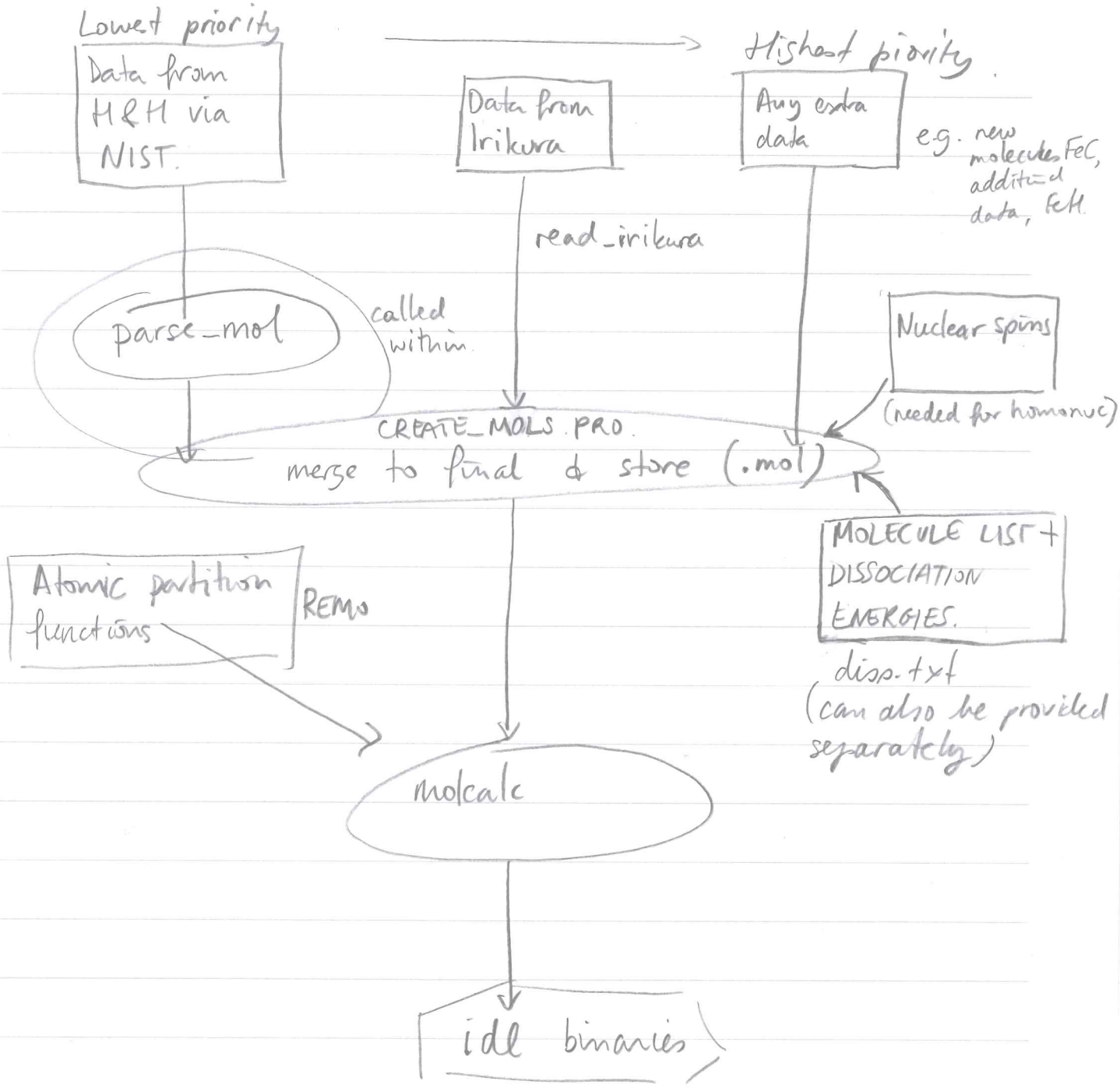

Everything need to calculate a specific molecule should be in .mol file, since best for simplicity.

Problems arising in parsing molecule list
(ie. html → dat)

BeS $^{1}\Sigma$ which should be $(B\,^{1}\Sigma^{+})$

HBr missing superscript
$(^{1}\Sigma^{+}, ^{1}\Pi)$
also need to deal with these double labels.

For BeS, a hard fix was put in parse_mol.
For HBr, "
specifically in relabel routine

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A Stellar Journey

Following molecules not in NIST, but in diss.tot

HeH^+ (SET)	TiC	CS^- (SET)	TiF
CH^+ (SET)	FeC		VF
ScH^+	NiC	FeS	CoF
TiH^+		CoS	
VH^+	ScN	NiS	TiCl
CrH^+	CrN	ZnS	VCl
MnH^+			
FeH^+	TiO^+		CuSc (SET)
CoH^+	ZrO^+		
NiH^+			
CuH^+			

These have no states:

ScH	CN^-	CoO	ClF
TiH		ZnO	CrF
VH	CS^-	LaO	
FeH			AuSi
PdH	VN	BO^-	
			VS
HS^-			
		CrCl	
		CoCl	