Full wwPDB X-ray Structure Validation Report (i)

Aug 8, 2023 – 06:59 PM EDT

PDB ID	:	1PGZ
Title	:	Crystal Structure of UP1 Complexed With d(TTAGGGTTAG(6-MI)G); A Human Telomeric Repeat Containing 6-methyl-8-(2-deoxy-beta-ribofuranosyl)isoxanthopteridine (6-MI)
Authors	:	Myers, J.C.; Moore, S.A.; Shamoo, Y.
Deposited on	:	2003-05-28
Resolution	:	2.60 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 (i)) were used in the production of this report:

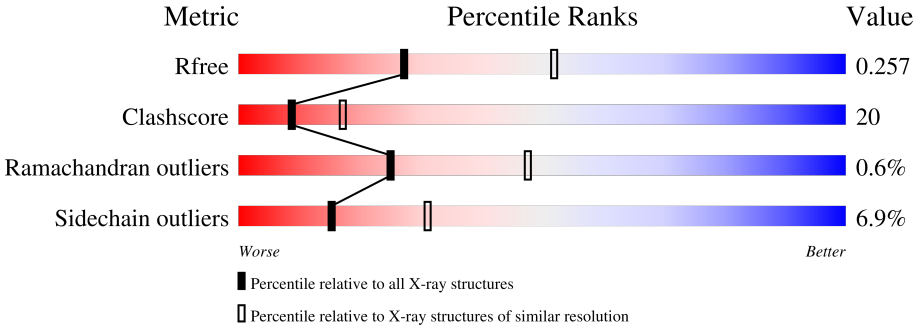
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 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 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)

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%

Mol	Chain	Length	Quality of chain
1	B	12	75% 8% 17%
2	A	195	63% 26% 5% 6%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	6MI	B	211	X	-	-	-

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1724 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 DNA chain called 5'-D(*T*TP*AP*GP*GP*GP*TP*TP*AP*GP*(6MI)P*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	B	10	212	102	41	60	9	0	0	0

- Molecule 2 is a protein called Heterogeneous nuclear ribonucleoprotein A1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	A	183	1466	913	267	280	6	0	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	B	4	4	4	0	0
3	A	42	Total	O	0	0
			42	42		

3 Residue-property plots (i)

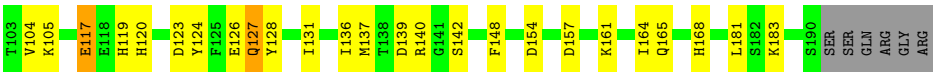
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: 5'-D(*T*TP*AP*GP*GP*GP*TP*TP*AP*GP*(6MI)P*G)-3'

Chain B:

- Molecule 2: Heterogeneous nuclear ribonucleoprotein A1

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	51.62Å 51.62Å 171.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.80 – 2.60 19.80 – 2.00	Depositor EDS
% Data completeness (in resolution range)	83.6 (19.80-2.60) 78.2 (19.80-2.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	1.34 (at 2.01Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.235 , 0.269 0.222 , 0.257	Depositor DCC
R_{free} test set	607 reflections (4.42%)	wwPDB-VP
Wilson B-factor (Å^2)	24.0	Xtriage
Anisotropy	0.179	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 36.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.43$, $< L^2 > = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.88	EDS
Total number of atoms	1724	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.65% 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: 6MI

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	B	0.41	0/210	0.62	0/324
2	A	0.40	0/1494	0.63	0/2006
All	All	0.40	0/1704	0.63	0/2330

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	B	2	0

There are no bond length outliers.

There are no bond angle outliers.

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	211	6MI	C3',C4'

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	B	212	0	114	0	0
2	A	1466	0	1435	66	0
3	A	42	0	0	3	0
3	B	4	0	0	0	0
All	All	1724	0	1549	66	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 20.

All (66) 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:A:78:LYS:HE2	2:A:81:GLY:HA2	1.30	1.09
2:A:117:GLU:H	2:A:120:HIS:HD2	1.25	0.84
2:A:13:LEU:HD11	2:A:164:ILE:HD13	1.60	0.82
2:A:23:PHE:CB	2:A:53:ARG:HH22	2.03	0.71
2:A:78:LYS:CE	2:A:81:GLY:HA2	2.16	0.70
2:A:97:ARG:HA	2:A:97:ARG:HE	1.58	0.68
2:A:126:GLU:HG3	2:A:131:ILE:HD12	1.76	0.67
2:A:23:PHE:HB2	2:A:53:ARG:HH12	1.60	0.65
2:A:23:PHE:HB3	3:A:199:HOH:O	2.00	0.60
2:A:117:GLU:H	2:A:120:HIS:CD2	2.14	0.60
2:A:64:THR:OG1	2:A:67:GLU:HG3	2.02	0.60
2:A:13:LEU:CD1	2:A:164:ILE:HD13	2.31	0.59
2:A:65:VAL:HA	2:A:68:VAL:CG1	2.33	0.59
2:A:139:ASP:OD1	2:A:142:SER:HB3	2.02	0.58
2:A:23:PHE:HB2	2:A:53:ARG:HH22	1.68	0.58
2:A:65:VAL:HA	2:A:68:VAL:HG13	1.86	0.57
2:A:93:GLU:O	2:A:96:GLN:HB2	2.03	0.57
2:A:64:THR:HG1	2:A:67:GLU:HG3	1.70	0.57
2:A:26:THR:O	2:A:27:ASP:C	2.44	0.56
2:A:88:ARG:NH2	2:A:161:LYS:HD3	2.21	0.55
2:A:164:ILE:HD12	2:A:165:GLN:N	2.22	0.55
2:A:127:GLN:HG3	2:A:128:TYR:CD1	2.42	0.55
2:A:9:GLU:OE2	2:A:64:THR:HA	2.05	0.54
2:A:183:LYS:O	2:A:183:LYS:HD2	2.08	0.53
2:A:105:LYS:HE3	2:A:154:ASP:O	2.07	0.53
2:A:47:ARG:HA	2:A:55:ARG:HG3	1.90	0.53
2:A:65:VAL:O	2:A:68:VAL:HG13	2.09	0.53
2:A:139:ASP:CG	2:A:142:SER:HB3	2.30	0.51
2:A:165:GLN:HE21	2:A:165:GLN:HA	1.77	0.49
2:A:47:ARG:HB3	2:A:54:SER:HA	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:92:ARG:HG3	2:A:92:ARG:HH11	1.78	0.48
2:A:9:GLU:HG2	2:A:14:ARG:HD3	1.96	0.47
2:A:31:ARG:O	2:A:35:GLU:HG3	2.15	0.46
2:A:140:ARG:C	2:A:142:SER:H	2.18	0.46
2:A:23:PHE:HB2	2:A:53:ARG:NH1	2.28	0.46
2:A:102:LEU:HD11	2:A:181:LEU:CD2	2.45	0.46
2:A:40:LEU:HA	2:A:61:THR:O	2.16	0.46
2:A:137:MET:HG3	2:A:148:PHE:CE1	2.52	0.45
2:A:157:ASP:O	2:A:161:LYS:HG3	2.17	0.45
2:A:164:ILE:HD12	2:A:164:ILE:C	2.37	0.45
2:A:119:HIS:CE1	2:A:120:HIS:CE1	3.05	0.44
2:A:26:THR:OG1	2:A:28:GLU:HB2	2.18	0.43
2:A:139:ASP:HB3	2:A:142:SER:HB3	1.99	0.43
2:A:124:TYR:OH	2:A:168:HIS:ND1	2.41	0.43
2:A:47:ARG:HB2	2:A:53:ARG:O	2.17	0.43
2:A:51:THR:C	2:A:53:ARG:H	2.22	0.43
2:A:165:GLN:HA	2:A:165:GLN:NE2	2.33	0.43
2:A:65:VAL:CA	2:A:68:VAL:HG13	2.49	0.42
2:A:48:ASP:OD2	2:A:49:PRO:HD2	2.19	0.42
2:A:9:GLU:CG	2:A:14:ARG:HD3	2.49	0.42
2:A:82:ARG:NH1	2:A:83:VAL:O	2.52	0.42
2:A:51:THR:C	2:A:53:ARG:N	2.73	0.42
2:A:99:GLY:C	2:A:102:LEU:HD22	2.40	0.42
2:A:136:ILE:HB	3:A:219:HOH:O	2.19	0.42
2:A:26:THR:O	2:A:28:GLU:N	2.53	0.42
2:A:99:GLY:O	2:A:102:LEU:CD2	2.68	0.42
2:A:23:PHE:HB2	2:A:53:ARG:NH2	2.33	0.41
2:A:97:ARG:HA	2:A:97:ARG:NE	2.32	0.41
2:A:92:ARG:HG3	3:A:198:HOH:O	2.20	0.41
2:A:102:LEU:CD2	2:A:102:LEU:H	2.34	0.41
2:A:99:GLY:O	2:A:102:LEU:HD22	2.21	0.41
2:A:97:ARG:HA	2:A:98:PRO:HD3	1.87	0.41
2:A:102:LEU:HG	2:A:104:VAL:HG13	2.02	0.41
2:A:13:LEU:HD12	2:A:13:LEU:HA	1.93	0.41
2:A:41:THR:N	2:A:61:THR:O	2.47	0.40
2:A:127:GLN:HE21	2:A:127:GLN:HB2	1.70	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
2	A	181/195 (93%)	170 (94%)	10 (6%)	1 (1%)	25 47

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	28	GLU

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
2	A	159/170 (94%)	148 (93%)	11 (7%)	15 31

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	9	GLU
2	A	13	LEU
2	A	47	ARG
2	A	53	ARG
2	A	66	GLU
2	A	68	VAL
2	A	96	GLN
2	A	102	LEU
2	A	117	GLU
2	A	123	ASP

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Mol	Chain	Res	Type
2	A	127	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	12	GLN
2	A	50	ASN
2	A	96	GLN
2	A	119	HIS
2	A	120	HIS
2	A	127	GLN
2	A	165	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)

1 non-standard protein/DNA/RNA residue is 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	$\#\|Z\| > 2$
1	6MI	B	211	1	23,27,28	2.16	7 (30%)	27,40,43	5.09	14 (51%)

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
1	6MI	B	211	1	2/2/4/4	2/7/21/22	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	211	6MI	C3M-N4M	7.56	1.42	1.32
1	B	211	6MI	C7M-N6M	3.33	1.41	1.33
1	B	211	6MI	C8A-N1M	2.79	1.43	1.37
1	B	211	6MI	C8A-N8M	2.50	1.41	1.37
1	B	211	6MI	C5M-N6M	2.33	1.42	1.38
1	B	211	6MI	C4A-N4M	2.15	1.41	1.37
1	B	211	6MI	C2M-C3M	-2.08	1.41	1.46

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	211	6MI	C2M-C3M-N4M	-15.91	118.78	123.83
1	B	211	6MI	O4'-C1'-N1M	10.72	119.08	108.29
1	B	211	6MI	C2'-C1'-N1M	10.54	128.49	116.01
1	B	211	6MI	C3M-C2M-N1M	9.36	119.77	115.67
1	B	211	6MI	O3'-C3'-C4'	4.91	128.90	110.10
1	B	211	6MI	O3'-C3'-C2'	4.58	127.27	110.90
1	B	211	6MI	O4'-C4'-C5'	3.78	121.83	109.37
1	B	211	6MI	C4'-O4'-C1'	-3.11	101.93	109.45
1	B	211	6MI	C4A-N4M-C3M	3.09	121.78	116.21
1	B	211	6MI	C3I-C3M-N4M	3.09	120.41	116.72
1	B	211	6MI	O2M-C2M-C3M	-2.93	120.13	124.52
1	B	211	6MI	C3I-C3M-C2M	2.69	120.80	117.56
1	B	211	6MI	C5'-C4'-C3'	2.41	128.93	114.74
1	B	211	6MI	N8M-C7M-N6M	-2.33	118.97	123.32

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	211	6MI	C3'
1	B	211	6MI	C4'

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	211	6MI	C3'-C4'-C5'-O5'
1	B	211	6MI	O4'-C1'-N1M-C8A

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)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.