Table 4. Residues predicted to be functionally divergent in clathrin heavy chain

Residue no. (bovine CHC17)	**In CHC17 sequences**	**In CHC22 sequences**	**Protein domain**
139	Conserved V	M, V, Q, or A	N-terminal domain
200	S, G, or R	Conserved A	N-terminal domain
206	Conserved M	I, V, S, or M	N-terminal domain
266	I or V	I or V	N-terminal domain
370	A, N, or T	Conserved T	Linker region
576	S, T, or M	A or S	Distal leg segment
864	A or S	Conserved S	Distal leg segment
1212	D or E	D or E	Proximal leg segment
1382	P, A or R	Conserved P	Proximal leg segment
1408	I or V	Conserved L	Proximal leg segment
1440	S or T	S, F, or T	Proximal leg segment
1473	T, I, or S	Conserved E	Proximal leg segment
1494	Conserved S	S, A, T, or G	Proximal leg segment
1555	Q, S, or A	Conserved Q	Trimerization domain
1559	Q, V, S, or D	Conserved E	Trimerization domain
1561	E, N, or D	Conserved G	Trimerization domain