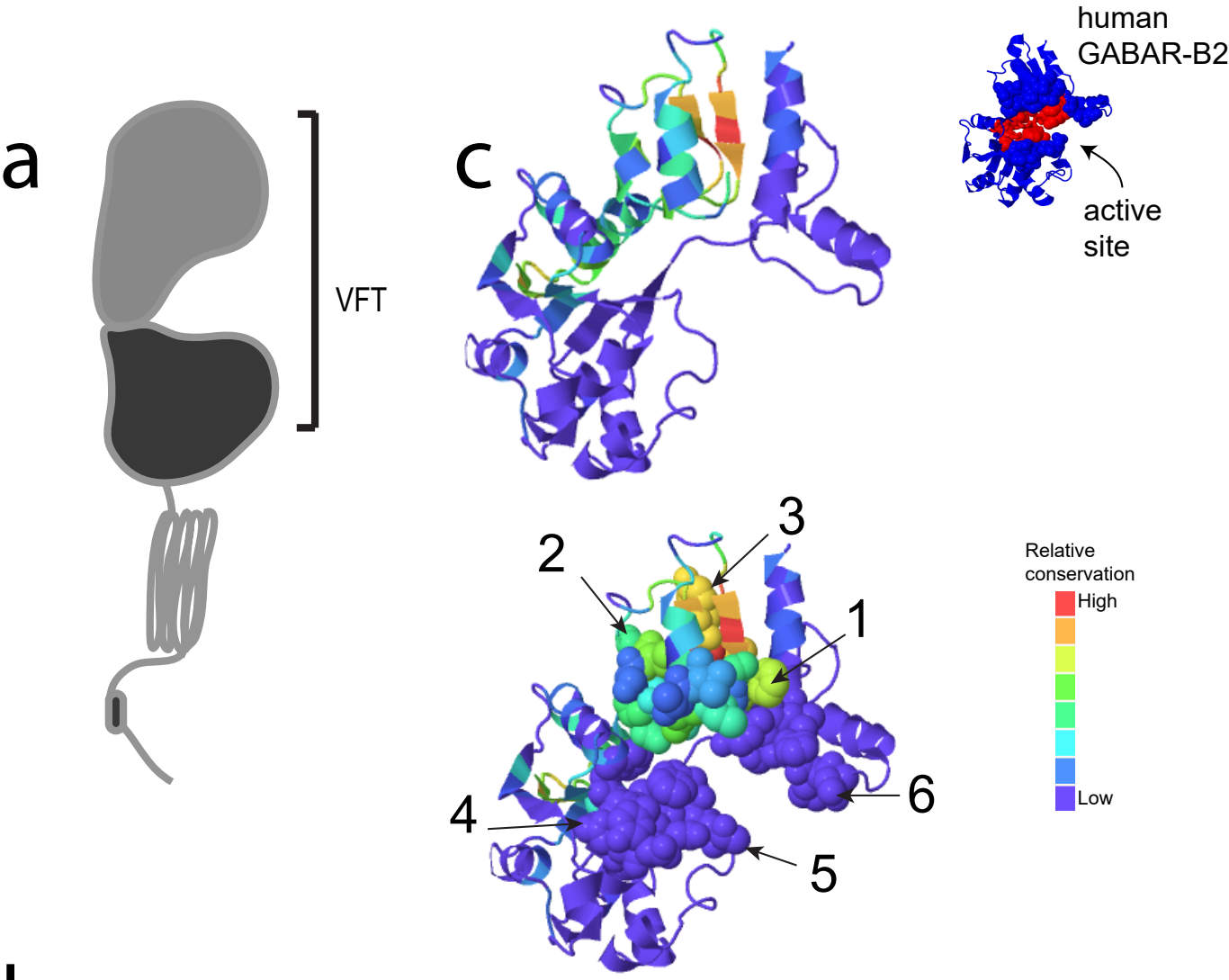

b

	1	2	3	4	5	6
	* *	* * *	*	*	*	*
Hsa_GABAR-B2	GGVCPSV	FAATTPVLA	FRTVPSD	GQFDQNMA	IPGWYE	EGPSKFHGY
Dre_GABAR-B2	GGVCPSV	FAATTPVLA	FRTVPSD	GQFDENLA	IPGWYQ	QETSKFHGF
Dme_NP001287456.1	GAACTHV	YADTHPMFT	FRVVPSE	GNFNEHFA	IMATYS	SEYSRFHGY
Em0016g375a	DGGCNTV	FGSSSPSLS	YRTIPSE	AWMYEDQA	LPGWYT	TNMHSYVPF
Em0016g376a	GGGCSSS	FGSSSPTLT	FRTIPSE	IWMYEDKA	LPGWYS	SAVSKYMRF
Em0020g696a	GADCSVS	PLSTSPQLE	LRTVASD	VNTYPTHA	YFAWYP	PSLQDQVPY
Em0013g539a	GCGCSVA	YFSESAALS	FRTNPSG	SRLFETES	FQDWYT	T----QIEY