

flags_pssm

```
-parser:script_vars blade4=# comma separated list of protein names and  
pssm paths, e.g. 1bf6A:pssm/blade4/1bf6A.pssm,1bf6B:pssm/  
blade4/1bf6B.pssm  
-parser:script_vars blade5=# comma separated list of protein names and  
pssm paths, e.g. 1bf6A:pssm/blade5/1bf6A.pssm,1bf6B:pssm/  
blade5/1bf6B.pssm  
-parser:script_vars blade6=# comma separated list of protein names and  
pssm paths, e.g. 1bf6A:pssm/blade6/1bf6A.pssm,1bf6B:pssm/  
blade6/1bf6B.pssm  
-parser:script_vars blade7=# comma separated list of protein names and  
pssm paths, e.g. 1bf6A:pssm/blade7/1bf6A.pssm,1bf6B:pssm/  
blade7/1bf6B.pssm
```

flags_pross

```
-ex1  
-ex2  
  
-nodelay  
-use_input_sc  
-extrachi_cutoff 8  
-ignore_unrecognized_res  
-chemical:exclude_patches LowerDNA UpperDNA Cterm_amidation  
SpecialRotamer VirtualBB ShoveBB VirtualDNAPhosphate VirtualNTerm  
CTermConnect sc_orbitals pro_hydroxylated_case1 pro_hydroxylated_case2  
ser_phosphorylated thr_phosphorylated tyr_phosphorylated tyr_sulfated  
lys_dimethylated lys_monomethylated lys_trimethylated lys_acetylated  
glu_carboxylated cys_acetylated tyr_diiodinated N_acetylated  
C_methylamidated MethylatedProteinCterm  
-jd2:ntrials 5  
-overwrite  
-out:file:fullatom  
-pdb_comments true ## this is the mover reads the comments in the  
input pdb file. The comments contain the pdb segments comprising the  
input pdb  
  
-out:path:pdb pdb/  
-mute protocols.toolbox.task_operations.SeqprofConsensusOperation  
-no_nstruct_label  
#-mute devel.splice.Splice_constraints  
#-mute devel.splice.SpliceSegment  
#-mute protocols.rosetta_scripts.RosettaScriptsParser  
#-mute core.pack.rotamer_set.SampleRotamersFromPDB_RotamerSetOperation  
#-mute all
```

```
-unmute protocols.jd2.JobDistributor
-unmute devel.splice.util
-unmute protocols.simple_filters.ScoreTypeFilter

-parser:protocol filterscan_auto_xds.xml
@flags_pssm
```

flags_pross1

```
-ex1
-ex2

-nodelay
-use_input_sc
-extrachi_cutoff 8
-ignore_unrecognized_res
-chemical:exclude_patches LowerDNA UpperDNA Cterm_amidation
SpecialRotamer VirtualBB ShoveBB VirtualDNAPhosphate VirtualNTerm
CTermConnect sc_orbitals pro_hydroxylated_case1 pro_hydroxylated_case2
ser_phosphorylated thr_phosphorylated tyr_phosphorylated tyr_sulfated
lys_dimethylated lys_monomethylated lys_trimethylated lys_acetylated
glu_carboxylated cys_acetylated tyr_diiodinated N_acetylated
C_methylamidated MethylatedProteinCterm
-jd2:ntrials 5
-overwrite
-out:file:fullatom
-pdb_comments true ## this is the mover reads the comments in the
input pdb file. The comments contain the pdb segments comprising the
input pdb

-out:path:pdb pdb/
-mute protocols.toolbox.task_operations.SeqprofConsensusOperation
-no_nstruct_label
#-mute devel.splice.Splice_constraints
#-mute devel.splice.SpliceSegment
#-mute protocols.rosetta_scripts.RosettaScriptsParser
#-mute core.pack.rotamer_set.SampleRotamersFromPDB_RotamerSetOperation
#-mute all
-unmute protocols.jd2.JobDistributor
-unmute devel.splice.util
-unmute protocols.simple_filters.ScoreTypeFilter
```

```
-parser:protocol filterscan_auto_xds.xml
@flags_pssm
```

```
flags_pross2
```

```
-ex1
```

```
-ex2
```

```
-nodelay
```

```
-use_input_sc
```

```
-extrachi_cutoff 8
```

```
-ignore_unrecognized_res
```

```
-chemical:exclude_patches LowerDNA UpperDNA Cterm_amidation
```

```
SpecialRotamer VirtualBB ShoveBB VirtualDNAPhosphate VirtualNTerm
```

```
CtermConnect sc_orbitals pro_hydroxylated_case1 pro_hydroxylated_case2
```

```
ser_phosphorylated thr_phosphorylated tyr_phosphorylated tyr_sulfated
```

```
lys_dimethylated lys_monomethylated lys_trimethylated lys_acetylated
```

```
glu_carboxylated cys_acetylated tyr_diodinated N_acetylated
```

```
C_methylamidated MethylatedProteinCterm
```

```
-jd2:ntrials 5
```

```
-overwrite
```

```
-out:file:fullatom
```

```
-pdb_comments true ## this is the mover reads the comments in the
input pdb file. The comments contain the pdb segments comprising the
input pdb
```

```
-out:path:pdb pdb/
```

```
-mute protocols.toolbox.task_operations.SeqprofConsensusOperation
```

```
-no_nstruct_label
```

```
#-mute devel.splice.Splice_constraints
```

```
#-mute devel.splice.SpliceSegment
```

```
#-mute protocols.rosetta_scripts.RosettaScriptsParser
```

```
#-mute core.pack.rotamer_set.SampleRotamersFromPDB_RotamerSetOperation
```

```
#-mute all
```

```
-unmute protocols.jd2.JobDistributor
```

```
-unmute devel.splice.util
```

```
-unmute protocols.simple_filters.ScoreTypeFilter
```

```
-parser:protocol design_auto_xsd.xml
```

```
@flags_pssm
```

flags_splice_in

```
-ex1
-ex2
-nodelay
-use_input_sc
-extrachi_cutoff 8
-ignore_unrecognized_res
-chemical:exclude_patches LowerDNA UpperDNA Cterm_amidation
SpecialRotamer VirtualBB ShoveBB VirtualDNAPhosphate VirtualNTerm
CTermConnect sc_orbitals pro_hydroxylated_case1 pro_hydroxylated_case2
ser_phosphorylated thr_phosphorylated tyr_phosphorylated tyr_sulfated
lys_dimethylated lys_monomethylated lys_trimethylated lys_acetylated
glu_carboxylated cys_acetylated tyr_diiodinated N_acetylated
C_methylamidated MethylatedProteinCterm
-jd2:ntrials 5
-overwrite
-out:file:fullatom
-pdb_comments true ## this is the mover reads the comments in the
input pdb file. The comments contain the pdb segments comprising the
input pdb

-parser:protocol splice_in_xsd.xml
-parser:script_vars start_pdb=2vc5B_ppk.pdb

#-mute all
-out:path:pdb pdb/
@flags_pssm
-no_nstruct_label
```