wwPDB EM Validation Summary Report

Nov 24, 2025 – 01:33 PM EST

PDB ID	:	9YOQ / pdb_00009yoq
EMDB ID	:	EMD-73269
Title	:	Core module of ctSAGA
Authors	:	Mattoo, R.U.H.; Chen, D.H.; Bushnell, D.A.; Tamir, S.; Kornberg, R.D.
Deposited on	:	2025-10-13
Resolution	:	2.60 Å(reported)

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

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

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

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

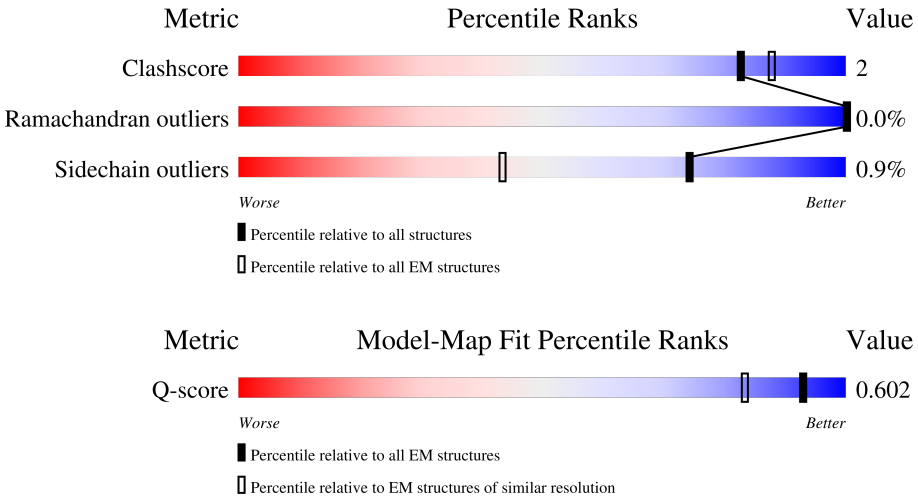
EMDB validation analysis	:	0.0.1.dev129
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.46

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 2.60 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	8728 (2.10 - 3.10)

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	3893	5% 94%
2	B	1192	19% 80%
3	C	433	5% 37% 60%
4	D	767	16% 66% 32%

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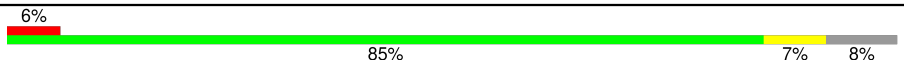
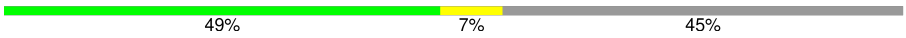
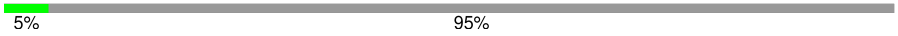
Mol	Chain	Length	Quality of chain
5	E	480	
6	G	204	
7	H	485	
8	I	770	
9	K	1360	
10	Q	1273	
11	F	277	

2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 41791 atoms, of which 20646 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 Non-specific serine/threonine protein kinase.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	225	3656	1184	1790	323	350	9	0	0

- Molecule 2 is a protein called Spt20-like SEP domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
2	B	236	3915	1269	1952	332	355	7	0	0

- Molecule 3 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	C	174	2888	911	1446	255	271	5	0	0

- Molecule 4 is a protein called Transcription initiation factor TFIID subunit 5.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	D	523	8240	2632	4096	730	762	20	0	0

- Molecule 5 is a protein called Transcription initiation factor TFIID subunit 6.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	E	443	6959	2193	3519	598	639	10	0	0

- Molecule 6 is a protein called Transcription initiation factor TFIID subunit 10.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
6	G	113	1751	553	874	156	164	4	0	0

- Molecule 7 is a protein called Putative transcriptional coactivator HFI1 protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	H	254	Total	C	H	N	O	S	0	0
			3898	1238	1920	346	382	12		

- Molecule 8 is a protein called Transcription initiation factor TFIID subunit 12.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	I	133	Total	C	H	N	O	S	0	0
			2078	642	1053	187	191	5		

- Molecule 9 is a protein called Putative transcriptional activator protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	K	370	Total	C	H	N	O	S	0	0
			5982	1888	2978	543	564	9		

- Molecule 10 is a protein called SCA7 domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	Q	62	Total	C	H	N	O	S	0	0
			950	303	472	86	88	1		

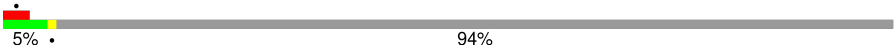
- Molecule 11 is a protein called Putative transcription initiation factor.

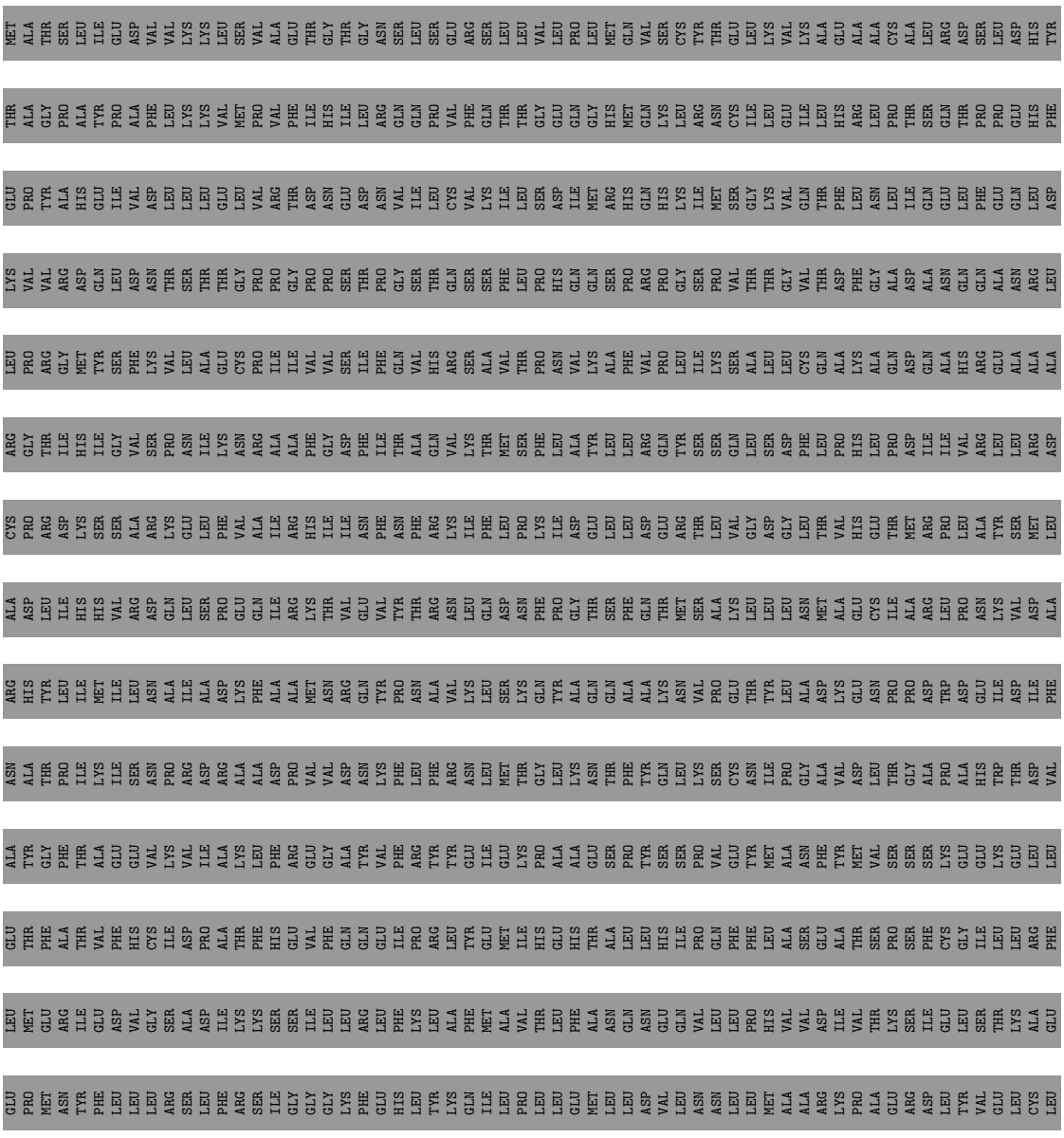
Mol	Chain	Residues	Atoms						AltConf	Trace
11	F	123	Total	C	H	N	O	S	0	0
			1474	586	546	172	169	1		

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: Non-specific serine/threonine protein kinase

Chain A: 



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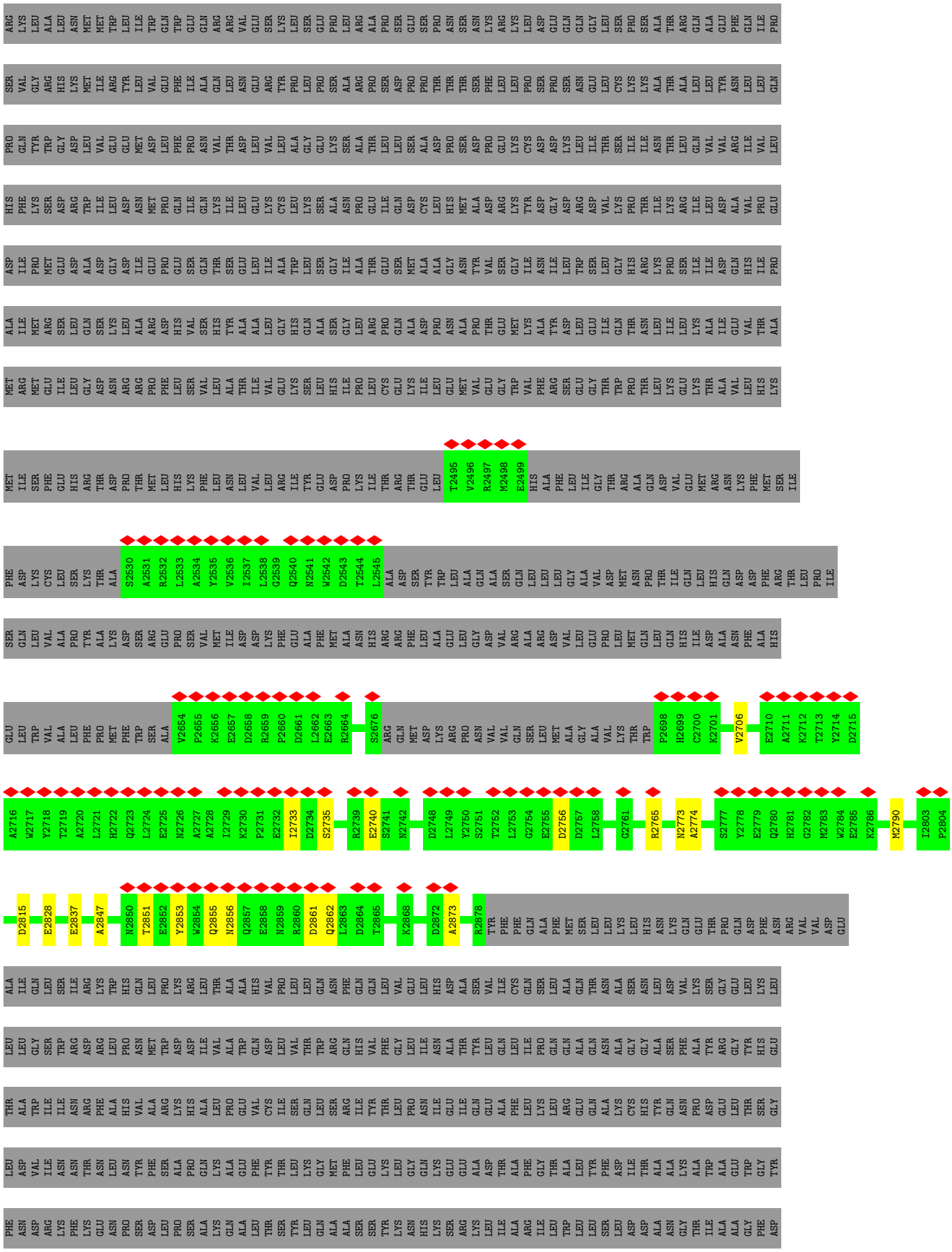
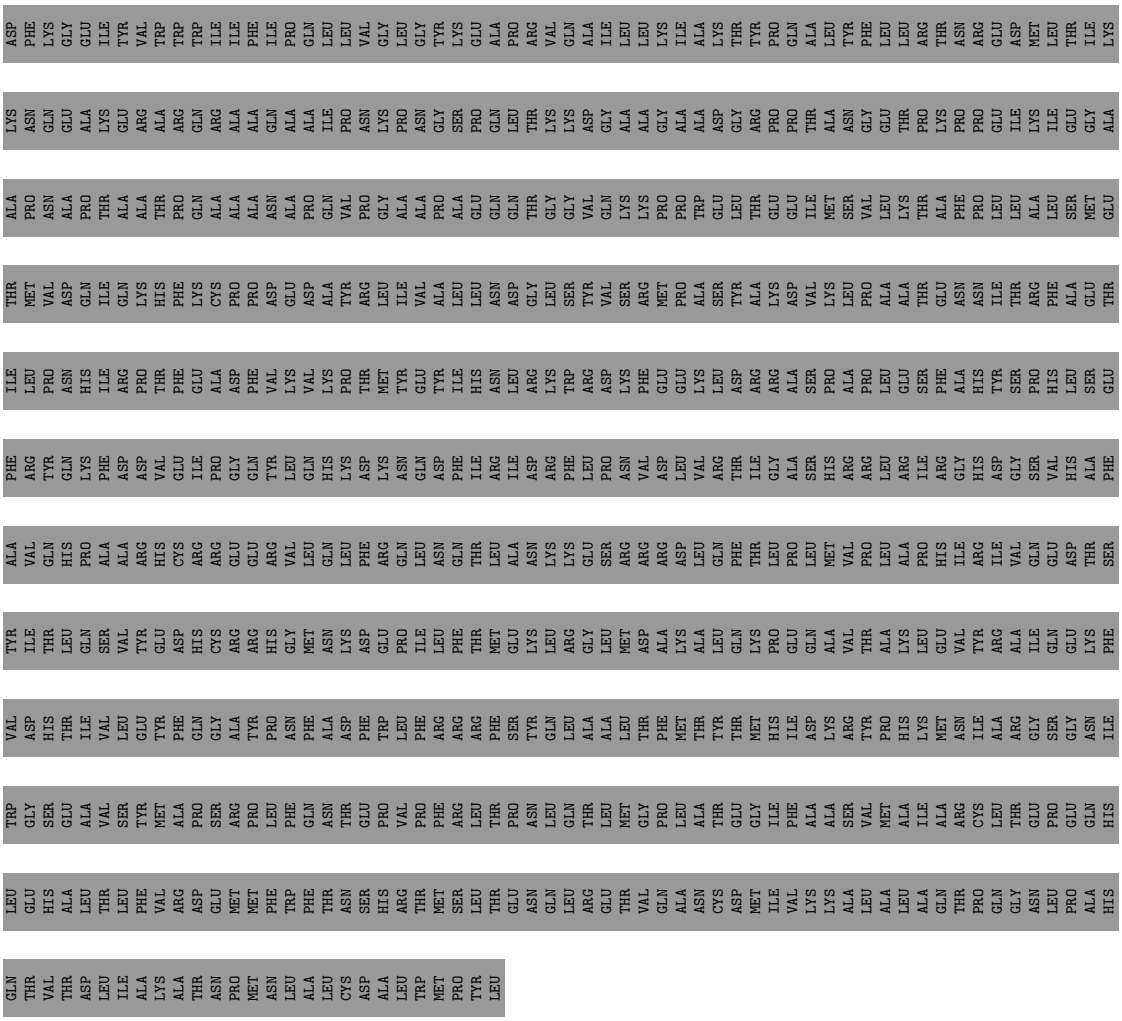
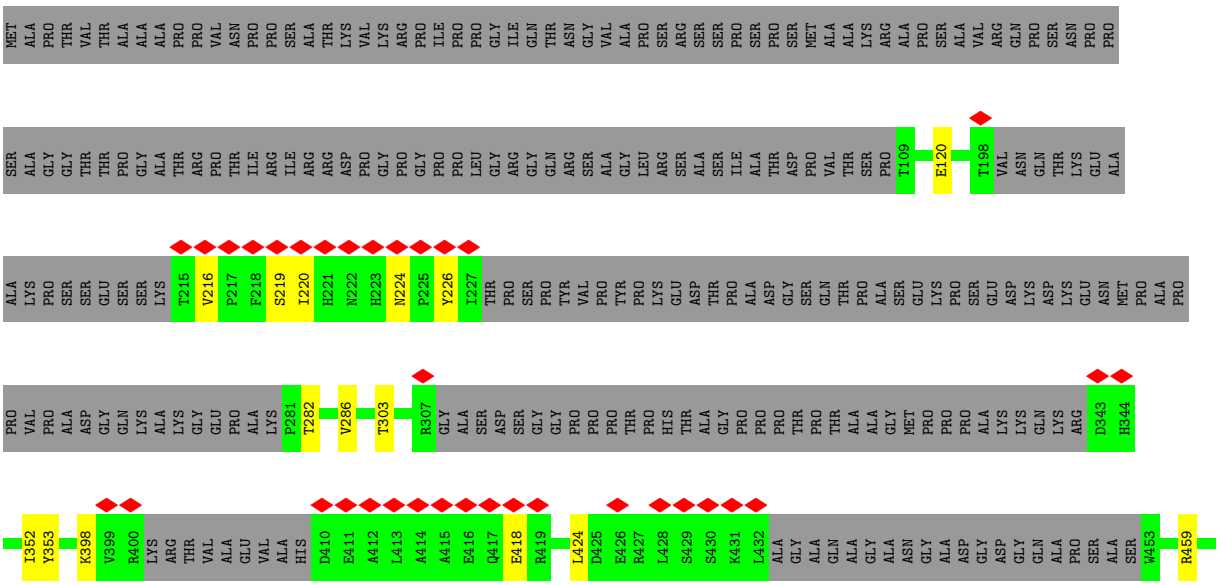
SER ILE GLU ALA ILE ALA ALA GLN ALA GLU VAL TRP GLU LEU LEU GLU PRO HIS LYS LYS HIS ILE LEU GLY PRO ILE TYR ALA LYS PRO LEU ARG ALA LEU PRO PHE ALA ILE GLN ILE GLY TYR ILE ASP ALA VAL THR TYR TYR MET SER LEU LYS ARG ASP PHE VAL PRO
PHE ASP GLU ASN LEU ASN ARG LEU LEU MET GLU SER LEU ASP ALA SER ASP GLU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

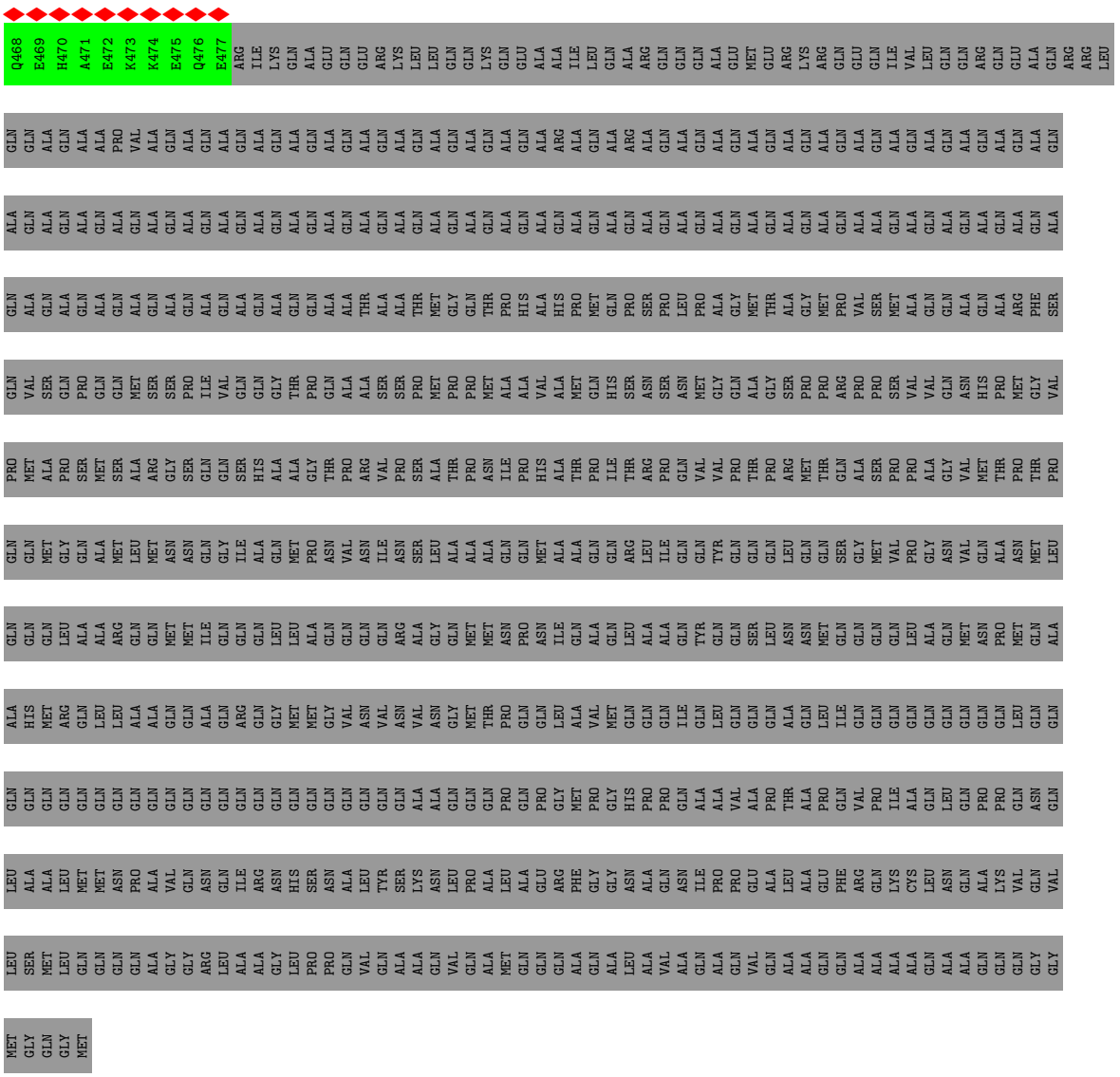

T2495 V2496 R2497 M2498 E2499
S2530 A2531 R2532 L2533 A2534 Y2535 V2536 I2537 L2538 G2539 Q2540 N2541 W2542 D2543 T2544 L2545
V2654 P2655 K2656 E2657 D2658 R2659 P2660 D2661 L2662 E2663 R2664 S2676
P2698 H2699 C2700 K2701 V2706 E2710 A2711 K2712 T2713 Y2714 D2715
A2716 W2717 Y2718 T2719 A2720 L2721 H2722 Q2723 L2724 E2725 N2726 A2727 A2728 I2729 K2730 P2731 E2732 I2733 D2734 S2735 R2739 E2740 S2741 N2742 D2748 L2749 Y2750 S2751 T2752 L2753 G2754 E2755 D2756 D2757 L2768 G2761 R2765 N2773 A2774 S2777 Y2778 E2779 Q2780 H2781 G2782 M2783 W2784 E2785 K2786 M2790 I2803 P2804
D2815 E2828 E2837 A2847 N2850 T2851 E2852 Y2853 W2854 Q2855 N2856 Q2857 E2858 N2859 R2860 D2861 Q2862 L2863 D2864 T2865 K2868 D2872 A2873 R2878



• Molecule 2: Spt20-like SEP domain-containing protein

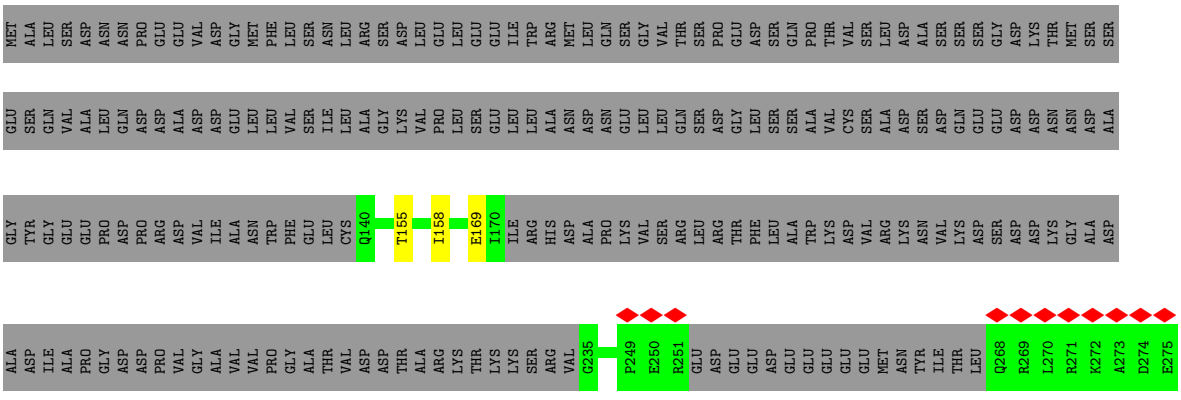
Chain B:

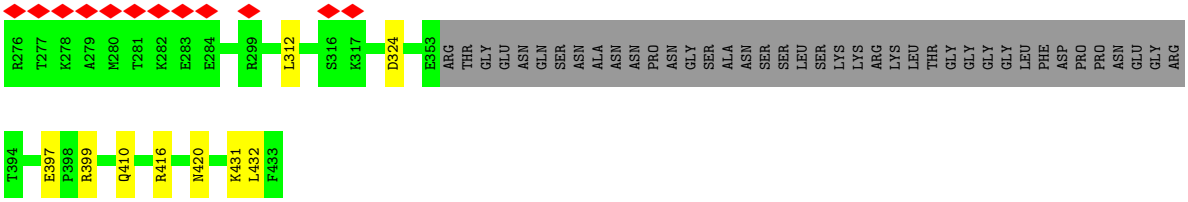




• Molecule 3: Uncharacterized protein

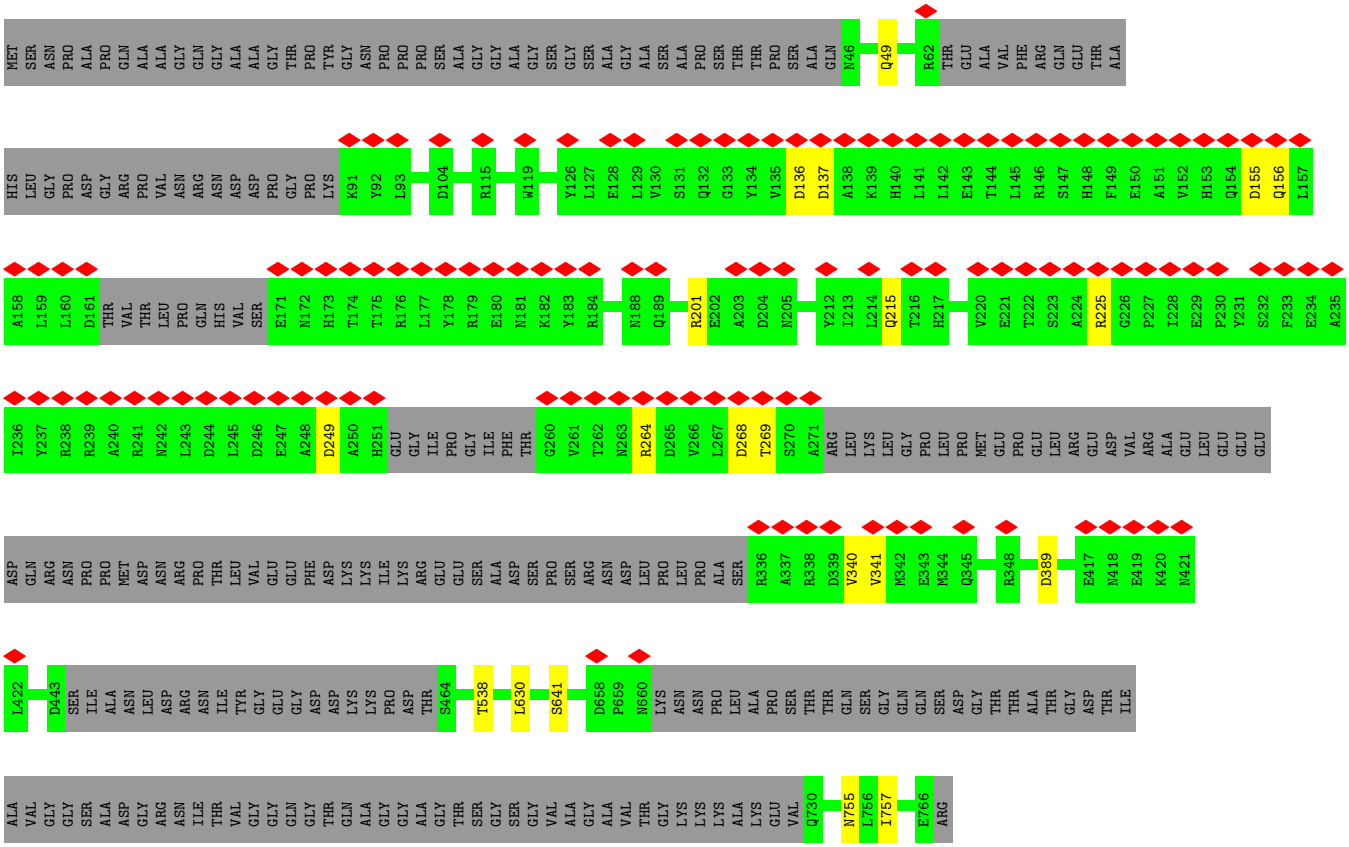
Chain C:





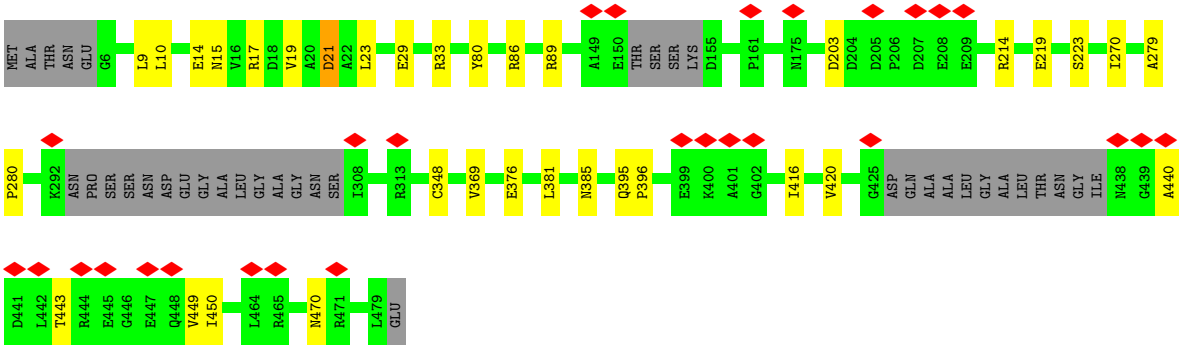
• Molecule 4: Transcription initiation factor TFIID subunit 5

Chain D:



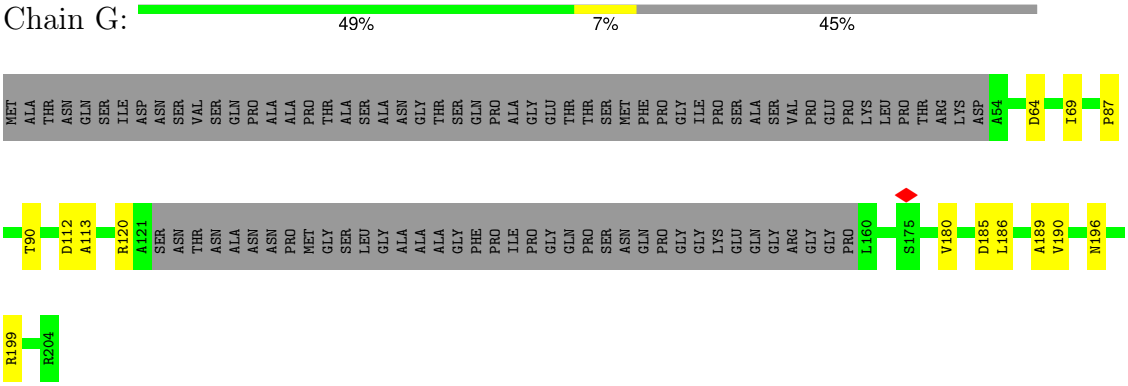
• Molecule 5: Transcription initiation factor TFIID subunit 6

Chain E:



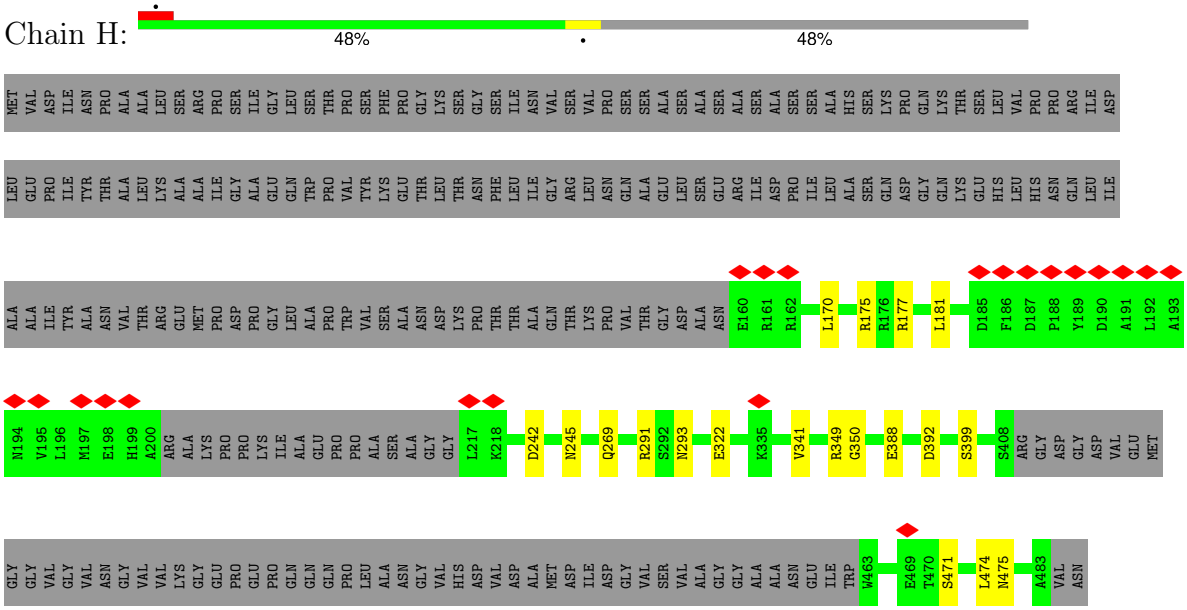
• Molecule 6: Transcription initiation factor TFIID subunit 10

Chain G:



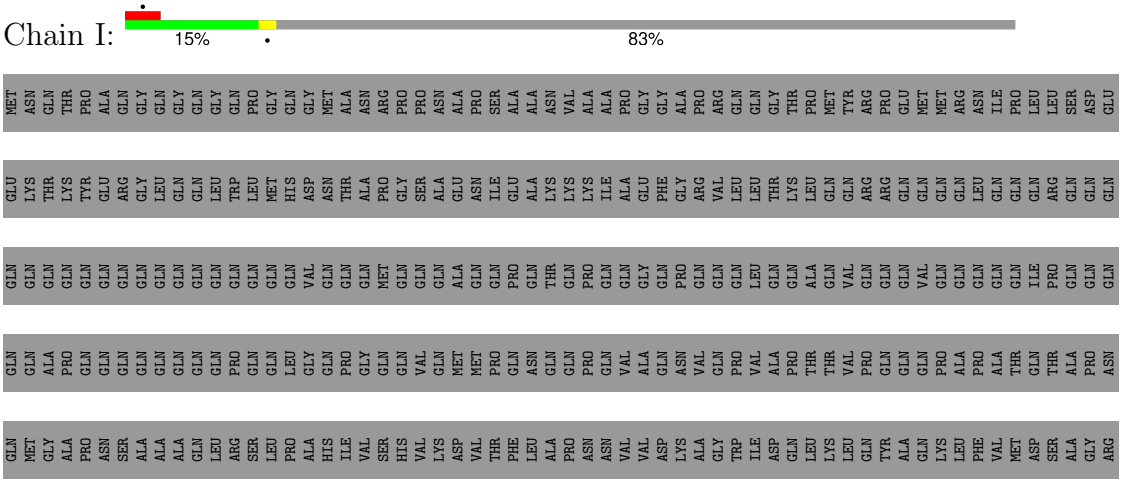
• Molecule 7: Putative transcriptional coactivator HFI1 protein

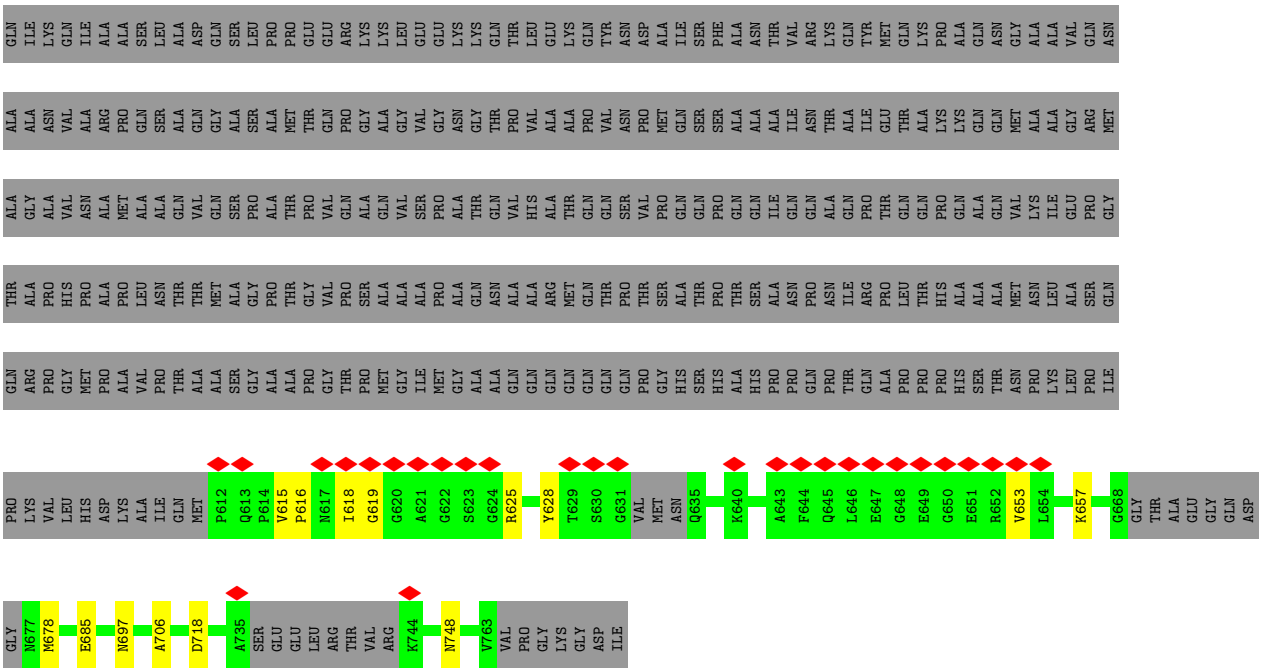
Chain H:



• Molecule 8: Transcription initiation factor TFIID subunit 12

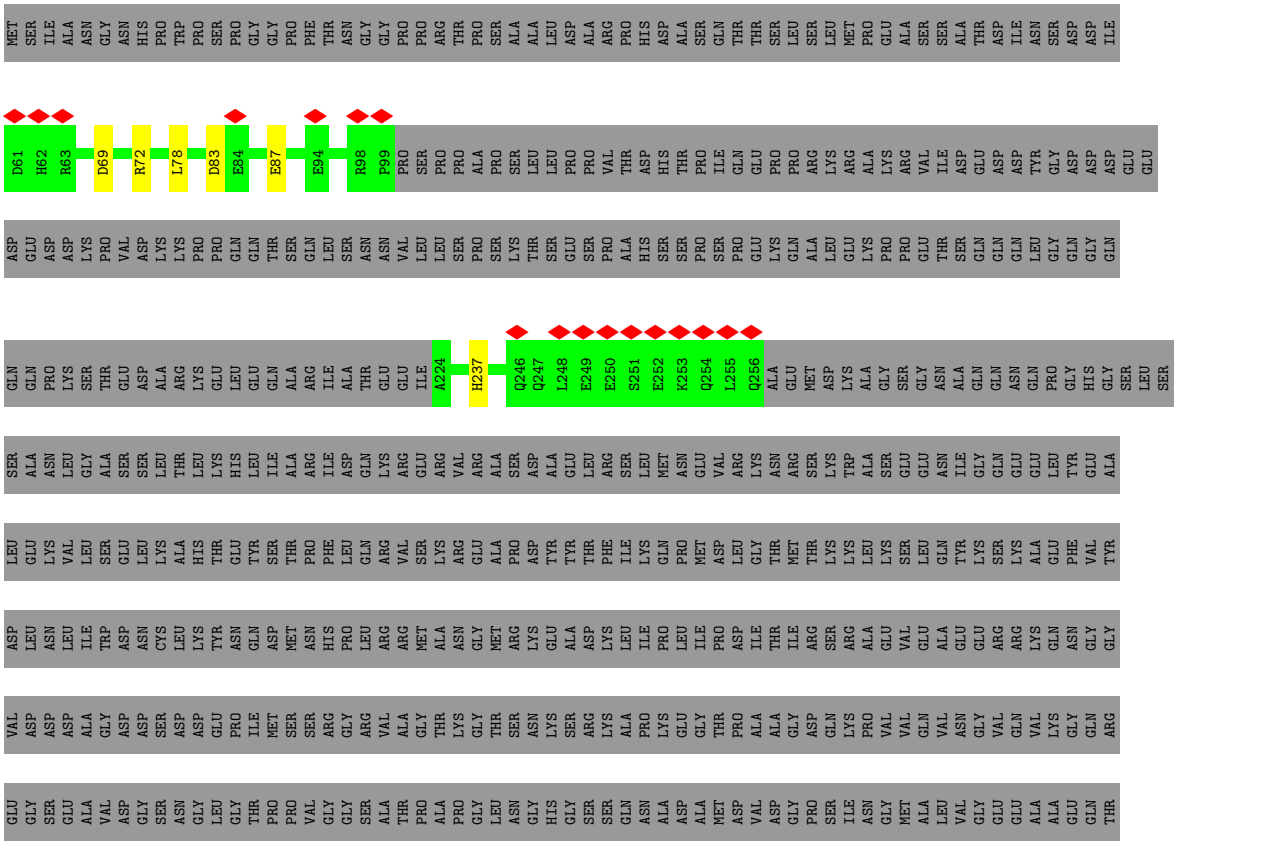
Chain I:

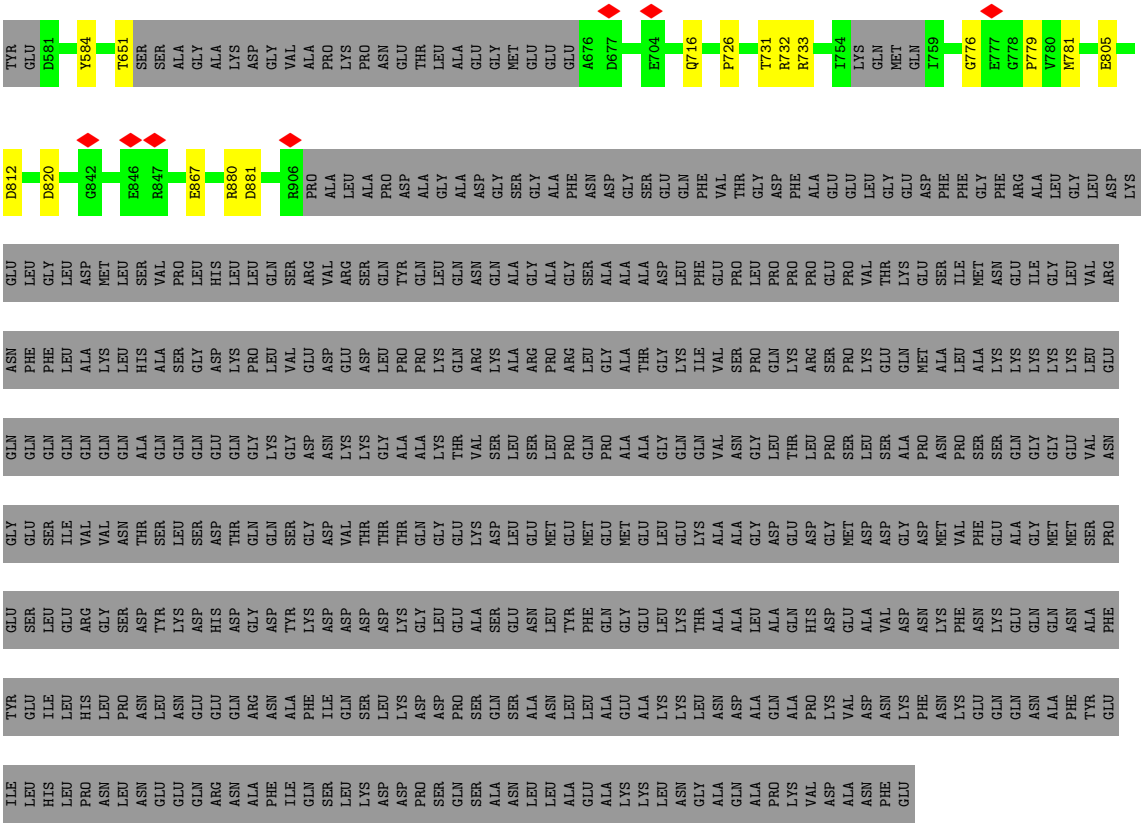




• Molecule 9: Putative transcriptional activator protein

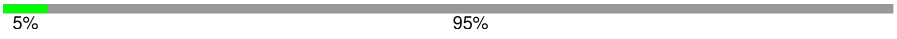
Chain K:

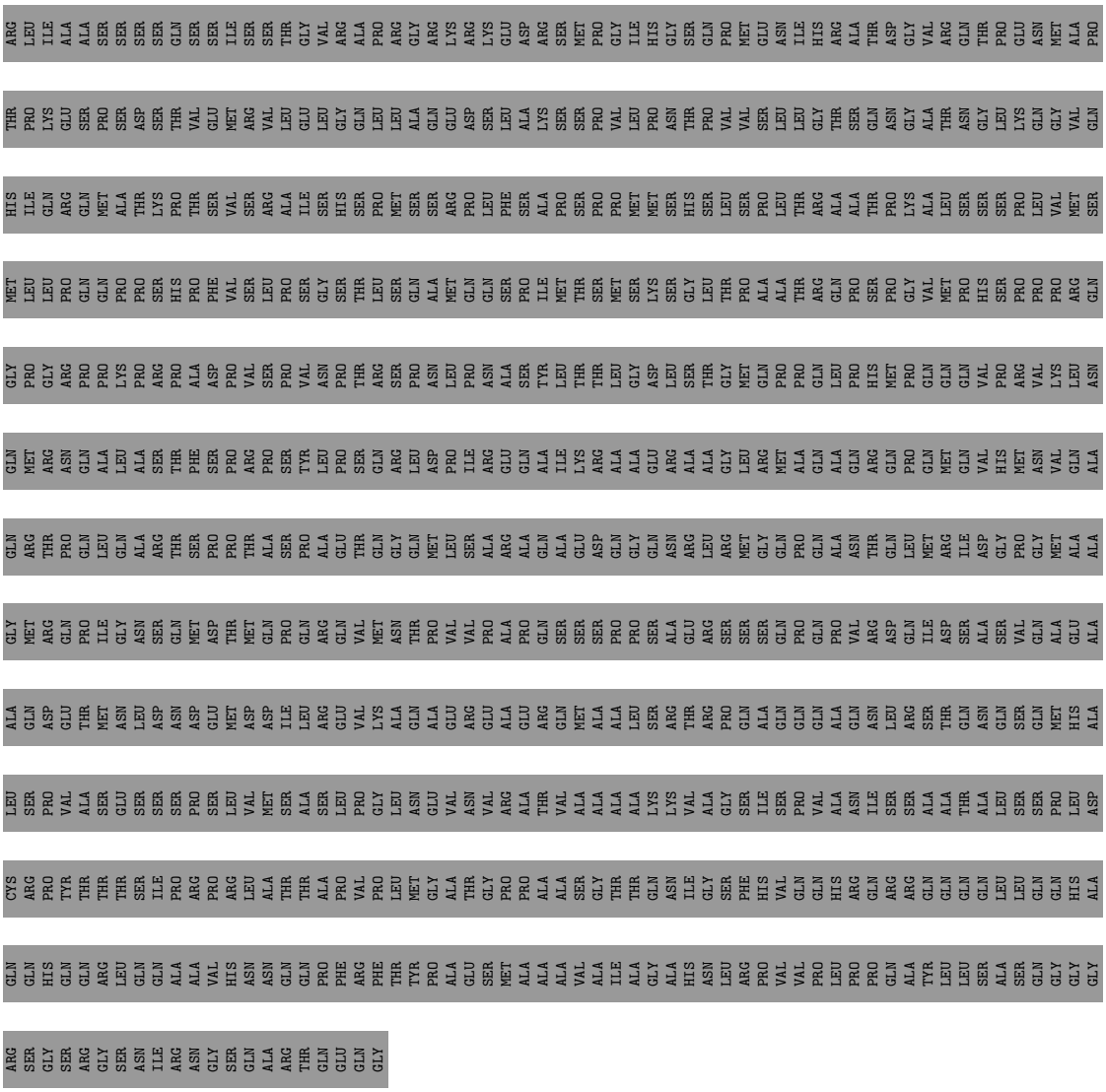




• Molecule 10: SCA7 domain-containing protein

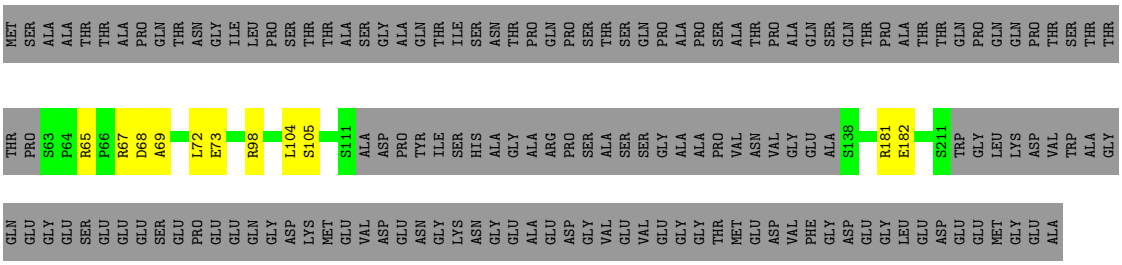
Chain Q:





• Molecule 11: Putative transcription initiation factor

Chain F:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1734991	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	68.9	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	8.384	Depositor
Minimum map value	-5.913	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.128	Depositor
Recommended contour level	0.8	Depositor
Map size (Å)	374.76, 374.76, 374.76	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.041, 1.041, 1.041	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	0.08	0/1912	0.20	0/2593
2	B	0.11	0/2016	0.23	0/2730
3	C	0.11	0/1467	0.24	0/1967
4	D	0.11	0/4235	0.29	0/5730
5	E	0.12	0/3505	0.25	0/4767
6	G	0.16	0/893	0.36	0/1205
7	H	0.12	0/2018	0.25	0/2721
8	I	0.13	0/1039	0.27	0/1400
9	K	0.13	0/3059	0.25	0/4119
10	Q	0.13	0/489	0.25	0/667
11	F	0.12	0/946	0.28	0/1279
All	All	0.12	0/21579	0.26	0/29178

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	1866	1790	1787	15	0
2	B	1963	1952	1946	11	0
3	C	1442	1446	1441	6	0
4	D	4144	4096	4088	12	0
5	E	3440	3519	3515	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	G	877	874	872	11	0
7	H	1978	1920	1917	9	0
8	I	1025	1053	1050	10	0
9	K	3004	2978	2973	12	0
10	Q	478	472	471	0	0
11	F	928	546	934	9	0
All	All	21145	20646	20994	96	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 2.

The worst 5 of 96 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)
11:F:65:ARG:NH1	11:F:73:GLU:OE1	2.11	0.83
1:A:2756:ASP:OD1	8:I:628:TYR:OH	1.96	0.83
7:H:293:ASN:O	7:H:349:ARG:NH2	2.14	0.81
1:A:2837:GLU:OE1	2:B:459:ARG:NH1	2.15	0.80
5:E:23:LEU:CD1	11:F:104:LEU:HD11	2.12	0.79

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	217/3893 (6%)	213 (98%)	4 (2%)	0	100	100
2	B	224/1192 (19%)	222 (99%)	2 (1%)	0	100	100
3	C	166/433 (38%)	162 (98%)	4 (2%)	0	100	100
4	D	509/767 (66%)	489 (96%)	20 (4%)	0	100	100
5	E	435/480 (91%)	427 (98%)	8 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	G	109/204 (53%)	106 (97%)	3 (3%)	0	100	100
7	H	248/485 (51%)	240 (97%)	8 (3%)	0	100	100
8	I	125/770 (16%)	123 (98%)	1 (1%)	1 (1%)	16	34
9	K	360/1360 (26%)	355 (99%)	5 (1%)	0	100	100
10	Q	60/1273 (5%)	60 (100%)	0	0	100	100
11	F	119/277 (43%)	116 (98%)	3 (2%)	0	100	100
All	All	2572/11134 (23%)	2513 (98%)	58 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	I	697	ASN

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	198/3412 (6%)	196 (99%)	2 (1%)	73	88
2	B	218/928 (24%)	216 (99%)	2 (1%)	75	90
3	C	156/377 (41%)	155 (99%)	1 (1%)	84	94
4	D	450/635 (71%)	448 (100%)	2 (0%)	89	96
5	E	375/401 (94%)	371 (99%)	4 (1%)	70	86
6	G	89/157 (57%)	88 (99%)	1 (1%)	70	86
7	H	206/387 (53%)	202 (98%)	4 (2%)	52	75
8	I	112/620 (18%)	112 (100%)	0	100	100
9	K	318/1138 (28%)	315 (99%)	3 (1%)	75	90
10	Q	50/1047 (5%)	48 (96%)	2 (4%)	27	52
11	F	94/212 (44%)	94 (100%)	0	100	100
All	All	2266/9314 (24%)	2245 (99%)	21 (1%)	74	90

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	H	392	ASP
9	K	820	ASP
10	Q	351	LYS
9	K	867	GLU
9	K	78	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
5	E	241	GLN
8	I	700	HIS
8	I	677	ASN
9	K	706	GLN
3	C	410	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)

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.

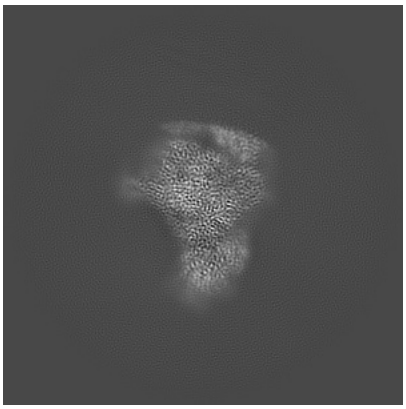
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-73269. These allow visual inspection of the internal detail of the map and identification of artifacts.

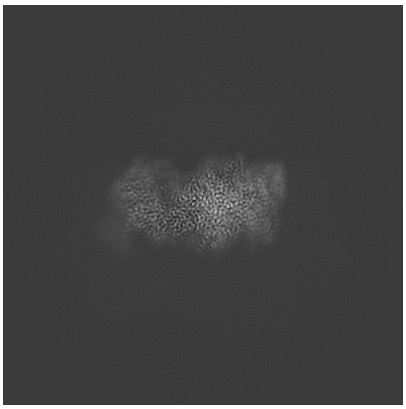
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

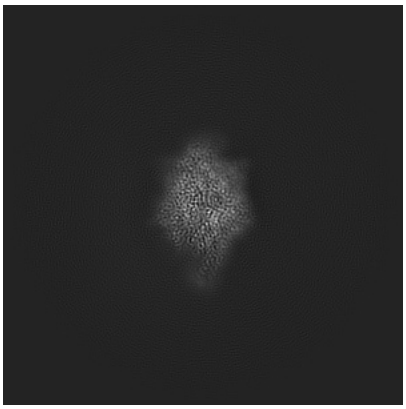
6.1.1 Primary map



X

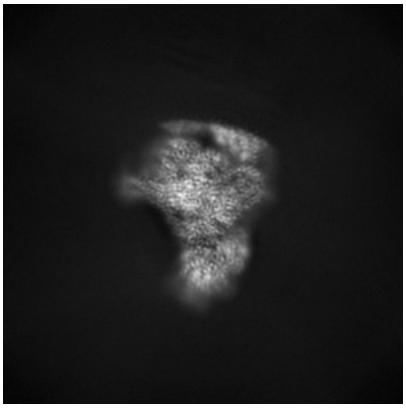


Y

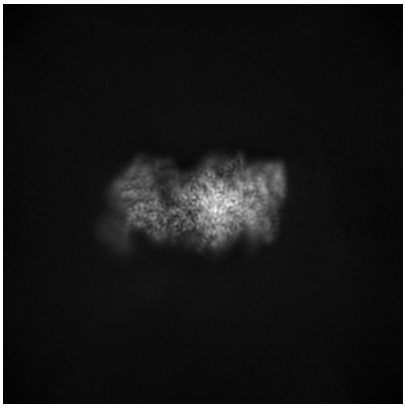


Z

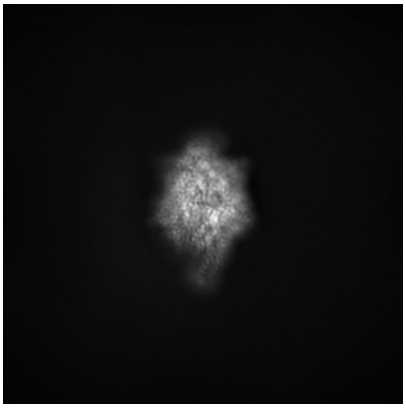
6.1.2 Raw map



X



Y

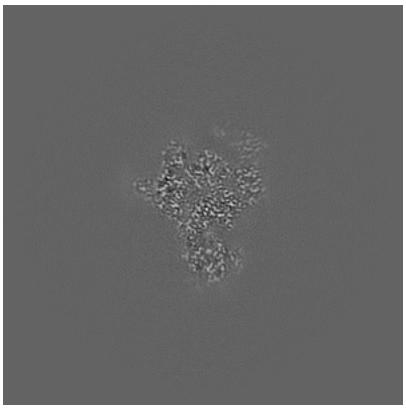


Z

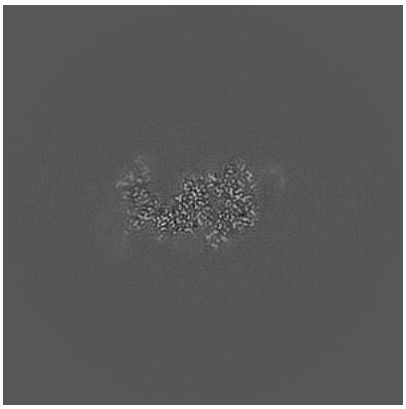
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

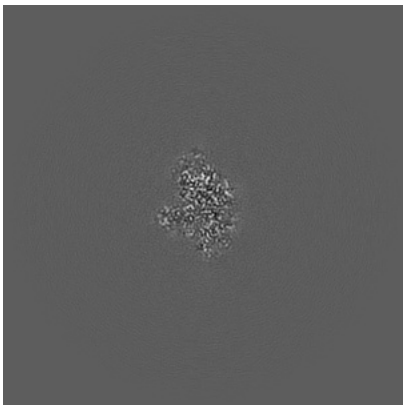
6.2.1 Primary map



X Index: 180

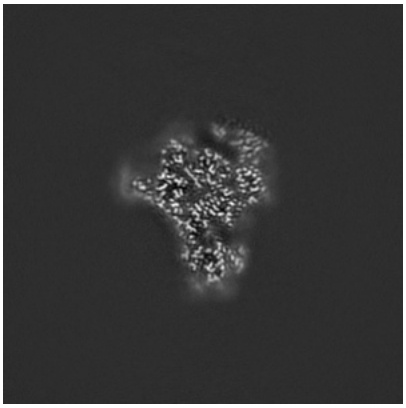


Y Index: 180

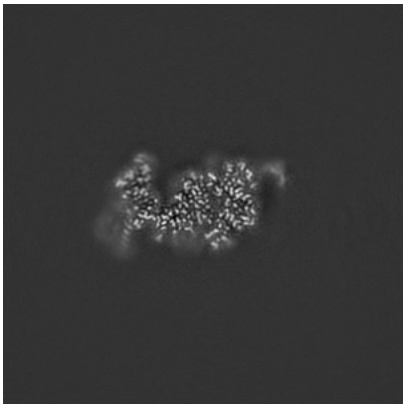


Z Index: 180

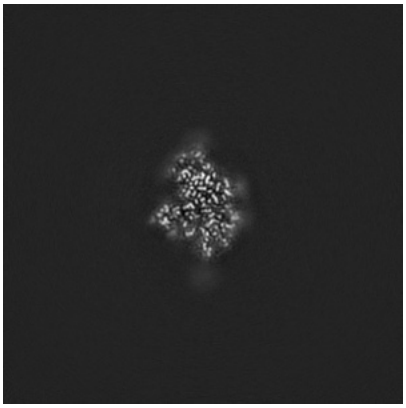
6.2.2 Raw map



X Index: 180



Y Index: 180

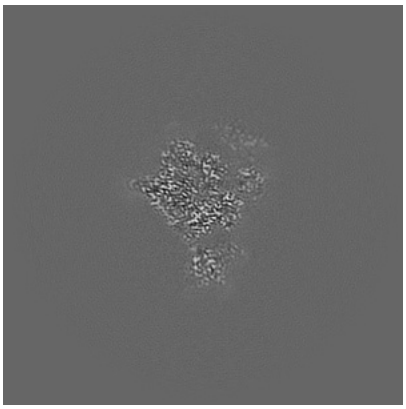


Z Index: 180

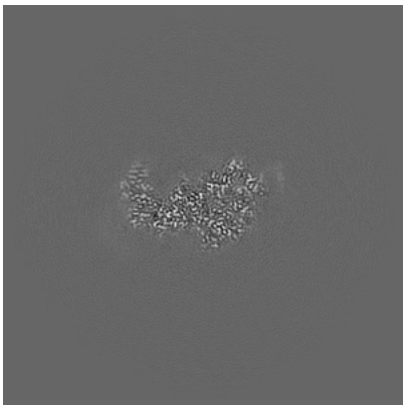
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

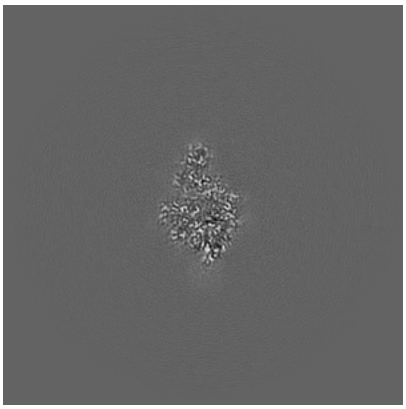
6.3.1 Primary map



X Index: 185

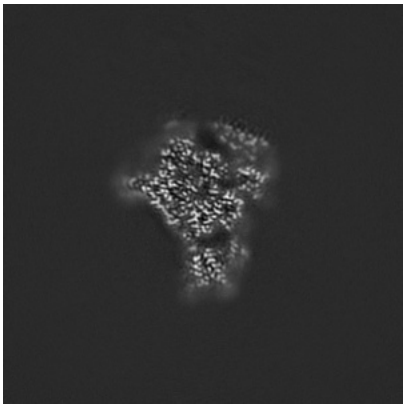


Y Index: 175

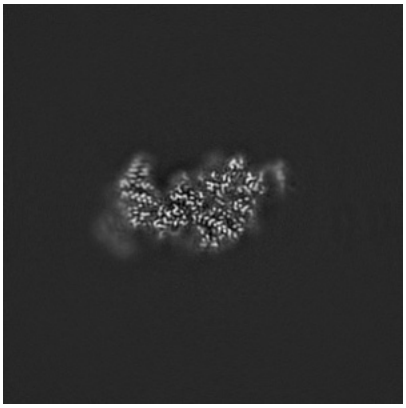


Z Index: 190

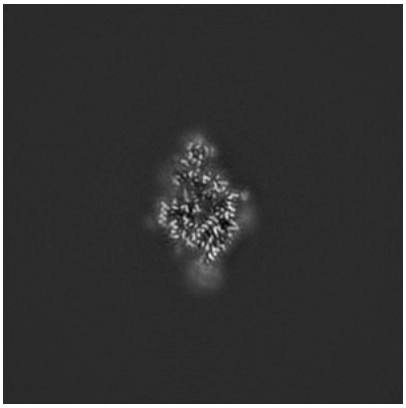
6.3.2 Raw map



X Index: 185



Y Index: 175

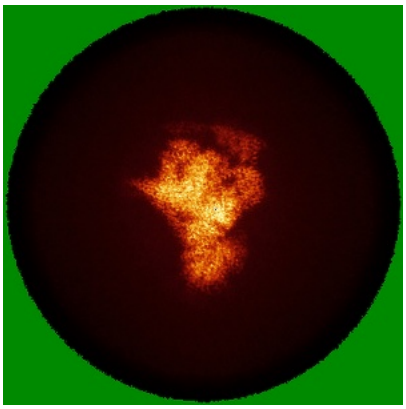


Z Index: 189

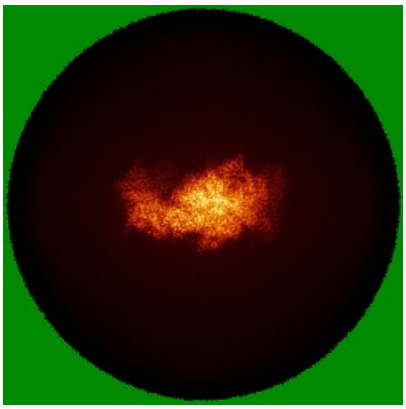
The images above show the largest variance slices of the map in three orthogonal directions.

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

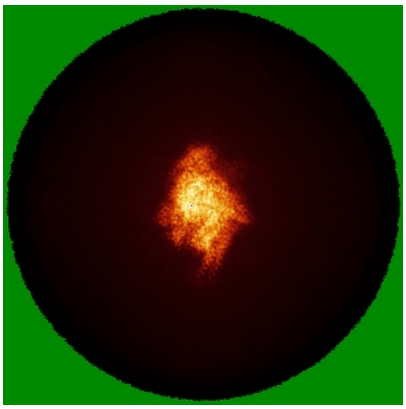
6.4.1 Primary map



X

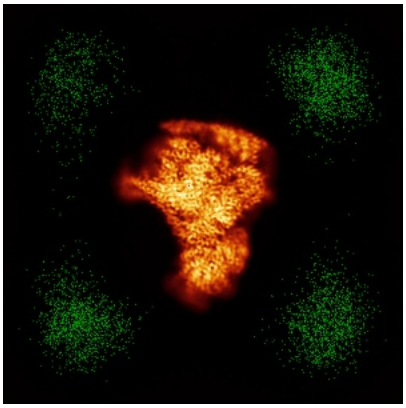


Y

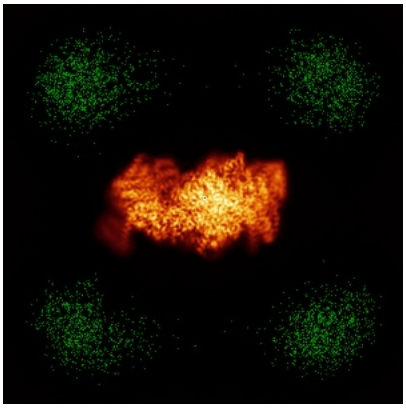


Z

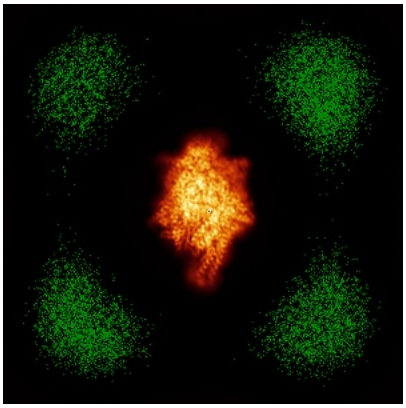
6.4.2 Raw map



X



Y

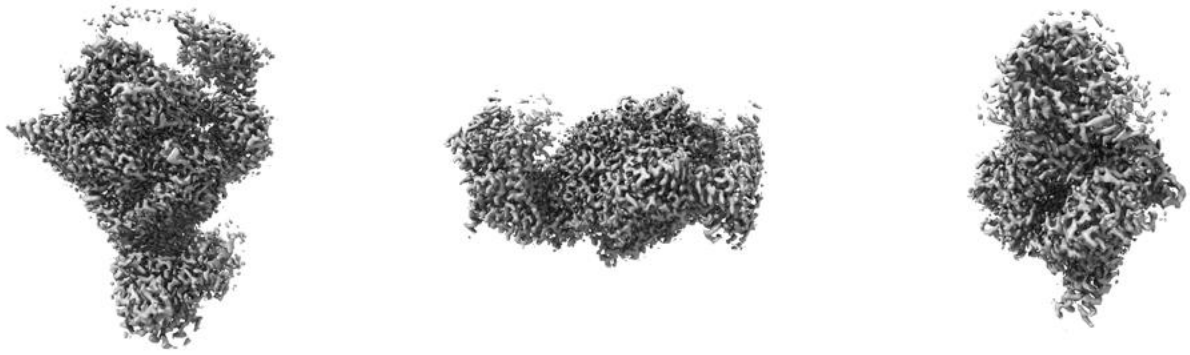


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map

X Y Z

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

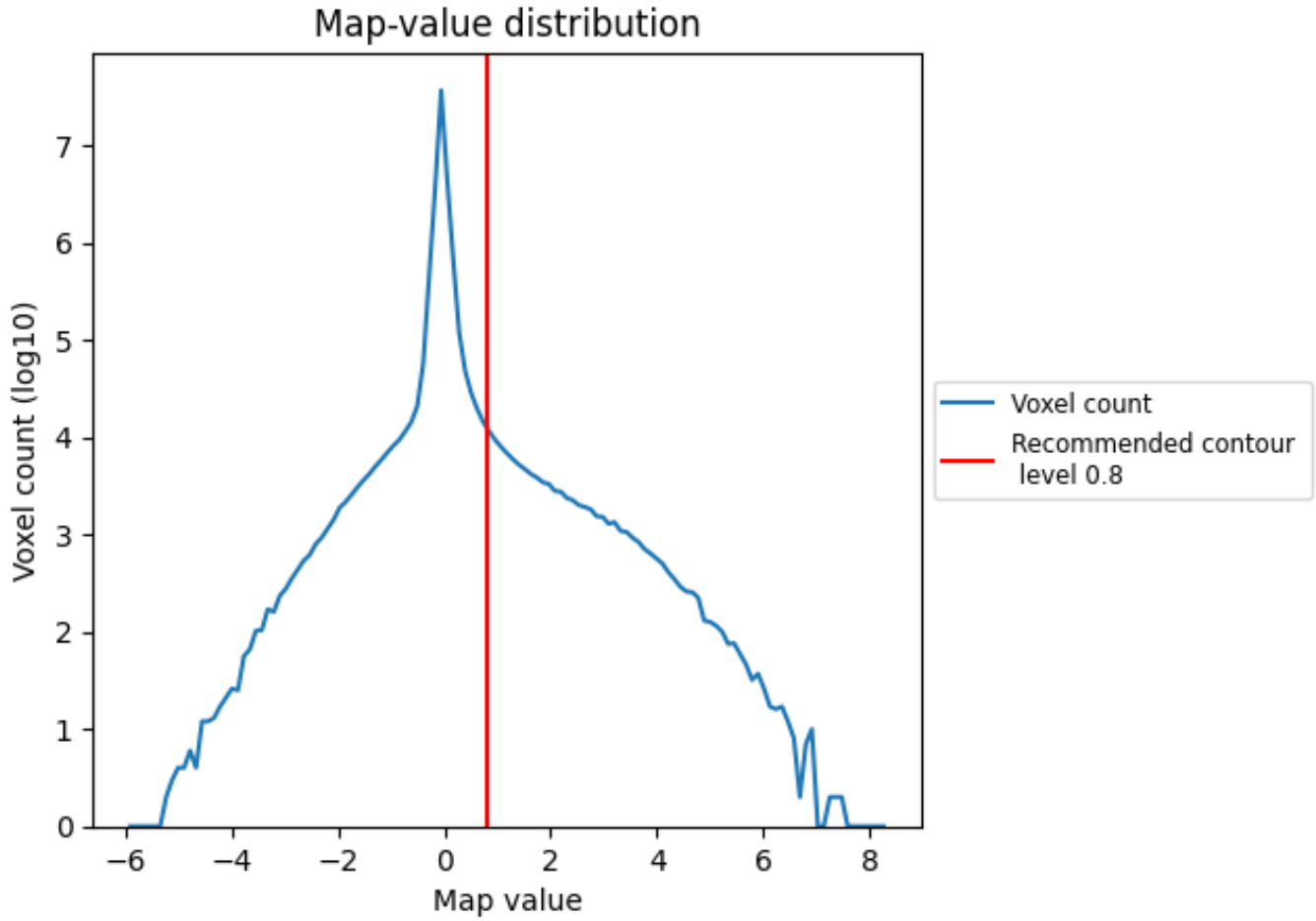
6.6 Mask visualisation (i)

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

7 Map analysis

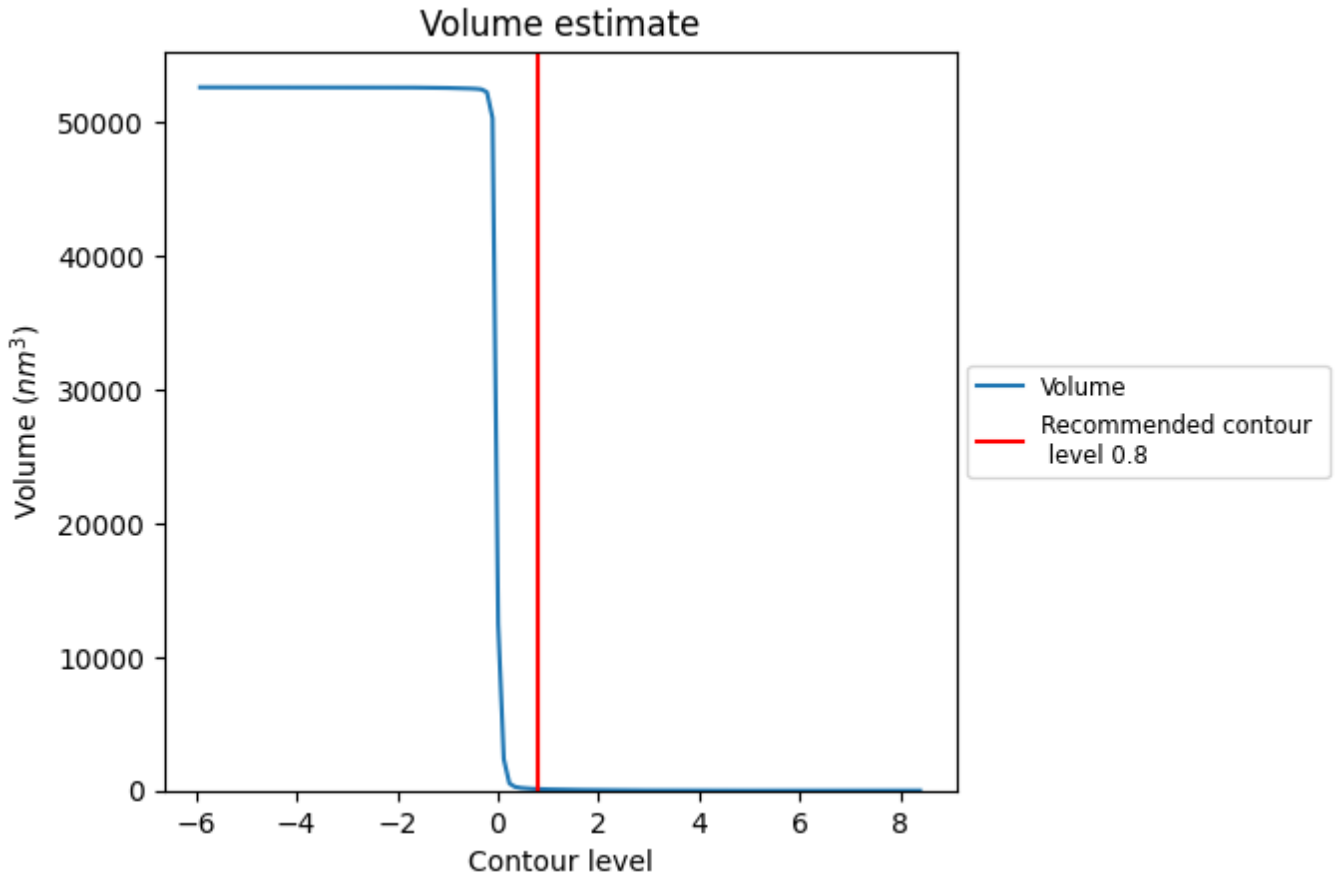
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

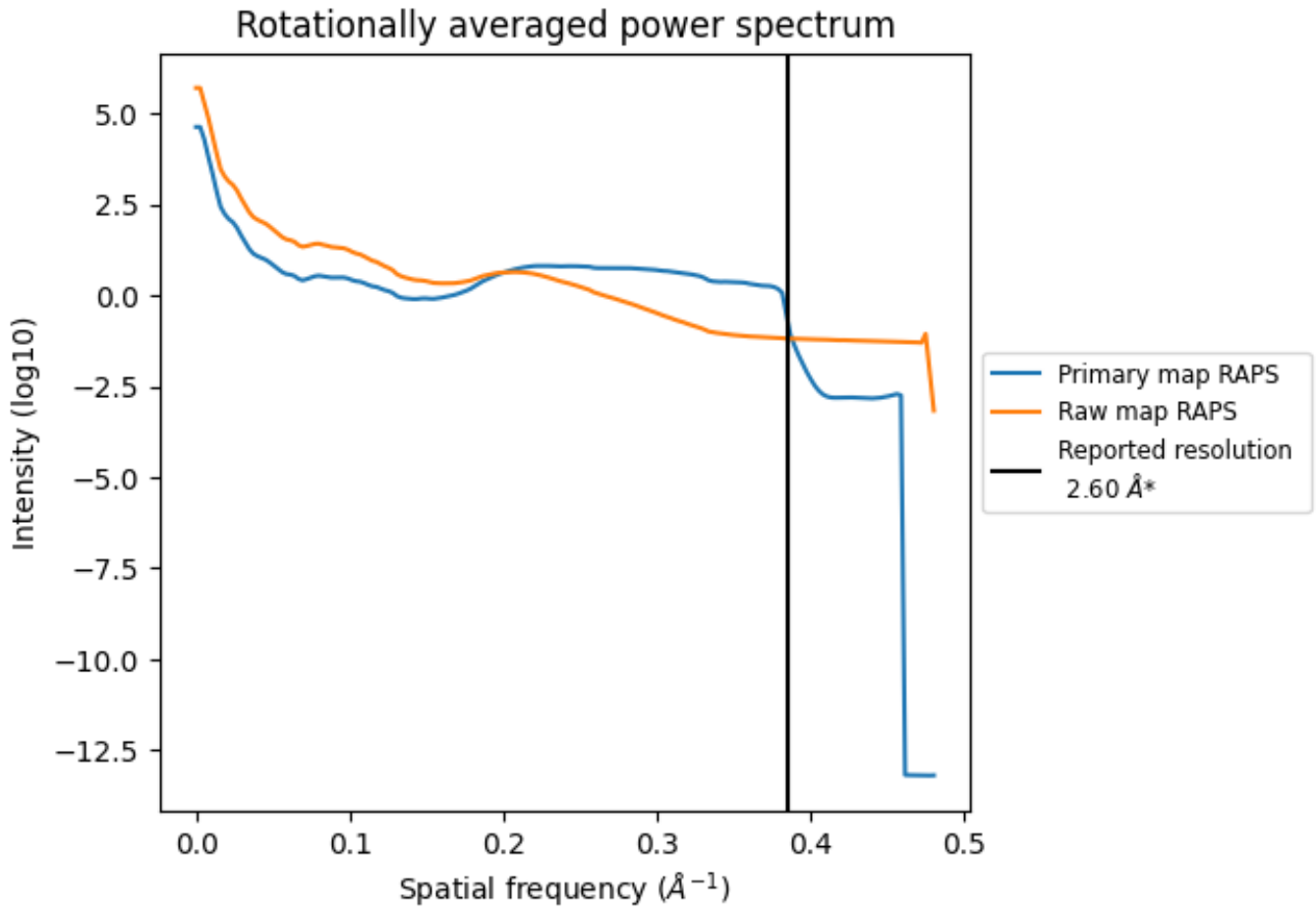
7.2 Volume estimate (i)



The volume at the recommended contour level is 115 nm^3; this corresponds to an approximate mass of 104 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)

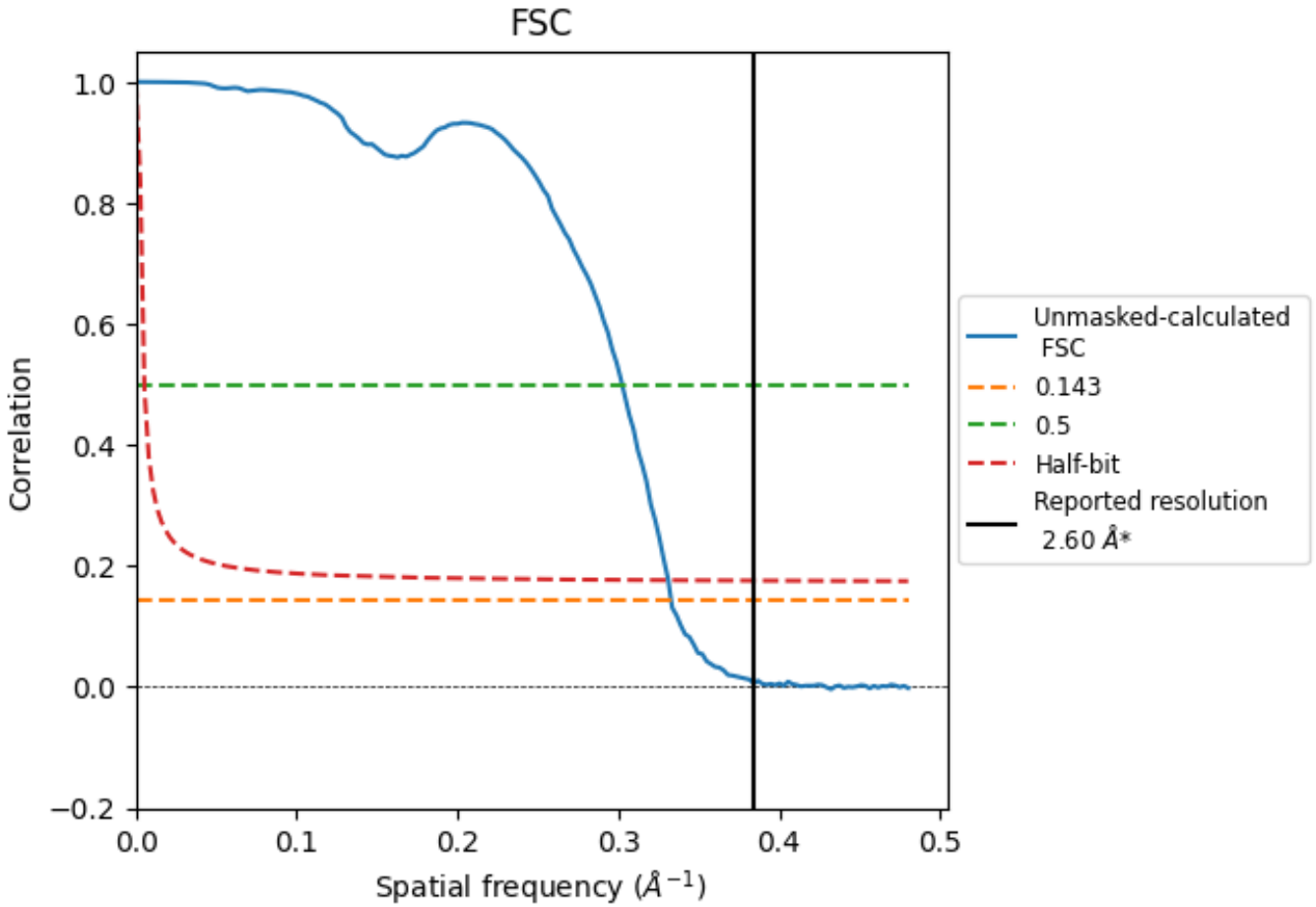


*Reported resolution corresponds to spatial frequency of 0.385 $Å^{-1}$

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 0.385 Å^{-1}

8.2 Resolution estimates (i)

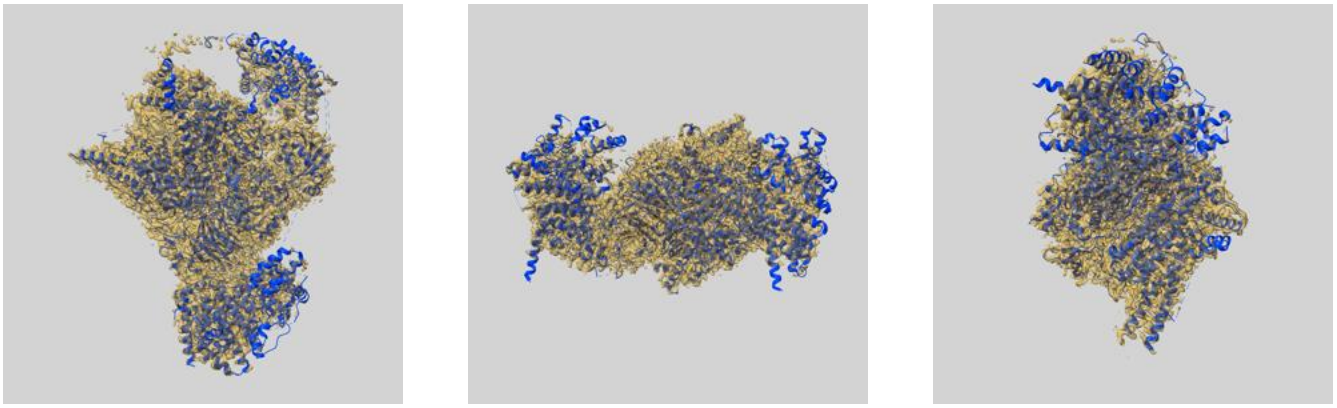
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.00	3.31	3.02

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.00 differs from the reported value 2.6 by more than 10 %

9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-73269 and PDB model 9YOQ. Per-residue inclusion information can be found in section 3 on page 6.

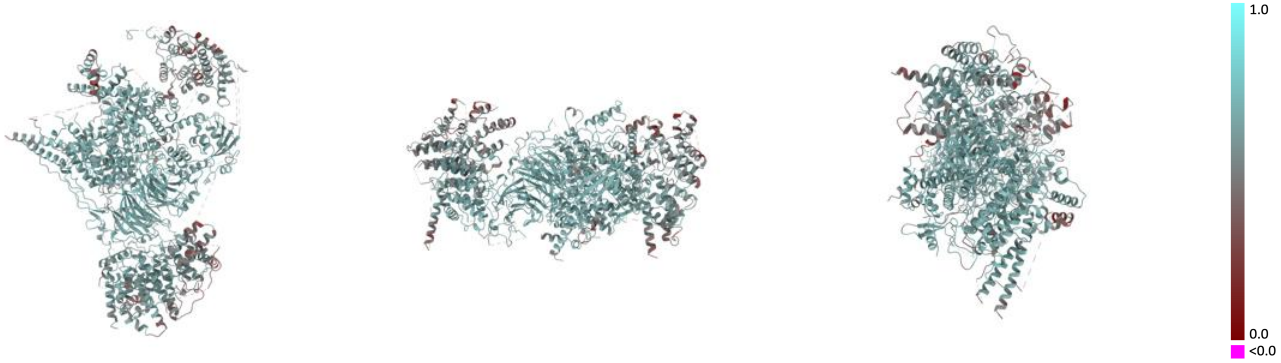
9.1 Map-model overlay



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.8 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.

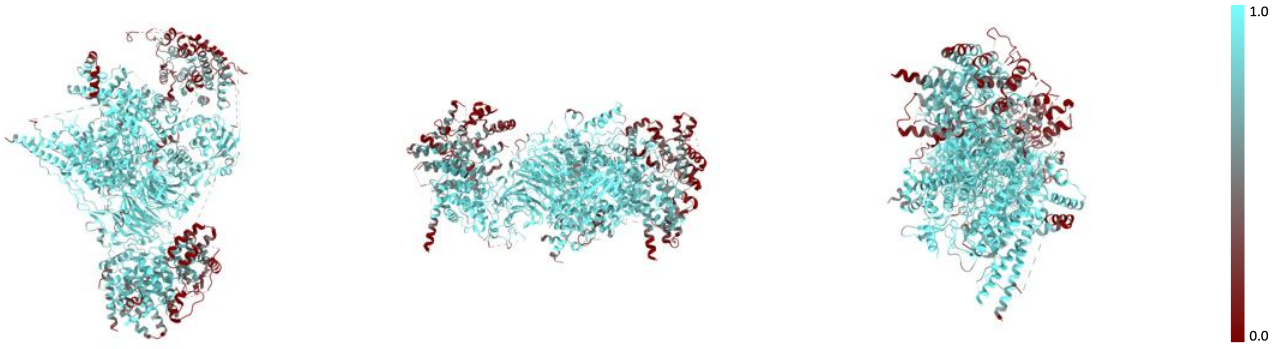
9.2 Q-score mapped to coordinate model (i)



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.

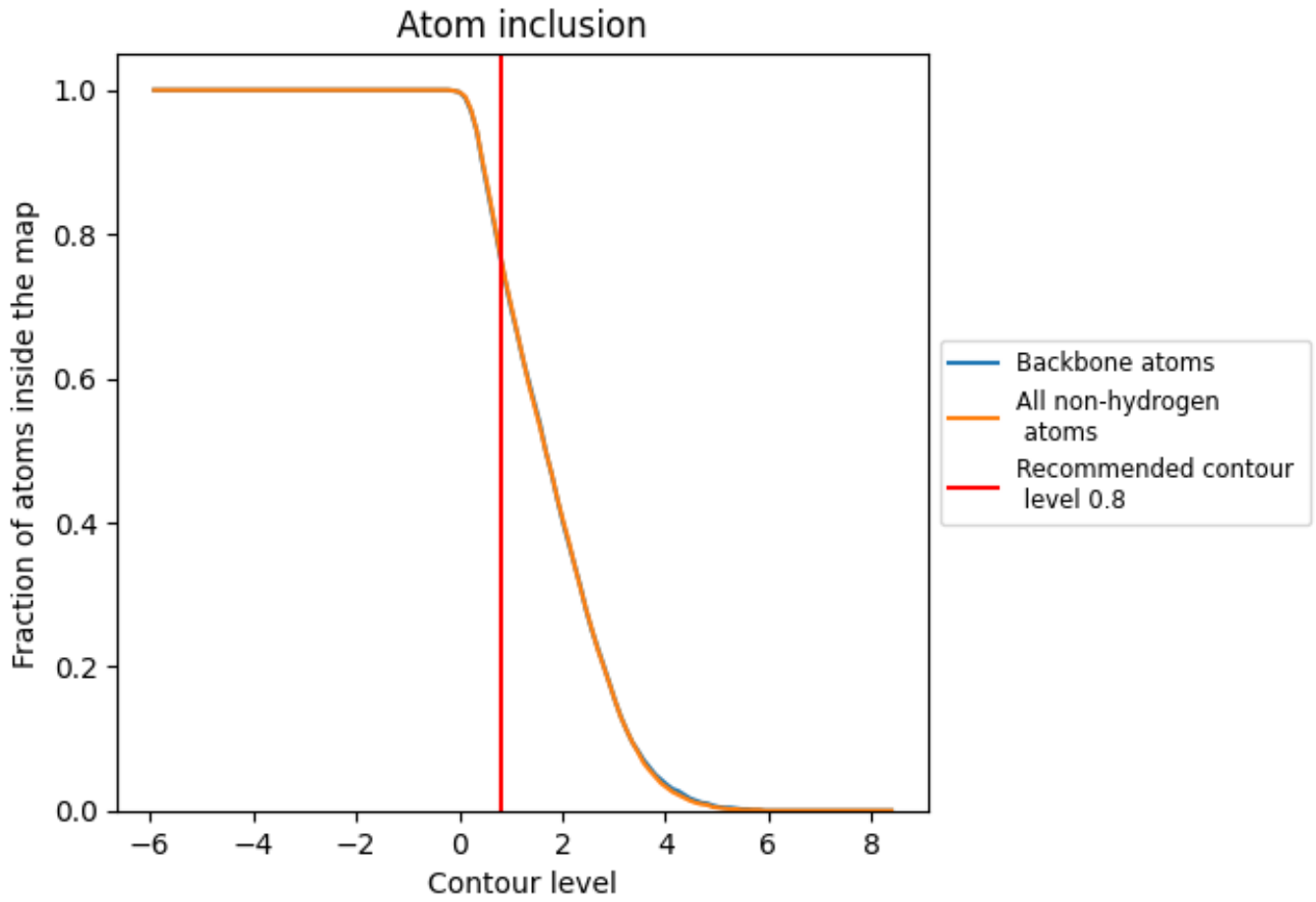
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.8).

9.4 Atom inclusion (i)



At the recommended contour level, 77% of all backbone atoms, 77% 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 (0.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7710	0.6020
A	0.4300	0.5200
B	0.7470	0.5970
C	0.7780	0.5890
D	0.7100	0.6010
E	0.8570	0.6150
F	0.9450	0.6540
G	0.9400	0.6390
H	0.8370	0.6140
I	0.7280	0.5910
K	0.8380	0.6110
Q	0.8830	0.6310