wwPDB X-ray Structure Validation Summary Report (i)

May 13, 2020 – 12:10 pm BST

PDB ID	:	4YOZ
Title	:	p107 pocket domain in complex with HPV E7 peptide
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Deposited on	:	2015-03-12
Resolution	:	2.25 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

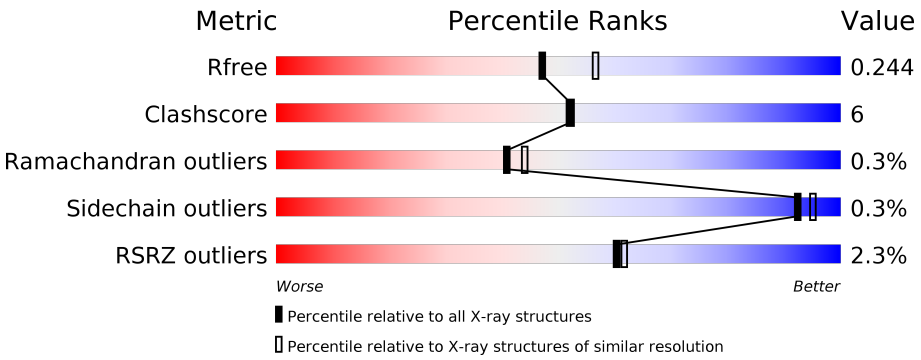
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.25 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	2391 (2.26-2.22)
Clashscore	141614	2539 (2.26-2.22)
Ramachandran outliers	138981	2489 (2.26-2.22)
Sidechain outliers	138945	2490 (2.26-2.22)
RSRZ outliers	127900	2353 (2.26-2.22)

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 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	371	2% 78% 14% 8%
2	B	9	22% 78% 11% 11%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3012 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 Retinoblastoma-like protein 1,Retinoblastoma-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	342	2801	1803	478	502	18	0	0	0

There are 45 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	388	GLY	-	expression tag	UNP P28749
A	389	GLU	-	expression tag	UNP P28749
A	390	PHE	-	expression tag	UNP P28749
A	594	PRO	-	linker	UNP P28749
A	773	ASN	-	linker	UNP P28749
A	774	ASN	-	linker	UNP P28749
A	775	PHE	-	linker	UNP P28749
A	776	GLU	-	linker	UNP P28749
A	779	ASN	ILE	conflict	UNP P28749
A	?	-	PRO	deletion	UNP P28749
A	?	-	ARG	deletion	UNP P28749
A	?	-	GLU	deletion	UNP P28749
A	?	-	VAL	deletion	UNP P28749
A	?	-	VAL	deletion	UNP P28749
A	?	-	ALA	deletion	UNP P28749
A	?	-	TYR	deletion	UNP P28749
A	?	-	ASN	deletion	UNP P28749
A	?	-	LYS	deletion	UNP P28749
A	?	-	ASN	deletion	UNP P28749
A	?	-	ILE	deletion	UNP P28749
A	?	-	ASN	deletion	UNP P28749
A	?	-	ASP	deletion	UNP P28749
A	?	-	ASP	deletion	UNP P28749
A	?	-	PHE	deletion	UNP P28749
A	?	-	GLU	deletion	UNP P28749
A	?	-	MET	deletion	UNP P28749
A	?	-	ILE	deletion	UNP P28749

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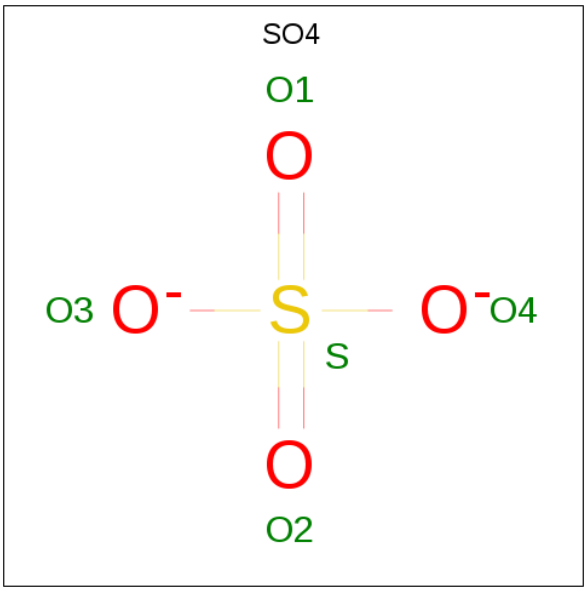
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ASP	deletion	UNP P28749
A	?	-	CYS	deletion	UNP P28749
A	?	-	ASP	deletion	UNP P28749
A	?	-	LEU	deletion	UNP P28749
A	?	-	GLU	deletion	UNP P28749
A	?	-	ASP	deletion	UNP P28749
A	?	-	ALA	deletion	UNP P28749
A	?	-	THR	deletion	UNP P28749
A	?	-	LYS	deletion	UNP P28749
A	?	-	THR	deletion	UNP P28749
A	?	-	PRO	deletion	UNP P28749
A	?	-	ASP	deletion	UNP P28749
A	?	-	CYS	deletion	UNP P28749
A	?	-	SER	deletion	UNP P28749
A	?	-	SER	deletion	UNP P28749
A	?	-	GLY	deletion	UNP P28749
A	?	-	PRO	deletion	UNP P28749
A	?	-	VAL	deletion	UNP P28749

- Molecule 2 is a protein called HPV E7 peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	9	80	51	11	17	1	0	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0

- Molecule 4 is water.

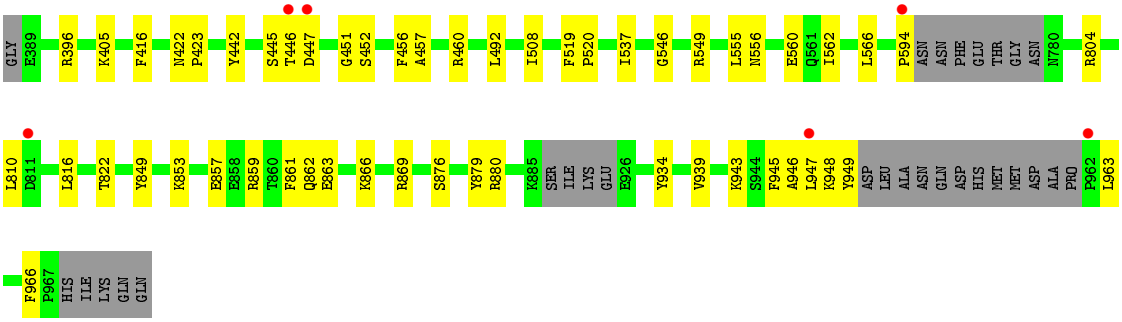
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	110	Total O 110 110	0	0
4	B	1	Total O 1 1	0	0

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: Retinoblastoma-like protein 1,Retinoblastoma-like protein 1

Chain A:



- Molecule 2: HPV E7 peptide

Chain B:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	99.69Å 76.55Å 74.68Å 90.00° 120.32° 90.00°	Depositor
Resolution (Å)	57.20 – 2.25 57.20 – 2.25	Depositor EDS
% Data completeness (in resolution range)	92.7 (57.20-2.25) 90.7 (57.20-2.25)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.57 (at 2.25Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.184 , 0.240 0.187 , 0.244	Depositor DCC
R_{free} test set	2000 reflections (9.28%)	wwPDB-VP
Wilson B-factor (Å^2)	24.1	Xtriage
Anisotropy	0.219	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 51.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	3012	wwPDB-VP
Average B, all atoms (Å^2)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.79% 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)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.29	0/2861	0.45	1/3866 (0.0%)
2	B	0.31	0/81	0.90	1/109 (0.9%)
All	All	0.29	0/2942	0.47	2/3975 (0.1%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	594	PRO	CA-N-CD	-8.62	99.44	111.50
2	B	28	LEU	CA-CB-CG	7.10	131.63	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	2801	0	2822	31	0
2	B	80	0	68	1	0
3	A	20	0	0	1	0
4	A	110	0	0	0	0
4	B	1	0	0	0	0
All	All	3012	0	2890	32	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 32 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:822:THR:HG22	1:A:945:PHE:HZ	1.60	0.66
1:A:508:ILE:HD11	1:A:555:LEU:HD11	1.76	0.65
1:A:810:LEU:O	1:A:859:ARG:NH1	2.30	0.63
1:A:946:ALA:O	1:A:948:LYS:N	2.34	0.60
1:A:442:TYR:CE2	1:A:452:SER:HB2	2.39	0.57

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	334/371 (90%)	325 (97%)	8 (2%)	1 (0%)	41	44
2	B	7/9 (78%)	7 (100%)	0	0	100	100
All	All	341/380 (90%)	332 (97%)	8 (2%)	1 (0%)	41	44

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	947	LEU

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	315/342 (92%)	314 (100%)	1 (0%)	92 95
2	B	9/9 (100%)	9 (100%)	0	100 100
All	All	324/351 (92%)	323 (100%)	1 (0%)	92 95

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	861	PHE

Some 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 carbohydrates in this entry.

5.6 Ligand geometry (i)

4 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	$\#\|Z\| > 2$
3	SO4	A	1002	-	4,4,4	0.15	0	6,6,6	0.09	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	SO4	A	1001	-	4,4,4	0.15	0	6,6,6	0.20	0
3	SO4	A	1004	-	4,4,4	0.14	0	6,6,6	0.07	0
3	SO4	A	1003	-	4,4,4	0.15	0	6,6,6	0.05	0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1002	SO4	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	342/371 (92%)	0.00	6 (1%)	68	69	13, 32, 60, 77	0
2	B	9/9 (100%)	1.26	2 (22%)	0	0	50, 55, 92, 112	0
All	All	351/380 (92%)	0.03	8 (2%)	60	61	13, 32, 62, 112	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	29	ASN	4.5
1	A	594	PRO	4.5
2	B	28	LEU	3.7
1	A	446	THR	3.5
1	A	447	ASP	2.7

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. 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
3	SO4	A	1004	5/5	0.86	0.13	99,100,102,104	0
3	SO4	A	1002	5/5	0.93	0.10	67,70,74,78	0
3	SO4	A	1003	5/5	0.93	0.13	79,80,81,83	0
3	SO4	A	1001	5/5	0.99	0.12	20,26,27,30	0

6.5 Other polymers (i)

There are no such residues in this entry.