



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 17, 2017 – 10:51 AM EDT

PDB ID : 5J5Y
Title : Translation initiation factor 4E in complex with m2(7,2'O)GppCCl2ppG mRNA 5' cap analog
Authors : Warminski, M.; Nowak, E.; Rydzik, A.M.; Kowalska, J.; Jemielity, J.; Nowotny, M.
Deposited on : unknown
Resolution : 1.75 Å(reported)

This is a wwPDB X-ray 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/XrayValidationReportHelp>

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:

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20029824
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20029824

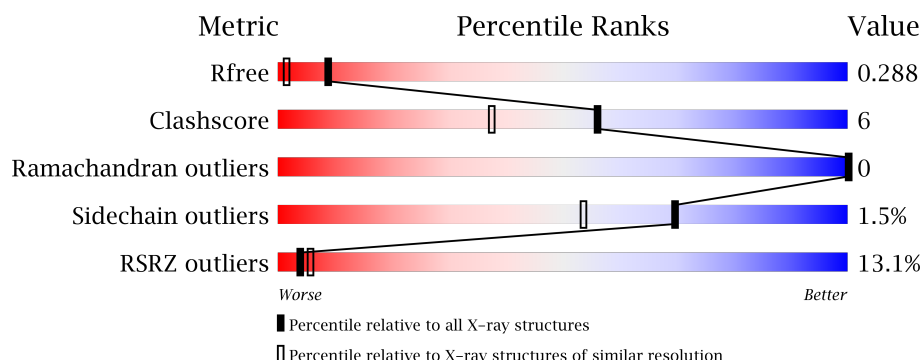
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	1762 (1.76-1.76)
Clashscore	112137	1889 (1.76-1.76)
Ramachandran outliers	110173	1868 (1.76-1.76)
Sidechain outliers	110143	1868 (1.76-1.76)
RSRZ outliers	101464	1770 (1.76-1.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	190	<div> <div>85%</div> <div>11%</div> <div>•</div> </div>
1	B	190	<div> <div>85%</div> <div>10%</div> <div>5%</div> </div>
1	C	190	<div> <div>23%</div> <div>67%</div> <div>14%</div> <div>18%</div> </div>
1	D	190	<div> <div>23%</div> <div>68%</div> <div>16%</div> <div>•</div> <div>15%</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	6G6	A	300	X	-	-	-

2 Entry composition i

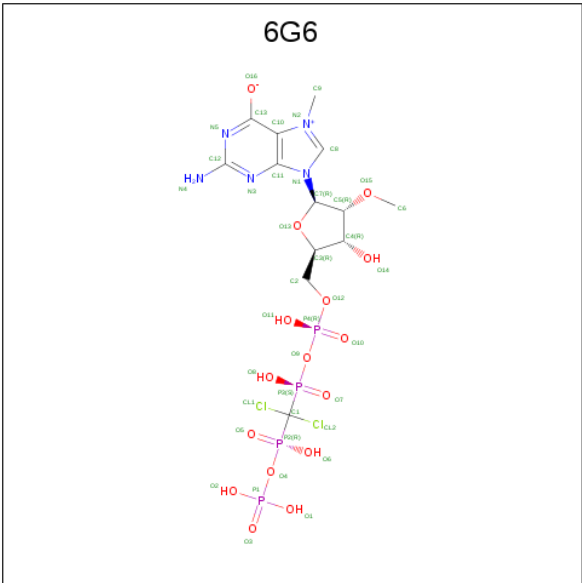
There are 4 unique types of molecules in this entry. The entry contains 5784 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Eukaryotic translation initiation factor 4E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	182	Total	C	N	O	S	0	3	0
			1499	960	261	272	6			
1	B	181	Total	C	N	O	S	0	3	0
			1484	950	255	273	6			
1	C	155	Total	C	N	O	S	0	2	0
			1197	767	204	220	6			
1	D	162	Total	C	N	O	S	0	2	0
			1251	795	220	232	4			

- Molecule 2 is 2-amino-9-{5-O-[(R)-{[(S)-{dichloro[(R)-hydroxy(phosphonooxy)phosphoryl]methyl}(hydroxy)phosphoryl]oxy}(hydroxy)phosphoryl]-2-O-methyl-beta-D-ribofuranosyl}-7-methyl-9H-purin-7-ium-6-olate (three-letter code: 6G6) (formula: C₁₃H₂₁Cl₂N₅O₁₆P₄).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	0	0
			36	13	2	5	13		

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	B	1	Total	C	Cl	N	O	P	0	0
			40	13	2	5	16	4		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			6	3	3		

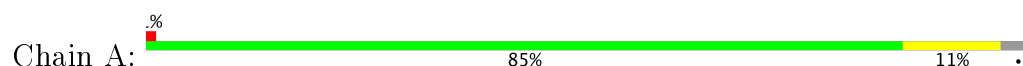
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	101	Total	O	0	1
			102	102		
4	B	111	Total	O	0	1
			112	112		
4	C	28	Total	O	0	0
			28	28		
4	D	29	Total	O	0	0
			29	29		

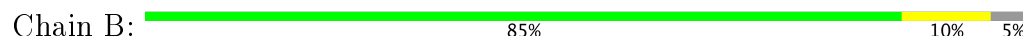
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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 electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

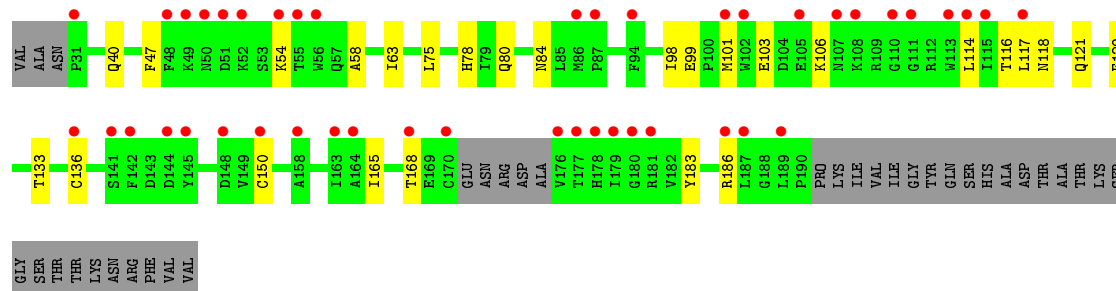
- Molecule 1: Eukaryotic translation initiation factor 4E



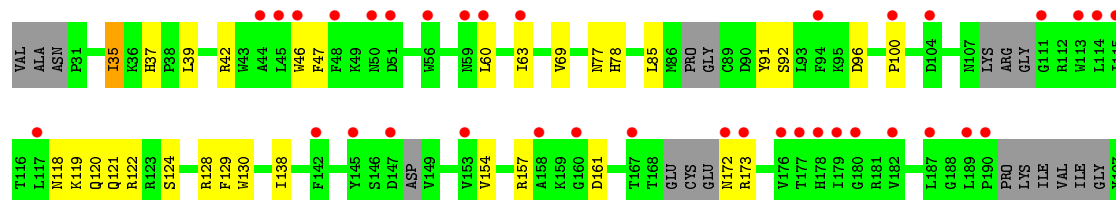
- Molecule 1: Eukaryotic translation initiation factor 4E



- Molecule 1: Eukaryotic translation initiation factor 4E



- Molecule 1: Eukaryotic translation initiation factor 4E



Q198	S199	H200	A201	D202	T203	ALA	THR	LYS	SER	GLY	SER	THR	THR	LYS	N213	R214	F215	V216	VAL
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	38.04Å 38.06Å 146.74Å 88.36° 95.63° 103.54°	Depositor
Resolution (Å)	37.00 – 1.75 37.00 – 1.75	Depositor EDS
% Data completeness (in resolution range)	90.6 (37.00-1.75) 88.4 (37.00-1.75)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.63 (at 1.75Å)	Xtriage
Refinement program	PHENIX (1.10_2152: ???)	Depositor
R, R_{free}	0.236 , 0.286 0.239 , 0.288	Depositor DCC
R_{free} test set	3556 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	18.9	Xtriage
Anisotropy	0.536	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 72.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.085 for -h,-k,h+1	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5784	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.71% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, 6G6

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	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.49	1/1543 (0.1%)	0.65	0/2090
1	B	0.43	0/1532	0.61	0/2077
1	C	0.36	1/1233 (0.1%)	0.50	0/1679
1	D	0.32	0/1281	0.53	0/1737
All	All	0.41	2/5589 (0.0%)	0.58	0/7583

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	B	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	99	GLU	C-N	7.02	1.47	1.34
1	C	99	GLU	C-N	5.61	1.45	1.34

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	90	ASP	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	1499	0	1445	11	0
1	B	1484	0	1415	11	0
1	C	1197	0	1082	16	0
1	D	1251	0	1113	23	0
2	A	36	0	0	1	0
2	B	40	0	0	0	0
3	B	6	0	8	1	0
4	A	102	0	0	0	0
4	B	112	0	0	2	0
4	C	28	0	0	1	0
4	D	29	0	0	1	0
All	All	5784	0	5063	61	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 61 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)
1:A:118:ASN:H	1:A:121:GLN:HE21	1.37	0.72
1:B:60:LEU:HD21	1:B:100:PRO:HG2	1.75	0.68
1:A:103:GLU:OE1	2:A:300:6G6:N4	2.26	0.68
1:D:128:ARG:HH11	1:D:129:PHE:HE1	1.43	0.66
1:C:133:THR:HG23	1:C:165:ILE:HD11	1.77	0.65

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	181/190 (95%)	172 (95%)	9 (5%)	0	100	100
1	B	180/190 (95%)	176 (98%)	4 (2%)	0	100	100
1	C	153/190 (80%)	144 (94%)	9 (6%)	0	100	100
1	D	150/190 (79%)	136 (91%)	14 (9%)	0	100	100
All	All	664/760 (87%)	628 (95%)	36 (5%)	0	100	100

There are no Ramachandran outliers to report.

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 X-ray entries followed by that with respect to entries of similar resolution.

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	158/169 (94%)	155 (98%)	3 (2%)	62	41
1	B	156/169 (92%)	155 (99%)	1 (1%)	89	82
1	C	116/169 (69%)	115 (99%)	1 (1%)	82	71
1	D	119/169 (70%)	116 (98%)	3 (2%)	53	28
All	All	549/676 (81%)	541 (98%)	8 (2%)	70	53

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	148	ASP
1	D	202	ASP
1	D	35	ILE
1	A	199	SER
1	C	40	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	121	GLN
1	A	155	ASN
1	B	120	GLN
1	C	80	GLN
1	D	120	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	6G6	A	300	-	30,34,42	78.37	9 (30%)	25,54,69	14.82	11 (44%)
2	6G6	B	301	-	35,42,42	1.11	4 (11%)	33,69,69	1.36	6 (18%)
3	GOL	B	302	-	5,5,5	0.33	0	5,5,5	0.43	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
2	6G6	A	300	-	1/1/6/9	0/22/39/58	1/3/3/3
2	6G6	B	301	-	-	1/34/58/58	0/3/3/3
3	GOL	B	302	-	-	0/4/4/4	0/0/0/0

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	300	6G6	P2-O4	-5.75	1.51	1.58
2	B	301	6G6	P2-O6	-2.45	1.51	1.56
2	B	301	6G6	P3-O8	-2.38	1.51	1.56
2	A	300	6G6	P3-O8	-2.12	1.50	1.54
2	B	301	6G6	P3-O9	2.07	1.60	1.58

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	300	6G6	O13-C7-N1	-57.17	11.44	107.78
2	A	300	6G6	O12-C2-C3	-35.78	12.83	111.76
2	A	300	6G6	O13-C3-C4	-22.34	67.65	104.80
2	A	300	6G6	P1-O4-P2	-18.83	65.89	132.38
2	A	300	6G6	O4-P1-O3	-4.73	82.36	111.44

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	300	6G6	C7

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	301	6G6	C6-O15-C5-C7

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	300	6G6	C3-C4-C5-C7-O13

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	300	6G6	1	0
3	B	302	GOL	1	0

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 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	182/190 (95%)	0.20	2 (1%) 80 86	14, 25, 47, 67	0
1	B	181/190 (95%)	0.15	0 100 100	13, 25, 47, 69	0
1	C	155/190 (81%)	1.41	44 (28%) 1 1	28, 51, 81, 101	0
1	D	162/190 (85%)	1.44	43 (26%) 1 1	25, 56, 80, 93	0
All	All	680/760 (89%)	0.76	89 (13%) 4 6	13, 36, 74, 101	0

The worst 5 of 89 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	145	TYR	6.9
1	C	179	ILE	6.4
1	D	179	ILE	5.7
1	A	211	THR	5.5
1	C	108	LYS	5.3

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	6G6	B	301	40/40	0.93	0.10	-0.15	18,29,61,65	2
3	GOL	B	302	6/6	0.81	0.10	-0.76	43,47,48,50	0
2	6G6	A	300	36/40	0.92	0.09	-0.88	14,30,47,55	2

6.5 Other polymers [i](#)

There are no such residues in this entry.