wwPDB EM Validation Summary Report (i)

Mar 8, 2026 – 09:22 AM UTC

PDB ID	:	7Z8J / pdb_00007z8j
EMDB ID	:	EMD-14553
Title	:	Cytoplasmic dynein (A2) bound to BICDR1
Authors	:	Chaaban, S.; Carter, A.P.
Deposited on	:	2022-03-17
Resolution	:	3.93 Å(reported)

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

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

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

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

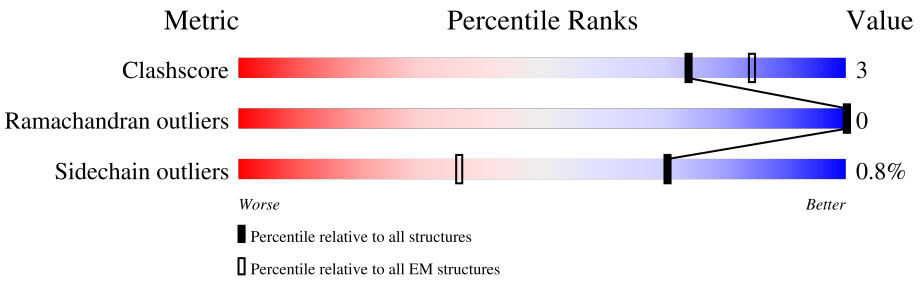
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

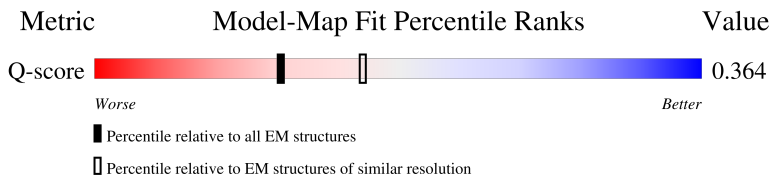
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.93 Å.

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





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	7811 (3.43 - 4.43)

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	X	577	11% 14% • 84%
1	x	577	14% 15% • 84%
2	f	4646	6% 13% • 85%
2	m	4646	• 10% • 89%

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Mol	Chain	Length	Quality of chain
2	n	4646	97%
3	h	638	5%, 50%, 6%, 44%
3	o	638	50%, 6%, 44%
4	j	492	40%, 47%, 50%
4	r	492	97%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 20189 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 BICD family-like cargo adapter 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	X	93	797	488	153	154	2	0	0
1	x	93	797	488	153	154	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	f	674	5545	3521	994	1009	21	0	0
2	m	524	4333	2751	789	780	13	0	0
2	n	126	1068	667	211	186	4	0	0

- Molecule 3 is a protein called Cytoplasmic dynein 1 intermediate chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	h	358	2804	1769	490	530	15	0	0
3	o	358	2808	1771	490	532	15	0	0

- Molecule 4 is a protein called Cytoplasmic dynein 1 light intermediate chain 2.

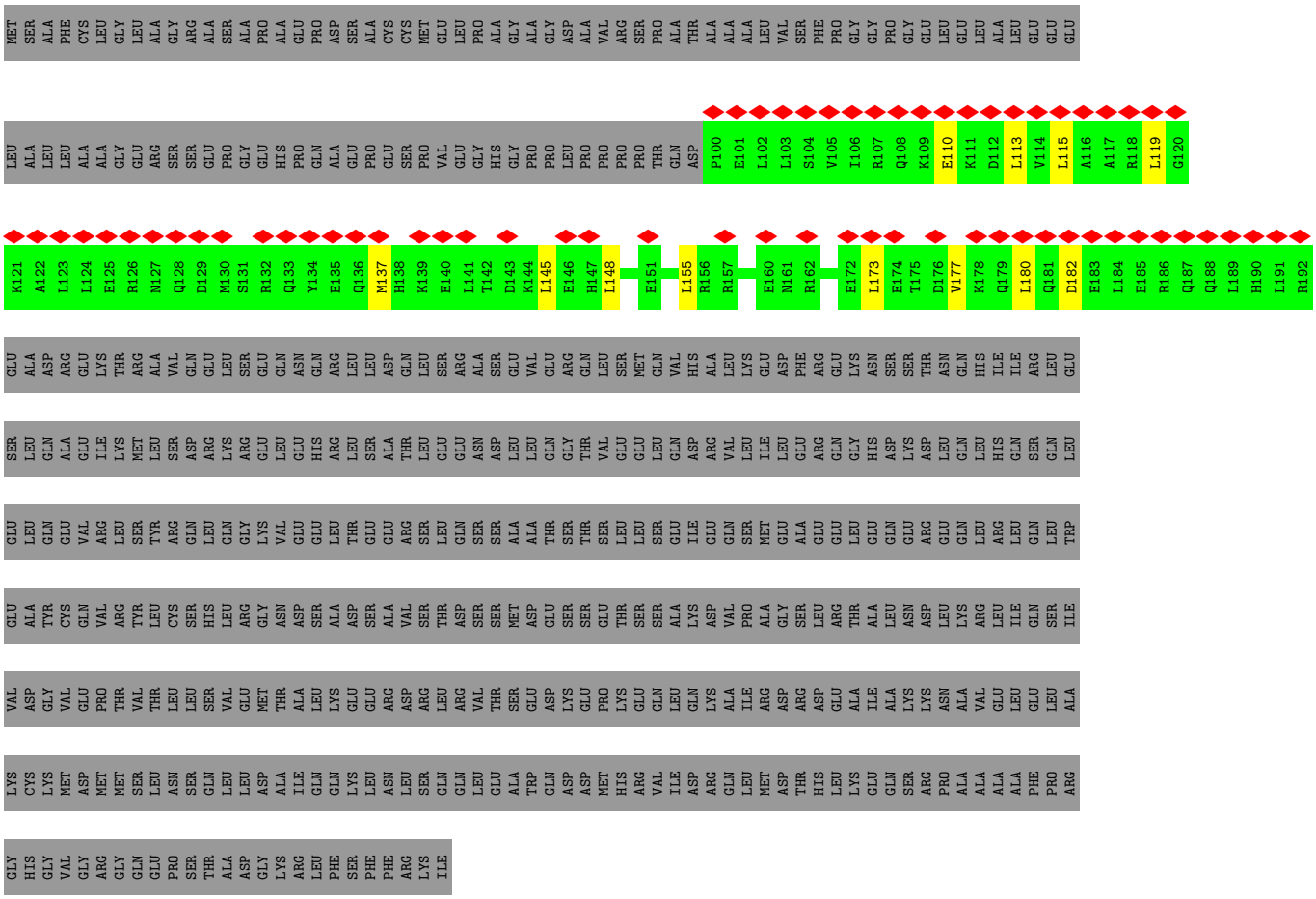
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	j	247	1981	1278	331	362	10	0	0
4	r	14	Total	C	N	O		0	0
			56	28	14	14			

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.

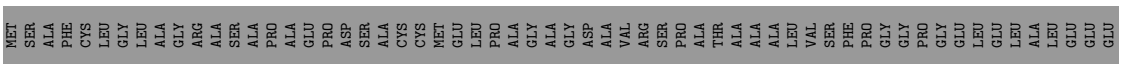
- Molecule 1: BICD family-like cargo adapter 1

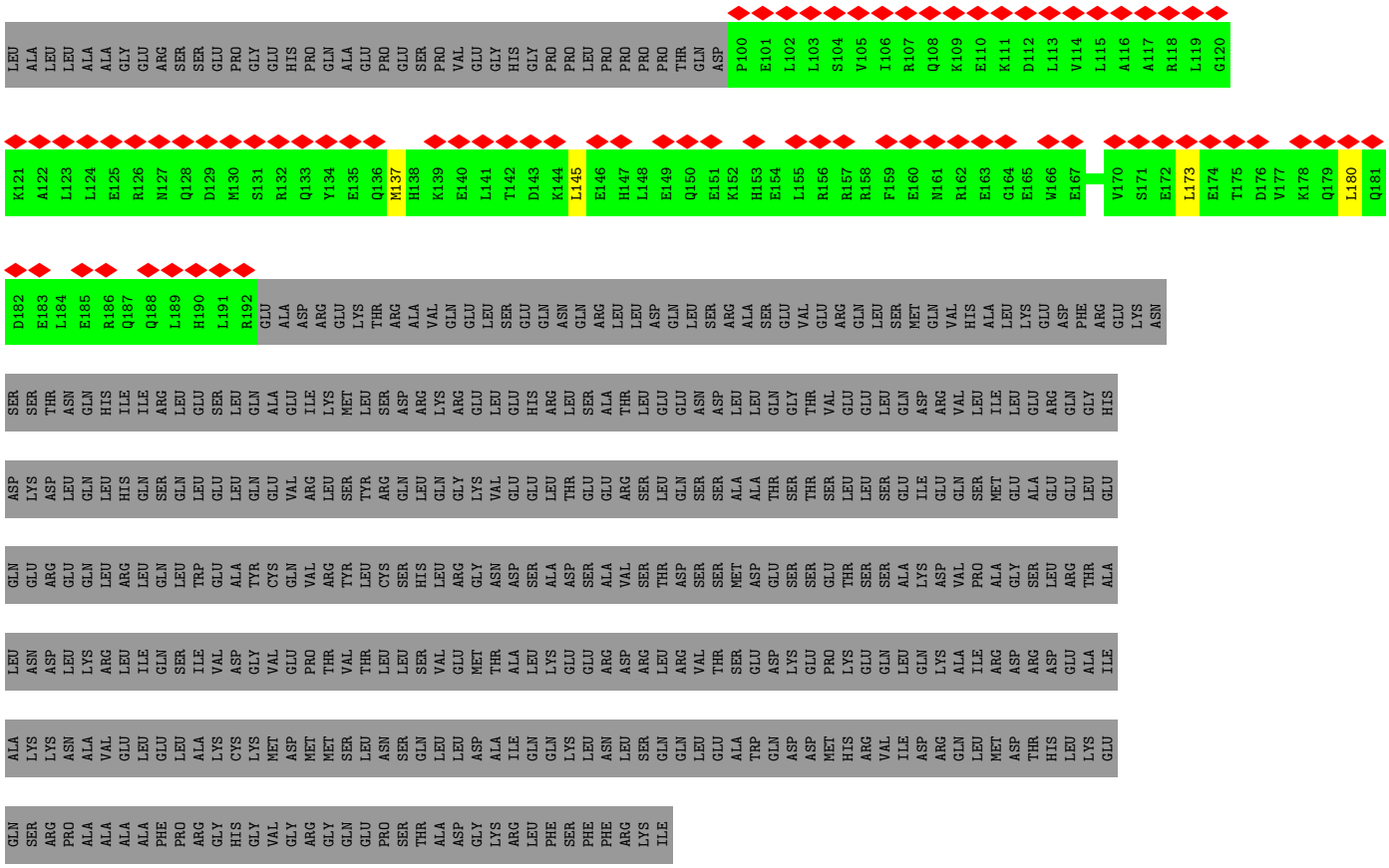
Chain X:



- Molecule 1: BICD family-like cargo adapter 1

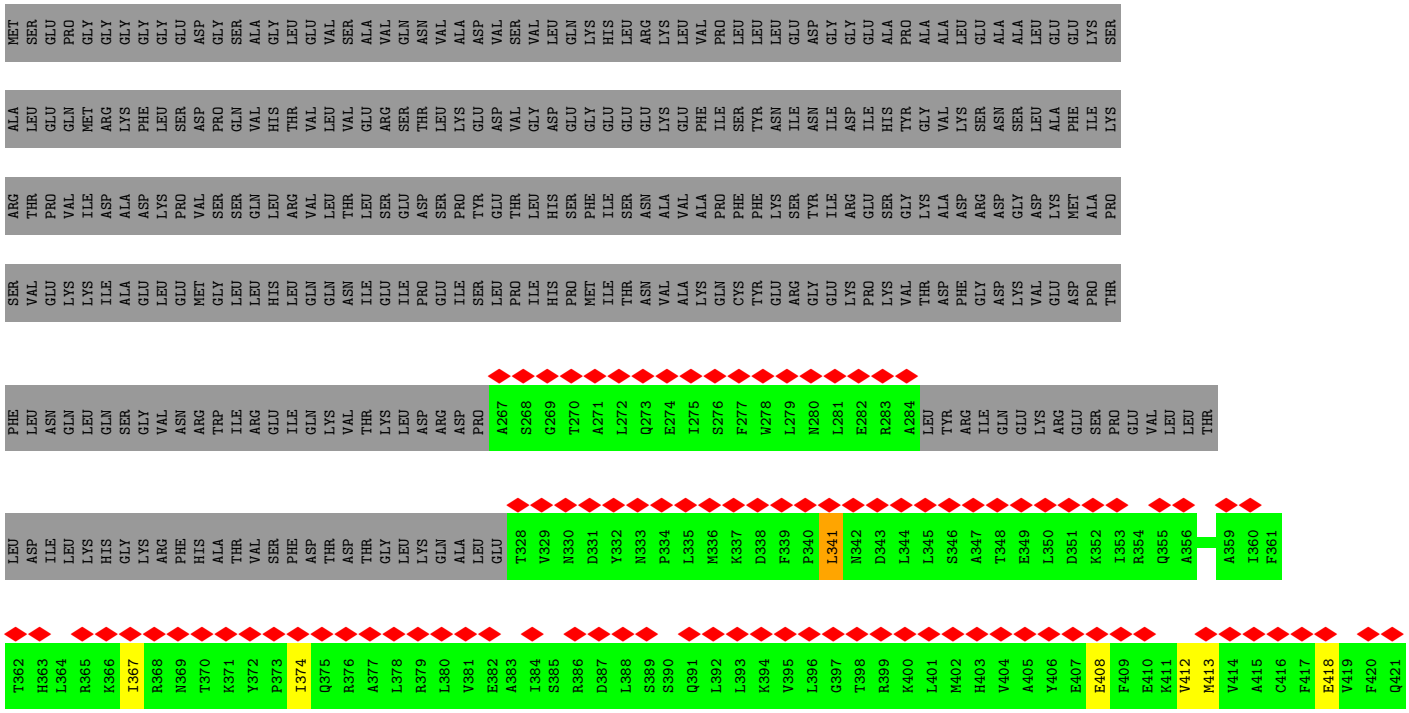
Chain x:

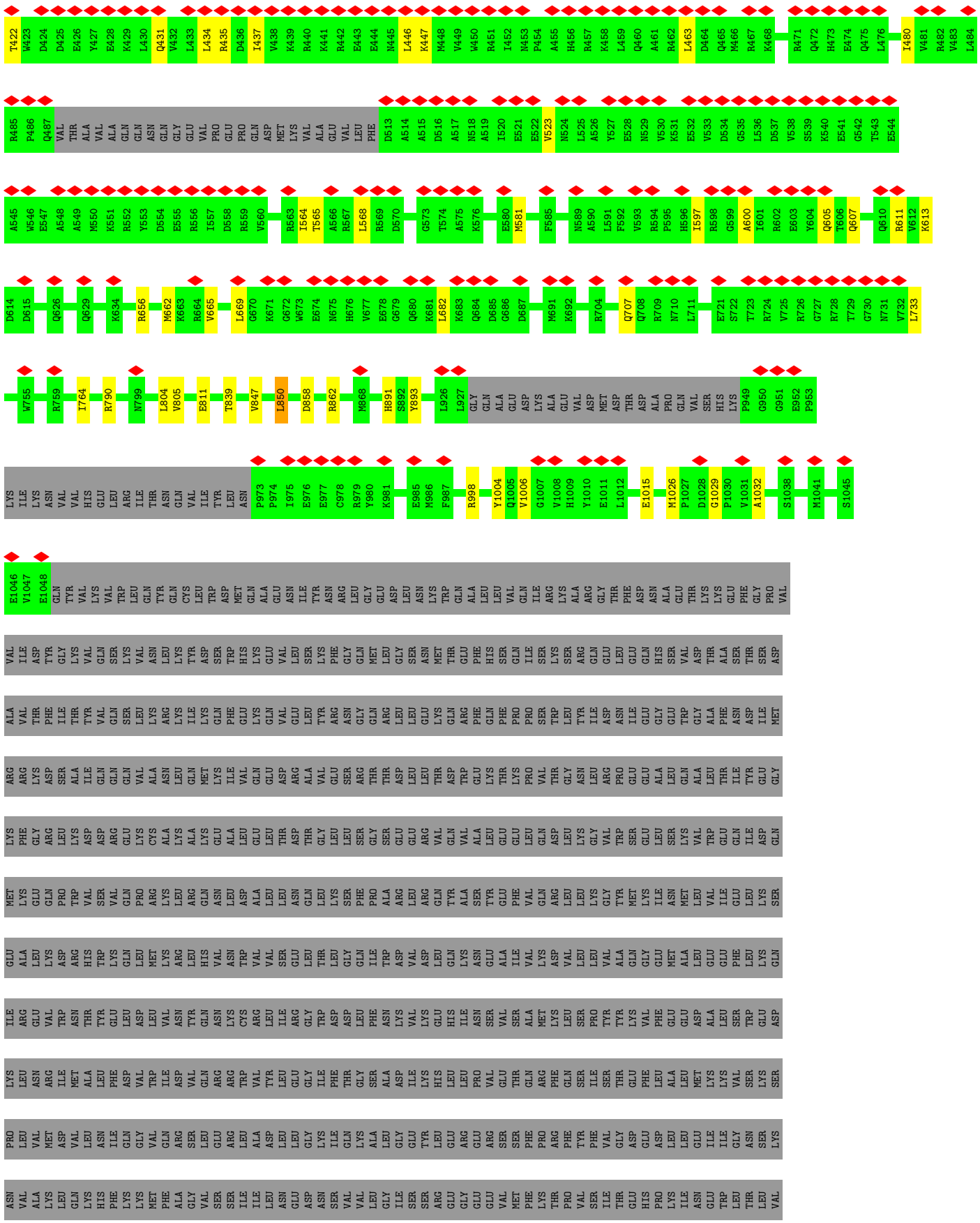




- Molecule 2: Cytoplasmic dynein 1 heavy chain 1

Chain f: 6% 13% • 85%




T422 W423 D424 D425 E426 Y427 E428 K429 L430 Q431 V432 L433 L434 R435 D436 I437 V438 K439 R440 K441 R442 E443 E444 N445 L446 K447 M448 V449 W450 R451 I452 N453 P454 A455 H456 R457 K458 L459 Q460 A461 R462 L463 D464 Q465 M466 R467 K468 R471 Q472 H473 E474 Q475 L476 I480 V481 R482 V483 L484
R485 P486 Q487 VAL THR ALA VAL ALA GLN ASN GLN GLY GLU VAL PRO GLU PRO GLN ASP MET LYS VAL ALA GLU VAL LEU PHE D513 A514 A515 D516 A517 N518 A519 I520 E521 E522 V523 N524 L525 A526 Y527 E528 N529 V530 K531 E532 V533 D534 G535 L536 D537 V538 S539 K540 E541 G542 T543 E544
A545 W546 E547 A548 A549 M550 K551 R552 Y553 D554 E555 R556 I557 D558 R559 V560 R563 I564 T565 A566 R567 L568 R569 D570 G573 T574 A575 K576 E580 M581 F585 N589 A590 L591 F592 V593 R594 P595 H596 I597 R598 G599 A600 I601 R602 E603 Y604 Q605 T606 Q607 Q610 R611 V612 K613
D614 D615 Q626 Q629 K634 R656 M662 K663 R664 V665 L669 G670 K671 G672 W673 E674 N675 H676 V677 E678 G679 Q680 K681 L682 K683 Q684 D685 G686 D687 M691 K692 R704 Q707 Q708 R709 N710 L711 E721 S722 T723 R724 V725 R726 G727 R728 T729 G730 N731 V732 L733
W755 R759 I764 R790 N799 L804 V805 E811 T839 V847 L850 D858 R862 M868 H991 S892 Y893 L926 L927 GLY GLN ALA GLU ASP LYS ALA GLU VAL ASP MET ASP THR ASP ALA PRO GLN VAL SER HIS LYS P949 G950 G951 E952 P953
LYS ILE LYS ASN VAL VAL HIS GLU LEU ARG ILE THR ASN GLN VAL ILE TYR LEU ASN P973 P974 I975 E976 E977 C978 R979 Y980 K981 E985 M986 F987 R998 Y1004 Q1005 V1006 G1007 V1008 H1009 Y1010 E1011 L1012 E1015 M1026 P1027 D1028 G1029 P1030 V1031 A1032 S1038 M1041 S1045
E1046 V1047 E1048 GLN TYR VAL LYS VAL TRP LEU GLN TYR GLN CYS LEU TRP ASP MET GLN ALA GLU ASN ILE TYR 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
VAL ILE ASP TYR GLY LYS VAL GLN SER LYS VAL ASN LEU LYS TYR 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 GLU LEU GLU GLN HIS SER VAL ASP THR ALA SER THR SER ASP
ALA VAL THR PHE ILE THR TYR VAL GLN SER LEU LYS ARG LYS ILE LYS GLN PHE GLU LYS GLN VAL 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 MET
ARG ARG LYS ASP SER ALA ILE GLN GLN GLN VAL ALA ASN LEU GLN MET LYS ILE VAL GLN GLU ASP ARG ALA VAL GLU SER ARG THR THR ASP LEU LEU THR ASP TRP GLU LYS THR LYS PRO VAL THR GLY ASN LEU ARG PRO GLU GLU ALA LEU GLN GLN ALA LEU THR ILE TYR GLU GLY
LYS PHE GLY ARG LEU LYS ASP ARG GLU LYS CYS ALA LYS ALA LYS GLN LEU ALA LEU GLU LEU THR ASP THR GLY LYS SER GLU GLU ARG VAL GLN VAL ALA LEU GLU LEU GLU GLN ASP LEU GLY VAL TRP SER GLU LEU ILE ASP LYS VAL ALA ALA LEU ILE ASP ASP GLN
MET LYS GLU GLN PRO TRP VAL SER VAL GLN PRO ARG LYS LEU ARG GLN ASN LEU ASP ALA LEU LEU ASN GLN LEU LYS SER PHE PRO ALA ARG LEU ARG GLN TYR ALA SER TYR GLU PHE VAL GLN ARG LEU LEU LYS GLY TYR MET 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 GLU LEU GLN ILE ASN GLU ALA ILE VAL LYS ASP VAL LEU LEU LEU VAL ALA GLN GLY GLU MET ALA LEU GLU 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 TYR TYR LYS VAL PHE GLU GLU ASP ALA LEU SER TRP GLU ILE
LYS LEU ASN ARG ILE MET ALA LEU PHE ASP VAL TRP ILE ASP VAL GLN ARG ARG TRP VAL TYR LEU GLU 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
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 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 ASN GLU ASP ASN SER VAL VAL LEU GLY ILE SER SER ARG GLU GLY GLU GLU VAL MET 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 THR ALA

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

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

GLY VAL 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 SER VAL ARG GLY GLU LEU GLN 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 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 SER ARG CYS GLY MET VAL TRP PHE SER

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

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

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

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

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

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

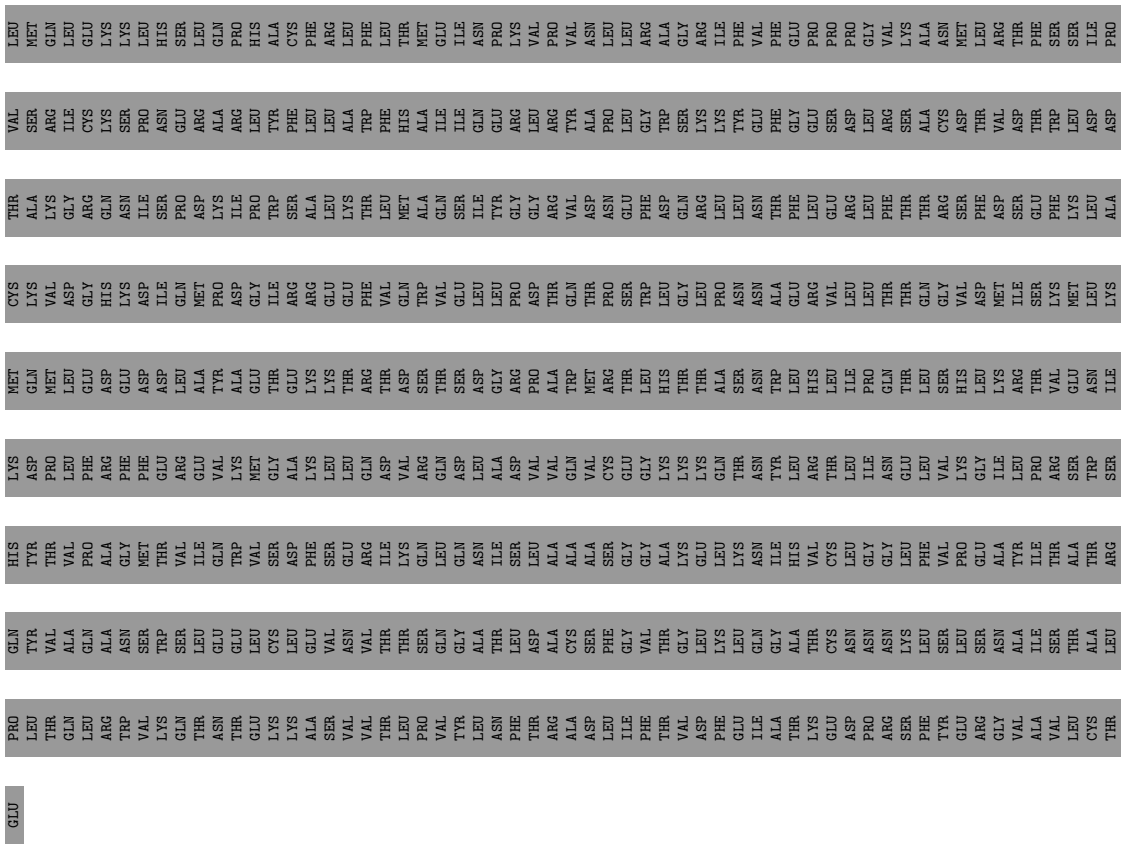
THR ALA CYS SER SER ILE TYR PHE THR MET GLU SER LEU LYS GLN ILE HIS PHE LEU TYR GLN TYR SER LEU GLN PHE PHE LEU ASP ILE TYR HIS ASN VAL LEU TYR GLU ASN PRO ASN LEU LYS GLY VAL THR ASP HIS THR GLN ARG LEU SER ILE ILE THR LYS ASP LEU PHE GLN

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

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

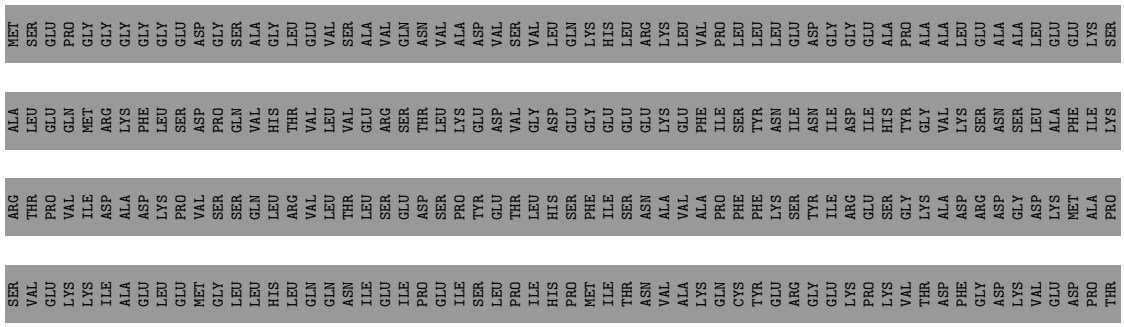
ALA ILE HIS ARG LEU LEU LEU ILE GLN ALA PHE ARG PRO ASP ARG LEU LEU ALA MET ALA HIS MET PHE VAL SER THR ASN LEU GLY GLU SER PHE MET SER ILE MET GLU GLN PRO LEU ASP LEU THR HIS ILE VAL GLY THR GLU VAL LYS PRO ASN THR PRO VAL LEU MET CYS SER

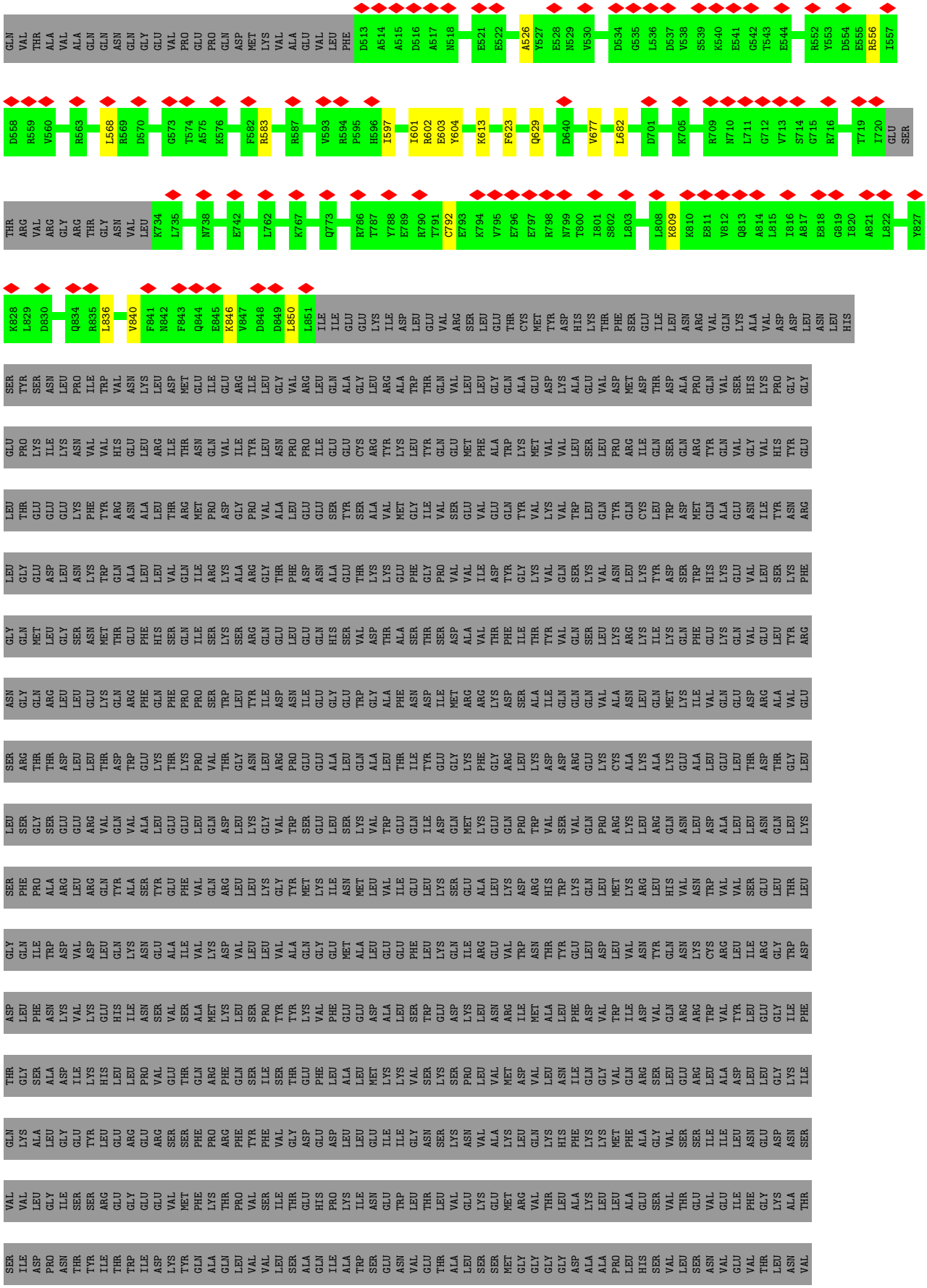
VAL PRO GLY TYR ASP ALA SER GLY HIS VAL GLU ASP LEU ALA ALA GLU GLN ASN THR GLN ILE THR SER ILE ALA ILE GLY SER ALA GLU GLY PHE ASN GLN ALA ASP LYS ALA ILE ASN THR ALA VAL LYS SER GLY ARG TRP VAL MET LEU LYS ASN VAL HIS LEU ALA PRO GLY TRP



- Molecule 2: Cytoplasmic dynein 1 heavy chain 1

Chain m: 10% 89%




GLN VAL THR ALA VAL ALA GLN GLN ASN GLN GLY GLU VAL PRO GLU PRO GLN ASP MET LYS VAL ALA GLU VAL LEU PHE D513 A514 A515 D516 A517 N518 E521 E522 A526 Y527 E528 N529 V530 D534 G535 L536 D537 V538 S539 K540 E541 G542 T543 E544 R552 Y553 D554 E555 R556 I557
D558 R559 V560 R563 L568 R569 D570 G573 T574 A575 K576 F582 R583 R587 V593 R594 P595 H596 I597 I601 R602 E603 Y604 K613 F623 Q629 D640 V677 L682 D701 K705 R709 N710 L711 G712 V713 S714 G715 R716 T719 I720 GLU SER
THR ARG VAL ARG GLY ARG THR GLY ASN VAL LEU K734 L735 N738 E742 L762 K767 Q773 R786 T787 Y788 E789 R790 T791 C792 E793 K794 V795 E796 E797 R798 N799 T800 I801 S802 L803 L808 L809 K810 E811 V812 Q813 A814 L815 I816 A817 E818 G819 I820 A821 L822 Y827
K828 L829 D830 Q834 R835 L836 V840 F841 N842 F843 Q844 E845 K846 V847 D848 D849 L850 L851 ILE ILE ILE GLU GLU LYS ILE ASP LEU GLU VAL ARG SER LEU GLU THR CYS MET TYR ASP HIS LYS THR PHE SER GLU ILE LEU ASN ARG VAL GLN LYS ALA VAL ASP ASP LEU ASN LEU HIS
SER TYR SER ASN LEU PRO ILE TRP VAL ASN LYS LEU ASP MET GLU ILE GLU ARG LEU GLN ALA GLY LEU ARG ALA TRP THR GLN 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 LYS PHE TYR ARG ASN ALA LEU THR ARG MET PRO ASP GLY PRO VAL ALA LEU GLU GLU SER TYR SER ALA VAL MET GLY ILE VAL SER GLU VAL GLU GLN TYR VAL LYS VAL TRP LEU GLN TYR GLN CYS LEU TRP ASP MET GLN ALA GLU ASN ILE TYR 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 VAL ILE ASP TYR GLY LYS VAL GLN SER LYS VAL ASN LEU LYS TYR 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 GLU LEU GLN HIS SER VAL ASP THR ALA SER THR SER ASP ALA VAL THR PHE ILE THR TYR VAL GLN SER LEU LYS ARG LYS ILE LYS GLN PHE GLU LYS GLN VAL GLU 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 MET ARG ARG LYS ASP SER ALA ILE GLN GLN GLN VAL ALA ASN LEU GLN MET LYS ILE ILE GLN VAL GLU GLU ASP ARG ALA VAL GLU
SER ARG THR THR ASP TRP GLU LYS THR LYS PRO VAL THR GLY ASN LEU ARG PRO GLU 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 ALA LYS GLU LEU THR ASP THR GLY LEU
LEU SER GLY SER GLU GLU ARG VAL GLN VAL ALA LEU GLU GLU LEU GLN ASP LEU LYS GLY VAL TRP SER GLU LEU SER LYS VAL TRP GLU GLN ILE ASP GLN MET LYS GLU GLN PRO TRP VAL SER VAL GLN PRO ARG LYS LEU ARG GLN ASN LEU LEU ASP LEU LEU LYS
SER PHE PRO ALA ARG LEU ARG GLN TYR ALA SER TYR GLU PHE VAL GLN ARG LEU LEU LYS GLY TYR MET LYS ILE ASN MET LEU VAL ILE GLU GLU LEU LYS SER GLU GLU ALA LYS ASP ARG HIS TRP LYS GLN LEU HIS VAL ASN TRP VAL VAL SER GLU THR LEU
GLY GLN ILE TRP ASP VAL ASP LEU GLN LYS ASN GLU ALA ILE ILE VAL LYS ASP VAL LEU LEU GLY GLU MET ALA LEU VAL GLU PHE LEU LYS GLN ILE ARG GLU VAL TRP ASN THR TYR GLU LEU ASP LYS ASN TYR GLN ASN LYS CYS ARG LEU VAL ILE ARG GLY THR TRP
ASP LEU PHE ASN LYS VAL LYS GLU HIS ILE ASN SER VAL SER MET ALA LYS LEU ASP ASP LEU SER TRP GLU LYS VAL PHE LEU ASN GLU GLU ASP ALA LEU LYS LEU ASN ARG ILE MET LEU PHE ASP VAL ALA LEU SER TRP LYS LEU ASP ARG LEU HIS VAL ASP VAL ALA LEU LEU GLU GLY THR ILE
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 LYS HIS PHE ILE GLN GLY VAL VAL GLN ARG GLN ARG ARG TRP VAL TYR 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 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 VAL ILE ILE ASN LEU GLU ASP
VAL VAL LEU GLY ILE SER SER ARG GLU GLY GLY GLU 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 VAL GLU ILE PHE GLY LYS ALA THR
SER ILE ASP PRO ASN THR TYR ILE THR TRP ILE ASP LYS TYR GLN VAL LEU VAL SER ALA GLN ILE ALA TRP SER GLU ASN VAL GLU THR ALA LEU SER SER MET GLY GLY GLY GLY ASP ALA ALA PRO LEU HIS SER VAL LEU SER ASN VAL GLU VAL LEU THR LEU ASN VAL

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

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

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

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

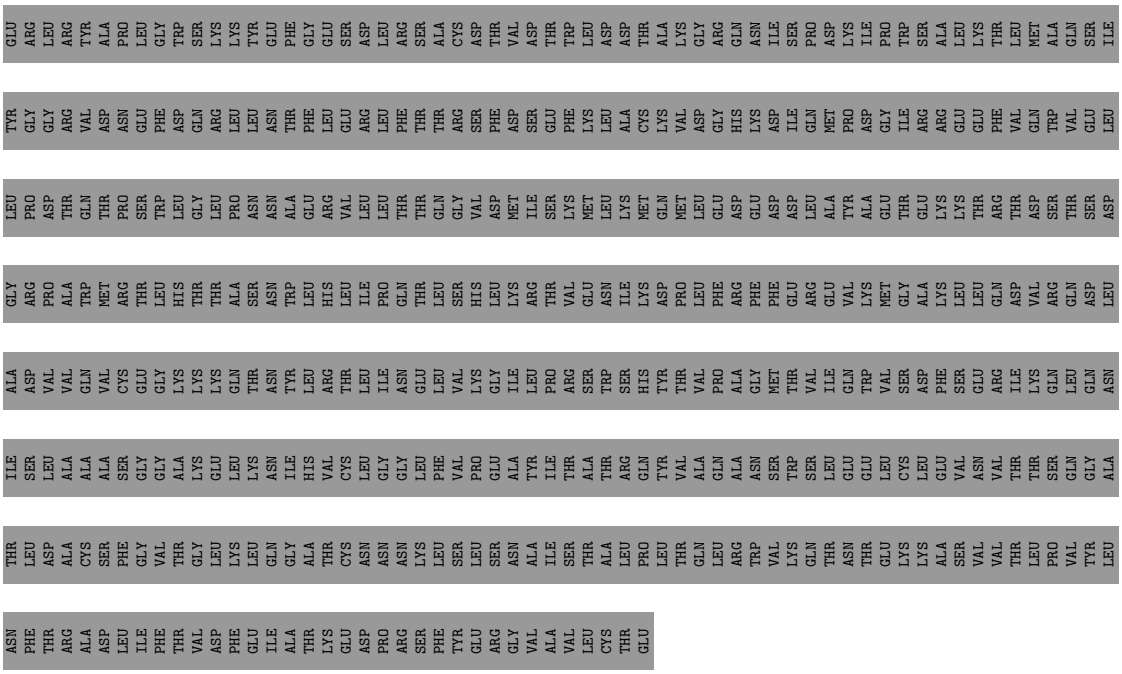
LEU LYS GLY THR VAL GLY GLU PRO THR TYR ASP ALA GLU PHE GLN HIS PHE LEU ARG GLY ASN GLU ILE VAL LEU SER ALA GLY SER THR PRO ARG ILE GLN GLY LEU THR VAL GLU GLN ALA GLU ALA VAL VAL ARG LEU SER CYS LEU PRO ALA PHE LYS ASP LEU ILE ALA LYS VAL

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

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

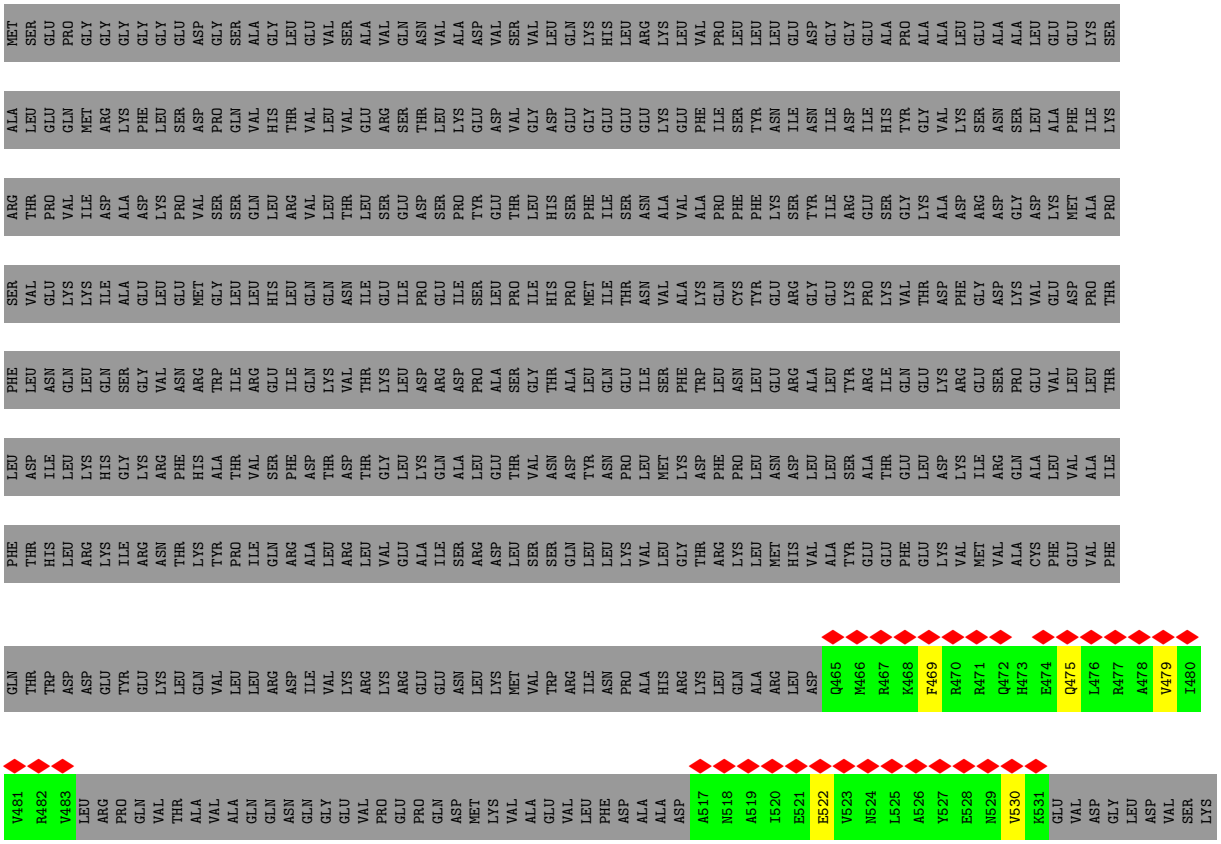
GLY SER ALA GLU GLY PHE ASN GLN ALA ASP LYS ALA ILE ASN THR ALA VAL LYS SER GLY ARG TRP VAL MET LEU LYS ASN VAL HIS LEU ALA PRO GLY TRP LEU MET GLN LEU GLU LYS LYS LEU HIS SER LEU GLN PRO HIS ALA CYS PHE ARG LEU PHE LEU THR MET GLU ILE ASN

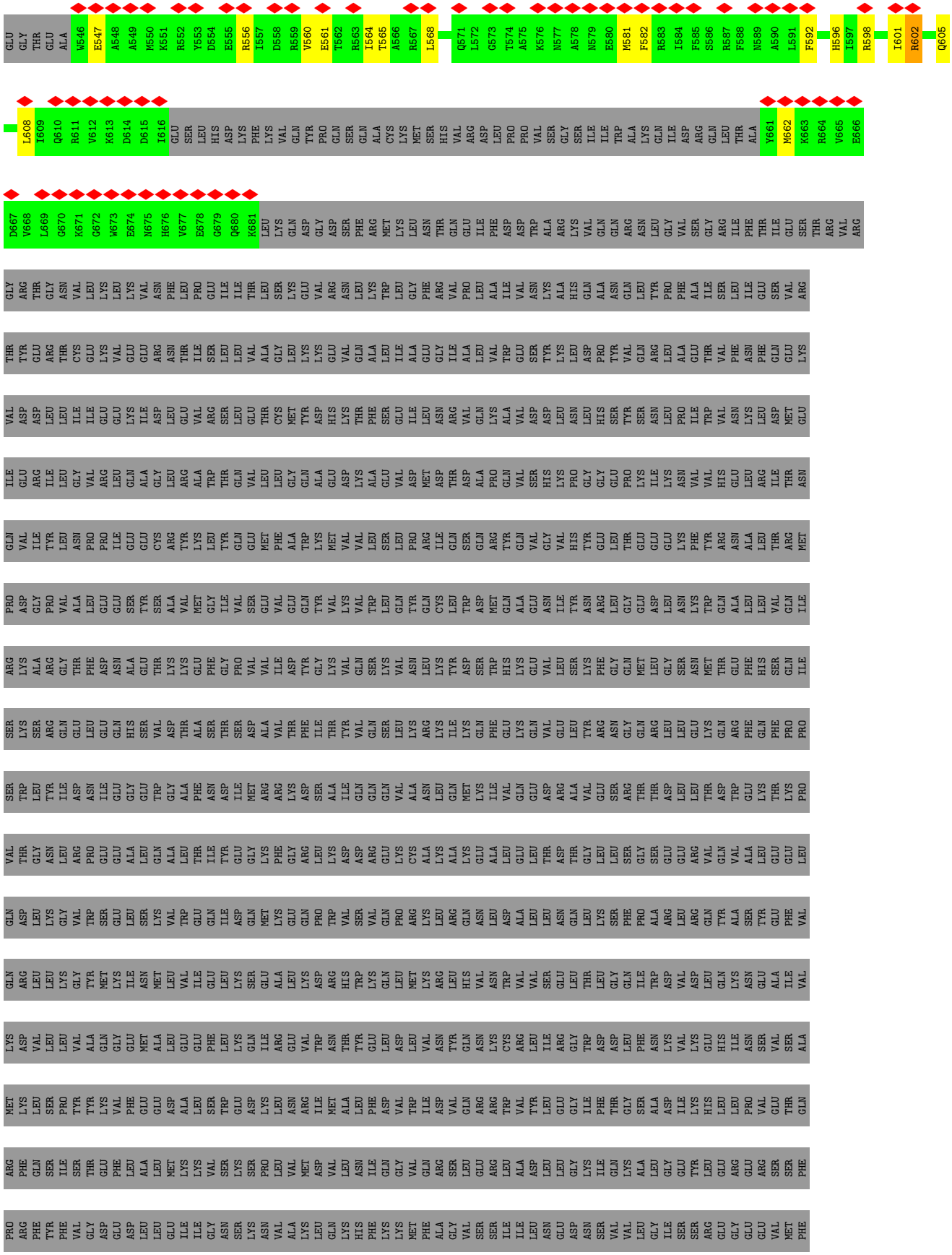
PRO LYS VAL PRO VAL ASN LEU LEU ARG ALA GLY ARG ILE PHE VAL PHE GLU PRO PRO PRO GLY VAL LYS ALA ASN MET LEU ARG THR PHE SER SER ILE PRO VAL SER ARG ILE CYS LYS SER PRO ASN GLU ARG ALA ARG LEU TYR PHE LEU LEU ALA TRP PHE HIS ALA ILE ILE GLN



• Molecule 2: Cytoplasmic dynein 1 heavy chain 1

Chain n: 97%




GLU GLY THR GLU ALA W546 E547 A548 A549 M550 K551 R552 Y553 D554 E555 R556 I557 D558 R559 V560 E561 T562 R563 I564 T565 A566 R567 L568 Q571 L572 G573 T574 A575 K576 N577 A578 N579 E580 M581 F582 R583 I584 F585 S586 R587 F588 N589 A590 L591 F592 H596 I597 R598 I601 R602 Q605
L608 I609 Q610 R611 V612 K613 D614 D615 I616 GLU SER LEU HIS ASP LYS PHE LYS VAL GLN TYR PRO GLN SER GLN ALA CYS LYS MET SER HIS VAL ARG ASP LEU PRO VAL SER GLY SER ILE ILE TRP ALA LYS GLN ILE ASP ARG GLN LEU THR ALA Y661 M662 K663 R664 V665 E666
D667 V668 L669 G670 K671 G672 W673 E674 N675 H676 V677 E678 G679 Q680 K681 LEU LYS GLN ASP GLY ASP SER PHE ARG MET LYS LEU ASN THR GLN GLU ILE PHE ASP ASP TRP ALA ARG LYS VAL GLN GLN ARG ASN GLN LEU TYR PRO GLY VAL SER GLY ARG ILE PHE THR ILE GLU SER THR ARG VAL ARG
GLY ARG THR GLY ASN VAL LEU LYS LEU LYS VAL ASN PHE LEU PRO GLU ILE ILE THR LEU SER LYS GLU VAL ARG ASN LEU LYS TRP LEU GLY PHE ARG VAL PRO LEU ALA ILE VAL ASN LYS ALA HIS GLN ALA ASN GLN LEU TYR PRO PHE ALA ILE SER LEU ILE GLU SER VAL ARG
THR TYR GLU ARG THR CYS GLU LYS VAL GLU GLU ARG ASN THR ILE SER LEU LEU VAL ALA GLY LEU LYS LYS GLU VAL GLN ALA LEU ILE ALA GLU GLY ILE ALA LEU VAL TRP GLU SER TYR LYS LEU ASP PRO TYR VAL GLN ARG LEU ALA GLU THR VAL PHE ASN PHE GLN GLU LYS
VAL ASP ASP LEU LEU ILE ILE GLU GLU LYS ILE ASP LEU GLU VAL ARG SER LEU GLU THR CYS MET TYR ASP HIS LYS THR PHE SER GLU ILE LEU ASN ARG VAL GLN LYS ALA VAL ASP ASP LEU ASN LEU HIS SER TYR SER ASN LEU PRO ILE TRP VAL ASN LYS LEU MET GLU
ILE GLU ARG ILE LEU GLY VAL ARG LEU GLN ALA GLY LEU ARG ALA TRP THR GLN 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 GLU GLU LYS 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 SER ALA VAL MET GLY ILE VAL SER GLU VAL GLU GLN TYR VAL LYS VAL TRP LEU GLN TYR GLN CYS LEU TRP ASP MET GLN ALA GLU ASN ILE TYR 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 VAL ILE ASP TYR GLY LYS VAL GLN SER LYS VAL ASN LEU LYS TYR 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 GLU GLN HIS SER VAL ASP THR ALA SER THR SER ASP ALA VAL THR PHE ILE THR TYR VAL GLN SER LEU LYS ARG LYS ILE LYS GLN PHE GLU LYS GLN VAL GLU LEU TYR ARG ASN GLY GLN ARG LEU LEU GLU 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 MET ARG ARG LYS ASP SER ALA ILE GLN GLN GLN VAL ALA ASN LEU LYS ASN LEU GLN LYS ILE LYS GLN MET LYS ILE VAL GLN GLU ASP ARG ALA VAL GLU SER ARG THR THR ASP LEU LEU THR LYS PRO
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 ALA ALA LYS GLU LEU THR ASP THR GLY LEU LEU GLY SER GLU GLU ARG VAL GLN GLU GLU LEU
GLN ASP LEU LYS GLY VAL TRP SER GLU LEU SER LYS VAL TRP GLU GLN ILE ASP GLN MET LYS GLU GLN PRO TRP VAL SER VAL GLN GLN PRO ARG LYS LYS LEU ARG LEU HIS GLN ASN LEU ASP ASP ALA LEU LEU ASN GLN LYS SER PHE PRO ALA ARG LEU ARG GLN TYR ALA SER GLU GLU PHE VAL
GLN ARG LEU LEU LYS GLY TYR MET LYS ILE ASN MET ARG LEU GLU VAL ILE GLU LYS SER GLU ALA LEU LYS ASP HIS ARG LYS LEU VAL ASN TRP VAL VAL SER GLU LEU THR LEU GLY GLN ILE TRP ASP VAL ALA LEU GLU GLU LEU
LYS ASP VAL LEU LEU VAL ALA GLN GLY GLU MET ALA LEU GLU 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 ASP ASP LYS ARG GLN ILE ASP LEU 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 ILE LEU LEU ASN ARG ILE MET ALA LEU PHE ASP VAL GLN ARG ARG TRP VAL TYR LEU GLU GLY ILE PHE THR GLY SER ALA ASP LEU LYS GLU HIS LEU LEU PRO VAL GLU THR GLN
ARG PHE GLN SER ILE SER THR TYR LYS LYS VAL LEU ASN ILE ILE ILE GLY VAL LEU LYS SER PRO LEU VAL MET ASP VAL LEU ASN ILE GLN LYS ALA LEU GLU GLY VAL SER ARG LEU GLU ARG LEU ALA ASP LEU LEU GLY GLU ILE GLU GLU ARG GLU ARG SER SER PHE
PRO ARG PHE TYR PHE VAL GLY ASP GLU ASP LEU ILE ILE GLY ASN SER LYS ASN VAL ALA LYS LEU GLN LYS HIS PHE LYS LYS MET PHE ALA SER SER LEU GLU THR ILE ILE LEU ASN GLU ASP ASN SER VAL VAL LEU GLY ILE SER SER ARG GLU GLY GLU VAL MET 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 VAL GLU THR ALA LEU SER SER MET GLY GLY GLY ASP ALA ALA PRO LEU HIS SER VAL LEU SER ASN VAL GLU VAL THR LEU ASN VAL LEU ALA ASP SER VAL LEU MET GLU GLN PRO LEU ARG 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 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 SER ILE GLN MET ALA ASN ALA LYS PHE
ASN TYR GLY PHE GLU TYR LEU GLY VAL GLN ASP LYS LEU VAL GLN THR PRO LEU THR ASP ARG CYS TYR LEU THR MET THR GLN ALA LEU GLU 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 ASP GLN ALA MET GLY ARG ILE PHE VAL ALA GLY LEU CYS GLN VAL GLY ALA TRP GLY CYS PHE ASP GLU PHE ASN ARG LEU GLU GLU ARG ARG ALA VAL SER ALA GLN VAL GLN CYS ILE GLN GLU ALA LEU ARG GLU HIS SER
ASN PRO ASN TYR ASP LYS THR 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 SER HIS TYR ASP PHE ILE THR MET LEU 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 SER GLN SER HIS TYR ASP PHE GLY LEU ARG ALA LEU LEU LYS SER VAL LEU LEU LEU LEU LEU 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 ILE ALA GLU ASN LEU PRO PHE 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 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 MET TRP VAL GLU LYS VAL LEU GLN LEU TYR GLN ILE THR GLN ILE ASN HIS GLY LEU LEU MET MET VAL GLY PRO SER
GLY SER GLY LYS SER MET ALA TRP ARG VAL LEU LEU LYS ARG LEU GLU GLU ALA LEU LYS ALA 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 GLU LEU LEU PHE THR HIS VAL LEU ARG LYS
ILE ILE ASP SER VAL ARG GLY GLU LEU GLN LYS ARG GLN TRP ILE VAL PHE ASP GLY ASP VAL ASP PRO GLU TRP VAL GLU ASN LEU ASN SER VAL LEU ASP LYS LYS LYS ASN LYS LEU LEU THR THR LEU PRO ASN GLY GLU ARG LEU LEU SER LEU PRO ASN VAL ARG ILE MET PHE GLU VAL GLN
ASP LEU LYS TYR ALA THR LEU LEU ALA THR VAL SER ARG CYS GLY MET VAL TRP PHE SER GLU ASP VAL SER THR ASP MET ILE PHE ASN ASN PHE LEU ALA ARG LEU ARG SER ILE PRO LEU ASP GLU GLY GLU ASP GLU ALA CRG CYS LEU GLU GLY GLU GLY GLU
GLU ALA ALA SER PRO MET LEU GLN ILE GLN ARG ASP ALA ALA THR ILE MET GLN PRO TYR PHE THR SER ASN GLY LEU VAL THR LYS ALA LEU GLU HIS ALA PHE GLN LEU GLU HIS GLN ARG ARG SER LEU LEU PHE SER LEU GLY GLY SER LEU LEU ARG CYS
ARG ASN VAL ALA GLN TYR ASN ALA ASN HIS PRO ASP PHE PRO MET GLN ILE GLU GLN TYR ARG TYR ILE GLN ARG TYR ALA ILE LEU TRP ARG ALA LEU VAL TYR ALA LEU GLY GLU TYR ILE LEU ILE GLN ARG ARG ARG LYS MET ARG ALA GLU LEU GLY LEU ILE THR THR VAL PRO LEU
PRO THR ALA PRO ASN ILE ILE ASP TYR GLU VAL PRO ILE ILE GLU VAL SER ILE SER TRP PRO TRP GLN ALA LYS VAL PRO GLN ILE GLU VAL GLU THR HIS LYS VAL ALA ALA PRO ASP ASP VAL ARG THR THR ASP LEU ASP THR VAL VAL ARG HIS GLU ILE THR TRP LEU
GLU HIS LYS PRO LEU VAL CYS GLY PRO PRO GLY SER GLY LYS THR MET THR LEU PHE SER ALA LEU LEU ARG ALA 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 THR GLU GLU TYR ARG THR TRP LEU
GLY VAL VAL LEU ALA PRO VAL GLN LEU PRO GLY LYS TRP LEU VAL LEU PHE CYS ASP GLU HIS GLY GLY PHE TYR ARG 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 THR ASP PRO LYS ARG PHE LEU ARG HIS VAL PRO VAL VAL TYR VAL ASP TYR PRO GLY PRO ALA SER LEU THR THR PHE ASN ARG ALA MET LEU ARG LEU ILE PRO LEU LEU ILE
GLU PRO LEU THR ALA ALA MET VAL THR TYR ILE ILE ARG HIS TYR ILE TYR SER PRO ARG GLU MET THR ARG TRP VAL ARG GLY ILE PHE GLU ALA LEU ARG PRO LEU GLU THR THR LEU LEU PRO VAL GLU LYS ARG ILE TRP ALA
HIS GLU ALA LEU ARG LEU VAL GLU ASP ARG GLU GLU ARG ARG TRP THR ASP GLU ASN ILE ASP THR VAL ALA LEU LYS HIS PHE PRO ASN ILE ASP ARG GLU LYS ALA MET SER ARG PRO ILE LEU TYR SER ASN TRP LEU SER VAL 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 VAL PRO LEU VAL LEU PHE ASN GLU VAL LEU ASP HIS VAL LEU ARG ILE ASP ARG ILE PHE 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 ASP LEU ARG THR VAL LEU ARG ARG SER GLY CYS LYS ASN GLU LYS ILE 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 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 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 ILE 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 VAL LYS ASN ALA ALA ALA ASN ASP LYS LEU LYS LYS MET VAL LYS ASP

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

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

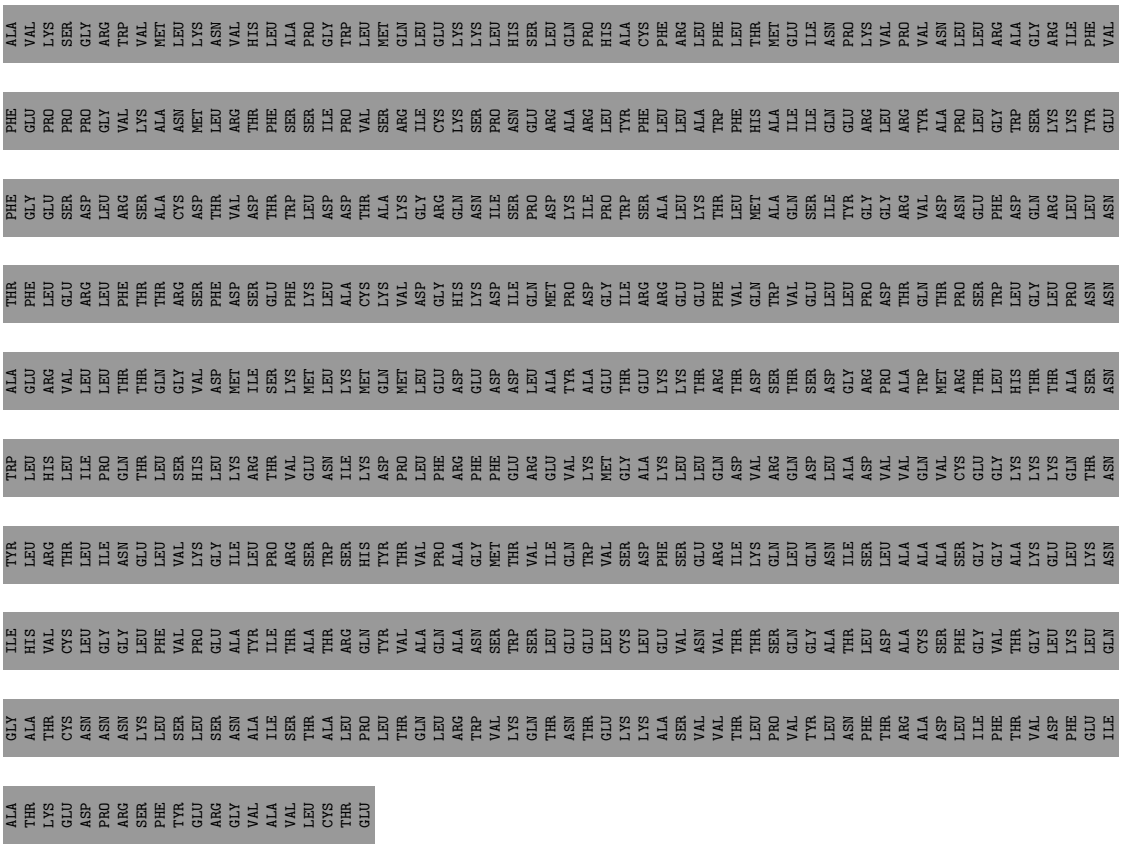
THR ASP ILE VAL MET GLN GLU VAL GLU THR VAL SER GLN GLN TYR LEU PRO LEU SER THR ALA CYS SER SER ILE TYR PHE THR MET GLU SER LEU LYS GLN ILE HIS PHE LEU TYR GLN TYR SER LEU GLN PHE PHE LEU ASP ILE TYR HIS ASN VAL LEU TYR GLU ASN PRO ASN LEU

LYS GLY VAL THR ASP HIS THR GLN ARG LEU SER 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 ASP ALA GLU PHE GLN

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

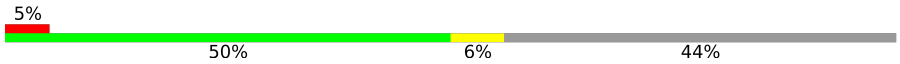
GLU GLN THR VAL PRO TYR LEU TRP SER GLU GLU THR PRO ALA THR PRO ILE GLY GLN ALA ILE HIS ARG LEU LEU LEU ILE GLN ALA PHE ARG PRO ASP ARG LEU LEU ALA MET ALA HIS MET PHE VAL SER THR ASN LEU GLY GLU SER PHE MET SER ILE MET GLU GLN PRO LEU ASP

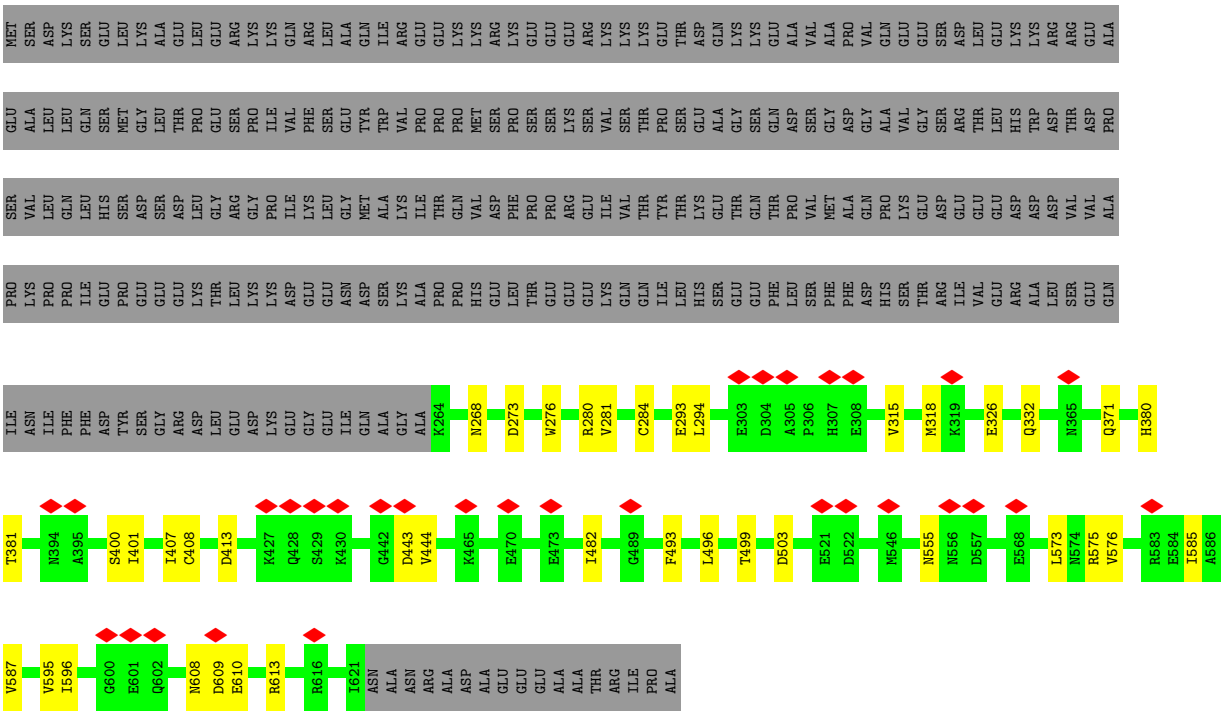
LEU THR HIS ILE VAL GLY THR GLU VAL LYS PRO ASN THR PRO VAL LEU MET CYS SER VAL PRO GLY TYR ASP ALA SER GLY HIS VAL GLU ASP LEU ALA ALA GLU GLN ASN THR GLN ILE THR SER ILE ALA ILE GLY SER ALA GLU GLY PHE ASN GLN ALA ASP LYS ALA ILE ASN THR



• Molecule 3: Cytoplasmic dynein 1 intermediate chain 2

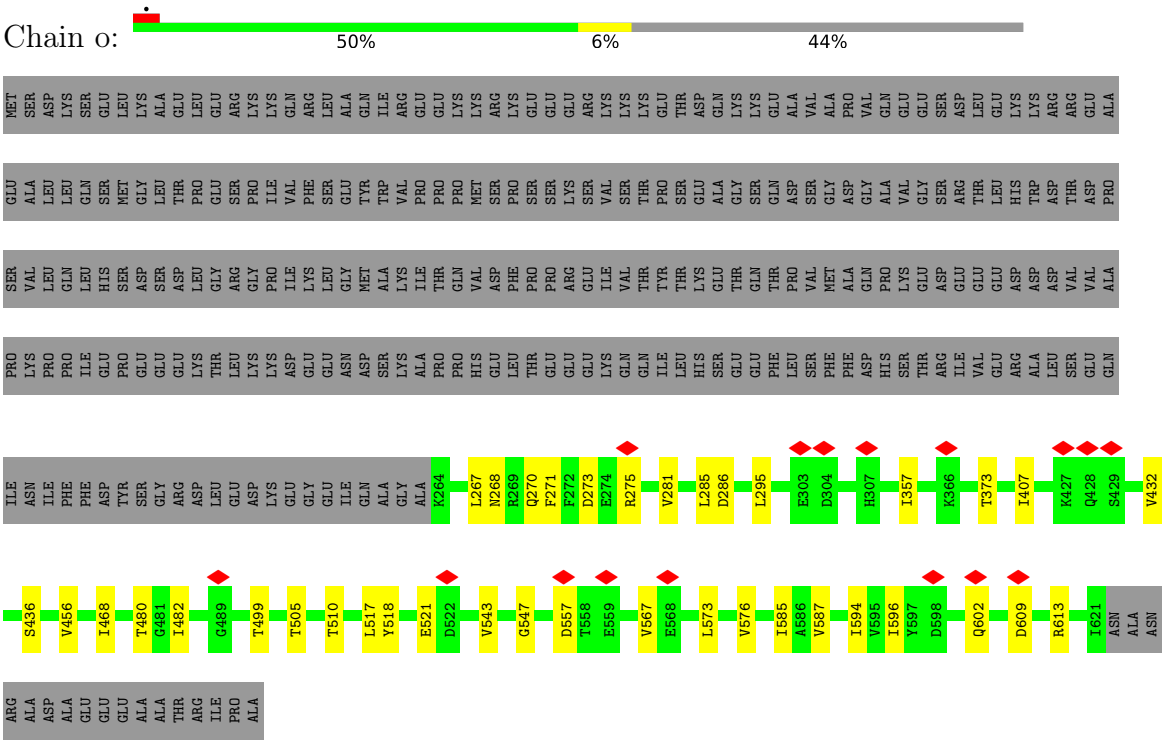
Chain h:





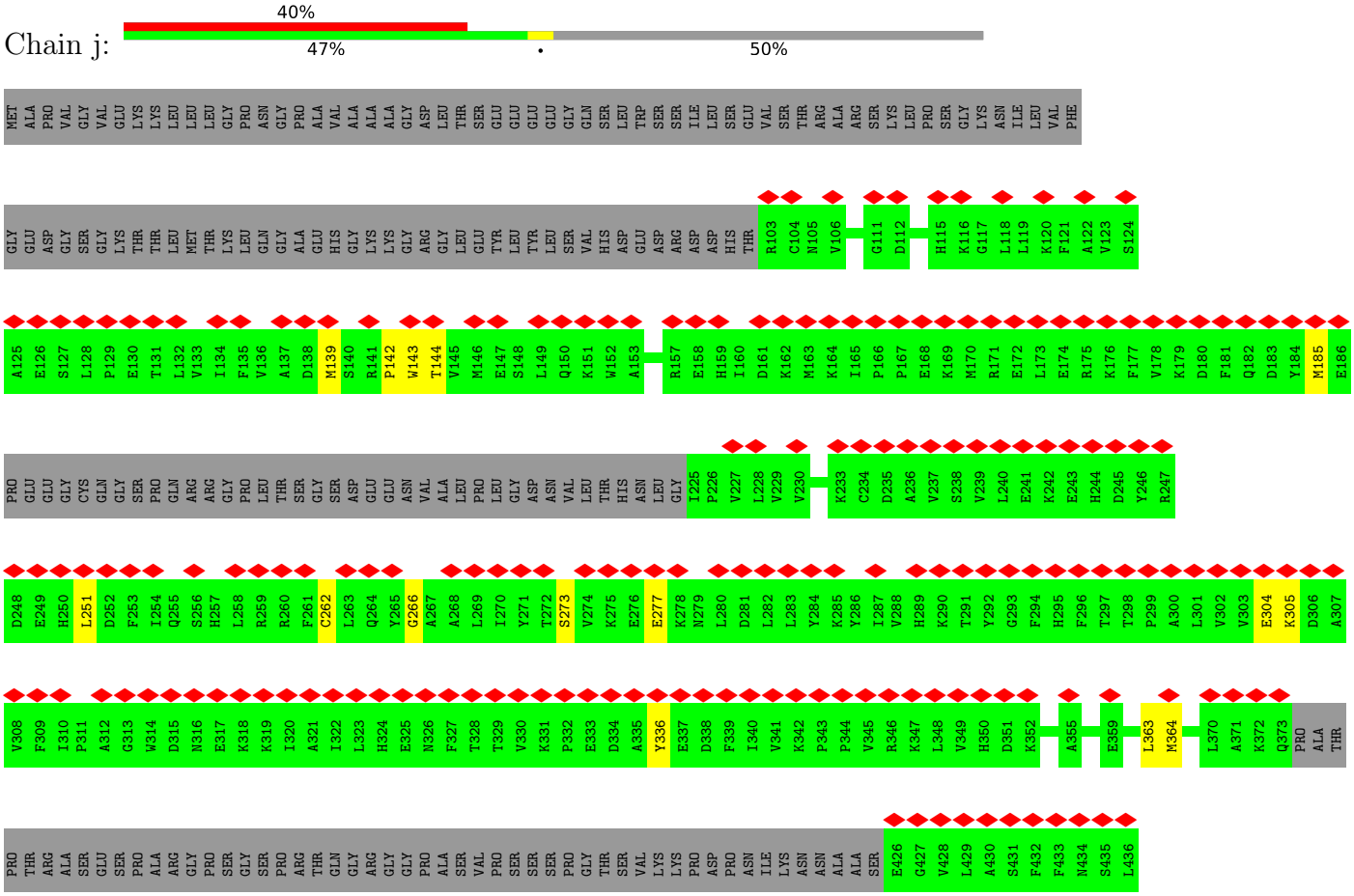
• Molecule 3: Cytoplasmic dynein 1 intermediate chain 2

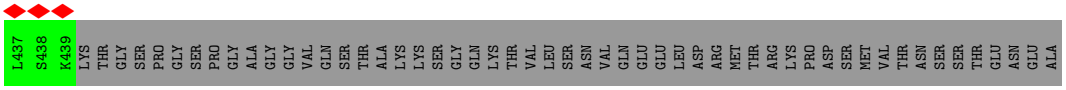
Chain o:



• Molecule 4: Cytoplasmic dynein 1 light intermediate chain 2

Chain j:





• Molecule 4: Cytoplasmic dynein 1 light intermediate chain 2

Chain r: 97%

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	78061	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	53	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.021	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.00128	Depositor
Map size (Å)	955.776, 955.776, 955.776	wwPDB
Map dimensions	768, 768, 768	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2445, 1.2445, 1.2445	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	X	0.51	0/805	0.86	0/1072
1	x	0.33	0/805	0.62	0/1072
2	f	0.39	0/5641	0.57	0/7605
2	m	0.29	0/4403	0.49	0/5927
2	n	0.39	0/1081	0.62	0/1442
3	h	0.37	0/2883	0.54	0/3932
3	o	0.41	0/2887	0.55	0/3938
4	j	0.18	0/2026	0.40	0/2731
4	r	0.12	0/55	0.28	0/67
All	All	0.36	0/20586	0.55	0/27786

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	X	797	0	797	6	0
1	x	797	0	797	3	0
2	f	5545	0	5644	34	0
2	m	4333	0	4444	25	0
2	n	1068	0	1079	13	0
3	h	2804	0	2670	24	0
3	o	2808	0	2673	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	j	1981	0	1950	10	0
4	r	56	0	15	0	0
All	All	20189	0	20069	129	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 3.

The worst 5 of 129 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)
3:o:547:GLY:HA2	3:o:573:LEU:HD23	1.68	0.75
2:m:483:VAL:HG23	2:m:484:LEU:HD22	1.67	0.75
2:m:792:CYS:SG	2:m:809:LYS:NZ	2.63	0.70
2:n:592:PHE:O	2:n:598:ARG:NH2	2.27	0.67
2:f:581:MET:SD	2:f:611:ARG:NH1	2.67	0.67

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	X	91/577 (16%)	91 (100%)	0	0	100	100
1	x	91/577 (16%)	91 (100%)	0	0	100	100
2	f	664/4646 (14%)	651 (98%)	13 (2%)	0	100	100
2	m	516/4646 (11%)	502 (97%)	14 (3%)	0	100	100
2	n	118/4646 (2%)	115 (98%)	3 (2%)	0	100	100
3	h	356/638 (56%)	343 (96%)	13 (4%)	0	100	100
3	o	356/638 (56%)	342 (96%)	14 (4%)	0	100	100
4	j	241/492 (49%)	236 (98%)	5 (2%)	0	100	100

Continued on next page...

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	r	12/492 (2%)	12 (100%)	0	0	100	100
All	All	2445/17352 (14%)	2383 (98%)	62 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	X	87/503 (17%)	83 (95%)	4 (5%)	24	48
1	x	87/503 (17%)	86 (99%)	1 (1%)	65	74
2	f	603/4125 (15%)	598 (99%)	5 (1%)	73	77
2	m	468/4125 (11%)	467 (100%)	1 (0%)	87	88
2	n	110/4125 (3%)	107 (97%)	3 (3%)	39	60
3	h	308/557 (55%)	306 (99%)	2 (1%)	78	81
3	o	309/557 (56%)	307 (99%)	2 (1%)	78	81
4	j	213/422 (50%)	213 (100%)	0	100	100
All	All	2185/14917 (15%)	2167 (99%)	18 (1%)	70	77

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	n	602	ARG
1	x	145	LEU
3	o	407	ILE
2	f	850	LEU
2	n	601	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
3	h	495	HIS
3	h	570	ASN
1	x	150	GLN
3	o	419	GLN
3	o	523	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

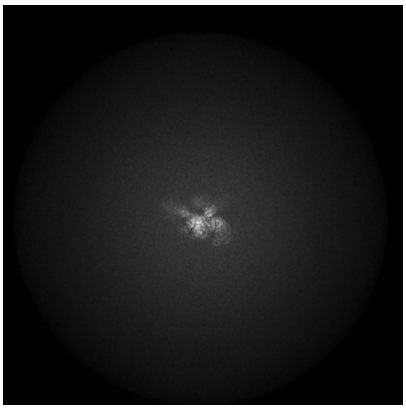
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-14553. These allow visual inspection of the internal detail of the map and identification of artifacts.

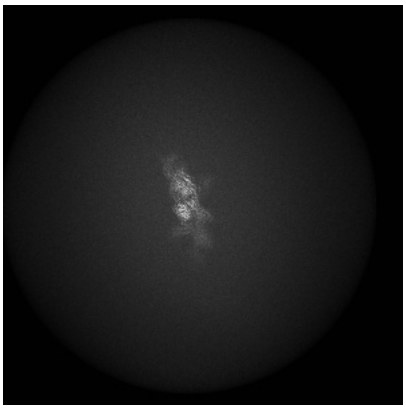
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

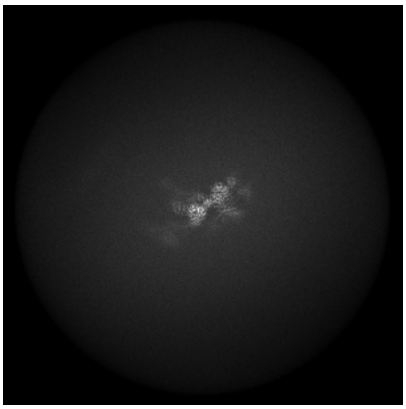
6.1.1 Primary map



X

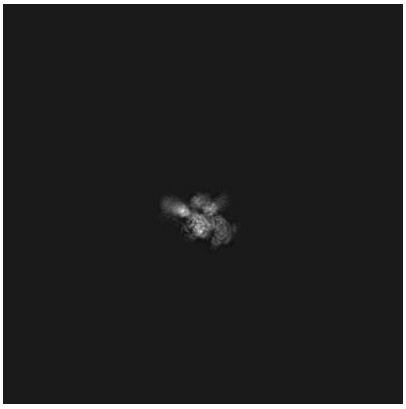


Y



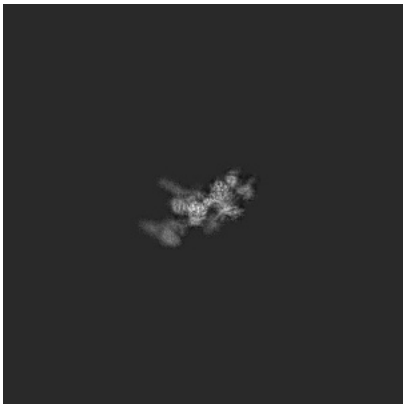
Z

6.1.2 Raw map



X

Y

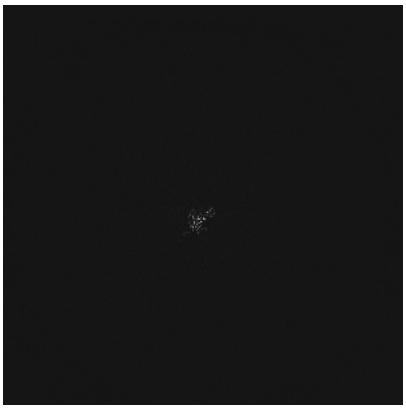


Z

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

6.2 Central slices (i)

6.2.1 Primary map

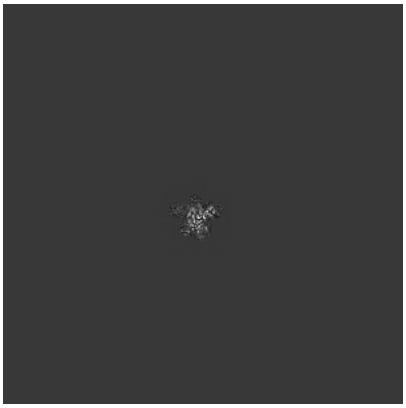


X Index: 384

Y Index: 384

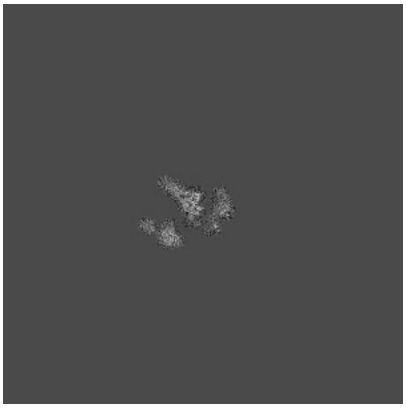
Z Index: 384

6.2.2 Raw map



X Index: 384

Y Index: 384

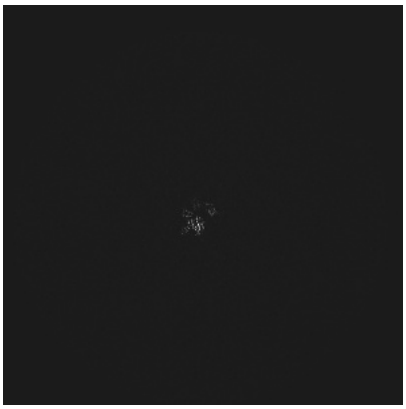


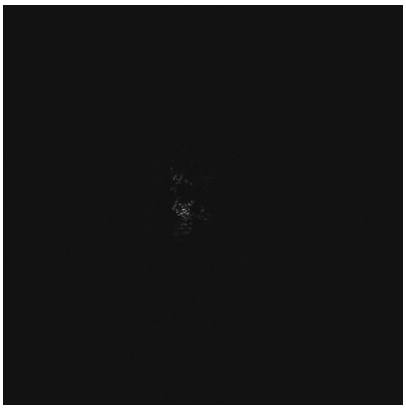
Z Index: 384

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

6.3 Largest variance slices (i)

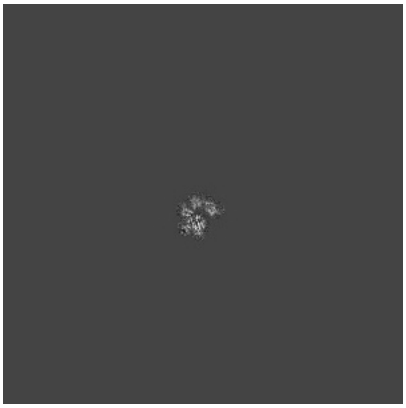
6.3.1 Primary map

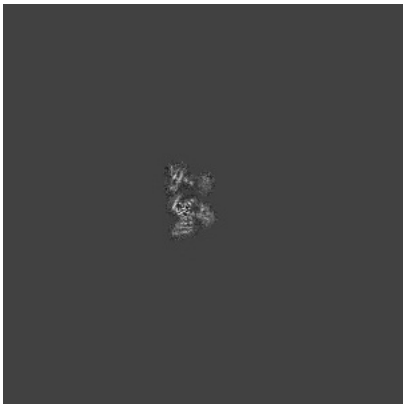

X Index: 374


Y Index: 375

Z Index: 349

6.3.2 Raw map


X Index: 374

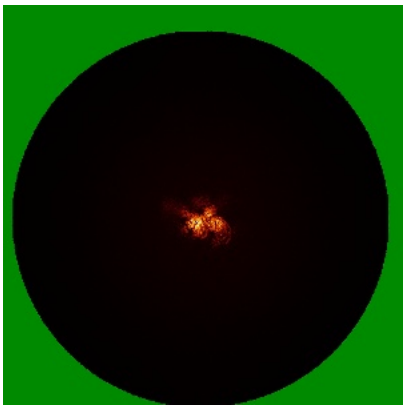

Y Index: 375

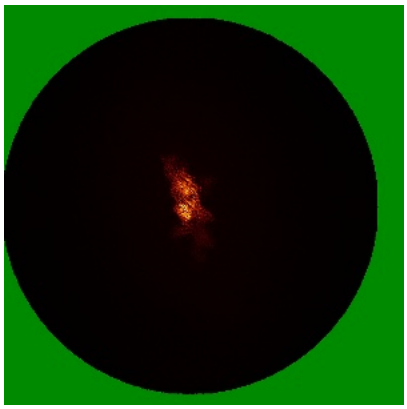
Z Index: 349

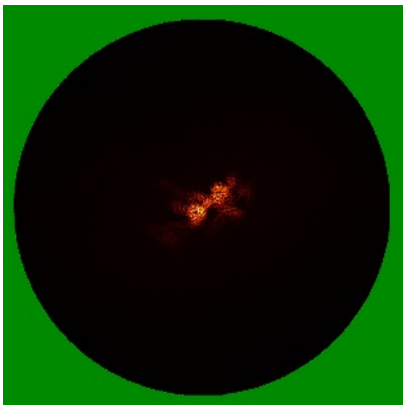
The images above show the largest variance slices of the map in three orthogonal directions.

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

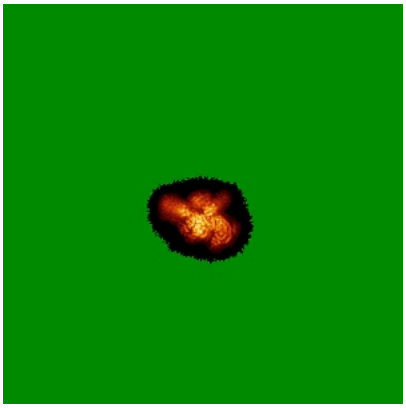
6.4.1 Primary map

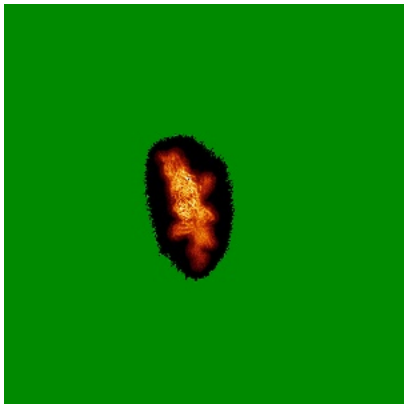

X

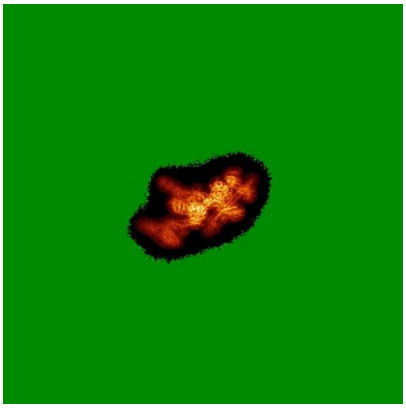

Y


Z

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 0.00128. 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.

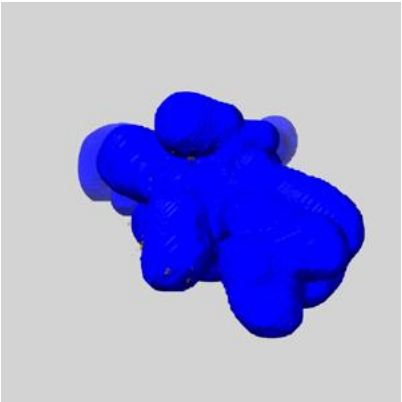
6.6 Mask visualisation (i)

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

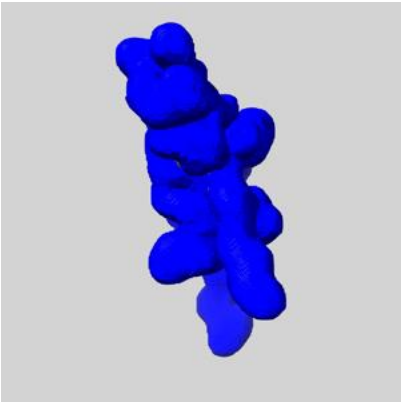
A mask typically either:

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

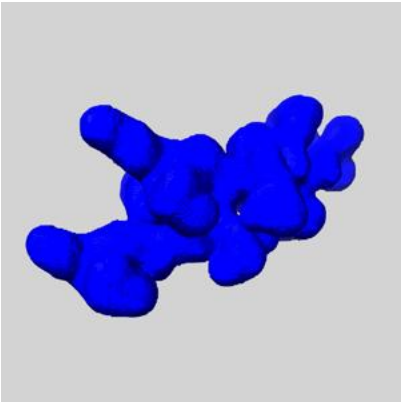
6.6.1 emd_14553_msk_1.map (i)



X



Y

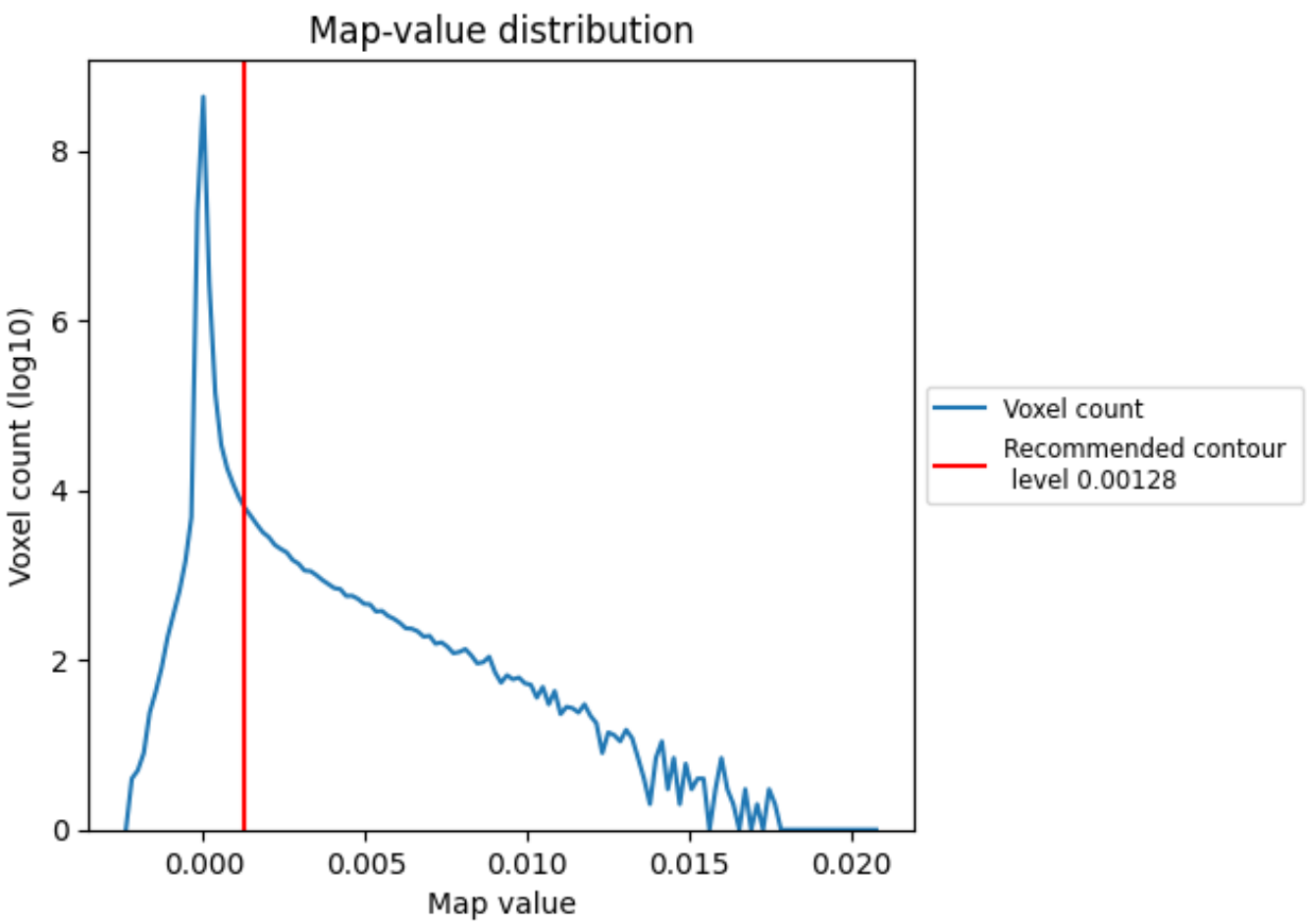


Z

7 Map analysis (i)

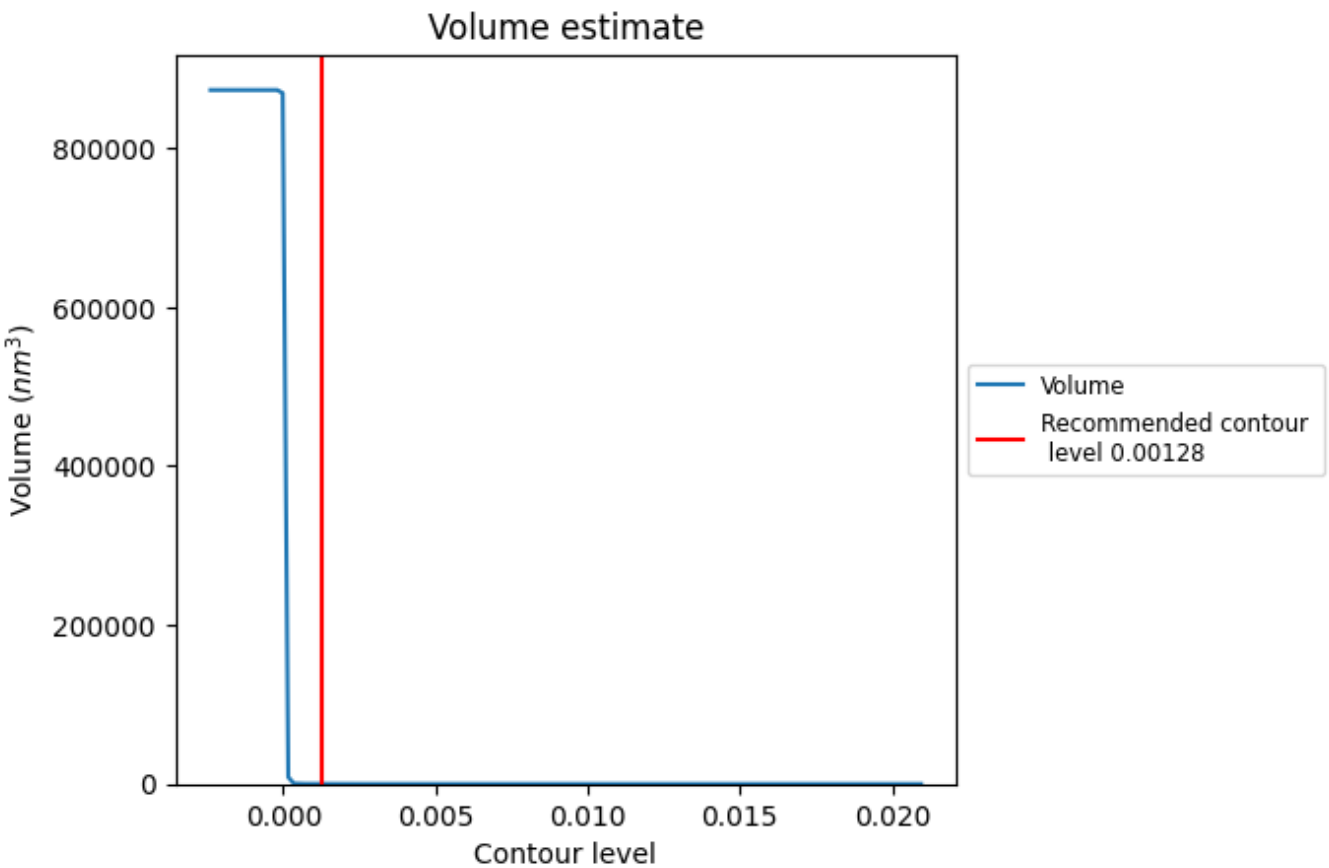
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

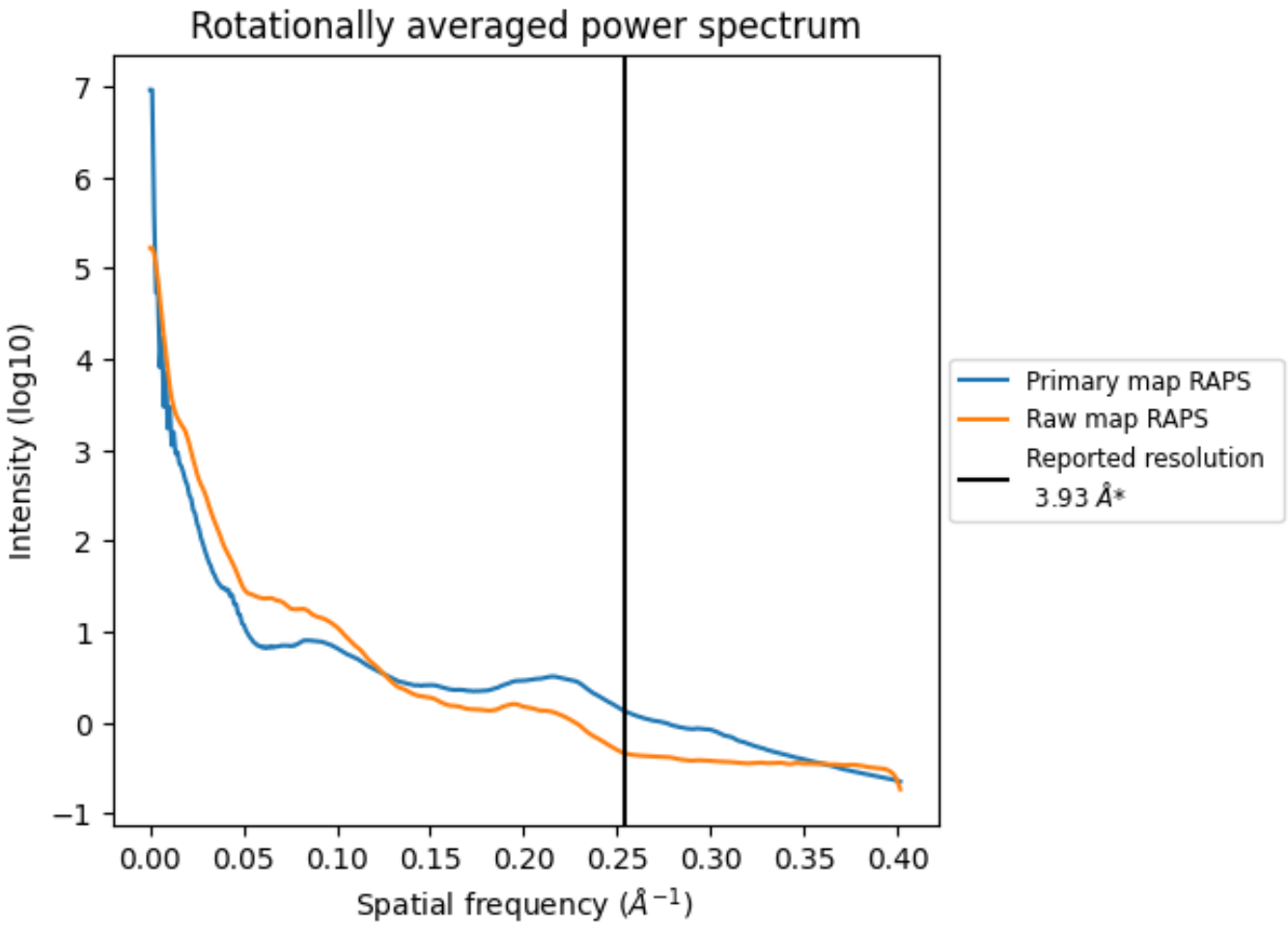
7.2 Volume estimate (i)



The volume at the recommended contour level is 85 nm^3; this corresponds to an approximate mass of 77 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)

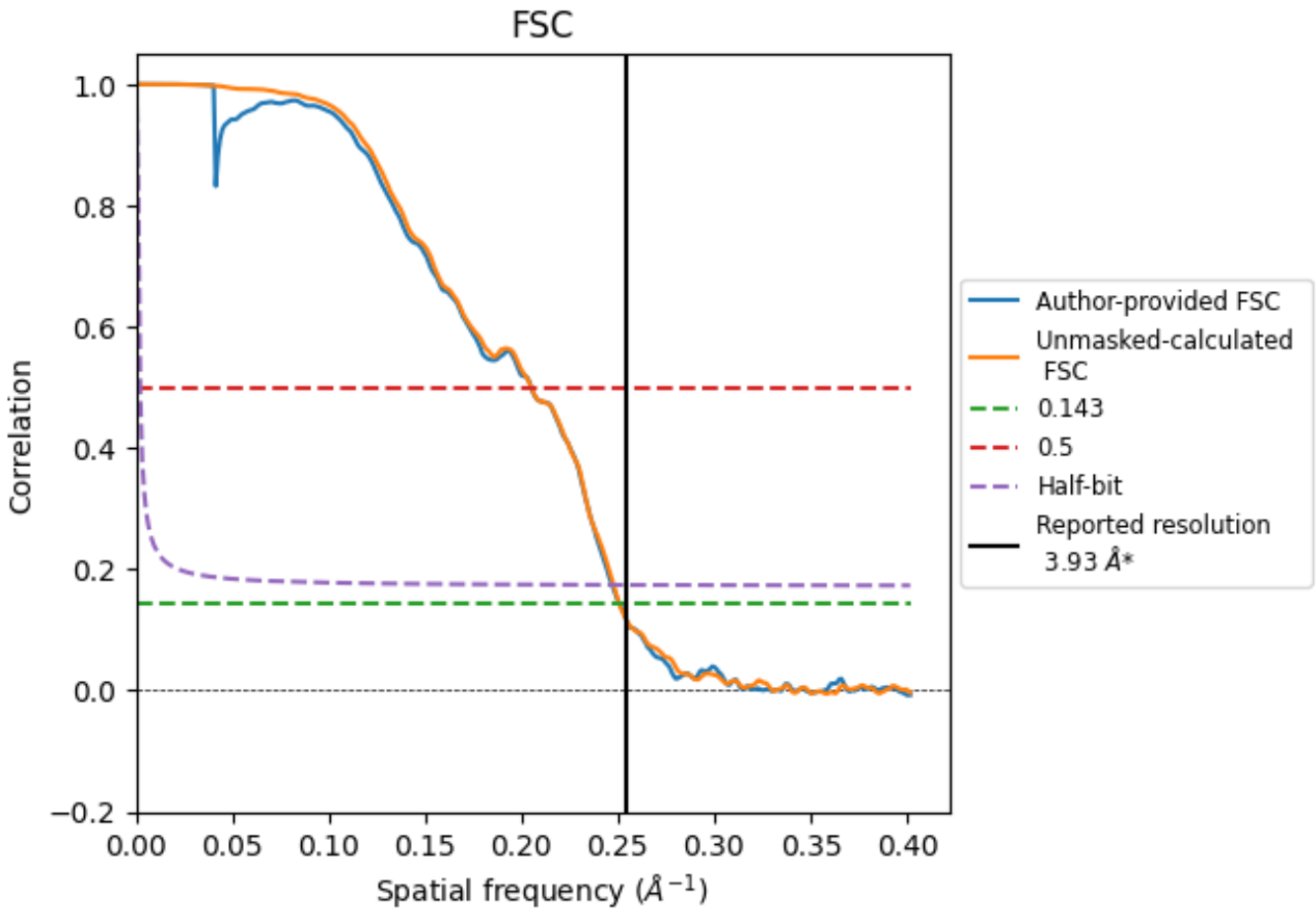


*Reported resolution corresponds to spatial frequency of 0.254 Å^{-1}

8 Fourier-Shell correlation (i)

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 (i)



*Reported resolution corresponds to spatial frequency of 0.254 Å^{-1}

8.2 Resolution estimates (i)

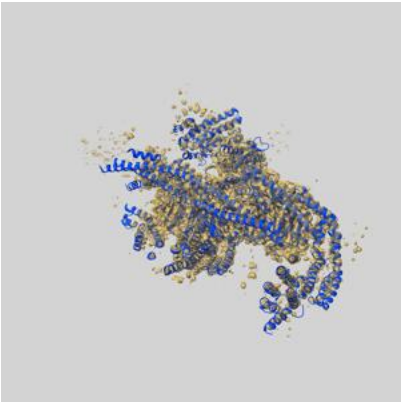
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.93	-	-
Author-provided FSC curve	3.99	4.88	4.05
Unmasked-calculated*	3.99	4.88	4.04

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

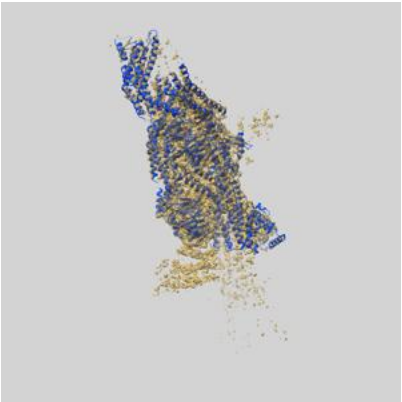
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-14553 and PDB model 7Z8J. Per-residue inclusion information can be found in section 3 on page 5.

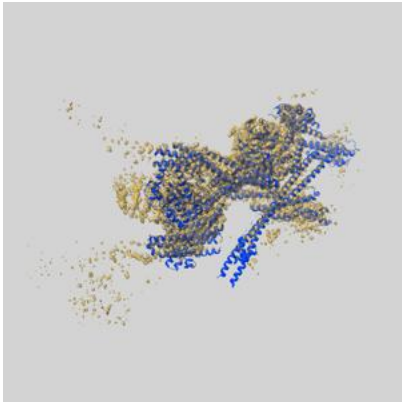
9.1 Map-model overlay (i)



X



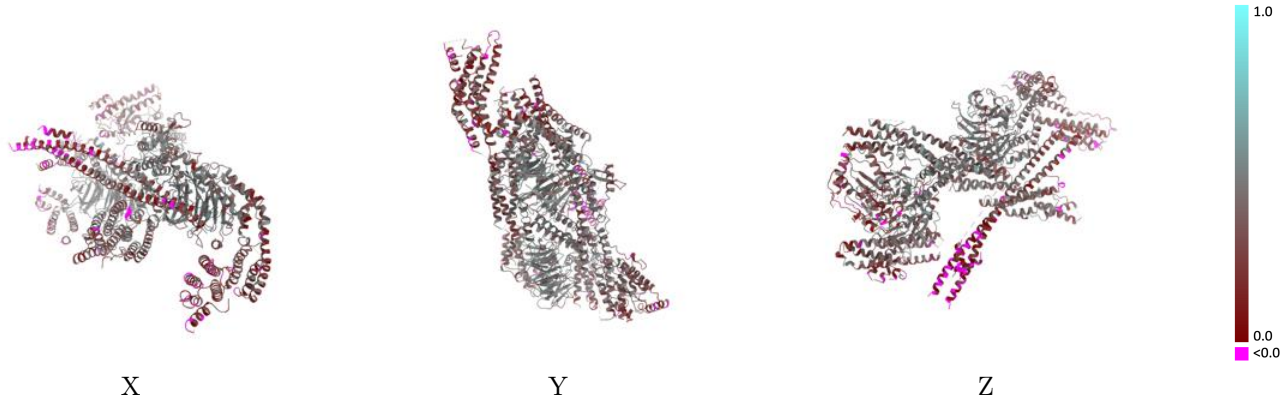
Y



Z

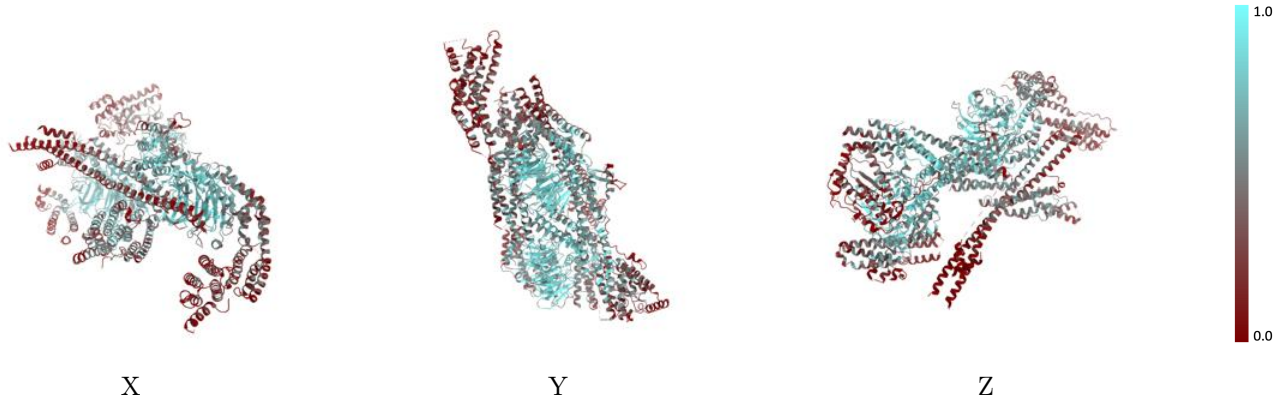
The images above show the 3D surface view of the map at the recommended contour level 0.00128 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



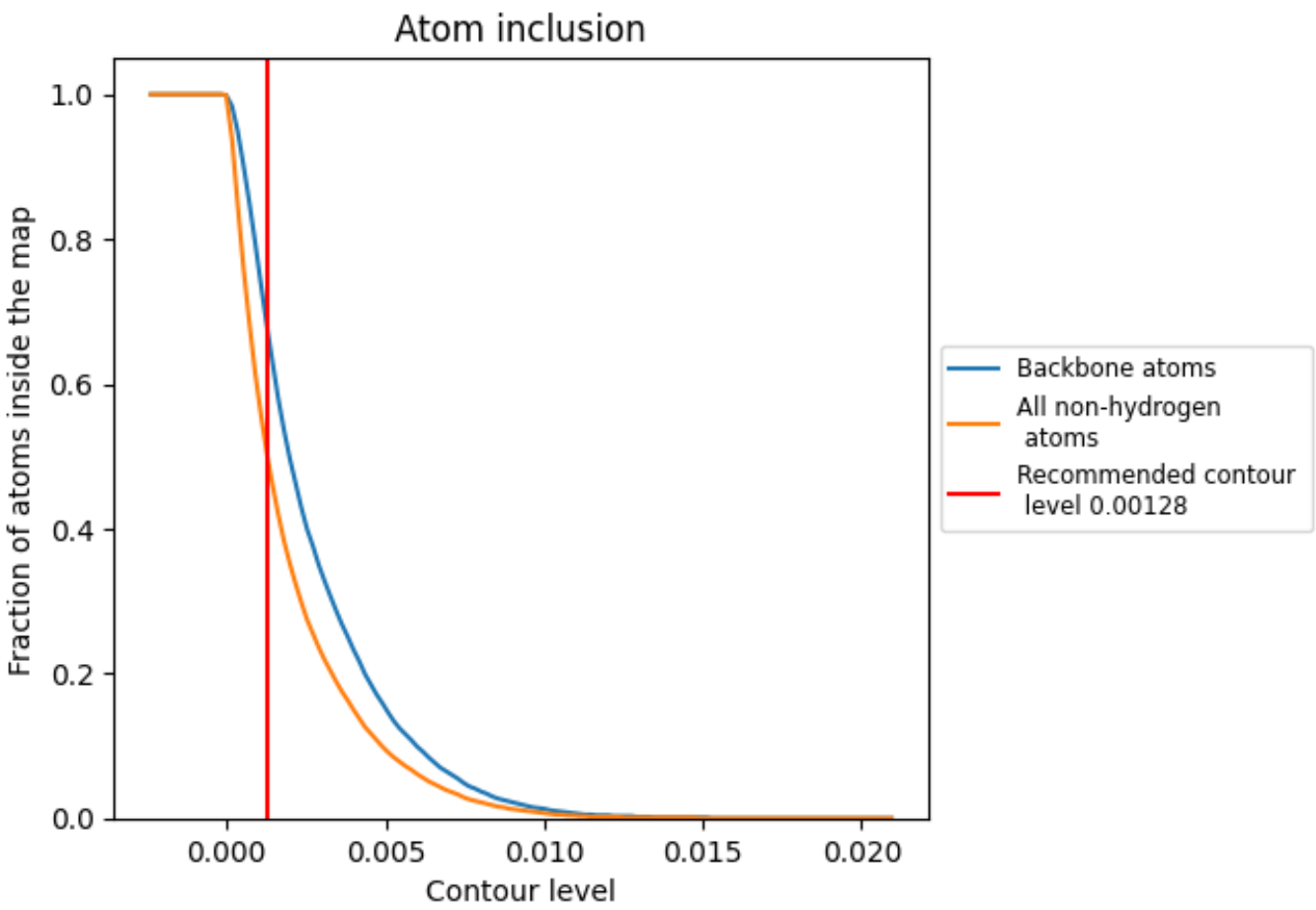
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00128).

9.4 Atom inclusion (i)



At the recommended contour level, 68% of all backbone atoms, 50% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.00128) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4990	0.3640
X	0.2690	0.2190
f	0.4550	0.3510
h	0.7210	0.4520
j	0.2100	0.2700
m	0.5350	0.3820
n	0.2230	0.2710
o	0.7800	0.4690
r	0.0000	0.1370
x	0.1900	0.2020