Full wwPDB X-ray Structure Validation Report (i)

Sep 20, 2023 – 10:52 AM EDT

PDB ID	:	5HUW
Title	:	Structure of HSV-1 Large Terminase NLS bound to importin alpha
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Deposited on	:	2016-01-27
Resolution	:	1.95 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

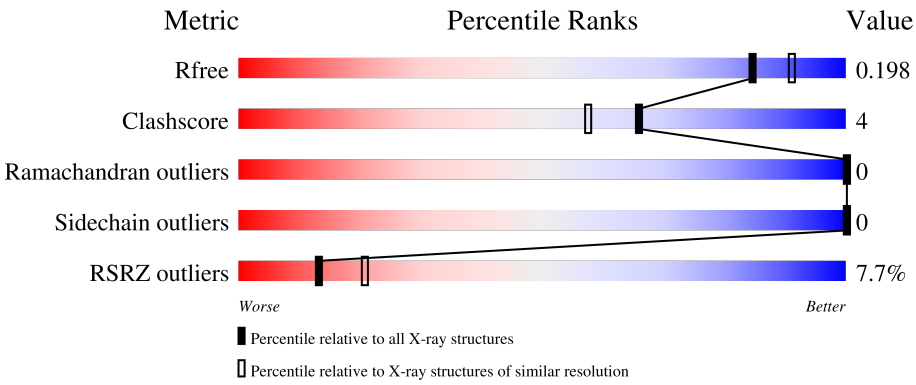
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 1.95 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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	C	528	5%, 74%, 6%, 20%
2	A	12	8%, 75%, 8%, 17%
2	B	12	33%, 33%, 17%, 50%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3691 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 Importin subunit alpha-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	C	423	3236	2061	550	615	10	0	1	0

- Molecule 2 is a protein called HSV1 large terminase NLS.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	A	10	76	48	16	12	0	0	0
2	B	6	48	31	11	6	0	0	0

- Molecule 3 is water.

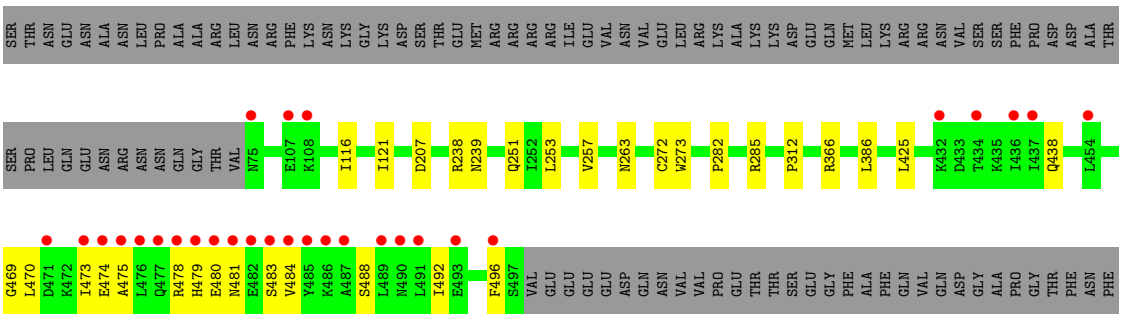
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	C	317	317	317	0	0
3	A	13	13	13	0	0
3	B	1	1	1	0	0

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.

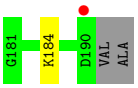
- Molecule 1: Importin subunit alpha-1

Chain C:



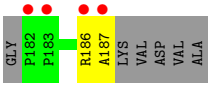
- Molecule 2: HSV1 large terminase NLS

Chain A:



- Molecule 2: HSV1 large terminase NLS

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	78.26Å 90.73Å 97.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.94 – 1.95 45.36 – 1.94	Depositor EDS
% Data completeness (in resolution range)	99.7 (14.94-1.95) 93.4 (45.36-1.94)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	2.79 (at 1.94Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.173 , 0.195 0.176 , 0.198	Depositor DCC
R_{free} test set	2013 reflections (3.89%)	wwPDB-VP
Wilson B-factor (Å^2)	29.6	Xtriage
Anisotropy	0.257	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 54.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	3691	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.42% 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	C	0.40	0/3295	0.55	0/4490
2	A	0.36	0/77	0.56	0/101
2	B	0.33	0/49	0.65	0/63
All	All	0.39	0/3421	0.55	0/4654

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	C	3236	0	3307	25	0
2	A	76	0	86	3	0
2	B	48	0	58	2	0
3	A	13	0	0	0	0
3	B	1	0	0	1	0
3	C	317	0	0	4	0
All	All	3691	0	3451	27	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.

All (27) 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:B:186:ARG:NH1	3:B:201:HOH:O	2.11	0.82
1:C:366:ARG:NH2	3:C:601:HOH:O	2.12	0.82
1:C:263:ASN:HB3	3:C:638:HOH:O	1.93	0.68
1:C:469:GLY:O	1:C:473:ILE:HG13	1.96	0.64
1:C:479:HIS:HB3	1:C:484:VAL:HG21	1.80	0.64
1:C:238:ARG:NE	2:A:184:LYS:HE3	2.16	0.60
1:C:475:ALA:O	1:C:478:ARG:HG3	2.06	0.56
1:C:386:LEU:HD21	1:C:425:LEU:HD13	1.89	0.55
1:C:238:ARG:CZ	2:A:184:LYS:HE3	2.37	0.54
1:C:479:HIS:HE1	1:C:481:ASN:HB3	1.73	0.53
3:C:819:HOH:O	2:B:187:ALA:HA	2.08	0.53
1:C:479:HIS:CE1	1:C:481:ASN:HB3	2.47	0.50
1:C:488:SER:O	1:C:492:ILE:HG12	2.13	0.49
1:C:282:PRO:HD2	1:C:285:ARG:HG3	1.96	0.48
1:C:239:ASN:OD1	2:A:184:LYS:NZ	2.47	0.48
1:C:438:GLN:NE2	1:C:483:SER:HB3	2.29	0.47
1:C:475:ALA:O	1:C:478:ARG:CG	2.62	0.47
1:C:207:ASP:OD1	1:C:251:GLN:NE2	2.48	0.47
1:C:285:ARG:HD2	3:C:714:HOH:O	2.16	0.45
1:C:272:CYS:HB3	1:C:312:PRO:HB2	1.99	0.44
1:C:116:ILE:HG12	1:C:121:ILE:HD11	1.99	0.43
1:C:253:LEU:O	1:C:257:VAL:HG23	2.20	0.42
1:C:273:TRP:CD2	1:C:312:PRO:HB3	2.53	0.42
1:C:474:GLU:HA	1:C:474:GLU:OE1	2.19	0.42
1:C:470:LEU:O	1:C:474:GLU:HG2	2.20	0.41
1:C:480:GLU:OE1	1:C:481:ASN:HA	2.21	0.41
1:C:470:LEU:HD13	1:C:496:PHE:CD1	2.57	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	C	422/528 (80%)	412 (98%)	10 (2%)	0	100	100
2	A	8/12 (67%)	8 (100%)	0	0	100	100
2	B	4/12 (33%)	3 (75%)	1 (25%)	0	100	100
All	All	434/552 (79%)	423 (98%)	11 (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	C	356/448 (80%)	356 (100%)	0	100	100
2	A	8/9 (89%)	8 (100%)	0	100	100
2	B	5/9 (56%)	5 (100%)	0	100	100
All	All	369/466 (79%)	369 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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	C	423/528 (80%)	0.20	29 (6%)	16	25	23, 34, 93, 144	0
2	A	10/12 (83%)	0.06	1 (10%)	7	11	30, 43, 60, 88	0
2	B	6/12 (50%)	4.38	4 (66%)	0	0	76, 88, 116, 118	0
All	All	439/552 (79%)	0.26	34 (7%)	13	21	23, 34, 94, 144	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	183	PRO	8.6
2	B	182	PRO	6.7
1	C	485	TYR	6.1
1	C	478	ARG	5.7
1	C	483	SER	5.7
1	C	486	LYS	5.5
1	C	474	GLU	5.5
1	C	476	LEU	5.3
1	C	481	ASN	5.1
1	C	482	GLU	5.0
1	C	475	ALA	4.9
2	B	187	ALA	4.6
1	C	108	LYS	4.6
1	C	489	LEU	4.2
1	C	496	PHE	4.1
1	C	479	HIS	4.1
1	C	432	LYS	3.9
1	C	484	VAL	3.6
1	C	493	GLU	3.6
1	C	480	GLU	3.5
2	B	186	ARG	3.4
1	C	434	THR	3.3
1	C	477	GLN	3.3

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Mol	Chain	Res	Type	RSRZ
1	C	487	ALA	3.0
1	C	437	ILE	2.9
1	C	491	LEU	2.9
2	A	190	ASP	2.6
1	C	473	ILE	2.5
1	C	107	GLU	2.4
1	C	436	ILE	2.3
1	C	75	ASN	2.2
1	C	490	ASN	2.1
1	C	471	ASP	2.1
1	C	454	LEU	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.