



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 13, 2023 – 09:24 PM JST

PDB ID : 5Y6Z
Title : Crystal structure of the coxsackievirus A16 polymerase elongation complex
Authors : Bi, P.; Shu, B.; Gong, P.
Deposited on : 2017-08-15
Resolution : 2.50 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

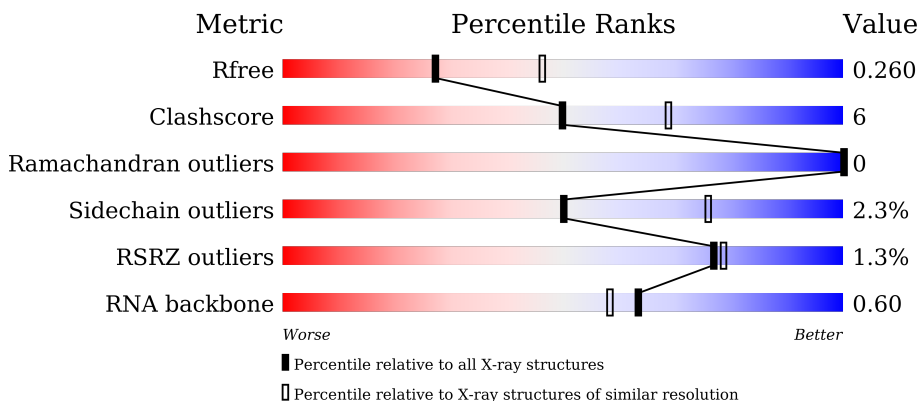
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)
RNA backbone	3102	1008 (2.84-2.16)

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 of the lower 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 $\leq 5\%$. 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	468	 84% 13% 3%
1	E	468	 83% 15% 2%
2	B	33	 15% 30% 3% 55%
2	F	33	 24% 27% 45%

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Mol	Chain	Length	Quality of chain
3	C	14	 79% 7% 14%
3	G	14	 57% 29% 14%

2 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 8885 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 Genome polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	457	3612	2317	602	675	18	0	0	0
1	E	460	3635	2332	607	677	19	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	463	HIS	-	expression tag	UNP L7WS61
A	464	HIS	-	expression tag	UNP L7WS61
A	465	HIS	-	expression tag	UNP L7WS61
A	466	HIS	-	expression tag	UNP L7WS61
A	467	HIS	-	expression tag	UNP L7WS61
A	468	HIS	-	expression tag	UNP L7WS61
E	463	HIS	-	expression tag	UNP L7WS61
E	464	HIS	-	expression tag	UNP L7WS61
E	465	HIS	-	expression tag	UNP L7WS61
E	466	HIS	-	expression tag	UNP L7WS61
E	467	HIS	-	expression tag	UNP L7WS61
E	468	HIS	-	expression tag	UNP L7WS61

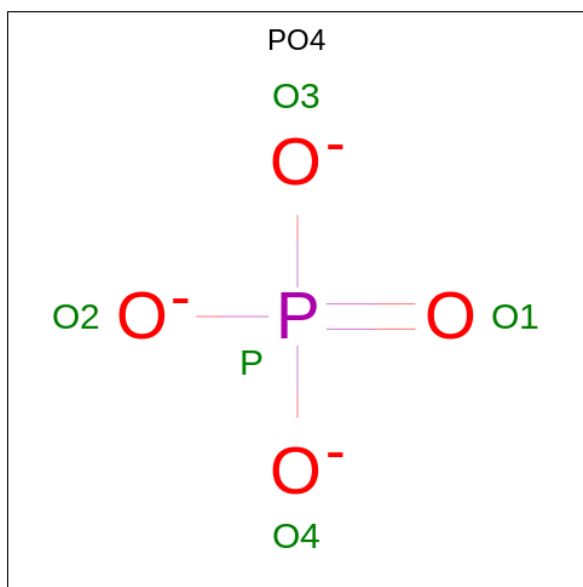
- Molecule 2 is a RNA chain called Template RNA (33-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	B	15	316	141	53	107	15	0	0	0
2	F	18	368	162	65	123	18	0	0	0

- Molecule 3 is a RNA chain called Product RNA (14-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	12	Total	C	N	O	P	0	0	0
			260	116	50	82	12			
3	G	12	Total	C	N	O	P	0	0	0
			260	116	50	82	12			

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			5	4	1		
4	B	1	Total	O	P	0	0
			5	4	1		
4	C	1	Total	O	P	0	0
			5	4	1		
4	G	1	Total	O	P	0	0
			5	4	1		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 6 3 3	0	0
5	B	1	Total C O 6 3 3	0	0
5	C	1	Total C O 6 3 3	0	0
5	E	1	Total C O 6 3 3	0	0
5	E	1	Total C O 6 3 3	0	0
5	F	1	Total C O 6 3 3	0	0

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	E	1	Total Mg 1 1	0	0

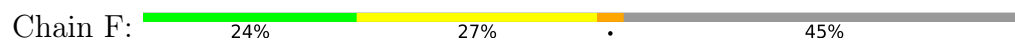
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	147	Total O 147 147	0	0
7	B	25	Total O 25 25	0	0

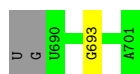
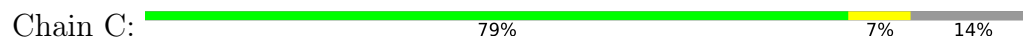
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	C	23	Total O 23 23	0	0
7	E	145	Total O 145 145	0	0
7	F	21	Total O 21 21	0	0
7	G	16	Total O 16 16	0	0



- Molecule 3: Product RNA (14-MER)



- Molecule 3: Product RNA (14-MER)



4 Data and refinement statistics i

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	93.72Å 93.72Å 167.51Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	32.83 – 2.50 46.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.1 (32.83-2.50) 99.3 (46.00-2.50)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.12 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.10_2155	Depositor
R, R_{free}	0.218 , 0.259 0.219 , 0.260	Depositor DCC
R_{free} test set	2773 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	41.5	Xtriage
Anisotropy	0.653	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 34.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	0.000 for -h,-k,l 0.419 for h,-h-k,-l 0.000 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8885	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.34% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, GOL, PO4

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	0.42	0/3706	0.58	1/5040 (0.0%)
1	E	0.43	0/3731	0.59	0/5073
2	B	0.57	0/351	0.94	0/544
2	F	0.54	0/409	0.99	0/634
3	C	0.59	0/291	1.14	0/452
3	G	0.59	0/291	1.00	0/452
All	All	0.45	0/8779	0.68	1/12195 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	229	LEU	CA-CB-CG	5.01	126.82	115.30

There are no chirality outliers.

There are no planarity outliers.

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	A	3612	0	3491	37	0
1	E	3635	0	3508	42	0
2	B	316	0	162	6	0
2	F	368	0	184	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	260	0	131	1	0
3	G	260	0	131	4	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
4	C	5	0	0	0	0
4	G	5	0	0	1	0
5	A	6	0	8	0	0
5	B	6	0	8	1	0
5	C	6	0	8	0	0
5	E	12	0	16	1	0
5	F	6	0	8	1	0
6	E	1	0	0	0	0
7	A	147	0	0	3	0
7	B	25	0	0	1	0
7	C	23	0	0	0	0
7	E	145	0	0	6	0
7	F	21	0	0	0	0
7	G	16	0	0	0	0
All	All	8885	0	7655	91	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 91 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)
2:F:600:G:H22	5:F:701:GOL:H12	1.47	0.79
1:E:17:ILE:HG21	1:E:155:SER:HB3	1.67	0.77
1:E:39:LYS:HE2	1:E:165:LEU:HD21	1.66	0.75
1:A:17:ILE:HG21	1:A:155:SER:HB3	1.69	0.74
1:E:128:ARG:NH2	7:E:601:HOH:O	2.03	0.74

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 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	453/468 (97%)	444 (98%)	9 (2%)	0	100	100
1	E	456/468 (97%)	444 (97%)	12 (3%)	0	100	100
All	All	909/936 (97%)	888 (98%)	21 (2%)	0	100	100

There are no Ramachandran outliers to report.

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 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	387/413 (94%)	378 (98%)	9 (2%)	50	76
1	E	389/413 (94%)	380 (98%)	9 (2%)	50	76
All	All	776/826 (94%)	758 (98%)	18 (2%)	50	76

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	273	HIS
1	E	410	ASN
1	E	365	ASN
1	A	376	LYS
1	E	228	SER

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

Mol	Chain	Res	Type
1	A	270	ASN
1	A	365	ASN
1	E	18	ASN
1	E	56	GLN
1	E	270	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	14/33 (42%)	2 (14%)	0
2	F	15/33 (45%)	2 (13%)	0
3	C	11/14 (78%)	0	0
3	G	11/14 (78%)	0	0
All	All	51/94 (54%)	4 (7%)	0

All (4) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	598	A
2	B	602	C
2	F	583	G
2	F	599	G

There are no RNA pucker outliers to report.

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 11 ligands modelled in this entry, 1 is monoatomic - leaving 10 for Mogul analysis.

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	$\# Z > 2$
4	PO4	C	801	-	4,4,4	0.88	0	6,6,6	0.51	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	PO4	G	801	-	4,4,4	0.98	0	6,6,6	0.80	0
4	PO4	A	501	-	4,4,4	0.61	0	6,6,6	0.79	0
5	GOL	B	702	-	5,5,5	0.40	0	5,5,5	0.42	0
4	PO4	B	701	-	4,4,4	0.85	0	6,6,6	0.48	0
5	GOL	E	502	-	5,5,5	0.36	0	5,5,5	0.28	0
5	GOL	E	503	-	5,5,5	0.32	0	5,5,5	0.95	0
5	GOL	F	701	-	5,5,5	0.41	0	5,5,5	0.57	0
5	GOL	C	802	-	5,5,5	0.32	0	5,5,5	0.46	0
5	GOL	A	502	-	5,5,5	0.36	0	5,5,5	0.50	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
5	GOL	B	702	-	-	4/4/4/4	-
5	GOL	E	503	-	-	4/4/4/4	-
5	GOL	E	502	-	-	2/4/4/4	-
5	GOL	F	701	-	-	0/4/4/4	-
5	GOL	C	802	-	-	2/4/4/4	-
5	GOL	A	502	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	502	GOL	O1-C1-C2-C3
5	B	702	GOL	O1-C1-C2-O2
5	B	702	GOL	O1-C1-C2-C3
5	B	702	GOL	C1-C2-C3-O3
5	C	802	GOL	C1-C2-C3-O3

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	801	PO4	1	0
5	B	702	GOL	1	0
5	E	503	GOL	1	0
5	F	701	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	457/468 (97%)	-0.03	7 (1%) 73 75	30, 42, 62, 81	0
1	E	460/468 (98%)	-0.01	5 (1%) 80 82	30, 43, 63, 87	0
2	B	15/33 (45%)	-0.15	1 (6%) 17 18	35, 42, 91, 107	0
2	F	18/33 (54%)	-0.00	0 100 100	36, 53, 96, 99	0
3	C	12/14 (85%)	-0.19	0 100 100	35, 48, 80, 86	0
3	G	12/14 (85%)	-0.01	0 100 100	39, 48, 85, 91	0
All	All	974/1030 (94%)	-0.02	13 (1%) 77 79	30, 43, 65, 107	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	364	PHE	3.3
1	A	313	THR	2.9
1	E	125	VAL	2.8
1	A	157	TYR	2.8
1	E	4	GLN	2.4

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 monosaccharides 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. 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	B-factors(Å ²)	Q<0.9
4	PO4	A	501	5/5	0.80	0.15	50,54,65,72	5
5	GOL	F	701	6/6	0.86	0.14	46,49,52,55	6
5	GOL	A	502	6/6	0.88	0.13	46,47,50,57	0
5	GOL	E	503	6/6	0.89	0.10	44,47,56,60	0
6	MG	E	501	1/1	0.89	0.13	57,57,57,57	1
5	GOL	C	802	6/6	0.91	0.18	38,43,44,46	6
4	PO4	B	701	5/5	0.91	0.31	62,64,73,80	5
5	GOL	B	702	6/6	0.93	0.14	40,41,45,48	6
5	GOL	E	502	6/6	0.94	0.13	49,51,56,57	0
4	PO4	G	801	5/5	0.95	0.13	38,43,48,57	5
4	PO4	C	801	5/5	0.96	0.15	42,43,47,53	5

6.5 Other polymers [i](#)

There are no such residues in this entry.