Full wwPDB EM Validation Report ⓘ

Jun 20, 2024 – 02:27 pm BST

PDB ID	:	8QRL
EMDB ID	:	EMD-18439
Title	:	mt-SSU assembly intermediate in GTPBP8 knock-out cells, state 2
Authors	:	Valentin Gese, G.; Cipullo, M.; Rorbach, J.; Hallberg, B.M.
Deposited on	:	2023-10-09
Resolution	:	3.34 Å(reported)

This is a Full wwPDB EM Validation 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:

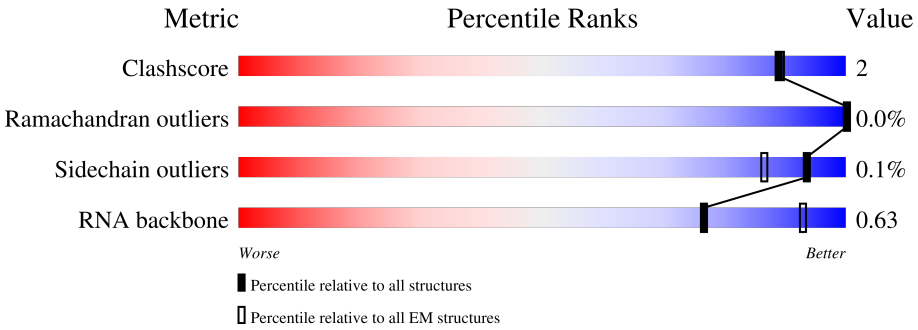
EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.34 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	955	81% 18%
2	B	296	71% 5% 24%
3	C	167	8% 74% 5% 21%
4	D	430	9% 76% 20%
5	E	125	18% 92% 6%
6	F	242	29% 81% 15%
7	G	396	18% 78% 17%

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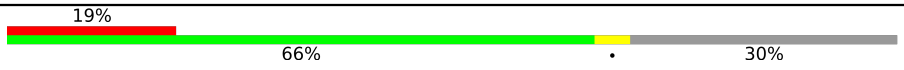
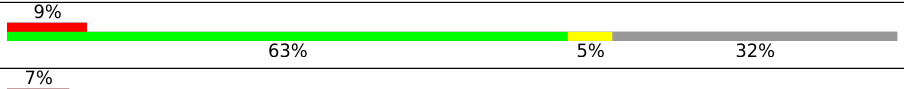
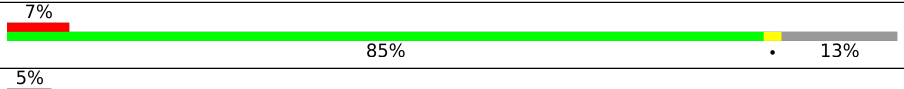
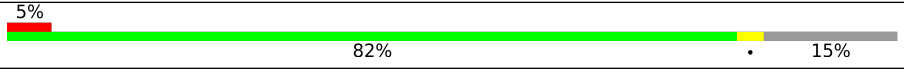
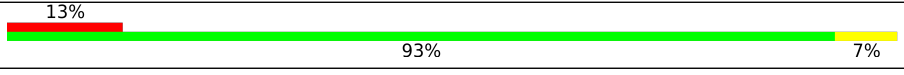
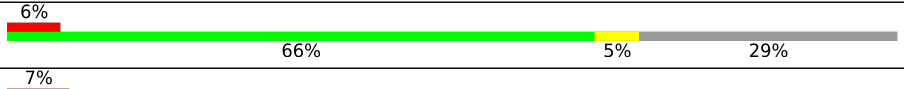
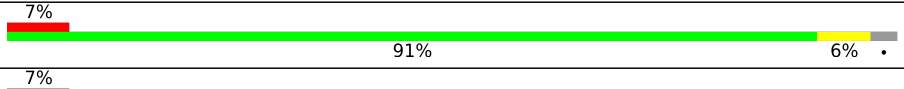
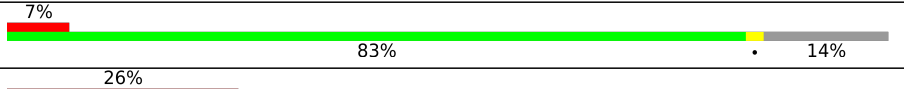
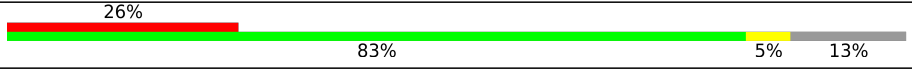
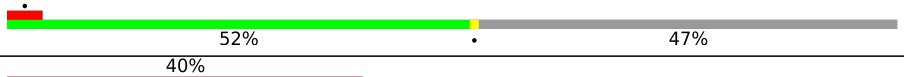
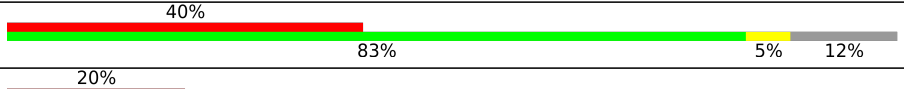
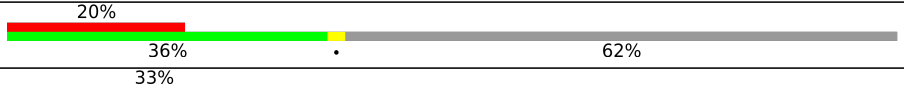
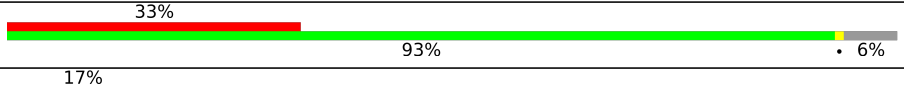
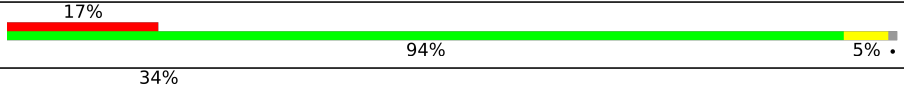
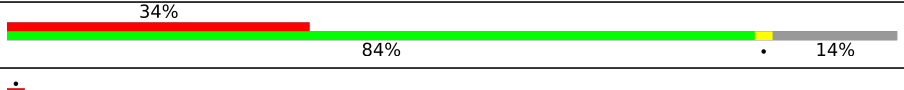
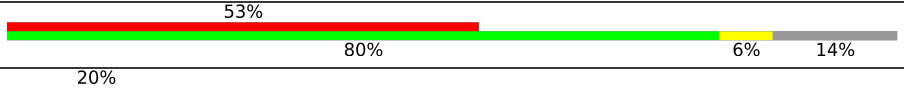
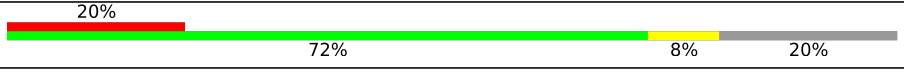
Mol	Chain	Length	Quality of chain
8	H	201	
9	I	194	
10	J	138	
11	K	128	
12	L	257	
13	M	137	
14	N	130	
15	O	258	
16	P	142	
17	Q	86	
18	R	360	
19	S	190	
20	T	173	
21	U	205	
22	V	414	
23	W	187	
24	X	398	
25	Y	395	
26	Z	106	
27	0	218	
28	1	323	
29	3	199	
30	4	689	
31	8	407	

2 Entry composition

There are 40 unique types of molecules in this entry. The entry contains 70955 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
			Total	C	N	O	P		
1	A	951	20198	9060	3636	6551	951	0	0

There is a discrepancy between the modelled and reference sequences:

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	118	936	592	168	172	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	205	Total	C	N	O	S	15	0
			1804	1158	324	311	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	327	Total	C	N	O	S	0	0
			2688	1710	477	487	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
			1020	642	192	182	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	184	5F0	ASN	conflict	UNP P82912

- 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	193	Total	C	N	O	S	0	0
			1592	1014	294	277	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	278	Total	C	N	O	S	0	0
			2256	1430	386	429	11		

- Molecule 29 is a protein called Aurora kinase A-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	3	71	Total	C	N	O	S	0	0
			629	403	135	90	1		

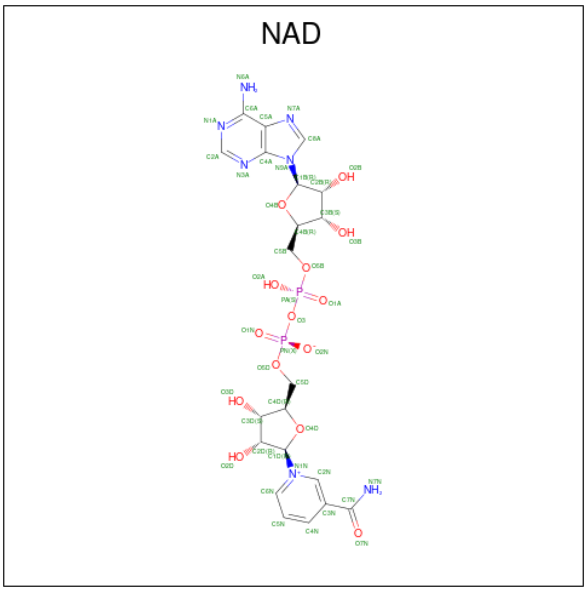
- Molecule 30 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	590	Total	C	N	O	S	0	0
			4775	3056	809	882	28		

- Molecule 31 is a protein called 12S rRNA N4-methylcytidine (m4C) methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	8	326	Total	C	N	O	S	0	0
			2546	1610	456	466	14		

- Molecule 32 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



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

- Molecule 33 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
33	A	61	Total	Mg	0
			61	61	
33	B	1	Total	Mg	0
			1	1	
33	X	1	Total	Mg	0
			1	1	
33	3	1	Total	Mg	0
			1	1	

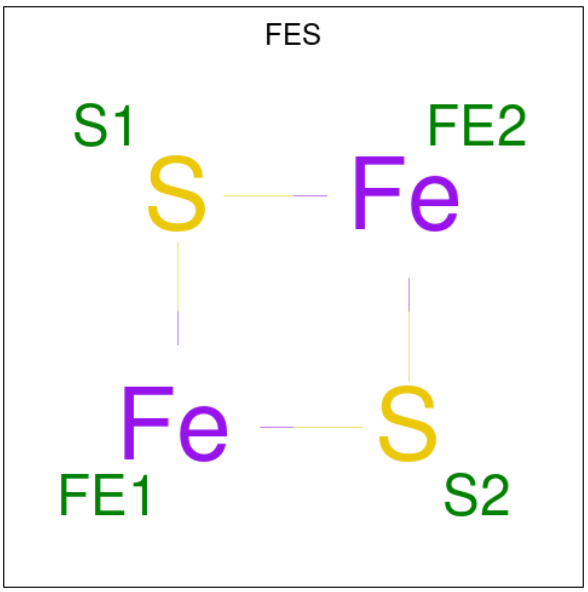
- Molecule 34 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
34	A	16	Total	K	0
			16	16	

- Molecule 35 is ZINC ION (three-letter code: ZN) (formula: Zn).

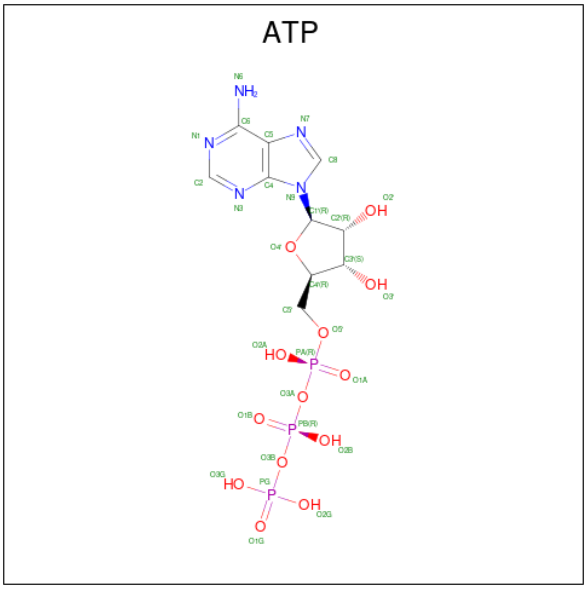
Mol	Chain	Residues	Atoms		AltConf
35	O	1	Total	Zn	0
			1	1	

- Molecule 36 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2).



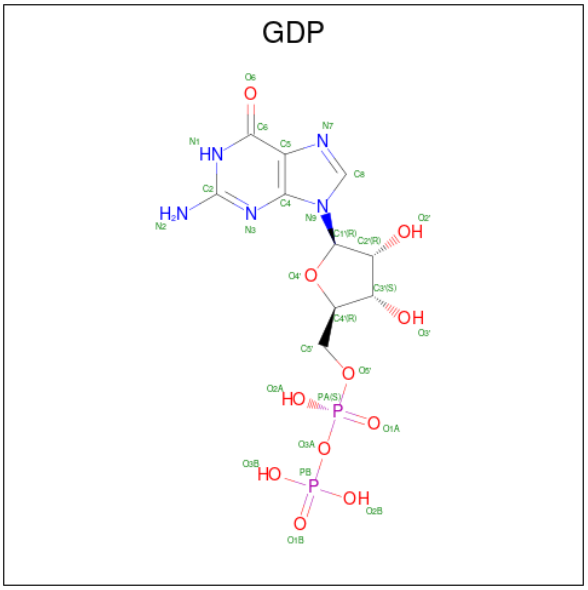
Mol	Chain	Residues	Atoms			AltConf
36	P	1	Total	Fe	S	0
			4	2	2	
36	T	1	Total	Fe	S	0
			4	2	2	

- Molecule 37 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



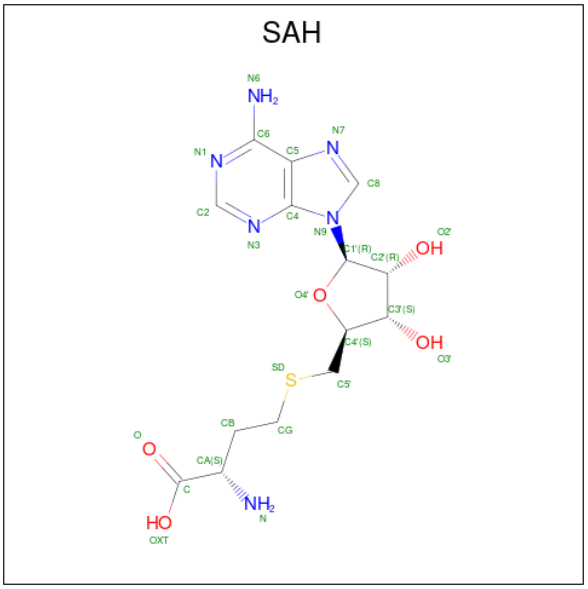
Mol	Chain	Residues	Atoms					AltConf
37	X	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 38 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					AltConf
38	X	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 39 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: $C_{14}H_{20}N_6O_5S$).



Mol	Chain	Residues	Atoms					AltConf
39	8	1	Total	C	N	O	S	0
			26	14	6	5	1	

- Molecule 40 is water.

Mol	Chain	Residues	Atoms		AltConf
40	A	1296	Total	O	0
			1296	1296	
40	B	81	Total	O	0
			81	81	
40	C	60	Total	O	0
			60	60	
40	D	72	Total	O	0
			72	72	
40	E	4	Total	O	0
			4	4	
40	F	24	Total	O	0
			24	24	
40	G	60	Total	O	0
			60	60	
40	H	32	Total	O	0
			32	32	
40	I	14	Total	O	0
			14	14	
40	J	28	Total	O	0
			28	28	
40	K	45	Total	O	0
			45	45	
40	L	23	Total	O	0
			23	23	
40	M	44	Total	O	0
			44	44	
40	N	28	Total	O	0
			28	28	
40	O	56	Total	O	0
			56	56	
40	P	9	Total	O	0
			9	9	
40	Q	14	Total	O	0
			14	14	
40	R	45	Total	O	0
			45	45	
40	S	25	Total	O	0
			25	25	

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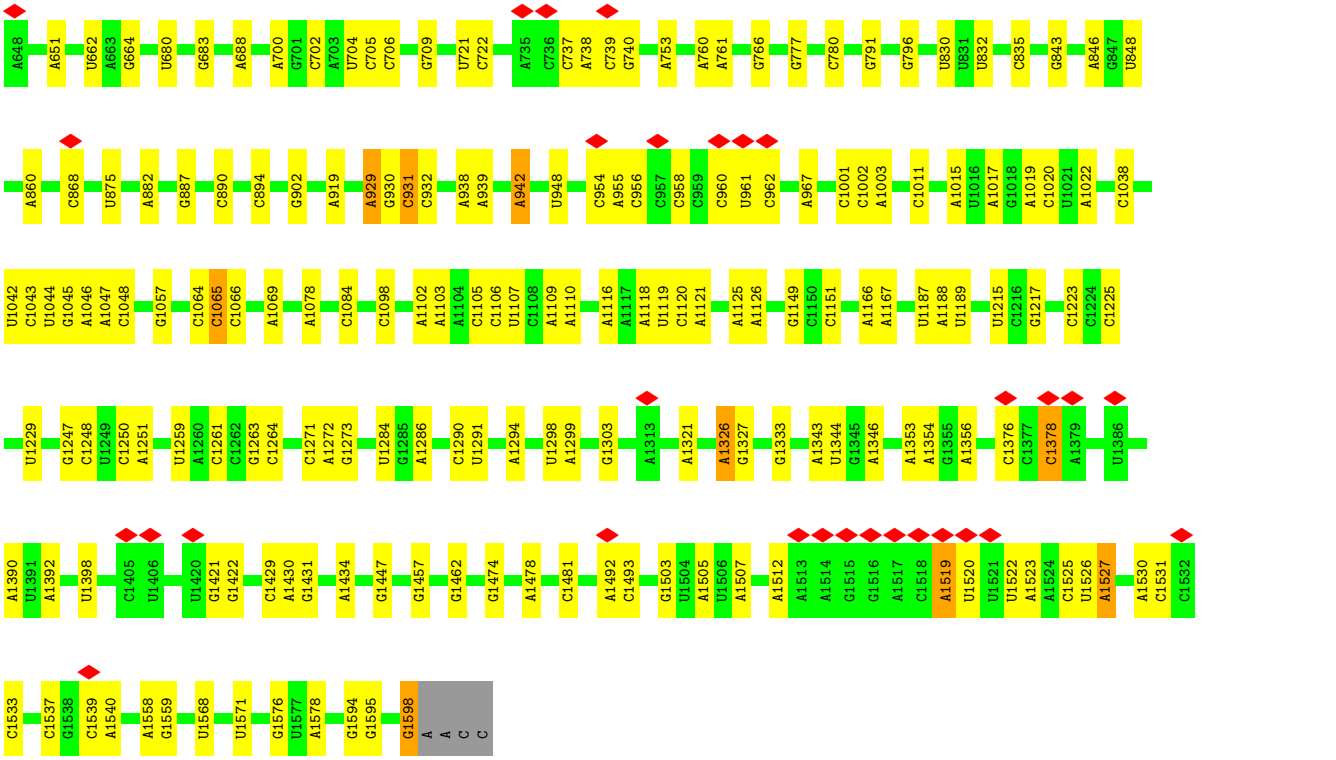
Mol	Chain	Residues	Atoms	AltConf
40	T	40	Total O 40 40	0
40	U	15	Total O 15 15	0
40	V	2	Total O 2 2	0
40	W	13	Total O 13 13	0
40	X	32	Total O 32 32	0
40	Y	3	Total O 3 3	0
40	Z	19	Total O 19 19	0
40	0	26	Total O 26 26	0
40	1	26	Total O 26 26	0
40	3	9	Total O 9 9	0
40	4	7	Total O 7 7	0

3 Residue-property plots (i)

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

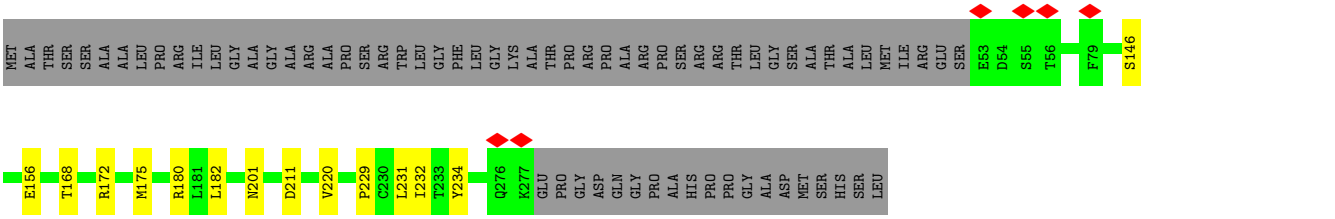
• Molecule 1: 12S mitochondrial rRNA

Chain A:



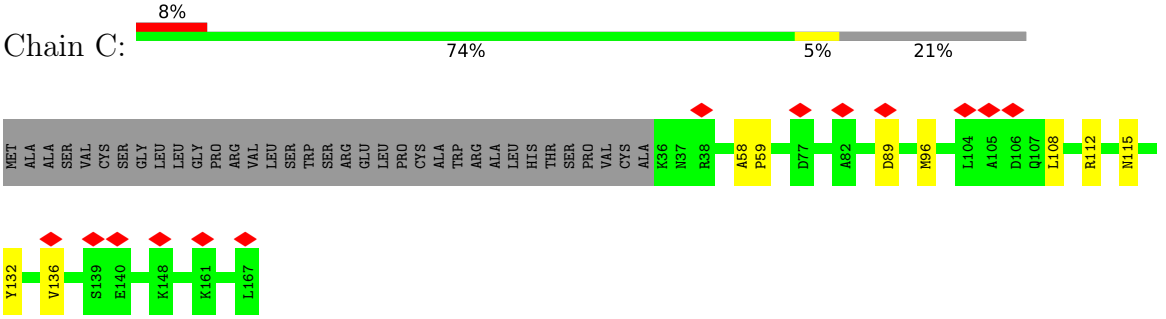
• Molecule 2: 28S ribosomal protein S2, mitochondrial

Chain B:



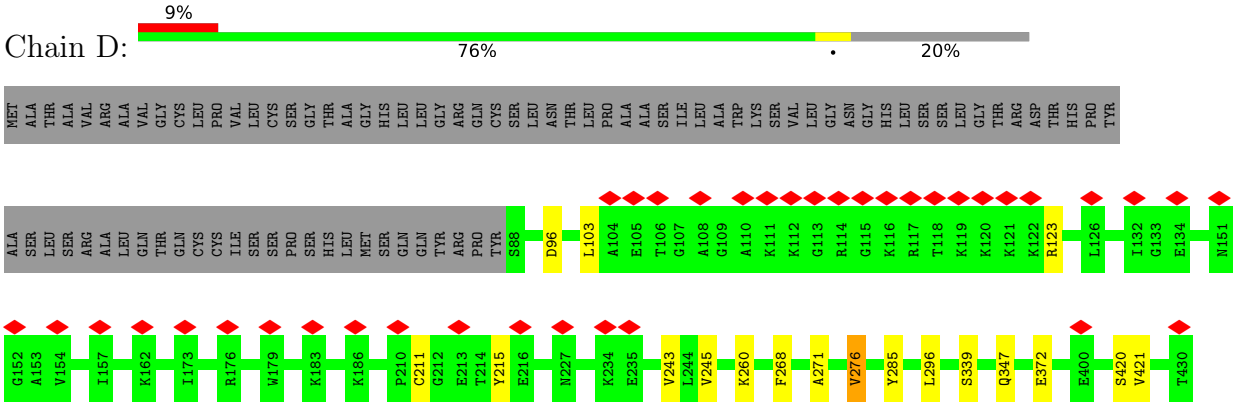
• Molecule 3: 28S ribosomal protein S24, mitochondrial

Chain C:



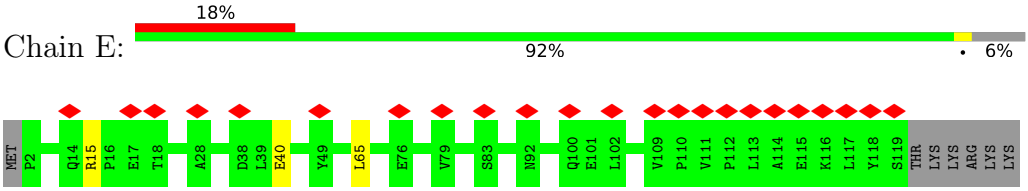
• Molecule 4: 28S ribosomal protein S5, mitochondrial

Chain D:



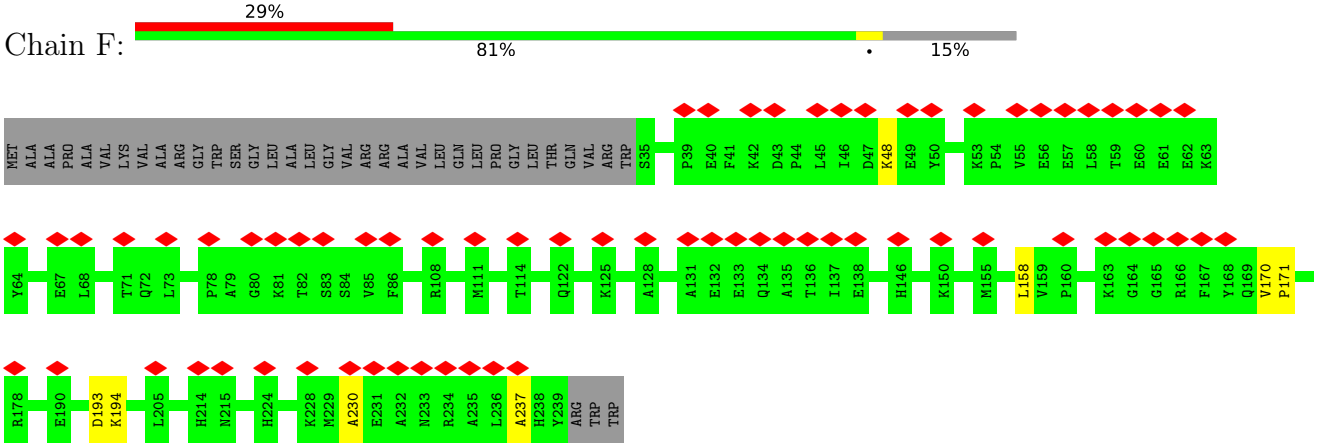
• Molecule 5: 28S ribosomal protein S6, mitochondrial

Chain E:



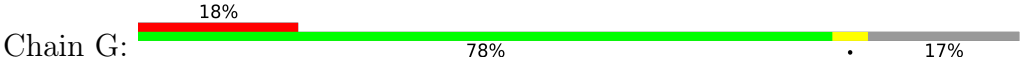
• Molecule 6: 28S ribosomal protein S7, mitochondrial

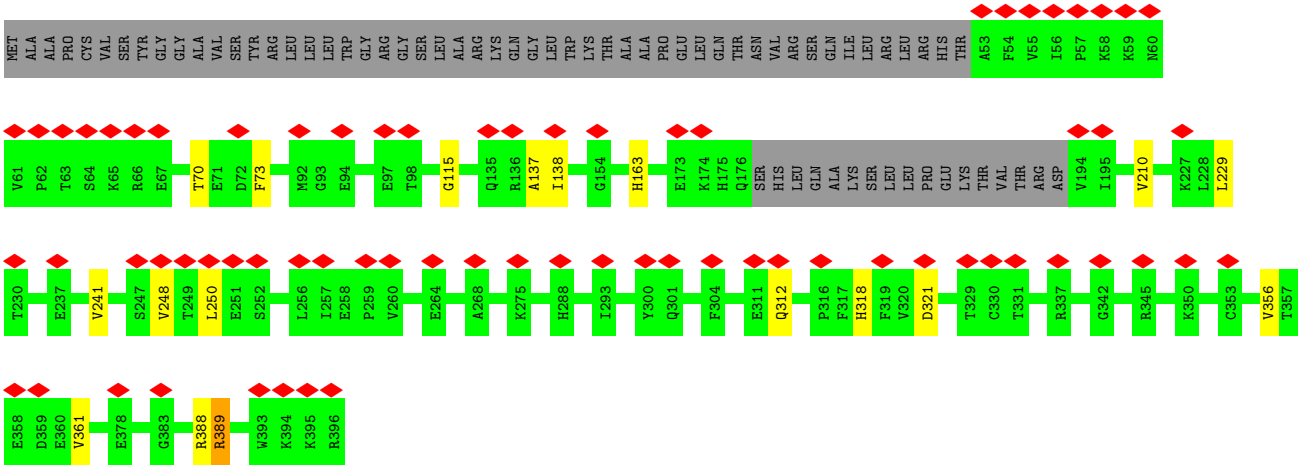
Chain F:



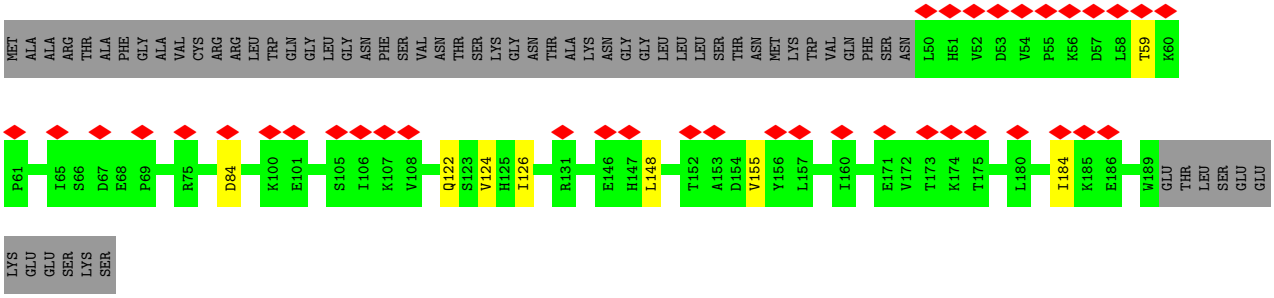
• Molecule 7: 28S ribosomal protein S9, mitochondrial

Chain G:

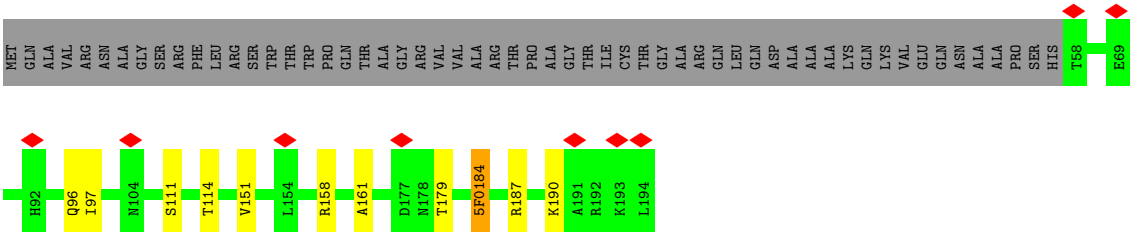




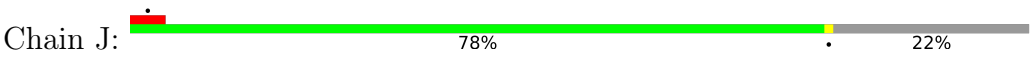
• Molecule 8: 28S ribosomal protein S10, mitochondrial

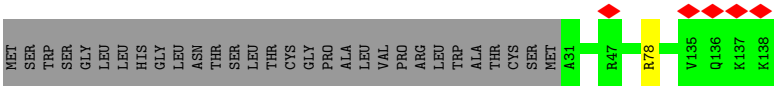


• Molecule 9: 28S ribosomal protein S11, mitochondrial

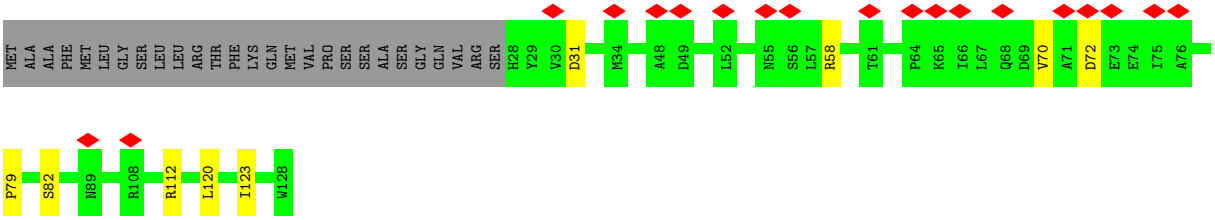


• Molecule 10: 28S ribosomal protein S12, mitochondrial



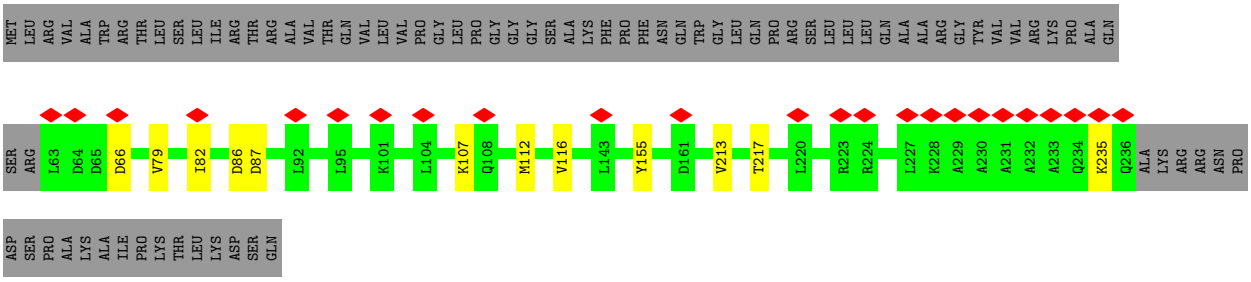


• Molecule 11: 28S ribosomal protein S14, mitochondrial



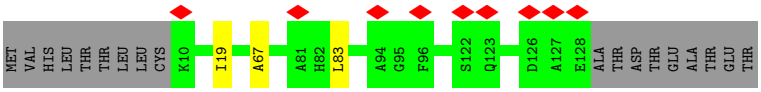
• Molecule 12: 28S ribosomal protein S15, mitochondrial

Chain L:



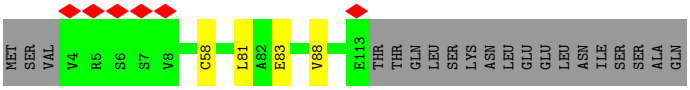
• Molecule 13: 28S ribosomal protein S16, mitochondrial

Chain M:



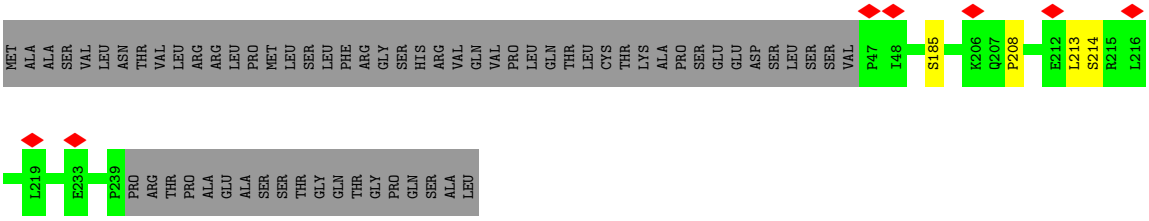
• Molecule 14: 28S ribosomal protein S17, mitochondrial

Chain N:



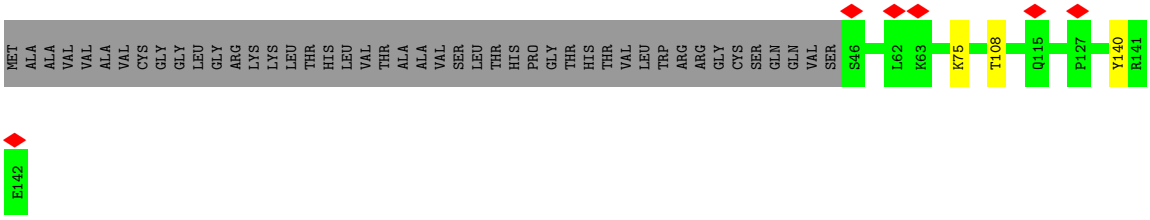
• Molecule 15: 28S ribosomal protein S18b, mitochondrial

Chain O:

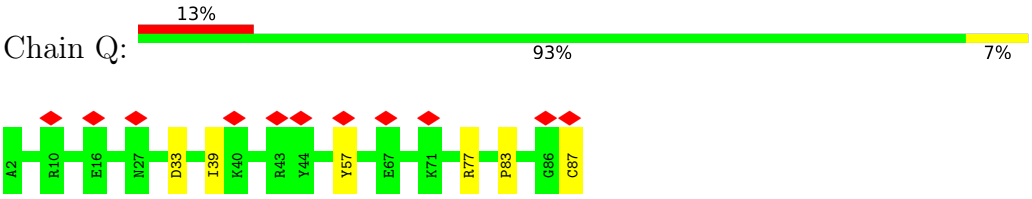


• Molecule 16: 28S ribosomal protein S18c, mitochondrial

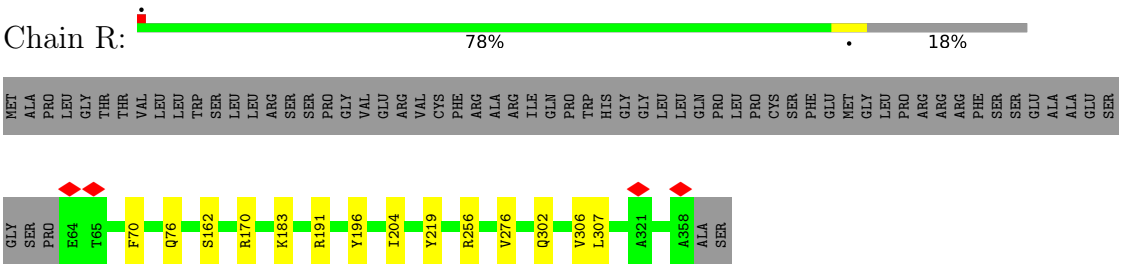
Chain P:



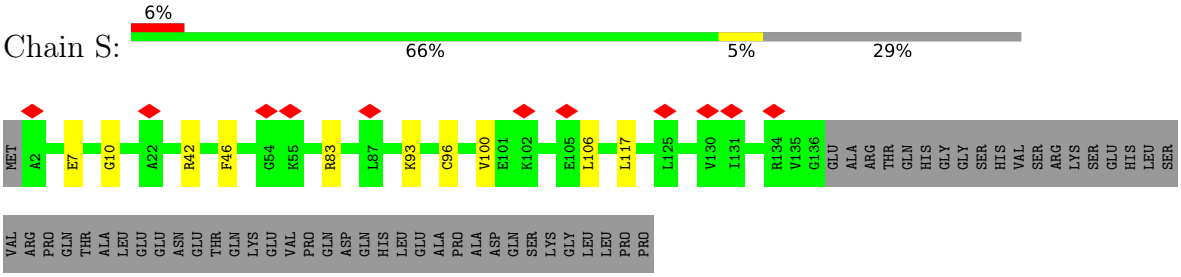
• Molecule 17: 28S ribosomal protein S21, mitochondrial



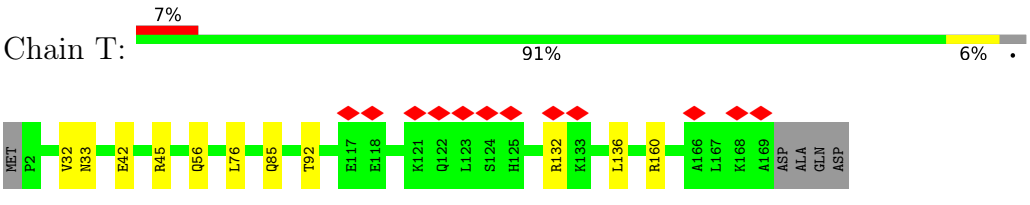
• Molecule 18: 28S ribosomal protein S22, mitochondrial



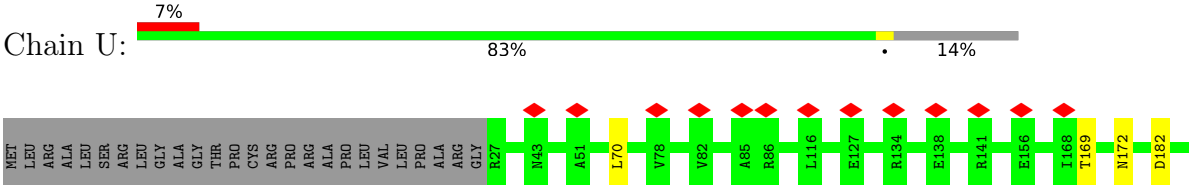
• Molecule 19: 28S ribosomal protein S23, mitochondrial

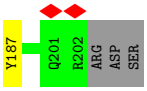


• Molecule 20: 28S ribosomal protein S25, mitochondrial



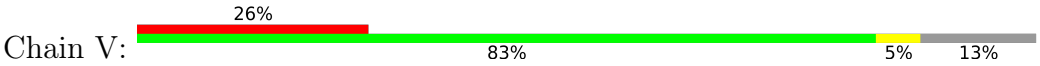
• Molecule 21: 28S ribosomal protein S26, mitochondrial

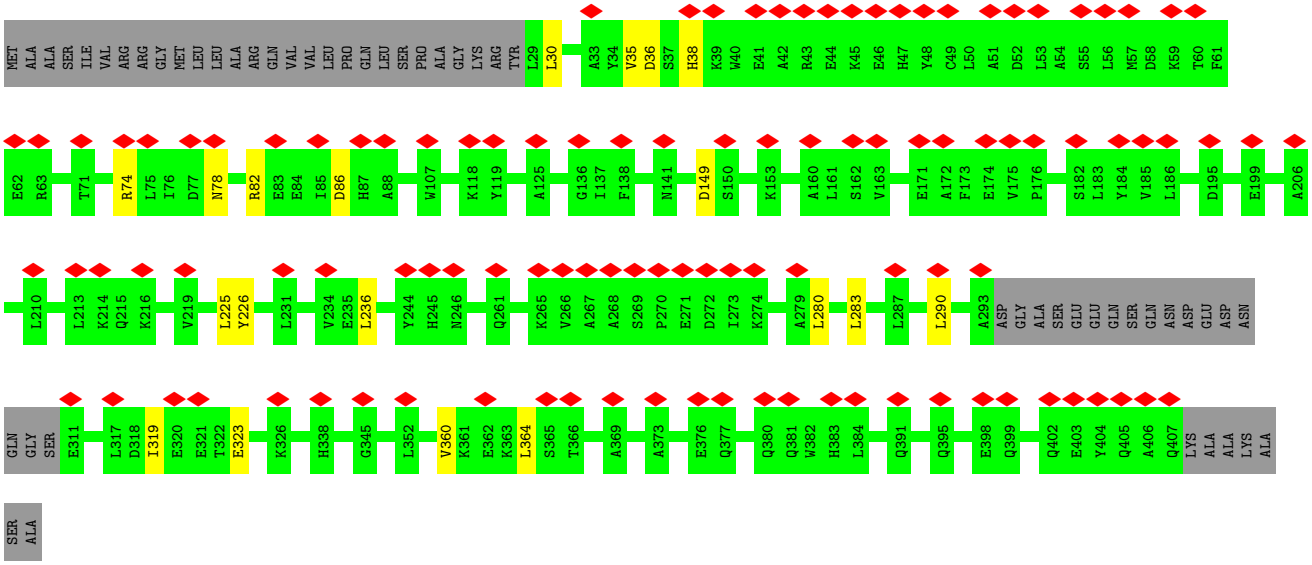




• Molecule 22: 28S ribosomal protein S27, mitochondrial

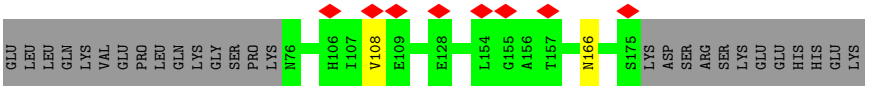
Chain V:





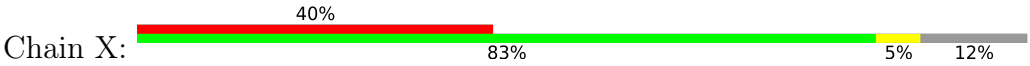
• Molecule 23: 28S ribosomal protein S28, mitochondrial

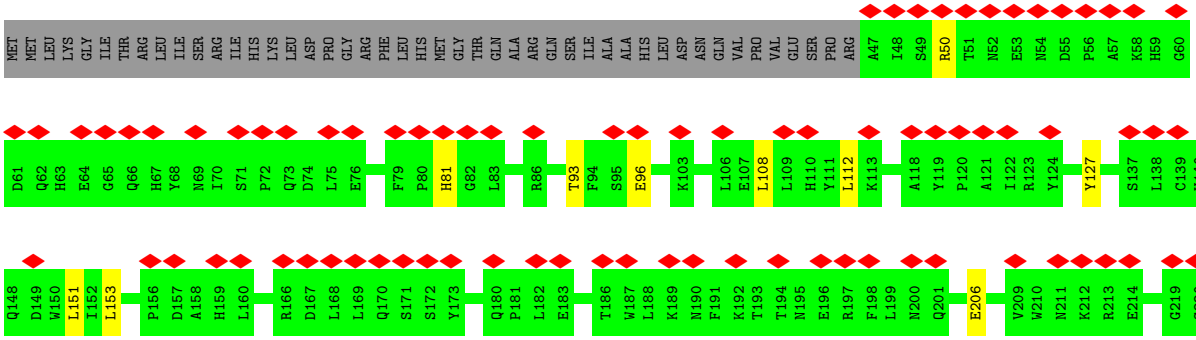
Chain W:

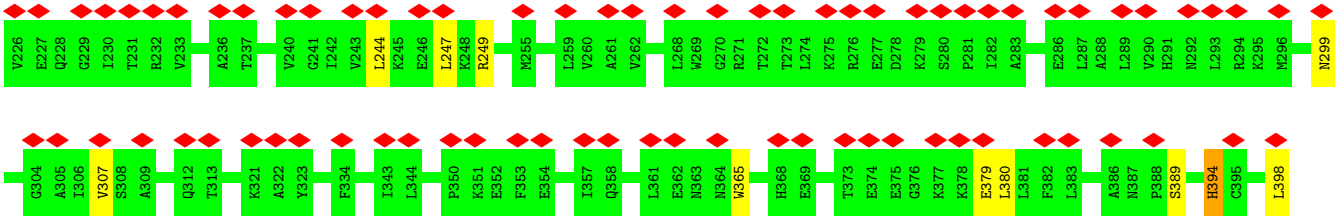


• Molecule 24: 28S ribosomal protein S29, mitochondrial

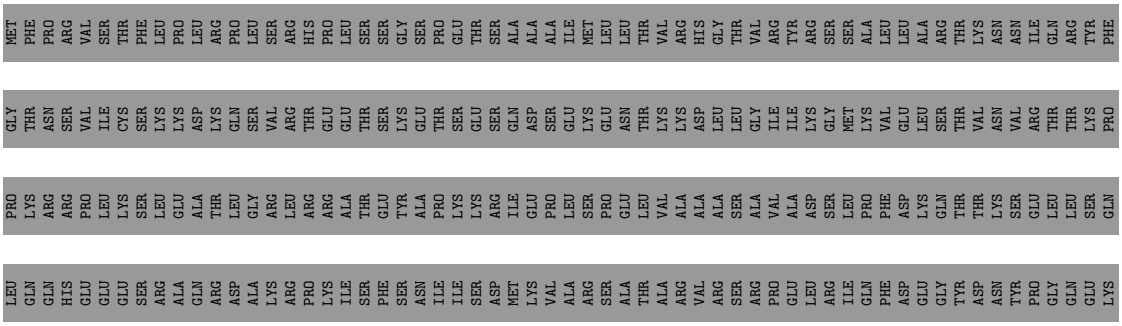
Chain X:

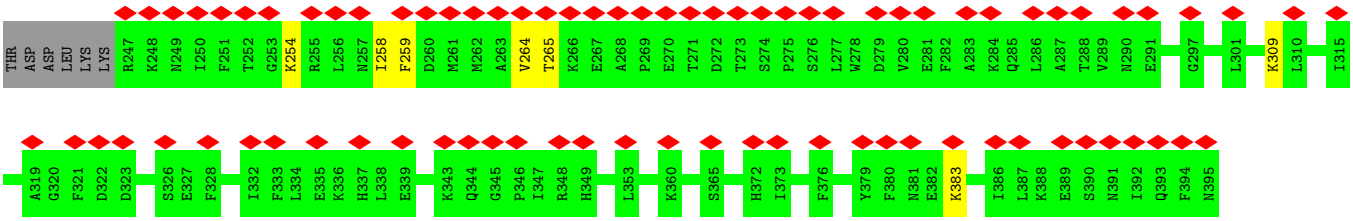




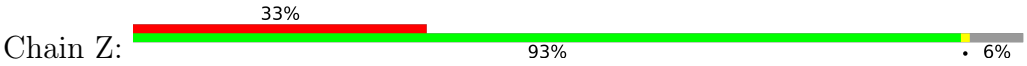


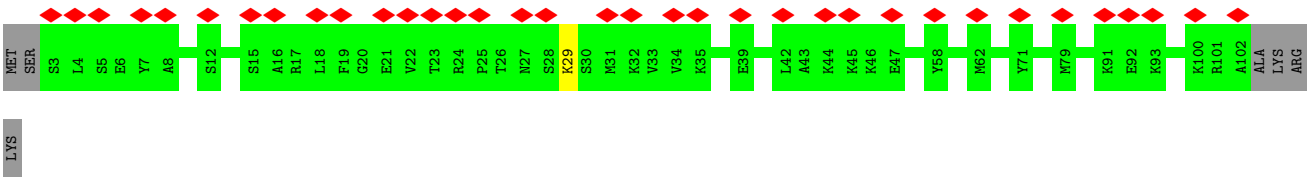
• Molecule 25: 28S ribosomal protein S31, mitochondrial



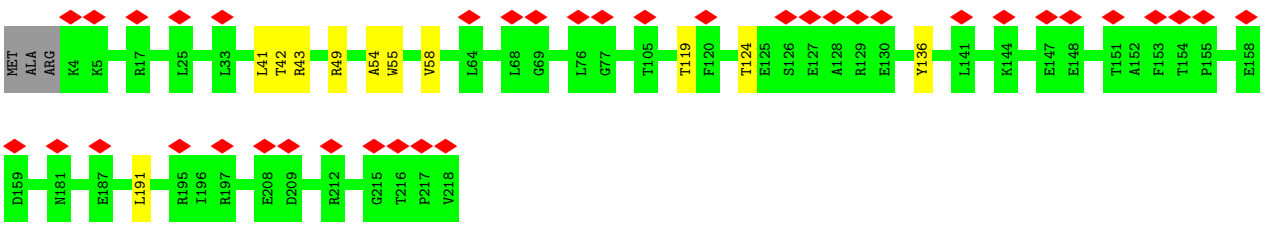


• Molecule 26: 28S ribosomal protein S33, mitochondrial



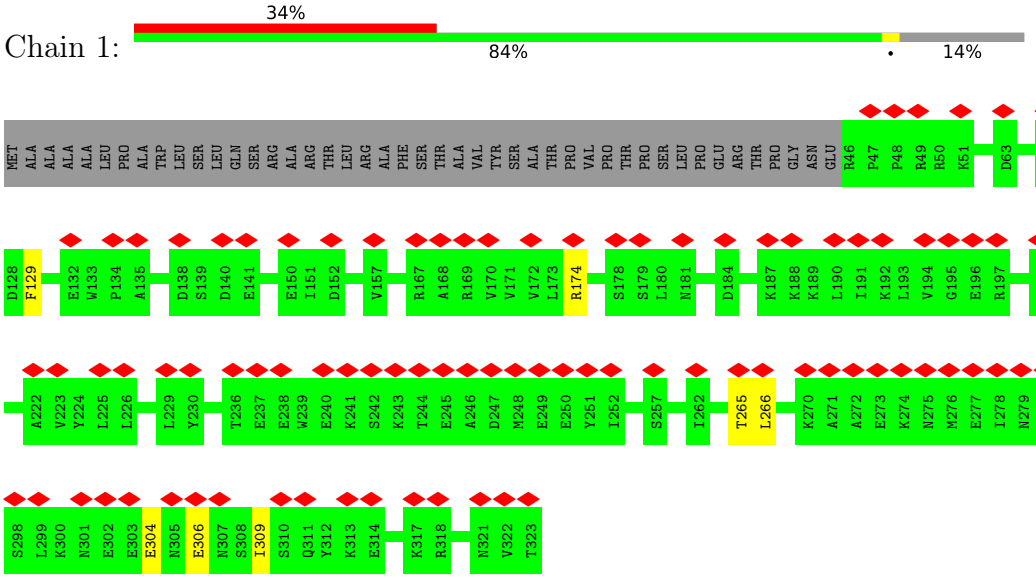


• Molecule 27: 28S ribosomal protein S34, mitochondrial



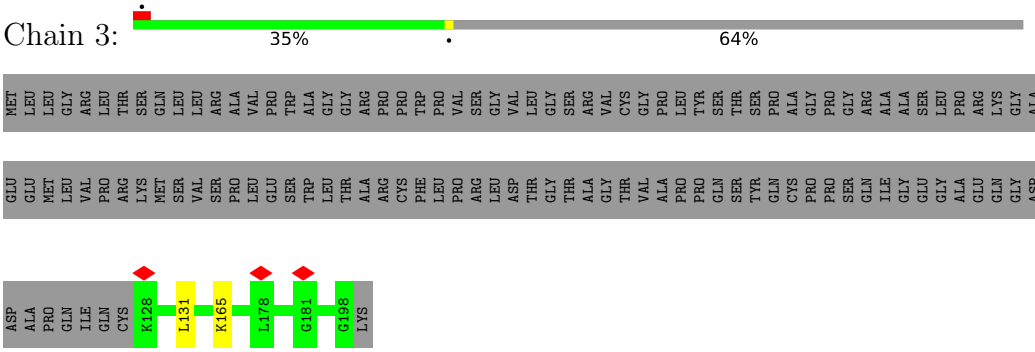
• Molecule 28: 28S ribosomal protein S35, mitochondrial

Chain 1:



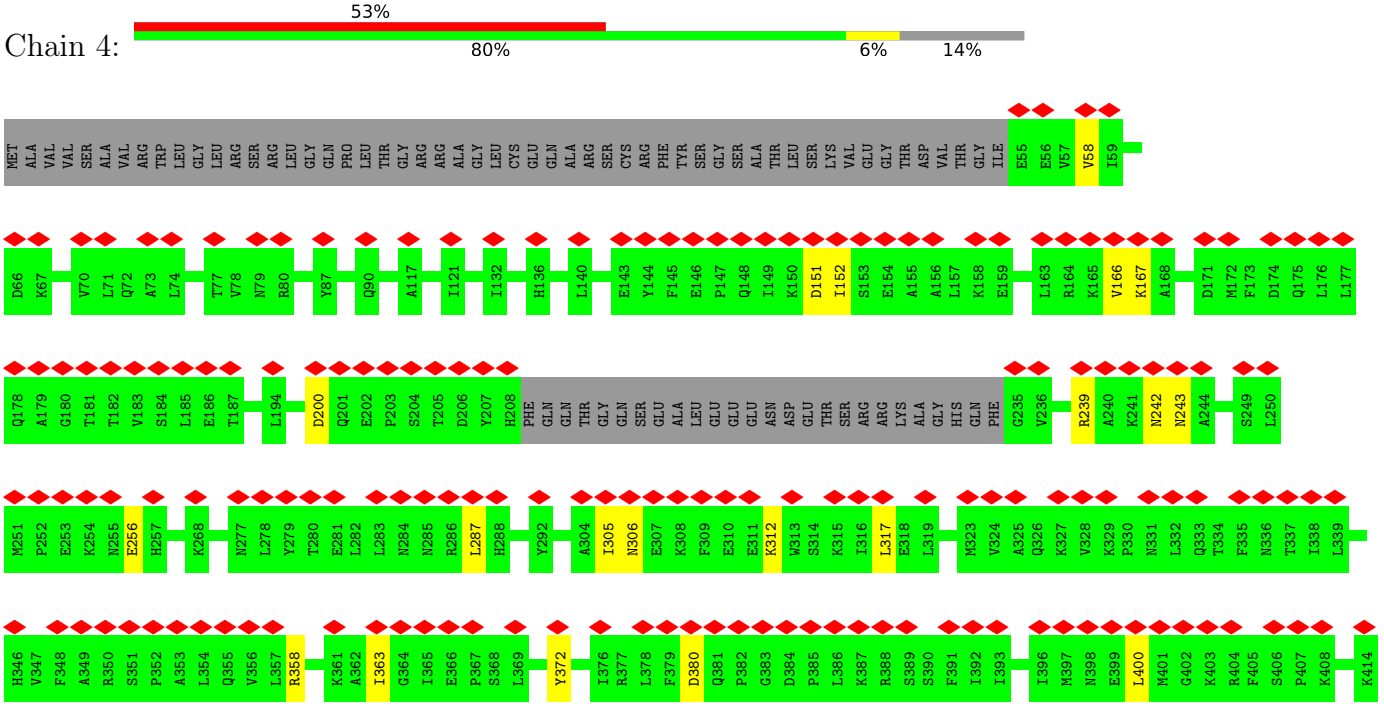
• Molecule 29: Aurora kinase A-interacting protein

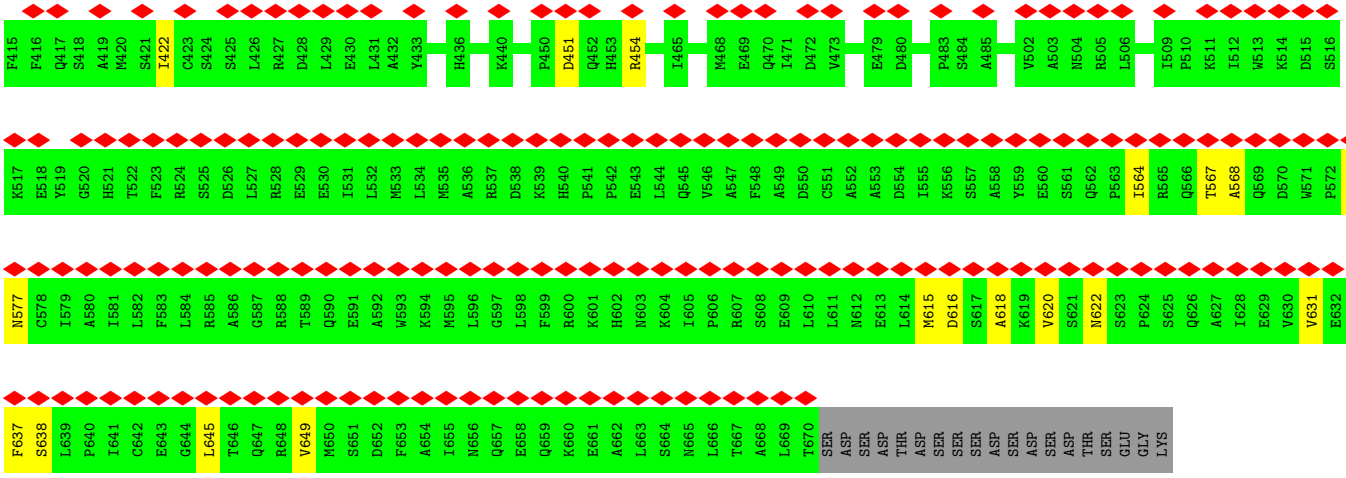
Chain 3:



• Molecule 30: Pentatricopeptide repeat domain-containing protein 3, mitochondrial

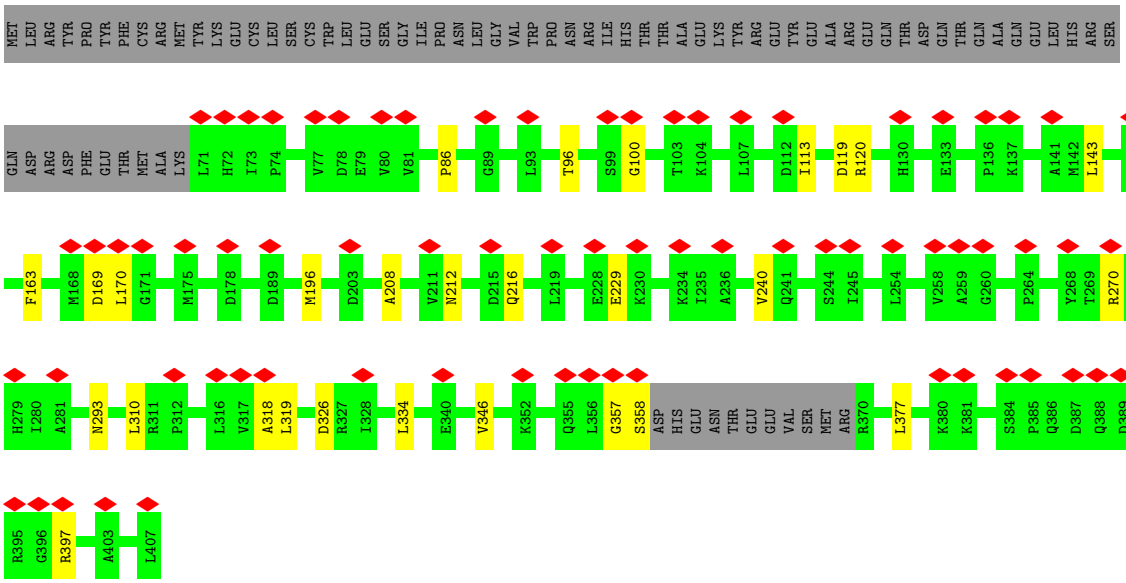
Chain 4:





• Molecule 31: 12S rRNA N4-methylcytidine (m4C) methyltransferase

Chain 8:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	32577	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 ($e^-/Å^2$)	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	0.621	Depositor
Minimum map value	-0.187	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.125	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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MA6, 5MC, NAD, SAH, 5MU, 5F0, ATP, MG, B8T, FES, AYA, GDP, K

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	0.26	0/22468	0.68	0/34978
2	B	0.25	0/1871	0.42	0/2531
3	C	0.26	0/1113	0.41	0/1505
4	D	0.25	0/2783	0.42	0/3724
5	E	0.24	0/953	0.42	0/1289
6	F	0.24	0/1846	0.37	0/2482
7	G	0.25	0/2746	0.40	0/3681
8	H	0.25	0/1178	0.42	0/1598
9	I	0.25	0/1030	0.44	0/1386
10	J	0.26	0/855	0.46	0/1148
11	K	0.23	0/880	0.41	0/1182
12	L	0.24	0/1477	0.37	0/1974
13	M	0.25	0/963	0.42	0/1295
14	N	0.26	0/886	0.45	0/1199
15	O	0.25	0/1648	0.40	0/2243
16	P	0.27	0/798	0.42	0/1070
17	Q	0.24	0/748	0.38	0/994
18	R	0.25	0/2456	0.38	0/3317
19	S	0.26	0/1138	0.40	0/1533
20	T	0.25	0/1402	0.40	0/1883
21	U	0.23	0/1510	0.37	0/2025
22	V	0.23	0/3030	0.35	0/4093
23	W	0.25	0/801	0.41	0/1079
24	X	0.25	0/2921	0.39	0/3954
25	Y	0.24	0/1280	0.37	0/1725
26	Z	0.25	0/857	0.38	0/1141
27	0	0.24	0/1834	0.41	0/2484
28	1	0.25	0/2304	0.38	0/3117
29	3	0.24	0/640	0.38	0/844
30	4	0.24	0/4883	0.36	0/6608
31	8	0.24	0/2590	0.40	0/3492
All	All	0.25	0/71889	0.51	0/101574

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
9	I	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	I	184	5F0	Mainchain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	20198	0	10253	55	0
2	B	1828	0	1815	10	0
3	C	1083	0	1088	6	0
4	D	2731	0	2804	13	0
5	E	936	0	954	3	0
6	F	1804	0	1868	5	0
7	G	2688	0	2687	15	0
8	H	1152	0	1183	8	0
9	I	1020	0	1053	7	0
10	J	839	0	887	1	0
11	K	862	0	885	6	0
12	L	1453	0	1540	7	0
13	M	942	0	965	2	0
14	N	868	0	928	3	0
15	O	1592	0	1557	3	0
16	P	781	0	806	3	0
17	Q	744	0	758	6	0
18	R	2409	0	2428	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	S	1111	0	1115	8	0
20	T	1371	0	1393	8	0
21	U	1488	0	1499	5	0
22	V	2969	0	2961	11	0
23	W	789	0	802	2	0
24	X	2849	0	2843	17	0
25	Y	1246	0	1197	6	0
26	Z	839	0	858	1	0
27	0	1787	0	1796	8	0
28	1	2256	0	2288	6	0
29	3	629	0	702	2	0
30	4	4775	0	4779	25	0
31	8	2546	0	2615	22	0
32	A	44	0	26	0	0
33	3	1	0	0	0	0
33	A	61	0	0	0	0
33	B	1	0	0	0	0
33	X	1	0	0	0	0
34	A	16	0	0	0	0
35	O	1	0	0	0	0
36	P	4	0	0	0	0
36	T	4	0	0	0	0
37	X	31	0	12	0	0
38	X	28	0	12	0	0
39	8	26	0	19	1	0
40	0	26	0	0	0	0
40	1	26	0	0	1	0
40	3	9	0	0	0	0
40	4	7	0	0	0	0
40	A	1296	0	0	10	0
40	B	81	0	0	1	0
40	C	60	0	0	1	0
40	D	72	0	0	2	0
40	E	4	0	0	0	0
40	F	24	0	0	0	0
40	G	60	0	0	2	0
40	H	32	0	0	0	0
40	I	14	0	0	1	0
40	J	28	0	0	0	0
40	K	45	0	0	1	0
40	L	23	0	0	0	0
40	M	44	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
40	N	28	0	0	0	0
40	O	56	0	0	0	0
40	P	9	0	0	0	0
40	Q	14	0	0	1	0
40	R	45	0	0	0	0
40	S	25	0	0	2	0
40	T	40	0	0	2	0
40	U	15	0	0	0	0
40	V	2	0	0	0	0
40	W	13	0	0	0	0
40	X	32	0	0	0	0
40	Y	3	0	0	0	0
40	Z	19	0	0	0	0
All	All	70955	0	59376	231	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.

All (231) 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)
12:L:112:MET:O	12:L:116:VAL:HG22	1.82	0.78
1:A:1353:A:N1	40:A:1805:HOH:O	2.18	0.76
30:4:200:ASP:OD2	30:4:243:ASN:N	2.20	0.75
30:4:451:ASP:OD1	30:4:454:ARG:NH1	2.22	0.73
1:A:1217:G:O6	40:A:1801:HOH:O	2.07	0.72
1:A:1217:G:N7	40:A:1820:HOH:O	2.27	0.67
17:Q:87:CYS:O	40:Q:101:HOH:O	2.16	0.63
1:A:1294:A:OP1	2:B:201:ASN:ND2	2.32	0.63
1:A:1321:A:OP2	40:A:1803:HOH:O	2.16	0.62
19:S:42:ARG:NH2	40:S:202:HOH:O	2.32	0.62
27:0:41:LEU:HD13	27:0:55:TRP:CG	2.35	0.61
2:B:211:ASP:OD2	40:B:401:HOH:O	2.16	0.61
31:8:163:PHE:O	31:8:310:LEU:HD12	2.00	0.61
19:S:10:GLY:O	40:S:201:HOH:O	2.16	0.60
1:A:942:A:N6	1:A:1047:A:OP2	2.33	0.59
4:D:420:SER:O	40:D:501:HOH:O	2.17	0.59
21:U:70:LEU:CD2	27:0:191:LEU:HD11	2.33	0.59
24:X:153:LEU:HD21	24:X:244:LEU:HD22	1.83	0.59
31:8:86:PRO:HB3	31:8:113:ILE:HD12	1.84	0.59
1:A:1078:A:O2'	31:8:326:ASP:OD2	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:70:PHE:O	18:R:76:GLN:NE2	2.36	0.59
20:T:33:ASN:OD1	40:T:301:HOH:O	2.17	0.58
1:A:700:A:N1	1:A:709:G:O2'	2.32	0.58
7:G:312:GLN:NE2	40:G:404:HOH:O	2.37	0.58
1:A:1272:A:N1	1:A:1303:G:O2'	2.30	0.58
22:V:236:LEU:HD12	22:V:290:LEU:HD13	1.87	0.57
1:A:1346:A:OP2	40:A:1804:HOH:O	2.16	0.57
1:A:1038:C:HO2'	12:L:155:TYR:HH	1.51	0.57
24:X:151:LEU:HD23	24:X:247:LEU:HD22	1.85	0.57
4:D:285:TYR:OH	4:D:372:GLU:OE2	2.17	0.57
28:1:304:GLU:OE1	28:1:309:ILE:HD11	2.04	0.57
1:A:702:C:OP1	1:A:848:U:O2'	2.22	0.56
1:A:948:U:OP2	1:A:1045:G:N1	2.37	0.56
4:D:347:GLN:NE2	40:D:505:HOH:O	2.39	0.56
1:A:843:G:N2	1:A:846:A:OP2	2.35	0.56
1:A:1066:C:O2'	9:I:187:ARG:O	2.23	0.56
7:G:115:GLY:O	40:G:401:HOH:O	2.18	0.56
20:T:132:ARG:NH1	20:T:136:LEU:O	2.39	0.56
12:L:86:ASP:OD1	12:L:87:ASP:N	2.39	0.55
1:A:1046:A:O2'	1:A:1048:C:OP2	2.17	0.55
31:8:196:MET:SD	31:8:293:ASN:ND2	2.80	0.55
25:Y:259:PHE:HB2	30:4:363:ILE:HD11	1.89	0.55
30:4:151:ASP:OD1	30:4:152:ILE:N	2.40	0.54
31:8:229:GLU:OE1	31:8:270:ARG:NH1	2.40	0.54
25:Y:258:ILE:HD11	30:4:317:LEU:HD22	1.88	0.54
15:O:208:PRO:HG2	15:O:213:LEU:HD21	1.89	0.54
30:4:631:VAL:HG21	30:4:649:VAL:HG21	1.90	0.54
1:A:1084:C:H1'	31:8:346:VAL:HG11	1.90	0.54
17:Q:83:PRO:HA	23:W:108:VAL:HG21	1.89	0.54
31:8:119:ASP:O	31:8:143:LEU:HD12	2.07	0.54
1:A:1434:A:OP1	7:G:389:ARG:NE	2.41	0.53
3:C:115:ASN:ND2	25:Y:309:LYS:O	2.39	0.53
6:F:158[A]:LEU:HD23	6:F:171[A]:PRO:HA	1.90	0.53
1:A:760:A:N1	1:A:780:C:O2'	2.36	0.53
2:B:156:GLU:OE1	7:G:163:HIS:ND1	2.41	0.53
7:G:229:LEU:HD21	7:G:241:VAL:HG11	1.90	0.53
15:O:185:SER:O	18:R:183:LYS:NZ	2.41	0.53
1:A:1333:G:N7	40:A:1830:HOH:O	2.33	0.53
1:A:1598:G:OP2	17:Q:57:TYR:OH	2.26	0.52
31:8:318:ALA:O	31:8:319:LEU:HD12	2.09	0.52
24:X:151:LEU:CD2	24:X:247:LEU:HD22	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:106:LEU:HB2	19:S:117:LEU:HD11	1.90	0.52
11:K:120:LEU:HB3	11:K:123:ILE:HD12	1.92	0.52
17:Q:77:ARG:NH1	23:W:166:ASN:OD1	2.43	0.51
6:F:48:LYS:NZ	7:G:321:ASP:OD1	2.36	0.51
27:0:42:THR:HG22	27:0:49:ARG:HG2	1.92	0.51
27:0:54:ALA:O	27:0:58:VAL:HG23	2.10	0.51
24:X:380:LEU:HD23	24:X:394:HIS:CD2	2.45	0.51
1:A:706:C:OP1	27:0:43:ARG:NE	2.41	0.51
1:A:1530:A:N1	1:A:1531:C:N4	2.59	0.51
30:4:615:MET:HG3	30:4:645:LEU:HD11	1.92	0.51
21:U:70:LEU:HD21	27:0:191:LEU:HD11	1.93	0.51
31:8:208:ALA:O	31:8:212:ASN:ND2	2.44	0.50
31:8:390:VAL:HG13	31:8:397:ARG:HB2	1.93	0.50
24:X:108:LEU:HD23	24:X:141:VAL:HG21	1.94	0.50
30:4:239:ARG:O	30:4:242:ASN:ND2	2.44	0.50
31:8:318:ALA:C	31:8:319:LEU:HD12	2.32	0.49
22:V:35:VAL:HG12	22:V:35:VAL:O	2.12	0.49
1:A:1398:U:OP1	26:Z:29:LYS:NZ	2.30	0.49
6:F:170[B]:VAL:HG13	6:F:237:ALA:HA	1.94	0.49
22:V:360:VAL:HG13	22:V:364:LEU:HD22	1.95	0.49
1:A:662:U:OP2	4:D:339:SER:OG	2.30	0.49
18:R:276:VAL:HG11	18:R:307:LEU:HD12	1.94	0.49
30:4:567:THR:HG22	30:4:568:ALA:N	2.28	0.49
30:4:615:MET:HE1	30:4:649:VAL:HG22	1.95	0.49
1:A:887:G:N7	40:A:1839:HOH:O	2.35	0.49
1:A:1392:A:N7	40:A:1837:HOH:O	2.35	0.49
9:I:179:THR:HG21	17:Q:39:ILE:HD13	1.95	0.49
1:A:1057:G:H4'	1:A:1578:A:H4'	1.94	0.49
11:K:31:ASP:OD2	40:K:201:HOH:O	2.20	0.49
31:8:216:GLN:CG	31:8:240:VAL:HG21	2.42	0.49
1:A:664:G:O2'	1:A:1166:A:N1	2.41	0.48
20:T:56:GLN:OE1	40:T:302:HOH:O	2.20	0.48
30:4:380:ASP:HB2	30:4:422:ILE:HD11	1.95	0.48
24:X:108:LEU:HD21	24:X:307:VAL:CG1	2.44	0.48
18:R:219:TYR:O	18:R:256:ARG:NH1	2.46	0.48
12:L:213:VAL:O	12:L:217:THR:HG23	2.13	0.48
11:K:58:ARG:NE	11:K:72:ASP:OD1	2.39	0.48
24:X:380:LEU:HD21	24:X:398:LEU:CD1	2.44	0.48
27:0:119:THR:OG1	27:0:124:THR:HG22	2.14	0.47
9:I:190:LYS:NZ	40:I:202:HOH:O	2.47	0.47
30:4:564:ILE:HG22	30:4:564:ILE:O	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:4:256:GLU:HG3	30:4:287:LEU:HD22	1.96	0.47
1:A:929:A:O4'	4:D:421:VAL:HG13	2.14	0.47
30:4:372:TYR:CE2	30:4:400:LEU:HD21	2.49	0.47
1:A:1429:C:OP1	7:G:388:ARG:NH2	2.45	0.47
20:T:32:VAL:HG22	20:T:76:LEU:HD22	1.96	0.47
31:8:100:GLY:N	39:8:501:SAH:O	2.47	0.47
24:X:206:GLU:OE2	24:X:249:ARG:NH2	2.46	0.47
30:4:58:VAL:HG23	30:4:58:VAL:O	2.14	0.47
7:G:318:HIS:NE2	24:X:379:GLU:OE2	2.47	0.47
14:N:58:CYS:SG	14:N:81:LEU:HD22	2.55	0.47
22:V:225:LEU:HD21	22:V:280:LEU:HD23	1.96	0.47
1:A:1431:G:O2'	1:A:1457:G:O6	2.26	0.46
18:R:162:SER:O	18:R:170:ARG:NH2	2.45	0.46
30:4:618:ALA:O	30:4:622:ASN:N	2.48	0.46
31:8:272:ASP:OD1	31:8:273:LEU:N	2.45	0.46
2:B:220:VAL:HG22	2:B:234:TYR:HB2	1.97	0.46
2:B:172:ARG:O	2:B:175:MET:HG2	2.15	0.46
1:A:1125:A:N1	40:A:1845:HOH:O	2.36	0.46
1:A:1259:U:H6	1:A:1326:A:HO2'	1.61	0.46
5:E:40:GLU:OE1	21:U:187:TYR:OH	2.31	0.46
8:H:148:LEU:H	8:H:148:LEU:HD23	1.79	0.46
31:8:120:ARG:NH2	31:8:293:ASN:O	2.49	0.46
7:G:248:VAL:O	7:G:250:LEU:N	2.47	0.46
13:M:19:ILE:HB	13:M:83:LEU:HD23	1.96	0.46
22:V:225:LEU:HD11	22:V:283:LEU:HD22	1.97	0.46
1:A:1263:G:N7	40:A:1847:HOH:O	2.36	0.46
25:Y:264:VAL:HG12	25:Y:265:THR:N	2.30	0.46
1:A:1017:A:O2'	16:P:108:THR:OG1	2.30	0.45
18:R:302:GLN:O	18:R:306:VAL:HG23	2.16	0.45
30:4:631:VAL:CG2	30:4:649:VAL:HG21	2.46	0.45
31:8:216:GLN:HG3	31:8:240:VAL:HG21	1.98	0.45
1:A:894:C:H41	10:J:78:ARG:NH1	2.15	0.45
3:C:89:ASP:OD1	3:C:112:ARG:NH2	2.42	0.45
6:F:193:ASP:OD1	6:F:194:LYS:N	2.50	0.45
15:O:214:SER:OG	22:V:319:ILE:HG23	2.17	0.45
30:4:615:MET:CE	30:4:649:VAL:HG22	2.46	0.45
21:U:169:THR:N	21:U:172:ASN:OD1	2.46	0.45
1:A:738:A:H2'	1:A:740:G:C4	2.52	0.45
1:A:1102:A:H5'	1:A:1576:G:H4'	1.99	0.45
11:K:70:VAL:HG11	25:Y:383:LYS:HE3	1.97	0.45
1:A:1523:A:O2'	1:A:1527:A:N1	2.39	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:245:VAL:HG22	4:D:271:ALA:HB1	1.99	0.45
1:A:705:C:OP2	27:0:136:TYR:OH	2.30	0.45
22:V:74:ARG:O	22:V:78:ASN:ND2	2.46	0.45
1:A:1519:A:N7	12:L:235:LYS:NZ	2.62	0.44
25:Y:254:LYS:O	30:4:358:ARG:NH1	2.51	0.44
3:C:96:MET:HB2	3:C:108:LEU:HD11	2.00	0.44
9:I:97:ILE:HD11	9:I:161:ALA:HB1	2.00	0.44
16:P:140:TYR:OH	17:Q:33:ASP:OD1	2.30	0.44
1:A:1298:U:H2'	1:A:1299:A:C8	2.52	0.44
1:A:1298:U:O2'	2:B:182:LEU:HD23	2.17	0.44
20:T:92:THR:HG22	20:T:92:THR:O	2.18	0.44
22:V:30:LEU:HD12	22:V:149:ASP:HB2	1.99	0.44
1:A:875:U:O2'	1:A:882:A:N1	2.40	0.44
1:A:1378:C:O2	24:X:389:SER:OG	2.30	0.44
1:A:1478:A:C2	29:3:131:LEU:HD21	2.53	0.43
7:G:70:THR:HG23	7:G:73:PHE:H	1.82	0.43
4:D:103:LEU:HD11	4:D:123:ARG:HB2	2.00	0.43
5:E:15:ARG:NH2	21:U:182:ASP:OD1	2.48	0.43
24:X:112:LEU:CD1	24:X:141:VAL:HG13	2.49	0.43
24:X:380:LEU:HD21	24:X:398:LEU:HD12	2.01	0.43
4:D:96:ASP:OD1	4:D:123:ARG:NH1	2.51	0.43
8:H:155:VAL:HG21	28:1:129:PHE:CB	2.48	0.43
19:S:7:GLU:OE1	19:S:7:GLU:N	2.48	0.43
30:4:637:PHE:O	30:4:638:SER:OG	2.29	0.43
1:A:1003:A:O2'	9:I:96:GLN:OE1	2.36	0.43
7:G:356:VAL:HG23	7:G:361:VAL:HG23	2.01	0.43
8:H:184:ILE:O	8:H:184:ILE:HG22	2.18	0.43
18:R:162:SER:O	18:R:170:ARG:NH1	2.52	0.43
31:8:169:ASP:OD1	31:8:170:LEU:N	2.51	0.43
1:A:1044:U:OP1	1:A:1110:A:O2'	2.32	0.43
2:B:231:LEU:HD21	19:S:46:PHE:HB2	2.00	0.43
4:D:243:VAL:HG11	4:D:268:PHE:CD1	2.54	0.43
28:1:174:ARG:NH1	40:1:403:HOH:O	2.41	0.43
3:C:112:ARG:NH1	40:C:205:HOH:O	2.51	0.43
24:X:299:ASN:ND2	28:1:265:THR:OG1	2.51	0.43
30:4:305:ILE:O	30:4:312:LYS:NZ	2.47	0.42
30:4:616:ASP:O	30:4:620:VAL:HG23	2.19	0.42
2:B:229:PRO:HA	2:B:232:ILE:HD12	2.00	0.42
5:E:65:LEU:HD21	16:P:75:LYS:HD3	2.01	0.42
31:8:229:GLU:OE2	31:8:270:ARG:NH2	2.52	0.42
4:D:243:VAL:HG11	4:D:268:PHE:HD1	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:210:VAL:HG12	7:G:210:VAL:O	2.19	0.42
22:V:82:ARG:NH2	22:V:86:ASP:OD1	2.52	0.42
8:H:148:LEU:HD23	8:H:148:LEU:N	2.34	0.42
31:8:96:THR:HG21	31:8:169:ASP:O	2.19	0.42
7:G:137:ALA:O	7:G:138:ILE:C	2.57	0.42
8:H:59:THR:O	8:H:59:THR:HG23	2.18	0.42
30:4:305:ILE:HG22	30:4:306:ASN:N	2.35	0.42
7:G:250:LEU:O	7:G:250:LEU:HG	2.19	0.42
19:S:96:CYS:O	19:S:100:VAL:HG23	2.20	0.42
2:B:180:ARG:NH1	4:D:211:CYS:SG	2.87	0.42
1:A:1264:C:H1'	8:H:124:VAL:HG13	2.02	0.42
4:D:215:TYR:CD2	4:D:276:VAL:HG21	2.54	0.42
1:A:930:G:O2'	1:A:931:C:OP2	2.26	0.42
1:A:1286:A:OP1	4:D:260:LYS:NZ	2.51	0.42
9:I:111:SER:OG	9:I:114:THR:HG23	2.20	0.42
14:N:83:GLU:OE1	20:T:85:GLN:NE2	2.42	0.42
14:N:88:VAL:O	14:N:88:VAL:HG13	2.19	0.41
19:S:83:ARG:NH1	19:S:93:LYS:O	2.53	0.41
8:H:122:GLN:O	11:K:112:ARG:NH1	2.53	0.41
12:L:66:ASP:OD1	12:L:107:LYS:NZ	2.43	0.41
22:V:236:LEU:HD21	22:V:323:GLU:HB3	2.02	0.41
30:4:573:ALA:O	30:4:577:ASN:ND2	2.53	0.41
2:B:146:SER:O	2:B:168:THR:HA	2.20	0.41
22:V:36:ASP:OD1	22:V:38:HIS:ND1	2.53	0.41
1:A:683:G:OP1	20:T:160:ARG:NH1	2.54	0.41
6:F:158[A]:LEU:HD21	6:F:230:ALA:HA	2.03	0.41
11:K:79:PRO:O	11:K:82:SER:OG	2.26	0.41
1:A:1149:G:OP2	29:3:165:LYS:NZ	2.51	0.41
3:C:58:ALA:HB1	3:C:59:PRO:CD	2.51	0.41
13:M:67:ALA:HB2	18:R:196:TYR:CE1	2.56	0.41
18:R:191:ARG:HG3	18:R:204:ILE:HG23	2.03	0.41
19:S:106:LEU:CB	19:S:117:LEU:HD11	2.51	0.41
20:T:42:GLU:OE1	20:T:45:ARG:NH2	2.45	0.41
9:I:151:VAL:HG21	9:I:158:ARG:HG3	2.03	0.41
7:G:115:GLY:N	8:H:84:ASP:OD2	2.54	0.40
24:X:93:THR:HG21	24:X:365:TRP:CZ3	2.56	0.40
12:L:79:VAL:HG21	12:L:82:ILE:HD13	2.03	0.40
24:X:50:ARG:NH2	24:X:96:GLU:OE2	2.42	0.40
31:8:216:GLN:HG2	31:8:240:VAL:HG21	2.03	0.40
31:8:357:GLY:O	31:8:358:SER:C	2.59	0.40
3:C:132:TYR:O	3:C:136:VAL:HG23	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:108:LEU:HD21	24:X:307:VAL:HG13	2.03	0.40
24:X:127:TYR:OH	28:1:306:GLU:OE2	2.38	0.40
31:8:334:LEU:HD21	31:8:377:LEU:HD11	2.03	0.40
1:A:1064:C:HO2'	1:A:1065:C:H5	1.69	0.40
28:1:266:LEU:HD11	28:1:289:ILE:HD11	2.02	0.40
30:4:166:VAL:HG23	30:4:167:LYS:N	2.36	0.40

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%)	222 (100%)	1 (0%)	0	100	100
3	C	130/167 (78%)	127 (98%)	3 (2%)	0	100	100
4	D	341/430 (79%)	334 (98%)	7 (2%)	0	100	100
5	E	116/125 (93%)	116 (100%)	0	0	100	100
6	F	218/242 (90%)	212 (97%)	6 (3%)	0	100	100
7	G	323/396 (82%)	316 (98%)	7 (2%)	0	100	100
8	H	138/201 (69%)	136 (99%)	1 (1%)	1 (1%)	22	57
9	I	134/194 (69%)	131 (98%)	3 (2%)	0	100	100
10	J	106/138 (77%)	104 (98%)	2 (2%)	0	100	100
11	K	99/128 (77%)	98 (99%)	1 (1%)	0	100	100
12	L	172/257 (67%)	172 (100%)	0	0	100	100
13	M	117/137 (85%)	117 (100%)	0	0	100	100
14	N	108/130 (83%)	108 (100%)	0	0	100	100
15	O	191/258 (74%)	189 (99%)	2 (1%)	0	100	100
16	P	95/142 (67%)	94 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	Q	84/86 (98%)	84 (100%)	0	0	100	100
18	R	293/360 (81%)	286 (98%)	7 (2%)	0	100	100
19	S	133/190 (70%)	132 (99%)	1 (1%)	0	100	100
20	T	166/173 (96%)	164 (99%)	2 (1%)	0	100	100
21	U	174/205 (85%)	174 (100%)	0	0	100	100
22	V	358/414 (86%)	353 (99%)	5 (1%)	0	100	100
23	W	98/187 (52%)	97 (99%)	1 (1%)	0	100	100
24	X	350/398 (88%)	345 (99%)	5 (1%)	0	100	100
25	Y	147/395 (37%)	146 (99%)	1 (1%)	0	100	100
26	Z	98/106 (92%)	97 (99%)	1 (1%)	0	100	100
27	0	213/218 (98%)	212 (100%)	1 (0%)	0	100	100
28	1	276/323 (85%)	273 (99%)	3 (1%)	0	100	100
29	3	69/199 (35%)	69 (100%)	0	0	100	100
30	4	586/689 (85%)	579 (99%)	7 (1%)	0	100	100
31	8	322/407 (79%)	316 (98%)	6 (2%)	0	100	100
All	All	5878/7591 (77%)	5803 (99%)	74 (1%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	H	126	ILE

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	
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%)	284 (99%)	2 (1%)	84	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
5	E	100/107 (94%)	100 (100%)	0	100 100
6	F	195/209 (93%)	195 (100%)	0	100 100
7	G	285/342 (83%)	284 (100%)	1 (0%)	91 95
8	H	130/180 (72%)	130 (100%)	0	100 100
9	I	104/146 (71%)	104 (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	174/230 (76%)	174 (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%)	324 (100%)	1 (0%)	92 96
23	W	87/158 (55%)	87 (100%)	0	100 100
24	X	311/351 (89%)	309 (99%)	2 (1%)	86 92
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%)	188 (100%)	0	100 100
28	1	256/291 (88%)	256 (100%)	0	100 100
29	3	65/166 (39%)	65 (100%)	0	100 100
30	4	527/609 (86%)	527 (100%)	0	100 100
31	8	275/350 (79%)	275 (100%)	0	100 100
All	All	5234/6593 (79%)	5228 (100%)	6 (0%)	93 97

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	276	VAL

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Mol	Chain	Res	Type
4	D	296	LEU
7	G	389	ARG
22	V	226	TYR
24	X	81	HIS
24	X	394	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
6	F	113	GLN
6	F	146	HIS
9	I	96	GLN
9	I	98	GLN
12	L	162	GLN
20	T	33	ASN
22	V	134	GLN
25	Y	290	ASN
28	1	185	HIS
30	4	129	GLN
30	4	285	ASN
31	8	343	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	947/955 (99%)	117 (12%)	0

All (117) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	651	A
1	A	680	U
1	A	688	A
1	A	704	U
1	A	721	U
1	A	722	C
1	A	737	C
1	A	739	C
1	A	753	A
1	A	761	A

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Mol	Chain	Res	Type
1	A	766	G
1	A	777	G
1	A	791	G
1	A	796	G
1	A	830	U
1	A	832	U
1	A	835	C
1	A	860	A
1	A	868	C
1	A	890	C
1	A	902	G
1	A	919	A
1	A	929	A
1	A	931	C
1	A	932	C
1	A	938	A
1	A	939	A
1	A	942	A
1	A	954	C
1	A	955	A
1	A	956	C
1	A	958	C
1	A	960	C
1	A	961	U
1	A	962	C
1	A	967	A
1	A	1001	C
1	A	1002	C
1	A	1011	C
1	A	1015	A
1	A	1019	A
1	A	1020	C
1	A	1022	A
1	A	1042	U
1	A	1043	C
1	A	1065	C
1	A	1069	A
1	A	1098	C
1	A	1103	A
1	A	1105	C
1	A	1106	C
1	A	1107	U

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Mol	Chain	Res	Type
1	A	1109	A
1	A	1116	A
1	A	1118	A
1	A	1119	U
1	A	1120	C
1	A	1121	A
1	A	1126	A
1	A	1151	C
1	A	1167	A
1	A	1187	U
1	A	1188	A
1	A	1189	U
1	A	1215	U
1	A	1223	C
1	A	1225	C
1	A	1229	U
1	A	1247	G
1	A	1248	C
1	A	1250	C
1	A	1251	A
1	A	1261	C
1	A	1271	C
1	A	1273	G
1	A	1284	U
1	A	1290	C
1	A	1291	U
1	A	1326	A
1	A	1327	G
1	A	1343	A
1	A	1344	U
1	A	1354	A
1	A	1356	A
1	A	1376	C
1	A	1378	C
1	A	1390	A
1	A	1421	G
1	A	1422	G
1	A	1430	A
1	A	1447	G
1	A	1462	G
1	A	1474	G
1	A	1481	C

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Mol	Chain	Res	Type
1	A	1492	A
1	A	1493	C
1	A	1503	G
1	A	1505	A
1	A	1507	A
1	A	1512	A
1	A	1519	A
1	A	1520	U
1	A	1522	U
1	A	1525	C
1	A	1526	U
1	A	1527	A
1	A	1533	C
1	A	1537	C
1	A	1539	C
1	A	1540	A
1	A	1558	A
1	A	1559	G
1	A	1568	U
1	A	1571	U
1	A	1594	G
1	A	1595	G
1	A	1598	G

There are no RNA pucker outliers to report.

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

7 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	18,26,27	0.72	0	19,38,41	0.61	0
1	5MU	A	1076	1	19,22,23	0.30	0	28,32,35	0.37	0
9	5F0	I	184	9	8,8,9	0.58	0	7,9,11	1.04	1 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	B8T	A	1486	1	19,22,23	0.33	0	26,31,34	0.33	0
1	MA6	A	1584	1	18,26,27	0.74	0	19,38,41	0.56	0
1	5MC	A	1488	1	18,22,23	0.33	0	26,32,35	0.46	0
17	AYA	Q	2	17	6,7,8	0.76	0	5,8,10	0.48	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	-	2/7/29/30	0/3/3/3
1	5MU	A	1076	1	-	0/7/25/26	0/2/2/2
9	5F0	I	184	9	-	0/9/9/10	-
1	B8T	A	1486	1	-	0/7/27/28	0/2/2/2
1	MA6	A	1584	1	-	1/7/29/30	0/3/3/3
1	5MC	A	1488	1	-	0/7/25/26	0/2/2/2
17	AYA	Q	2	17	-	0/4/6/8	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	I	184	5F0	O-C-CB	-2.33	118.63	125.43

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1584	MA6	C5-C6-N6-C9
1	A	1583	MA6	O4'-C4'-C5'-O5'
1	A	1583	MA6	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 87 ligands modelled in this entry, 81 are monoatomic - leaving 6 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	$\#\|Z\| > 2$
32	NAD	A	1701	33	42,48,48	0.58	0	50,73,73	0.56	1 (2%)
37	ATP	X	501	33	26,33,33	0.76	0	31,52,52	0.64	0
36	FES	P	201	16,5	0,4,4	-	-	-		
39	SAH	8	501	-	24,28,28	0.70	0	25,40,40	0.79	1 (4%)
36	FES	T	201	13,20	0,4,4	-	-	-		
38	GDP	X	503	-	24,30,30	0.88	2 (8%)	30,47,47	0.65	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
32	NAD	A	1701	33	-	2/26/62/62	0/5/5/5
37	ATP	X	501	33	-	0/18/38/38	0/3/3/3
36	FES	P	201	16,5	-	-	0/1/1/1
39	SAH	8	501	-	-	4/11/31/31	0/3/3/3
36	FES	T	201	13,20	-	-	0/1/1/1
38	GDP	X	503	-	-	0/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	X	503	GDP	C5-C6	-2.13	1.43	1.47
38	X	503	GDP	C8-N7	-2.01	1.31	1.35

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
39	8	501	SAH	C5-C6-N6	2.32	123.88	120.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	A	1701	NAD	C5A-C6A-N6A	2.31	123.86	120.35

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
39	8	501	SAH	OXT-C-CA-N
39	8	501	SAH	OXT-C-CA-CB
39	8	501	SAH	O-C-CA-CB
39	8	501	SAH	O-C-CA-N
32	A	1701	NAD	PA-O3-PN-O1N
32	A	1701	NAD	PA-O3-PN-O2N

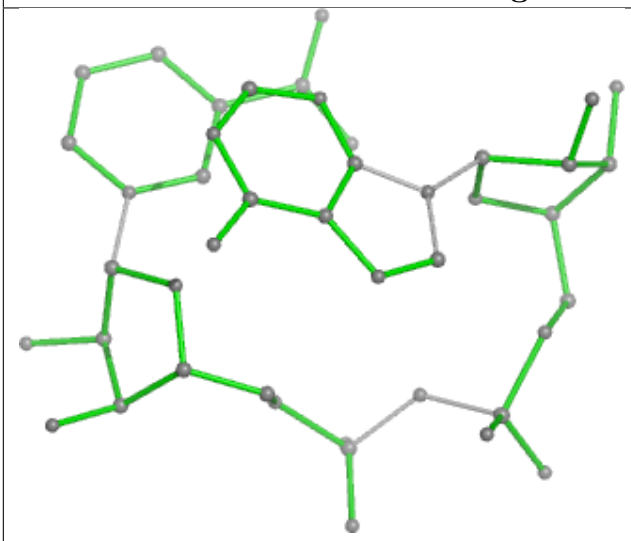
There are no ring outliers.

1 monomer is involved in 1 short contact:

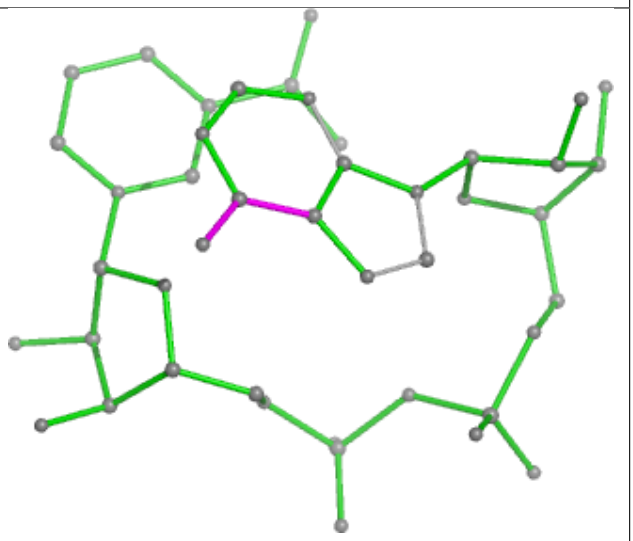
Mol	Chain	Res	Type	Clashes	Symm-Clashes
39	8	501	SAH	1	0

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 then 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.

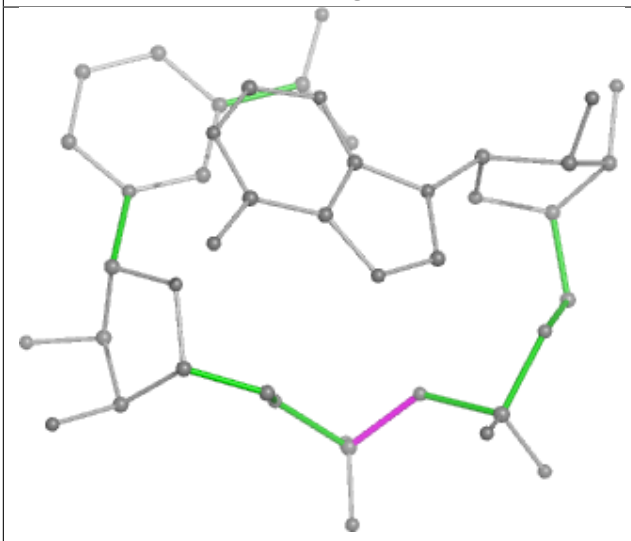
Ligand NAD A 1701



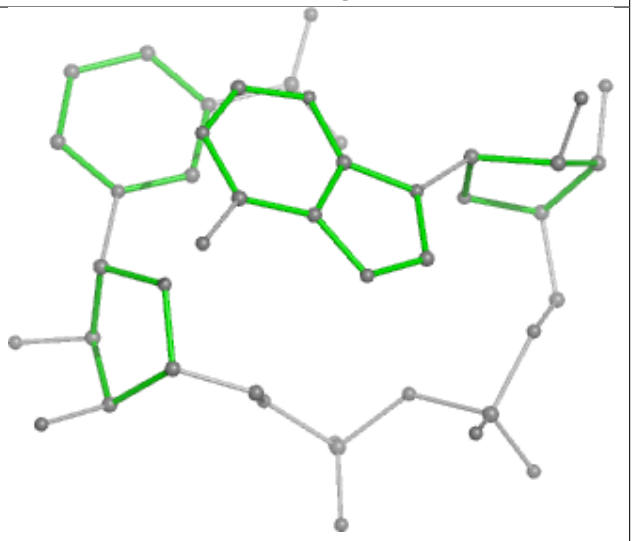
Bond lengths



Bond angles

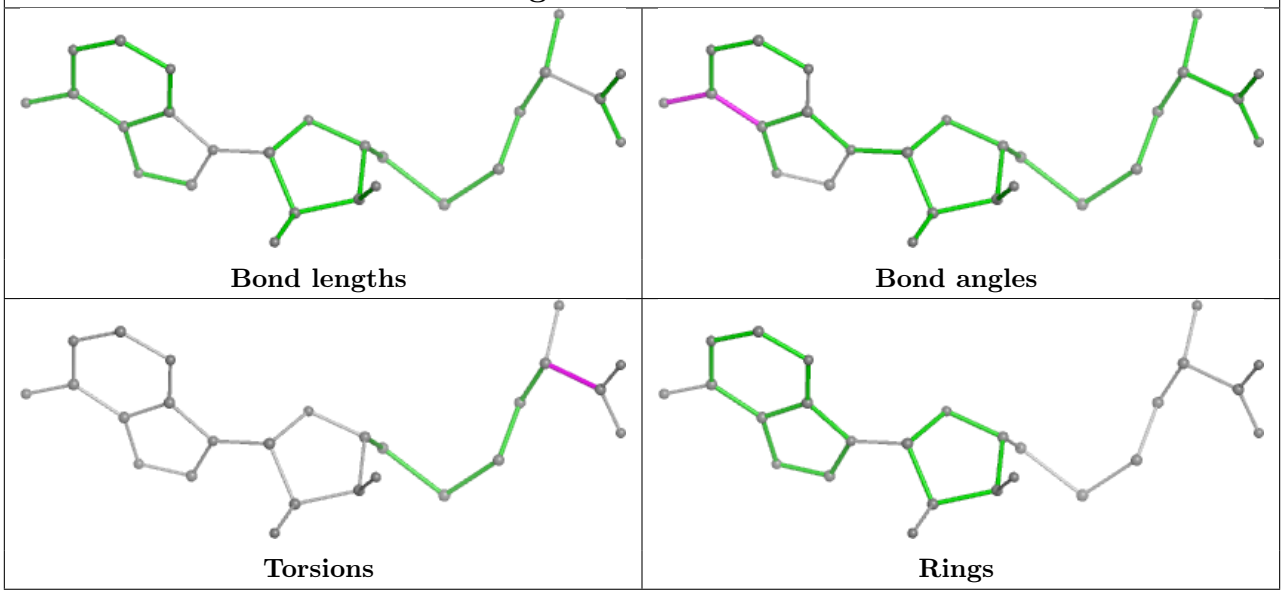


Torsions

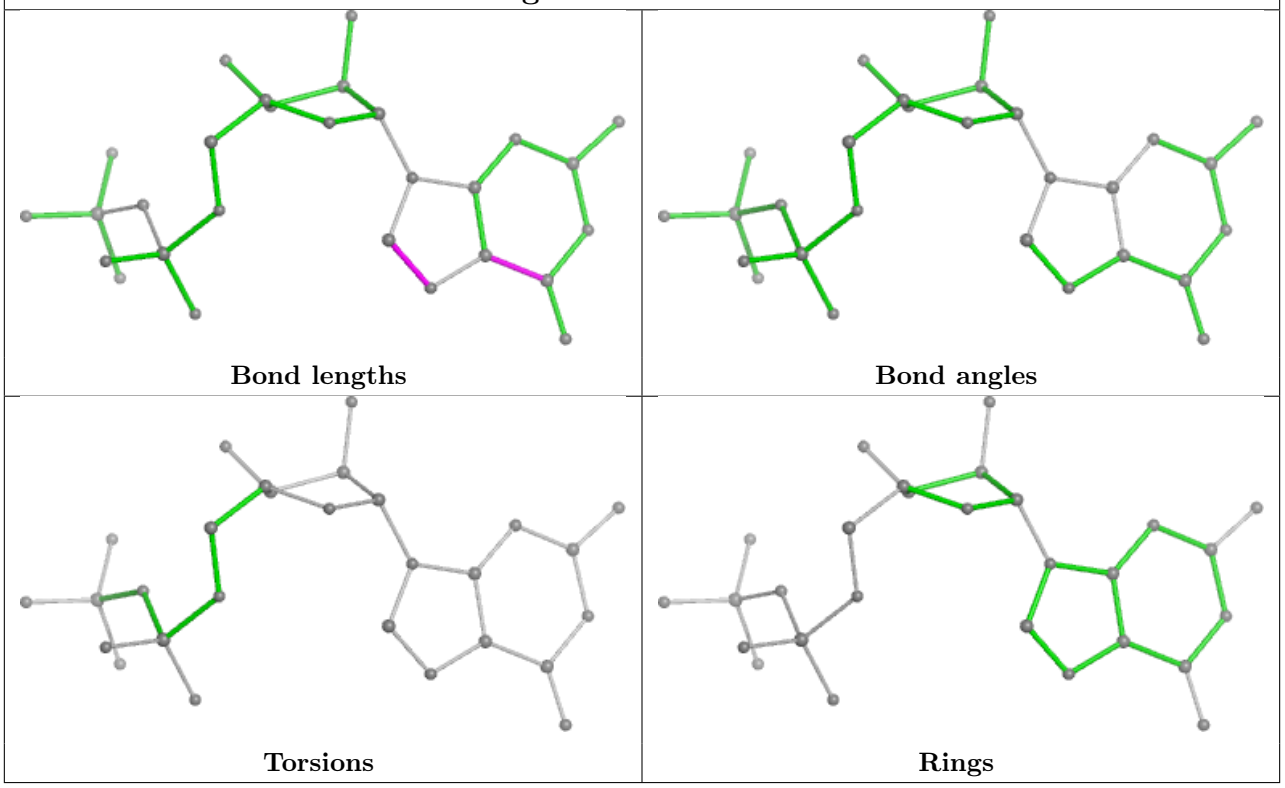


Rings

Ligand SAH 8 501



Ligand GDP X 503



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.

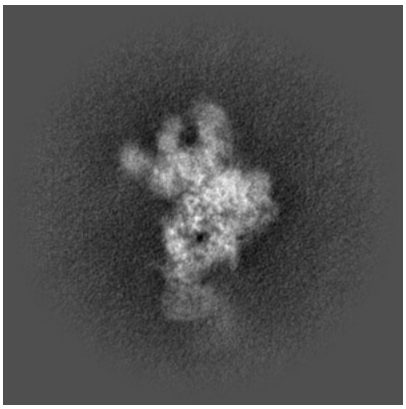
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-18439. These allow visual inspection of the internal detail of the map and identification of artifacts.

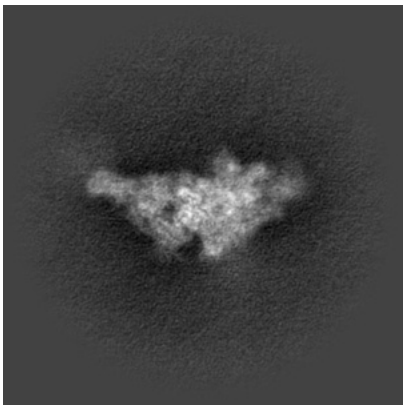
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

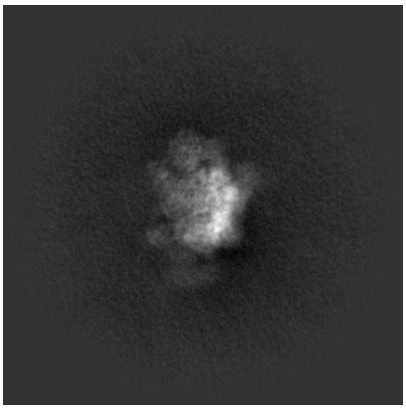
6.1.1 Primary map



X

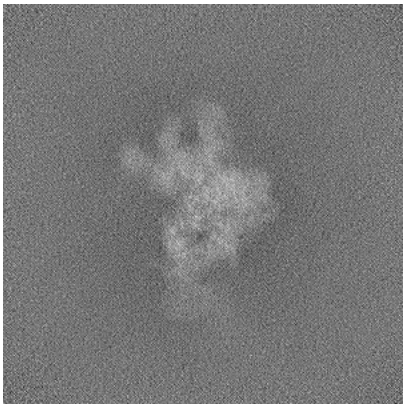


Y

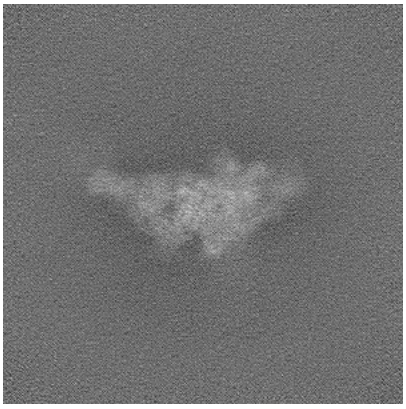


Z

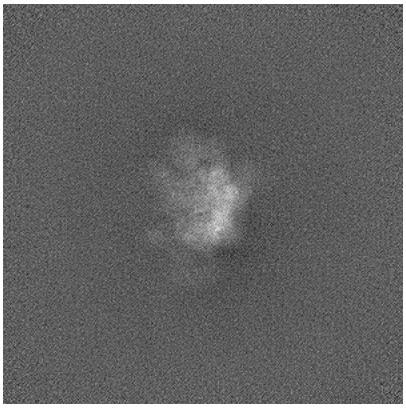
6.1.2 Raw map



X



Y

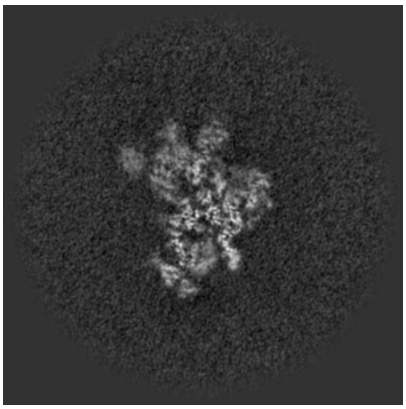


Z

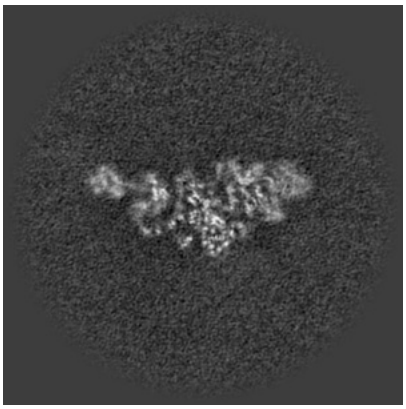
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

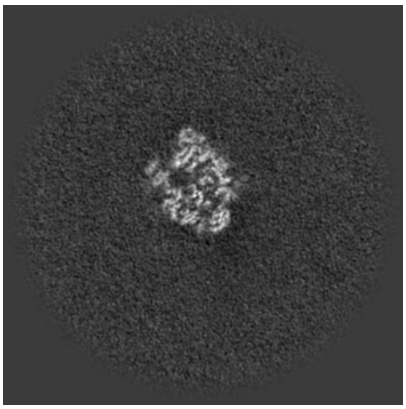
6.2.1 Primary map



X Index: 256

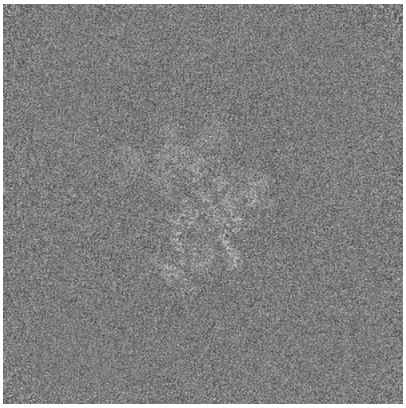


Y Index: 256

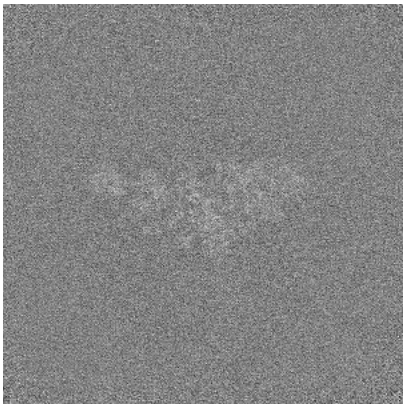


Z Index: 256

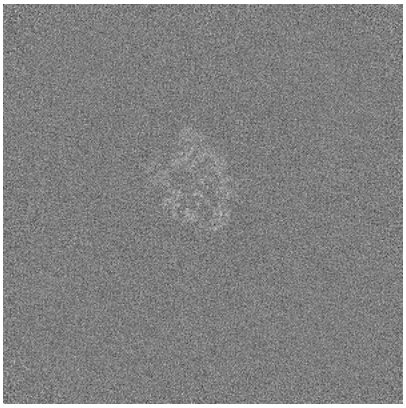
6.2.2 Raw map



X Index: 256



Y Index: 256

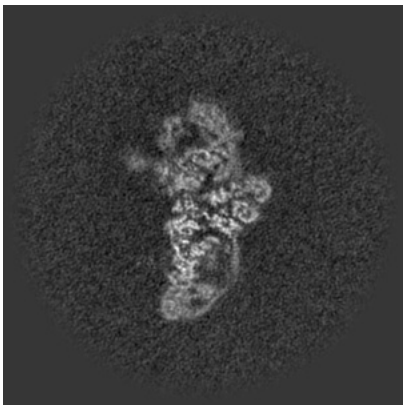


Z Index: 256

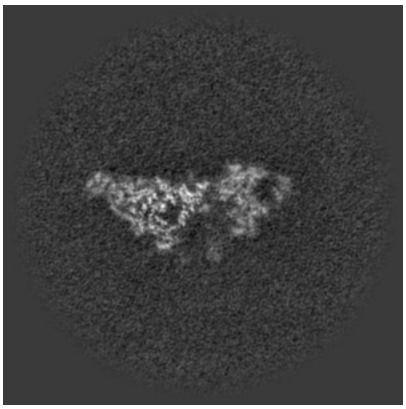
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

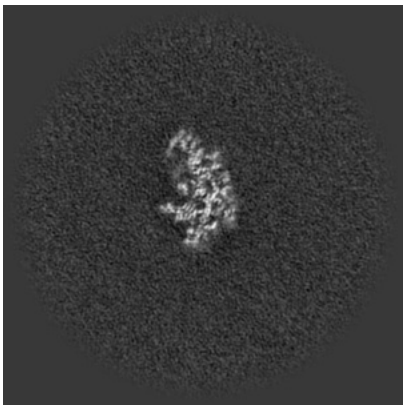
6.3.1 Primary map



X Index: 272

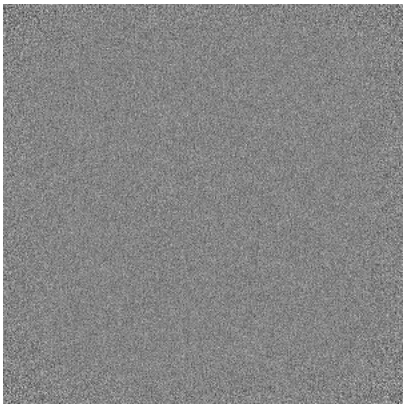


Y Index: 228

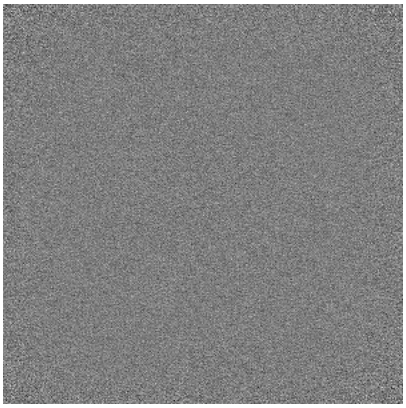


Z Index: 239

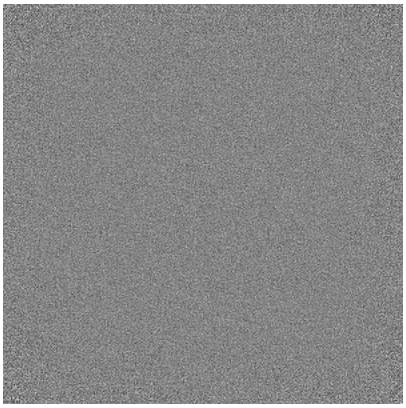
6.3.2 Raw map



X Index: 0



Y Index: 0

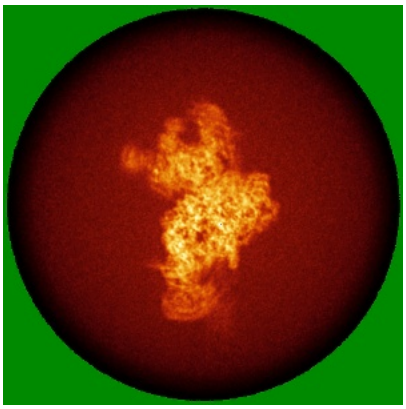


Z Index: 0

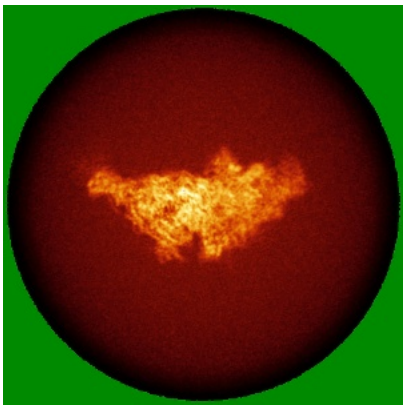
The images above show the largest variance slices of the map in three orthogonal directions.

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

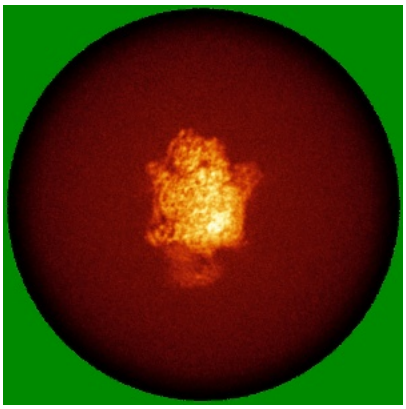
6.4.1 Primary map



X

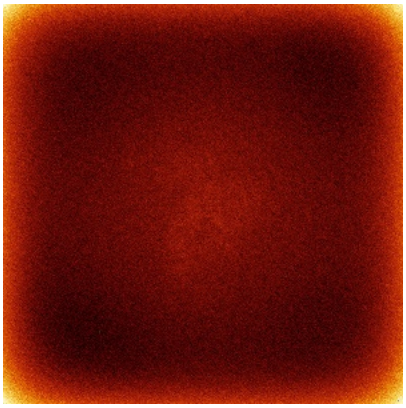


Y

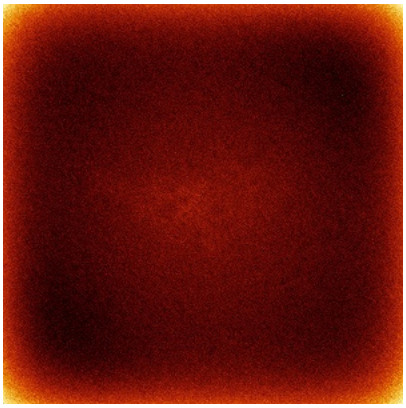


Z

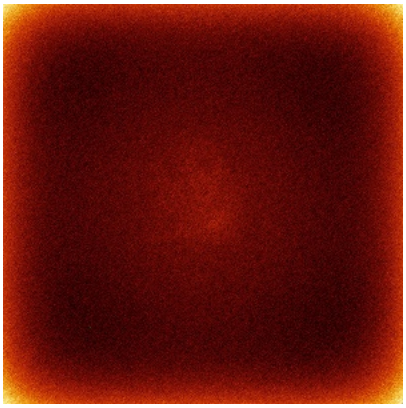
6.4.2 Raw map



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

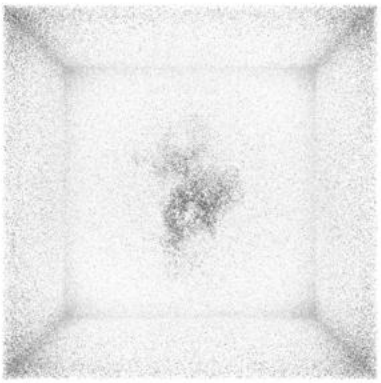
X

Y

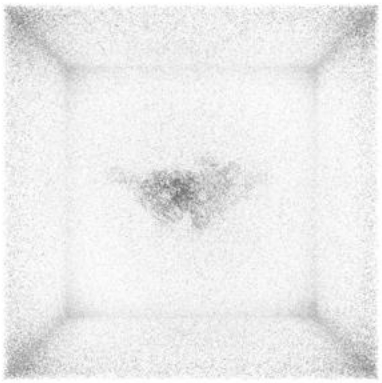
Z

The images above show the 3D surface view of the map at the recommended contour level 0.125. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

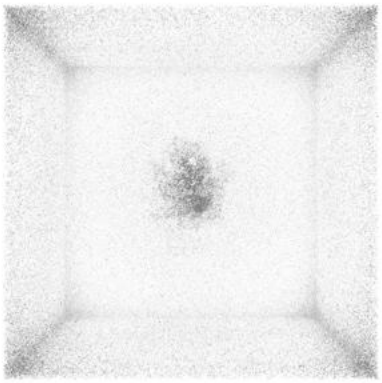
6.5.2 Raw map



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.

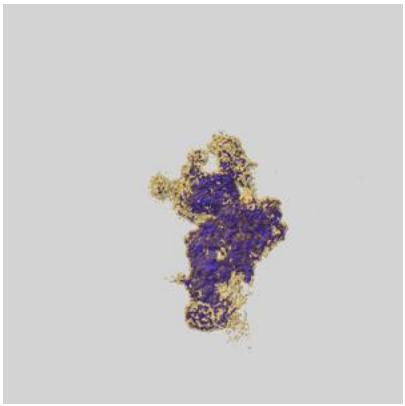
6.6 Mask visualisation (i)

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

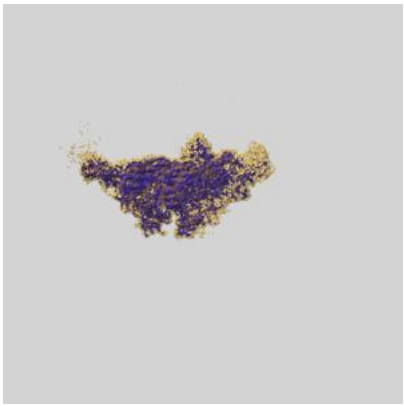
A mask typically either:

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

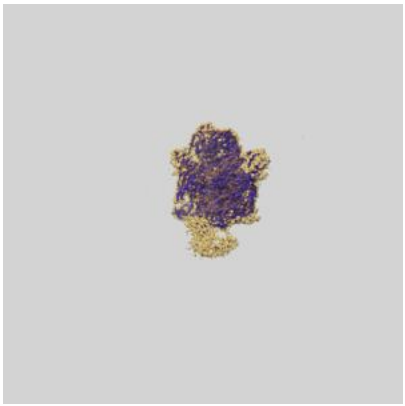
6.6.1 emd_18439_msk_1.map (i)



X



Y

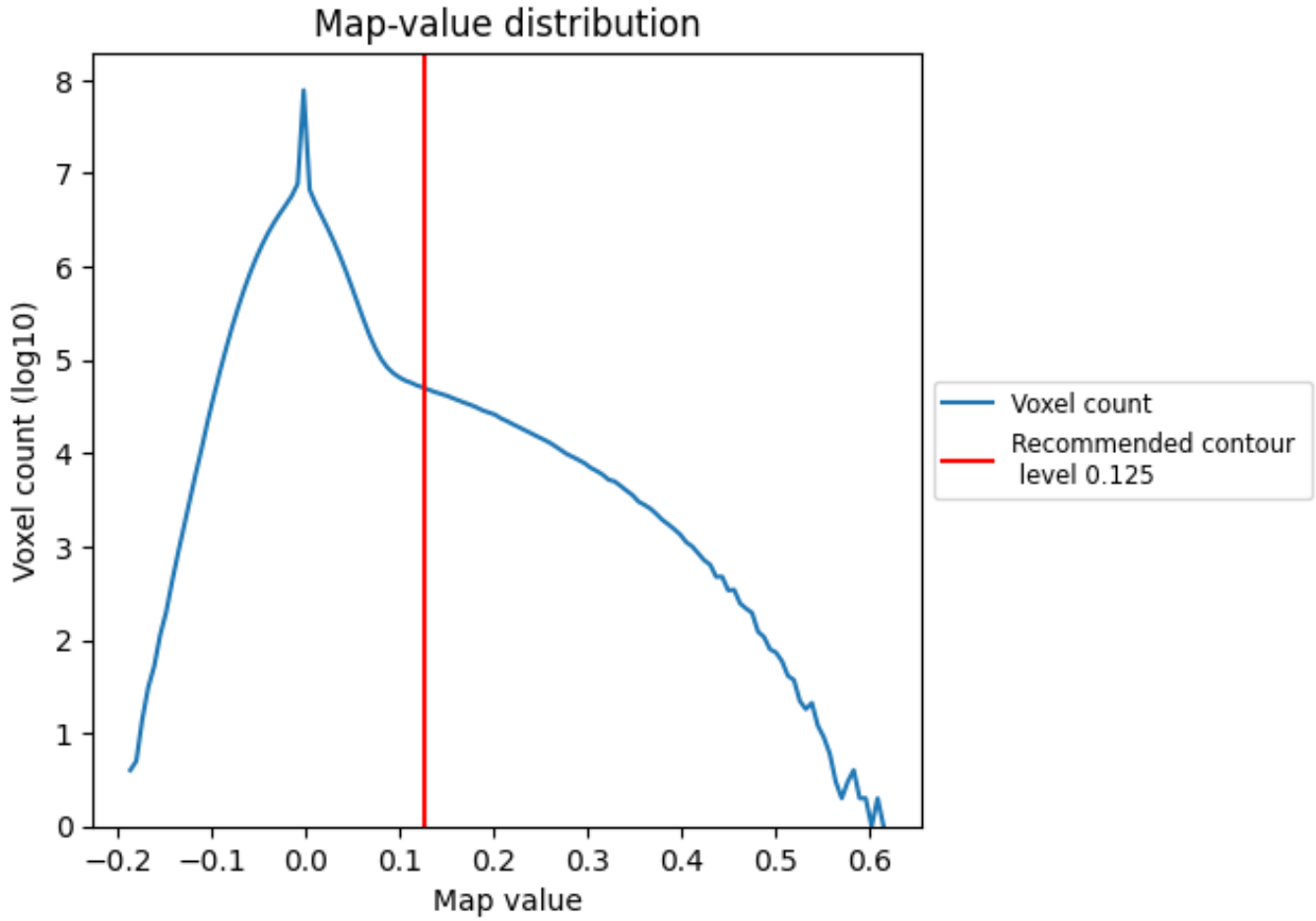


Z

7 Map analysis

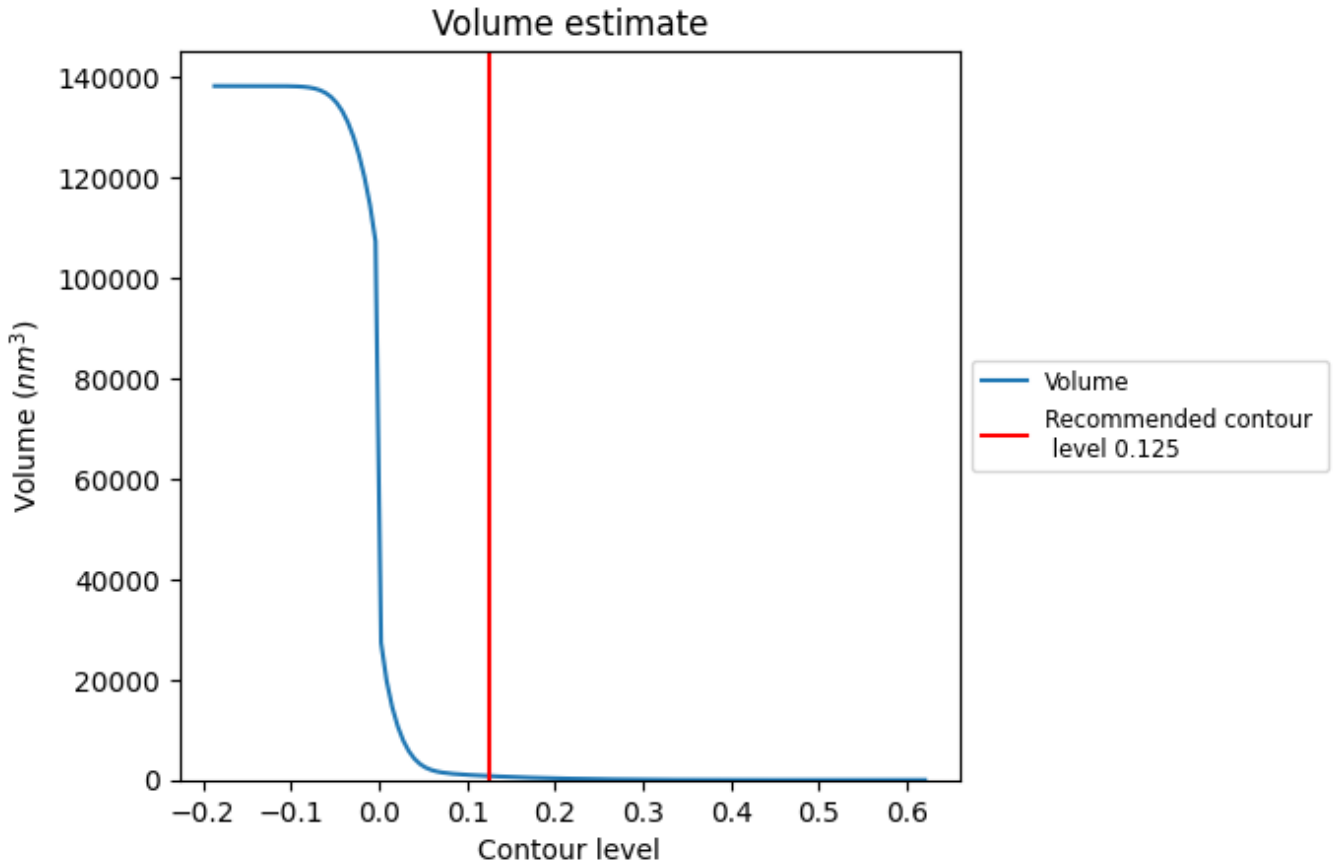
This section contains the results of statistical analysis of the map.

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.

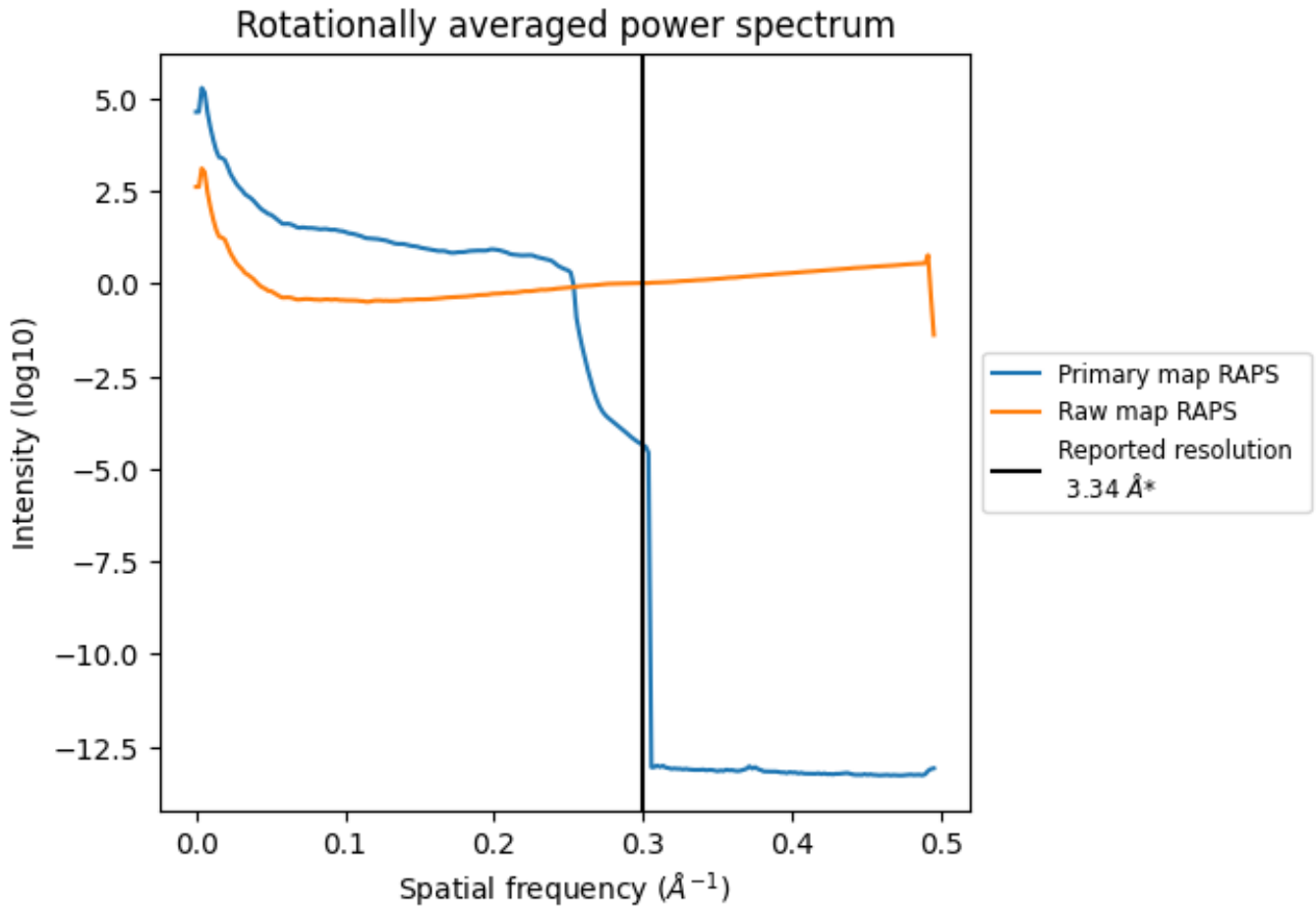
7.2 Volume estimate



The volume at the recommended contour level is 788 nm^3; this corresponds to an approximate mass of 712 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)

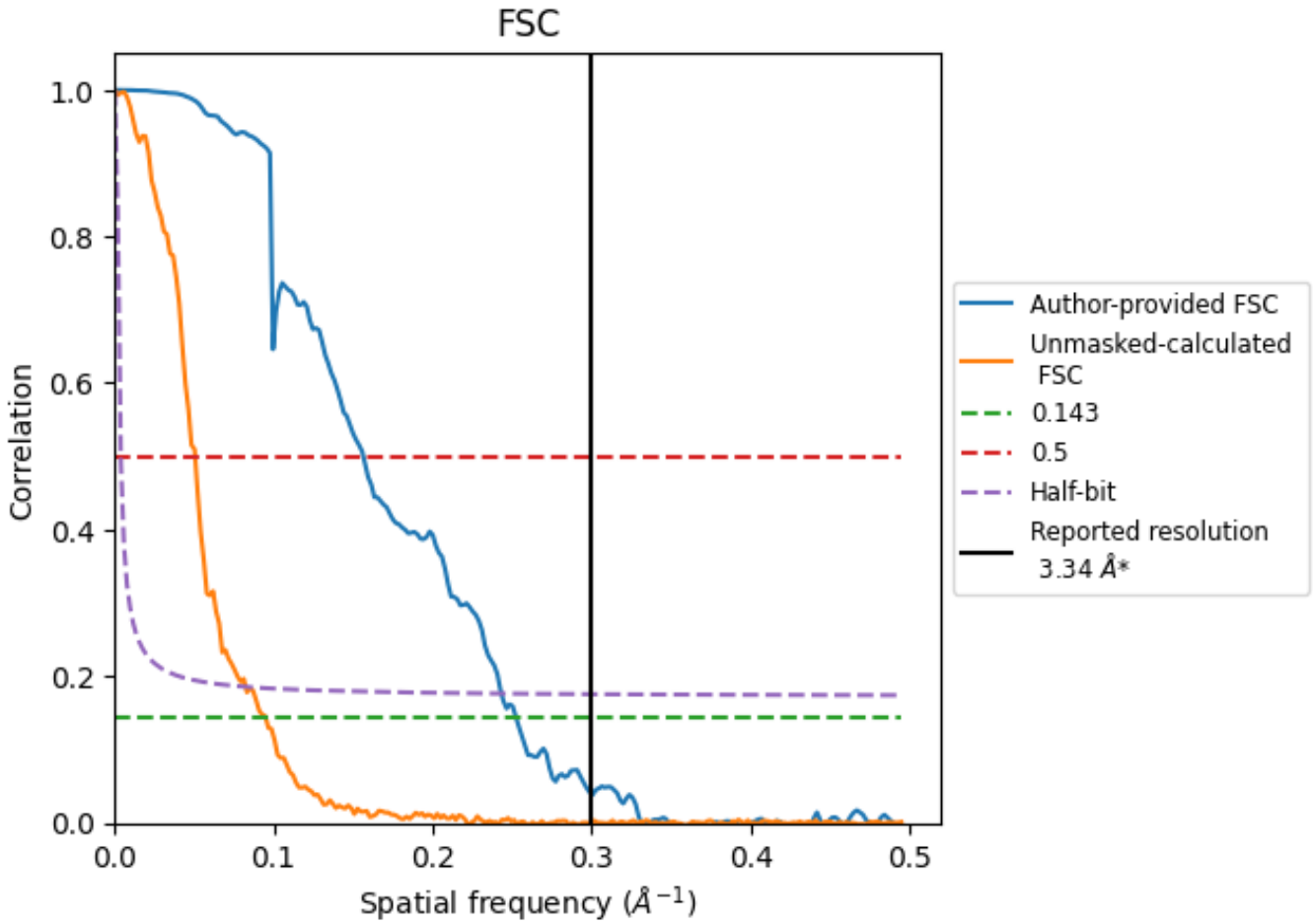


*Reported resolution corresponds to spatial frequency of 0.299 $Å^{-1}$

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 0.299 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.34	-	-
Author-provided FSC curve	3.96	6.39	4.11
Unmasked-calculated*	10.53	19.76	12.14

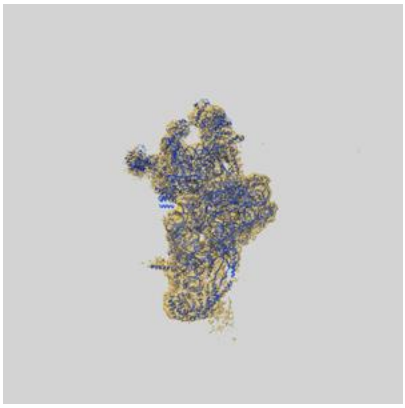
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.96 differs from the reported value 3.34 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 10.53 differs from the reported value 3.34 by more than 10 %

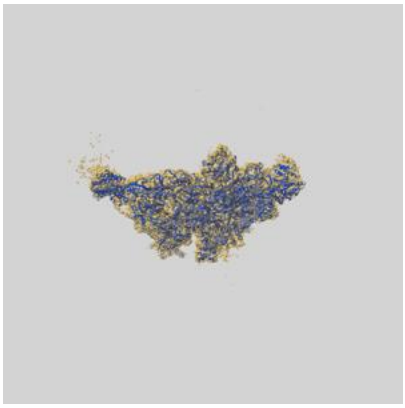
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-18439 and PDB model 8QRL. Per-residue inclusion information can be found in section 3 on page 14.

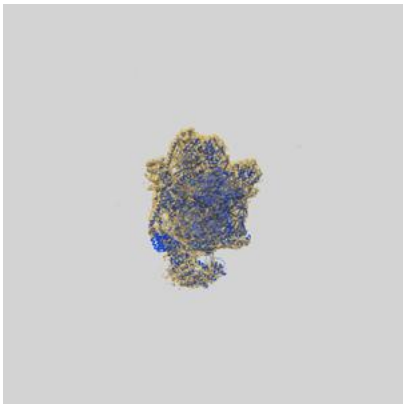
9.1 Map-model overlay



X



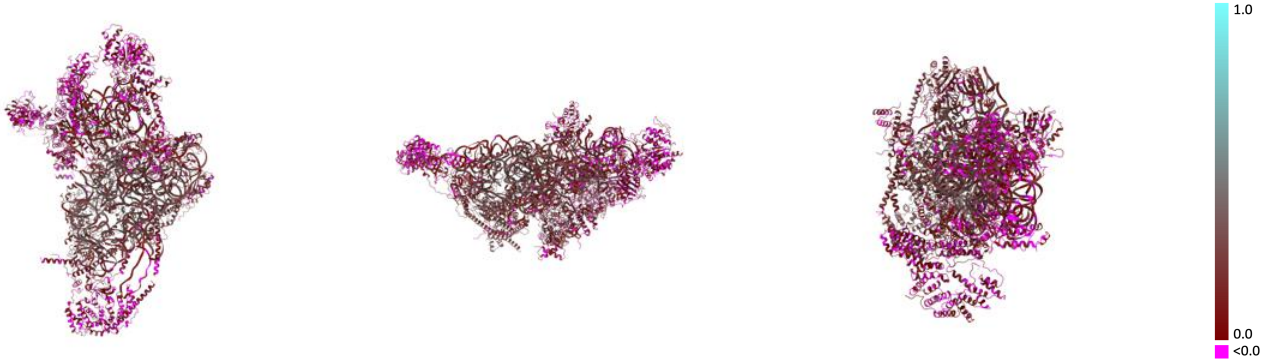
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.125 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.

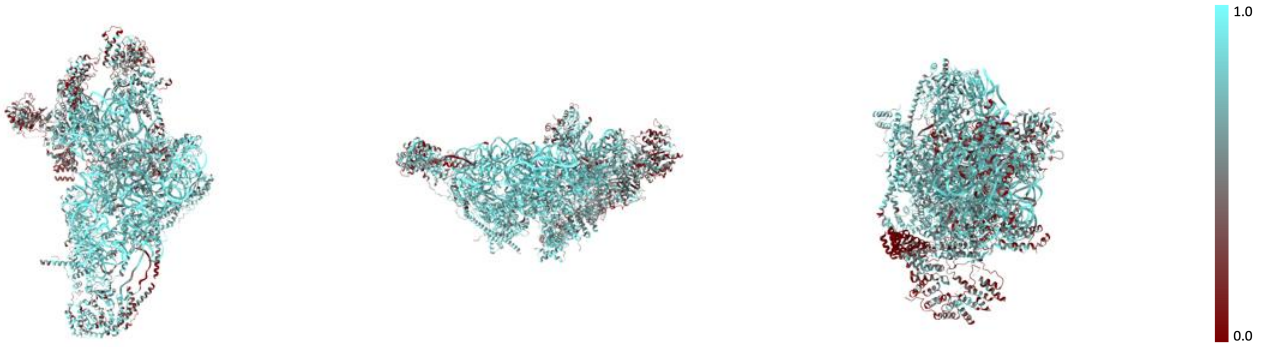
9.2 Q-score mapped to coordinate model (i)



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.

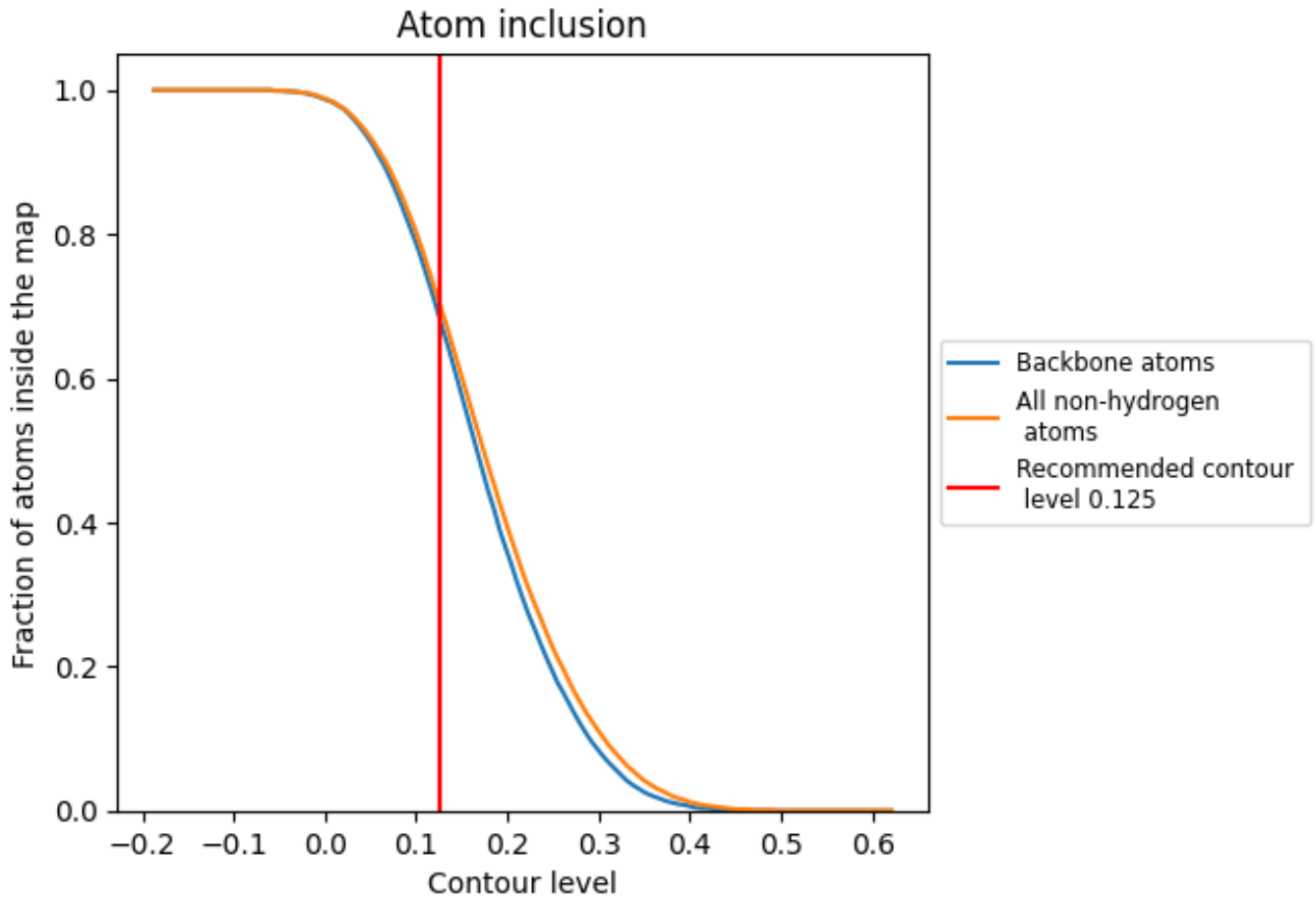
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.125).

9.4 Atom inclusion (i)



At the recommended contour level, 69% of all backbone atoms, 71% 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 (0.125) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7070	0.1830
0	0.6840	0.1160
1	0.5090	0.0940
3	0.7230	0.2440
4	0.3320	0.0530
8	0.6200	0.1360
A	0.8980	0.2480
B	0.7720	0.2430
C	0.7180	0.2240
D	0.7090	0.2540
E	0.6650	0.1750
F	0.5490	0.1250
G	0.6120	0.1390
H	0.5810	0.1140
I	0.7650	0.1900
J	0.7680	0.2830
K	0.6930	0.1030
L	0.7120	0.2250
M	0.8030	0.2390
N	0.7840	0.2700
O	0.8130	0.2650
P	0.7770	0.2070
Q	0.6950	0.1770
R	0.8150	0.2830
S	0.7360	0.1940
T	0.7440	0.2930
U	0.7370	0.1910
V	0.6100	0.0280
W	0.7220	0.1850
X	0.4710	0.0460
Y	0.4100	0.0350
Z	0.5790	0.1110