wwPDB EM Validation Summary Report

May 25, 2025 – 01:43 PM EDT

PDB ID	:	6UXV / pdb_00006uxv
EMDB ID	:	EMD-20933
Title	:	SWI/SNF Body Module
Authors	:	He, Y.; Han, Y.
Deposited on	:	2019-11-08
Resolution	:	4.70 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:

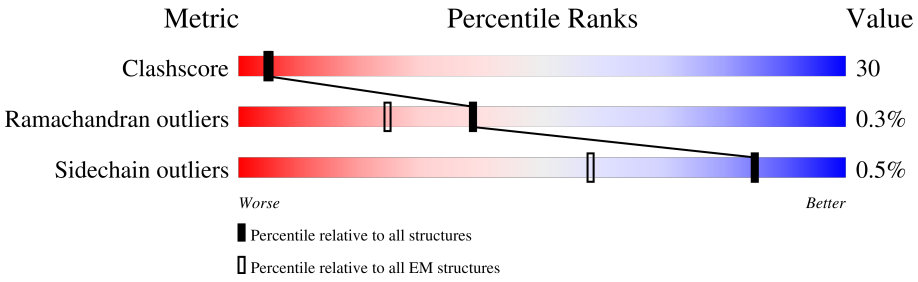
EMDB validation analysis	:	0.0.1.dev118
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.70 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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

Mol	Chain	Length	Quality of chain
1	A	1703	92%
2	B	1314	5% 15% 22% 63%
3	C	905	5% 10% 17% 73%
4	D	825	8% 11% 81%
4	E	825	8% 9% 83%
4	F	825	16% 11% 73%
4	G	825	14% 10% 76%
5	H	566	10% 19% 27% 55%

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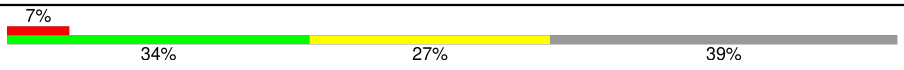
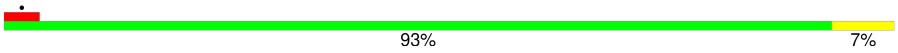
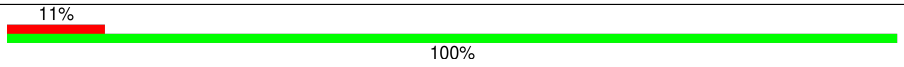
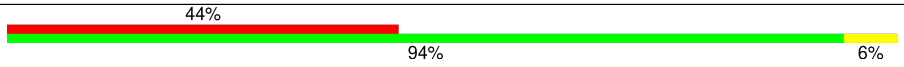
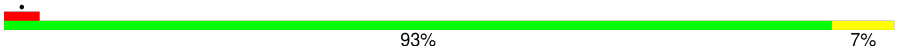
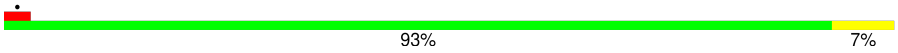
Mol	Chain	Length	Quality of chain
6	I	179	
7	J	67	
8	K	28	
9	L	18	
9	O	18	
10	M	83	
11	N	30	

2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 16649 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 regulatory protein SNF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	140	Total	C	N	O	S	0	0
			1133	715	196	220	2		

- Molecule 2 is a protein called SWI/SNF chromatin-remodeling complex subunit SWI1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	482	Total	C	N	O	S	0	0
			3890	2519	637	723	11		

- Molecule 3 is a protein called SWI/SNF chromatin-remodeling complex subunit SNF5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	245	Total	C	N	O	S	0	0
			2005	1256	346	395	8		

- Molecule 4 is a protein called SWI/SNF complex subunit SWI3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	159	Total	C	N	O	S	0	0
			1322	853	225	239	5		
4	E	139	Total	C	N	O	S	0	0
			1152	746	198	205	3		
4	F	221	Total	C	N	O	S	0	0
			1583	987	287	304	5		
4	G	197	Total	C	N	O	S	0	0
			1435	904	258	268	5		

- Molecule 5 is a protein called Transcription regulatory protein SNF12.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	257	Total	C	N	O	S	0	0
			2085	1323	355	400	7		

- Molecule 6 is a protein called Transcription regulatory protein SNF6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	109	Total	C	N	O	S	0	0
			818	504	155	156	3		

- Molecule 7 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	J	67	Total	C	N	O	0	0
			336	201	67	68		

- Molecule 8 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	K	28	Total	C	N	O	0	0
			141	84	28	29		

- Molecule 9 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	L	18	Total	C	N	O	0	0
			91	54	18	19		
9	O	18	Total	C	N	O	0	0
			91	54	18	19		

- Molecule 10 is a protein called SWI/SNF global transcription activator complex subunit SWP82.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	M	83	Total	C	N	O	0	0
			416	249	83	84		

- Molecule 11 is a protein called Unknown protein.

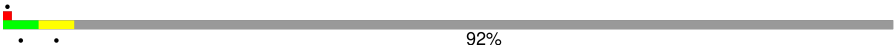
Mol	Chain	Residues	Atoms				AltConf	Trace
11	N	30	Total	C	N	O	0	0
			151	90	30	31		

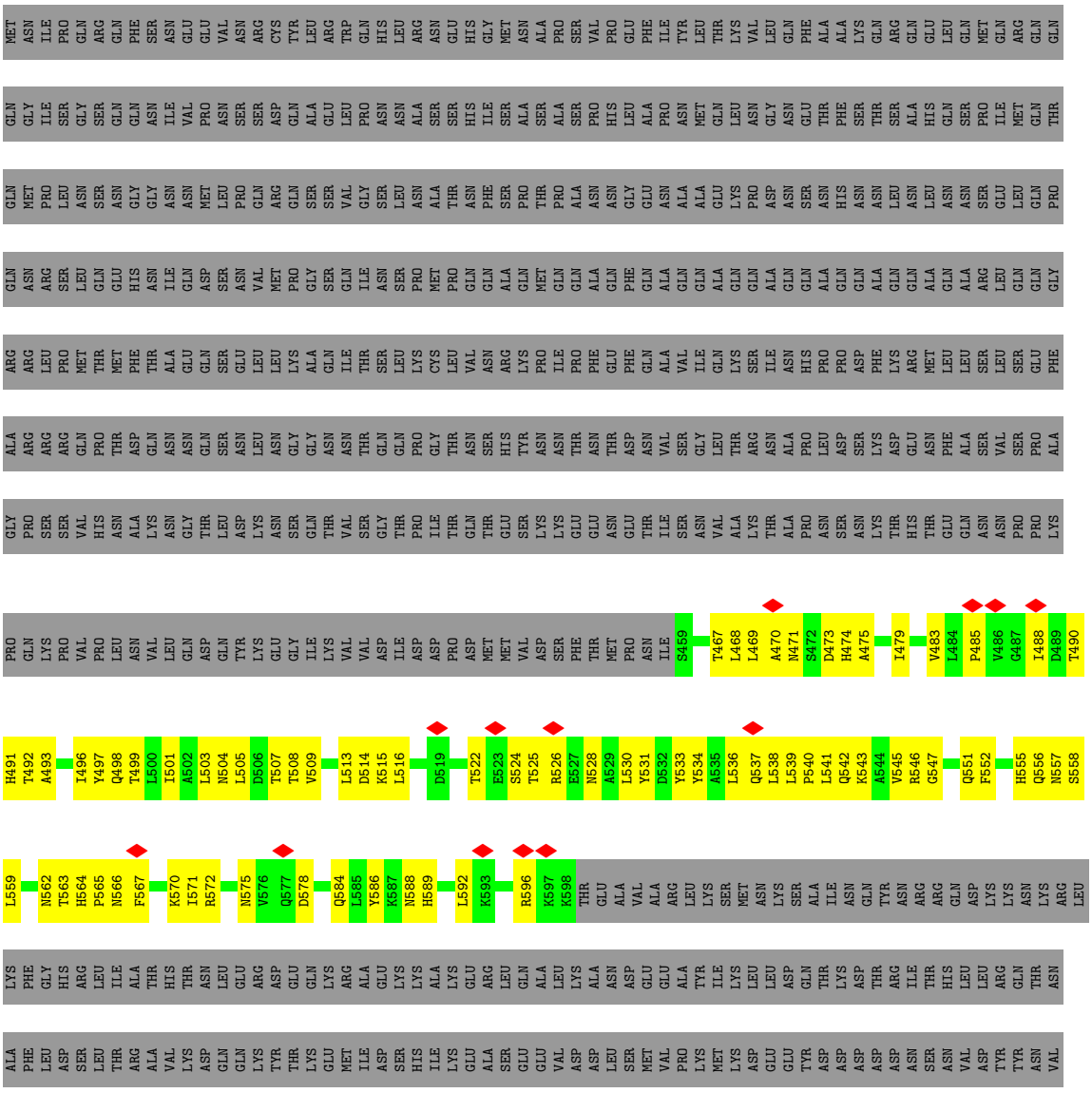
3 Residue-property plots (i)

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 regulatory protein SNF2

Chain A:





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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

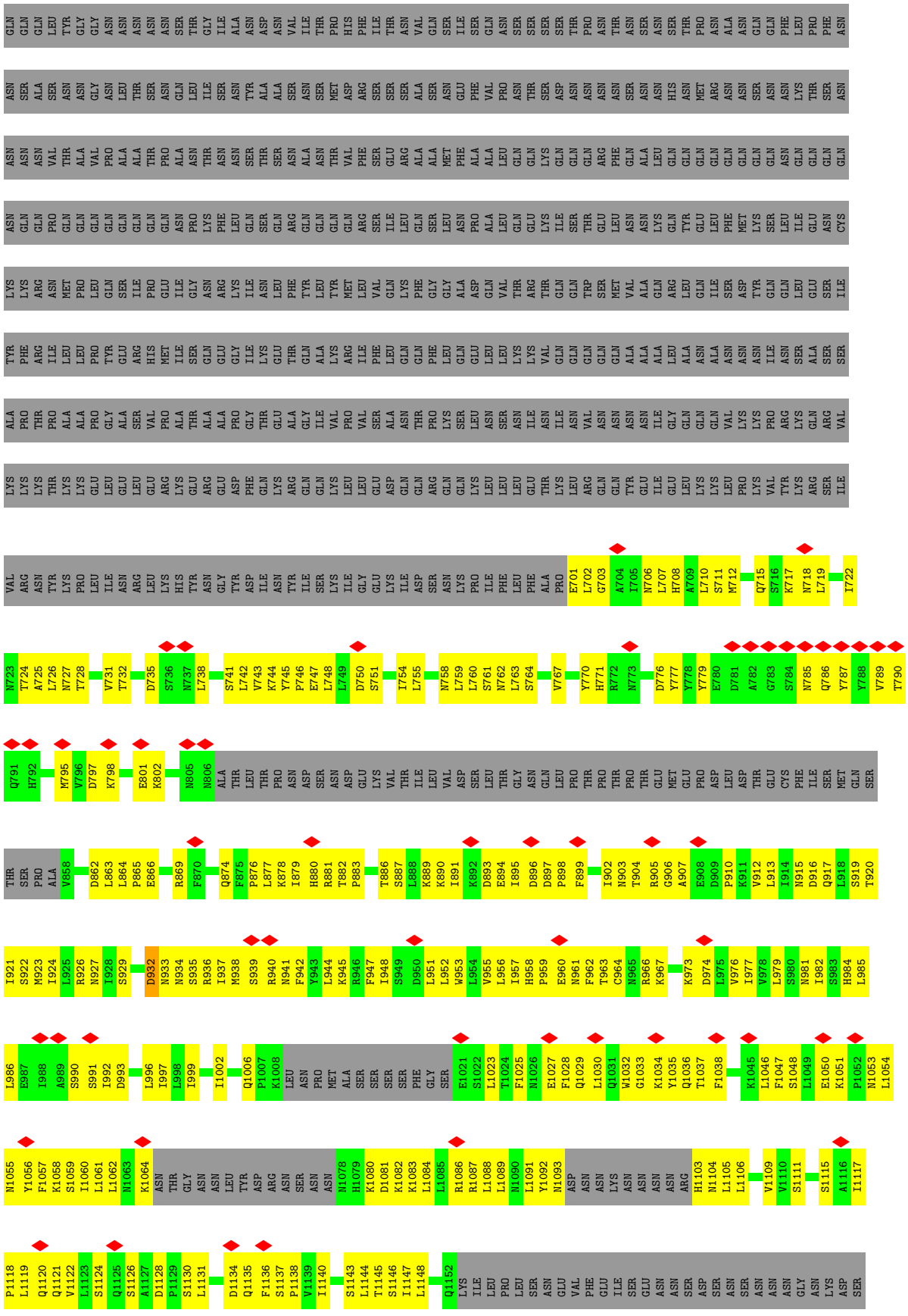
- Molecule 2: SWI/SNF chromatin-remodeling complex subunit SWI1

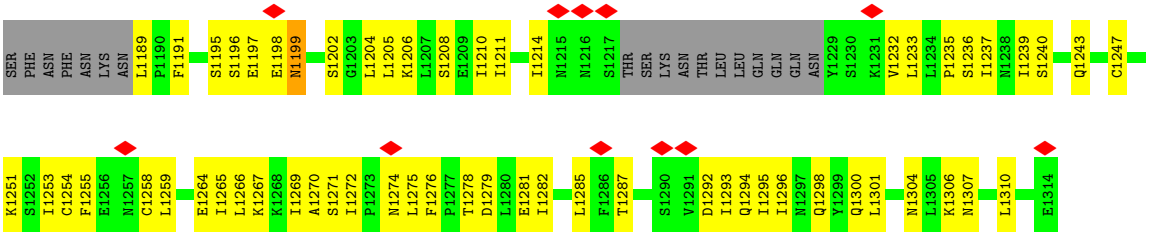
Chain B:

MET ASP PHE PHE ASN LEU ASN ASN ASN ASN ASN ASN ASN ASN THR THR THR THR THR THR THR THR ASN ASN ASN ASN THR ASN ASN ASN ASN THR ASN ASN ASN ASN ASN PRO ALA ASN ASN THR ASN ASN ASN ASN SER THR GLY HIS SER SER ASN THR ASN ASN ASN THR ASN ASN

ASN ASN THR ASN THR GLY ALA SER GLY VAL ASP ASP PHE GLN ASN PHE PHE ASP PRO LYS PRO PHE ASP GLN ASN LEU ASP SER ASN ASN ASN ASN SER ASN SER ASN ASN ASN ASP ASN ASN ASN SER ASN THR VAL ALA SER SER THR ASN PHE THR SER PRO THR ALA VAL VAL ASN

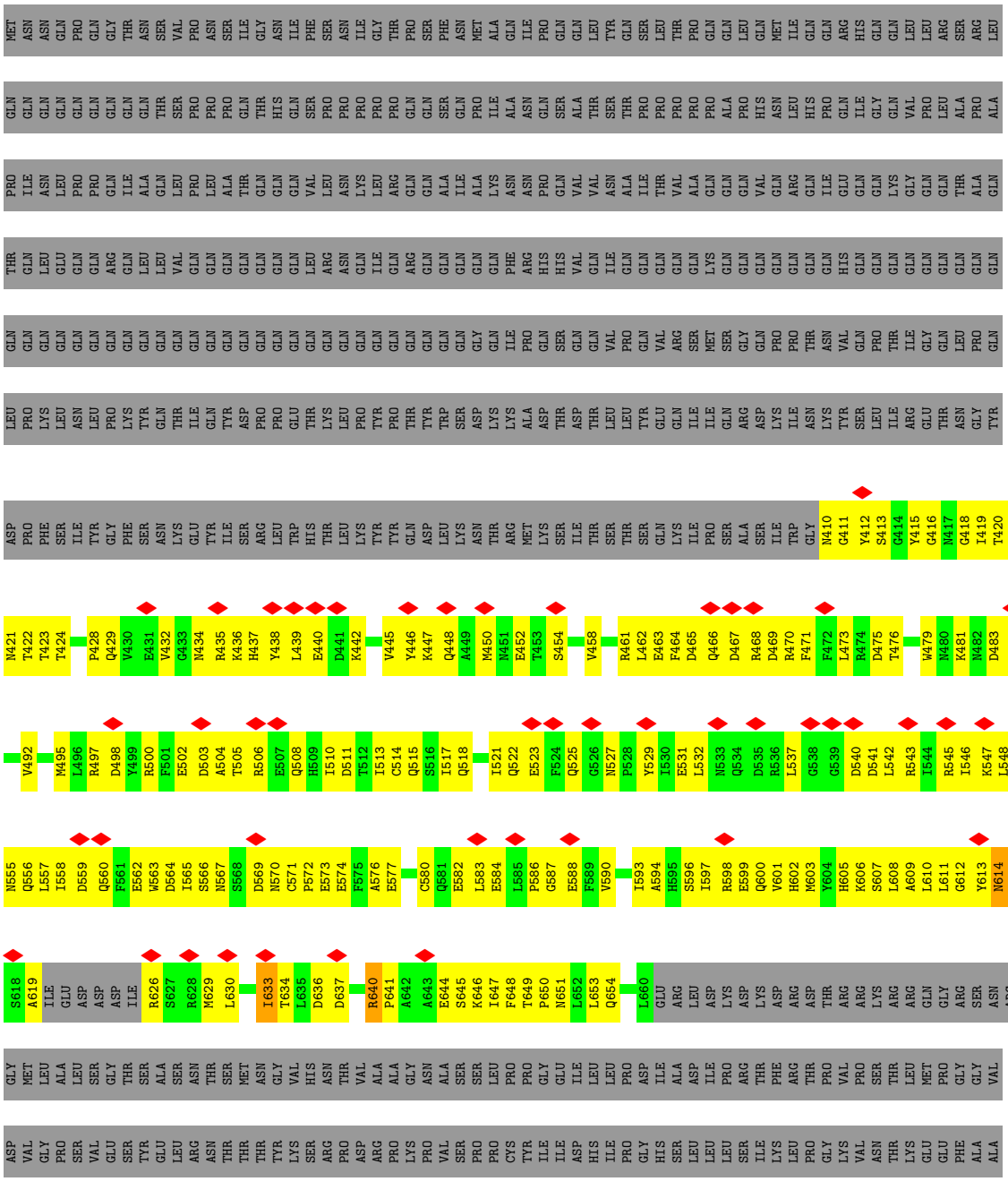
ASN ALA ALA PRO ALA ASN VAL THR GLY GLY LYS ALA ALA ASN PHE ILE GLN ASN GLN SER PRO GLN PHE ASN SER PRO TYR ASP SER ASN ASN SER ASN THR ASN LEU ASN SER LEU SER PRO GLN ALA ILE LEU ALA LYS ASN SER ILE ILE ASP SER SER ASN LEU PRO LEU GLN ALA

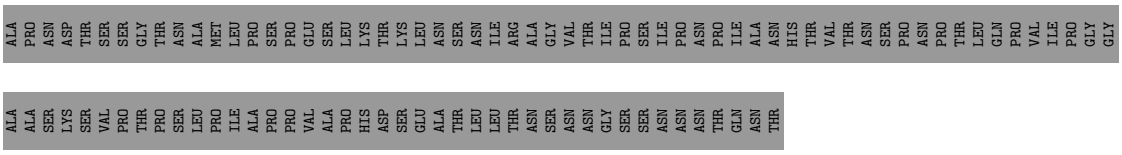




• Molecule 3: SWI/SNF chromatin-remodeling complex subunit SNF5

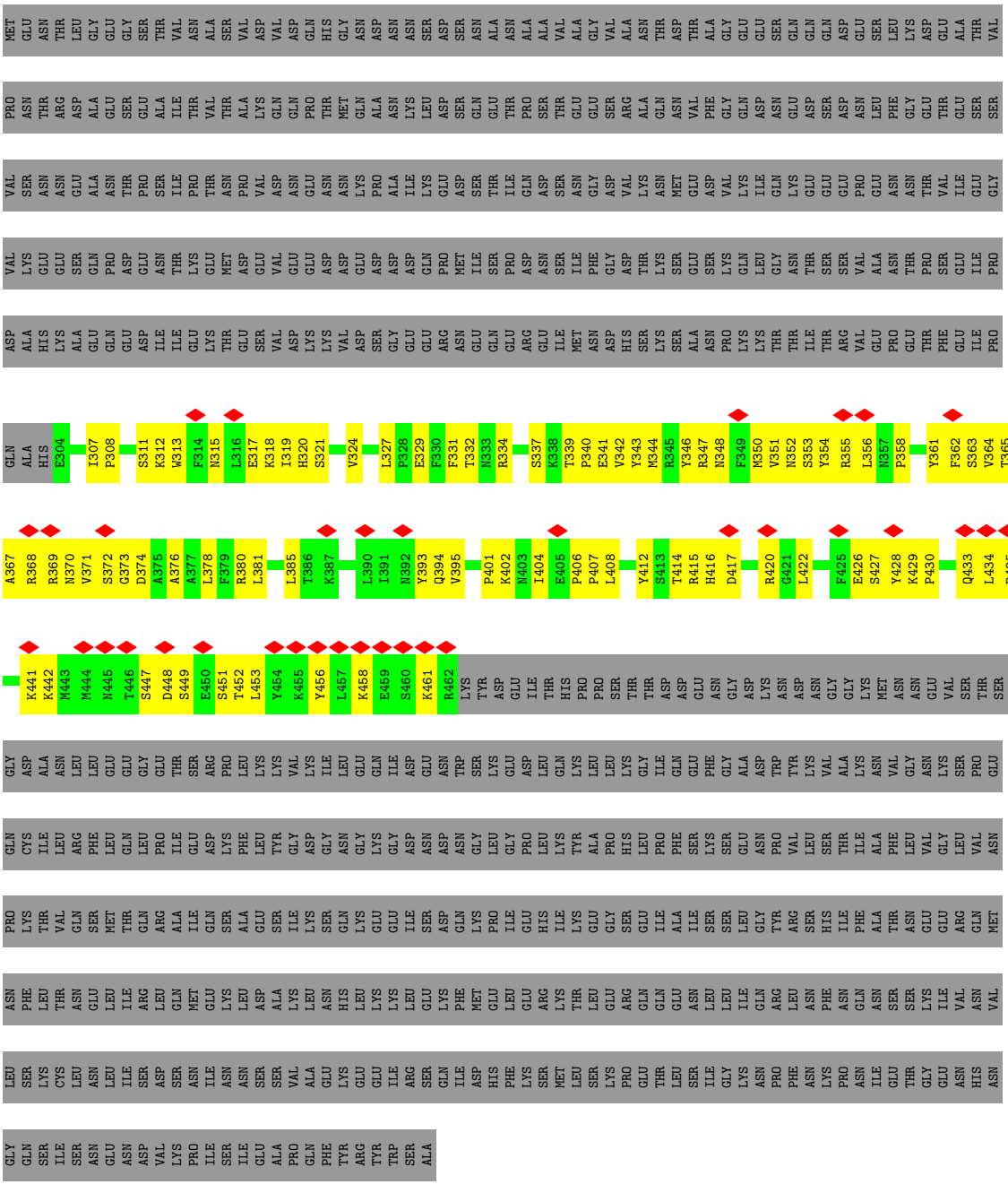
Chain C:





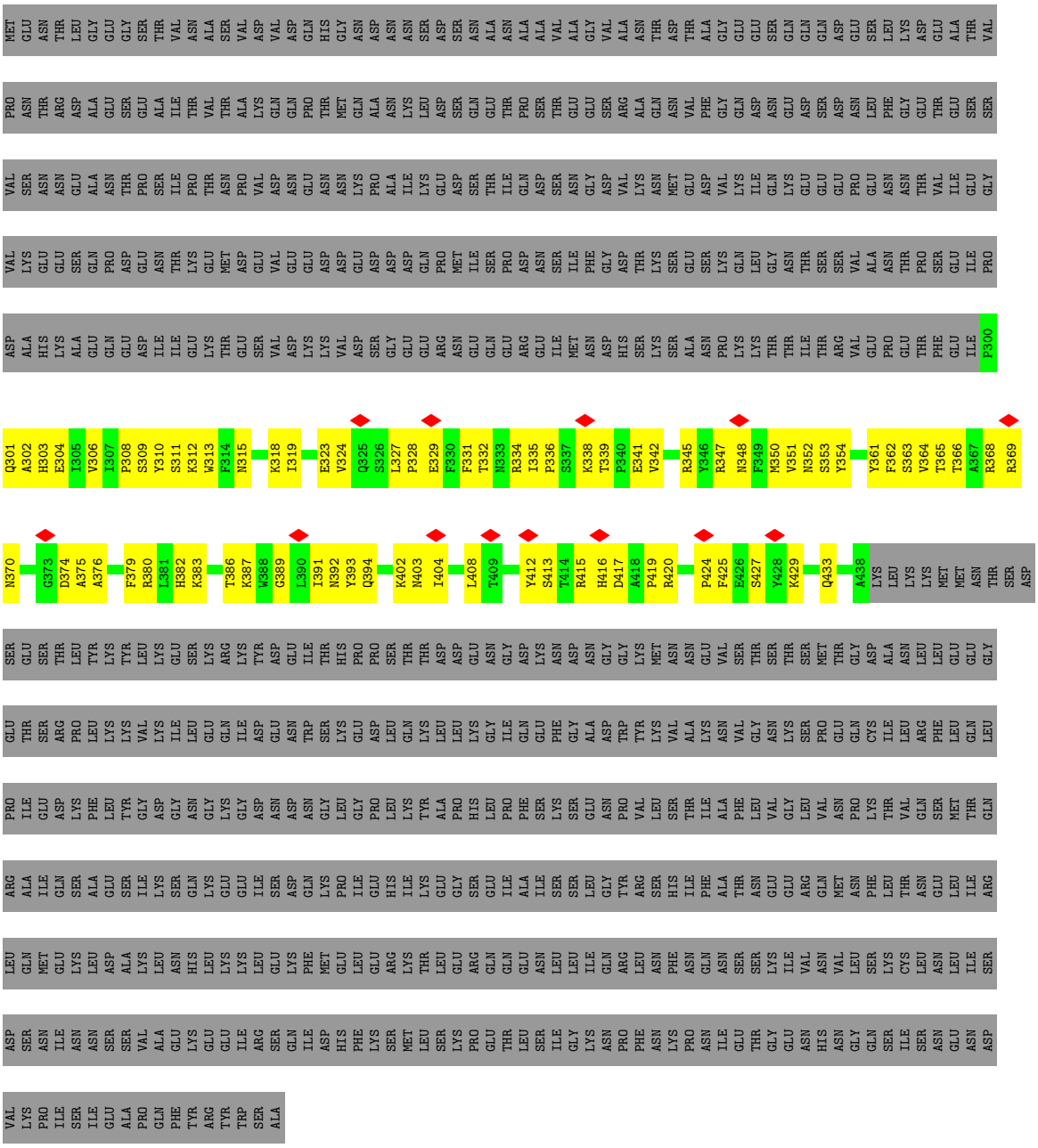
• Molecule 4: SWI/SNF complex subunit SWI3

Chain D:



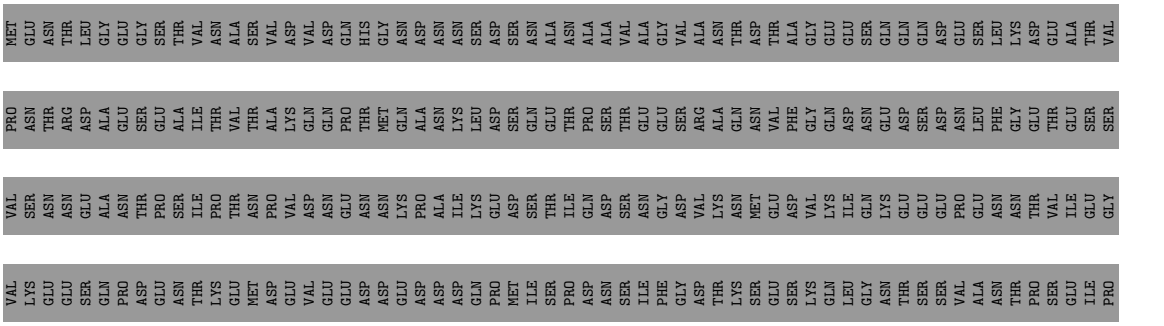
• Molecule 4: SWI/SNF complex subunit SWI3

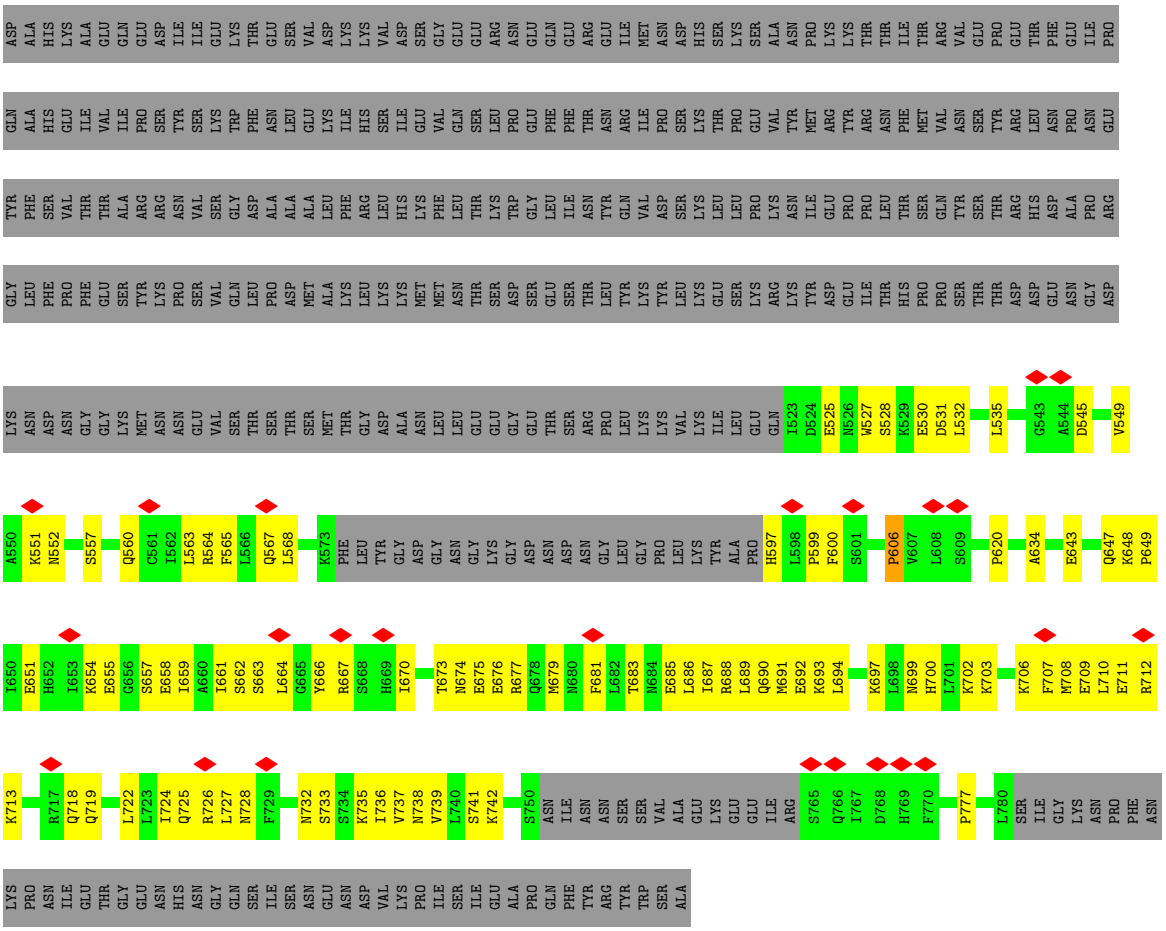
Chain E:



• Molecule 4: SWI/SNF complex subunit SWI3

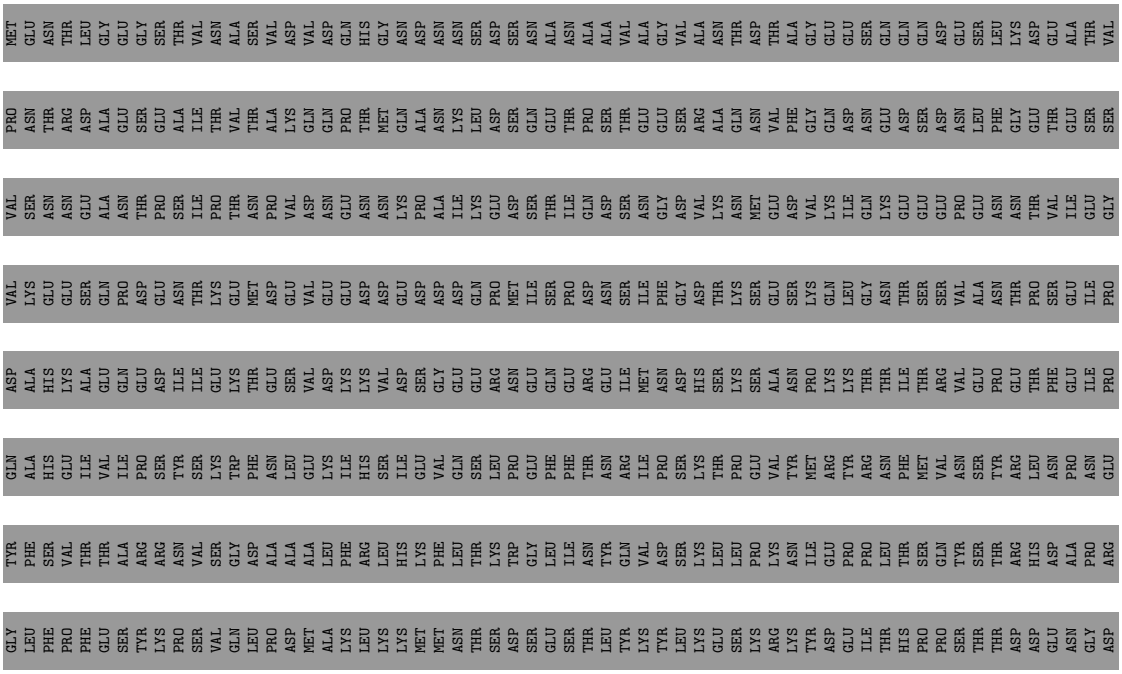
Chain F:

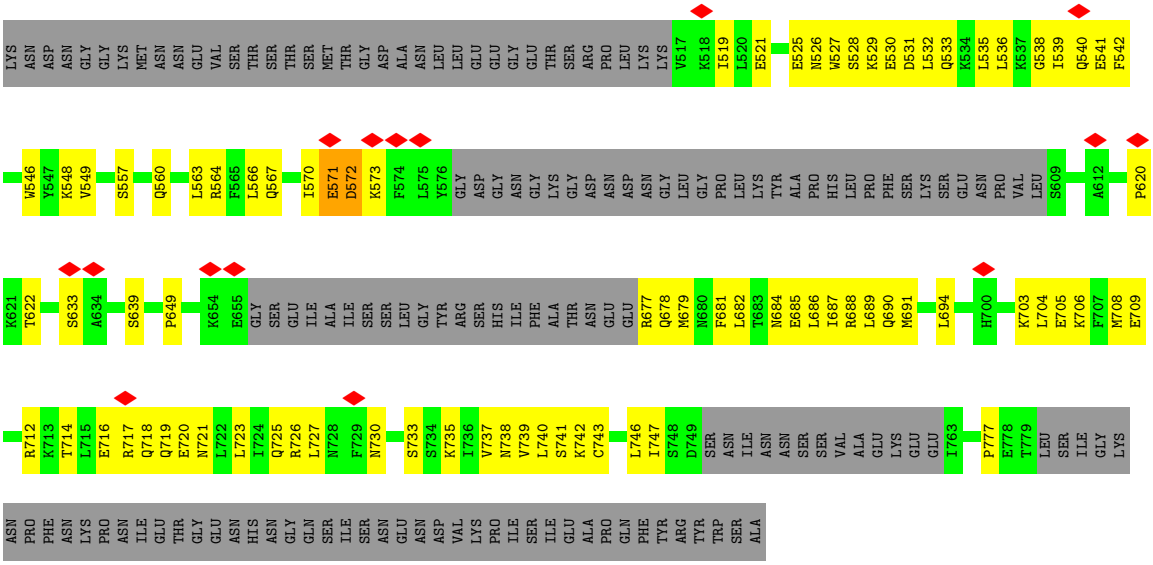




• Molecule 4: SWI/SNF complex subunit SWI3

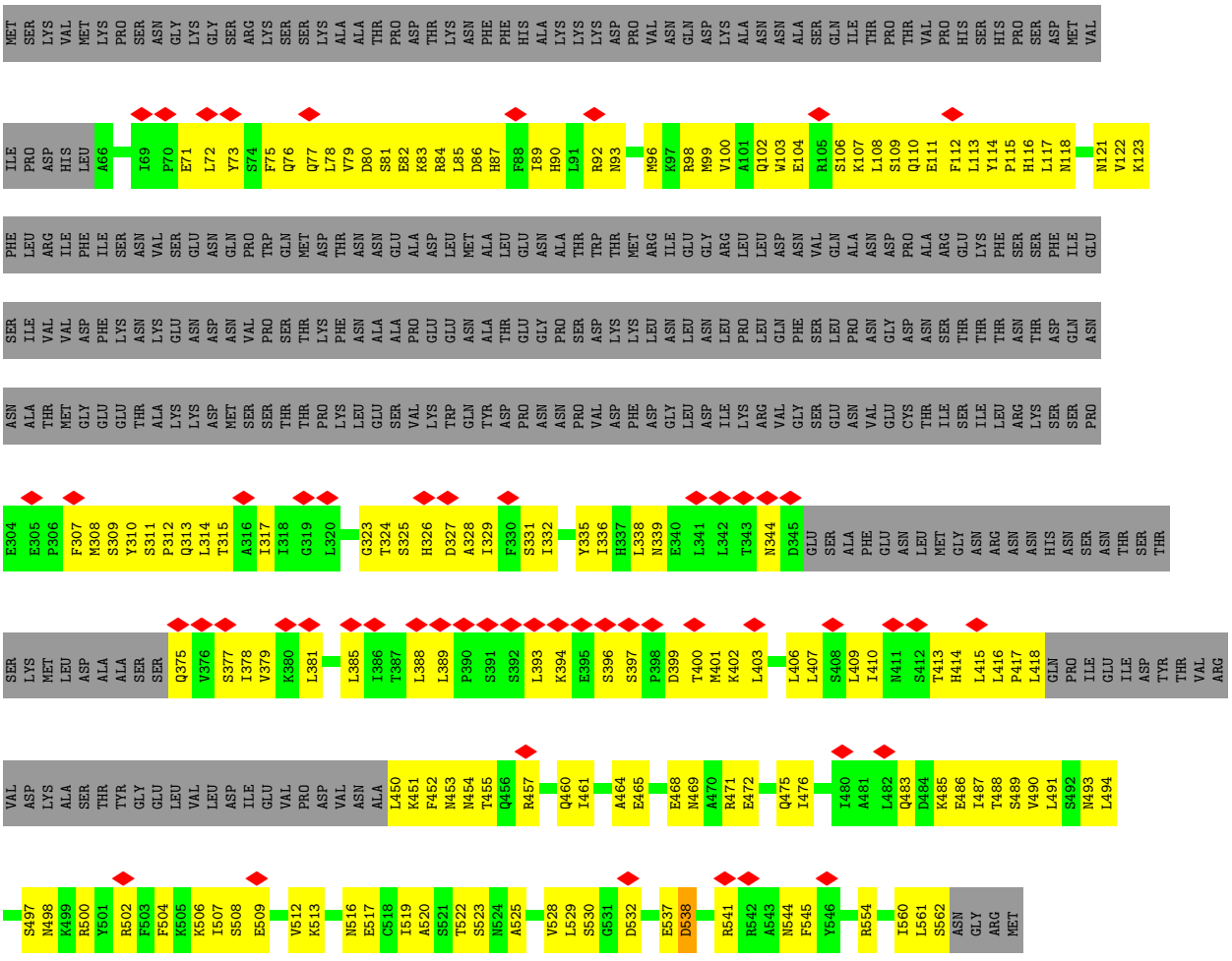
Chain G:





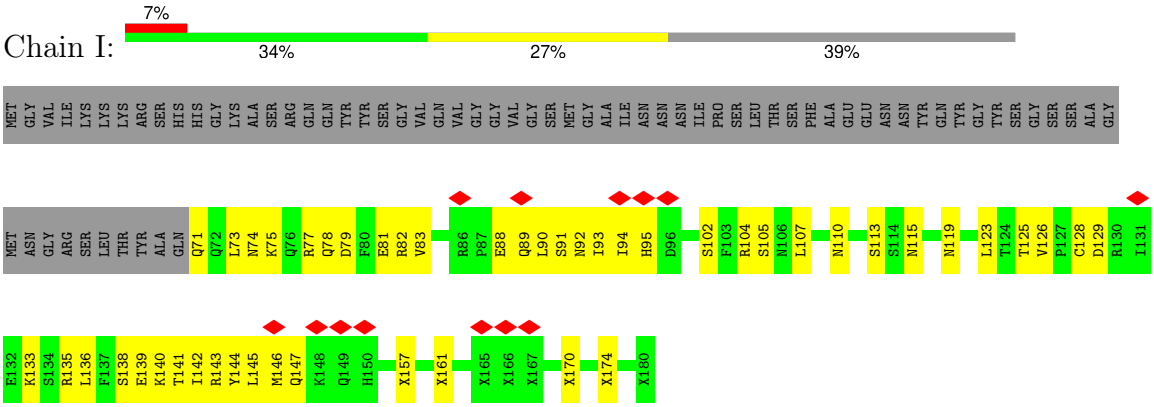
• Molecule 5: Transcription regulatory protein SNF12

Chain H:



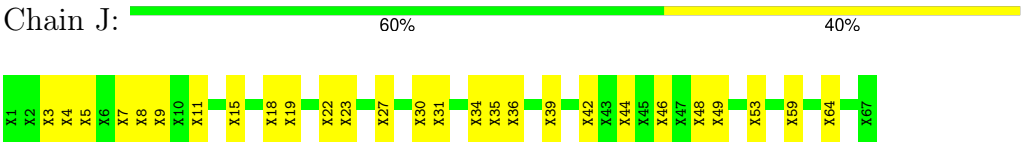
• Molecule 6: Transcription regulatory protein SNF6

Chain I:



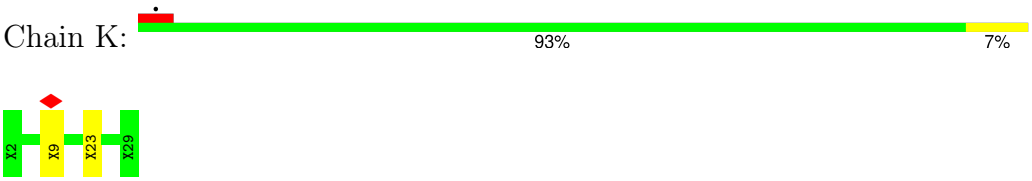
• Molecule 7: Unknown protein

Chain J:



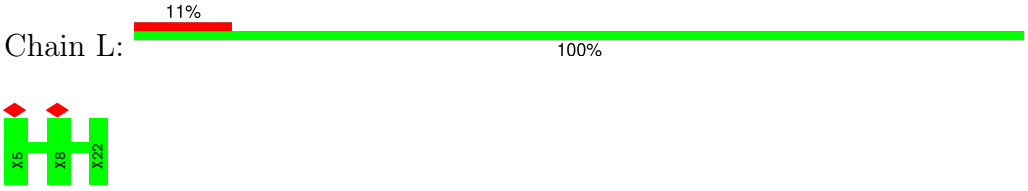
• Molecule 8: Unknown protein

Chain K:



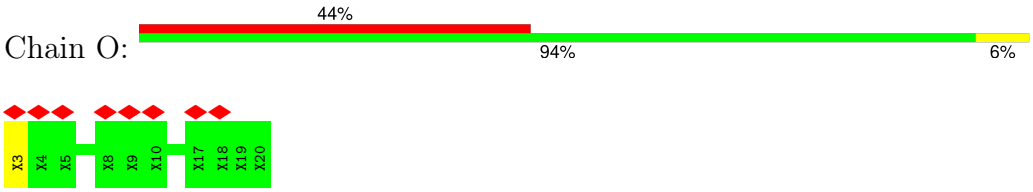
• Molecule 9: Unknown protein

Chain L:



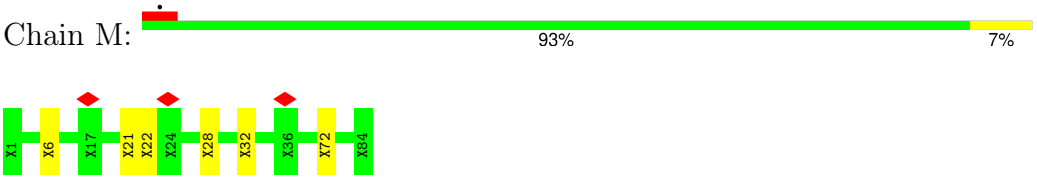
• Molecule 9: Unknown protein

Chain O:



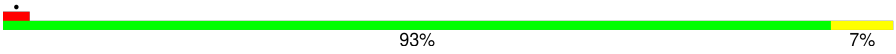
• Molecule 10: SWI/SNF global transcription activator complex subunit SWP82

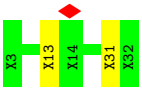
Chain M:



• Molecule 11: Unknown protein

Chain N:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	61518	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY; CTF amplitude correction was performed following 3D auto refinement in relion.	Depositor
Microscope	JEOL 3200FS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	76.5	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	0.093	Depositor
Minimum map value	-0.040	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	430.08002, 430.08002, 430.08002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.12, 1.12, 1.12	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.31	0/1154	0.46	0/1572
2	B	0.35	0/3958	0.53	0/5364
3	C	0.31	0/2040	0.64	2/2756 (0.1%)
4	D	0.26	0/1359	0.45	0/1838
4	E	0.34	0/1189	0.53	0/1616
4	F	0.29	0/1596	0.58	5/2154 (0.2%)
4	G	0.32	0/1446	0.58	3/1949 (0.2%)
5	H	0.33	1/2119 (0.0%)	0.47	0/2856
6	I	0.29	0/682	0.45	0/913
All	All	0.32	1/15543 (0.0%)	0.53	10/21018 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	H	544	ASN	CA-C	-5.00	1.44	1.52

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	640	ARG	CA-C-N	10.75	133.28	119.84
3	C	640	ARG	C-N-CA	10.75	133.28	119.84
4	F	649	PRO	N-CA-CB	8.31	110.58	103.35
4	F	606	PRO	N-CA-CB	7.99	111.64	103.25
4	F	599	PRO	N-CA-CB	7.17	110.36	103.19

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	776	ASP	Peptide
2	B	932	ASP	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1133	0	1122	88	0
2	B	3890	0	4008	263	0
3	C	2005	0	1939	171	0
4	D	1322	0	1325	100	0
4	E	1152	0	1137	87	0
4	F	1583	0	1397	78	0
4	G	1435	0	1294	63	0
5	H	2085	0	2104	149	0
6	I	818	0	708	68	0
7	J	336	0	70	18	0
8	K	141	0	33	3	0
9	L	91	0	21	0	0
9	O	91	0	21	2	0
10	M	416	0	92	4	0
11	N	151	0	41	3	0
All	All	16649	0	15312	945	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 30.

The worst 5 of 945 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)
4:D:412:TYR:CD1	5:H:560:ILE:HG23	1.62	1.34
4:D:412:TYR:CD1	5:H:560:ILE:CG2	2.12	1.32
4:D:412:TYR:CG	5:H:560:ILE:HG21	1.93	1.02
1:A:570:LYS:HE2	6:I:90:LEU:H	1.25	0.98

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:412:TYR:HD1	5:H:560:ILE:HG23	1.16	0.95

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	138/1703 (8%)	118 (86%)	20 (14%)	0	100	100
2	B	468/1314 (36%)	364 (78%)	104 (22%)	0	100	100
3	C	241/905 (27%)	176 (73%)	63 (26%)	2 (1%)	16	54
4	D	157/825 (19%)	131 (83%)	26 (17%)	0	100	100
4	E	137/825 (17%)	113 (82%)	24 (18%)	0	100	100
4	F	215/825 (26%)	186 (86%)	27 (13%)	2 (1%)	14	51
4	G	189/825 (23%)	164 (87%)	24 (13%)	1 (0%)	25	64
5	H	249/566 (44%)	217 (87%)	32 (13%)	0	100	100
6	I	78/179 (44%)	67 (86%)	11 (14%)	0	100	100
All	All	1872/7967 (24%)	1536 (82%)	331 (18%)	5 (0%)	38	72

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	F	606	PRO
3	C	614	ASN
4	G	572	ASP
4	F	648	LYS
3	C	612	GLY

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	A	129/1520 (8%)	129 (100%)	0	100 100
2	B	460/1218 (38%)	459 (100%)	1 (0%)	92 94
3	C	222/823 (27%)	220 (99%)	2 (1%)	75 83
4	D	150/751 (20%)	150 (100%)	0	100 100
4	E	129/751 (17%)	129 (100%)	0	100 100
4	F	138/751 (18%)	138 (100%)	0	100 100
4	G	127/751 (17%)	126 (99%)	1 (1%)	79 85
5	H	239/517 (46%)	235 (98%)	4 (2%)	56 73
6	I	79/133 (59%)	79 (100%)	0	100 100
All	All	1673/7215 (23%)	1665 (100%)	8 (0%)	85 90

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	H	562	SER
5	H	561	LEU
5	H	494	LEU
4	G	571	GLU
5	H	538	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
5	H	102	GLN
5	H	118	ASN
6	I	76	GLN
2	B	1260	ASN
2	B	1243	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
6	I	1
10	M	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	I	150:HIS	C	152:UNK	N	20.17
1	M	22:UNK	C	24:UNK	N	7.86

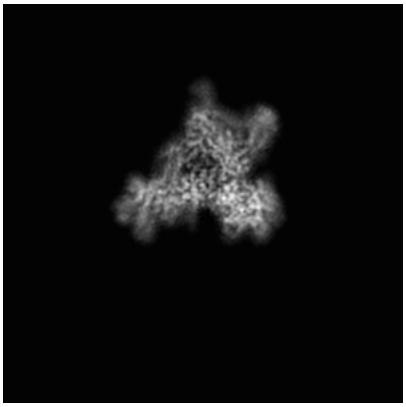
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-20933. These allow visual inspection of the internal detail of the map and identification of artifacts.

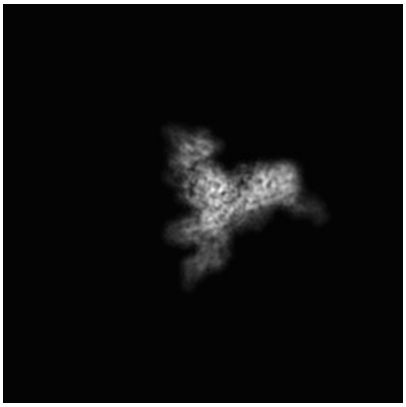
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

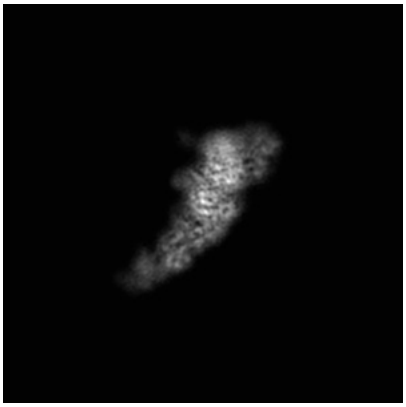
6.1.1 Primary map



X



Y



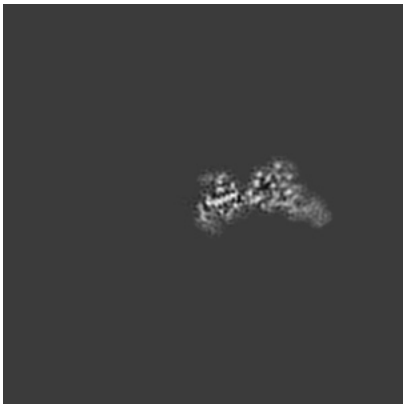
Z

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

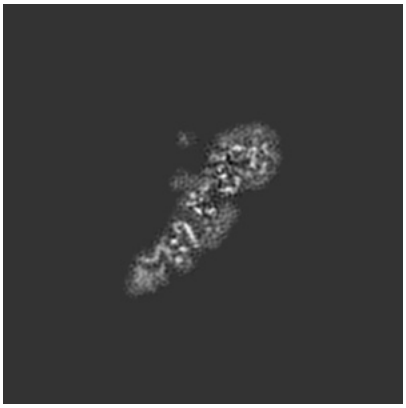
6.2 Central slices

6.2.1 Primary map

X Index: 192



Y Index: 192

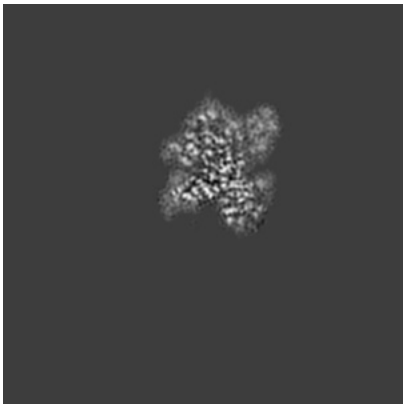


Z Index: 192

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

6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 204

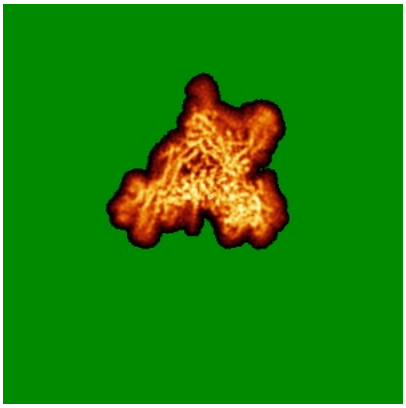
Y Index: 218

Z Index: 197

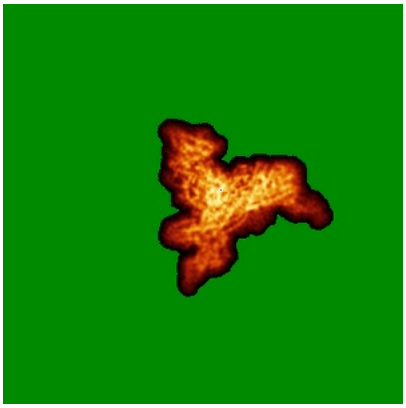
The images above show the largest variance slices of the map in three orthogonal directions.

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

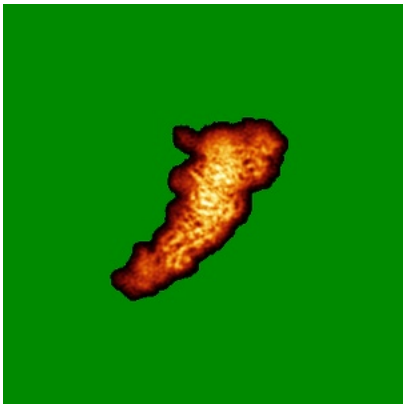
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

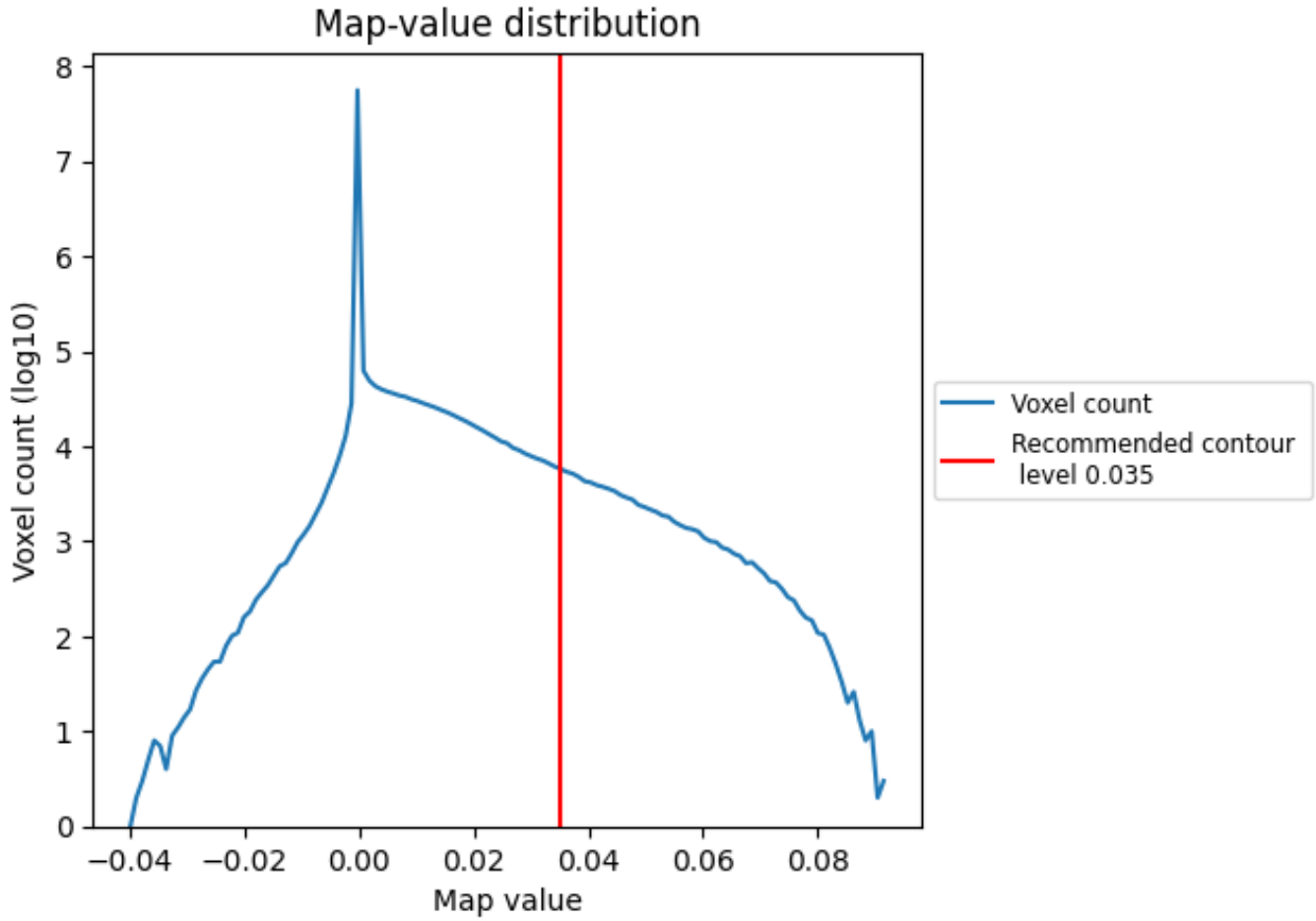
6.6 Mask visualisation (i)

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

7 Map analysis

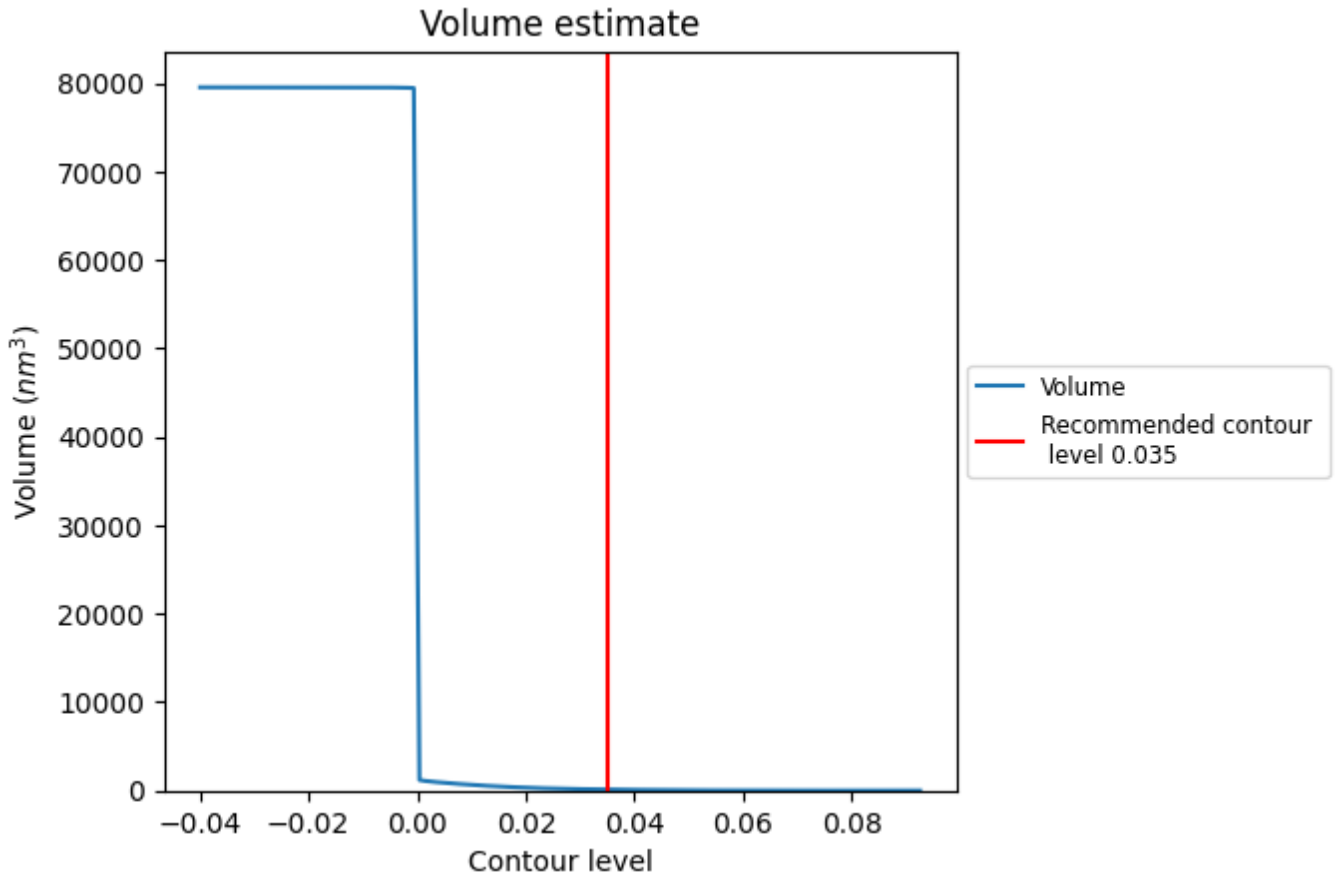
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

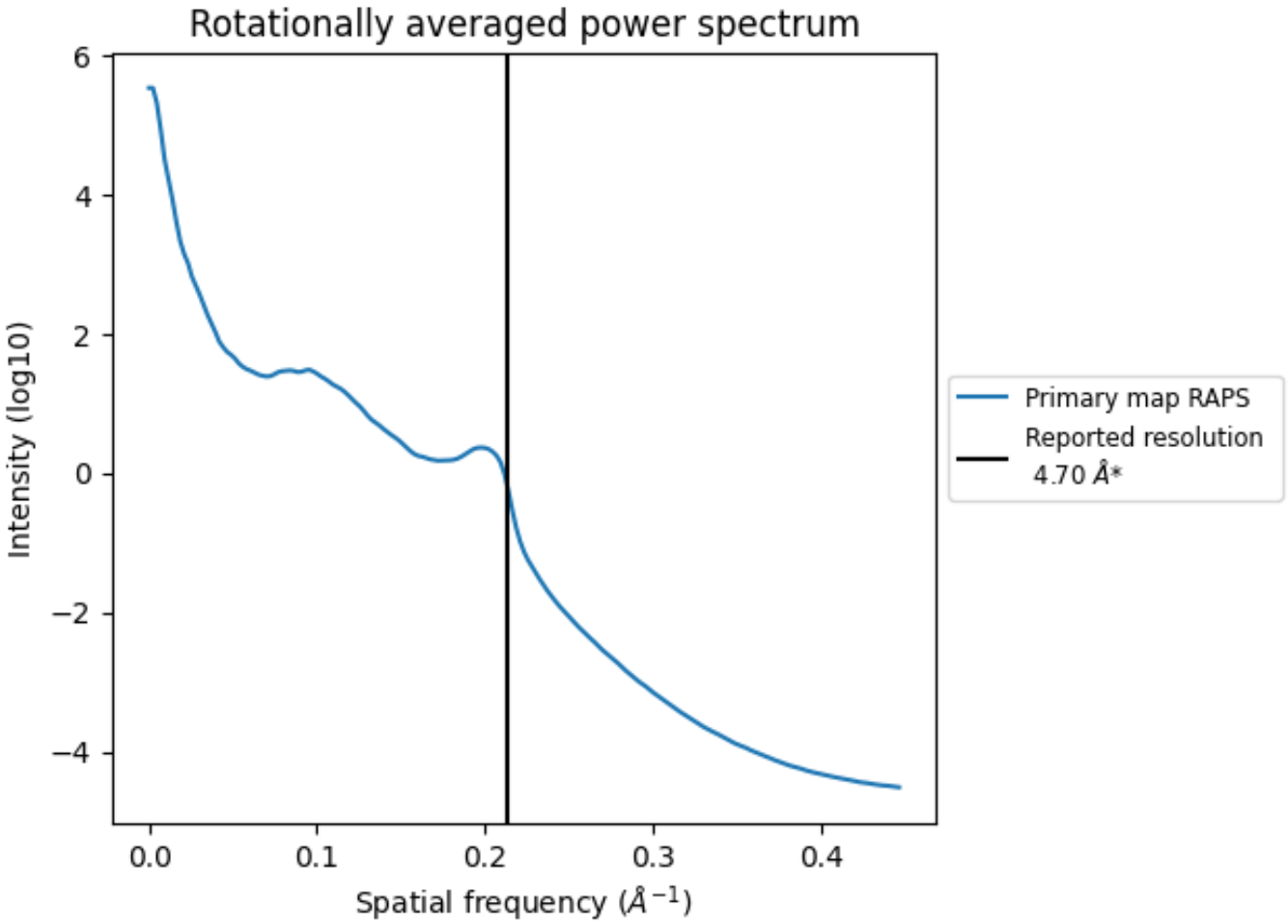
7.2 Volume estimate (i)



The volume at the recommended contour level is 118 nm^3; this corresponds to an approximate mass of 107 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)

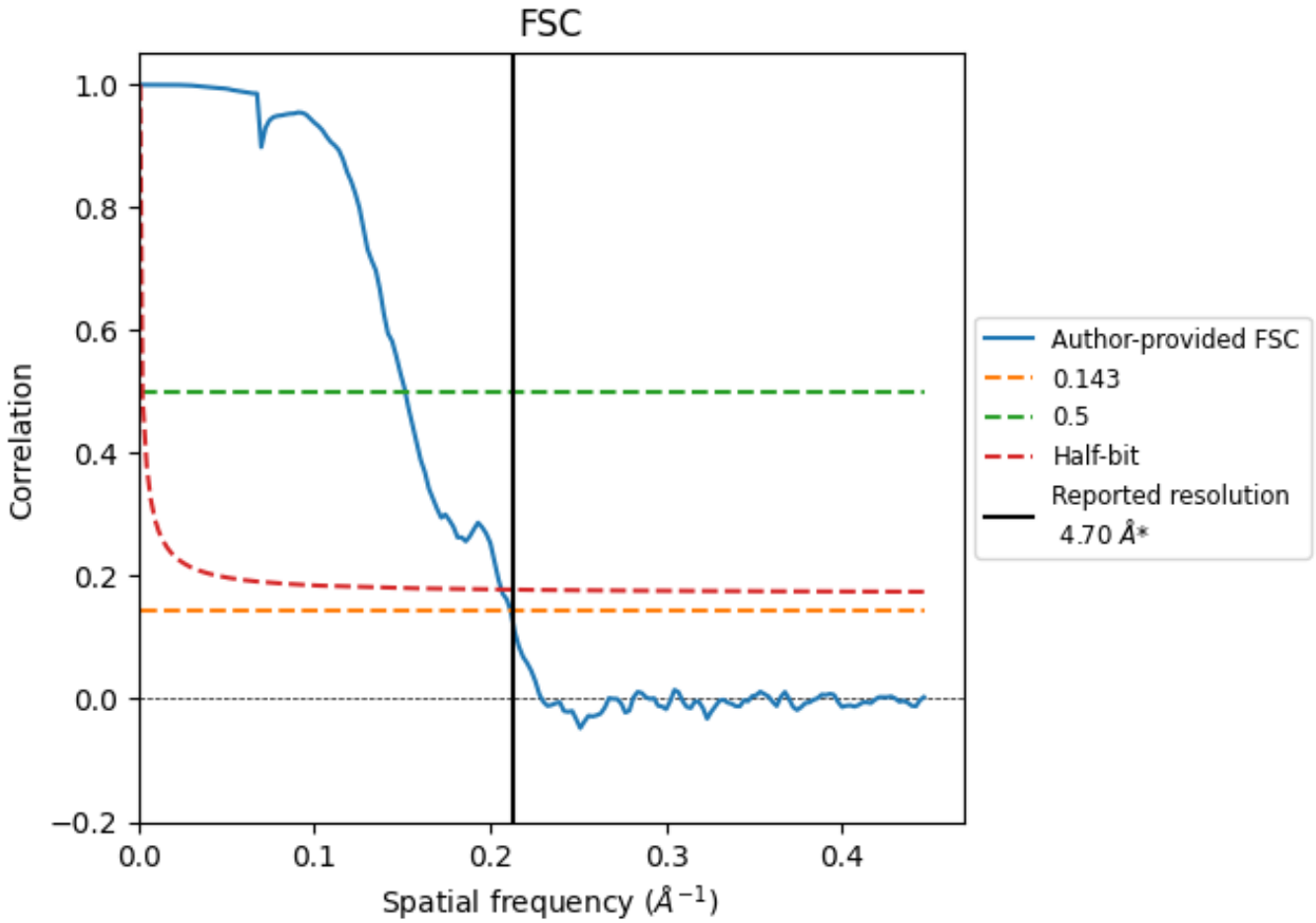


*Reported resolution corresponds to spatial frequency of 0.213 $Å^{-1}$

8 Fourier-Shell correlation

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

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.213 Å^{-1}

8.2 Resolution estimates (i)

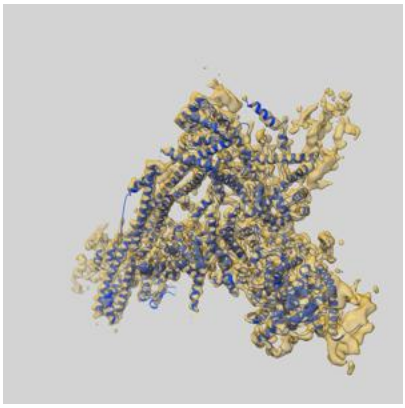
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.70	-	-
Author-provided FSC curve	4.73	6.60	4.85
Unmasked-calculated*	-	-	-

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

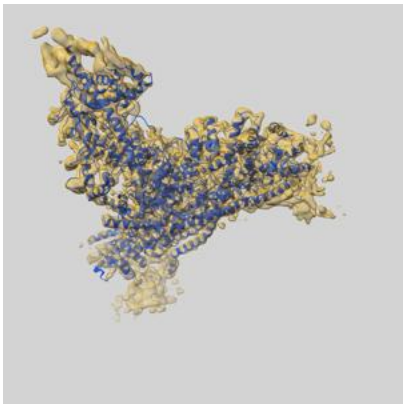
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-20933 and PDB model 6UXV. Per-residue inclusion information can be found in section 3 on page 6.

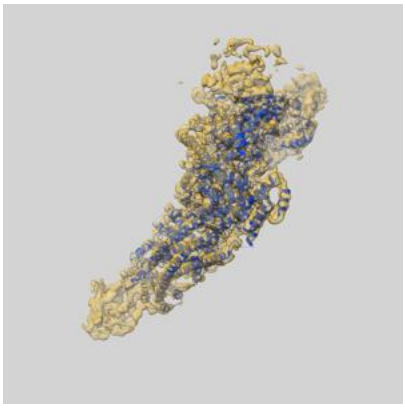
9.1 Map-model overlay



X



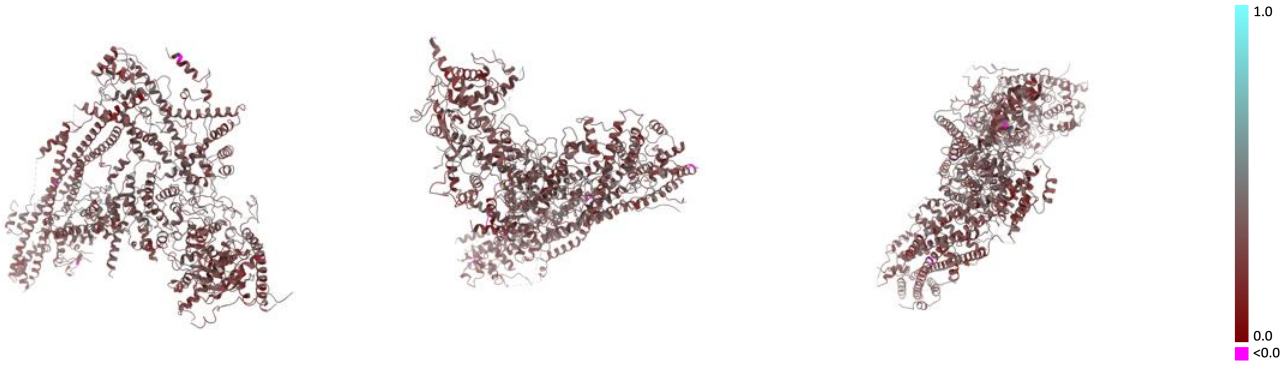
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.035 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.

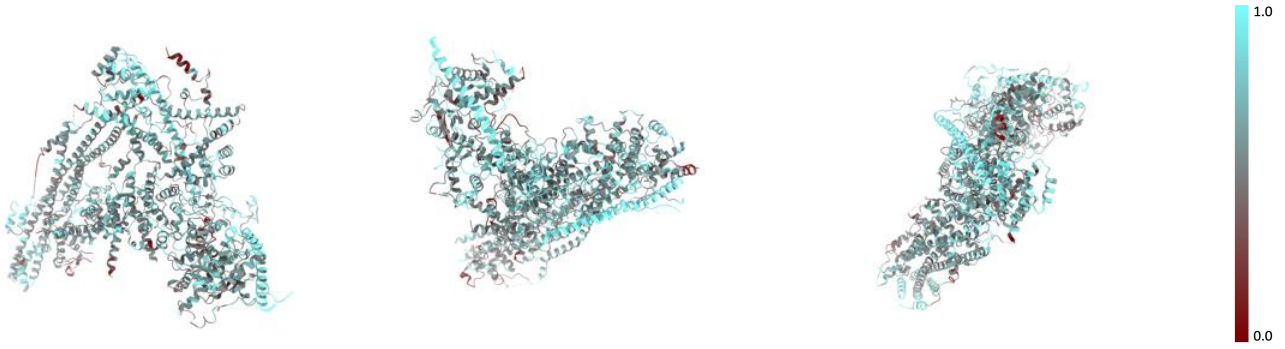
9.2 Q-score mapped to coordinate model



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.

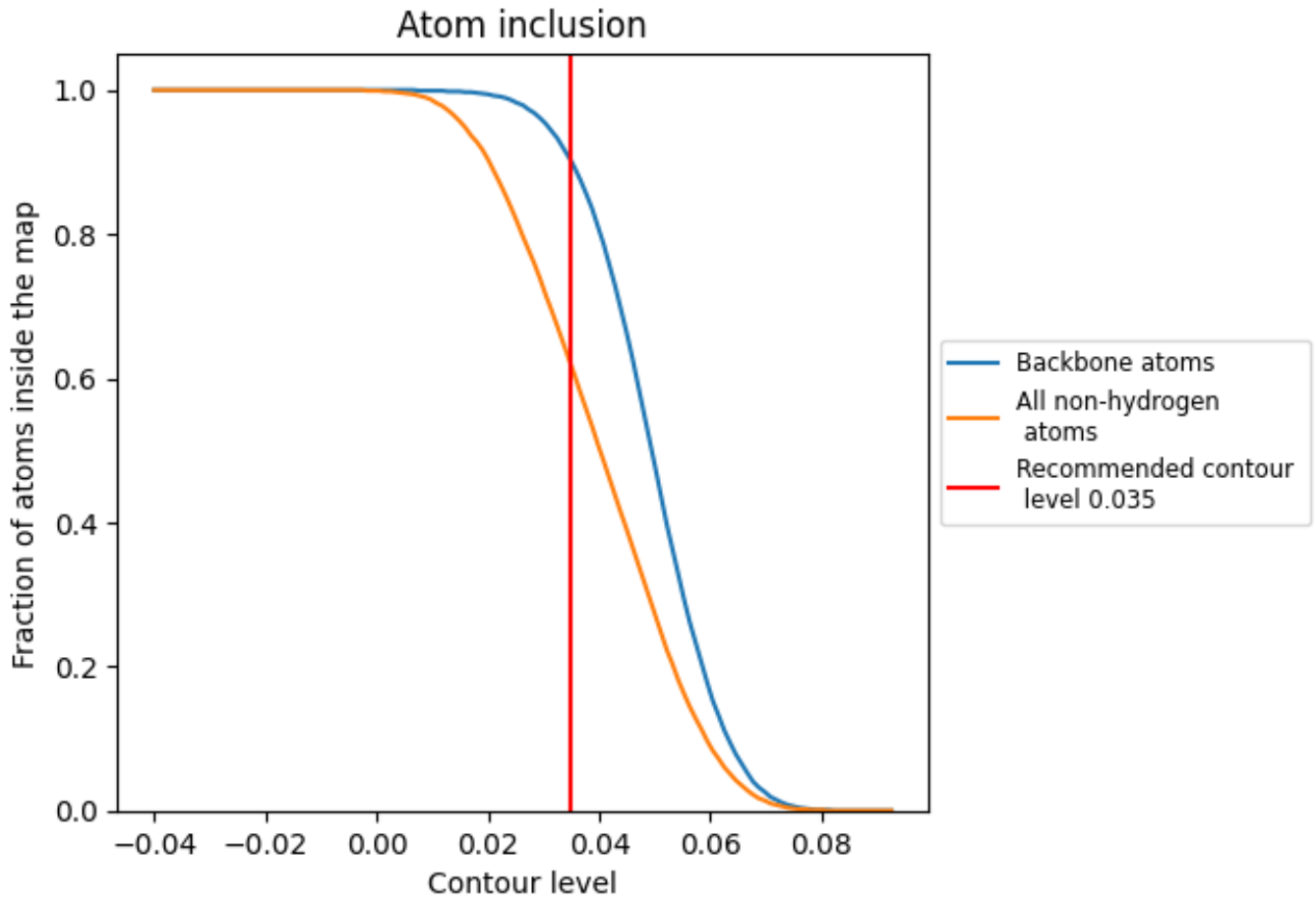
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.035).

9.4 Atom inclusion (i)



At the recommended contour level, 90% of all backbone atoms, 62% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6170	0.3220
A	0.6270	0.3330
B	0.5990	0.3360
C	0.5540	0.3140
D	0.5780	0.3070
E	0.6410	0.3420
F	0.6220	0.2950
G	0.6530	0.3150
H	0.5500	0.2930
I	0.6320	0.3310
J	0.9170	0.3710
K	0.8650	0.4030
L	0.7580	0.2930
M	0.8650	0.3650
N	0.8740	0.4630
O	0.4400	0.1680