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PDB ID	:	5IT9
EMDB ID	:	EMD-8124
Title	:	Structure of the yeast Kluyveromyces lactis small ribosomal subunit in complex with the cricket paralysis virus IRES.
Authors	:	Murray, J.; Savva, C.G.; Shin, B.S.; Dever, T.E.; Ramakrishnan, V.; Fernandez, I.S.
Deposited on	:	2016-03-16
Resolution	:	3.80 Å(reported)
This is	a I	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. dev 43
MolProbity	:	4.02b-467
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)	:	2.31.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.80 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	EM structures		
	(#Entries)	(#Entries)		
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 $\geq=3, 2, 1$ 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	А	206	87%	12%
2	В	214	91%	8%
3	С	217	88%	12% •
4	D	223	88%	12%
5	Е	260	<u> </u>	9% •
6	F	206	88%	11%
7	G	226	88%	11%
8	Н	184	9% 86%	14%



Mol	Chain	Length	Quality of chain	
9	Ι	200	80%	14% 6%
10	J	182	83%	15% •
11	K	96	86%	14%
12	L	155	14%	10%
13	M	199	60%	0%
14	N	150	12%	970
14	N	107	91%	9% •
15	0	127	91%	7% •
16	Р	123	85%	15% •
17	Q	141	89%	10% •
18	R	129	85%	14% •
19	S	145	83%	15% ·
20	Т	143	8%	10% •
21	U	106	92%	8%
22	V	87	87%	13%
23	W	129	• 85%	14% •
24	Х	145	6 87%	11% ••
25	Y	134	84%	15% •
26	77	70	29%	
26	Z	70	86%	13% •
27	a	100	80%	16% •
28	b	82	90%	10%
29	с	63	95%	5%
30	d	53	92%	8%
31	е	55	25% 87%	13%
32	f	69	64%	17% •
33	g	324	92%	6% •



Mol	Chain	Length	Quality of chain					
	-		13%		_			
34	2	1780	55%	44%	•			
			69%					
35	i	192	44%	55%	•			



2 Entry composition (i)

There are 37 unique types of molecules in this entry. The entry contains 80144 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 Ribosomal protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	А	206	Total 1616	C 1035	N 285	0 294	${S \over 2}$	0	0

• Molecule 2 is a protein called Ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	В	214	Total 1722	C 1089	N 313	0 317	${ m S} { m 3}$	0	0

• Molecule 3 is a protein called Ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	С	217	Total 1629	C 1041	N 287	O 297	$\frac{S}{4}$	0	0

• Molecule 4 is a protein called Ribosomal protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	223	Total 1744	C 1108	N 313	0 318	${S \atop 5}$	0	0

• Molecule 5 is a protein called Ribosomal protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Е	260	Total 2078	C 1322	N 393	O 359	${S \over 4}$	0	0

• Molecule 6 is a protein called Ribosomal protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	206	Total 1609	C 1008	N 298	O 300	${ m S} { m 3}$	0	0



• Molecule 7 is a protein called Ribosomal protein eS6.

Mol	Chain	Residues		Ate	oms			AltConf	Trace
7	G	226	Total 1812	C 1134	N 348	O 326	${f S}$ 4	0	0

• Molecule 8 is a protein called Ribosomal protein eS7.

Mol	Chain	Residues		Ato	ms	AltConf	Trace	
8	Н	184	Total	С	N	Ō	0	0
0	11	104	1483	950	270	263	0	0

• Molecule 9 is a protein called Ribosomal protein eS8.

Mol	Chain	Residues		At	oms	AltConf	Trace		
9	Ι	188	Total 1493	C 926	N 301	O 265	S 1	0	0

• Molecule 10 is a protein called Ribosomal protein uS4.

Mol	Chain	Residues		At	oms			AltConf	Trace
10	J	182	Total 1471	C 929	N 287	0 254	S 1	0	0

• Molecule 11 is a protein called Ribosomal protein eS10.

Mol	Chain	Residues		At	oms			AltConf	Trace
11	K	96	Total 809	C 533	N 129	0 146	S 1	0	0

• Molecule 12 is a protein called Ribosomal protein uS17.

Mol	Chain	Residues		At	AltConf	Trace			
12	L	155	Total 1248	C 798	N 237	O 210	${ m S} { m 3}$	0	0

• Molecule 13 is a protein called Ribosomal protein eS12.

Mol	Chain	Residues		Ato	ms	AltConf	Trace	
13	М	122	Total 922	C 575	N 167	O 180	0	0

• Molecule 14 is a protein called Ribosomal protein uS15.



Mol	Chain	Residues		At	oms			AltConf	Trace
14	Ν	150	Total 1187	C 756	N 223	O 206	${ m S} { m 2}$	0	0

• Molecule 15 is a protein called Ribosomal protein uS14.

Mol	Chain	Residues		At	AltConf	Trace			
15	0	127	Total 942	C 578	N 188	0 173	${ m S} { m 3}$	0	0

• Molecule 16 is a protein called Ribosomal protein uS19.

Mol	Chain	Residues		At	AltConf	Trace			
16	Р	123	Total 980	C 628	N 179	0 168	${ m S}{ m 5}$	0	0

• Molecule 17 is a protein called Ribosomal protein uS9.

Mol	Chain	Residues		Ato	\mathbf{ms}		AltConf	Trace
17	0	1/1	Total	С	Ν	Ο	0	0
11	Q	141	1105	709	204	192	0	0

• Molecule 18 is a protein called Ribosomal protein eS17.

Mol	Chain	Residues		At	AltConf	Trace			
18	R	129	Total 1031	C 641	N 193	0 194	${ m S} { m 3}$	0	0

• Molecule 19 is a protein called Ribosomal protein uS13.

Mol	Chain	Residues		At	oms	AltConf	Trace		
19	S	145	Total 1193	С 741	N 240	0 210	${ m S} { m 2}$	0	0

• Molecule 20 is a protein called Ribosomal protein eS19.

Mol	Chain	Residues		Ato	ms	AltConf	Trace	
20	Т	143	Total 1110	C 693	N 210	O 207	0	0

• Molecule 21 is a protein called Ribosomal protein uS10.



Mol	Chain	Residues		At	oms	AltConf	Trace		
21	U	106	Total 845	C 540	N 152	O 152	S 1	0	0

• Molecule 22 is a protein called Ribosomal protein eS21.

Mol	Chain	Residues		At	oms	AltConf	Trace		
22	V	87	Total 687	C 424	N 126	0 135	${S \over 2}$	0	0

• Molecule 23 is a protein called Ribosomal protein uS8.

Mol	Chain	Residues		At	oms	AltConf	Trace		
23	W	129	Total 1021	C 651	N 187	0 180	${ m S} { m 3}$	0	0

• Molecule 24 is a protein called Ribosomal protein uS21.

Mol	Chain	Residues		At	oms	AltConf	Trace		
24	Х	145	Total 1127	C 713	N 219	0 192	${ m S} { m 3}$	0	0

• Molecule 25 is a protein called Ribosomal protein eS24.

Mol	Chain	Residues		Ato	ms	AltConf	Trace	
25	Y	134	Total 1061	C 665	N 207	O 189	0	0

• Molecule 26 is a protein called Ribosomal protein eS25.

Mol	Chain	Residues		Ate	oms	AltConf	Trace		
26	Ζ	70	Total 558	C 355	N 104	0 98	S 1	0	0

• Molecule 27 is a protein called Ribosomal protein eS26.

Mol	Chain	Residues		At	oms	AltConf	Trace		
27	a	100	Total 798	C 491	N 170	0 131	${ m S}{ m 6}$	0	0

• Molecule 28 is a protein called Ribosomal protein eS27.



Mol	Chain	Residues		At	oms	AltConf	Trace		
28	b	82	Total 617	C 384	N 113	0 114	S 6	0	0

• Molecule 29 is a protein called Ribosomal protein eS28.

Mol	Chain	Residues		Atc	\mathbf{ms}	AltConf	Trace		
29	с	63	Total 494	C 305	N 98	0 90	S 1	0	0

• Molecule 30 is a protein called Ribosomal protein eS29.

Mol	Chain	Residues		Atc	\mathbf{ms}	AltConf	Trace		
30	d	53	Total 446	C 280	N 89	O 76	S 1	0	0

• Molecule 31 is a protein called Ribosomal protein eS30.

Mol	Chain	Residues		Ato	\mathbf{ms}			AltConf	Trace
31	0	55	Total	С	N	Ō	S	0	0
51	C		443	276	90	76	1	0	0

• Molecule 32 is a protein called Ribosomal protein eS31.

Mol	Chain	Residues	Atoms			AltConf	Trace		
32	f	69	Total 549	C 352	N 102	0 91	$\frac{S}{4}$	0	0

• Molecule 33 is a protein called Ribosomal protein RACK1.

Mol	Chain	Residues		At	\mathbf{oms}			AltConf	Trace
33	g	318	Total 2466	C 1561	N 430	0 470	${ m S}{ m 5}$	0	0

• Molecule 34 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms			AltConf	Trace		
34	2	1780	Total 37797	C 16892	N 6658	0 12467	Р 1780	0	0

• Molecule 35 is a RNA chain called Cricket paralysis virus IRES RNA.



Mol	Chain	Residues	Atoms			AltConf	Trace		
35	i	192	Total 3968	C 1774	N 669	O 1333	Р 192	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
i	6176	C	U	conflict	GB 8895506

• Molecule 36 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
36	G	1	Total Mg 1 1	0
36	Ν	1	Total Mg 1 1	0
36	Т	1	Total Mg 1 1	0
36	Х	1	Total Mg 1 1	0
36	2	76	TotalMg7676	0

• Molecule 37 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
37	a	1	Total Zn 1 1	0
37	b	1	Total Zn 1 1	0
37	f	1	Total Zn 1 1	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.

 \bullet Molecule 1: Ribosomal protein uS2





• Molecule 5: Ribosomal protein eS4







 \bullet Molecule 7: Ribosomal protein eS6

Chain G: 88% 11%



 \bullet Molecule 8: Ribosomal protein eS7





• Molecule 9: Ribosomal protein eS8







 \bullet Molecule 20: Ribosomal protein eS19





• Molecule 33: Ribosomal protein RACK1

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	54481	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.973	Depositor
Minimum map value	-0.641	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.042	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	375.2, 375.2, 375.2	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.34, 1.34, 1.34	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: MG, ZN

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	ond lengths	Bond angles		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.39	0/1656	0.77	0/2264	
2	В	0.38	0/1747	0.71	0/2353	
3	С	0.37	0/1659	0.71	0/2252	
4	D	0.36	0/1769	0.70	0/2378	
5	Е	0.36	0/2122	0.67	0/2861	
6	F	0.38	0/1628	0.79	0/2198	
7	G	0.46	2/1835~(0.1%)	0.80	2/2451~(0.1%)	
8	Н	0.38	0/1507	0.73	0/2028	
9	Ι	0.40	0/1519	0.79	0/2033	
10	J	0.44	1/1495~(0.1%)	0.90	3/2001~(0.1%)	
11	Κ	0.40	0/831	0.68	0/1123	
12	L	0.36	0/1276	0.67	0/1718	
13	М	0.40	0/929	0.76	0/1255	
14	Ν	0.40	0/1210	0.84	0/1628	
15	0	0.40	0/953	0.77	0/1279	
16	Р	0.53	1/1000~(0.1%)	0.80	1/1343~(0.1%)	
17	Q	0.38	0/1125	0.75	1/1510~(0.1%)	
18	R	0.40	0/1042	0.84	0/1399	
19	S	0.45	1/1212~(0.1%)	0.81	2/1629~(0.1%)	
20	Т	0.36	0/1129	0.75	0/1520	
21	U	0.35	0/857	0.69	0/1158	
22	V	0.37	0/696	0.69	0/938	
23	W	0.40	0/1039	0.81	0/1399	
24	Х	0.39	0/1145	0.81	1/1526~(0.1%)	
25	Y	0.39	0/1075	0.77	0/1433	
26	Ζ	0.42	0/567	0.81	1/762~(0.1%)	
27	a	0.40	0/810	0.82	0/1084	
28	b	0.34	$0/\overline{627}$	0.67	0/847	
29	с	0.37	0/496	0.73	0/666	
30	d	0.38	0/457	0.64	0/607	
31	е	0.36	0/450	0.68	0/599	
32	f	0.42	0/562	0.67	0/751	

Mal	Chain	Bo	ond lengths	Bond angles		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
33	g	0.35	0/2521	0.58	0/3431	
34	2	0.34	14/42269~(0.0%)	0.78	26/65862~(0.0%)	
35	i	0.34	1/4425~(0.0%)	0.72	1/6875~(0.0%)	
All	All	0.37	20/85640~(0.0%)	0.76	38/125161~(0.0%)	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	А	0	2
7	G	0	1
10	J	0	1
15	0	0	1
17	Q	0	2
22	V	0	1
23	W	0	1
26	Ζ	0	1
27	a	0	1
34	2	0	7
All	All	0	18

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	2	1073	G	C2-N2	-13.62	1.21	1.34
34	2	1074	С	C4-N4	11.59	1.44	1.33
34	2	1072	G	C2-N2	10.69	1.45	1.34
34	2	1073	G	N1-C2	-10.45	1.29	1.37
34	2	1073	G	C6-O6	-10.32	1.14	1.24
34	2	934	U	O3'-P	-10.18	1.49	1.61
35	i	6109	С	O3'-P	-9.66	1.49	1.61
34	2	1044	С	C2-O2	7.30	1.31	1.24
7	G	154	ARG	CA-C	7.19	1.71	1.52
34	2	1073	G	C6-N1	-7.07	1.34	1.39
34	2	8	U	O3'-P	-7.04	1.52	1.61
34	2	520	А	O3'-P	-6.29	1.53	1.61
34	2	77	U	O3'-P	6.25	1.68	1.61
34	2	1069	С	O3'-P	-6.04	1.53	1.61
16	Р	19	GLY	N-CA	5.95	1.54	1.46
7	G	154	ARG	N-CA	5.81	1.57	1.46

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	2	883	А	O3'-P	-5.39	1.54	1.61
34	2	1044	С	N1-C2	5.21	1.45	1.40
10	J	170	GLY	CA-C	5.07	1.59	1.51
19	S	93	ASN	N-CA	5.00	1.56	1.46

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
34	2	1073	G	N1-C2-N2	-16.67	101.20	116.20
34	2	1074	С	C2'-C3'-O3'	11.15	134.03	109.50
34	2	1074	С	N1-C1'-C2'	-9.84	101.17	112.00
26	Z	68	ARG	N-CA-C	-8.17	88.93	111.00
34	2	78	А	C4'-C3'-O3'	7.94	128.88	113.00
34	2	1044	С	N1-C2-O2	7.40	123.34	118.90
34	2	1044	С	C2-N1-C1'	7.22	126.74	118.80
34	2	78	А	C5'-C4'-C3'	7.09	127.34	116.00
34	2	1073	G	N1-C6-O6	-7.08	115.65	119.90
34	2	1082	G	P-O3'-C3'	-6.52	111.88	119.70
34	2	911	U	N1-C1'-C2'	6.41	122.34	114.00
34	2	1076	С	N1-C1'-C2'	-6.38	104.98	112.00
34	2	1074	С	C3'-C2'-C1'	6.34	106.58	101.50
34	2	1044	С	C6-N1-C1'	-6.13	113.44	120.80
34	2	511	А	O5'-P-OP1	6.07	117.98	110.70
34	2	1534	G	C2'-C3'-O3'	6.04	123.36	113.70
34	2	78	А	P-O5'-C5'	6.00	130.51	120.90
34	2	1083	А	O5'-P-OP2	-5.93	100.37	105.70
24	Х	64	PRO	CA-N-CD	-5.82	103.36	111.50
34	2	267	С	N1-C1'-C2'	-5.81	105.61	112.00
34	2	113	U	C2'-C3'-O3'	5.76	122.92	113.70
7	G	155	ASP	CB-CA-C	-5.71	98.99	110.40
35	i	6212	U	N1-C1'-C2'	-5.47	105.98	112.00
34	2	930	С	O4'-C1'-N1	5.46	112.57	108.20
19	S	30	TYR	CB-CA-C	5.43	121.26	110.40
17	Q	52	LEU	CA-CB-CG	5.35	127.61	115.30
34	2	828	А	C2'-C3'-O3'	5.29	122.17	113.70
19	S	93	ASN	N-CA-C	5.20	125.04	111.00
10	J	176	ARG	N-CA-CB	5.18	119.92	110.60
34	2	78	А	O4'-C4'-C3'	-5.12	98.88	104.00
10	J	170	GLY	N-CA-C	5.09	125.81	113.10
10	J	49	LEU	CA-CB-CG	5.08	126.98	115.30
34	2	1628	U	C4'-C3'-O3'	5.08	123.16	113.00
34	2	963	U	C2'-C3'-O3'	5.07	121.82	113.70

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
16	Р	20	VAL	N-CA-C	5.05	124.63	111.00
34	2	1073	G	N3-C2-N2	5.05	123.43	119.90
34	2	511	А	P-O5'-C5'	5.02	128.93	120.90
7	G	208	TYR	CA-CB-CG	-5.01	103.87	113.40

There are no chirality outliers.

All (18) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
34	2	1044	С	Sidechain
34	2	1073	G	Sidechain
34	2	1074	С	Sidechain
34	2	1269	G	Sidechain
34	2	1439	С	Sidechain
34	2	561	G	Sidechain
34	2	583	С	Sidechain
1	А	164	ASN	Peptide
1	А	168	HIS	Peptide
7	G	155	ASP	Peptide
10	J	66	ASP	Peptide
15	0	122	PRO	Peptide
17	Q	40	GLN	Peptide
17	Q	49	TYR	Peptide
22	V	13	VAL	Peptide
23	W	75	ILE	Peptide
26	Ζ	68	ARG	Sidechain
27	a	83	ILE	Peptide

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.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
1	А	204/206~(99%)	168~(82%)	25~(12%)	11 (5%)	2	22
2	В	212/214~(99%)	174 (82%)	32~(15%)	6 (3%)	5	35
3	С	215/217~(99%)	187 (87%)	21 (10%)	7 (3%)	4	32
4	D	221/223~(99%)	198 (90%)	17 (8%)	6 (3%)	5	35
5	Е	258/260~(99%)	214 (83%)	36 (14%)	8 (3%)	4	33
6	F	204/206~(99%)	174 (85%)	21 (10%)	9 (4%)	2	25
7	G	224/226~(99%)	186 (83%)	29 (13%)	9 (4%)	3	28
8	Н	182/184~(99%)	155 (85%)	16 (9%)	11 (6%)	1	20
9	Ι	184/200~(92%)	154 (84%)	22 (12%)	8 (4%)	2	26
10	J	180/182~(99%)	151 (84%)	17 (9%)	12 (7%)	1	19
11	К	94/96~(98%)	80 (85%)	7 (7%)	7 (7%)	1	16
12	L	153/155~(99%)	129 (84%)	17 (11%)	7 (5%)	2	24
13	М	120/122~(98%)	94 (78%)	21 (18%)	5 (4%)	3	26
14	Ν	148/150~(99%)	130 (88%)	14 (10%)	4 (3%)	5	35
15	Ο	125/127~(98%)	108 (86%)	11 (9%)	6 (5%)	2	24
16	Р	121/123~(98%)	96 (79%)	16 (13%)	9(7%)	1	16
17	Q	139/141~(99%)	122 (88%)	12 (9%)	5 (4%)	3	30
18	R	127/129~(98%)	106 (84%)	14 (11%)	7 (6%)	2	22
19	S	143/145~(99%)	119 (83%)	17 (12%)	7 (5%)	2	24
20	Т	141/143~(99%)	126 (89%)	10 (7%)	5 (4%)	3	31
21	U	104/106~(98%)	93~(89%)	7~(7%)	4 (4%)	3	29
22	V	85/87~(98%)	69 (81%)	10 (12%)	6 (7%)	1	17
23	W	127/129~(98%)	107 (84%)	14 (11%)	6 (5%)	2	24
24	Х	143/145~(99%)	121 (85%)	15 (10%)	7 (5%)	2	24
25	Y	132/134~(98%)	113 (86%)	9~(7%)	10 (8%)	1	15
26	Z	68/70~(97%)	58 (85%)	5 (7%)	5 (7%)	1	16
27	a	98/100 (98%)	74 (76%)	13 (13%)	11 (11%)	0	7
28	b	80/82~(98%)	64 (80%)	12 (15%)	4 (5%)	2	23
29	с	61/63~(97%)	55 (90%)	6 (10%)	0	100	100
30	d	51/53~(96%)	41 (80%)	10 (20%)	0	100	100

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	Pe	erc	entil	es
31	е	53/55~(96%)	47 (89%)	3~(6%)	3~(6%)		1	21	
32	f	67/69~(97%)	50 (75%)	11 (16%)	6 (9%)		1	12	
33	g	312/324~(96%)	261 (84%)	44 (14%)	7 (2%)		6	39	
All	All	4776/4866 (98%)	4024 (84%)	534 (11%)	218 (5%)		4	24	

All (218) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	130	ALA
2	В	100	PHE
3	С	149	TRP
4	D	164	VAL
6	F	59	SER
6	F	206	GLY
7	G	154	ARG
8	Н	32	PRO
8	Н	64	VAL
8	Н	74	GLN
9	Ι	10	LYS
10	J	121	SER
11	Κ	88	PRO
12	L	105	LYS
14	Ν	24	ALA
14	Ν	133	SER
15	0	91	SER
16	Р	20	VAL
16	Р	29	PRO
17	Q	40	GLN
17	Q	138	PHE
18	R	26	MET
18	R	121	VAL
19	S	92	VAL
20	Т	11	ALA
21	U	107	THR
21	U	118	ILE
22	V	30	SER
23	W	83	ILE
24	Х	42	PRO
24	X	64	PRO
24	Х	131	SER
25	Y	30	PRO

Mol	Chain	Res	Type
25	Y	60	PHE
26	Ζ	73	GLY
26	Ζ	104	ALA
27	a	18	VAL
27	a	75	ILE
27	a	81	ALA
27	a	86	VAL
28	b	21	LEU
32	f	143	HIS
1	А	26	ALA
1	А	72	ASP
1	А	94	GLY
3	С	141	VAL
3	С	153	LEU
4	D	217	VAL
5	Е	38	LEU
5	Е	195	ILE
5	Е	201	HIS
7	G	122	GLU
8	Н	10	SER
8	Н	13	PRO
8	Н	53	GLY
8	Н	132	PRO
9	Ι	11	ARG
9	Ι	153	ILE
10	J	65	LYS
10	J	118	LEU
11	Κ	81	ASN
11	K	83	PRO
12	L	5	LEU
12	L	7	VAL
12	L	55	ASP
13	М	48	GLY
13	М	82	VAL
13	М	85	ALA
16	Р	12	PHE
16	Р	101	VAL
17	Q	27	GLY
18	R	127	VAL
19	S	26	ILE
19	S	51	ASP
20	Т	43	ASN

Mol	Chain	Res	Type
22	V	22	ARG
23	W	5	SER
23	W	57	ARG
23	W	120	HIS
24	Х	130	VAL
25	Y	64	TYR
27	a	10	ARG
27	a	83	ILE
27	a	85	ARG
32	f	89	LYS
32	f	97	LYS
32	f	111	GLU
33	g	293	ASP
1	А	35	PRO
2	В	209	ASN
3	С	41	VAL
3	С	111	ASP
4	D	44	THR
4	D	93	ASP
5	Е	80	THR
5	Е	95	THR
5	Е	120	SER
5	Е	205	PHE
6	F	53	VAL
6	F	101	MET
7	G	89	ASN
8	Н	29	ASN
9	Ι	22	ARG
9	Ι	40	THR
9	Ι	52	ASN
10	J	97	LEU
10	J	171	ARG
12	L	133	LYS
13	М	78	PRO
15	0	18	ARG
15	0	124	ASP
17	Q	116	LEU
20	Т	50	SER
22	V	4	ASP
22	V	44	ARG
23	W	107	SER
25	Y	61	ARG

Mol	Chain	Res	Type
25	Y	63	GLN
27	a	8	ASN
31	е	11	ALA
31	е	61	SER
32	f	88	PRO
33	g	4	SER
33	g	244	LYS
1	А	9	LEU
1	А	39	LYS
1	А	103	THR
1	А	167	LYS
1	А	193	GLN
2	В	148	ASN
2	В	210	VAL
5	Ε	77	ARG
6	F	83	ARG
7	G	165	GLY
7	G	173	PRO
7	G	177	ARG
8	Н	110	GLN
9	Ι	116	HIS
10	J	35	GLY
10	J	120	LYS
10	J	147	MET
15	0	51	ASP
16	Р	28	MET
16	Р	80	LEU
16	Р	121	ILE
17	Q	115	THR
18	R	100	LEU
20	Т	39	THR
21	U	21	LYS
25	Y	34	ASN
26	Ζ	56	THR
26	Ζ	57	TYR
$\overline{27}$	a	16	GLY
28	b	3	LEU
32	f	106	TYR
33	g	168	ASP
1	A	68	PRO
2	В	190	PRO
3	С	44	THR

Mol	Chain	Res	Type
3	С	65	SER
6	F	40	GLN
6	F	52	ASP
6	F	102	ASN
7	G	8	PRO
7	G	70	PRO
7	G	224	ALA
10	J	18	PRO
10	J	67	PRO
10	J	122	VAL
10	J	134	ILE
11	K	54	PHE
11	K	87	PHE
11	K	94	GLY
12	L	30	LYS
14	N	70	LYS
15	0	114	ARG
18	R	72	LYS
19	S	14	ILE
19	S	144	ARG
21	U	71	PRO
24	Х	4	GLY
25	Y	51	GLU
25	Y	133	ASN
28	b	62	VAL
31	е	47	VAL
2	В	221	PRO
4	D	4	ILE
11	K	2	LEU
12	L	113	PRO
14	N	3	ARG
15	0	25	ASP
16	Р	69	GLU
19	S	12	GLN
20	Т	45	LEU
22	V	46	ILE
22	V	82	VAL
24	X	144	ARG
25	Y	31	ASN
26	Z	62	VAL
27	a	84	VAL
33	g	139	GLY

Mol	Chain	Res	Type
27	a	36	ILE
33	g	278	ILE
6	F	77	GLY
8	Н	8	ILE
13	М	97	ILE
18	R	38	ILE
18	R	124	VAL
23	W	76	SER
4	D	163	PRO
8	Н	98	ILE
9	Ι	39	GLY
24	Х	63	GLN
28	b	39	GLY
33	g	31	PRO
16	Р	53	PRO
19	S	76	PRO
25	Y	29	HIS

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	Perce	entiles
1	А	174/174~(100%)	160 (92%)	14 (8%)	12	42
2	В	196/196~(100%)	182 (93%)	14 (7%)	14	45
3	С	176/176~(100%)	154 (88%)	22 (12%)	4	24
4	D	185/185~(100%)	165 (89%)	20 (11%)	6	30
5	Ε	223/223~(100%)	204 (92%)	19 (8%)	10	40
6	F	174/174~(100%)	158 (91%)	16 (9%)	9	35
7	G	192/192~(100%)	175~(91%)	17 (9%)	9	38
8	Н	164/164~(100%)	149 (91%)	15~(9%)	9	36
9	Ι	148/158~(94%)	126~(85%)	22~(15%)	3	18
10	J	153/153~(100%)	135 (88%)	18 (12%)	5	26
11	K	88/88~(100%)	82 (93%)	6(7%)	16	47

Mol	Chain	Analysed	Rotameric	Outliers	Per	rce	entiles
12	L	136/136~(100%)	126~(93%)	10 (7%)	1	.3	44
13	М	97/97~(100%)	91~(94%)	6~(6%)	1	.8	49
14	Ν	127/127~(100%)	116 (91%)	11 (9%)	1	.0	38
15	Ο	96/96~(100%)	90~(94%)	6 (6%)	1	.8	49
16	Р	105/106~(99%)	96 (91%)	9~(9%)	1	.0	40
17	Q	117/117~(100%)	109~(93%)	8 (7%)	1	6	47
18	R	$117/117\ (100\%)$	104 (89%)	13 (11%)	(6	29
19	S	128/128~(100%)	111 (87%)	17 (13%)	4	4	22
20	Т	$117/117 \ (100\%)$	106 (91%)	11 (9%)	8	8	35
21	U	96/96~(100%)	92~(96%)	4 (4%)	3	80	58
22	V	73/73~(100%)	69 (94%)	4 (6%)	2	21	53
23	W	110/110 (100%)	97~(88%)	13 (12%)	į	5	26
24	Х	120/120~(100%)	105 (88%)	15 (12%)	4	4	24
25	Y	108/108~(100%)	94 (87%)	14 (13%)	4	4	23
26	Ζ	60/60~(100%)	55~(92%)	5 (8%)	1	.1	40
27	a	85/85~(100%)	73~(86%)	12 (14%)	•	3	21
28	b	72/72~(100%)	68 (94%)	4 (6%)	2	21	52
29	с	55/55~(100%)	52 (94%)	3 (6%)	2	21	53
30	d	46/46~(100%)	42 (91%)	4 (9%)	1	.0	38
31	е	49/49~(100%)	45 (92%)	4 (8%)	1	1	40
32	f	58/60~(97%)	48 (83%)	10 (17%)	4	2	13
33	g	265/270~(98%)	251 (95%)	14 (5%)	2	22	54
All	All	4110/4128 (100%)	3730 (91%)	380 (9%)	1	.3	35

All (380) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	9	LEU
1	А	21	ARG
1	А	32	HIS
1	А	56	LYS
1	А	59	LEU
1	А	79	ARG
1	А	108	THR

Mol	Chain	Res	Type
1	А	109	ASN
1	А	135	GLU
1	А	146	LEU
1	А	151	SER
1	А	177	LEU
1	А	198	MET
1	А	205	ARG
2	В	47	LEU
2	В	48	VAL
2	В	70	LEU
2	В	84	VAL
2	В	96	LEU
2	В	100	PHE
2	В	120	LEU
2	В	127	VAL
2	В	167	VAL
2	В	179	SER
2	В	181	LEU
2	В	191	GLU
2	В	194	ASN
2	В	228	LEU
3	С	43	VAL
3	С	49	LEU
3	С	51	LYS
3	С	58	ILE
3	С	59	GLU
3	С	71	PHE
3	С	86	MET
3	С	92	GLN
3	С	93	LYS
3	С	94	GLN
3	C	99	GLN
3	C	100	ARG
3	С	111	ASP
3	C	122	THR
3	C	142	ILE
3	C	145	ARG
3	С	149	TRP
3	C	166	LYS
3	C	167	CYS
3	C	190	LYS
3	С	223	ILE

Mol	Chain	Res	Type
3	С	235	TRP
4	D	5	ILE
4	D	7	LYS
4	D	11	LEU
4	D	17	PHE
4	D	51	ARG
4	D	65	ARG
4	D	101	GLN
4	D	113	LEU
4	D	122	VAL
4	D	134	CYS
4	D	135	GLU
4	D	141	LYS
4	D	143	ARG
4	D	146	ARG
4	D	157	LEU
4	D	162	GLN
4	D	173	ARG
4	D	178	ARG
4	D	179	GLN
4	D	222	VAL
5	Е	6	LYS
5	Е	9	LEU
5	Е	11	ARG
5	Е	18	TRP
5	Е	37	LYS
5	Е	38	LEU
5	Е	42	LEU
5	Е	51	ARG
5	Е	68	ARG
5	Е	77	ARG
5	Е	79	ASP
5	Е	123	LEU
5	Е	133	LYS
5	Е	143	ASP
5	Е	187	ARG
5	Е	208	VAL
5	Е	225	VAL
5	Е	245	LYS
5	Е	247	THR
6	F	81	ASN
6	F	94	ARG

Mol	Chain	Res	Type
6	F	101	MET
6	F	114	ARG
6	F	121	GLU
6	F	158	ARG
6	F	165	SER
6	F	173	SER
6	F	186	PHE
6	F	187	ARG
6	F	188	ASN
6	F	192	ILE
6	F	196	LEU
6	F	210	SER
6	F	211	TYR
6	F	220	GLU
7	G	52	ILE
7	G	75	LEU
7	G	92	ARG
7	G	96	SER
7	G	97	VAL
7	G	136	LYS
7	G	141	ILE
7	G	152	ASP
7	G	153	VAL
7	G	155	ASP
7	G	159	ARG
7	G	164	LYS
7	G	178	LEU
7	G	180	THR
7	G	182	GLN
7	G	183	ARG
7	G	215	ARG
8	Н	11	GLN
8	Н	16	LEU
8	Н	24	PHE
8	Н	27	LEU
8	Н	33	GLU
8	Н	47	ARG
8	Н	80	GLU
8	Н	81	LEU
8	Н	93	LEU
8	Н	114	ARG
8	Н	122	HIS

Mol	Chain	Res	Type
8	Н	126	LEU
8	Н	129	LEU
8	Н	139	ARG
8	Н	174	ASN
9	Ι	8	ARG
9	Ι	10	LYS
9	Ι	24	LYS
9	Ι	25	ARG
9	Ι	29	LEU
9	Ι	35	ASN
9	Ι	62	THR
9	Ι	66	SER
9	Ι	72	VAL
9	Ι	75	LYS
9	Ι	77	ARG
9	Ι	86	SER
9	Ι	96	LEU
9	Ι	107	THR
9	Ι	138	LYS
9	Ι	140	THR
9	Ι	144	TRP
9	Ι	159	SER
9	Ι	160	GLN
9	Ι	161	PHE
9	Ι	170	ILE
9	Ι	190	LEU
10	J	8	TYR
10	J	11	THR
10	J	28	LEU
10	J	30	LEU
10	J	37	LYS
10	J	49	LEU
10	J	61	THR
10	J	64	GLU
10	J	69	ARG
10	J	89	ASP
10	J	97	LEU
10	J	126	ARG
10	J	132	ARG
10	J	145	SER
10	J	149	ARG
10	J	153	GLU

Mol	Chain	Res	Type
10	J	175	LYS
10	J	176	ARG
11	К	15	LEU
11	K	40	LEU
11	K	59	PHE
11	К	76	LEU
11	K	80	LEU
11	K	86	ILE
12	L	8	GLN
12	L	10	GLU
12	L	80	MET
12	L	83	THR
12	L	84	ILE
12	L	87	ARG
12	L	94	VAL
12	L	101	GLU
12	L	105	LYS
12	L	136	ARG
13	М	55	LEU
13	М	67	LEU
13	М	69	GLN
13	М	91	TRP
13	М	104	ARG
13	М	105	LYS
14	N	3	ARG
14	N	12	SER
14	N	25	TRP
14	N	36	GLN
14	Ν	64	LYS
14	N	88	LEU
14	N	89	TYR
14	N	115	LEU
14	N	121	ARG
14	N	139	TRP
14	N	142	GLU
15	0	53	ASP
15	Ο	67	VAL
15	0	71	CYS
15	0	114	ARG
15	0	124	ASP
15	0	127	ARG
16	Р	17	TYR



Mol	Chain	Res	Type
16	Р	40	ARG
16	Р	52	LYS
16	Р	57	MET
16	Р	77	ARG
16	Р	79	HIS
16	Р	84	ILE
16	Р	111	MET
16	Р	127	ARG
17	Q	8	GLN
17	Q	19	VAL
17	Q	46	PHE
17	Q	53	LEU
17	Q	55	VAL
17	Q	121	SER
17	Q	128	LYS
17	Q	142	TYR
18	R	6	THR
18	R	16	LEU
18	R	17	ILE
18	R	27	ASP
18	R	36	ASP
18	R	45	ARG
18	R	47	ARG
18	R	66	VAL
18	R	67	ARG
18	R	88	VAL
18	R	127	VAL
18	R	128	ARG
18	R	130	ARG
19	S	16	ARG
19	S	25	ASN
19	S	36	ARG
19	S	38	VAL
19	S	41	ARG
19	S	49	LYS
19	S	73	MET
19	S	74	GLN
19	S	85	PHE
19	S	93	ASN
19	S	96	LYS
19	S	100	SER
19	S	105	LEU



Mol	Chain	Res	Type
19	S	126	ARG
19	S	128	PHE
19	S	131	LEU
19	S	144	ARG
20	Т	45	LEU
20	Т	53	TRP
20	Т	57	ARG
20	Т	63	ARG
20	Т	68	ARG
20	Т	85	ASN
20	Т	86	ARG
20	Т	100	ILE
20	Т	102	ARG
20	Т	124	ILE
20	Т	139	THR
21	U	52	LYS
21	U	84	MET
21	U	94	GLU
21	U	103	ILE
22	V	12	TYR
22	V	33	GLN
22	V	38	GLN
22	V	50	TYR
23	W	6	VAL
23	W	7	LEU
23	W	11	LEU
23	W	15	ASN
23	W	19	LYS
23	W	23	ARG
23	W	24	GLN
23	W	25	VAL
23	W	28	ARG
23	W	61	ILE
23	W	66	ASN
23	W	70	ASN
23	W	107	SER
24	Х	9	LEU
24	Х	17	VAL
24	Х	19	ARG
24	Х	63	GLN
24	Х	64	PRO
24	Х	70	LYS



Mol	Chain	Res	Type
24	Х	73	ARG
24	Х	93	LEU
24	Х	98	GLU
24	Х	99	ASN
24	Х	102	VAL
24	Х	107	PHE
24	Х	109	ARG
24	Х	114	LYS
24	Х	130	VAL
25	Y	3	ASP
25	Y	6	THR
25	Y	15	ASN
25	Y	29	HIS
25	Y	31	ASN
25	Y	35	VAL
25	Y	46	GLU
25	Y	57	VAL
25	Y	74	LEU
25	Y	98	GLU
25	Y	110	GLN
25	Y	113	ASN
25	Y	116	LYS
25	Y	125	ILE
26	Ζ	49	ARG
26	Ζ	59	TYR
26	Ζ	63	SER
26	Ζ	68	ARG
26	Ζ	97	LYS
27	a	1	MET
27	a	5	ARG
27	a	7	SER
27	a	8	ASN
27	a	18	VAL
27	a	30	VAL
27	a	32	LYS
27	a	33	ASP
27	a	34	LYS
27	a	39	MET
27	a	64	LEU
27	a	75	ILE
28	b	7	LEU
28	b	9	HIS



Mol	Chain	Res	Type
28	b	26	GLN
28	b	67	THR
29	с	16	LEU
29	с	32	PHE
29	С	56	LEU
30	d	21	CYS
30	d	40	ARG
30	d	45	GLU
30	d	49	ASP
31	е	17	GLN
31	е	22	GLU
31	е	33	ARG
31	е	53	LYS
32	f	82	LYS
32	f	89	LYS
32	f	99	LYS
32	f	103	LEU
32	f	106	TYR
32	f	113	LYS
32	f	117	LEU
32	f	120	GLU
32	f	136	ARG
32	f	139	CYS
33	g	27	SER
33	g	43	LEU
33	g	55	PHE
33	g	60	ARG
33	g	67	HIS
33	g	99	ASN
33	g	175	VAL
33	g	188	LEU
33	g	244	LYS
33	g	273	GLU
33	g	275	GLU
33	g	292	GLN
33	g	299	LEU
33	g	321	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

		1000	L JPC
1 A	7	92	HIS



Mol	Chain	Res	Type
1	А	109	ASN
2	В	160	HIS
5	Е	224	ASN
6	F	141	ASN
6	F	202	ASN
7	G	4	ASN
7	G	190	GLN
14	Ν	78	ASN
15	0	29	HIS
16	Р	79	HIS
16	Р	98	ASN
17	Q	83	GLN
19	S	89	GLN
20	Т	25	GLN
23	W	92	ASN
24	Х	18	HIS
24	Х	22	ASN
24	Х	63	GLN
24	Х	79	ASN
25	Y	29	HIS
25	Y	34	ASN
28	b	49	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	2	1778/1780~(99%)	767~(43%)	111~(6%)
35	i	184/192~(95%)	107~(58%)	0
All	All	1962/1972~(99%)	874 (44%)	111 (5%)

All (874) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	2	2	А
34	2	3	U
34	2	4	С
34	2	5	U
34	2	9	U
34	2	10	G
34	2	14	С
34	2	17	С



Mol	Chain	Res	Type
34	2	25	С
34	2	26	А
34	2	32	U
34	2	34	G
34	2	39	А
34	2	40	А
34	2	42	G
34	2	45	U
34	2	47	А
34	2	51	А
34	2	57	G
34	2	59	С
$\overline{34}$	2	60	U
$\overline{34}$	2	61	A
34	2	63	G
$\overline{34}$	2	64	U
34	2	65	А
34	2	66	U
34	2	67	А
34	2	68	А
34	2	69	G
34	2	71	А
34	2	72	A
34	2	73	U
34	2	74	U
34	2	75	U
34	2	76	А
34	2	77	U
$\overline{34}$	2	78	A
34	2	80	A
34	2	81	G
34	2	82	U
34	2	86	A
$\overline{34}$	2	93	A
34	2	101	U
$\overline{34}$	2	104	A
34	2	111	U
$\overline{34}$	2	113	U
34	2	114	C
$\overline{34}$	2	115	G
34	2	123	G
34	2	124	A



Mol	Chain	Res	Type
34	2	125	U
34	2	127	G
34	2	129	U
34	2	130	С
34	2	131	С
34	2	132	U
34	2	133	U
34	2	134	U
34	2	136	С
34	2	137	U
34	2	138	А
34	2	139	С
34	2	140	A
34	2	141	U
$\overline{34}$	2	146	A
$\overline{34}$	2	148	C
$\overline{34}$	2	149	U
34	2	150	G
34	2	152	G
34	2	153	G
34	2	154	U
34	2	155	А
34	2	157	U
34	2	158	U
34	2	159	С
34	2	160	U
34	2	161	А
34	2	167	А
34	2	169	U
34	2	170	А
34	2	173	U
34	2	175	С
34	2	176	U
34	2	177	U
34	2	178	А
34	2	180	A
34	2	183	С
34	2	184	U
34	2	186	G
34	2	187	А
34	2	190	C
34	2	191	U



Mol	Chain	Res	Type
34	2	192	U
34	2	194	G
34	2	195	G
34	2	198	G
34	2	199	А
34	2	203	G
34	2	205	А
34	2	210	U
34	2	217	А
34	2	218	А
34	2	220	А
34	2	224	А
34	2	225	А
34	2	226	U
34	2	228	U
34	2	230	U
34	2	231	U
34	2	232	С
34	2	233	G
34	2	234	G
34	2	235	А
34	2	239	С
34	2	240	U
34	2	241	U
34	2	249	С
34	2	253	А
34	2	256	А
34	2	259	U
34	2	264	А
34	2	265	А
34	2	266	U
34	2	267	С
34	2	268	G
34	2	269	С
34	2	270	A
34	2	274	С
34	2	275	С
34	2	276	U
34	2	277	U
34	2	278	G
34	2	279	U
34	2	280	G



Mol	Chain	Res	Type
34	2	284	G
34	2	286	G
34	2	288	U
34	2	294	А
34	2	298	А
34	2	301	U
34	2	305	U
34	2	308	С
34	2	309	С
34	2	311	А
34	2	312	U
34	2	313	С
34	2	314	А
34	2	315	A
34	2	319	U
34	2	320	C
34	2	321	G
34	2	322	А
34	2	328	G
34	2	332	А
34	2	336	G
34	2	337	С
34	2	342	С
34	2	351	А
34	2	359	А
34	2	360	С
34	2	374	U
34	2	377	А
34	2	382	G
34	2	389	G
34	2	392	С
34	2	397	G
34	2	399	A
34	2	400	A
34	2	401	С
34	2	403	G
34	2	406	A
34	2	410	С
34	2	411	A
34	2	412	U
34	2	414	С
34	2	415	A



Mol	Chain	Res	Type
34	2	416	А
34	2	417	G
34	2	419	А
34	2	421	G
34	2	422	G
34	2	423	С
34	2	424	А
34	2	425	G
34	2	433	G
34	2	436	А
34	2	438	U
34	2	442	С
34	2	443	С
34	2	444	A
34	2	447	С
34	2	452	U
34	2	458	G
34	2	459	А
34	2	460	G
34	2	463	А
34	2	467	А
34	2	474	А
34	2	476	А
34	2	479	G
34	2	480	А
34	2	483	С
34	2	490	C
34	2	491	А
34	2	492	U
34	2	493	U
34	2	494	C
34	2	497	G
34	2	499	C
34	2	500	U
34	2	503	U
34	2	504	A
34	2	505	А
34	2	506	U
34	2	507	U
34	2	509	G
34	2	510	A
34	2	512	U



Mol	Chain	Res	Type
34	2	513	G
34	2	514	А
34	2	516	U
34	2	518	С
34	2	521	U
34	2	524	А
34	2	526	А
34	2	527	U
34	2	532	U
34	2	533	А
34	2	534	А
34	2	535	С
34	2	536	G
34	2	537	A
34	2	538	G
34	2	539	G
34	2	540	А
34	2	541	А
34	2	542	С
34	2	543	А
34	2	544	А
34	2	545	С
34	2	547	G
34	2	548	G
34	2	550	G
34	2	551	G
34	2	553	С
34	2	554	A
34	2	556	G
34	2	557	U
34	2	558	С
34	2	561	G
34	2	564	С
34	2	565	С
34	2	570	G
$\overline{34}$	2	573	G
34	2	574	С
34	2	575	G
34	2	576	G
34	2	577	U
34	2	578	A
34	2	579	A



Mol	Chain	Res	Type
34	2	581	U
34	2	593	А
34	2	594	G
34	2	596	G
34	2	600	А
34	2	605	А
34	2	606	G
34	2	607	U
34	2	610	U
34	2	613	С
34	2	618	А
34	2	619	А
34	2	622	А
34	2	623	G
34	2	629	A
34	2	632	U
34	2	634	A
34	2	637	U
34	2	638	U
34	2	639	U
34	2	640	G
34	2	642	G
34	2	647	G
34	2	648	U
34	2	649	U
34	2	652	С
34	2	653	С
34	2	654	G
$\overline{34}$	2	655	G
34	2	677	G
34	2	678	U
34	2	679	U
34	2	683	C
34	2	684	A
34	2	691	U
34	2	694	U
34	2	695	U
34	2	696	C
34	2	697	С
34	2	698	U
34	2	701	U
34	2	704	С



Mol	Chain	Res	Type
34	2	705	U
34	2	708	С
34	2	709	С
34	2	710	U
34	2	712	U
34	2	713	А
34	2	714	С
34	2	716	C
34	2	717	С
34	2	718	U
34	2	719	U
34	2	722	G
34	2	724	G
34	2	725	U
34	2	727	С
34	2	731	С
34	2	732	G
34	2	733	А
34	2	734	A
34	2	735	С
34	2	736	С
34	2	737	А
34	2	738	G
34	2	740	A
34	2	741	С
34	2	742	U
34	2	743	U
34	2	754	А
34	2	756	А
34	2	765	G
34	2	766	U
34	2	767	U
34	2	769	A
34	2	771	A
34	2	774	A
34	2	778	G
34	2	779	A
34	2	780	A
34	2	781	A
34	2	782	G
34	2	785	С
34	2	786	G



Mol	Chain	Res	Type
34	2	787	А
34	2	788	А
34	2	789	U
34	2	792	А
34	2	793	U
34	2	794	U
34	2	795	А
34	2	802	А
34	2	806	А
34	2	809	G
34	2	811	А
34	2	812	U
34	2	813	A
34	2	815	G
34	2	817	С
34	2	819	U
34	2	820	U
34	2	821	U
34	2	822	G
34	2	823	G
34	2	825	U
34	2	826	С
34	2	828	А
34	2	829	U
34	2	830	U
34	2	831	U
34	2	832	U
34	2	834	U
34	2	837	G
34	2	840	U
34	2	842	U
34	2	844	G
34	2	845	G
34	2	848	С
34	2	849	A
34	2	852	G
34	2	855	A
34	2	859	U
34	2	860	U
34	2	861	A
34	2	862	A
34	2	863	U



Mol	Chain	Res	Type
34	2	872	U
34	2	875	G
34	2	876	G
34	2	884	G
34	2	885	U
34	2	887	U
34	2	894	G
34	2	895	U
34	2	897	А
34	2	903	G
34	2	904	А
34	2	905	А
34	2	906	A
34	2	908	U
34	2	909	C
34	2	910	U
34	2	912	G
34	2	913	G
34	2	914	А
34	2	915	U
34	2	919	U
34	2	920	U
34	2	927	U
34	2	928	А
34	2	929	А
34	2	931	U
34	2	932	А
34	2	934	U
34	2	935	G
34	2	936	С
34	2	939	A
34	2	941	G
34	2	943	A
34	2	944	U
34	2	950	A
34	2	958	U
34	2	959	U
34	2	964	U
34	2	965	A
34	2	969	A
34	2	972	A
34	2	980	U



Mol	Chain	Res	Type
34	2	981	U
34	2	983	G
34	2	985	G
34	2	987	А
34	2	990	G
34	2	991	А
34	2	992	А
34	2	993	G
34	2	994	А
34	2	999	С
34	2	1003	U
34	2	1004	А
34	2	1005	С
34	2	1009	С
34	2	1010	G
34	2	1011	U
34	2	1012	А
34	2	1013	G
34	2	1015	С
34	2	1020	С
34	2	1024	А
34	2	1026	А
34	2	1027	С
34	2	1028	U
34	2	1030	U
34	2	1031	G
34	2	1037	U
34	2	1038	А
34	2	1039	G
34	2	1041	G
34	2	1042	A
34	2	1044	С
34	2	1045	G
34	2	1046	G
34	2	1050	G
34	2	1051	U
34	2	1052	G
34	2	1056	U
34	2	1057	U
34	2	1058	С
34	2	1059	U
34	2	1060	U



Mol	Chain	Res	Type
34	2	1063	G
34	2	1070	U
34	2	1071	С
34	2	1073	G
34	2	1074	С
34	2	1075	А
34	2	1076	С
34	2	1080	A
34	2	1081	С
34	2	1082	G
34	2	1083	А
34	2	1084	G
34	2	1087	A
34	2	1090	A
34	2	1091	A
34	2	1092	A
34	2	1094	U
34	2	1096	U
34	2	1097	U
34	2	1098	U
34	2	1099	G
34	2	1100	G
34	2	1107	G
34	2	1108	G
34	2	1110	G
34	2	1113	G
34	2	1118	G
34	2	1121	G
34	2	1123	A
34	2	1130	А
34	2	1137	A
34	2	1142	A
34	2	1145	G
34	2	1149	G
34	2	1150	A
34	2	1157	С
34	2	1158	С
34	2	1159	A
34	2	1162	А
34	2	1163	G
34	2	1166	G
34	2	1174	U



Mol	Chain	Res	Type
34	2	1175	G
34	2	1183	А
34	2	1184	U
34	2	1185	U
34	2	1189	С
34	2	1190	U
34	2	1192	А
34	2	1193	А
34	2	1195	А
34	2	1196	С
34	2	1198	G
34	2	1199	G
34	2	1200	G
34	2	1201	A
34	2	1202	А
34	2	1203	A
34	2	1204	С
34	2	1211	G
34	2	1212	G
34	2	1213	U
34	2	1215	C
34	2	1216	А
34	2	1217	G
34	2	1218	A
34	2	1219	С
34	2	1222	А
34	2	1224	U
34	2	1226	А
34	2	1227	G
34	2	1228	G
34	2	1229	A
34	2	1230	U
34	2	1231	U
34	2	1234	С
34	2	$1\overline{236}$	G
34	2	1238	U
34	2	1240	G
34	2	1241	A
34	2	1242	G
34	2	1243	A
34	2	1244	G
34	2	1245	С



Mol	Chain	Res	Type
34	2	1247	С
34	2	1250	U
34	2	1253	U
34	2	1254	G
34	2	1257	U
34	2	1258	U
34	2	1259	U
34	2	1265	U
34	2	1266	G
34	2	1268	U
34	2	1269	G
34	2	1274	А
34	2	1282	U
34	2	1284	U
34	2	1296	G
34	2	1306	U
34	2	1310	U
34	2	1313	U
34	2	1314	U
34	2	1317	G
34	2	1319	U
34	2	1320	А
34	2	1321	A
34	2	1322	С
34	2	1324	А
34	2	1336	A
34	2	1339	U
34	2	1340	А
34	2	1343	А
34	2	1344	А
34	2	1345	A
34	2	1347	A
34	2	1349	G
34	2	1353	G
34	2	1356	G
34	2	1358	С
34	2	1359	А
34	2	1360	С
34	2	1361	U
34	2	1362	U
34	2	1363	G
34	2	1364	С



Mol	Chain	Res	Type
34	2	1366	G
34	2	1369	U
34	2	1370	G
34	2	1371	А
34	2	1374	С
34	2	1380	А
34	2	1388	U
34	2	1393	G
34	2	1396	U
34	2	1397	С
34	2	1398	A
34	2	1400	G
34	2	1404	A
34	2	1410	G
34	2	1411	U
34	2	1412	U
34	2	1413	U
34	2	1416	G
34	2	1417	G
34	2	1425	А
34	2	1426	G
34	2	1428	U
34	2	1430	U
34	2	1432	U
34	2	1433	G
34	2	1434	А
34	2	1435	U
34	2	1442	А
34	2	1443	G
34	2	1444	А
34	2	1445	C
34	2	1446	G
34	2	1449	C
34	2	1452	G
34	2	1454	C
34	2	1455	C
34	2	1456	G
34	2	1457	C
34	2	1458	A
34	2	$1\overline{461}$	С
34	2	1464	G
34	2	1467	А



Mol	Chain	Res	Type
34	2	1468	С
34	2	1469	А
34	2	1471	U
34	2	1475	G
34	2	1476	G
34	2	1481	А
34	2	1484	G
34	2	1485	А
34	2	1487	U
34	2	1488	А
34	2	1489	С
34	2	1490	А
34	2	1491	A
34	2	1492	С
34	2	1494	U
34	2	1495	U
34	2	1498	С
34	2	1502	G
34	2	1506	U
34	2	1507	С
34	2	1508	U
34	2	1509	G
34	2	1512	U
34	2	1513	А
34	2	1514	А
34	2	1519	G
34	2	1521	G
34	2	1522	А
34	2	1523	А
34	2	1527	С
34	2	1531	С
34	2	1532	G
34	2	1533	U
34	2	1534	G
34	2	1535	С
34	2	1537	G
34	2	1538	G
34	2	1540	G
34	2	1543	А
34	2	1552	U
34	2	1555	U
34	2	1557	А



Mol	Chain	Res	Type
34	2	1565	U
34	2	1566	С
34	2	1569	С
34	2	1570	G
34	2	1571	А
34	2	1580	U
34	2	1583	U
34	2	1588	G
34	2	1589	С
34	2	1594	С
34	2	1595	А
34	2	1597	С
34	2	1598	А
34	2	1599	G
34	2	1602	U
34	2	1603	G
34	2	1605	G
34	2	1612	А
34	2	1614	G
34	2	1616	С
34	2	1623	С
34	2	1626	U
34	2	1629	А
34	2	1633	A
34	2	1635	С
34	2	1640	G
34	2	1643	G
34	2	1655	U
34	2	1656	G
34	2	1667	U
34	2	1676	А
34	2	1679	А
34	2	1682	U
34	2	1685	U
34	2	1686	U
34	2	1687	А
34	2	1688	G
34	2	1692	А
34	2	1693	G
34	2	1694	G
34	2	1696	G
34	2	1697	G



Mol	Chain	Res	Type
34	2	1698	С
34	2	1699	А
34	2	1700	А
34	2	1701	С
34	2	1702	U
34	2	1703	С
34	2	1706	U
34	2	1707	С
34	2	1708	U
34	2	1709	С
34	2	1710	А
34	2	1711	G
34	2	1712	А
34	2	1725	G
34	2	1730	А
34	2	1740	U
34	2	1743	G
34	2	1748	А
34	2	1753	А
34	2	1754	А
34	2	1755	G
34	2	1756	U
34	2	1758	G
34	2	1759	U
34	2	1763	А
34	2	1764	А
34	2	1766	G
34	2	1767	U
34	2	1770	С
34	2	1774	А
34	2	1776	G
34	2	1777	U
34	2	1778	G
34	2	1779	A
34	2	1780	А
34	2	1781	С
34	2	1784	G
34	2	1789	A
34	2	1790	G
34	2	1791	G
34	2	1792	A
34	2	1793	U



Mol	Chain	Res	Type
34	2	1794	С
34	2	1796	U
34	2	1798	А
35	i	6033	А
35	i	6034	А
35	i	6037	U
35	i	6039	А
35	i	6044	G
35	i	6046	U
35	i	6049	U
35	i	6052	А
35	i	6053	U
35	i	6056	А
35	i	6058	U
35	i	6061	U
35	i	6062	G
35	i	6063	А
35	i	6067	G
35	i	6068	U
35	i	6075	А
35	i	6076	U
35	i	6077	U
35	i	6079	С
35	i	6080	A
35	i	6081	А
35	i	6084	А
35	i	6086	U
35	i	6087	G
35	i	6088	С
35	i	6090	А
35	i	6094	U
35	i	6098	А
35	i	6099	U
35	i	6101	U
35	i	6102	А
35	i	6104	G
35	i	6105	U
35	i	6106	U
35	i	6107	А
35	i	6108	G
35	i	6109	С
35	i	6110	U



Mol	Chain	Res	Type
35	i	6112	U
35	i	6114	U
35	i	6118	U
35	i	6119	U
35	i	6121	А
35	i	6122	С
35	i	6123	G
35	i	6124	U
35	i	6128	А
35	i	6129	G
35	i	6130	G
35	i	6132	U
35	i	6133	G
35	i	6135	С
35	i	6136	U
35	i	6137	А
35	i	6138	G
35	i	6139	U
35	i	6140	G
35	i	6142	С
35	i	6143	А
35	i	6144	G
35	i	6145	С
35	i	6146	С
35	i	6147	С
35	i	6148	С
35	i	6149	A
35	i	6153	U
35	i	6154	А
35	i	6155	U
35	i	6157	С
35	i	6158	А
35	i	6159	G
35	i	6160	G
35	i	6162	А
35	i	6163	G
35	i	6165	С
35	i	6166	С
35	i	6168	С
35	i	6169	U
35	i	6170	С
35	i	6171	U



Mol	Chain	Res	Type
35	i	6172	G
35	i	6173	С
35	i	6174	G
35	i	6176	С
35	i	6178	U
35	i	6179	U
35	i	6180	U
35	i	6181	С
35	i	6183	G
35	i	6184	А
35	i	6186	U
35	i	6187	А
35	i	6192	G
35	i	6197	А
35	i	6198	А
35	i	6199	А
35	i	6200	А
35	i	6202	С
35	i	6210	U
35	i	6211	U
35	i	6212	U
35	i	6213	А
35	i	6218	С
35	i	6219	U
35	i	6220	А
35	i	6221	С

All (111) RNA pucker outliers are listed below:

Mol	Chain	Chain Res T	
34	2	3	U
34	2	44	U
34	2	59	С
34	2	63	G
34	2	65	А
34	2	66	U
34	2	70	С
34	2	71	А
34	2	72	А
34	2	73	U
34	2	129	U
34	2	130	С



Mol	Chain	Res	Type
34	2	137	U
34	2	139	С
34	2	148	С
34	2	149	U
34	2	157	U
34	2	169	U
34	2	177	U
34	2	186	G
34	2	216	А
34	2	217	А
34	2	239	С
34	2	248	U
34	2	258	U
34	2	262	С
34	2	263	G
34	2	264	А
34	2	265	А
34	2	269	С
34	2	271	U
34	2	277	U
34	2	279	U
34	2	321	G
34	2	399	А
34	2	454	С
34	2	497	G
34	2	509	G
34	2	513	G
34	2	532	U
34	2	537	A
34	2	542	С
34	2	556	G
34	2	557	U
34	2	563	G
34	2	564	С
34	2	576	G
34	2	577	U
34	2	578	А
34	2	579	А
34	2	605	А
34	2	621	А
34	2	638	U
34	2	695	U



Mol	Chain	Res	Type
34	2	700	С
34	2	704	С
34	2	708	С
34	2	710	U
34	2	721	U
34	2	740	А
34	2	766	U
34	2	779	А
34	2	792	А
34	2	794	U
34	2	809	G
34	2	811	А
34	2	826	С
34	2	828	A
34	2	854	А
34	2	862	А
34	2	884	G
34	2	909	С
34	2	911	U
34	2	912	G
34	2	913	G
34	2	927	U
34	2	963	U
34	2	1003	U
34	2	1010	G
34	2	1027	С
34	2	1044	С
34	2	1060	U
34	2	1073	G
34	2	1080	А
34	2	1083	А
34	2	1107	G
34	2	1184	U
34	2	1189	С
34	2	1195	А
34	2	1217	G
34	2	1230	U
34	2	1243	А
34	2	1264	G
34	2	1343	А
34	2	1429	С
34	2	1455	С



Mol	Chain	Res	Type
34	2	1470	С
34	2	1491	А
34	2	1501	А
34	2	1532	G
34	2	1534	G
34	2	1556	U
34	2	1598	А
34	2	1613	С
34	2	1628	U
34	2	1634	С
34	2	1655	U
34	2	1678	G
34	2	1763	А
34	2	1765	G
34	2	1791	G

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)

Of 83 ligands modelled in this entry, 83 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.



5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
34	2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	657:C	O3'	676:G	Р	17.80



6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-8124. 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



X Index: 140





Z Index: 140

6.2.2 Raw map



X Index: 140

Y Index: 140



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: 143





Z Index: 149

6.3.2 Raw map



X Index: 145

Y Index: 148

Z Index: 149

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 0.1. 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.



Mask visualisation (i) 6.5

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

$emd_{8124}_{msk_1.map}$ (i) 6.5.1




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 800 $\rm nm^3;$ this corresponds to an approximate mass of 722 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 0.263 ${\rm \AA^{-1}}$



8 Fourier-Shell correlation (i)

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

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.263 ${\rm \AA}^{-1}$



8.2 Resolution estimates (i)

$\begin{bmatrix} Bosolution ostimato (Å) \end{bmatrix}$	Estimation criterion (FSC cut-off)		
resolution estimate (A)	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.79	4.28	3.86
Unmasked-calculated*	4.27	6.68	4.38

*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 4.27 differs from the reported value 3.8 by more than 10 %



9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-8124 and PDB model 5IT9. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay (i)



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)



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 (0.1).



9.4 Atom inclusion (i)



At the recommended contour level, 77% of all backbone atoms, 67% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	$\mathbf{Q} extsf{-score}$
All	0.6727	0.3140
2	0.7327	0.3170
А	0.7336	0.3460
В	0.6394	0.2850
С	0.7758	0.4200
D	0.6473	0.3370
E	0.7457	0.4160
F	0.6266	0.3370
G	0.5483	0.2380
Н	0.6774	0.3140
Ι	0.6050	0.2830
J	0.7472	0.3750
K	0.5854	0.2920
L	0.7021	0.3730
М	0.3190	0.1150
Ν	0.7504	0.3290
0	0.7366	0.3850
Р	0.5352	0.2530
Q	0.6926	0.3620
R	0.6371	0.3090
S	0.3877	0.1730
Т	0.6577	0.3360
U	0.5892	0.3210
V	0.7541	0.3810
W	0.8200	0.4430
X	0.8038	0.4260
Y	0.6693	0.3120
Z	0.5230	0.2640
a	0.7457	0.3880
b	0.7016	0.3450
С	0.6013	0.3480
d	0.7518	0.4040
e	0.6294	0.3100
f	0.3500	0.1300
g	0.5951	0.3310
i	0.2964	0.1530

0.0 <.00

