
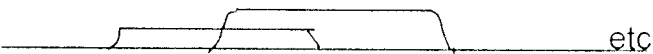


Mark Scheme 2815/02
June 2005

Abbreviations, annotations and conventions used in the Mark Scheme		
Question	Expected Answers	Marks
	/ = alternative and acceptable answers for the same marking point ; = separates marking points NOT = answers which are not worthy of credit () = words which are not essential to gain credit _____ = (underlining) key words which must be used to gain credit ecf = error carried forward AW = alternative wording ora = or reverse argument	
(a)	Any two from Specific ✓ More reactive/effective/faster ✓ More sensitive to changes of pH/temperature ✓ Milder conditions ✓ Cleaner product ✓ But not active site. AW in each case.	2
(b)	Allow uncharged structure/zwitterion ✓ for CONH and ✓ for the rest(correct). Must be a genuine attempt to link them. $\text{HOC}_6\text{H}_4\text{CH}_2\text{CH}(\text{NH}_2)\text{CONHCH}(\text{COOH})\text{CH}_2\text{C}_6\text{H}_4\text{OH}$ Or displayed in part or full.	2
(c)	Phenylalanine – van der Waals ✓ using benzene/phenyl/arene ring. ✓ AW Tyrosine – hydrogen bonding ✓ using the OH/phenol. ✓ AW Accept van der Waals again here for 1 mark. The structural feature mark only follows from a correct attraction. Ignore any reference to ionic attraction using the terminal COO^- and NH_3^+ .	4
(d)	Any 6 marks. AW throughout. <ul style="list-style-type: none"> • Correct use of term transcription/translation. ✓ • A different t-RNA, (with a different amino acid), will be brought up to altered m-RNA triplet. ✓ • Example of one transcription eg $\text{ATA (in DNA)} \rightarrow \text{UAU (in m-RNA)}$ Or $\text{AAA(in DNA)} \rightarrow \text{UUU (in m-RNA)} \checkmark$ <ul style="list-style-type: none"> • Translation of normal RNA eg UAU Tyr ✓ • Translation of changed RNA UUU Phe ✓ Do not give the second translation if same acid. <ul style="list-style-type: none"> • New amino acid has a different sidechain ✓ • then an important part of the tertiary structure/active site/shape may be changed. ✓ For one of these two marks accept reference to degeneracy of the triplet code. Accept also a base change which results in a new stop code rather than new amino acid	6
	Question total	14

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(2) (a)(i)	<p>Their diagram should show two bridges, either as –S-S- or as lines. Give ✓ for one bridge; ✓ for other bridge which will require a loop/spiral/crossover.</p> <p>Eg </p> <p>or  etc</p> <p>Accept any one bridge (even if wrong structure) eg –SH---HS-</p>	<p>2</p>
(ii)	<p>In primary structure it is a peptide/amide link ✓ In bridges it is a disulphide link (bond between S atoms) ✓ Either -CONH- or –S-S- for third mark ✓ (But if both given and one incorrectly then CON) If only structures without names give 2 marks. Fish back to part (i) for correct –S-S- if no structure.</p>	<p>3</p>
(b)	<p>Link between S and Zn ✓; dative/covalent ✓ or Link between Zinc ion (Zn^{2+}) and $COO^-/COOH$; ionic/covalent ✓ AW In either case must have first mark to score the second</p>	<p>2</p>
	<p>Question total</p>	<p>7</p>

