Full wwPDB EM Validation Report

Aug 26, 2026 – 11:41 pm BST

PDB ID	:	7PNY / pdb_00007pny
EMDB ID	:	EMD-13556
Title	:	Assembly intermediate of human mitochondrial ribosome small subunit without mS37 in complex with RBFA and METTL15 conformation b
Authors	:	Itoh, Y.; Khawaja, A.; Rorbach, J.; Amunts, A.
Deposited on	:	2021-09-08
Resolution	:	3.06 Å(reported)
Based on initial model	:	6RW4

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 (i) symbol.

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

The following versions of software and data (see references (1)) were used in the production of this report:

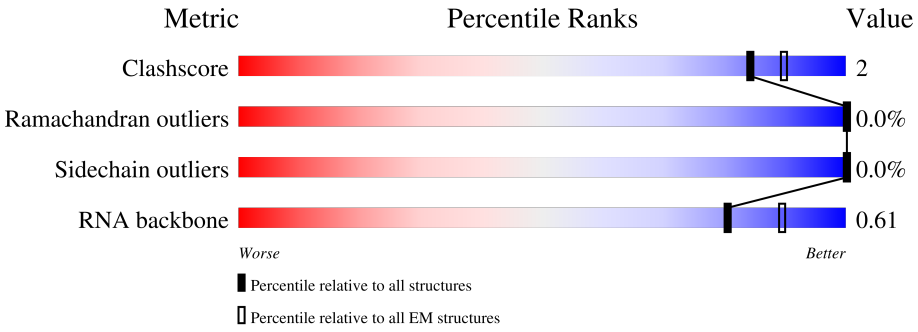
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data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

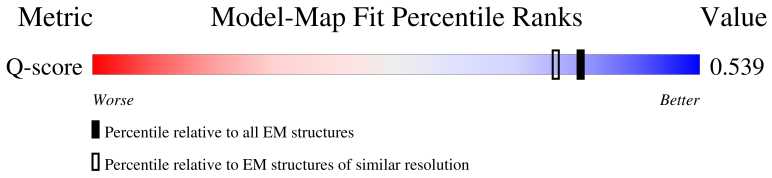
1 Overall quality at a glance

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

The reported resolution of this entry is 3.06 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.





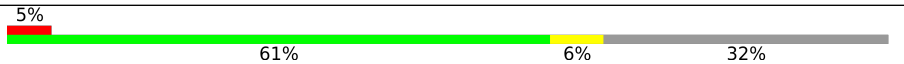
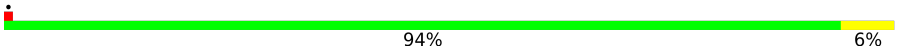
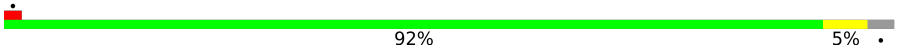
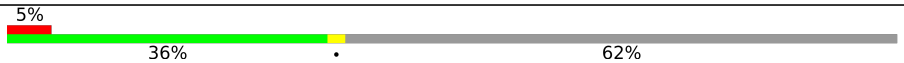
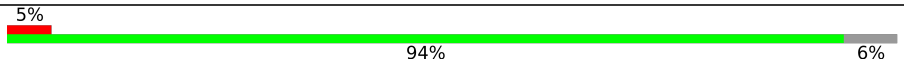
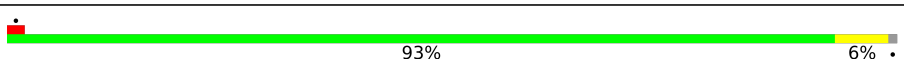
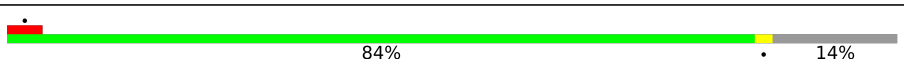
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13976 (2.56 - 3.56)

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	78% 20%
2	B	296	73% 24%
3	C	167	74% 5% 21%

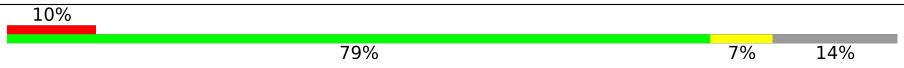
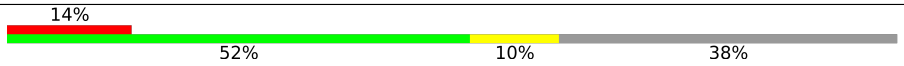
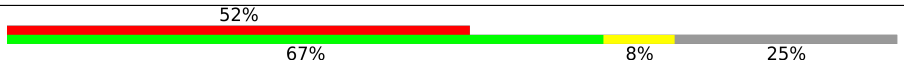
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Mol	Chain	Length	Quality of chain
4	D	430	
5	E	125	
6	F	242	
7	G	396	
8	H	201	
9	I	194	
10	J	138	
11	K	128	
12	L	257	
13	M	137	
14	N	130	
15	O	258	
16	P	142	
17	Q	86	
18	R	360	
19	S	190	
20	T	173	
21	U	205	
22	V	414	
23	W	187	
24	X	398	
25	Y	395	
26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

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Mol	Chain	Length	Quality of chain
29	3	199	
30	4	689	
31	a	343	
32	b	407	

2 Entry composition

There are 41 unique types of molecules in this entry. The entry contains 132175 atoms, of which 60960 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	H	N	O	P		
1	A	951	30467	9060	10269	3636	6551	951	0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
2	B	225	3644	1164	1816	331	323	10	0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	C	132	2172	699	1089	195	185	4	0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	D	343	5536	1713	2805	518	487	13	0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	E	118	1891	592	955	168	172	4	0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
6	F	205	3673	1158	1869	324	311	11	15	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	327	Total	C	H	N	O	S	0	0
			5378	1710	2690	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	H	N	O	S	0	0
			2336	745	1184	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	H	N	O	S	0	0
			2081	642	1061	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	H	N	O	S	0	0
			1727	521	888	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	H	N	O	S	0	0
			1748	537	886	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	H	N	O	S	0	0
			2994	925	1541	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	H	N	O	S	0	0
			1908	594	966	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	H	N	O	S	0	0
			1797	562	929	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	H	N	O	S	0	0
			3149	1014	1557	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	H	N	O	S	0	0
			1588	501	807	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	H	N	O	S	0	0
			1502	460	758	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	H	N	O	S	0	0
			4838	1533	2429	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	H	N	O	S	0	0
			2227	716	1116	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	H	N	O	S	0	0
			2765	877	1394	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	H	N	O	S	0	0
			2988	916	1500	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	H	N	O	S	0	0
			5933	1904	2964	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	H	N	O	S	0	0
			1592	498	803	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	H	N	O	S	0	0
			5694	1822	2845	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	H	N	O	S	0	0
			2444	801	1198	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	H	N	O	S	0	0
			1699	534	860	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	H	N	O	S	0	0
			3584	1130	1797	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	H	N	O	S	0	0
			4545	1430	2289	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	H	N	O	S	0	0
			1331	403	702	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	H	N	O	S	0	0
			9556	3056	4781	809	882	28		

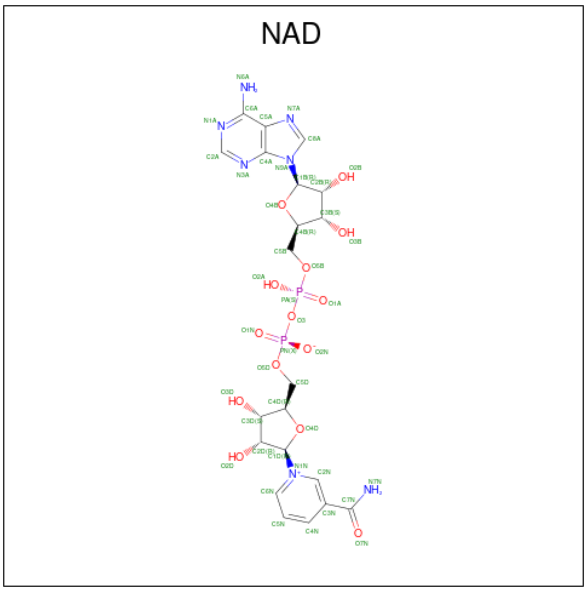
- Molecule 31 is a protein called Putative ribosome-binding factor A, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	a	211	Total	C	H	N	O	S	0	0
			3361	1050	1679	298	325	9		

- Molecule 32 is a protein called 12S rRNA N4-methylcytidine (m4C) methyltransferase.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	b	307	Total	C	H	N	O	S	0	0
			4856	1517	2463	426	437	13		

- Molecule 33 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms						AltConf
33	A	1	Total	C	H	N	O	P	0
			70	21	26	7	14	2	

- Molecule 34 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
34	A	58	Total	Mg	0
			58	58	
34	B	1	Total	Mg	0
			1	1	
34	X	1	Total	Mg	0
			1	1	
34	3	1	Total	Mg	0
			1	1	

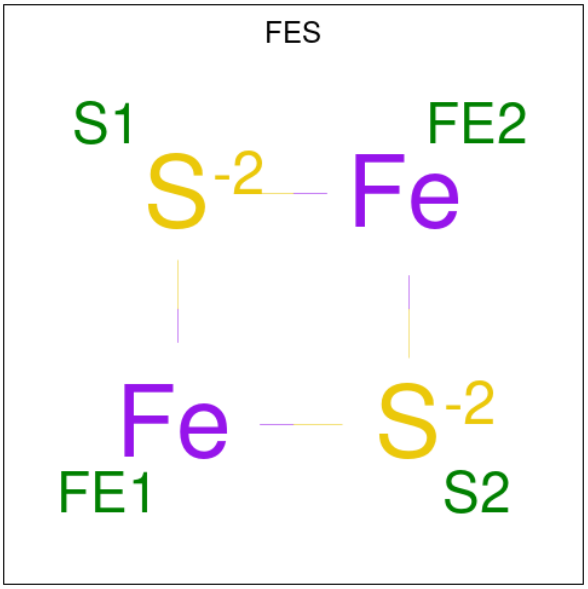
- Molecule 35 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
35	A	20	Total	K	0
			20	20	

- Molecule 36 is ZINC ION (CCD ID: ZN) (formula: Zn).

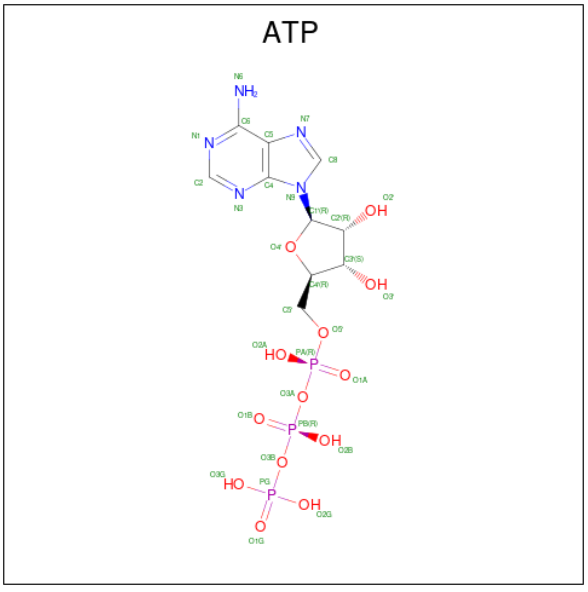
Mol	Chain	Residues	Atoms		AltConf
36	O	1	Total	Zn	0
			1	1	

- Molecule 37 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2) (labeled as "Ligand of Interest" by depositor).



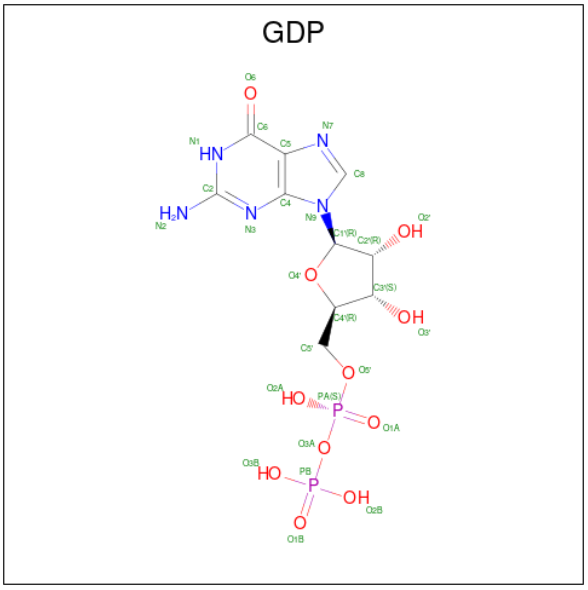
Mol	Chain	Residues	Atoms			AltConf
37	P	1	Total	Fe	S	0
			4	2	2	
37	T	1	Total	Fe	S	0
			4	2	2	

- Molecule 38 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



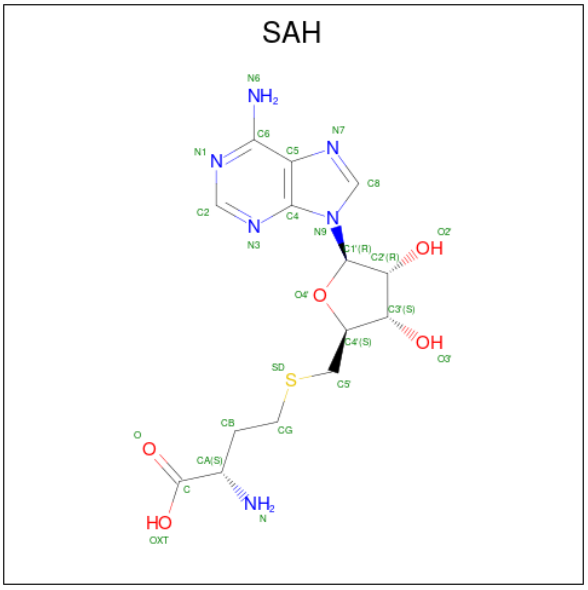
Mol	Chain	Residues	Atoms						AltConf
38	X	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	

- Molecule 39 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms						AltConf
39	X	1	Total	C	H	N	O	P	0
			40	10	12	5	11	2	

- Molecule 40 is S-ADENOSYL-L-HOMOCYSTEINE (CCD ID: SAH) (formula: $C_{14}H_{20}N_6O_5S$).



Mol	Chain	Residues	Atoms						AltConf
40	b	1	Total	C	H	N	O	S	0
			46	14	20	6	5	1	

- Molecule 41 is water.

Mol	Chain	Residues	Atoms		AltConf
41	A	611	Total	O	0
			611	611	
41	B	14	Total	O	0
			14	14	
41	C	30	Total	O	0
			30	30	
41	D	14	Total	O	0
			14	14	
41	E	1	Total	O	0
			1	1	
41	F	5	Total	O	0
			5	5	
41	G	16	Total	O	0
			16	16	
41	H	23	Total	O	0
			23	23	
41	I	3	Total	O	0
			3	3	
41	J	7	Total	O	0
			7	7	
41	K	16	Total	O	0
			16	16	
41	L	10	Total	O	0
			10	10	
41	M	21	Total	O	0
			21	21	
41	N	16	Total	O	0
			16	16	
41	O	9	Total	O	0
			9	9	
41	P	2	Total	O	0
			2	2	
41	Q	5	Total	O	0
			5	5	
41	R	4	Total	O	0
			4	4	
41	S	5	Total	O	0
			5	5	

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Mol	Chain	Residues	Atoms	AltConf
41	T	10	Total O 10 10	0
41	U	4	Total O 4 4	0
41	X	3	Total O 3 3	0
41	Y	6	Total O 6 6	0
41	Z	15	Total O 15 15	0
41	0	7	Total O 7 7	0
41	1	13	Total O 13 13	0
41	3	5	Total O 5 5	0
41	4	4	Total O 4 4	0
41	a	3	Total O 3 3	0

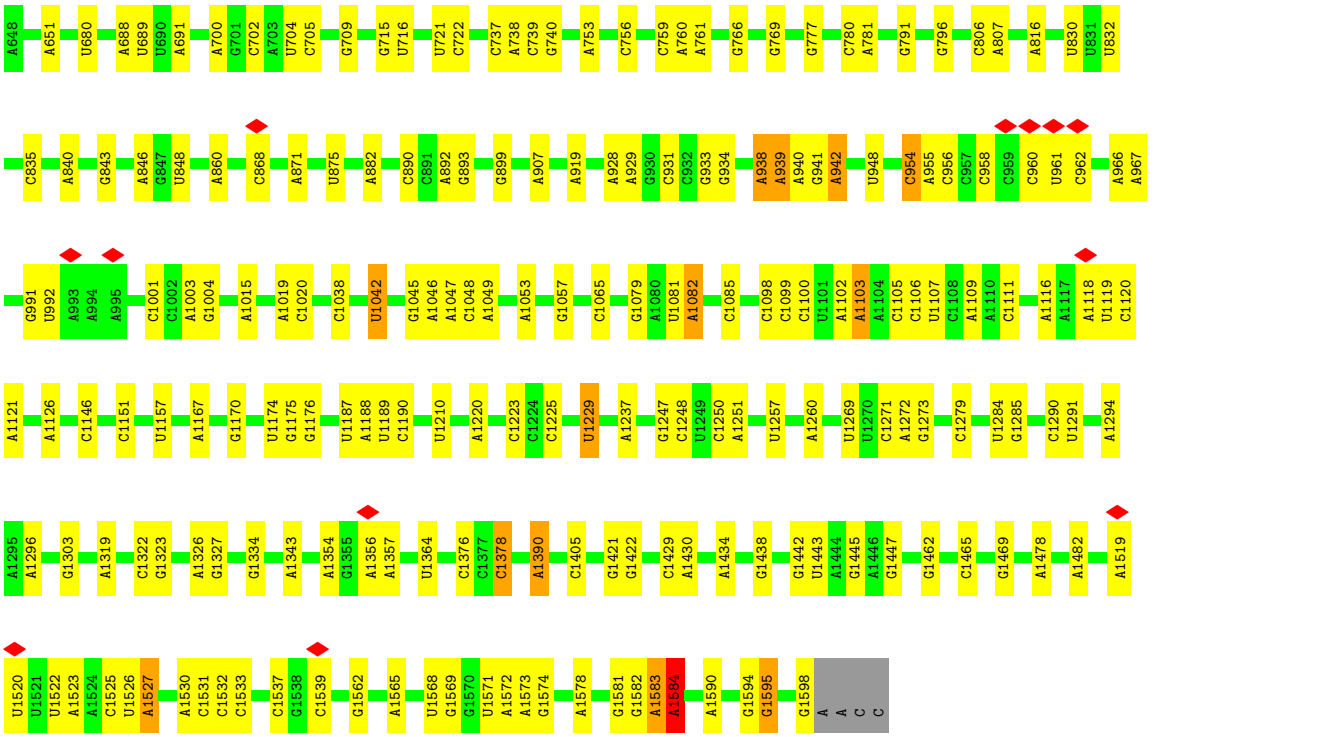
3 Residue-property plots (i)

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:

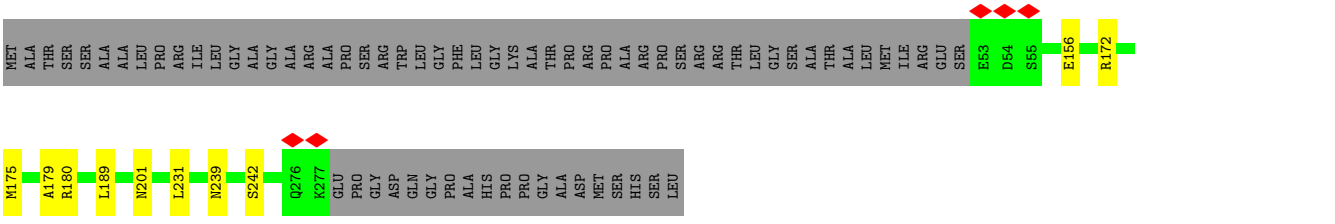




• Molecule 2: 28S ribosomal protein S2, mitochondrial

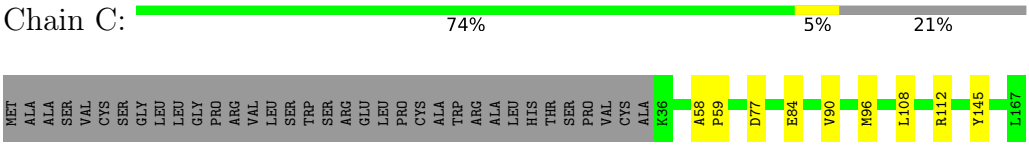
Chain B:





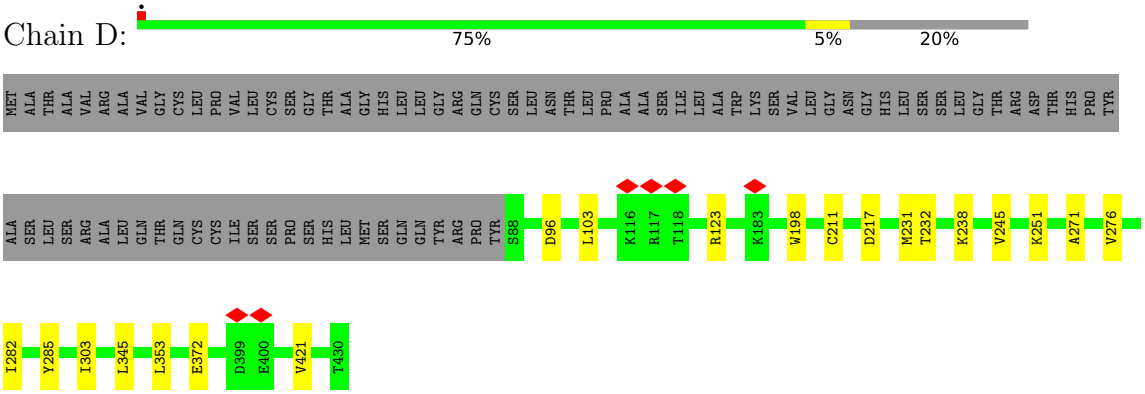
• Molecule 3: 28S ribosomal protein S24, mitochondrial

Chain C:



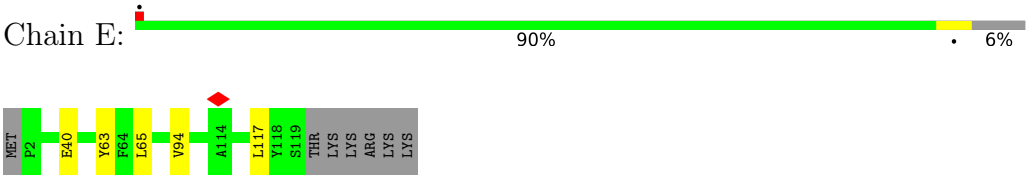
• Molecule 4: 28S ribosomal protein S5, mitochondrial

Chain D:



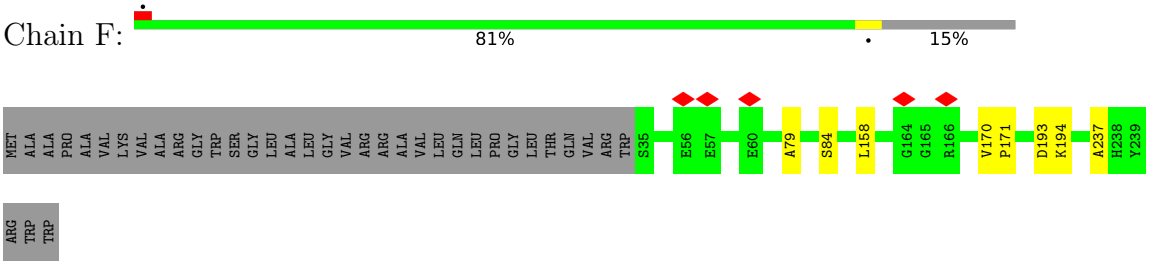
• Molecule 5: 28S ribosomal protein S6, mitochondrial

Chain E:



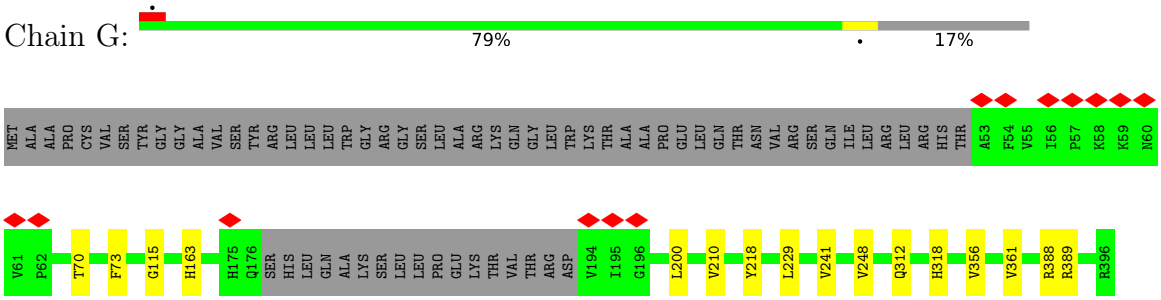
• Molecule 6: 28S ribosomal protein S7, mitochondrial

Chain F:



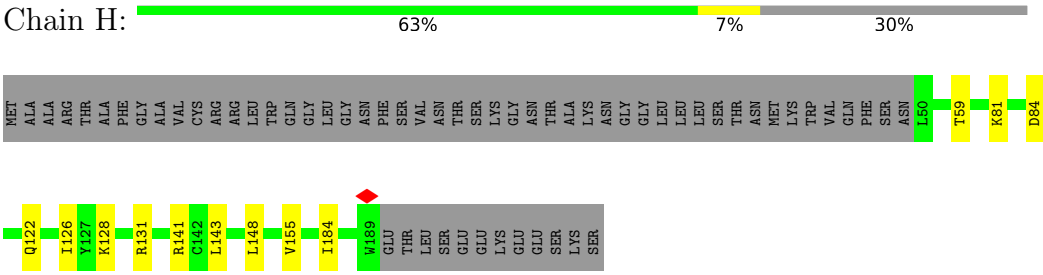
• Molecule 7: 28S ribosomal protein S9, mitochondrial

Chain G:



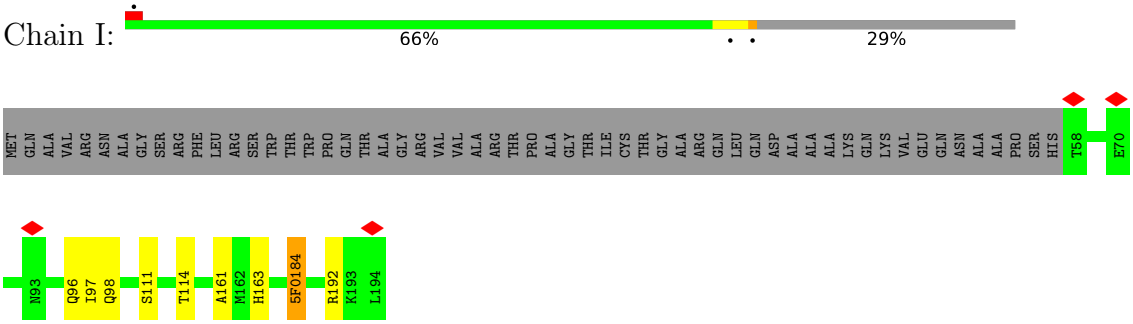
• Molecule 8: 28S ribosomal protein S10, mitochondrial

Chain H:



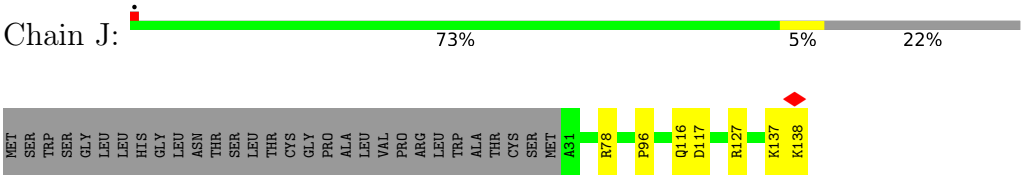
• Molecule 9: 28S ribosomal protein S11, mitochondrial

Chain I:



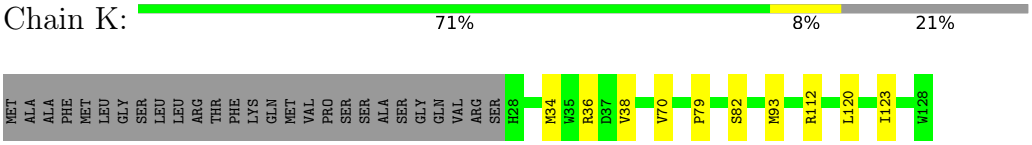
• Molecule 10: 28S ribosomal protein S12, mitochondrial

Chain J:



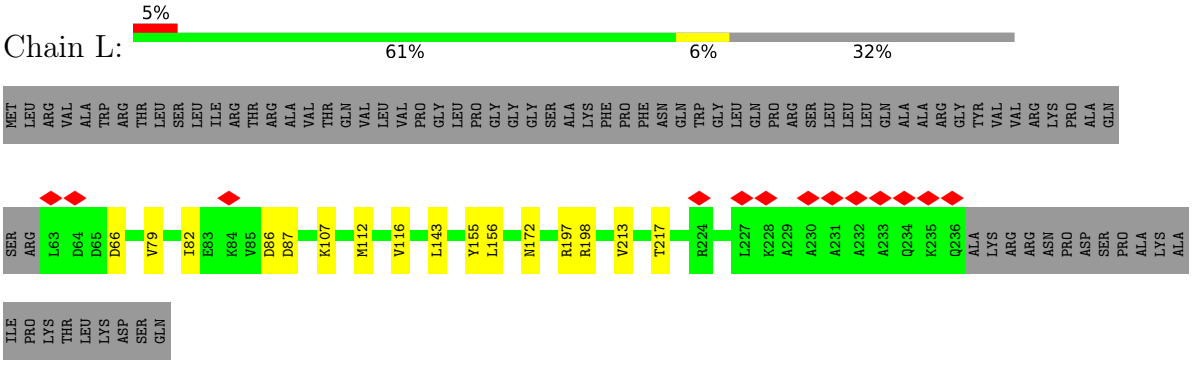
• Molecule 11: 28S ribosomal protein S14, mitochondrial

Chain K:



• Molecule 12: 28S ribosomal protein S15, mitochondrial

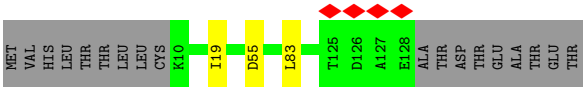
Chain L:



• Molecule 13: 28S ribosomal protein S16, mitochondrial

Chain M:

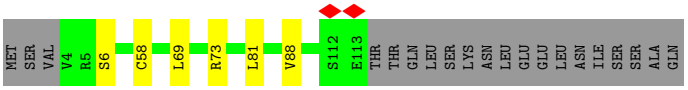




• Molecule 14: 28S ribosomal protein S17, mitochondrial

Chain N:

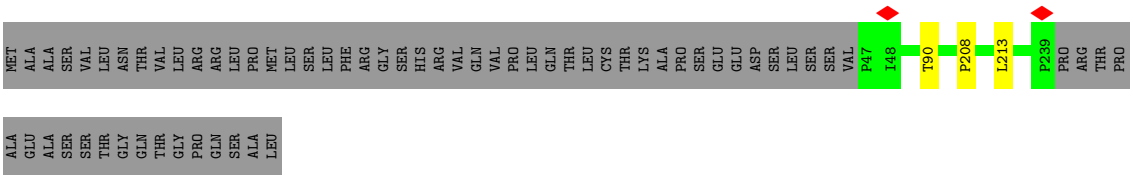




• Molecule 15: 28S ribosomal protein S18b, mitochondrial

Chain O:

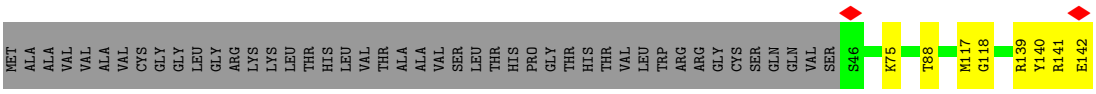




• Molecule 16: 28S ribosomal protein S18c, mitochondrial

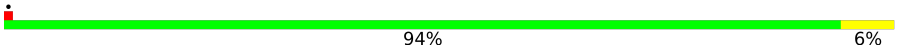
Chain P:

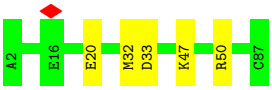




• Molecule 17: 28S ribosomal protein S21, mitochondrial

Chain Q:

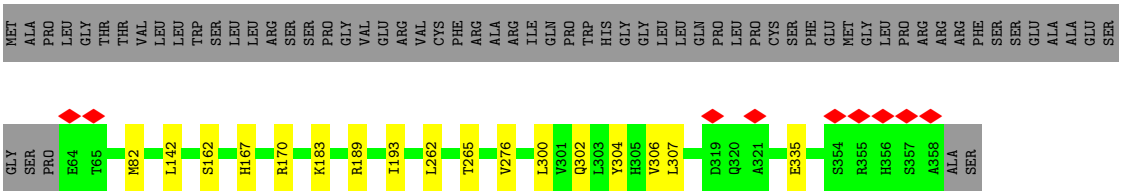




• Molecule 18: 28S ribosomal protein S22, mitochondrial

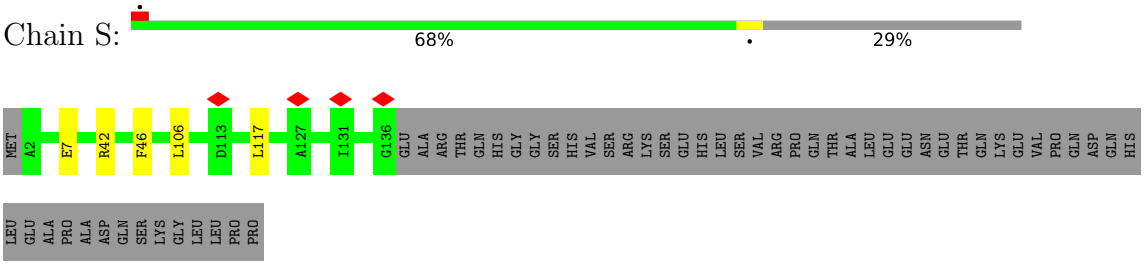
Chain R:





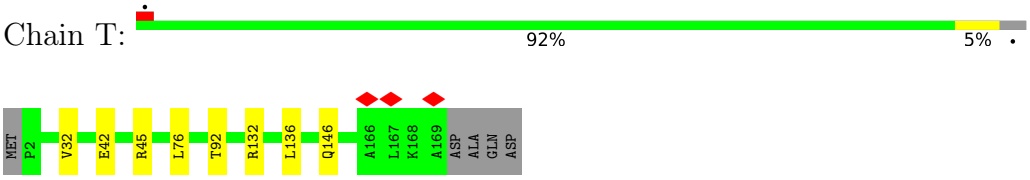
• Molecule 19: 28S ribosomal protein S23, mitochondrial

Chain S:



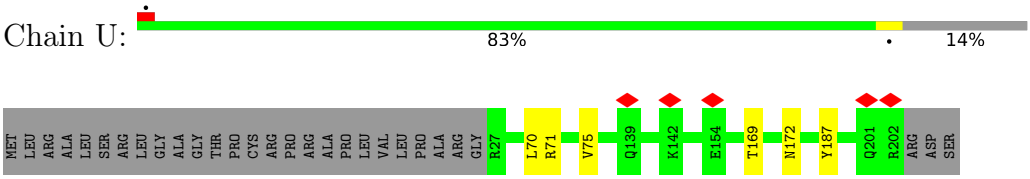
• Molecule 20: 28S ribosomal protein S25, mitochondrial

Chain T:



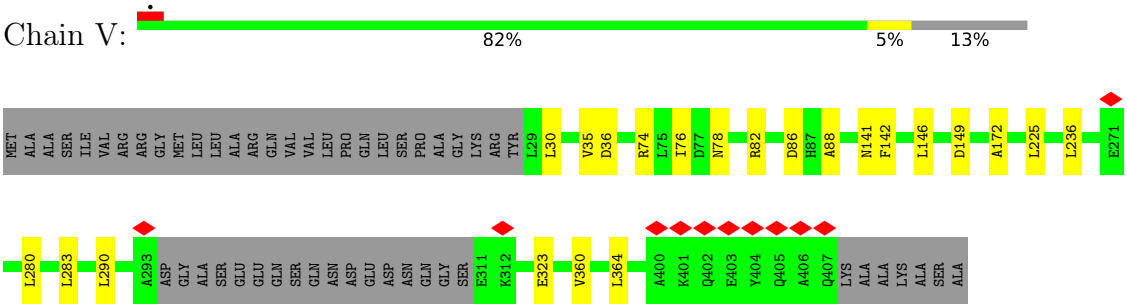
• Molecule 21: 28S ribosomal protein S26, mitochondrial

Chain U:



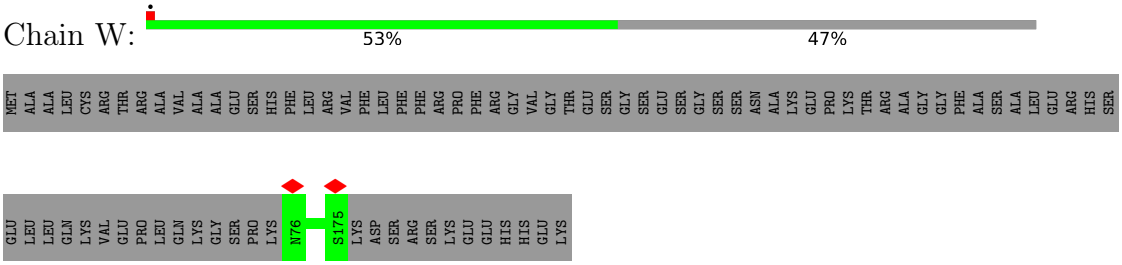
• Molecule 22: 28S ribosomal protein S27, mitochondrial

Chain V:



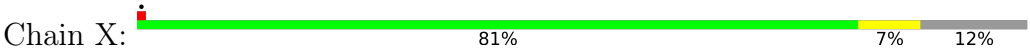
• Molecule 23: 28S ribosomal protein S28, mitochondrial

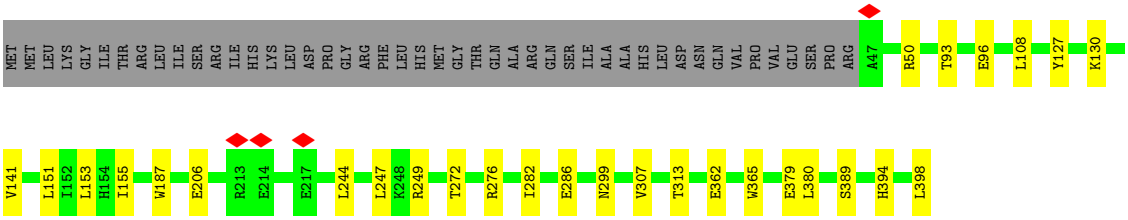
Chain W:



• Molecule 24: 28S ribosomal protein S29, mitochondrial

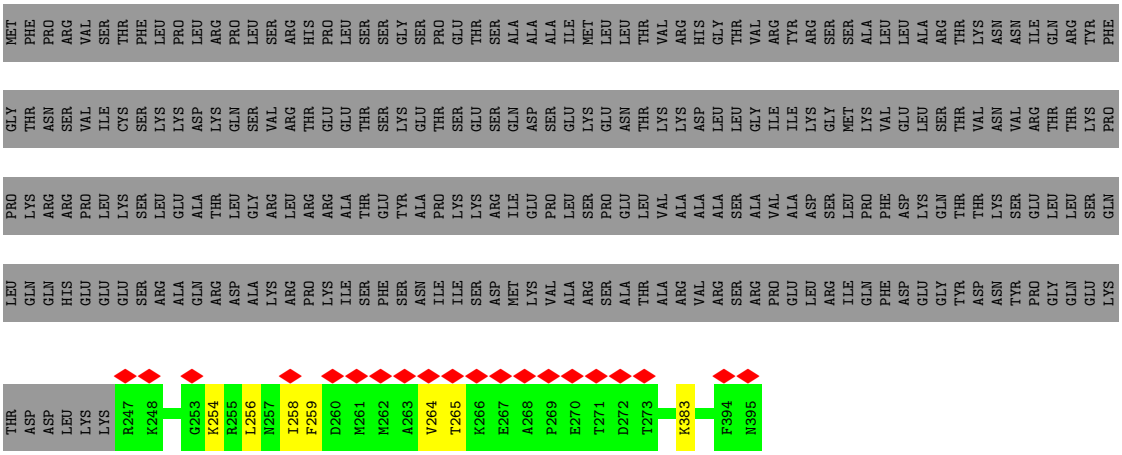
Chain X:





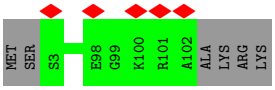
• Molecule 25: 28S ribosomal protein S31, mitochondrial



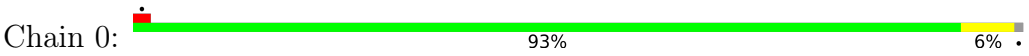


• Molecule 26: 28S ribosomal protein S33, mitochondrial



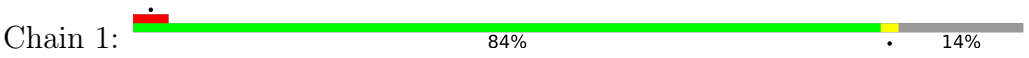


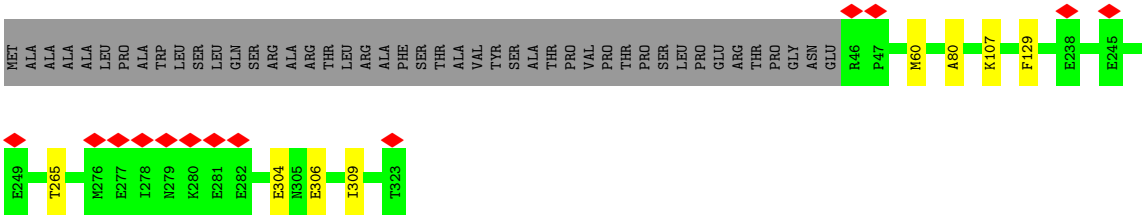
• Molecule 27: 28S ribosomal protein S34, mitochondrial





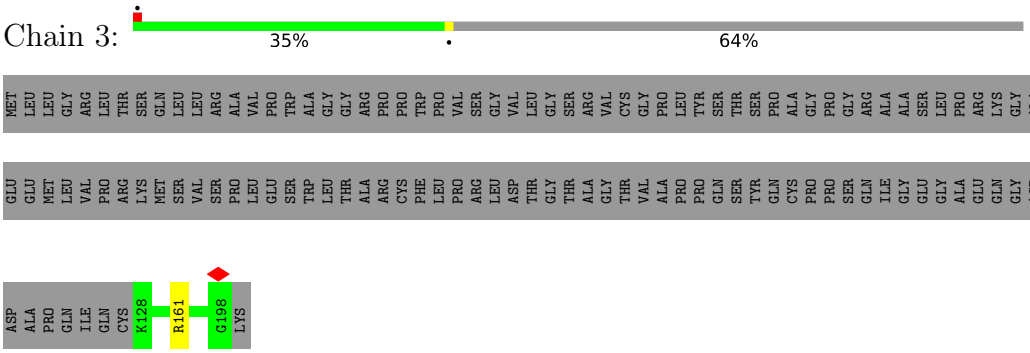
• Molecule 28: 28S ribosomal protein S35, mitochondrial





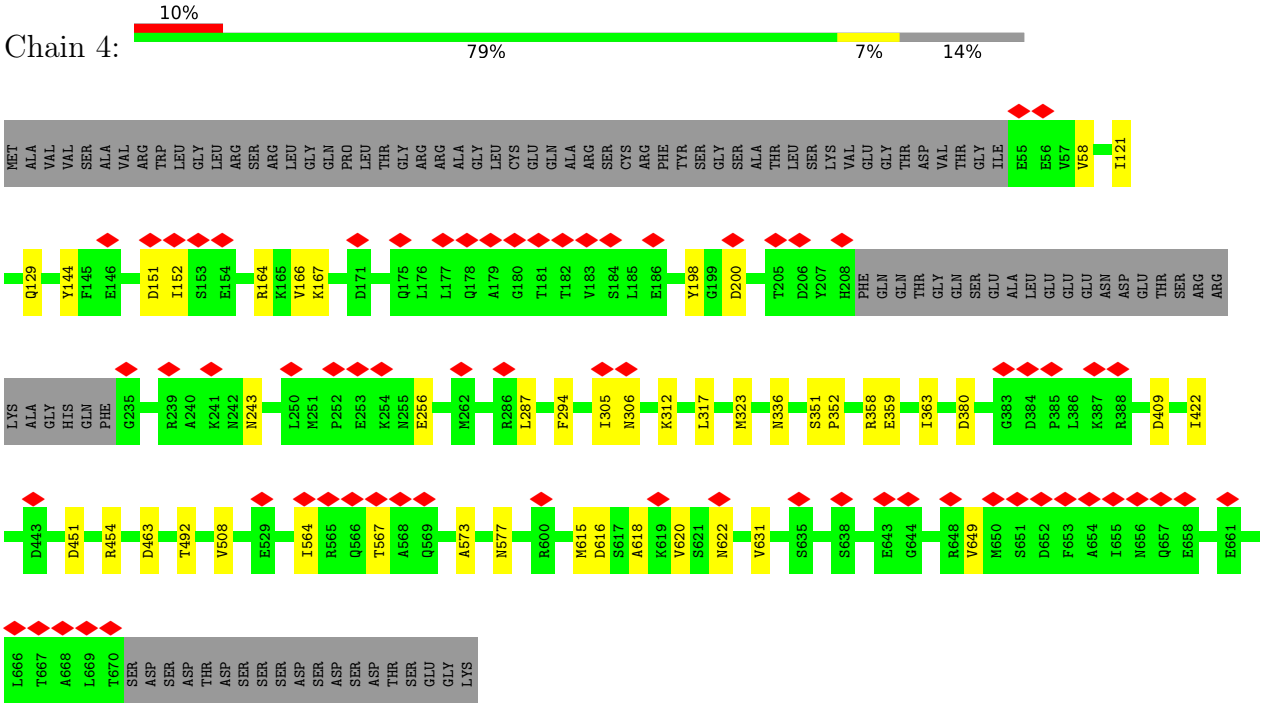
• Molecule 29: Aurora kinase A-interacting protein

Chain 3:



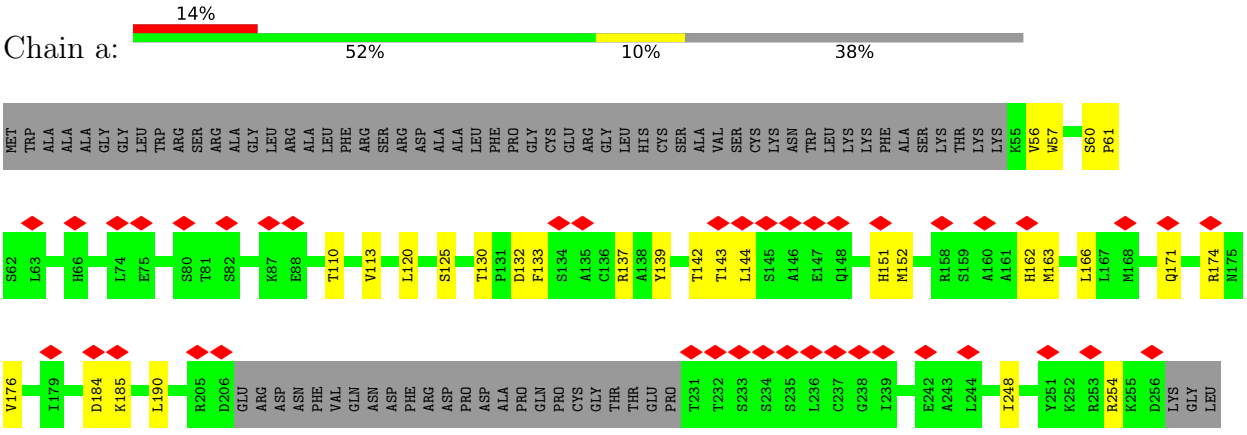
• Molecule 30: Pentatricopeptide repeat domain-containing protein 3, mitochondrial

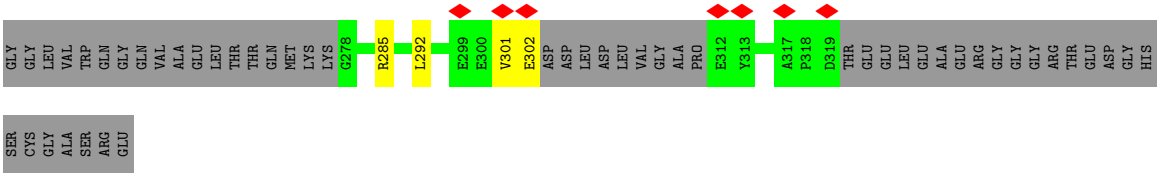
Chain 4:



• Molecule 31: Putative ribosome-binding factor A, mitochondrial

Chain a:

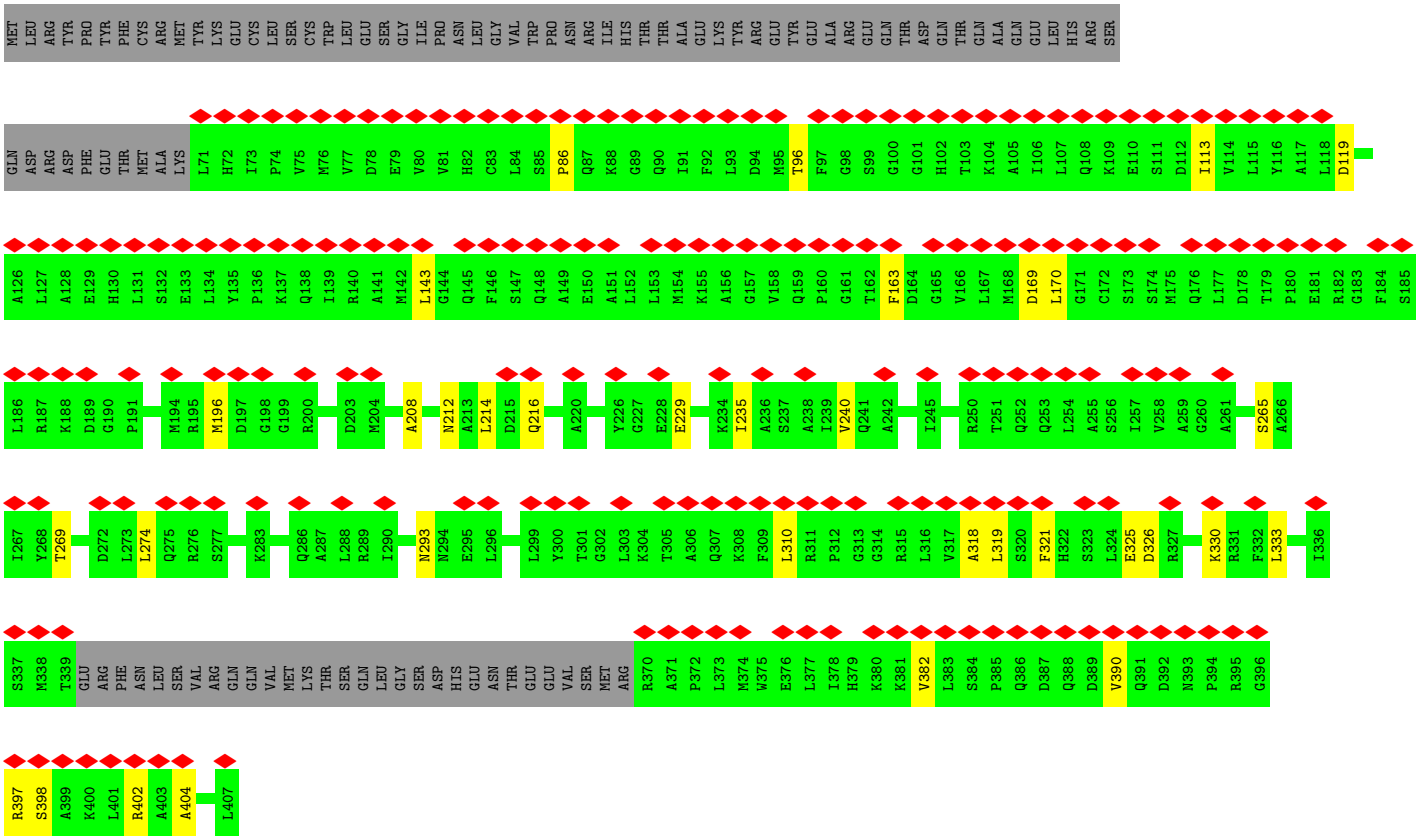




• Molecule 32: 12S rRNA N4-methylcytidine (m4C) methyltransferase

Chain b:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	33779	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	31	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	165000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.470	Depositor
Minimum map value	-0.756	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	388.80002, 388.80002, 388.80002	wwPDB
Map dimensions	540, 540, 540	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.72, 0.72, 0.72	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, 5F0, GDP, NAD, AYA, MG, ZN, K, B8T, 5MC, SAH, FES, ATP, MA6

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	0.12	0/22468	0.20	0/34978
2	B	0.12	0/1871	0.28	0/2531
3	C	0.13	0/1113	0.27	0/1505
4	D	0.12	0/2783	0.27	0/3724
5	E	0.11	0/953	0.27	0/1289
6	F	0.10	0/1846	0.24	0/2482
7	G	0.11	0/2746	0.26	0/3681
8	H	0.14	0/1178	0.27	0/1598
9	I	0.11	0/1030	0.26	0/1386
10	J	0.14	0/855	0.31	0/1148
11	K	0.15	0/880	0.32	0/1182
12	L	0.11	0/1477	0.25	0/1974
13	M	0.14	0/963	0.30	0/1295
14	N	0.13	0/886	0.28	0/1199
15	O	0.11	0/1648	0.27	0/2243
16	P	0.13	0/798	0.30	0/1070
17	Q	0.12	0/748	0.32	0/994
18	R	0.10	0/2456	0.24	0/3317
19	S	0.12	0/1138	0.25	0/1533
20	T	0.12	0/1402	0.27	0/1883
21	U	0.12	0/1510	0.27	0/2025
22	V	0.09	0/3030	0.23	0/4093
23	W	0.11	0/801	0.25	0/1079
24	X	0.11	0/2921	0.26	0/3954
25	Y	0.10	0/1280	0.24	0/1725
26	Z	0.12	0/857	0.26	0/1141
27	0	0.13	0/1834	0.30	0/2484
28	1	0.11	0/2304	0.25	0/3117
29	3	0.13	0/640	0.33	0/844
30	4	0.10	0/4883	0.24	0/6608
31	a	0.12	0/1710	0.28	0/2302
32	b	0.09	0/2436	0.26	0/3287

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
All	All	0.11	0/73445	0.24	0/103671

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	10269	10255	72	0
2	B	1828	1816	1815	7	0
3	C	1083	1089	1088	7	0
4	D	2731	2805	2804	14	0
5	E	936	955	954	5	0
6	F	1804	1869	1868	6	0
7	G	2688	2690	2687	12	0
8	H	1152	1184	1183	13	0
9	I	1020	1061	1053	7	0
10	J	839	888	887	4	0
11	K	862	886	885	7	0
12	L	1453	1541	1540	10	0
13	M	942	966	965	2	0
14	N	868	929	928	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	O	1592	1557	1557	2	0
16	P	781	807	806	7	0
17	Q	744	758	758	6	0
18	R	2409	2429	2428	10	0
19	S	1111	1116	1115	4	0
20	T	1371	1394	1393	5	0
21	U	1488	1500	1499	4	0
22	V	2969	2964	2961	13	0
23	W	789	803	802	0	0
24	X	2849	2845	2843	22	0
25	Y	1246	1198	1197	6	0
26	Z	839	860	858	0	0
27	0	1787	1797	1796	8	0
28	1	2256	2289	2288	8	0
29	3	629	702	702	1	0
30	4	4775	4781	4779	30	0
31	a	1682	1679	1675	28	0
32	b	2393	2463	2457	23	0
33	A	44	26	26	0	0
34	3	1	0	0	0	0
34	A	58	0	0	0	0
34	B	1	0	0	0	0
34	X	1	0	0	0	0
35	A	20	0	0	0	0
36	O	1	0	0	0	0
37	P	4	0	0	0	0
37	T	4	0	0	0	0
38	X	31	12	12	0	0
39	X	28	12	12	0	0
40	b	26	20	19	0	0
41	0	7	0	0	0	0
41	1	13	0	0	1	0
41	3	5	0	0	0	0
41	4	4	0	0	0	0
41	A	611	0	0	12	0
41	B	14	0	0	0	0
41	C	30	0	0	1	0
41	D	14	0	0	1	0
41	E	1	0	0	0	0
41	F	5	0	0	0	0
41	G	16	0	0	0	0
41	H	23	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
41	I	3	0	0	0	0
41	J	7	0	0	0	0
41	K	16	0	0	0	0
41	L	10	0	0	1	0
41	M	21	0	0	0	0
41	N	16	0	0	0	0
41	O	9	0	0	1	0
41	P	2	0	0	0	0
41	Q	5	0	0	0	0
41	R	4	0	0	1	0
41	S	5	0	0	1	0
41	T	10	0	0	0	0
41	U	4	0	0	0	0
41	X	3	0	0	0	0
41	Y	6	0	0	0	0
41	Z	15	0	0	0	0
41	a	3	0	0	1	0
All	All	71215	60960	60895	290	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 (290) 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	1.83	0.79
1:A:899:G:O2'	1:A:907:A:N1	2.16	0.77
30:4:200:ASP:OD2	30:4:243:ASN:N	2.24	0.70
1:A:1573:A:N7	41:A:1809:HOH:O	2.23	0.70
1:A:1003:A:O2'	9:I:96:GLN:OE1	2.09	0.69
1:A:705:C:OP2	27:0:136:TYR:OH	2.09	0.69
1:A:769:G:OP2	14:N:73:ARG:NH2	2.25	0.69
1:A:948:U:OP2	1:A:1045:G:N1	2.25	0.68
1:A:1257:U:O2'	1:A:1260:A:OP2	2.06	0.68
1:A:689:U:OP1	41:A:1802:HOH:O	2.13	0.67
15:O:90:THR:O	41:O:401:HOH:O	2.11	0.67
1:A:939:A:OP1	41:A:1801:HOH:O	2.12	0.66
1:A:1099:C:N3	41:A:1818:HOH:O	2.29	0.66
1:A:691:A:N7	1:A:716:U:O2'	2.28	0.66
1:A:942:A:N6	1:A:1047:A:OP2	2.29	0.65
12:L:172:ASN:OD1	41:L:301:HOH:O	2.14	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1038:C:HO2'	12:L:155:TYR:HH	1.44	0.64
1:A:1046:A:O2'	1:A:1048:C:OP2	2.13	0.64
1:A:1157:U:OP2	41:A:1803:HOH:O	2.15	0.64
1:A:1378:C:O2	24:X:389:SER:OG	2.15	0.63
1:A:1429:C:OP1	7:G:388:ARG:NH2	2.32	0.63
1:A:1085:C:OP1	9:I:192:ARG:NE	2.32	0.62
1:A:1102:A:OP1	41:A:1804:HOH:O	2.16	0.61
32:b:163:PHE:O	32:b:310:LEU:HD12	2.01	0.61
27:0:41:LEU:HD13	27:0:55:TRP:CG	2.35	0.61
9:I:163:HIS:CE1	31:a:144:LEU:HD22	2.35	0.61
1:A:1272:A:N1	1:A:1303:G:O2'	2.31	0.60
1:A:941:G:O2'	1:A:1109:A:OP2	2.18	0.60
1:A:840:A:N7	41:A:1822:HOH:O	2.31	0.60
30:4:564:ILE:HG22	30:4:567:THR:HB	1.84	0.60
32:b:86:PRO:HB3	32:b:113:ILE:HD12	1.84	0.59
32:b:265:SER:O	32:b:269:THR:HG23	2.02	0.59
24:X:380:LEU:HD21	24:X:398:LEU:HD12	1.83	0.59
27:0:42:THR:HG22	27:0:49:ARG:HG2	1.83	0.59
19:S:42:ARG:O	41:S:201:HOH:O	2.17	0.59
1:A:1443:U:O2'	1:A:1445:G:N7	2.29	0.59
18:R:262:LEU:O	18:R:265:THR:OG1	2.18	0.59
6:F:79:ALA:O	7:G:312:GLN:NE2	2.35	0.58
13:M:55:ASP:OD2	20:T:146:GLN:NE2	2.35	0.58
32:b:196:MET:SD	32:b:293:ASN:ND2	2.77	0.58
1:A:1530:A:N1	1:A:1531:C:N4	2.50	0.58
7:G:210:VAL:HG12	7:G:210:VAL:O	2.03	0.58
1:A:1049:A:OP1	12:L:198:ARG:NE	2.36	0.58
1:A:1279:C:O2'	1:A:1296:A:N1	2.30	0.57
31:a:130:THR:HG22	31:a:137:ARG:NH1	2.19	0.57
32:b:321:PHE:O	32:b:398:SER:OG	2.22	0.57
1:A:1364:U:O2'	1:A:1390:A:OP1	2.21	0.56
4:D:285:TYR:OH	4:D:372:GLU:OE2	2.17	0.56
3:C:90:VAL:HG21	11:K:93:MET:HE1	1.86	0.56
30:4:129:GLN:NE2	30:4:144:TYR:OH	2.37	0.55
1:A:843:G:N2	1:A:846:A:OP2	2.38	0.55
31:a:130:THR:HG22	31:a:137:ARG:CZ	2.36	0.55
22:V:236:LEU:HD12	22:V:290:LEU:HD13	1.88	0.54
24:X:108:LEU:HD23	24:X:141:VAL:HG21	1.89	0.54
1:A:1079:G:N2	1:A:1562:G:O3'	2.39	0.54
6:F:170[B]:VAL:HG13	6:F:237:ALA:HA	1.89	0.54
3:C:112:ARG:O	41:C:202:HOH:O	2.19	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:b:119:ASP:O	32:b:143:LEU:HD12	2.07	0.54
32:b:321:PHE:N	32:b:325:GLU:OE1	2.41	0.54
30:4:451:ASP:OD1	30:4:454:ARG:NH1	2.41	0.53
12:L:86:ASP:OD1	12:L:87:ASP:N	2.41	0.53
24:X:276:ARG:NH2	24:X:286:GLU:OE1	2.42	0.53
30:4:336:ASN:ND2	30:4:409:ASP:OD2	2.38	0.53
32:b:318:ALA:C	32:b:319:LEU:HD12	2.34	0.53
2:B:156:GLU:OE1	7:G:163:HIS:ND1	2.39	0.53
5:E:117:LEU:HD13	31:a:56:VAL:CG2	2.38	0.53
30:4:151:ASP:OD1	30:4:152:ILE:N	2.41	0.53
1:A:1146:C:OP1	29:3:161:ARG:NH1	2.39	0.53
31:a:56:VAL:HG12	31:a:57:TRP:H	1.74	0.53
31:a:163:MET:HA	31:a:166:LEU:HD12	1.91	0.53
31:a:120:LEU:HD22	31:a:152:MET:CG	2.39	0.53
31:a:162:HIS:CE1	31:a:166:LEU:HD11	2.44	0.53
19:S:106:LEU:HB2	19:S:117:LEU:HD11	1.91	0.52
22:V:141:ASN:ND2	22:V:172:ALA:O	2.36	0.52
1:A:966:A:N3	41:A:1825:HOH:O	2.34	0.52
31:a:56:VAL:HG12	31:a:57:TRP:N	2.24	0.52
25:Y:259:PHE:HB2	30:4:363:ILE:HD11	1.92	0.52
32:b:318:ALA:O	32:b:319:LEU:HD12	2.09	0.52
27:0:54:ALA:O	27:0:58:VAL:HG23	2.09	0.52
1:A:1004:G:O2'	9:I:98:GLN:NE2	2.42	0.52
14:N:6:SER:OG	14:N:69:LEU:O	2.26	0.52
32:b:382:VAL:HG11	32:b:402:ARG:CZ	2.40	0.52
1:A:875:U:O2'	1:A:882:A:N1	2.37	0.51
1:A:1210:U:O2'	31:a:254:ARG:NH1	2.44	0.51
5:E:40:GLU:OE1	21:U:187:TYR:OH	2.28	0.51
8:H:92:GLU:OE1	8:H:141:ARG:NH1	2.42	0.51
1:A:760:A:N1	1:A:780:C:O2'	2.36	0.51
18:R:189:ARG:NH2	41:R:401:HOH:O	2.41	0.51
1:A:1057:G:H4'	1:A:1578:A:H4'	1.93	0.51
6:F:158[A]:LEU:HD23	6:F:171[A]:PRO:HA	1.91	0.51
24:X:380:LEU:HD21	24:X:398:LEU:CD1	2.41	0.51
32:b:382:VAL:HG23	32:b:382:VAL:O	2.10	0.51
7:G:229:LEU:HD21	7:G:241:VAL:HG11	1.93	0.51
11:K:34:MET:O	11:K:38:VAL:HG23	2.10	0.51
18:R:162:SER:O	18:R:170:ARG:NH1	2.43	0.51
30:4:631:VAL:HG21	30:4:649:VAL:HG21	1.92	0.50
4:D:198:TRP:CD2	31:a:292:LEU:HD13	2.46	0.50
24:X:299:ASN:ND2	28:1:265:THR:OG1	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:151:LEU:HD23	24:X:247:LEU:HD22	1.93	0.50
30:4:256:GLU:HG3	30:4:287:LEU:HD22	1.94	0.50
31:a:120:LEU:HD21	31:a:151:HIS:ND1	2.27	0.50
1:A:934:G:O2'	1:A:940:A:N1	2.36	0.50
1:A:1595:G:O6	17:Q:50:ARG:NH2	2.44	0.49
15:O:208:PRO:HG2	15:O:213:LEU:HD21	1.95	0.49
21:U:169:THR:N	21:U:172:ASN:OD1	2.43	0.49
22:V:35:VAL:HG12	22:V:35:VAL:O	2.11	0.49
1:A:929:A:H1'	4:D:421:VAL:HG22	1.94	0.49
4:D:245:VAL:HG22	4:D:271:ALA:HB1	1.94	0.49
7:G:200:LEU:O	7:G:218:TYR:OH	2.23	0.49
31:a:285:ARG:NH1	41:a:401:HOH:O	2.46	0.49
8:H:148:LEU:HD23	8:H:148:LEU:H	1.78	0.49
20:T:132:ARG:NH1	20:T:136:LEU:O	2.46	0.49
30:4:631:VAL:CG2	30:4:649:VAL:HG21	2.42	0.48
32:b:216:GLN:CG	32:b:240:VAL:HG21	2.43	0.48
1:A:954:C:O2	1:A:1111:C:O2'	2.29	0.48
22:V:225:LEU:HD11	22:V:283:LEU:HD22	1.96	0.48
5:E:94:VAL:CG1	16:P:117:MET:HE1	2.44	0.48
24:X:50:ARG:NE	24:X:362:GLU:OE1	2.46	0.48
2:B:179:ALA:CB	2:B:189:LEU:HD21	2.43	0.48
24:X:151:LEU:CD2	24:X:247:LEU:HD22	2.44	0.48
13:M:19:ILE:HB	13:M:83:LEU:HD23	1.96	0.48
31:a:301:VAL:O	31:a:302:GLU:C	2.57	0.48
31:a:184:ASP:O	31:a:185:LYS:HB3	2.14	0.48
7:G:318:HIS:NE2	24:X:379:GLU:OE2	2.47	0.48
32:b:216:GLN:HG3	32:b:240:VAL:HG21	1.94	0.48
2:B:180:ARG:NH1	4:D:211:CYS:SG	2.86	0.47
7:G:70:THR:HG23	7:G:73:PHE:H	1.79	0.47
10:J:116:GLN:OE1	10:J:116:GLN:N	2.42	0.47
31:a:60:SER:N	31:a:61:PRO:HD3	2.29	0.47
31:a:113:VAL:HG13	31:a:166:LEU:HD13	1.95	0.47
8:H:155:VAL:HG21	28:1:129:PHE:CB	2.44	0.47
30:4:615:MET:CE	30:4:649:VAL:HG22	2.44	0.47
9:I:111:SER:OG	9:I:114:THR:HG23	2.14	0.47
3:C:58:ALA:HB1	3:C:59:PRO:CD	2.44	0.47
16:P:88:THR:OG1	17:Q:33:ASP:OD2	2.22	0.47
20:T:42:GLU:OE1	20:T:45:ARG:NH2	2.46	0.47
24:X:153:LEU:HD21	24:X:244:LEU:HD22	1.97	0.47
25:Y:264:VAL:HG12	25:Y:265:THR:N	2.29	0.47
30:4:463:ASP:OD1	30:4:492:THR:HG22	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:4:573:ALA:O	30:4:577:ASN:ND2	2.46	0.47
1:A:1590:A:OP2	17:Q:47:LYS:NZ	2.36	0.47
8:H:108:VAL:HG22	8:H:143:LEU:HD23	1.97	0.47
18:R:276:VAL:HG11	18:R:307:LEU:HD12	1.97	0.47
24:X:272:THR:OG1	24:X:282:ILE:O	2.31	0.47
30:4:58:VAL:HG23	30:4:58:VAL:O	2.15	0.47
30:4:618:ALA:O	30:4:622:ASN:N	2.48	0.47
11:K:120:LEU:HB3	11:K:123:ILE:HD12	1.97	0.47
4:D:282:ILE:HD12	4:D:353:LEU:HB3	1.97	0.46
12:L:213:VAL:O	12:L:217:THR:HG23	2.15	0.46
31:a:171:GLN:O	31:a:174:ARG:NH1	2.39	0.46
1:A:1176:G:OP2	41:A:1807:HOH:O	2.21	0.46
19:S:7:GLU:OE1	19:S:7:GLU:N	2.43	0.46
24:X:108:LEU:HD21	24:X:307:VAL:CG1	2.46	0.46
30:4:615:MET:HE1	30:4:649:VAL:HG22	1.96	0.46
31:a:176:VAL:O	31:a:176:VAL:HG13	2.15	0.46
32:b:333:LEU:HD22	32:b:404:ALA:HB3	1.98	0.46
28:1:60:MET:HE1	28:1:80:ALA:O	2.16	0.46
32:b:333:LEU:HD22	32:b:404:ALA:CB	2.46	0.46
1:A:928:A:N3	4:D:421:VAL:HG11	2.31	0.46
27:0:119:THR:OG1	27:0:124:THR:HG22	2.16	0.46
32:b:208:ALA:O	32:b:212:ASN:ND2	2.49	0.46
32:b:229:GLU:CD	32:b:235:ILE:HD12	2.39	0.46
6:F:237:ALA:HB3	31:a:190:LEU:HD13	1.97	0.46
31:a:120:LEU:HD22	31:a:152:MET:HG3	1.98	0.46
31:a:120:LEU:HD22	31:a:152:MET:HG2	1.96	0.45
1:A:1229:U:O2'	1:A:1442:G:O4'	2.34	0.45
31:a:110:THR:HG23	31:a:110:THR:O	2.16	0.45
1:A:1523:A:O2'	1:A:1527:A:N1	2.36	0.45
1:A:1103:A:N7	1:A:1574:G:O2'	2.45	0.45
1:A:1319:A:N3	41:A:1832:HOH:O	2.36	0.45
7:G:248:VAL:O	7:G:248:VAL:HG13	2.17	0.45
4:D:303:ILE:CD1	4:D:345:LEU:HD12	2.47	0.45
18:R:302:GLN:O	18:R:306:VAL:HG23	2.16	0.45
1:A:1269:U:O2	41:A:1805:HOH:O	2.18	0.45
14:N:58:CYS:SG	14:N:81:LEU:HD22	2.57	0.45
12:L:143:LEU:HD12	12:L:156:LEU:HD22	1.98	0.45
22:V:30:LEU:HD12	22:V:149:ASP:HB2	1.98	0.45
1:A:715:G:O2'	1:A:816:A:O2'	2.29	0.44
1:A:1569:G:OP2	1:A:1572:A:O2'	2.36	0.44
22:V:236:LEU:HD21	22:V:323:GLU:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:206:GLU:OE2	24:X:249:ARG:NH2	2.50	0.44
32:b:326:ASP:O	32:b:330:LYS:N	2.42	0.44
2:B:231:LEU:HD21	19:S:46:PHE:HB2	2.00	0.44
6:F:193:ASP:OD1	6:F:194:LYS:N	2.51	0.44
16:P:140:TYR:OH	17:Q:33:ASP:OD1	2.20	0.44
20:T:32:VAL:HG22	20:T:76:LEU:HD22	1.99	0.44
20:T:92:THR:O	20:T:92:THR:HG22	2.17	0.44
1:A:702:C:OP1	1:A:848:U:O2'	2.35	0.44
24:X:50:ARG:NH2	24:X:96:GLU:OE2	2.43	0.44
31:a:132:ASP:O	31:a:133:PHE:HB2	2.18	0.44
3:C:96:MET:HB2	3:C:108:LEU:HD11	1.99	0.44
25:Y:258:ILE:HD11	30:4:317:LEU:HD22	1.99	0.44
8:H:148:LEU:HD23	8:H:148:LEU:N	2.32	0.44
18:R:167:HIS:HB3	18:R:193:ILE:HD13	1.98	0.44
2:B:172:ARG:O	2:B:175:MET:HG2	2.17	0.44
4:D:103:LEU:HD11	4:D:123:ARG:HB2	1.99	0.44
18:R:170:ARG:O	18:R:189:ARG:NH1	2.47	0.44
24:X:127:TYR:HH	28:1:306:GLU:CD	2.26	0.44
1:A:781:A:N1	12:L:197:ARG:NH2	2.63	0.44
8:H:184:ILE:O	8:H:184:ILE:HG22	2.18	0.44
30:4:294:PHE:HB3	30:4:323:MET:HE2	1.99	0.44
1:A:1322:C:H2'	1:A:1323:G:O4'	2.18	0.44
2:B:239:ASN:ND2	2:B:242:SER:OG	2.51	0.44
11:K:70:VAL:HG11	25:Y:383:LYS:HE3	2.00	0.44
31:a:143:THR:HG22	31:a:144:LEU:N	2.33	0.44
32:b:390:VAL:HG13	32:b:397:ARG:HB2	2.00	0.44
9:I:97:ILE:HD11	9:I:161:ALA:HB1	2.00	0.43
27:0:37:ASP:O	27:0:41:LEU:N	2.48	0.43
1:A:938:A:H5"	1:A:1170:G:H4'	1.99	0.43
1:A:1237:A:OP1	11:K:36:ARG:NH2	2.41	0.43
25:Y:256:LEU:HD12	30:4:359:GLU:OE1	2.18	0.43
28:1:304:GLU:OE1	28:1:309:ILE:HD11	2.18	0.43
30:4:200:ASP:OD1	30:4:200:ASP:N	2.51	0.43
32:b:96:THR:HG21	32:b:169:ASP:O	2.18	0.43
24:X:93:THR:HG21	24:X:365:TRP:CZ3	2.53	0.43
24:X:380:LEU:HD23	24:X:394:HIS:CD2	2.53	0.43
1:A:1175:G:O2'	1:A:1482:A:N1	2.51	0.43
8:H:122:GLN:O	11:K:112:ARG:NH1	2.51	0.43
30:4:305:ILE:O	30:4:312:LYS:NZ	2.48	0.43
1:A:1532:C:O4'	27:0:21:LEU:HD21	2.18	0.43
1:A:806:C:OP2	1:A:807:A:N6	2.40	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1562:G:O2'	1:A:1583:MA6:N1	2.52	0.43
7:G:356:VAL:HG23	7:G:361:VAL:HG23	2.00	0.43
22:V:225:LEU:HD21	22:V:280:LEU:HD23	2.01	0.43
16:P:141:ARG:O	16:P:142:GLU:C	2.61	0.43
31:a:142:THR:HG22	31:a:143:THR:N	2.33	0.43
32:b:169:ASP:OD1	32:b:170:LEU:N	2.52	0.43
4:D:232:THR:HG21	4:D:238:LYS:HD3	2.01	0.42
6:F:84:SER:OG	24:X:379:GLU:OE1	2.36	0.42
9:I:163:HIS:NE2	17:Q:20:GLU:OE1	2.45	0.42
21:U:70:LEU:CD2	27:0:191:LEU:HD11	2.49	0.42
5:E:63:TYR:OH	16:P:118:GLY:O	2.23	0.42
3:C:145:TYR:CG	30:4:121:ILE:HD13	2.54	0.42
4:D:217:ASP:OD2	4:D:251:LYS:NZ	2.44	0.42
14:N:88:VAL:O	14:N:88:VAL:HG13	2.19	0.42
1:A:1581:G:N2	1:A:1584:MA6:OP2	2.48	0.42
18:R:304:TYR:OH	18:R:335:GLU:OE1	2.32	0.42
22:V:360:VAL:HG13	22:V:364:LEU:HD22	2.00	0.42
30:4:164:ARG:NH1	30:4:198:TYR:OH	2.52	0.42
8:H:59:THR:O	8:H:59:THR:HG23	2.20	0.42
1:A:1081:U:H5'	1:A:1082:A:O5'	2.20	0.42
1:A:1334:G:OP2	41:A:1808:HOH:O	2.22	0.42
4:D:303:ILE:HD11	4:D:345:LEU:HD12	2.01	0.42
22:V:74:ARG:O	22:V:78:ASN:ND2	2.51	0.42
24:X:155:ILE:HD13	24:X:187:TRP:HE1	1.84	0.42
10:J:96:PRO:O	10:J:127:ARG:NH2	2.45	0.42
16:P:139:ARG:O	17:Q:32:MET:HE1	2.20	0.42
30:4:380:ASP:HB2	30:4:422:ILE:HD11	2.01	0.42
30:4:305:ILE:HG22	30:4:306:ASN:N	2.34	0.42
1:A:700:A:N1	1:A:709:G:O2'	2.44	0.42
12:L:66:ASP:OD1	12:L:107:LYS:NZ	2.42	0.42
1:A:1434:A:OP1	7:G:389:ARG:NE	2.52	0.41
3:C:77:ASP:O	8:H:81:LYS:NZ	2.44	0.41
4:D:96:ASP:OD2	41:D:501:HOH:O	2.22	0.41
5:E:65:LEU:HD21	16:P:75:LYS:HD3	2.02	0.41
22:V:76:ILE:HD13	22:V:88:ALA:HB1	2.01	0.41
30:4:616:ASP:O	30:4:620:VAL:HG23	2.20	0.41
30:4:351:SER:HB3	30:4:352:PRO:HD3	2.02	0.41
1:A:1294:A:OP1	2:B:201:ASN:ND2	2.53	0.41
1:A:1174:U:O2'	4:D:231:MET:O	2.39	0.41
30:4:166:VAL:HG23	30:4:167:LYS:N	2.36	0.41
30:4:508:VAL:O	30:4:508:VAL:HG12	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1583:MA6:N6	1:A:1584:MA6:H103	2.36	0.41
3:C:84:GLU:OE1	3:C:84:GLU:N	2.51	0.41
25:Y:254:LYS:O	30:4:358:ARG:NH1	2.54	0.41
31:a:248:ILE:HG23	32:b:214:LEU:HD21	2.03	0.41
8:H:155:VAL:HG21	28:1:129:PHE:HB3	2.03	0.41
22:V:236:LEU:HD21	22:V:323:GLU:CB	2.51	0.41
8:H:128:LYS:O	8:H:131:ARG:NE	2.46	0.41
11:K:79:PRO:O	11:K:82:SER:OG	2.24	0.41
18:R:82:MET:HE1	18:R:300:LEU:HD13	2.02	0.41
24:X:130:LYS:NZ	24:X:313:THR:OG1	2.42	0.41
32:b:274:LEU:HG	32:b:274:LEU:O	2.20	0.41
22:V:142:PHE:CE1	22:V:146:LEU:HD11	2.56	0.41
1:A:1053:A:N1	1:A:1100:C:O2'	2.50	0.40
1:A:1478:A:N1	1:A:1565:A:O2'	2.48	0.40
1:A:1581:G:H2'	1:A:1583:MA6:OP2	2.21	0.40
7:G:115:GLY:N	8:H:84:ASP:OD2	2.54	0.40
10:J:78:ARG:NE	10:J:117:ASP:OD2	2.51	0.40
12:L:79:VAL:HG21	12:L:82:ILE:HD13	2.04	0.40
22:V:82:ARG:NH2	22:V:86:ASP:OD1	2.52	0.40
24:X:108:LEU:HD21	24:X:307:VAL:HG13	2.03	0.40
1:A:756:C:O2'	1:A:759:C:OP1	2.31	0.40
1:A:955:A:O4'	1:A:1042:U:H1'	2.22	0.40
10:J:137:LYS:O	10:J:138:LYS:C	2.64	0.40
18:R:142:LEU:HD21	18:R:183:LYS:HE3	2.02	0.40
8:H:155:VAL:HG21	28:1:129:PHE:HB2	2.04	0.40
31:a:125:SER:N	31:a:139:TYR:O	2.54	0.40
21:U:71:ARG:O	21:U:75:VAL:HG23	2.21	0.40
28:1:107:LYS:O	41:1:401:HOH:O	2.22	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%)	211 (97%)	7 (3%)	0	100	100
7	G	323/396 (82%)	319 (99%)	4 (1%)	0	100	100
8	H	138/201 (69%)	136 (99%)	1 (1%)	1 (1%)	18	45
9	I	134/194 (69%)	132 (98%)	2 (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%)	93 (98%)	2 (2%)	0	100	100
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%)	346 (99%)	4 (1%)	0	100	100
25	Y	147/395 (37%)	146 (99%)	1 (1%)	0	100	100
26	Z	98/106 (92%)	96 (98%)	2 (2%)	0	100	100
27	0	213/218 (98%)	212 (100%)	1 (0%)	0	100	100
28	1	276/323 (85%)	271 (98%)	5 (2%)	0	100	100
29	3	69/199 (35%)	69 (100%)	0	0	100	100
30	4	586/689 (85%)	580 (99%)	6 (1%)	0	100	100
31	a	203/343 (59%)	196 (97%)	7 (3%)	0	100	100
32	b	303/407 (74%)	295 (97%)	8 (3%)	0	100	100
All	All	6062/7934 (76%)	5979 (99%)	82 (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%)	285 (100%)	1 (0%)	86 85
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%)	285 (100%)	0	100 100
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%)	86 85
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%)	311 (100%)	0	100	100
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	a	186/288 (65%)	186 (100%)	0	100	100
32	b	257/350 (73%)	257 (100%)	0	100	100
All	All	5402/6881 (78%)	5400 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	276	VAL
22	V	36	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (45) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	37	ASN
3	C	81	HIS
3	C	116	GLN
3	C	154	HIS
4	D	356	GLN
4	D	361	GLN
6	F	113	GLN
6	F	147	GLN
6	F	207	HIS
7	G	176	GLN
7	G	308	GLN
7	G	312	GLN
8	H	109	HIS
9	I	87	HIS
9	I	98	GLN
10	J	105	HIS
13	M	16	HIS
15	O	111	HIS

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Mol	Chain	Res	Type
16	P	137	ASN
19	S	66	HIS
20	T	54	GLN
22	V	134	GLN
22	V	145	ASN
22	V	237	GLN
23	W	121	HIS
24	X	67	HIS
24	X	69	ASN
24	X	110	HIS
24	X	235	ASN
24	X	257	HIS
24	X	302	HIS
26	Z	82	GLN
27	0	32	GLN
27	0	192	ASN
27	0	194	GLN
27	0	207	GLN
28	1	185	HIS
28	1	231	HIS
29	3	140	HIS
29	3	141	HIS
30	4	129	GLN
30	4	322	HIS
31	a	90	HIS
31	a	183	GLN
32	b	212	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	950/955 (99%)	112 (11%)	0

All (112) 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

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Mol	Chain	Res	Type
1	A	722	C
1	A	737	C
1	A	738	A
1	A	739	C
1	A	740	G
1	A	753	A
1	A	761	A
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	871	A
1	A	890	C
1	A	892	A
1	A	893	G
1	A	919	A
1	A	931	C
1	A	933	G
1	A	938	A
1	A	939	A
1	A	942	A
1	A	954	C
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	991	G
1	A	992	U
1	A	1001	C
1	A	1015	A
1	A	1019	A
1	A	1020	C
1	A	1042	U
1	A	1065	C
1	A	1082	A

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Mol	Chain	Res	Type
1	A	1098	C
1	A	1103	A
1	A	1105	C
1	A	1106	C
1	A	1107	U
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	1190	C
1	A	1220	A
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	1271	C
1	A	1273	G
1	A	1284	U
1	A	1285	G
1	A	1290	C
1	A	1291	U
1	A	1326	A
1	A	1327	G
1	A	1343	A
1	A	1354	A
1	A	1356	A
1	A	1357	A
1	A	1376	C
1	A	1378	C
1	A	1390	A
1	A	1405	C
1	A	1421	G

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Mol	Chain	Res	Type
1	A	1422	G
1	A	1430	A
1	A	1438	G
1	A	1447	G
1	A	1462	G
1	A	1465	C
1	A	1469	G
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	1568	U
1	A	1571	U
1	A	1582	G
1	A	1584	MA6
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	5MU	A	1076	1	19,22,23	0.29	0	28,32,35	0.32	0
17	AYA	Q	2	17	6,7,8	0.75	0	5,8,10	0.68	0
1	B8T	A	1486	1	19,22,23	0.31	0	26,31,34	0.32	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	MA6	A	1584	1	23,26,27	0.30	0	34,38,41	0.59	1 (2%)
1	MA6	A	1583	1	23,26,27	0.30	0	34,38,41	0.57	1 (2%)
9	5F0	I	184	9	8,8,9	0.56	0	7,9,11	1.04	1 (14%)
1	5MC	A	1488	1	18,22,23	0.32	0	26,32,35	0.47	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	5MU	A	1076	1	-	0/7/25/26	0/2/2/2
17	AYA	Q	2	17	-	0/4/6/8	-
1	B8T	A	1486	1	-	0/7/27/28	0/2/2/2
1	MA6	A	1584	1	-	1/11/29/30	0/3/3/3
1	MA6	A	1583	1	-	0/11/29/30	0/3/3/3
9	5F0	I	184	9	-	0/9/9/10	-
1	5MC	A	1488	1	-	0/7/25/26	0/2/2/2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	I	184	5F0	O-C-CB	-2.37	118.51	125.43
1	A	1583	MA6	C2-N1-C6	2.37	117.34	111.75
1	A	1584	MA6	C2-N1-C6	2.33	117.26	111.75

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1584	MA6	C4'-C5'-O5'-P

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1584	MA6	2	0
1	A	1583	MA6	3	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 88 ligands modelled in this entry, 82 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	$\#\|Z\|>2$
38	ATP	X	501	34	29,33,33	0.49	0	44,52,52	0.49	0
39	GDP	X	502	-	28,30,30	0.43	0	44,47,47	0.41	0
37	FES	P	201	5,16	0,4,4	-	-	-		
40	SAH	b	501	-	27,28,28	0.40	0	38,40,40	0.44	0
37	FES	T	201	13,20	0,4,4	-	-	-		
33	NAD	A	1701	35	45,48,48	0.38	0	63,73,73	0.40	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
38	ATP	X	501	34	-	0/22/38/38	0/3/3/3
39	GDP	X	502	-	-	0/16/32/32	0/3/3/3
37	FES	P	201	5,16	-	-	0/1/1/1
40	SAH	b	501	-	-	5/15/31/31	0/3/3/3
37	FES	T	201	13,20	-	-	0/1/1/1
33	NAD	A	1701	35	-	1/30/62/62	0/5/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

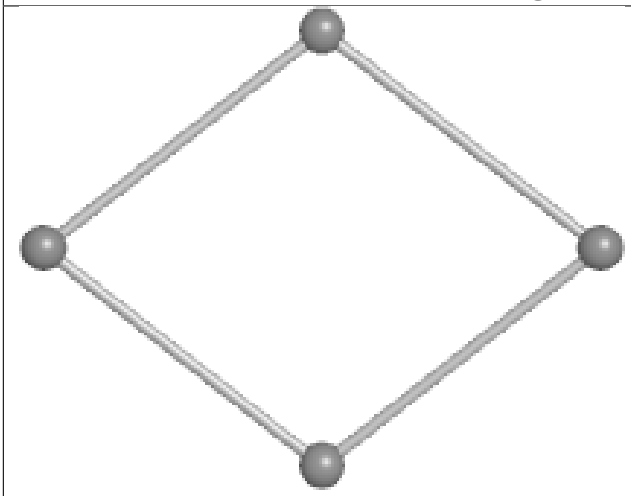
Mol	Chain	Res	Type	Atoms
40	b	501	SAH	OXT-C-CA-N
40	b	501	SAH	O-C-CA-CB
40	b	501	SAH	OXT-C-CA-CB
40	b	501	SAH	O-C-CA-N
40	b	501	SAH	C2'-C1'-N9-C8
33	A	1701	NAD	PA-O3-PN-O2N

There are no ring outliers.

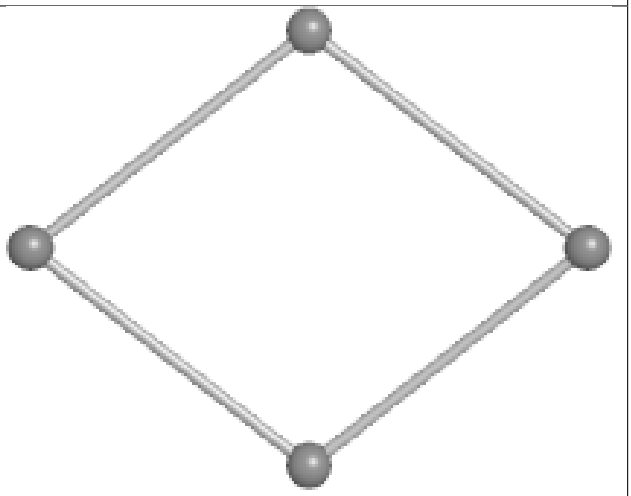
No monomer is involved in short contacts.

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.

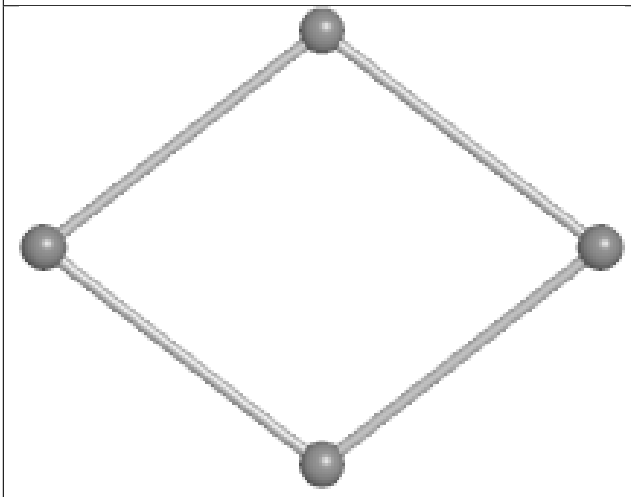
Ligand FES P 201



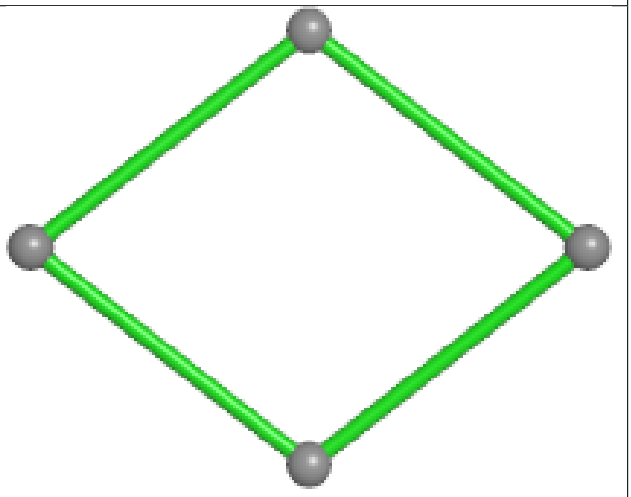
Bond lengths



Bond angles

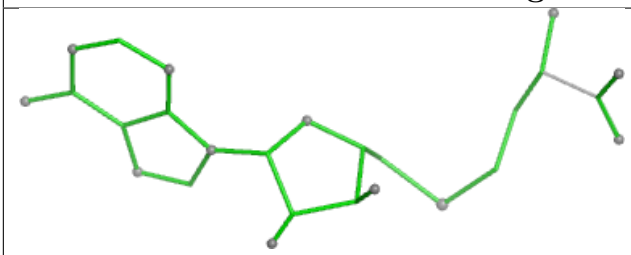


Torsions

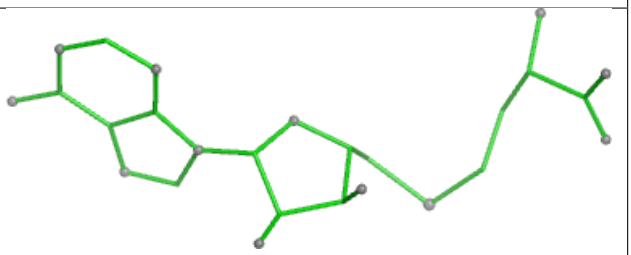


Rings

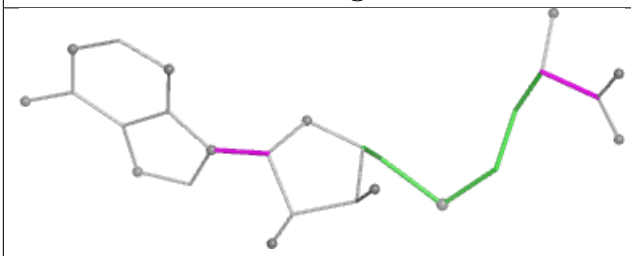
Ligand SAH b 501



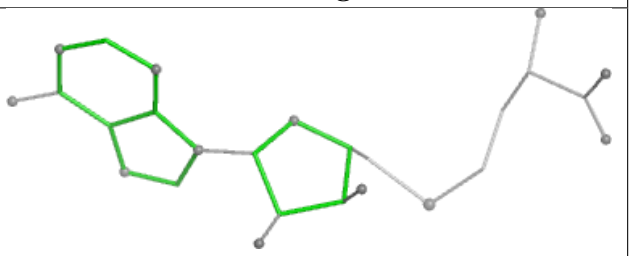
Bond lengths



Bond angles

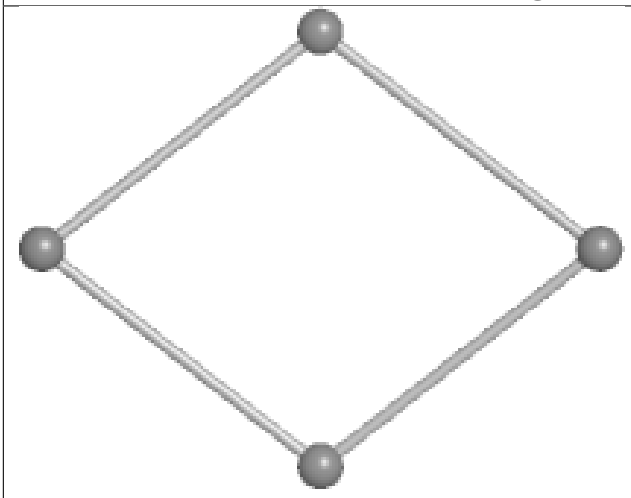


Torsions

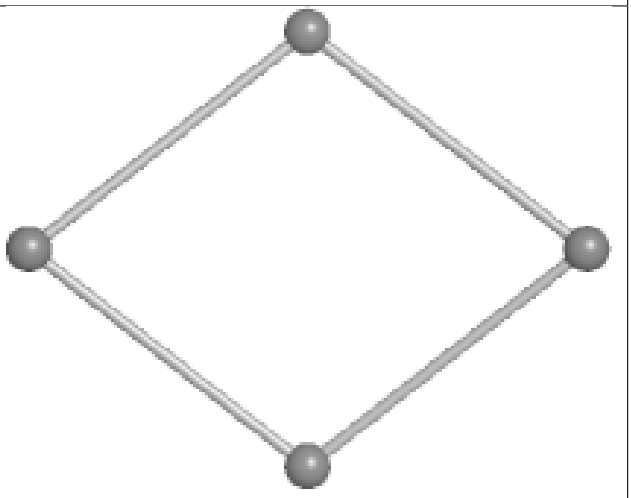


Rings

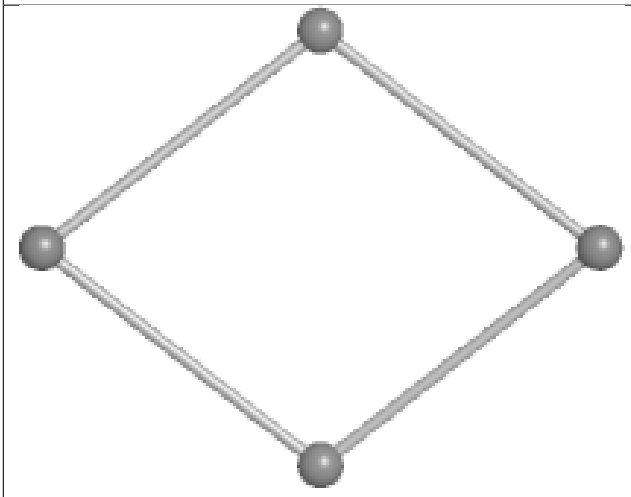
Ligand FES T 201



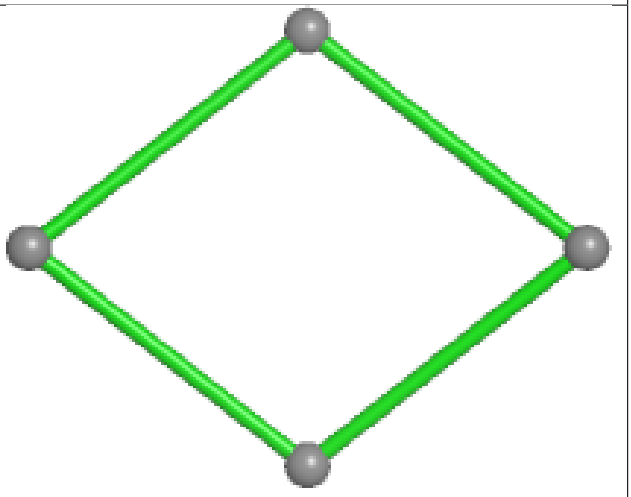
Bond lengths



Bond angles

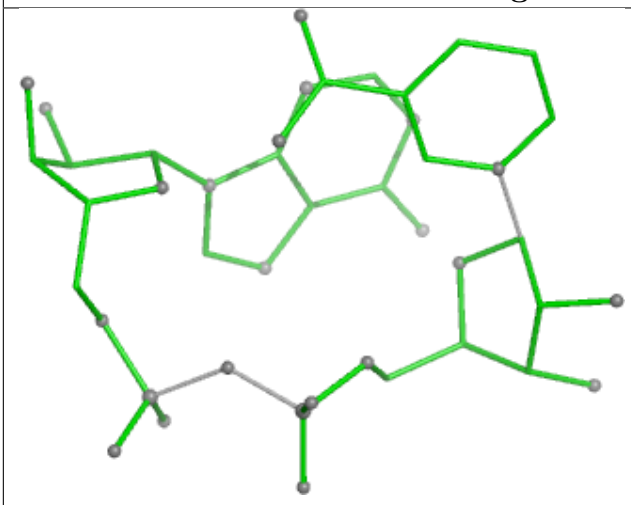


Torsions

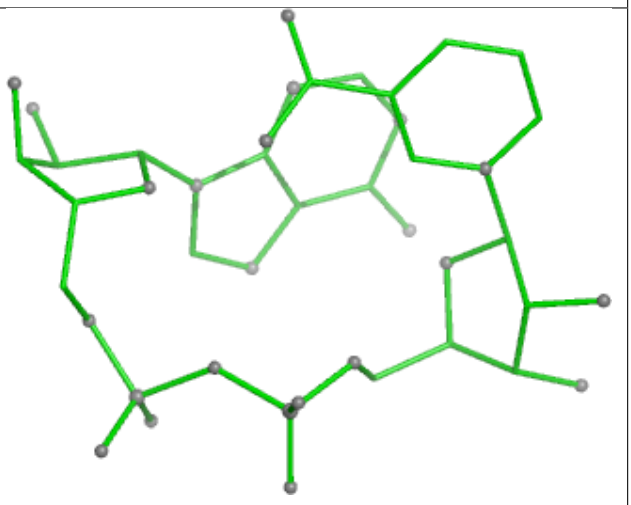


Rings

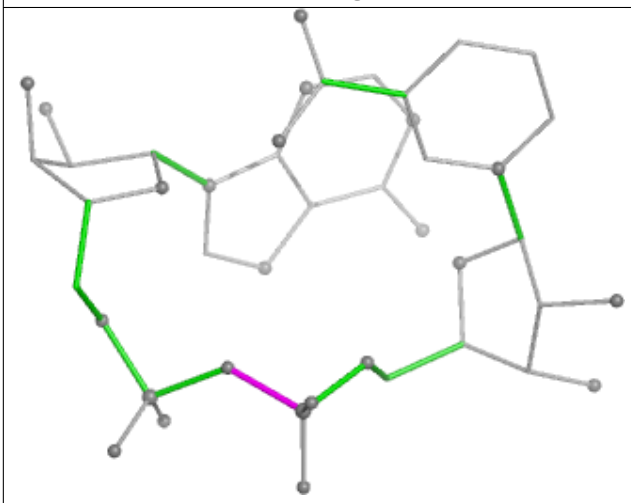
Ligand NAD A 1701



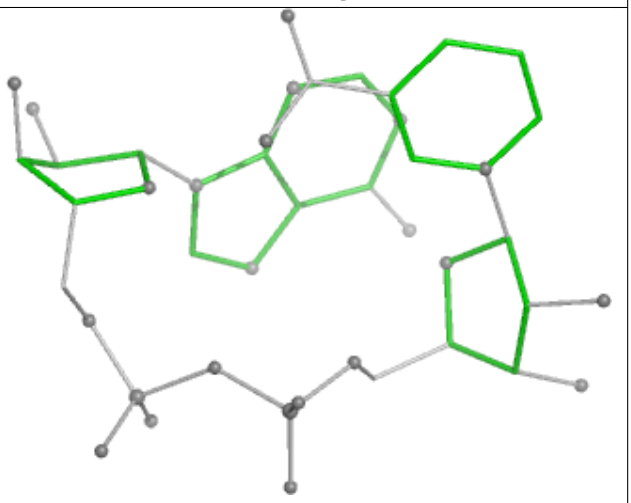
Bond lengths



Bond angles



Torsions



Rings

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.

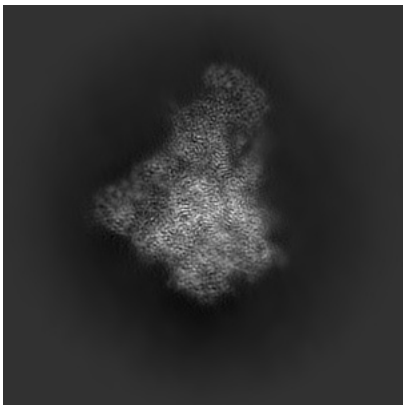
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-13556. These allow visual inspection of the internal detail of the map and identification of artifacts.

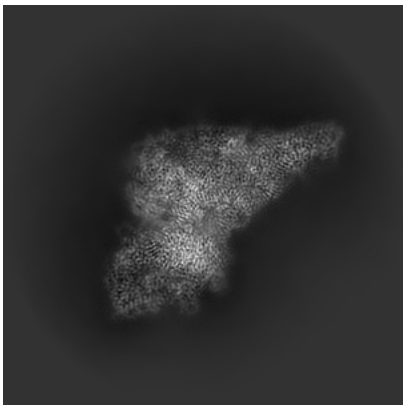
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

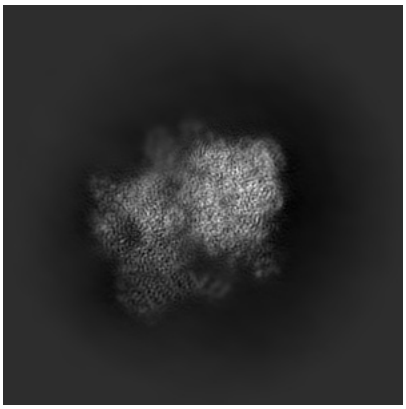
6.1.1 Primary map



X

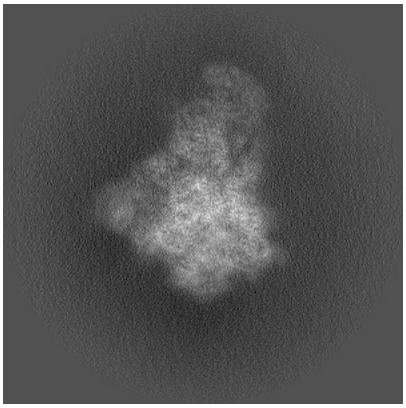


Y

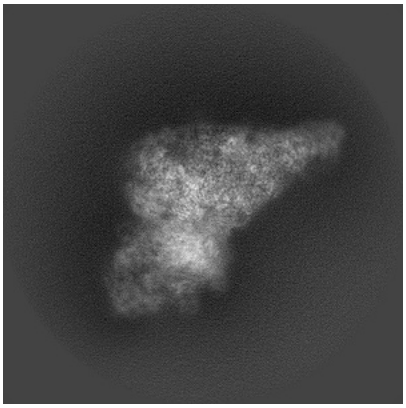


Z

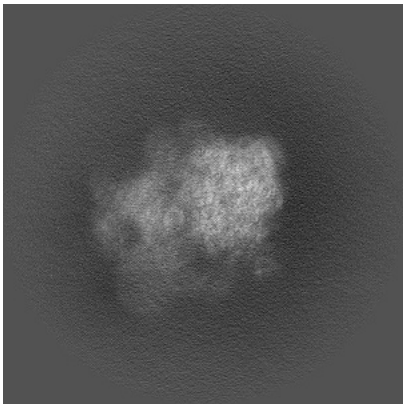
6.1.2 Raw map



X



Y

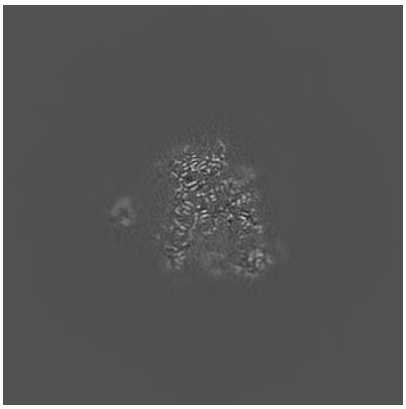


Z

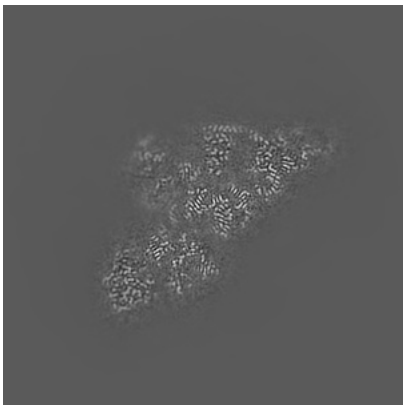
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

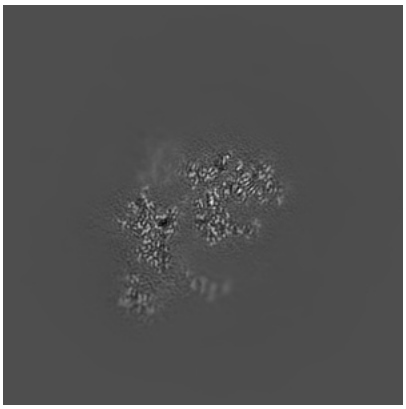
6.2.1 Primary map



X Index: 270

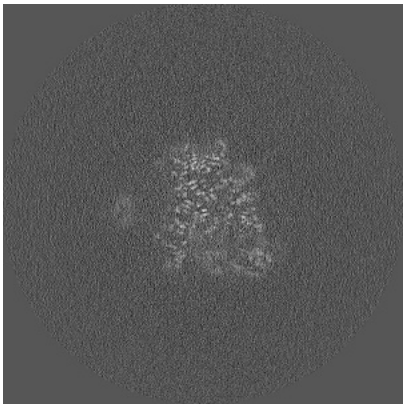


Y Index: 270

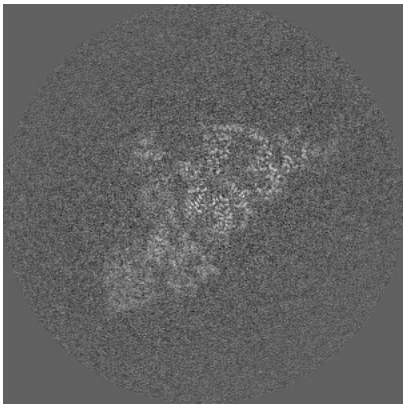


Z Index: 270

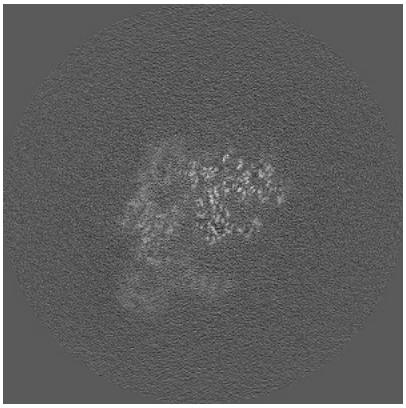
6.2.2 Raw map



X Index: 240



Y Index: 240

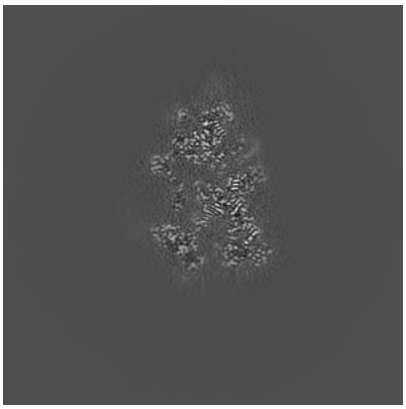


Z Index: 240

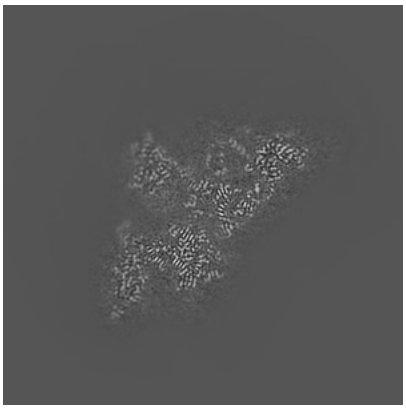
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

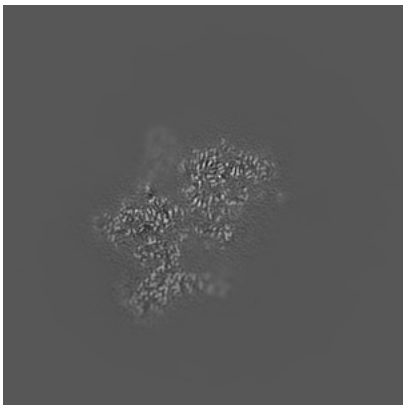
6.3.1 Primary map



X Index: 318

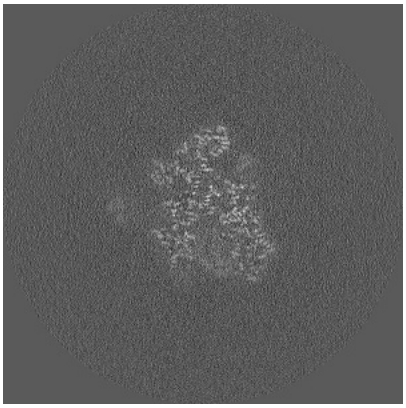


Y Index: 260

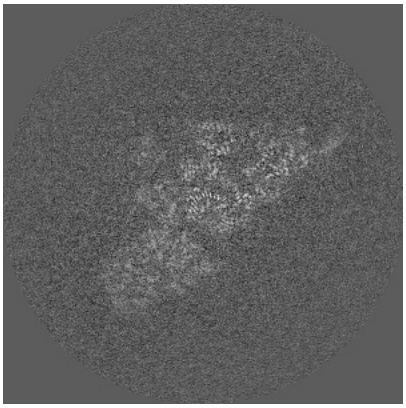


Z Index: 253

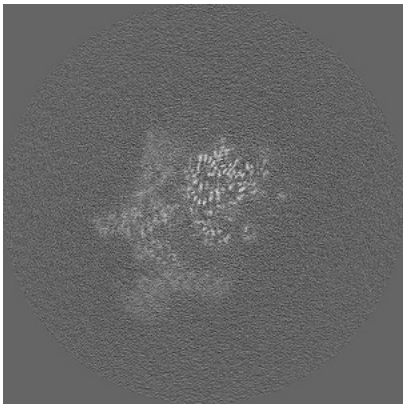
6.3.2 Raw map



X Index: 252



Y Index: 244

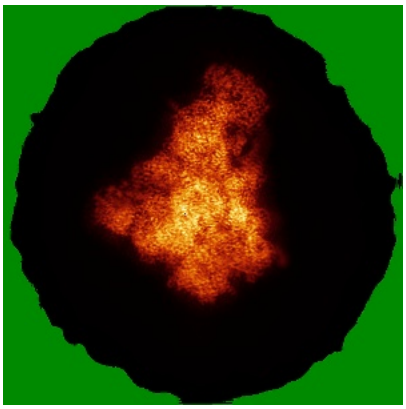


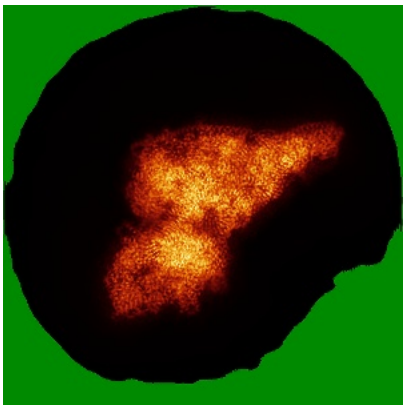
Z Index: 231

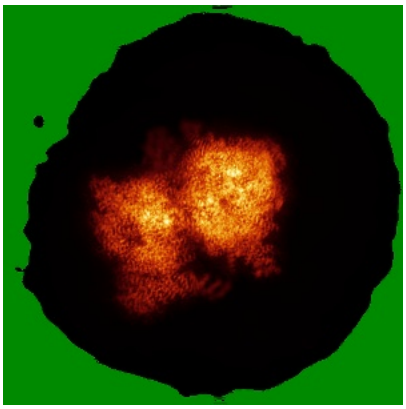
The images above show the largest variance slices of the map in three orthogonal directions.

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

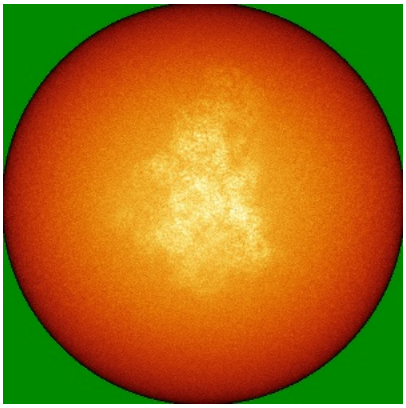
6.4.1 Primary map

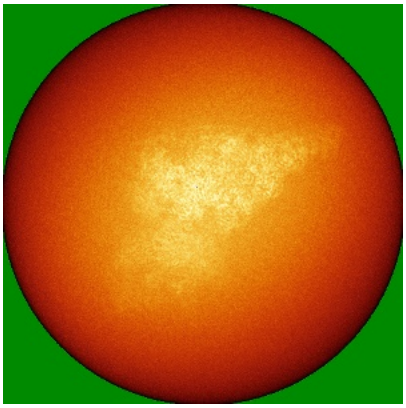

X

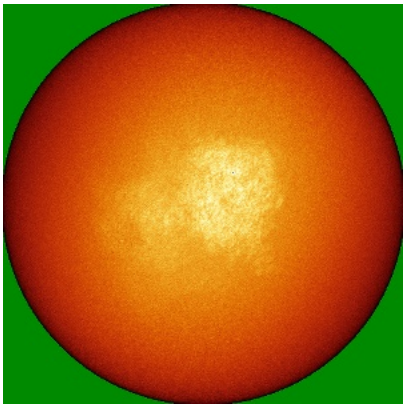

Y


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)

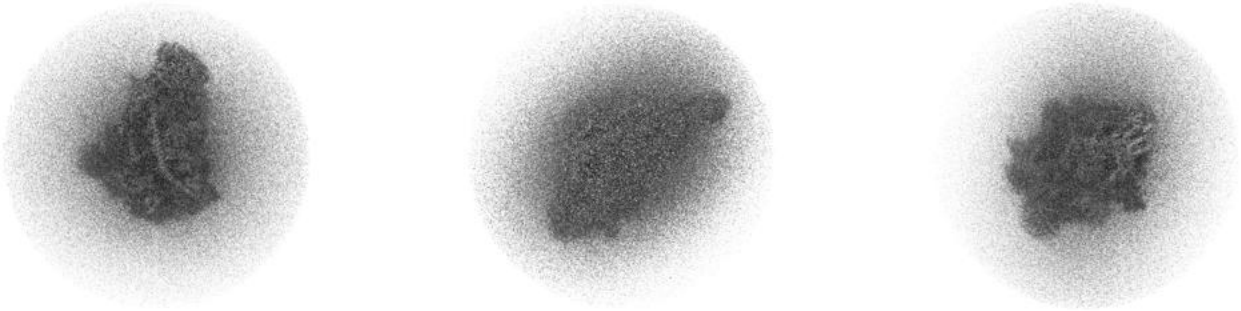
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. 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.

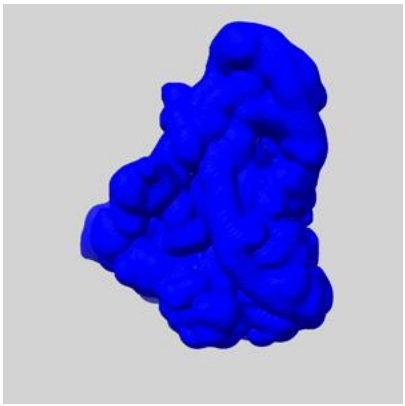
6.6 Mask visualisation

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

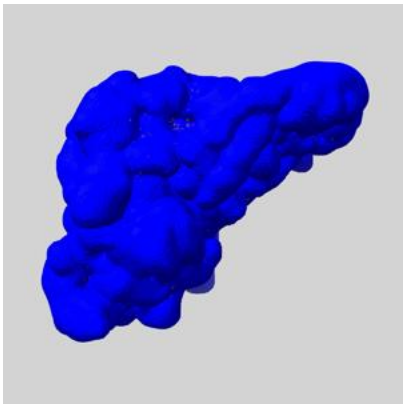
A mask typically either:

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

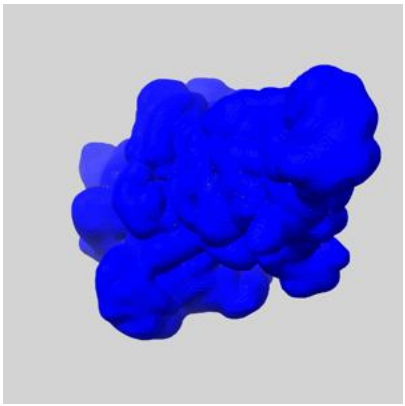
6.6.1 emd_13556_msk_1.map



X



Y

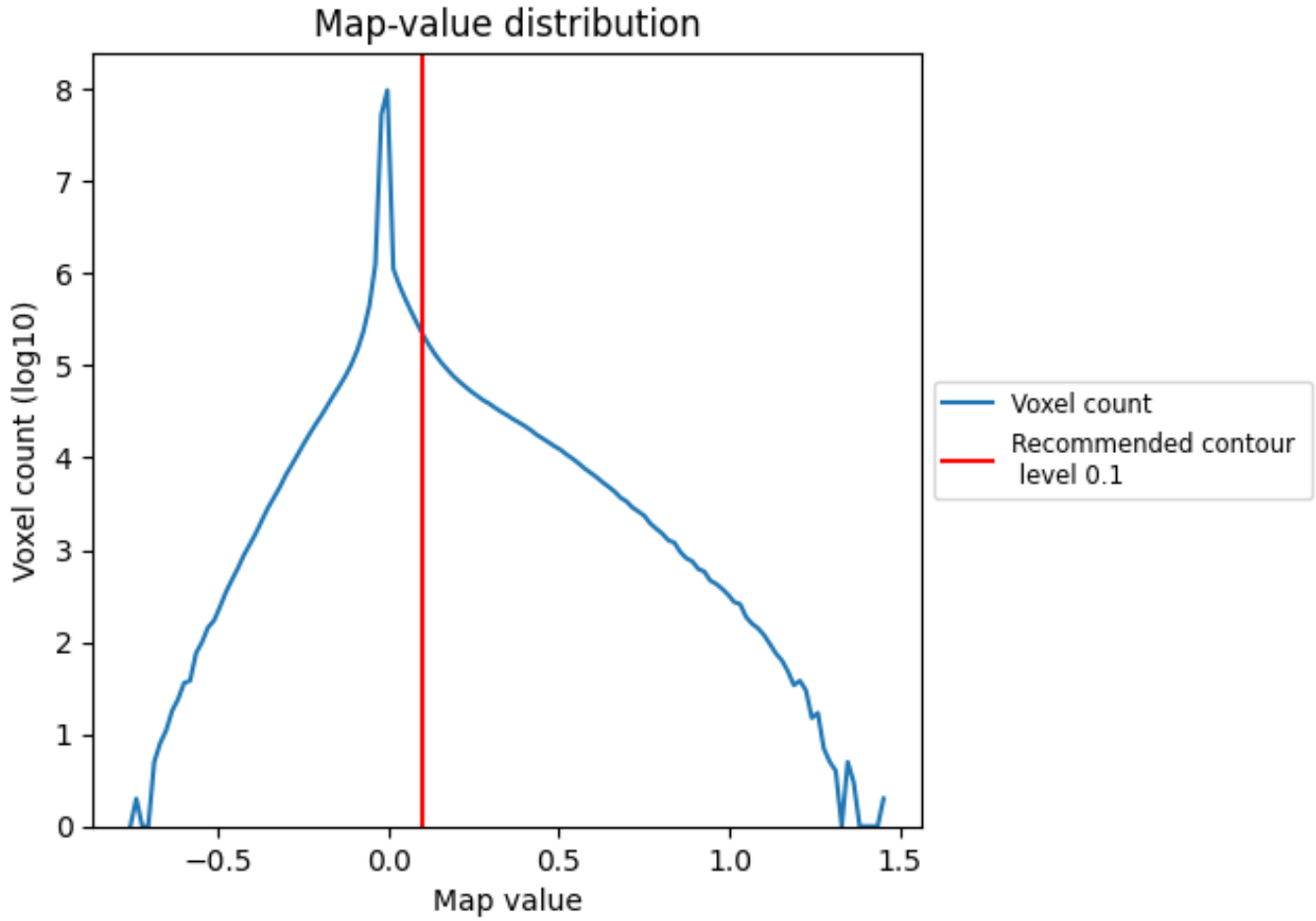


Z

7 Map analysis

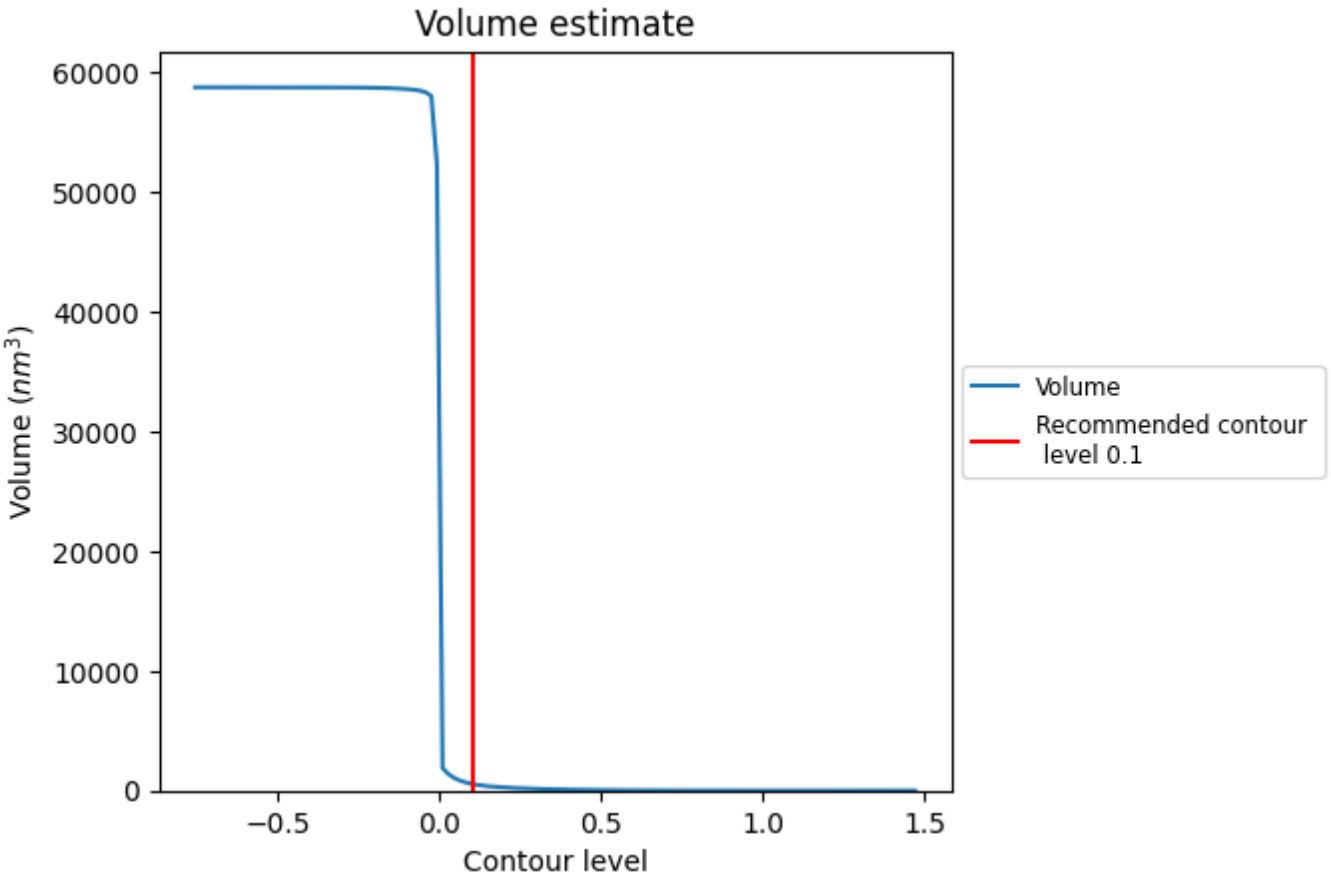
This section contains the results of statistical analysis of the map.

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.

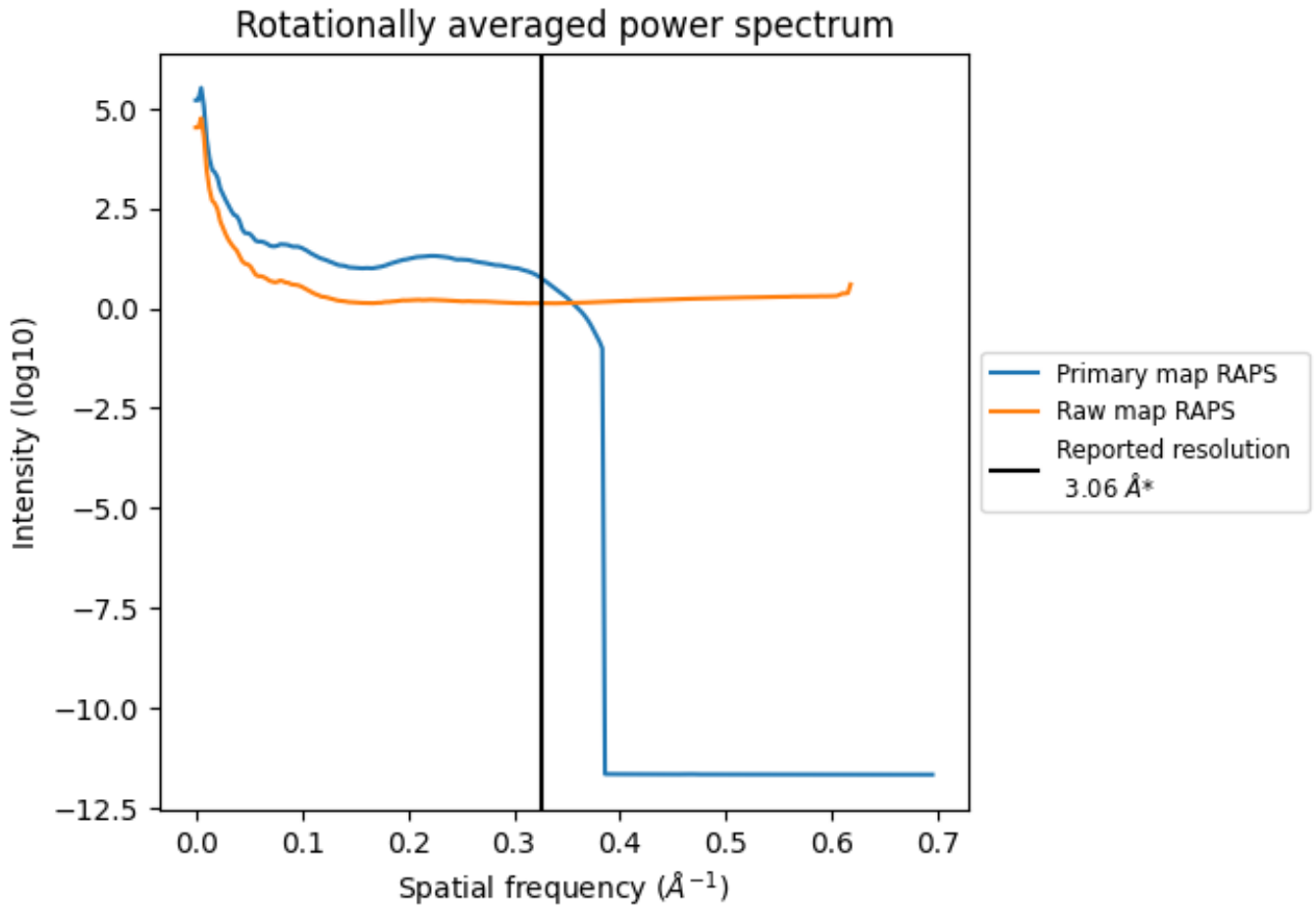
7.2 Volume estimate



The volume at the recommended contour level is 557 nm^3; this corresponds to an approximate mass of 503 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)

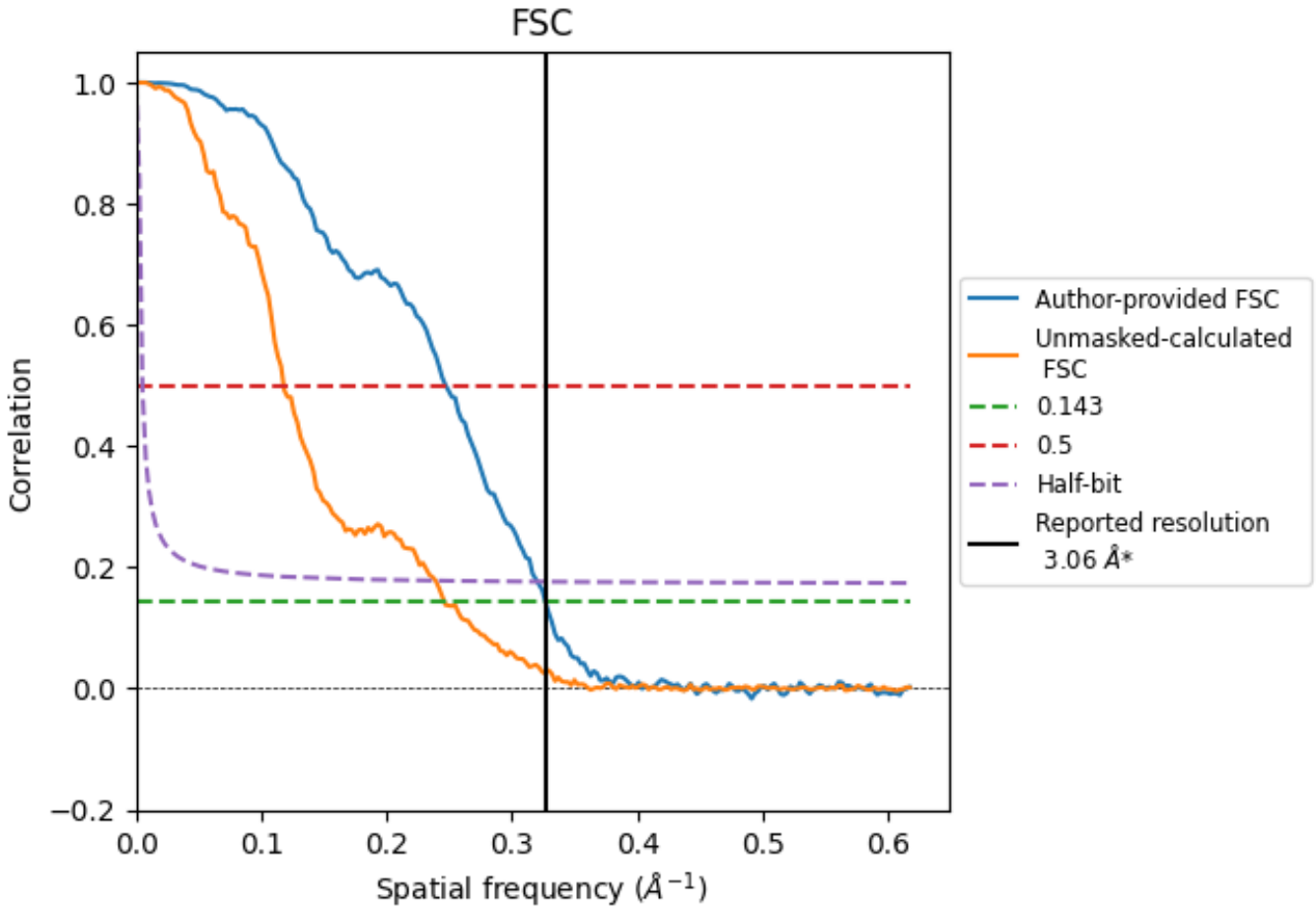


*Reported resolution corresponds to spatial frequency of 0.327 $Å^{-1}$

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 0.327 Å^{-1}

8.2 Resolution estimates (i)

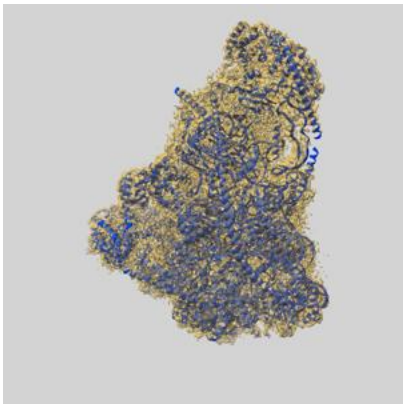
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.06	-	-
Author-provided FSC curve	3.06	4.05	3.12
Unmasked-calculated*	4.07	8.49	4.18

*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 4.07 differs from the reported value 3.06 by more than 10 %

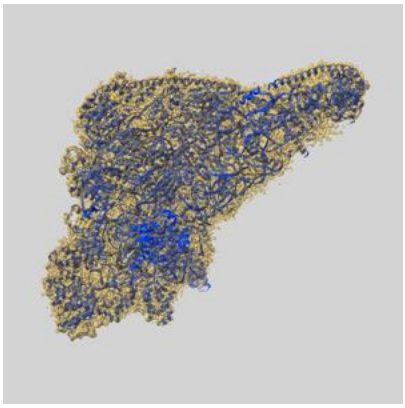
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-13556 and PDB model 7PNY. Per-residue inclusion information can be found in section 3 on page 15.

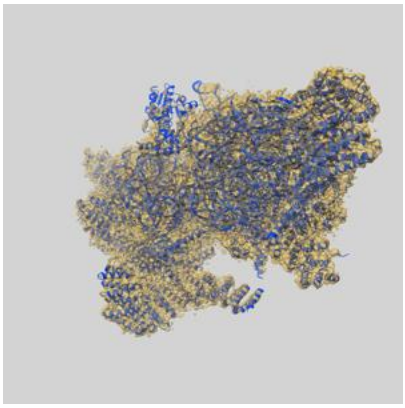
9.1 Map-model overlay



X



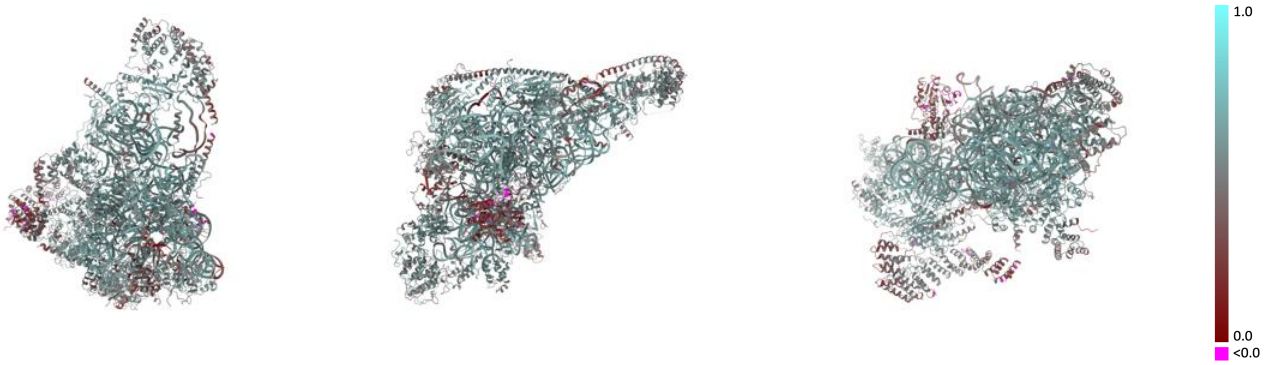
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.1 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.

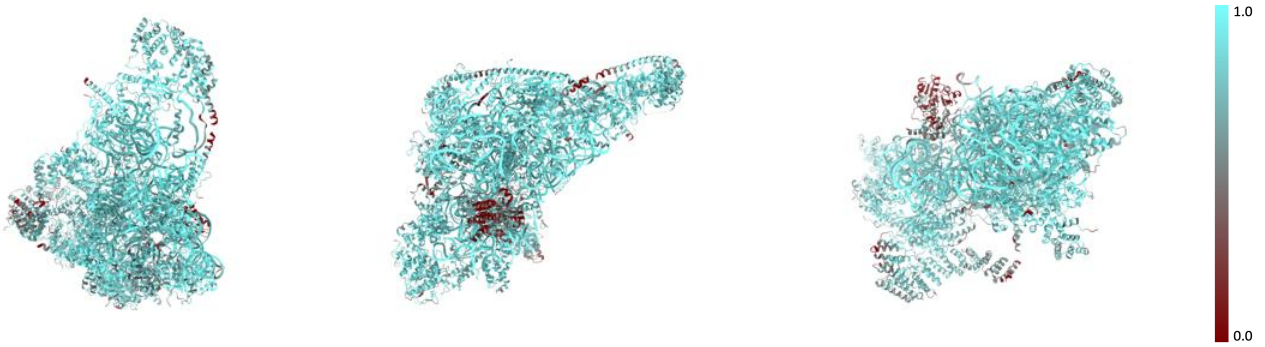
9.2 Q-score mapped to coordinate model (i)



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.

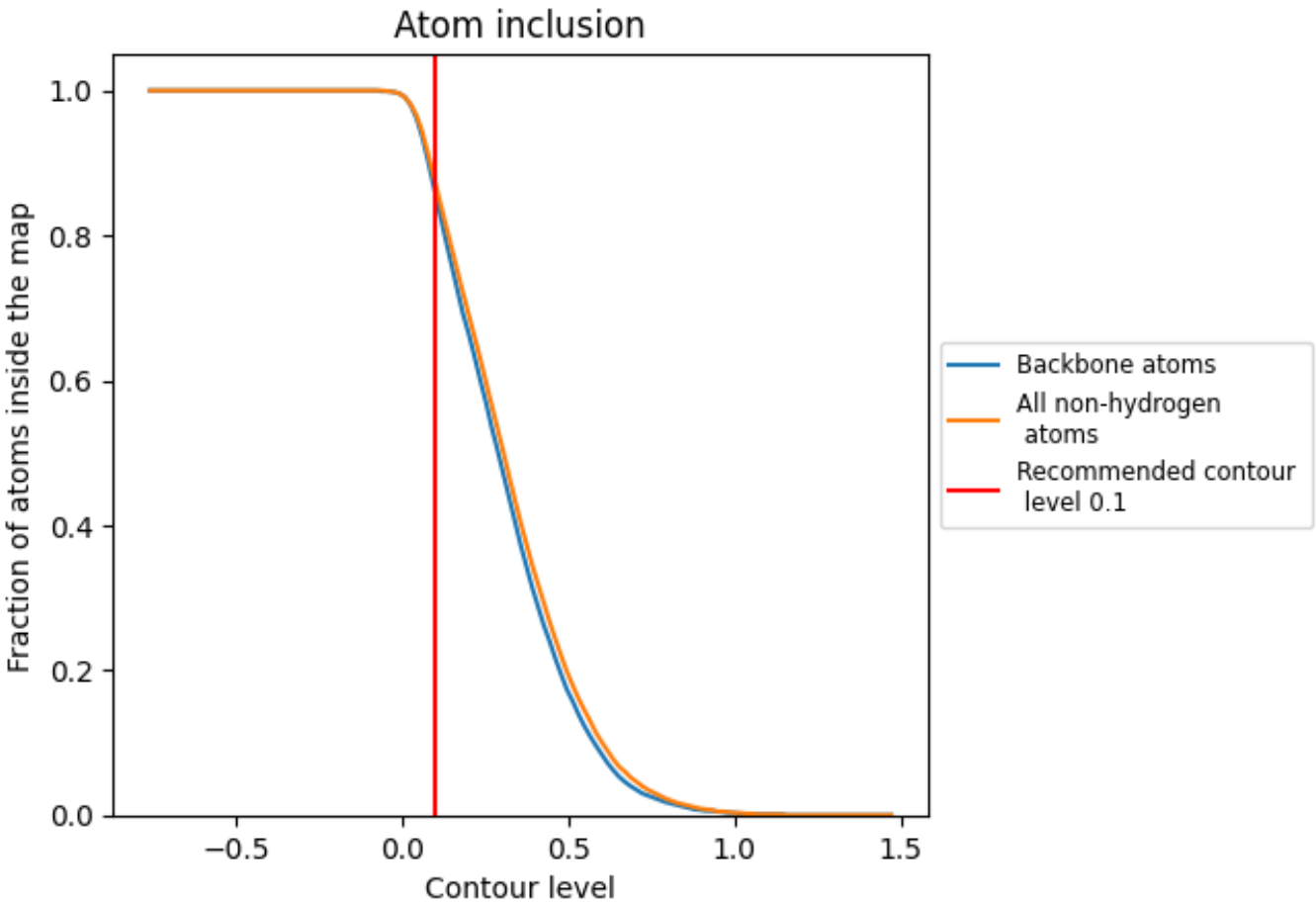
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.1).

9.4 Atom inclusion (i)



At the recommended contour level, 86% of all backbone atoms, 87% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8740	0.5390
0	0.9010	0.5570
1	0.8430	0.5310
3	0.9200	0.5750
4	0.7240	0.4260
A	0.9660	0.5990
B	0.9300	0.5910
C	0.9720	0.6270
D	0.8980	0.5640
E	0.8960	0.5550
F	0.8520	0.5090
G	0.8580	0.5380
H	0.9100	0.5880
I	0.8380	0.4860
J	0.9410	0.5860
K	0.9600	0.6300
L	0.8720	0.5510
M	0.9260	0.6110
N	0.9460	0.6110
O	0.9250	0.5870
P	0.9220	0.5670
Q	0.9270	0.5690
R	0.8650	0.5330
S	0.8340	0.5070
T	0.9180	0.5840
U	0.8190	0.5030
V	0.8130	0.4880
W	0.8920	0.5530
X	0.8870	0.5460
Y	0.7610	0.4930
Z	0.8940	0.5620
a	0.5720	0.3250
b	0.2650	0.2160

