

wwPDB EM Validation Summary Report (i)

Nov 30, 2022 – 03:48 pm GMT

PDB ID 7ZM8 : EMDB ID EMD-14792 : Title : CryoEM structure of mitochondrial complex I from Chaetomium thermophilum (inhibited by DDM) - membrane arm Authors Laube, E.; Kuehlbrandt, W. : 2022-04-19 Deposited on Resolution 2.76 Å(reported) : Based on initial models 6RFR, 6RFQ :

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 (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.dev43
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.76 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)	$\mathop{\mathrm{EM}}\limits_{(\#\mathrm{Entries})}$		
Ramachandran outliers	154571	4023		
Sidechain outliers	154315	3826		

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 $\geq=3, 2, 1$ and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq=5\%$ The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain	
1	1	378	99%	
2	2	571	98%	·
3	3	146	6 9% 3	1%
4	4	542	90%	• 9%
5	5	679	• 98%	·
6	6	224	84%	16%
7	8	86	90%	10%
8	9	785	13% 87%	
9	D	86	98%	



Mol	Chain	Length	Quality of chain	
10	J	199	<u>5%</u> 94%	6%
11	L	89	98%	·
12	Q	141	60%	40%
13	R	99	99%	·
14	S	143	50% 5	50%
15	U	186	89%	• 10%
16	W	121	83%	17%
17	Х	191	97%	•
18	a	815	18% 82%	
19	b	94	84%	• 15%
20	с	93	• 69%	31%
21	d	105	95%	5%
22	е	46	80%	• 17%
23	g	82	94%	6%
24	i	93	87%	13%
25	j	75	97%	•
26	n	184	73%	27%

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2 Entry composition (i)

There are 32 unique types of molecules in this entry. The entry contains 37030 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

• Molecule 1 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	378	Total 2848	C 1914	N 430	0 494	S 10	0	0

• Molecule 2 is a protein called NADH dehydrogenase subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	558	Total 4456	C 2993	N 672	O 780	S 11	0	0

• Molecule 3 is a protein called NADH-ubiquinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	101	Total 790	С 541	N 115	0 132	${ m S} { m 2}$	0	0

• Molecule 4 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	494	Total 3904	C 2650	N 572	O 670	S 12	0	0

• Molecule 5 is a protein called NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	670	Total 5276	C 3552	N 793	0 906	$\frac{\mathrm{S}}{25}$	0	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	445	ARG	-	insertion	UNP G1DJA3
5	446	LEU	-	insertion	UNP G1DJA3
5	447	ALA	-	insertion	UNP G1DJA3



Chain	Residue	Modelled	Actual	Comment	Reference
5	448	ILE	-	insertion	UNP G1DJA3
5	449	ASP	-	insertion	UNP G1DJA3
5	450	ASN	-	insertion	UNP G1DJA3
5	451	PHE	-	insertion	UNP G1DJA3
5	452	PHE	-	insertion	UNP G1DJA3
5	453	SER	-	insertion	UNP G1DJA3
5	454	ALA	-	insertion	UNP G1DJA3
5	455	GLN	-	insertion	UNP G1DJA3
5	456	ALA	-	insertion	UNP G1DJA3
5	457	ILE	-	insertion	UNP G1DJA3
5	458	LYS	-	insertion	UNP G1DJA3

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• Molecule 6 is a protein called NADH-ubiquinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	189	Total 1460	C 985	N 219	O 250	S 6	0	0

• Molecule 7 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7.

Mol	Chain	Residues		At	oms	AltConf	Trace		
7	8	77	Total 654	C 405	N 125	0 118	S 6	0	0

• Molecule 8 is a protein called Subunit NDUFS5 of NADH-ubiquinone oxidoreductase (Complex I).

Mol	Chain	Residues		At	oms			AltConf	Trace
8	9	102	Total 802	C 497	N 146	0 153	S 6	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
9	100	VAL	-	insertion	UNP G0SG48

• Molecule 9 is a protein called Subunit NDUFA1 of NADH-ubiquinone oxidoreductase (Complex I).



Mol	Chain	Residues		At	oms			AltConf	Trace
9	D	85	Total 678	C 432	N 127	0 115	$\frac{S}{4}$	0	0

• Molecule 10 is a protein called NADH-ubiquinone oxidoreductase-like protein.

Mol	Chain	Residues		At	oms			AltConf	Trace
10	J	188	Total 1408	C 892	N 263	O 251	${ m S} { m 2}$	0	0

• Molecule 11 is a protein called NADH-ubiquinone oxidoreductase chain 4L.

Mol	Chain	Residues		At	oms			AltConf	Trace
11	L	87	Total 673	C 453	N 102	0 115	${ m S} { m 3}$	0	0

• Molecule 12 is a protein called Acyl carrier protein.

Mol	Chain	Residues		At	oms			AltConf	Trace
12	Q	85	Total 670	C 421	N 109	0 139	S 1	0	0

• Molecule 13 is a protein called Complex I-B22.

Mol	Chain	Residues		At	oms	AltConf	Trace		
13	R	98	Total 807	C 520	N 149	0 137	S 1	0	0

• Molecule 14 is a protein called Complex I-ESSS.

Mol	Chain	Residues		Ator	\mathbf{ns}	AltConf	Trace	
14	S	72	Total	C	N	0	0	0
			598	393	96	109		

• Molecule 15 is a protein called NADH-ubiquinone oxidoreductase.

Mol	Chain	Residues		At	oms			AltConf	Trace
15	U	167	Total 1353	C 852	N 252	0 240	S 9	0	0

• Molecule 16 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13.



Mol	Chain	Residues		At	oms			AltConf	Trace
16	W	101	Total 825	$\begin{array}{c} \mathrm{C} \\ 527 \end{array}$	N 156	O 140	${ m S} { m 2}$	0	0

• Molecule 17 is a protein called NADH-ubiquinone oxidoreductase-like protein.

Mol	Chain	Residues		At	oms			AltConf	Trace
17	Х	186	Total 1467	C 934	N 266	O 259	S 8	0	0

• Molecule 18 is a protein called NADH dehydrogenase (Ubiquinone)-like protein.

Mol	Chain	Residues		At	AltConf	Trace			
18	a	143	Total 1167	C 750	N 195	O 217	${ m S}{ m 5}$	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	166	VAL	ALA	conflict	UNP GORXU4
a	168	ALA	MET	conflict	UNP GORXU4
a	?	-	GLU	deletion	UNP GORXU4
a	?	-	GLY	deletion	UNP GORXU4
a	?	-	ASP	deletion	UNP GORXU4
a	?	-	PRO	deletion	UNP GORXU4
a	?	-	ASP	deletion	UNP GORXU4
a	?	-	PRO	deletion	UNP GORXU4

• Molecule 19 is a protein called Subunit NDUFC2 of NADH-ubiquinone oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
19	b	80	Total 675	C 440	N 124	O 109	${ m S} { m 2}$	0	0

• Molecule 20 is a protein called Subunit NDUFB3 of NADH-ubiquinone oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
20	с	64	Total 510	C 332	N 90	O 86	S 2	0	0

• Molecule 21 is a protein called Subunit NDUFB10 of NADH-ubiquinone oxidoreductase



(Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
21	d	100	Total 827	C 526	N 146	0 151	$\frac{S}{4}$	0	0

• Molecule 22 is a protein called Subunit NDUFB2 of NADH-ubiquinone oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
22	e	38	Total	С	Ν	0	S	0	0
	Ũ	00	320	217	58	44	1	Ŭ	0

• Molecule 23 is a protein called Subunit NDUFA3 of NADH-ubiquinone oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
23	g	77	Total 604	C 395	N 104	0 104	S 1	0	0

• Molecule 24 is a protein called Subunit NDUFB6 of NADH-ubiquinone oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
24	i	81	Total 686	C 453	N 119	0 112	${ m S} { m 2}$	0	0

• Molecule 25 is a protein called Subunit NDUFB4 of NADH-ubiquinone oxidoreductase (Complex I).

Mol	Chain	Residues		At	AltConf	Trace			
25	j	73	Total 603	C 391	N 108	0 101	${ m S} { m 3}$	0	0

• Molecule 26 is a protein called Subunit NDUFB5 of NADH-ubiquinone oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
26	n	135	Total 1068	C 683	N 189	0 195	S 1	0	0

There are 52 discrepancies between the modelled and reference sequences:



Chain	Residue	Modelled	Actual	Comment	Reference
n	1	MET	-	initiating methionine	UNP G0S086
n	2	LEU	-	insertion	UNP G0S086
n	3	ALA	-	insertion	UNP G0S086
n	4	LEU	-	insertion	UNP G0S086
n	5	ARG	-	insertion	UNP G0S086
n	6	GLN	-	insertion	UNP G0S086
n	7	ARG	-	insertion	UNP G0S086
n	8	ALA	-	insertion	UNP G0S086
n	9	ALA	-	insertion	UNP G0S086
n	10	LEU	-	insertion	UNP G0S086
n	11	LEU	-	insertion	UNP G0S086
n	12	ALA	-	insertion	UNP G0S086
n	13	ARG	-	insertion	UNP G0S086
n	14	ARG	-	insertion	UNP G0S086
n	15	VAL	-	insertion	UNP G0S086
n	16	ARG	-	insertion	UNP G0S086
n	17	PRO	-	insertion	UNP G0S086
n	18	THR	-	insertion	UNP G0S086
n	19	VAL	-	insertion	UNP G0S086
n	20	VAL	-	insertion	UNP G0S086
n	21	VAL	-	insertion	UNP G0S086
n	22	PRO	-	insertion	UNP G0S086
n	23	ARG	-	insertion	UNP G0S086
n	24	ASN	-	insertion	UNP G0S086
n	25	ALA	-	insertion	UNP G0S086
n	26	ARG	-	insertion	UNP G0S086
n	27	THR	-	insertion	UNP G0S086
n	28	TYR	-	insertion	UNP G0S086
n	29	ALA	-	insertion	UNP G0S086
n	30	SER	-	insertion	UNP G0S086
n	31	SER	-	insertion	UNP G0S086
n	32	HIS	-	insertion	UNP G0S086
n	33	ASP	-	insertion	UNP G0S086
n	34	HIS	-	insertion	UNP G0S086
n	35	ASP	-	insertion	UNP G0S086
n	36	HIS	-	insertion	UNP G0S086
n	37	HIS	-	insertion	UNP G0S086
n	38	ASP	-	insertion	UNP G0S086
n	39	HIS	-	insertion	UNP G0S086
n	40	HIS	-	insertion	UNP G0S086
n	41	HIS	-	insertion	UNP G0S086
n	42	ASP	-	insertion	UNP G0S086
n	43	HIS	-	insertion	UNP G0S086



Chain	Residue	Modelled	Actual	Comment	Reference
n	44	GLY	-	insertion	UNP G0S086
n	45	HIS	-	insertion	UNP G0S086
n	46	ASN	-	insertion	UNP G0S086
n	47	VAL	-	insertion	UNP G0S086
n	48	GLU	-	insertion	UNP G0S086
n	49	GLU	-	insertion	UNP G0S086
n	50	PRO	-	insertion	UNP G0S086
n	51	LEU	-	insertion	UNP G0S086
n	52	GLY	-	insertion	UNP G0S086

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• Molecule 27 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (three-letter code: 3PE) (formula: $C_{41}H_{82}NO_8P$).



Mol	Chain	Residues		Ato	\mathbf{ms}			AltConf
27	1	1	Total	С	Ν	Ο	Р	0
21	T	1	39	29	1	8	1	0
27	5	1	Total	С	Ν	Ο	Р	0
21	5	1	127	97	3	24	3	0
27	ц	1	Total	С	Ν	Ο	Р	0
21	0	1	127	97	3	24	3	0
97	и	1	Total	С	Ν	Ο	Р	0
21	5	1	127	97	3	24	3	0
97	W	1	Total	С	Ν	Ο	Р	0
21	vv	1	76	56	2	16	2	0
97		1	Total	С	Ν	Ο	Р	0
21	vv	1	76	56	2	16	2	0



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Mol	Chain	Residues	Atoms					AltConf
97	;	1	Total	С	Ν	Ο	Р	0
21	1	L	43	33	1	8	1	0

• Molecule 28 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: PC1) (formula: $C_{44}H_{88}NO_8P$).



Mol	Chain	Residues		Ato	oms			AltConf
28	1	1	Total	С	Ν	Ο	Р	0
20	T	T	33	23	1	8	1	0
28	2	1	Total	С	Ν	Ο	Р	0
20	2	T	45	35	1	8	1	0
20	F	1	Total	С	Ν	Ο	Р	0
20	5	L	85	65	2	16	2	0
20	<u> </u>	1	Total	С	Ν	Ο	Р	0
20	5		85	65	2	16	2	U

- Molecule 29 is DODECYL-BETA-D-MALTOSIDE (three-letter code: LMT) (formula: $\rm C_{24}H_{46}O_{11}).$





Mol	Chain	Residues	Atoms	AltConf
29	1	1	Total C O 70 48 22	0
29	1	1	Total C O 70 48 22	0
29	2	1	Total C O 140 96 44	0
29	2	1	Total C O 140 96 44	0
29	2	1	Total C O 140 96 44	0
29	2	1	Total C O 140 96 44	0
29	3	1	Total C O 70 48 22	0
29	3	1	Total C O 70 48 22	0
29	4	1	Total C O 31 20 11	0
29	5	1	Total C O 35 24 11	0
29	J	1	Total C O 70 48 22	0
29	J	1	Total C O 70 48 22	0
29	a	1	Total C O 35 24 11	0
29	g	1	Total C O 34 23 11	0



• Molecule 30 is CARDIOLIPIN (three-letter code: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



Mol	Chain	Residues	A	4ton	ns		AltConf
30	2	1	Total	С	0	Р	0
30	2	I	69	50	17	2	0
30	Л	1	Total	С	Ο	Р	0
30	D	I	65	46	17	2	0
30	q	1	Total	С	Ο	Р	0
30	G	I	61	42	17	2	0
30	v	1	Total	С	Ο	Р	0
30	Λ	I	129	91	34	4	0
30	v	1	Total	С	0	Р	0
- 50	Λ		129	91	34	4	

• Molecule 31 is S-[2-({N-[(2S)-2-hydroxy-3,3-dimethyl-4-(phosphonooxy)butanoyl]-beta-alan yl}amino)ethyl] tetradecanethioate (three-letter code: ZMP) (formula: $C_{25}H_{49}N_2O_8PS$).





Mol	Chain	Residues	Atoms					AltConf	
91	0	1	Total	С	Ν	Ο	Р	S	0
	Q		36	25	2	7	1	1	0

• Molecule 32 is water.

Mol	Chain	Residues	Atoms	AltConf
32	1	36	Total O 36 36	0
32	2	122	Total O 122 122	0
32	3	6	Total O 6 6	0
32	4	96	Total O 96 96	0
32	5	71	Total O 71 71	0
32	6	21	TotalO2121	0
32	9	18	Total O 18 18	0
32	D	23	TotalO2323	0
32	J	3	Total O 3 3	0
32	L	5	Total O 5 5	0
32	Q	3	Total O 3 3	0



Mol	Chain	Residues	Atoms	AltConf
32	R	16	Total O 16 16	0
32	S	7	Total O 7 7	0
32	U	19	Total O 19 19	0
32	W	35	Total O 35 35	0
32	Х	37	Total O 37 37	0
32	a	12	Total O 12 12	0
32	b	6	Total O 6 6	0
32	с	1	Total O 1 1	0
32	d	18	Total O 18 18	0
32	g	2	$\begin{array}{cc} \text{Total} & \text{O} \\ 2 & 2 \end{array}$	0
32	i	5	$\begin{array}{cc} \text{Total} & \text{O} \\ 5 & 5 \end{array}$	0
32	j	18	Total O 18 18	0
32	n	28	Total O 28 28	0

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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: NADH-ubiquinone oxidoreductase chain 1







• Molecule 6: NADH-ubiquinone oxidoreductase chain 6



• Molecule 7: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7



• Molecule 8: Subunit NDUFS5 of NADH-ubiquinone oxidoreductase (Complex I)





• Molecule 9: Subunit NDUFA1 of NADH-ubiquinone oxidoreductase (Complex I)

Chain D:		98%		I
MET P2 P2 V81 X86				
• Molecule 10: N	ADH-ubiquinone ox	xidoreductase-like p	protein	
Chain J:		94%	6%	
•	• • • •• ••	•		
MET PALA PILA PILE GLU GLU GLU GLU HIS GLU HIS HIS MIL2	D70 R105 S128 G132 F134 F134 K135 R136	0137 0198 ALA		
• Molecule 11: N	ADH-ubiquinone ox	xidoreductase chain	4L	
Chain L:		98%		
MET N2 Y88 LYS				
• Molecule 12: A	cyl carrier protein			
Chain O:	60%		40%	I
MET PHE SER SER VAL LEU LEU SER ALA ALA	ALA THR THR THR ILE SER PRO PRO PRO ALA ALA ALA LYS	PHE PHE ALA ALA ALA PRO PRO SER VAL THR THR THR TLE TLE	PRO LYS ALA ALA ALA SER TTRP GGLN VAL ILE ILE TLE CYS CYS SER SER	ASN E57 E63
A91 H141				
Moleculo 12. C	lomplar I D99			
• Molecule 15. C	omplex 1-D22			
Chain R:		99%		l
RE3				
• Molecule 14: C	omplex I-ESSS			
~	L			
Chain S:	50%		50%	
MET ASP GLY GLY GLY PRO PRO PRO PHE ALA ALA PHE PHE PHE	ALA ARG GLN GLN GLY FRO GLY LYS CLY SER SER SER SER SER ALA PRO VAL	THR ARG LEU ALA ALA ALA ALA ALA ALA SER ARG SER ALA SER THR YAL	SER SER LYS ALA ALA LEU THR PLE ARG PHE PHE PHE SER	THR THR GLN ARG





• Molecule 15: NADH-ubiquinone oxidoreductase





MET PRO HIS SER ASP GLY CLY SER ARG CLV GLY	ARG VAL VAL LEU GLN GLN GLN GLN GLN GLN GLN ALA ARG GLN ALA ARG GLN GLU GLU GLU GLU GLU GLU GLU	ALA PHE OLIY MET MET ASN ASN PRO DLU ALA ASN ASN ASN ASN ASN ASN ASN ASN ASN AS
VAL THR PRO PRO LEU PHE ALA ALA ALA ASN GLN SER SER VAL	ASN PRO ULEU VLLU VLL VLLU VLL VLLU VLL VLLU VLL VLL	ASP THR THR THR THR THR THR THR THR ALA ALA ALA ALA ALA ALA ALA ALA ALA CU THR CU N CU CU CU CU
PRO ALA PRO PRO SER ASN ALA ALA ASN ASN GLU GLU VAL	ILE ILE THR SER CLEU CLEU CLEU CLEU CLEU CLEU CLEU CLEU	PHE THR PRO ALA ALA ALA ARG ARG ASP ARG ASP ARG ARG ARG ARG ARG CLU CLN CLN CLN CLN
VAL VAL GLN GLY GLY GLY PHE ALA CLU CLU THR THR YAL	GLU SER TLE GLN	
• Molecule 19: S	ubunit NDUFC2 of NADH-ubiquino	ne oxidoreductase (Complex I)
Chain b:	84%	• 15%
MET V2 F28 B1 ALA ALA ALA ALA ALA ALA ALA ALA ALA	SER SER ALA ALA ALA ALA	
• Molecule 20: S	ubunit NDUFB3 of NADH-ubiquino	ne oxidoreductase (Complex I)
Chain c:	69%	31%
MET GLN PRO TTHR ARC ASN ASN GLY GLY	K13 H76 PHE PHE PHE LEU LU ASP ASP ASP ASP ASP ASP ASP ASP	
• Molecule 21: S	Subunit NDUFB10 of NADH-ubiquin	one oxidoreductase (Complex I)
Chain d:	95%	5%
MET P2 E101 ASN GLN GLN GLN		
• Molecule 22: S	ubunit NDUFB2 of NADH-ubiquino	ne oxidoreductase (Complex I)
Chain e:	80%	• 17%
MET ALA ALA GLY GLY GLN GLN HIS H13 P44 P44 P44 P44 P44	ASP	
• Molecule 23: S	ubunit NDUFA3 of NADH-ubiquino	ne oxidoreductase (Complex I)
Chain g:	94%	6%
MET SER ALA 14 14 ASP ASP ASN		
• Molecule 24: S	ubunit NDUFB6 of NADH-ubiquino	ne oxidoreductase (Complex I)
Chain i:	87%	13%



• Molecule 25: Subunit NDUFB4 of NADH-ubiquinone oxidoreductase (Complex I)

Chain j:	97%	
MET ALA G3 R75		
• Molecul	e 26: Subunit NDUFB5 of NADH-ubiquinone o	xidoreductase (Complex I)
Chain n:	73%	27%
MET LEU ALA LEU ARG GLN ARG	ALA ALA LEU LEU LEU ARG ARG ARG ARG VAL VAL VAL VAL VAL VAL VAL VAL ARG ASN ASN ASN ASN ASN ASN ASN ASS ASS ASS	HIS 044 C75 D92 D92 A175 A175 A175 A178 A178 A178 A178 A178 A178 A178 A178



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	37767	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	45	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.887	Depositor
Minimum map value	-1.296	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.140	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	153.4554, 154.48529, 277.04364	wwPDB
Map dimensions	269, 150, 149	wwPDB
Map angles $(^{\circ})$	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.029902, 1.029902, 1.029902	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: LMT, 3PE, PC1, ZMP, CDL

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).

Mal	Chain	Bo	nd lengths	Bond	angles
	Ullaili	RMSZ	# Z > 5	RMSZ	# Z > 5
1	1	0.49	0/2917	0.62	0/3991
2	2	0.50	0/4562	0.64	0/6205
3	3	0.47	0/811	0.57	0/1105
4	4	0.50	0/4002	0.66	0/5454
5	5	0.44	0/5418	0.58	0/7376
6	6	0.49	0/1487	0.63	0/2026
7	8	0.39	0/667	0.49	0/892
8	9	0.51	0/819	0.69	0/1105
9	D	0.44	0/674	0.66	0/911
10	J	0.38	0/1435	0.56	0/1940
11	L	0.48	0/680	0.62	0/921
12	Q	0.37	0/680	0.47	0/922
13	R	0.47	0/832	0.68	0/1133
14	S	0.48	0/622	0.59	0/850
15	U	0.51	1/1390~(0.1%)	0.73	0/1885
16	W	0.48	0/844	0.69	0/1139
17	Х	0.51	0/1506	0.72	0/2036
18	а	0.36	0/1204	0.52	0/1632
19	b	0.42	0/693	0.60	0/929
20	с	0.37	0/529	0.52	0/720
21	d	0.44	0/845	0.62	0/1137
22	е	0.51	0/335	0.68	0/454
23	g	0.49	0/624	0.66	0/857
24	i	0.40	0/715	0.51	0/971
25	j	0.46	0/617	0.60	0/830
26	n	0.45	0/1100	0.63	0/1491
All	All	0.47	1/36008~(0.0%)	0.62	0/48912

All (1) bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	U	90	HIS	C-N	5.03	1.45	1.34

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	Perce	entiles
1	1	376/378~(100%)	359~(96%)	16 (4%)	1 (0%)	41	60
2	2	554/571~(97%)	540 (98%)	14 (2%)	0	100	100
3	3	97/146~(66%)	95~(98%)	2 (2%)	0	100	100
4	4	490/542~(90%)	473 (96%)	17 (4%)	0	100	100
5	5	668/679~(98%)	637~(95%)	30 (4%)	1 (0%)	51	75
6	6	185/224~(83%)	180 (97%)	5 (3%)	0	100	100
7	8	75/86~(87%)	73~(97%)	2(3%)	0	100	100
8	9	100/785~(13%)	98~(98%)	2 (2%)	0	100	100
9	D	79/86~(92%)	75~(95%)	4 (5%)	0	100	100
10	J	186/199~(94%)	183 (98%)	3 (2%)	0	100	100
11	L	85/89~(96%)	83 (98%)	2 (2%)	0	100	100
12	Q	83/141 (59%)	82 (99%)	1 (1%)	0	100	100
13	R	96/99~(97%)	92 (96%)	4 (4%)	0	100	100
14	S	70/143~(49%)	68 (97%)	2 (3%)	0	100	100



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
15	U	165/186~(89%)	163 (99%)	2 (1%)	0	100	100
16	W	99/121~(82%)	99 (100%)	0	0	100	100
17	Х	184/191~(96%)	178 (97%)	6 (3%)	0	100	100
18	a	141/815~(17%)	137 (97%)	4 (3%)	0	100	100
19	b	78/94~(83%)	76~(97%)	1 (1%)	1 (1%)	12	21
20	с	62/93~(67%)	60 (97%)	2(3%)	0	100	100
21	d	98/105~(93%)	93~(95%)	5 (5%)	0	100	100
22	е	36/46~(78%)	35~(97%)	1 (3%)	0	100	100
23	g	75/82~(92%)	72~(96%)	3 (4%)	0	100	100
24	i	79/93~(85%)	73~(92%)	6 (8%)	0	100	100
25	j	71/75~(95%)	69~(97%)	2 (3%)	0	100	100
26	n	133/184 (72%)	127 (96%)	6 (4%)	0	100	100
All	All	4365/6253~(70%)	4220 (97%)	142 (3%)	3 (0%)	54	75

Continued from previous page...

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
19	b	28	PHE
1	1	228	ILE
5	5	350	VAL

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric Outliers		Percentiles		
1	1	297/326~(91%)	295~(99%)	2(1%)	84 89		
2	2	509/518~(98%)	508 (100%)	1 (0%)	93 96		
3	3	83/128~(65%)	83 (100%)	0	100 100		
4	4	431/477~(90%)	426 (99%)	5 (1%)	71 82		
5	5	581/596~(98%)	579~(100%)	2(0%)	92 95		



Mol	Chain	Analysed	Rotameric	Outliers	Perce	entiles	
6	6	167/203~(82%)	166 (99%)	1 (1%)	86	90	
7	8	68/75~(91%)	68 (100%)	0	100	100	
8	9	84/687~(12%)	84 (100%)	0	100	100	
9	D	68/69~(99%)	67~(98%)	1 (2%)	65	78	
10	J	131/146~(90%)	131 (100%)	0	100	100	
11	L	74/76~(97%)	74 (100%)	0	100	100	
12	Q	74/119~(62%)	74 (100%)	0	100	100	
13	R	87/89~(98%)	87 (100%)	0	100	100	
14	S	58/111~(52%)	58 (100%)	0	100	100	
15	U	148/167~(89%)	148 (100%)	0	100	100	
16	W	84/102~(82%)	84 (100%)	0	100	100	
17	Х	143/152~(94%)	143 (100%)	0	100	100	
18	a	123/697~(18%)	123 (100%)	0	100	100	
19	b	66/74~(89%)	66 (100%)	0	100	100	
20	с	47/80~(59%)	47 (100%)	0	100	100	
21	d	87/94~(93%)	87 (100%)	0	100	100	
22	е	30/35~(86%)	29 (97%)	1 (3%)	38	58	
23	g	65/69~(94%)	65 (100%)	0	100	100	
24	i	69/78~(88%)	69 (100%)	0	100	100	
25	j	63/64~(98%)	63 (100%)	0	100	100	
26	n	108/150~(72%)	108 (100%)	0	100	100	
All	All	3745/5382 (70%)	3732 (100%)	13 (0%)	92	95	

Continued from previous page...

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	4	354	TYR
5	5	340	PHE
22	е	43	HIS
6	6	198	VAL
9	D	81	VAL

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such side chains are listed below:



Mol	Chain	Res	Type
6	6	182	ASN
26	n	84	HIS
14	S	117	GLN
26	n	126	HIS
18	a	101	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

31 ligands 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).

Mal	Mol Type Chain B		Dog	Tink	Bo	ond leng	ths	Bond angles			
	туре	Unain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
28	PC1	5	702	-	39, 39, 53	0.40	0	45,47,61	0.54	0	
29	LMT	1	403	-	36,36,36	1.10	2 (5%)	47,47,47	1.06	2 (4%)	
29	LMT	2	605	-	36,36,36	0.39	0	47,47,47	0.69	0	
29	LMT	g	101	-	35,35,36	1.10	2 (5%)	46,46,47	1.07	3 (6%)	
27	3PE	i	101	-	42,42,50	0.92	4 (9%)	45,47,55	1.08	2 (4%)	
28	PC1	1	402	-	32,32,53	0.34	0	38,40,61	0.39	0	
29	LMT	2	602	-	36,36,36	0.36	0	47,47,47	0.72	1 (2%)	
30	CDL	Х	201	-	52,52,99	0.37	0	58,64,111	0.45	0	
28	PC1	5	703	-	44,44,53	0.33	0	50,52,61	0.36	0	



Mal	Tuno	Chain	Dog	Link	Bo	ond leng	ths	Bo	ond ang	les
	Type	Ullalli	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
29	LMT	3	201	-	36,36,36	0.37	0	47,47,47	0.69	0
29	LMT	3	202	-	36,36,36	0.39	0	47,47,47	0.99	2 (4%)
29	LMT	2	603	-	36,36,36	0.40	0	47,47,47	0.74	0
29	LMT	4	601	-	32,32,36	1.19	2 (6%)	43,43,47	0.88	0
31	ZMP	Q	201	12	29,35,36	0.17	0	34,42,45	0.39	0
27	3PE	5	704	-	41,41,50	0.94	4 (9%)	44,46,55	1.16	2 (4%)
29	LMT	2	604	-	36,36,36	0.39	0	47,47,47	0.82	0
27	3PE	5	706	-	42,42,50	0.29	0	44,46,55	0.34	0
29	LMT	J	201	-	36,36,36	1.13	2(5%)	47,47,47	1.16	3 (6%)
30	CDL	Х	202	-	75,75,99	0.33	0	81,87,111	0.35	0
30	CDL	2	601	-	$68,\!68,\!99$	0.34	0	74,80,111	0.42	0
30	CDL	S	201	-	60,60,99	0.31	0	66,72,111	0.42	0
28	PC1	2	606	-	44,44,53	1.00	3 (6%)	$50,\!52,\!61$	1.18	2 (4%)
27	3PE	W	201	-	39,39,50	0.30	0	42,44,55	0.34	0
27	3PE	5	701	-	40,40,50	0.94	4 (10%)	$43,\!45,\!55$	1.19	3 (6%)
29	LMT	a	901	-	36,36,36	0.35	0	47,47,47	0.83	1 (2%)
30	CDL	D	101	-	64,64,99	0.33	0	70,76,111	0.41	0
29	LMT	J	202	-	36,36,36	0.40	0	47,47,47	0.73	1 (2%)
27	3PE	W	202	-	35,35,50	1.00	4 (11%)	38,40,55	1.19	2 (5%)
29	LMT	5	705	-	36,36,36	1.10	2 (5%)	47,47,47	1.31	5 (10%)
29	LMT	1	404	-	36,36,36	1.13	2 (5%)	47,47,47	0.94	2 (4%)
27	3PE	1	401	-	38,38,50	0.33	0	41,43,55	0.54	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
28	PC1	5	702	-	-	10/43/43/57	-
29	LMT	1	403	-	-	10/21/61/61	0/2/2/2
29	LMT	2	605	-	-	10/21/61/61	0/2/2/2
29	LMT	g	101	-	-	6/20/60/61	0/2/2/2
27	3PE	i	101	-	-	20/46/46/54	-
28	PC1	1	402	-	-	7/36/36/57	-
29	LMT	2	602	-	-	8/21/61/61	0/2/2/2
30	CDL	Х	201	-	-	22/63/63/110	-
28	PC1	5	703	-	-	11/48/48/57	-



Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
29	LMT	3	201	-	-	2/21/61/61	0/2/2/2
29	LMT	3	202	-	-	8/21/61/61	0/2/2/2
29	LMT	2	603	-	_	6/21/61/61	0/2/2/2
29	LMT	4	601	-	_	9/17/57/61	0/2/2/2
31	ZMP	Q	201	12	-	11/40/42/43	-
27	3PE	5	704	-	-	17/45/45/54	-
29	LMT	2	604	-	-	8/21/61/61	0/2/2/2
27	3PE	5	706	-	-	15/45/45/54	-
29	LMT	J	201	-	-	11/21/61/61	0/2/2/2
30	CDL	Х	202	-	-	17/86/86/110	-
30	CDL	2	601	-	-	26/79/79/110	-
30	CDL	S	201	-	-	20/70/70/110	-
28	PC1	2	606	-	-	19/48/48/57	-
27	3PE	W	201	-	-	6/43/43/54	-
27	3PE	5	701	-	-	14/44/44/54	-
29	LMT	a	901	-	-	7/21/61/61	0/2/2/2
30	CDL	D	101	-	-	21/75/75/110	-
29	LMT	J	202	-	-	5/21/61/61	0/2/2/2
27	3PE	W	202	-	-	14/39/39/54	-
29	LMT	5	705	-	-	7/21/61/61	0/2/2/2
29	LMT	1	404	-	-	8/21/61/61	0/2/2/2
27	3PE	1	401	-	-	18/42/42/54	-

Continued from previous page...

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\operatorname{\AA})$
29	J	201	LMT	O5'-C1'	3.38	1.50	1.41
29	4	601	LMT	O5'-C1'	3.30	1.50	1.41
29	J	201	LMT	O5B-C1B	3.29	1.50	1.41
29	4	601	LMT	O5B-C1B	3.28	1.50	1.41
29	1	404	LMT	O5B-C1B	3.28	1.50	1.41

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
28	2	606	PC1	O21-C21-C22	4.76	121.77	111.50
27	5	704	3PE	O21-C21-C22	4.43	121.04	111.50



	$f \rightarrow f \rightarrow$						
Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
27	5	701	3PE	O21-C21-C22	4.11	120.35	111.50
27	W	202	3PE	O21-C21-C22	3.77	119.62	111.50
27	i	101	3PE	O21-C21-C22	3.64	119.35	111.50

Continued from previous page...

There are no chirality outliers.

5 of 373 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
27	1	401	3PE	C1-O11-P-O14
27	1	401	3 PE	C11-O13-P-O12
27	5	701	3PE	O13-C11-C12-N
27	5	704	3PE	C1-O11-P-O14
27	5	704	3PE	C11-O13-P-O12

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.







































5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-14792. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections (i)

6.1.1 Primary map



6.1.2 Raw map



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



6.2 Central slices (i)

6.2.1 Primary map







Z Index: 134

6.2.2 Raw map



X Index: 256

Y Index: 256

Z Index: 256

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



6.3 Largest variance slices (i)

6.3.1 Primary map





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



6.4 Orthogonal surface views (i)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



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.

6.5 Mask visualisation (i)

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



7 Map analysis (i)

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

7.1 Map-value distribution (i)



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



7.2 Volume estimate (i)



The volume at the recommended contour level is 319 nm^3 ; this corresponds to an approximate mass of 288 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)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.



8 Fourier-Shell correlation (i)

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

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.362 ${\rm \AA^{-1}}$



8.2 Resolution estimates (i)

$\begin{bmatrix} Bosolution ostimato (Å) \end{bmatrix}$	Estim	Estimation criterion (FSC cut-off			
resolution estimate (A)	0.143	0.5	Half-bit		
Reported by author	2.76	-	-		
Author-provided FSC curve	2.76	3.24	2.84		
Unmasked-calculated*	4.44	8.53	6.51		

*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 4.44 differs from the reported value 2.76 by more than 10 %



9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-14792 and PDB model 7ZM8. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.



9.2 Q-score mapped to coordinate model (i)



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

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.12).



9.4 Atom inclusion (i)



At the recommended contour level, 89% of all backbone atoms, 89% of all non-hydrogen atoms, are inside the map.



9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8900	0.6040
1	0.8439	0.5810
2	0.9374	0.6370
3	0.8263	0.5680
4	0.9595	0.6430
5	0.9224	0.6160
6	0.8881	0.6040
8	0.8320	0.5480
9	0.8418	0.5700
D	0.9255	0.6300
J	0.7415	0.5350
L	0.9427	0.6260
Q	0.8086	0.5280
R	0.8555	0.5780
S	0.9064	0.5980
U	0.9198	0.6170
W	0.8585	0.6000
Х	0.9258	0.6210
a	0.8651	0.5740
b	0.8710	0.6010
С	0.8458	0.5580
d	0.9217	0.6170
е	0.8058	0.5490
g	0.8675	0.5910
i	0.8590	0.5860
j	0.9396	0.6250
n	0.8292	0.5680



<0.0

