# Case 6:

Brentuximab Vedotin

```
QIQLQQSGPE VVKPGASVKI
SCKASGYTFT DYYITWVKQK
PGQGLEWIGW ...

QIQLQQSGPE VVKPGASVKI
SCKASGYTFT DYYITWVKQK
PGQGLEWIGW ...
```

**Modified**

New Protein
New Substance
Amino Acid Sequence
Monoclonal Antibody
Glycosylation
Variable substitution
Modification

# Premise:

Well-populated System

Protein NOT registered
Modified Cysteine Residue NOT registered

GINAS

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*Register New:*

Substance | Product

Single Substance | Mixture Substance | Specified Substance | Not Sure

Chemical | Protein | Nucleic Acid | Structurally Diverse | Polymer

## Add Name

*Name:*

Brentuximab Vedotin

*Language:* English

*Domain:* Drug

*Name Type:* Official Name

*Public Domain:*

*Naming Org:* INN

*Deprecated:*

*Official Jurisdiction:* US NL CA DE

Add / Select References

*(0 references)*

Please select a reference.

Cancel Done

## Add Name

*Name:*

Brentuximab Vedotin

*Language:* English

*Domain:* Drug

*Name Type:* Official Name

*Public Domain:* ☑

*Naming Org:* INN

*Deprecated:* ☐

*Official Jurisdiction:* US NL CA DE

Add / Select References

*(1 reference)*

| *Type* | *Citation* | *URL* |
|---|---|---|
| INN List | Proposed List 103 | http://whqlibdoc.who... |

Cancel Done

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*Enter Names for Substance:*

| Name: | Type: | Language: | Domain: | Preferred: |
|---|---|---|---|---|
| Brentuximab Vedotin | Official | English | Drug | ☑ |
| Brentuximabum Vedoti... | Official | Latin | Drug | ☐ |
| брентуксимаб ведотин | Official | Russian | Drug | ☐ |
| برانتوكسيماب فيدوتين | Official | Arabic | Drug | ☐ |

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## Register New Protein:

Protein Type: Monoclonal Antibody

Protein subtype: IGG2

## Sequence Origin:

Source Organism Type: Human

## Amino Acid Sequence:

Total number of Subunits: 4

### Subunit 1:

Length: 446

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPG
```

N-Terminus (Duplicate Below) C-Terminus

### Subunit 2:

Length: 0

Disulfide Bridges 0 | Glycosylation 0 | Modifications 0

Add / Select References (0 references)

## Amino Acid Sequence:

Total number of Subunits: 4

### Subunit 2:

Length: 446

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPG
```

N-Terminus (Duplicate Below) C-Terminus

### Subunit 3:

Length: 0

Disulfide Bridges 0 | Glycosylation 0 | Modifications 0

Add / Select References (0 references)

## Amino Acid Sequence:

Total number of Subunits: 4

### Subunit 3:

Length: 218

```
DIVLTQSPAS LAVSLGQRAT ISCKASQSVD FDGDSYMNWY QQKPGQPPKV
LIYAASNLES GIPARFSGSG SGTDFTLNIH PVEEEDAATY YCQQSNEDPW
TFGGGTKLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV
THQGLSSPVT KSFNRGEC
```

N-Terminus (Duplicate Below) C-Terminus

### Subunit 4:

Length: 0

N-Terminus C-Terminus

Disulfide Bridges 0 | Glycosylation 0 | Modifications 0

Add / Select References (0 references)

## Amino Acid Sequence:

Total number of Subunits: 4

### Subunit 3:

Length: 218

```
DIVLTQSPAS LAVSLGQRAT ISCKASQSVD FDGDSYMNWY QQKPGQPPKV
LIYAASNLES GIPARFSGSG SGTDFTLNIH PVEEEDAATY YCQQSNEDPW
TFGGGTKLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV
THQGLSSPVT KSFNRGEC
```

N-Terminus (Duplicate Below) C-Terminus

### Subunit 4:

Length: 218

```
DIVLTQSPAS LAVSLGQRAT ISCKASQSVD FDGDSYMNWY QQKPGQPPKV
LIYAASNLES GIPARFSGSG SGTDFTLNIH PVEEEDAATY YCQQSNEDPW
TFGGGTKLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV
```

Disulfide Bridges 0 | Glycosylation 0 | Modifications 0

Add / Select References (0 references)

# Disulfide Bridges

**Subunit 1:** *Length: 446*

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
```

32 cysteine residues unspecified

*From:* *To:*

*Add disulfide bridge*

Done

# Disulfide Bridges

**Subunit 1:**

(1-22)
(click to select)

*Length: 446*

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
```

32 cysteine residues unspecified

| *From:* | | *To:* | | |
|---|---|---|---|---|
| 1-22 | Select | | Select | ✖ |

*Add disulfide bridge* ✚

Done

# Disulfide Bridges

**Subunit 1:**

(1-96)
(click to select)

*Length: 446*

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
```

30 cysteine residues unspecified

| *From:* | | *To:* | | |
|---|---|---|---|---|
| 1-22 | Select | 1-96 | Select | ✖ |

*Add disulfide bridge* ✚

Done

# Disulfide Bridges

**Subunit 1:** *Length: 446*

(1-144)
(click to select)

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQR
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
```

30 cysteine residues unspecified

| From: | | To: | |
|---|---|---|---|
| 1-22 | Select | 1-96 | Select |
| 1-144 | Select | | Select |

*Add disulfide bridge*

Done

# Disulfide Bridges

**Subunit 1:** *Length: 446*

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCAR
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
```

(1-200)
(click to select)

28 cysteine residues unspecified

| From: | | To: | |
|---|---|---|---|
| 1-22 | Select | 1-96 | Select |
| 1-144 | Select | 1-200 | Select |

*Add disulfide bridge*

Done

# Disulfide Bridges

**Subunit 1:** *Length: 446*

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAKT TPPSVYPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
```

(1-220)
(click to select)

24 cysteine residues unspecified

| From: | | To: | |
|---|---|---|---|
| 1-367 | Select | 1-425 | Select |
| 1-220 | Select | | Select |

*Add disulfide bridge*

Done

# Disulfide Bridges

**Subunit 3:** *Length: 218*

```
DIVLTQSPAS LAVSLGQRAT ISCKASQSVD FDGDSYMNWY QQKPGQPPKV
LIYAASNLES GIPARFSGSG SGTDFTLNIH PVEEEDAATY YCQQSNEDPW
TFGGGTKLEI KRTVLAAPSV IIFPPSDEQLK SGTASVVCLL NNFYPREAKV
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV
THQGLSSPVT KSFNRGEC
```

(3-218)
(click to select)

N-Terminus C-Terminus

22 cysteine residues unspecified

| From: | | To: | |
|---|---|---|---|
| 1-367 | Select | 1-425 | Select |
| 1-220 | Select | 3-218 | Select |

*Add disulfide bridge*

Done

# Disulfide Bridges

**Subunit 1:** *Length: 446*

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTS(1-226)F MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KG(click to select)SKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
```

24 cysteine residues unspecified

| From: | | To: | |
|---|---|---|---|
| 1-367 | Select | 1-425 | Select |
| 1-220 | Select | 3-218 | Select |
| 1-226 | Select | | Select |

*Add disulfide bridge*

Done

# Disulfide Bridges

**Subunit 2:** *Length: 446*

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTS(2-226) MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KG(click to select)SKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
```

22 cysteine residues unspecified

| From: | | To: | |
|---|---|---|---|
| 1-367 | Select | 1-425 | Select |
| 1-220 | Select | 3-218 | Select |
| 1-226 | Select | 2-226 | Select |

*Add disulfide bridge*

Done

# Disulfide Bridges

**Subunit 2:** *Length: 446*

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAKT TAPSVYPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
```

(2-220)
(click to select)

10 cysteine residues unspecified

| *From:* | | *To:* | |
|---|---|---|---|
| 2-367 | Select | 2-425 | Select |
| 2-220 | Select | | Select |

*Add disulfide bridge*

Done

# Disulfide Bridges

**Subunit 4:** *Length: 218*

```
DIVLTQSPAS LAVSLGQRAT ISCKASQSVD FDGDSYMNWY QQKPGQPPKV
LIYAASNLES GIPARFSGSG SGTDFTLNIH PVEEEDAATY YCQQSNEDPW
TFGGGTKLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV
THQGLSSPVT KSFNRGEC
```

(4-218)
(click to select)

N-Terminus C-Terminus

8 cysteine residues unspecified

| From: | | To: | |
|---|---|---|---|
| 2-367 | Select | 2-425 | Select |
| 2-220 | Select | 4-218 | Select |

*Add disulfide bridge*

Done

# Disulfide Bridges

**Subunit 4:** *Length: 218*

```
DIVLTQSPAS LAVSLGQRAT ISCKASQSVD FDGDSYMNWY QQKPGQPPKV
LIYAASNLES GIPARFSGSG SGTDFTLNIH PVEEEDAATY YCQQSNEDPW
TFGGGTKLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV
THQGLSSPVT KSFNRGEC
```

(4-198)
(click to select)

N-Terminus C-Terminus

0 cysteine residues unspecified

| From: | | To: | |
|---|---|---|---|
| 4-23 | Select | 4-92 | Select |
| 4-138 | Select | 4-198 | Select |

*Add disulfide bridge*

Done

## Amino Acid Sequence:

Total number of Subunits: 4

### Subunit 1:

Length: 446

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPG
```

N-Terminus (Duplicate Below) C-Terminus

### Subunit 2:

Length: 446

Disulfide Bridges 16 | Glycosylation 0 | Modifications 0

Add / Select References (0 references)

GINAS

Peryeat logout

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*Amino Acid Sequence:*

*Total number of Subunits:* 4

Subunit 1: *Length: 446*

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQP
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYT
```

N-Terminus (Duplicate Below) C-Terminus

Structural 0

Agent 0

Physical 0

Modifications 0

Subunit 2: *Length: 446*

Disulfide Bridges 16

Glycosylation 0

Add / Select References *(0 references)*

GINAS

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Home Search Download Register Admin

*Amino Acid Sequence:*

*Total number of Subunits:* 4

Subunit 1: *Length: 446*

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQP
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYT
```

N-Terminus (Duplicate Below) C-Terminus

Structural 0 | Add New

Agent 0

Physical 0

Modifications 0

Subunit 2: *Length: 446*

Disulfide Bridges 16 | Glycosylation 0

Add / Select References *(0 references)*

## Structural Modification

*Type:* Amino Acid Replacement

*Location:* Residue-Specific

*Residue:* C (Cysteine)

*Extent:* Partial

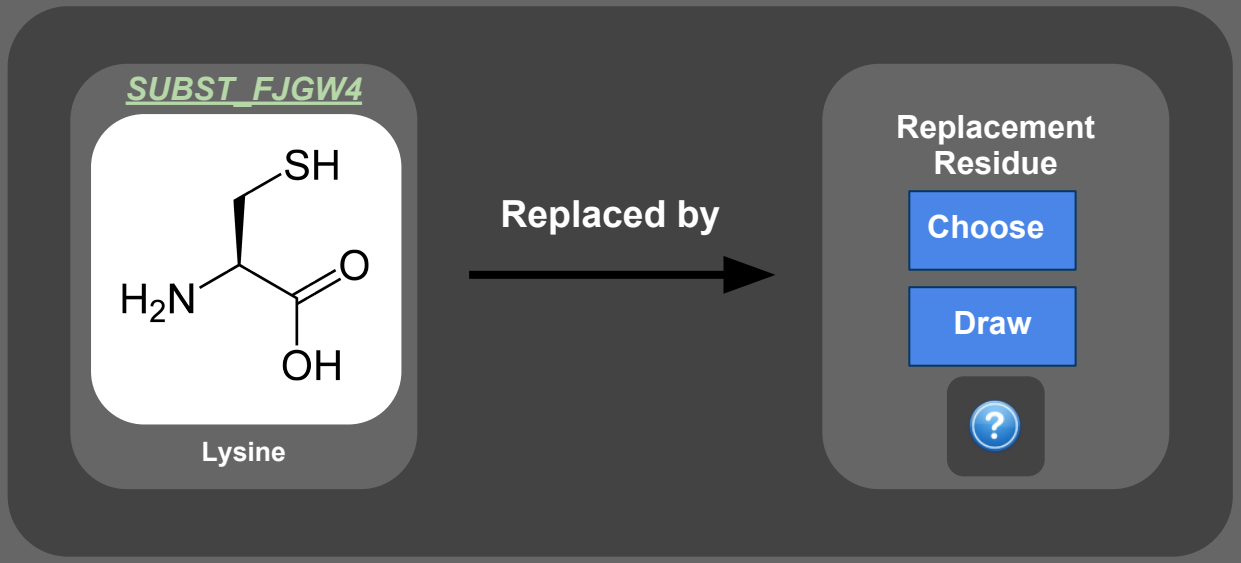
Number

| | *Avg:* | *Low:* | *High:* |
|---|---|---|---|
| Residues Replaced: | 4 | 3 | 5 |

Cancel Next

# Structural Modification

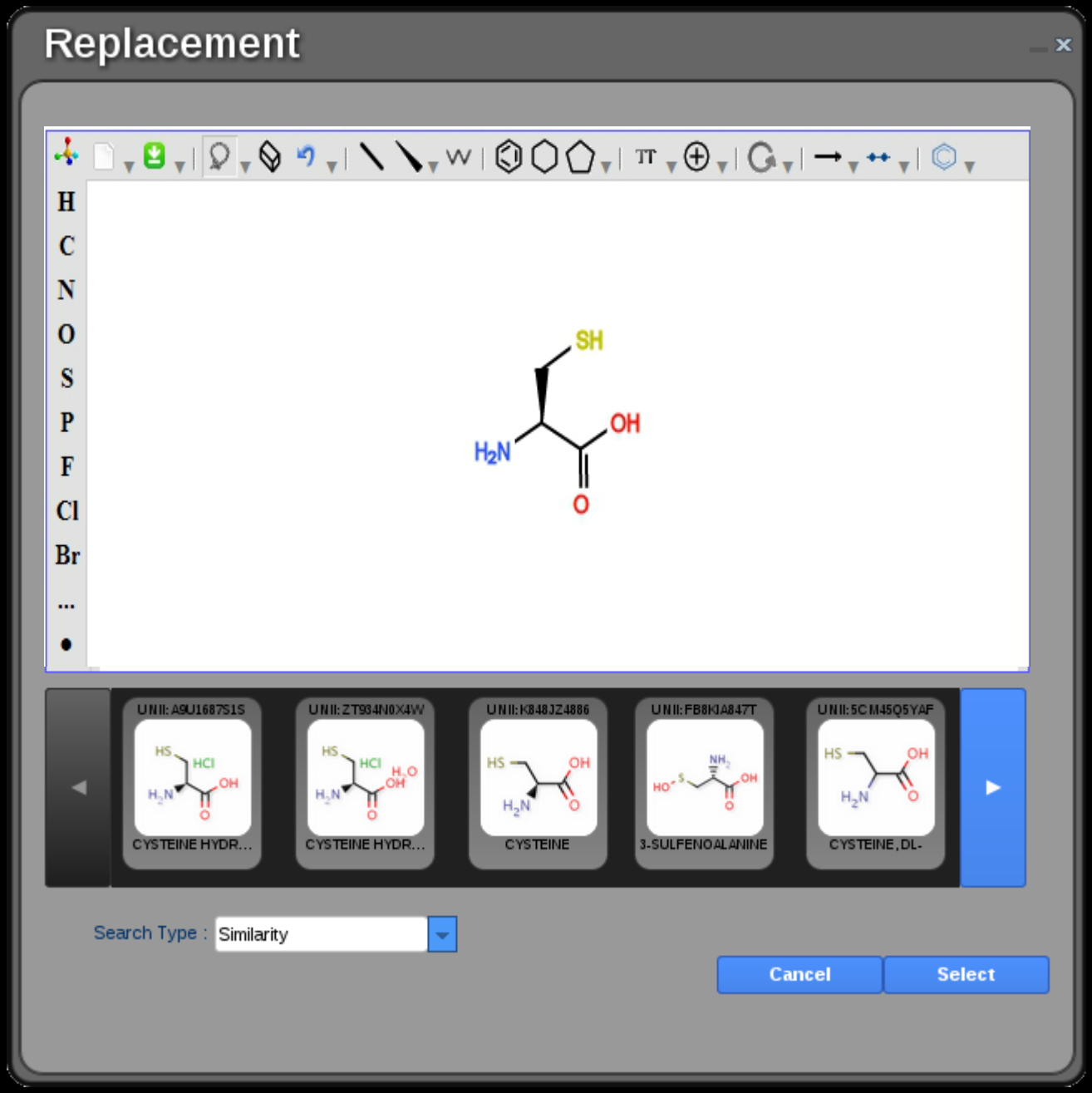
*Replacement :*



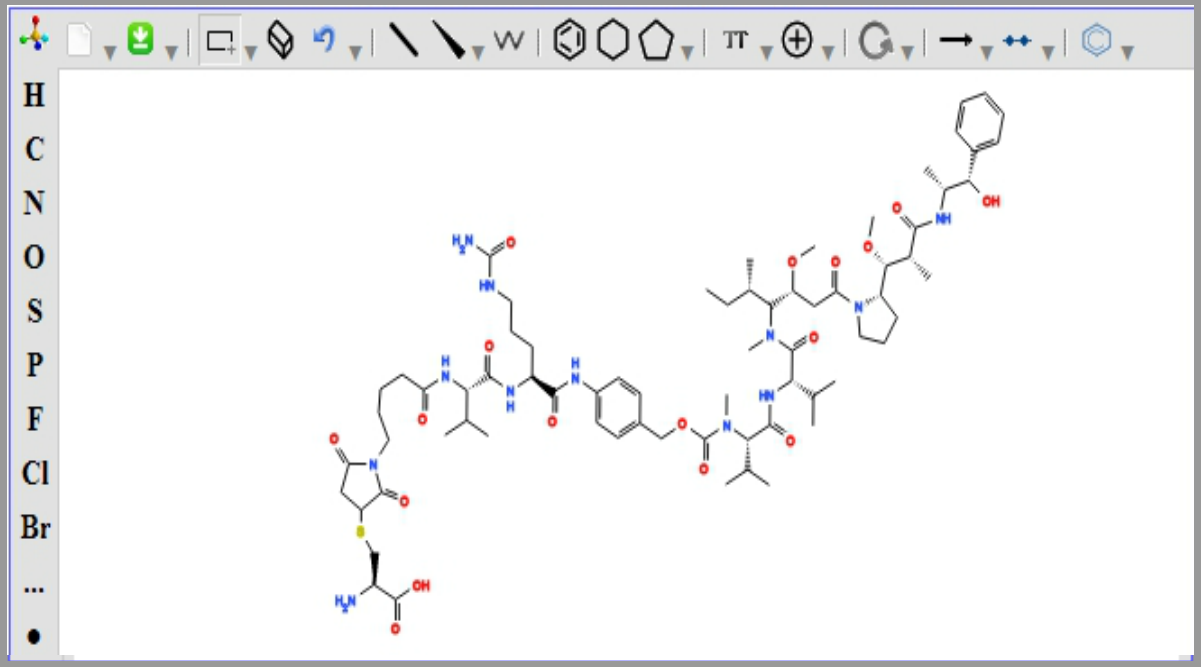

Previous

Cancel

Finish


Replacement
H
C
N
O
S
P
F
Cl
Br
...
SH
OH
H2N
O
UNII: A9U1687S1S
CYSTEINE HYDR...
UNII: ZT934N0X4W
CYSTEINE HYDR...
UNII: K848JZ4886
CYSTEINE
UNII: FB8KJA847T
3-SULFENOALANINE
UNII: 5CM45Q5YAF
CYSTEINE, DL-
Search Type :
Similarity
Cancel
Select

# Replacement




Search Type : Similarity

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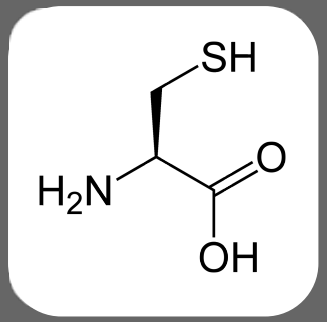
# Structural Modification

***Replacement :***

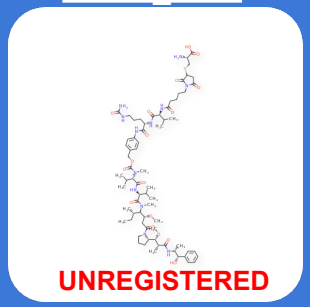
***SUBST_FJGW4***




Cysteine

**Replaced by**

***NSUB_5832***



**UNREGISTERED**

**TO BE NAMED**

Previous

Cancel

Finish

## Amino Acid Sequence:

Total number of Subunits: 4

### Subunit 1:

Length: 446

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPG
```

N-Terminus (Duplicate Below) C-Terminus

### Subunit 2:

Length: 446

Disulfide Bridges 16 | Glycosylation 0 | Modifications 1

Add / Select References (0 references)

GINAS

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*Amino Acid Sequence:*

*Total number of Subunits:* 4

Subunit 1: *Length: 446*

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
LPPSRDELTK NQVSLTCL PENN YKTTPPVLDS
DGSFFLYSKL TVDKSRWQ TQKS LSLSPG
```

N-Terminus C-Terminus

| | |
|---|---|
| C-Glycosylation | 0 |
| N-Glycosylation | 0 |
| O-Glycosylation | 0 |

Subunit 2: *Length: 446*

Disulfide Bridges 16 | Glycosylation 0 | Modifications 1

Add / Select References *(0 references)*

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*Amino Acid Sequence:*

*Total number of Subunits:* 4

Subunit 1: *Length: 446*

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
LPPSRDELTK NQVSLTCL PENN YKTTPPVLDS
DGSFFLYSKL TVDKSRWQ TQKS LSLSPG
```

N-Terminus C-Terminus

C-Glycosylation 0

N-Glycosylation 0

O-Glycosylation 0

*Add New*

Subunit 2: *Length: 446*

Disulfide Bridges 16

Glycosylation 0

Modifications 1

Add / Select References

*(0 references)*

# N-Glycosylation

**Subunit 1:** *Length: 447*

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
```

2 predicted N-Glycosylation sites unmarked

*Add Glycosylation Site*

Glycosylation Type

**Mammalian**

**Done**

# N-Glycosylation

**Subunit 1:** *Length: 447*

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
```

(1-297)
(click to select)

1 predicted N-Glycosylation sites unmarked

***Site:***

1-297 | Select

***Add Glycosylation Site***

Glycosylation Type

**Mammalian**

**Done**

# N-Glycosylation

**Subunit 2:** *Length: 447*

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
```

(2-297)
(click to select)

0 predicted N-Glycosylation sites unmarked

***Site:***

| | | |
|---|---|---|
| 1-297 | Select | ✖ |
| 2-297 | Select | ✖ |
| *Add Glycosylation Site* | | ✚ |

Glycosylation Type

Mammalian

Done

GINAS

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## Amino Acid Sequence:

Total number of subunits: 4

Notes: <none>
(click to edit)

### Subunit 1:

Length: 446

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPG
```

N-Terminus (Duplicate Below) C-Terminus

### Subunit 2:

Length: 446

Disulfide Bridges 16 | Glycosylation 2 | Modifications 1

Add / Select References (0 references)

GINAS

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## Amino Acid Sequence:

Total number of subunits: 4

Notes: <none>
(click to edit)

### Subunit 1:

Length: 446

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPG
```

N-Terminus (Duplicate Below) C-Terminus

### Subunit 2:

Length: 446

Disulfide Bridges 16 | Glycosylation 2 | Modifications 1

Add / Select References (0 references)

## Add / Modify Note

Subunit 1 is "Heavy chain"

Remove

Cancel

Save

## Amino Acid Sequence:

Notes: Subunit 1 is "Heavy chain"
(click to edit)

Total Number of Subunits: 4

### Subunit 1:

Length: 446

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPG
```

N-Terminus (Duplicate Below) C-Terminus

### Subunit 2:

Length: 446

Disulfide Bridges 16 | Glycosylation 2 | Modifications 1

Add / Select References (0 references)

***Modifications:***

***Are there more modifications to the substance?*** Yes No

GINAS

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*Ready to Register new Substance* *(pending 1 component registration)*

Sequence 4 | Modifications 1 | Disulfide Bridges 16 | Glycosylation 2

Subunit 1: *Length: 446*

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
```

Names 9 | References 2 | Relationships 0 | Notes 4 | Properties 0

| *Name* | *Lang.* | *Dom.* | *Type* | *Preferred:* |
|---|---|---|---|---|
| Brentuximab Vedotin | English | Drug | Official | ☑ |
| Brentuximabum Vedoti... | Latin | Drug | Official | ☐ |

Register Component | Register Substance

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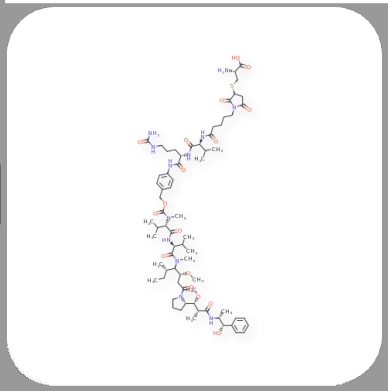
UNREGISTERED MOIETY



Moiety 1 of 1

Defined Stereocenters: 13

Total Stereocenters: 13

E / Z centers: 0

Charge: 0

Molecular Formula:

$C_{70}H_{11}0N_{12}O_{17}S$

Molecular Weight:

1423.7692

## Stereochemistry

Achiral | Absolute | Mixed | Racemic | Epimeric | Unknown

## Optical Activity

( + / - ) | ( + ) | ( - ) | None | Unspecified

*Is there atropisomerism?* Yes No

## Structure References

Add / Select References *(1 reference)*

| Type | Citation | URL |
|---|---|---|
| INN List | Proposed List 101 | http://whqlibdoc.who... |

GINAS

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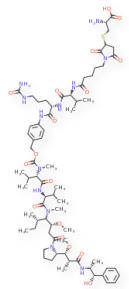
*Ready to Register new Substance*



Absolute

| | |
|---|---|
| Molecular Formula: | $C_{70}H_{11}0N_{12}O_{17}S$ |
| Molecular Weight: | 1423.7692 |

| | |
|---|---|
| Defined Stereocenters: | 13 |
| Total Stereocenters: | 13 |
| E / Z centers: | 0 |
| Charge: | 0 |

Names 0 | References 2 | Relationships 1 | Notes 0 | Properties 0

| Name | Lang. | Dom. | Type | Preferred: |
|---|---|---|---|---|
| Vedotin, Cysteine ... | English | Drug | Common | ✓ |

Add Reference

Register Substance

GINAS

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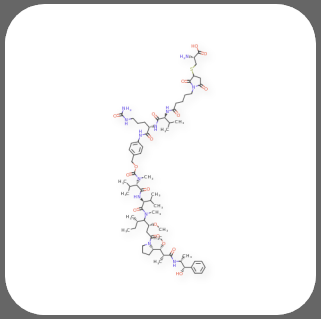
**Successfully submitted *Single Protein Substance:***

***SUBST_753C2***



**Vedotin, Cysteine ...**

***Is there a more specific physical form of this substance?*** Yes No

**In progress:**

***Brentuximab Vedotin*** Resume Registration

GINAS

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*Ready to Register new Substance*

Sequence 4 | Modifications 1 | Disulfide Bridges 16 | Glycosylation 2

Subunit 1: *Length: 446*

```
QIQLQQSGPE VVKPGASVKI SCKASGYTFT DYYITWVKQK PGQGLEWIGW
IYPGSGNTKY NEKFKGKATL TVDTSSSTAF MQLSSLTSED TAVYFCANYG
NYWFAYWGQG TQVTVSAAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
```

Names 9 | References 2 | Relationships 1 | Notes 4 | Properties 0

| *Name* | *Lang.* | *Dom.* | *Type* | *Preferred:* |
|---|---|---|---|---|
| Brentuximab Vedotin | English | Drug | Official | ☑ |
| Brentuximabum Vedoti... | Latin | Drug | Official | ☐ |

Register Substance

GINAS

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**Successfully submitted *Single Protein Substance:***

***SUBST_G9823***

```
QIQLQQSGPE VVKPGASVKI
SCKASGYTFT DYYITWVKQK
PGQGLEWIGW ...

QIQLQQSGPE VVKPGASVKI
SCKASGYTFT DYYITWVKQK
PGQGLEWIGW ...
```

Modified

**Brentuximab Vedotin**

***Is there a more specific physical form of this substance?*** Yes No ?