



wwPDB NMR Structure Validation Summary Report ⓘ

Feb 12, 2017 – 07:47 pm GMT

PDB ID : 1RF8
Title : Solution structure of the yeast translation initiation factor eIF4E in complex with m7GDP and eIF4GI residues 393 to 490
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Deposited on : 2003-11-07

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

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

A user guide is available at

<http://wwpdb.org/validation/2016/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	trunk28760
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

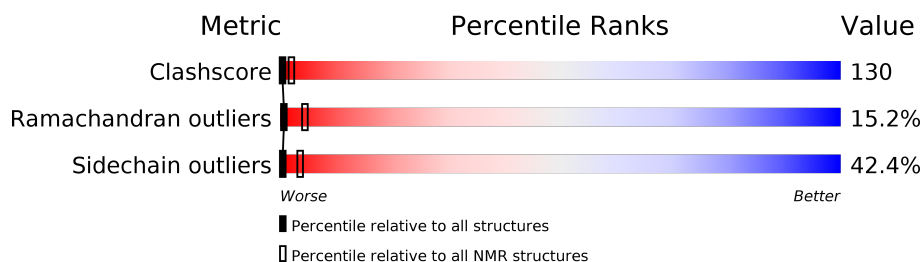
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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)	NMR archive (#Entries)
Clashscore	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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	213	
2	B	100	

2 Ensemble composition and analysis

This entry contains 11 models. Model 2 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:22-A:50, A:56-A:188, A:193-A:202, A:210-A:213, B:234-B:308 (251)	0.77	2

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 2 clusters. No single-model clusters were found.

Cluster number	Models
1	1, 4, 5, 9, 10, 11
2	2, 3, 6, 7, 8

3 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5073 atoms, of which 2506 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Eukaryotic translation initiation factor 4E.

Mol	Chain	Residues	Atoms						Trace
1	A	213	Total	C	H	N	O	S	0
			3371	1089	1663	285	329	5	

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	120	CYS	ARG	CONFLICT	UNP P07260
A	132	CYS	ARG	CONFLICT	UNP P07260
A	169	CYS	SER	CONFLICT	UNP P07260
A	200	CYS	SER	CONFLICT	UNP P07260

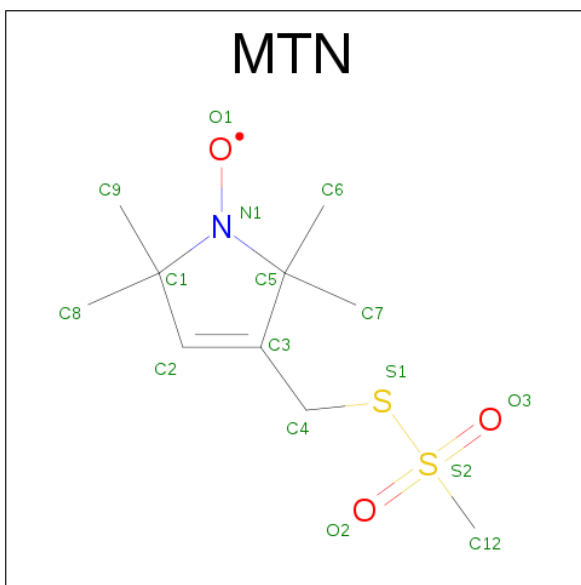
- Molecule 2 is a protein called Eukaryotic initiation factor 4F subunit p150.

Mol	Chain	Residues	Atoms						Trace
2	B	100	Total	C	H	N	O	S	0
			1550	498	768	123	160	1	

There are 2 discrepancies between the modelled and reference sequences:

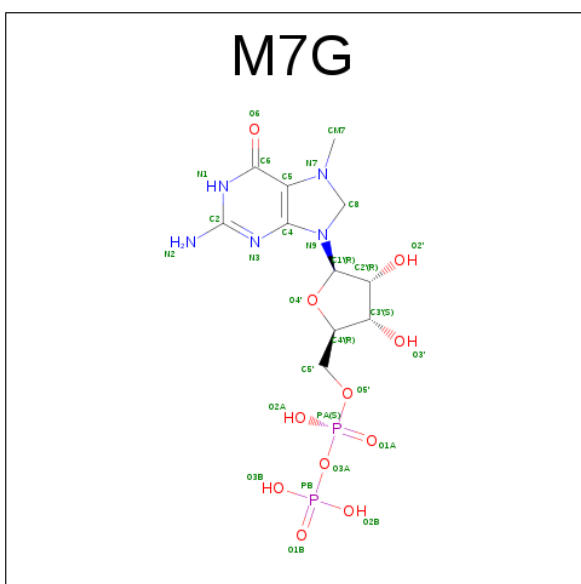
Chain	Residue	Modelled	Actual	Comment	Reference
B	215	GLY	-	CLONING ARTIFACT	UNP P39935
B	216	SER	-	CLONING ARTIFACT	UNP P39935

- Molecule 3 is S-[(1-OXYL-2,2,5,5-TETRAMETHYL-2,5-DIHYDRO-1H-PYRROL-3-YL)METHYL] METHANESULFONOTHIOATE (three-letter code: MTN) (formula: C₁₀H₁₈NO₃S₂).



Mol	Chain	Residues	Atoms					
3	A	1	Total 27	C 9	H 15	N 1	O 1	S 1
3	A	1	Total 27	C 9	H 15	N 1	O 1	S 1
3	A	1	Total 27	C 9	H 15	N 1	O 1	S 1
3	A	1	Total 27	C 9	H 15	N 1	O 1	S 1

- Molecule 4 is 7N-METHYL-8-HYDROGUANOSINE-5'-DIPHOSPHATE (three-letter code: M7G) (formula: $\text{C}_{11}\text{H}_{19}\text{N}_5\text{O}_{11}\text{P}_2$).



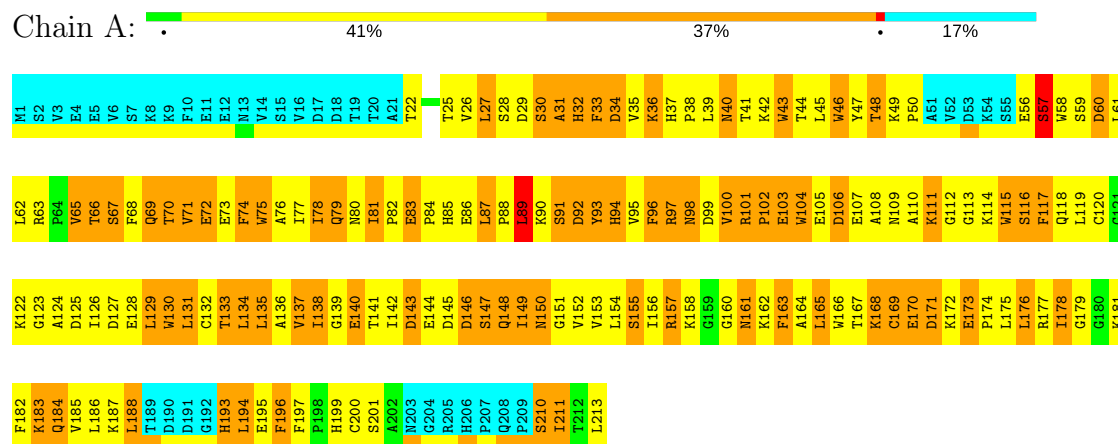
Mol	Chain	Residues	Atoms					
			Total	C	H	N	O	P
4	A	1	44	11	15	5	11	2

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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 outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: Eukaryotic translation initiation factor 4E



- Molecule 2: Eukaryotic initiation factor 4F subunit p150

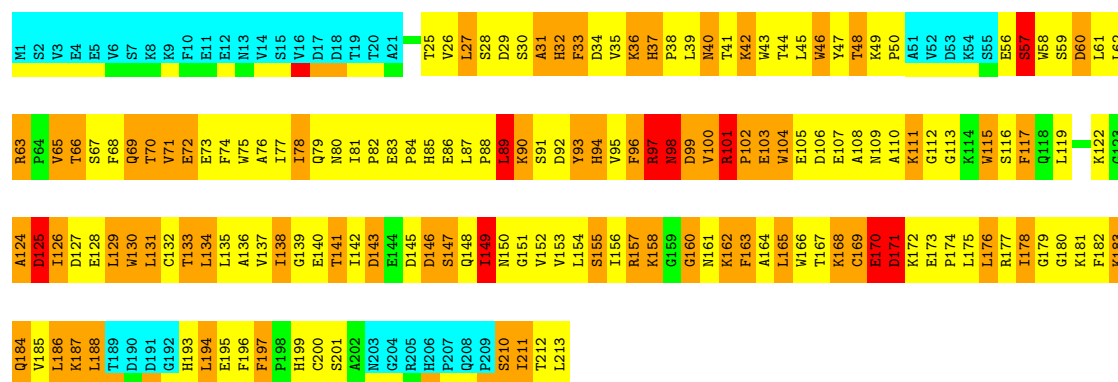


4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 2. Colouring as in section 4.1 above.

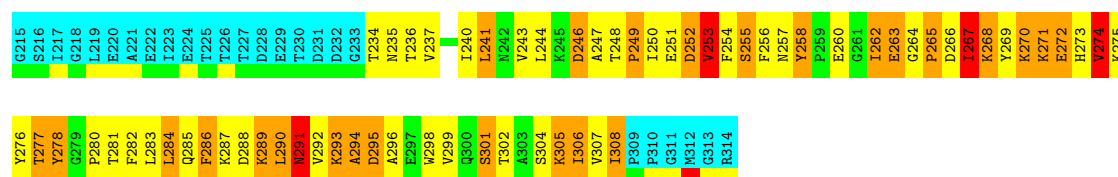
- Molecule 1: Eukaryotic translation initiation factor 4E





• Molecule 2: Eukaryotic initiation factor 4F subunit p150

Chain B: 10% 35% 26% 25%



5 Refinement protocol and experimental data overview

Of the 50 calculated structures, 11 were deposited, based on the following criterion: *structures with the least restraint violations*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
X-PLOR	structure solution	3.851
X-PLOR	refinement	3.851

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality [i](#)

6.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MTN, M7G

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1428	1403	1397	438±19
2	B	605	608	606	188±21
3	A	48	60	60	2±2
4	A	29	15	16	16±4
All	All	23210	22946	22869	5990

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 130.

5 of 2848 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:250:ILE:HD11	2:B:256:PHE:CE1	1.14	1.77	8	8
1:A:135:LEU:HD21	2:B:283:LEU:HD13	1.13	1.15	8	3
1:A:35:VAL:CG1	2:B:250:ILE:HD12	1.07	1.79	7	7
2:B:250:ILE:HD11	2:B:256:PHE:CZ	1.07	1.84	7	11
1:A:149:ILE:HD11	1:A:167:THR:HG22	1.07	1.10	11	5

6.3 Torsion angles [i](#)

6.3.1 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 NMR 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	175/213 (82%)	110±4 (63±2%)	39±4 (22±2%)	25±3 (14±2%)	1 5
2	B	75/100 (75%)	50±2 (67±3%)	12±2 (16±3%)	13±3 (17±4%)	0 3
All	All	2750/3443 (80%)	1767 (64%)	564 (21%)	419 (15%)	1 4

5 of 93 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	B	252	ASP	11
2	B	253	VAL	11
1	A	169	CYS	11
2	B	267	ILE	11
2	B	272	GLU	11

6.3.2 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 NMR 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	158/191 (83%)	87±4 (55±3%)	71±4 (45±3%)	0 2
2	B	68/87 (78%)	43±2 (63±3%)	25±2 (37±3%)	1 7
All	All	2486/3058 (81%)	1432 (58%)	1054 (42%)	0 3

5 of 194 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	48	THR	11
2	B	253	VAL	11

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Mol	Chain	Res	Type	Models (Total)
2	B	305	LYS	11
1	A	117	PHE	11
1	A	183	LYS	11

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.6 Ligand geometry ⓘ

5 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds 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 is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
3	MTN	A	320	1	10,12,16	1.12±0.01	0±0 (0±0%)
3	MTN	A	321	1	10,12,16	1.12±0.01	0±0 (0±0%)
3	MTN	A	322	1	10,12,16	1.12±0.00	0±0 (0±0%)
3	MTN	A	323	1	10,12,16	1.12±0.00	0±0 (0±0%)
4	M7G	A	325	-	27,31,31	1.67±0.02	1±0 (3±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of 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 angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is

considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
3	MTN	A	320	1	11,20,27	1.47±0.01	0±0 (0±0%)
3	MTN	A	321	1	11,20,27	1.47±0.01	0±0 (0±0%)
3	MTN	A	322	1	11,20,27	1.47±0.01	0±0 (0±0%)
3	MTN	A	323	1	11,20,27	1.47±0.01	0±0 (0±0%)
4	M7G	A	325	-	27,49,49	1.05±0.02	0±0 (0±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
3	MTN	A	320	1	-	0±0,0,25,29	0±0,1,1,1
3	MTN	A	321	1	-	0±0,0,25,29	0±0,1,1,1
3	MTN	A	322	1	-	0±0,0,25,29	0±0,1,1,1
3	MTN	A	323	1	-	0±0,0,25,29	0±0,1,1,1
4	M7G	A	325	-	-	0±0,16,44,44	0±0,3,3,3

All unique bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
4	A	325	M7G	C8-N9	6.96	1.35	1.45	5	11

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided