

A Coding diversity in gH

AA #	7	12	15	16	110	124	127	129	130	138	147	150	170	284*	292	305	307	368	369**	370**	371	372	392	400	584	582	649	667	670	
17 Ref	F	I	V	A	P	P	P	T	V	E	S	H	A	E	V	G	N	P	A	G	A	E	Q	A	N	A	L	S	I	N
F	Y	V
H129	V
McKr
KOS	.	L	.	S	.	.	I	.	A	.	T	S
HF10	.	A	A	.	T	.	A
CR38	.	L	.	S	.	.	I	.	A	.	T
E03	D	A	T	L	E	.	S	.	.	.	H	T
E06	A	S	P	.	K	.	H
E07	T	S	A
E08	T	A	S	P	.	K	.	H	L	.	.
E10	A	S	P	.	K	.	H
E11	A	S	P	.	K	.	H
E12	T	A	F	.	.
E13	T	A
E14	A
E15	A	S	P	.	K	.	H
E19	T	A
E22	D	A	D	T	L	E	.	S	.	.	H
E23	A	S	P	.	K	.	H
E25	G	A	S	P	.	K	.	H
E35	A	S	P	.	K	.	H
R11	.	.	V	S	A	.	T	.	A
R62	.	.	S	.	.	.	Q	A	.	T	V	.
S23	.	.	S	.	.	.	Q	A	.	T	V	.
S25	.	.	S	.	.	.	Q	A	.	T	V	.

B Coding diversity in UL42

AA #	8	13	92	210	231	284*	335	336	337	349	350	352	377	378	404	405	423	434	441	442	450	451	477	481	483
17 Ref	V	P	R	F	S	G	G	S	S	S	Q	S	L	H	R	A	A	S	A	A	R	S	G	T	Y
F	.	H	.	.	A	S	Y	H	S
H129	A	S	Y	H
McKr	.	H	.	I	K
KOS	A	S	.	T
HF10	N
CR38	V	S
E03	.	.	S	S	D	.	P
E06	.	H	S	.	N	S	Y
E07	.	H	S	Y
E08	S	A
E10	.	H	S	S	Y
E11	.	H	S	S	Y
E12	S
E13	S
E14	L	.	P	S	Y	Q	N	.	A	.	.	.
E15	.	H	S	S	Y
E19	S	A
E22	.	H	S	S	Y
E23	.	H	S	S	Y
E25	.	H	S	S	Y
E35	.	H	S	S	Y
R11	A	.	L	.	.	S	Y
R62	M	L	.	.	.	S	.	S	.	GR	.	V
S23	M	L	.	.	.	S	.	S	.	GR	.	V
S25	M	L	.	.	.	S	.	S	.	GR	.	V

Positively selected residues in HSV-1 proteins gH and UL42

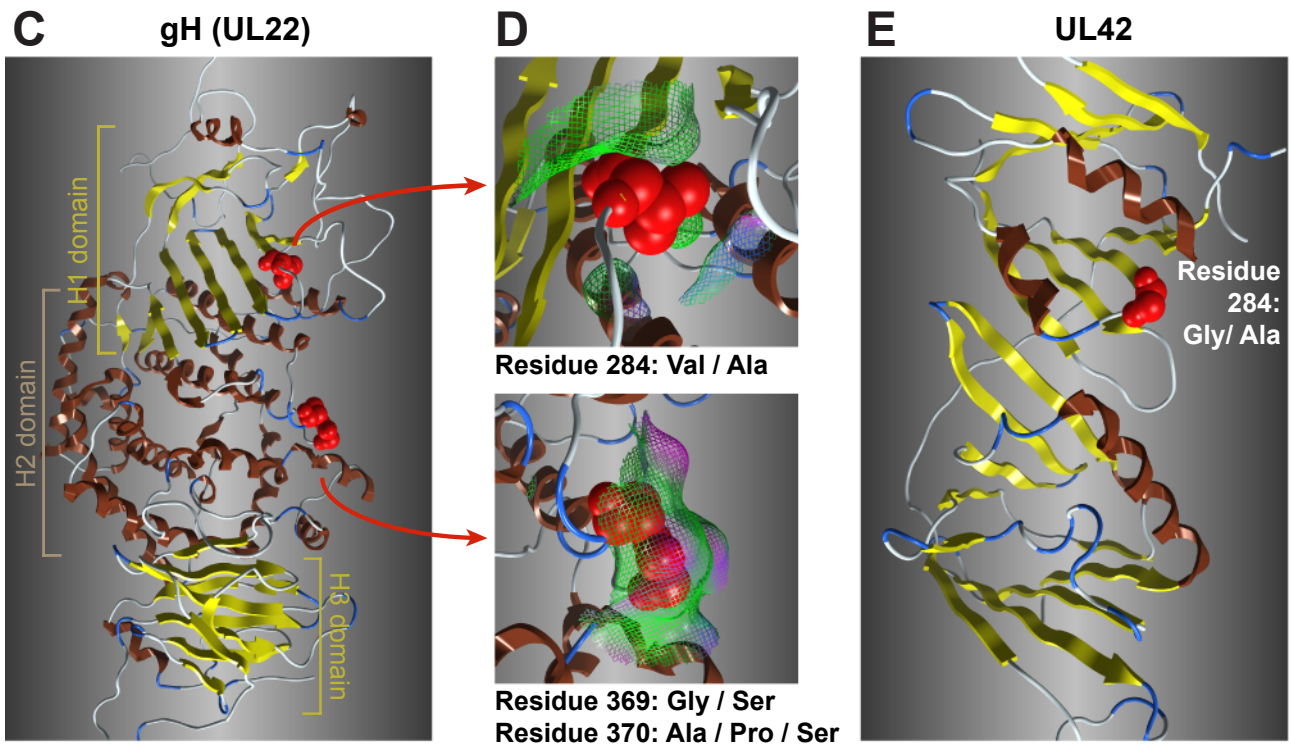


Figure 7. Coding diversity and positive selection of residues in the HSV-1 entry protein gH and the DNA-binding protein UL42.

Szpara *et al.* (2013) JVI. Evolution and diversity in human herpes simplex virus genomes.