



wwPDB EM Validation Summary Report ⓘ

Apr 16, 2024 – 02:59 am BST

PDB ID : 7PO0
EMDB ID : EMD-13558
Title : Assembly intermediate of human mitochondrial ribosome small subunit without mS37 in complex with RBFA and IF3
Authors : Itoh, Y.; Khawaja, A.; Rorbach, J.; Amunts, A.
Deposited on : 2021-09-08
Resolution : 2.90 Å(reported)
Based on initial model : 6RW4

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

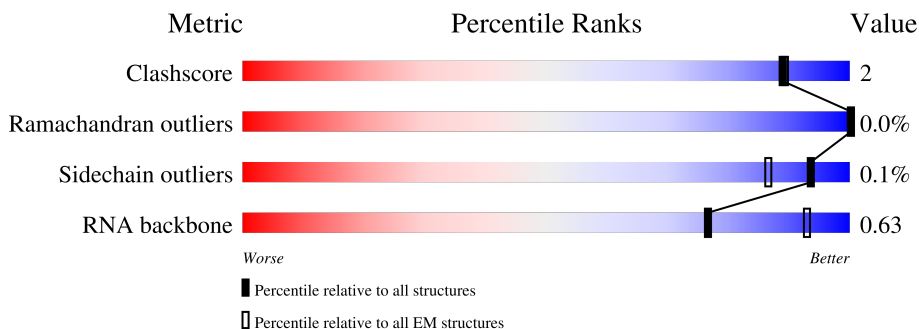
EMDB validation analysis : 0.0.1.dev92
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

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 2.90 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	955	81% (green), 18% (yellow), 1% (orange), 0% (red), 0% (grey)
2	B	296	74% (green), 24% (grey), 2% (yellow), 0% (orange), 0% (red)
3	C	167	75% (green), 21% (grey), 4% (yellow), 0% (orange), 0% (red)
4	D	430	77% (green), 20% (grey), 3% (yellow), 0% (orange), 0% (red)
5	E	125	93% (green), 6% (grey), 1% (yellow), 0% (orange), 0% (red)
6	F	242	81% (green), 15% (grey), 4% (yellow), 0% (orange), 0% (red)
7	G	396	78% (green), 17% (grey), 5% (yellow), 0% (orange), 0% (red)

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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	278	
32	a	343	

2 Entry composition [i](#)

There are 40 unique types of molecules in this entry. The entry contains 130256 atoms, of which 59850 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	
			Total	C	H	N	O			S
7	G	327	5378	1710	2690	477	487	14	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
8	H	140	2336	745	1184	194	210	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
9	I	137	2081	642	1061	192	182	4	0	0

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	
			Total	C	H	N	O			S
10	J	108	1727	521	888	169	143	6	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
11	K	101	1748	537	886	179	141	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
12	L	174	2994	925	1541	270	251	7	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
13	M	119	1908	594	966	185	157	6	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
14	N	110	1797	562	929	156	147	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
15	O	193	3149	1014	1557	294	277	7	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
16	P	97	1588	501	807	134	138	8	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
17	Q	86	1502	460	758	150	126	8	0	0

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	
			Total	C	H	N	O			S
18	R	295	4838	1533	2429	413	455	8	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
19	S	135	2227	716	1116	198	196	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
20	T	168	2765	877	1394	239	244	11	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
21	U	176	2988	916	1500	301	267	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
22	V	362	5933	1904	2964	495	558	12	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
23	W	100	1592	498	803	141	146	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
24	X	352	5694	1822	2845	499	517	11	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
25	Y	149	2444	801	1198	207	234	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
26	Z	100	1699	534	860	153	148	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
27	0	215	3584	1130	1797	339	313	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
28	1	278	4545	1430	2289	386	429	11	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
29	3	71	1331	403	702	135	90	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
30	4	590	9556	3056	4781	809	882	28	0	0

- Molecule 31 is a protein called Mitochondrial translational initiation factor 3, isoform CRA_ a.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
31	8	191	3132	953	1589	289	293	8	0	0

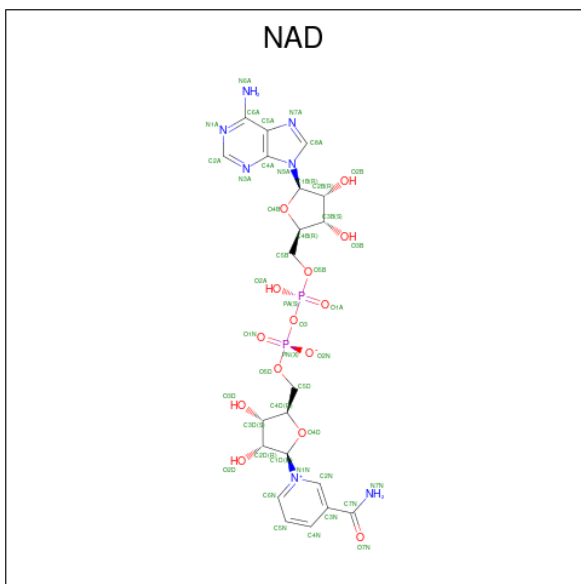
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
8	68	ILE	THR	variant	UNP A0A024RDQ7

- Molecule 32 is a protein called Putative ribosome-binding factor A, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
32	a	184	2927	919	1463	258	280	7	0	0

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



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

- Molecule 34 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
34	A	61	Total	Mg	0
			61	61	
34	B	1	Total	Mg	0
			1	1	
34	X	1	Total	Mg	0
			1	1	
34	3	1	Total	Mg	0
			1	1	
34	8	1	Total	Mg	0
			1	1	

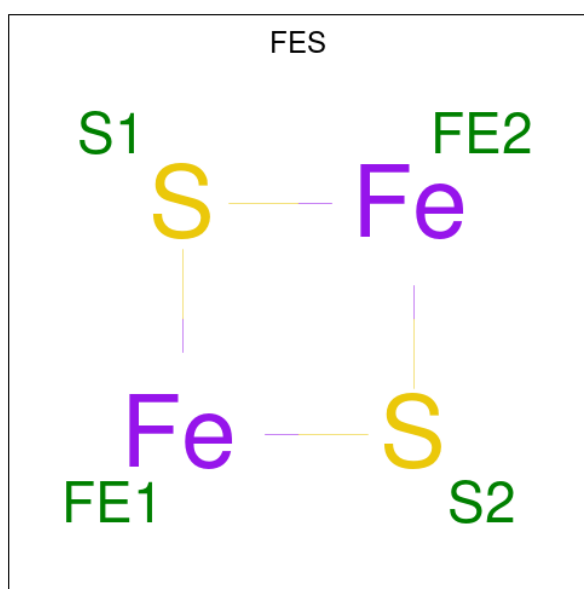
- Molecule 35 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	AltConf
35	A	17	Total K 17 17	0

- Molecule 36 is ZINC ION (three-letter code: ZN) (formula: Zn).

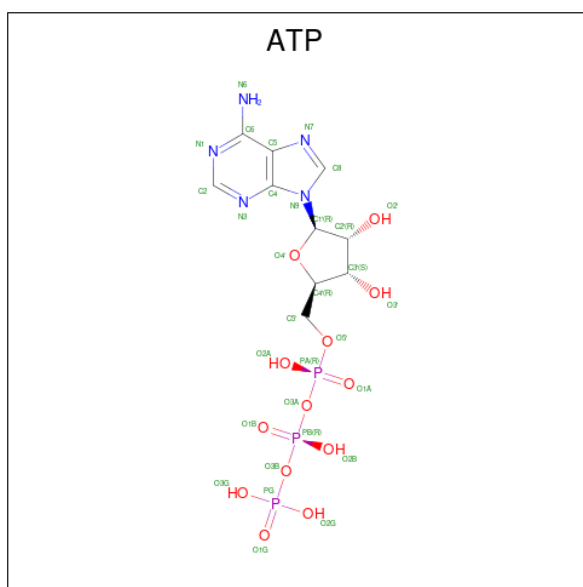
Mol	Chain	Residues	Atoms	AltConf
36	O	1	Total Zn 1 1	0

- Molecule 37 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂) (labeled as "Ligand of Interest" by depositor).



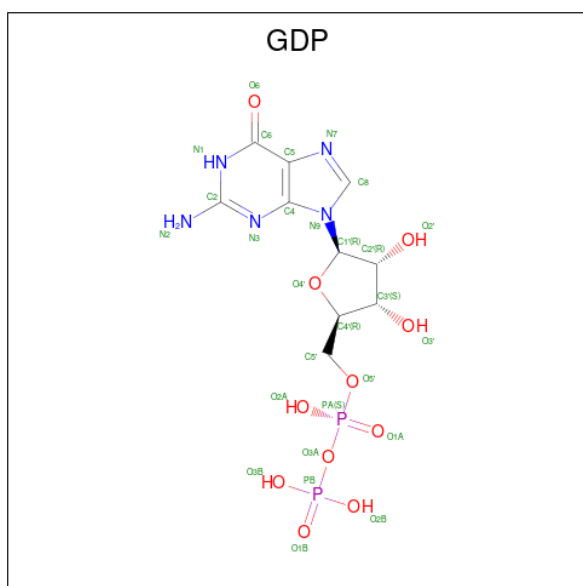
Mol	Chain	Residues	Atoms	AltConf
37	P	1	Total Fe S 4 2 2	0
37	T	1	Total Fe S 4 2 2	0

- Molecule 38 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



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

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



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

- Molecule 40 is water.

Mol	Chain	Residues	Atoms		AltConf
40	A	751	Total 751	O 751	0
40	B	31	Total 31	O 31	0
40	C	30	Total 30	O 30	0
40	D	34	Total 34	O 34	0
40	F	11	Total 11	O 11	0
40	G	39	Total 39	O 39	0
40	H	34	Total 34	O 34	0
40	I	7	Total 7	O 7	0
40	J	12	Total 12	O 12	0
40	K	37	Total 37	O 37	0
40	L	3	Total 3	O 3	0
40	M	14	Total 14	O 14	0
40	N	5	Total 5	O 5	0
40	O	24	Total 24	O 24	0
40	P	2	Total 2	O 2	0
40	Q	7	Total 7	O 7	0
40	R	17	Total 17	O 17	0
40	S	9	Total 9	O 9	0
40	T	12	Total 12	O 12	0
40	U	5	Total 5	O 5	0
40	V	6	Total 6	O 6	0
40	W	1	Total 1	O 1	0

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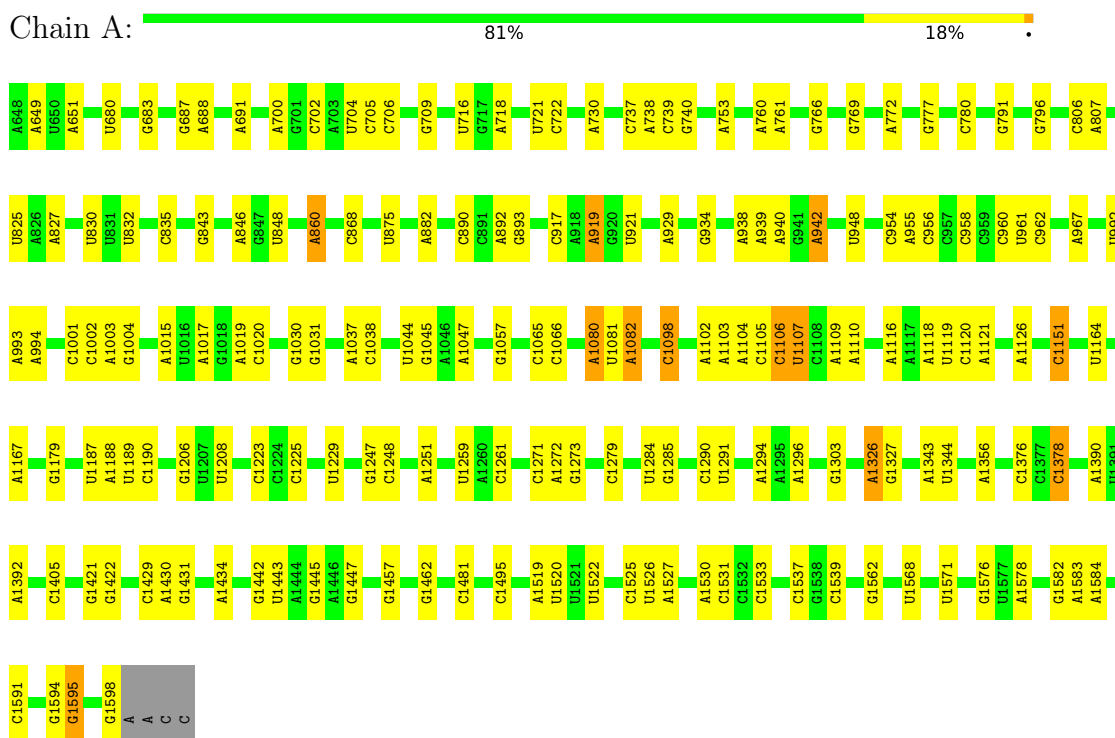
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Mol	Chain	Residues	Atoms		AltConf
40	X	9	Total 9	O 9	0
40	Y	1	Total 1	O 1	0
40	Z	18	Total 18	O 18	0
40	0	13	Total 13	O 13	0
40	1	19	Total 19	O 19	0
40	3	7	Total 7	O 7	0
40	4	3	Total 3	O 3	0
40	8	3	Total 3	O 3	0
40	a	2	Total 2	O 2	0

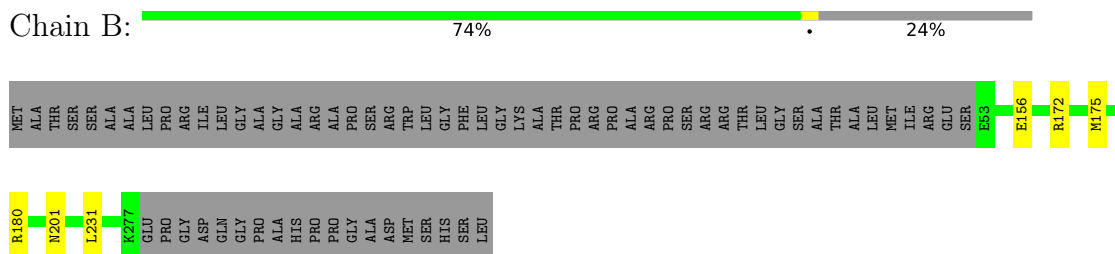
3 Residue-property plots

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

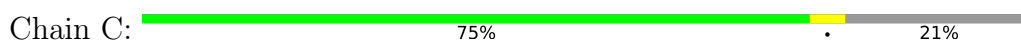
- Molecule 1: 12S mitochondrial rRNA

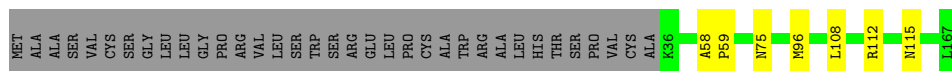


- Molecule 2: 28S ribosomal protein S2, mitochondrial



- Molecule 3: 28S ribosomal protein S24, mitochondrial





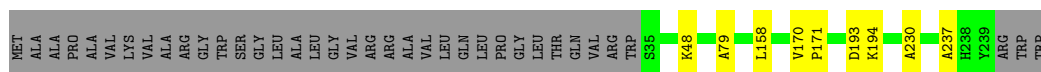
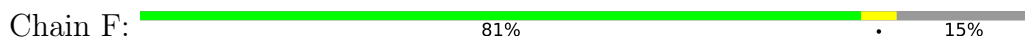
• Molecule 4: 28S ribosomal protein S5, mitochondrial



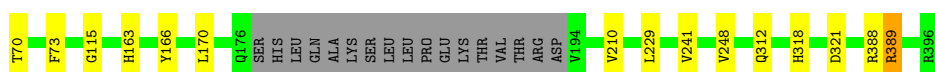
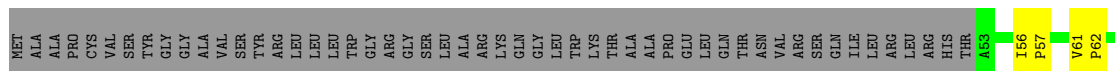
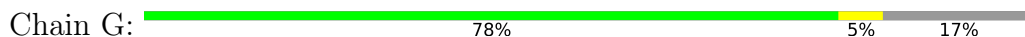
• Molecule 5: 28S ribosomal protein S6, mitochondrial



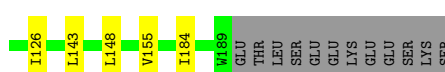
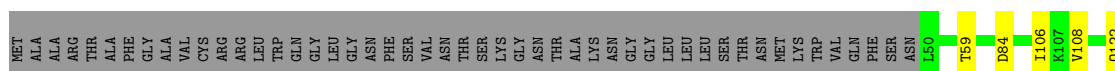
• Molecule 6: 28S ribosomal protein S7, mitochondrial



• Molecule 7: 28S ribosomal protein S9, mitochondrial

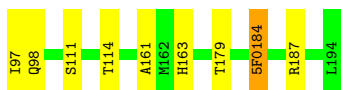
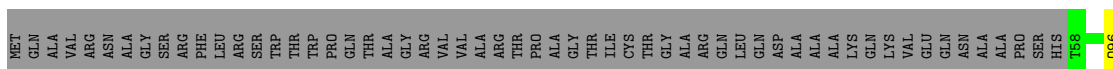


• Molecule 8: 28S ribosomal protein S10, mitochondrial

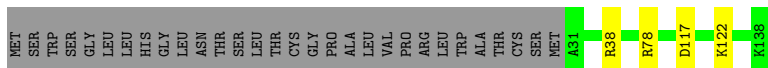


• Molecule 9: 28S ribosomal protein S11, mitochondrial

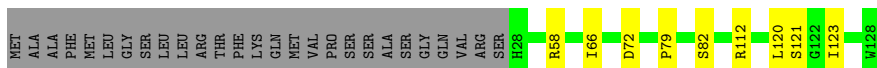




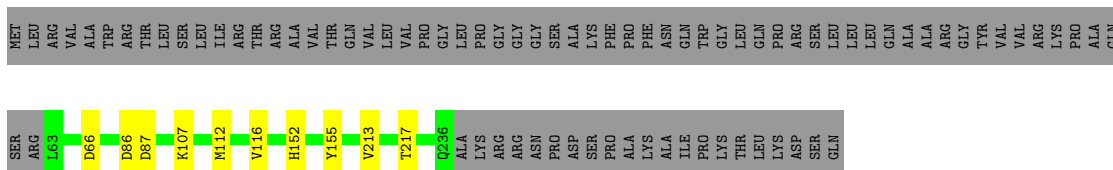
- Molecule 10: 28S ribosomal protein S12, mitochondrial



- Molecule 11: 28S ribosomal protein S14, mitochondrial



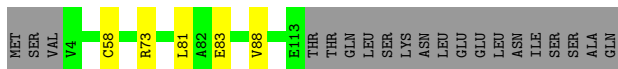
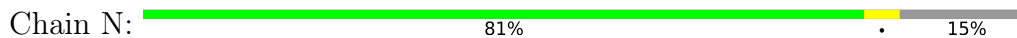
- Molecule 12: 28S ribosomal protein S15, mitochondrial



- Molecule 13: 28S ribosomal protein S16, mitochondrial

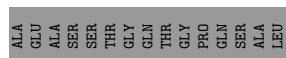
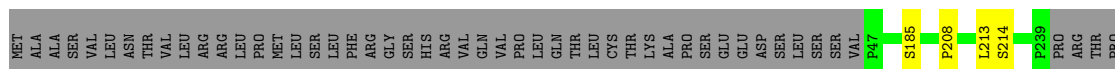


- Molecule 14: 28S ribosomal protein S17, mitochondrial

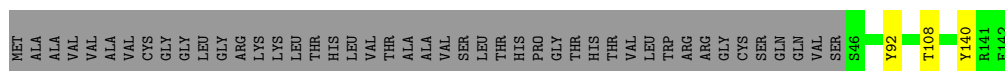


- Molecule 15: 28S ribosomal protein S18b, mitochondrial





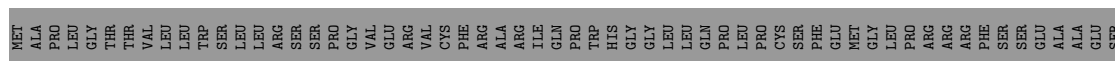
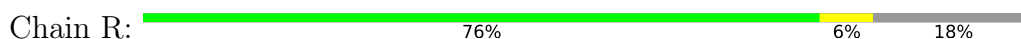
- Molecule 16: 28S ribosomal protein S18c, mitochondrial



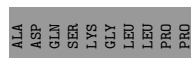
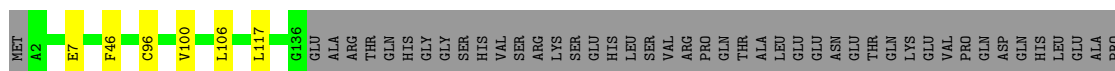
- Molecule 17: 28S ribosomal protein S21, mitochondrial



- Molecule 18: 28S ribosomal protein S22, mitochondrial



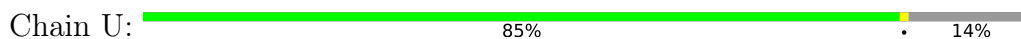
- Molecule 19: 28S ribosomal protein S23, mitochondrial



- Molecule 20: 28S ribosomal protein S25, mitochondrial

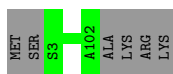


- Molecule 21: 28S ribosomal protein S26, mitochondrial



- Molecule 26: 28S ribosomal protein S33, mitochondrial

Chain Z:  94% 6%




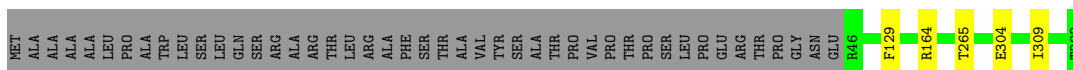
- Molecule 27: 28S ribosomal protein S34, mitochondrial

Chain 0:  93% 6%



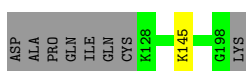
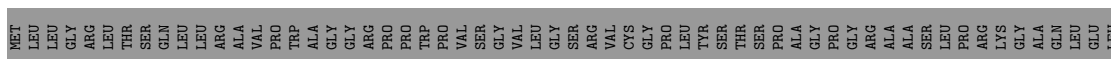
- Molecule 28: 28S ribosomal protein S35, mitochondrial

Chain 1:  85% 14%




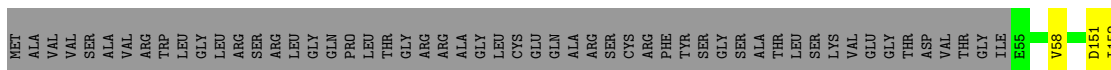
- Molecule 29: Aurora kinase A-interacting protein

Chain 3:  35% 64%



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

Chain 4:  81% 5% 14%



- Molecule 31: Mitochondrial translational initiation factor 3, isoform CRA_a

Chain 8:  66% 31%

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

THR GLN ASN GLU GLY LYS LYS ASN K72 D81 E92 T156 I220 V230 Q231 C238 V239 T262 LEU ASN LYS ASP ASP GLY ASN ASP LYS GLU SER ASN ASN LEU TLE ALA SER HIS GLN

● Molecule 32: Putative ribosome-binding factor A, mitochondrial

Chain a: 53% 46%

MET TRP ALA ALA GLY LEU TRP LYS SER ARG PRO ALA GLY LEU ARG ALA THR LEU LYS K55 V56 W57 D206 GLU

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

VAL ALA GLU THR GLN MET LYS G278 V301 GLU ASP LEU ASP LEU VAL GLY ALA PRO E312 D319 THR GLU LEU GLU ALA ARG GLY ARG THR GLU ASP HIS GLY ARG THR ASP HIS SER CYS GLY ARG ARG GLU

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	70599	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 ($e^-/\text{\AA}^2$)	31	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	165000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

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, MG, NAD, ATP, 5F0, GDP, B8T, K, FES, MA6, 5MU, AYA, 5MC

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	0.67	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	0.25	0/953	0.41	0/1289
6	F	0.24	0/1846	0.36	0/2482
7	G	0.25	0/2746	0.39	0/3681
8	H	0.25	0/1178	0.42	0/1598
9	I	0.25	0/1030	0.43	0/1386
10	J	0.27	0/855	0.46	0/1148
11	K	0.23	0/880	0.41	0/1182
12	L	0.24	0/1477	0.36	0/1974
13	M	0.25	0/963	0.43	0/1295
14	N	0.25	0/886	0.44	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	0.39	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	0.42	0/1079
24	X	0.24	0/2921	0.39	0/3954
25	Y	0.24	0/1280	0.37	0/1725
26	Z	0.25	0/857	0.39	0/1141
27	0	0.24	0/1834	0.41	0/2484
28	1	0.24	0/2304	0.38	0/3117
29	3	0.24	0/640	0.38	0/844
30	4	0.23	0/4883	0.36	0/6608
31	8	0.23	0/1560	0.39	0/2089
32	a	0.23	0/1491	0.39	0/2012

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.25	0/72350	0.51	0/102183

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	10253	52	0
2	B	1828	1816	1815	5	0
3	C	1083	1089	1088	6	0
4	D	2731	2805	2804	8	0
5	E	936	955	954	1	0
6	F	1804	1869	1868	7	0
7	G	2688	2690	2687	14	0
8	H	1152	1184	1183	9	0
9	I	1020	1061	1053	7	0
10	J	839	888	887	3	0
11	K	862	886	885	6	0
12	L	1453	1541	1540	6	0
13	M	942	966	965	1	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	3	0
16	P	781	807	806	3	0
17	Q	744	758	758	6	0
18	R	2409	2429	2428	13	0
19	S	1111	1116	1115	4	0
20	T	1371	1394	1393	6	0
21	U	1488	1500	1499	3	0
22	V	2969	2964	2961	12	0
23	W	789	803	802	2	0
24	X	2849	2845	2843	17	0
25	Y	1246	1198	1197	6	0
26	Z	839	860	858	0	0
27	0	1787	1797	1796	10	0
28	1	2256	2289	2288	4	0
29	3	629	702	702	1	0
30	4	4775	4781	4779	23	0
31	8	1543	1589	1587	5	0
32	a	1464	1463	1460	0	0
33	A	44	26	26	1	0
34	3	1	0	0	0	0
34	8	1	0	0	0	0
34	A	61	0	0	0	0
34	B	1	0	0	0	0
34	X	1	0	0	0	0
35	A	17	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	0	13	0	0	0	0
40	1	19	0	0	0	0
40	3	7	0	0	0	0
40	4	3	0	0	0	0
40	8	3	0	0	0	0
40	A	751	0	0	3	0
40	B	31	0	0	0	0
40	C	30	0	0	2	0
40	D	34	0	0	0	0
40	F	11	0	0	0	0
40	G	39	0	0	0	0
40	H	34	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
40	I	7	0	0	0	0
40	J	12	0	0	0	0
40	K	37	0	0	0	0
40	L	3	0	0	0	0
40	M	14	0	0	0	0
40	N	5	0	0	0	0
40	O	24	0	0	0	0
40	P	2	0	0	0	0
40	Q	7	0	0	0	0
40	R	17	0	0	0	0
40	S	9	0	0	0	0
40	T	12	0	0	0	0
40	U	5	0	0	0	0
40	V	6	0	0	0	0
40	W	1	0	0	0	0
40	X	9	0	0	0	0
40	Y	1	0	0	0	0
40	Z	18	0	0	0	0
40	a	2	0	0	0	0
All	All	70406	59850	59789	200	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 200 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)
30:4:200:ASP:OD2	30:4:243:ASN:N	2.14	0.81
12:L:112:MET:O	12:L:116:VAL:HG22	1.90	0.70
1:A:1294:A:OP1	2:B:201:ASN:ND2	2.25	0.70
1:A:1272:A:N1	1:A:1303:G:O2'	2.24	0.68
1:A:1208:U:OP2	40:A:1801:HOH:O	2.11	0.67

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%)	318 (98%)	5 (2%)	0	100	100
8	H	138/201 (69%)	136 (99%)	1 (1%)	1 (1%)	22	54
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%)	107 (99%)	1 (1%)	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
17	Q	84/86 (98%)	84 (100%)	0	0	100	100
18	R	293/360 (81%)	287 (98%)	6 (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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	0	213/218 (98%)	212 (100%)	1 (0%)	0	100	100
28	1	276/323 (85%)	272 (99%)	4 (1%)	0	100	100
29	3	69/199 (35%)	68 (99%)	1 (1%)	0	100	100
30	4	586/689 (85%)	580 (99%)	6 (1%)	0	100	100
31	8	189/278 (68%)	188 (100%)	1 (0%)	0	100	100
32	a	178/343 (52%)	171 (96%)	7 (4%)	0	100	100
All	All	5923/7805 (76%)	5847 (99%)	75 (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%)	286 (100%)	0	100	100
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	97
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	323 (99%)	2 (1%)	86	96
23	W	87/158 (55%)	87 (100%)	0	100	100
24	X	311/351 (89%)	309 (99%)	2 (1%)	86	96
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	172/247 (70%)	172 (100%)	0	100	100
32	a	161/288 (56%)	160 (99%)	1 (1%)	86	96
All	All	5292/6778 (78%)	5286 (100%)	6 (0%)	93	98

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

Mol	Chain	Res	Type
24	X	81	HIS
24	X	394	HIS
32	a	57	TRP
22	V	36	ASP
7	G	389	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
30	4	257	HIS

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Mol	Chain	Res	Type
31	8	118	GLN
32	a	288	GLN
32	a	151	HIS
23	W	121	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	947/955 (99%)	114 (12%)	0

5 of 114 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	649	A
1	A	651	A
1	A	680	U
1	A	687	G
1	A	688	A

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	$\# Z > 2$
9	5F0	I	184	9	8,8,9	0.55	0	7,9,11	1.07	1 (14%)
17	AYA	Q	2	17	6,7,8	0.78	0	5,8,10	0.50	0
1	B8T	A	1486	1	19,22,23	0.32	0	26,31,34	0.32	0
1	MA6	A	1583	1	18,26,27	0.76	0	19,38,41	0.59	0
1	5MU	A	1076	1	19,22,23	0.31	0	28,32,35	0.33	0
1	5MC	A	1488	1	18,22,23	0.32	0	26,32,35	0.44	0
1	MA6	A	1584	1	18,26,27	0.75	0	19,38,41	0.58	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
9	5F0	I	184	9	-	0/9/9/10	-
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	1583	1	-	0/7/29/30	0/3/3/3
1	5MU	A	1076	1	-	0/7/25/26	0/2/2/2
1	5MC	A	1488	1	-	0/7/25/26	0/2/2/2
1	MA6	A	1584	1	-	1/7/29/30	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	184	5F0	O-C-CB	-2.39	118.46	125.43

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 2 short contacts:

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 88 ligands modelled in this entry, 83 are monoatomic - leaving 5 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
39	GDP	X	502	-	24,30,30	0.88	1 (4%)	30,47,47	0.63	0
37	FES	T	201	13,20	0,4,4	-	-	-	-	-
38	ATP	X	501	34	26,33,33	0.76	0	31,52,52	0.64	0
33	NAD	A	1701	34	42,48,48	0.57	0	50,73,73	0.56	1 (2%)
37	FES	P	201	5,16	0,4,4	-	-	-	-	-

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
39	GDP	X	502	-	-	0/12/32/32	0/3/3/3
37	FES	T	201	13,20	-	-	0/1/1/1
38	ATP	X	501	34	-	0/18/38/38	0/3/3/3
33	NAD	A	1701	34	-	1/26/62/62	0/5/5/5
37	FES	P	201	5,16	-	-	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	X	502	GDP	C5-C6	-2.13	1.43	1.47

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	A	1701	NAD	C5A-C6A-N6A	2.29	123.83	120.35

There are no chirality outliers.

All (1) torsion outliers are listed below:

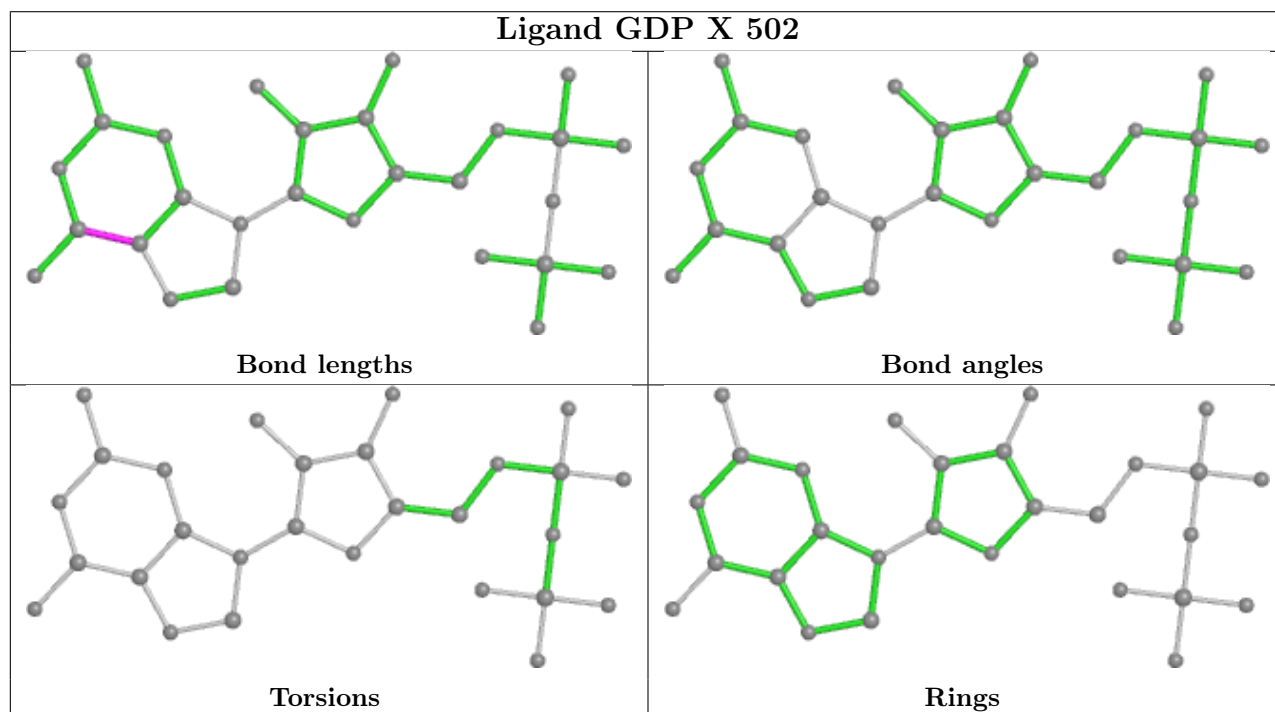
Mol	Chain	Res	Type	Atoms
33	A	1701	NAD	PA-O3-PN-O2N

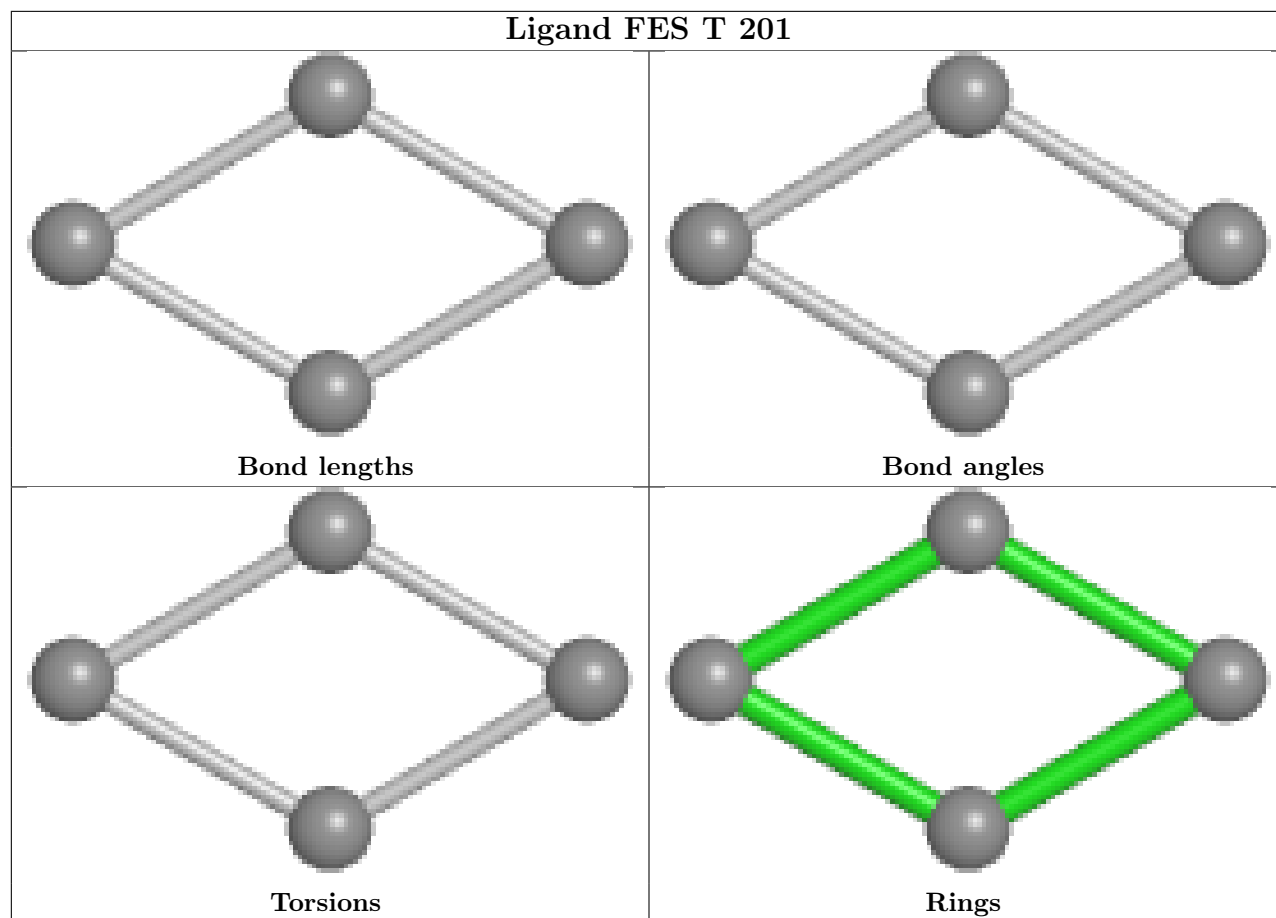
There are no ring outliers.

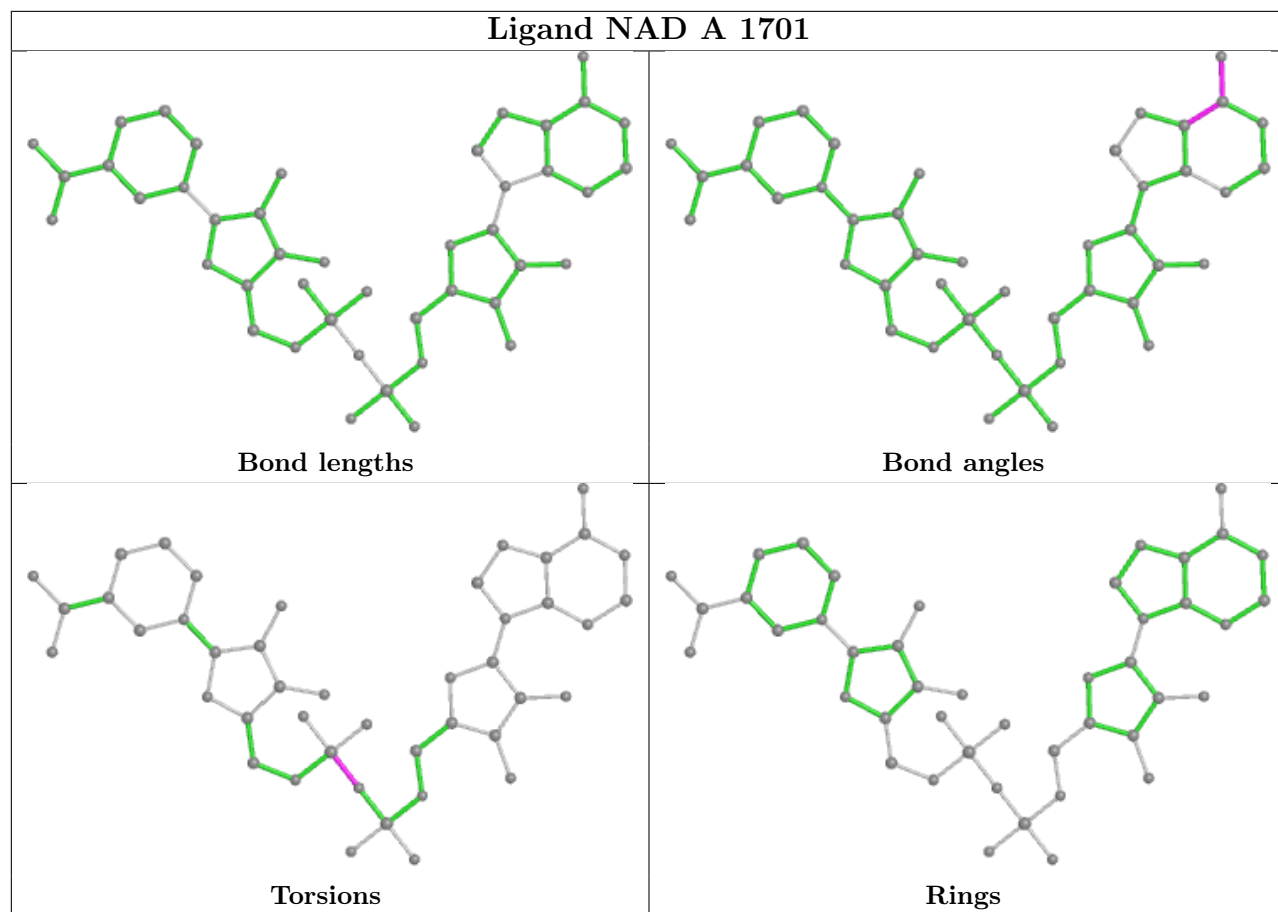
1 monomer is involved in 1 short contact:

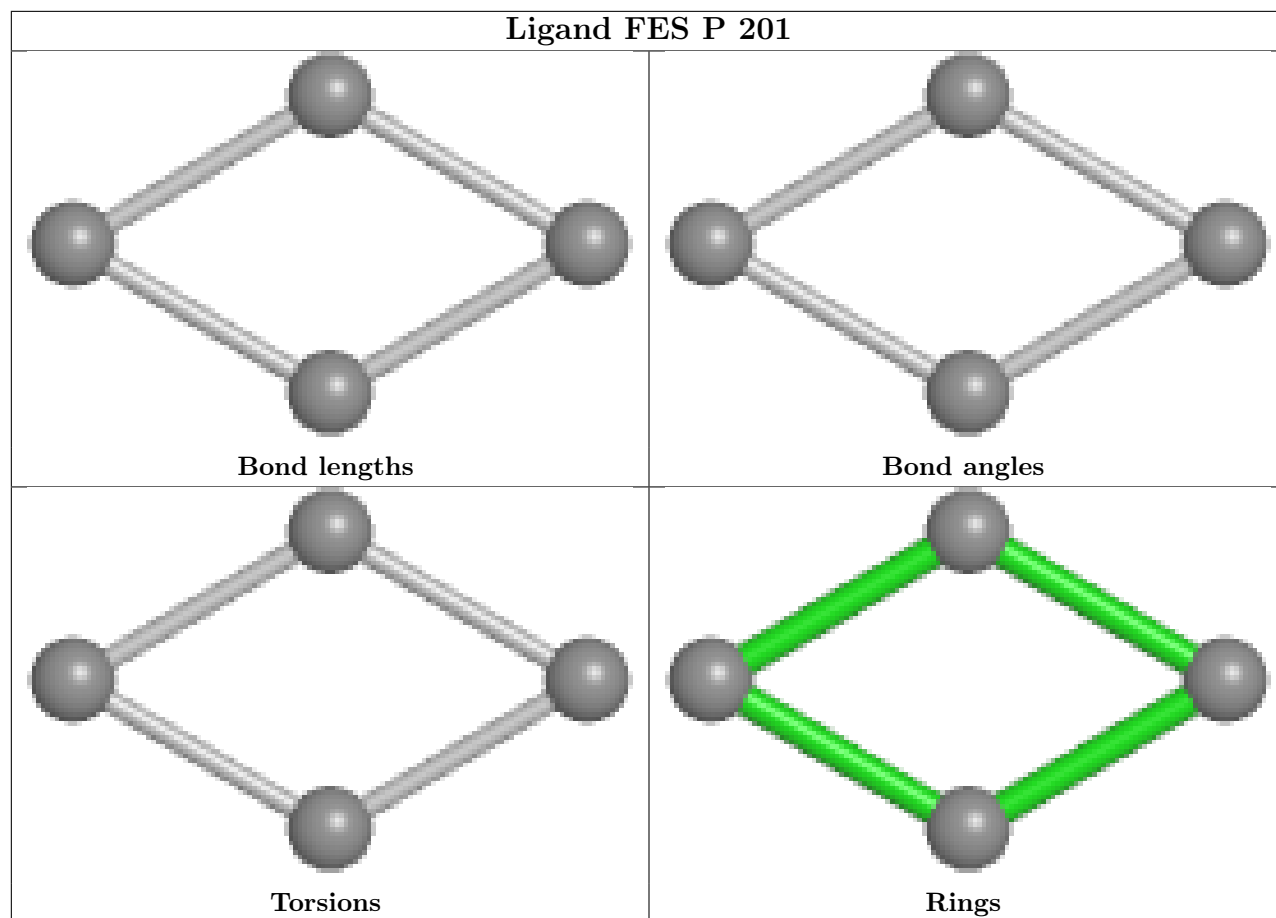
Mol	Chain	Res	Type	Clashes	Symm-Clashes
33	A	1701	NAD	1	0

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 than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-13558. 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

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis

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

7.1 Map-value distribution

This section was not generated.

7.2 Volume estimate versus contour level

This section was not generated.

7.3 Rotationally averaged power spectrum

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.