



wwPDB EM Validation Summary Report ⓘ

Aug 23, 2026 – 04:12 pm BST

PDB ID : 8QRN / pdb_00008qrn
EMDB ID : EMD-18443
Title : mt-SSU in GTPBP8 knock-out cells, state 4
Authors : Valentin Gese, G.; Cipullo, M.; Rorbach, J.; Hallberg, B.M.
Deposited on : 2023-10-09
Resolution : 2.98 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:

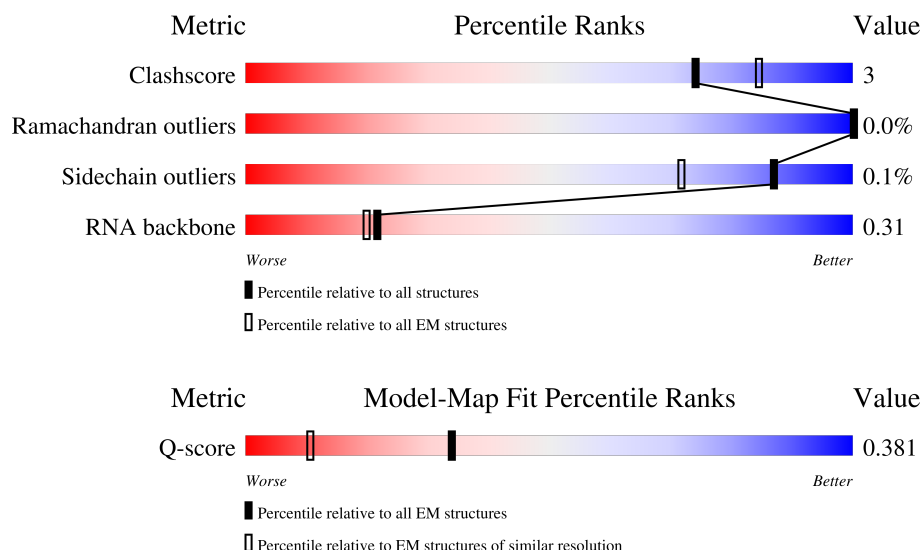
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.50

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 2.98 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.



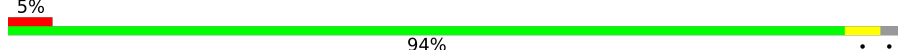
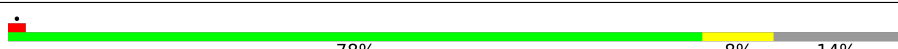
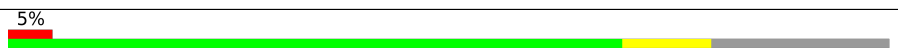
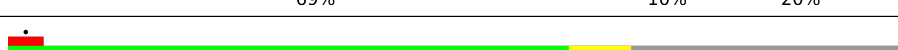
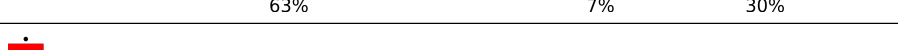
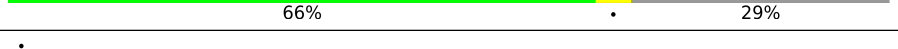
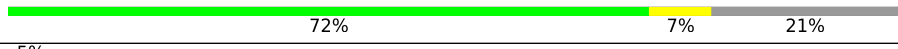
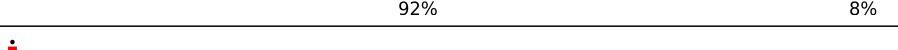
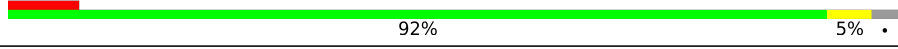
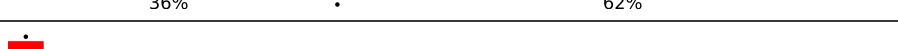
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13236 (2.48 - 3.48)

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 $\leq 5\%$. 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	955	
2	B	296	
3	C	167	

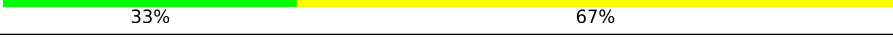
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Mol	Chain	Length	Quality of chain
4	D	430	
5	E	125	
6	F	242	
7	G	396	
8	H	201	
9	I	194	
10	J	138	
11	K	128	
12	L	257	
13	M	137	
14	N	130	
15	O	258	
16	P	142	
17	Q	86	
18	R	360	
19	S	190	
20	T	173	
21	U	205	
22	V	414	
23	W	187	
24	X	398	
25	Y	395	
26	Z	106	
27	0	218	
28	1	323	

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Mol	Chain	Length	Quality of chain
29	2	117	
30	3	199	
31	4	689	
32	5	71	
33	7	691	
34	6	3	

2 Entry composition [i](#)

There are 46 unique types of molecules in this entry. The entry contains 73195 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 RNA chain called 12S mitochondrial rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	955	Total	C	N	O	P	0	0
			20282	9098	3652	6577	955		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	709	G	A	variant	GB OM714795.1

- Molecule 2 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	225	Total	C	N	O	S	0	0
			1828	1164	331	323	10		

- Molecule 3 is a protein called 28S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	132	Total	C	N	O	S	0	0
			1083	699	195	185	4		

- Molecule 4 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	343	Total	C	N	O	S	0	0
			2731	1713	518	487	13		

- Molecule 5 is a protein called 28S ribosomal protein S6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	122	Total	C	N	O	S	0	0
			972	614	177	177	4		

- Molecule 6 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	208	Total	C	N	O	S	0	0
			1725	1104	312	298	11		

- Molecule 7 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	316	Total	C	N	O	S	0	0
			2596	1649	459	474	14		

- Molecule 8 is a protein called 28S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	140	Total	C	N	O	S	0	0
			1152	745	194	210	3		

- Molecule 9 is a protein called 28S ribosomal protein S11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	137	Total	C	N	O	S	0	0
			1019	641	193	181	4		

- Molecule 10 is a protein called 28S ribosomal protein S12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	108	Total	C	N	O	S	0	0
			839	521	169	143	6		

- Molecule 11 is a protein called 28S ribosomal protein S14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	101	Total	C	N	O	S	0	0
			862	537	179	141	5		

- Molecule 12 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	174	Total	C	N	O	S	0	0
			1453	925	270	251	7		

- Molecule 13 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	119	Total	C	N	O	S	0	0
			942	594	185	157	6		

- Molecule 14 is a protein called 28S ribosomal protein S17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	110	Total	C	N	O	S	0	0
			868	562	156	147	3		

- Molecule 15 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	194	Total	C	N	O	S	0	0
			1599	1019	295	278	7		

- Molecule 16 is a protein called 28S ribosomal protein S18c, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	97	Total	C	N	O	S	0	0
			781	501	134	138	8		

- Molecule 17 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	86	Total	C	N	O	S	0	0
			744	460	150	126	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	50	ARG	CYS	variant	UNP P82921

- Molecule 18 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	295	Total	C	N	O	S	0	0
			2409	1533	413	455	8		

- Molecule 19 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	135	Total	C	N	O	S	0	0
			1111	716	198	196	1		

- Molecule 20 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	168	Total	C	N	O	S	0	0
			1371	877	239	244	11		

- Molecule 21 is a protein called 28S ribosomal protein S26, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	176	Total	C	N	O	S	0	0
			1488	916	301	267	4		

- Molecule 22 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	362	Total	C	N	O	S	0	0
			2969	1904	495	558	12		

- Molecule 23 is a protein called 28S ribosomal protein S28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	100	Total	C	N	O	S	0	0
			789	498	141	146	4		

- Molecule 24 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	352	Total	C	N	O	S	0	0
			2849	1822	499	517	11		

- Molecule 25 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	149	Total	C	N	O	S	0	0
			1246	801	207	234	4		

- Molecule 26 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	100	Total	C	N	O	S	0	0
			839	534	153	148	4		

- Molecule 27 is a protein called 28S ribosomal protein S34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	0	215	Total	C	N	O	S	0	0
			1787	1130	339	313	5		

- Molecule 28 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	1	276	Total	C	N	O	S	0	0
			2238	1419	381	427	11		

- Molecule 29 is a protein called Coiled-coil-helix-coiled-coil-helix domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	2	117	Total	C	N	O	S	0	0
			935	579	182	166	8		

- Molecule 30 is a protein called Aurora kinase A-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	3	70	Total	C	N	O	S	0	0
			625	401	134	89	1		

- Molecule 31 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	4	588	Total	C	N	O	S	0	0
			4768	3053	808	879	28		

- Molecule 32 is a RNA chain called fMet-tRNA^{Met}.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	5	71	Total	C	N	O	P	0	0
			1504	674	264	495	71		

- Molecule 33 is a protein called Translation initiation factor IF-2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	7	571	Total	C	N	O	S	0	0
			4432	2785	779	851	17		

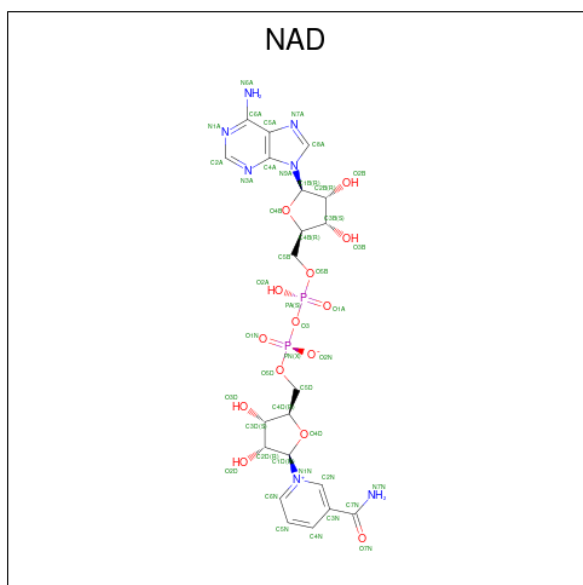
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
7	37	MET	-	initiating methionine	UNP P46199

- Molecule 34 is a RNA chain called mRNA.

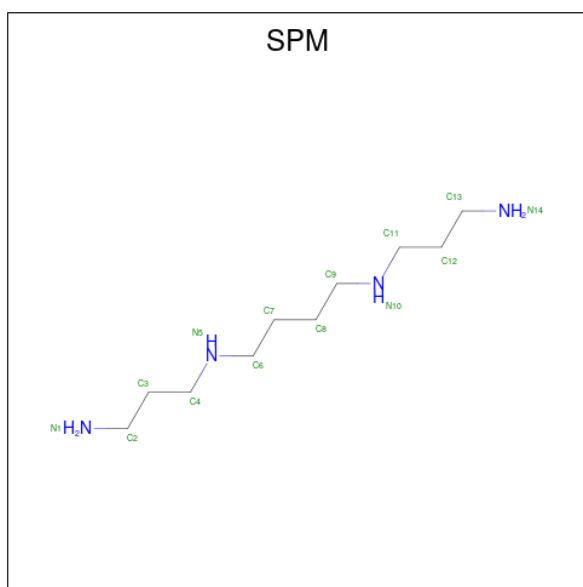
Mol	Chain	Residues	Atoms					AltConf	Trace
34	6	3	Total	C	N	O	P	0	0
			64	29	12	20	3		

- Molecule 35 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



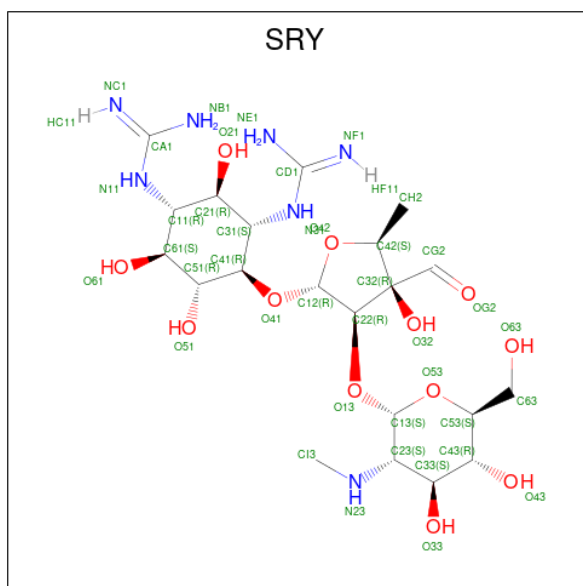
Mol	Chain	Residues	Atoms					AltConf
35	A	1	Total	C	N	O	P	0
			44	21	7	14	2	

- Molecule 36 is SPERMINE (CCD ID: SPM) (formula: $C_{10}H_{26}N_4$).



Mol	Chain	Residues	Atoms			AltConf
36	A	1	Total	C	N	0
			14	10	4	

- Molecule 37 is STREPTOMYCIN (CCD ID: SRY) (formula: $C_{21}H_{39}N_7O_{12}$).



Mol	Chain	Residues	Atoms				AltConf
37	A	1	Total	C	N	O	0
			40	21	7	12	

- Molecule 38 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
38	A	54	Total 54	Mg 54	0
38	B	1	Total 1	Mg 1	0
38	X	1	Total 1	Mg 1	0
38	3	1	Total 1	Mg 1	0
38	7	1	Total 1	Mg 1	0

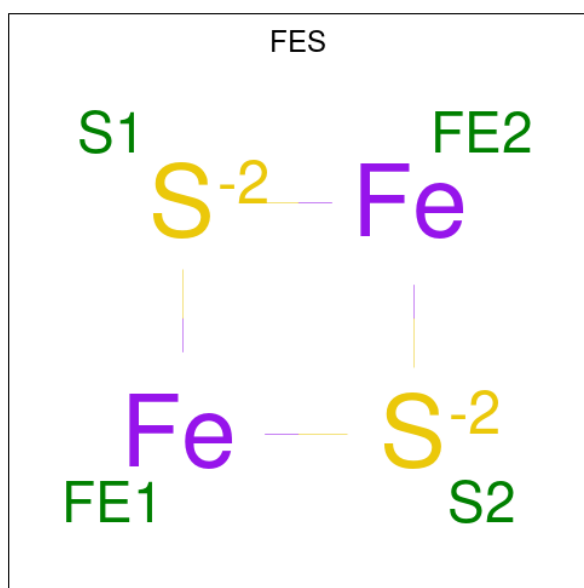
- Molecule 39 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
39	A	17	Total 17	K 17	0
39	7	1	Total 1	K 1	0

- Molecule 40 is ZINC ION (CCD ID: ZN) (formula: Zn).

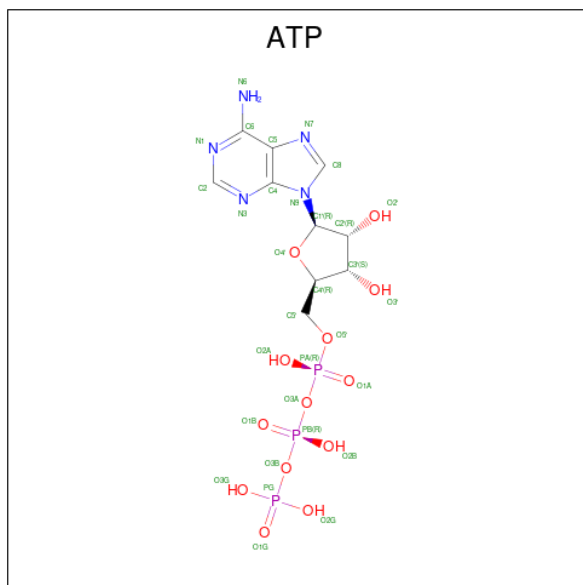
Mol	Chain	Residues	Atoms		AltConf
40	O	1	Total 1	Zn 1	0

- Molecule 41 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).



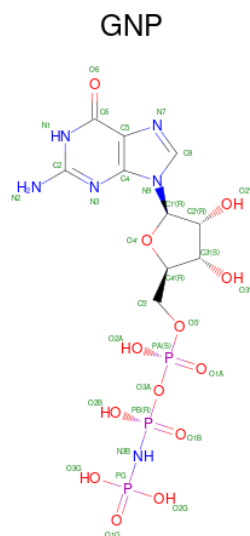
Mol	Chain	Residues	Atoms			AltConf
41	P	1	Total	Fe	S	0
			4	2	2	
41	T	1	Total	Fe	S	0
			4	2	2	

- Molecule 42 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



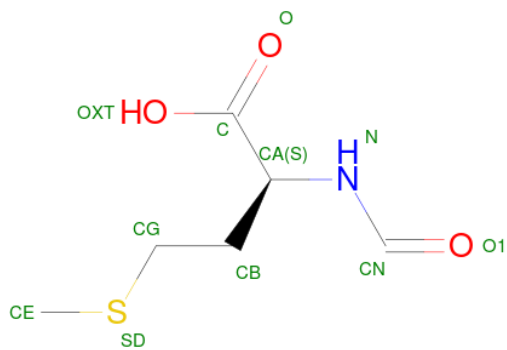
Mol	Chain	Residues	Atoms					AltConf
42	X	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 43 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$).



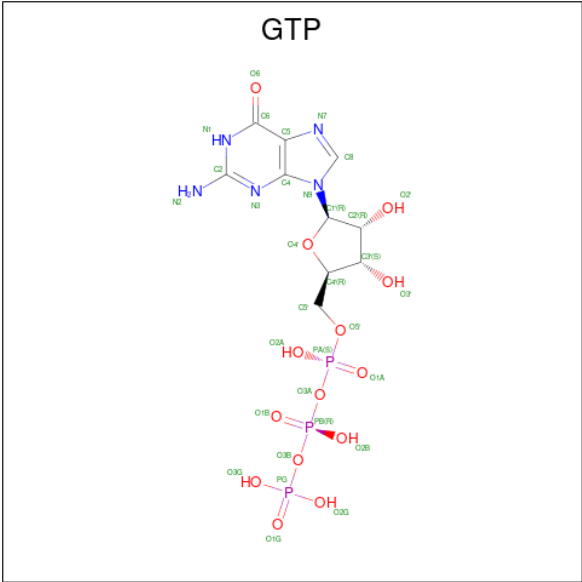
Mol	Chain	Residues	Atoms					AltConf
43	X	1	Total	C	N	O	P	0
			32	10	6	13	3	

- Molecule 44 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: $\text{C}_6\text{H}_{11}\text{NO}_3\text{S}$).



Mol	Chain	Residues	Atoms					AltConf
44	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

- Molecule 45 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $\text{C}_{10}\text{H}_{16}\text{N}_5\text{O}_{14}\text{P}_3$).



Mol	Chain	Residues	Atoms					AltConf
45	7	1	Total	C	N	O	P	0
			32	10	5	14	3	

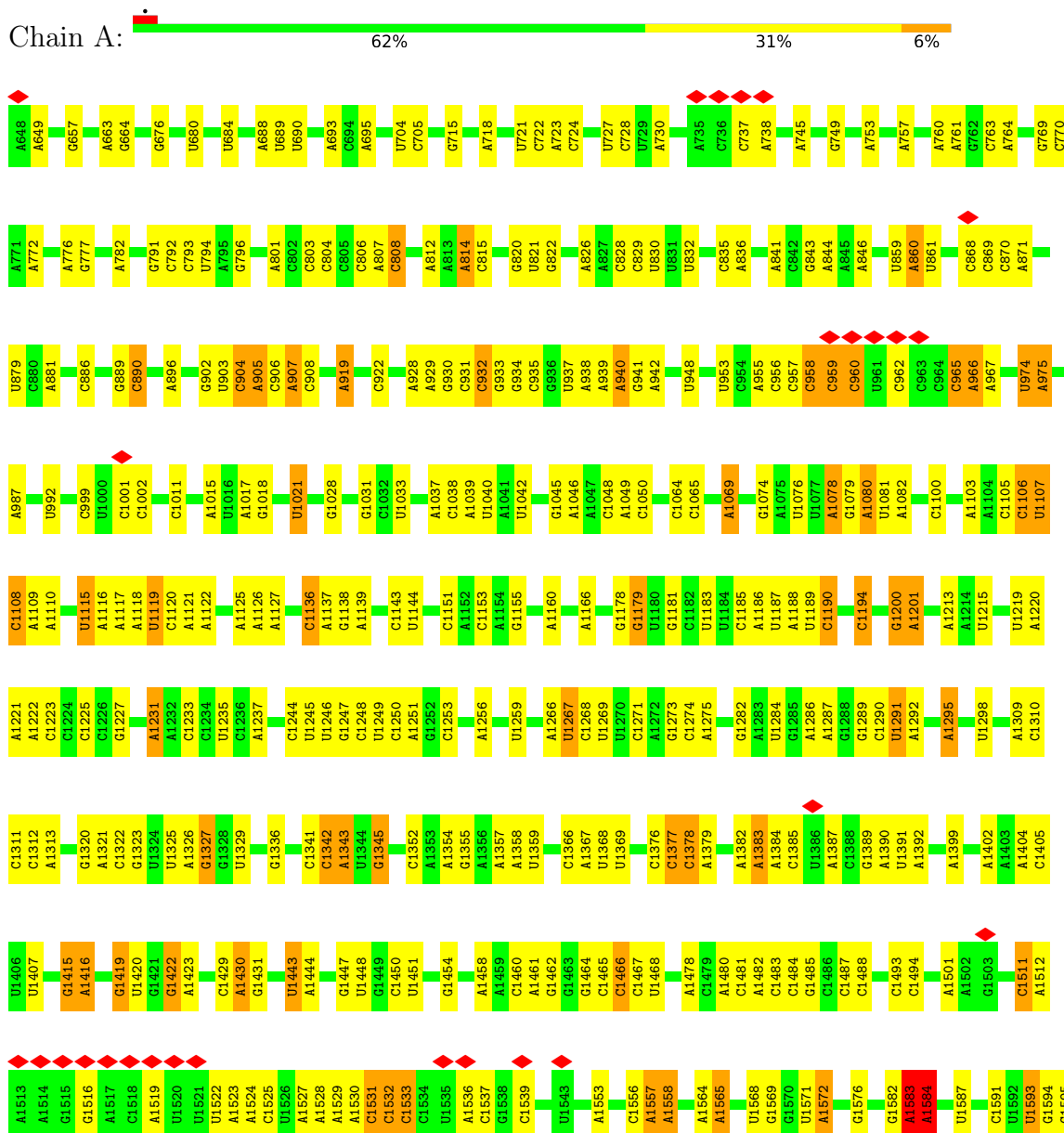
- Molecule 46 is water.

Mol	Chain	Residues	Atoms		AltConf
46	5	6	Total	O	0
			6	6	
46	7	1	Total	O	0
			1	1	

3 Residue-property plots

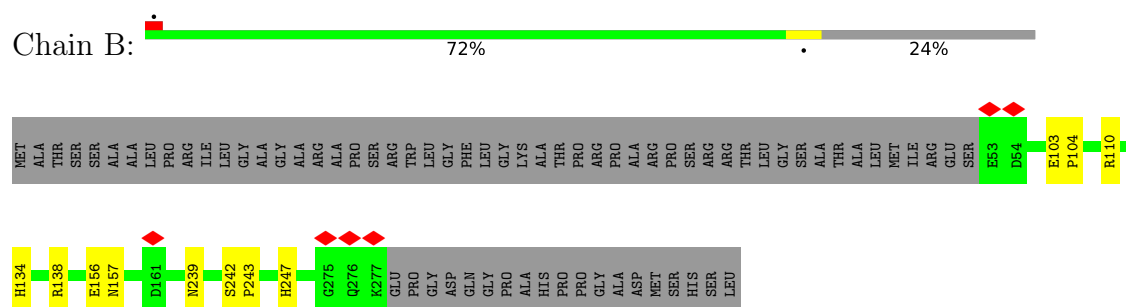
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 12S mitochondrial rRNA

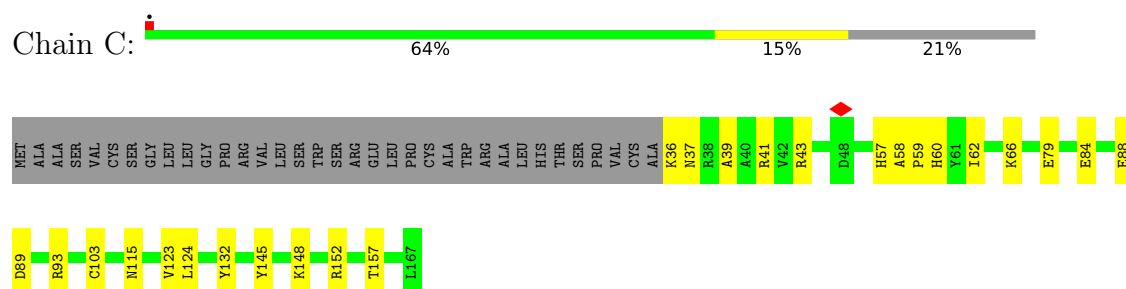


G1598
A1599
A1600
C1601
C1602

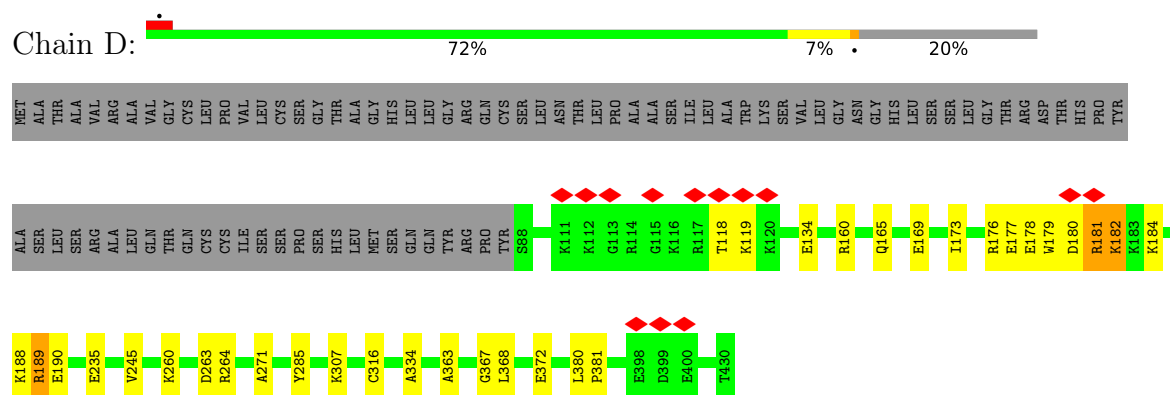
- Molecule 2: 28S ribosomal protein S2, mitochondrial



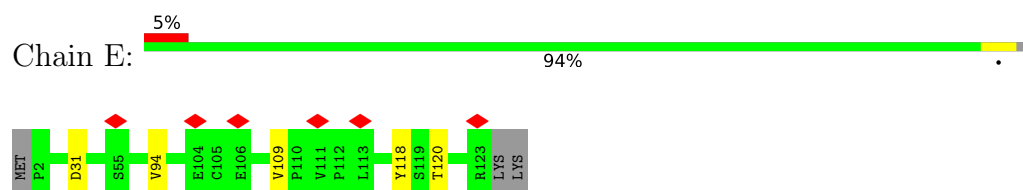
- Molecule 3: 28S ribosomal protein S24, mitochondrial



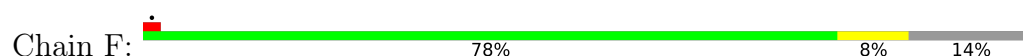
- Molecule 4: 28S ribosomal protein S5, mitochondrial

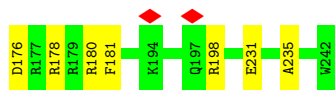


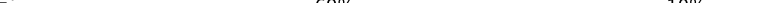
- Molecule 5: 28S ribosomal protein S6, mitochondrial

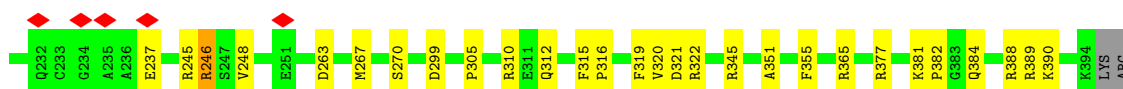


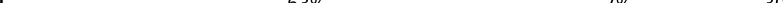
- Molecule 6: 28S ribosomal protein S7, mitochondrial



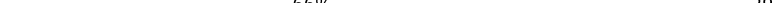


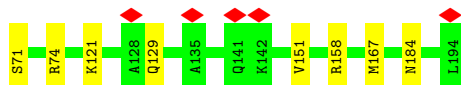
- Chain G: 

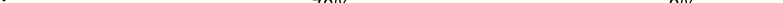


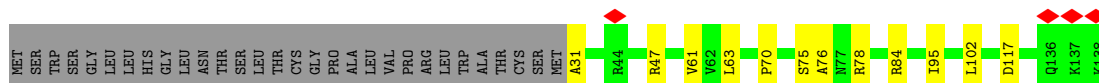
- Chain H: 



- Chain I:  66% 29%

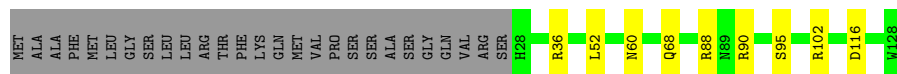


- Chain J:  70% 9% 22%



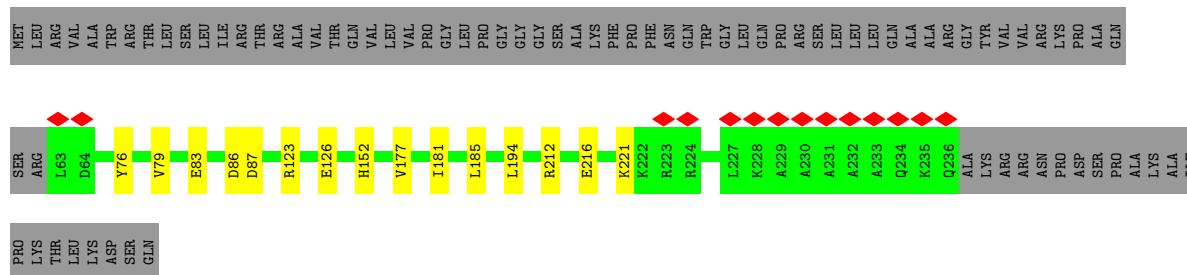
- Molecule 11: 28S ribosomal protein S14, mitochondrial

Chain K:  72% 7% 21%



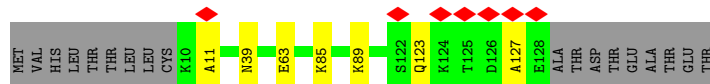
- Molecule 12: 28S ribosomal protein S15, mitochondrial

Chain L:  5% 62% 6% 32%



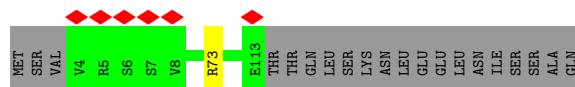
- Molecule 13: 28S ribosomal protein S16, mitochondrial

Chain M:  5% 82% 5% 13%



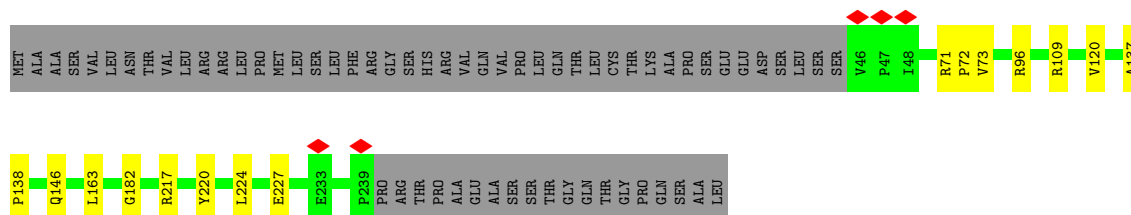
- Molecule 14: 28S ribosomal protein S17, mitochondrial

Chain N:  5% 84% 15%



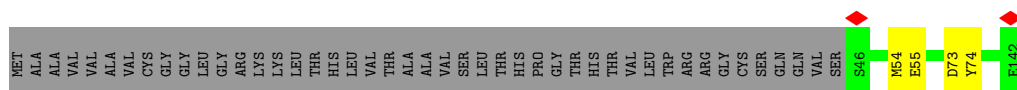
- Molecule 15: 28S ribosomal protein S18b, mitochondrial

Chain O:  69% 6% 25%

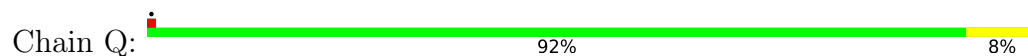


- Molecule 16: 28S ribosomal protein S18c, mitochondrial

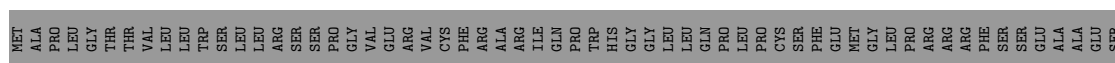
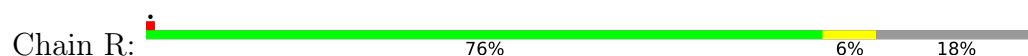
Chain P:  65% 32%



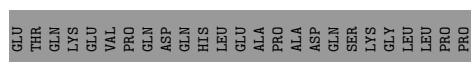
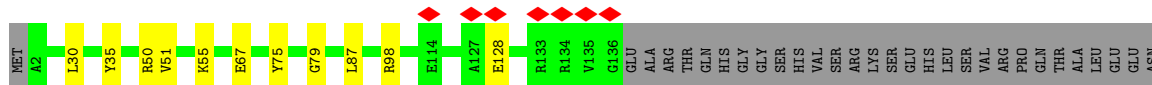
- Molecule 17: 28S ribosomal protein S21, mitochondrial



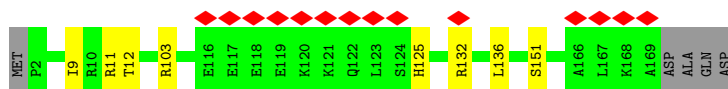
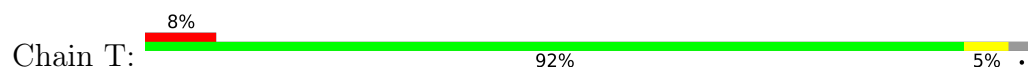
- Molecule 18: 28S ribosomal protein S22, mitochondrial



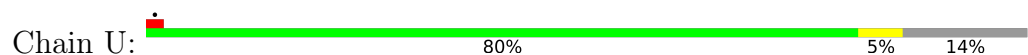
- Molecule 19: 28S ribosomal protein S23, mitochondrial



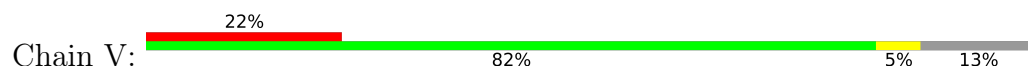
- Molecule 20: 28S ribosomal protein S25, mitochondrial

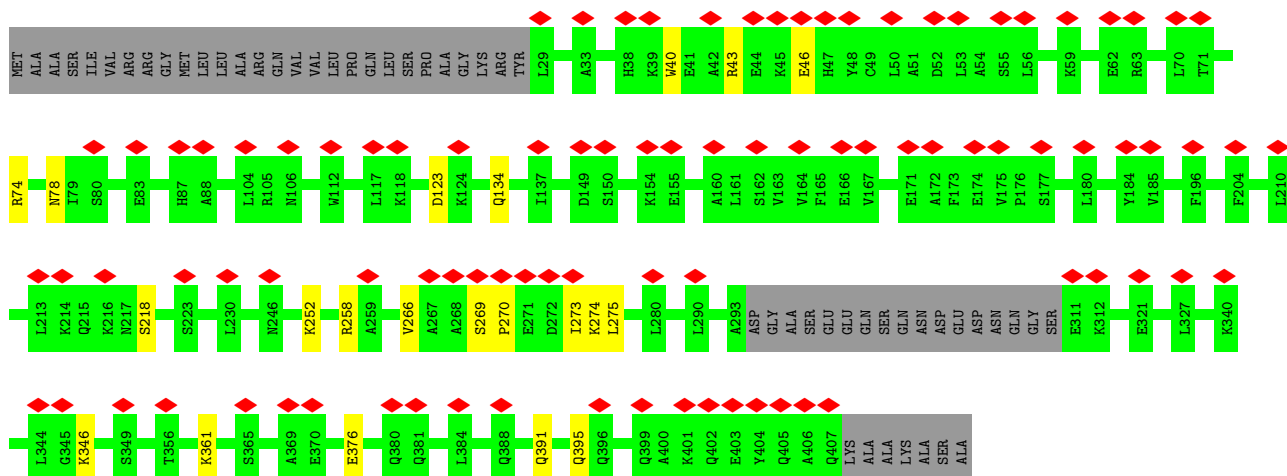


- Molecule 21: 28S ribosomal protein S26, mitochondrial



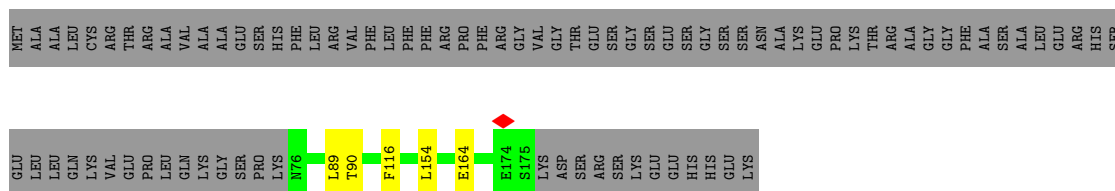
- Molecule 22: 28S ribosomal protein S27, mitochondrial





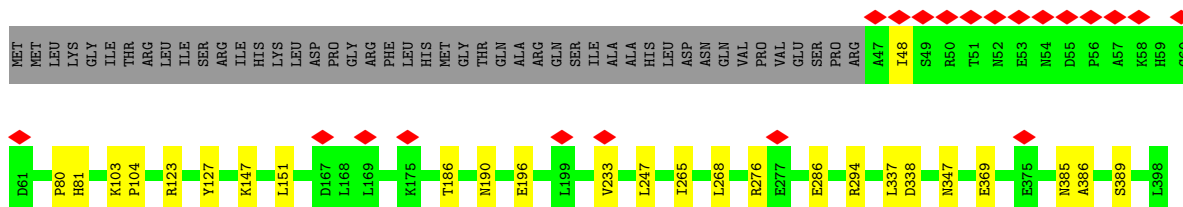
- Molecule 23: 28S ribosomal protein S28, mitochondrial

Chain W: 51% 47%



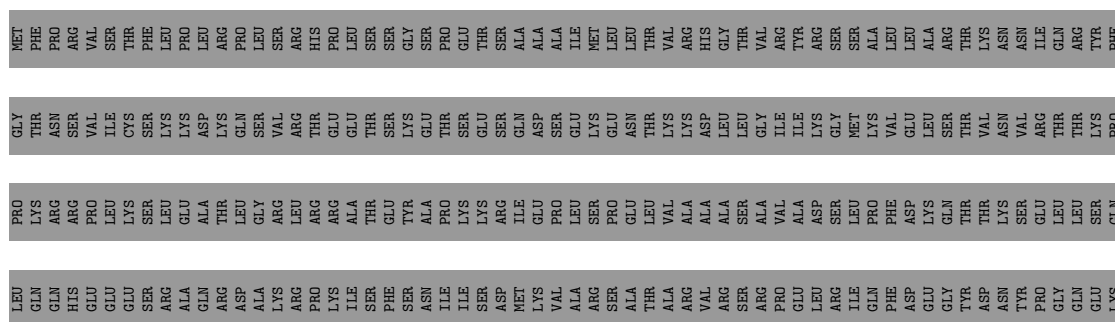
- Molecule 24: 28S ribosomal protein S29, mitochondrial

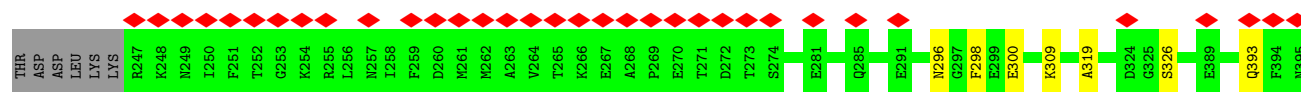
Chain X: 5% 82% 7% 12%



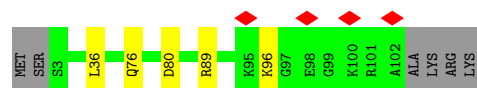
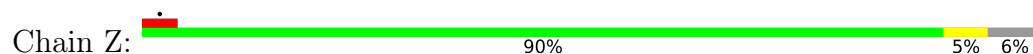
- Molecule 25: 28S ribosomal protein S31, mitochondrial

Chain Y: 9% 36% 62%

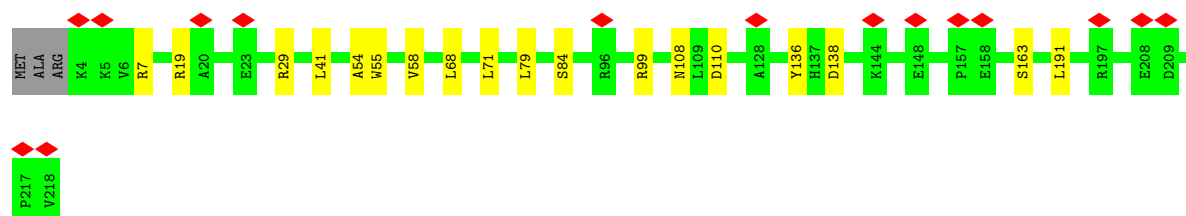
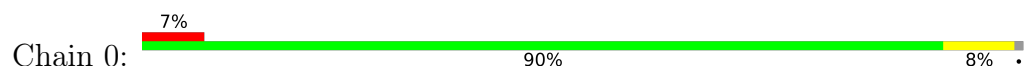




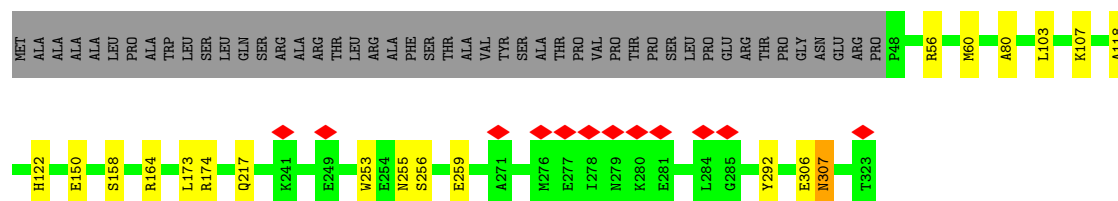
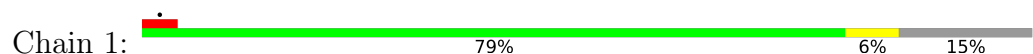
- Molecule 26: 28S ribosomal protein S33, mitochondrial



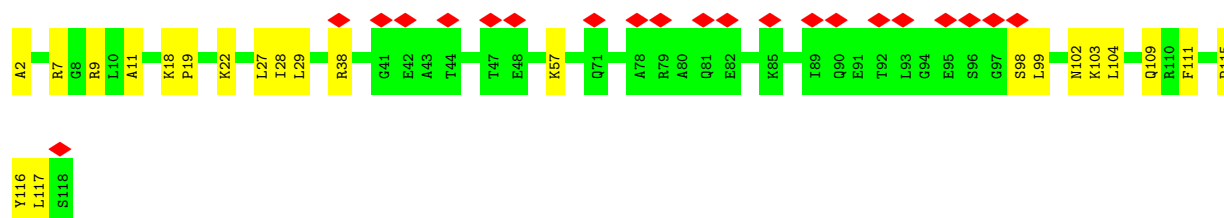
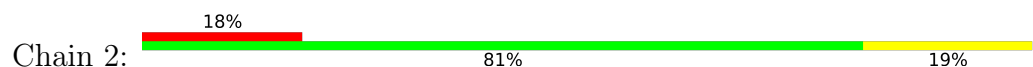
- Molecule 27: 28S ribosomal protein S34, mitochondrial



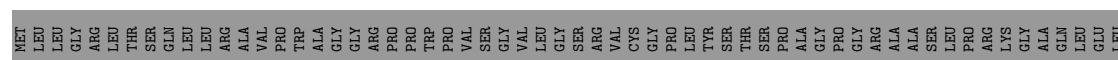
- Molecule 28: 28S ribosomal protein S35, mitochondrial

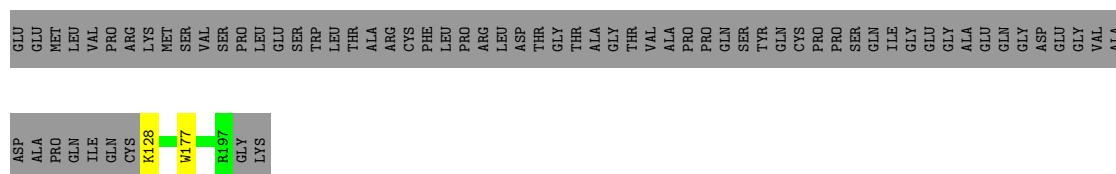


- Molecule 29: Coiled-coil-helix-coiled-coil-helix domain-containing protein 1

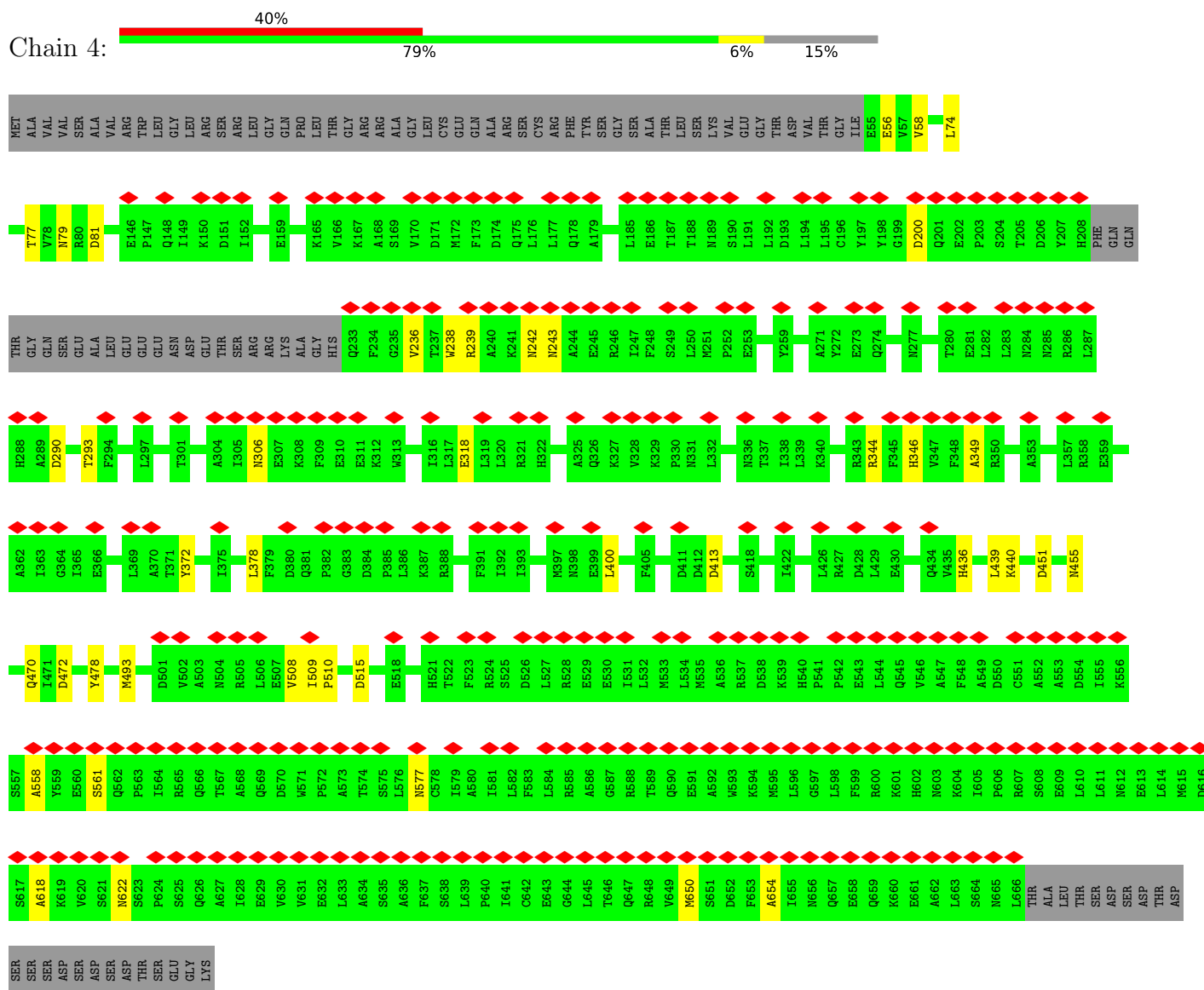


- Molecule 30: Aurora kinase A-interacting protein

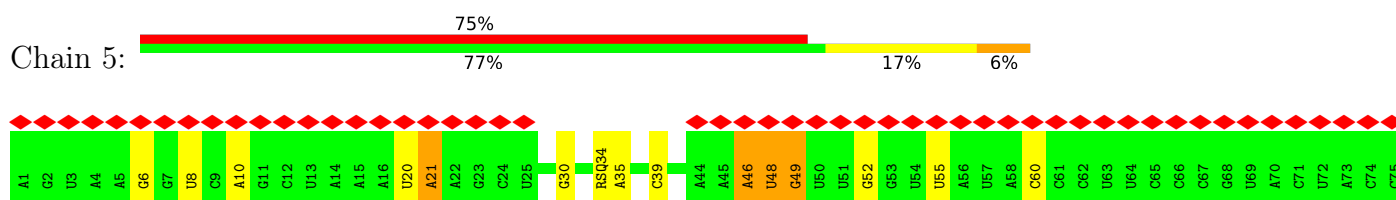




- Molecule 31: Pentatricopeptide repeat domain-containing protein 3, mitochondrial



- Molecule 32: fMet-tRNA^{Met}



Chain 6:



A legend for Chain 6 showing three colored squares with labels: a yellow square for A1, a green square for A2, and a yellow square for A3.

Color	Label
Yellow	A1
Green	A2
Yellow	A3

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	36448	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.565	Depositor
Minimum map value	-0.661	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.048	Depositor
Recommended contour level	0.16	Depositor
Map size (Å)	517.12, 517.12, 517.12	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.01, 1.01, 1.01	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, ATP, B8T, 5MC, MG, RSQ, NAD, GTP, ZN, FES, MA6, K, GNP, SPM, SRY, FME, AYA

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	0/22562	0.38	0/35124
2	B	0.32	0/1871	0.38	0/2531
3	C	0.39	0/1113	0.41	0/1505
4	D	0.37	0/2783	0.52	4/3724 (0.1%)
5	E	0.27	0/989	0.36	0/1335
6	F	0.72	0/1767	0.76	0/2373
7	G	0.34	0/2652	0.41	0/3556
8	H	0.36	0/1178	0.37	0/1598
9	I	0.26	0/1039	0.35	0/1400
10	J	0.34	0/855	0.38	0/1148
11	K	0.40	0/880	0.42	0/1182
12	L	0.30	0/1477	0.36	0/1974
13	M	0.34	0/963	0.41	0/1295
14	N	0.32	0/886	0.33	0/1199
15	O	0.31	0/1655	0.36	0/2254
16	P	0.32	0/798	0.36	0/1070
17	Q	0.33	0/748	0.44	0/994
18	R	0.26	0/2456	0.33	0/3317
19	S	0.26	0/1138	0.33	0/1533
20	T	0.32	0/1402	0.38	0/1883
21	U	0.24	0/1510	0.37	0/2025
22	V	0.19	0/3030	0.32	0/4093
23	W	0.27	0/801	0.33	0/1079
24	X	0.26	0/2921	0.35	0/3954
25	Y	0.27	0/1280	0.32	0/1725
26	Z	0.31	0/857	0.36	0/1141
27	0	0.26	0/1834	0.39	0/2484
28	1	0.30	0/2285	0.35	0/3090
29	2	0.25	0/941	0.38	0/1257
30	3	0.30	0/636	0.45	0/839
31	4	0.21	0/4877	0.34	0/6598
32	5	0.29	0/1654	0.38	0/2568

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	7	0.09	0/4502	0.25	0/6073
34	6	0.62	0/71	0.91	0/108
All	All	0.31	0/76411	0.38	4/108029 (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
4	D	0	2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	182	LYS	N-CA-C	-9.99	100.38	111.07
4	D	180	ASP	N-CA-C	5.70	117.97	111.02
4	D	190	GLU	N-CA-C	-5.25	99.63	110.80
4	D	182	LYS	N-CA-CB	5.17	117.50	110.01

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	181	ARG	Sidechain
4	D	189	ARG	Sidechain

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	20282	0	10297	156	0
2	B	1828	0	1815	8	0
3	C	1083	0	1088	16	0
4	D	2731	0	2804	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	972	0	1000	9	0
6	F	1725	0	1769	21	0
7	G	2596	0	2580	31	0
8	H	1152	0	1183	10	0
9	I	1019	0	1059	5	0
10	J	839	0	887	10	0
11	K	862	0	885	7	0
12	L	1453	0	1540	10	0
13	M	942	0	965	5	0
14	N	868	0	928	1	0
15	O	1599	0	1565	9	0
16	P	781	0	806	2	0
17	Q	744	0	758	6	0
18	R	2409	0	2428	16	0
19	S	1111	0	1115	13	0
20	T	1371	0	1393	7	0
21	U	1488	0	1499	7	0
22	V	2969	0	2961	14	0
23	W	789	0	802	5	0
24	X	2849	0	2843	18	0
25	Y	1246	0	1197	6	0
26	Z	839	0	858	4	0
27	0	1787	0	1796	12	0
28	1	2238	0	2269	14	0
29	2	935	0	969	44	0
30	3	625	0	699	2	0
31	4	4768	0	4766	26	0
32	5	1504	0	764	11	0
33	7	4432	0	4502	37	0
34	6	64	0	33	7	0
35	A	44	0	26	3	0
36	A	14	0	26	1	0
37	A	40	0	39	1	0
38	3	1	0	0	0	0
38	7	1	0	0	0	0
38	A	54	0	0	0	0
38	B	1	0	0	0	0
38	X	1	0	0	0	0
39	7	1	0	0	0	0
39	A	17	0	0	0	0
40	O	1	0	0	0	0
41	P	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
41	T	4	0	0	0	0
42	X	31	0	12	0	0
43	X	32	0	13	0	0
44	5	10	0	10	1	0
45	7	32	0	12	0	0
46	5	6	0	0	0	0
46	7	1	0	0	0	0
All	All	73195	0	62961	426	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 426 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)
1:A:1106:C:O4'	29:2:19:PRO:HG3	1.55	1.06
1:A:1190:C:H1'	1:A:1468:U:N3	1.72	1.05
1:A:1600:A:N6	29:2:99:LEU:O	1.97	0.97
1:A:1593:U:OP1	29:2:22:LYS:HD3	1.65	0.96
23:W:154:LEU:HB3	29:2:29:LEU:HG	1.47	0.96

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	
2	B	223/296 (75%)	212 (95%)	11 (5%)	0	100	100
3	C	130/167 (78%)	127 (98%)	3 (2%)	0	100	100
4	D	341/430 (79%)	326 (96%)	14 (4%)	1 (0%)	36	67
5	E	120/125 (96%)	116 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	206/242 (85%)	203 (98%)	3 (2%)	0	100	100
7	G	312/396 (79%)	300 (96%)	12 (4%)	0	100	100
8	H	138/201 (69%)	136 (99%)	1 (1%)	1 (1%)	18	50
9	I	135/194 (70%)	126 (93%)	8 (6%)	1 (1%)	18	50
10	J	106/138 (77%)	100 (94%)	6 (6%)	0	100	100
11	K	99/128 (77%)	99 (100%)	0	0	100	100
12	L	172/257 (67%)	168 (98%)	4 (2%)	0	100	100
13	M	117/137 (85%)	116 (99%)	1 (1%)	0	100	100
14	N	108/130 (83%)	101 (94%)	7 (6%)	0	100	100
15	O	192/258 (74%)	184 (96%)	8 (4%)	0	100	100
16	P	95/142 (67%)	93 (98%)	2 (2%)	0	100	100
17	Q	84/86 (98%)	83 (99%)	1 (1%)	0	100	100
18	R	293/360 (81%)	287 (98%)	6 (2%)	0	100	100
19	S	133/190 (70%)	130 (98%)	3 (2%)	0	100	100
20	T	166/173 (96%)	164 (99%)	2 (1%)	0	100	100
21	U	174/205 (85%)	171 (98%)	3 (2%)	0	100	100
22	V	358/414 (86%)	350 (98%)	8 (2%)	0	100	100
23	W	98/187 (52%)	93 (95%)	5 (5%)	0	100	100
24	X	350/398 (88%)	344 (98%)	6 (2%)	0	100	100
25	Y	147/395 (37%)	145 (99%)	2 (1%)	0	100	100
26	Z	98/106 (92%)	94 (96%)	4 (4%)	0	100	100
27	0	213/218 (98%)	207 (97%)	6 (3%)	0	100	100
28	1	274/323 (85%)	260 (95%)	14 (5%)	0	100	100
29	2	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
30	3	68/199 (34%)	65 (96%)	3 (4%)	0	100	100
31	4	584/689 (85%)	563 (96%)	21 (4%)	0	100	100
33	7	569/691 (82%)	558 (98%)	11 (2%)	0	100	100
All	All	6218/7992 (78%)	6034 (97%)	181 (3%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	I	184	ASN

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Mol	Chain	Res	Type
8	H	126	ILE
4	D	188	LYS

5.3.2 Protein sidechains ⓘ

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	
2	B	198/249 (80%)	198 (100%)	0	100	100
3	C	115/143 (80%)	115 (100%)	0	100	100
4	D	286/357 (80%)	286 (100%)	0	100	100
5	E	104/107 (97%)	104 (100%)	0	100	100
6	F	185/209 (88%)	185 (100%)	0	100	100
7	G	275/342 (80%)	273 (99%)	2 (1%)	76	87
8	H	130/180 (72%)	130 (100%)	0	100	100
9	I	105/147 (71%)	105 (100%)	0	100	100
10	J	93/118 (79%)	93 (100%)	0	100	100
11	K	91/113 (80%)	91 (100%)	0	100	100
12	L	158/226 (70%)	158 (100%)	0	100	100
13	M	97/113 (86%)	97 (100%)	0	100	100
14	N	96/115 (84%)	96 (100%)	0	100	100
15	O	175/230 (76%)	175 (100%)	0	100	100
16	P	88/123 (72%)	88 (100%)	0	100	100
17	Q	78/78 (100%)	78 (100%)	0	100	100
18	R	264/318 (83%)	264 (100%)	0	100	100
19	S	116/164 (71%)	116 (100%)	0	100	100
20	T	153/157 (98%)	153 (100%)	0	100	100
21	U	152/174 (87%)	152 (100%)	0	100	100
22	V	325/364 (89%)	325 (100%)	0	100	100
23	W	87/158 (55%)	87 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	X	311/351 (89%)	310 (100%)	1 (0%)	86	91
25	Y	137/357 (38%)	137 (100%)	0	100	100
26	Z	90/95 (95%)	90 (100%)	0	100	100
27	0	188/190 (99%)	187 (100%)	1 (0%)	81	89
28	1	254/291 (87%)	253 (100%)	1 (0%)	84	90
29	2	100/100 (100%)	100 (100%)	0	100	100
30	3	65/166 (39%)	65 (100%)	0	100	100
31	4	526/609 (86%)	525 (100%)	1 (0%)	87	92
33	7	481/587 (82%)	481 (100%)	0	100	100
All	All	5523/6931 (80%)	5517 (100%)	6 (0%)	87	94

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
27	0	79	LEU
28	1	307	ASN
31	4	577	ASN
7	G	248	VAL
7	G	246	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
15	O	166	HIS
31	4	243	ASN
19	S	66	HIS
24	X	140	HIS
18	R	214	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	954/955 (99%)	283 (29%)	10 (1%)
32	5	70/71 (98%)	11 (15%)	0
34	6	2/3 (66%)	0	0
All	All	1026/1029 (99%)	294 (28%)	10 (0%)

5 of 294 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	649	A
1	A	657	G
1	A	676	G
1	A	680	U
1	A	688	A

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1531	C
1	A	1532	C
1	A	1557	A
1	A	1246	U
1	A	1342	C

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

8 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	MA6	A	1583	1	23,26,27	0.80	1 (4%)	34,38,41	2.13	9 (26%)
1	B8T	A	1486	1	19,22,23	0.39	0	26,31,34	0.38	0
17	AYA	Q	2	17	6,7,8	1.39	1 (16%)	5,8,10	1.13	0
1	MA6	A	1584	1	23,26,27	0.81	1 (4%)	34,38,41	2.13	9 (26%)
29	AYA	2	2	29	6,7,8	1.37	1 (16%)	5,8,10	1.36	1 (20%)
1	5MC	A	1488	1	18,22,23	0.34	0	26,32,35	0.60	0
1	5MU	A	1076	1	19,22,23	1.12	3 (15%)	28,32,35	2.17	8 (28%)
32	RSQ	5	34	32,34	20,23,24	0.43	0	26,33,36	0.42	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.

'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MA6	A	1583	1	-	0/11/29/30	0/3/3/3
1	B8T	A	1486	1	-	0/7/27/28	0/2/2/2
17	AYA	Q	2	17	-	1/4/6/8	-
1	MA6	A	1584	1	-	1/11/29/30	0/3/3/3
29	AYA	2	2	29	-	0/4/6/8	-
1	5MC	A	1488	1	-	0/7/25/26	0/2/2/2
1	5MU	A	1076	1	-	0/7/25/26	0/2/2/2
32	RSQ	5	34	32,34	-	0/9/27/28	0/2/2/2

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	Q	2	AYA	CA-N	-2.93	1.43	1.46
29	2	2	AYA	CA-N	-2.81	1.43	1.46
1	A	1076	5MU	C4-C5	-2.68	1.40	1.44
1	A	1076	5MU	C2-N1	-2.64	1.34	1.38
1	A	1584	MA6	C5-N7	-2.17	1.34	1.39

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1076	5MU	C4-N3-C2	-5.71	119.95	127.35
1	A	1584	MA6	C5-C4-N3	-5.44	119.65	126.75
1	A	1583	MA6	C5-C4-N3	-4.87	120.40	126.75
1	A	1583	MA6	N1-C2-N3	-4.77	121.14	128.60
1	A	1076	5MU	N3-C2-N1	4.71	121.15	114.89

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	Q	2	AYA	C-CA-N-CT
1	A	1584	MA6	C4'-C5'-O5'-P

There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1583	MA6	3	0
1	A	1584	MA6	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1488	5MC	1	0
32	5	34	RSQ	6	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 86 ligands modelled in this entry, 77 are monoatomic - leaving 9 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
43	GNP	X	403	-	33,34,34	1.28	5 (15%)	46,54,54	0.95	1 (2%)
36	SPM	A	1702	-	13,13,13	0.15	0	12,12,12	1.15	0
45	GTP	7	801	39,38	30,34,34	0.50	0	46,54,54	0.50	0
37	SRY	A	1703	-	40,42,42	0.78	2 (5%)	49,63,63	1.33	6 (12%)
42	ATP	X	402	38	29,33,33	1.26	4 (13%)	44,52,52	1.91	11 (25%)
41	FES	P	201	5,16	0,4,4	-	-	-	-	-
44	FME	5	101	32	8,9,10	0.54	0	7,9,11	0.31	0
41	FES	T	201	20,13	0,4,4	-	-	-	-	-
35	NAD	A	1701	38	45,48,48	0.94	2 (4%)	63,73,73	1.63	10 (15%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
43	GNP	X	403	-	-	5/18/38/38	0/3/3/3
36	SPM	A	1702	-	-	0/11/11/11	-
45	GTP	7	801	39,38	-	0/22/38/38	0/3/3/3
37	SRY	A	1703	-	-	1/20/87/87	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
42	ATP	X	402	38	-	0/22/38/38	0/3/3/3
41	FES	P	201	5,16	-	-	0/1/1/1
44	FME	5	101	32	-	0/7/9/11	-
41	FES	T	201	20,13	-	-	0/1/1/1
35	NAD	A	1701	38	-	1/30/62/62	0/5/5/5

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	X	403	GNP	PB-O3A	4.27	1.64	1.59
42	X	402	ATP	C5-C4	4.08	1.46	1.39
43	X	403	GNP	PB-O1B	3.04	1.51	1.46
37	A	1703	SRY	CD1-N31	2.97	1.38	1.33
43	X	403	GNP	PG-N3B	2.94	1.71	1.63

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	X	402	ATP	C5-C4-N3	-5.97	118.96	126.75
35	A	1701	NAD	C5A-C4A-N3A	-5.89	119.07	126.75
42	X	402	ATP	N3-C4-N9	4.69	134.81	127.08
37	A	1703	SRY	C12-O42-C42	-4.62	101.11	108.38
35	A	1701	NAD	N3A-C4A-N9A	4.33	134.22	127.08

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
43	X	403	GNP	PG-N3B-PB-O3A
43	X	403	GNP	PA-O3A-PB-O1B
43	X	403	GNP	PA-O3A-PB-O2B
43	X	403	GNP	PG-N3B-PB-O1B
37	A	1703	SRY	C13-C23-N23-CI3

There are no ring outliers.

4 monomers are involved in 6 short contacts:

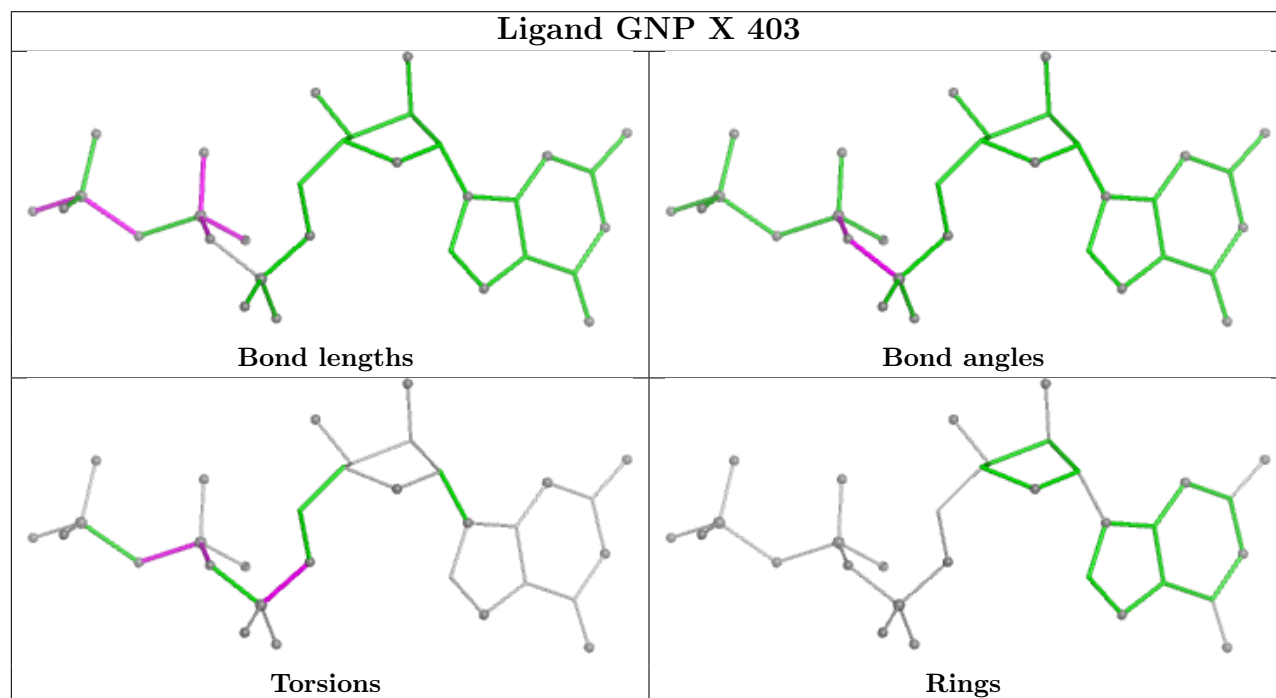
Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	A	1702	SPM	1	0
37	A	1703	SRY	1	0
44	5	101	FME	1	0

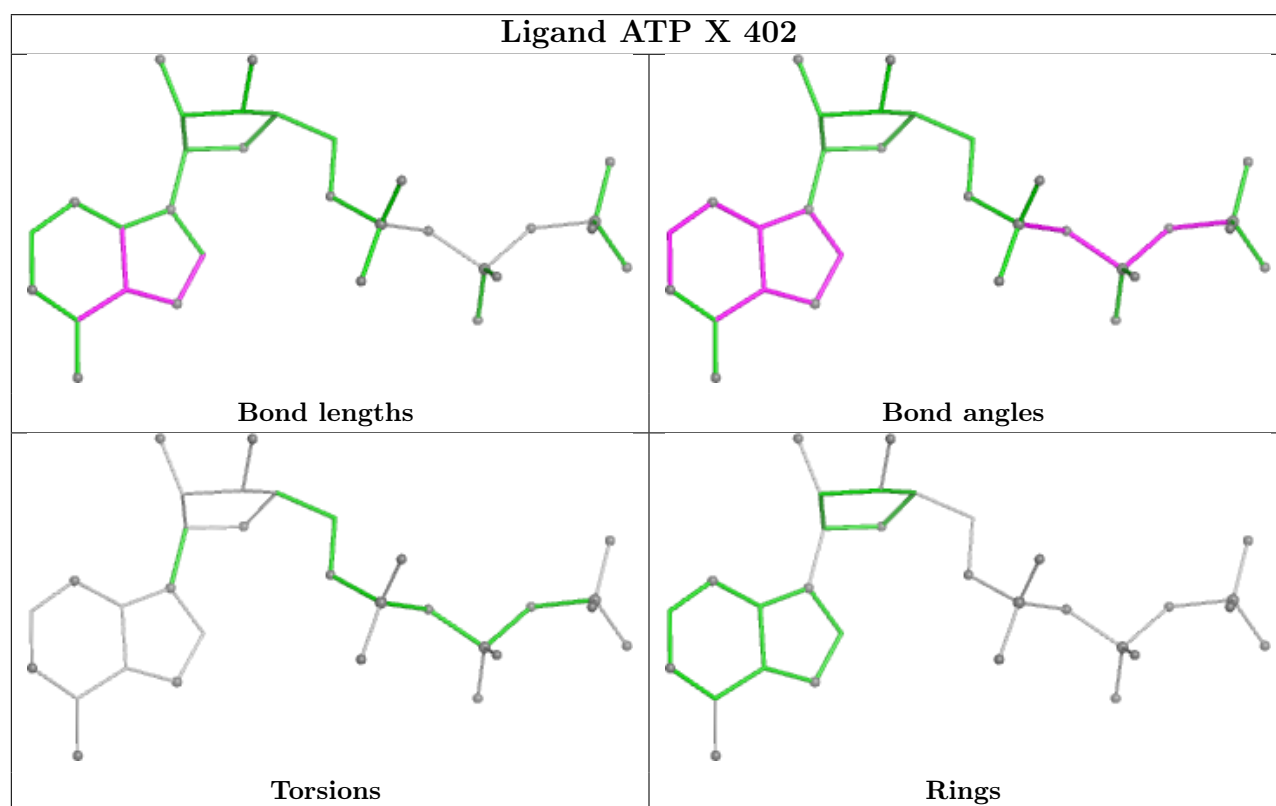
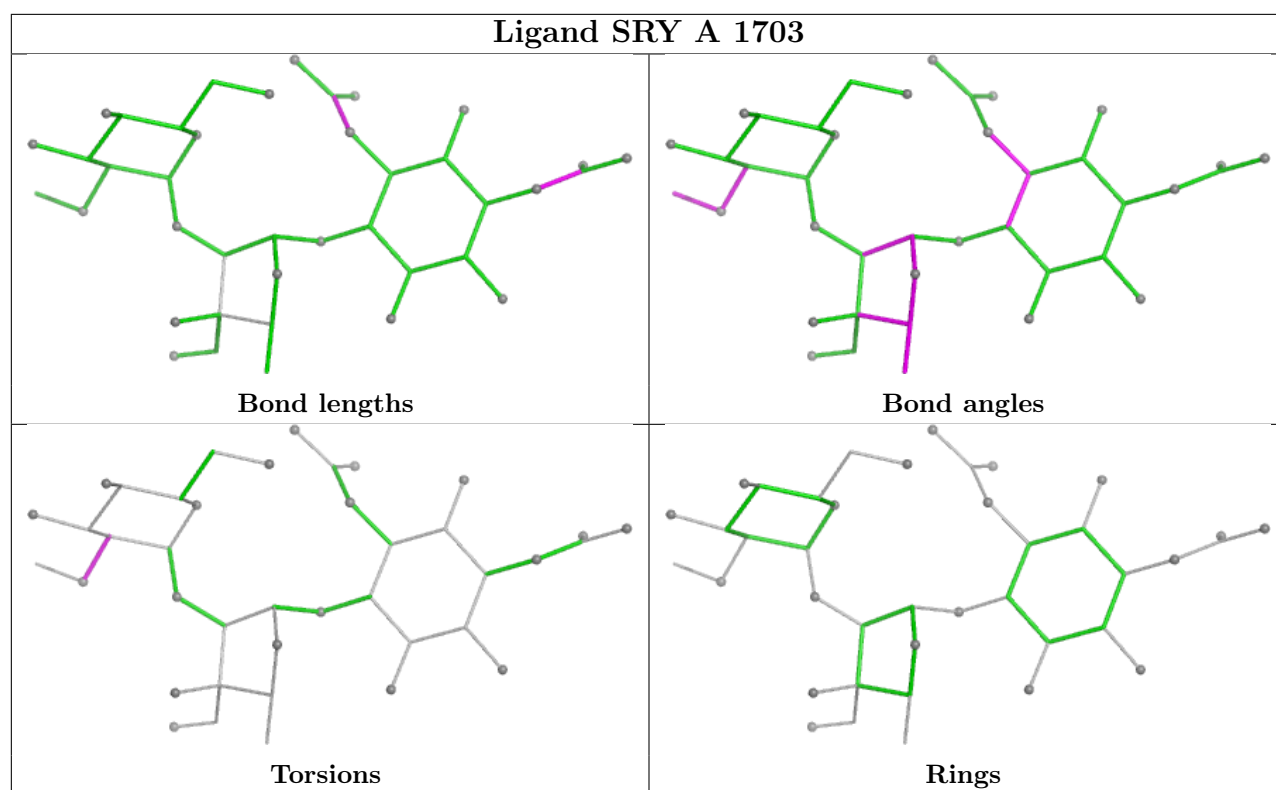
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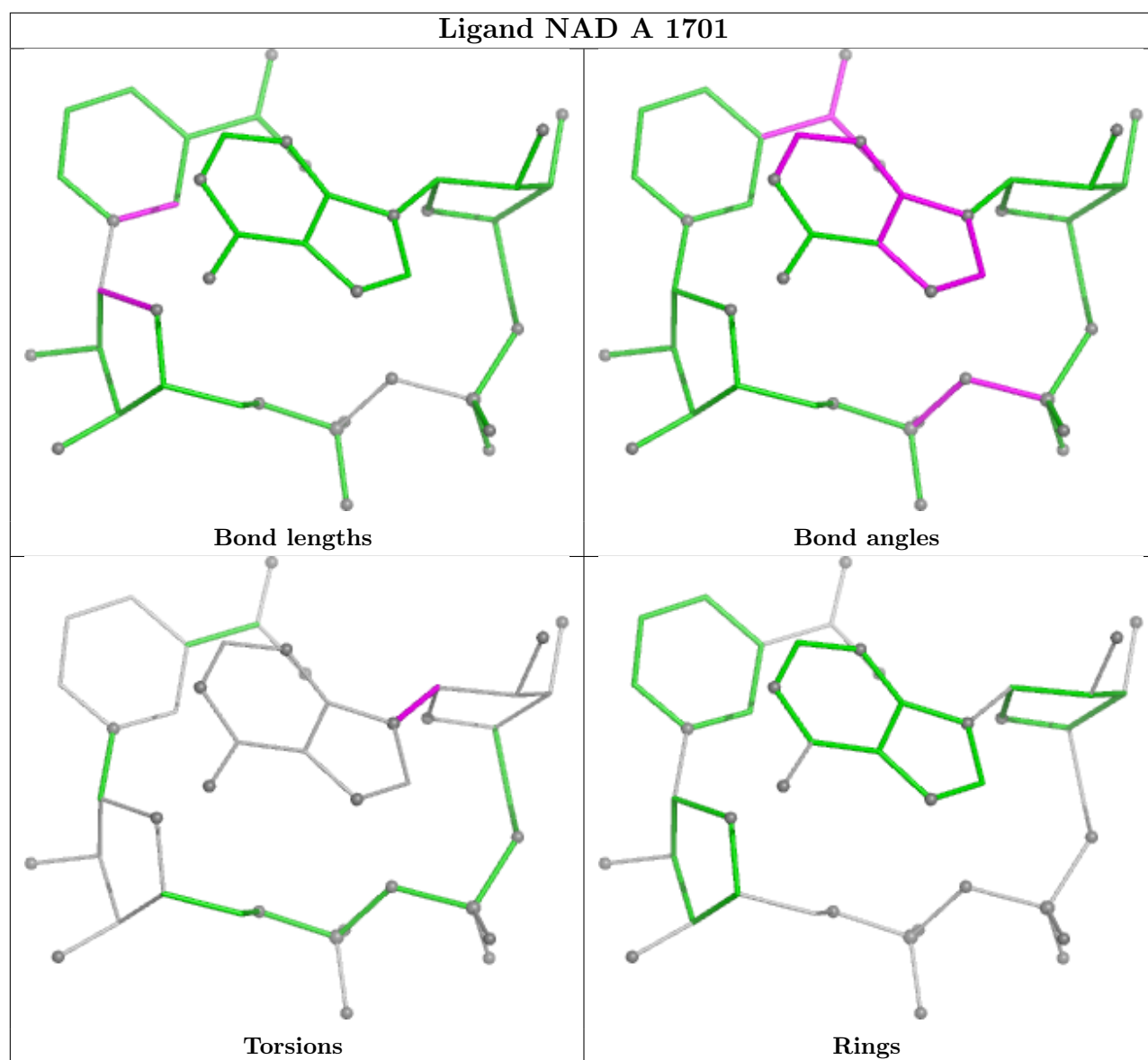
Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
35	A	1701	NAD	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







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.

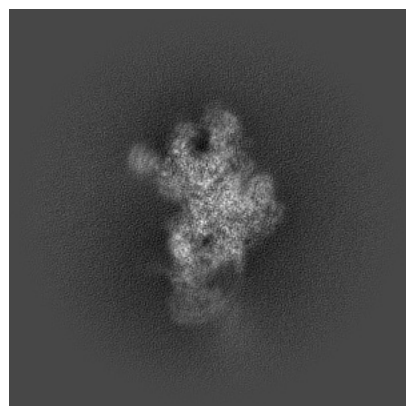
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18443. These allow visual inspection of the internal detail of the map and identification of artifacts.

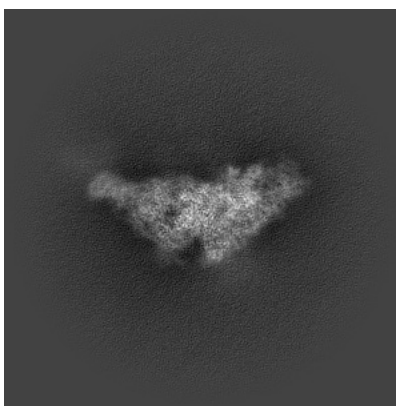
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

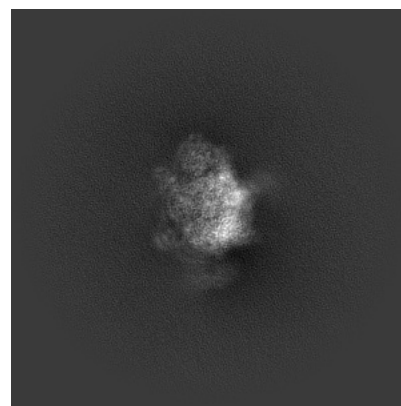
6.1.1 Primary map



X

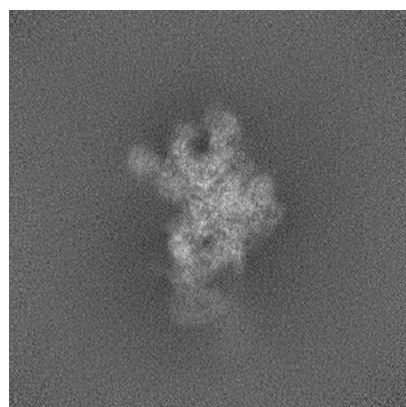


Y

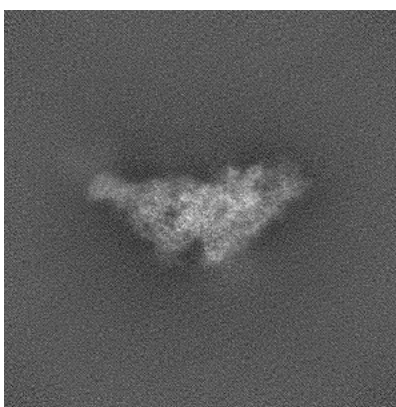


Z

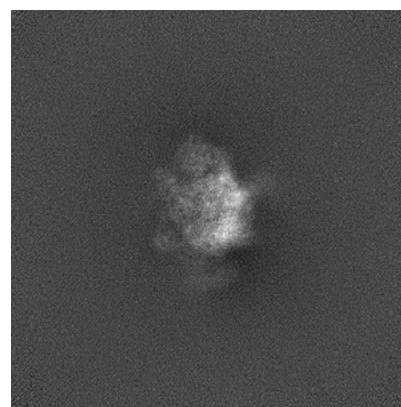
6.1.2 Raw map



X



Y

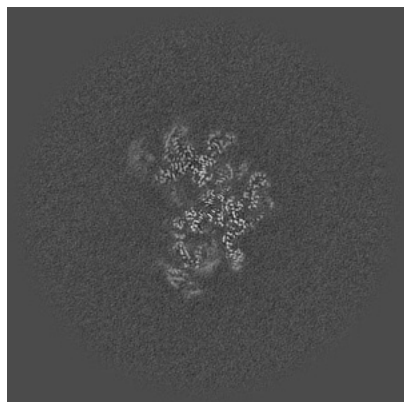


Z

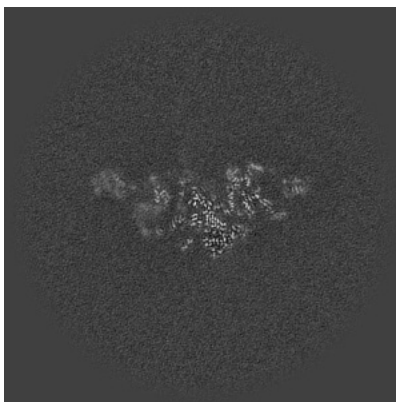
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

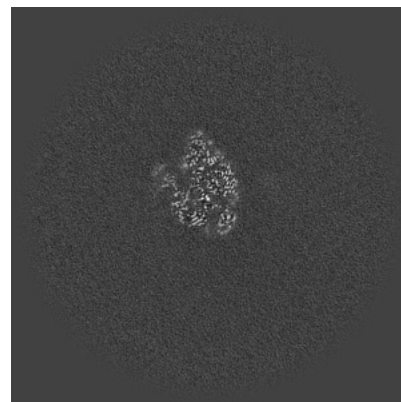
6.2.1 Primary map



X Index: 256

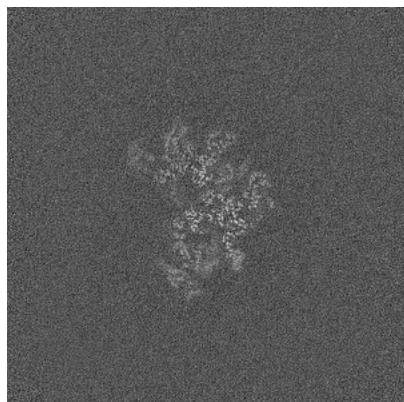


Y Index: 256

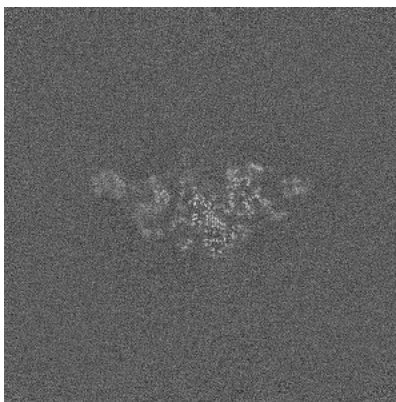


Z Index: 256

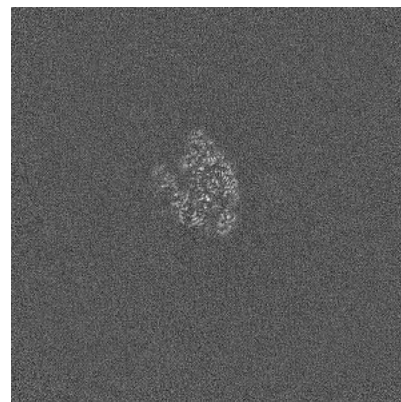
6.2.2 Raw map



X Index: 256



Y Index: 256

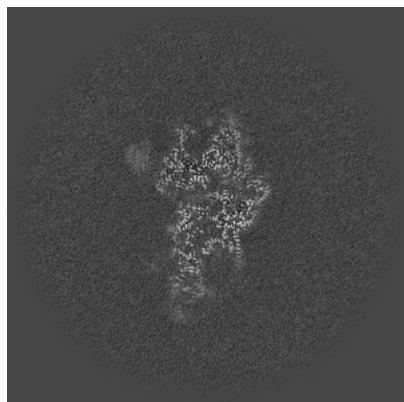


Z Index: 256

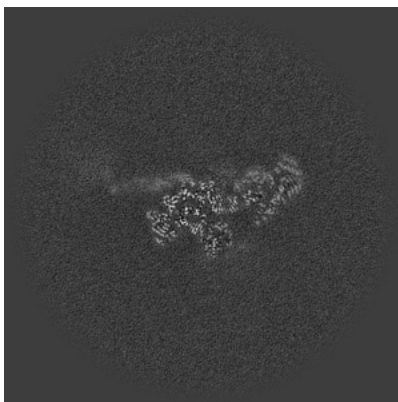
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

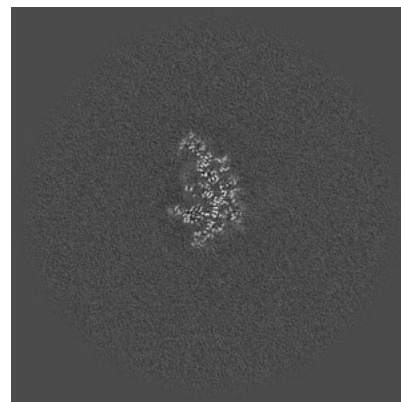
6.3.1 Primary map



X Index: 268

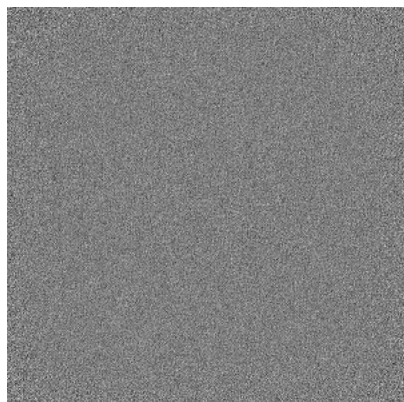


Y Index: 277

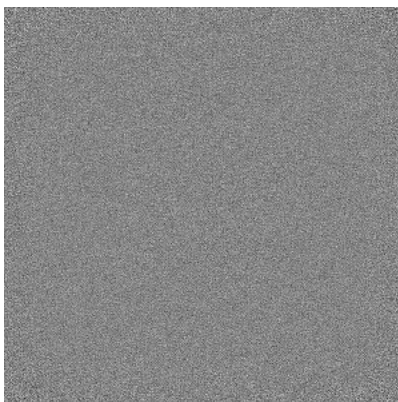


Z Index: 240

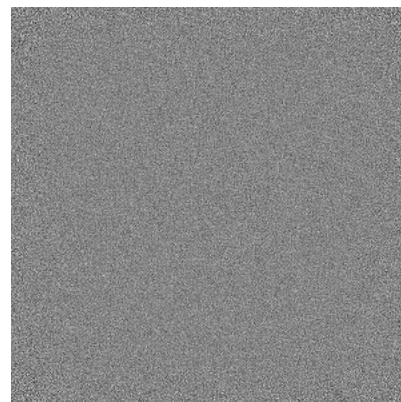
6.3.2 Raw map



X Index: 0



Y Index: 0

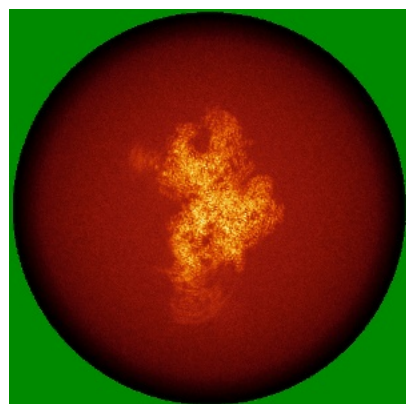


Z Index: 0

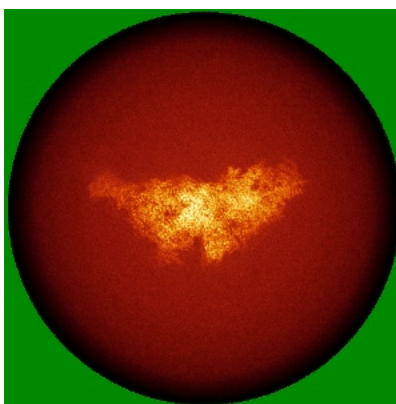
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

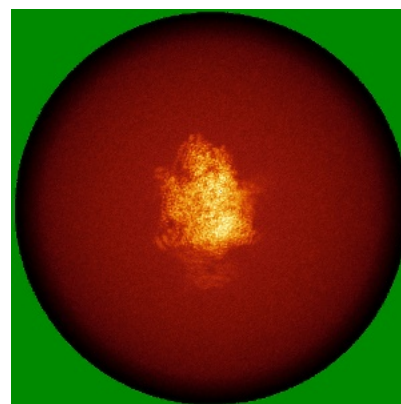
6.4.1 Primary map



X

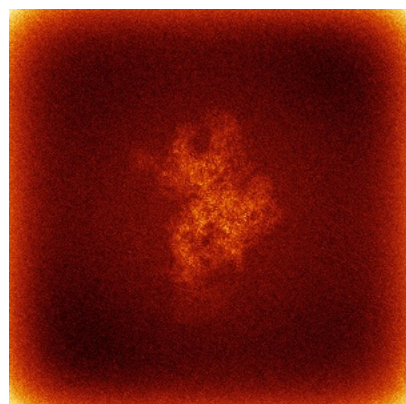


Y

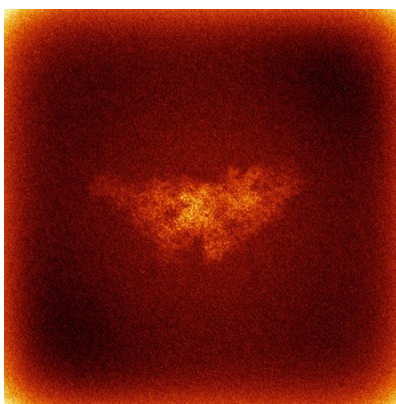


Z

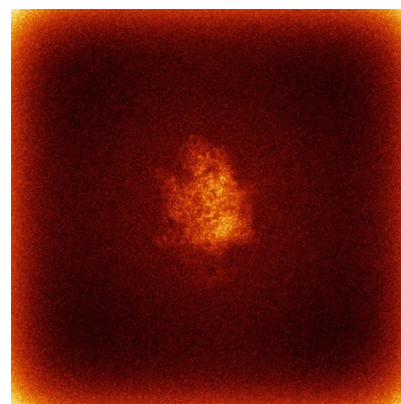
6.4.2 Raw map



X



Y

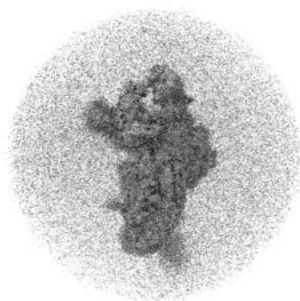


Z

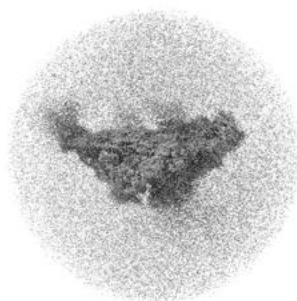
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

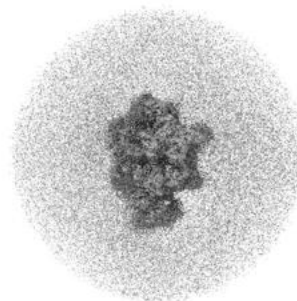
6.5.1 Primary map



X



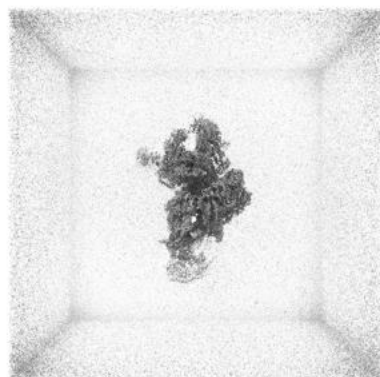
Y



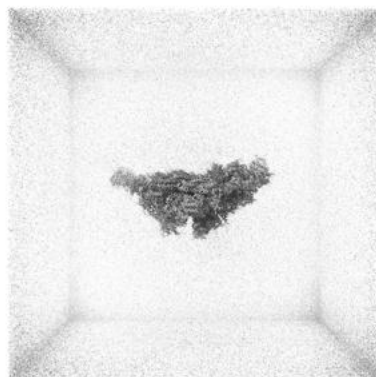
Z

The images above show the 3D surface view of the map at the recommended contour level 0.16. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

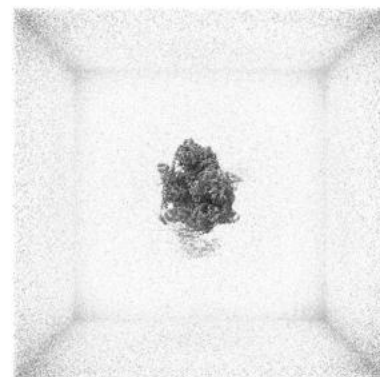
6.5.2 Raw map



X



Y



Z

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

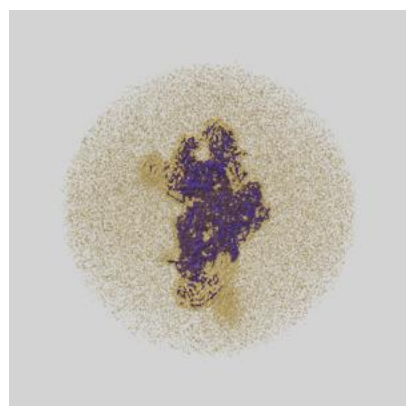
6.6 Mask visualisation [i](#)

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

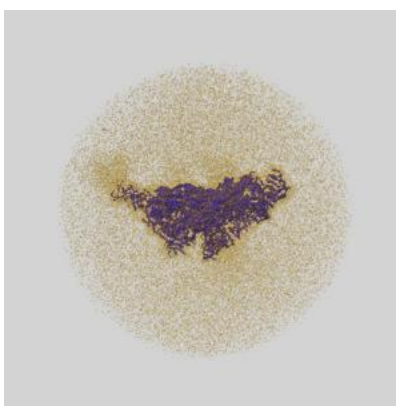
A mask typically either:

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

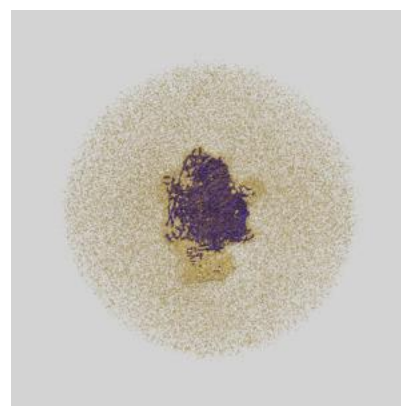
6.6.1 emd_18443_msk_1.map [i](#)



X



Y

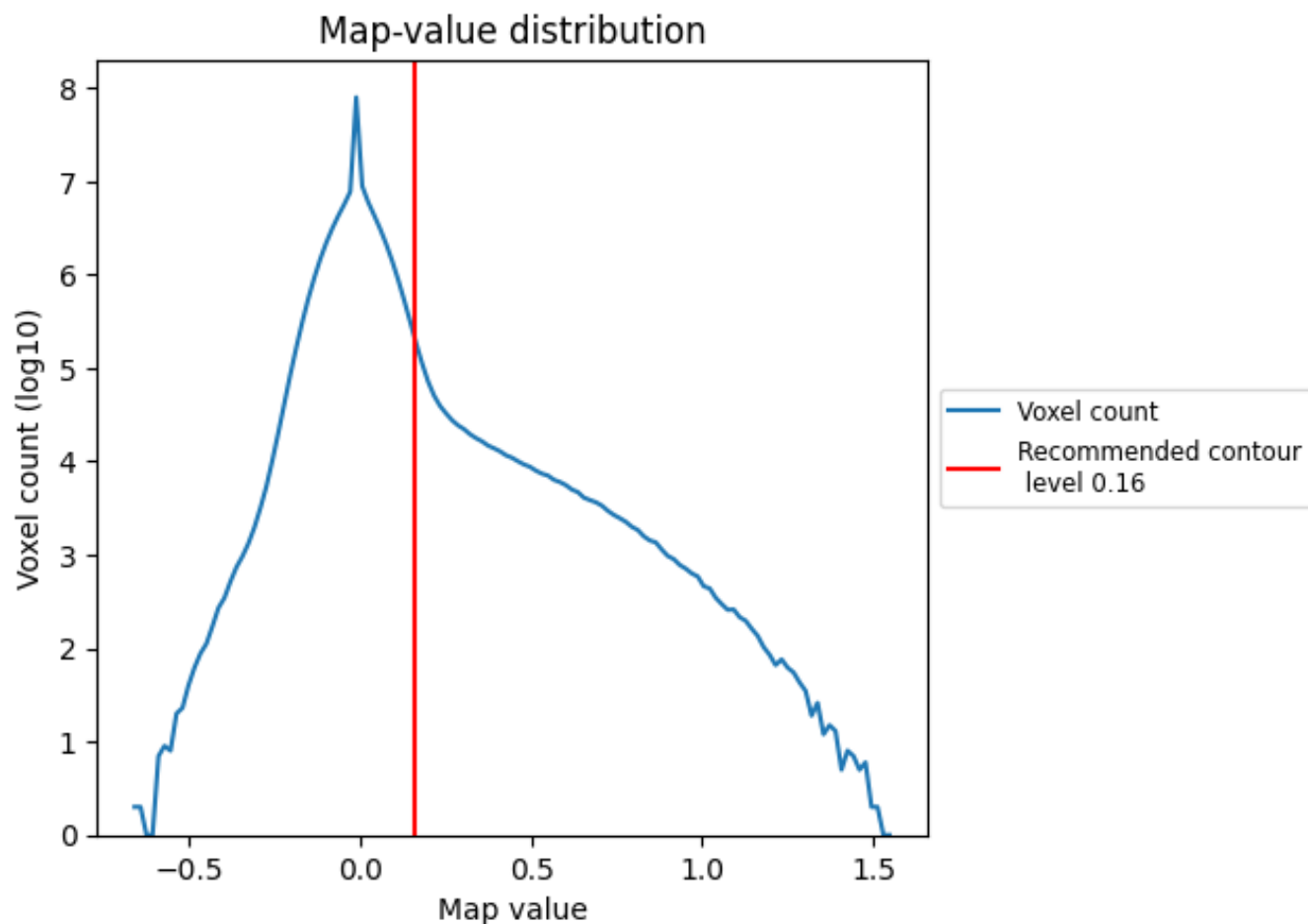


Z

7 Map analysis [i](#)

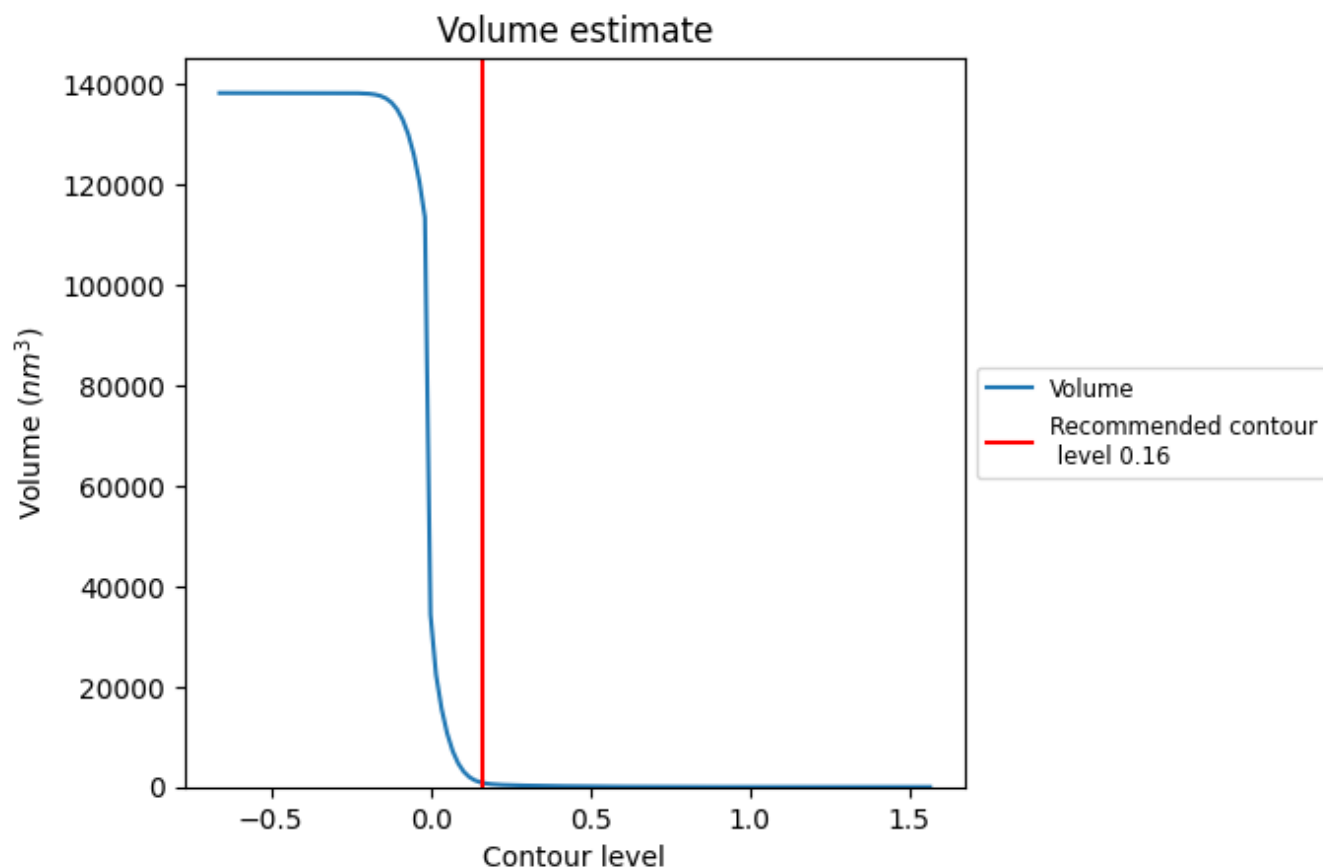
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

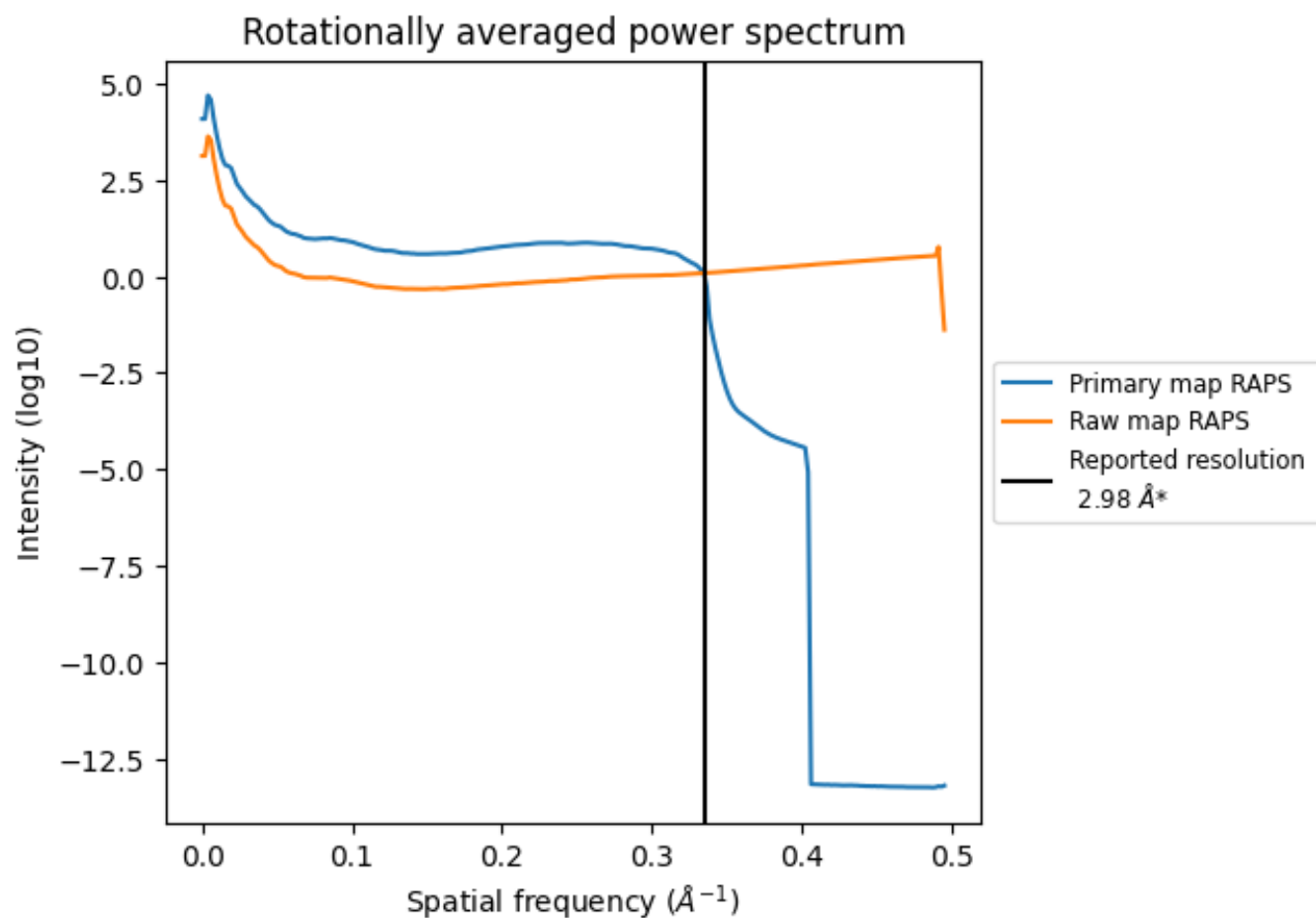
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 883 nm^3 ; this corresponds to an approximate mass of 798 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 ⓘ

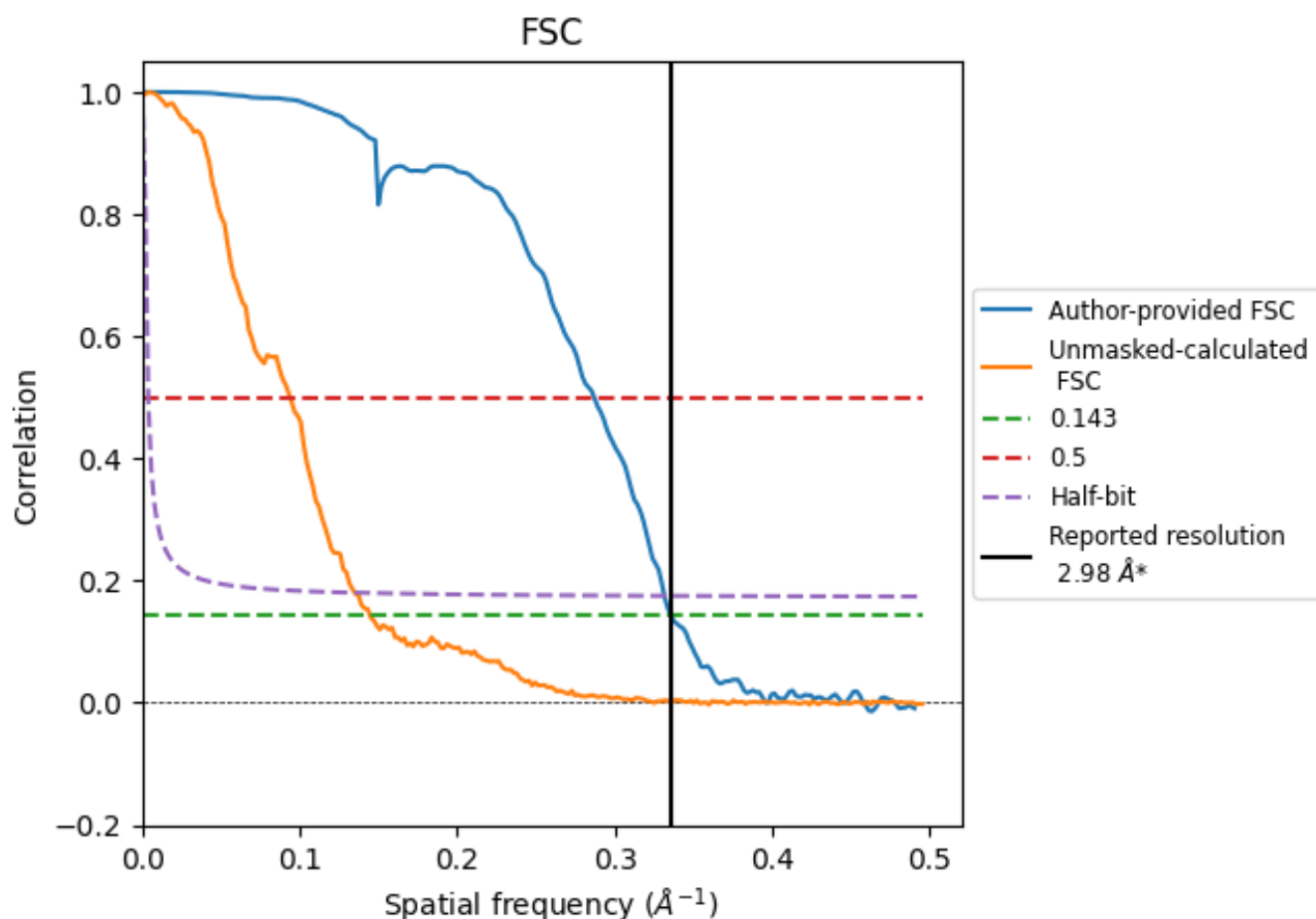


*Reported resolution corresponds to spatial frequency of 0.336 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.336 Å⁻¹

8.2 Resolution estimates [i](#)

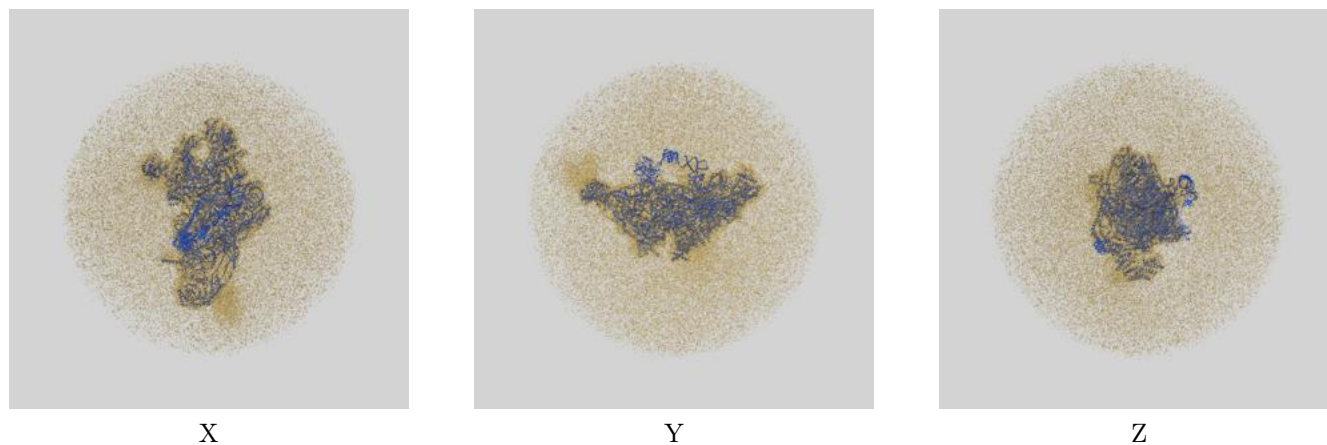
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.98	-	-
Author-provided FSC curve	2.98	3.49	3.02
Unmasked-calculated*	6.92	10.66	7.41

*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 6.92 differs from the reported value 2.98 by more than 10 %

9 Map-model fit [i](#)

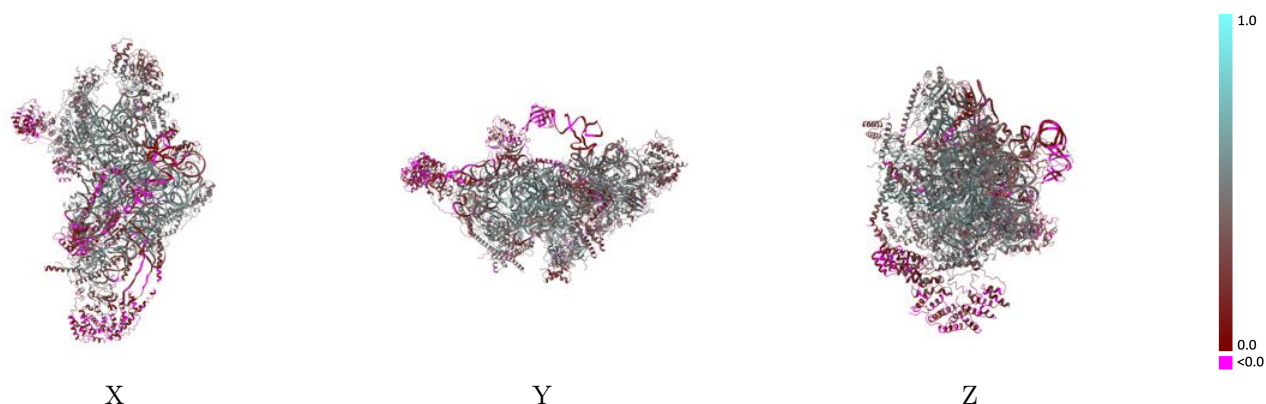
This section contains information regarding the fit between EMDB map EMD-18443 and PDB model 8QRN. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



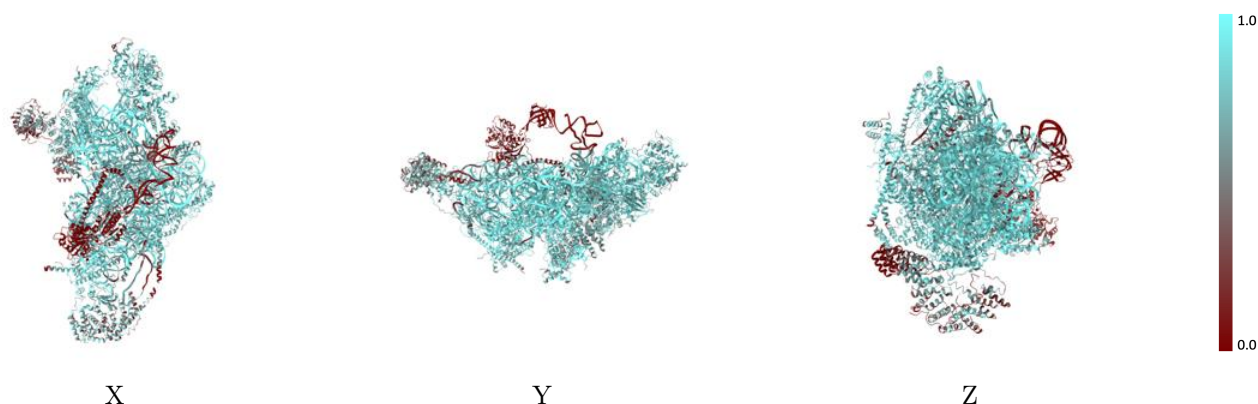
The images above show the 3D surface view of the map at the recommended contour level 0.16 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



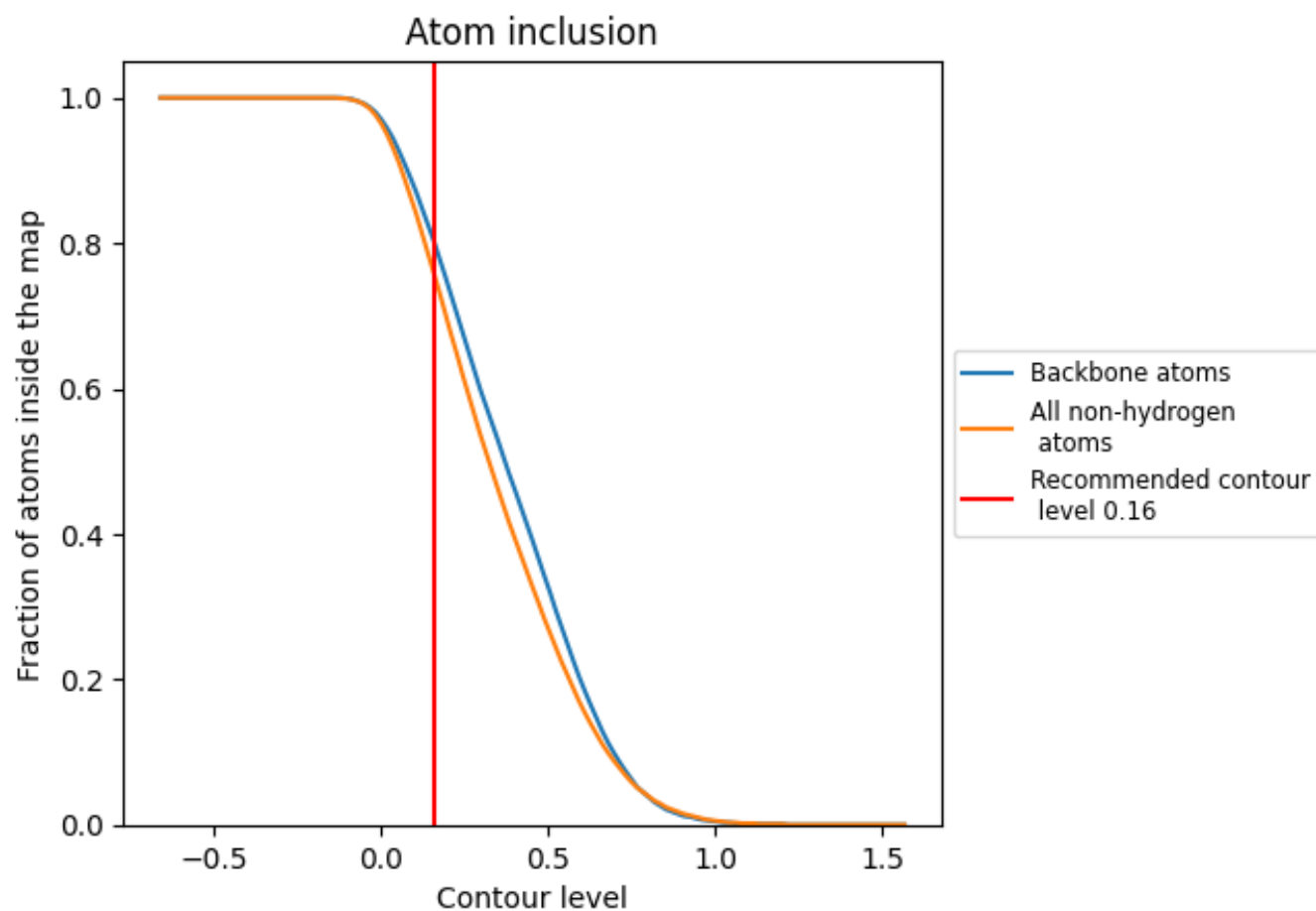
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.16).

9.4 Atom inclusion ⓘ



At the recommended contour level, 80% of all backbone atoms, 75% 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 (0.16) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7540	 0.3810
0	 0.7390	 0.2910
1	 0.7960	 0.4140
2	 0.6570	 0.2840
3	 0.8510	 0.4560
4	 0.4510	 0.1610
5	 0.2190	 0.1570
6	 0.7660	 0.4950
7	 0.0450	 0.1020
A	 0.9260	 0.4720
B	 0.8970	 0.5100
C	 0.8850	 0.5290
D	 0.8440	 0.4890
E	 0.8240	 0.4240
F	 0.8320	 0.4530
G	 0.7990	 0.4090
H	 0.8120	 0.4640
I	 0.7700	 0.3010
J	 0.8170	 0.4410
K	 0.9060	 0.5190
L	 0.8190	 0.4290
M	 0.8240	 0.4390
N	 0.8530	 0.4620
O	 0.8630	 0.4440
P	 0.8730	 0.4700
Q	 0.8860	 0.4940
R	 0.8530	 0.4090
S	 0.8110	 0.4000
T	 0.8210	 0.4430
U	 0.8040	 0.3770
V	 0.5690	 0.1020
W	 0.8660	 0.4760
X	 0.7710	 0.3640
Y	 0.6730	 0.3400
Z	 0.8370	 0.4580

