wwPDB EM Validation Summary Report (i)

Mar 9, 2026 – 07:02 PM UTC

PDB ID	:	6LTH / pdb_00006lth
EMDB ID	:	EMD-0968
Title	:	Structure of human BAF Base module
Authors	:	He, S.; Wu, Z.; Tian, Y.; Yu, Z.; Yu, J.; Wang, X.; Li, J.; Liu, B.; Xu, Y.
Deposited on	:	2020-01-22
Resolution	:	3.00 Å(reported)

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

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

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

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

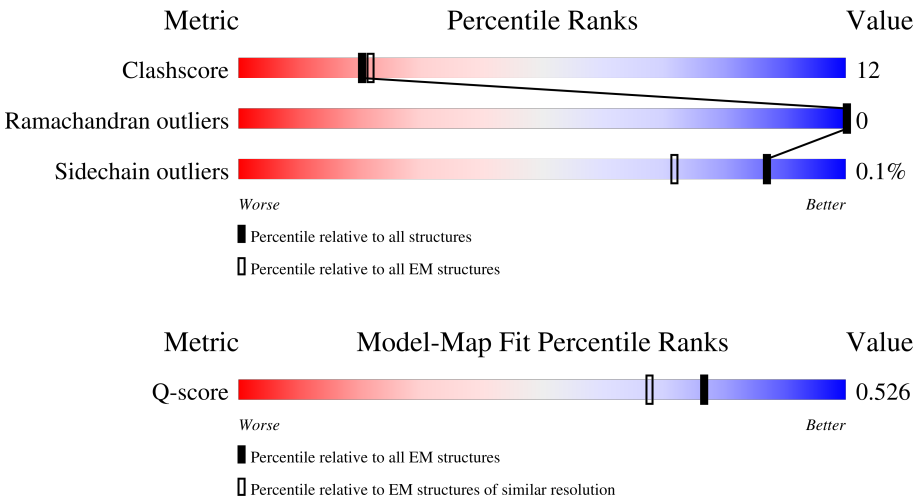
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14081 (2.50 - 3.50)

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

Mol	Chain	Length	Quality of chain
1	I	1647	5% • 93%
2	L	2285	15% 6% 80%
3	M	385	51% 16% 33%
4	N	1214	14% 8% 79%

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Mol	Chain	Length	Quality of chain
4	O	1214	19% 8% 73%
5	P	515	5% 30% 16% 54%
6	Q	411	10% 17% 9% 74%
7	R	391	13% 5% 82%

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 14970 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 Transcription activator BRG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	I	120	1022	632	208	180	2	0	0

- Molecule 2 is a protein called AT-rich interactive domain-containing protein 1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	L	466	3670	2341	620	688	21	0	0

- Molecule 3 is a protein called SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	M	259	2070	1318	341	401	10	0	0

- Molecule 4 is a protein called SWI/SNF complex subunit SMARCC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	N	261	2120	1346	374	388	12	0	0
4	O	325	2632	1676	458	485	13	0	0

- Molecule 5 is a protein called SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	P	239	2015	1281	362	361	11	0	0

- Molecule 6 is a protein called SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	Q	105	860	530	161	165	4	0	0

- Molecule 7 is a protein called Zinc finger protein ubi-d4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	R	70	580	361	112	102	5	0	0

- Molecule 8 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

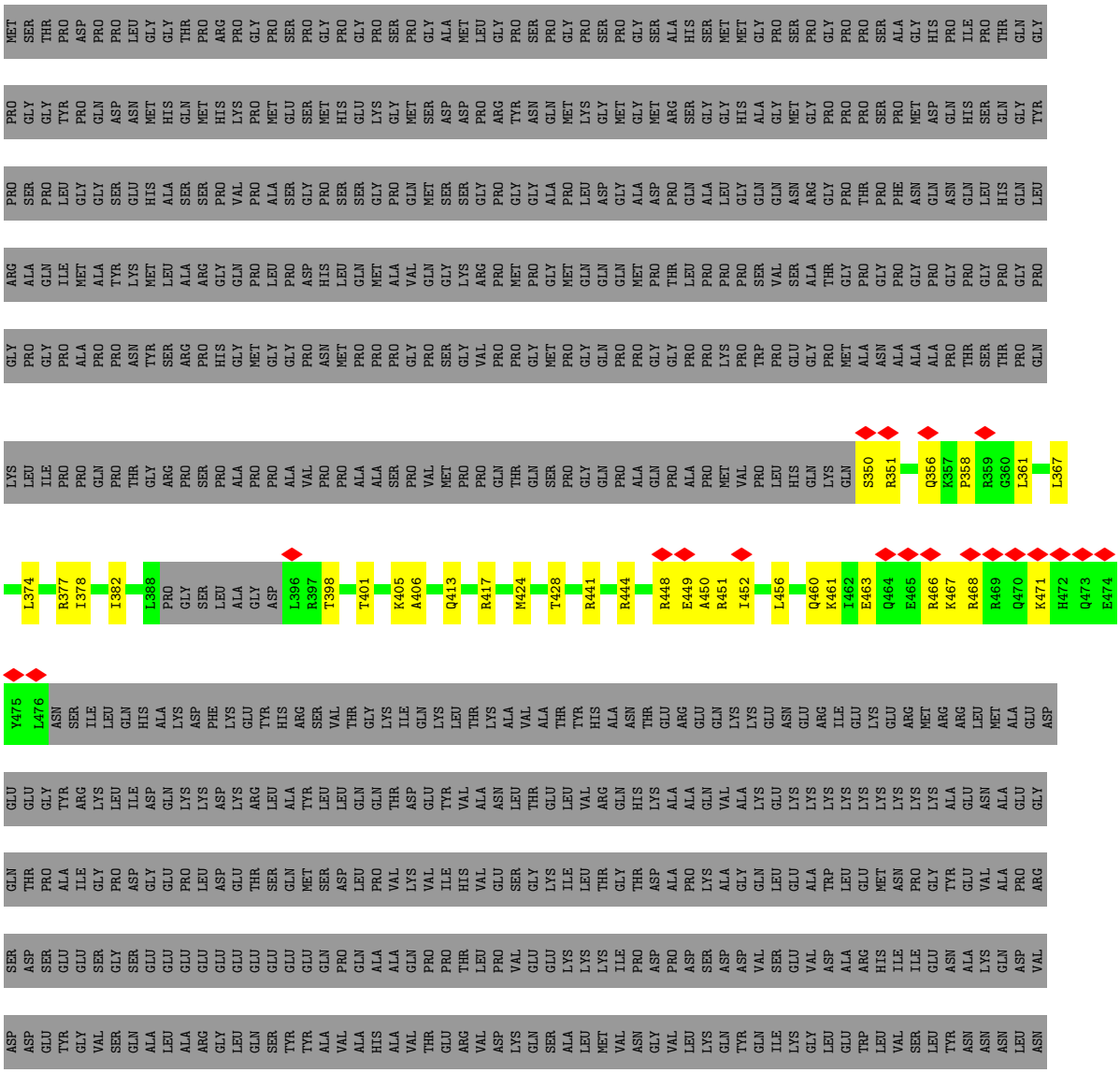
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
8	L	1	1	1	0

3 Residue-property plots (i)

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

- Molecule 1: Transcription activator BRG1

Chain I: 5% 93%



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

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

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

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

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

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

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

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

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

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

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

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

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

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

ARG PRO SER ARG GLY SER ARG ALA LYS PRO VAL VAL SER ASP ASP ASP SER GLU GLU GLU GLN GLU GLU ASP ARG SER GLY SER GLY SER GLU GLU ASP

• Molecule 2: AT-rich interactive domain-containing protein 1A

Chain L:

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

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

PRO GLY GLY GLY GLY GLY SER SER ASP GLY VAL GLY ALA PRO PRO HIS SER ALA ALA ALA ALA LEU PRO PRO PRO ALA TYR GLY PHE GLY GLN PRO TYR GLY ARG SER PRO SER ALA VAL ALA ALA ALA ALA ALA ALA VAL PHE HIS GLN GLN HIS GLY GLY GLN GLN SER PRO GLY

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

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

SER PRO SER SER ALA ARG GLY TYR GLN GLY TYR PRO GLY GLY ASP TYR SER GLY GLY PRO GLN ASP GLY GLY ALA GLY LYS GLY PRO ALA ASP MET ALA SER GLN CYS TRP GLY ALA ALA ALA ALA ALA ALA ALA ALA ALA ALA ALA SER GLY GLY ALA GLN GLN ARG SER HIS HIS ALA

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

PRO TYR GLY SER GLN THR PRO GLN ARG TYR PRO MET THR MET GLN GLY ARG ALA GLN SER ALA MET GLY GLY LEU SER TYR THR GLN GLN ILE PRO PRO TYR GLY GLN GLN GLY PRO SER GLY TYR GLY GLN GLN GLY GLN THR PRO TYR TYR ASN GLN GLN SER PRO HIS PRO GLN GLN

GLN GLN PRO PRO TYR SER GLN GLN PRO PRO SER GLN THR PRO HIS ALA GLN PRO SER TYR GLN GLN GLN PRO GLN SER GLN PRO PRO GLN LEU GLN SER SER GLN PRO PRO TYR SER GLN GLN PRO SER GLN PRO PRO HIS GLN GLN SER PRO ALA PRO TYR PRO SER GLN GLN SER THR

THR GLN GLN HIS PRO GLN SER GLN PRO PRO TYR SER GLN PRO GLN ALA GLN SER PRO TYR GLN GLN GLN GLN PRO GLN GLN PRO ALA PRO SER THR LEU SER GLN GLN ALA ALA TYR PRO GLN PRO GLN SER GLN GLN SER GLN GLN THR ALA TYR SER GLN GLN ARG PHE PRO PRO PRO

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

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

GLY ASN GLN MET PRO PRO ARG PRO PRO SER GLY GLN SER ASP SER ILE MET HIS PRO SER MET ASN GLN SER SER ILE ALA GLN ASP ARG GLY TYR MET GLN ARG ASN PRO GLN MET PRO GLN TYR SER SER PRO GLN PRO GLY SER ALA LEU SER PRO ARG GLN PRO SER GLY GLY GLN

ILE HIS THR GLY MET GLY SER TYR GLN GLN ASN SER MET GLY SER TYR GLY PRO GLN GLY GLY GLN TYR GLY PRO GLN GLY GLY TYR PRO ARG GLN PRO ASN TYR ASN ALA LEU PRO ASN ALA ASN TYR PRO SER ALA GLY MET ALA GLY GLY ILE ASN PRO MET GLY ALA GLY GLY GLN

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

MET HIS VAL ALA ALA ASN SER ILE GLN ASN ARG PRO PRO GLY TYR PRO ASN MET ASN GLN GLY GLY MET MET GLY THR GLY PRO PRO TYR GLY GLN GLY ILE ASN SER MET ALA GLY MET ILE ASN PRO GLN GLY PRO PRO TYR SER MET GLY GLY THR MET ALA ASN ASN SER ALA GLY

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

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

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

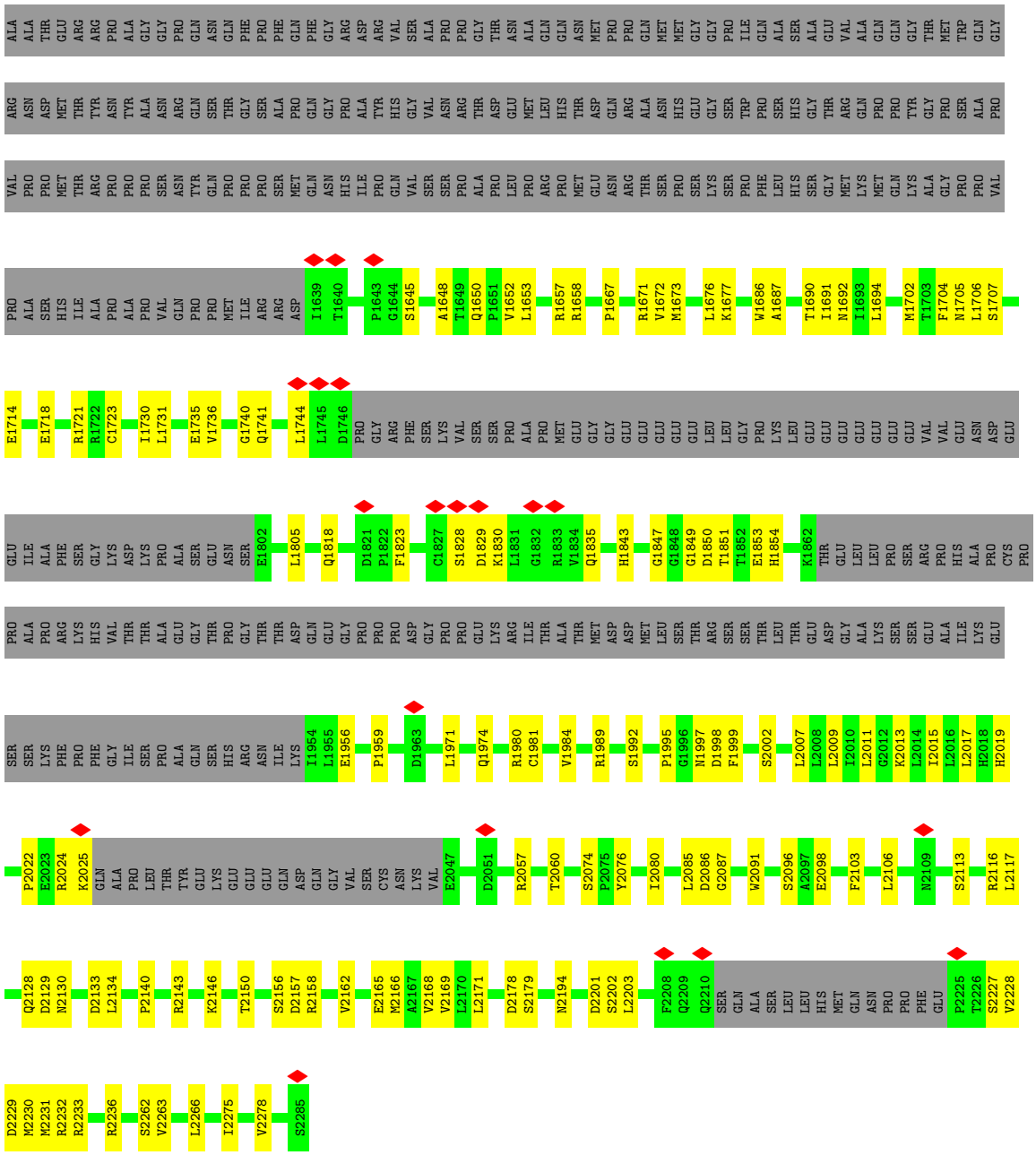
MET GLN GLY PRO GLN THR PRO GLN SER THR SER SER SER MET ALA GLU GLY GLY ASP LEU LYS PRO PRO THR PRO ALA SER THR PRO HIS SER GLN ILE PRO PRO LEU PRO GLY MET SER ARG SER ASN SER VAL GLY ILE GLN ASP ALA PHE ASN ASP GLY SER ASP SER THR PHE GLN

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

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

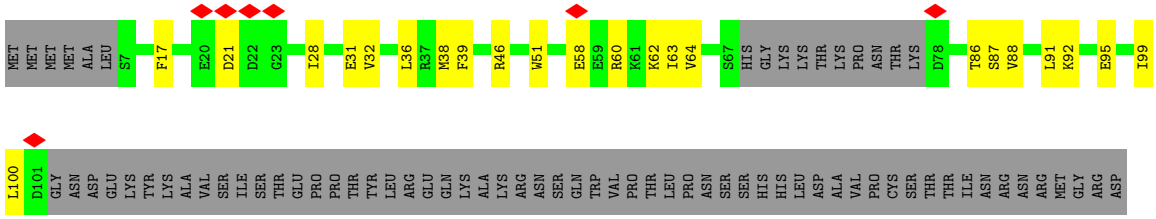
PRO SER ARG TYR PRO PRO GLN GLN GLN GLN GLN GLN GLN GLN ARG HIS ASP SER TYR GLY ASN GLN PHE SER THR GLN GLY THR PRO SER GLY SER PRO PHE PRO SER GLN GLN THR THR MET TYR GLN GLN GLN GLN GLN ASN TYR LYS ARG PRO MET ASP GLY THR TYR GLY PRO PRO

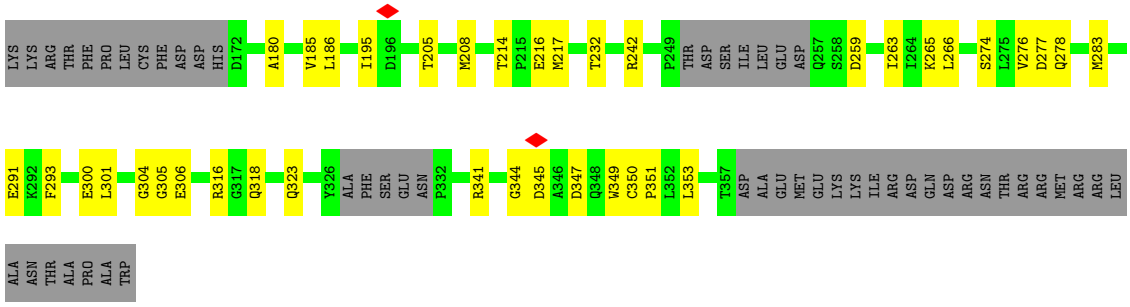
ALA LYS ARG HIS GLU GLY GLU MET TYR SER VAL PRO TYR SER THR GLY GLN GLY GLN PRO GLN GLN GLN GLN LEU PRO PRO ALA GLN PRO GLN PRO ALA SER GLN GLN GLN ALA ALA GLN PRO SER PRO GLN GLN ASP VAL TYR ASN GLN TYR GLY ASN ALA TYR PRO ALA THR ALA THR



• Molecule 3: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1

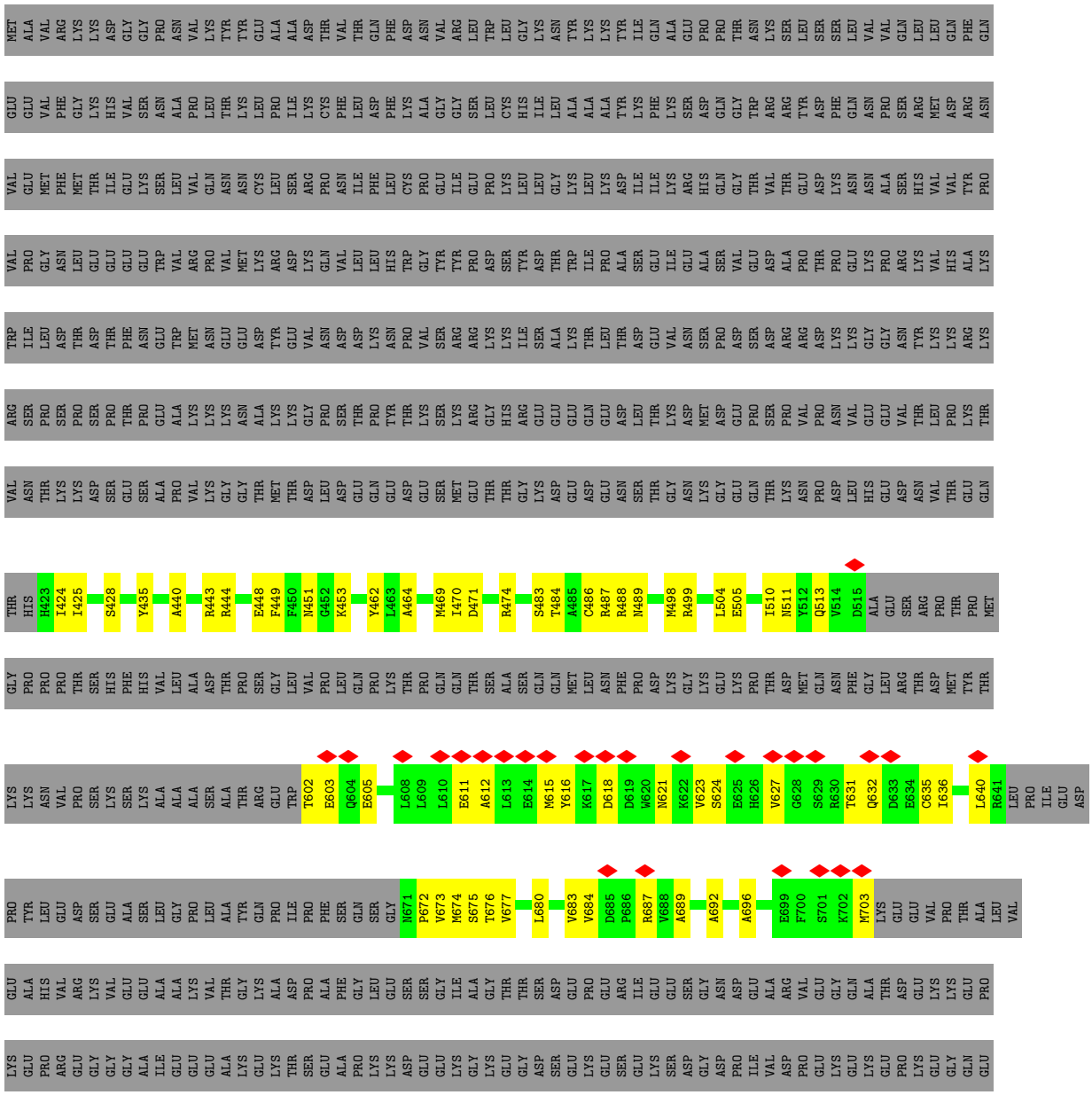
Chain M:

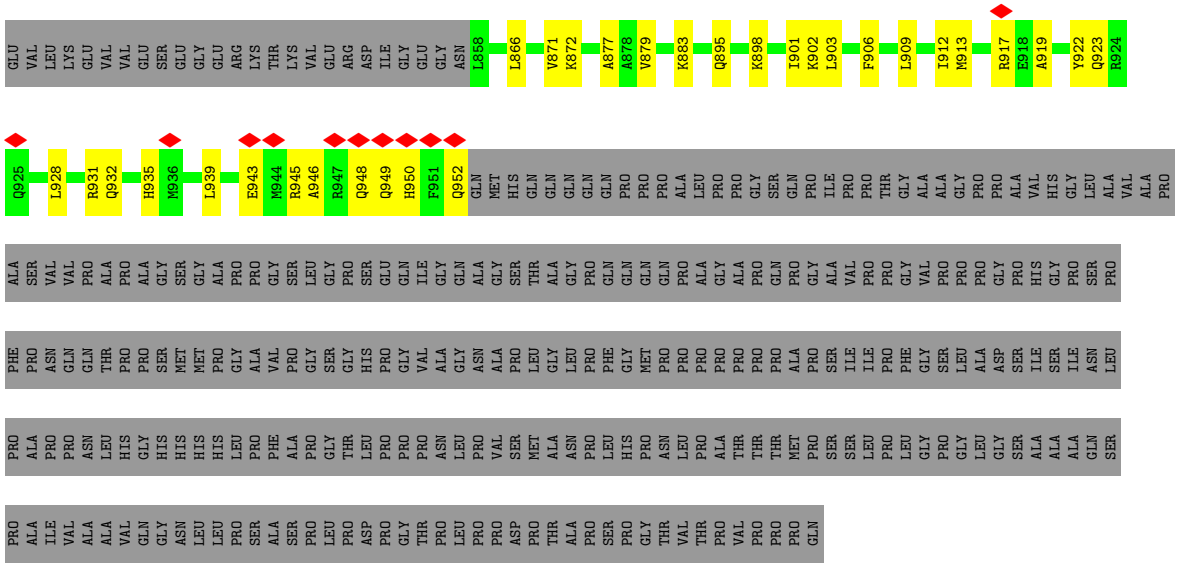




- Molecule 4: SWI/SNF complex subunit SMARCC2

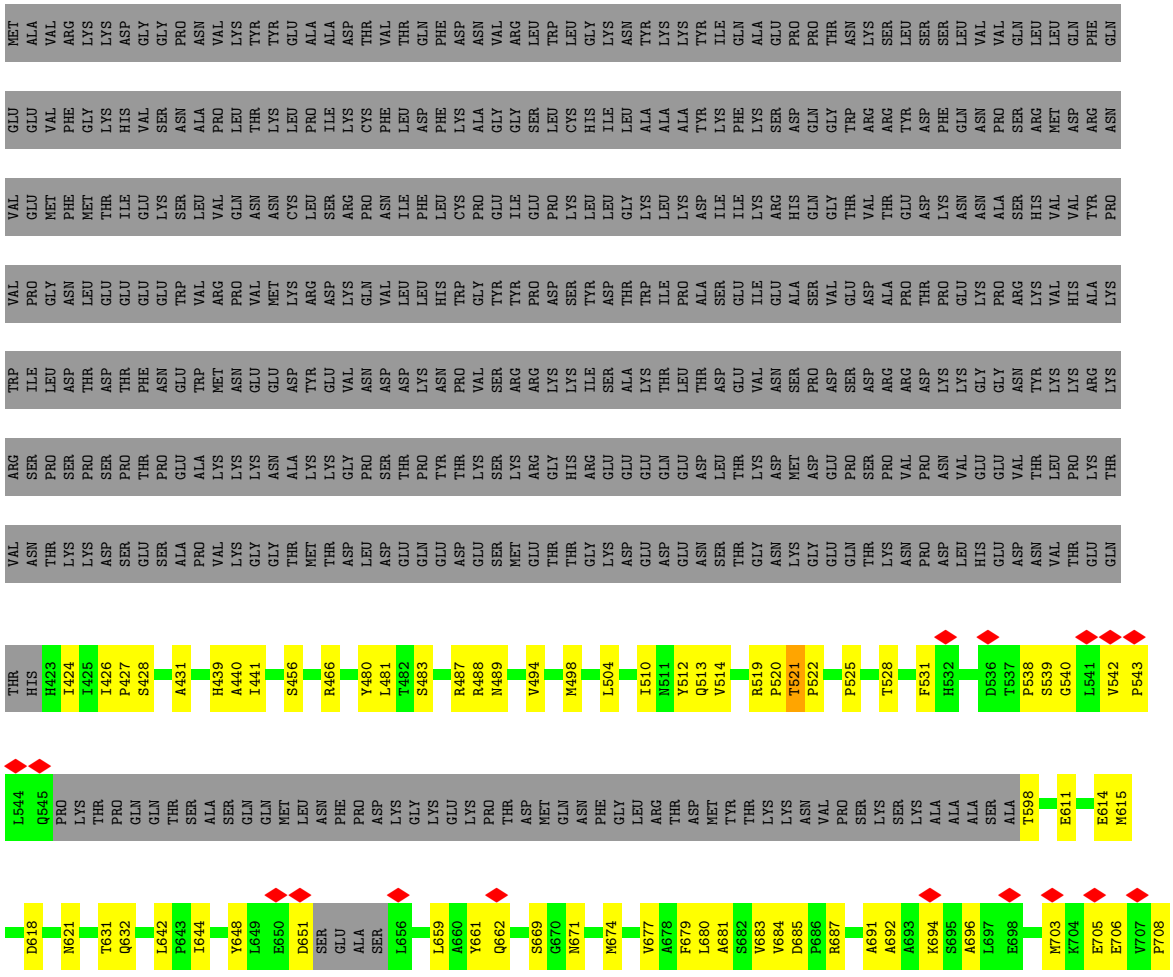
Chain N: 14% 8% 79%

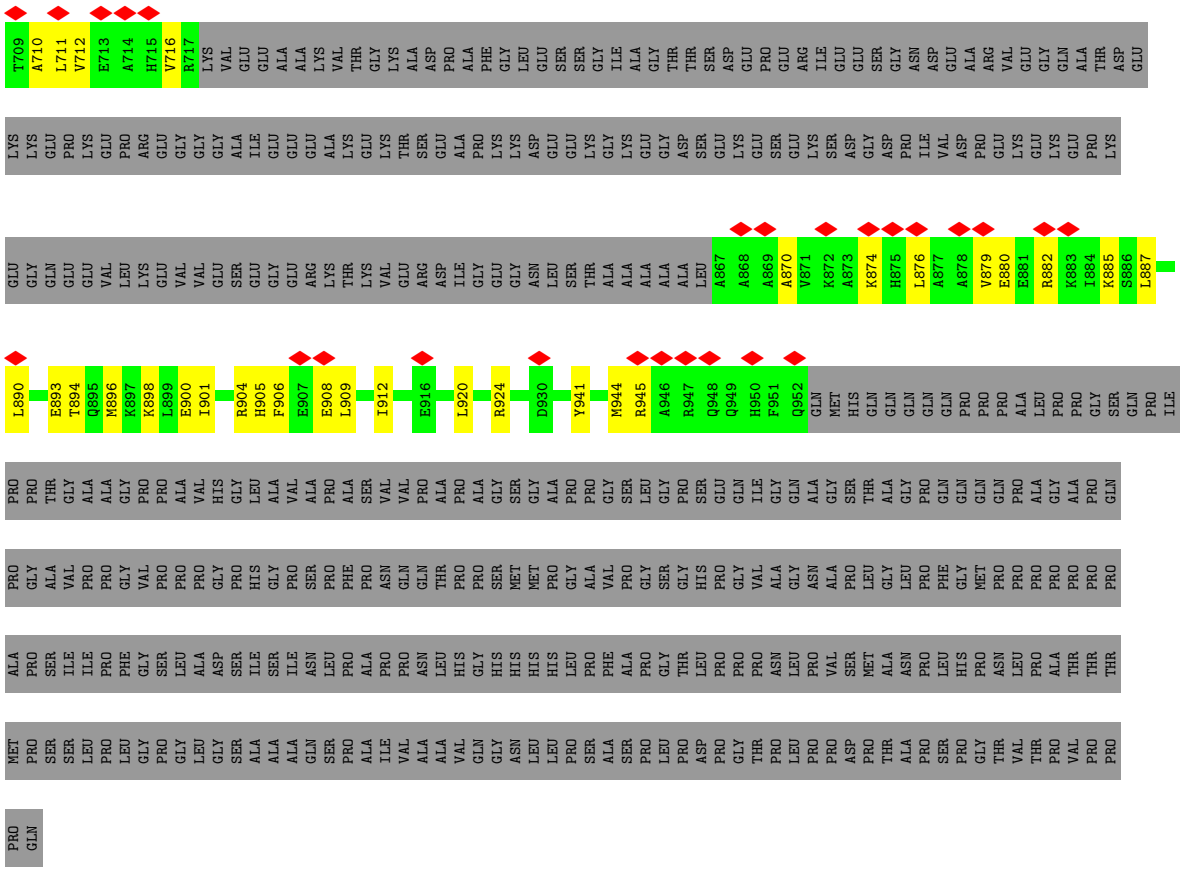




- Molecule 4: SWI/SNF complex subunit SMARCC2

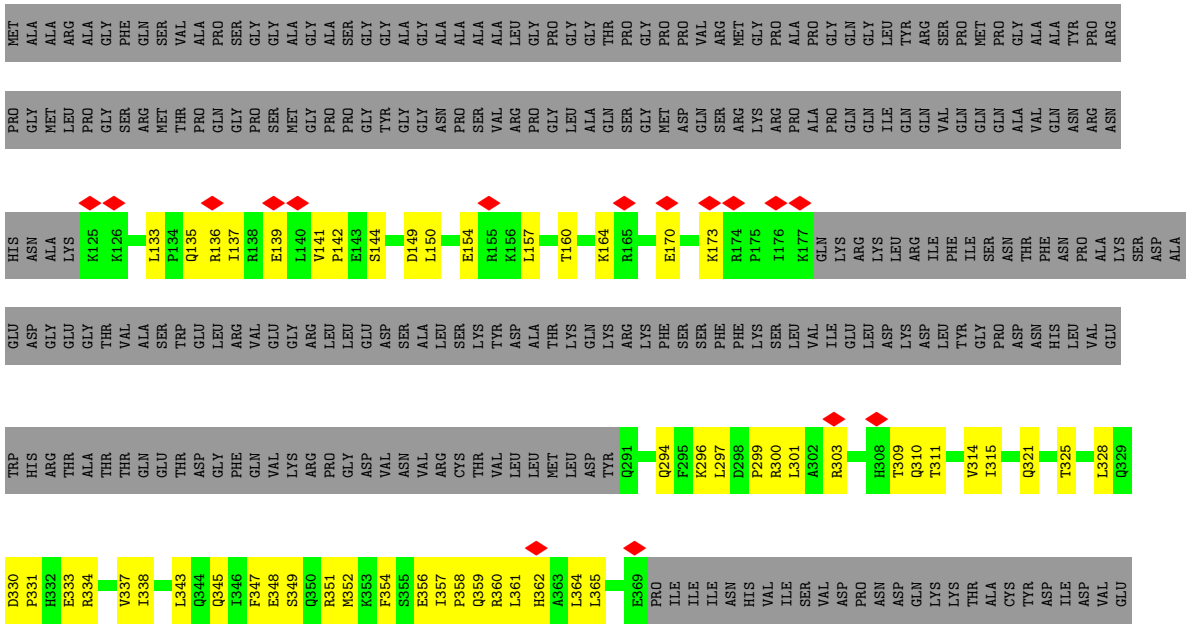
Chain O:

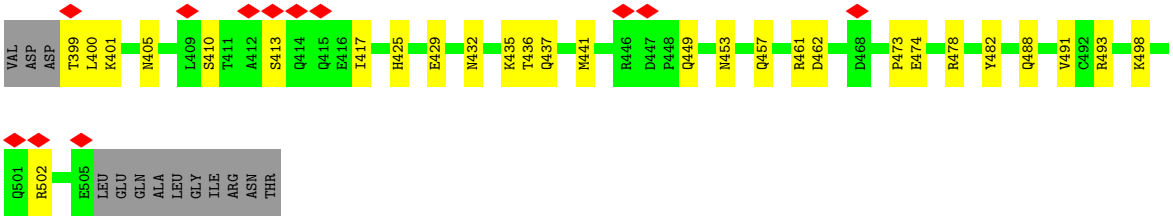




• Molecule 5: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1

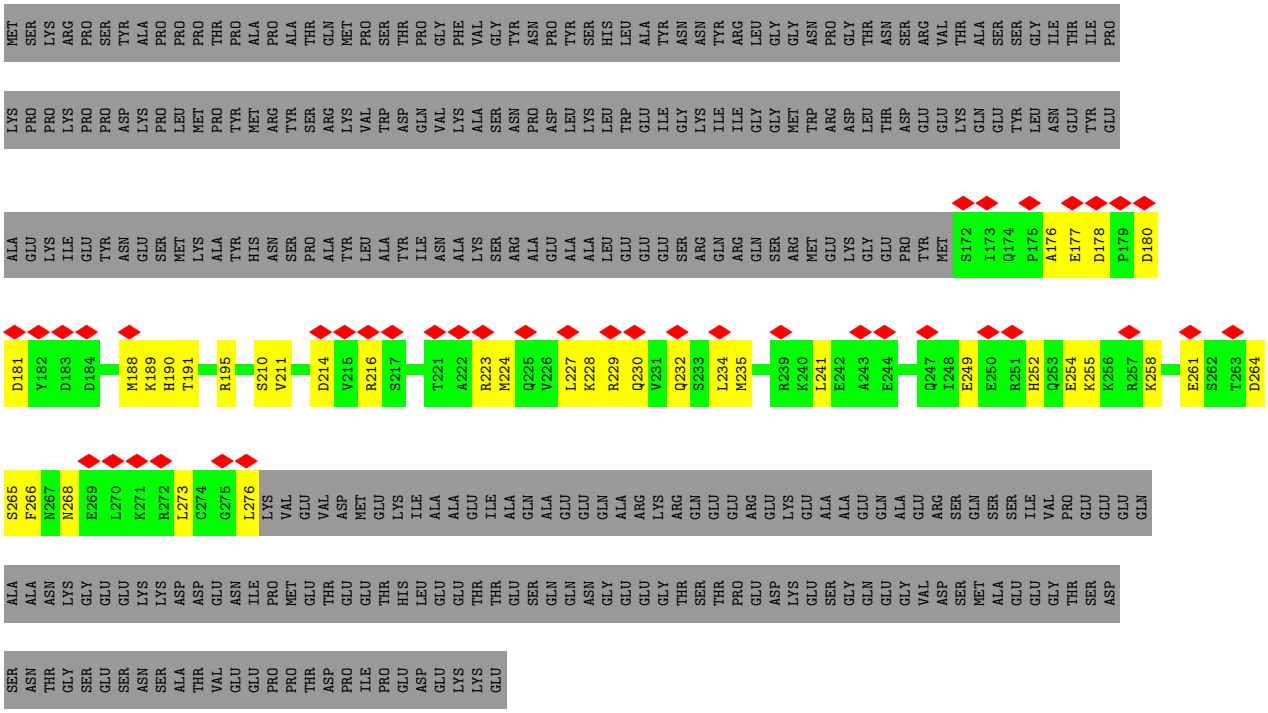
Chain P: 5% 30% 16% 54%





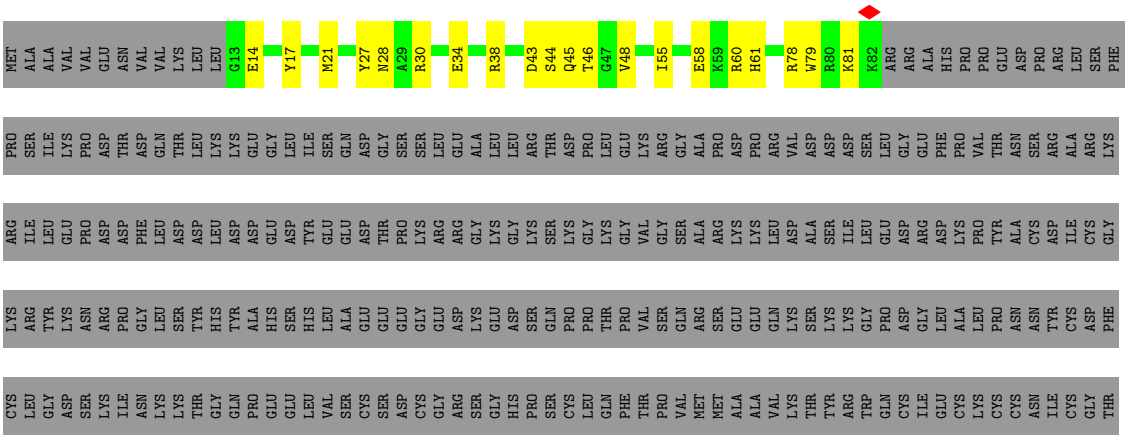
• Molecule 6: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1

Chain Q:



• Molecule 7: Zinc finger protein ubi-d4

Chain R:



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

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	197606	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 ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	4.938	Depositor
Minimum map value	-2.357	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.046	Depositor
Recommended contour level	1	Depositor
Map size (Å)	532.48, 532.48, 532.48	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	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: 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	I	0.24	0/1029	0.54	0/1370
2	L	0.25	0/3739	0.40	0/5070
3	M	0.26	0/2110	0.45	2/2856 (0.1%)
4	N	0.27	0/2158	0.44	0/2908
4	O	0.25	0/2692	0.46	0/3646
5	P	0.24	0/2055	0.45	0/2764
6	Q	0.24	0/871	0.49	0/1168
7	R	0.25	0/595	0.46	0/799
All	All	0.25	0/15249	0.45	2/20581 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	M	304	GLY	CA-C-N	-5.01	112.36	121.32
3	M	304	GLY	C-N-CA	-5.01	112.36	121.32

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	I	1022	0	1092	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	L	3670	0	3724	92	0
3	M	2070	0	2036	43	0
4	N	2120	0	2116	81	0
4	O	2632	0	2606	95	0
5	P	2015	0	2046	71	0
6	Q	860	0	864	31	0
7	R	580	0	557	20	0
8	L	1	0	0	0	0
All	All	14970	0	15041	366	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 12.

The worst 5 of 366 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)
2:L:1818:GLN:HA	4:O:428:SER:HB3	1.49	0.93
2:L:2263:VAL:HG22	5:P:358:PRO:HD3	1.64	0.79
5:P:352:MET:HE3	5:P:360:ARG:HG2	1.63	0.79
2:L:2157:ASP:OD1	2:L:2158:ARG:N	2.17	0.77
4:N:612:ALA:O	4:N:616:TYR:HB2	1.85	0.77

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	I	116/1647 (7%)	113 (97%)	3 (3%)	0	100	100
2	L	456/2285 (20%)	434 (95%)	22 (5%)	0	100	100
3	M	249/385 (65%)	239 (96%)	10 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	N	253/1214 (21%)	247 (98%)	6 (2%)	0	100	100
4	O	317/1214 (26%)	303 (96%)	14 (4%)	0	100	100
5	P	233/515 (45%)	220 (94%)	13 (6%)	0	100	100
6	Q	103/411 (25%)	96 (93%)	7 (7%)	0	100	100
7	R	68/391 (17%)	61 (90%)	7 (10%)	0	100	100
All	All	1795/8062 (22%)	1713 (95%)	82 (5%)	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	I	110/1422 (8%)	110 (100%)	0	100	100
2	L	418/1845 (23%)	417 (100%)	1 (0%)	87	92
3	M	230/346 (66%)	230 (100%)	0	100	100
4	N	222/1030 (22%)	222 (100%)	0	100	100
4	O	282/1030 (27%)	281 (100%)	1 (0%)	84	90
5	P	223/442 (50%)	223 (100%)	0	100	100
6	Q	98/361 (27%)	98 (100%)	0	100	100
7	R	59/344 (17%)	59 (100%)	0	100	100
All	All	1642/6820 (24%)	1640 (100%)	2 (0%)	87	93

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	1692	ASN
4	O	521	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
5	P	135	GLN
5	P	457	GLN
5	P	321	GLN
5	P	405	ASN
6	Q	238	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

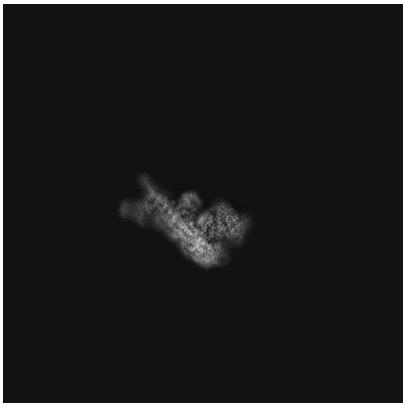
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-0968. These allow visual inspection of the internal detail of the map and identification of artifacts.

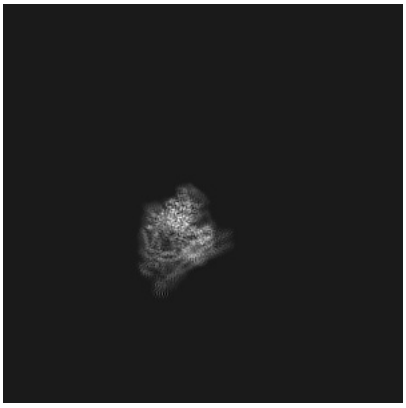
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

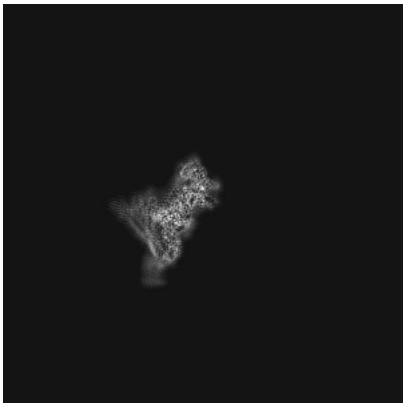
6.1.1 Primary map



X



Y

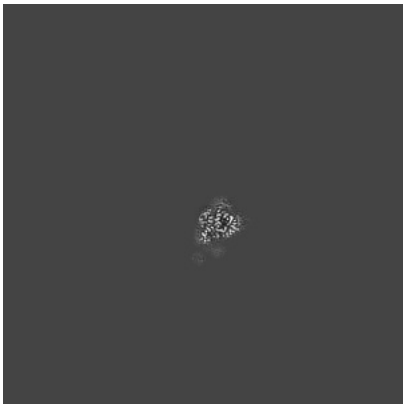


Z

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

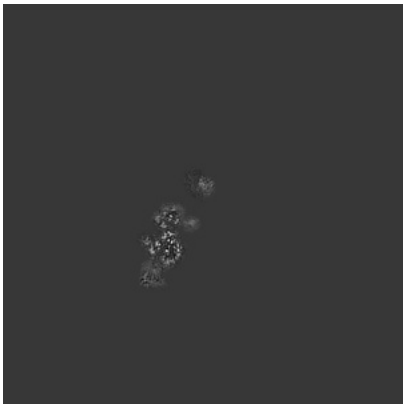
6.2 Central slices (i)

6.2.1 Primary map



X Index: 256

Y Index: 256

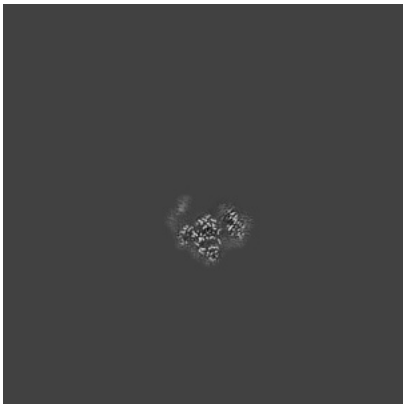


Z Index: 256

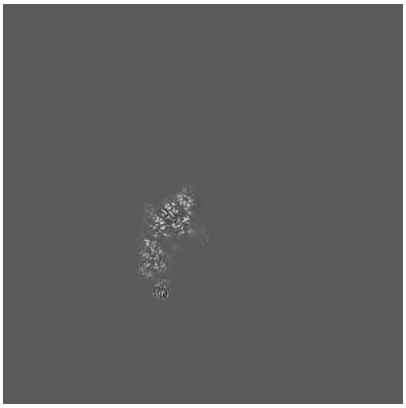
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

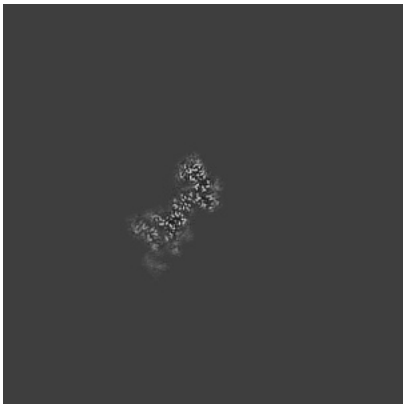
6.3.1 Primary map



X Index: 238



Y Index: 255

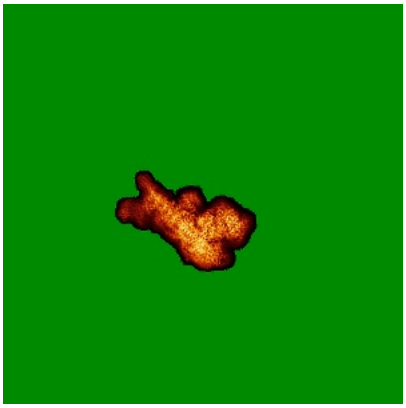


Z Index: 231

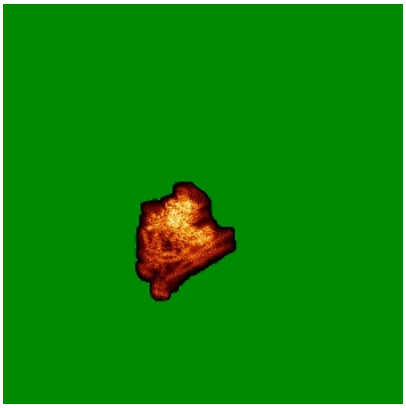
The images above show the largest variance slices of the map in three orthogonal directions.

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

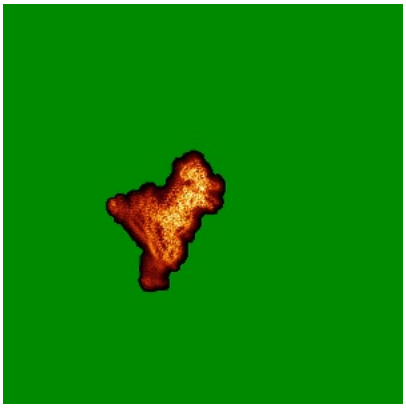
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views (i)

This section was not generated.

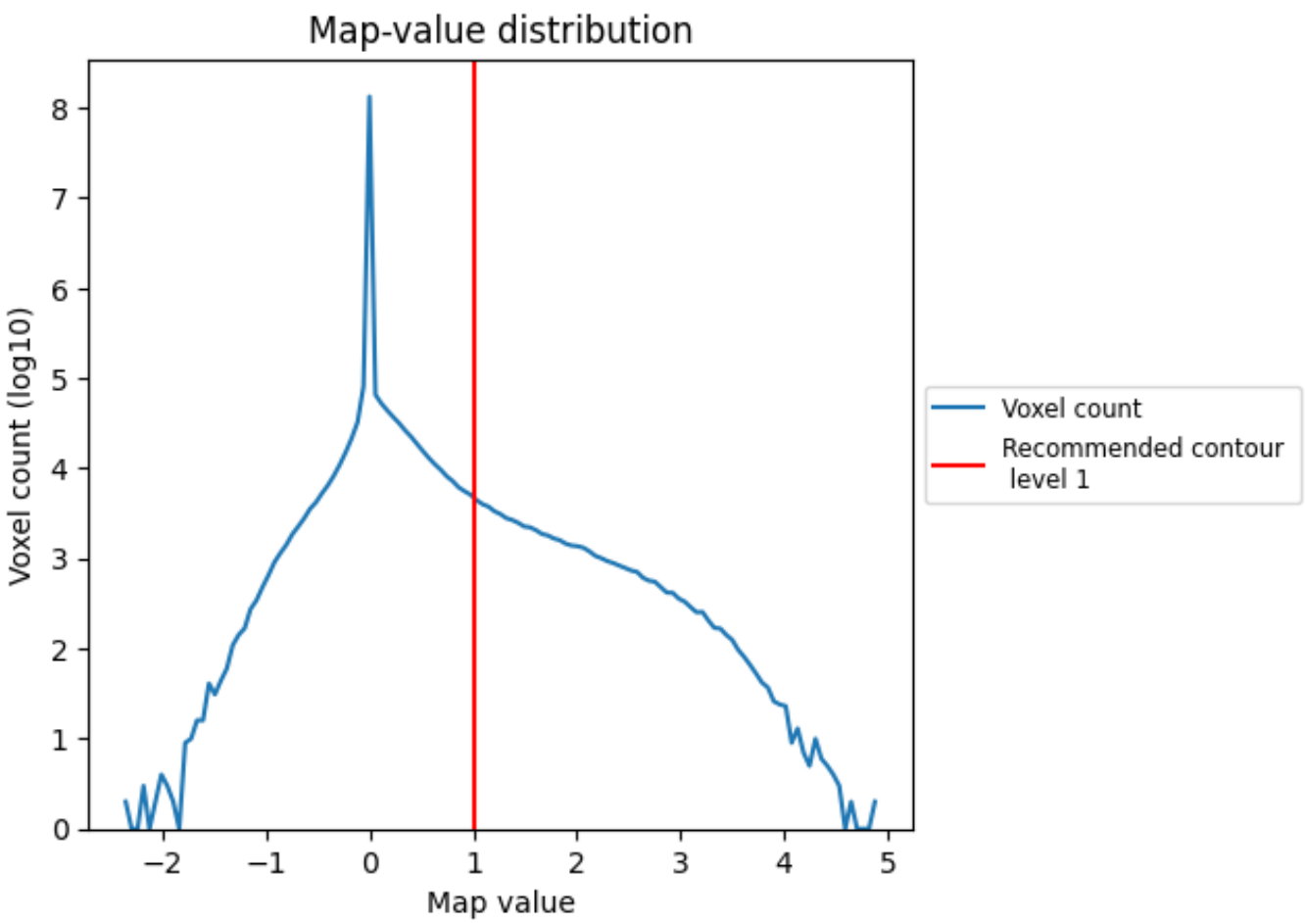
6.6 Mask visualisation (i)

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

7 Map analysis (i)

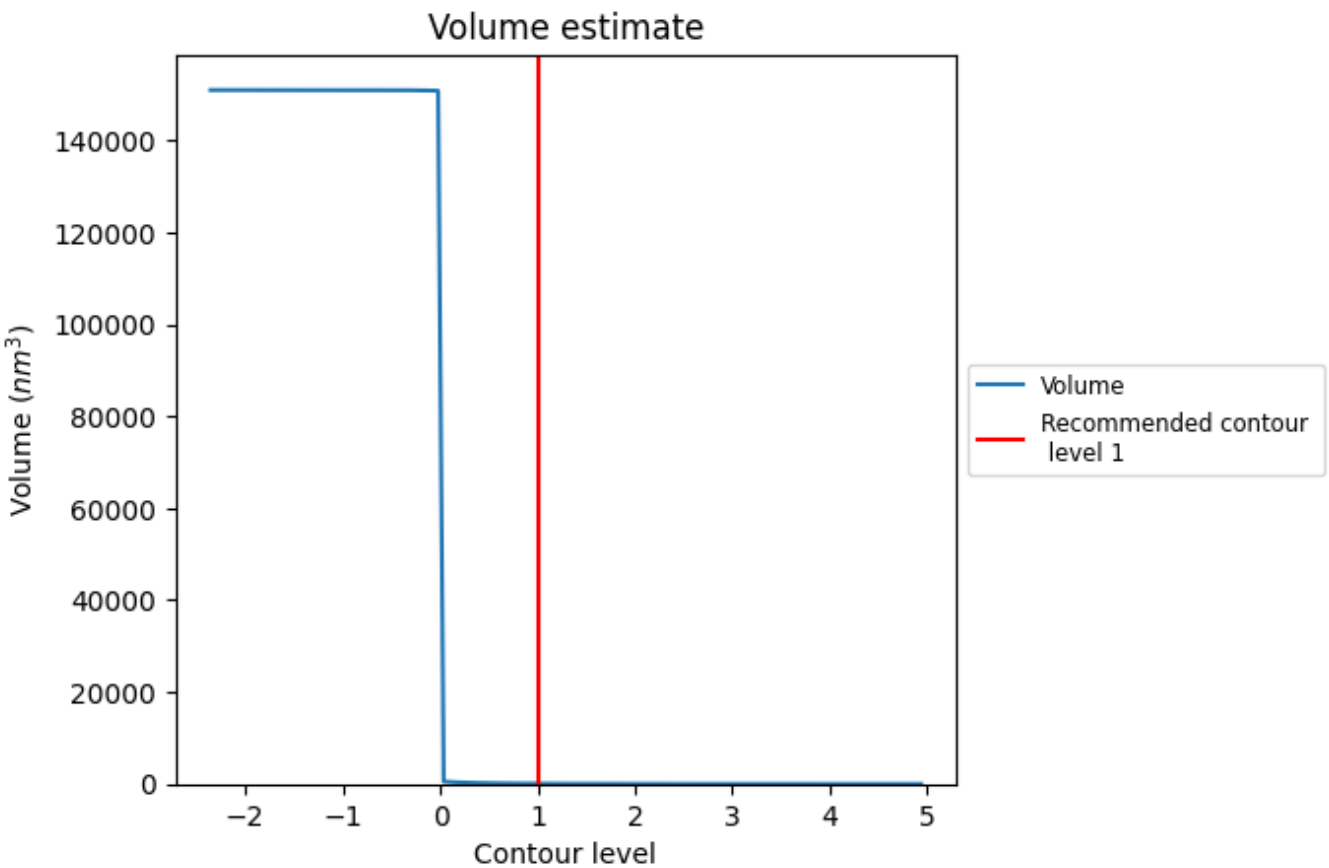
This section contains the results of statistical analysis of the map.

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.

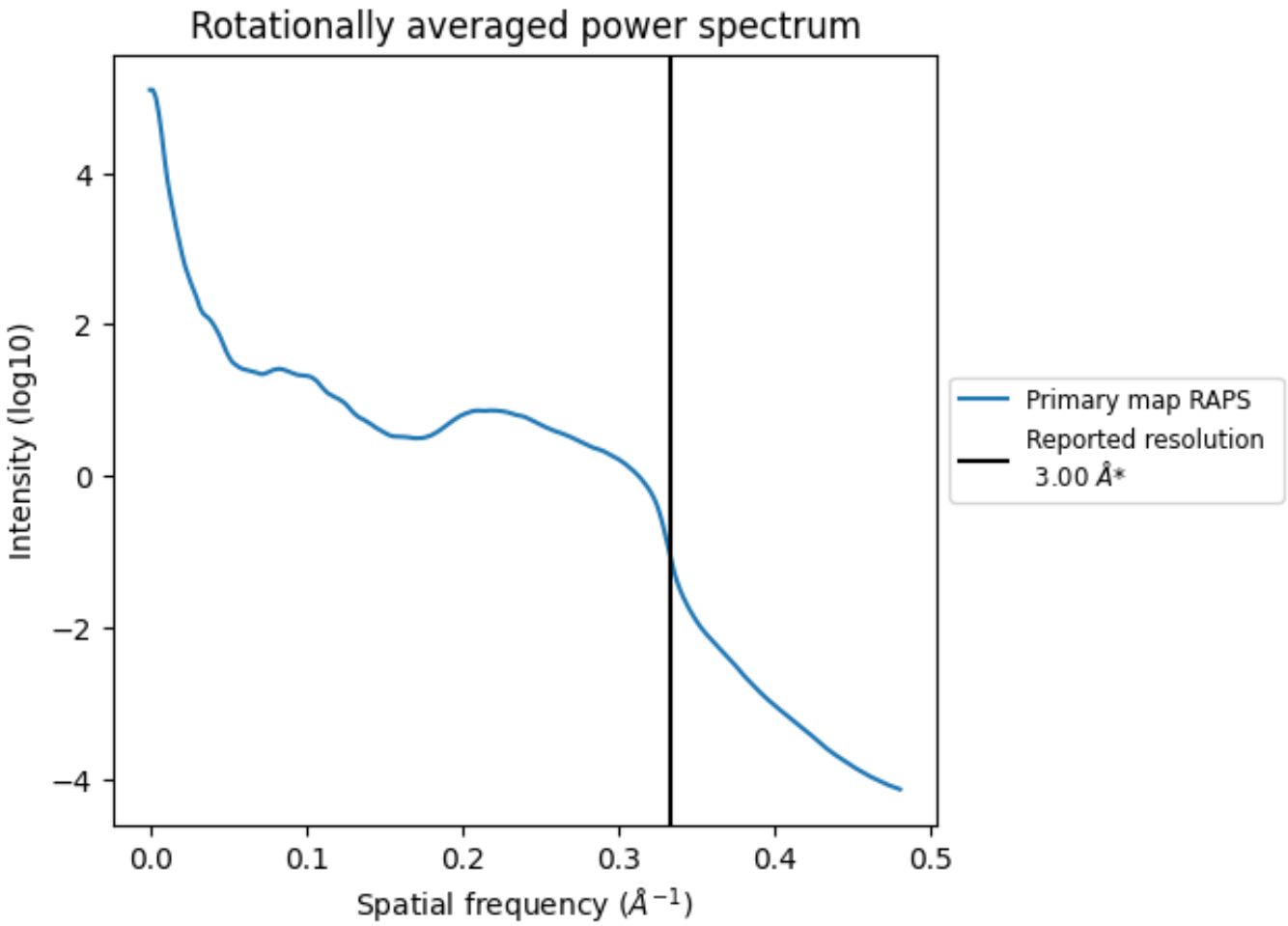
7.2 Volume estimate (i)



The volume at the recommended contour level is 70 nm^3; this corresponds to an approximate mass of 63 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 0.333 Å^{-1}

8 Fourier-Shell correlation (i)

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

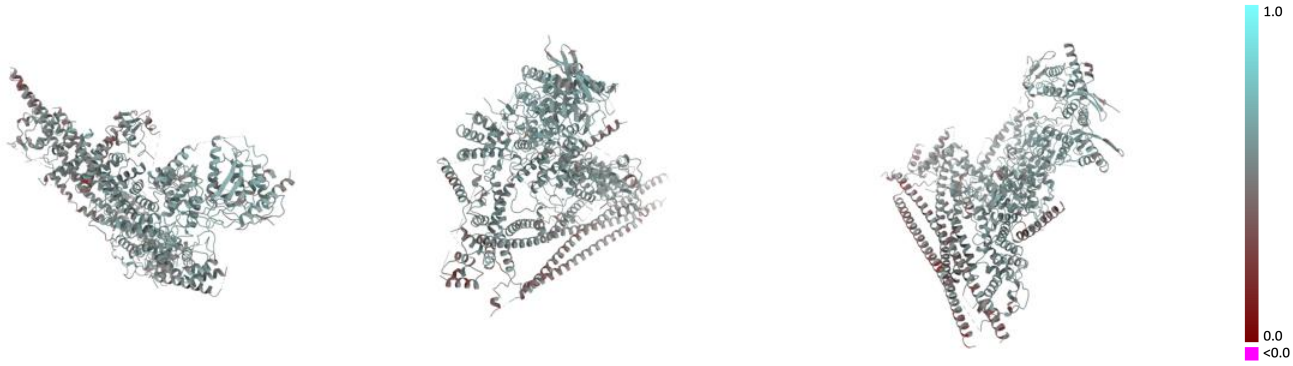
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-0968 and PDB model 6LTH. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay (i)

This section was not generated.

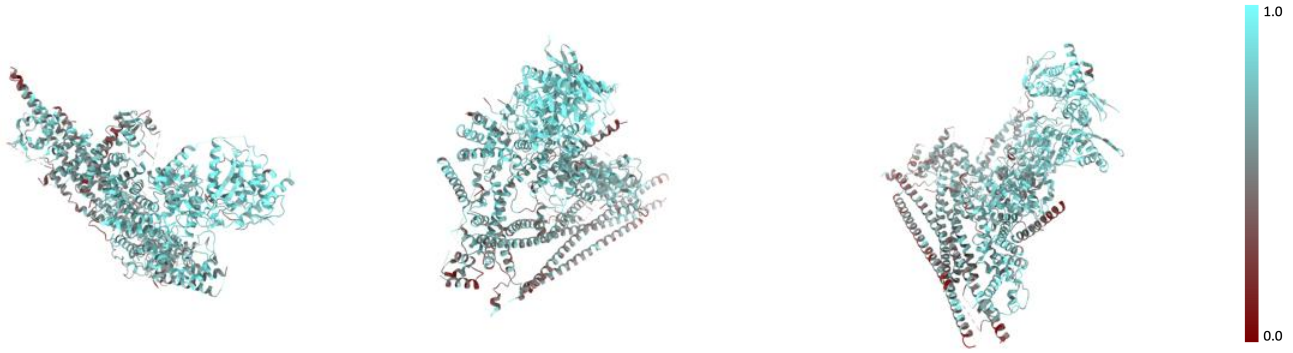
9.2 Q-score mapped to coordinate model (i)



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.

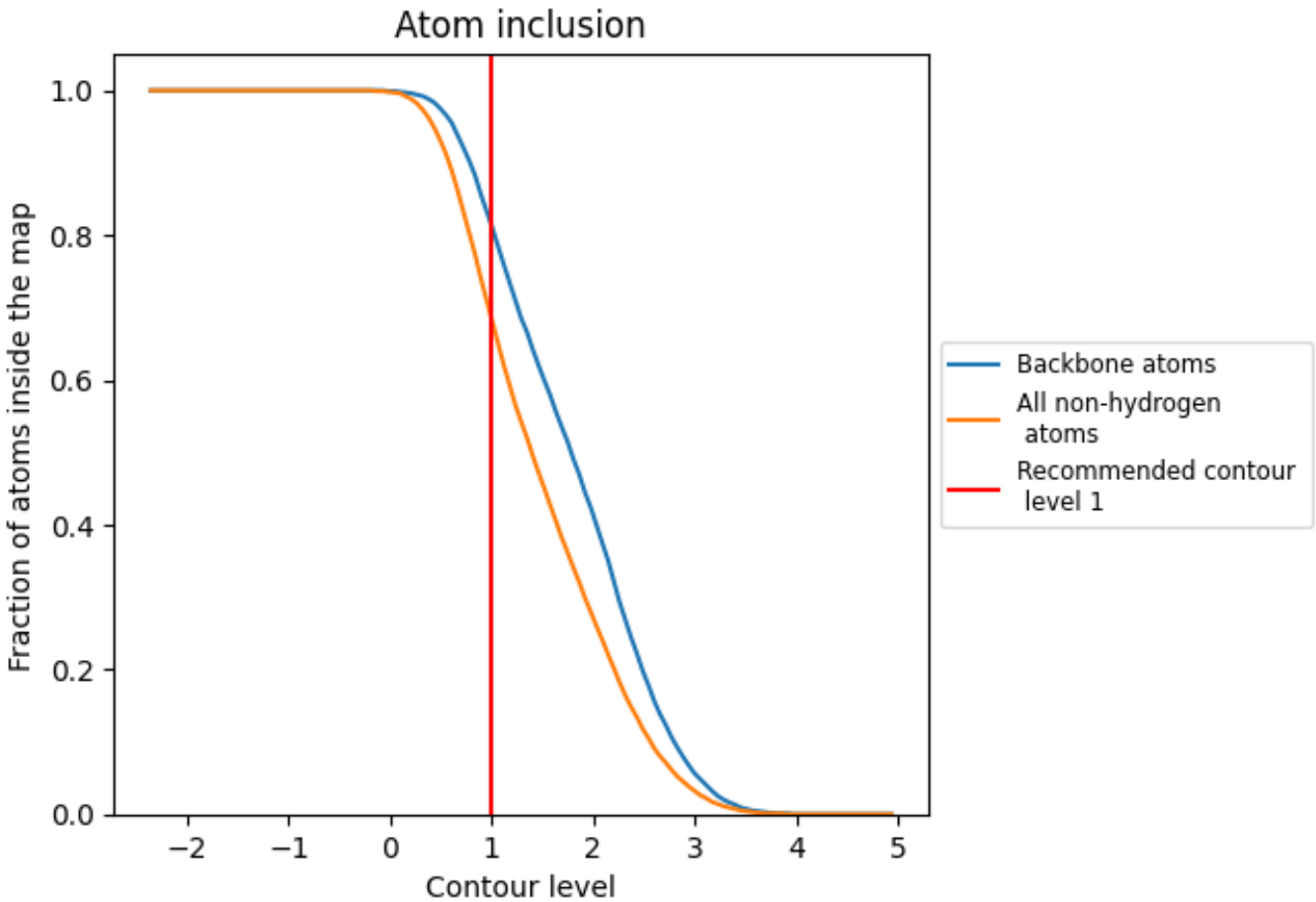
9.3 Atom inclusion mapped to coordinate model (i)



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 (1).

9.4 Atom inclusion (i)



At the recommended contour level, 81% of all backbone atoms, 68% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6830	0.5260
I	0.6160	0.4980
L	0.7200	0.5540
M	0.7340	0.5400
N	0.6610	0.5130
O	0.6820	0.5150
P	0.6630	0.5170
Q	0.5070	0.4540
R	0.8090	0.5670