wwPDB EM Validation Summary Report (i)

Mar 2, 2026 – 12:22 AM UTC

PDB ID	:	8GHN / pdb_00008ghn
EMDB ID	:	EMD-40037
Title	:	Composite model of the yeast Hir Complex with Asf1/H3/H4
Authors	:	Kim, H.J.; Murakami, K.
Deposited on	:	2023-03-10
Resolution	:	2.96 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:

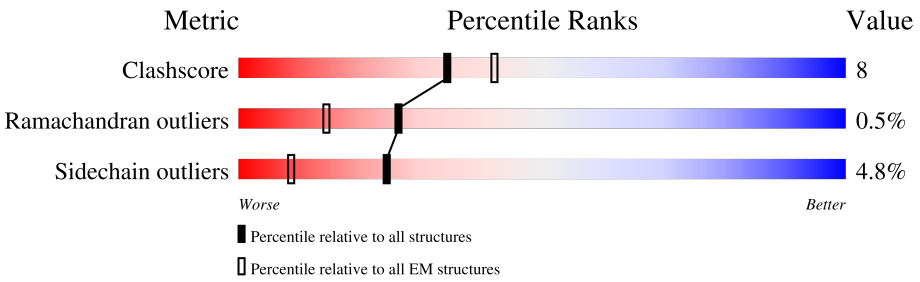
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

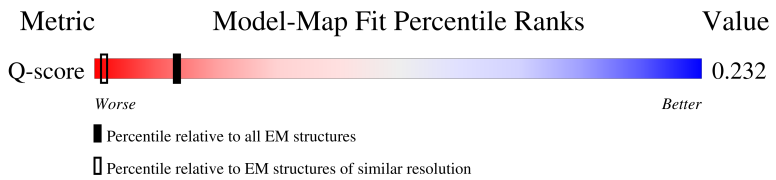
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.96 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	13155 (2.46 - 3.46)

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	840	8% 70% 9% • 21%
1	G	840	5% 67% 9% • 22%
2	B	875	• 71% 20% • 9%
2	C	875	• 34% 7% • 57%

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Mol	Chain	Length	Quality of chain
2	H	875	71% 19% 9%
2	I	875	37% 5% 57%
3	D	1648	8% 71% 18% 7%
3	J	1648	11% 71% 18% 7%
4	E	625	17% 80%
4	F	625	6% 93%
4	K	625	16% 80%
4	L	625	9% 90%
5	M	136	51% 47%
6	N	103	69% 7% 24%
7	O	279	14% 53% 45%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 59784 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 Protein HIR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	667	5272	3363	902	985	22	0	0
1	G	651	5155	3289	880	964	22	0	0

- Molecule 2 is a protein called Protein HIR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	800	6359	4053	1061	1214	31	0	0
2	C	377	3022	1936	498	571	17	0	0
2	H	800	6359	4053	1061	1214	31	0	0
2	I	377	3022	1936	498	571	17	0	0

- Molecule 3 is a protein called Histone transcription regulator 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	D	1533	12616	8119	2086	2364	47	0	0
3	J	1533	12617	8119	2086	2365	47	0	0

- Molecule 4 is a protein called Histone promoter control protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	126	1012	651	162	198	1	0	0
4	F	43	362	240	53	69		0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	K	126	1012	651	162	198	1	0	0
4	L	64	Total	C	N	O		0	0
			540	356	76	108			

- Molecule 5 is a protein called Histone H3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	M	72	584	369	110	105	0	0

- Molecule 6 is a protein called Histone H4.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	N	78	618	391	119	108	0	0

- Molecule 7 is a protein called Histone chaperone.

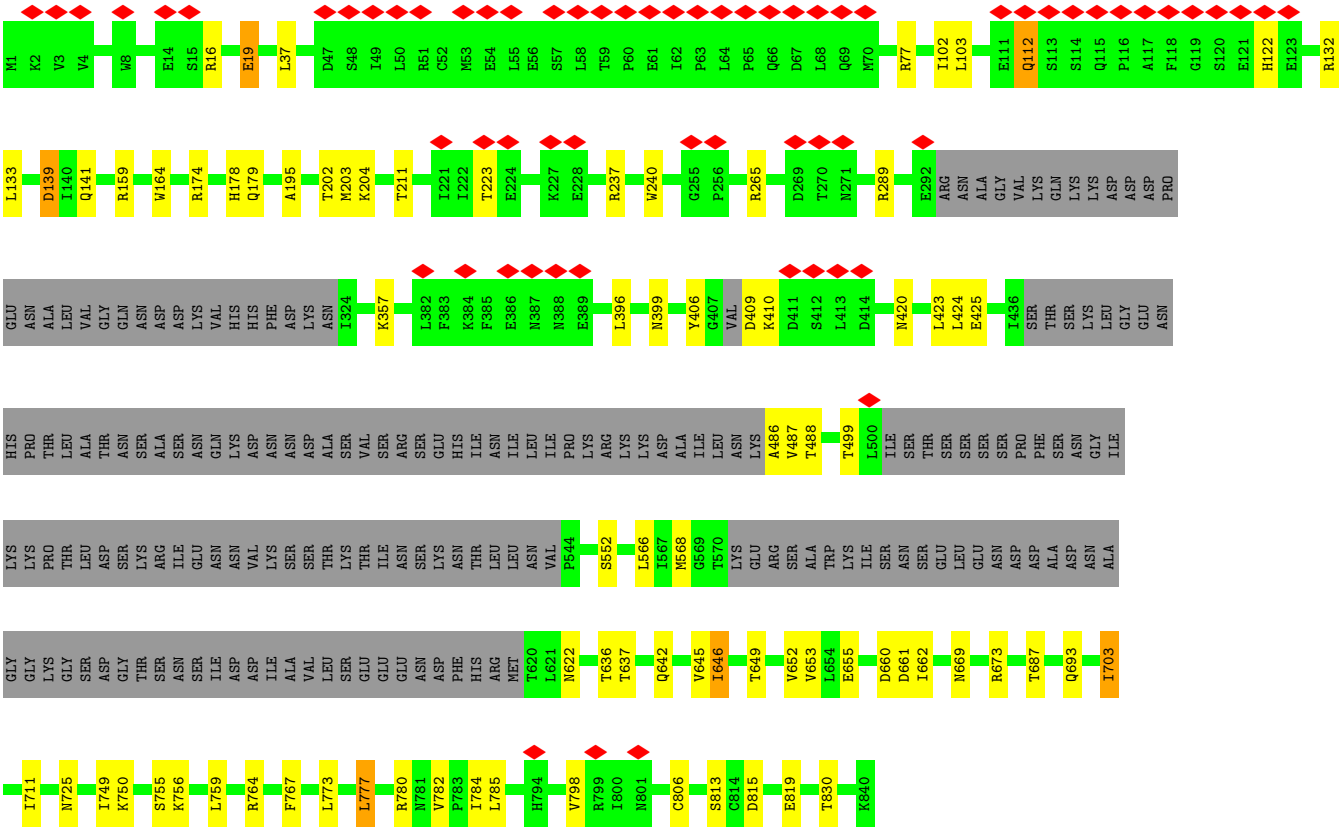
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	O	154	1234	793	200	238	3	0	0

3 Residue-property plots (i)

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

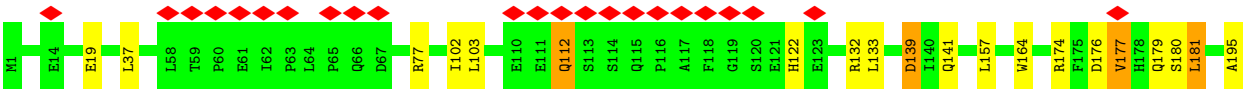
- Molecule 1: Protein HIR1

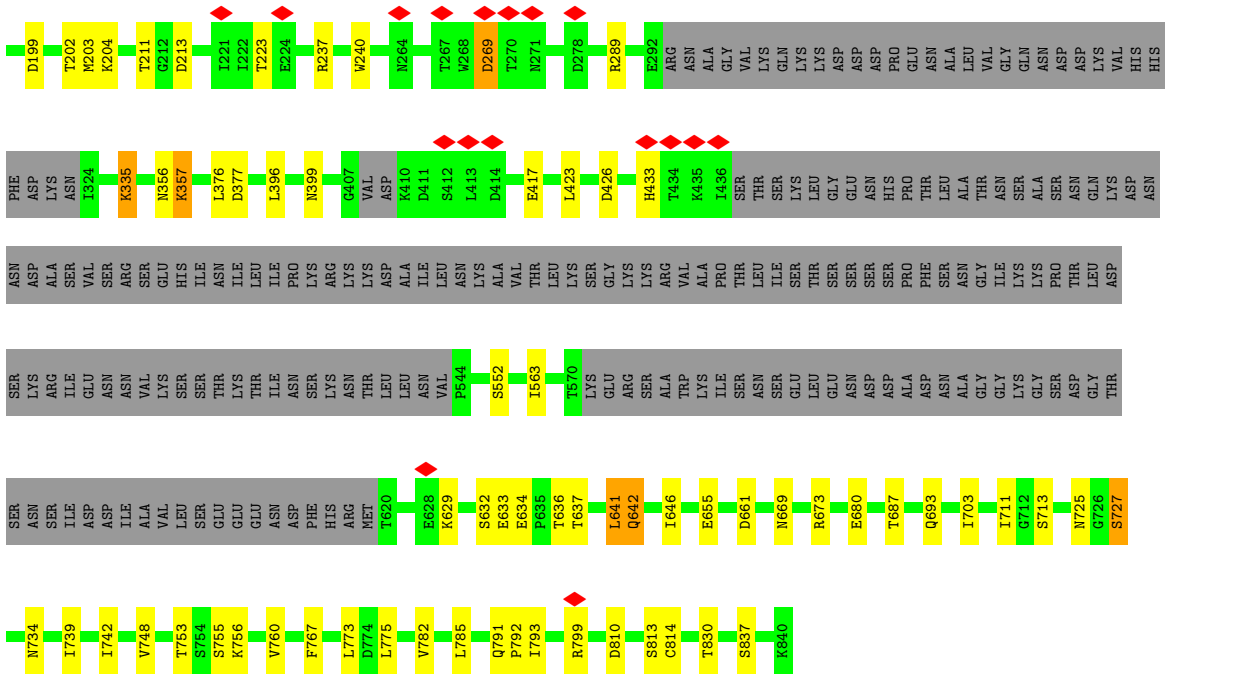
Chain A:



- Molecule 1: Protein HIR1

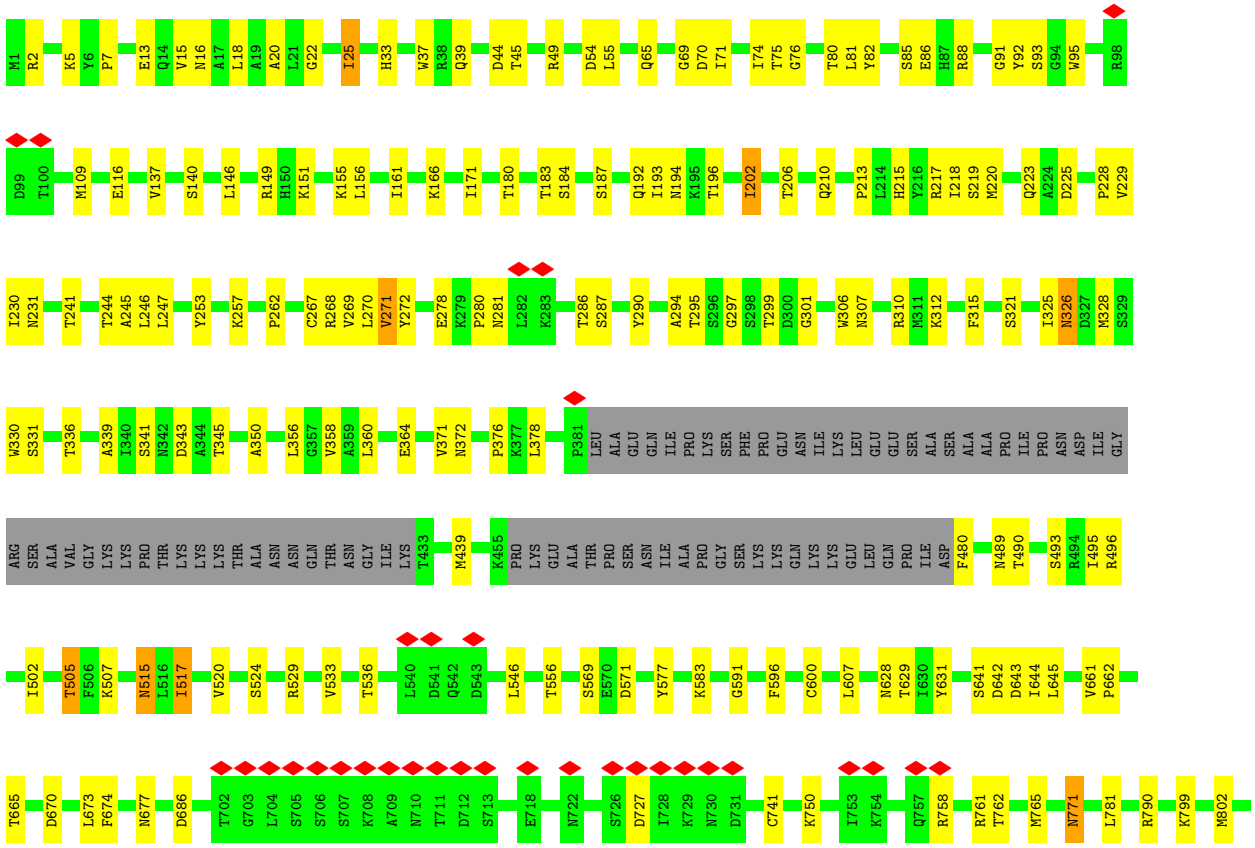
Chain G:





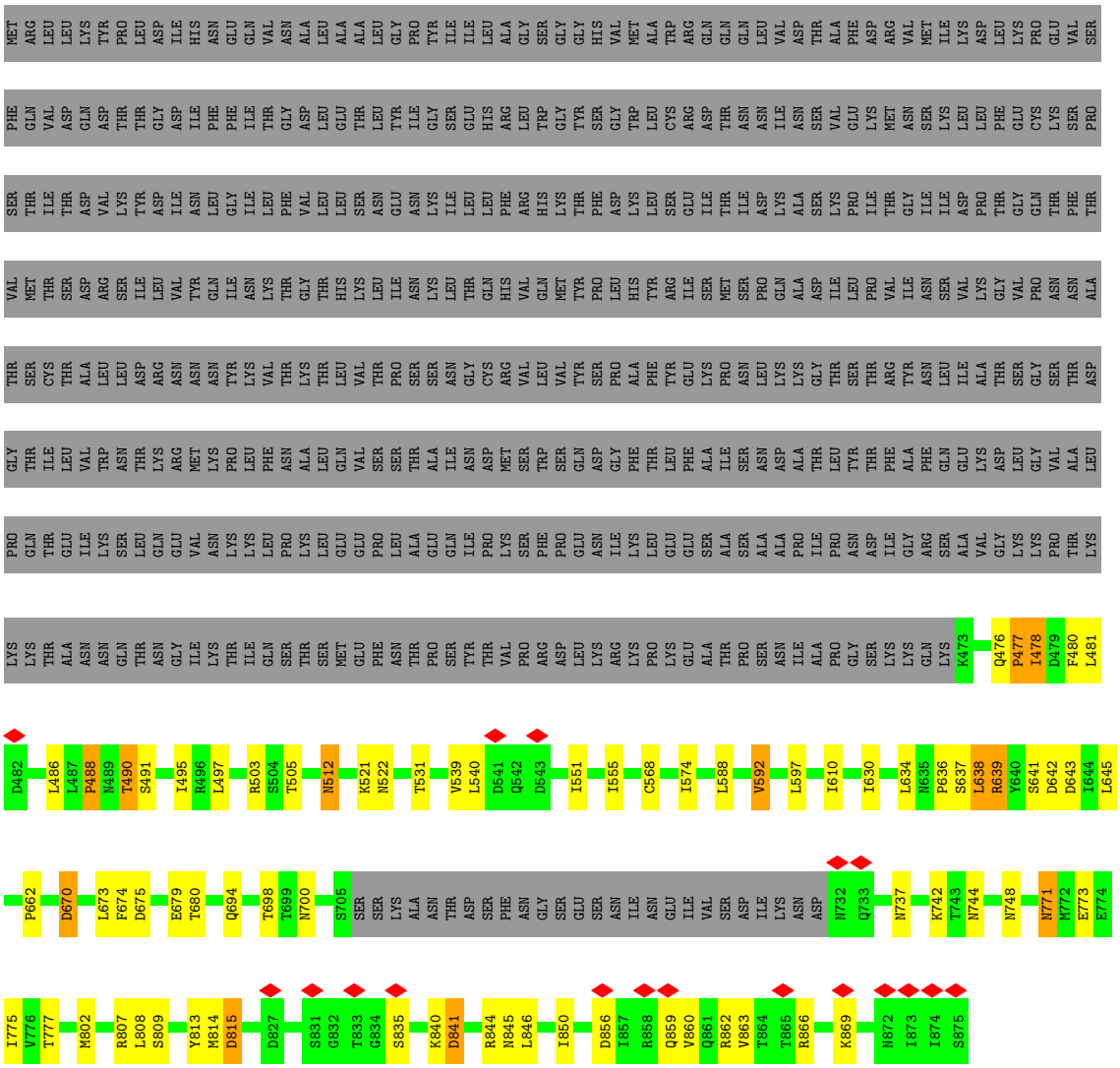
- Molecule 2: Protein HIR2

Chain B:



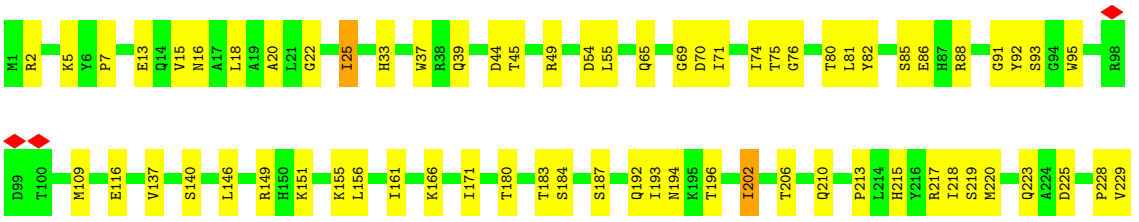
• Molecule 2: Protein HIR2

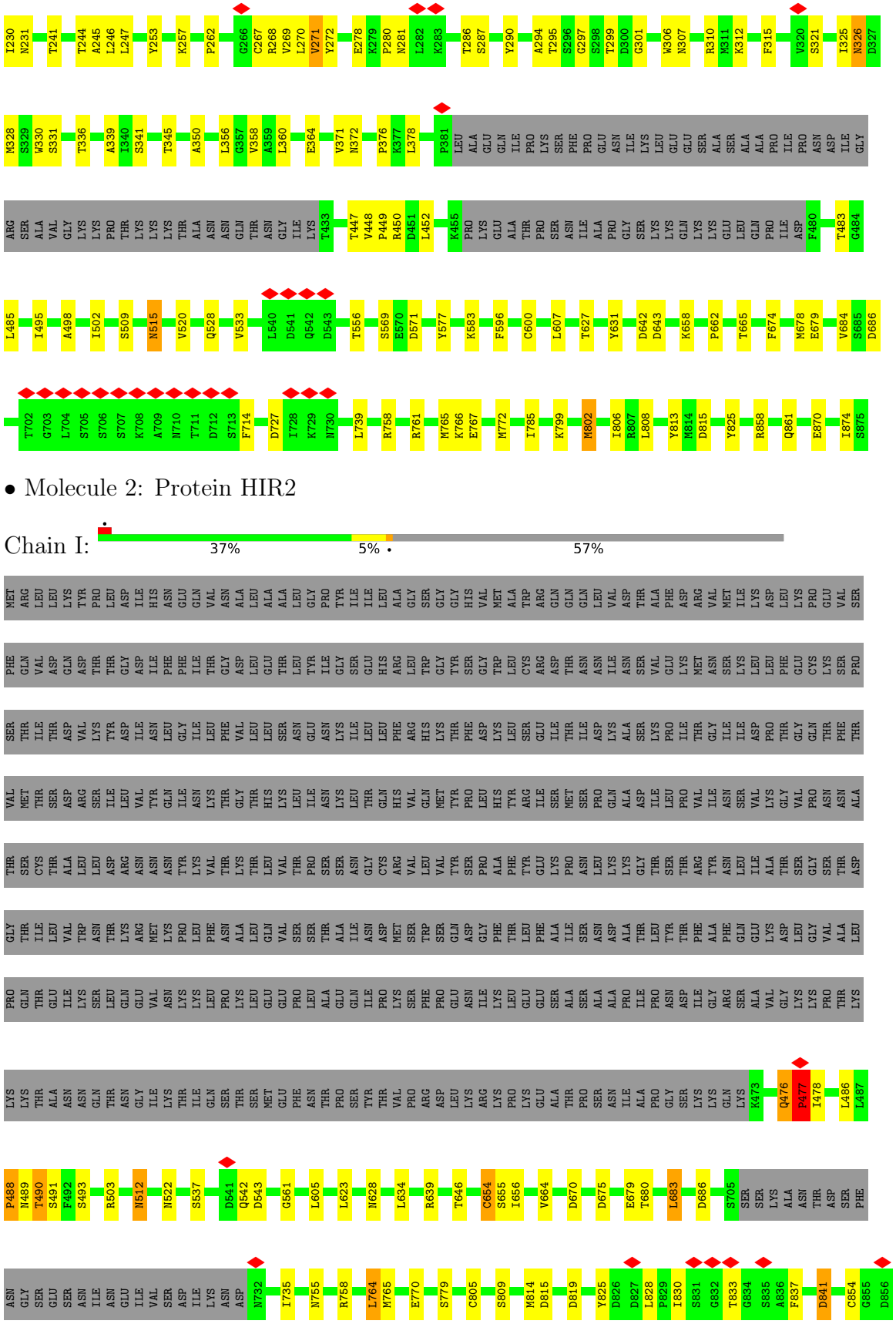
Chain C:



• Molecule 2: Protein HIR2

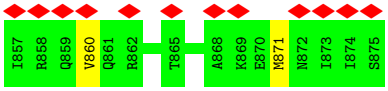
Chain H:





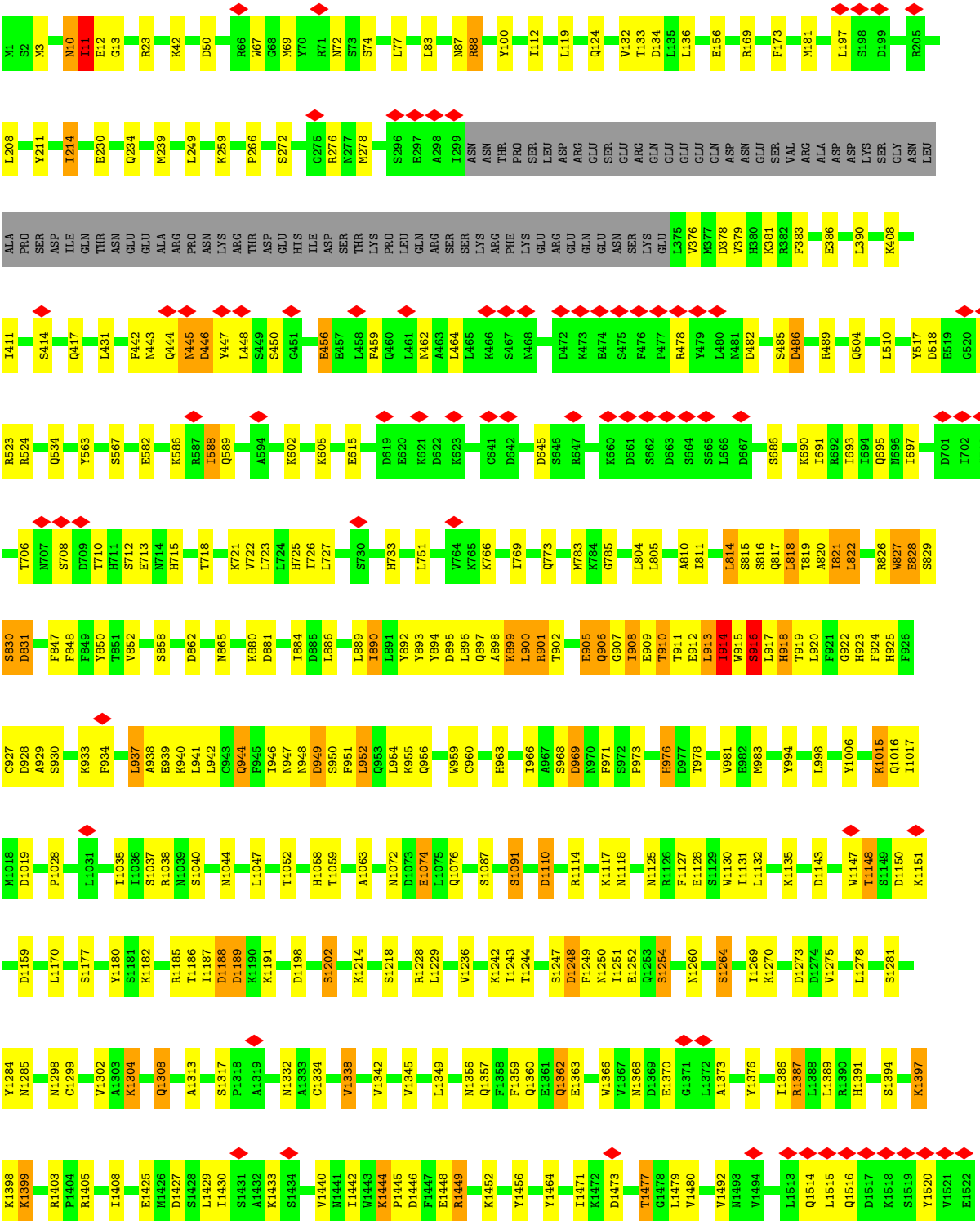
- Molecule 2: Protein HIR2

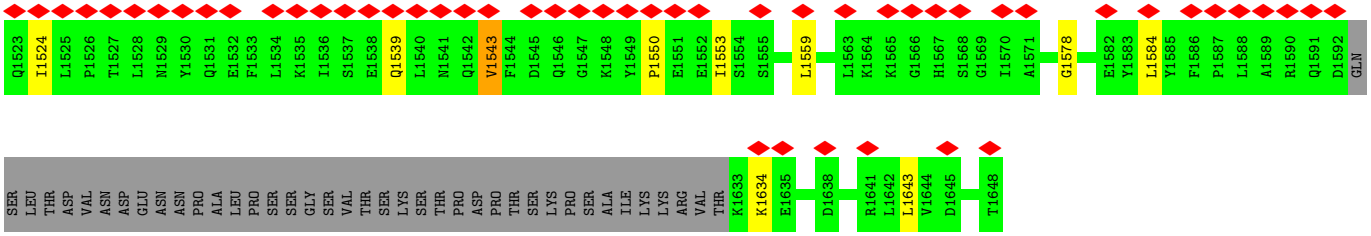
Chain I: 37% 5% 57%



- Molecule 3: Histone transcription regulator 3

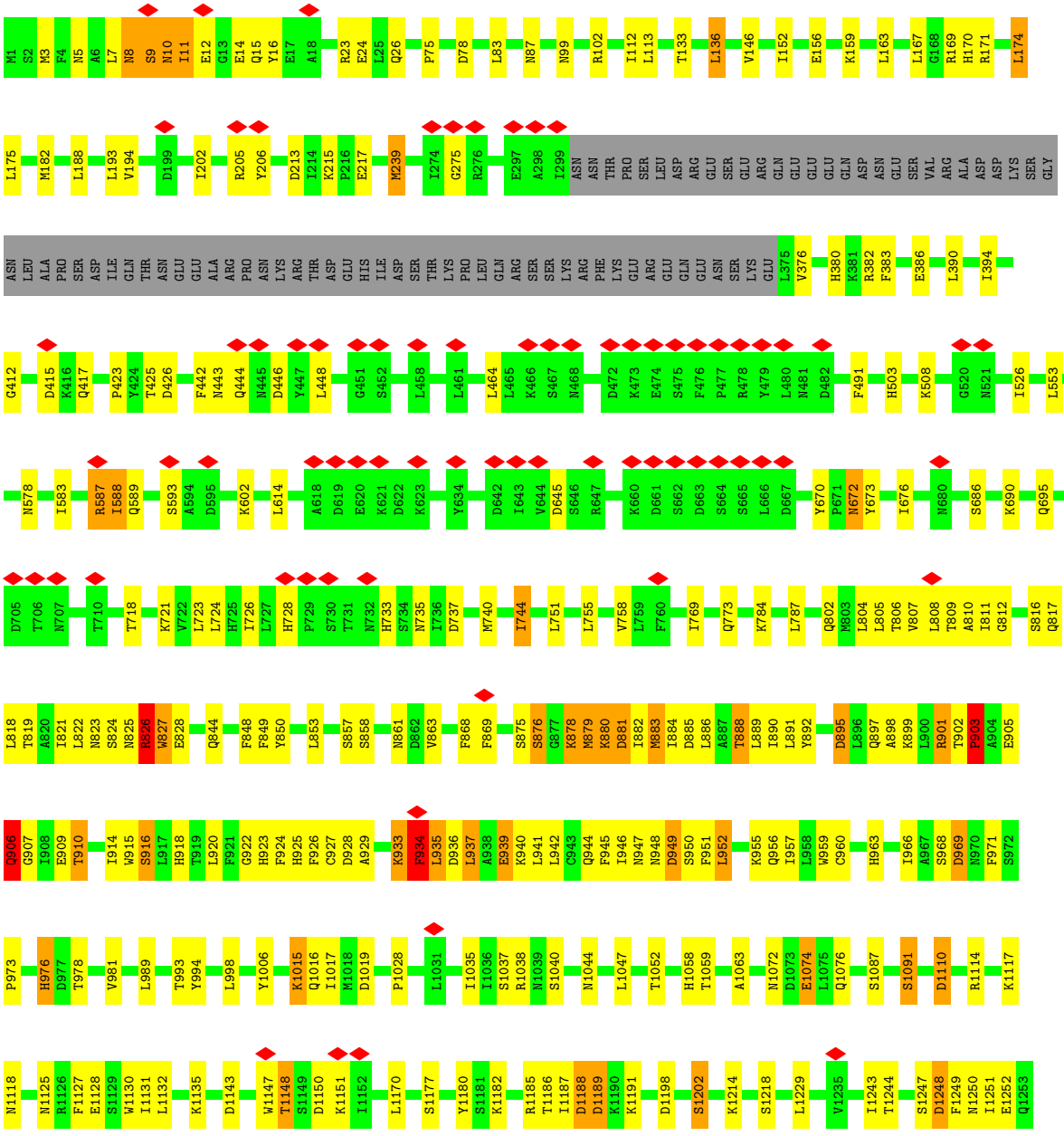
Chain D:

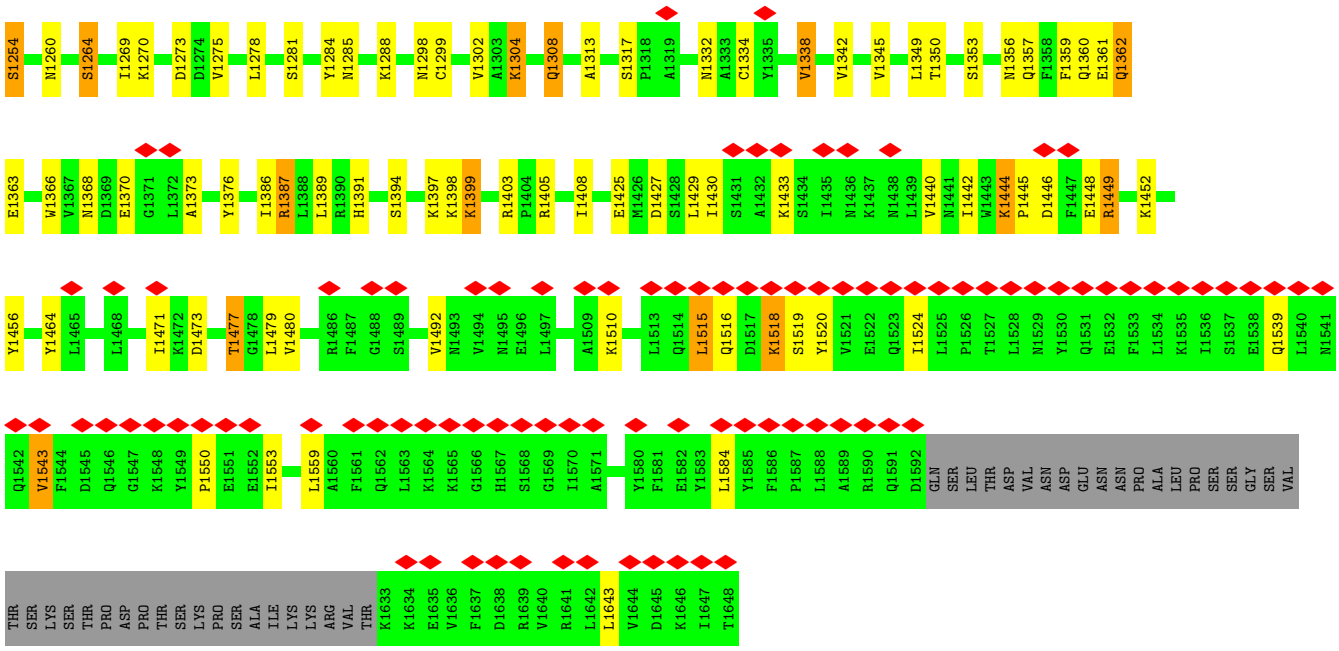




• Molecule 3: Histone transcription regulator 3

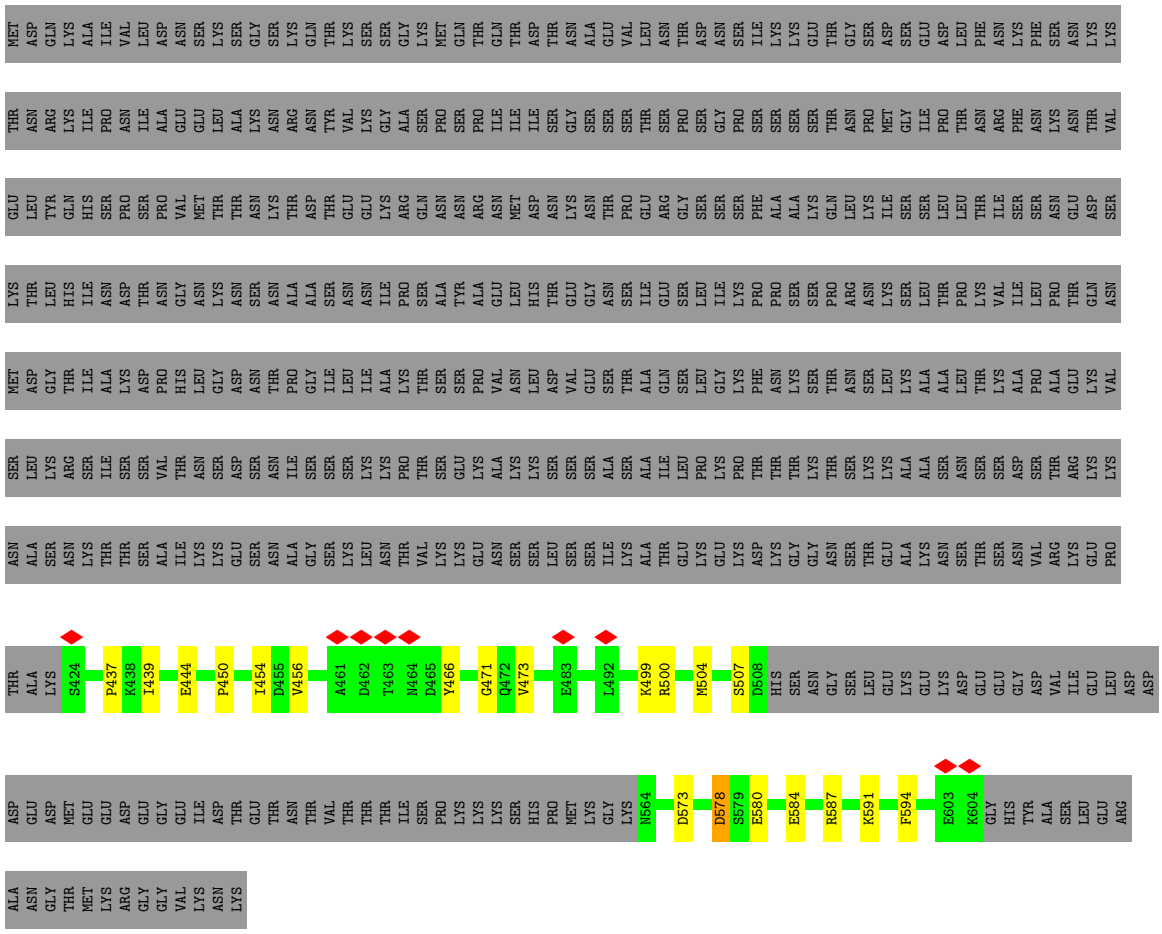
Chain J:





- Molecule 4: Histone promoter control protein 2

Chain E:



- Molecule 4: Histone promoter control protein 2

Chain F: 6% 93%

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

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

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

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

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

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

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

THR ALA LYS SER PRO LYS ARG GLU LEU VAL ALA ALA PRO THR VAL SER PRO PRO LYS ILE LEU GLN THR ALA GLU THR LYS ALA LYS GLU PRO SER I452 L453 I454 D455 V456 P457 L458 Y459 Q460 A461 D462 T463 N464 D465 Y466 L467 D468 E469 N470 G471 L480 E483 K484 Y485 H486 PRO LYS

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

THR THR ILE SER PRO LYS LYS LYS SER HIS PRO MET LYS GLY LYS ASN LEU ILE GLY LYS TYR ASP VAL GLU ASP PRO PHE ILE ASP ASP SER GLU LEU LEU TRP GLU GLU GLN ARG ALA ALA THR K591 D592 F598 GLY PRO LEU ILE GLU LYS GLY HIS TYR ALA SER LEU GLU ARG

ALA ASN GLY THR MET LYS ARG GLY GLY VAL LYS ASN LYS

- Molecule 4: Histone promoter control protein 2

Chain K: 16% 80%

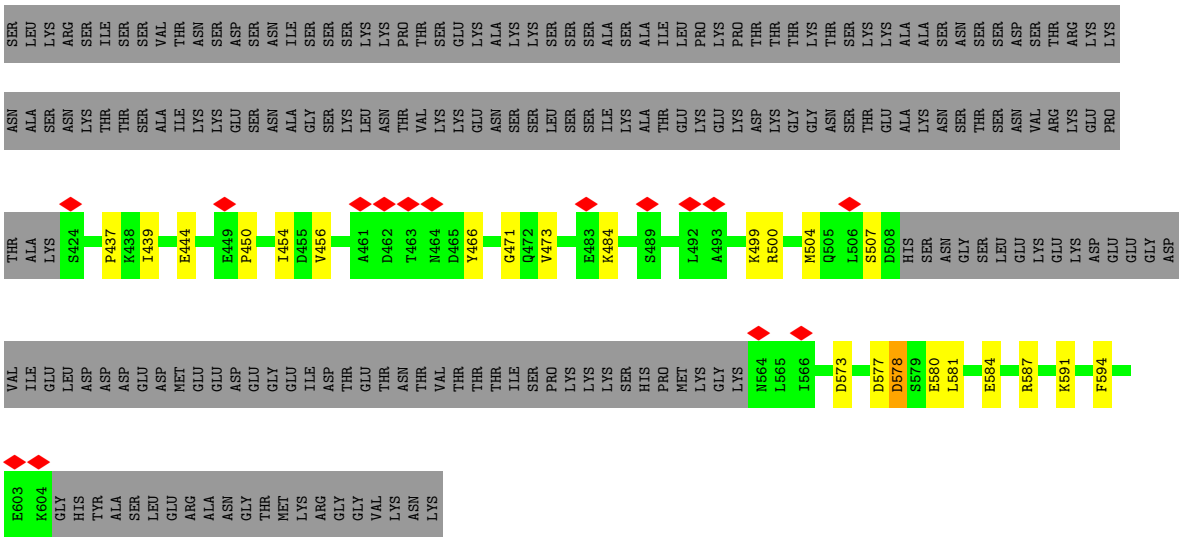
MET ASP GLN LYS ALA ILE VAL LEU ASP ASN SER LYS SER GLY SER LYS GLN THR LYS SER SER GLY LYS MET GLN THR GLN THR ASP THR ASN ALA GLU VAL LEU ASN THR ASP ASN SER ILE LYS LYS GLU THR GLY SER ASP SER GLU ASP LEU PHE ASN LYS PHE SER ASN LYS LYS

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

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

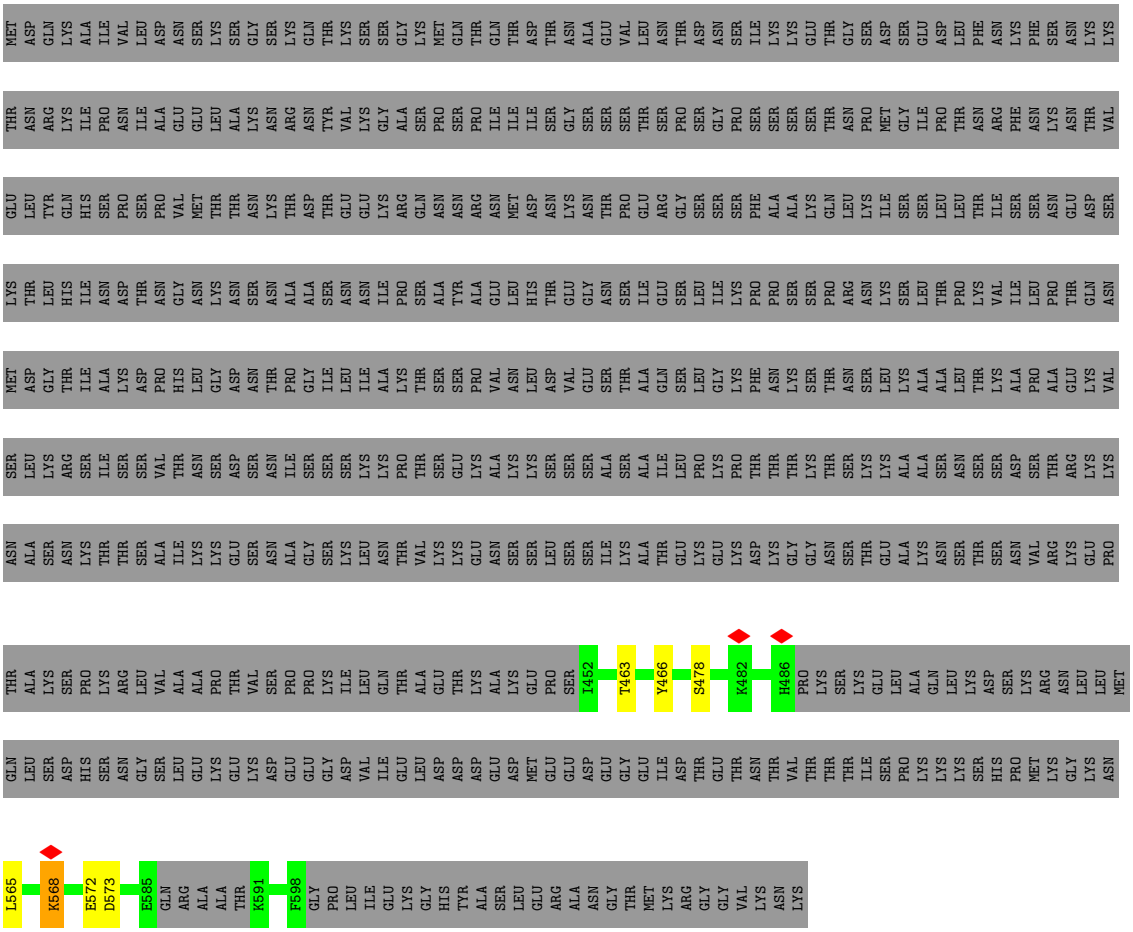
LYS THR LEU HIS ILE ASN ASP THR ASN GLY ASN LYS ASN SER ASN ALA ALA SER ASN ASN ILE PRO SER ALA TYR ALA GLU LEU HIS THR GLU GLY ASN SER ILE GLU SER LEU ILE LYS PRO PRO SER SER PRO ARG ASN LYS SER LEU THR PRO LYS VAL ILE LEU PRO THR GLN ASN

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



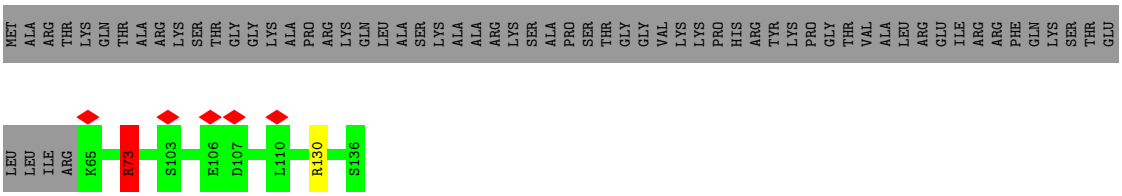
- Molecule 4: Histone promoter control protein 2

Chain L: 9% 90%



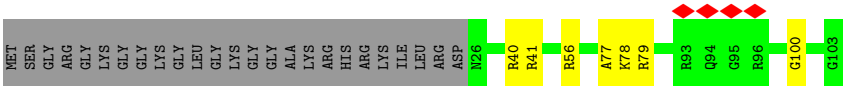
- Molecule 5: Histone H3

Chain M: 51% 47%



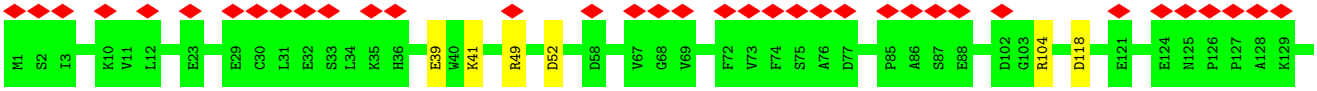
• Molecule 6: Histone H4

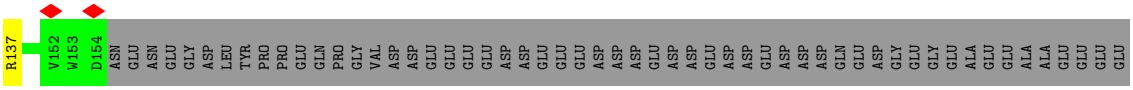
Chain N:

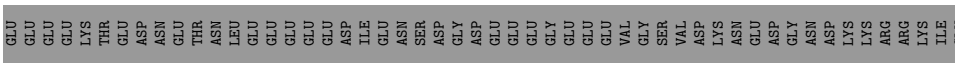


• Molecule 7: Histone chaperone

Chain O:







4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	639629	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 ($e^-/Å^2$)	42	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.190	Depositor
Minimum map value	0.000	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	723.52, 754.8, 618.8	wwPDB
Map dimensions	532, 555, 455	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.36, 1.36, 1.36	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.63	0/5386	1.06	7/7300 (0.1%)
1	G	0.63	0/5269	1.08	12/7144 (0.2%)
2	B	0.23	0/6482	0.54	0/8786
2	C	0.27	0/3080	0.66	3/4171 (0.1%)
2	H	0.23	0/6482	0.53	3/8786 (0.0%)
2	I	0.29	0/3080	0.71	5/4171 (0.1%)
3	D	0.30	0/12889	0.64	9/17409 (0.1%)
3	J	0.31	1/12890 (0.0%)	0.62	11/17410 (0.1%)
4	E	0.22	0/1032	0.48	0/1397
4	F	0.78	0/370	1.26	0/500
4	K	0.22	0/1032	0.48	0/1397
4	L	0.78	0/552	1.22	0/747
5	M	0.84	0/590	1.44	2/789 (0.3%)
6	N	0.87	0/625	1.44	3/837 (0.4%)
7	O	0.74	0/1263	1.22	2/1722 (0.1%)
All	All	0.41	1/61022 (0.0%)	0.76	57/82566 (0.1%)

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	C	0	2
2	I	0	1
3	D	0	4
3	J	0	4
4	F	0	1
4	L	0	1
5	M	0	1
6	N	0	2
7	O	0	2
All	All	0	18

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	J	194	VAL	C-N	5.05	1.40	1.33

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	588	ILE	N-CA-C	-9.78	103.15	112.83
1	G	642	GLN	CA-CB-CG	9.00	132.09	114.10
2	I	871	MET	N-CA-C	-8.65	102.74	113.38
1	G	791	GLN	CA-CB-CG	7.93	129.97	114.10
1	G	174	ARG	NE-CZ-NH2	7.27	125.74	119.20

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	476	GLN	Peptide
2	C	636	PRO	Peptide
3	D	10	ASN	Peptide
3	D	444	GLN	Peptide
3	D	445	ASN	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	5272	0	5314	82	0
1	G	5155	0	5180	55	0
2	B	6359	0	6419	114	0
2	C	3022	0	3048	44	0
2	H	6359	0	6419	113	0
2	I	3022	0	3048	31	0
3	D	12616	0	12567	284	0
3	J	12617	0	12567	278	0
4	E	1012	0	1019	14	0
4	F	362	0	345	3	0
4	K	1012	0	1019	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	L	540	0	504	6	0
5	M	584	0	614	1	0
6	N	618	0	660	23	0
7	O	1234	0	1219	1	0
All	All	59784	0	59942	965	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 965 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:D:10:ASN:CA	3:D:11:ILE:HG22	1.26	1.61
3:D:1634:LYS:HD3	6:N:78:LYS:CB	1.29	1.61
3:D:10:ASN:CB	3:D:11:ILE:HG22	1.27	1.59
3:D:10:ASN:HB3	3:D:11:ILE:CG2	1.22	1.57
3:D:379:VAL:HG21	3:D:923:HIS:CD2	1.45	1.48

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	655/840 (78%)	620 (95%)	32 (5%)	3 (0%)	24	49
1	G	641/840 (76%)	600 (94%)	38 (6%)	3 (0%)	24	49
2	B	794/875 (91%)	768 (97%)	26 (3%)	0	100	100
2	C	373/875 (43%)	353 (95%)	15 (4%)	5 (1%)	9	26
2	H	794/875 (91%)	764 (96%)	29 (4%)	1 (0%)	48	72
2	I	373/875 (43%)	357 (96%)	14 (4%)	2 (0%)	24	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	D	1527/1648 (93%)	1445 (95%)	72 (5%)	10 (1%)	18	40
3	J	1527/1648 (93%)	1455 (95%)	59 (4%)	13 (1%)	14	34
4	E	122/625 (20%)	118 (97%)	4 (3%)	0	100	100
4	F	39/625 (6%)	39 (100%)	0	0	100	100
4	K	122/625 (20%)	118 (97%)	4 (3%)	0	100	100
4	L	58/625 (9%)	55 (95%)	3 (5%)	0	100	100
5	M	70/136 (52%)	68 (97%)	2 (3%)	0	100	100
6	N	76/103 (74%)	74 (97%)	2 (3%)	0	100	100
7	O	152/279 (54%)	148 (97%)	4 (3%)	0	100	100
All	All	7323/11494 (64%)	6982 (95%)	304 (4%)	37 (0%)	26	49

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	477	PRO
2	C	478	ILE
2	C	488	PRO
3	D	11	ILE
2	I	488	PRO

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	596/753 (79%)	574 (96%)	22 (4%)	30	55
1	G	583/753 (77%)	557 (96%)	26 (4%)	24	50
2	B	727/790 (92%)	697 (96%)	30 (4%)	27	53
2	C	343/790 (43%)	326 (95%)	17 (5%)	22	47
2	H	727/790 (92%)	701 (96%)	26 (4%)	31	56
2	I	343/790 (43%)	325 (95%)	18 (5%)	21	46
3	D	1419/1528 (93%)	1333 (94%)	86 (6%)	17	40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	J	1420/1528 (93%)	1328 (94%)	92 (6%)	15	37
4	E	114/557 (20%)	112 (98%)	2 (2%)	51	72
4	F	40/557 (7%)	39 (98%)	1 (2%)	42	66
4	K	114/557 (20%)	112 (98%)	2 (2%)	51	72
4	L	60/557 (11%)	58 (97%)	2 (3%)	33	58
5	M	62/113 (55%)	62 (100%)	0	100	100
6	N	65/81 (80%)	65 (100%)	0	100	100
7	O	142/252 (56%)	141 (99%)	1 (1%)	76	87
All	All	6755/10396 (65%)	6430 (95%)	325 (5%)	24	48

5 of 325 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	J	174	LEU
3	J	1229	LEU
3	J	817	GLN
3	J	933	LYS
3	J	1386	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 82 such sidechains are listed below:

Mol	Chain	Res	Type
3	J	246	ASN
3	J	1260	ASN
3	J	417	GLN
3	J	735	ASN
4	K	476	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.

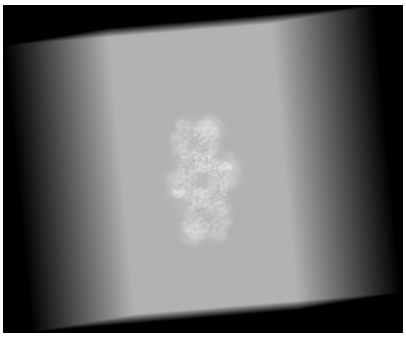
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-40037. These allow visual inspection of the internal detail of the map and identification of artifacts.

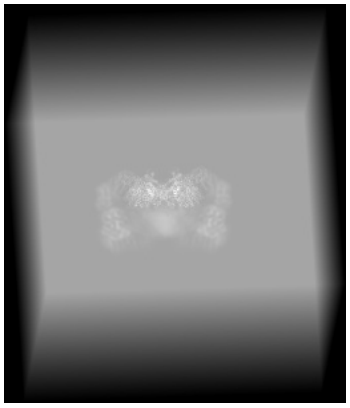
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

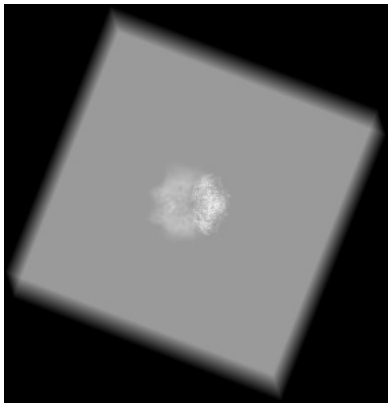
6.1.1 Primary map



X



Y

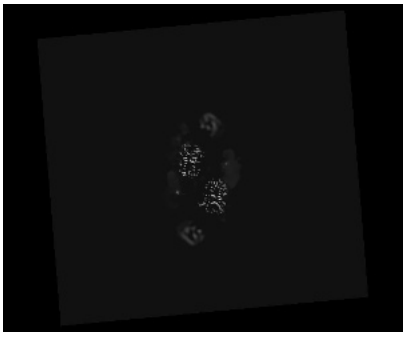


Z

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

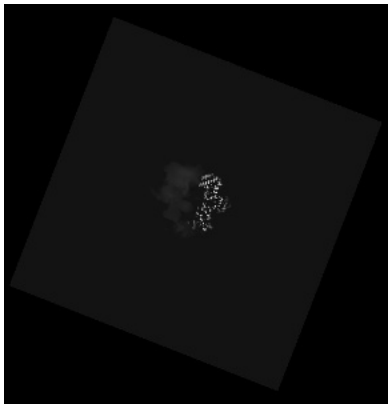
6.2 Central slices (i)

6.2.1 Primary map



X Index: 266

Y Index: 277

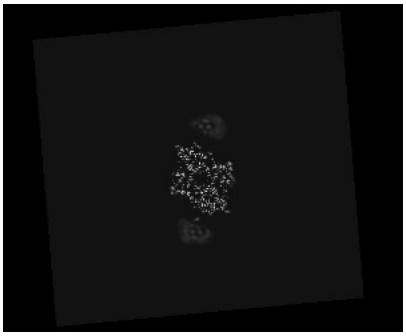


Z Index: 227

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

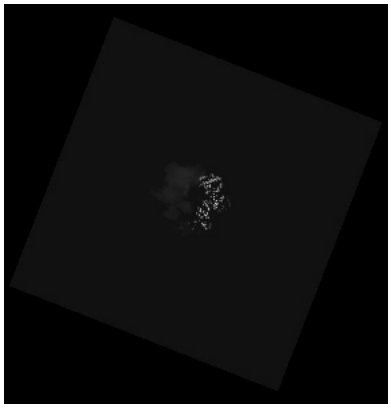
6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 282

Y Index: 285

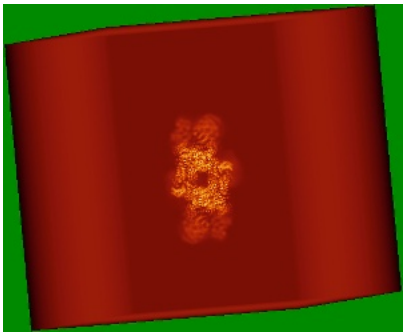


Z Index: 229

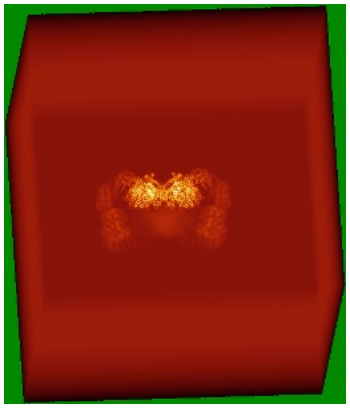
The images above show the largest variance slices of the map in three orthogonal directions.

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

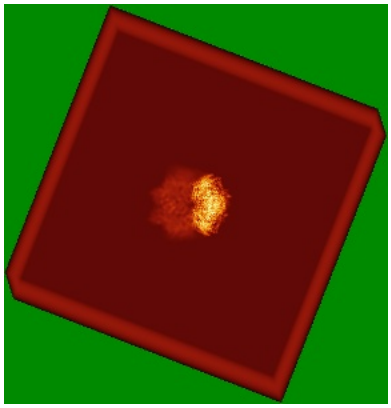
6.4.1 Primary map



X



Y

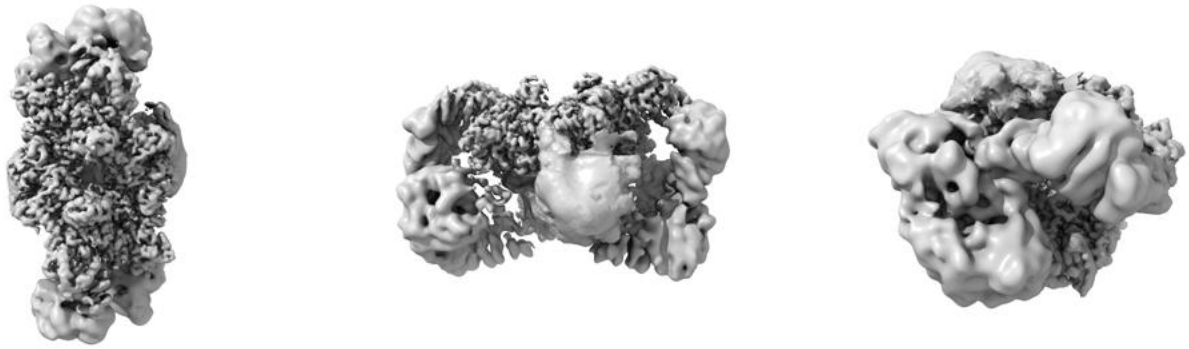


Z

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 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

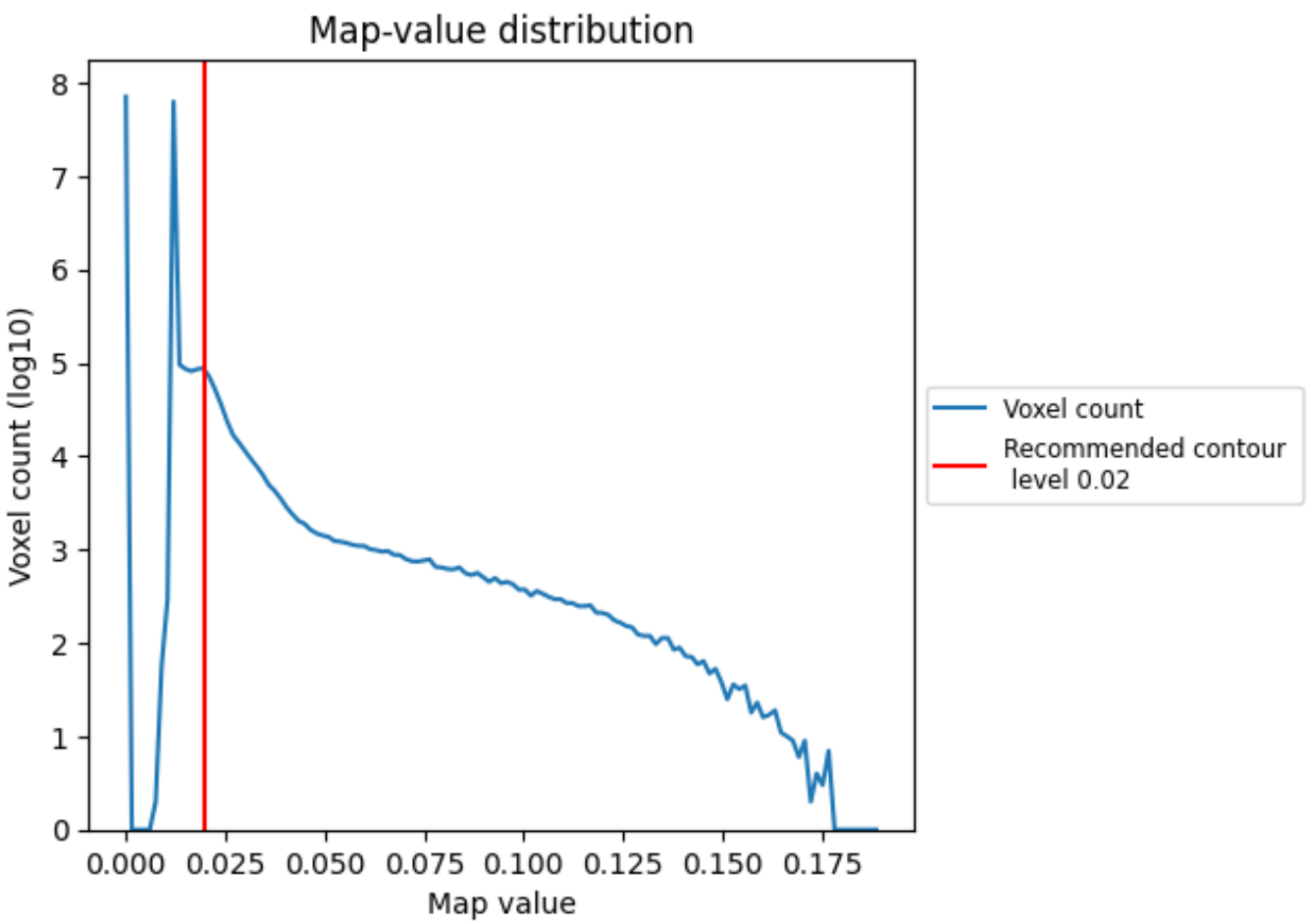
6.6 Mask visualisation (i)

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

7 Map analysis (i)

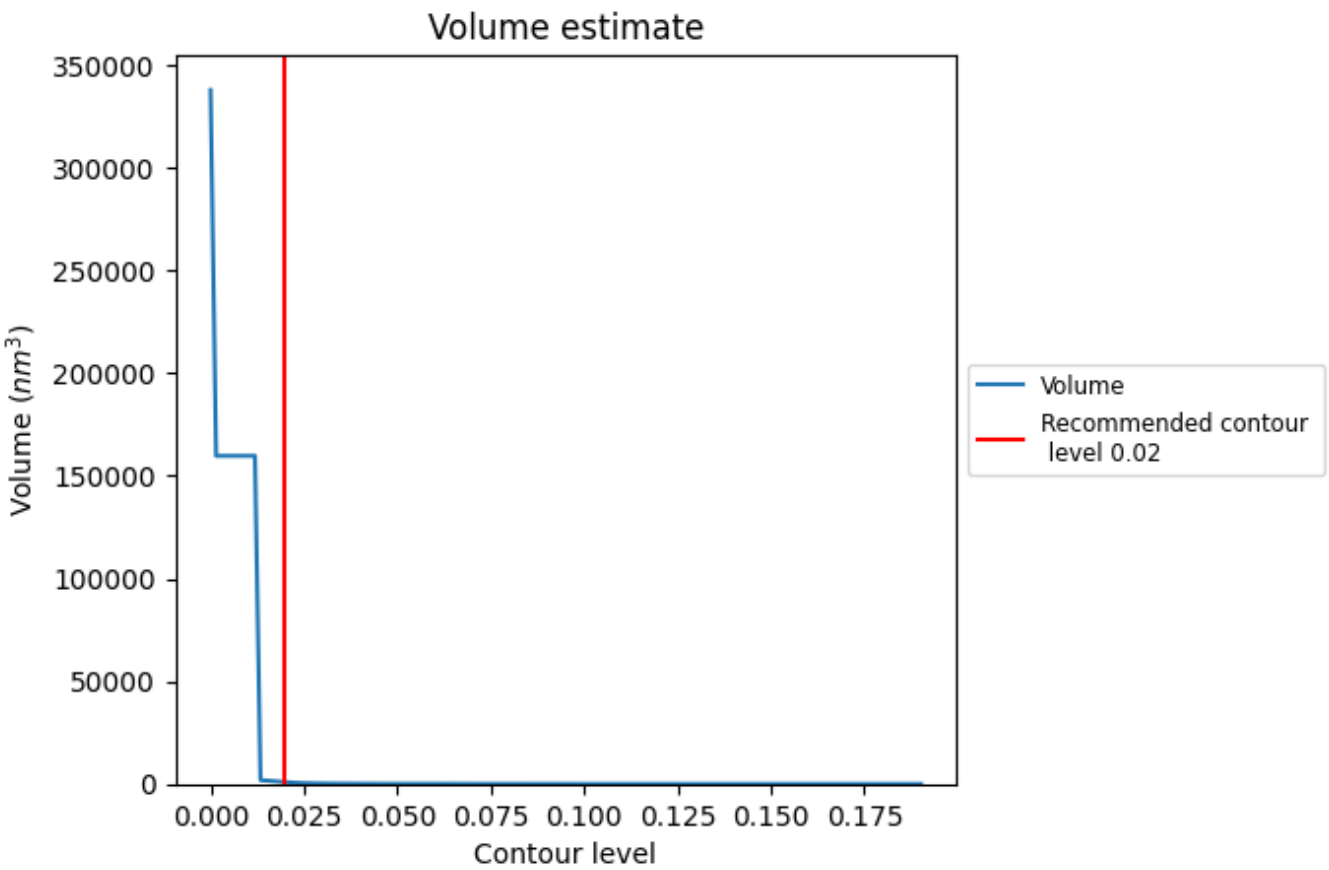
This section contains the results of statistical analysis of the map.

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 910 nm^3; this corresponds to an approximate mass of 822 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)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

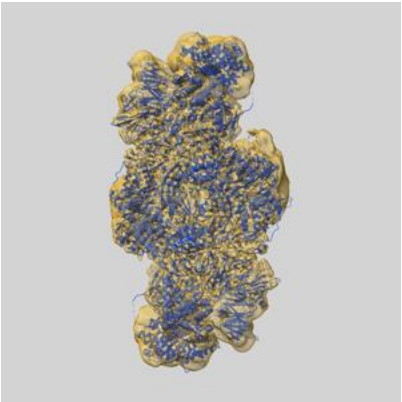
8 Fourier-Shell correlation (i)

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

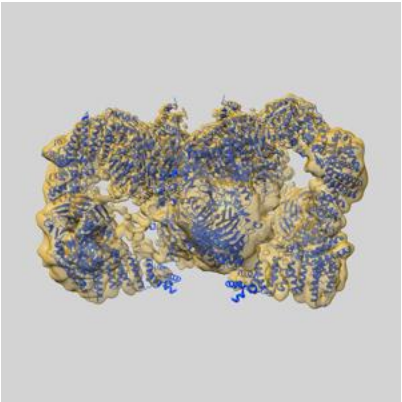
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-40037 and PDB model 8GHN. Per-residue inclusion information can be found in section 3 on page 6.

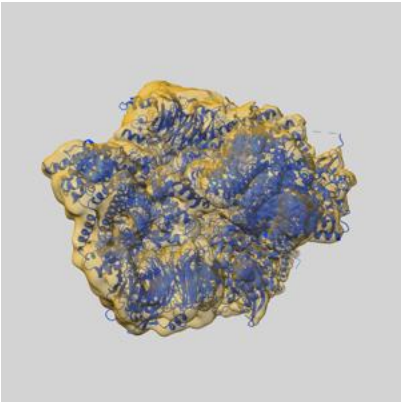
9.1 Map-model overlay (i)



X



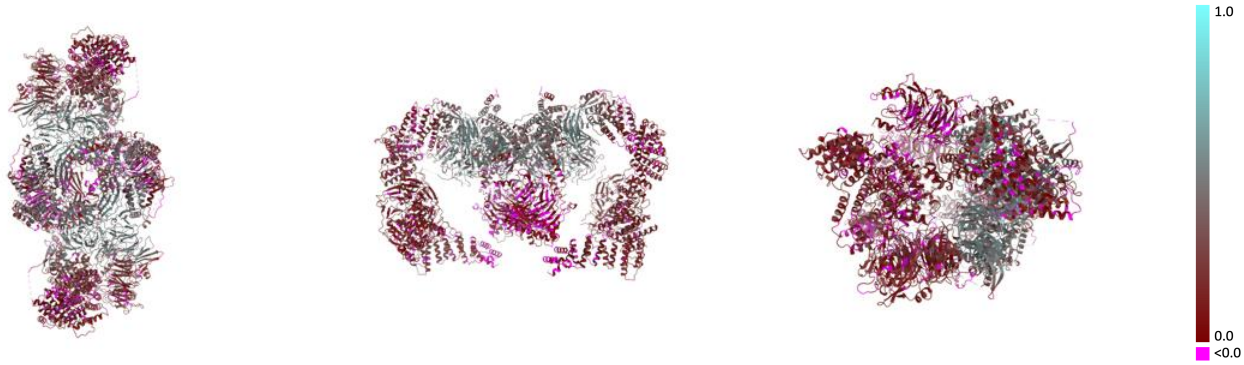
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

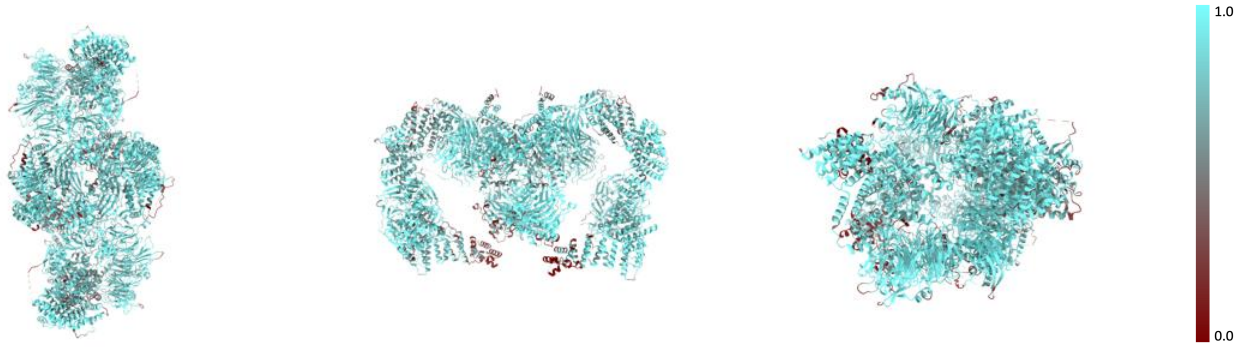
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

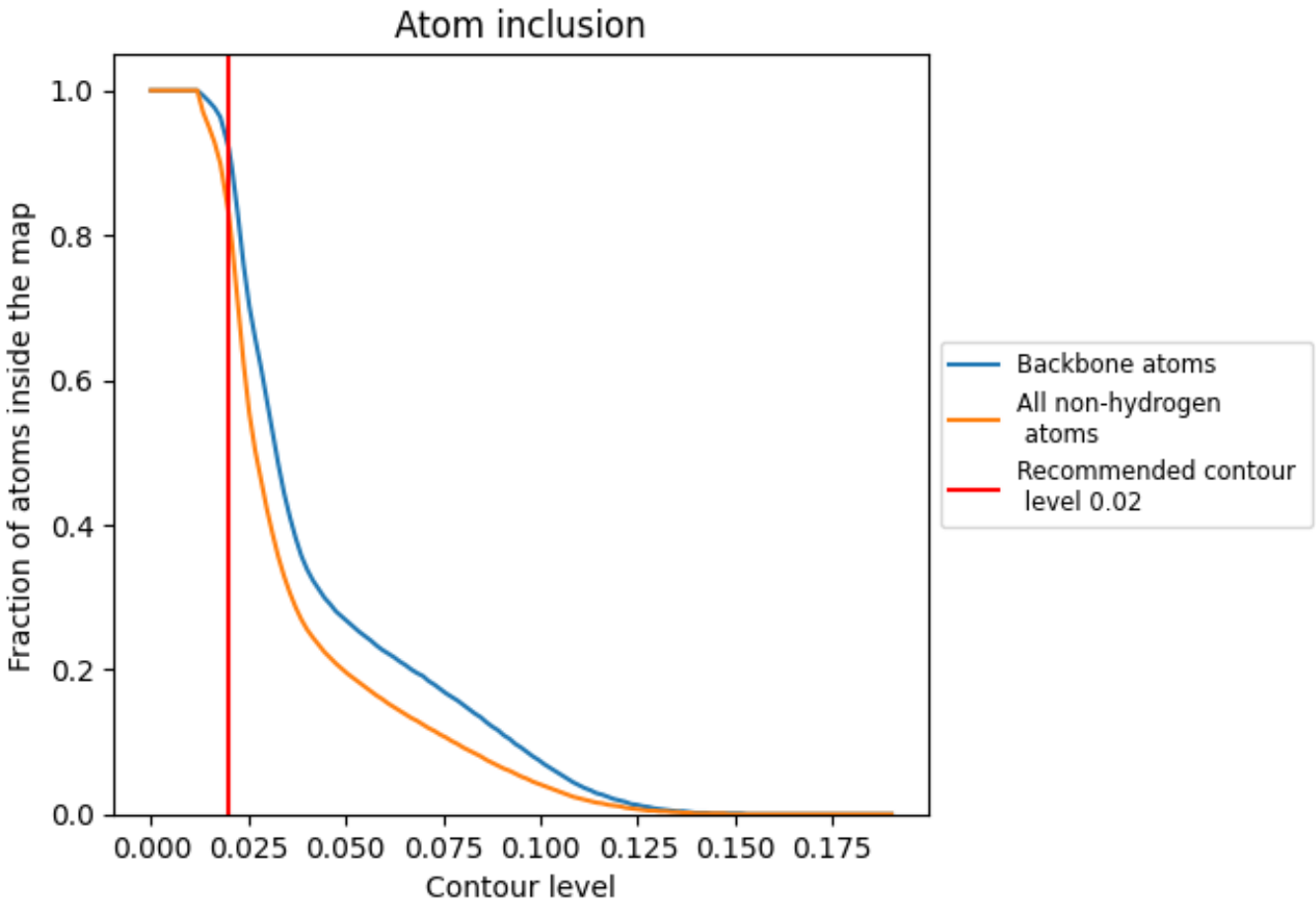
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

9.4 Atom inclusion (i)



At the recommended contour level, 92% of all backbone atoms, 83% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8290	0.2320
A	0.8490	0.2160
B	0.8800	0.3060
C	0.8750	0.4510
D	0.8060	0.1860
E	0.8510	0.1440
F	0.4610	-0.0110
G	0.8980	0.2180
H	0.8720	0.2980
I	0.8660	0.4540
J	0.7590	0.1820
K	0.8010	0.1290
L	0.9060	0.0290
M	0.8920	0.0190
N	0.8910	0.0470
O	0.7220	0.0400