Full wwPDB X-ray Structure Validation Report (i)

Sep 30, 2021 – 12:49 PM EDT

PDB ID	:	7LGA
Title	:	PEG10 CA-like C-terminal domain
Authors	:	Zurowska, K.; Pornillos, O.; Ganser-Pornillos, B.K.
Deposited on	:	2021-01-19
Resolution	:	1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 (i) symbol.

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

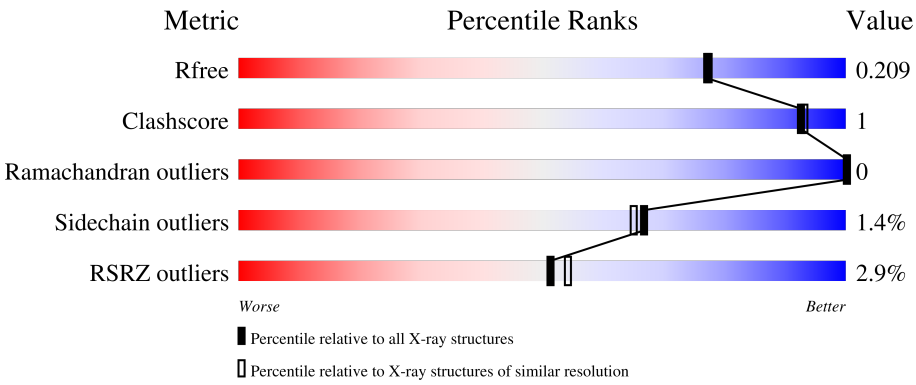
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 <=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	101	.% 81% • 16%
1	B	101	2% 78% 6% 16%
1	D	101	4% 87% • 10%
1	E	101	3% 82% • 15%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 5652 atoms, of which 2692 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 Retrotransposon-derived protein PEG10.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S	Se			
1	A	85	1366	423	682	132	126	1	2	0	0	0
1	B	85	1340	418	667	129	123	1	2	0	1	0
1	D	91	1377	431	677	136	130	1	2	0	0	0
1	E	86	1344	420	666	129	126	1	2	0	0	0

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	152	GLY	-	expression tag	UNP Q86TG7
A	153	HIS	-	expression tag	UNP Q86TG7
A	154	HIS	-	expression tag	UNP Q86TG7
A	155	HIS	-	expression tag	UNP Q86TG7
A	156	HIS	-	expression tag	UNP Q86TG7
A	157	HIS	-	expression tag	UNP Q86TG7
A	158	HIS	-	expression tag	UNP Q86TG7
A	159	GLY	-	expression tag	UNP Q86TG7
A	160	SER	-	expression tag	UNP Q86TG7
A	239	ARG	-	expression tag	UNP Q86TG7
A	240	ARG	-	expression tag	UNP Q86TG7
A	241	LEU	-	expression tag	UNP Q86TG7
A	242	ALA	-	expression tag	UNP Q86TG7
A	243	ARG	-	expression tag	UNP Q86TG7
A	244	ALA	-	expression tag	UNP Q86TG7
A	245	ALA	-	expression tag	UNP Q86TG7
A	246	ALA	-	expression tag	UNP Q86TG7
A	247	ALA	-	expression tag	UNP Q86TG7
A	248	ARG	-	expression tag	UNP Q86TG7
A	249	LYS	-	expression tag	UNP Q86TG7
A	250	PRO	-	expression tag	UNP Q86TG7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	251	ARG	-	expression tag	UNP Q86TG7
A	252	SER	-	expression tag	UNP Q86TG7
B	152	GLY	-	expression tag	UNP Q86TG7
B	153	HIS	-	expression tag	UNP Q86TG7
B	154	HIS	-	expression tag	UNP Q86TG7
B	155	HIS	-	expression tag	UNP Q86TG7
B	156	HIS	-	expression tag	UNP Q86TG7
B	157	HIS	-	expression tag	UNP Q86TG7
B	158	HIS	-	expression tag	UNP Q86TG7
B	159	GLY	-	expression tag	UNP Q86TG7
B	160	SER	-	expression tag	UNP Q86TG7
B	239	ARG	-	expression tag	UNP Q86TG7
B	240	ARG	-	expression tag	UNP Q86TG7
B	241	LEU	-	expression tag	UNP Q86TG7
B	242	ALA	-	expression tag	UNP Q86TG7
B	243	ARG	-	expression tag	UNP Q86TG7
B	244	ALA	-	expression tag	UNP Q86TG7
B	245	ALA	-	expression tag	UNP Q86TG7
B	246	ALA	-	expression tag	UNP Q86TG7
B	247	ALA	-	expression tag	UNP Q86TG7
B	248	ARG	-	expression tag	UNP Q86TG7
B	249	LYS	-	expression tag	UNP Q86TG7
B	250	PRO	-	expression tag	UNP Q86TG7
B	251	ARG	-	expression tag	UNP Q86TG7
B	252	SER	-	expression tag	UNP Q86TG7
D	152	GLY	-	expression tag	UNP Q86TG7
D	153	HIS	-	expression tag	UNP Q86TG7
D	154	HIS	-	expression tag	UNP Q86TG7
D	155	HIS	-	expression tag	UNP Q86TG7
D	156	HIS	-	expression tag	UNP Q86TG7
D	157	HIS	-	expression tag	UNP Q86TG7
D	158	HIS	-	expression tag	UNP Q86TG7
D	159	GLY	-	expression tag	UNP Q86TG7
D	160	SER	-	expression tag	UNP Q86TG7
D	239	ARG	-	expression tag	UNP Q86TG7
D	240	ARG	-	expression tag	UNP Q86TG7
D	241	LEU	-	expression tag	UNP Q86TG7
D	242	ALA	-	expression tag	UNP Q86TG7
D	243	ARG	-	expression tag	UNP Q86TG7
D	244	ALA	-	expression tag	UNP Q86TG7
D	245	ALA	-	expression tag	UNP Q86TG7
D	246	ALA	-	expression tag	UNP Q86TG7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	247	ALA	-	expression tag	UNP Q86TG7
D	248	ARG	-	expression tag	UNP Q86TG7
D	249	LYS	-	expression tag	UNP Q86TG7
D	250	PRO	-	expression tag	UNP Q86TG7
D	251	ARG	-	expression tag	UNP Q86TG7
D	252	SER	-	expression tag	UNP Q86TG7
E	152	GLY	-	expression tag	UNP Q86TG7
E	153	HIS	-	expression tag	UNP Q86TG7
E	154	HIS	-	expression tag	UNP Q86TG7
E	155	HIS	-	expression tag	UNP Q86TG7
E	156	HIS	-	expression tag	UNP Q86TG7
E	157	HIS	-	expression tag	UNP Q86TG7
E	158	HIS	-	expression tag	UNP Q86TG7
E	159	GLY	-	expression tag	UNP Q86TG7
E	160	SER	-	expression tag	UNP Q86TG7
E	239	ARG	-	expression tag	UNP Q86TG7
E	240	ARG	-	expression tag	UNP Q86TG7
E	241	LEU	-	expression tag	UNP Q86TG7
E	242	ALA	-	expression tag	UNP Q86TG7
E	243	ARG	-	expression tag	UNP Q86TG7
E	244	ALA	-	expression tag	UNP Q86TG7
E	245	ALA	-	expression tag	UNP Q86TG7
E	246	ALA	-	expression tag	UNP Q86TG7
E	247	ALA	-	expression tag	UNP Q86TG7
E	248	ARG	-	expression tag	UNP Q86TG7
E	249	LYS	-	expression tag	UNP Q86TG7
E	250	PRO	-	expression tag	UNP Q86TG7
E	251	ARG	-	expression tag	UNP Q86TG7
E	252	SER	-	expression tag	UNP Q86TG7

- Molecule 2 is water.

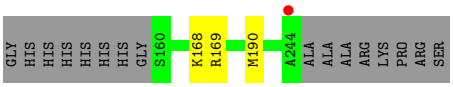
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	81	81	81	0	0
			Total	O		
2	B	48	48	48	0	0
			Total	O		
2	D	47	47	47	0	0
			Total	O		
2	E	49	49	49	0	0

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 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.

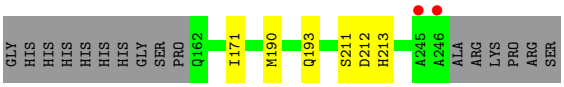
• Molecule 1: Retrotransposon-derived protein PEG10

Chain A:



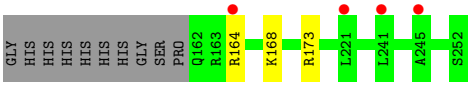
• Molecule 1: Retrotransposon-derived protein PEG10

Chain B:



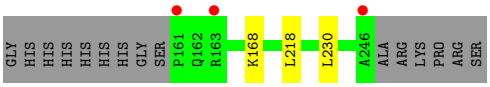
• Molecule 1: Retrotransposon-derived protein PEG10

Chain D:



• Molecule 1: Retrotransposon-derived protein PEG10

Chain E:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	51.60Å 70.29Å 52.69Å 90.00° 98.10° 90.00°	Depositor
Resolution (Å)	41.89 – 1.90 41.89 – 1.90	Depositor EDS
% Data completeness (in resolution range)	83.6 (41.89-1.90) 91.2 (41.89-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.14 (at 1.89Å)	Xtriage
Refinement program	PHENIX 1.18_3845	Depositor
R, R_{free}	0.182 , 0.209 0.182 , 0.209	Depositor DCC
R_{free} test set	1984 reflections (7.16%)	wwPDB-VP
Wilson B-factor (Å^2)	17.5	Xtriage
Anisotropy	0.055	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.42 , 53.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.027 for l,-k,h	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	5652	wwPDB-VP
Average B, all atoms (Å^2)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.43% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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)

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	0.36	0/692	0.51	0/926
1	B	0.37	0/683	0.53	0/915
1	D	0.30	0/707	0.48	0/949
1	E	0.34	0/686	0.50	0/920
All	All	0.34	0/2768	0.51	0/3710

There are no bond length outliers.

There are no bond angle outliers.

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	684	682	682	2	0
1	B	673	667	667	4	0
1	D	700	677	677	3	0
1	E	678	666	666	1	0
2	A	81	0	0	2	0
2	B	48	0	0	0	0
2	D	47	0	0	1	0
2	E	49	0	0	0	0
All	All	2960	2692	2692	8	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 1.

All (8) 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:E:218:LEU:HD21	1:E:230:LEU:HD11	1.77	0.67
1:B:190:MSE:O	1:B:193:GLN:HG2	2.07	0.54
1:A:169:ARG:NH2	2:A:303:HOH:O	2.45	0.49
1:A:190:MSE:HE2	2:A:370:HOH:O	2.13	0.49
1:B:212:ASP:OD2	1:D:173:ARG:NH1	2.47	0.43
1:B:211:SER:HG	1:B:213:HIS:CE1	2.37	0.42
1:D:164:ARG:NH2	2:D:301:HOH:O	2.51	0.42
1:B:212:ASP:CG	1:D:173:ARG:HH12	2.22	0.40

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	83/101 (82%)	83 (100%)	0	0	100	100
1	B	84/101 (83%)	84 (100%)	0	0	100	100
1	D	89/101 (88%)	88 (99%)	1 (1%)	0	100	100
1	E	84/101 (83%)	84 (100%)	0	0	100	100
All	All	340/404 (84%)	339 (100%)	1 (0%)	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	72/82 (88%)	71 (99%)	1 (1%)	67	65
1	B	68/82 (83%)	67 (98%)	1 (2%)	65	62
1	D	68/82 (83%)	67 (98%)	1 (2%)	65	62
1	E	69/82 (84%)	68 (99%)	1 (1%)	67	65
All	All	277/328 (84%)	273 (99%)	4 (1%)	67	65

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	168	LYS
1	B	171	ILE
1	D	168	LYS
1	E	168	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)

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.

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	83/101 (82%)	0.01	1 (1%)	79	81	6, 16, 40, 55	0
1	B	83/101 (82%)	0.01	2 (2%)	59	62	8, 20, 49, 70	0
1	D	89/101 (88%)	0.15	4 (4%)	33	36	9, 26, 52, 58	0
1	E	84/101 (83%)	0.14	3 (3%)	42	45	8, 22, 56, 70	0
All	All	339/404 (83%)	0.08	10 (2%)	51	54	6, 21, 52, 70	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	244	ALA	4.4
1	B	246	ALA	3.9
1	E	161	PRO	3.7
1	D	221	LEU	2.9
1	D	245	ALA	2.8
1	E	163	ARG	2.3
1	D	241	LEU	2.3
1	B	245	ALA	2.3
1	E	246	ALA	2.1
1	D	164	ARG	2.0

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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.