wwPDB EM Validation Summary Report (i)

Mar 5, 2026 – 09:41 PM UTC

PDB ID	:	7KZN / pdb_00007kzn
EMDB ID	:	EMD-23083
Title	:	Outer dynein arm core subcomplex from C. reinhardtii
Authors	:	Walton, T.; Wu, H.; Brown, A.B.
Deposited on	:	2020-12-10
Resolution	:	4.00 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

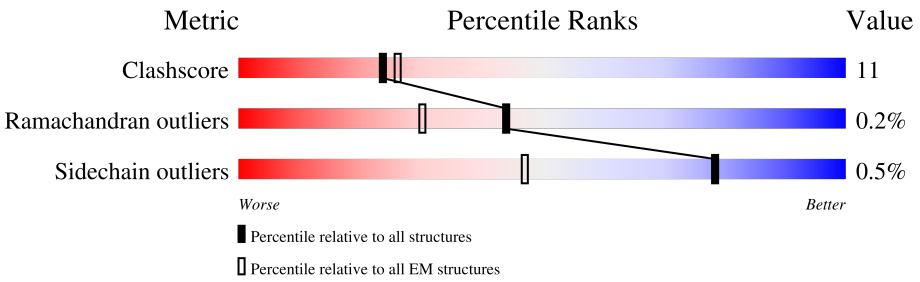
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

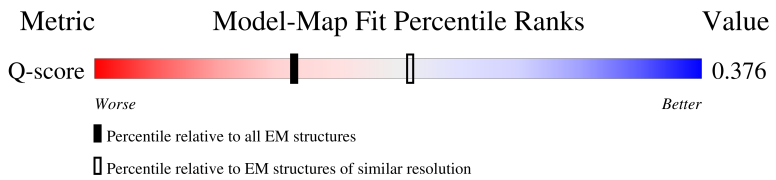
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	7587 (3.50 - 4.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	4503	6% 7% 93%
2	B	4568	11% 85%
3	C	4485	17% 5% 78%
4	D	683	47% 19% 33%

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Mol	Chain	Length	Quality of chain
5	E	567	53% 29% 16%
6	F	136	13% 74% 26%
7	G	159	9% 67% 20% 13%
8	H	120	71% 5% 24%
9	I	105	72% 25%
10	J	100	78% 16% 6%
11	K	91	64% 26% 10%
11	L	91	65% 25% 10%
11	M	91	59% 31% 10%
11	N	91	8% 80% 10% 10%
12	O	117	12% 81% 17%
13	P	103	72% 22% 5%
14	X	121	100%
15	Y	168	99%
16	Z	184	18% 62% 23% 15%

2 Entry composition (i)

There are 16 unique types of molecules in this entry. The entry contains 31205 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Heavy chain alpha.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	A	315	1544	914	315	315	0	0

- Molecule 2 is a protein called Flagellar outer dynein arm heavy chain beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	683	5028	3180	878	946	24	0	0

- Molecule 3 is a protein called Dynein gamma chain, flagellar outer arm.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	965	7293	4574	1296	1386	37	0	0

- Molecule 4 is a protein called Dynein, 78 kDa intermediate chain, flagellar outer arm.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	456	3609	2297	610	678	24	0	0

- Molecule 5 is a protein called Dynein, 70 kDa intermediate chain, flagellar outer arm.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	474	3697	2332	623	725	17	0	0

- Molecule 6 is a protein called Flagellar outer dynein arm light chain 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	F	100	495	295	100	100	0	0

- Molecule 7 is a protein called Dynein 18 kDa light chain, flagellar outer arm.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	138	1089	677	183	220	9	0	0

- Molecule 8 is a protein called Dynein 11 kDa light chain, flagellar outer arm.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	H	91	451	269	91	91	0	0

- Molecule 9 is a protein called Dynein light chain roadblock LC7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	103	827	525	148	153	1	0	0

- Molecule 10 is a protein called Dynein light chain roadblock LC7b.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	94	741	466	133	140	2	0	0

- Molecule 11 is a protein called Dynein 8 kDa light chain, flagellar outer arm.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	82	671	433	112	122	4	0	0
11	L	82	671	433	112	122	4	0	0
11	M	82	671	433	112	122	4	0	0
11	N	82	Total	C	N	O		0	0
			407	243	82	82			

- Molecule 12 is a protein called Dynein light chain 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	O	97	481	286	97	98	0	0

- Molecule 13 is a protein called Dynein light chain 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	P	98	805	523	128	146	8	0	0

- Molecule 14 is a protein called DC1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	X	121	605	363	121	121	0	0

- Molecule 15 is a protein called DC2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	Y	168	840	504	168	168	0	0

- Molecule 16 is a protein called Outer dynein arm-docking complex protein DC3.

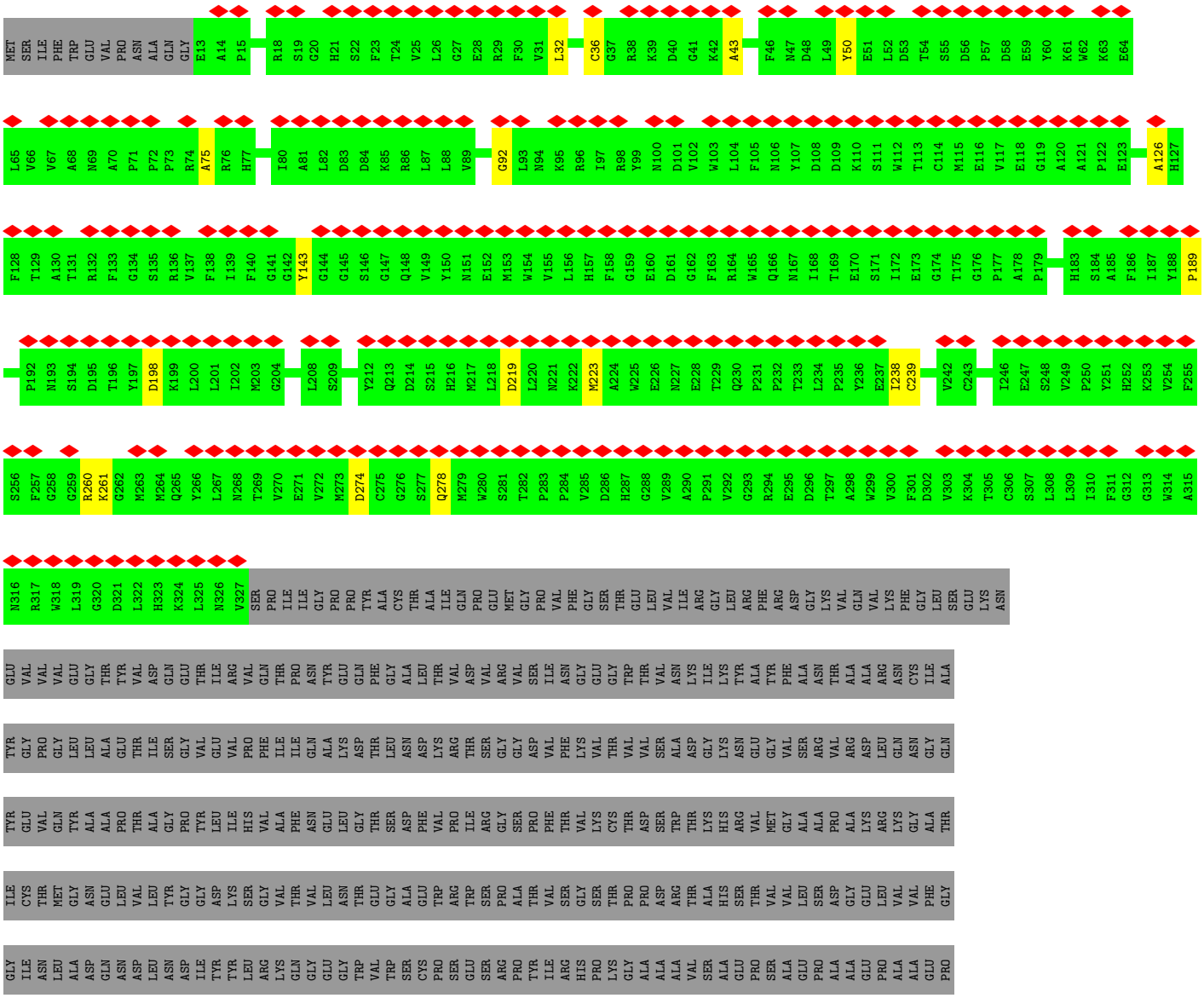
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	Z	157	1280	798	221	252	9	0	0

3 Residue-property plots (i)

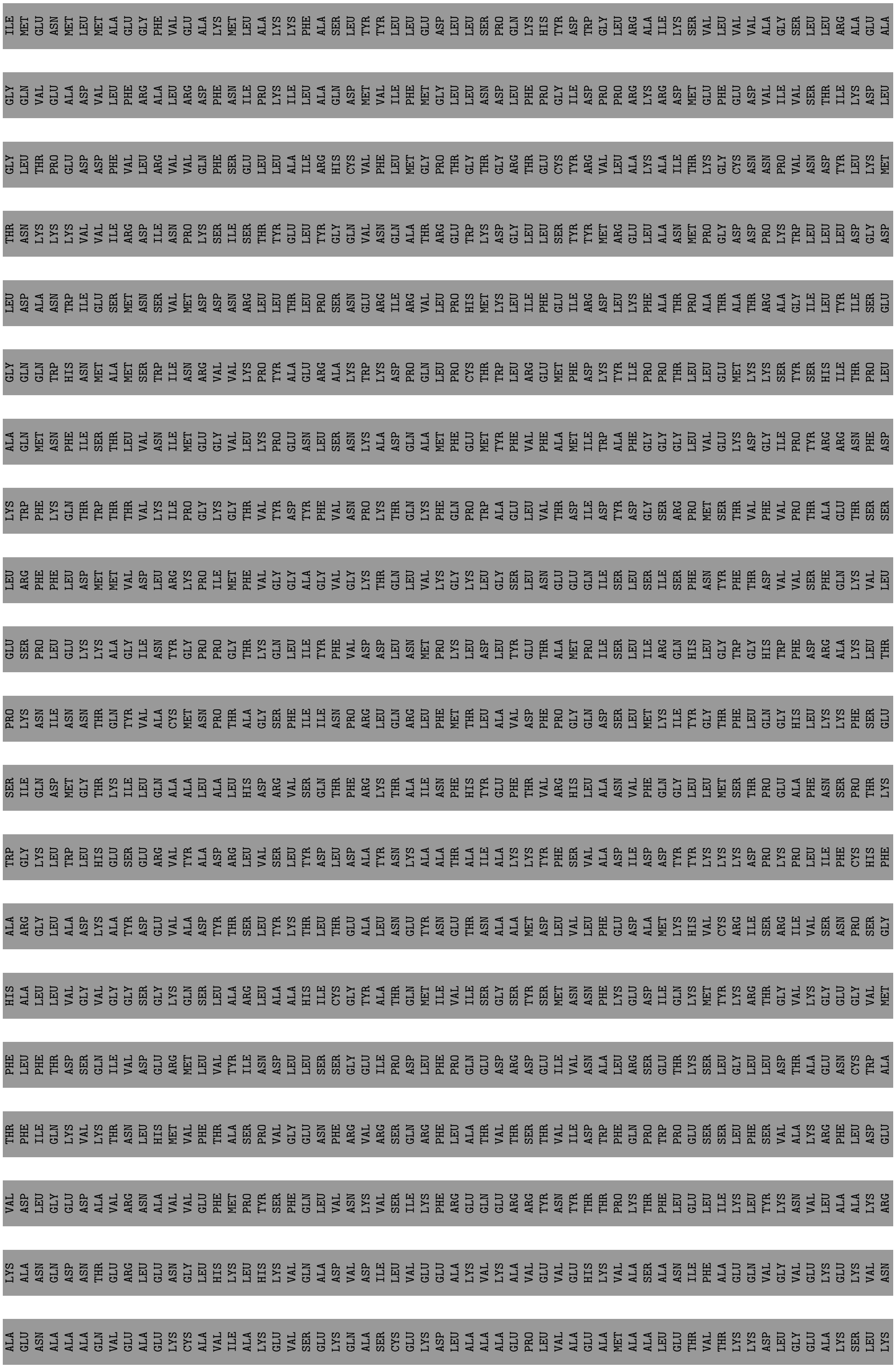
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Heavy chain alpha

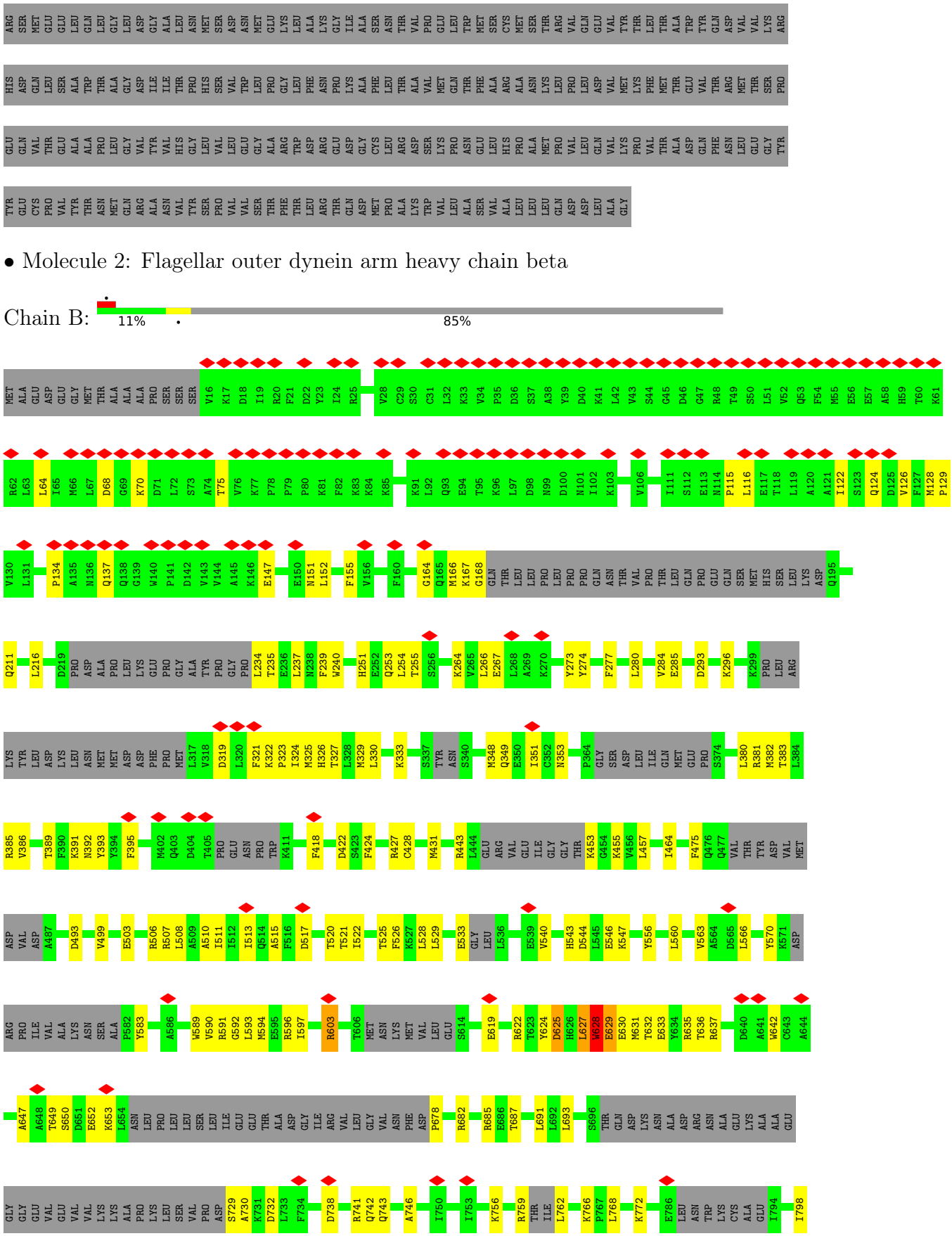
Chain A: 6% 7% 93%



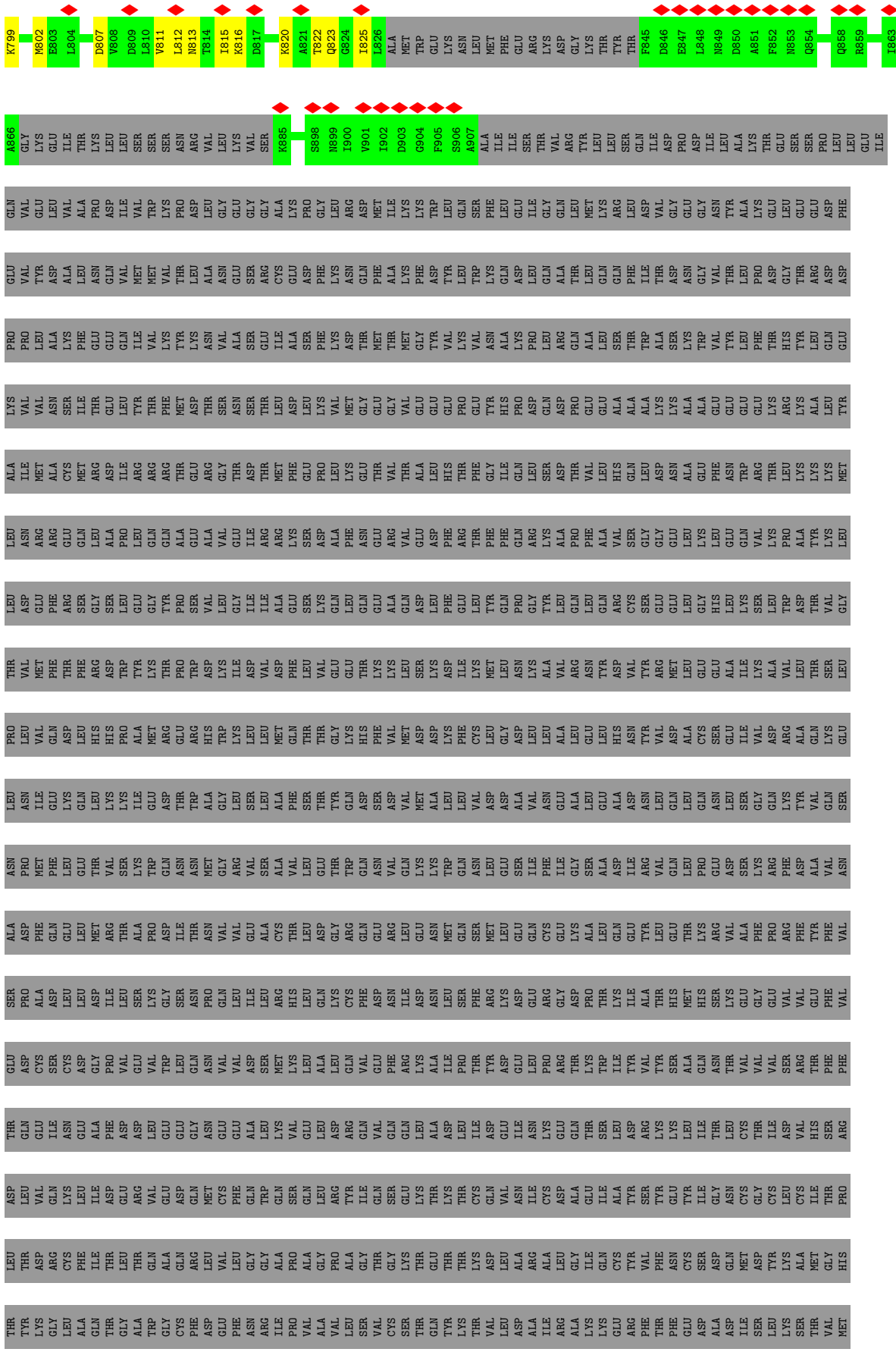
LYS HIS PRO ALA VAL GLU HIS TRP SER PHE ILE ALA ALA ASP GLY VAL GLU MET PRO LEU GLU GLY THR SER ALA PHE ILE THR MET VAL ASN PRO GLY TYR ILE LYS ARG ALA GLU LEU GLY THR VAL GLN LYS LYS LYS THR GLY ARG GLN LEU
MET GLY ASP ILE PHE LYS GLY LEU ALA ALA SER GLY SER TRP GLY CYS PHE ASP GLU PHE ASN ARG LEU VAL PRO GLU VAL CYS SER VAL GLN TYR LYS CYS VAL THR ASP SER ALA LEU GLY LYS LYS THR MET LEU PRO GLY ARG GLY LYS ASP LEU GLU VAL GLY VAL
ILE THR PRO LEU THR ASP ARG ILE TYR ILE THR ALA THR GLN ALA CYS TRP LEU SER LEU GLY THR ALA PRO ALA GLY LYS ASP ARG GLY THR THR GLU THR ASP SER ALA GLN LEU GLY LYS SER VAL TYR VAL GLY ASN GLN LYS ASP LEU ALA ALA ARG THR
HIS SER ARG ASP MET VAL LEU ALA VAL ILE ILE GLU ALA ALA GLY ASP ALA ASP GLN PRO ASP SER PHE GLN TRP VAL SER GLN LEU ARG SER TYR TRP ASP ARG ASP ILE SER ASP CYS ARG ILE ARG ILE CYS ASP ALA SER PHE PRO TYR GLY TYR GLU TYR LEU GLY ASN GLY ARG ASP VAL
ILE TYR TRP CYS LEU GLU VAL GLU GLN ALA PHE THR GLU MET ALA ARG GLY ASP LYS ILE ILE ALA MET SER LYS GLN GLN THR VAL LYS GLN LEU ILE GLU VAL THR ARG THR ASP LEU PRO LEU PHE ASP PRO ASP ARG ILE THR LYS ILE MET ASN MET ILE THR ILE ASP ASN
PRO PHE SER SER PRO LEU PRO LEU GLU ASN LYS VAL GLU GLN TYR MET VAL ASP ASP ILE ILE ALA LYS MET ARG ASN GLU LEU ARG MET VAL LEU LYS ALA SER VAL GLU ASP TYR PRO SER LYS PRO ARG ASP LYS TRP LEU PHE ASP TRP PRO SER GLN ILE VAL GLN GLN
PRO PHE SER ALA ASP LEU LEU ASP ILE LEU SER ASN GLY ASN ASN PRO MET ARG VAL GLN ILE HIS MET ASN LYS CYS PHE GLN ALA ILE ASP LYS LEU ARG LEU ASP SER GLU GLU GLU VAL VAL PRO GLY ARG ARG PRO LYS ALA LEU GLU SER ARG ARG ALA PHE PRO ARG PHE TYR VAL
ASP THR GLU VAL LYS LYS VAL LEU ARG GLU PHE GLN GLN LEU LYS ASN ASP CYS VAL SER CYS CYS ASN ARG GLU GLY LEU TYR ALA ASN LEU GLU THR GLN GLU ARG GLU LEU GLU ILE CYS LYS LYS ALA LEU ASN ASP TYR MET GLU SER LYS ARG ARG PHE ALA ALA PHE
TYR MET ALA THR PHE LYS ASP GLU ILE LEU LEU GLY TRP GLN LYS LYS LEU ASN ASP VAL ASN GLN ILE MET ALA GLU ILE GLN ARG TRP GLN LEU LEU TYR LEU ARG ASP VAL ALA ASP PHE GLU ILE HIS SER CYS LEU PHE ILE HIS SER GLU GLU VAL LYS LYS GLU GLU ALA
ALA GLN LYS GLU GLU LYS MET GLU ILE ALA LYS ILE ARG ARG ASP ASP THR TRP THR ARG VAL GLU GLN PHE HIS ARG HIS LYS ASP TYR ASP VAL HIS THR ARG GLU GLU ASP ASP LEU LEU ALA LEU GLU LEU GLU ASP PHE GLU ALA LEU GLU ASP ASN GLN VAL GLN VAL GLN GLY MET ILE ALA ASN ARG
VAL SER VAL PRO LEU VAL ALA ASP LEU ARG SER PRO ALA MET ARG ASP ARG HIS TRP GLU GLN LEU MET ALA THR THR LYS MET THR PHE ASN VAL LYS ASP PRO ASN VAL PHE LYS LEU ASP PRO LEU LEU ALA LEU GLU LEU HIS LYS PHE GLU GLU GLU VAL GLU ILE VAL ASP ARG
THR ALA VAL LEU CYS GLU LEU GLN PHE GLN ASP TRP ARG GLN THR LEU TRP SER ASP ILE ARG THR ASP ILE MET GLU GLU GLY ALA LYS GLN PHE VAL LYS GLU VAL LYS SER LEU HIS LYS LYS VAL ARG ASP GLU ASP VAL PHE ARG GLY VAL ASP GLN VAL VAL LYS ASN PHE LEU
PHE ASP GLY ALA TYR PRO LEU LEU ASP ALA ALA ALA HIS GLU LEU ALA GLU LEU LYS LYS GLU CYS ASP ARG LEU SER GLU LEU ALA SER VAL PHE GLU PHE PRO VAL THR VAL ALA ILE LYS GLU VAL MET VAL LYS ASP VAL TRP ASP
ALA ALA ALA HIS LYS TRP ASP GLU ILE LYS LYS ALA GLN PRO GLN VAL LYS THR ASP VAL GLU PRO ILE GLN ALA ALA LYS GLY GLU ASP ILE LYS LYS GLU ILE GLU THR PHE ALA ALA LYS VAL ARG ASN TYR ARG ALA ASP PHE ARG ARG ARG GLY PHE PHE LYS TYR ALA THR GLY
SER PRO GLU LYS LEU SER LYS ASP PHE GLU GLU LEU LYS ARG LEU LEU ASP ALA LEU PHE GLN VAL LYS SER GLN THR ASP PHE GLU LEU GLN ARG SER GLN THR ASP LEU LEU ILE ASP GLN LEU HIS GLU ALA PHE ALA GLN LEU ALA GLU GLU LYS VAL PRO GLY ILE ASN LYS MET GLU LYS ARG LEU GLU
PHE ASP GLU GLU LEU LEU ASP ALA ALA ALA HIS GLU LEU LEU LYS LYS ALA ALA ASP ARG LEU SER GLU LEU ALA ALA SER VAL PHE GLU PHE PRO VAL THR VAL ALA ILE LYS LYS VAL ARG ASP GLU ASP VAL PHE ARG GLY VAL ASP GLN VAL VAL LYS ASP VAL TRP ASP
THR ALA VAL LEU CYS GLU LEU GLN PHE GLN ASP TRP ARG GLN THR LEU TRP SER ASP ILE ARG THR ASP ILE MET GLU GLU GLY ALA LYS GLN PHE VAL LYS GLU VAL LYS SER LEU HIS LYS LYS VAL ARG ASP GLU ASP VAL PHE ARG GLY VAL ASP GLN VAL VAL LYS ASN PHE LEU
VAL SER VAL PRO LEU VAL ALA ASP LEU ARG SER PRO ALA MET ARG ASP ARG HIS TRP GLU GLN LEU MET ALA THR THR LYS MET THR PHE ASN VAL LYS ASP PRO ASN VAL PHE LYS LEU ASP PRO LEU LEU ALA LEU GLU LEU HIS LYS PHE GLU GLU GLU VAL GLY GLU ILE VAL ASP ARG
ALA GLN LYS GLU GLU LYS MET GLU ILE ALA LYS ILE ARG ARG ASP ASP THR TRP THR ARG VAL GLU GLN PHE HIS ARG HIS LYS ASP TYR ASP VAL HIS THR ARG GLU GLU ASP ASP LEU LEU ALA LEU GLU LEU GLU ASP PHE GLU ALA LEU GLU ASP ASN GLN VAL GLN VAL GLN GLY MET ILE ALA ASN ARG
TYR MET ALA THR PHE LYS ASP GLU ILE LEU LEU GLY TRP GLN LYS LYS LEU ASN ASP VAL ASN GLN ILE MET ALA GLU ILE GLN ARG TRP GLN LYS LYS LEU ASN ASP VAL ALA ASP VAL GLU GLN PHE HIS SER CYS LEU PHE ILE HIS SER GLU GLU VAL LYS LYS GLU LEU PRO GLN ALA ALA ILE
ASP THR GLU VAL LYS LYS VAL LEU ARG GLU PHE GLN GLN LEU LYS ASN ASP CYS VAL SER CYS CYS ASN ARG GLU GLY LEU TYR ALA ASN LEU GLU THR GLN GLU ARG GLU LEU GLU ILE CYS LYS LYS ALA LEU ASN ASP TYR MET GLU SER LYS ARG ARG PHE PHE PRO ARG PHE TYR PHE
VAL SER SER ALA ASP LEU LEU ASP ILE LEU SER ASN GLY ASN ASN PRO MET ARG VAL GLN ILE HIS MET ASN LYS CYS PHE GLN ALA ILE ASP LYS LEU ARG LEU ASP SER GLU GLU GLU VAL VAL PRO GLY ARG ARG PRO LYS ALA LEU GLY MET GLU SER GLN GLU ARG ALA THR GLU ILE GLU TYR VAL
PRO PHE SER SER PRO LEU PRO LEU GLU ASN LYS VAL GLU GLN TYR MET VAL ASP ASN ILE ILE ALA LYS MET ARG ASN GLU LEU ARG MET VAL LEU LYS ALA SER VAL GLU ASP TYR PRO SER LYS PRO ARG ASP LYS TRP LEU PHE ASP TRP PRO SER GLN ILE VAL ALA ILE LEU ASN
ILE TYR TRP CYS LEU GLU VAL GLU GLN ALA PHE THR GLU MET ALA ARG GLY ASP LYS ILE ILE ALA MET SER LYS GLN GLN THR VAL LYS GLN LEU ILE GLU VAL THR ARG THR ASP LEU ARG PRO ASP ARG ILE THR ILE MET ASN MET ILE THR ILE ASP ALA
HIS SER ARG ASP MET VAL LEU ALA VAL ILE ILE GLU ALA ALA GLY ASP ALA ASP GLN PRO ASP SER PHE GLN TRP VAL SER GLN LEU ARG SER TYR TRP ASP ARG ASP ILE SER ASP CYS ARG ILE ARG ILE CYS ASP ALA SER PHE PRO TYR GLY TYR GLU TYR LEU GLY ASN GLY ARG ASP VAL
ILE THR PRO LEU THR ASP ARG ILE TYR ILE THR ALA THR GLN ALA CYS TRP LEU SER LEU GLY LYS ASP LEU SER ALA GLN LEU GLY LYS LYS THR MET LEU PRO GLY ARG GLY LYS THR GLU THR THR LYS ASP LEU SER ALA ALA GLN LEU GLY LYS LYS THR MET VAL TYR VAL PHE ASN CYS SER PRO GLU MET ASP TYR ARG THR
MET GLY ASP ILE PHE LYS GLY LEU ALA ALA SER GLY SER TRP GLY CYS PHE ASP GLU PHE ASN ARG LEU VAL PRO GLU VAL CYS SER VAL GLN TYR LYS CYS VAL THR ASP SER ALA LEU GLY LYS LYS THR MET LEU PRO GLY ARG GLY LYS LYS THR GLU TYR ILE LYS ASP VAL GLU
LYS HIS PRO ALA VAL GLU HIS TRP SER PHE ILE ALA ALA ASP GLY VAL GLU MET PRO LEU GLU GLU GLY THR SER ALA PHE ILE THR MET ASN PRO GLY TYR ILE LYS ARG ALA GLU LEU PRO GLU SER LEU LYS ALA LEU PHE ARG PRO ILE THR VAL MET VAL PRO ASP ARG GLN LEU



LYS PRO PRO PRO GLY VAL ASP ASP ILE THR ALA VAL VAL ILE ILE LEU LEU GLU ASN ASN PRO LYS ASP LYS SER TRP GLN ALA ALA GLN LYS LEU MET ASN ASN VAL ASP LYS PHE LEU GLU ARG VAL LYS SER PHE LYS SER VAL ILE ASP ALA GLY GLN VAL ALA ARG LYS THR VAL
ASP ALA CYS ARG PRO TYR LEU ALA LEU GLU TRP PHE ASN ARG GLU ALA ILE GLY LYS LYS SER ALA ALA ALA ALA ALA GLY LEU CYS GLU TRP ALA VAL ASN ILE ILE LYS TYR TYR ASP VAL VAL GLN GLU VAL GLU PRO LYS ARG GLN GLU LEU ALA ALA ALA ALA GLU GLU
ALA ASN VAL THR LEU ALA ALA VAL GLU GLU GLU LYS VAL ALA ALA LEU LEU LEU ASN ALA LYS VAL GLN GLU LEU LEU GLN GLN TYR LYS GLU ALA ASN ASP ASP LYS GLU ALA ALA ILE ARG GLU SER GLU ARG CYS GLN ARG LYS LEU ILE ASN ARG LEU ILE ALA ALA LEU
GLY GLU ARG TRP ALA LEU THR VAL GLU GLN LEU ARG LYS SER TYR GLU VAL LEU THR GLY ASP MET LEU LEU LEU PRO SER ALA LEU LEU ALA ALA PHE VAL SER TYR TYR ALA GLN LEU ILE ASP ASP TRP ILE LEU PHE LEU ARG GLU GLU ARG LEU ILE ASN ALA LEU THR GLU
GLY ILE THR ASP PRO LEU LYS VAL LEU VAL ASP ASP ALA LEU VAL ALA GLY TRP ILE ARG GLU GLY LEU PRO SER ASP PRO THR SER VAL GLN ASN GLY THR ILE LEU LEU THR ASN SER GLU ARG ALA GLN LEU ILE MET MET ASP PRO GLN LEU GLN GLY GLY ILE LEU TRP ILE LYS GLU THR GLU
SER LYS ASN ASN LEU GLN VAL THR ARG MET GLY ALA SER ASN MET LEU GLN VAL MET GLU ARG ALA ILE GLU ALA GLY HIS SER VAL LEU VAL GLU ASN MET GLY GLU THR ILE ASP ALA ILE GLU ASN PRO ILE ILE THR ARG SER LYS LYS GLY GLY LYS PHE LEU GLU TYR TYR LYS LYS
LEU GLY ASP LYS GLU CYS GLU TYR ASN LYS ASN PHE ARG LEU PHE LEU HIS THR LYS LEU SER ASN PRO HIS TYR PRO PRO GLU ILE GLN ALA GLU THR THR LEU LEU ILE ASN PHE THR VAL THR GLU ALA GLY LEU GLU GLU ASP GLN LEU LEU ALA LEU ARG PRO ASP
LEU GLU GLU THR LYS THR GLN LEU ILE ILE GLN ASN THR GLU PHE THR ILE LYS LEU LYS GLU LEU GLU ASP GLY LEU LYS LEU SER THR ALA GLU GLU GLY ASP ILE THR GLU ASP VAL ALA LEU ILE GLU SER LEU GLU ASP ALA LYS ARG VAL SER THR GLU ILE SER GLU LYS
VAL LYS GLU SER ARG GLU THR GLU ALA ALA ILE ASN GLU ASN ARG ASN LYS TYR ARG THR VAL ALA ALA ARG GLY ALA MET LEU PHE PHE LEU LEU ASN SER LEU LYS ILE HIS ALA PHE TYR GLN PHE SER LEU ASN ALA PHE VAL THR VAL PHE SER ARG GLY LEU ASP ALA
PRO GLY GLY ARG LYS LYS GLY LEU LYS LYS THR PRO SER LEU ARG ASP GLN PRO MET ASP HIS GLN SER LEU MET GLU LYS ALA ARG ARG SER SER GLY VAL GLY ASP ARG ARG PRO SER GLN GLU GLY LEU PRO GLY PRO GLU ALA SER GLN ALA SER LEU ALA GLU SER GLN
GLY GLY ARG GLY SER GLN VAL GLY ASP ALA ALA GLU ASP ASP ASP GLU SER PHE ALA MET ALA PRO GLU ALA LEU GLU GLN ARG LEU VAL ASN LEU LEU GLU THR CYS THR PHE THR VAL TYR ASN TYR THR ARG ARG GLY LEU PHE ASP ARG ASP LYS LEU ILE VAL LEU LEU LEU
THR PHE THR ILE LEU LEU ARG SER GLN SER ALA ALA VAL ASP ALA SER GLU TYR GLU ALA LEU CYS ARG GLY MET ARG ASN PRO THR PRO PRO PRO ILE THR ASP ASP LEU SER ARG TRP MET ALA GLU SER GLN TRP ALA ALA LEU ASP VAL LEU LEU THR THR LEU PRO CYS PHE ALA HIS LEU ALA
LYS ASP MET GLU LYS ASN SER ASP ASP TRP PHE ASN TRP CYS ASN ASN GLU ALA ALA ALA ARG ALA PRO MET PRO GLY GLU TRP GLY LYS LEU THR GLU PHE ARG GLN LEU LEU ILE ILE ARG ALA LEU ARG PRO LEU LYS GLU ILE HIS HIS MET MET
GLY SER ASP TYR VAL ASN GLN ASP ALA PHE SER PRO ALA ALA MET MET ASP GLU SER SER SER ALA THR PRO ILE PHE PHE ILE LEU PHE PRO GLY TYR SER PRO SER LYS GLU ILE GLU VAL TYR ALA ASN LYS CYS GLY TYR SER VAL ALA ASN GLY LEU LEU ILE ILE SER MET
GLY GLN GLY GLN GLU ALA ALA PRO ALA GLU ALA ALA VAL LEU ASP ASP LYS ASP LYS TYR THR ARG GLU GLY GLY TRP VAL PHE LEU ASP VAL HIS LEU MET GLN GLY TRP ILE PRO LYS LEU GLU ILE ALA ALA ARG LYS LEU GLU ARG CYS PHE ASP PHE ARG CYS ASP PHE PHE ALA ALA PRO
ILE ASN GLY ALA PRO HIS ALA ASN ILE ILE PRO GLU SER ILE LEU GLN THR CYS ILE LYS ILE SER ASN GLU PRO PRO SER ASP MET LYS SER ASN MET ARG ALA PHE ALA ALA ALA PHE THR PRO GLU CYS ASP ARG PRO ALA VAL ARG ALA PHE THR ARG ILE ILE
LEU PHE GLY LEU CYS PHE TYR HIS SER LEU LEU LEU GLY VAL GLY SER GLY SER GLY LEU LEU GLY PHE CYS ARG GLY ASP VAL GLU ALA HIS PRO ASP PHE ARG CYS PHE PHE GLY ASP LEU THR THR CYS GLY ASP VAL LEU TYR ASN TYR GLU ALA SER THR PRO GLY ILE
TRP ARG ASP LEU GLN TYR MET PHE GLY GLU VAL PHE TYR GLY GLY HIS ILE THR ASP SER MET ASP ARG ARG CYS CYS THR THR TYR LEU GLU VAL LEU ILE ARG ASN GLU ILE LEU PRO LYS GLY ASN PRO ASP GLU VAL GLU ALA TRP GLU ALA PRO THR GLU LEU GLU ALA PRO GLY
PHE PHE ALA PRO LYS PRO VAL ASP TYR PRO THR VAL SER LEU GLU SER PRO VAL VAL MET HIS PRO ASN ALA GLU LEU LEU LEU THR THR SER LEU GLY GLU THR LYS THR VAL GLU GLU VAL GLY GLY GLY GLY GLY GLY
GLY GLY GLY GLY GLY GLY GLU ASN ALA VAL ARG GLN ALA LEU GLU THR PHE LYS GLU ARG VAL LYS GLU LYS THR PRO PHE VAL VAL ALA LEU GLN GLU ALA THR ARG MET ASN ALA LEU LEU SER GLU MET LYS



• Molecule 2: Flagellar outer dynein arm heavy chain beta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E803
L804
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D809
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V811
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N813
T814
I815
K816
D817
K820
A821
T822
Q823
G824
I825
L826
ALA MET TRP GLU LYS ASN LEU MET PHE GLU ARG LYS ASP GLY LYS THR TYR THR
F845
D846
E847
L848
N849
D850
A851
F852
N853
Q854
Q858
R859
I863
R864
D865
A866
GLY LYS GLU ILE THR LYS LEU LEU SER SER SER ASN ARG VAL LEU LYS VAL SER
K885
S898
N899
I900
V901
I902
D903
G904
F905
S906
A907
ALA ILE ILE SER THR VAL ARG TYR LEU LEU SER GLN ILE ASP PRO ASP ILE LEU ALA LYS LYS THR ASP PHE
GLN VAL GLU LEU VAL ALA PRO ASP ILE VAL TRP LYS PRO ASP LEU GLY GLU GLY GLY LYS PRO GLY LEU ARG ASP MET ILE LYS LYS TRP LEU GLN SER PHE LEU GLU ILE GLY GLN LEU MET LYS ARG LEU ASP VAL GLY GLU GLY ASN TYR ALA LYS GLU LEU GLU GLU ASP
GLU VAL TYR ASP ALA LEU ASN GLN VAL MET MET VAL THR LEU ALA ASN GLU SER ARG CYS GLU ASP PHE LYS ASN GLN PHE ALA LYS PHE ASP TYR LEU TRP LYS GLN ASP LEU GLN ALA THR LEU GLN GLN PHE ILE THR ASP ASN GLY VAL THR LEU PRO ASP GLY THR ARG ASP
PRO PRO LEU ALA LYS PHE GLU GLU GLN ILE VAL LYS TYR LYS ASN VAL ALA SER GLU ILE ALA SER PHE LYS ASP THR MET THR MET GLY TYR VAL LYS VAL ASN ALA LYS PRO LEU ARG GLN ALA LEU SER THR TRP ALA SER LYS TRP VAL TYR LEU PHE THR HIS TYR LEU GLN GLU
LYS VAL VAL ASN SER ILE THR GLU LEU TYR THR PHE MET ASP THR SER ASN SER THR LEU ASP LEU LYS VAL MET GLY GLU GLY GLY VAL GLU GLU PRO GLU TYR HIS PRO ASP GLN ASP PRO GLU GLU ALA ALA ALA ALA LYS LYS ALA ALA GLU GLU GLU GLU LYS ARG LYS ALA LEU TYR
ALA ILE MET ALA CYS MET ARG ASP ILE ARG ARG THR GLU ARG GLY THR ASP THR MET PHE GLU PRO LEU LYS GLU THR VAL THR ALA LEU HIS THR PHE GLY ILE GLN LEU SER ASP THR VAL LEU HIS GLN LEU ASP ASN ALA GLU PHE ASN TRP ARG THR LEU LYS LYS LYS MET
LEU ASN ARG ARG GLU GLN GLN LEU ALA PRO LEU GLN GLN ALA GLU ALA VAL GLU GLU ILE ARG LYS SER ASP ALA PHE ASN GLU ARG VAL THR ALA GLU ASP PHE ARG THR PHE PHE GLN ARG LYS ALA PRO PHE ALA VAL SER GLY GLY GLU LEU LYS LEU GLU GLN VAL LYS PRO ALA TYR LYS LEU
LEU ASP GLU PHE ARG SER GLY SER LEU GLU GLU GLY TYR PRO SER VAL LEU GLY ILE ILE ALA GLU SER LYS GLN LEU GLN GLN GLU ALA GLN ASP LEU PHE GLU LEU TYR GLN PRO GLY TYR LEU GLN LEU GLN ARG CYS SER GLU GLU LEU GLY HIS LEU LYS SER LEU TRP ASP THR VAL GLY
THR VAL MET PHE THR PHE ARG ASP TRP TYR LYS THR PRO TRP ASP PHE LEU VAL GLU GLU THR LYS LYS LEU SER LYS ASP ILE LYS MET LEU ASN LYS ALA VAL ARG ASN TYR ASP VAL TYR ARG MET LEU GLU GLU ALA ILE LYS ALA LEU THR SER LEU
PRO LEU VAL GLN ASP LEU HIS HIS PRO ALA MET MET ARG GLU ARG HIS TRP LYS LEU LEU MET GLN THR THR GLY LYS HIS PHE VAL MET ASP ASP LYS PHE CYS LEU LEU GLY ASP LEU LEU ALA LEU GLU LEU HIS ASN TYR VAL ASP ALA CYS SER GLU ILE VAL ASP ARG ALA GLN LYS GLU
LEU ASN ILE GLU LYS GLN LEU LYS LYS ILE GLU ASP THR TRP ALA GLY LEU SER LEU ALA PHE SER THR TYR GLN ASP SER ASP VAL MET ALA LEU LEU VAL ASN GLU ALA LEU GLU ALA LEU GLU LEU ASP ASN VAL LEU GLN LEU GLN GLN ASN LEU LEU SER GLY GLN LYS TYR ARG VAL GLN
ASN PRO MET PHE LEU GLU THR VAL SER LYS TRP GLN ASN ASN MET GLY ARG VAL SER ALA VAL LEU GLU THR TRP GLN ASN VAL GLN LYS LYS TRP GLN ASN ASN GLU LYS SER ALA ASP ILE ARG VAL GLN LEU GLU PRO GLU ASP SER LYS ARG PHE ASP ALA ALA VAL ASN
ALA ASP PHE GLN GLU LEU MET ARG THR ALA PRO ASP ILE THR ASN VAL VAL GLU ALA CYS THR LEU ASP GLY ARG GLN GLU ARG ILE GLU ASN MET GLN SER ASP LEU GLU ILE CYS GLU LYS ALA LEU GLN GLN GLU TYR LEU GLU VAL PHE PHE VAL
SER PRO ALA ASP LEU LEU SER ASP ILE LEU LEU ILE LEU ARG HIS LEU GLN LYS CYS PHE ASP ASN ILE ASP ASN LEU SER PHE ARG LYS ASP GLU ARG GLY ASP PRO THR LYS ILE ALA TYR VAL GLU PHE GLU GLY LYS THR HIS MET HIS SER LYS GLU GLY GLU VAL VAL PHE VAL
GLU ASP CYS SER CYS ASP GLY PRO VAL GLU LEU TRP LEU GLN ASN VAL VAL ALA SER MET LYS LEU LEU ALA LEU GLN VAL GLU PHE ARG LYS ALA ILE PRO THR TYR ASP LEU GLU LEU PRO ARG THR LYS LEU ILE TYR VAL TYR SER ALA LYS GLU VAL VAL VAL SER ARG THR PHE PHE
THR GLN GLU ILE ASN GLU ALA PHE ASP ASP LEU GLU GLU GLU ALA LEU LYS VAL LEU LEU ASP ARG GLN VAL GLU LEU ALA ASP LEU ILE ASP GLU ILE ASN LYS GLU GLN THR SER LEU ASP ARG LYS LYS LEU ILE THR LEU CYS THR ILE ASP VAL HIS SER ARG
ASP LEU VAL GLN LYS LEU ILE ASP GLU GLN ARG VAL GLU ASP GLN MET CYS PHE GLN TRP GLN SER VAL GLU LYS THR THR LYS THR CYS GLN VAL ASN ILE CYS ASP ALA GLU ILE GLN THR SER LEU ALA TYR SER TYR GLU TYR ILE LYS ASN CYS THR ILE ASP VAL HIS SER PRO
LEU THR ASP ARG CYS PHE ILE ILE THR LEU THR GLN ALA GLN ARG LEU VAL LEU GLY GLY ALA PRO ALA GLY THR LYS THR GLU THR THR LYS ASP LEU ALA ARG ALA ALA LEU GLY GLY ILE GLN CYS TYR VAL PHE ASN CYS SER ASP GLN MET ASP TYR LYS ALA ALA ILE THR LEU CYS ASN GLY CYS THR ILE ASP ARG THR PHE
THR TYR LYS GLY LEU ALA GLN THR GLY ALA TRP GLY CYS PHE ASP GLN VAL LEU THR GLN GLU VAL ASN ARG ILE ALA PRO VAL ALA ALA VAL LEU SER VAL CYS SER THR GLN TYR LYS THR VAL LEU ASP ALA ILE ARG ALA LYS LYS GLU ARG PHE THR PHE GLU ASP ALA ASP ILE SER LEU LYS SER THR VAL MET

ALA PHE ILE THR MET ASN PRO GLY TYR PRO GLY ARG ALA GLU LEU PRO GLU SER LEU LYS ALA LEU PHE ARG PRO VAL SER MET VAL VAL PRO ASP LEU ALA LEU ILE CYS GLU ILE MET LEU MET ALA GLU GLY PHE GLN MET SER LYS ILE LEU SER ARG LYS PHE VAL ILE LEU TYR

LYS LEU CYS GLU ASP LEU LEU SER LYS SER ARG HIS TYR ASP TRP LYS LEU ARG ALA ILE LYS THR THR LEU TYR VAL ALA GLY GLY MET LYS ARG ALA ALA PRO GLU LEU SER GLU ASP LYS VAL LEU LEU ARG ALA LEU ARG ASP PHE ASN LEU GLY LYS LEU THR ALA ASP ASP THR

SER ILE PHE MET GLY LEU LEU ASN ASP LEU PHE PRO LYS THR LEU GLU LEU VAL PRO ARG ALA LEU ASP LYS ALA PHE ASP GLU ALA ALA HIS LYS ALA ALA THR GLU LEU GLY TYR GLN PRO ASP ASP GLN PHE LEU LEU LYS ILE SER GLN LEU ARG GLU LEU PHE VAL VAL ARG TRP

SER VAL PHE LEU LEU GLY ALA ALA GLY CYS GLY LYS THR ALA VAL TRP ARG THR LEU LEU ARG ALA GLN ASN SER SER GLY GLU LYS THR ILE TYR GLN ALA VAL ASN PRO LYS ALA VAL THR ARG ASN GLU LEU TYR GLY TYR LEU HIS PRO ALA THR ARG GLU TRP LYS GLU GLY LEU

MET SER VAL THR PHE ARG ASN MET ALA ASN ASN LYS THR ASN LYS HIS GLN TRP ILE VAL LEU ASP GLY ASP ILE ASP ALA GLU TRP ILE GLU SER MET ASN THR VAL MET ASP ASP ASN LYS MET LEU THR LEU ALA SER ASN GLU ARG ILE PRO LEU THR PRO SER MET ARG LEU LEU

LEU GLU ILE ASN HIS MET VAL HIS CYS SER PRO ALA THR VAL SER ARG GLY GLY VAL ILE PHE ILE ASN ALA ASP ASP VAL GLY TRP GLN PRO VAL VAL ALA SER TRP ILE ASP LYS LEU GLU ALA ALA GLU TYR ARG PRO LEU LEU THR ALA LEU PHE THR LYS TYR VAL ASP PRO CYS

LEU GLU HIS CYS ARG ARG ASN PHE LYS THR VAL VAL PRO LEU PRO ALA VAL ASN GLN ALA MET THR ILE CYS LYS ILE LEU GLU GLY ILE LEU PRO LYS GLU THR VAL ARG GLY ALA PRO PRO ASP LYS LYS LEU LEU HIS TYR HIS PHE VAL PHE ALA CYS VAL TRP ALA PHE GLY

GLY CYS MET LEU VAL ASP LYS VAL THR ASP TYR ARG THR GLN PHE SER LYS TRP TRP VAL SER GLU TRP LYS ASP VAL GLN PHE PRO GLU LYS GLY LEU VAL TYR ASP TYR TYR VAL ASP GLU GLN ASN CYS ILE MET VAL PRO TRP GLU ASP ARG VAL THR LYS PHE GLN TYR ILE PRO

GLY ASP PHE THR SER LEU PHE VAL PRO THR VAL GLU THR THR ARG LEU THR TYR PHE LEU ASP SER LEU VAL SER ASN LYS HIS TYR ALA MET PHE VAL GLY ASN THR GLY THR GLY LYS SER ALA ILE MET VAL ASN LYS LEU ARG ASN MET ASP THR GLU THR MET SER PHE TYR THR

ILE ASN MET ASN SER LEU SER GLU ALA PRO ALA LEU GLN VAL ILE LEU GLU GLN PRO LEU GLU LYS LYS SER GLY VAL ARG TYR GLY PRO PRO GLY SER ARG ARG MET VAL TYR PHE VAL ASP ASP MET ASN MET PRO LEU VAL ASP LYS TYR ASP THR GLN SER SER ILE GLU LEU LEU

ARG GLN MET VAL ASP TYR HIS GLY TRP TYR ASP LYS VAL LYS ILE GLN LEU LYS GLU ILE ILE ASN CYS GLN MET ALA ALA CYS MET ASN PRO THR ALA GLY SER PHE ASN ILE THR PRO ARG MET GLN ARG HIS PHE VAL THR PHE ALA VAL GLN MET PRO ASN ALA GLU ILE THR ARG

ALA MET TYR TYR GLN ILE ILE ASP GLY HIS PHE SER SER PHE ASP VAL ASP VAL ALA LYS MET SER ASN LYS LEU VAL ASP ALA THR CYS GLU LEU HIS ARG ASN VAL MET HIS ASN PHE LEU PRO SER ALA VAL LYS PHE HIS TYR GLN PHE ASN LEU ARG ASP LEU SER ASN ILE THR

GLN GLY LEU THR ARG ALA ILE LYS GLU TYR TYR ARG GLU PRO VAL LYS VAL ALA ARG LEU TRP VAL HIS GLU CYS GLU ARG VAL PHE ARG ASP ARG MET ILE ASN GLU ALA ASP MET ALA LYS PHE ASP GLU PHE ARG VAL ALA VAL THR LYS LYS PHE PHE ASP ASP CYS GLY GLY MET

VAL ALA ILE GLU GLU ARG PRO LEU ILE TYR ALA SER HIS ALA SER MET THR THR TYR THR PRO GLU ASP VAL PRO VAL TYR ASN ALA LEU SER SER TYR ASP VAL LEU ARG LYS THR LEU GLU ASP LYS LEU ARG GLU TYR ASN GLU SER ASN ALA VAL MET ASP LEU VAL LEU PHE GLN GLN

ALA MET GLU HIS VAL THR ARG ILE ALA ARG ILE ILE ASP LEU PRO ARG GLY ASN ALA MET LEU VAL GLY VAL GLY GLY SER GLY LYS GLN SER LEU ALA ARG LEU ALA SER TYR ILE CYS GLY TYR GLU VAL TYR GLN ILE SER VAL SER SER THR TYR GLY ILE ASN ASP PHE LYS GLU

ASN LEU LEU GLY LEU TYR ARG LYS ALA GLY THR LYS GLY THR PRO ILE THR PHE LEU MET THR ASP ASN GLN ILE VAL LYS GLU GLY PHE LEU VAL TYR ILE ASN ASP LEU LEU SER THR GLY TYR ILE ALA ASP LEU PHE THR PRO GLU ASP LYS GLU ALA PHE THR ASN ALA VAL ARG

ASN GLU VAL LYS ALA ALA GLY ILE LEU ASP SER ALA GLU ASN CYS TRP ASP PHE PHE ILE ASP LYS VAL ARG LYS PHE LEU HIS ILE VAL LEU CYS PHE SER PRO VAL GLY ASP LYS PHE ARG ILE ARG ALA ARG GLN PHE PRO ALA LEU VAL ASN CYS THR MET PHE ASP TRP PHE HIS

GLY TRP PRO GLY GLU ALA LEU VAL SER VAL ALA GLN ARG PHE LEU VAL ASP VAL PRO ASN MET GLU GLU VAL VAL ARG GLU ASN ILE ALA TYR HIS MET ALA TYR ALA HIS GLN CYS VAL SER GLU ALA SER GLU ARG PHE LYS GLU ALA PHE ARG ARG TYR ASN TYR THR THR PRO LYS

SER TYR LEU GLU LEU ILE SER LEU TYR LYS MET LEU LEU GLN LEU LYS ARG ASP ASP LEU ARG ARG SER LYS GLU ARG LEU GLU ASN GLY ILE ASP LYS ILE ALA GLN ALA ALA GLN VAL THR ASP LEU GLN ARG VAL LEU LYS GLU GLU GLN ILE VAL VAL ASP GLU LYS ALA

GLN THR ASP GLU LEU ILE VAL SER ILE GLY LYS GLU LYS ALA ILE VAL ASP GLN ALA VAL GLU ALA GLY ARG GLU ASP GLU GLU ALA ALA THR ALA LEU GLN THR GLU VAL SER ALA PHE GLN ALA GLU CYS GLU ARG ASP LEU LEU GLU ALA GLU PRO ILE ILE ALA GLN ALA GLU ALA

ALA LEU ASN SER LEU ASN LYS LYS GLU LEU SER GLU LEU LYS SER PHE GLY SER PRO ALA ALA GLU ILE VAL GLN VAL ALA ALA ALA CYS LEU VAL LEU THR CYS GLY GLY LYS ILE PRO LYS ASP ARG ASP TRP ASN ALA GLY LYS LYS MET MET ALA ASP VAL ASN SER PHE LEU SER

SER LEU MET ASN PHE ASP LYS ASP ASN VAL PRO VAL VAL CYS VAL GLU VAL VAL GLU LYS ASP TYR ILE SER ASN PRO GLY PHE THR PRO ASP ASN ILE LYS GLY LYS SER ALA ALA CYS ALA GLY LEU CYS SER TRP VAL ILE ASN ILE CYS LYS TYR PHE ARG ILE TYR GLN VAL VAL

ALA PRO LYS ARG ALA ALA LEU ALA GLU ALA ASN LYS LYS LEU ASP THR ALA ASN LYS LYS LEU LYS VAL ILE ARG ASP GLU VAL LYS ARG LEU GLN ASP ARG VAL ALA LEU LEU GLU GLN SER LEU MET LYS ALA THR GLU ASP LYS ASN ALA ALA ILE ALA GLN ALA ASP ARG THR ALA

ARG LYS ALA GLN MET ALA GLU ARG LEU ILE ASN GLY LEU SER GLY GLU ASN THR ARG TRP GLY ALA GLU ILE LYS ARG LEU GLU SER LEU GLU GLY ARG LEU VAL GLY ASP VAL LEU ILE ALA SER ALA PHE VAL SER TYR ALA GLY PRO PHE ASN MET GLN PHE ARG LYS SER LEU VAL

ASP GLU LYS TRP LEU PRO ASP ILE ILE GLU ARG GLN ILE PRO MET THR GLN GLY ILE ARG PRO LEU ASP LEU LEU THR ASP ASP ALA THR LYS ALA LYS TRP ALA ASN GLU GLY LEU PRO THR ASP PRO LEU SER VAL GLU ASN GLY ALA ILE MET SER ASN ALA SER ARG TRP ALA LEU

MET ILE ASP PRO GLN LEU GLN GLY ILE LYS TRP ILE ILE ASN LYS GLU THR ASN ASN GLY LEU VAL ILE ILE GLN GLN SER GLN PRO LYS TYR ILE ASP GLN VAL ILE ASN CYS ILE GLU ASN GLY TRP PRO LEU LEU ILE GLU ASN LEU PRO VAL ASP ILE ASP ALA VAL LEU ASP PRO

VAL ILE GLY LYS MET THR ILE LYS LYS GLY ARG ASN ILE ILE MET LYS ILE GLY ASP ALA GLU VAL GLN TYR ASP SER ARG PHE ARG LEU TYR LEU GLN THR LYS LEU SER ASN PRO HIS PHE LYS PRO GLU VAL ALA ALA GLN THR THR LEU VAL ASN PHE CYS VAL THR GLU LYS GLY

LEU GLU ASP GLN LEU LEU ALA LEU VAL VAL ASP HIS GLU ARG PRO ASP LEU GLN GLU GLN ALA ALA GLY LEU VAL ARG SER LEU ASN GLU TYR ASN ILE THR LEU VAL GLU LEU GLU ASN ASN LEU LEU PHE ASN LEU ALA ASN ALA THR GLY ASN ILE LEU GLU ASN ILE GLU LEU ILE

GLU GLY LEU GLU GLU THR LYS ARG THR ALA VAL GLU ILE GLU GLU LYS VAL LYS LEU ALA LYS GLN THR GLU ILE GLN ILE ALA LYS ALA ARG GLU VAL TYR ARG PRO VAL ALA THR ARG GLY SER LEU THR TYR PHE LEU ILE ASP ASN LEU ASN ALA LEU ASP ARG VAL TYR HIS TYR

SER MET ALA ASN PHE VAL PHE VAL LEU LYS LYS GLY MET ASP MET THR PRO GLY GLY LYS ASP GLU SER LYS VAL PRO LEU ALA GLU ARG LEU ASN GLN GLU VAL ASP LEU ASP LYS ARG VAL GLU LEU LEU VAL GLU THR THR CYS PHE VAL LEU ILE GLY TYR VAL ALA GLN GLY LEU

PHE GLU ARG HIS LYS LEU ILE VAL ALA THR GLN LEU CYS MET GLN ILE LEU ARG SER ARG GLY GLU LEU HIS TYR ALA LYS PHE GLU TYR LEU LEU ARG GLY PRO LYS VAL MET GLY ALA ASP ASN PRO LEU HIS ASP TRP VAL SER ASP SER VAL TRP GLY SER VAL GLN ALA LEU LYS

GLU LEU ASP ASP TYR GLN GLY LEU PRO GLU ASP LEU ILE GLY SER SER LYS ARG TRP ARG GLU TRP MET GLU LEU GLU ARG PRO GLU ASP GLU PRO LEU PRO GLY ASP TRP LYS ARG MET GLN GLU PHE ASP LYS LEU LEU LEU PHE ARG ALA LEU ARG PRO ASP ARG LEU THR SER ALA

MET GLY ARG PHE VAL THR ASN MET LEU GLY ALA LYS TYR VAL THR SER GLN PRO TYR ASP LEU GLU ARG SER TYR GLN ASP ALA SER PRO GLY THR PRO ILE PHE VAL PHE LEU SER PRO GLY VAL ASP VAL ALA GLY SER VAL GLU ALA LEU GLY LYS LYS LEU GLY PHE THR LEU ASP

ASN GLY LYS TYR ALA SER VAL SER LEU GLY GLN GLY GLN GLU PRO ILE ALA MET ASP ARG LEU SER ALA ALA HIS LYS ASN GLY GLY TRP VAL LEU LEU GLN ASN ILE HIS LEU THR ILE ASP TRP THR THR ASN GLN LEU ASP LYS LYS VAL ASP LYS LEU VAL GLU GLY ALA HIS PRO

ASP PHE ARG LEU PHE LEU SER ALA GLU PRO PRO PRO SER LEU GLU ARG GLY LEU PRO ILE SER LEU LEU GLN ASN SER ILE LYS LEU THR ASN GLU PRO PRO GLU GLY LEU LYS ALA ASN LEU ARG ARG ALA TRP ASN ASN PHE ASN GLU GLU ILE LEU GLU SER CYS ALA LYS GLN ALA

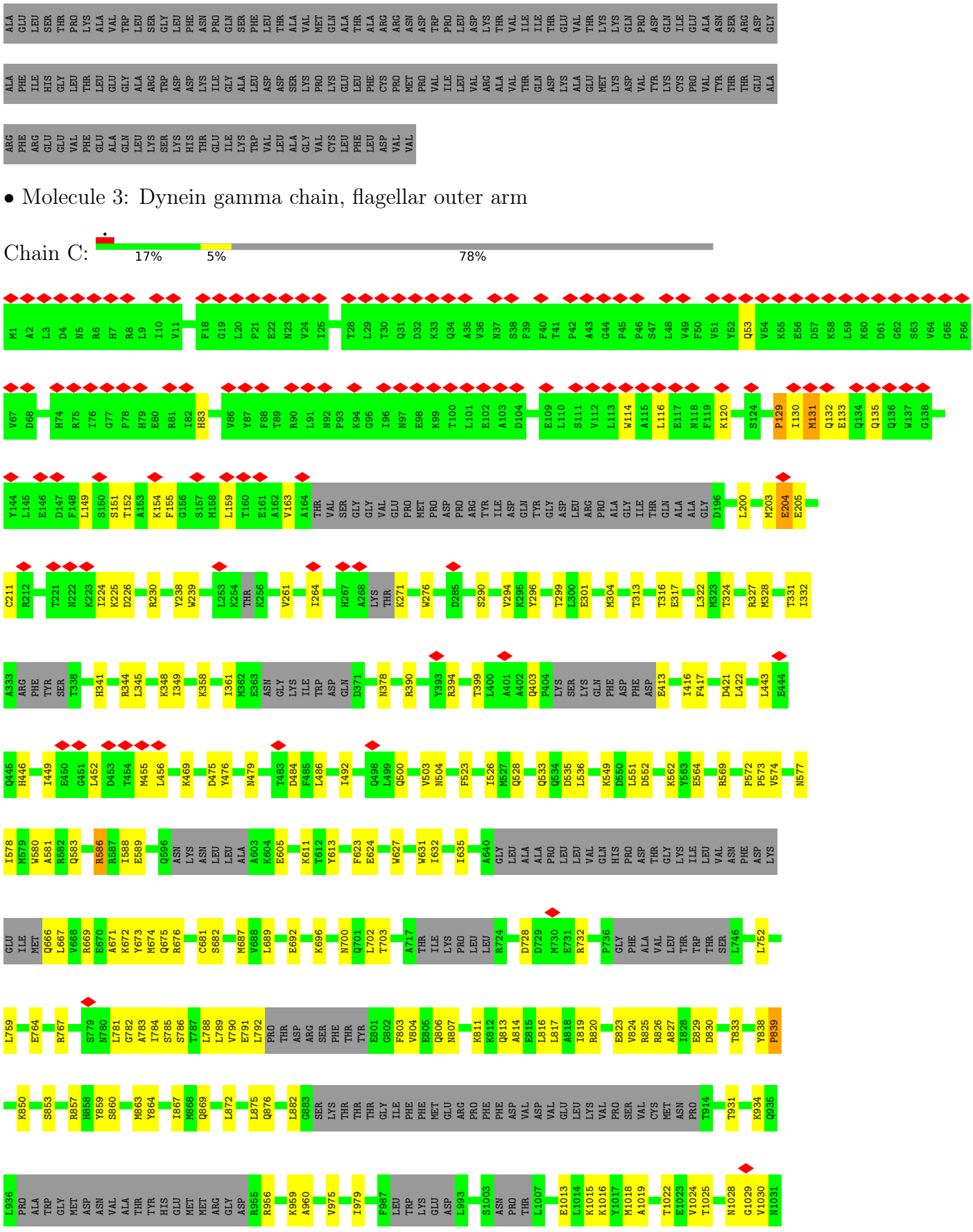
GLU PHE ARG ALA ILE VAL PHE ALA LEU CYS TYR PHE HIS ALA ALA LEU LEU GLU ARG LYS LYS PHE GLY VAL GLY ASN LEU PRO GLY ALA ARG SER GLY ILE GLY TRP ASN MET ASN TYR PRO PHE ASN THR GLY ASP LEU LEU CYS CYS GLY GLN THR ALA ASN ASN TYR LEU GLU ASN

ASN VAL LYS VAL PRO TRP GLU ASP LEU ARG TYR ASN PHE GLY GLU ILE MET TYR GLY GLY HIS ILE VAL GLU ASP TYR ASP ARG ARG LEU ALA MET CYS TYR LEU ARG LYS TYR VAL ASN GLU GLY LEU LEU ASP ASN MET GLU PHE PHE PRO GLY PHE ALA MET PRO PRO ASN THR ALA

ASN HIS ARG GLN VAL LEU GLU PHE ILE ASP GLU VAL MET PRO PRO GLU THR PRO LEU ALA PHE GLY LEU HIS PRO ASN ALA GLU ILE GLY PHE LYS LEU ARG GLU ALA GLU SER PHE CYS ASN SER LEU VAL GLN LEU GLN PRO ARG GLU SER SER GLY GLU GLY GLY MET SER ALA GLU

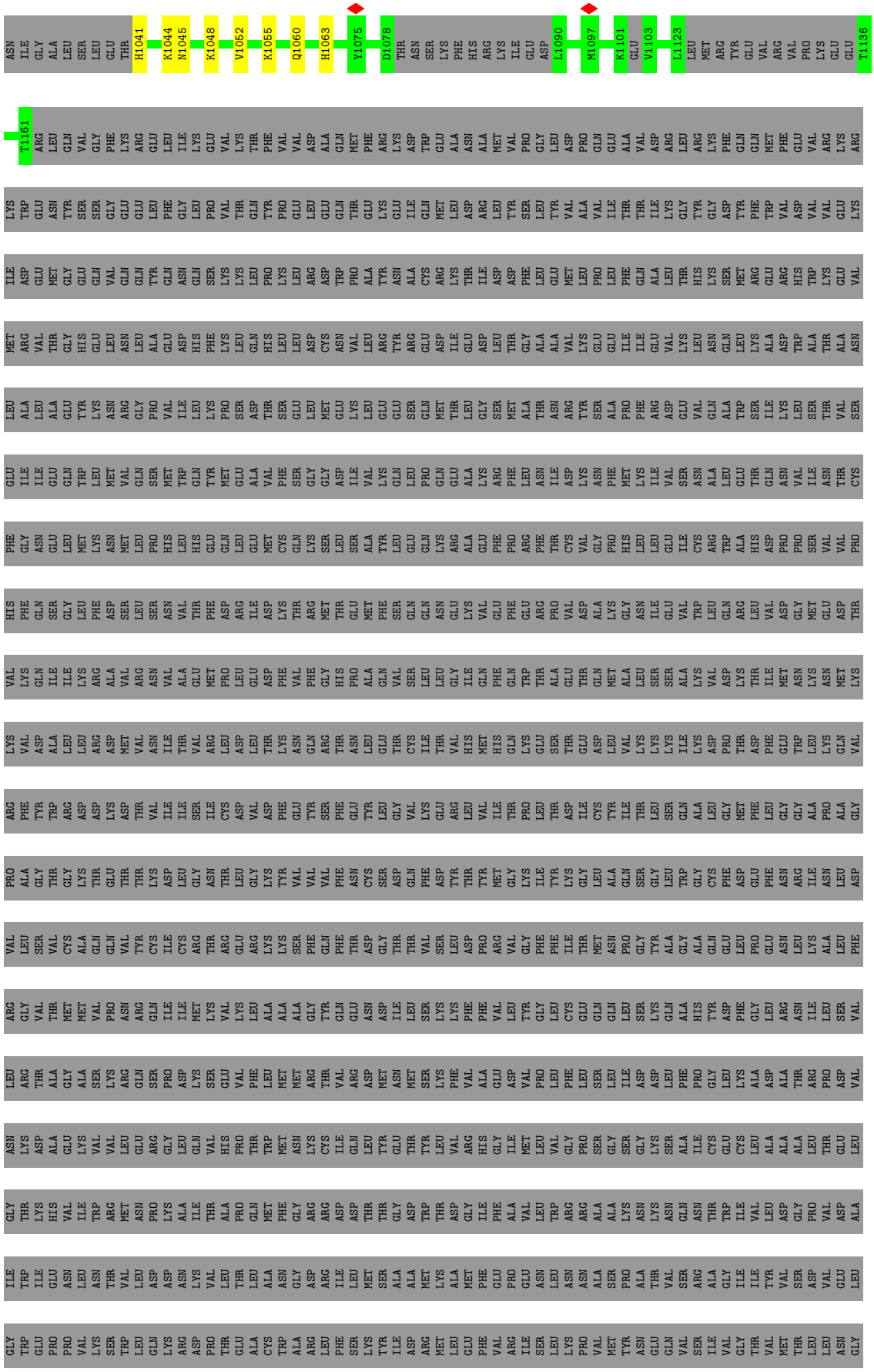
GLU ARG ALA LYS LEU VAL LEU ASP GLU VAL VAL ASP LYS LEU PRO ASP ILE PHE ASP MET GLU ASP VAL ARG SER LYS ILE ASN PRO ASP ASP PRO ASN MET PRO PHE VAL MET VAL ALA ILE GLN GLU SER GLU ARG MET ASN MET LEU LEU ALA GLU MET LYS ARG SER LEU LEU GLU

LEU ASP LEU GLY LEU LYS GLY ASP LEU THR MET THR GLU PRO MET GLU ARG LEU LEU LYS ALA LEU ALA THR ASP ALA VAL PRO GLY SER TRP ARG ASN LEU ALA TYR PRO SER LEU ARG PRO LEU GLY SER TRP LEU GLY ASN LEU LEU ALA ARG HIS ALA GLN LEU VAL ASP TRP THR



• Molecule 3: Dynein gamma chain, flagellar outer arm

Chain C: 17% 5% 78%


ASN ILE GLY ALA LEU SER LEU GLU THR H1041 K1044 N1045 K1048 V1052 K1055 Q1060 H1063 Y1075 D1078 THR ASN SER LYS PHE HIS ARG LYS ILE GLU ASP L1090 M1097 K1101 GLU V1103 L1123 LEU MET ARG TYR GLU VAL ARG VAL PRO LYS GLU GLU T1136
T1161 ARG LEU GLN VAL GLY PHE LYS ARG GLU GLU LEU ILE ILE GLU VAL LYS THR PHE VAL VAL ASP ALA GLN MET PHE ARG LYS ASP TRP GLU ALA ASN ALA ALA MET VAL PRO GLY LEU ASP PRO GLN GLU ALA VAL ASP ARG LEU ARG LYS PHE GLN GLN GLN MET PHE GLU VAL ASP ARG LYS SER MET PHE GLU VAL ARG LYS
LYS TRP GLU ASN TYR SER SER GLY GLU GLU GLU LEU PHE LYS PRO VAL THR GLN TYR PRO GLU LEU GLU GLN THR GLU LYS GLU ILE GLN MET LEU ASP ARG LEU TYR SER LEU TYR VAL ALA VAL ILE THR THR ILE LYS GLY TYR GLY ASP TYR PHE TRP VAL ASP TYR GLY LYS LYS
ILE ASP GLU MET GLY GLU GLN GLN VAL GLN GLN TYR GLN ASN GLN SER LYS LYS LEU PRO VAL THR ARG ASP TRP PRO ALA TYR ASN ALA CYS ARG LYS THR ILE ASP ARG LEU MET LEU PRO LEU PHE GLN ALA LEU THR HIS LYS SER MET ARG GLU ARG HIS TRP LYS GLU VAL
MET ARG VAL THR GLY HIS GLU LEU ASN LEU ALA GLU ASP HIS PHE LYS LEU GLN HIS LEU LEU ASP CYS ASN VAL LEU ARG TYR ARG GLU ASP ILE GLU ASP LEU THR GLY ALA ALA VAL LYS GLU GLU ILE ILE GLU VAL LYS ASP ALA THR ALA ASN
LEU ALA LEU ALA GLU TYR LYS ASN ARG GLY PRO VAL ILE LEU LYS PRO LEU SER GLU LEU GLU MET GLU LYS LEU GLU GLU SER GLN MET THR LEU GLY LEU ARG ASN THR ARG GLY TYR SER ALA PRO PHE ARG ASP GLU VAL GLN GLN ILE CYS ARG TRP ALA HIS ASP PRO PRO SER VAL VAL PRO
GLU ILE ILE GLU GLN TRP LEU MET VAL GLN SER MET TRP GLN TYR MET GLU ALA VAL PHE SER GLY GLY ASP ILE VAL LYS GLN LEU PRO GLN GLU ALA LYS ARG PHE LEU ASN ILE ASP LYS ARG PRO GLN LYS ARG ALA TYR LEU GLU GLN LYS ARG PHE THR CYS VAL GLY PRO HIS LEU LEU GLU ILE CYS ARG TRP ALA HIS ASP PRO PRO SER VAL VAL PRO
PHE GLY ASN GLU LEU MET LYS ASN MET LEU PRO HIS LEU HIS GLU GLN LEU GLU MET CYS GLN LYS SER LEU SER ALA TYR LEU GLU GLN LYS ARG ALA GLU PHE PRO ARG PHE THR CYS VAL GLY PRO HIS LEU LEU GLU VAL SER ASN ALA LEU GLU THR GLN GLN ASN VAL GLY ASN ILE GLU VAL ARG ALA ALA HIS ASP PRO PRO SER VAL VAL PRO
HIS PHE GLN SER GLY LEU PHE ASP SER LEU SER ASN VAL THR PHE ASP ARG ILE ASP LYS THR ARG MET THR GLU MET PHE SER GLN GLN GLN ASN GLU LYS VAL GLU PHE GLU ARG PRO VAL ASP ALA LYS GLY ASN ILE GLU VAL TRP LEU GLN ARG LEU VAL ASP GLY MET GLU VAL ASP THR
VAL LYS GLN ILE ILE LYS ARG ARG ALA VAL ARG ASN VAL ALA GLU MET PRO LEU GLU ASP PHE VAL PHE GLY HIS PRO ALA GLN VAL SER LEU LEU GLY ILE GLN PHE PRO GLU THR ALA GLU THR GLU GLU GLU ASP GLN MET ALA LEU SER SER ALA LYS VAL ASP LYS LYS ILE LYS ASP PRO THR ASP LYS ASN MET LYS
LYS VAL ASP ALA LEU LEU ARG ASP MET VAL ASN ILE THR VAL ARG LEU ASP LEU THR LYS ASN GLN ARG THR ASN LEU GLU THR CYS ILE THR VAL HIS MET HIS GLN LYS GLU SER THR GLU ASP LEU VAL LYS LYS LYS ILE LYS ASP PRO LYS LEU LYS GLN VAL
ARG PHE TYR TRP ARG ASP ASP ASP LYS ASP THR ASN ILE ILE SER ILE CYS ASP VAL ASP PHE GLU TYR LEU GLY VAL LYS GLU ARG LEU LEU THR ASP ILE CYS TYR ILE THR LEU SER GLN ALA LEU GLY MET PHE ASP GLU LEU ALA LEU GLY
PRO ALA GLY THR GLY LYS THR THR LYS ASP ASN GLY THR THR LYS ASN GLN ASN CYS SER ASP GLN PHE ASP TYR THR THR PHE ASN CYS SER ASP GLN PHE ASP TYR THR THR LYS GLY GLY LEU ALA GLN SER GLY LEU TRP GLY CYS PHE ASP GLU PHE ASN ARG ILE ASN LEU ASP
VAL LEU SER VAL CYS ALA GLN GLN VAL TYR CYS ILE CYS ARG THR ILE LYS LYS ARG ARG ARG LYS LYS ILE ILE SER PHE GLN PHE THR ASP GLY THR THR VAL SER LEU ASP PHE PHE ILE THR MET ASN PRO GLY TYR ALA GLY ALA ALA HIS GLY CYS GLU CYS LYS ILE
ARG GLY VAL THR MET MET VAL PRO ASN ARG GLN ILE ILE MET LYS VAL LYS LEU ALA ALA ALA GLY TYR GLN GLU ASN ASP ILE LEU SER LYS LYS PHE PHE VAL LEU TYR GLY LEU CYS GLU GLN GLN LEU SER LYS GLN ALA HIS TYR ASP PHE GLY LEU LYS ALA ASP ALA THR ARG ASN ILE LEU SER VAL
LEU ARG THR ALA GLY ALA SER LYS ARG GLN SER PRO VAL ASP ALA SER GLU VAL PHE LEU MET MET ARG THR VAL ARG ASP MET ASN MET SER LYS PHE VAL ARG ASP ILE LEU LEU ILE ASP ASP LEU PHE PRO GLY LEU LYS ALA ASP ALA THR ARG PRO VAL
ASN LYS ASP ALA GLU LYS VAL VAL ARG GLU GLU ARG GLY VAL LEU GLU VAL HIS PRO THR TRP MET ASN LYS CYS ILE GLN LEU TYR GLU THR TYR LEU VAL ARG HIS GLY ILE MET LEU VAL GLY PRO SER GLY LYS SER ALA ILE CYS GLU CYS LEU ALA ALA LEU THR GLU LEU
GLY THR LYS HIS VAL ILE TRP ARG MET ASN PRO LYS ALA ILE THR ALA PRO GLN MET PHE GLY ARG ARG ASP ASP THR THR GLY ASP TRP THR ASP GLY ILE PHE GLU PRO VAL VAL LEU TRP ARG ARG ALA ALA LYS ASN LYS ASN GLN VAL LEU ASP GLY PRO VAL ASP ALA
ILE TRP ILE GLU ASN LEU VAL THR ILE LEU LEU ASP ASP ASN LYS VAL LEU THR LEU ASN ALA ALA ILE LEU MET MET SER ALA ALA MET LYS ASP ASN ASN ALA ILE ILE LEU ASN ASN ALA SER PRO ALA THR VAL SER ARG ALA ILE VAL LYS GLU GLU LEU
GLY TRP GLU PRO PRO VAL LYS SER TRP LYS ARG LEU PHE SER LYS TYR ILE ASP ARG MET LEU GLU PHE VAL ARG ILE SER LEU LYS PRO VAL MET TYR ASN GLU GLN VAL SER ILE VAL GLY THR VAL MET THR LEU VAL GLY THR ASN ASN GLN ASN THR TRP ILE ILE VAL LEU ASP PRO VAL GLU LEU GLY

TYR LEU LYS SER MET LYS GLU ALA GLY THR ALA MET ASN ASP ALA LYS TYR GLU ARG VAL PHE LEU TYR CYS MET THR TRP SER LEU GLY GLY LEU LEU GLU MET LYS GLU ARG PRO LEU PHE ASP GLN GLU LEU ARG THR PHE ALA HIS ASN MET PRO PRO LYS GLU GLU ASP SER ASP

THR ILE PHE GLU PHE LEU VAL ASN THR THR ASP ALA GLU TRP LEU HIS TRP ARG HIS CYS VAL PRO VAL TRP THR TYR PRO LYS ASN GLU GLU LYS PRO GLN TYR ALA GLN LEU VAL ILE PRO THR LEU ASP SER VAL ARG TYR GLY ALA LEU LEU ASN LEU SER TYR ASN VAL ASP LYS

ALA THR LEU LEU VAL GLY GLY PRO GLY THR ALA LYS THR ASN THR ILE ASN GLN PHE ILE SER LYS PHE ASN ALA GLU THR THR ALA ASN LYS THR ILE THR PHE SER SER LEU THR THR PRO GLY ILE PHE GLN MET SER ILE GLU GLY ALA VAL GLU LYS ARG GLN GLY ARG THR PHE

GLY PRO PRO GLY GLY LYS GLN MET CYS ILE PHE VAL ASP ASP ILE SER MET PRO TYR ILE ASN GLU TRP GLY HIS GLN VAL THR ASN GLU ILE VAL ARG GLN LEU LEU GLU GLN GLY GLY MET TYR SER LEU GLU LYS PRO ILE GLY ASP MET LYS PHE ILE THR ASP VAL ARG TYR VAL

ALA ALA MET ASN THR PRO GLY GLY GLY LYS ASN ASP ILE PRO ASN ARG LEU LYS ARG GLN PHE ALA ILE PHE ASN VAL PRO LEU PRO SER VAL ALA ALA ILE ASN GLY ILE PHE GLY LYS LEU VAL GLU GLY ARG PHE SER ARG ASP VAL PHE CYS GLU GLU VAL VAL TYR VAL ALA SER

LYS LEU VAL PRO LEU THR ILE THR LEU TRP ASN ARG ILE GLN THR LYS MET LEU PRO THR PRO ALA LYS PHE HIS TYR LEU PHE ASN MET ARG GLU LEU SER LYS VAL PHE GLN GLY VAL ILE LEU ALA THR ARG ASP ARG PHE ASN LEU ALA ALA GLY ASP SER ALA VAL PHE GLY GLY

ASN VAL ALA SER PRO GLU GLY TYR LEU LEU GLY LEU TRP ILE HIS GLU CYS ARG ARG VAL PHE SER ASP LYS LEU ILE SER TYR GLU ASP LYS ASN TRP VAL ASP LYS ALA VAL PHE ASP LEU CYS ARG ASP ASN PHE SER SER ASP LEU VAL LYS GLN VAL GLU GLU PRO ILE TYR PHE

VAL ASP PHE LEU ARG GLU PRO ALA VAL MET MET ARG PRO VAL GLU ILE VAL THR PRO HIS PRO SER PHE TYR TYR SER VAL PRO GLY GLY LEU PRO GLU VAL ARG ALA ARG VAL GLU GLY LEU GLN ARG LYS PHE ASN GLU GLU SER LYS VAL MET LYS LEU GLU LEU VAL LEU PHE THR

ASP CYS VAL THR HIS LEU MET ARG ILE THR ARG LEU LEU ALA TRP PRO GLY LEU GLY LEU LEU VAL GLY VAL GLY GLY SER GLY LYS GLN SER LEU SER ARG LEU SER ALA TYR ILE ALA GLY PRO THR PHE TYR ILE THR LYS THR TYR ASN VAL SER ASN LEU PHE GLU HIS ILE LYS

GLY LEU TYR LYS ILE ALA GLY PHE LYS GLY GLN PRO VAL TYR PHE ILE PHE THR ASP ALA GLU VAL LYS ASP GLU GLY PHE LEU GLU TYR ILE ASN GLN ILE LEU MET THR GLY GLU VAL ALA GLY LEU LEU THR LYS GLU ASP GLN ASP MET ILE VAL ASN ASP ILE ARG PRO VAL MET

LYS HIS GLN ALA PRO GLY ILE LEU ASP THR TYR ASP ASN LEU TYR ASN PHE PHE LEU ASN ARG VAL ARG ASP ASN LEU HIS VAL VAL LEU CYS PHE SER PRO VAL GLY ALA LYS PHE ALA ARG ARG ALA GLN GLN PHE PRO GLY LEU ILE ASN GLY CYS THR ILE ASP TRP PHE CYS PRO

GLY PRO LYS LYS ARG LEU THR SER VAL SER GLY LYS PHE ILE ASP LYS PHE THR MET ALA CYS PRO LYS GLU VAL LYS ASN GLN LEU GLU LEU LEU MET GLY HIS ALA HIS VAL PHE VAL THR ALA ALA CYS LYS GLU TYR PHE GLU LYS TYR ARG ARG TYR VAL TYR VAL THR PRO LYS

SER TYR LEU SER PHE LEU GLN GLY TYR LYS GLU LEU TYR ALA LYS LYS TRP SER PHE THR LYS GLU LEU ALA TYR GLN ILE GLU VAL ALA CYS GLN LYS MET PHE GLU PRO LYS ALA ASP VAL ASN LYS MET LYS ALA GLU LEU ALA VAL LYS ASN GLN THR ALA VAL SER ALA LYS GLU

ALA GLU ALA LEU LEU LYS GLN ILE SER GLU SER THR ALA ILE ALA GLU LYS GLU LYS GLN LYS VAL ALA ALA ILE VAL ASP ALA VAL THR LYS LYS ALA SER GLU ILE ALA THR VAL LYS ASP ASP ALA GLU ARG ASP LEU ALA ALA ALA LYS PRO ALA LEU ASP ALA ALA LEU GLU ALA

LEU ASN SER ILE LYS ASP GLY ASP ILE LYS ASN LEU LYS ALA LEU LYS LYS PRO PRO GLN ILE ILE THR ARG ILE PHE ASP CYS VAL LEU VAL LEU ARG MET LEU PRO VAL THR LYS ALA GLU TYR THR ASP GLU LYS GLY ARG MET VAL GLN VAL GLY ASN TYR PRO GLU ALA GLN LYS

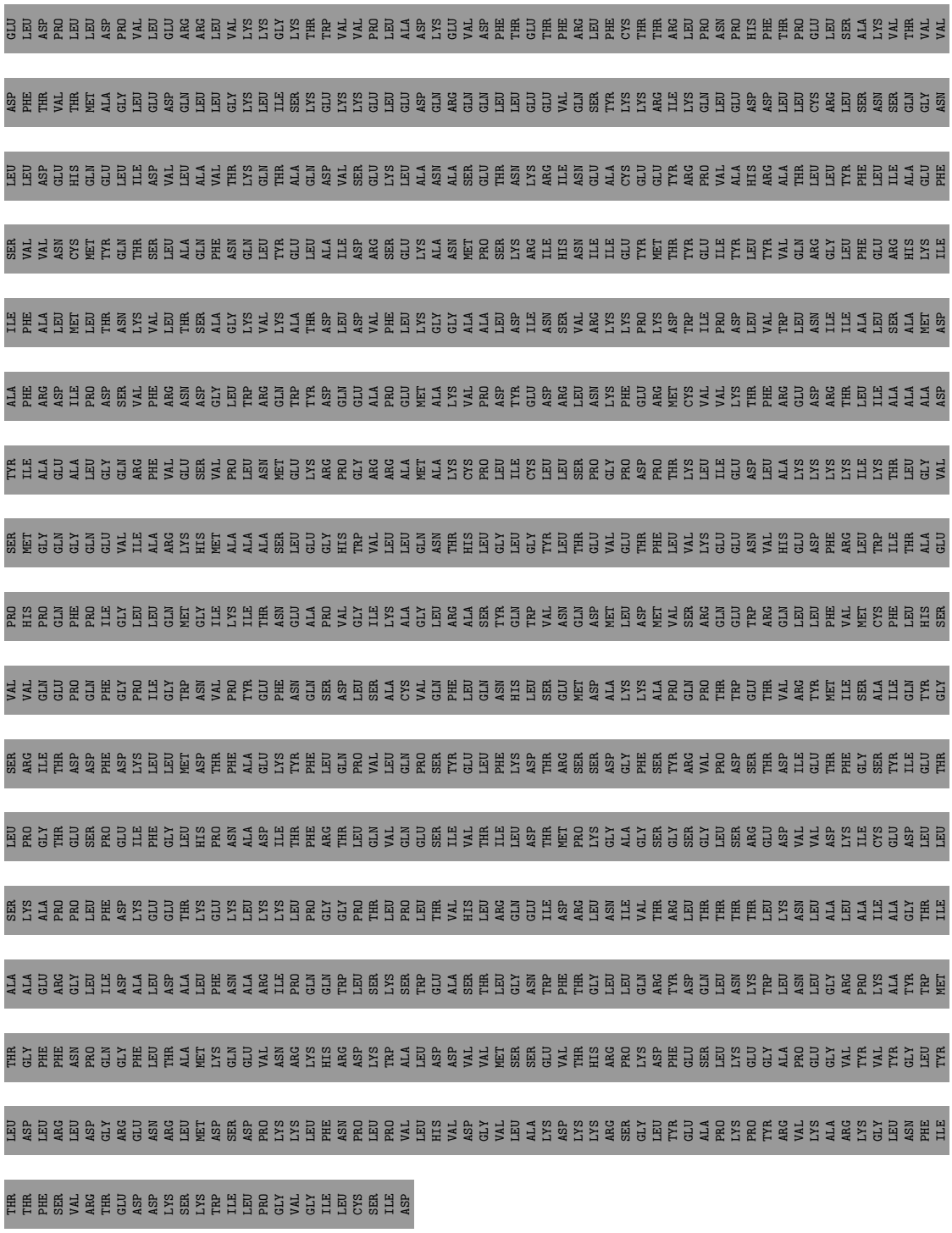
MET MET ASN GLN MET SER PHE LEU GLN ASP LEU LYS ASP PHE ALA LYS GLU GLN ILE ASN ASP GLU THR VAL GLU LEU LEU GLU PRO TYR PHE MET SER GLU ASP PHE THR PHE GLU ASN ALA GLN LYS GLY SER GLY ASN VAL ALA GLY LEU CYS ASN TRP ALA GLU SER MET ALA LYS

TYR HIS ASN VAL ALA LYS VAL VAL GLU PRO LYS ILE ALA LYS LEU ARG GLU ALA GLU ALA GLU LEU LYS LEU ALA THR LYS GLU LYS ASN ALA ALA GLU GLU ARG MET ALA LYS VAL GLN ALA LYS LEU ASP GLU MET GLN ALA GLN PHE ASP ALA ALA MET ALA HIS LYS GLN ALA LEU

GLU ASP ASP ALA ALA ALA THR GLN ARG LYS MET ASP SER ALA ASN ALA LEU ILE GLY ALA LEU ALA GLY GLU GLU ALA ARG TRP THR ALA GLN SER LYS GLU PHE ASP VAL GLN ILE GLN ARG LEU THR GLY ASP CYS ALA LEU ALA SER ALA PHE VAL SER TYR LEU GLY PRO PHE ASN

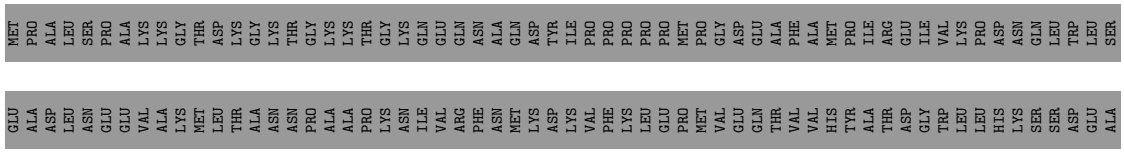
LYS GLU PHE ARG GLU LEU LEU LEU ASN ARG ASP PHE TYR GLY ASP CYS MET LYS LEU ASN VAL PRO VAL THR PRO HIS LEU GLN ILE THR LYS PHE LEU VAL ASP ASP SER GLU VAL GLY GLU TRP ASN LEU GLN GLY LEU PRO THR ASP GLU LEU SER ILE GLN ASN GLY ILE MET VAL

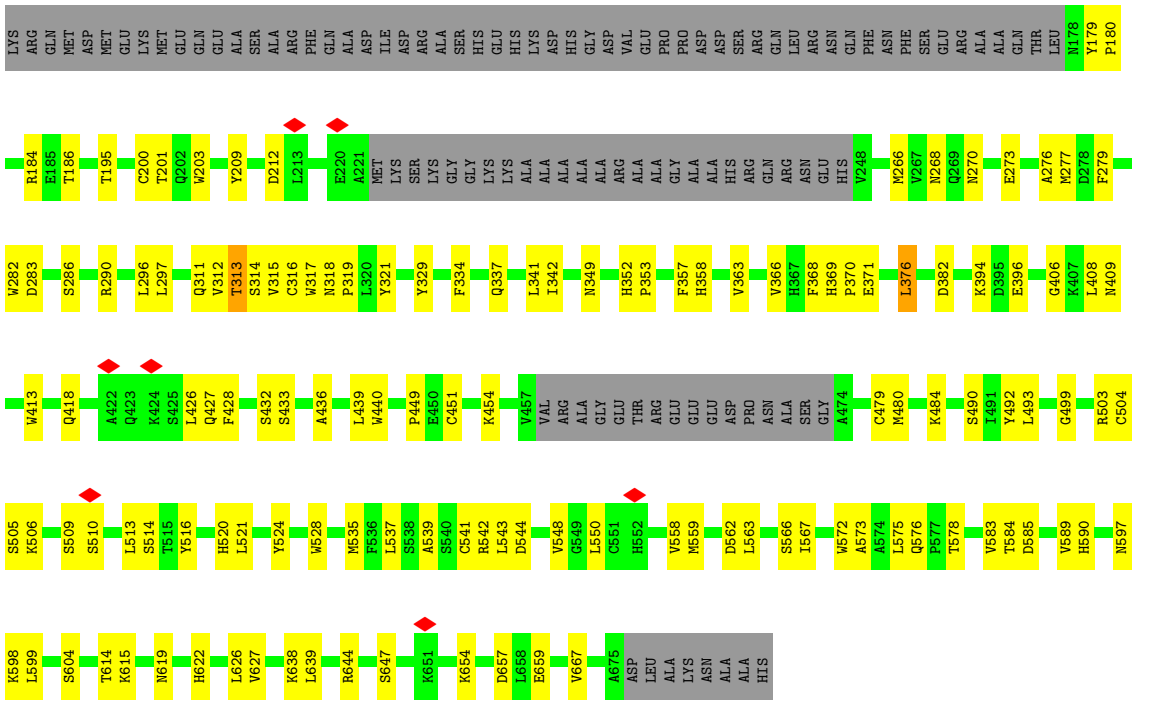
THR ARG ALA SER ARG TYR PRO VAL LEU VAL ASP PRO GLN GLY GLN GLY ARG GLU TRP ILE LYS ASN ARG GLU GLU ALA ASN GLN LEU LYS THR THR GLN LEU ASN ASP LYS LEU PHE ARG ASN HIS LEU GLU GLU CYS LEU ALA PHE GLY ARG PRO LEU LEU ILE GLU ASN ILE GLU GLU



• Molecule 4: Dynein, 78 kDa intermediate chain, flagellar outer arm

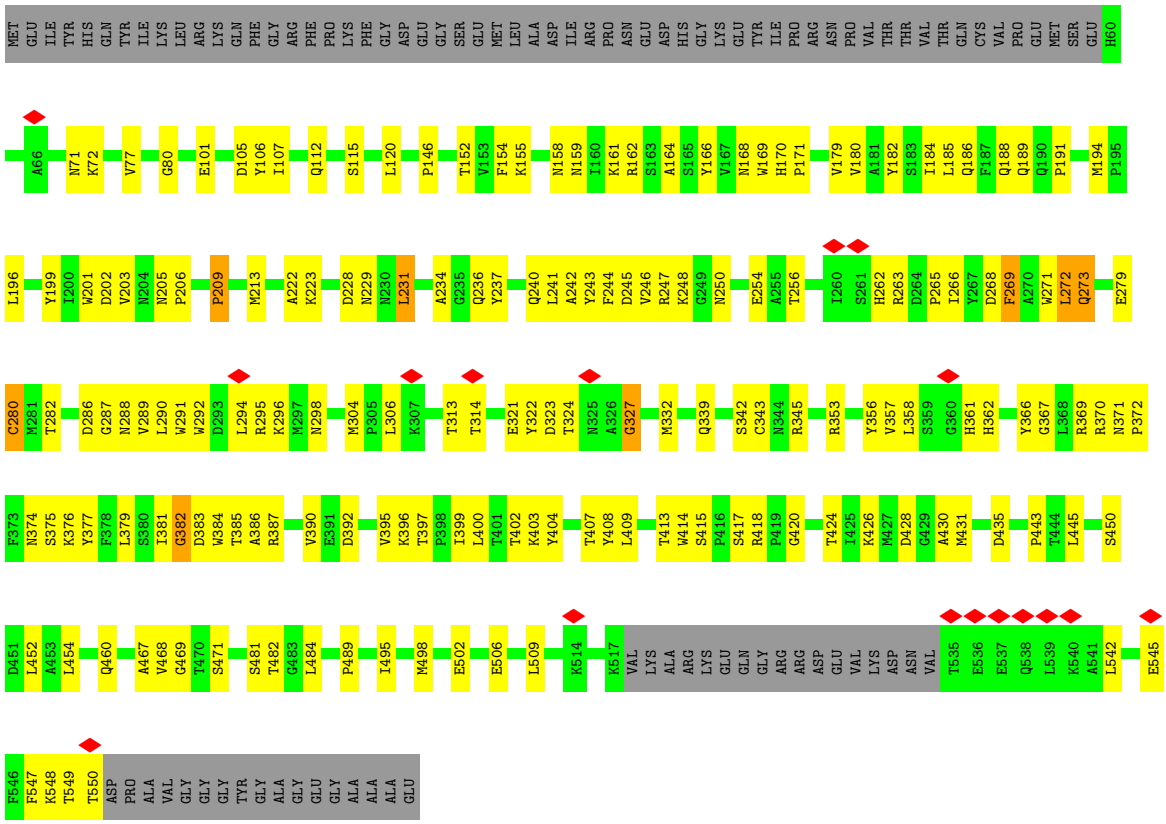
Chain D:





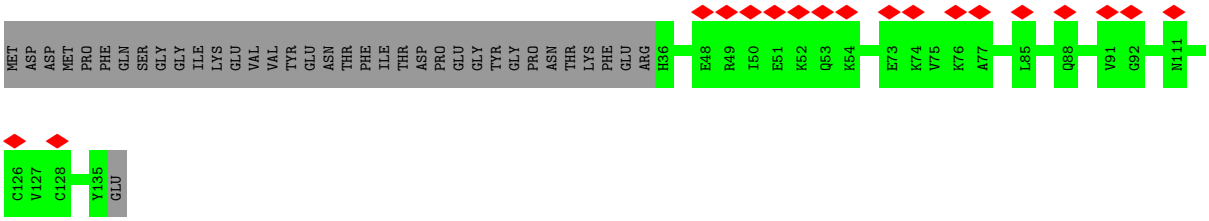
- Molecule 5: Dynein, 70 kDa intermediate chain, flagellar outer arm

Chain E: 53% 29% • 16%



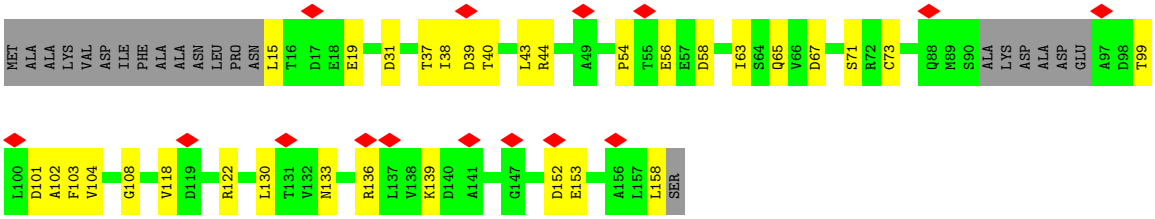
- Molecule 6: Flagellar outer dynein arm light chain 2

Chain F: 13% 74% 26%



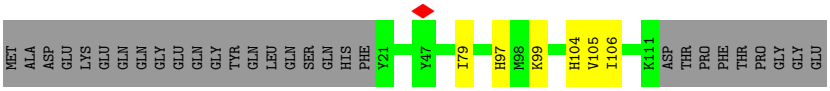
• Molecule 7: Dynein 18 kDa light chain, flagellar outer arm

Chain G: 9% 67% 20% 13%



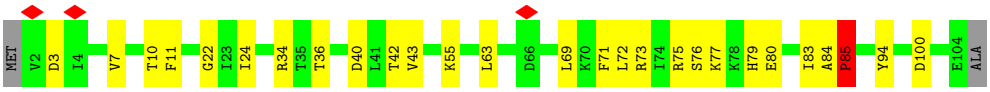
• Molecule 8: Dynein 11 kDa light chain, flagellar outer arm

Chain H: 71% 5% 24%



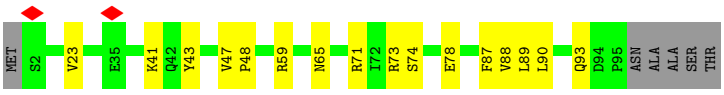
• Molecule 9: Dynein light chain roadblock LC7a

Chain I: 72% 25%



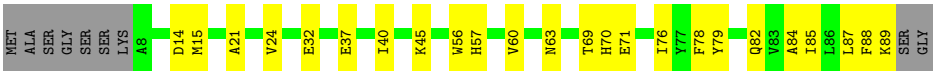
• Molecule 10: Dynein light chain roadblock LC7b

Chain J: 78% 16% 6%



• Molecule 11: Dynein 8 kDa light chain, flagellar outer arm

Chain K: 64% 26% 10%

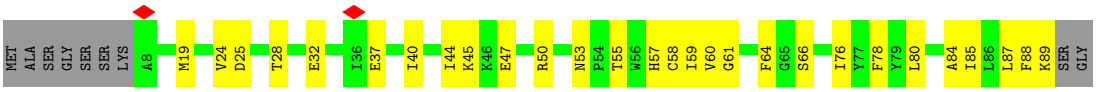


• Molecule 11: Dynein 8 kDa light chain, flagellar outer arm

Chain L:

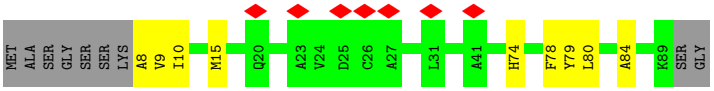
• Molecule 11: Dynein 8 kDa light chain, flagellar outer arm

Chain M:



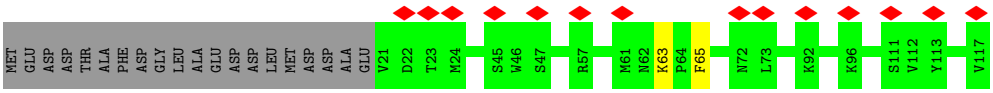
• Molecule 11: Dynein 8 kDa light chain, flagellar outer arm

Chain N:



• Molecule 12: Dynein light chain 9

Chain O:

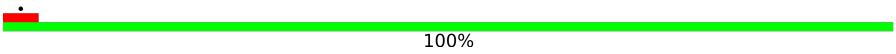


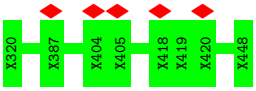
• Molecule 13: Dynein light chain 10

Chain P:

• Molecule 14: DC1

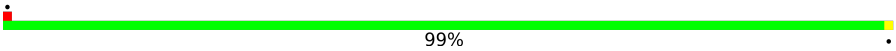
Chain X:

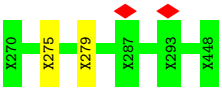




• Molecule 15: DC2

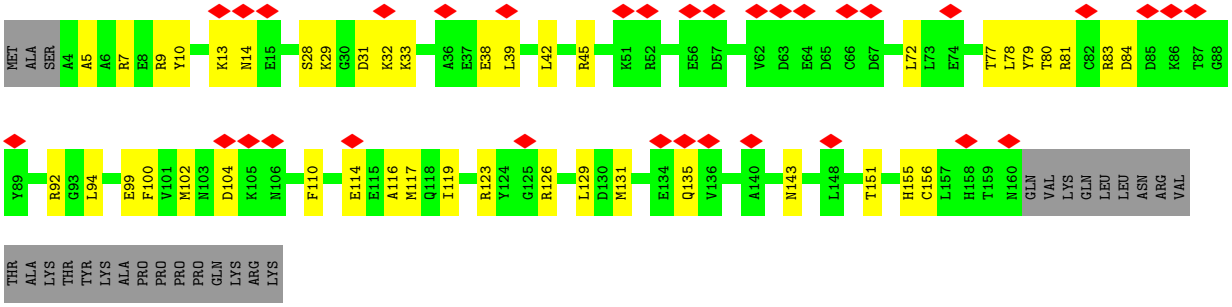
Chain Y:





• Molecule 16: Outer dynein arm-docking complex protein DC3

Chain Z:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=0°, rise=82 Å, axial sym=C1	Depositor
Number of segments used	485694	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	61.48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.150	Depositor
Minimum map value	-0.004	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0125	Depositor
Map size (Å)	353.6, 353.6, 353.6	wwPDB
Map dimensions	260, 260, 260	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.36, 1.36, 1.36	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	A	0.13	0/1543	0.40	0/2140
2	B	0.39	0/5090	0.75	3/6881 (0.0%)
3	C	0.41	0/7381	0.75	5/9958 (0.1%)
4	D	0.67	1/3699 (0.0%)	1.02	7/5023 (0.1%)
5	E	0.64	0/3784	1.01	7/5152 (0.1%)
6	F	0.18	0/494	0.60	0/687
7	G	0.27	0/1098	0.60	0/1471
8	H	0.20	0/450	0.42	0/626
9	I	0.50	0/840	0.89	1/1133 (0.1%)
10	J	0.52	0/752	0.76	0/1019
11	K	0.41	0/687	0.74	0/926
11	L	0.44	0/687	0.80	0/926
11	M	0.37	0/687	0.81	0/926
11	N	0.16	0/406	0.42	0/565
12	O	0.21	0/480	0.66	0/666
13	P	0.49	0/823	0.95	0/1108
16	Z	0.23	0/1299	0.55	0/1745
All	All	0.46	1/30200 (0.0%)	0.80	23/40952 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	314	SER	CA-CB	-5.44	1.44	1.53

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	129	PRO	CA-N-CD	-8.06	100.72	112.00
3	C	455	MET	CB-CG-SD	-6.99	91.72	112.70
3	C	586	ARG	CA-CB-CG	6.88	127.85	114.10
2	B	603	ARG	CB-CG-CD	6.84	127.04	111.30
4	D	184	ARG	N-CA-CB	6.46	122.09	111.62

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1544	0	701	10	0
2	B	5028	0	4588	124	0
3	C	7293	0	6812	149	0
4	D	3609	0	3534	94	0
5	E	3697	0	3534	136	0
6	F	495	0	221	0	0
7	G	1089	0	1072	22	0
8	H	451	0	204	3	0
9	I	827	0	841	21	0
10	J	741	0	750	14	0
11	K	671	0	654	20	0
11	L	671	0	654	19	0
11	M	671	0	654	24	0
11	N	407	0	192	5	0
12	O	481	0	230	1	0
13	P	805	0	801	20	0
14	X	605	0	129	0	0
15	Y	840	0	181	1	0
16	Z	1280	0	1239	25	0
All	All	31205	0	26991	633	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

The worst 5 of 633 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:79:ILE:O	8:H:105:VAL:HA	1.63	0.99
2:B:382:MET:O	2:B:386:VAL:HG23	1.69	0.92
2:B:503:GLU:HG2	4:D:510:SER:HB2	1.56	0.88
4:D:200:CYS:HG	13:P:89:TYR:HH	1.23	0.84

Continued on next page...

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:627:LEU:HG	2:B:631:MET:HE2	1.61	0.82

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	313/4503 (7%)	279 (89%)	34 (11%)	0	100	100
2	B	647/4568 (14%)	615 (95%)	31 (5%)	1 (0%)	43	75
3	C	925/4485 (21%)	858 (93%)	65 (7%)	2 (0%)	43	75
4	D	450/683 (66%)	387 (86%)	63 (14%)	0	100	100
5	E	470/567 (83%)	371 (79%)	94 (20%)	5 (1%)	11	44
6	F	98/136 (72%)	94 (96%)	4 (4%)	0	100	100
7	G	134/159 (84%)	125 (93%)	9 (7%)	0	100	100
8	H	89/120 (74%)	77 (86%)	12 (14%)	0	100	100
9	I	101/105 (96%)	89 (88%)	11 (11%)	1 (1%)	12	45
10	J	92/100 (92%)	81 (88%)	11 (12%)	0	100	100
11	K	80/91 (88%)	73 (91%)	7 (9%)	0	100	100
11	L	80/91 (88%)	72 (90%)	8 (10%)	0	100	100
11	M	80/91 (88%)	73 (91%)	7 (9%)	0	100	100
11	N	80/91 (88%)	68 (85%)	12 (15%)	0	100	100
12	O	95/117 (81%)	92 (97%)	3 (3%)	0	100	100
13	P	96/103 (93%)	89 (93%)	7 (7%)	0	100	100
16	Z	155/184 (84%)	136 (88%)	19 (12%)	0	100	100
All	All	3985/16194 (25%)	3579 (90%)	397 (10%)	9 (0%)	44	75

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	625	ASP
5	E	298	ASN
9	I	85	PRO
5	E	295	ARG
3	C	114	TRP

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	463/3998 (12%)	459 (99%)	4 (1%)	70	76
3	C	701/3945 (18%)	699 (100%)	2 (0%)	86	85
4	D	401/584 (69%)	397 (99%)	4 (1%)	68	76
5	E	400/489 (82%)	398 (100%)	2 (0%)	81	82
7	G	121/136 (89%)	121 (100%)	0	100	100
9	I	90/91 (99%)	90 (100%)	0	100	100
10	J	83/87 (95%)	83 (100%)	0	100	100
11	K	70/76 (92%)	70 (100%)	0	100	100
11	L	70/76 (92%)	70 (100%)	0	100	100
11	M	70/76 (92%)	70 (100%)	0	100	100
13	P	86/90 (96%)	85 (99%)	1 (1%)	63	73
16	Z	138/162 (85%)	138 (100%)	0	100	100
All	All	2693/9810 (28%)	2680 (100%)	13 (0%)	78	82

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	273	GLU
4	D	297	LEU
13	P	20	LEU
5	E	273	GLN

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Mol	Chain	Res	Type
5	E	279	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
5	E	205	ASN
7	G	53	ASN
5	E	374	ASN
7	G	65	GLN
3	C	528	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
15	Y	3

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Mol	Chain	Number of breaks
14	X	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	X	396:UNK	C	403:UNK	N	28.65
1	Y	387:UNK	C	394:UNK	N	22.26
1	Y	420:UNK	C	424:UNK	N	12.82
1	X	345:UNK	C	348:UNK	N	10.08
1	Y	281:UNK	C	284:UNK	N	6.72

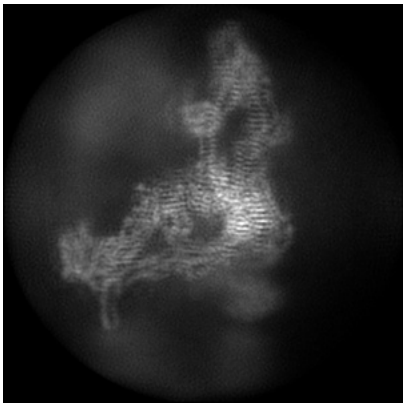
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-23083. These allow visual inspection of the internal detail of the map and identification of artifacts.

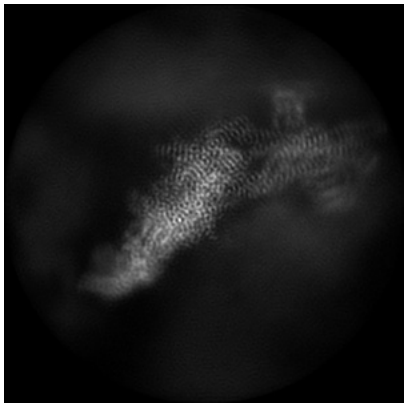
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

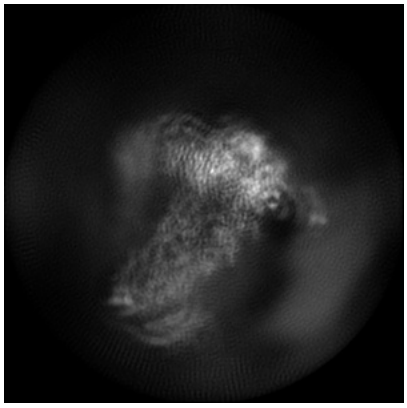
6.1.1 Primary map



X



Y

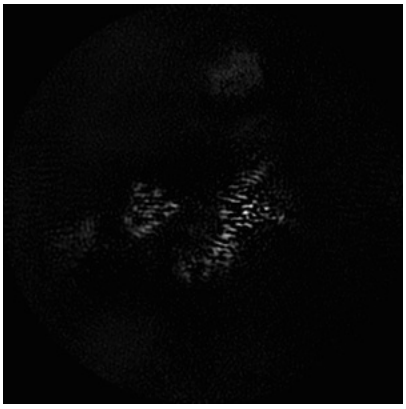


Z

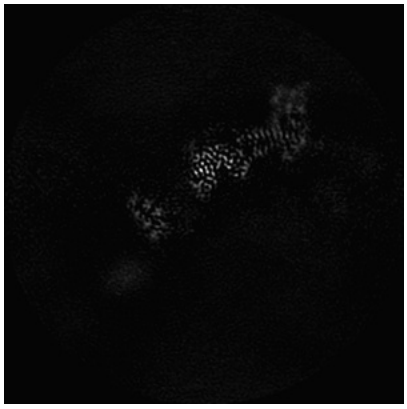
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

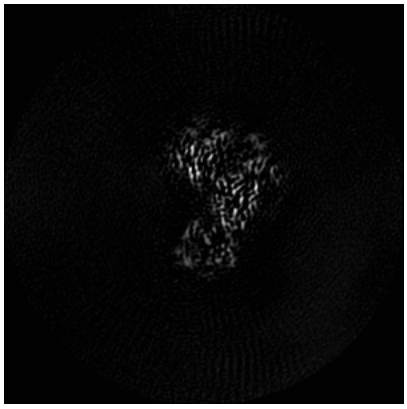
6.2.1 Primary map



X Index: 130



Y Index: 130

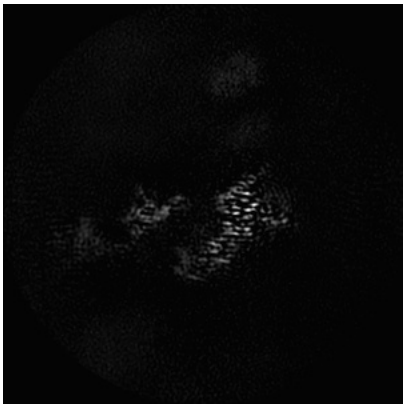


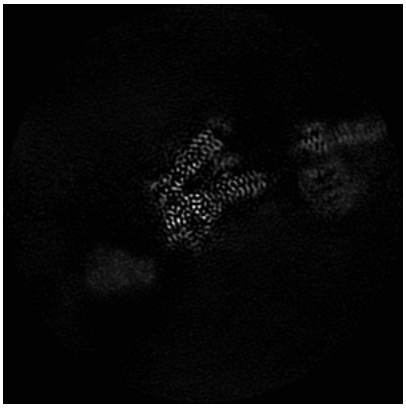
Z Index: 130

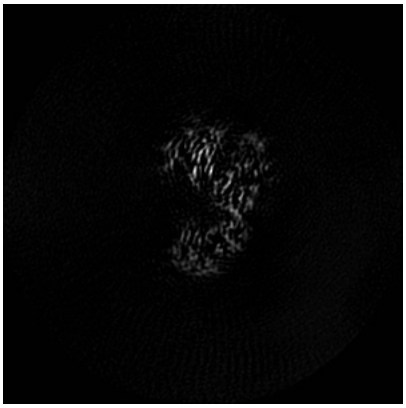
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map


X Index: 127

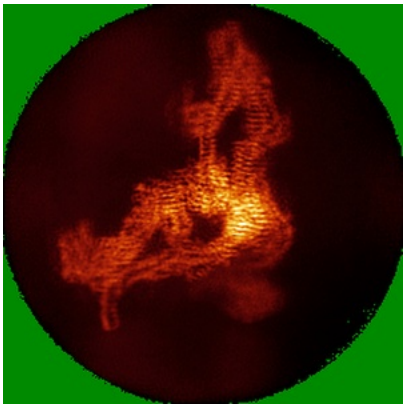

Y Index: 152

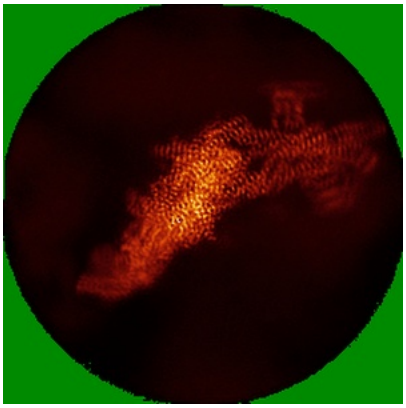

Z Index: 126

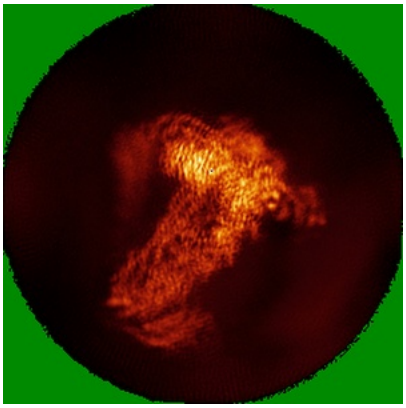
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map


X


Y


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0125. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

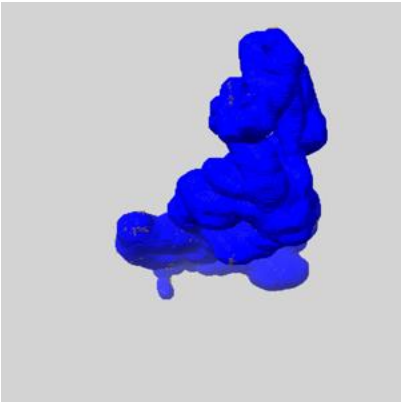
6.6 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

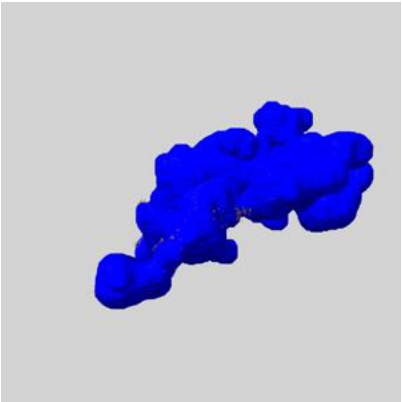
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

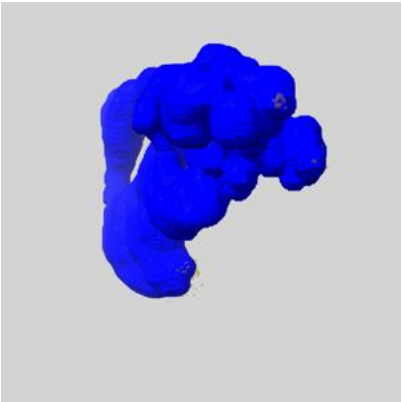
6.6.1 emd_23083_msk_1.map (i)



X



Y

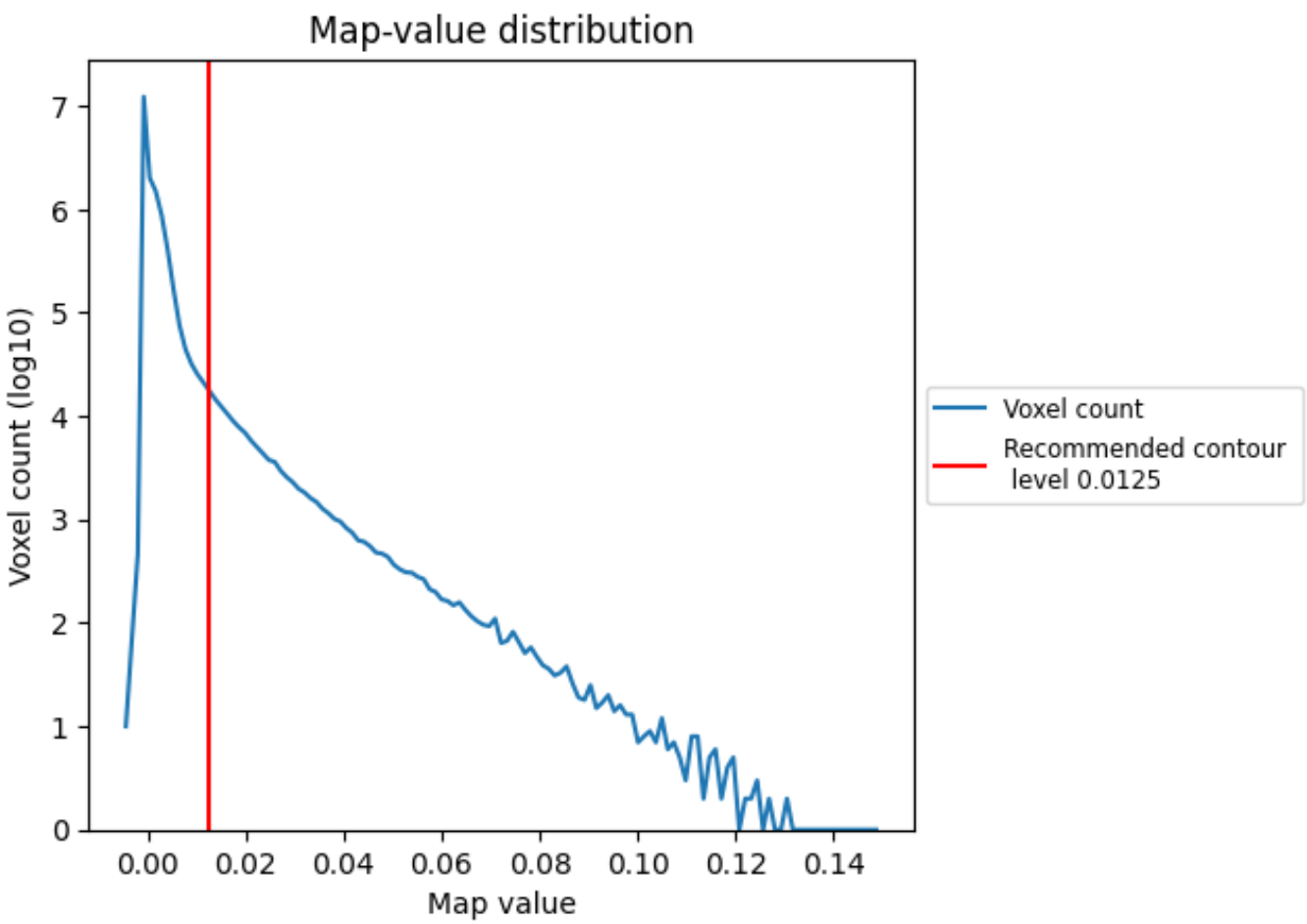


Z

7 Map analysis (i)

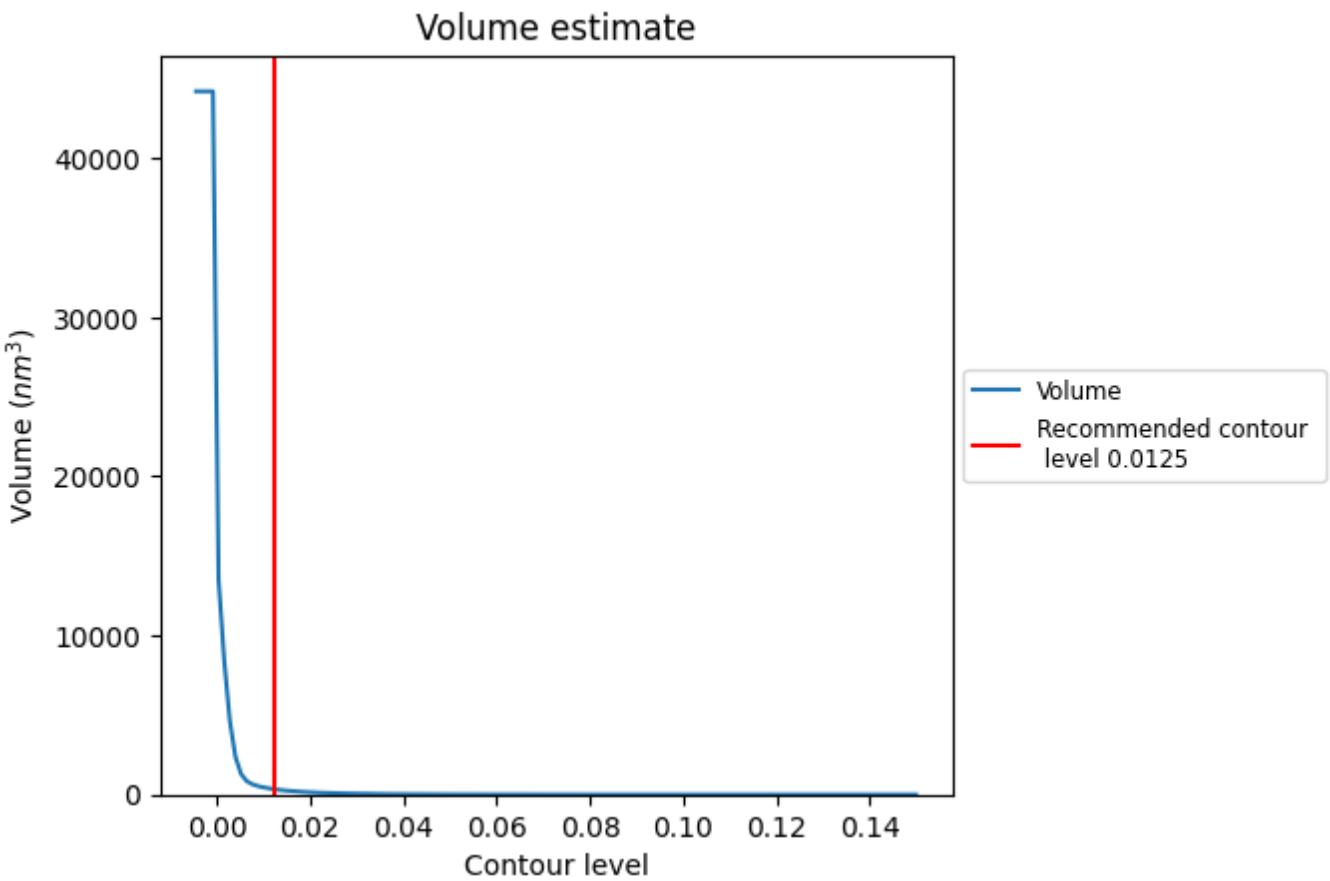
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

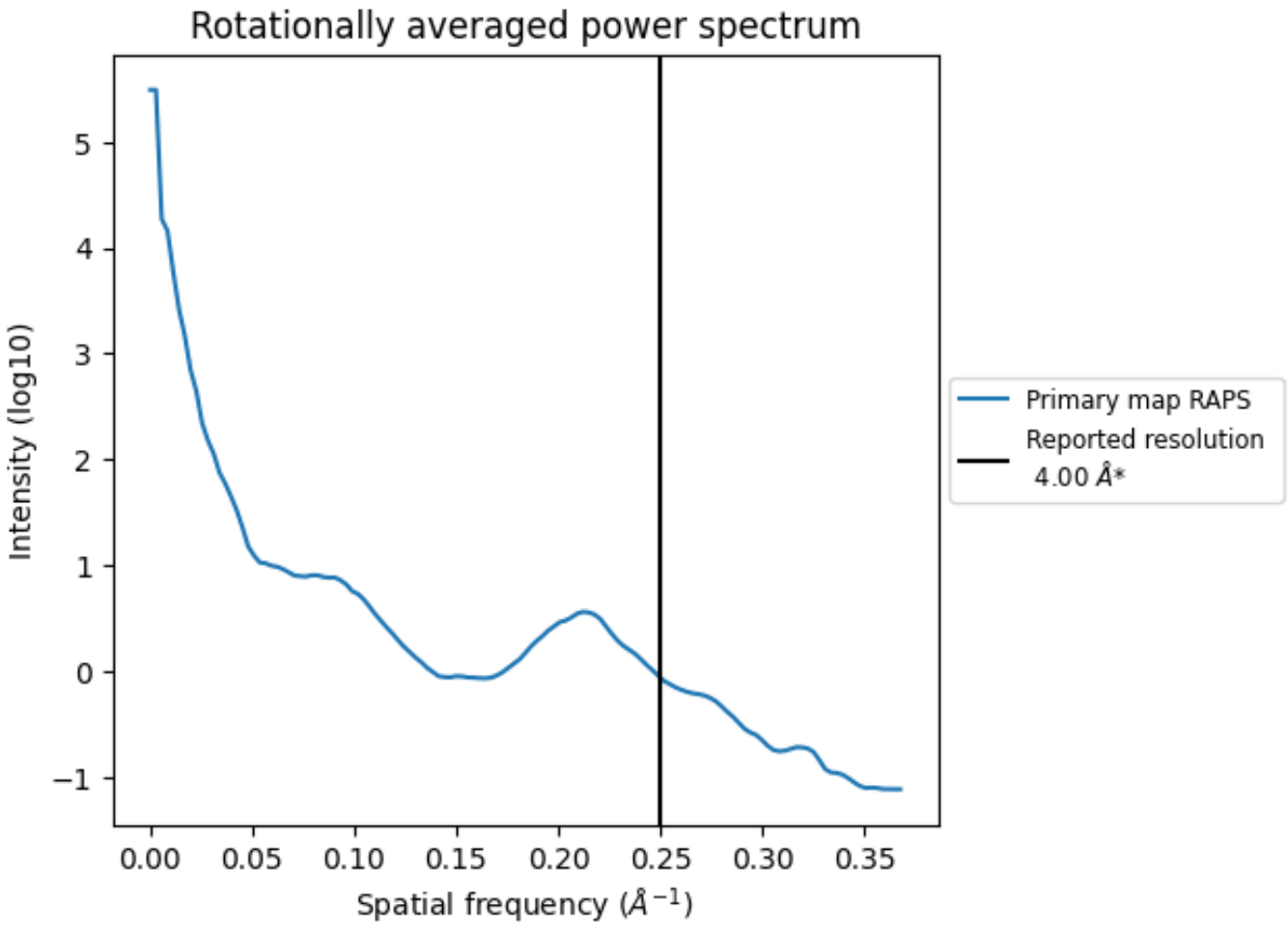
7.2 Volume estimate (i)



The volume at the recommended contour level is 330 nm^3; this corresponds to an approximate mass of 298 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.250 Å^{-1}

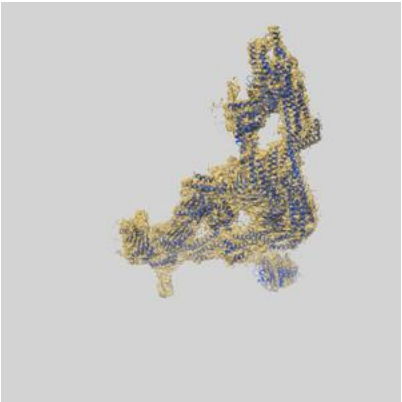
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

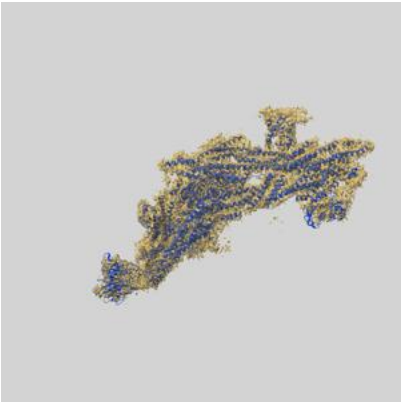
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-23083 and PDB model 7KZN. Per-residue inclusion information can be found in section 3 on page 7.

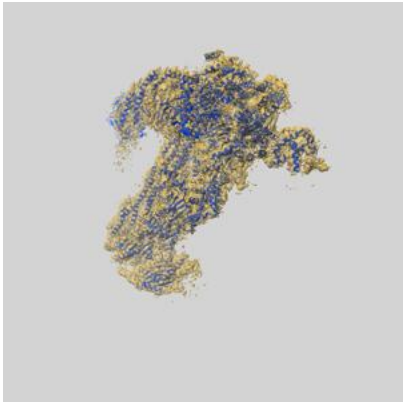
9.1 Map-model overlay (i)



X



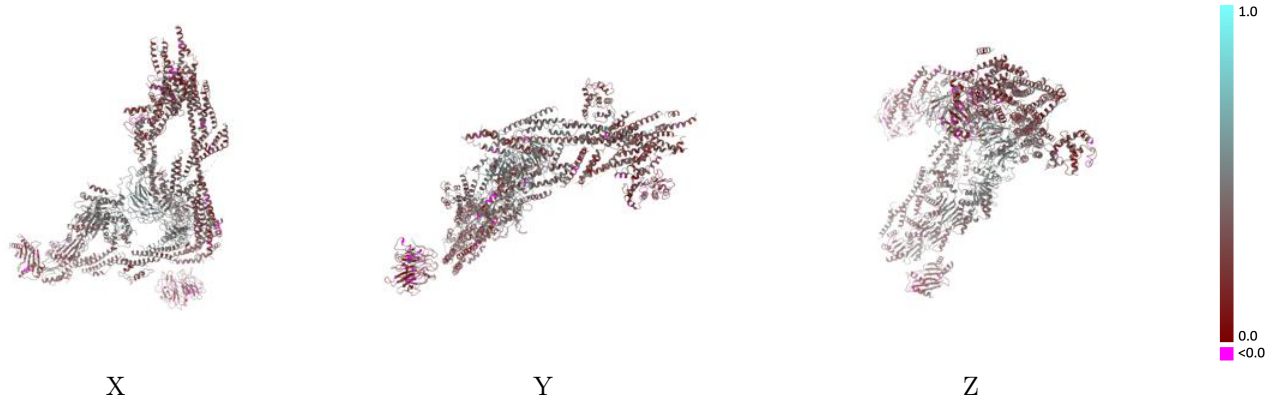
Y



Z

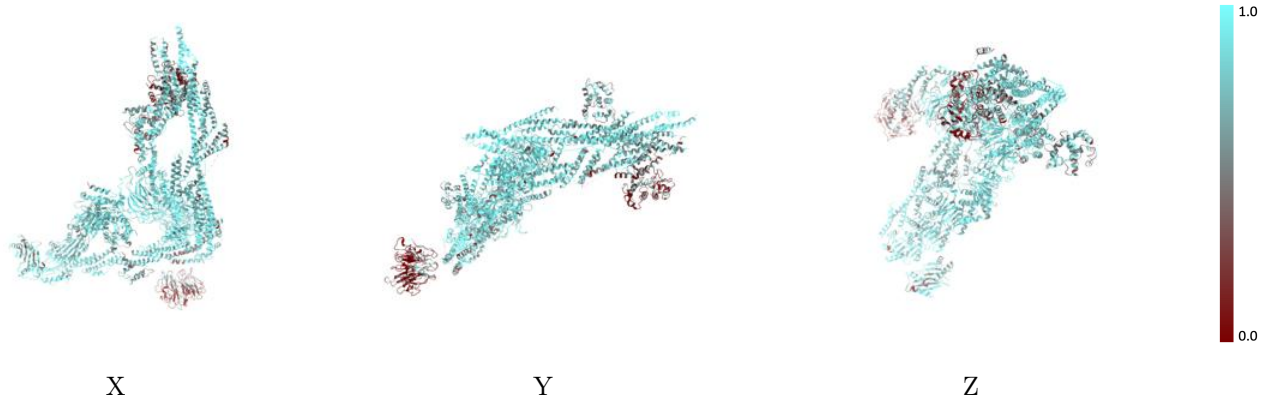
The images above show the 3D surface view of the map at the recommended contour level 0.0125 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



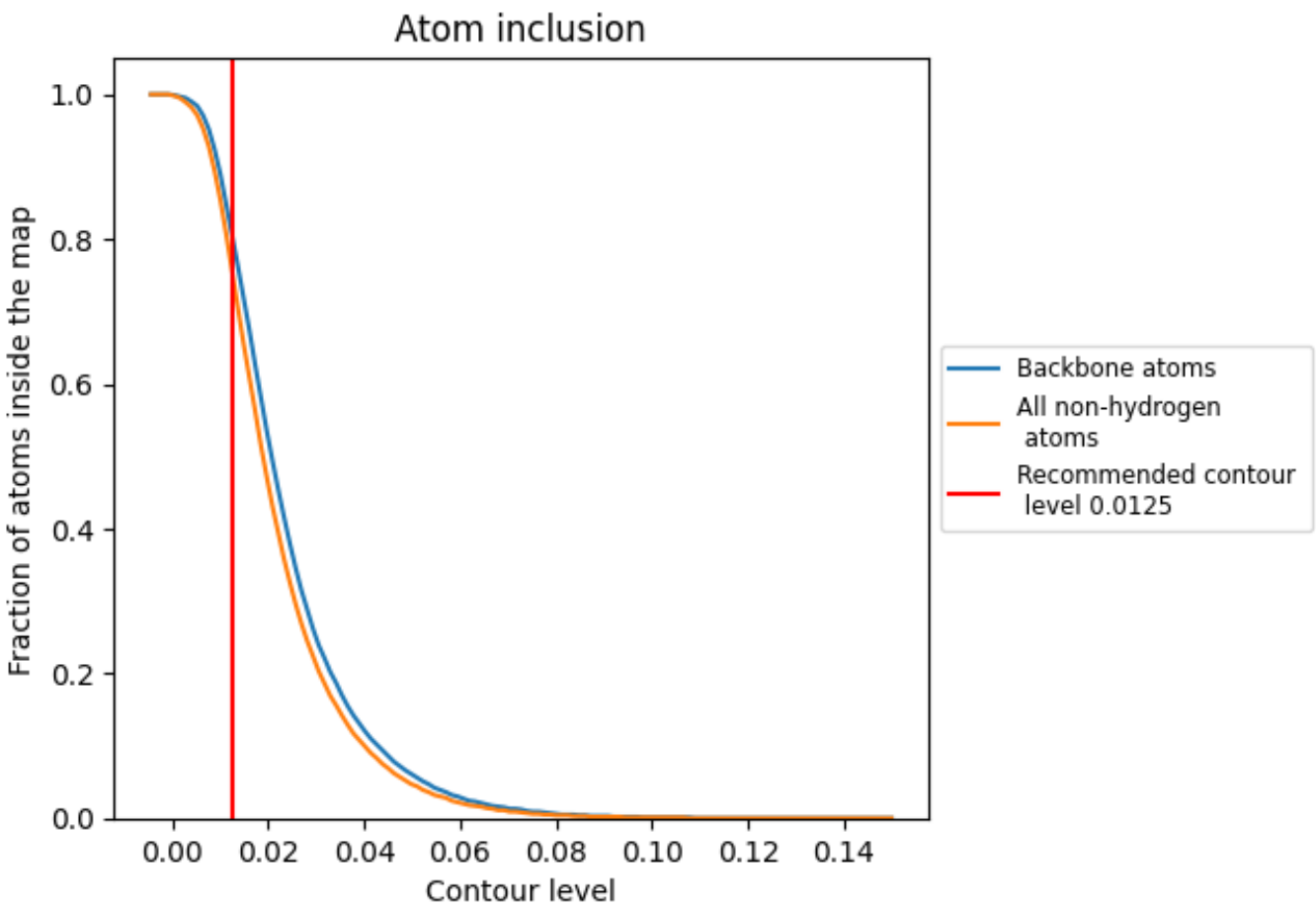
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0125).

9.4 Atom inclusion (i)



At the recommended contour level, 80% of all backbone atoms, 76% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.0125) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7550	0.3760
A	0.2160	0.2390
B	0.6780	0.3280
C	0.7650	0.3780
D	0.8840	0.4800
E	0.8440	0.4280
F	0.7310	0.2340
G	0.7040	0.3780
H	0.9200	0.3880
I	0.8290	0.4610
J	0.8890	0.4840
K	0.8310	0.4030
L	0.7850	0.3470
M	0.8430	0.3440
N	0.8620	0.3230
O	0.7800	0.2730
P	0.7850	0.4020
X	0.8350	0.3370
Y	0.8840	0.3590
Z	0.6070	0.2890