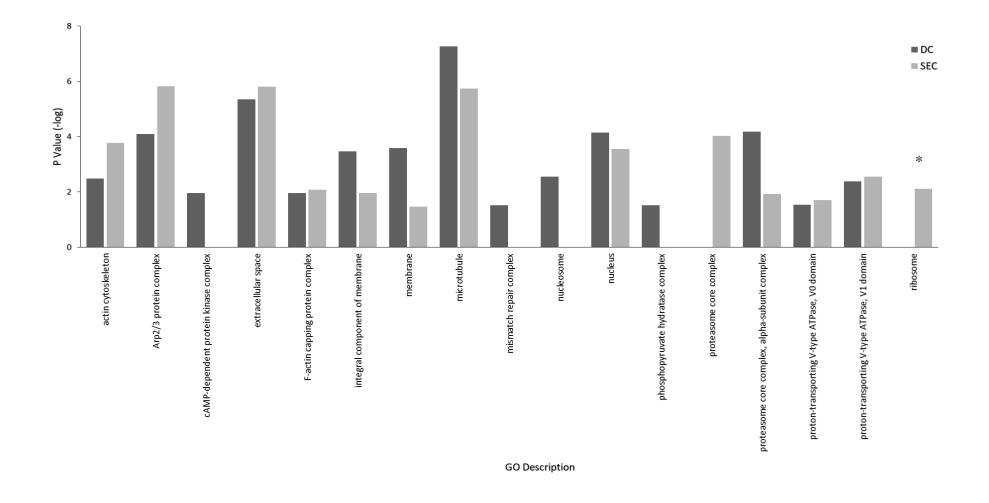
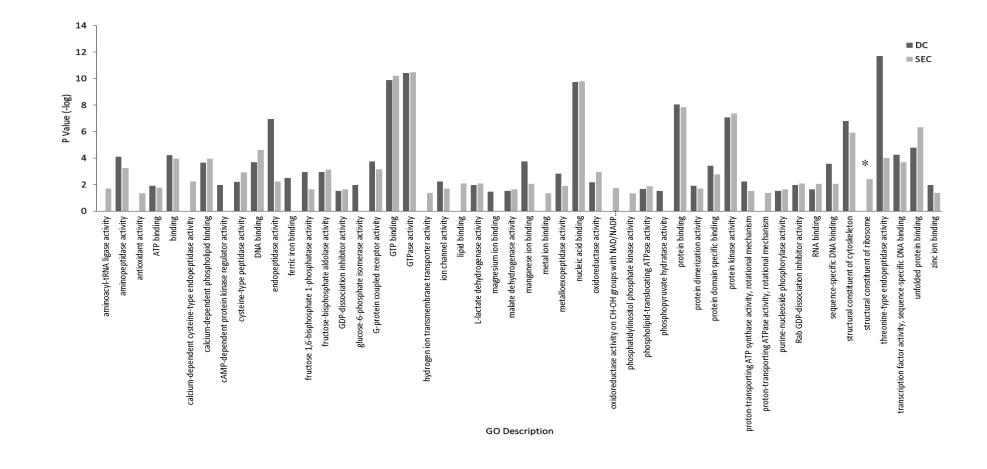


Gene enrichment analysis comparison between SEC and DC *F. hepatica* EV purification methods within biological process categories against the *F. hepatica* genome. Significant processes lower than 0.05 probability, presented using -log transformation were identified by asterisks. Data analysed using GOATOOLS in python software.



Gene enrichment analysis comparison between SEC and DC purification methods within cellular component categories against the *F. hepatica* genome. Significant processes lower than 0.05 probability, presented using -log transformation were identified by asterisks. Data analysed using GOATOOLS in python software.



Gene enrichment analysis comparison between SEC and DC purification methods within molecular function categories against the *F. hepatica* genome. Significant processes lower than 0.05 probability, presented using -log transformation were identified by asterisks. Data analysed using GOATOOLS in python software.