wwPDB X-ray Structure Validation Summary Report (i)

Jun 23, 2024 – 02:53 AM EDT

PDB ID	:	6JTQ
Title	:	RVD HA specifically contacts 5mC through van der Waals interactions
Authors	:	Liu, L.; Yi, C.
Deposited on	:	2019-04-11
Resolution	:	2.48 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

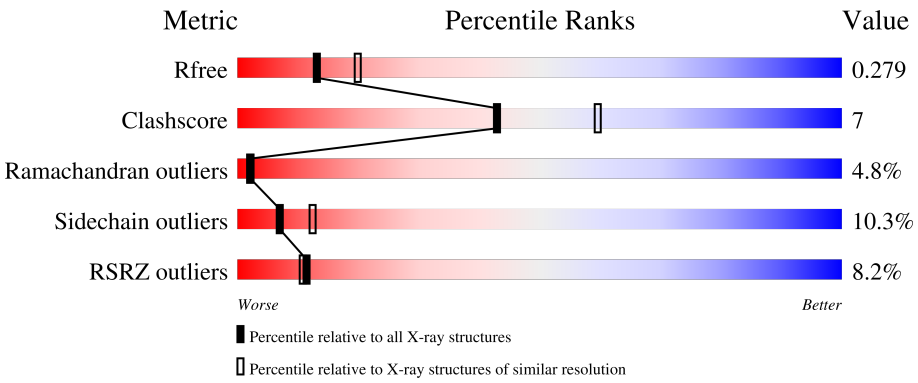
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.48 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	5857 (2.50-2.46)
Clashscore	141614	6594 (2.50-2.46)
Ramachandran outliers	138981	6469 (2.50-2.46)
Sidechain outliers	138945	6471 (2.50-2.46)
RSRZ outliers	127900	5738 (2.50-2.46)

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	499	2%, 81%, 16%, •
1	B	499	15%, 72%, 18%, 8%, •
2	C	17	6%, 88%, 12%
2	I	17	88%, 12%
3	D	17	6%, 100%

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Mol	Chain	Length	Quality of chain
3	J	17	6% 88% 12%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 8704 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 TAL effector.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	497	3605	2253	673	667	12	0	0	0
1	B	497	3605	2253	673	667	12	0	0	0

- Molecule 2 is a DNA chain called DNA (5'-D(*TP*GP*TP*CP*CP*CP*TP*TP*(5CM)P*GP*CP*GP*TP*CP*TP*CP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	I	17	336	163	50	107	16	0	0	0
2	C	17	336	163	50	107	16	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	J	17	355	167	79	93	16	0	0	0
3	D	17	355	167	79	93	16	0	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	51	51	51	0	0
4	I	13	13	13	0	0
4	J	1	1	1	0	0

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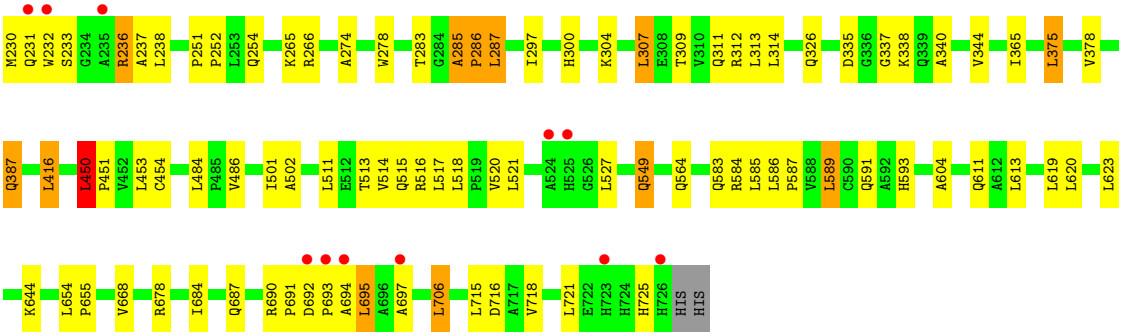
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	B	33	33	33	0	0
			Total	O		
4	C	14	14	14	0	0

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.

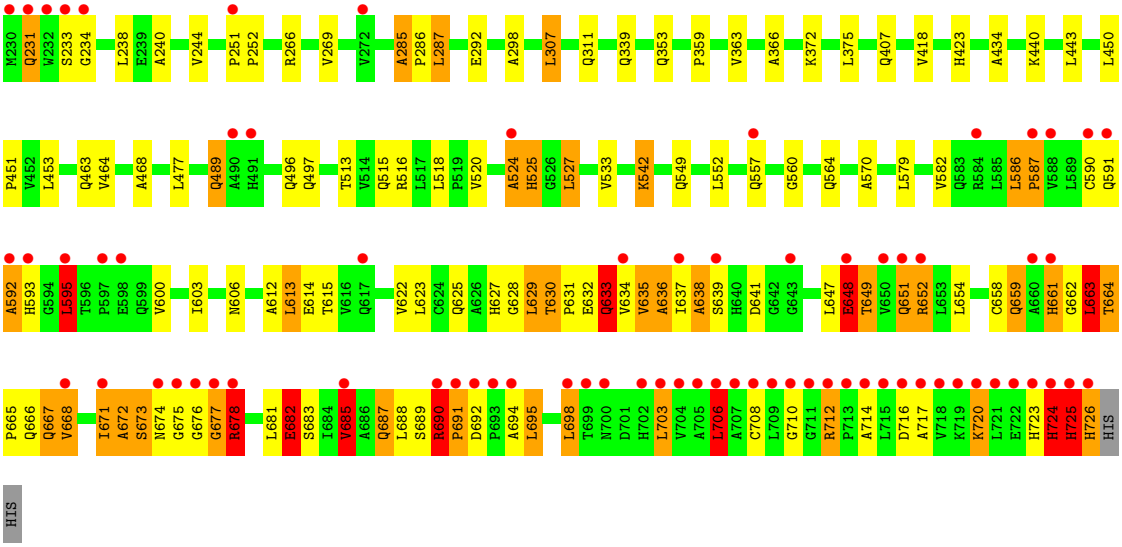
• Molecule 1: TAL effector

Chain A:



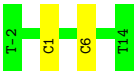
• Molecule 1: TAL effector

Chain B:



• Molecule 2: DNA (5'-D(*TP*GP*TP*CP*CP*CP*TP*TP*(5CM)P*GP*CP*GP*TP*CP*TP *CP*T)-3')

Chain I:

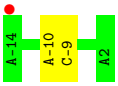


• Molecule 2: DNA (5'-D(*TP*GP*TP*CP*CP*CP*TP*TP*(5CM)P*GP*CP*GP*TP*CP*TP*CP*T)-3')

Chain C:

• Molecule 3: DNA (5'-D(*AP*GP*AP*GP*AP*CP*GP*CP*GP*AP*AP*GP*GP*GP*AP*CP*A)-3')

Chain J:



• Molecule 3: DNA (5'-D(*AP*GP*AP*GP*AP*CP*GP*CP*GP*AP*AP*GP*GP*GP*AP*CP*A)-3')

Chain D:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	85.79Å 88.02Å 89.35Å 90.00° 104.77° 90.00°	Depositor
Resolution (Å)	50.00 – 2.48 43.20 – 2.48	Depositor EDS
% Data completeness (in resolution range)	91.8 (50.00-2.48) 91.8 (43.20-2.48)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.19 (at 2.48Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.218 , 0.283 0.220 , 0.279	Depositor DCC
R_{free} test set	2095 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	34.9	Xtriage
Anisotropy	0.102	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 36.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.024 for l,-k,h	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	8704	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 6.59% 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: 5CM

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	0.64	0/3660	0.83	5/5001 (0.1%)
1	B	0.69	0/3660	0.92	8/5001 (0.2%)
2	C	0.52	0/349	1.01	0/533
2	I	0.53	0/349	0.95	1/533 (0.2%)
3	D	0.46	0/402	0.78	0/620
3	J	0.49	0/402	0.82	0/620
All	All	0.64	0/8822	0.88	14/12308 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4
1	B	0	15
All	All	0	19

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	595	LEU	CA-CB-CG	8.11	133.95	115.30
1	B	724	HIS	N-CA-CB	6.56	122.41	110.60
1	A	416	LEU	CA-CB-CG	6.12	129.38	115.30
1	A	450	LEU	CA-CB-CG	5.79	128.62	115.30
1	B	629	LEU	CA-CB-CG	5.76	128.54	115.30

There are no chirality outliers.

5 of 19 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	236	ARG	Peptide
1	A	237	ALA	Peptide
1	A	251	PRO	Peptide
1	A	694	ALA	Peptide
1	B	234	GLY	Peptide

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	3605	0	3734	39	3
1	B	3605	0	3734	78	4
2	C	336	0	195	2	0
2	I	336	0	195	0	0
3	D	355	0	189	0	0
3	J	355	0	189	1	0
4	A	51	0	0	0	0
4	B	33	0	0	2	0
4	C	14	0	0	0	0
4	I	13	0	0	0	0
4	J	1	0	0	0	0
All	All	8704	0	8236	114	4

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 7.

The worst 5 of 114 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:B:613:LEU:O	1:B:615:THR:N	2.13	0.80
1:B:672:ALA:HB3	1:B:675:GLY:HA3	1.66	0.77
1:B:648:GLU:HA	1:B:652:ARG:HB2	1.67	0.77
1:B:678:ARG:HG2	1:B:681:LEU:HD12	1.65	0.77
1:A:274:ALA:HB2	1:A:304:LYS:HG3	1.69	0.75

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:230:MET:O	1:B:233:SER:N[1_656]	1.95	0.25
1:A:231:GLN:O	1:B:231:GLN:C[1_656]	1.98	0.22
1:A:231:GLN:O	1:B:231:GLN:O[1_656]	2.00	0.20
1:B:595:LEU:N	1:B:725:HIS:O[2_545]	2.13	0.07

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	495/499 (99%)	454 (92%)	32 (6%)	9 (2%)	8 13
1	B	495/499 (99%)	401 (81%)	55 (11%)	39 (8%)	1 0
All	All	990/998 (99%)	855 (86%)	87 (9%)	48 (5%)	2 2

5 of 48 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	285	ALA
1	B	285	ALA
1	B	524	ALA
1	B	586	LEU
1	B	592	ALA

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	379/384 (99%)	346 (91%)	33 (9%)	10 18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	B	379/384 (99%)	334 (88%)	45 (12%)	5 9
All	All	758/768 (99%)	680 (90%)	78 (10%)	7 12

5 of 78 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	635	VAL
1	B	698	LEU
1	B	652	ARG
1	B	682	GLU
1	B	724	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	321	HIS
1	B	687	GLN
1	B	496	GLN
1	B	723	HIS
1	B	599	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

2 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
2	5CM	C	6	3,2	18,21,22	1.73	2 (11%)	24,30,33	1.28	2 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	5CM	I	6	3,2	18,21,22	1.63	3 (16%)	24,30,33	1.65	5 (20%)

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
2	5CM	C	6	3,2	-	0/7/21/22	0/2/2/2
2	5CM	I	6	3,2	-	0/7/21/22	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	6	5CM	C5-C4	6.38	1.48	1.44
2	I	6	5CM	C5-C4	5.65	1.48	1.44
2	C	6	5CM	C6-C5	2.99	1.39	1.34
2	I	6	5CM	C6-N1	-2.64	1.33	1.38
2	I	6	5CM	C6-C5	2.25	1.38	1.34

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	I	6	5CM	C5-C4-N3	-4.14	117.51	121.75
2	I	6	5CM	C5A-C5-C6	-3.35	118.31	122.85
2	C	6	5CM	C5A-C5-C6	-3.31	118.38	122.85
2	C	6	5CM	C5A-C5-C4	2.75	125.03	120.51
2	I	6	5CM	C5-C4-N4	2.74	125.25	121.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	497/499 (99%)	0.02	11 (2%) 62 64	17, 38, 76, 130	0
1	B	497/499 (99%)	0.81	73 (14%) 2 2	17, 41, 136, 282	0
2	C	16/17 (94%)	-0.21	1 (6%) 20 20	20, 28, 73, 155	0
2	I	16/17 (94%)	-0.57	0 100 100	19, 25, 72, 100	0
3	D	17/17 (100%)	-0.25	1 (5%) 22 22	28, 42, 74, 130	0
3	J	17/17 (100%)	-0.19	1 (5%) 22 22	27, 41, 82, 145	0
All	All	1060/1066 (99%)	0.37	87 (8%) 11 11	17, 39, 106, 282	0

The worst 5 of 87 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	230	MET	25.7
1	B	717	ALA	17.7
1	B	706	LEU	14.9
1	B	713	PRO	14.4
1	B	707	ALA	14.2

6.2 Non-standard residues in protein, DNA, RNA chains (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
2	5CM	I	6	20/21	0.98	0.14	21,24,27,28	0
2	5CM	C	6	20/21	0.98	0.11	20,22,25,26	0

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.