



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:15 AM UTC

PDB ID : 7PEL / pdb_00007pel
EMDB ID : EMD-11052
Title : CryoEM structure of simian T-cell lymphotropic virus intasome in complex with PP2A regulatory subunit B56 gamma
Authors : Barski, M.; Pye, V.E.; Nans, A.; Cherepanov, P.; Maertens, G.N.
Deposited on : 2021-08-10
Resolution : 3.34 Å (reported)
Based on initial models : 6TOQ, 6TJU, 5JJA, 6QBW

This is a wwPDB EM Validation Summary Report for a publicly released PDB/EMDB entry.

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

A user guide is available at

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

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 : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

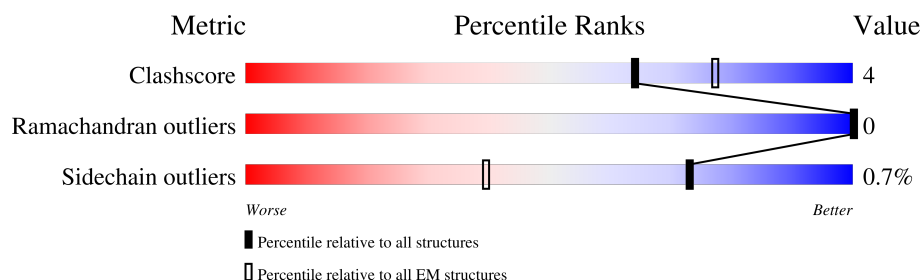
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.34 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	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	301	75% 10% • 14%
1	B	301	88% 5% 8%
1	D	301	75% 10% • 14%
1	E	301	87% 5% 8%
2	C	697	38% 5% 58%
2	F	697	38% 5% 58%
3	K	30	40% 30% 30%
3	M	30	40% 30% 30%
4	L	28	43% 25% 32%

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Mol	Chain	Length	Quality of chain
4	N	28	 39% 29% 32%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14998 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 Pol protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	258	Total	C	N	O	S	0	0
			2053	1307	384	355	7		
1	B	278	Total	C	N	O	S	0	0
			2208	1399	417	384	8		
1	D	258	Total	C	N	O	S	0	0
			2053	1307	384	355	7		
1	E	278	Total	C	N	O	S	0	0
			2208	1399	417	384	8		

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q4QY51
A	-2	PRO	-	expression tag	UNP Q4QY51
A	-1	GLU	-	expression tag	UNP Q4QY51
A	0	PHE	-	expression tag	UNP Q4QY51
B	-3	GLY	-	expression tag	UNP Q4QY51
B	-2	PRO	-	expression tag	UNP Q4QY51
B	-1	GLU	-	expression tag	UNP Q4QY51
B	0	PHE	-	expression tag	UNP Q4QY51
D	-3	GLY	-	expression tag	UNP Q4QY51
D	-2	PRO	-	expression tag	UNP Q4QY51
D	-1	GLU	-	expression tag	UNP Q4QY51
D	0	PHE	-	expression tag	UNP Q4QY51
E	-3	GLY	-	expression tag	UNP Q4QY51
E	-2	PRO	-	expression tag	UNP Q4QY51
E	-1	GLU	-	expression tag	UNP Q4QY51
E	0	PHE	-	expression tag	UNP Q4QY51

- Molecule 2 is a protein called Isoform 3 of PC4 and SFRS1-interacting protein,Isoform Gamma-2 of Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	296	Total	C	N	O	S	0	0
			2423	1593	397	425	8		
2	F	296	Total	C	N	O	S	0	0
			2423	1593	397	425	8		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-316	SER	-	expression tag	UNP O75475
C	10	PHE	-	linker	UNP O75475
F	-316	SER	-	expression tag	UNP O75475
F	10	PHE	-	linker	UNP O75475

- Molecule 3 is a DNA chain called DNA (5'-D(*AP*CP*TP*GP*TP*GP*TP*TP*TP*GP*GP*CP*GP*CP*TP*TP*CP*TP*CP*TP*C)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
3	K	21	Total	C	N	O	P	0	0
			422	204	66	132	20		
3	M	21	Total	C	N	O	P	0	0
			422	204	66	132	20		

- Molecule 4 is a DNA chain called DNA (5'-D(*GP*AP*GP*AP*GP*AP*AP*GP*CP*GP*CP*CP*AP*AP*AP*CP*AP*CP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	19	Total	C	N	O	P	0	0
			391	185	85	103	18		
4	N	19	Total	C	N	O	P	0	0
			391	185	85	103	18		

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

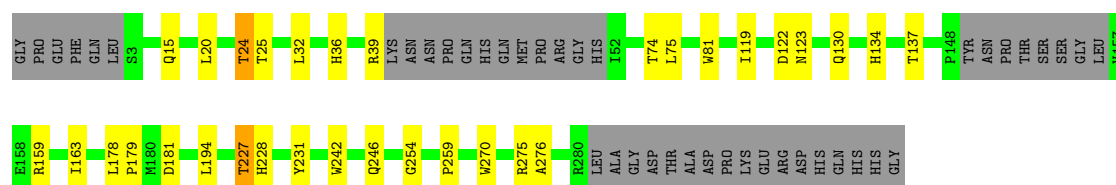
Mol	Chain	Residues	Atoms		AltConf
5	A	1	Total	Zn	0
			1	1	
5	B	1	Total	Zn	0
			1	1	
5	D	1	Total	Zn	0
			1	1	
5	E	1	Total	Zn	0
			1	1	

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. 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: Pol protein

Chain A: 



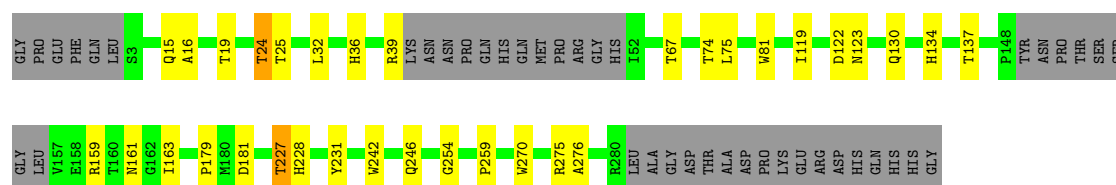
- Molecule 1: Pol protein

Chain B: 



- Molecule 1: Pol protein

Chain D: 



- Molecule 1: Pol protein

Chain E: 



- Molecule 2: Isoform 3 of PC4 and SFRS1-interacting protein,Isoform Gamma-2 of Serine/threonine-phosphatase 2A 56 kDa regulatory subunit gamma isoform

Chain C: 

- Molecule 3: DNA (5'-D(*AP*CP*TP*GP*TP*GP*TP*TP*TP*GP*GP*CP*GP*CP*TP*TP*CP*TP*CP*TP*C)-3')

A1		G6		T9 G10 G11 C12 G13		C17 T18 C19	T20 C21	DC	DC	DG	DG	DA	DG	DA	DG	DA
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- | |
|--------------------------------|
| A1 |
| G6 |
| T9
G10
G11
C12
G13 |
| C17
T18
C19 |
| T20
C21 |
| DC |
| DC |
| DG |
| DG |
| DA |
| DG |
| DA |
| DG |
| DA |

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| DT |
| DC |
| DT |
| DC |
| DT |
| DC |
| DC |
| DG |
| DG |
| G2 |
| A3 |
| G4 |
| A5 |
| G6 |
| C13 |
| A14 |
| A15 |
| A20 |

- | | | | | | | | | | | | | | | | | | | | |
|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|
| DT | DC | DT | DC | DT | DC | DC | DG | DG | G2 | A3 | G4 | A5 | G6 | C13 | A14 | A15 | A16 | C17 | A20 |
|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	161921	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.4	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.15	0/2116	0.33	0/2886
1	B	0.19	0/2279	0.34	0/3111
1	D	0.16	0/2116	0.33	0/2886
1	E	0.19	0/2279	0.34	0/3111
2	C	0.13	0/2488	0.33	0/3380
2	F	0.13	0/2488	0.33	0/3380
3	K	0.27	0/469	0.49	0/722
3	M	0.27	0/469	0.49	0/722
4	L	0.25	0/442	0.34	0/680
4	N	0.25	0/442	0.34	0/680
All	All	0.17	0/15588	0.35	0/21558

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

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	2053	0	2040	18	0
1	B	2208	0	2180	10	0
1	D	2053	0	2040	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2208	0	2180	11	0
2	C	2423	0	2422	21	0
2	F	2423	0	2422	20	0
3	K	422	0	242	6	0
3	M	422	0	242	7	0
4	L	391	0	211	6	0
4	N	391	0	211	7	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
All	All	14998	0	14190	119	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 4.

The worst 5 of 119 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:C:244:LYS:HD3	2:C:281:LEU:HD13	1.63	0.81
2:F:244:LYS:HD3	2:F:281:LEU:HD13	1.63	0.81
1:E:218:GLU:OE1	2:F:31:ARG:NH1	2.26	0.69
1:B:218:GLU:OE1	2:C:31:ARG:NH1	2.26	0.68
1:B:54:ARG:NH2	3:K:6:DG:OP1	2.28	0.67

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	252/301 (84%)	240 (95%)	12 (5%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	276/301 (92%)	269 (98%)	7 (2%)	0	100	100
1	D	252/301 (84%)	240 (95%)	12 (5%)	0	100	100
1	E	276/301 (92%)	269 (98%)	7 (2%)	0	100	100
2	C	292/697 (42%)	277 (95%)	15 (5%)	0	100	100
2	F	292/697 (42%)	277 (95%)	15 (5%)	0	100	100
All	All	1640/2598 (63%)	1572 (96%)	68 (4%)	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 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	222/258 (86%)	220 (99%)	2 (1%)	70	77
1	B	239/258 (93%)	239 (100%)	0	100	100
1	D	222/258 (86%)	220 (99%)	2 (1%)	70	77
1	E	239/258 (93%)	239 (100%)	0	100	100
2	C	265/628 (42%)	262 (99%)	3 (1%)	65	75
2	F	265/628 (42%)	262 (99%)	3 (1%)	65	75
All	All	1452/2288 (64%)	1442 (99%)	10 (1%)	73	79

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	88	THR
2	F	233	ASN
2	F	273	GLN
2	C	233	ASN
2	C	273	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	193	HIS
2	F	264	HIS
2	F	255	HIS
2	C	97	HIS
1	E	161	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.