



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:17 PM BST

PDB ID : 5ANC  
EMDB ID: : EMD-3145  
Title : Mechanism of eIF6 release from the nascent 60S ribosomal subunit  
Authors : Weis, F.; Giudice, E.; Churcher, M.; Jin, L.; Hilcenko, C.; Wong, C.C.;  
Traynor, D.; Kay, R.R.; Warren, A.J.  
Deposited on : 2015-09-06  
Resolution : 4.20 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.  
For rigid body fitted models, validation errors reported here could  
stem from errors in the original structure(s) used in the fitting.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

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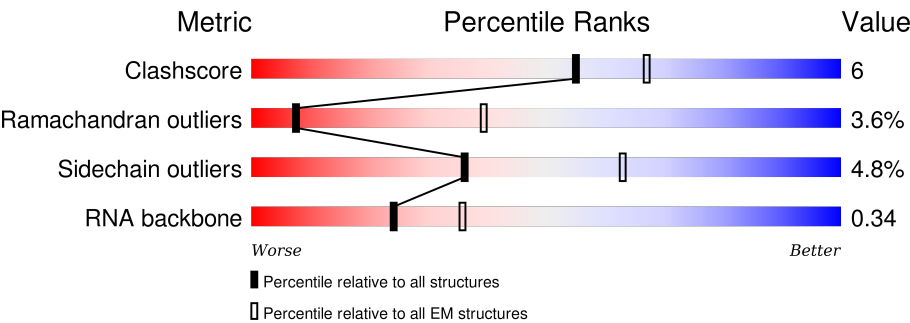
MolProbity : 4.02b-467  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk27241

# 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 4.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	398	<div><div>70%</div><div>26%</div><div>.</div><div>.</div></div>
2	B	188	<div><div>75%</div><div>24%</div><div>.</div></div>
3	C	205	<div><div>95%</div><div>5%</div></div>
4	D	166	<div><div>90%</div><div>10%</div></div>
5	E	136	<div><div>79%</div><div>18%</div><div>.</div></div>
6	F	217	<div><div>77%</div><div>20%</div><div>.</div></div>
7	G	69	<div><div>80%</div><div>19%</div><div>.</div></div>
8	H	52	<div><div>77%</div><div>19%</div><div>.</div></div>

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Mol	Chain	Length	Quality of chain
9	J	250	<div><div></div><div>86%</div><div>14%</div><div></div></div>
10	K	1120	<div><div></div><div>90%</div><div>9%</div><div></div></div>
11	N	3741	<div><div></div><div>13%</div><div>14%</div><div></div><div>69%</div></div>

## 2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 46807 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 60S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	398	Total	C	N	O	S	0	0
			3176	2018	599	547	12		

- Molecule 2 is a protein called 60S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	188	Total	C	N	O	S	0	0
			1491	944	264	277	6		

- Molecule 3 is a protein called 60S ACIDIC RIBOSOMAL PROTEIN P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	205	Total	C	N	O	S	0	0
			1571	998	271	294	8		

- Molecule 4 is a protein called 60S RIBOSOMAL PROTEIN L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	166	Total	C	N	O	S	0	0
			1245	790	220	228	7		

- Molecule 5 is a protein called 60S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	136	Total	C	N	O	S	0	0
			1017	640	188	181	8		

- Molecule 6 is a protein called 60S RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	217	Total	C	N	O	S	0	0
			1721	1079	332	297	13		

- Molecule 7 is a protein called 60S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	69	Total	C	N	O	S	0	0
			586	378	105	99	4		

- Molecule 8 is a protein called UBIQUITIN-60S RIBOSOMAL PROTEIN L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	52	Total	C	N	O	S	0	0
			427	269	88	64	6		

- Molecule 9 is a protein called RIBOSOME MATURATION PROTEIN SBDS.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	250	Total	C	N	O	S	0	0
			2015	1272	352	380	11		

- Molecule 10 is a protein called ELONGATION FACTOR TU GTP-BINDING DOMAIN-CONTAINING PROTEIN 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	1120	Total	C	N	O	S	0	0
			8800	5547	1518	1682	53		

- Molecule 11 is a RNA chain called 26S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N	1162	Total	C	N	O	P	0	0
			24758	11082	4431	8087	1158		

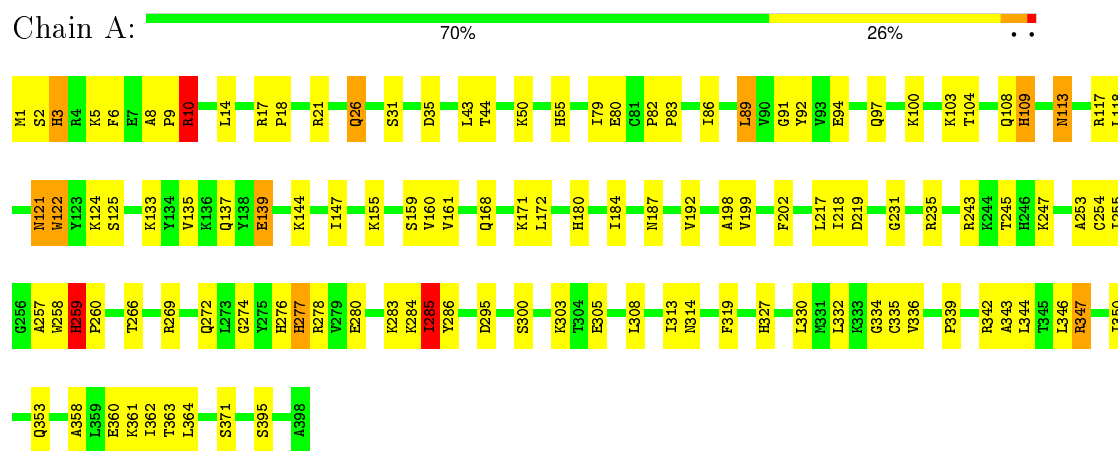
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	3119	C	G	CONFLICT	GB FR733594.

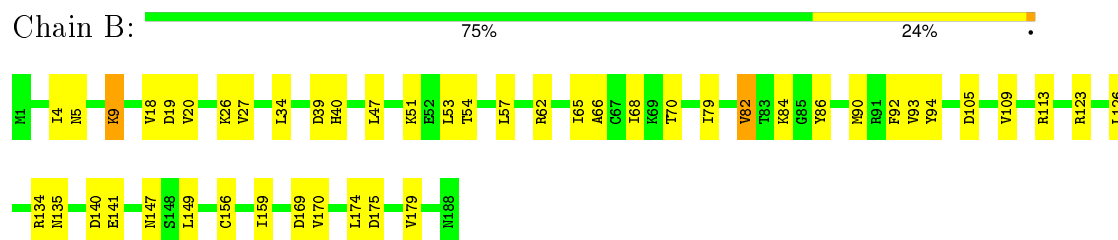
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

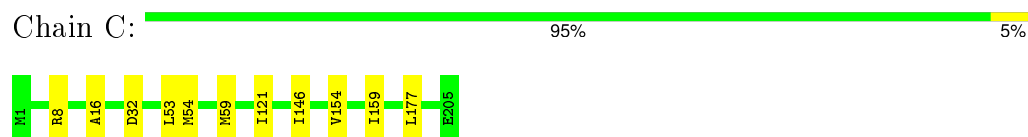
#### • Molecule 1: 60S RIBOSOMAL PROTEIN L3



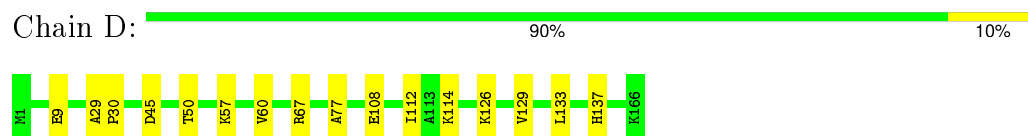
#### • Molecule 2: 60S RIBOSOMAL PROTEIN L9




#### • Molecule 3: 60S ACIDIC RIBOSOMAL PROTEIN P0

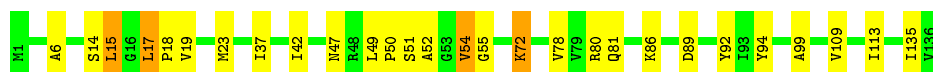


#### • Molecule 4: 60S RIBOSOMAL PROTEIN L12




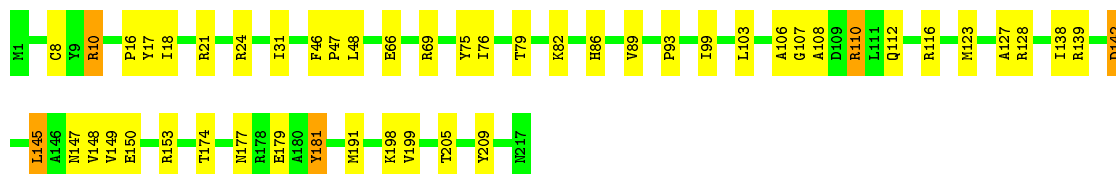
#### • Molecule 5: 60S RIBOSOMAL PROTEIN L23

Chain E:  79% 18%




- Molecule 6: 60S RIBOSOMAL PROTEIN L10

Chain F:  77% 20%




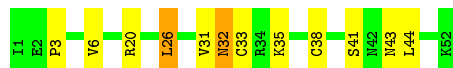
- Molecule 7: 60S RIBOSOMAL PROTEIN L24

Chain G:  80% 19%




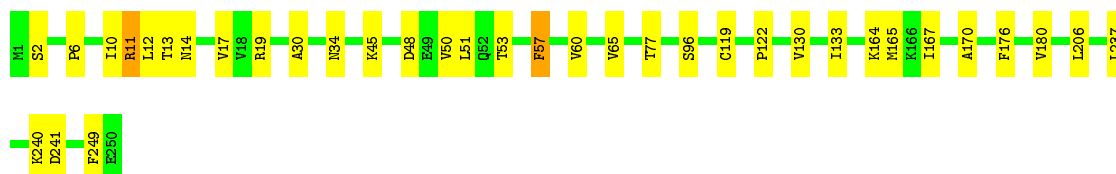
- Molecule 8: UBIQUITIN-60S RIBOSOMAL PROTEIN L40

Chain H:  77% 19%



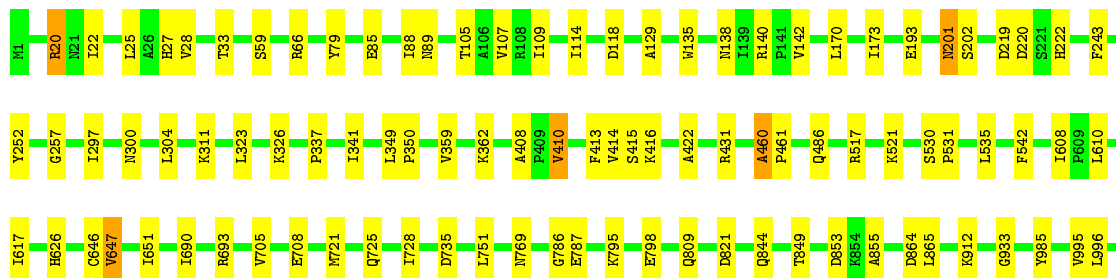
- Molecule 9: RIBOSOME MATURATION PROTEIN SBDS

Chain J:  86% 14%



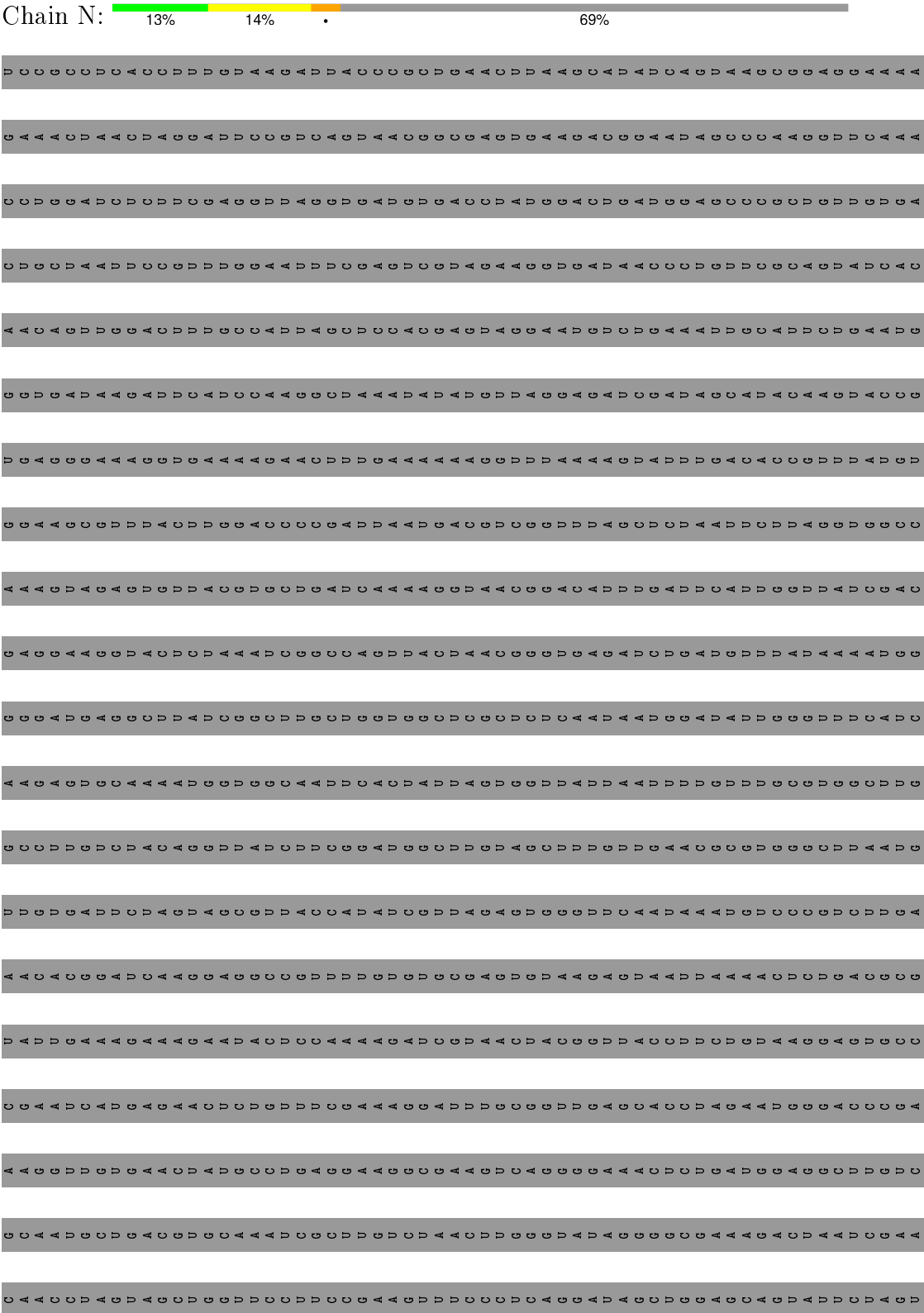
- Molecule 10: ELONGATION FACTOR TU GTP-BINDING DOMAIN-CONTAINING PROTEIN 1

Chain K:  90% 9%





• Molecule 11: 26S RIBOSOMAL RNA











0 0 0 0 0 0 0 0

## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	EACH PARTICLE, Not provided	Depositor
Microscope	OTHER	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	30	Depositor
Minimum defocus (nm)	2200	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4K X 4K)	Depositor

## 5 Model quality

### 5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z  > 2$	RMSZ	# $ Z  > 2$
1	A	0.57	0/3241	0.86	1/4339 (0.0%)
10	K	0.40	0/8969	0.63	0/12124
11	N	0.41	2/27702 (0.0%)	0.80	14/43160 (0.0%)
2	B	0.42	0/1510	0.73	0/2030
3	C	0.39	0/1592	0.55	0/2142
4	D	0.40	0/1265	0.57	0/1702
5	E	0.48	0/1032	0.81	1/1386 (0.1%)
6	F	0.51	0/1752	0.79	1/2345 (0.0%)
7	G	0.53	0/600	0.79	0/801
8	H	0.46	0/433	0.84	0/571
9	J	0.45	0/2038	0.74	1/2727 (0.0%)
All	All	0.43	2/50134 (0.0%)	0.76	18/73327 (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	A	0	5
11	N	0	1
6	F	0	1
9	J	0	1
All	All	0	8

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	N	1550	U	O3'-P	5.07	1.67	1.61
11	N	2405	A	O3'-P	5.07	1.67	1.61

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	N	1221	A	C5'-C4'-O4'	7.66	118.29	109.10
11	N	2625	C	C2'-C3'-O3'	7.09	125.10	109.50
11	N	1221	A	C5'-C4'-C3'	6.37	126.19	116.00
11	N	2515	G	C2'-C3'-O3'	6.20	123.62	113.70
11	N	3421	G	C2'-C3'-O3'	6.18	123.59	113.70

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	108	GLN	Peptide
1	A	122	TRP	Peptide
1	A	277	HIS	Peptide
1	A	5	LYS	Peptide
1	A	9	PRO	Peptide

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3176	0	3319	56	0
2	B	1491	0	1555	19	0
3	C	1571	0	1657	1	0
4	D	1245	0	1338	4	0
5	E	1017	0	1076	14	0
6	F	1721	0	1778	22	0
7	G	586	0	601	5	0
8	H	427	0	483	6	0
9	J	2015	0	2112	15	0
10	K	8800	0	8840	27	0
11	N	24758	0	12487	383	0
All	All	46807	0	35246	523	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 6.

The worst 5 of 523 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:N:3224:U:N3	11:N:3466:A:C6	2.39	0.90
11:N:3224:U:C4	11:N:3466:A:N6	2.42	0.88
11:N:3224:U:N3	11:N:3466:A:N6	2.23	0.87
11:N:1598:U:H2'	11:N:1599:U:C6	2.13	0.84
1:A:79:ILE:HG21	1:A:344:LEU:HD12	1.63	0.81

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	396/398 (100%)	313 (79%)	61 (15%)	22 (6%)	2	29
2	B	186/188 (99%)	159 (86%)	20 (11%)	7 (4%)	4	39
3	C	203/205 (99%)	168 (83%)	30 (15%)	5 (2%)	7	48
4	D	164/166 (99%)	131 (80%)	29 (18%)	4 (2%)	7	49
5	E	134/136 (98%)	113 (84%)	15 (11%)	6 (4%)	3	34
6	F	215/217 (99%)	171 (80%)	35 (16%)	9 (4%)	3	35
7	G	67/69 (97%)	52 (78%)	11 (16%)	4 (6%)	2	27
8	H	50/52 (96%)	41 (82%)	8 (16%)	1 (2%)	9	53
9	J	248/250 (99%)	214 (86%)	26 (10%)	8 (3%)	5	43
10	K	1118/1120 (100%)	939 (84%)	144 (13%)	35 (3%)	5	44
All	All	2781/2801 (99%)	2301 (83%)	379 (14%)	101 (4%)	7	41

5 of 101 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	44	THR
1	A	137	GLN
1	A	253	ALA

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Mol	Chain	Res	Type
1	A	259	HIS
1	A	395	SER

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	337/337 (100%)	305 (90%)	32 (10%)	11	44
2	B	168/168 (100%)	157 (94%)	11 (6%)	21	61
3	C	172/172 (100%)	168 (98%)	4 (2%)	58	83
4	D	139/139 (100%)	134 (96%)	5 (4%)	42	76
5	E	108/108 (100%)	102 (94%)	6 (6%)	26	66
6	F	180/180 (100%)	167 (93%)	13 (7%)	18	58
7	G	65/65 (100%)	61 (94%)	4 (6%)	23	62
8	H	48/48 (100%)	44 (92%)	4 (8%)	14	51
9	J	228/228 (100%)	218 (96%)	10 (4%)	35	71
10	K	975/975 (100%)	948 (97%)	27 (3%)	51	80
All	All	2420/2420 (100%)	2304 (95%)	116 (5%)	36	69

5 of 116 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	E	14	SER
6	F	82	LYS
10	K	721	MET
5	E	23	MET
6	F	10	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
9	J	52	GLN

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Mol	Chain	Res	Type
10	K	30	HIS
10	K	809	GLN
9	J	103	GLN
10	K	64	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	N	1159/3741 (30%)	362 (31%)	46 (3%)

5 of 362 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	N	1223	U
11	N	1225	G
11	N	1229	U
11	N	1231	U
11	N	1232	C

5 of 46 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	N	2625	C
11	N	2968	A
11	N	3457	U
11	N	2638	A
11	N	2676	U

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 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.