

wwPDB EM Validation Summary Report (i)

Aug 5, 2023 – 12:26 PM EDT

PDB ID	:	8FFZ
EMDB ID	:	EMD-29071
Title	:	TFIIIA-TFIIIC-Brf1-TBP complex bound to 5S rRNA gene
Authors	:	Talyzina, A.; He, Y.
Deposited on	:	2022-12-11
Resolution	:	3.80 Å(reported)

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:

:	0.0.1. dev 50
:	4.02b-467
:	20191225.v01 (using entries in the PDB archive December 25th 2019)
:	1.9.9
:	Engh & Huber (2001)
:	Parkinson et al. (1996)
:	2.35
	: : : : :

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.



Motric	Whole archive	EM structures		
INTEGI IC	$(\# {\rm Entries})$	$(\# { m Entries})$		
Clashscore	158937	4297		
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 >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Q	uality of chain	
1	А	451	10%	5%	30%
2	В	1160	11%		• 22%
3	С	1025	41%	-	• 22%
4	D	649	39%	60%	
5	Е	672	 75%		• 23%
6	F	588	8%	97%	•••
7	G	435	74%		• 23%
8	Н	736	45%	• 55%	

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Mol	Chain	Length		Quality of chain						
				52%						
9	Ι	171	9%	9%	12%					
				49%						
10	J	171	11%	71%	6%	12%				

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
11	ZN	А	505	-	-	Х	-
11	ZN	А	506	-	-	Х	-
11	ZN	А	507	-	-	Х	-
11	ZN	А	508	-	-	Х	-



2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 38962 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 Transcription factor IIIA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	А	314	Total 2597	C 1631	N 482	0 461	S 23	0	0

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	430	ALA	-	expression tag	UNP P39933
А	431	ASP	-	expression tag	UNP P39933
А	432	PRO	-	expression tag	UNP P39933
А	433	ASN	-	expression tag	UNP P39933
А	434	SER	-	expression tag	UNP P39933
А	435	SER	-	expression tag	UNP P39933
А	436	SER	-	expression tag	UNP P39933
А	437	VAL	-	expression tag	UNP P39933
А	438	ASP	-	expression tag	UNP P39933
А	439	LYS	-	expression tag	UNP P39933
А	440	LEU	-	expression tag	UNP P39933
А	441	ALA	-	expression tag	UNP P39933
А	442	ALA	-	expression tag	UNP P39933
А	443	ALA	-	expression tag	UNP P39933
А	444	LEU	-	expression tag	UNP P39933
А	445	GLU	-	expression tag	UNP P39933
А	446	HIS	-	expression tag	UNP P39933
A	447	HIS	-	expression tag	UNP P39933
А	448	HIS	-	expression tag	UNP P39933
A	449	HIS	-	expression tag	UNP P39933
A	450	HIS	-	expression tag	UNP P39933
A	451	HIS	-	expression tag	UNP P39933

• Molecule 2 is a protein called Transcription factor tau 138 kDa subunit.



Mol	Chain	Residues	Atoms					AltConf	Trace
2	В	005	Total	С	Ν	Ο	\mathbf{S}	0	0
	D	900	7330	4685	1255	1366	24	0	0

• Molecule 3 is a protein called Transcription factor tau 131 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	С	797	Total 6627	C 4242	N 1121	0 1237	S 27	0	0

• Molecule 4 is a protein called Transcription factor tau 95 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	262	Total 2070	C 1318	N 346	O 400	S 6	0	0

• Molecule 5 is a protein called Transcription factor tau 91 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Е	518	Total 4097	C 2623	N 678	O 779	S 17	0	0

• Molecule 6 is a protein called Transcription factor tau 60 kDa subunit.

Mol	Chain	Residues		At	oms			AltConf	Trace
6	F	585	Total 4743	C 3048	N 773	O 899	S 23	0	0

• Molecule 7 is a protein called Transcription factor tau 55 kDa subunit.

Mol	Chain	Residues		Atoms				AltConf	Trace
7	G	336	Total 2705	C 1734	N 448	0 511	S 12	0	0

• Molecule 8 is a protein called Transcription factor IIIB 70 kDa subunit,TATA-box-binding protein.

Mol	Chain	Residues		At	oms			AltConf	Trace
8	Н	328	Total 2593	C 1656	N 460	0 466	S 11	0	0

There are 16 discrepancies between the modelled and reference sequences:



Chain	Residue	Modelled	Actual	Comment	Reference
Н	383	ALA	-	linker	UNP P29056
Н	384	MET	-	linker	UNP P29056
Н	385	PRO	-	linker	UNP P29056
Н	386	TRP	-	linker	UNP P29056
Н	567	GLY	-	linker	UNP P13393
Н	568	SER	-	linker	UNP P13393
Н	569	GLY	-	linker	UNP P13393
Н	570	SER	-	linker	UNP P13393
Н	571	GLY	-	linker	UNP P13393
Н	572	SER	-	linker	UNP P13393
Н	573	GLY	-	linker	UNP P13393
Н	574	SER	-	linker	UNP P13393
Н	575	GLY	-	linker	UNP P13393
Н	576	SER	-	linker	UNP P13393
Н	577	GLY	-	linker	UNP P13393
Н	578	SER	-	linker	UNP P13393

• Molecule 9 is a DNA chain called DNA (151-MER).

Mol	Chain	Residues		A	toms			AltConf	Trace
9	Ι	151	Total 3090	C 1471	N 560	O 908	Р 151	0	0

• Molecule 10 is a DNA chain called DNA (151-MER).

Mol	Chain	Residues		Atoms				AltConf	Trace
10	J	151	Total 3101	C 1474	N 572	0 904	Р 151	0	0

• Molecule 11 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
11	А	9	Total Zn 9 9	0



3 Residue-property plots (i)

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

• Molecule 1: Transcription factor IIIA









\bullet Molecule 6: Transcription factor tau 60 kDa subunit
8% Chain F: 97% ··
MI P47 P47 P47 P47 P47 P47 P415 P415 P415 P415 P464 P464 P235 P227 P2
R431 R443 R443 R454 R448 R448 <t< td=""></t<>
\bullet Molecule 7: Transcription factor tau 55 kDa subunit
Chain G: 74% · 23%
M1 B31 B32 B32 B32 B97 B97 B97 B97 B97 B97 B97 B97
LLE LYS ARG ARG ARG ARG ARA ELYS SER RER ARA ARA ARA ARA ARA ARA ARA ARA A
ASN TILE OLIN OLIN OLIN OLIN OLIU OLIU ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP
• Molecule 8: Transcription factor IIIB 70 kDa subunit, TATA-box-binding protein
Chain H: 43% • 55%
MET PRO CYAL CYAL CYAL CYAL CYAL CYAL CYAL ASP CYAL CYAL CYAL CYAL CYAL CYAL CYAL CYAL
GLY SER ALA ALA ALA ALA ALA ALA ALA ALA SER SER SER SER SER ALA ALA ALA ALA ALA ALA ALA ALA ALA AL
ARG SER ASN ASN ASN ASN ASN ASN ASN ASN ASS ASE ASS ASS ASS ASS ASS ASS ASS ASS
H N N A R R F R R F Z R R F R R F R R F R R F R R F H N F H N F R R F R F R R R F R
F18 1141 1141 1141 1141 1141 1141 1141 1
H241 1242 1244 1244 1244 1244 1244 1244
LYS ASP ASP ASP ASP ASP ASP ASP CLU CLU CLU CLU CLU CLU CLU CLU CLU CLU
LLE ASP GLY GLY GLY GLU GLU GLU GLU GLU GLU GLU GLU GLU GLU

W O R L D W I D E PROTEIN DATA BANK





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	78512	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	60	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 $(6k \ge 4k)$	Depositor
Maximum map value	0.102	Depositor
Minimum map value	-0.060	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.016	Depositor
Map size (Å)	405.504, 405.504, 405.504	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.056, 1.056, 1.056	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

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	Bond	lengths	E	Bond angles
	Unain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.65	0/2665	0.97	11/3584~(0.3%)
2	В	0.64	0/7445	1.00	22/10016~(0.2%)
3	С	0.69	0/6761	1.03	22/9123~(0.2%)
4	D	0.59	0/2112	0.94	3/2851~(0.1%)
5	Е	0.63	0/4190	1.02	10/5685~(0.2%)
6	F	0.64	0/4854	1.01	10/6585~(0.2%)
7	G	0.67	0/2773	1.04	11/3761~(0.3%)
8	Н	0.71	0/2638	1.01	8/3549~(0.2%)
9	Ι	1.64	0/3464	2.42	284/5343~(5.3%)
10	J	1.64	0/3480	2.42	304/5370~(5.7%)
All	All	0.90	0/40382	1.39	685/55867~(1.2%)

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
2	В	0	3
3	С	0	4
4	D	0	3
5	Е	0	2
6	F	0	1
8	Н	0	1
9	Ι	0	17
10	J	0	12
All	All	0	45

There are no bond length outliers.



Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
9	Ι	94	DA	N1-C6-N6	-11.51	111.69	118.60
10	J	136	DA	N1-C6-N6	-10.81	112.12	118.60
10	J	36	DA	N1-C6-N6	-10.80	112.12	118.60
10	J	44	DA	N1-C6-N6	-9.90	112.66	118.60
9	Ι	147	DA	N1-C6-N6	-9.86	112.69	118.60

The worst 5 of 685 bond angle outliers are listed below:

There are no chirality outliers.

5 of 45 planarity outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	Group
1	А	45	ARG	Sidechain
1	А	62	ARG	Sidechain
2	В	1154	TYR	Sidechain
2	В	339	TYR	Sidechain
2	В	908	ARG	Sidechain

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	А	2597	0	2549	13	0
2	В	7330	0	7550	6	0
3	С	6627	0	6547	4	0
4	D	2070	0	2097	0	0
5	Е	4097	0	4072	2	0
6	F	4743	0	4705	1	0
7	G	2705	0	2653	0	0
8	Н	2593	0	2692	0	0
9	Ι	3090	0	1701	0	0
10	J	3101	0	1699	0	0
11	А	9	0	0	11	0
All	All	38962	0	36265	25	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 0.

The worst 5 of 25 close contacts within the same asymmetric unit are listed below, sorted by their



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:255:CYS:HG	11:A:507:ZN:ZN	0.77	0.95
1:A:367:CYS:HG	11:A:508:ZN:ZN	0.85	0.80
1:A:168:CYS:HG	11:A:505:ZN:ZN	0.98	0.74
1:A:227:CYS:HG	11:A:506:ZN:ZN	1.03	0.71
1:A:113:CYS:SG	11:A:503:ZN:ZN	1.86	0.64

clash magnitude.

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	Perce	ntiles
1	А	310/451~(69%)	285~(92%)	25~(8%)	0	100	100
2	В	883/1160 (76%)	842 (95%)	40 (4%)	1 (0%)	51	83
3	С	787/1025~(77%)	760 (97%)	27 (3%)	0	100	100
4	D	258/649~(40%)	245 (95%)	13 (5%)	0	100	100
5	Е	516/672~(77%)	484 (94%)	31 (6%)	1 (0%)	47	79
6	F	581/588~(99%)	541 (93%)	40 (7%)	0	100	100
7	G	328/435~(75%)	307~(94%)	19 (6%)	2(1%)	25	62
8	Н	322/736~(44%)	297 (92%)	24 (8%)	1 (0%)	41	74
All	All	3985/5716 (70%)	3761 (94%)	219 (6%)	5 (0%)	54	83

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	В	653	THR
7	G	122	GLU
8	Н	514	GLU
5	Е	227	ILE

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Mol	Chain	Res	Type
7	G	90	ILE

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	\mathbf{s}
1	А	297/422~(70%)	296 (100%)	1 (0%)	92 96	
2	В	825/1049~(79%)	820~(99%)	5 (1%)	86 92	
3	С	719/925~(78%)	718 (100%)	1 (0%)	93 97	
4	D	243/588~(41%)	242 (100%)	1 (0%)	91 95	
5	Ε	460/592~(78%)	459 (100%)	1 (0%)	93 97	
6	F	541/544~(99%)	538~(99%)	3~(1%)	86 92	
7	G	295/384~(77%)	295 (100%)	0	100 100	
8	Η	282/623~(45%)	281 (100%)	1 (0%)	91 95	
All	All	3662/5127~(71%)	3649 (100%)	13 (0%)	91 95	

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

Mol	Chain	\mathbf{Res}	Type
4	D	24	LEU
5	Е	291	LEU
8	Н	416	ARG
6	F	353	ARG
6	F	411	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

Of 9 ligands modelled in this entry, 9 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)

There are no chain breaks in this entry.



6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-29071. 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: 192



Y Index: 192



Z Index: 192

6.2.2 Raw map



X Index: 192

Y Index: 192

Z Index: 192

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: 193



Y Index: 191



Z Index: 210

6.3.2 Raw map



X Index: 192

Y Index: 191



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



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

6.4.1 Primary map



6.4.2 Raw map



The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.



6.5 Orthogonal surface views (i)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.016. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

6.6 Mask visualisation (i)

This section 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 242 $\rm nm^3;$ this corresponds to an approximate mass of 219 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	3.81	4.41	3.90	
Unmasked-calculated*	4.31	7.78	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 4.31 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-29071 and PDB model 8FFZ. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.016 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 (0.016).



9.4 Atom inclusion (i)



At the recommended contour level, 68% of all backbone atoms, 57% 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 (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score	
All	0.5740	0.3330	1.0
А	0.6860	0.3460	
В	0.6810	0.3740	
С	0.4290	0.3050	
D	0.8220	0.4710	
Е	0.7600	0.4400	
F	0.7160	0.4110	
G	0.7440	0.4030	
Н	0.0000	0.0300	0.0
Ι	0.4050	0.2330	<0.0
J	0.4080	0.2290	

