

Can you spot a cancer mutation?

How does cancer develop, and how can geneticists tell that a cell is cancerous? This teaching activity developed by the **Communication and Public Engagement team** from the Wellcome Trust Sanger Institute, UK, answers these and other related questions.

All cancers result from changes to the DNA sequence in some of our cells. Because the genetic material within cells is exposed to mutagens such as UV radiation, it can accumulate mistakes during replication. Occasionally, one of these mutations alters the function of a critical gene, providing a growth advantage to the cell in which it has occurred and its offspring; these cells will divide at a faster rate than their neighbours. Gradually, the DNA acquires more mutations, which can lead to the disruption of other key genes, resulting in particularly fast-growing and invasive cells. The result is tumour formation, the invasion of the surrounding tissue and eventually metastasis – the spread of the cancer to other parts of the body.

Genes that lead to the development of cancer when mutated are known as ‘cancer genes’.

Tumour suppressor genes (TSGs, Figure 1) encode the information for making proteins that normally slow down cell growth, preventing unnecessary division or promoting apoptosis (programmed cell death) if the cell’s DNA is damaged. Both copies of a TSG would have to be inactivated by mutation before this control of the cell cycle is lost. If one functional



- ✓ Biology
- ✓ Medicine
- ✓ Mutation
- ✓ Ages 15+

REVIEW

The teaching activities described in this article aim to actively involve advanced secondary-school biology students in a search for mutations that could potentially lead to cancer development, using real genomic data. The procedure is not a truly experimental one, so no real laboratory instruments are needed. Instead, the search is a theoretical one based on authentic data. All materials required to run the activity along with detailed directions can be freely downloaded from the programme website.

Apart from describing the various steps of the activity, the article and the supporting website include important information on what cancers are, what causes them, how they develop and how genomic information can be useful in developing treatments. Furthermore, several discussion points are suggested to enhance students’ understanding of cancer.

Michalis Hadjimarcou, Cyprus

copy remains, there is still a ‘brake’ on the cell’s growth.

Proto-oncogenes (Figure 2), in contrast, encode proteins that promote cell division and differentiation (specialisation). When these genes acquire mutations that either make the pro-

teins continually active or lead to the gene’s activity not being regulated anymore, they become oncogenes, promoting uncontrolled cell growth and division. For proto-oncogenes, a mutation in one copy of the gene can be enough to drive cancer develop-

Images courtesy of the Wellcome Trust Sanger Institute Communication and Public Engagement team

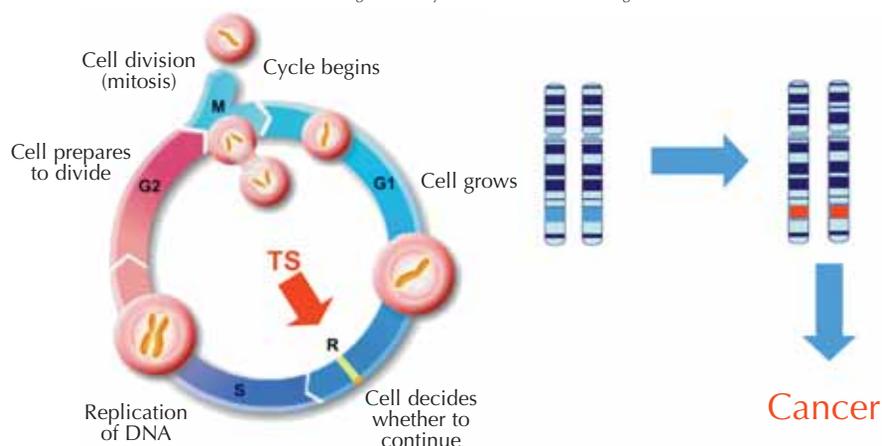


Figure 1: Tumour suppressor genes normally function to *prevent* cell growth and division. To lead to cancer, both copies of the gene would have to be mutated (marked in red)

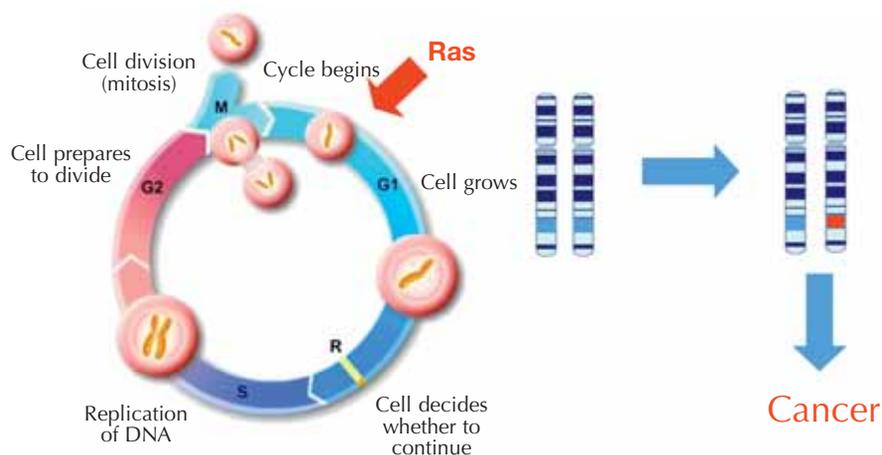


Figure 2: Proto-oncogenes normally function to *promote* cell growth and division in a controlled manner. A mutation in one copy of the gene (marked in red) can be enough to drive cancer development

Image courtesy of the Wellcome Trust Sanger Institute Communication and Public Engagement team

START																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
ATGACTGAATATAAAGCTGTGGTAGTGGGAGTGGGCTAGGCAAGAGTGGCTTGACGATACAGCTAATTCAGAAATCATTTTGTGGCAAAATATGATCCA																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
ACAATAGAGGATTCCTACAGGAAACAAGTAGTAATTGATGGGAAACCTGCTCTGGATATTCGACACAGCAGGTCAGAGGAGATACAGTCCATGAGG																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
GACCAGTACATGAGGACTGGGAGGGCTTCTTGTGATTTGCCATAAATAACTAAATCATTTGAGGATATTCACCATATAGAGAACAAATTAAGA																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
GTTAAGGACTCTGAAGATGTACTATGTTGCTAGTAGGAATAAATGATTTGGCTTCTAGACAGGTAGACACAAAACAGGCTCAGGACTTAACAAGAGTTAC																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
GGATTCCTTTTATTAAGACATCAGCAAGACAGACAGGTTGATGATGCTTCTATACATTAGTTGGAGAAATTCGAAACATAAAGAAAGATGAGGAAA																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000	1001	1002	1003	1004	1005	1006	1007	1008	1009	1010	1011	1012	1013	1014	1015	1016	1017	1018	1019	1020	1021	1022	1023	1024	1025	1026	1027	1028	1029	1030	1031	1032	1033	1034	1035	1036	1037	1038	1039	1040	1041	1042	1043	1044	1045	1046	1047	1048	1049	1050	1051	1052	1053	1054	1055	1056	1057	1058	1059	1060	1061	1062	1063	1064	1065	1066	1067	1068	1069	1070	1071	1072	1073	1074	1075	1076	1077	1078	1079	1080	1081	1082	1083	1084	1085	1086	1087	1088	1089	1090	1091	1092	1093	1094	1095	1096	1097	1098	1099	1100	1101	1102	1103	1104	1105	1106	1107	1108	1109	1110	1111	1112	1113	1114	1115	1116	1117	1118	1119	1120	1121	1122	1123	1124	1125	1126	1127	1128	1129	1130	1131	1132	1133	1134	1135	1136	1137	1138	1139	1140	1141	1142	1143	1144	1145	1146	1147	1148	1149	1150	1151	1152	1153	1154	1155	1156	1157	1158	1159	1160	1161	1162	1163	1164	1165	1166	1167	1168	1169	1170	1171	1172	1173	1174	1175	1176	1177	1178	1179	1180	1181	1182	1183	1184	1185	1186	1187	1188	1189	1190	1191	1192	1193	1194	1195	1196	1197	1198	1199	1200	1201	1202	1203	1204	1205	1206	1207	1208	1209	1210	1211	1212	1213	1214	1215	1216	1217	1218	1219	1220	1221	1222	1223	1224	1225	1226	1227	1228	1229	1230	1231	1232	1233	1234	1235	1236	1237	1238	1239	1240	1241	1242	1243	1244	1245	1246	1247	1248	1249	1250	1251	1252	1253	1254	1255	1256	1257	1258	1259	1260	1261	1262	1263	1264	1265	1266	1267	1268	1269	1270	1271	1272	1273	1274	1275	1276	1277	1278	1279	1280	1281	1282	1283	1284	1285	1286	1287	1288	1289	1290	1291	1292	1293	1294	1295	1296	1297	1298	1299	1300	1301	1302	1303	1304	1305	1306	1307	1308	1309	1310	1311	1312	1313	1314	1315	1316	1317	1318	1319	1320	1321	1322	1323	1324	1325	1326	1327	1328	1329	1330	1331	1332	1333	1334	1335	1336	1337	1338	1339	1340	1341	1342	1343	1344	1345	1346	1347	1348	1349	1350	1351	1352	1353	1354	1355	1356	1357	1358	1359	1360	1361	1362	1363	1364	1365	1366	1367	1368	1369	1370	1371	1372	1373	1374	1375	1376	1377	1378	1379	1380	1381	1382	1383	1384	1385	1386	1387	1388	1389	1390	1391	1392	1393	1394</

Amino acid code

- A - Alanine
- C - Cysteine
- D - Aspartic acid
- E - Glutamic acid
- F - Phenylalanine
- G - Glycine
- H - Histidine
- I - Isoleucine
- K - Lysine
- L - Leucine
- M - Methionine
- N - Asparagine
- P - Proline
- Q - Glutamine
- R - Arginine
- S - Serine
- T - Threonine
- V - Valine
- W - Tryptophan
- Y - Tyrosine

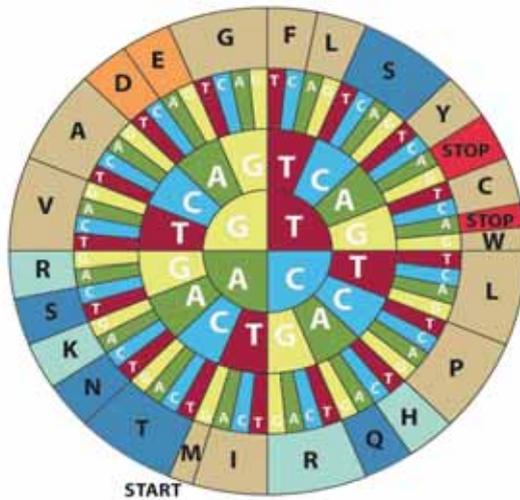


Figure 4: Use the codon wheel to translate DNA codons into amino acids. To decode a codon find the first letter of your sequence in the inner circle and work outwards to see the corresponding amino acid. For example, CAT codes for H (histidine). Note that this diagram uses the sense DNA codons (5' to 3')

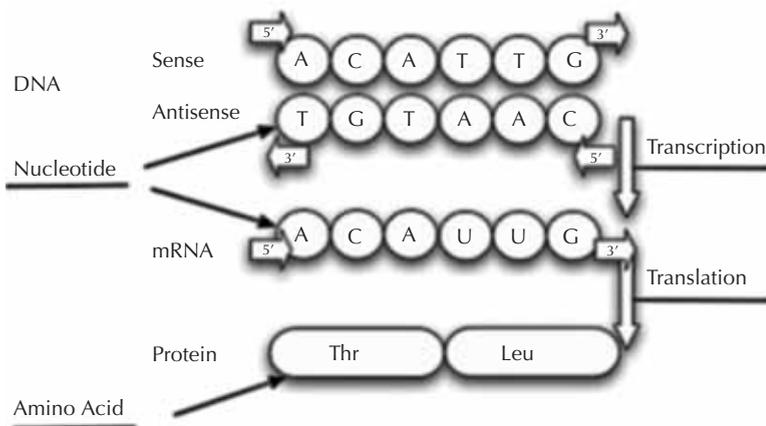


Figure 5: mRNA is synthesised from the antisense strand of DNA. The sense strand of DNA, used in this activity, has the same sequence as the corresponding mRNA strand, except that T is replaced by U

dents. For large groups (20 or more), use two sets of worksheets, providing double coverage of the gene.

- One *KRAS* gene sequence banner (KRAS_gene_banner.pdf; Figure 3) for the whole class, and one *KRAS* gene sheet (KRAS_genesheet_yg.pdf; Figure 3) per group of students. The gene sheet (printed on A3 or A4) requires little preparation time. The *KRAS* banner, printed on several sheets of paper that are then stuck

together, enables the results from the whole class to be displayed simultaneously.

- One codon wheel sheet (KRAS_codon_wheel.pdf or any other codon table for sense DNA, 5' to 3') per group, see Figures 4 and 5
- One summary sheet (KRAS_data_sheet.pdf) per group
- Pens

To use the banner, you will also need large arrows for marking muta-

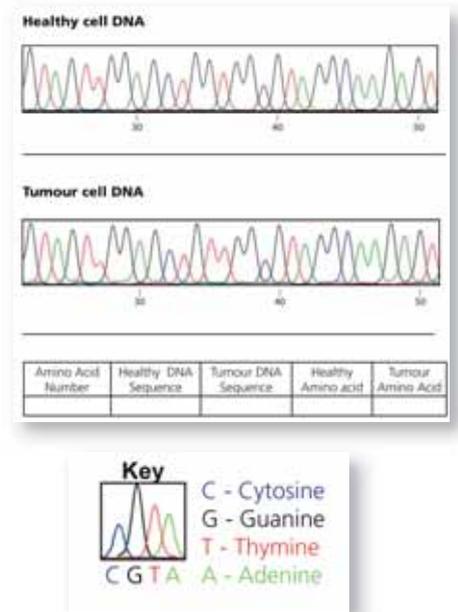


Figure 6: Example from a student worksheet

tions on the gene sequence, squares for marking regions which have been checked (KRAS_annotations.pdf), and reusable adhesive (e.g. Blu Tack®) for sticking arrows and squares to the gene sequence banner. Find out more about how to use this method in the downloadable teacher notes^{w6}.

In addition, you might find it helpful to have DNA, peptide and/or protein models to hand, and to use the Wellcome Trust Sanger Institute cancer animations (*Cancer: Rogue cells* and *Role of cancer genes*) on the *KRAS* activity website^{w6}.

Introduction to the activity

The *Investigating Cancer* presentation (available online^{w6}) provides students with an overview of cancer. It introduces the concept that cancer arises due to abnormalities in DNA sequence, explains the various causes of these mutations and introduces the worksheets and activity. Several sections of the presentation encourage student discussions (see the presentation notes^{w6}).

In the first part of the activity, students identify differences between *KRAS* gene sequences in healthy and

Image courtesy of C Brooksbank, European Bioinformatics Institute

Image courtesy of Cleopatra Kozłowski

Image courtesy of the Wellcome Trust Sanger Institute Communication and Public Engagement team

tumour cells on their worksheets, and mark these on the *KRAS* banner or gene sheet.

The worksheets have raw *KRAS* DNA sequencing traces from healthy and cancerous cell samples, represented as coloured line plots – one for each region of the gene. The four bases are represented on these plots by four different colours. Each coloured peak represents an individual DNA base:

Red: T

Green: A

Blue: C

Black: G (normally these peaks are yellow but this is not easy to read on paper)

There are 11 numbered worksheets in total, each showing two different regions of the *KRAS* gene. The six mutations in the *KRAS* gene are on worksheets one to six, so be sure to mix the sheets up before distributing them to the class. All must be completed to ensure full coverage of the gene. It is important to point out to the students that mutations are (relatively) rare, so not everyone will find one; this can be used to explore the importance of negative data and comprehensive coverage in scientific studies.

Identifying the mutations

Using the worksheets, the students will compare a section of DNA sequence from a healthy cell and a tumour cell from the same patient. The easiest way to identify whether a mutation has occurred is to write the DNA sequence below the coloured peaks (there is a colour key on the sheet to help) and to compare the written sequences.

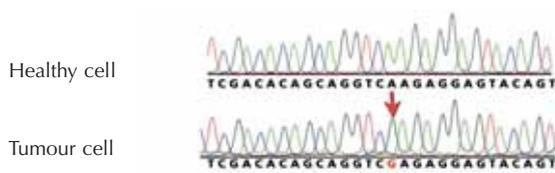


Figure 7: Identifying sequence mutations

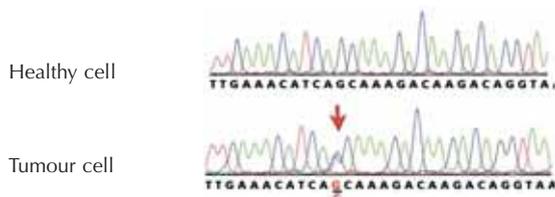
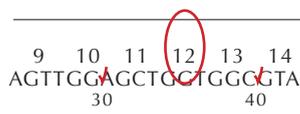


Figure 8: A heterozygous mutation

Figure 9: Ticking off the gene regions that have been checked, and marking any mutations



If one of the letters is different (a peak has changed colour), this indicates a mutation in the sequence. In Figure 7, the A in the DNA sequence from the healthy cell has been replaced by G in the tumour cell.

If the students find a double peak at one base position, this should be recorded with the two alternative bases at that position, one above the other. In the example below, the healthy DNA sequence has a G, whereas the tumour sequence has both G and C. This is not an insertion: it represents a heterozygous mutation where only one copy of the gene has substituted a C for a G. In this case the tumour sequence has replaced G with a C.

All students should indicate the gene regions they have checked by ticking off the relevant region on the gene sheet (see Figure 9).

Students who find a mutation should indicate the specific base by circling it on the gene sheet (see Figure 9) and make a note of which codon this lies in (in this example, codon 12).

They should also fill in the table at the base of the worksheet, using the codon wheel to translate the DNA sequence into the amino acid, as shown in Table 1:

Amino acid number	Healthy cell DNA sequence	Tumour cell DNA sequence	Healthy cell amino acid	Tumour cell amino acid
12	GGT	GTT	G (glycine)	V (valine)

Table 1: Mutations as listed on the individual worksheets

When all mutations have been found, record them on the summary data sheet (see Table 2).

Amino acid number	Healthy cell DNA sequence	Tumour cell DNA sequence	Healthy cell amino acid	Tumour cell amino acid
12	GGT	GTT	G (glycine)	V (valine)
13	GGC	GAC	G (glycine)	D (aspartic acid)
30	GAC	GAT	D (aspartic acid)	D (aspartic acid)
61	CAA	CGA	Q (glutamine)	R (arginine)
146	GCA	CCA	A (alanine)	P (proline)
173	GAT	GAC	D (aspartic acid)	D (aspartic acid)

Table 2: Mutations as recorded on the summary data sheet

Discussing the results

The results above are all single base substitutions. These mutations within the protein-coding region of the *KRAS* gene may be classified into one of three types, depending on the information encoded by the altered codon.

- Silent mutations code for the same amino acid.
- Missense mutations code for a different amino acid.
- Nonsense mutations code for a stop and can truncate the protein.

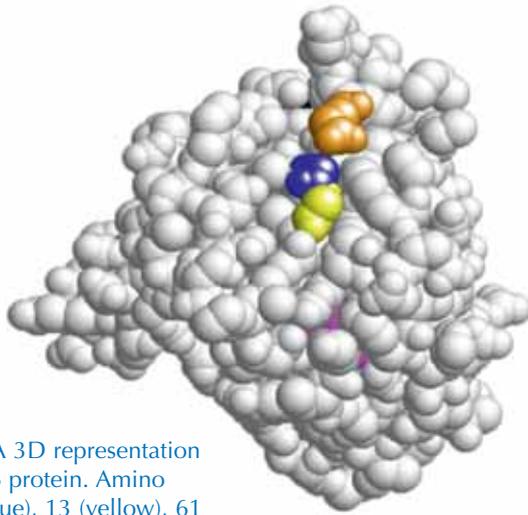


Figure 10: A 3D representation of the KRAS protein. Amino acids 12 (blue), 13 (yellow), 61 (orange) and 146 (pink) are those which carry mutations

Discuss whether the mutations are significant – will they have an impact on protein function or are they ‘silent’? In this activity, codons 30 and 173 are silent and therefore do not have a functional impact.

The presentation has a 3D space-fill image of the KRAS protein (Figure 10); slides 26–30 show where on the protein the significant mutations are, and you will notice they are all in the same region. Codons 12, 13 and 61 were the first mutations to be associated with oncogenic transformation in the KRAS protein; mutation 146 was only discovered in 2005. Use these slides to discuss the impact that the mutations could have on protein structure and KRAS’s function in growth signalling.

As an optional activity, the students can use RasMol, the molecular modelling software used to create the images on slides 26–30, to highlight the mutated amino acids in the protein structure. See the teacher notes^{w6} for details.

How does information like this influence our approach to cancer?

The teacher notes^{w6} contain a wealth of background information, using *KRAS* as an example, to stimulate dis-

cussion on how genomic information can be used to further our understanding of cancer and develop cancer treatments. Discussion points for students include:

- What experiments or approaches could be used to establish which cancers involve *KRAS* mutations?
- What could be the advantages of knowing this information?
- Cancer is a genetic disease: it is a result of changes in the DNA sequence. This is why many people believe that significant funding of research into cancer genetics is the best way of developing new cancer treatments and thus dealing with the disease. Cancer treatment and care for patients also requires large amounts of money (the UK National Health Service spent more than £2 billion on cancer care alone in 2000). Where and how do students think money should be spent?

Web references

w1 – Learn more about the Cancer Genome Project at the Wellcome Trust Sanger Institute here:
www.sanger.ac.uk/genetics/CGP

w2 – To learn more about the Wellcome Trust Sanger Institute in Hinxton, UK, a leader in the Human Genome Project, see: www.sanger.ac.uk

The institute offers visits for school classes, teachers and the general public, as well as teacher support and further opportunities to get involved. See:
www.sanger.ac.uk/about/engagement

w3 – The Yourgenome.org website was launched by the Sanger Institute to stimulate interest in and discussion on genetic research. It includes a section of varied and well developed resources for teachers, including the activity presented in this article. See:
www.yourgenome.org

w4 – The European Learning Laboratory for the Life Sciences (ELLS) at the European Molecular Biology Laboratory provides continuing professional development courses (LearningLABs) in molecular biology for European secondary-school science teachers. In March

Amino acid number	Healthy cell DNA sequence	Tumour cell DNA sequence	Healthy cell amino acid	Tumour cell amino acid	Type of mutation	Significant yes / no
12	GGT	GTT	G (glycine)	V (valine)	Point (missense)	yes
13	GCC	GAC	G (glycine)	D (aspartic acid)	Point (missense)	yes
30	GAC	GAT	D (aspartic acid)	D (aspartic acid)	Point (silent)	no
61	CAA	CGA	Q (glutamine)	R (arginine)	Point (missense)	yes
146	GCA	CCA	A (alanine)	P (proline)	Point (missense)	yes
173	GAT	GAC	D (aspartic acid)	D (aspartic acid)	Point (silent)	no

Table 3: Type of mutation, as recorded on the summary data sheet

2010, ELLS ran the first bioinformatics LearningLAB for teachers at the European Bioinformatics Institute in the UK. For information on ELLS courses, please go to: www.embl.org/ells

w5 – To find out more about the European Bioinformatics Institute, see: www.ebi.ac.uk

w6 – To download all materials for the KRAS activity and for more background information, see: www.yourgenome.org/teachers/kras.shtml

Resources

Websites for student reference and discussion

The Cancer Research UK website offers accessible information on all the major cancers and current research. See: <http://info.cancerresearchuk.org/cancerandresearch>

The *New Scientist* website has an area focusing on cancer, featuring the latest articles on cancer research developments and interactive animations demonstrating targeted cancer drug functions. See: www.newscientist.com/topic/cancer

Nature Milestones in Cancer offers a collection of selected review-type articles and an online library of recent research papers from Nature Publishing Group, available for download as PDFs. It also has a cancer timeline showing major milestones in cancer research. See: www.nature.com/milestones/milecancer

The Inside Cancer multimedia website created by the DNA Learning Center offers a multimedia guide to cancer biology, diagnosis and treatment. See: www.insidecancer.org

Recent news articles

The BBC News website has published an interesting article on how newly discovered genetic hotspots for bowel cancer might help doctors

to treat the disease better. See: <http://news.bbc.co.uk> or use the direct link: <http://tinyurl.com/28o7zgf>

Sample I (2009) First cancer genome sequences reveal how mutations lead to disease. *The Guardian*. See www.guardian.co.uk or use the direct link: <http://tinyurl.com/yeknj5x>

Roberts M (2009) Scientists crack 'entire genetic code' of cancer. *BBC News*. See <http://news.bbc.co.uk> or use the direct link: <http://tinyurl.com/yb59qcz>
This article includes a video interview with Professor Mike Stratton, leader of the Cancer Genome Project.

Further reading

Friday BB, Adjei AA (2005) K-ras as a target for cancer therapy. *Biochimica et Biophysica Acta – Reviews on Cancer* **1756**(2): 127-144. doi: 10.1016/j.bbcan.2005.08.001

Futreal A et al. (2004) A census of human cancer genes. *Nature Reviews Cancer* **4**: 177-183. doi: 10.1038/nrc1299

The author version of this paper can be freely viewed online. See: www.ncbi.nlm.nih.gov/pmc or use the direct link: <http://tinyurl.com/3x5hah6>

For a full catalogue of somatic cancer genes (COSMIC) described in the above paper and created by the Cancer Genome Project, see: www.sanger.ac.uk

Stratton MR, Campbell PJ, Futreal AP (2009) The cancer genome. *Nature* **458**: 719-724. doi: 10.1038/nature07943

Download the article free of charge from the *Science in School* website (www.scienceinschool.org/2010/issue15/cancer#resources), or subscribe to *Nature* today: www.nature.com/subscribe.

For more information on how genetic

mutations cause diseases, see:

Patterson L (2009) Getting a grip on genetic diseases. *Science in School* **13**: 53-58.

www.scienceinschool.org/2009/issue13/insight

For an interview with cancer researcher Joan Massagué, see:

Sherwood S (2008) On the trail of a cure of cancer. *Science in School* **8**: 56-59.

www.scienceinschool.org/2008/issue8/joanmassague

For a classroom activity to discuss the ethics of knowing what your genes have in store for you, including the possibility of cancer, see:

Strieth L et al. (2008) Meet the Gene Machine: stimulating bioethical discussions at school. *Science in School* **9**: 34-38.

www.scienceinschool.org/2008/issue9/genemachine

If you enjoyed this article, why not take a look at other medicine-related articles previously published in *Science in School*? See:

www.scienceinschool.org/medicine

The Wellcome Trust Sanger Institute Communication and Public Engagement programme communicates the nature, discoveries and wonder of science and its implications for individuals and society. It tries to make complex biomedical research accessible to a range of audiences, including school students and their teachers, through a visit programme, a range of collaborations, and the Yourgenome.org website^{w3}. For more information about the programme, see:

www.sanger.ac.uk/about/engagement; to contact the team, email pubengage@sanger.ac.uk.

