK*][WC*]

H[FWSCY*L]

[PGFSRACYIDTNVLH]I

[SPAT][LF]



CCAC

GTGG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

P[PRQLH]

[PGFSRACYIDTNVLH]H

[SPAT][T]

V[GEADV]

[PEGWRSA*KTQMVL]W

[SGCR][G]



ATGG

CCAT

GC content: **50 %**.

The overhang contains the start codon ATG.

Can form the following amino acids in 6 translation frames:

M[GEADV]

[PEGRSA*IKTQVL]W

[HDYN][G]

P[FWSCY*L]

[PGFSRACYIDTNVLH]H

[SPAT][MI]



CCCA

TGGG

GC content: **75 %**.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

P[RSIKTNM]

[PGFSRACYIDTNVLH]P

[SPAT][HQ]

W[GEADV]

[PGFSRACYIDTNVLH]G

[MVL][G]



CCGC

GCGG

GC content: **100 %**.

Can form the following amino acids in 6 translation frames:

P[PRQLH]

[PGFSRACYIDTNVLH]R

[SPAT][A]

A[GEADV]

[PEGWRSA*KTQMVL]R

[SGCR][G]



CCGG

CCGG

GC content: **100 %**.

The overhang is palindromic, cannot be used for DNA assembly.

Can form the following amino acids in 6 translation frames:

P[GEADV]

[PGFSRACYIDTNVLH]R

[SPAT][G]

P[GEADV]

[PGFSRACYIDTNVLH]R

[SPAT][G]



ACGG

CCGT

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

T[GEADV]

[PEGRSA*IKTQVL]R

[HDYN][G]

P[FWSCY*L]

[PGFSRACYIDTNVLH]R

[SPAT][V]



CCTC

GAGG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

P[PRQLH]

[PGFSRACYIDTNVLH]L

[SPAT][S]

E[GEADV]

[PEGWRSA*KTQMVL]R

[RG*][G]



CAGG

CCTG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

Q[GEADV]

[PGFSRACYIDTNVLH]R

[SPAT][G]

P[GEADV]

[PGFSRACYIDTNVLH]L

[SPAT][WC*]



AAGG

CCTT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

K[GEADV]

[PEGRSA*IKTQVL]R

[EQK*][G]

P[FWSCY*L]

[PGFSRACYIDTNVLH]L

[SPAT][LF]



CGAC

GTCG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

R[PRQLH]

[PGFSRACYIDTNVLH]D

[SPAT][T]

V[GEADV]

[PEGWRSA*KTQMVL]S

[SGCR][R]



CGCA

TGCG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

R[RSIKTNM]

[PGFSRACYIDTNVLH]A

[SPAT][HQ]

C[GEADV]

[PGFSRACYIDTNVLH]A

[MVL][R]



CGCC

GGCG

GC content: **100 %**.

Can form the following amino acids in 6 translation frames:

R[PRQLH]

[PGFSRACYIDTNVLH]A

[SPAT][P]

G[GEADV]

[PEGWRSA*KTQMVL]A

[RGW][R]



CGCG

CGCG

GC content: **100 %**.

The overhang is palindromic, cannot be used for DNA assembly.

Can form the following amino acids in 6 translation frames:

R[GEADV]

[PGFSRACYIDTNVLH]A

[SPAT][R]

R[GEADV]

[PGFSRACYIDTNVLH]A

[SPAT][R]



CGGA

TCCG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

R[RSIKTNM]

[PGFSRACYIDTNVLH]G

[SPAT][ED]

S[GEADV]

[PGFSRACYIDTNVLH]P

[IVFL][R]



CCCCG

CGGGG

GC content: **100 %**.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

P[GEADV]

[PGFSRACYIDTNVLH]P

[SPAT][R]

R[GEADV]

[PGFSRACYIDTNVLH]G

[SPAT][G]



CGTA

TACG

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

R[RSIKTNM]

[PGFSRACYIDTNVLH]V

[SPAT][Y*]

Y[GEADV]

[PGFSRACYIDTNVLH]T

[IVL][R]



AACG

CGTT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

N[GEADV]

[PEGRSA*IKTQVL]T

[EQK*][R]

R[FWSCY*L]

[PGFSRACYIDTNVLH]V

[SPAT][LF]



CTAC

GTAG

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

L[PRQLH]

[PGFSRACYIDTNVLH]Y

[SPAT][T]

V[GEADV]

[PEGWRSA*KTQMVL]*

[SGCR][RS]



CTAG

CTAG

GC content: **50 %**.

The overhang is palindromic, cannot be used for DNA assembly.

Can form the following amino acids in 6 translation frames:

L[GEADV]

[PGFSRACYIDTNVLH]*

[SPAT][RS]

L[GEADV]

[PGFSRACYIDTNVLH]*

[SPAT][RS]



ATAG

CTAT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

I[GEADV]

[PEGRSA*IKTQVL]*

[HDYN][RS]

L[FWSCY*L]

[PGFSRACYIDTNVLH]Y

[SPAT][MI]



CTCC

GGAG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

L[PRQLH]

[PGFSRACYIDTNVLH]S

[SPAT][P]

G[GEADV]

[PEGWRSA*KTQMVL]E

[RGW][RS]



CGAG

CTCG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

R[GEADV]

[PGFSRACYIDTNVLH]E

[SPAT][RS]

L[GEADV]

[PGFSRACYIDTNVLH]S

[SPAT][R]



AGAG

CTCT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

R[GEADV]

[PEGRSA*IKTQVL]E

[EQK*][RS]

L[FWSCY*L]

[PGFSRACYIDTNVLH]S

[SPAT][L]



CCAG

CTGG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

P[GEADV]

[PGFSRACYIDTNVLH]Q

[SPAT][RS]

L[GEADV]

[PGFSRACYIDTNVLH]W

[SPAT][G]



CTTC

GAAG

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

L[PRQLH]

[PGFSRACYIDTNVLH]F

[SPAT][S]

E[GEADV]

[PEGWRSA*KTQMVL]K

[RG*][RS]



CAAG

CTTG

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

Q[GEADV]

[PGFSRACYIDTNVLH]K

[SPAT][RS]

L[GEADV]

[PGFSRACYIDTNVLH]L

[SPAT][WC*]



AAAG

CTTT

GC content: **25 %**.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

K[GEADV]

[PEGRSA*IKTQVL]K

[EQK*][RS]

L[FWSCY*L]

[PGFSRACYIDTNVLH]F

[SPAT][LF]



GAAA

TTTC

GC content: **25 %**.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

E[RSIKTNM]

[PEGWRSA*KTQMVL]K

[RG*][KN]

F[PRQLH]

[PGFSRACYIDTNVLH]F

[IVFL][S]



GAAC

GTTC

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

E[PRQLH]

[PEGWRSA*KTQMVL]N

[RG*][T]

V[PRQLH]

[PEGWRSA*KTQMVL]F

[SGCR][S]



GACC

GGTC

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

D[PRQLH]

[PEGWRSA*KTQMVL]T

[RG*][P]

G[PRQLH]

[PEGWRSA*KTQMVL]V

[RGW][S]



CGTC

GACG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

R[PRQLH]

[PGFSRACYIDTNVLH]V

[SPAT][S]

D[GEADV]

[PEGWRSA*KTQMVL]T

[RG*][R]



AGTC

GACT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

S[PRQLH]

[PEGRSA*IKTQVL]V

[EQK*][S]

D[FWSCY*L]

[PEGWRSA*KTQMVL]T

[RG*][L]



GAGC

GCTC

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

E[PRQLH]

[PEGWRSA*KTQMVL]S

[RG*][A]

A[PRQLH]

[PEGWRSA*KTQMVL]L

[SGCR][S]



ACTC

GAGT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

T[PRQLH]

[PEGRSA*IKTQVL]L

[HDYN][S]

E[FWSCY*L]

[PEGWRSA*KTQMVL]S

[RG*][V]



GATC

GATC

GC content: 50 %.

The overhang is palindromic, cannot be used for DNA assembly.

Can form the following amino acids in 6 translation frames:

D[PRQLH]

[PEGWRSA*KTQMVL]I

[RG*][S]

D[PRQLH]

[PEGWRSA*KTQMVL]I

[RG*][S]



GCAA

TTGC

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

A[RSIKTNM]

[PEGWRSA*KTQMVL]Q

[SGCR][KN]

L[PRQLH]

[PGFSRACYIDTNVLH]C

[IVFL][A]



CTGC

GCAG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

L[PRQLH]

[PGFSRACYIDTNVLH]C

[SPAT][A]

A[GEADV]

[PEGWRSA*KTQMVL]Q

[SGCR][RS]



ATGC

GCAT

GC content: **50 %**.

The overhang contains the start codon ATG.

Can form the following amino acids in 6 translation frames:

M[PRQLH]

[PEGRSA*IKTQVL]C

[HDYN][A]

A[FWSCY*L]

[PEGWRSA*KTQMVL]H

[SGCR][MI]



GCCC

GGGC

GC content: **100 %**.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

A[PRQLH]

[PEGWRSA*KTQMVL]P

[SGCR][P]

G[PRQLH]

[PEGWRSA*KTQMVL]G

[RGW][A]



CGGC

GCCG

GC content: **100 %**.

Can form the following amino acids in 6 translation frames:

R[PRQLH]

[PGFSRACYIDTNVLH]G

[SPAT][A]

A[GEADV]

[PEGWRSA*KTQMVL]P

[SGCR][R]



AGGC

GCCT

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

R[PRQLH]

[PEGRSA*IKTQVL]G

[EQK*][A]

A[FWSCY*L]

[PEGWRSA*KTQMVL]P

[SGCR][L]



GCGA

TCGC

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

A[RSIKTNM]

[PEGWRSA*KTQMVL]R

[SGCR][ED]

S[PRQLH]

[PGFSRACYIDTNVLH]R

[IVFL][A]



GCGC

GCGC

GC content: **100 %**.

The overhang is palindromic, cannot be used for DNA assembly.

Can form the following amino acids in 6 translation frames:

A[PRQLH]

[PEGWRSA*KTQMVL]R

[SGCR][A]

A[PRQLH]

[PEGWRSA*KTQMVL]R

[SGCR][A]



GCTA

TAGC

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

A[RSIKTNM]

[PEGWRSA*KTQMVL]L

[SGCR][Y*]

*[PRQLH]

[PGFSRACYIDTNVLH]S

[IVL][A]



CAGC

GCTG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

Q[PRQLH]

[PGFSRACYIDTNVLH]S

[SPAT][A]

A[GEADV]

[PEGWRSA*KTQMVL]L

[SGCR][WC*]



AAGC

GCTT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

K[PRQLH]

[PEGRSA*IKTQVL]S

[EQK*][A]

A[FWSCY*L]

[PEGWRSA*KTQMVL]L

[SGCR][LF]



GGAC

GTCC

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

G[PRQLH]

[PEGWRSA*KTQMVL]D

[RGW][T]

V[PRQLH]

[PEGWRSA*KTQMVL]S

[SGCR][P]



GGCC

GGCC

GC content: **100 %**.

The overhang is palindromic, cannot be used for DNA assembly.

Can form the following amino acids in 6 translation frames:

G[PRQLH]

[PEGWRSA*KTQMVL]A

[RGW][P]

G[PRQLH]

[PEGWRSA*KTQMVL]A

[RGW][P]



GGGA

TCCC

GC content: **75 %**.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

G[RSIKTNM]

[PEGWRSA*KTQMVL]G

[RGW][ED]

S[PRQLH]

[PGFSRACYIDTNVLH]P

[IVFL][P]



CCCC

GGGG

GC content: **100 %**.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

P[PRQLH]

[PGFSRACYIDTNVLH]P

[SPAT][P]

G[GEADV]

[PEGWRSA*KTQMVL]G

[RGW][G]



ACCC

GGGT

GC content: **75 %**.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

T[PRQLH]

[PEGRSA*IKTQVL]P

[HDYN][P]

G[FWSCY*L]

[PEGWRSA*KTQMVL]G

[RGW][V]



GTAA

TTAC

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

V[RSIKTNM]

[PEGWRSA*KTQMVL]*

[SGCR][KN]

L[PRQLH]

[PGFSRACYIDTNVLH]Y

[IVFL][T]



GTAC

GTAC

GC content: 50 %.

The overhang is palindromic, cannot be used for DNA assembly.

Can form the following amino acids in 6 translation frames:

V[PRQLH]

[PEGWRSA*KTQMVL]Y

[SGCR][T]

V[PRQLH]

[PEGWRSA*KTQMVL]Y

[SGCR][T]



ATAC

GTAT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

I[PRQLH]

[PEGRSA*IKTQVL]Y

[HDYN][T]

V[FWSCY*L]

[PEGWRSA*KTQMVL]Y

[SGCR][MI]



GTCA

TGAC

GC content: **50 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

V[RSIKTNM]

[PEGWRSA*KTQMVL]S

[SGCR][HQ]

*[PRQLH]

[PGFSRACYIDTNVLH]D

[MVL][T]



AGAC

GTCT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

R[PRQLH]

[PEGRSA*IKTQVL]D

[EQK*][T]

V[FWSCY*L]

[PEGWRSA*KTQMVL]S

[SGCR][L]



GTGA

TCAC

GC content: **50 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

V[RSIKTNM]

[PEGWRSA*KTQMVL]*

[SGCR][ED]

S[PRQLH]

[PGFSRACYIDTNVLH]H

[IVFL][T]



GCAC

GTGC

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

A[PRQLH]

[PEGWRSA*KTQMVL]H

[SGCR][T]

V[PRQLH]

[PEGWRSA*KTQMVL]C

[SGCR][A]



ACAC

GTGT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

T[PRQLH]

[PEGRSA*IKTQVL]H

[HDYN][T]

V[FWSCY*L]

[PEGWRSA*KTQMVL]C

[SGCR][V]



GTTA

TAAC

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

V[RSIKTNM]

[PEGWRSA*KTQMVL]L

[SGCR][Y*]

*[PRQLH]

[PGFSRACYIDTNVLH]N

[IVL][T]



CTTA

TAAG

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

L[RSIKTNM]

[PGFSRACYIDTNVLH]L

[SPAT][Y*]

*[GEADV]

[PGFSRACYIDTNVLH]K

[IVL][RS]



GGTA

TACC

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

G[RSIKTNM]

[PEGWRSA*KTQMVL]V

[RGW][Y*]

Y[PRQLH]

[PGFSRACYIDTNVLH]T

[IVL][P]



CCTA

TAGG

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

P[RSIKTNM]

[PGFSRACYIDTNVLH]L

[SPAT][Y*]

*[GEADV]

[PGFSRACYIDTNVLH]R

[IVL][G]



TATA

TATA

GC content: 0 %.

The overhang is palindromic, cannot be used for DNA assembly.

Can form the following amino acids in 6 translation frames:

Y[RSIKTNM]

[PGFSRACYIDTNVLH]I

[IVL][Y*]

Y[RSIKTNM]

[PGFSRACYIDTNVLH]I

[IVL][Y*]



GATA

TATC

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

D[RSIKTNM]

[PEGWRSA*KTQMVL]I

[RG*][Y*]

Y[PRQLH]

[PGFSRACYIDTNVLH]I

[IVL][S]



CATA

TATG

GC content: **25 %**.

The overhang contains the start codon ATG.

Can form the following amino acids in 6 translation frames:

H[RSIKTNM]

[PGFSRACYIDTNVLH]I

[SPAT][Y*]

Y[GEADV]

[PGFSRACYIDTNVLH]M

[IVL][WC*]



TCAA

TTGA

GC content: **25 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

S[RSIKTNM]

[PGFSRACYIDTNVLH]Q

[IVFL][KN]

L[RSIKTNM]

[PGFSRACYIDTNVLH]*

[IVFL][ED]



CTGA

TCAG

GC content: **50 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

L[RSIKTNM]

[PGFSRACYIDTNVLH]*

[SPAT][ED]

S[GEADV]

[PGFSRACYIDTNVLH]Q

[IVFL][RS]



TCGA

TCGA

GC content: 50 %.

The overhang is palindromic, cannot be used for DNA assembly.

Can form the following amino acids in 6 translation frames:

S[RSIKTNM]

[PGFSRACYIDTNVLH]R

[IVFL][ED]

S[RSIKTNM]

[PGFSRACYIDTNVLH]R

[IVFL][ED]



CCGA

TCGG

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

P[RSIKTNM]

[PGFSRACYIDTNVLH]R

[SPAT][ED]

S[GEADV]

[PGFSRACYIDTNVLH]R

[IVFL][G]



TAGA

TCTA

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

*[RSIKTNM]

[PGFSRACYIDTNVLH]R

[IVL][ED]

S[RSIKTNM]

[PGFSRACYIDTNVLH]L

[IVFL][Y*]



GAGA

TCTC

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

E[RSIKTNM]

[PEGWRSA*KTQMVL]R

[RG*][ED]

S[PRQLH]

[PGFSRACYIDTNVLH]L

[IVFL][S]



AAGA

TCTT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

K[RSIKTNM]

[PEGRSA*IKTQVL]R

[EQK*][ED]

S[FWSCY*L]

[PGFSRACYIDTNVLH]L

[IVFL][LF]



TGAA

TTCA

GC content: **25 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

*[RSIKTNM]

[PGFSRACYIDTNVLH]E

[MVL][KN]

F[RSIKTNM]

[PGFSRACYIDTNVLH]S

[IVFL][HQ]



CTCA

TGAG

GC content: **50 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

L[RSIKTNM]

[PGFSRACYIDTNVLH]S

[SPAT][HQ]

*[GEADV]

[PGFSRACYIDTNVLH]E

[MVL][RS]



ATCA

TGAT

GC content: **25 %**.

The overhang contains a stop codon (TAA, TAG or TGA).

Can form the following amino acids in 6 translation frames:

I[RSIKTNM]

[PEGRSA*IKTQVL]S

[HDYN][HQ]

*[FWSCY*L]

[PGFSRACYIDTNVLH]D

[MVL][MI]



TGCA

TGCA

GC content: **50 %**.

The overhang is palindromic, cannot be used for DNA assembly.

Can form the following amino acids in 6 translation frames:

C[RSIKTNM]

[PGFSRACYIDTNVLH]A

[MVL][HQ]

C[RSIKTNM]

[PGFSRACYIDTNVLH]A

[MVL][HQ]



GGCA

TGCC

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

G[RSIKTNM]

[PEGWRSA*KTQMVL]A

[RGW][HQ]

C[PRQLH]

[PGFSRACYIDTNVLH]A

[MVL][P]



AGCA

TGCT

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

S[RSIKTNM]

[PEGRSA*IKTQVL]A

[EQK*][HQ]

C[FWSCY*L]

[PGFSRACYIDTNVLH]A

[MVL][L]



TCCA

TGGA

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

S[RSIKTNM]

[PGFSRACYIDTNVLH]P

[IVFL][HQ]

W[RSIKTNM]

[PGFSRACYIDTNVLH]G

[MVL][ED]



GCCA

TGGC

GC content: **75 %**.

Can form the following amino acids in 6 translation frames:

A[RSIKTNM]

[PEGWRSA*KTQMVL]P

[SGCR][HQ]

W[PRQLH]

[PGFSRACYIDTNVLH]G

[MVL][A]



TACA

TGTA

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

Y[RSIKTNM]

[PGFSRACYIDTNVLH]T

[IVL][HQ]

C[RSIKTNM]

[PGFSRACYIDTNVLH]V

[MVL][Y*]



GACA

TGTC

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

D[RSIKTNM]

[PEGWRSA*KTQMVL]T

[RG*][HQ]

C[PRQLH]

[PGFSRACYIDTNVLH]V

[MVL][S]



TTAA

TTAA

GC content: 0 %.

The overhang is palindromic, cannot be used for DNA assembly.

Can form the following amino acids in 6 translation frames:

L[RSIKTNM]

[PGFSRACYIDTNVLH]*

[IVFL][KN]

L[RSIKTNM]

[PGFSRACYIDTNVLH]*

[IVFL][KN]



CTAA

TTAG

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

L[RSIKTNM]

[PGFSRACYIDTNVLH]*

[SPAT][KN]

L[GEADV]

[PGFSRACYIDTNVLH]*

[IVFL][RS]



ATAA

TTAT

GC content: **0 %**.

Can form the following amino acids in 6 translation frames:

I[RSIKTNM]

[PEGRSA*IKTQVL]*

[HDYN][KN]

L[FWSCY*L]

[PGFSRACYIDTNVLH]Y

[IVFL][MI]



GGAA

TTCC

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

G[RSIKTNM]

[PEGWRSA*KTQMVL]E

[RGW][KN]

F[PRQLH]

[PGFSRACYIDTNVLH]S

[IVFL][P]



CGAA

TTCG

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

R[RSIKTNM]

[PGFSRACYIDTNVLH]E

[SPAT][KN]

F[GEADV]

[PGFSRACYIDTNVLH]S

[IVFL][R]



AGAA

TTCT

GC content: **25 %**.

Can form the following amino acids in 6 translation frames:

R[RSIKTNM]

[PEGRSA*IKTQVL]E

[EQK*][KN]

F[FWSCY*L]

[PGFSRACYIDTNVLH]S

[IVFL][L]



CCAA

TTGG

GC content: **50 %**.

Can form the following amino acids in 6 translation frames:

P[RSIKTNM]

[PGFSRACYIDTNVLH]Q

[SPAT][KN]

L[GEADV]

[PGFSRACYIDTNVLH]W

[IVFL][G]



TAAA

TTTA

GC content: 0 %.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

*[RSIKTNM]

[PGFSRACYIDTNVLH]K

[IVL][KN]

F[RSIKTNM]

[PGFSRACYIDTNVLH]L

[IVFL][Y*]



AAAA

TTTT

GC content: 0 %.

Has 3 identical bases in a row. However, this has not shown to be very important.

Can form the following amino acids in 6 translation frames:

K[RSIKTNM]

[PEGRSA*IKTQVL]K

[EQK*][KN]

F[FWSCY*L]

[PGFSRACYIDTNVLH]F

[IVFL][LF]

Appendix

The report consists of 3 sections: summary, overhangs, appendix.

Summary page(s)

The first page summarises the compendium.

Overhang pages

Each overhang is analysed separately. The result is summarised with a symbol:

☑ : good overhang

☒ : unusable palindromic sequence

Overhangs are unpaired nucleotides at the end of a double-stranded linear DNA molecule. Overhangs can be on either strand; 5' or 3' overhangs. After DNA ligation with another DNA with a complementary overhang, these remain in the sequence as fusion sites ("scars").

Overhang sets

Use the [GoldenHinges](#) Python package to generate a set of mutually compatible overhangs that can be used for DNA assembly.