wwPDB EM Validation Summary Report

May 2, 2026 – 01:30 PM EDT

PDB ID	:	9DGU / pdb_00009dgu
EMDB ID	:	EMD-46848
Title	:	structure of dynactin, dynein tail with two BICDR from dynein-dynactin-BICDR on microtubules
Authors	:	Rao, Q.; Chai, P.; Zhang, K.
Deposited on	:	2024-09-03
Resolution	:	7.10 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 ⓘ 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 ⓘ) were used in the production of this report:

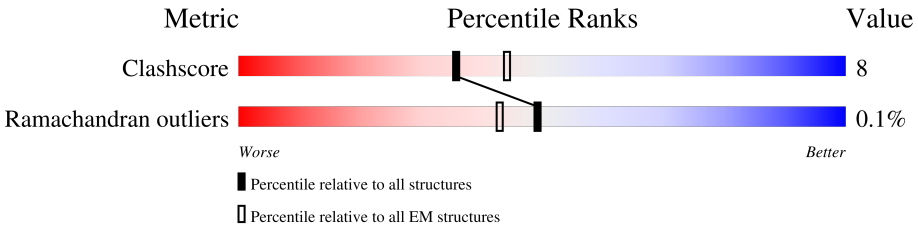
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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

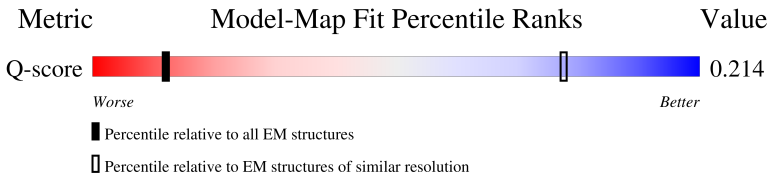
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 7.10 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	-
Q-score	-	25397	464 (6.60 - 7.60)

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	376	84% 14% •
1	B	376	84% 14% •
1	C	376	86% 14%
1	D	376	82% 16% •
1	E	376	86% 12% •

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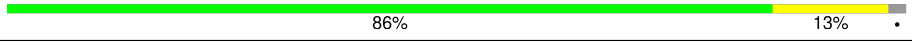
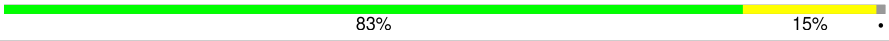
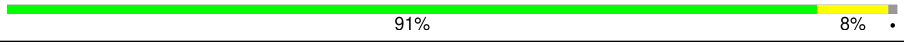
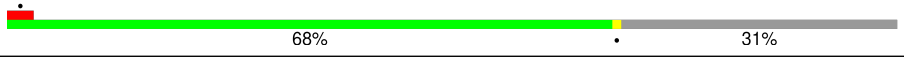
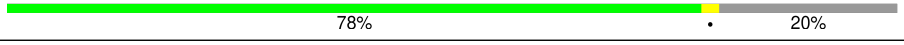
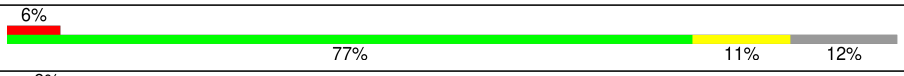
Mol	Chain	Length	Quality of chain
1	F	376	
1	G	376	
1	I	376	
2	H	375	
3	J	417	
4	K	286	
5	L	272	
6	M	405	
6	N	405	
6	P	405	
6	Q	405	
7	O	186	
7	R	186	
8	U	190	
9	V	182	
10	W	1281	
10	Z	1281	
11	Y	467	
12	a	577	
12	b	577	
12	c	577	
12	d	577	
13	e	4646	
13	f	4646	
13	m	4646	

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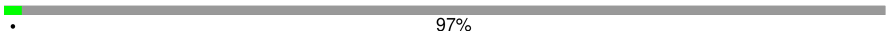
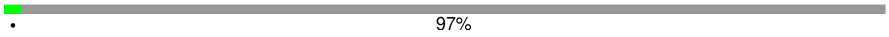
Mol	Chain	Length	Quality of chain
13	n	4646	
14	g	612	
14	h	612	
14	o	612	
14	p	612	
15	j	492	
15	q	492	

2 Entry composition (i)

There are 18 unique types of molecules in this entry. The entry contains 61911 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 Alpha-centractin.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	370	Total 1822	C 1082	N 370	O 370	0	0
1	B	370	Total 1822	C 1082	N 370	O 370	0	0
1	C	375	Total 1847	C 1097	N 375	O 375	0	0
1	D	370	Total 1822	C 1082	N 370	O 370	0	0
1	E	370	Total 1822	C 1082	N 370	O 370	0	0
1	F	370	Total 1822	C 1082	N 370	O 370	0	0
1	G	370	Total 1822	C 1082	N 370	O 370	0	0
1	I	370	Total 1822	C 1082	N 370	O 370	0	0

- Molecule 2 is a protein called Actin, cytoplasmic 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	H	370	Total 1822	C 1082	N 370	O 370	0	0

- Molecule 3 is a protein called Actin-related protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	J	379	Total 1868	C 1110	N 379	O 379	0	0

- Molecule 4 is a protein called F-actin-capping protein subunit alpha-1.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	K	278	Total 1378	C 822	N 278	O 278	0	0

- Molecule 5 is a protein called F-actin-capping protein subunit beta.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	L	269	Total 1327	C 789	N 269	O 269	0	0

- Molecule 6 is a protein called Dynactin subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	M	340	Total 1689	C 1009	N 340	O 340	0	0
6	N	280	Total 1394	C 834	N 280	O 280	0	0
6	P	325	Total 1612	C 962	N 325	O 325	0	0
6	Q	343	Total 1707	C 1021	N 343	O 343	0	0

- Molecule 7 is a protein called Dynactin subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	O	179	Total 888	C 530	N 179	O 179	0	0
7	R	170	Total 844	C 504	N 170	O 170	0	0

- Molecule 8 is a protein called Dynactin subunit 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	U	167	Total 822	C 488	N 167	O 167	0	0

- Molecule 9 is a protein called Dynactin subunit 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	V	179	Total 881	C 523	N 179	O 179	0	0

- Molecule 10 is a protein called Dynactin subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	W	152	Total 754	C 450	N 152	O 152	0	0
10	Z	192	Total 952	C 568	N 192	O 192	0	0

- Molecule 11 is a protein called Dynactin subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	Y	410	Total 2038	C 1218	N 410	O 410	0	0

- Molecule 12 is a protein called BICD family-like cargo adapter 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	a	207	Total 1030	C 616	N 207	O 207	0	0
12	b	207	Total 1030	C 616	N 207	O 207	0	0
12	c	240	Total 1194	C 714	N 240	O 240	0	0
12	d	269	Total 1339	C 801	N 269	O 269	0	0

- Molecule 13 is a protein called Cytoplasmic dynein 1 heavy chain 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	e	798	Total 3959	C 2363	N 798	O 798	0	0
13	f	808	Total 4009	C 2393	N 808	O 808	0	0
13	m	792	Total 3750	C 2166	N 792	O 792	0	0
13	n	755	Total 3566	C 2056	N 755	O 755	0	0

- Molecule 14 is a protein called Cytoplasmic dynein 1 intermediate chain 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	g	358	Total 1767	C 1051	N 358	O 358	0	0
14	h	358	Total 1767	C 1051	N 358	O 358	0	0

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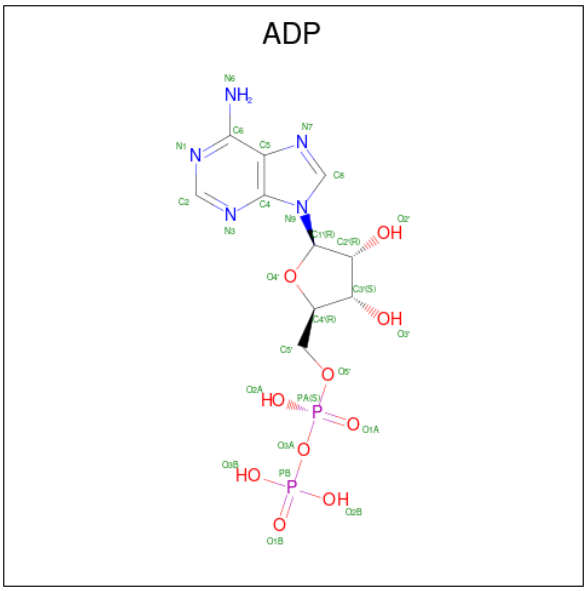
Mol	Chain	Residues	Atoms				AltConf	Trace
14	o	358	Total 1767	C 1051	N 358	O 358	0	0
14	p	358	Total 1767	C 1051	N 358	O 358	0	0

- Molecule 15 is a protein called Dynein light intermediate chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	j	14	Total 56	C 28	N 14	O 14	0	0
15	q	14	Total 56	C 28	N 14	O 14	0	0

- Molecule 16 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					AltConf
16	A	1	Total 27	C 10	N 5	O 10	P 2	0
16	B	1	Total 27	C 10	N 5	O 10	P 2	0
16	C	1	Total 27	C 10	N 5	O 10	P 2	0
16	D	1	Total 27	C 10	N 5	O 10	P 2	0
16	E	1	Total 27	C 10	N 5	O 10	P 2	0

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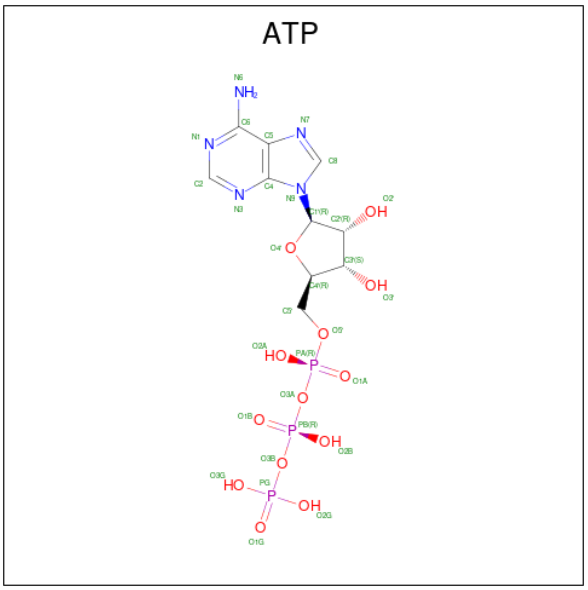
Mol	Chain	Residues	Atoms					AltConf
16	F	1	Total	C	N	O	P	0
			27	10	5	10	2	
16	G	1	Total	C	N	O	P	0
			27	10	5	10	2	
16	I	1	Total	C	N	O	P	0
			27	10	5	10	2	
16	J	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 17 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
17	H	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 18 is ZINC ION (CCD ID: ZN) (formula: Zn).

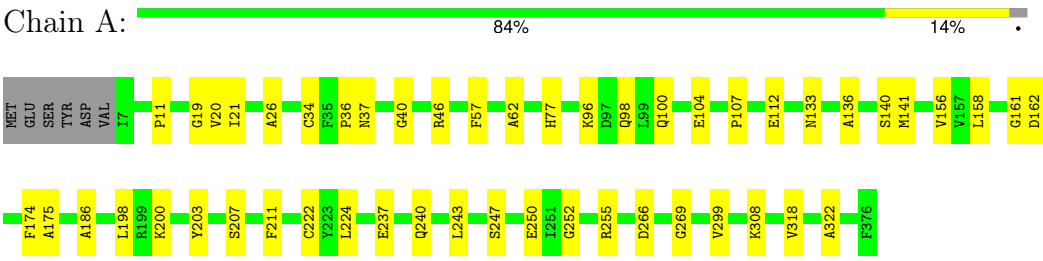
Mol	Chain	Residues	Atoms		AltConf
18	Y	3	Total	Zn	0
			3	3	

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.

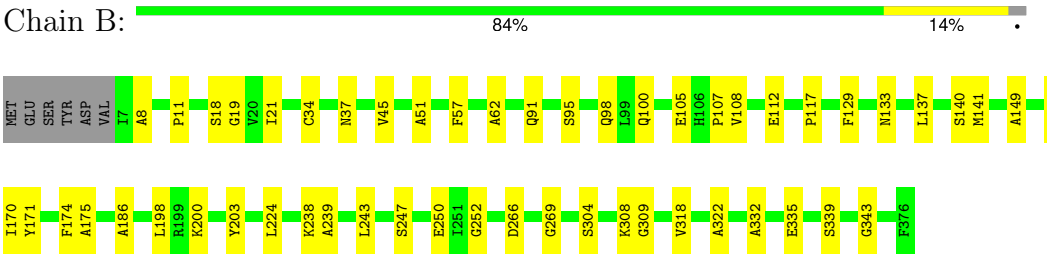
• Molecule 1: Alpha-centractin

Chain A:



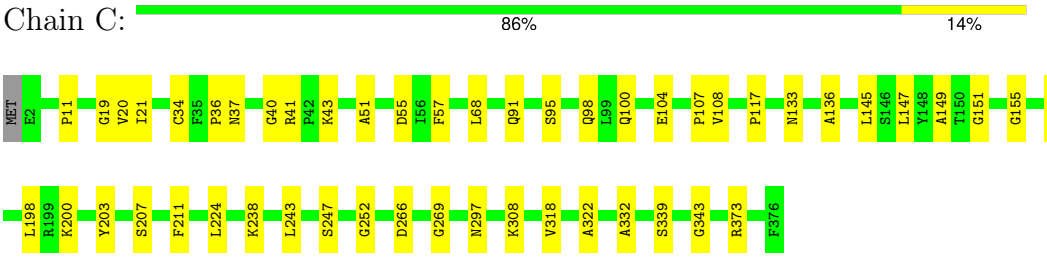
• Molecule 1: Alpha-centractin

Chain B:



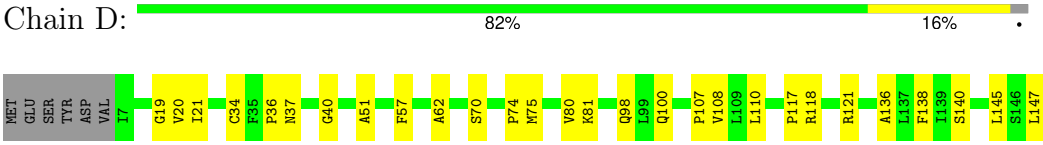
• Molecule 1: Alpha-centractin

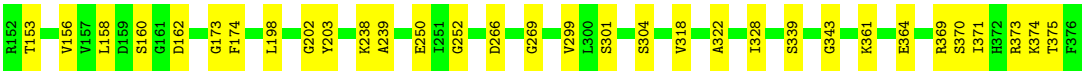
Chain C:



• Molecule 1: Alpha-centractin

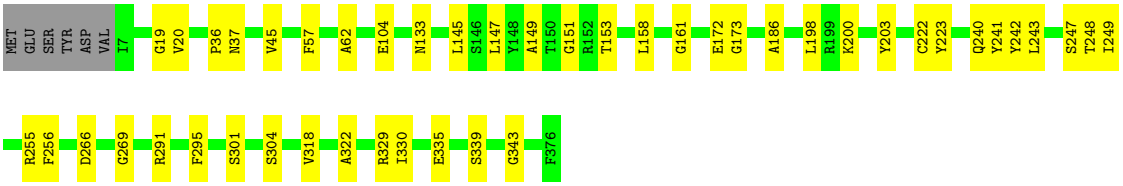
Chain D:





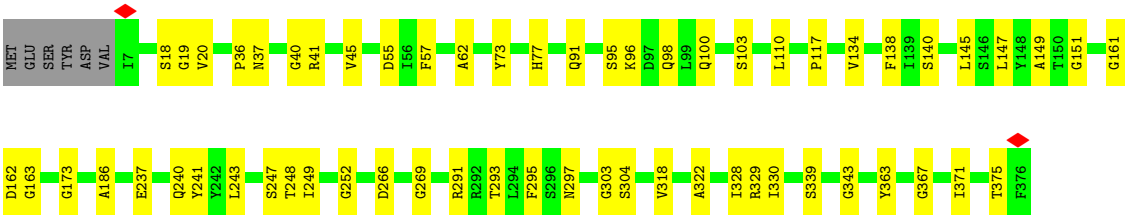
• Molecule 1: Alpha-centractin

Chain E:



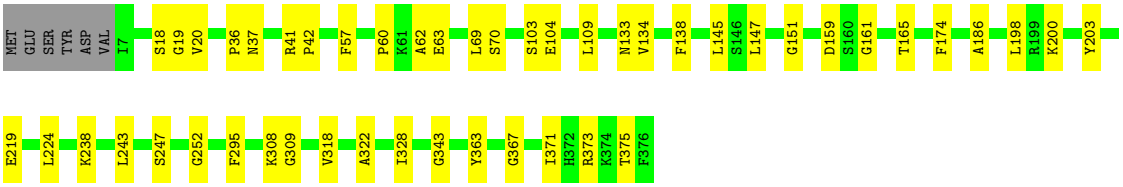
• Molecule 1: Alpha-centractin

Chain F:



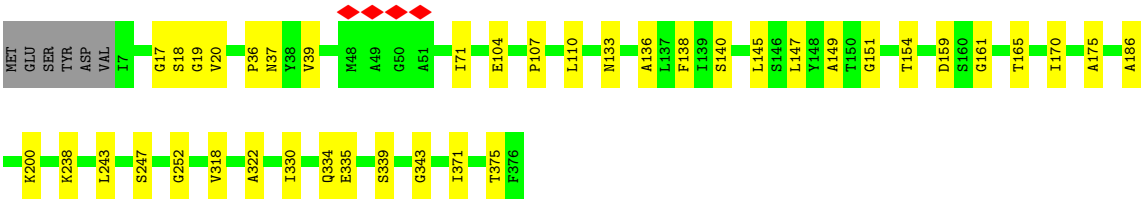
• Molecule 1: Alpha-centractin

Chain G:



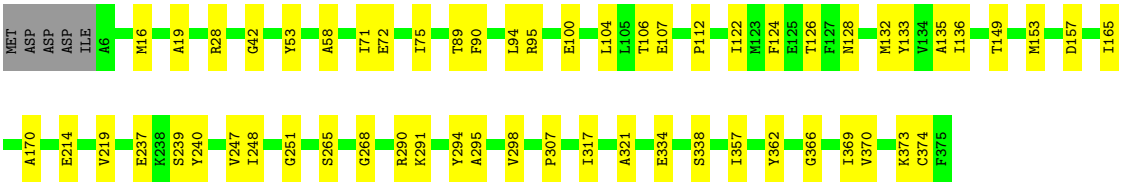
• Molecule 1: Alpha-centractin

Chain I:



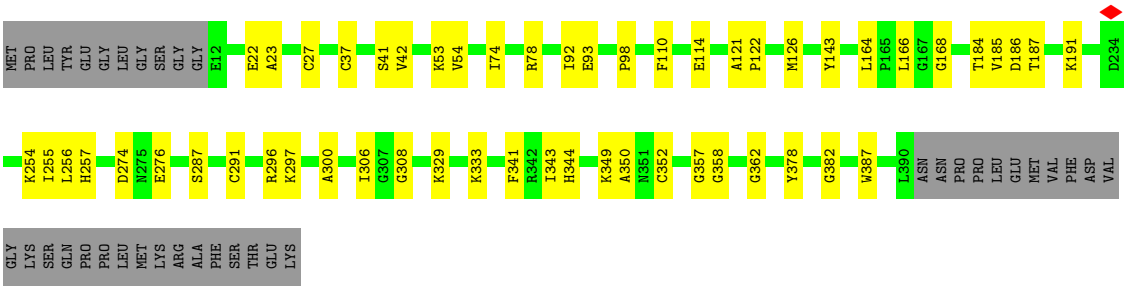
• Molecule 2: Actin, cytoplasmic 1

Chain H:



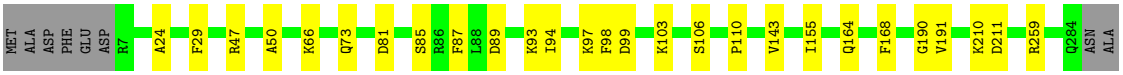
• Molecule 3: Actin-related protein 10

Chain J:



• Molecule 4: F-actin-capping protein subunit alpha-1

Chain K:

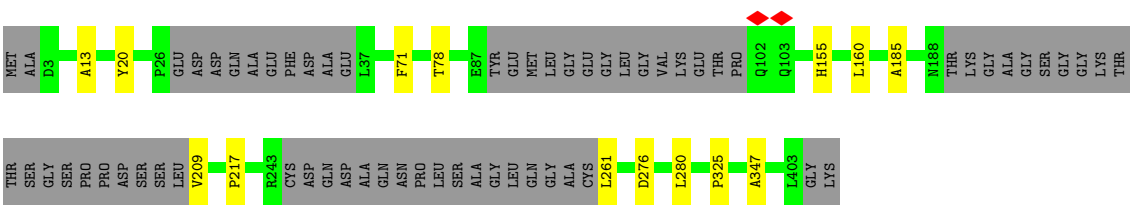


• Molecule 5: F-actin-capping protein subunit beta

Chain L:

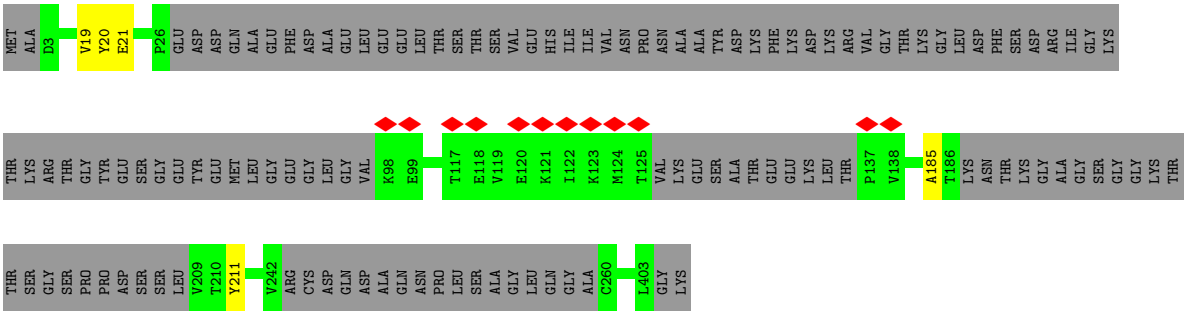
• Molecule 6: Dynactin subunit 2

Chain M:



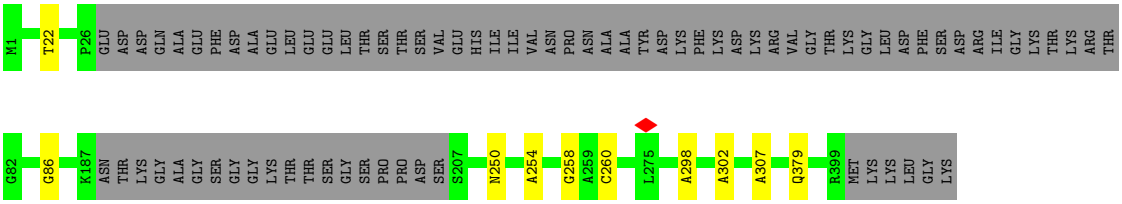
• Molecule 6: Dynactin subunit 2

Chain N:



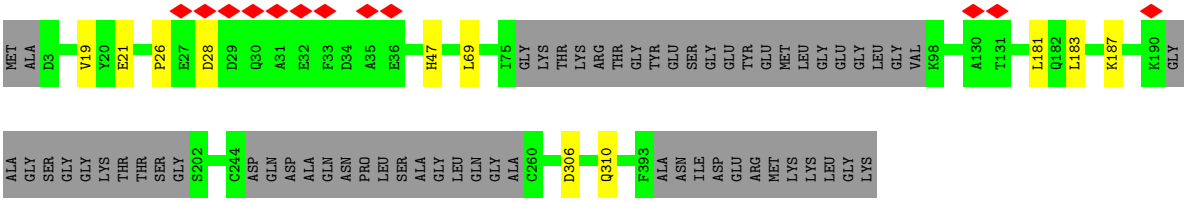
• Molecule 6: Dynactin subunit 2

Chain P:



• Molecule 6: Dynactin subunit 2

Chain Q:

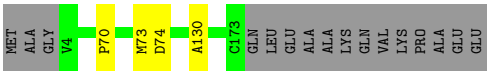


• Molecule 7: Dynactin subunit 3

Chain O:

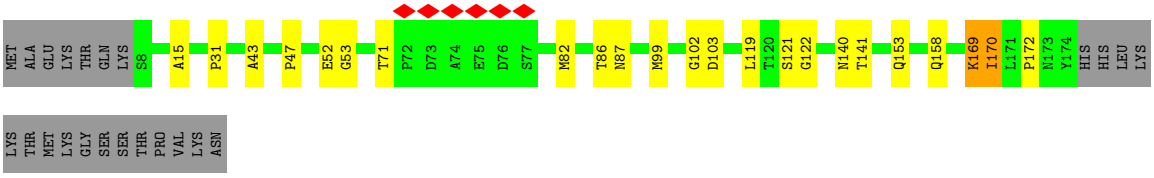
• Molecule 7: Dynactin subunit 3

Chain R:



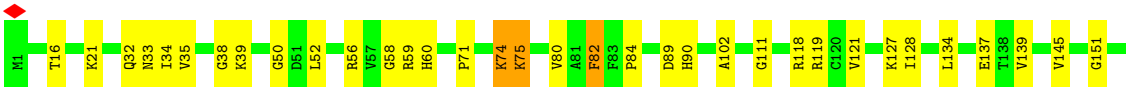
• Molecule 8: Dynactin subunit 6

Chain U:



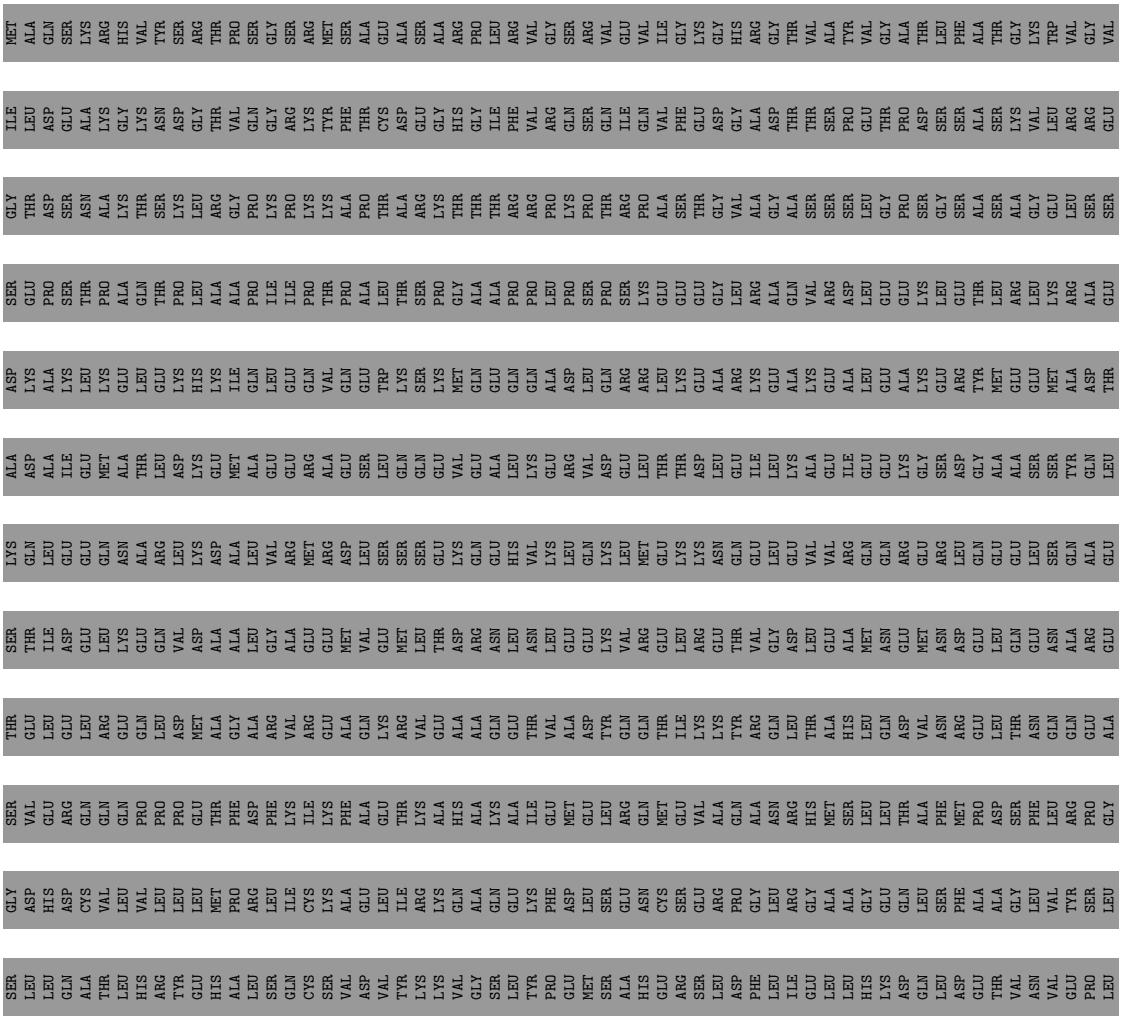
• Molecule 9: Dynactin subunit 5

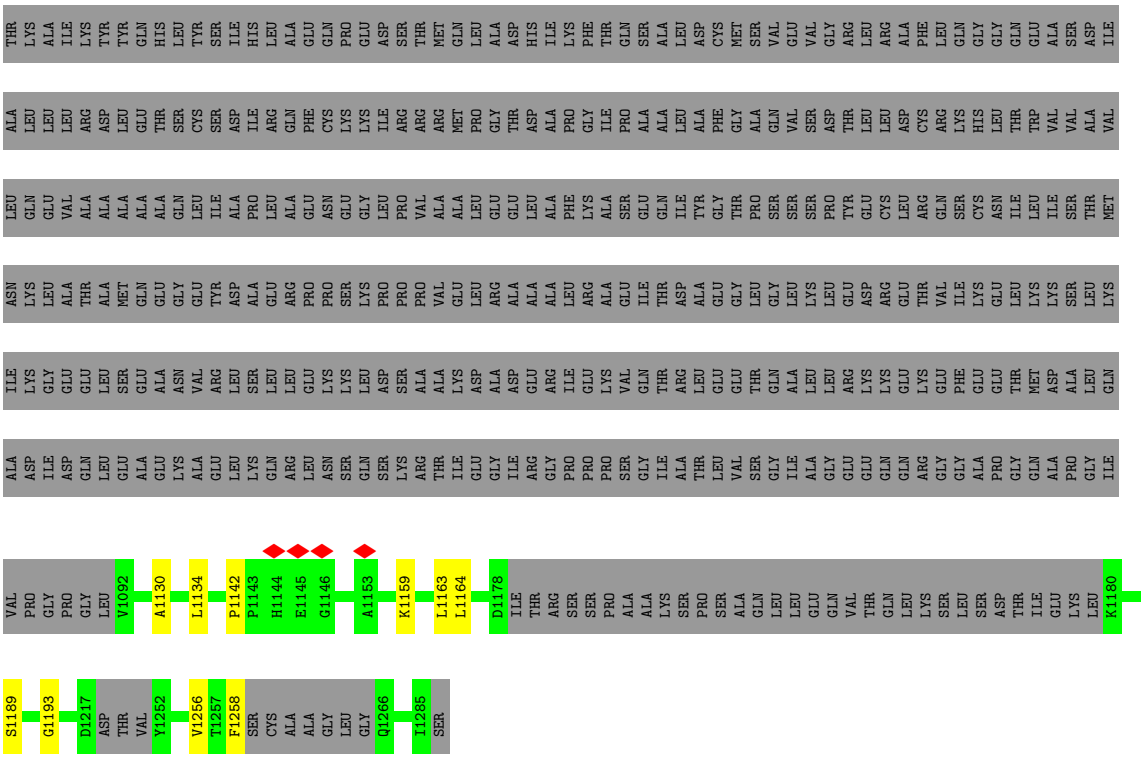
Chain V:



• Molecule 10: Dynactin subunit 1

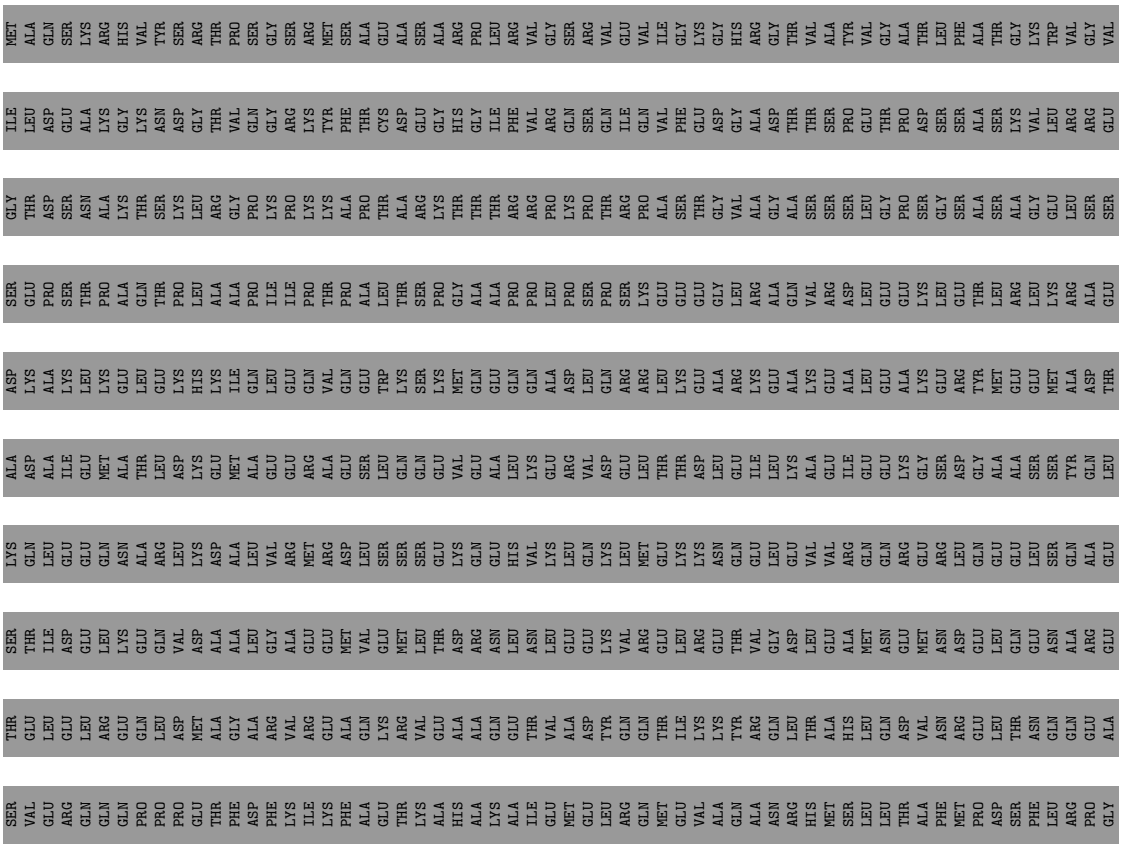
Chain W:

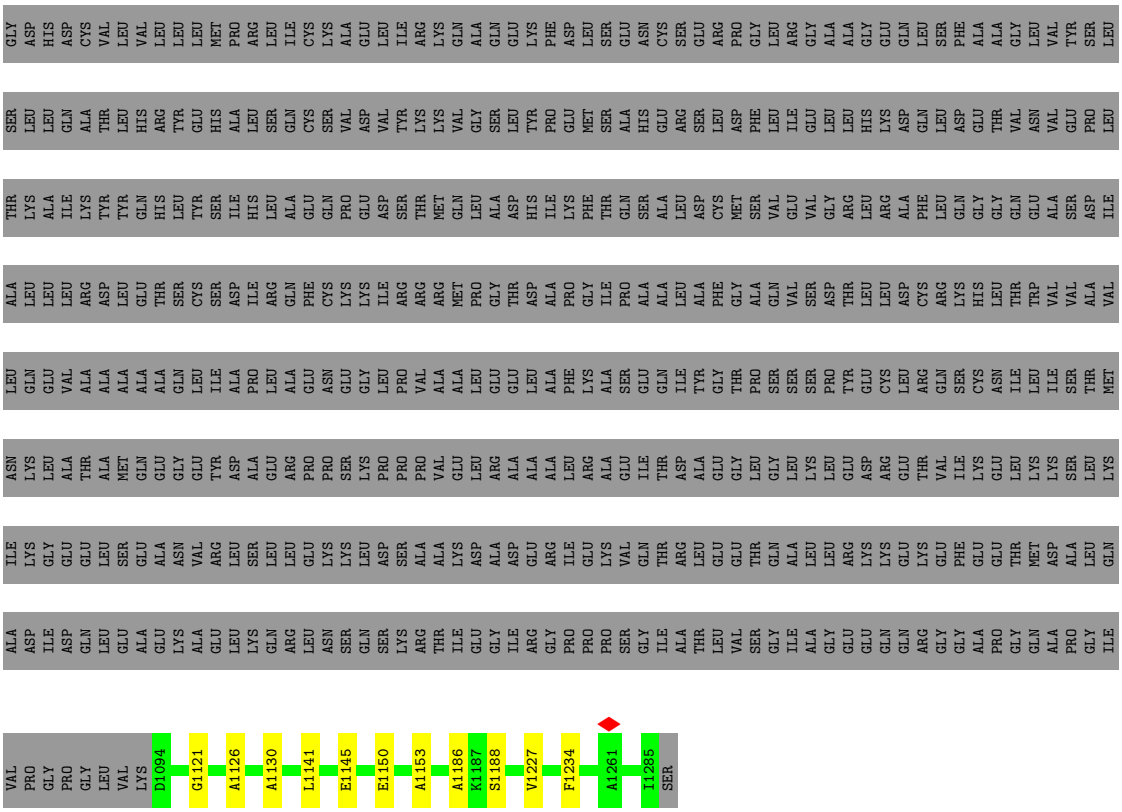




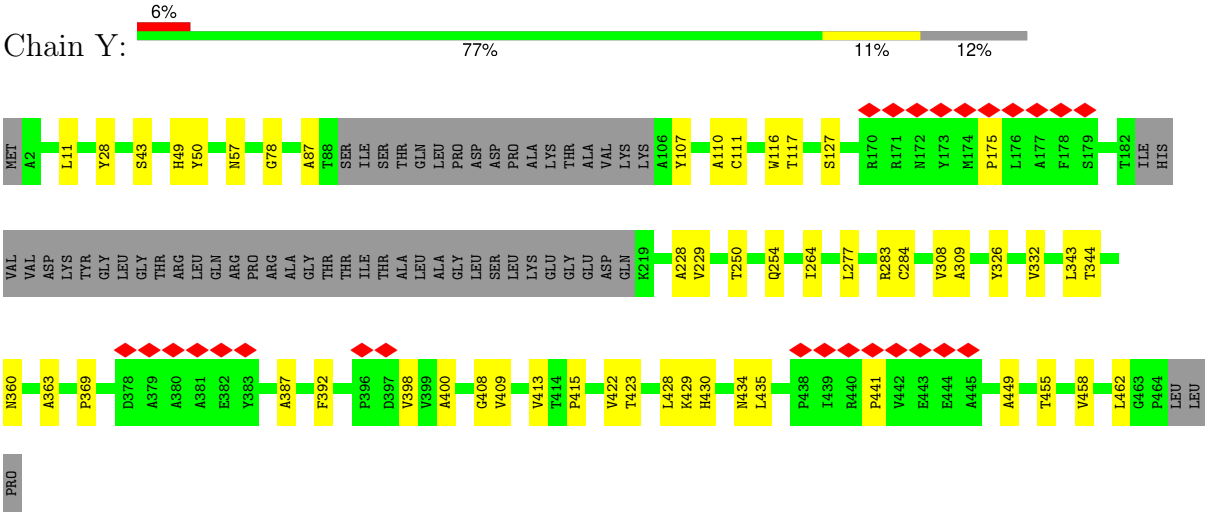
• Molecule 10: Dynactin subunit 1

Chain Z:

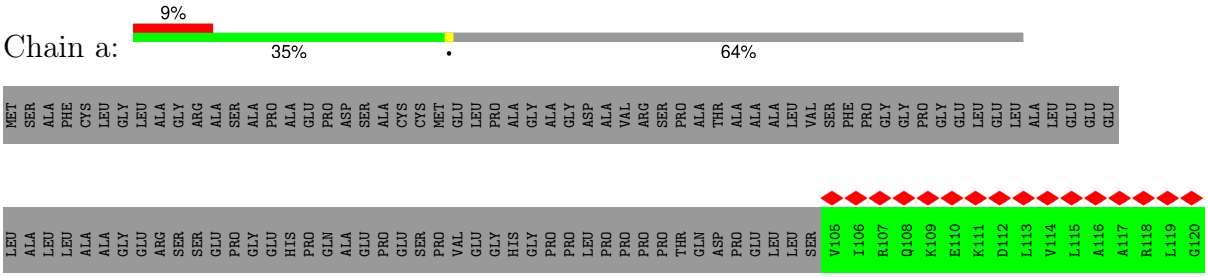


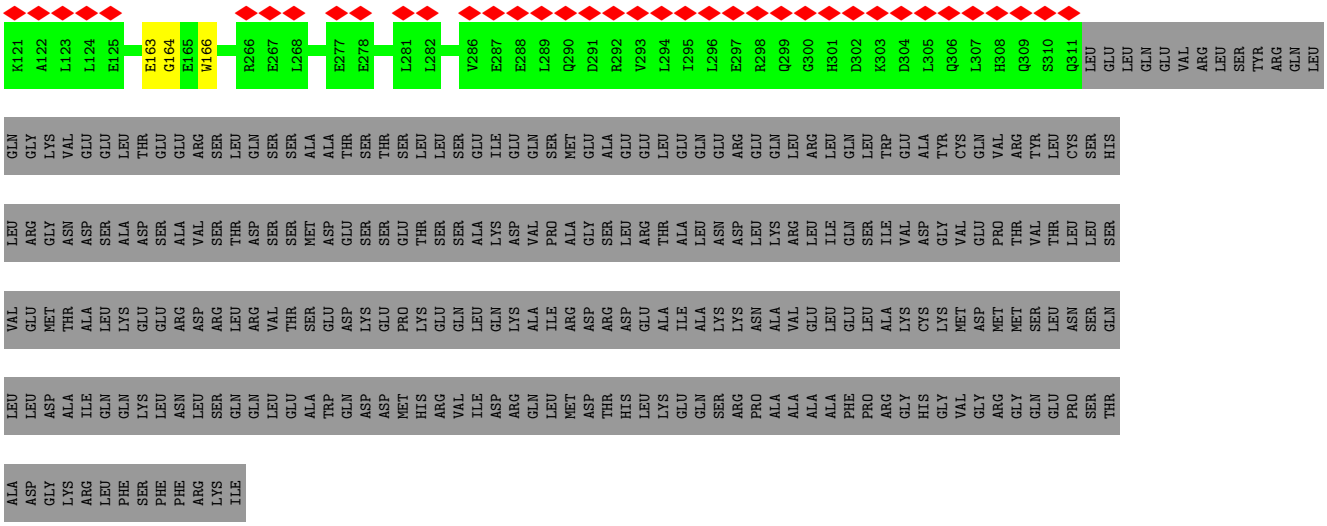


• Molecule 11: Dynactin subunit 4



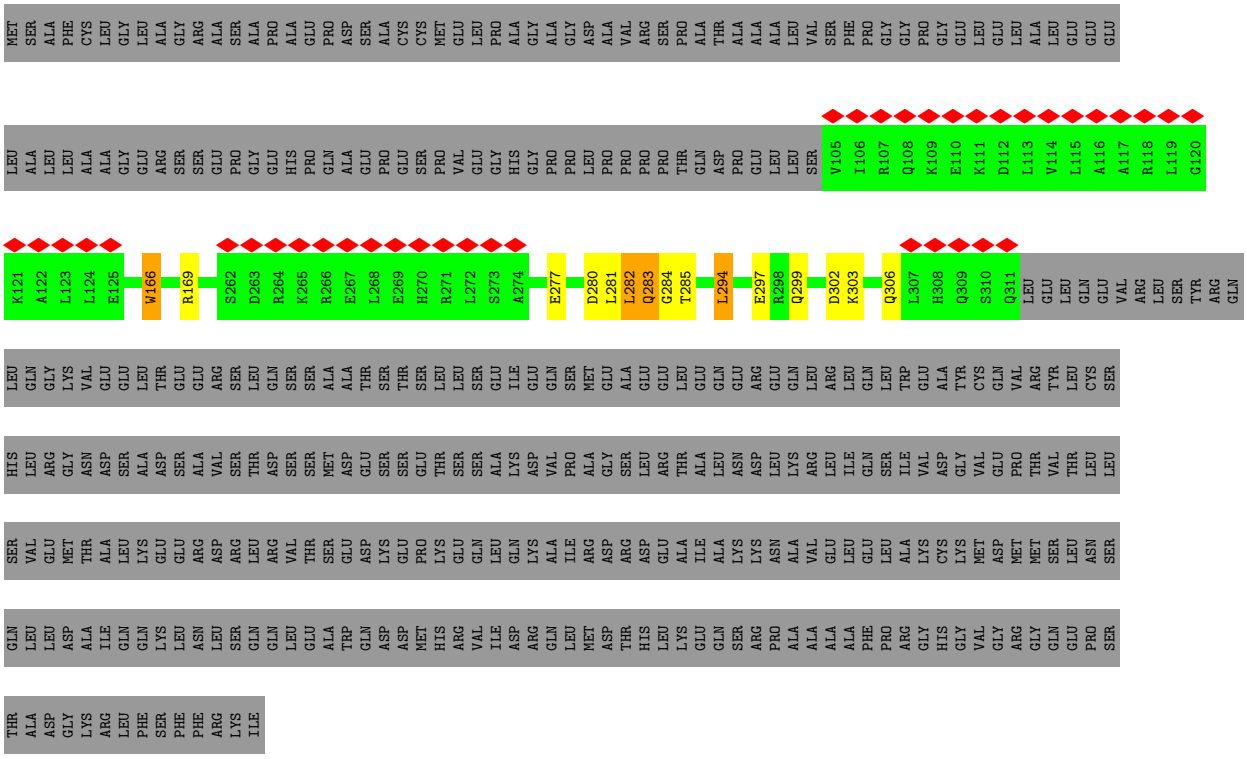
• Molecule 12: BICD family-like cargo adapter 1





• Molecule 12: BICD family-like cargo adapter 1

Chain b:

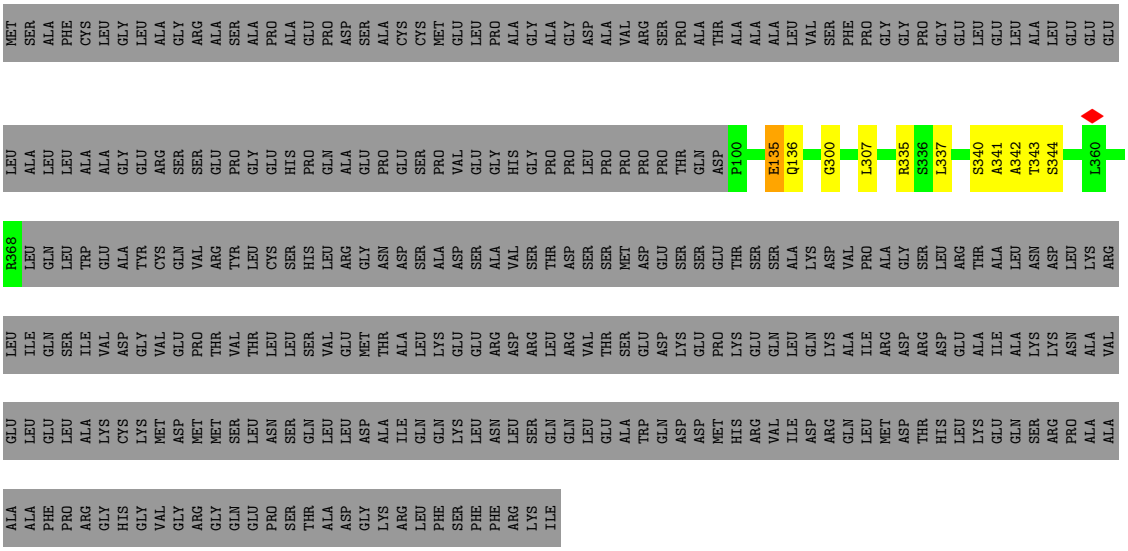


• Molecule 12: BICD family-like cargo adapter 1

Chain c:

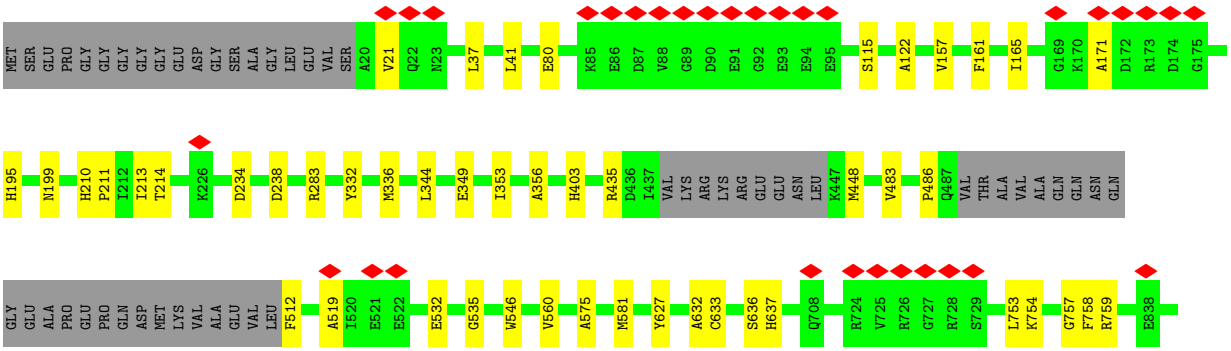
• Molecule 12: BICD family-like cargo adapter 1

Chain d:

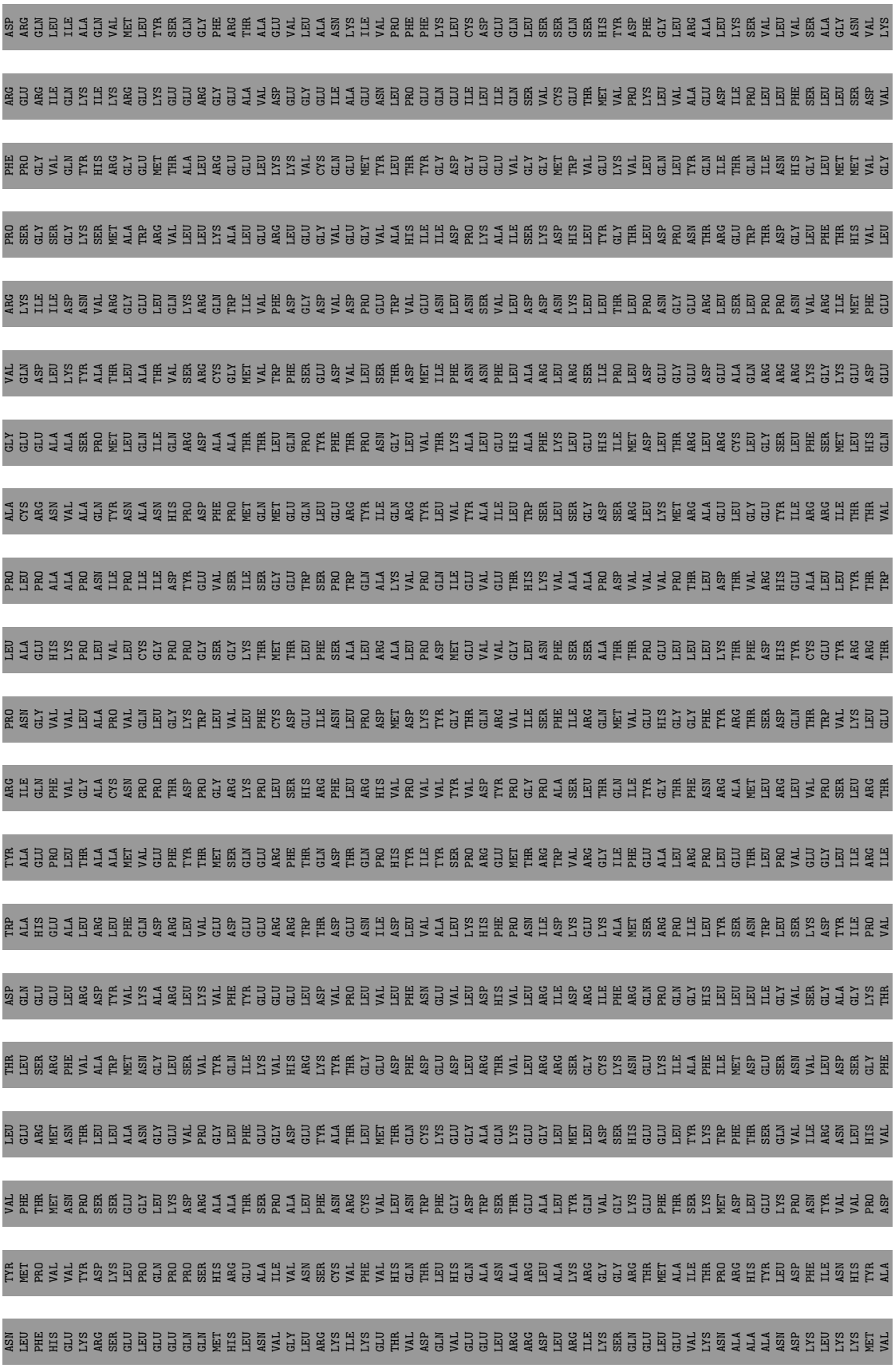


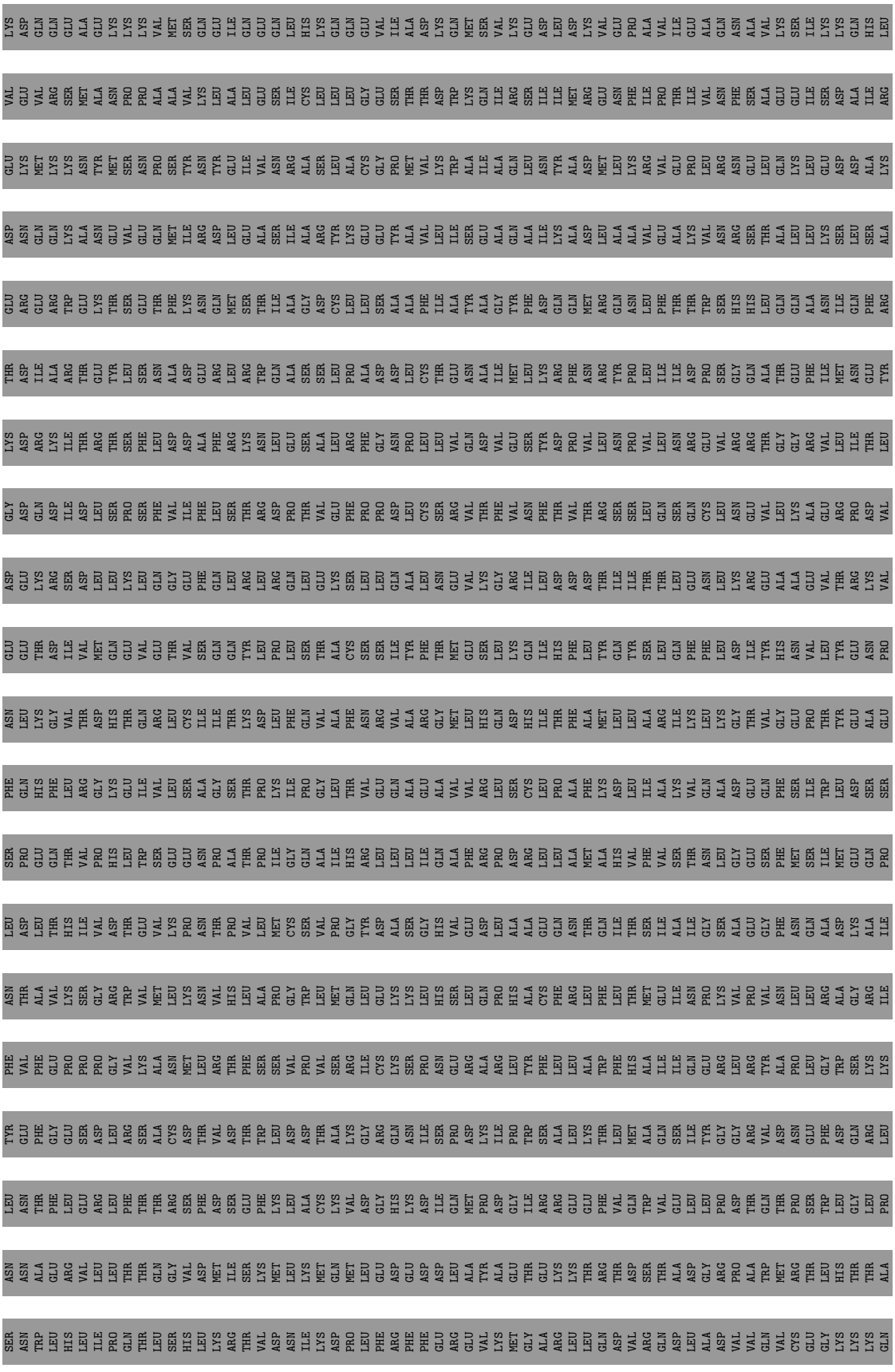
• Molecule 13: Cytoplasmic dynein 1 heavy chain 1

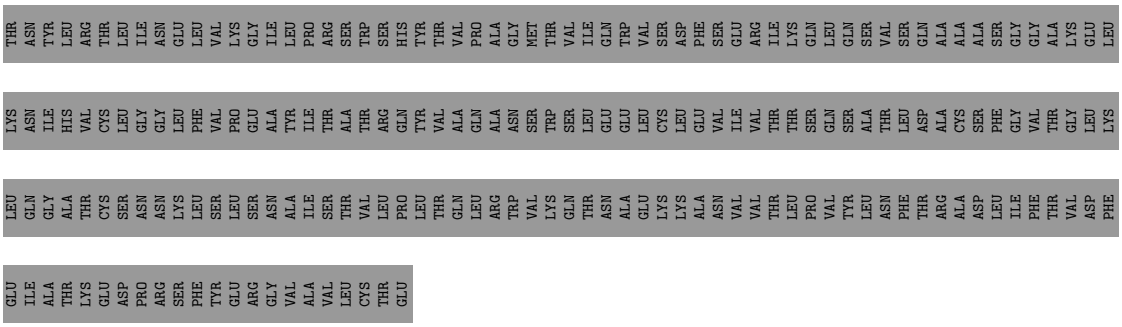
Chain e:

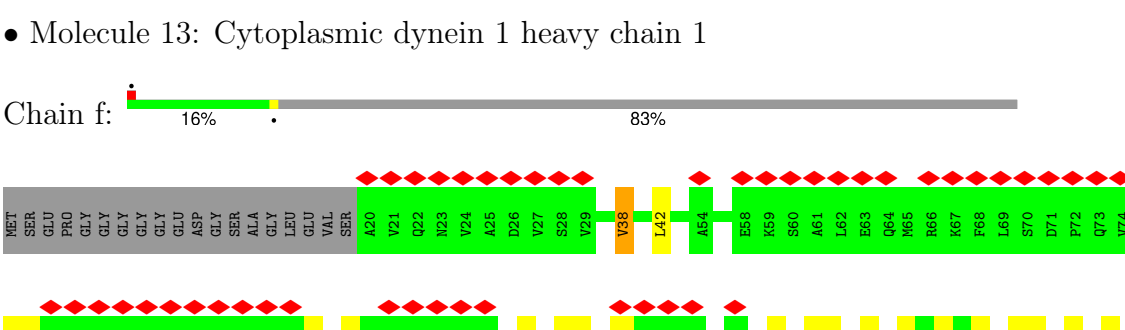


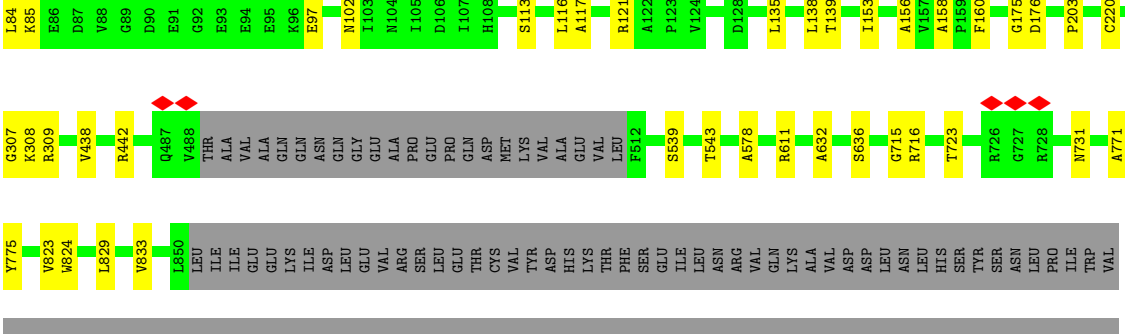
Q844
E845
D848
D849
L850

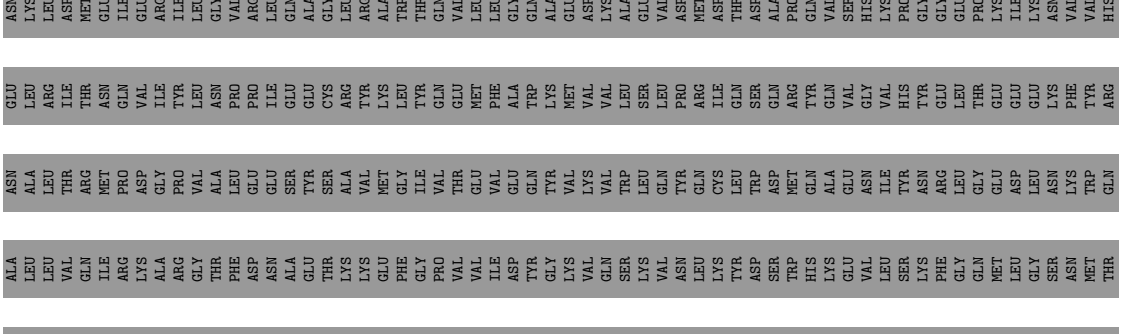

ASP ARG GLN LEU ILE ALA GLN VAL MET LEU TYR SER GLN GLY PHE ARG THR ALA GLU VAL LEU ALA ASN LYS ILE VAL PRO PHE PHE LYS LEU CYS ASP GLU GLN LEU SER SER GLN SER HIS TYR ASP PHE GLY LEU ARG ALA LEU LYS SER VAL LEU VAL SER ALA GLY ASN VAL LYS
ARG GLU ARG ILE GLN LYS ILE LYS ARG GLU LYS GLU GLU ARG GLY GLU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

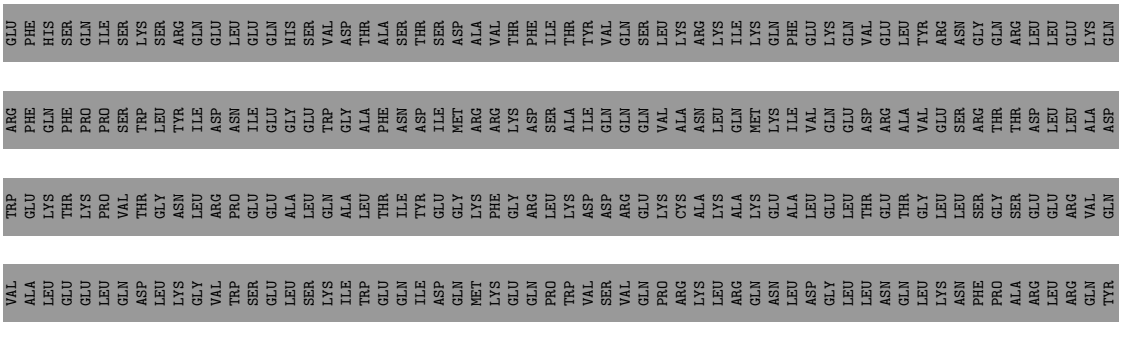






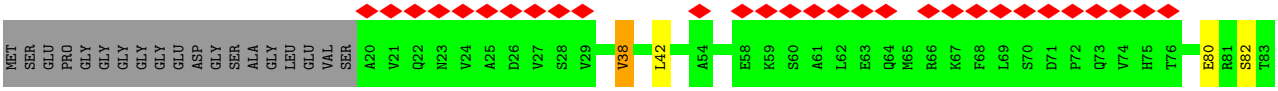


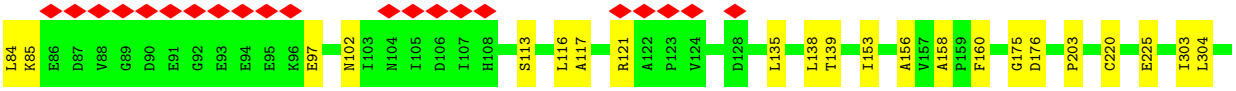


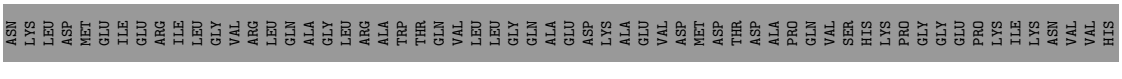


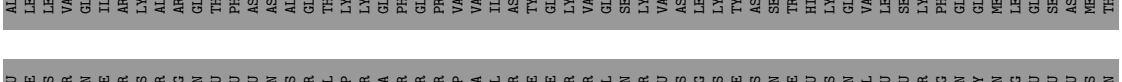
• Molecule 13: Cytoplasmic dynein 1 heavy chain 1

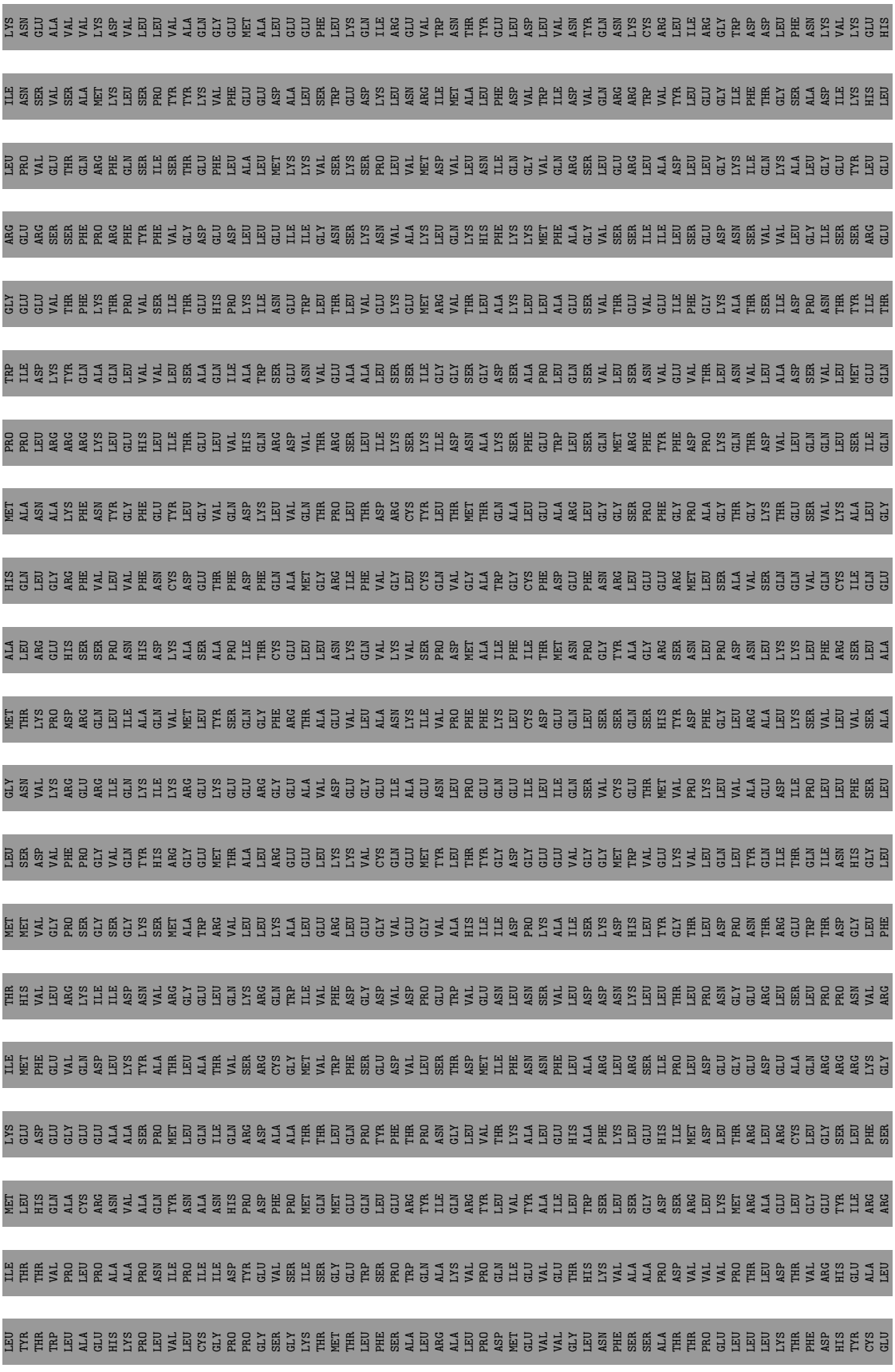
Chain f:







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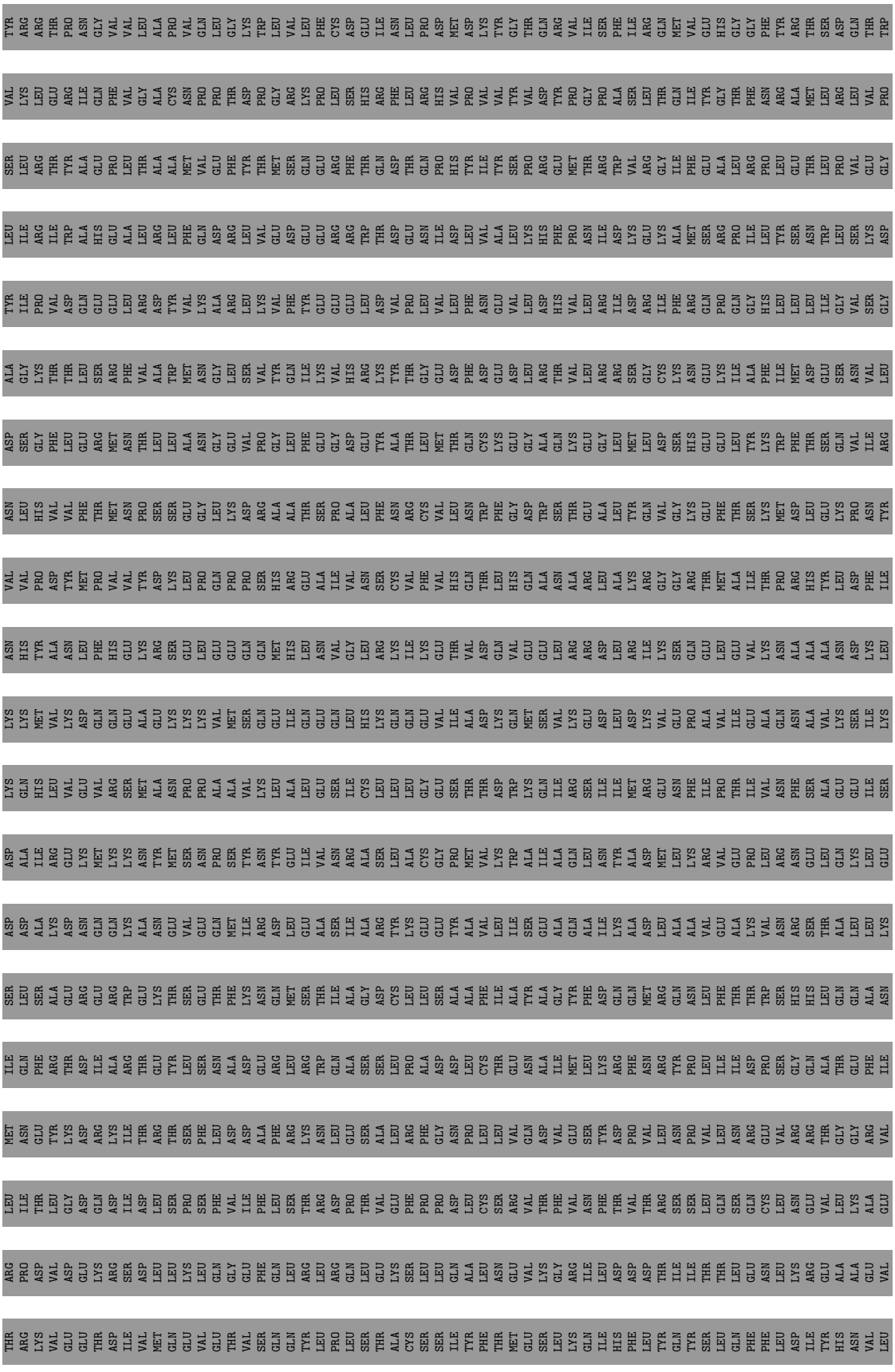
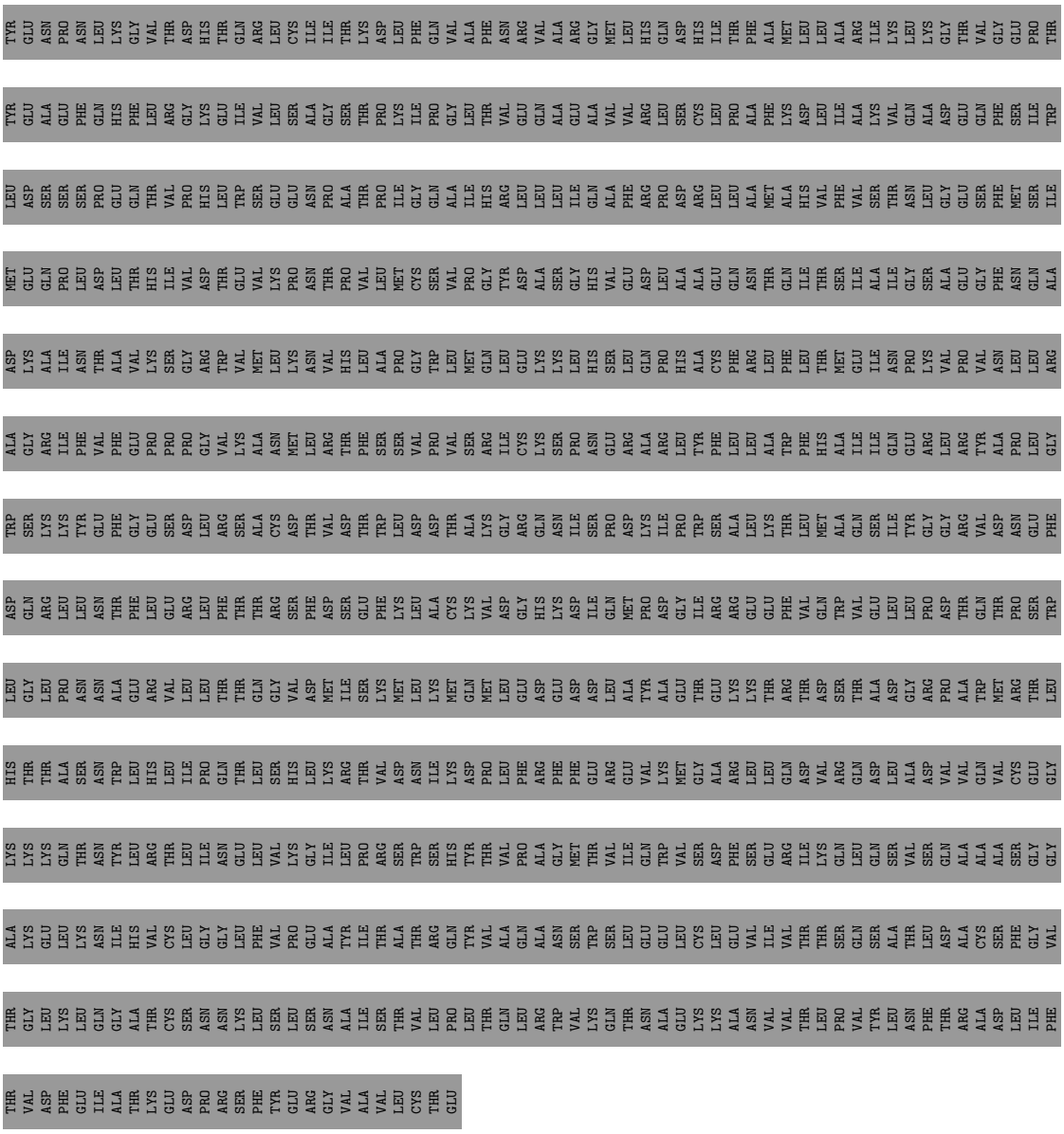
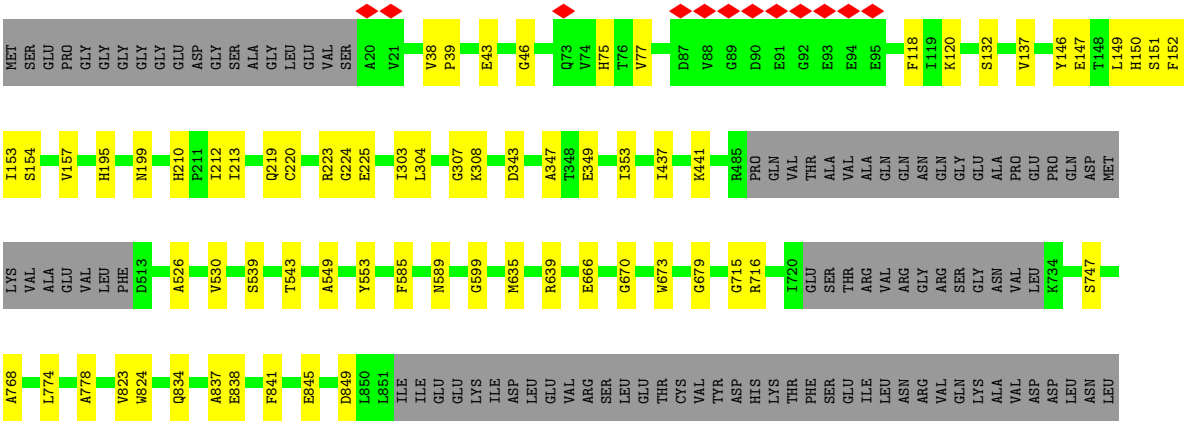
ILE ASN SER VAL SER ALA MET LYS LEU SER PRO TYR TYR LYS VAL PHE GLU GLU ASP LYS LEU ASN ARG ILE MET ALA LEU PHE ASP VAL TRP ILE ASP VAL GLN ARG ARG TRP VAL TYR LEU GLU GLY GLY ILE PHE THR GLY SER ALA ASP ILE LYS HIS LEU
LEU PRO VAL GLU THR GLN ARG PHE GLN SER ILE SER THR GLU PHE LEU ALA LEU MET LYS LYS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

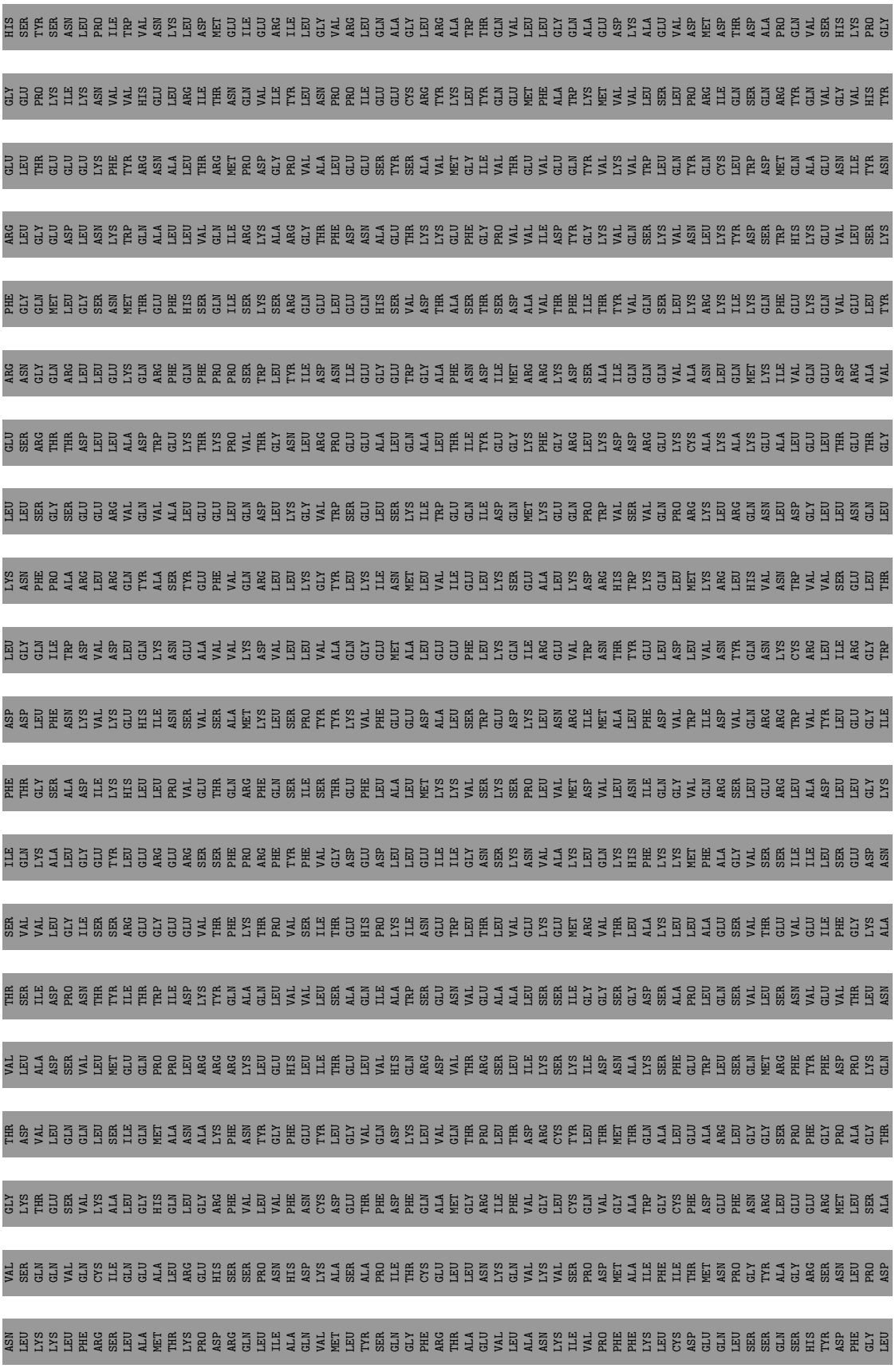

TYR ARG ARG THR PRO ASN GLY VAL VAL LEU LEU ALA PRO VAL GLN LEU GLY LYS TRP LEU VAL LEU PHE CYS ASP GLU ILE ASN LEU PRO ASP MET ASP LYS TYR GLY THR GLN ARG VAL ILE SER PHE ILE ARG GLN MET VAL GLU HIS GLY GLY PHE TYR ARG THR SER ASP GLN TRP
VAL LYS LEU GLU ARG ILE GLN PHE VAL GLY ALA CYS ASN PRO PRO THR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

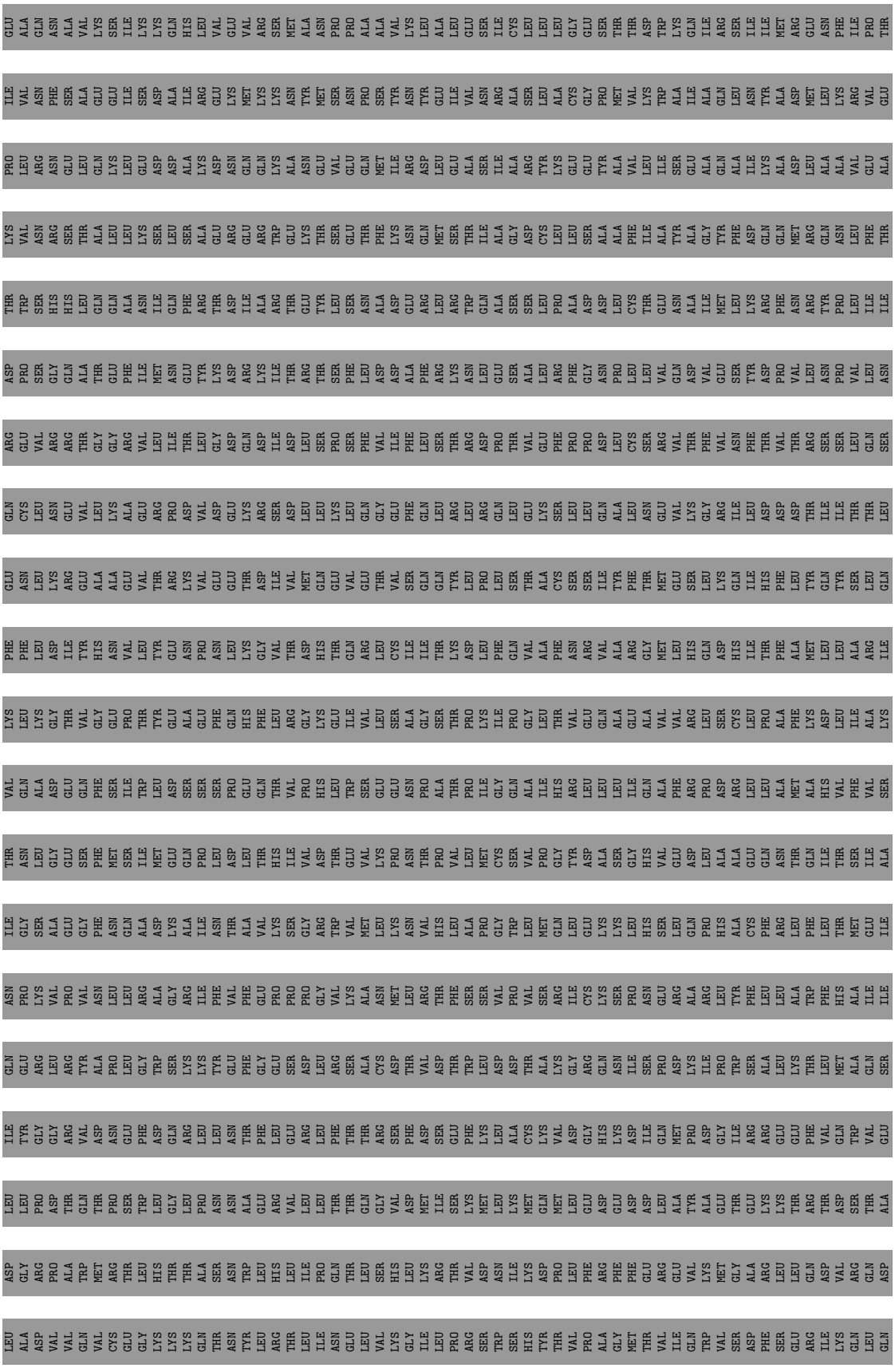


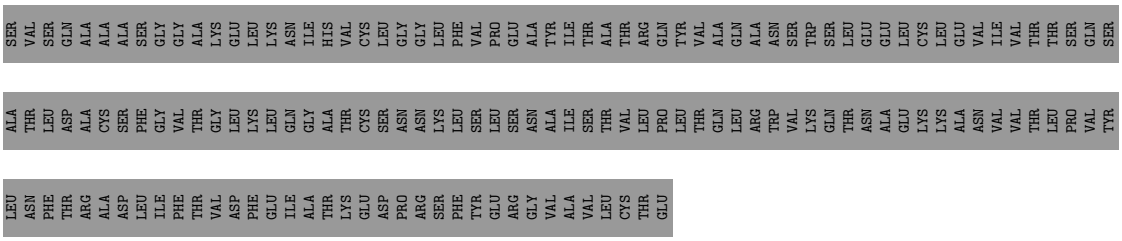
• Molecule 13: Cytoplasmic dynein 1 heavy chain 1

Chain m:



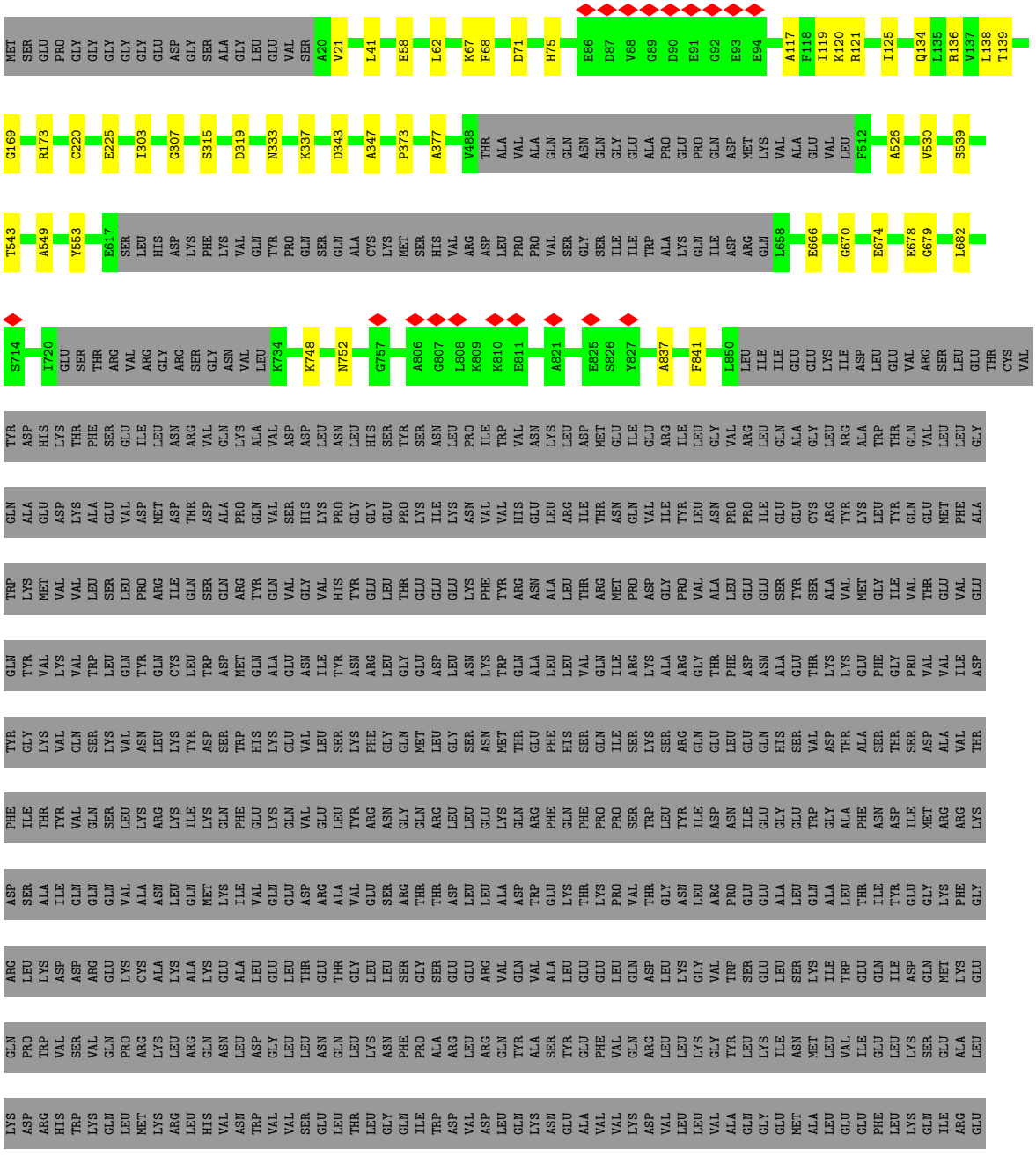

HIS SER TYR SER ASN LEU PRO ILE TRP VAL ASN LYS LEU ASP MET GLU ILE GLU ARG ILE LEU GLY VAL ARG LEU GLN ALA GLY LEU ARG ALA TRP THR GLN GLU VAL LEU LEU GLY GLN ALA GLU ASP LYS ALA GLU VAL ASP MET ASP THR ASP ALA PRO GLN VAL SER HIS LYS PRO GLY
GLY GLU PRO LYS ILE LYS ASN VAL VAL HIS GLU LEU ARG ILE THR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

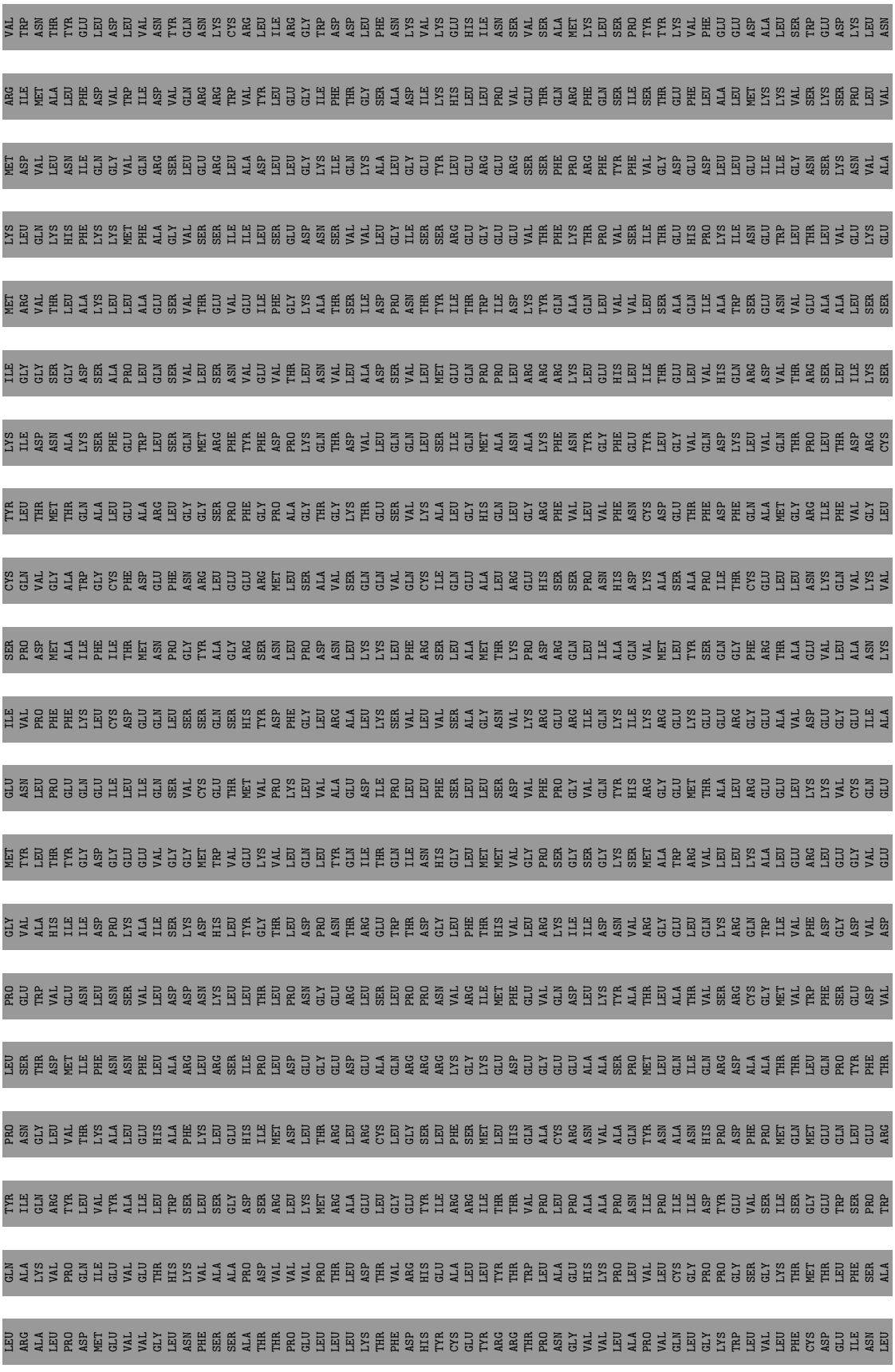

GLU ALA GLN ASN ALA VAL LYS SER ILE LYS LYS GLN HIS LEU VAL GLU VAL ARG SER MET ALA ASN PRO PRO ALA ALA VAL LYS LEU ALA LEU GLU SER ILE CYS LEU LEU LEU GLY GLU SER THR THR ASP TRP LYS GLN ILE ARG SER ILE ILE MET ARG GLU ASN PHE ILE PRO THR
ILE VAL ASN PHE SER ALA GLU GLU ILE SER ASP ALA ILE ARG GLU LYS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

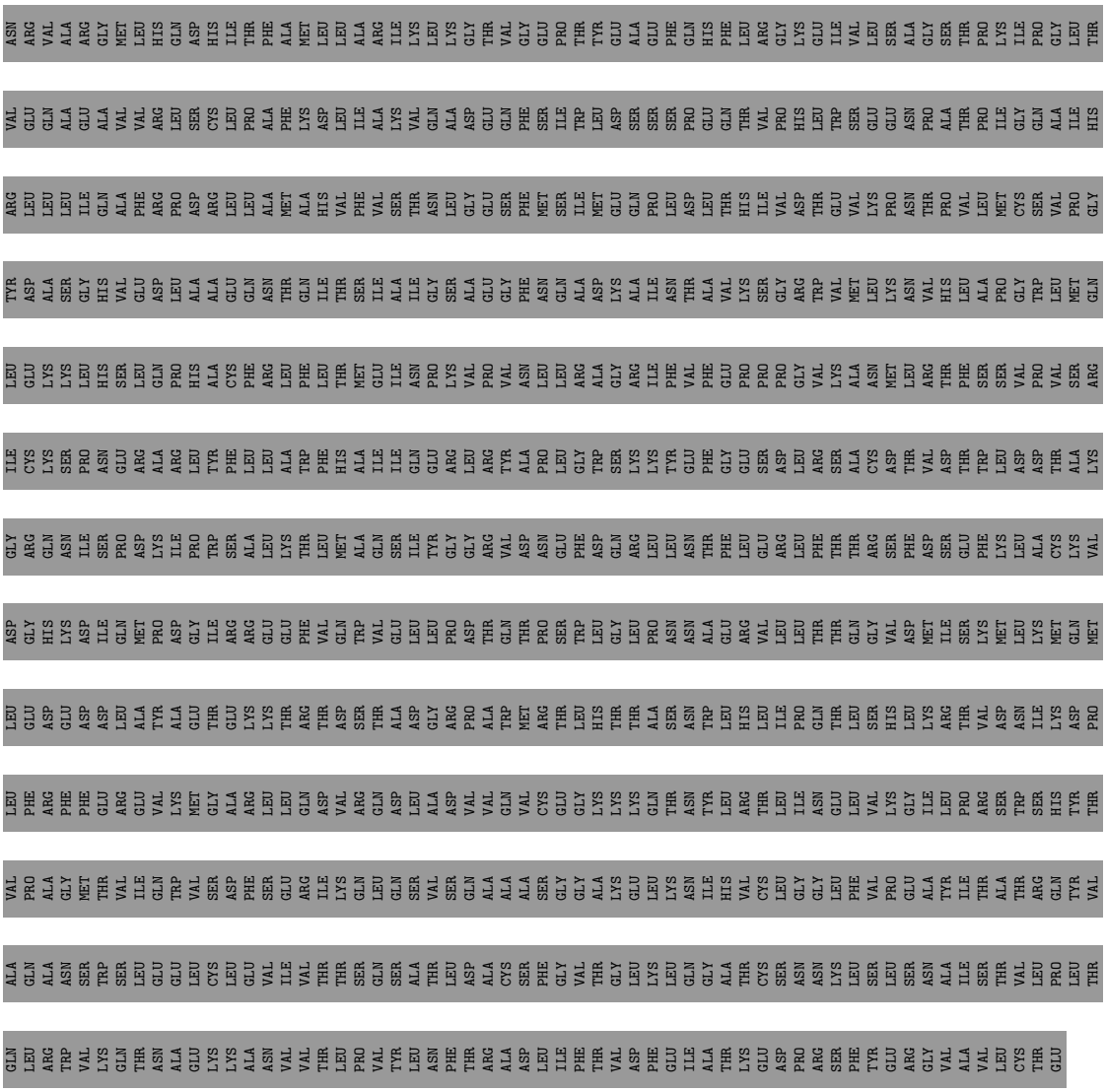


• Molecule 13: Cytoplasmic dynein 1 heavy chain 1

Chain n:

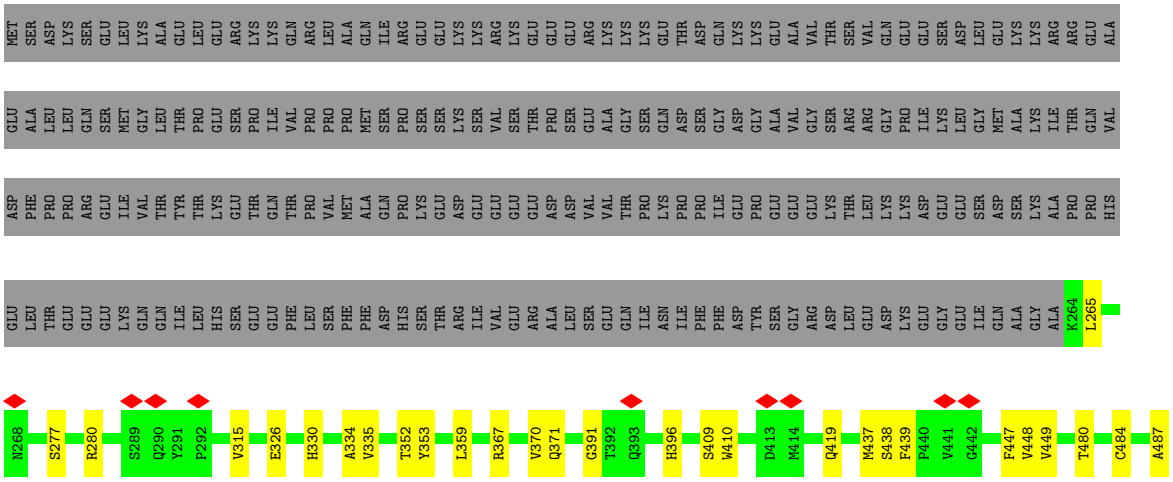


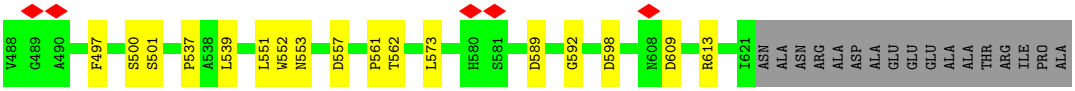

VAL TRP ASN THR TYR GLU LEU ASP LEU VAL ASN TYR GLN ASN LYS CYS ARG LEU ILE ARG GLY TRP ASP ASP LEU PHE ASN LYS VAL LYS GLU HIS ILE ASN SER VAL SER ALA MET LYS LEU SER PRO TYR TYR LYS VAL PHE GLU GLU ASP ALA LEU SER TRP GLU ASP LYS LEU ASN
ARG ILE MET ALA LEU PHE ASP VAL TRP ILE ASP VAL GLN ARG ARG TRP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



• Molecule 14: Cytoplasmic dynein 1 intermediate chain 2

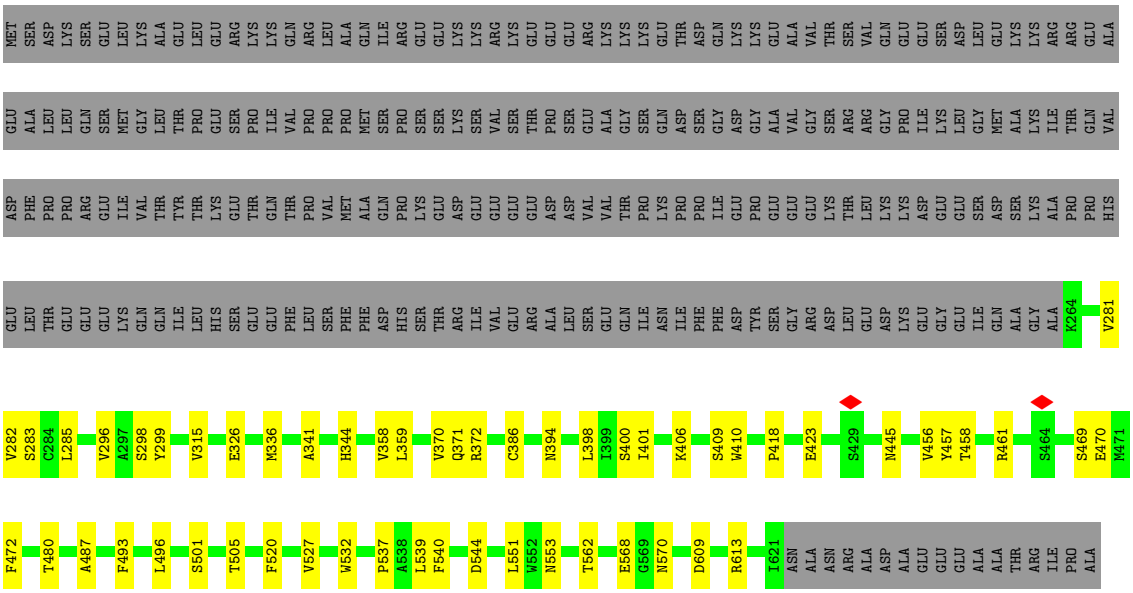
Chain g:





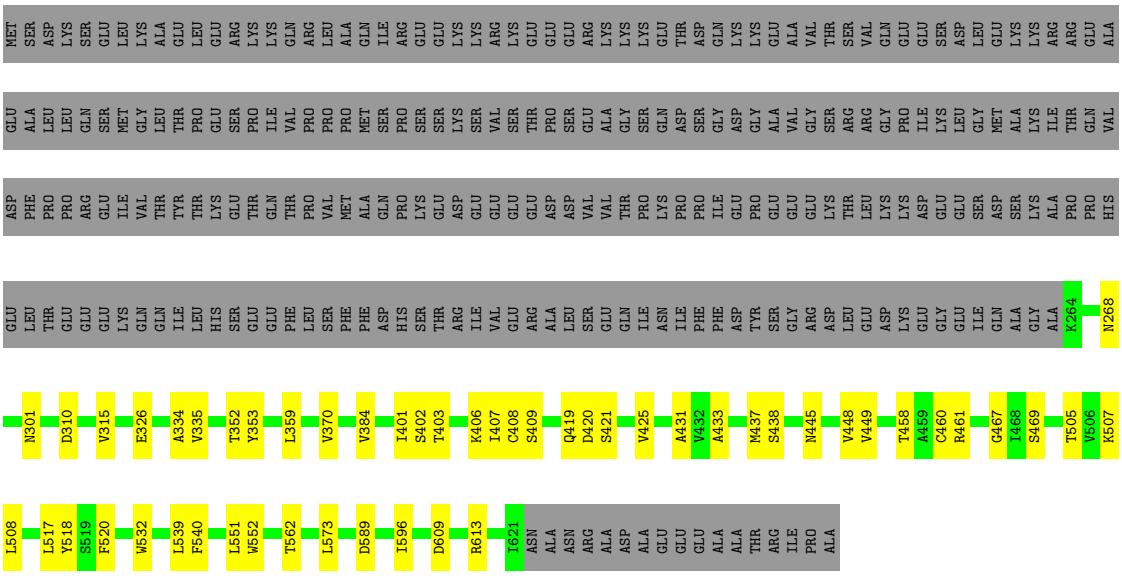
• Molecule 14: Cytoplasmic dynein 1 intermediate chain 2

Chain h:



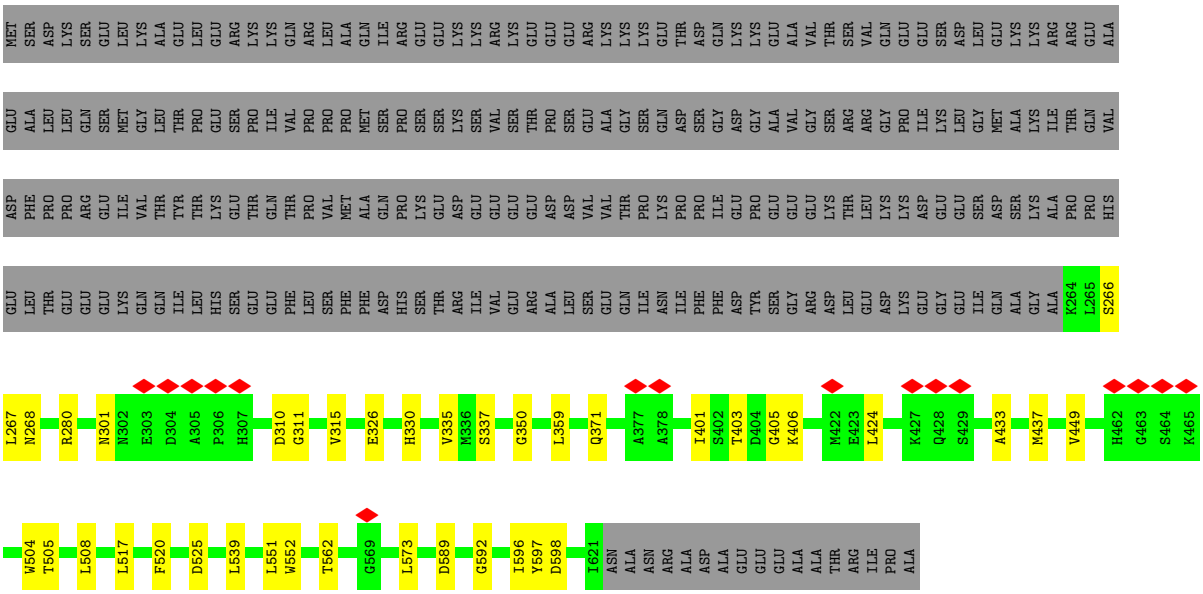
• Molecule 14: Cytoplasmic dynein 1 intermediate chain 2

Chain o:



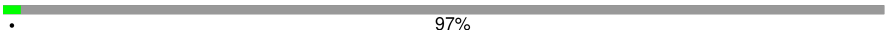
• Molecule 14: Cytoplasmic dynein 1 intermediate chain 2

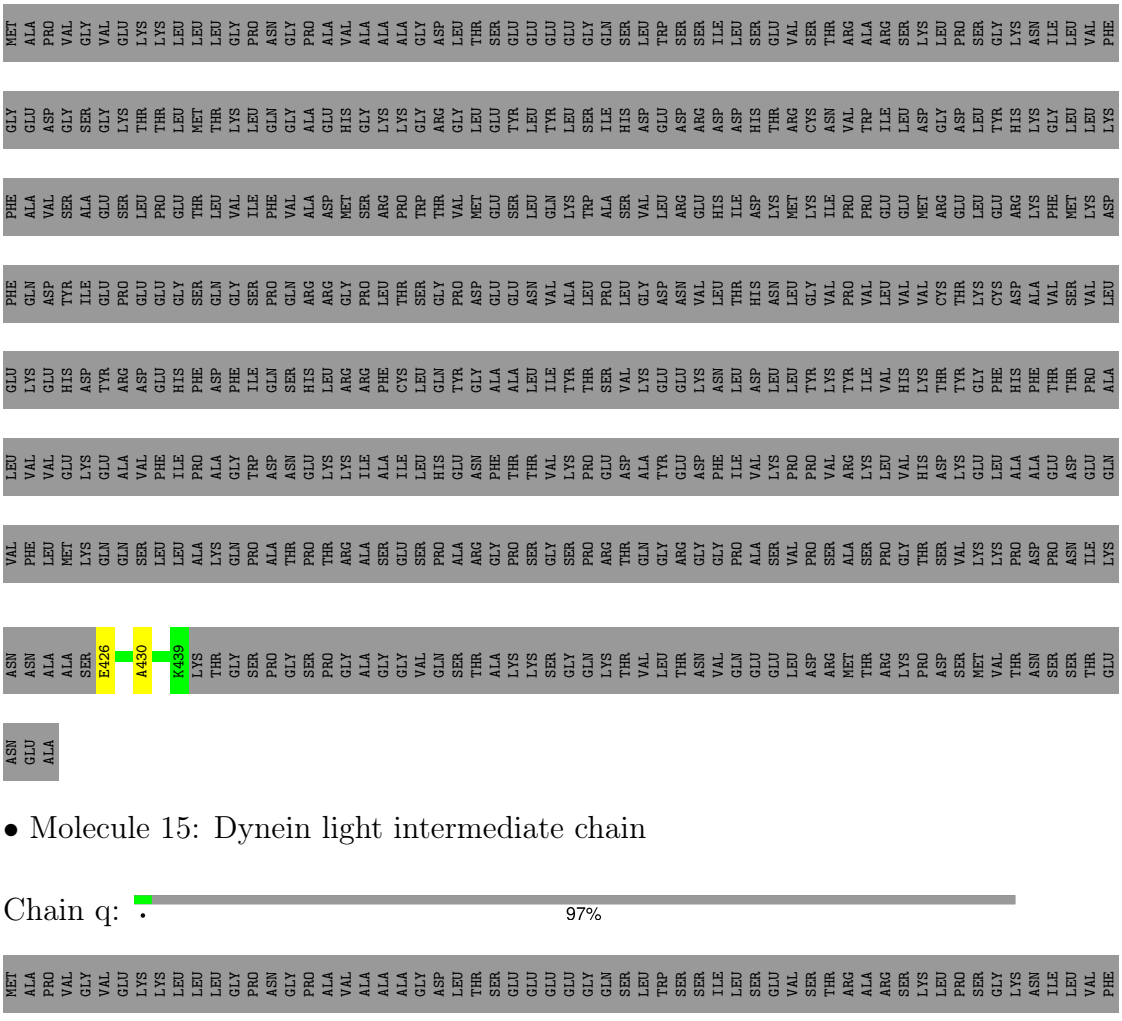
Chain p:



• Molecule 15: Dynein light intermediate chain

Chain j:





• Molecule 15: Dynein light intermediate chain

Chain q:

GLY GLU ASP GLY SER GLY LYS THR THR LEU MET THR LYS LEU GLN GLY ALA GLU HIS GLY LYS LYS GLY ARG GLY LEU GLU TYR LEU TYR LEU SER ILE HIS ASP GLU ASP ARG ASP ASP HIS THR ARG CYS ASN VAL TRP ILE LEU ASP GLY ASP LEU TYR HIS LYS GLY LEU LEU LYS
PHE ALA VAL SER ALA GLU SER LEU PRO GLU THR LEU VAL ILE PHE VAL ALA ASP MET SER ARG PRO TRP THR VAL MET GLU SER LEU GLN LYS TRP ALA SER VAL LEU ARG GLU HIS ILE ASP LYS MET LYS ILE PRO PRO GLU GLU MET ARG GLU LEU GLU ARG LYS PHE MET LYS ASP
PHE GLN ASP TYR ILE GLU PRO GLU GLU GLY SER GLN GLY SER PRO GLN ARG ARG GLY PRO LEU THR SER GLY PRO ASP GLU GLU ASN VAL ALA LEU PRO LEU GLY ASP ASN VAL LEU THR HIS ASN LEU GLY VAL PRO VAL LEU VAL VAL CYS THR LYS CYS ASP ALA VAL SER VAL LEU
GLU LYS GLU HIS ASP TYR ARG ASP GLU HIS PHE ASP PHE ILE GLN SER HIS LEU ARG ARG PHE CYS LEU GLN TYR GLY ALA ALA LEU ILE TYR THR SER VAL LYS GLU GLU LYS ASN LEU ASP LEU LEU TYR LYS TYR ILE VAL HIS LYS THR TYR GLY PHE HIS PHE THR THR PRO ALA
LEU VAL VAL GLU LYS GLU ALA VAL PHE ILE PRO ALA GLY TRP ASP ASN GLU LYS LYS ILE ALA ILE LEU HIS GLU ASN PHE THR THR VAL LYS PRO GLU ASP ALA TYR GLU ASP PHE ILE VAL LYS PRO PRO VAL ARG LYS LEU VAL HIS ASP LYS GLU LEU ALA ALA GLU ASP GLU GLN
VAL PHE LEU MET LYS GLN GLN SER LEU LEU ALA LYS GLN PRO ALA THR PRO THR ARG ALA SER GLU SER PRO ALA ARG GLY PRO SER GLY SER PRO ARG THR GLN GLY ARG GLY GLY PRO ALA SER VAL PRO SER ALA SER PRO GLY THR SER VAL LYS LYS PRO ASP PRO ASN ILE LYS
ASN ASN ALA ALA SER E426 S435 S438 K439 LYS THR GLY SER PRO GLY SER PRO GLY ALA GLY GLY VAL GLN SER THR ALA LYS LYS SER GLY GLN LYS THR VAL LEU THR ASN VAL GLN GLU GLU LEU ASP ARG MET THR ARG LYS PRO ASP SER MET VAL THR ASN SER SER THR
GLU ASN GLU ALA

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	10576	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.461	Depositor
Minimum map value	-0.215	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	666.62396, 666.62396, 666.62396	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.736, 1.736, 1.736	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ADP, ATP, ZN

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	0.25	0/1821	0.47	0/2531
1	B	0.28	0/1821	0.53	0/2531
1	C	0.26	0/1846	0.52	0/2566
1	D	0.26	0/1821	0.51	0/2531
1	E	0.25	0/1821	0.52	0/2531
1	F	0.32	1/1821 (0.1%)	0.56	0/2531
1	G	0.26	0/1821	0.51	0/2531
1	I	0.23	0/1821	0.50	0/2531
2	H	0.26	0/1821	0.49	2/2531 (0.1%)
3	J	0.23	0/1867	0.47	0/2596
4	K	0.24	0/1377	0.44	0/1919
5	L	0.25	0/1326	0.47	0/1844
6	M	0.18	0/1684	0.40	1/2343 (0.0%)
6	N	0.22	0/1389	0.42	0/1933
6	P	0.22	0/1609	0.45	0/2240
6	Q	0.21	0/1703	0.41	0/2373
7	O	0.20	0/887	0.42	0/1236
7	R	0.19	0/843	0.47	0/1175
8	U	0.40	1/821 (0.1%)	0.59	0/1140
9	V	0.36	0/880	0.82	5/1222 (0.4%)
10	W	0.17	0/750	0.36	0/1040
10	Z	0.26	0/951	0.47	0/1325
11	Y	0.25	0/2035	0.50	0/2837
12	a	0.28	0/1029	0.56	0/1436
12	b	1.19	3/1029 (0.3%)	1.26	6/1436 (0.4%)
12	c	0.25	0/1193	0.55	0/1665
12	d	0.32	0/1338	0.73	1/1868 (0.1%)
13	e	0.16	0/3956	0.39	0/5515
13	f	0.23	0/4007	0.52	0/5588
13	m	0.22	0/3747	0.46	0/5115
13	n	0.21	0/3562	0.41	0/4855
14	g	0.14	0/1766	0.32	0/2457

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
14	h	0.24	0/1766	0.50	0/2457
14	o	0.25	0/1766	0.48	0/2457
14	p	0.19	0/1766	0.46	0/2457
15	j	0.11	0/55	0.15	0/67
15	q	0.11	0/55	0.32	0/67
All	All	0.28	5/61571 (0.0%)	0.51	15/85477 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
8	U	0	2
9	V	0	3
12	b	0	1
All	All	0	6

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	b	282	LEU	C-N	31.58	1.72	1.33
12	b	283	GLN	N-CA	14.76	1.63	1.46
8	U	71	THR	C-O	-7.34	1.20	1.23
1	F	73	TYR	C-N	-6.43	1.28	1.33
12	b	282	LEU	CA-C	5.51	1.59	1.52

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
12	b	282	LEU	CA-C-N	23.93	152.24	120.65
12	b	282	LEU	C-N-CA	23.93	152.24	120.65
12	b	282	LEU	CA-C-O	-11.71	108.01	120.42
12	b	283	GLN	N-CA-C	7.36	118.99	110.97
9	V	74	LYS	N-CA-C	6.94	117.80	108.23

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	U	169	LYS	Peptide

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Mol	Chain	Res	Type	Group
8	U	170	ILE	Peptide
9	V	74	LYS	Peptide
9	V	75	LYS	Peptide
9	V	82	PHE	Peptide

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	1822	0	820	31	0
1	B	1822	0	820	34	0
1	C	1847	0	830	32	0
1	D	1822	0	820	41	0
1	E	1822	0	820	28	0
1	F	1822	0	820	38	0
1	G	1822	0	820	29	0
1	I	1822	0	820	25	0
2	H	1822	0	835	32	0
3	J	1868	0	823	35	0
4	K	1378	0	611	16	0
5	L	1327	0	585	16	0
6	M	1689	0	765	11	0
6	N	1394	0	632	6	0
6	P	1612	0	747	7	0
6	Q	1707	0	769	8	0
7	O	888	0	413	7	0
7	R	844	0	385	3	0
8	U	822	0	370	13	0
9	V	881	0	379	29	0
10	W	754	0	336	6	0
10	Z	952	0	434	6	0
11	Y	2038	0	886	44	0
12	a	1030	0	445	2	0
12	b	1030	0	444	21	0
12	c	1194	0	512	3	0
12	d	1339	0	579	20	0
13	e	3959	0	1773	30	0
13	f	4009	0	1794	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	m	3750	0	1534	37	0
13	n	3566	0	1454	24	0
14	g	1767	0	796	26	0
14	h	1767	0	796	29	0
14	o	1767	0	796	26	0
14	p	1767	0	796	20	0
15	j	56	0	15	1	0
15	q	56	0	15	1	0
16	A	27	0	12	1	0
16	B	27	0	12	3	0
16	C	27	0	12	2	0
16	D	27	0	12	3	0
16	E	27	0	12	2	0
16	F	27	0	12	5	0
16	G	27	0	12	2	0
16	I	27	0	12	1	0
16	J	27	0	12	5	0
17	H	31	0	12	3	0
18	Y	3	0	0	0	0
All	All	61911	0	27409	683	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 8.

The worst 5 of 683 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)
12:b:282:LEU:C	12:b:283:GLN:N	1.72	1.43
9:V:32:GLN:N	12:d:343:THR:H	1.60	0.99
9:V:32:GLN:H	12:d:343:THR:H	1.15	0.91
14:g:265:LEU:HA	14:g:598:ASP:O	1.73	0.88
9:V:33:ASN:H	12:d:343:THR:N	1.72	0.88

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	368/376 (98%)	347 (94%)	21 (6%)	0	100	100
1	B	368/376 (98%)	353 (96%)	15 (4%)	0	100	100
1	C	373/376 (99%)	354 (95%)	19 (5%)	0	100	100
1	D	368/376 (98%)	350 (95%)	18 (5%)	0	100	100
1	E	368/376 (98%)	348 (95%)	20 (5%)	0	100	100
1	F	368/376 (98%)	344 (94%)	24 (6%)	0	100	100
1	G	368/376 (98%)	350 (95%)	18 (5%)	0	100	100
1	I	368/376 (98%)	346 (94%)	22 (6%)	0	100	100
2	H	368/375 (98%)	346 (94%)	22 (6%)	0	100	100
3	J	377/417 (90%)	349 (93%)	28 (7%)	0	100	100
4	K	276/286 (96%)	261 (95%)	15 (5%)	0	100	100
5	L	267/272 (98%)	252 (94%)	15 (6%)	0	100	100
6	M	330/405 (82%)	310 (94%)	19 (6%)	1 (0%)	36	72
6	N	270/405 (67%)	258 (96%)	12 (4%)	0	100	100
6	P	319/405 (79%)	308 (97%)	11 (3%)	0	100	100
6	Q	335/405 (83%)	322 (96%)	13 (4%)	0	100	100
7	O	177/186 (95%)	169 (96%)	8 (4%)	0	100	100
7	R	168/186 (90%)	158 (94%)	10 (6%)	0	100	100
8	U	165/190 (87%)	146 (88%)	19 (12%)	0	100	100
9	V	177/182 (97%)	153 (86%)	23 (13%)	1 (1%)	21	59
10	W	144/1281 (11%)	135 (94%)	8 (6%)	1 (1%)	18	56
10	Z	190/1281 (15%)	179 (94%)	11 (6%)	0	100	100
11	Y	404/467 (86%)	358 (89%)	44 (11%)	2 (0%)	24	63
12	a	205/577 (36%)	203 (99%)	2 (1%)	0	100	100
12	b	205/577 (36%)	198 (97%)	6 (3%)	1 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	c	238/577 (41%)	234 (98%)	4 (2%)	0	100	100
12	d	267/577 (46%)	256 (96%)	11 (4%)	0	100	100
13	e	792/4646 (17%)	748 (94%)	44 (6%)	0	100	100
13	f	804/4646 (17%)	757 (94%)	45 (6%)	2 (0%)	43	78
13	m	786/4646 (17%)	751 (96%)	35 (4%)	0	100	100
13	n	747/4646 (16%)	714 (96%)	32 (4%)	1 (0%)	48	83
14	g	356/612 (58%)	348 (98%)	8 (2%)	0	100	100
14	h	356/612 (58%)	335 (94%)	21 (6%)	0	100	100
14	o	356/612 (58%)	333 (94%)	23 (6%)	0	100	100
14	p	356/612 (58%)	337 (95%)	19 (5%)	0	100	100
15	j	12/492 (2%)	12 (100%)	0	0	100	100
15	q	12/492 (2%)	12 (100%)	0	0	100	100
All	All	12408/34075 (36%)	11734 (95%)	665 (5%)	9 (0%)	49	83

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	M	217	PRO
10	W	1142	PRO
11	Y	175	PRO
11	Y	441	PRO
12	b	166	TRP

5.3.2 Protein sidechains

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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)

Of 13 ligands modelled in this entry, 3 are monoatomic - leaving 10 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
17	ATP	H	401	-	32,33,33	0.52	1 (3%)	48,52,52	0.35	0
16	ADP	C	800	-	28,29,29	1.37	5 (17%)	43,45,45	1.78	8 (18%)
16	ADP	I	800	-	28,29,29	1.39	4 (14%)	43,45,45	1.85	10 (23%)
16	ADP	E	800	-	28,29,29	1.40	5 (17%)	43,45,45	1.83	11 (25%)
16	ADP	J	800	-	28,29,29	1.42	6 (21%)	43,45,45	1.83	11 (25%)
16	ADP	G	800	-	28,29,29	1.38	4 (14%)	43,45,45	1.85	12 (27%)
16	ADP	B	800	-	28,29,29	1.38	4 (14%)	43,45,45	1.81	8 (18%)
16	ADP	A	800	-	28,29,29	1.39	4 (14%)	43,45,45	1.82	8 (18%)
16	ADP	F	800	-	28,29,29	1.39	4 (14%)	43,45,45	1.83	10 (23%)
16	ADP	D	800	-	28,29,29	1.39	4 (14%)	43,45,45	1.83	9 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
17	ATP	H	401	-	-	10/22/38/38	0/3/3/3
16	ADP	C	800	-	-	3/16/32/32	0/3/3/3
16	ADP	I	800	-	-	0/16/32/32	0/3/3/3
16	ADP	E	800	-	-	1/16/32/32	0/3/3/3
16	ADP	J	800	-	-	7/16/32/32	0/3/3/3
16	ADP	G	800	-	-	0/16/32/32	0/3/3/3
16	ADP	B	800	-	-	1/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
16	ADP	A	800	-	-	0/16/32/32	0/3/3/3
16	ADP	F	800	-	-	3/16/32/32	0/3/3/3
16	ADP	D	800	-	-	7/16/32/32	0/3/3/3

The worst 5 of 41 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	E	800	ADP	C5-C4	4.67	1.47	1.39
16	D	800	ADP	C5-C4	4.66	1.47	1.39
16	F	800	ADP	C5-C4	4.64	1.47	1.39
16	A	800	ADP	C5-C4	4.62	1.47	1.39
16	I	800	ADP	C5-C4	4.58	1.47	1.39

The worst 5 of 87 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
16	I	800	ADP	C5-C4-N3	-6.10	118.32	126.72
16	F	800	ADP	C5-C4-N3	-6.03	118.42	126.72
16	D	800	ADP	C5-C4-N3	-5.99	118.47	126.72
16	A	800	ADP	C5-C4-N3	-5.94	118.54	126.72
16	B	800	ADP	C5-C4-N3	-5.89	118.60	126.72

There are no chirality outliers.

5 of 32 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
16	B	800	ADP	C5'-O5'-PA-O3A
16	C	800	ADP	C5'-O5'-PA-O3A
16	D	800	ADP	PA-O3A-PB-O2B
16	D	800	ADP	PA-O3A-PB-O3B
16	D	800	ADP	C5'-O5'-PA-O2A

There are no ring outliers.

10 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	H	401	ATP	3	0
16	C	800	ADP	2	0
16	I	800	ADP	1	0
16	E	800	ADP	2	0

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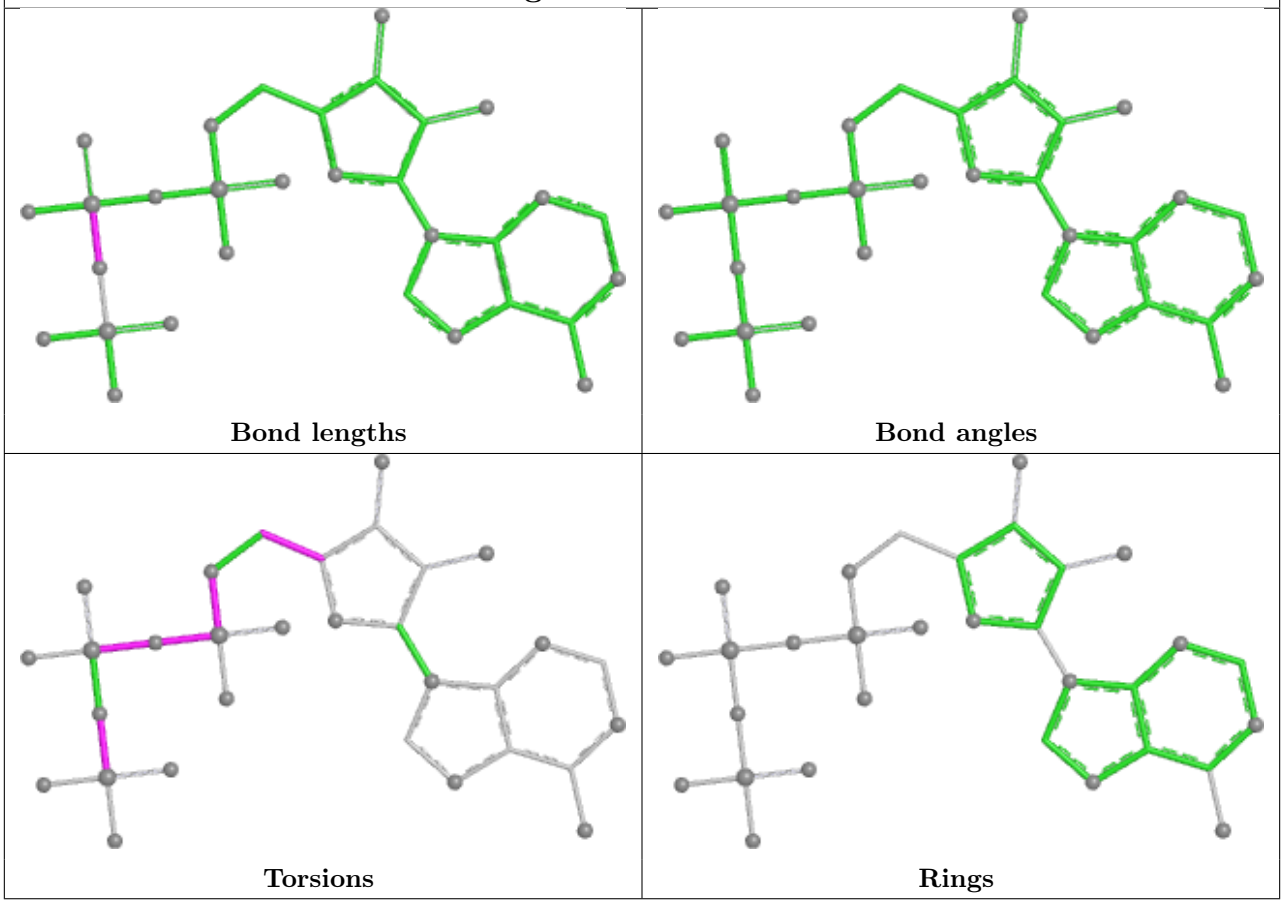
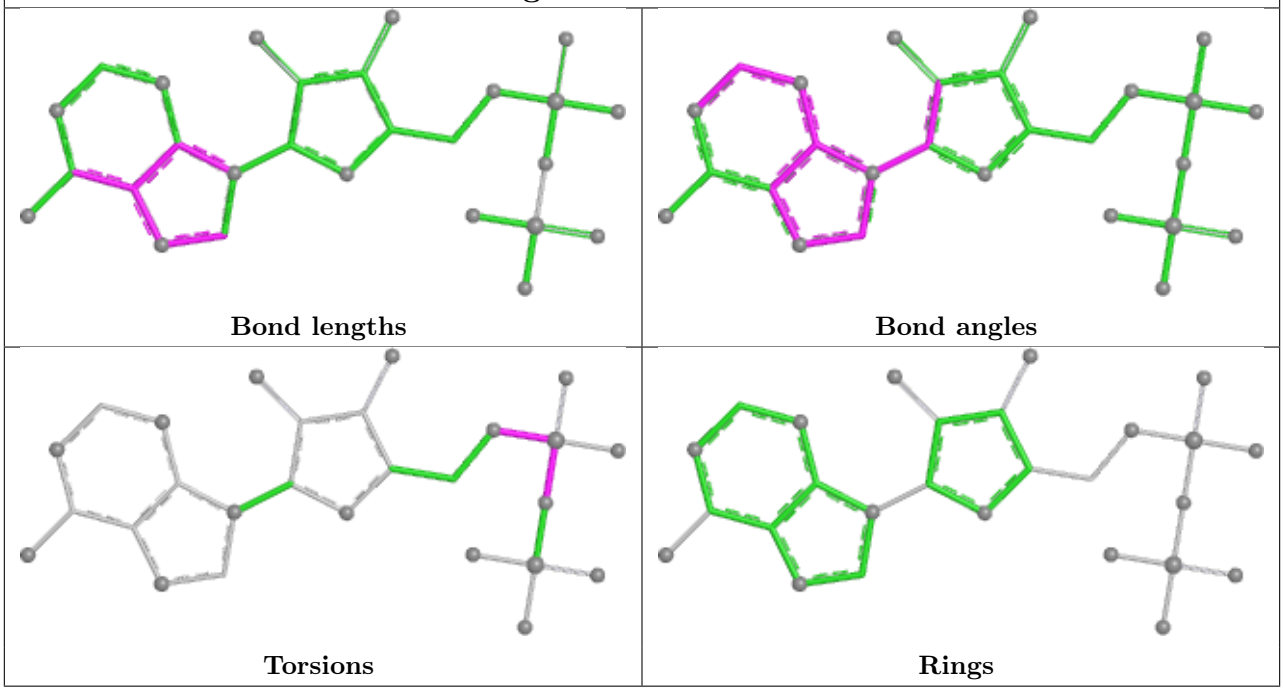
Mol	Chain	Res	Type	Clashes	Symm-Clashes
16	J	800	ADP	5	0
16	G	800	ADP	2	0
16	B	800	ADP	3	0
16	A	800	ADP	1	0
16	F	800	ADP	5	0
16	D	800	ADP	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

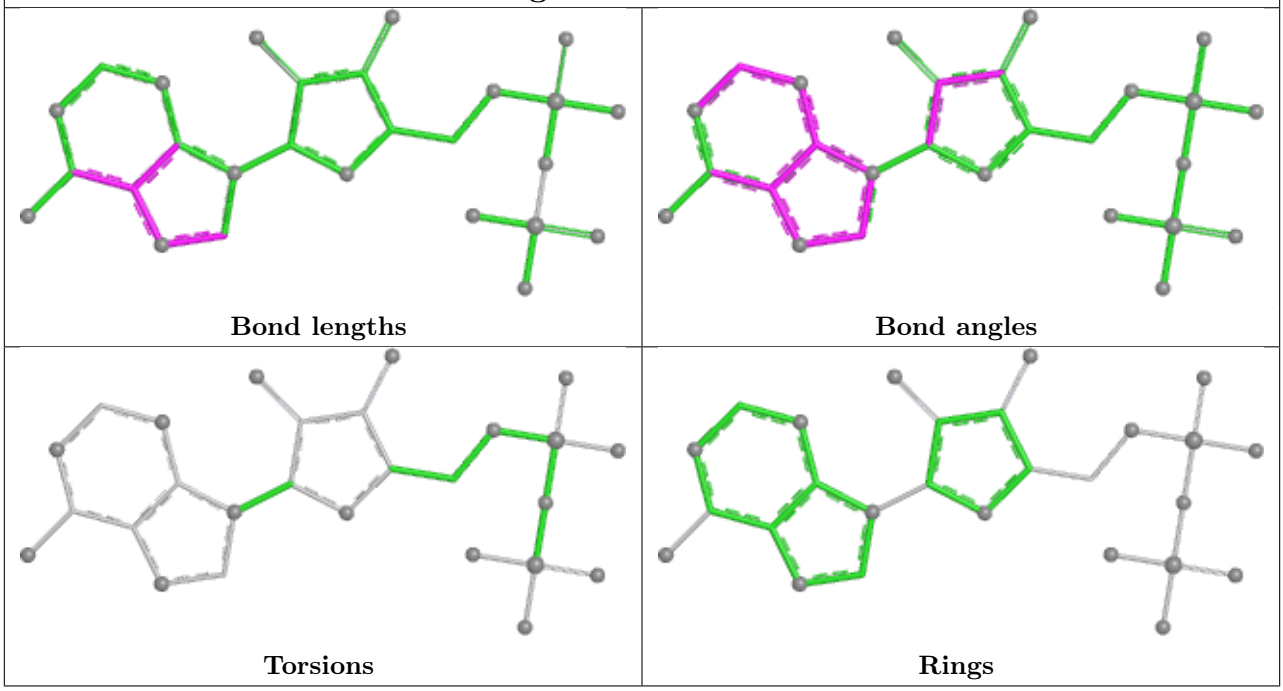
Ligand ATP H 401



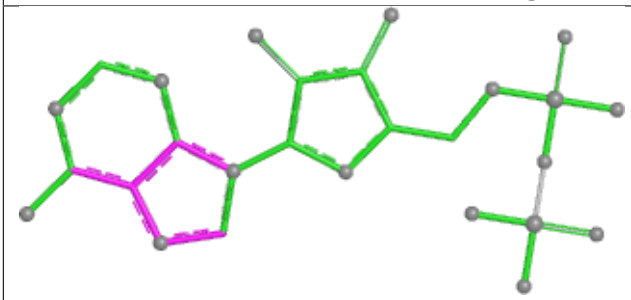
Ligand ADP C 800



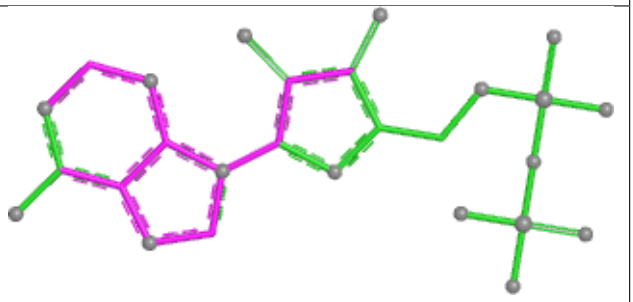
Ligand ADP I 800



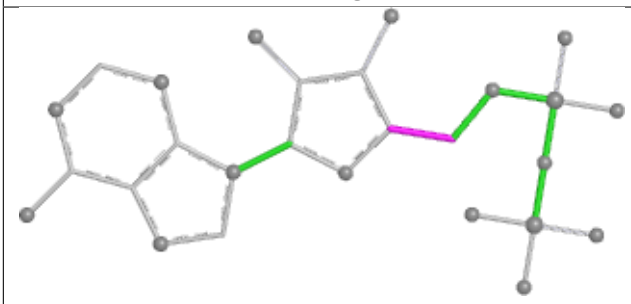
Ligand ADP E 800



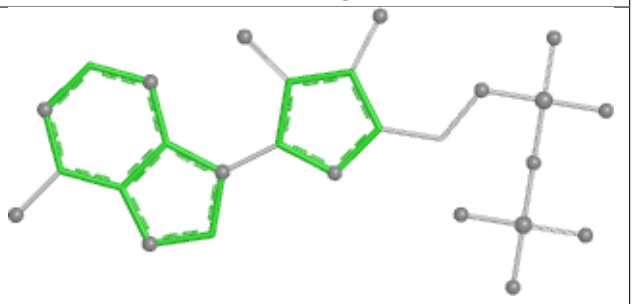
Bond lengths



Bond angles

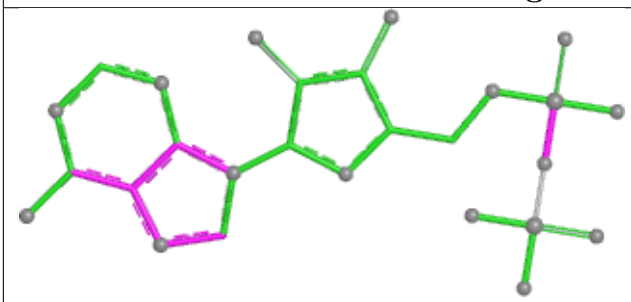


Torsions

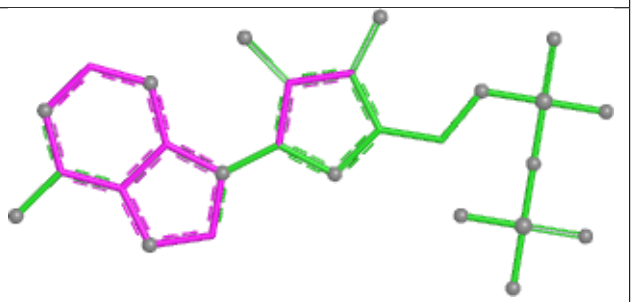


Rings

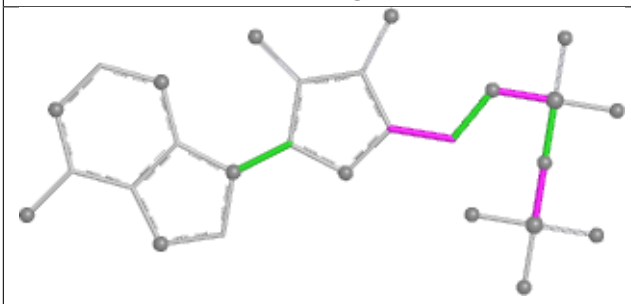
Ligand ADP J 800



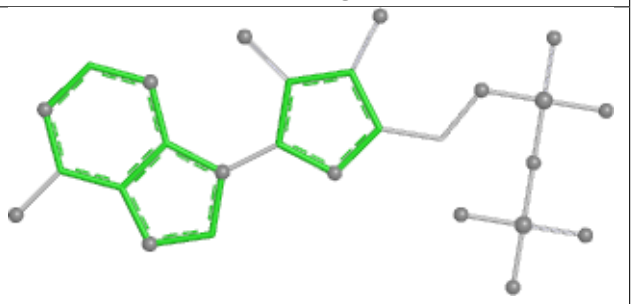
Bond lengths



Bond angles

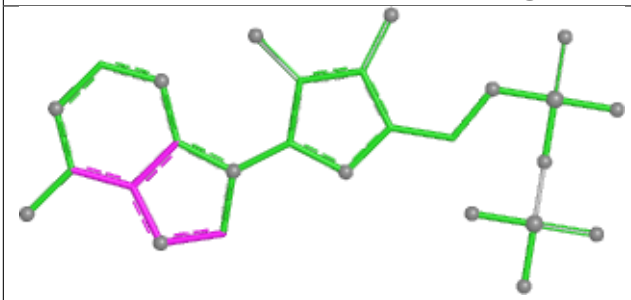


Torsions

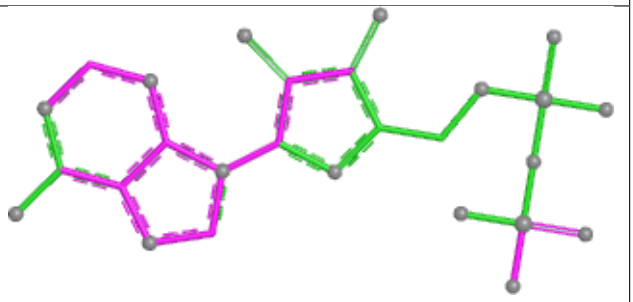


Rings

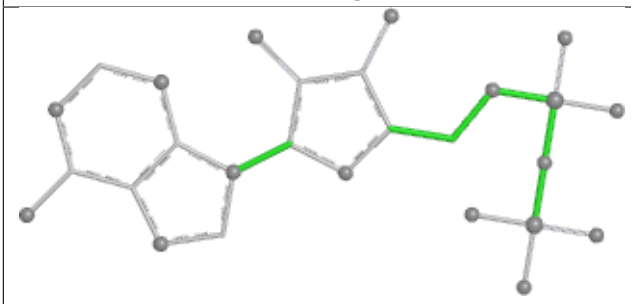
Ligand ADP G 800



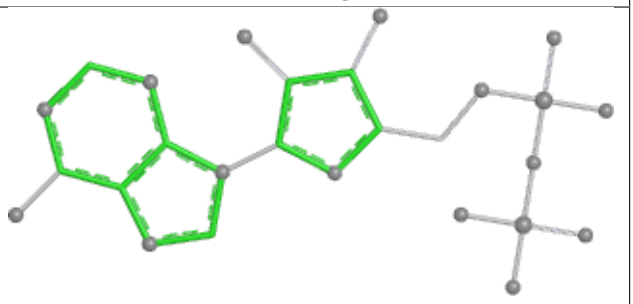
Bond lengths



Bond angles

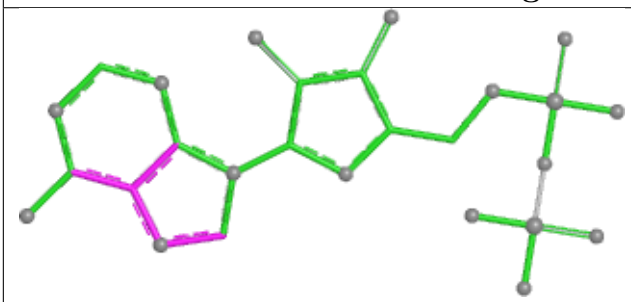


Torsions

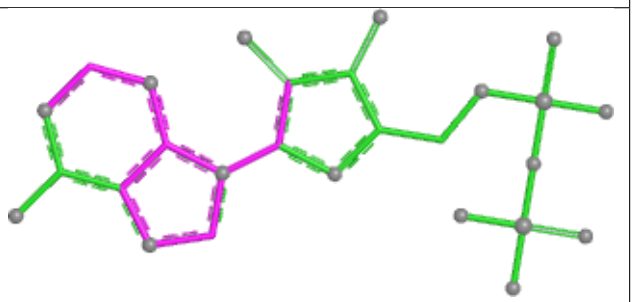


Rings

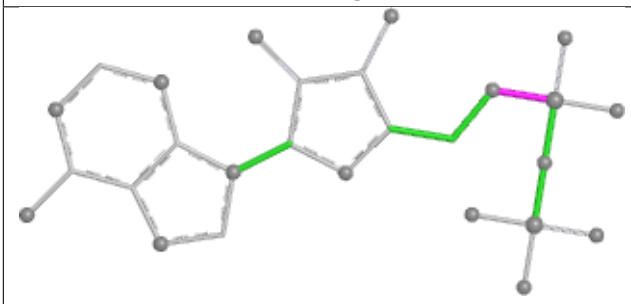
Ligand ADP B 800



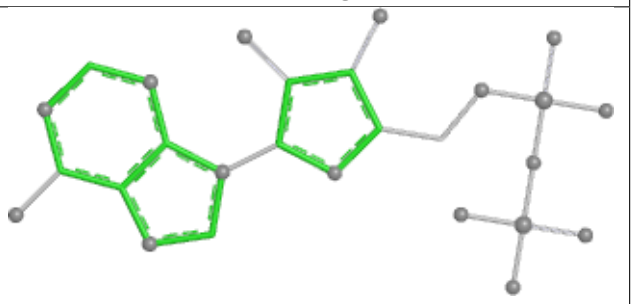
Bond lengths



Bond angles

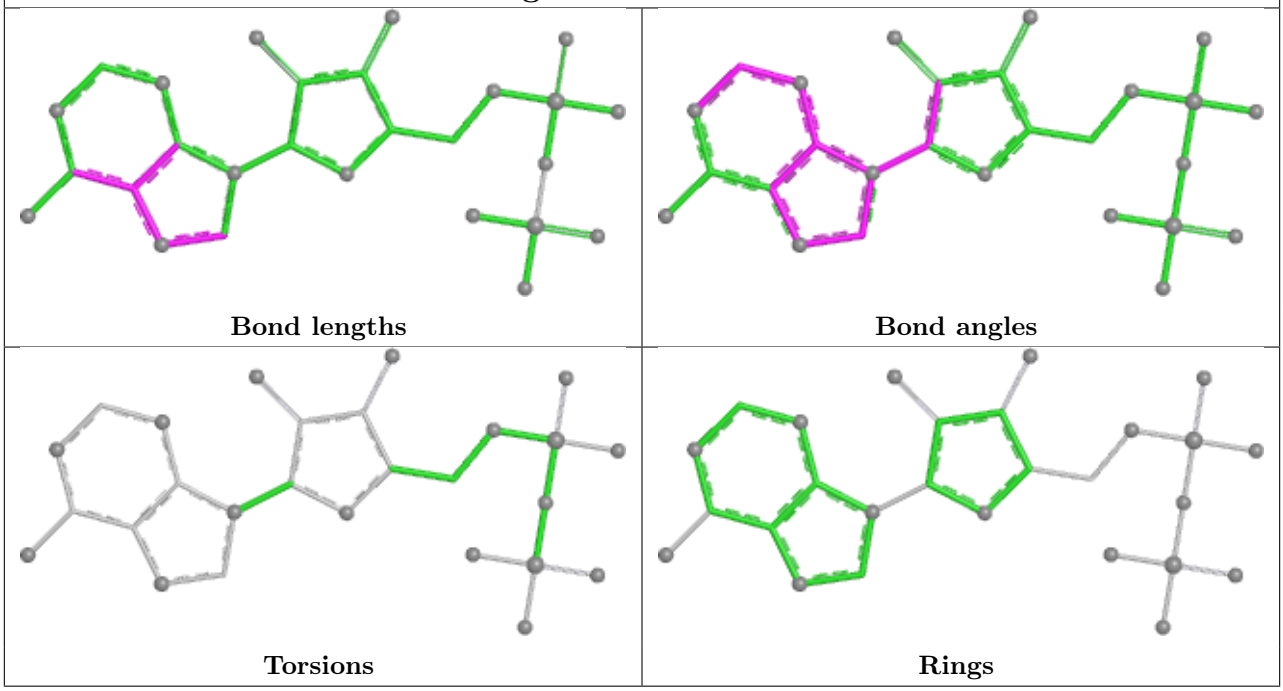


Torsions

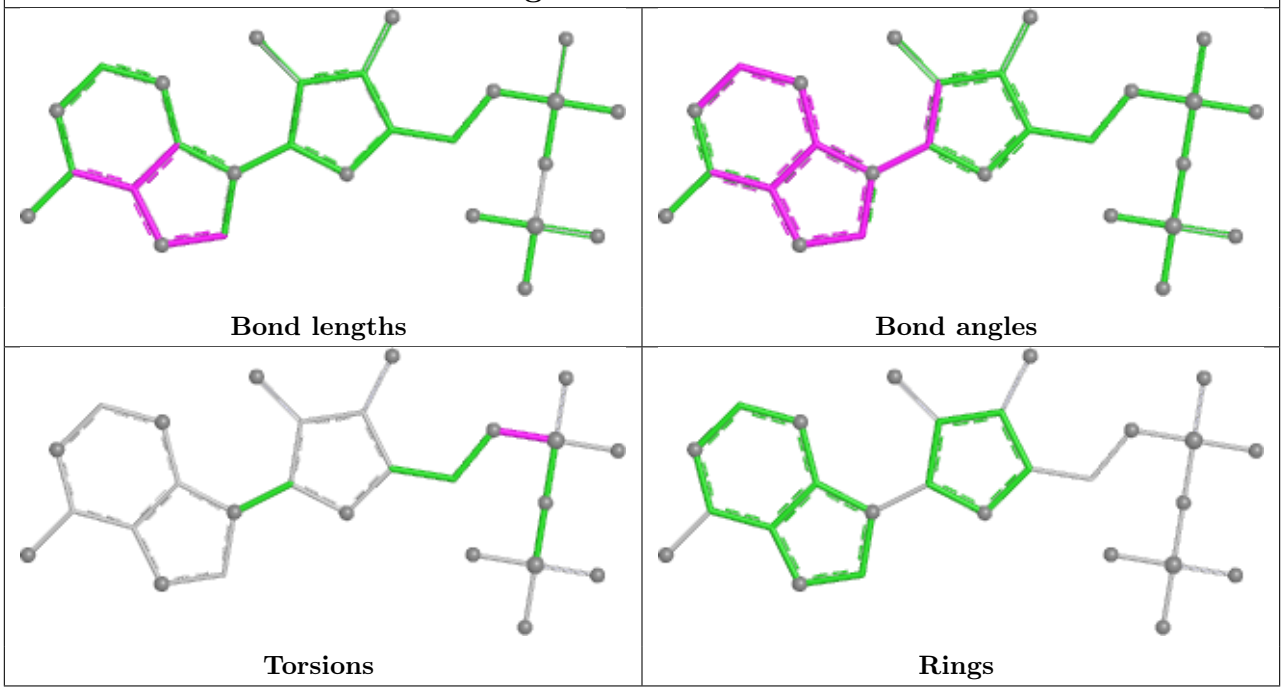


Rings

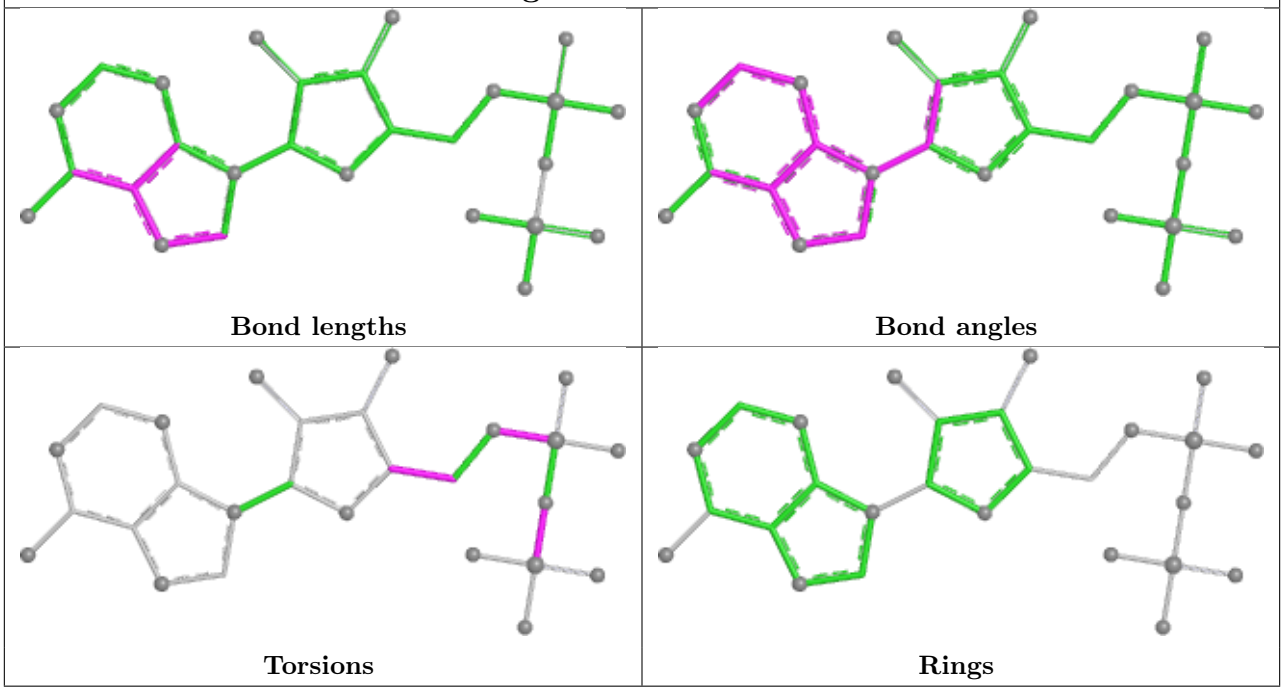
Ligand ADP A 800



Ligand ADP F 800



Ligand ADP D 800



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
12	b	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	b	282:LEU	C	283:GLN	N	1.72

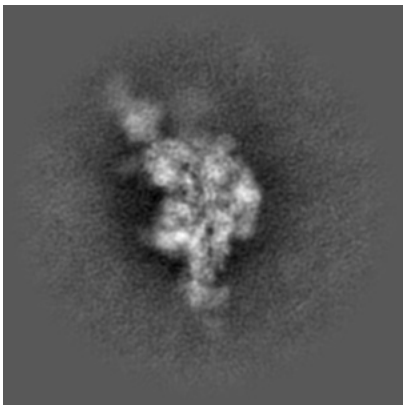
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-46848. These allow visual inspection of the internal detail of the map and identification of artifacts.

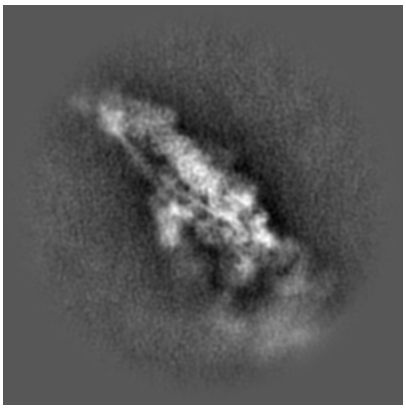
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

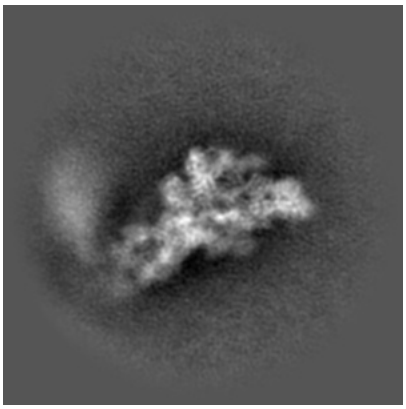
6.1.1 Primary map



X

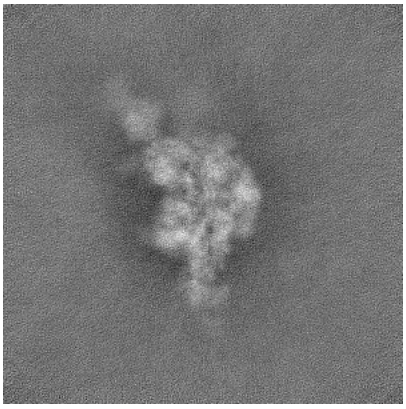


Y

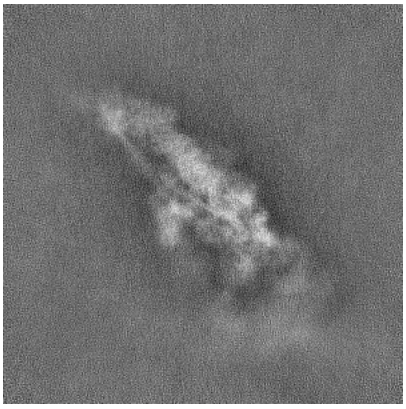


Z

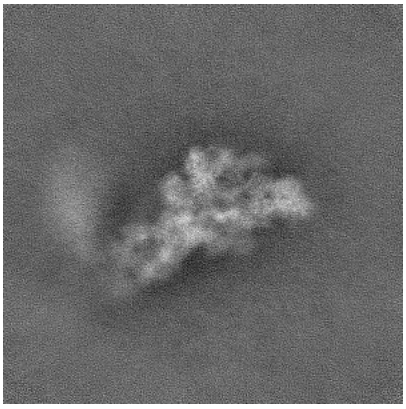
6.1.2 Raw map



X



Y

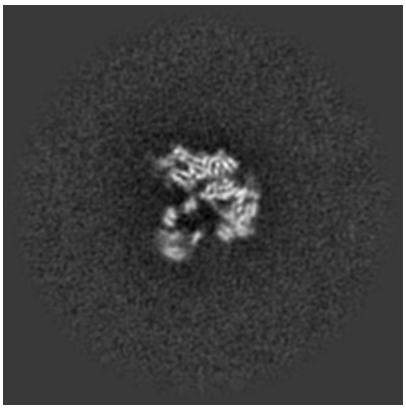


Z

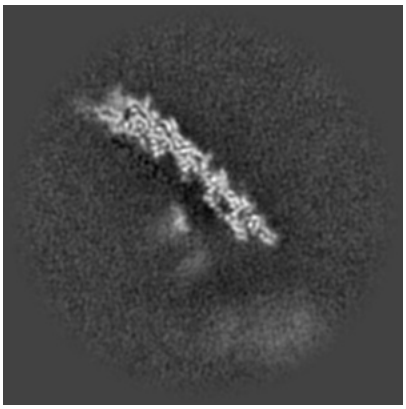
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

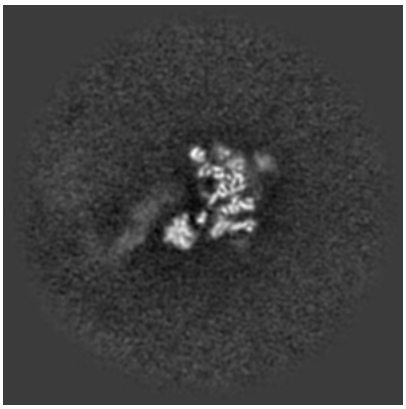
6.2.1 Primary map



X Index: 192

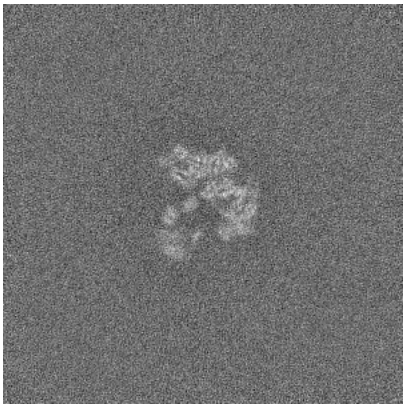


Y Index: 192

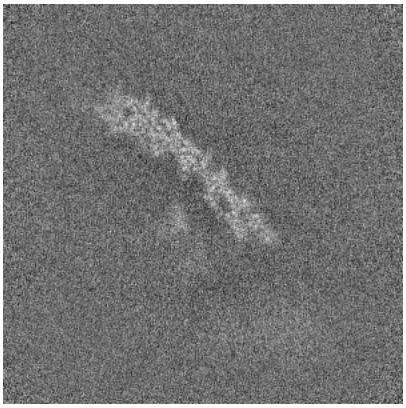


Z Index: 192

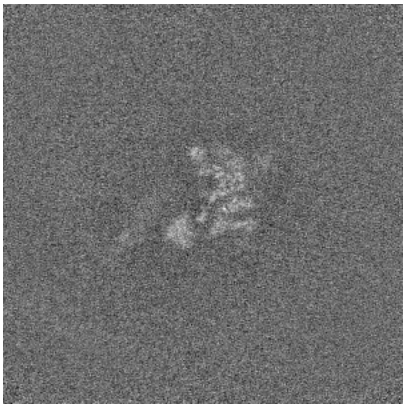
6.2.2 Raw map



X Index: 192



Y Index: 192

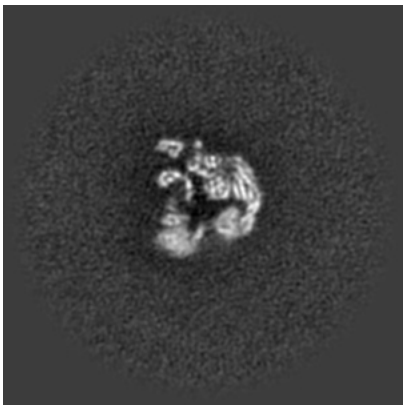


Z Index: 192

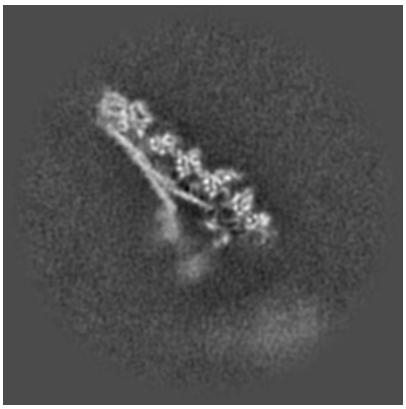
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

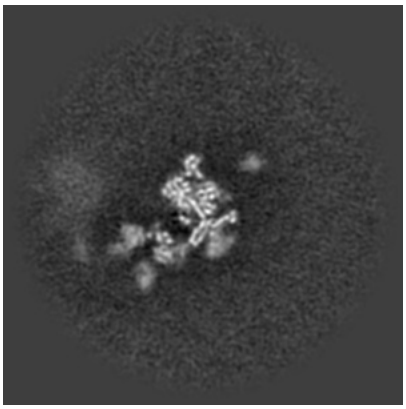
6.3.1 Primary map



X Index: 184

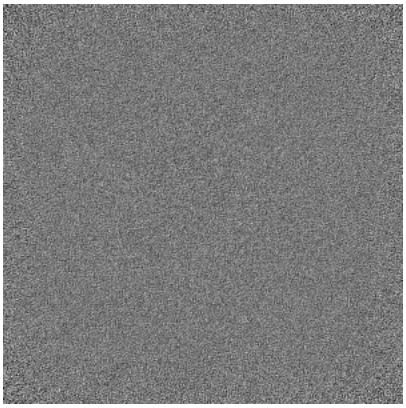


Y Index: 184

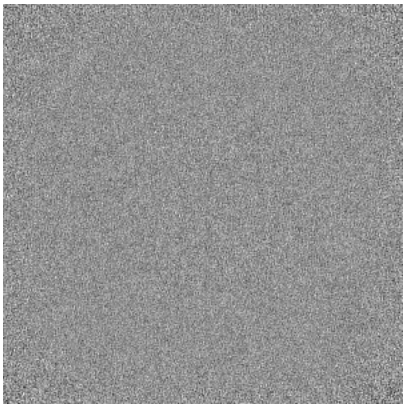


Z Index: 222

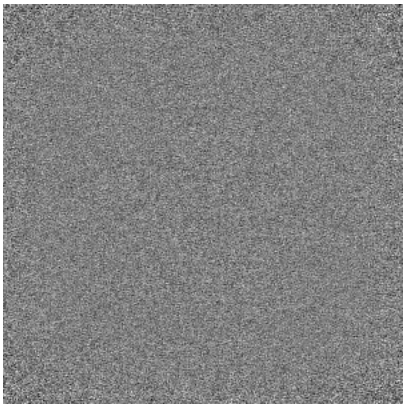
6.3.2 Raw map



X Index: 0



Y Index: 0

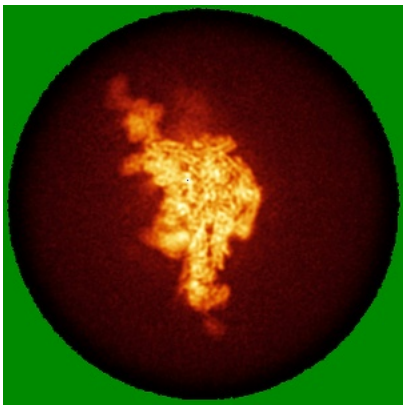


Z Index: 0

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



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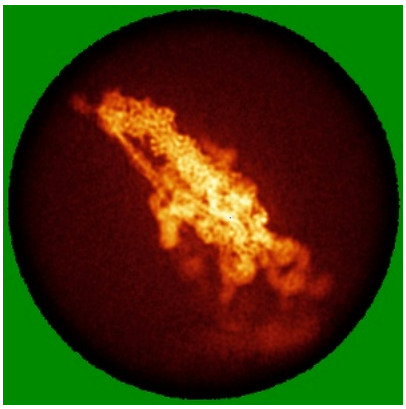
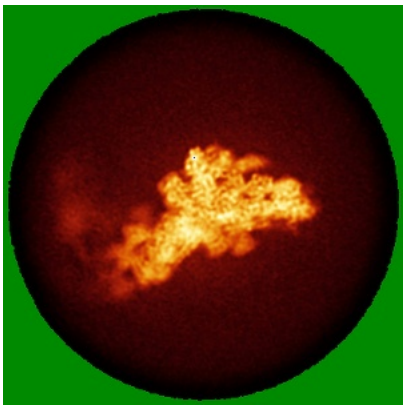
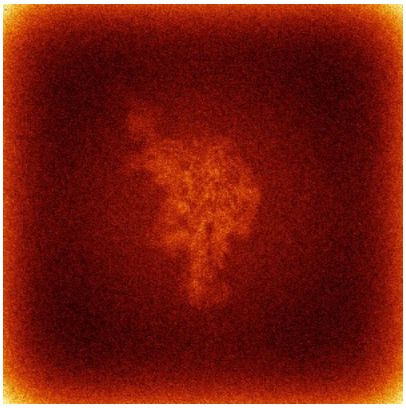


Y

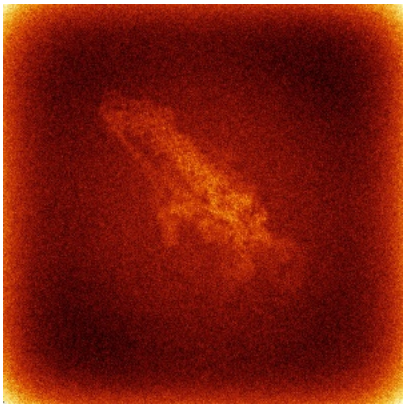


Z

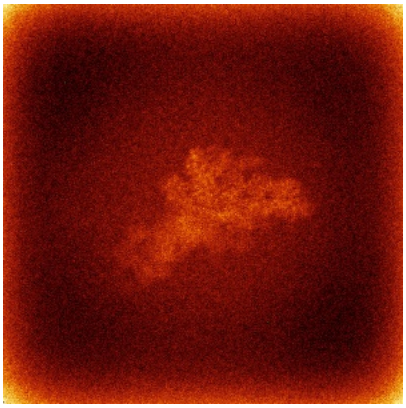
6.4.2 Raw map



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.

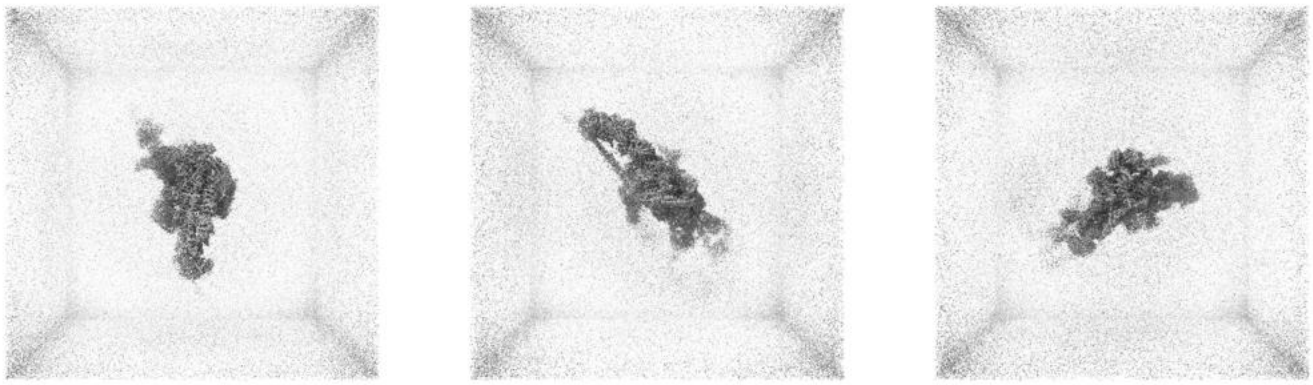
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

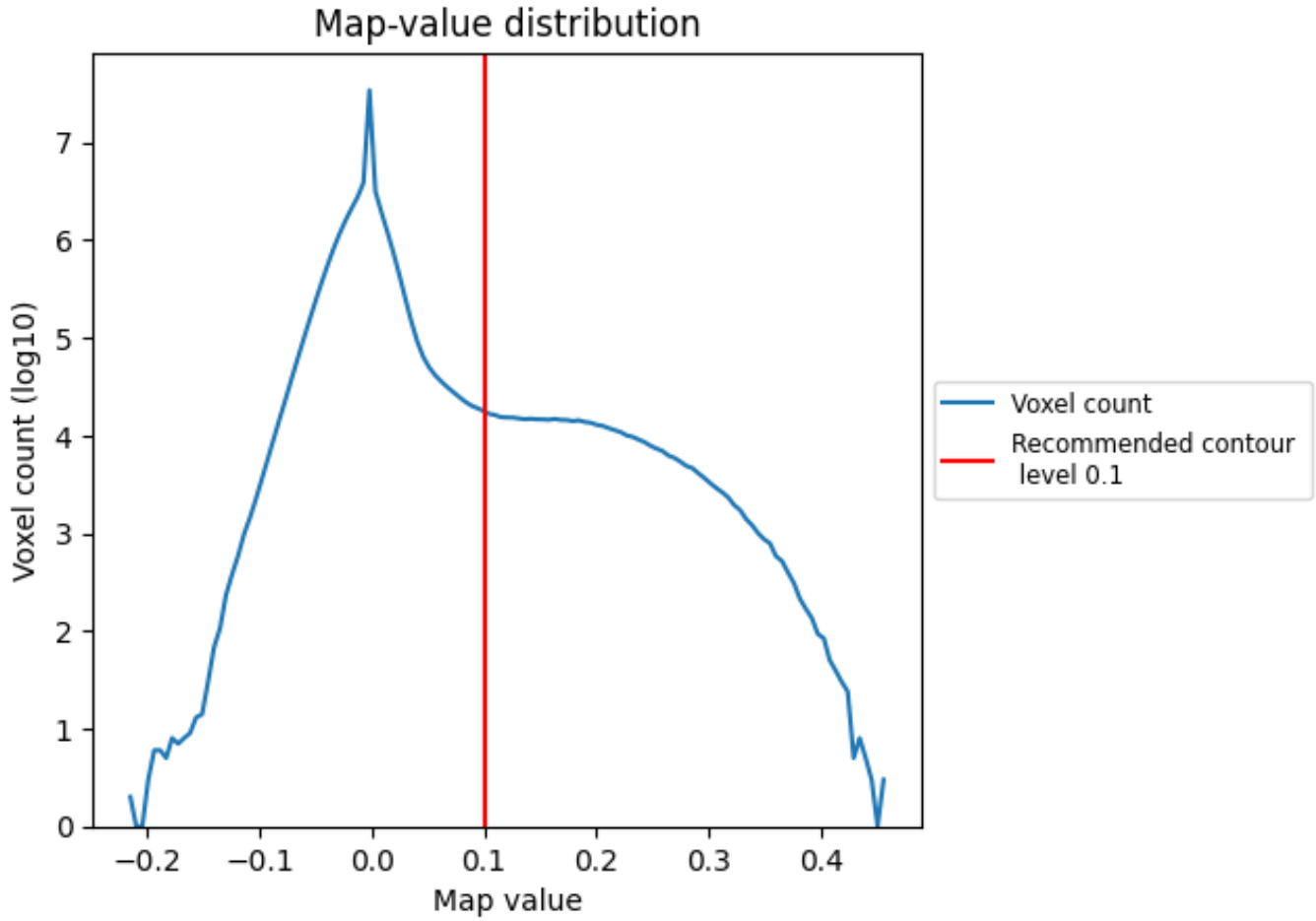
6.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

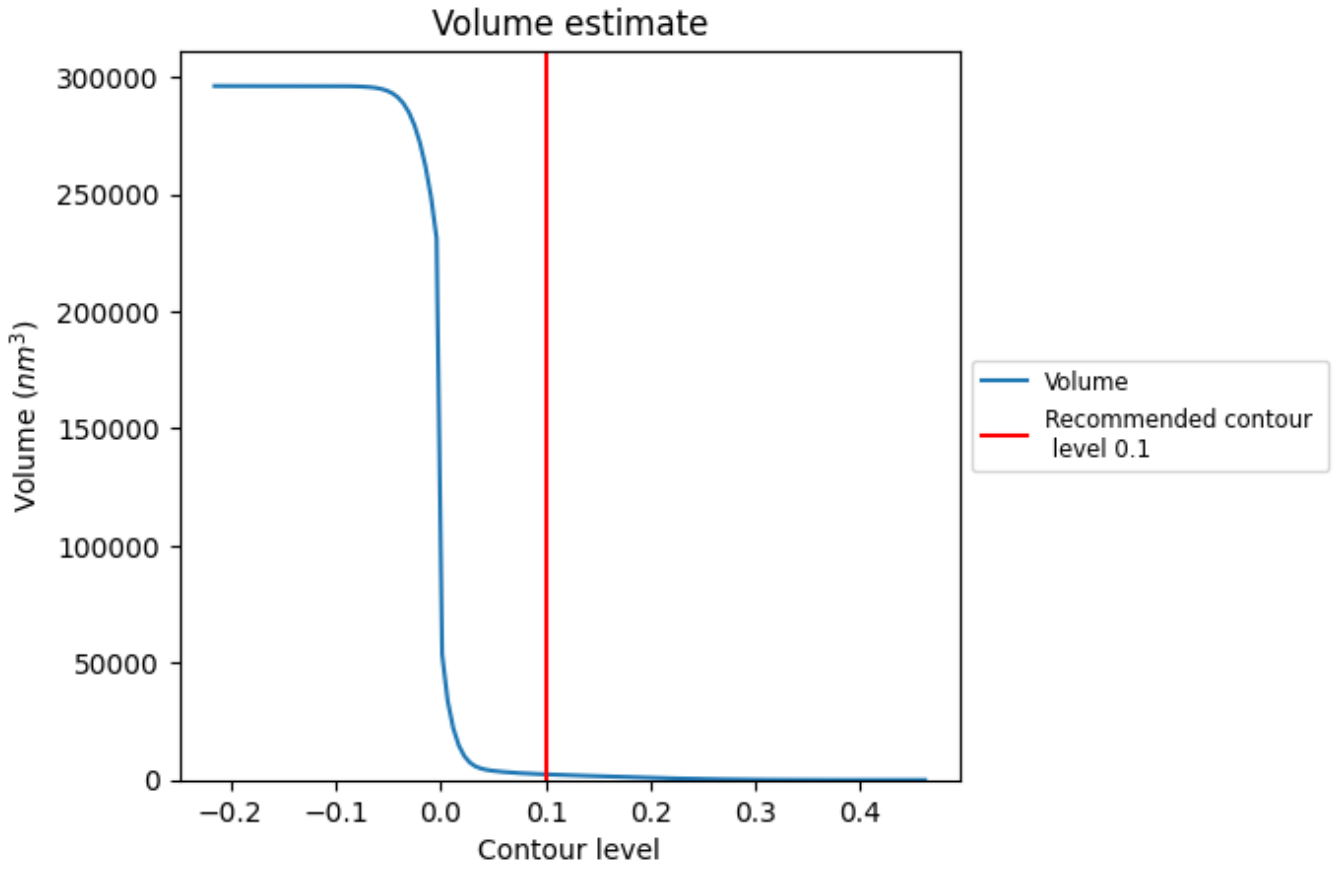
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

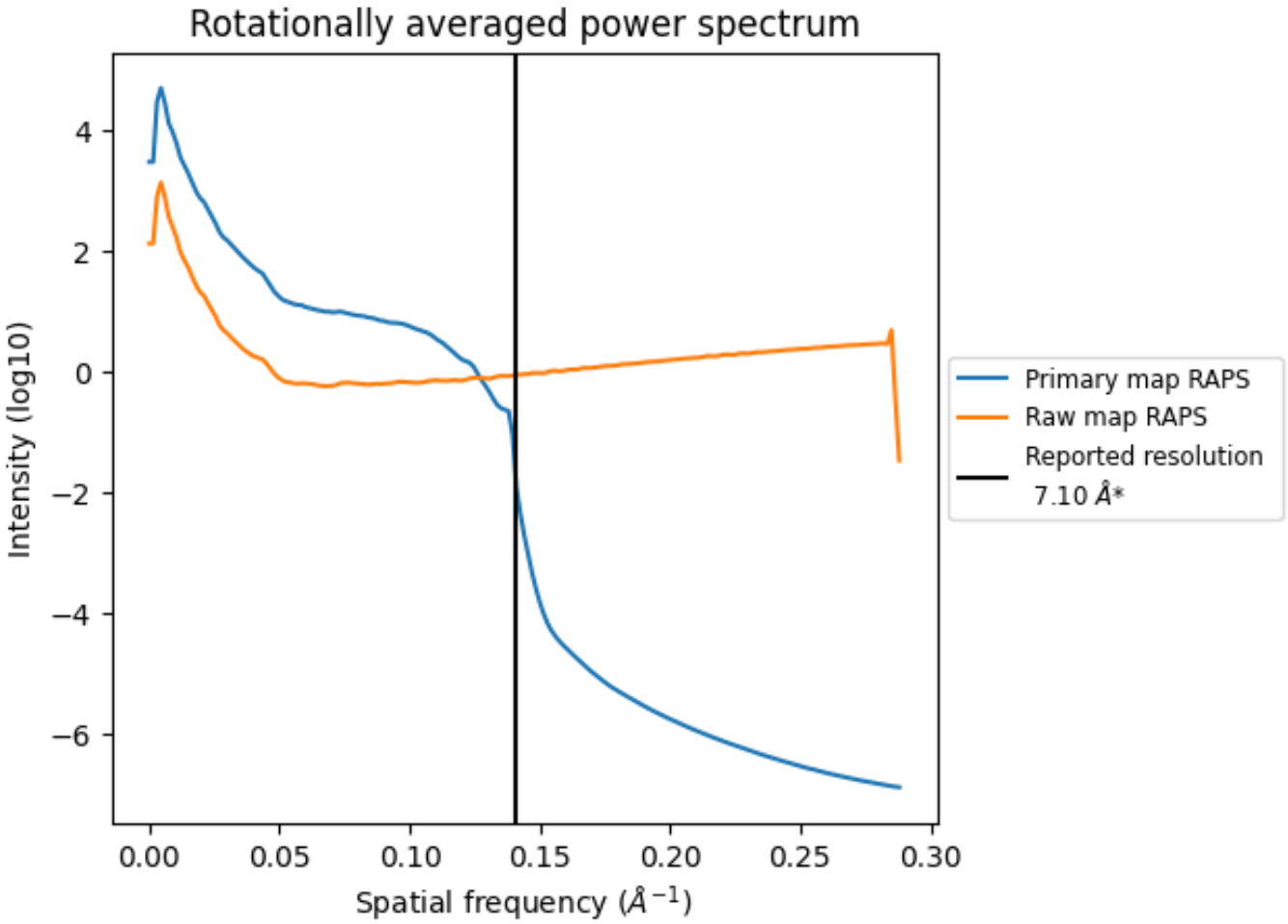
7.2 Volume estimate (i)



The volume at the recommended contour level is 2389 nm^3; this corresponds to an approximate mass of 2158 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)

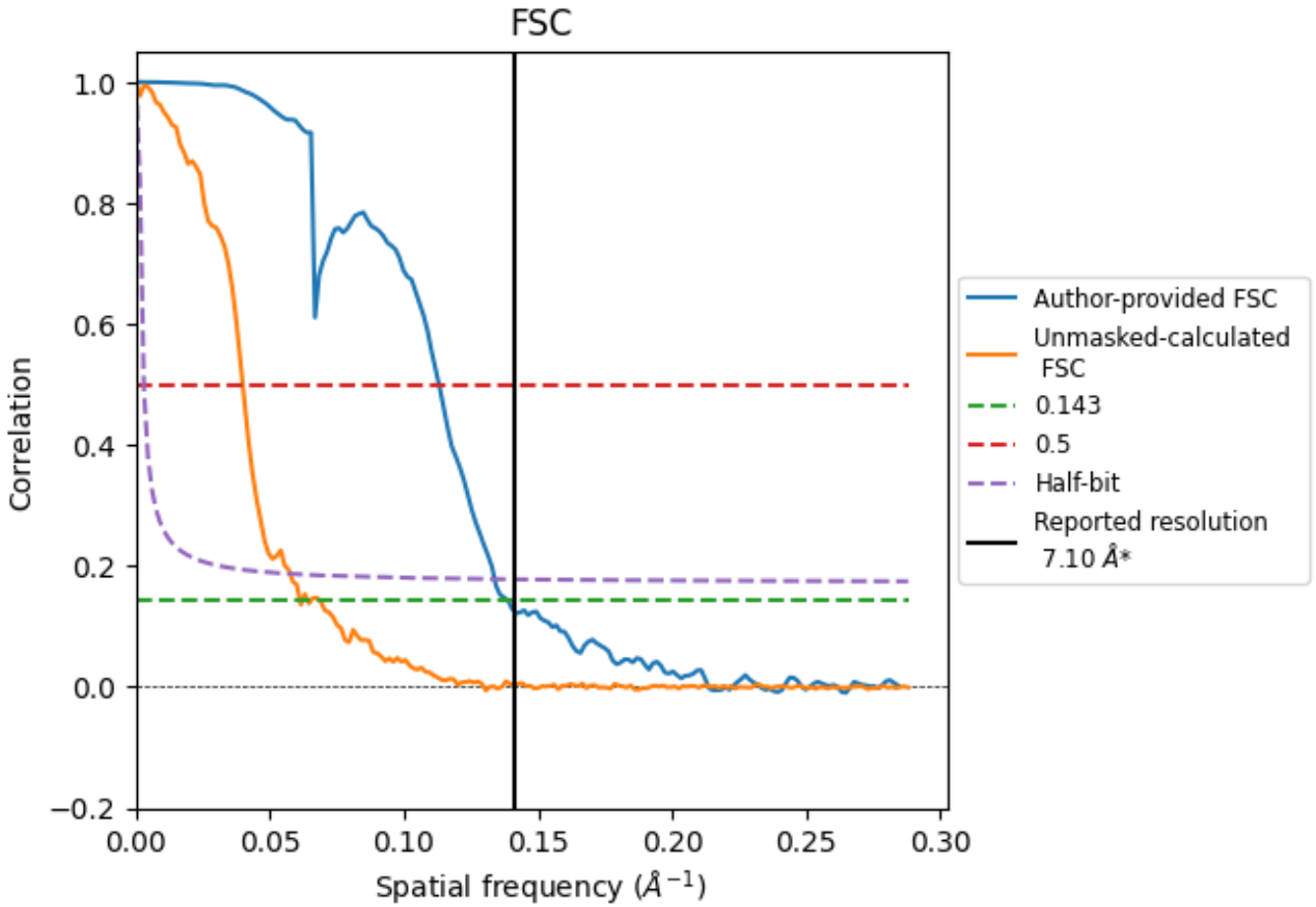


*Reported resolution corresponds to spatial frequency of 0.141 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.141 Å^{-1}

8.2 Resolution estimates (i)

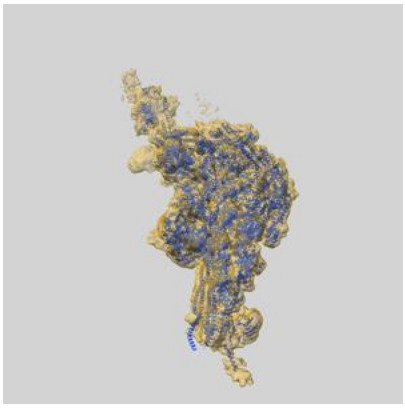
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.10	-	-
Author-provided FSC curve	7.21	8.85	7.48
Unmasked-calculated*	16.34	25.13	17.39

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 16.34 differs from the reported value 7.1 by more than 10 %

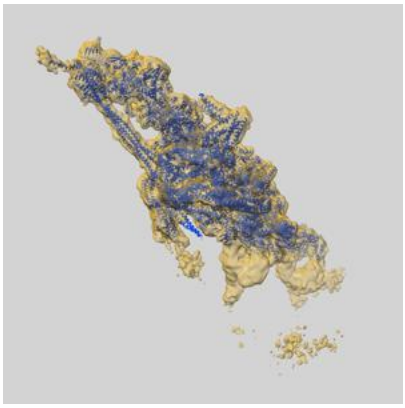
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-46848 and PDB model 9DGU. Per-residue inclusion information can be found in section 3 on page 10.

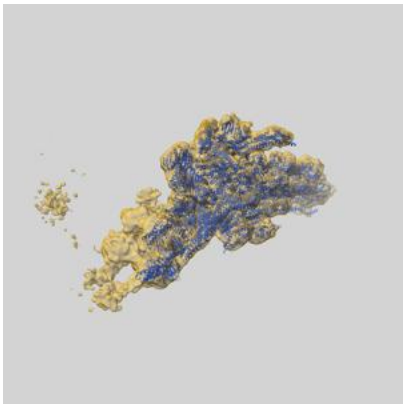
9.1 Map-model overlay



X



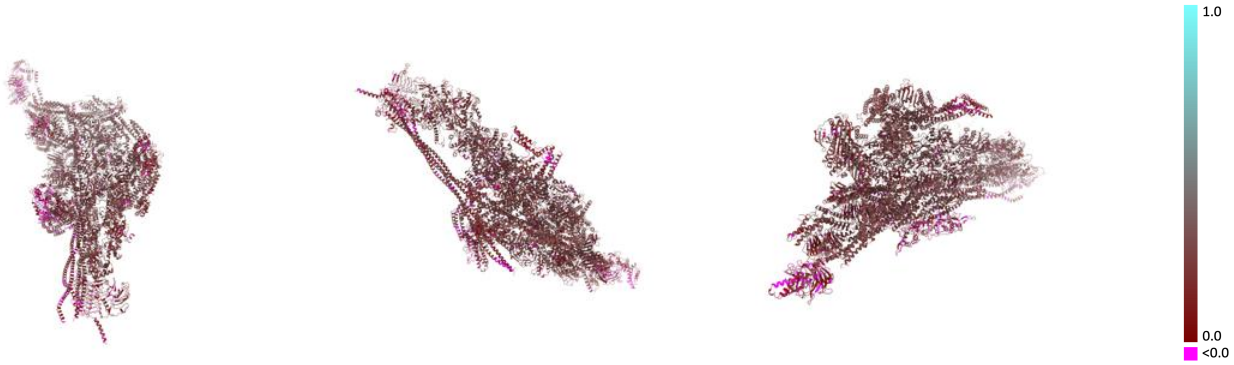
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.1 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.

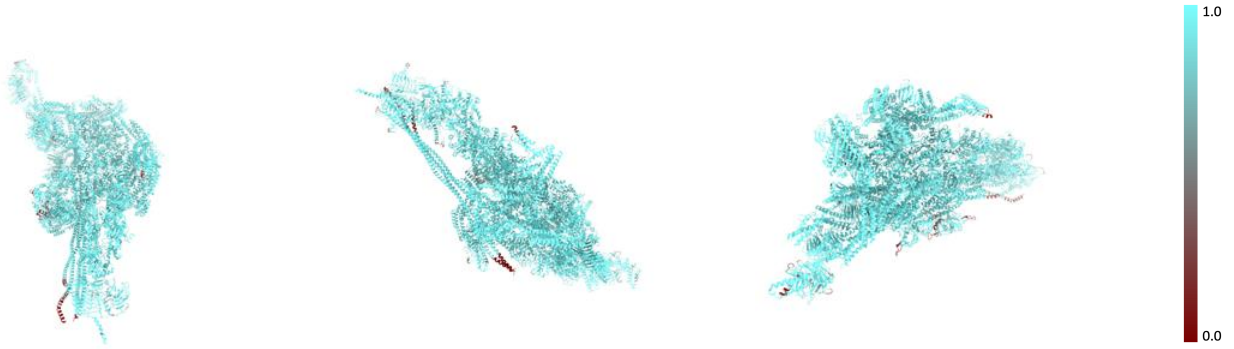
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

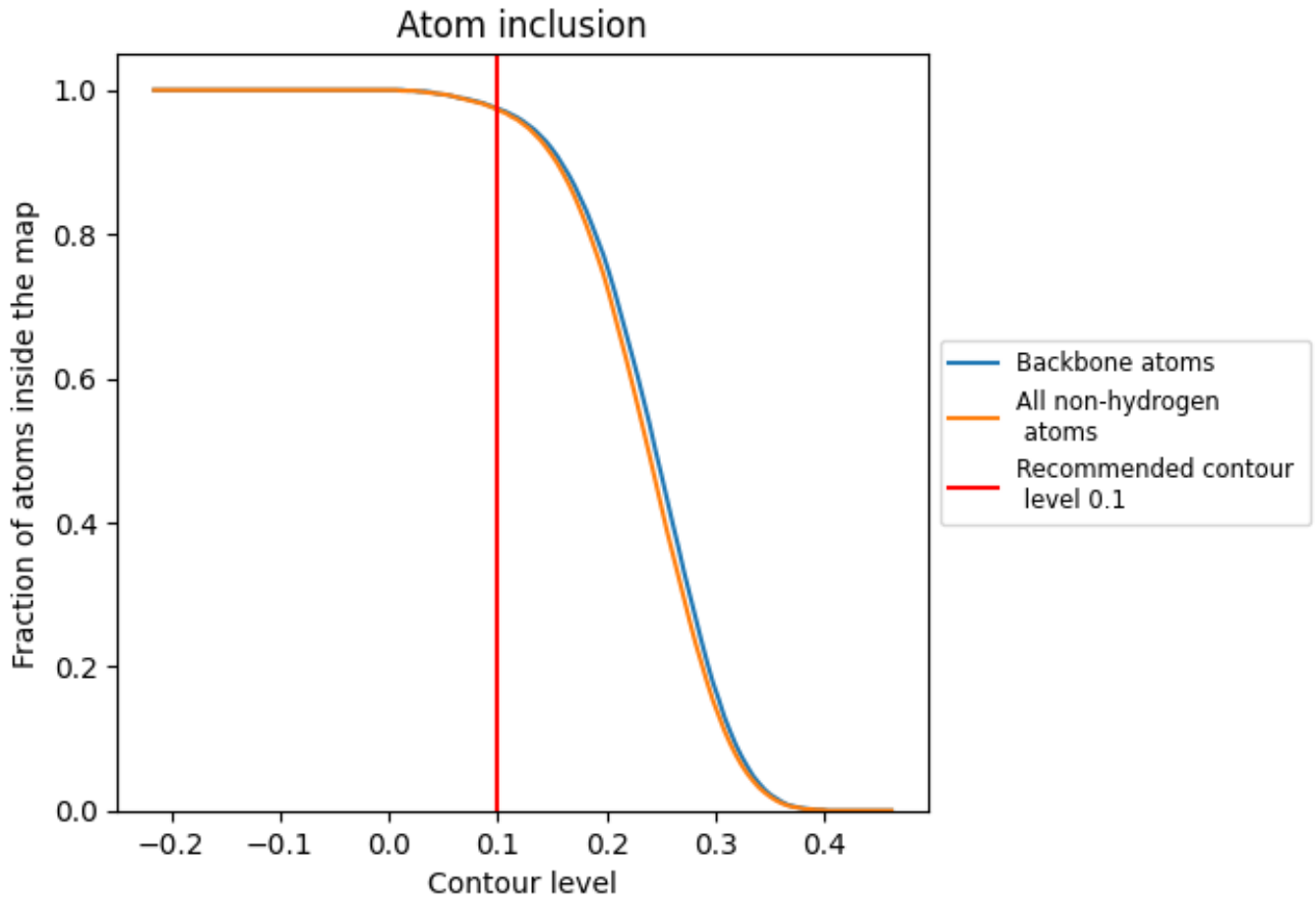
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.1).

9.4 Atom inclusion (i)



At the recommended contour level, 97% of all backbone atoms, 97% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9730	0.2140
A	0.9980	0.2410
B	1.0000	0.2500
C	0.9990	0.2550
D	1.0000	0.2490
E	0.9990	0.2580
F	0.9950	0.2520
G	1.0000	0.2590
H	1.0000	0.2560
I	0.9910	0.2330
J	0.9930	0.2400
K	1.0000	0.2440
L	0.9960	0.2480
M	0.9940	0.2260
N	0.9560	0.2210
O	0.9990	0.2380
P	0.9940	0.2510
Q	0.9590	0.2480
R	0.9990	0.2160
U	0.9680	0.1570
V	0.9900	0.1490
W	0.9630	0.2170
Y	0.9340	0.1750
Z	0.9960	0.2480
a	0.7410	0.1150
b	0.8060	0.1640
c	0.9950	0.2470
d	0.9930	0.2340
e	0.9530	0.1520
f	0.9320	0.2020
g	0.9610	0.1180
h	0.9960	0.1870
j	1.0000	0.2460
m	0.9830	0.2450
n	0.9730	0.2170

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Chain	Atom inclusion	Q-score
o	0.9970	0.1990
p	0.9490	0.0810
q	0.9460	0.2230