

DISTRIBUTION OF p53 MUTATION

Amino acids residues are shown using both 3 or 1 letter abbreviation

Yellow: codon number

White: wt codon

Light orange: 3 letter aa

light blue: 1 letter aa

The last lane shows the number of mutations found at this position in the UMD p53 database

The frequency of p53 mutations is colored coded:

Red: between 1 and 10 mutations

Green: between 11 and 100 mutations

Blue: > 100 mutations

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
ATG	GAG	GAG	CCG	CAG	TCA	GAT	CCT	AGC	GTC	GAG	CCC	CCT	CTG	AGT	CAG	GAA	ACA	TTT	TCA
Met	Glu	Glu	Pro	Gln	Ser	Asp	Pro	Ser	Val	Glu	Pro	Pro	Leu	Ser	Gln	Glu	Thr	Phe	Ser
M	E	E	P	Q	S	D	P	S	V	E	P	P	L	S	Q	E	T	F	S
0	0	0	0	2	0	1	1	0	1	6	1	0	0	1	0	1	0	0	0

21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
GAC	CTA	TGG	AAA	CTA	CTT	CCT	GAA	AAC	AAC	GTT	CTG	TCC	CCC	TTG	CCG	TCC	CAA	GCA	ATG
Asp	Leu	Trp	Lys	Leu	Leu	Pro	Glu	Asn	Asn	Val	Leu	Ser	Pro	Leu	Pro	Ser	Gln	Ala	Met
D	L	W	K	L	L	P	E	N	N	V	L	S	P	L	P	S	Q	A	M
1	1	0	1	1	2	1	2	2	1	1	0	3	1	5	9	4	4	1	3

41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
GAT	GAT	TTG	ATG	CTG	TCC	CCG	GAC	GAT	ATT	GAA	CAA	TGG	TTC	ACT	GAA	GAC	CCA	GGT	CCA
Asp	Asp	Leu	Met	Leu	Ser	Pro	Asp	Asp	Iso	Glu	Gln	Trp	Phe	Thr	Glu	Asp	Pro	Gly	Pro
D	D	L	M	L	S	P	D	D	I	E	Q	W	F	T	E	D	P	G	P
2	2	3	4	2	12	20	2	5	1	7	8	12	8	2	5	2	1	4	4

61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
GAT	GAA	GCT	CCC	AGA	ATG	CCA	GAG	GCT	GCT	CCC	CCC	GTG	GCC	CCT	GCA	CCA	GCA	GCT	CCT
Asp	Glu	Ala	Pro	Arg	Met	Pro	Glu	Ala	Ala	Pro	Pro	Val	Ala	Pro	Ala	Pro	Ala	Ala	Pro
D	E	A	P	R	M	P	E	A	A	P	P	V	A	P	A	P	A	A	P
5	11	1	2	6	2	5	11	9	2	9	CGC	8	2	4	17	4	1	3	4
											Arg								
											R								
											6								

81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
ACA	CCG	GCG	GCC	CCT	GCA	CCA	GCC	CCC	TCC	TGG	CCC	CTG	TCA	TCT	TCT	GTC	CCT	TCC	CAG
Thr	Pro	Ala	Ala	Pro	Ala	Pro	Ala	Pro	Ser	Trp	Pro	Leu	Ser	Ser	Ser	Val	Pro	Ser	Gln
T	P	A	A	P	A	P	A	P	S	W	P	L	S	S	S	V	P	S	Q
5	13	6	11	9	4	3	7	12	3	19	7	4	6	7	8	3	6	4	17

101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
AAA	ACC	TAC	CAG	GGC	AGC	TAC	GGT	TTC	CGT	CTG	GGC	TTC	TTG	CAT	TCT	GGG	ACA	GCC	AAG
Lys	Thr	Tyr	Gln	Gly	Ser	Tyr	Gly	Phe	Arg	Leu	Gly	Phe	Leu	His	Ser	Gly	Thr	Ala	Lys
K	T	Y	Q	G	S	Y	G	F	R	L	G	F	L	H	S	G	T	A	K
8	12	8	23	11	13	12	9	8	47	13	12	26	3	5	7	11	3	8	11

121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140
TCT	GTG	ACT	TGC	ACG	TAC	TCC	CCT	GCC	CTC	AAC	AAG	ATG	TTT	TGC	CAA	CTG	GCC	AAG	ACC
Ser	Val	Thr	Cys	Thr	Tyr	Ser	Pro	Ala	Leu	Asn	Lys	Met	Phe	Cys	Gln	Leu	Ala	Lys	Thr
S	V	T	C	T	Y	S	P	A	L	N	K	M	F	C	Q	L	A	K	T
6	6	3	11	24	60	44	23	17	54	34	141	40	49	208	84	32	110	41	36

141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160
TGC	CCT	GTG	CAG	CTG	TGG	GTT	GAT	TCC	ACA	CCC	CCG	CCC	GGC	ACC	CGC	GTC	CGC	GCC	ATG
Cys	Pro	Val	Gln	Leu	Trp	Val	Asp	Ser	Thr	Pro	Pro	Pro	Gly	Thr	Arg	Val	Arg	Ala	Met
C	P	V	Q	L	W	V	D	S	T	P	P	P	G	T	R	V	R	A	M
154	41	72	92	55	104	43	28	37	32	210	172	55	107	113	104	229	264	117	37

161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180
GCC	ATC	TAC	AAG	CAG	TCA	CAG	CAC	ATG	ACG	GAG	GTT	GTG	AGG	CGC	TGC	CCC	CAC	CAT	GAG
Ala	Iso	Tyr	Lys	Gln	Ser	Gln	His	Met	Thr	Glu	Val	Val	Arg	Arg	Cys	Pro	His	His	Glu
A	I	Y	K	Q	S	Q	H	M	T	E	V	V	R	R	C	P	H	H	E
112	51	195	66	60	58	67	66	33	37	56	66	200	77	1092	343	107	79	341	38

181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200
CGC	TGC	TCA	GAT	AGC	GAT	GGT	CTG	GCC	CCT	CCT	CAG	CAT	CTT	ATC	CGA	GTG	GAA	GGA	AAT
Arg	Cys	Ser	Asp	Ser	Asp	Gly	Leu	Ala	Pro	Pro	Gln	His	Leu	Iso	Arg	Val	Glu	Gly	Asn
R	C	S	D	S	D	G	L	A	P	P	Q	H	L	I	R	V	E	G	N
86	29	32	37	18	20	35	13	35	70	47	102	189	116	139	230	43	38	38	21

201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220
TTG	CGT	GTG	GAG	TAT	TTG	GAT	GAC	AGA	AAC	ACT	TTT	CGA	CAT	AGT	GTG	GTG	GTG	CCC	TAT
Leu	Arg	Val	Glu	Tyr	Leu	Asp	Asp	Arg	Asn	Thr	Phe	CGG	His	Ser	Val	Val	Val	Pro	Tyr
L	R	V	E	Y	L	D	D	R	N	T	F	Arg	H	S	V	V	V	P	Y
30	41	36	64	158	18	23	44	77	20	57	39								
												327							

221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240
GAG	CCG	CCT	GAG	GTT	GGC	TCT	GAC	TGT	ACC	ACC	ATC	CAC	TAC	AAC	TAC	ATG	TGT	AAC	AGT
Glu	Pro	Pro	Glu	Val	Gly	Ser	Asp	Cys	Thr	Thr	Iso	His	Tyr	Asn	Tyr	Met	Cys	Asn	Ser
E	P	P	E	V	G	S	D	C	T	T	I	H	Y	N	Y	M	C	N	S
39	27	18	41	24	31	27	44	42	33	23	58	29	167	56	130	214	197	130	70

241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260
TCC	TGC	ATG	GGC	GGC	ATG	AAC	CGG	AGG	CCC	ATC	CTC	ACC	ATC	ATC	ACA	CTG	GAA	GAC	TCC
Ser	Cys	Met	Gly	Gly	Met	Asn	Arg	Arg	Pro	Iso	Leu	Thr	Iso	Iso	Thr	Leu	Glu	Asp	Ser
S	C	M	G	G	M	N	R	R	P	I	L	T	I	I	T	L	E	D	S
208	198	55	227	718	135	82	1544	573	134	96	51	37	57	84	42	57	137	67	25

261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280
AGT	GGT	AAT	CTA	CTG	GGA	CGG	AAC	AGC	TTT	GAG	GTG	CGT	GTT	TGT	GCC	TGT	CCT	GGG	AGA
Ser	Gly	Asn	Leu	Leu	Gly	Arg	Asn	Ser	Phe	Glu	Val	Arg	Val	Cys	Ala	Cys	Pro	Gly	Arg
S	G	N	L	L	G	R	N	S	F	E	V	R	V	C	A	C	P	G	R
22	38	19	33	46	195	65	18	38	97	83	165	1425	98	168	72	93	268	73	231

281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300
GAC	CGG	CGC	ACA	GAG	GAA	GAG	AAT	CTC	CGC	AAG	AAA	GGG	GAG	CCT	CAC	CAC	GAG	CTG	CCC
Asp	Arg	Arg	Thr	Glu	Glu	Glu	Asn	Leu	Arg	Lys	Lys	Gly	Glu	Pro	His	His	Glu	Leu	Pro
D	R	R	T	E	E	E	N	L	R	K	K	G	E	P	H	H	E	L	P
178	616	103	30	200	152	65	23	30	73	28	34	34	74	23	30	21	90	27	27

301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320
CCA	GGG	AGC	ACT	AAG	CGA	GCA	CTG	CCC	AAC	AAC	ACC	AGC	TCC	TCT	CCC	CAG	CCA	AAG	AAG
Pro	Gly	Ser	Thr	Lys	Arg	Ala	Leu	Pro	Asn	Asn	Thr	Ser	Ser	Ser	Pro	Gln	Pro	Lys	Lys
P	G	S	T	K	R	A	L	P	N	N	T	S	S	S	P	Q	P	K	K
35	23	18	12	37	130	20	12	15	9	6	10	12	10	10	13	31	7	11	12

321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340
AAA	CCA	CTG	GAT	GGA	GAA	TAT	TTC	ACC	CTT	CAG	ATC	CGT	GGG	CGT	GAG	CGC	TTC	GAG	ATG
Lys	Pro	Leu	Asp	Gly	Glu	Tyr	Phe	Thr	Leu	Gln	Iso	Arg	Gly	Arg	Glu	Arg	Phe	Glu	Met
K	P	L	D	G	E	Y	F	T	L	Q	I	R	G	R	E	R	F	E	M
6	5	6	6	8	10	10	6	3	12	31	8	2	6	2	3	35	7	13	3

341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360
TTC	CGA	GAG	CTG	AAT	GAG	GCC	TTG	GAA	CTC	AAG	GAT	GCC	CAG	GCT	GGG	AAG	GAG	CCA	GGG
Phe	Arg	Glu	Leu	Asn	Glu	Ala	Leu	Glu	Leu	Lys	Asp	Ala	Gln	Ala	Gly	Lys	Glu	Pro	Gly
F	R	E	L	N	E	A	L	E	L	K	D	A	Q	A	G	K	E	P	G
7	65	5	4	2	5	3	3	7	0	0	1	1	2	2	4	0	2	0	4

361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380
GGG	AGC	AGG	GCT	CAC	TCC	AGC	CAC	CTG	AAG	TCC	AAA	AAG	GGT	CAG	TCT	ACC	TCC	CGC	CAT
Gly	Ser	Arg	Ala	His	Ser	Ser	His	Leu	Lys	Ser	Lys	Lys	Gly	Gln	Ser	Thr	Ser	Arg	His
G	S	R	A	H	S	S	H	L	K	S	K	K	G	Q	S	T	S	R	H
1	2	3	3	4	2	1	2	1	1	0	0	0	0	1	2	1	0	1	0

381	382	383	384	385	386	387	388	389	390	391	392	393
AAA	AAA	CTC	ATG	TTC	AAG	ACA	GAA	GGG	CCT	GAC	TCA	GAC
Lys	Lys	Leu	Met	Phe	Lys	Thr	Glu	Gly	Pro	Asp	Ser	Asp
K	K	L	M	F	K	T	E	G	P	D	S	D
1	0	0	0	1	0	1	0	0	1	0	0	0