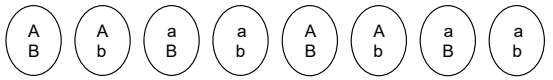
| | |
|---|---|
| 3(a)(i) | *if DNA or thymine stated within response, allow only H-bond mark (**ecf**)*<br><br>*any **two** from:*<br>(paired section) contains, complementary nucleotides / complementary bases / base pairs ;<br>adenine-uracil and guanine/cytosine ; **A** A/U and G/C<br>(paired by) hydrogen / H, bonds ; **I** strong (bonds) **ecf** from mp1<br>**R** if another bond also named<br>**I** phosphodiester bonds between, adjacent / AW, nucleotides |
| 3(a)(ii) | *any **two** from:*<br>(enzyme / Drosha / Dicer) active site is specific (to site on dsRNA) ;<br>*can apply in context of specific shaped active site or active site specific to a particular location*<br><br>detail of different active sites of Drosha and Dicer ;<br>site to be cleaved / AW, (only), fits into / can bind with / is complementary to (the specific) active site<br>forms enzyme-substrate complex at a particular site<br><br>Drosha and Dicer require different, conditions / cell locations, to function ;<br><br>AVP ; e.g. *suggestion that* Dicer too large to enter nucleus<br>Drosha exposed to degradation in cytoplasm |
| 3(b) | *any **two** from:*<br>mRNA is single-stranded and siRNA is double-stranded ;<br>**A** polynucleotide / chain, for strand<br><br>siRNA has paired and unpaired nucleotides<br>**or**<br>mRNA has, only unpaired nucleotides / no base pairing ;<br><br>mRNA codes for a, sequence of amino acids / protein ; **ora** for siRNA<br><br>mRNA has a longer sequence of nucleotides ;<br>**A** mRNA, is longer / has more nucleotides<br><br>AVP ; e.g. *ref. to* siRNA antiparallel / mRNA only 5' to 3'<br>mRNA has no H bonds |
| 3(c)(i) | *any **one** from:*<br>RISC must, align with / attach to / form H bonds with, (target) mRNA ;<br><br>(passenger strand needs to be, separated / released) to allow guide strand to, be exposed / bind to mRNA ; AW<br>**ora** e.g. (otherwise) guide strand cannot bind to mRNA<br>passenger strand prevents guide strand binding<br><br>guide strand has complementary sequence to target sequence of mRNA ;<br>**ora** passenger strand does not …. |





| | |
|---|---|
| 3(c)(ii) | *allow protein for polypeptide*<br>*points need the correct context of cleaved mRNA*<br><br>*any **three** from:*<br><br>*no protein formed*<br>**1** *idea that* mRNA may be degraded in cell before attaching to ribosome ;<br><br>**2** mRNA may not (be able to) attach to ribosome so no, polypeptide formed / translation ;<br><br>**3** cleaved mRNA results in loss of start, sequence / codon ;<br><br>*abnormal polypeptide formed*<br>**4** polypeptide chain is not released from ribosome ;<br>**A** cleaved mRNA results in loss of stop codon<br><br>**5** polypeptide chain degraded within cytoplasm / AW ;<br><br>**6** cleaved mRNA results in short(er) (polypeptide) chain being produced ;<br><br>**7** polypeptide does not, fold up / form correct tertiary structure / form correct 3D shape ; **I** tertiary structure changes<br><br>**8,9** AVP ; e.g. (results in) different R-group interactions / change in number of bonds that can form<br>active site / site of activity, changed / lost |



| | |
|---|---|
| 1(a)(i) | AABB AABb AaBB AaBb ; ; |
| 1(a)(ii) | long chocolate ; |
| 1(b) |  ;<br><br>**AB** / **Ab** / **aB** / **Ab**<br>**AB**: AABB, AABb, AaBB, AaBb<br>**Ab**: AABb, AAbb, AaBb, Aabb<br>**aB**: AaBB, AaBb, aaBB, aaBb<br>**Ab**: AaBb, Aabb, aaBb, aabb ;<br><br>*F2 offspring phenotype number ratio:*<br>**9** : **3** : **3** : **1** ;<br><br>short black / short chocolate / long black / long chocolate ;<br><br>*Mp 4 need phenotypes linked to genotypes by colour, symbol or initials* |
| 1(c) | **1** structural gene codes for, (named) structural / functional, protein / polypeptide ;<br>**2** regulatory gene codes for, transcription factor / repressor protein<br>**or**<br>regulatory gene, controls / helps / restricts, expression of (other) genes ; |