

# Full wwPDB X-ray Structure Validation Report (i)

### Feb 4, 2024 – 01:38 AM EST

PDB ID	:	1PUE
Title	:	PU.1 ETS DOMAIN-DNA COMPLEX
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Deposited on	:	1996-07-08
Resolution	:	2.10 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

The reported resolution of this entry is 2.10 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain						
1	А	16	69%	31%					
1	С	16	38%	62%					
2	В	16	50%	44%	6%				
2	D	16	56%	38%	6%				
3	Е	89	56%	35%	6% ••				
3	F	89	54%	33%	12% ·				



#### 1PUE

# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2928 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 DNA (5'-D(\*AP\*AP\*AP\*AP\*AP\*GP\*GP\*GP\*GP\*AP\* AP\*GP\*TP\*GP\*GP\*GP\*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Δ	16	Total	С	Ν	0	Р	0	0	0
1	I A		340	160	77	88	15	0		
1	С	16	Total	С	Ν	0	Р	0	0	0
		10	340	160	77	88	15	0	0	0

• Molecule 2 is a DNA chain called DNA (5'-D(\*TP\*CP\*CP\*CP\*AP\*CP\*TP\*TP\*CP\*CP\* CP\*CP\*TP\*TP\*TP\*T)-3').

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	В	16	Total	С	Ν	0	Р	0	0	0
	10	310	152	43	100	15	0	0	0	
0	Л	16	Total	С	Ν	0	Р	0	0	0
	2 D		310	152	43	100	15	0	0	0

• Molecule 3 is a protein called PROTEIN (TRANSCRIPTION FACTOR PU.1 (TF PU.1)).

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
2	F	<u> </u>	Total	С	Ν	0	S	0	0	0
່ <u>ບ</u>	9 L	00	738	475	135	125	3	0		0
2	Б	80	Total	С	Ν	0	S	0	0	0
3	3 F	- 69	747	481	136	127	3	0	0	U

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Е	228	GLU	GLN	conflict	UNP P17433
F	228	GLU	GLN	conflict	UNP P17433

• Molecule 4 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	15	Total O 15 15	0	0
4	В	21	TotalO2121	0	0
4	С	24	Total O 24 24	0	0
4	D	14	Total         O           14         14	0	0
4	Е	42	$\begin{array}{cc} \text{Total} & \text{O} \\ 42 & 42 \end{array}$	0	0
4	F	27	Total O 27 27	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. 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.

Note EDS was not executed.

• Molecule 1: DNA (5'-D(\*AP\*AP\*AP\*AP\*AP\*GP\*GP\*GP\*GP\*AP\*AP\*GP\*TP\*GP\*GP\*G) -3')

<ul> <li>Molecule 1: DNA (5'-D(*AP*AP*AP*AP*AP*GP*GP*GP*GP*AP*A-3')</li> <li>Chain C: 38% 62%</li> </ul>
• Molecule 1: DNA (5'-D(*AP*AP*AP*AP*AP*GP*GP*GP*GP*AP*A -3') Chain C: 38% 62%
Chain C: 38% 62%
A 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
• Molecule 2: DNA (5'-D(*TP*CP*CP*CP*AP*CP*TP*TP*CP*CP*CP)
Chain B: 50% 44% 6%
117 C18 C20 C26 C26 C26 C27 T28 T33 T32 T33
• Molecule 2: DNA (5'-D(*TP*CP*CP*CP*AP*CP*TP*TP*CP*CP*CP)
Chain D: 56% 38% 6%
117 123 124 123 124 123 123 123 123 123 123 123 123 123 123
• Molecule 3: PROTEIN (TRANSCRIPTION FACTOR PU.1 (TF PU.1)
Chain E: 56% 35% 6% •



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• Molecule 3: PROTEIN (TRANSCRIPTION FACTOR PU.1 (TF PU.1))





# 4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source	
Space group	C 1 2 1	Depositor	
Cell constants	89.10Å 101.90Å 55.60Å	Depositor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $111.20^{\circ}$ $90.00^{\circ}$	Depositor	
Resolution (Å)	6.00 - 2.10	Depositor	
% Data completeness	(Not available) $(6.00-2.10)$	Depositor	
(in resolution range)	(100 available) (0.00 2.10)		
$R_{merge}$	0.03	Depositor	
R <sub>sym</sub>	(Not available)	Depositor	
Refinement program	X-PLOR 3.1	Depositor	
$R, R_{free}$	0.225 , $0.287$	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	2928	wwPDB-VP	
Average B, all atoms $(Å^2)$	26.0	wwPDB-VP	



# 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).

Mal	Chain	Bo	nd lengths	Bond angles		
	Unain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.62	0/386	0.81	0/597	
1	С	0.71	0/386	0.75	0/597	
2	В	0.74	0/342	1.01	0/523	
2	D	0.81	0/342	0.99	1/523~(0.2%)	
3	Е	0.77	1/753~(0.1%)	1.09	5/999~(0.5%)	
3	F	0.61	0/762	0.86	1/1010~(0.1%)	
All	All	0.71	1/2971~(0.0%)	0.93	7/4249~(0.2%)	

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
2	В	0	4
2	D	0	4
All	All	0	8

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
3	Ε	186	ASP	CB-CG	10.79	1.74	1.51

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	Е	186	ASP	CB-CG-OD1	12.97	129.98	118.30
3	Е	186	ASP	OD1-CG-OD2	-8.51	107.13	123.30
3	Е	211	LEU	CA-CB-CG	7.83	133.31	115.30
3	Е	250	LEU	CA-CB-CG	7.13	131.69	115.30
3	F	211	LEU	CA-CB-CG	6.26	129.71	115.30
3	Е	234	LEU	CA-CB-CG	5.35	127.61	115.30
2	D	25	DC	OP2-P-O3'	5.02	116.25	105.20



There are no chirality outliers.

Mol	Chain	$\mathbf{Res}$	Type	Group
2	В	18	DC	Sidechain
2	В	27	DC	Sidechain
2	В	28	DC	Sidechain
2	В	30	DT	Sidechain
2	D	17	DT	Sidechain
2	D	23	DT	Sidechain
2	D	25	DC	Sidechain
2	D	26	DC	Sidechain

All (8) planarity outliers are listed below:

# 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	А	340	0	179	8	0
1	С	340	0	179	20	0
2	В	310	0	185	3	0
2	D	310	0	185	2	0
3	Е	738	0	767	29	0
3	F	747	0	778	49	0
4	А	15	0	0	1	0
4	В	21	0	0	1	0
4	С	24	0	0	0	0
4	D	14	0	0	0	0
4	Е	42	0	0	3	0
4	F	27	0	0	6	0
All	All	2928	0	2273	94	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 19.

All (94) 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:C:5:DA:H5"	3:F:249:LYS:NZ	1.82	0.93



	lo de page	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
3:E:248:LYS:HD2	3:E:251:THR:HG21	1.52	0.92
1:C:5:DA:H5"	3:F:249:LYS:HZ2	1.35	0.90
3:E:249:LYS:HG2	3:E:250:LEU:HD22	1.60	0.80
3:F:174:LEU:HD13	3:F:234:LEU:HD13	1.64	0.80
1:A:12:DG:H2"	1:A:13:DT:OP2	1.84	0.78
1:C:6:DG:H2"	1:C:7:DG:H5'	1.67	0.77
3:F:171:LYS:HG3	3:F:173:ARG:NH1	2.01	0.76
3:F:203:PHE:HB2	3:F:250:LEU:HB3	1.69	0.74
3:F:173:ARG:HD2	4:F:279:HOH:O	1.87	0.74
3:E:227:TYR:HB2	4:E:283:HOH:O	1.88	0.73
3:F:171:LYS:HZ3	3:F:173:ARG:HH12	1.36	0.73
3:F:199:GLY:HA3	3:F:259:LEU:HD11	1.71	0.73
3:F:236:ASN:ND2	4:F:266:HOH:O	2.22	0.72
1:C:5:DA:C5'	3:F:249:LYS:NZ	2.53	0.70
1:C:13:DT:H2"	1:C:14:DG:C8	2.26	0.70
3:F:171:LYS:NZ	3:F:173:ARG:HH12	1.92	0.66
3:E:192:TRP:HE1	3:E:202:GLN:HE21	1.43	0.65
3:F:213:HIS:HB2	4:F:267:HOH:O	1.97	0.64
3:E:246:VAL:HG22	3:E:251:THR:OG1	1.98	0.63
2:D:24:DT:H2"	2:D:25:DC:H5'	1.80	0.63
3:F:213:HIS:O	3:F:217:ILE:HG12	1.99	0.62
1:A:5:DA:H5"	3:E:249:LYS:HE3	1.82	0.61
3:E:255:SER:O	3:E:257:GLU:N	2.33	0.61
3:F:171:LYS:HG3	3:F:173:ARG:HH12	1.64	0.60
3:F:188:LYS:HE3	3:F:188:LYS:HA	1.82	0.60
3:E:195:ASP:HB3	3:E:200:THR:OG1	2.02	0.59
3:E:213:HIS:O	3:E:217:ILE:HG13	2.05	0.57
1:C:5:DA:H5"	3:F:249:LYS:HZ1	1.65	0.57
1:C:14:DG:C5'	3:F:222:ARG:HH12	2.18	0.56
3:E:257:GLU:HG2	3:E:257:GLU:O	2.06	0.56
1:C:9:DG:N7	3:F:232:ARG:NH1	2.52	0.56
2:B:20:DC:H2"	2:B:21:DA:C8	2.41	0.55
1:C:6:DG:OP1	3:F:249:LYS:O	2.24	0.55
1:C:15:DG:H2"	1:C:16:DG:H5"	1.89	0.54
3:F:248:LYS:O	3:F:251:THR:HG23	2.07	0.53
3:E:191:ILE:HD11	3:E:201:PHE:CD2	2.43	0.53
1:A:10:DA:N6	3:E:232:ARG:NH1	2.56	0.53
1:C:14:DG:H5'	3:F:222:ARG:NH1	2.23	0.53
3:F:196:LYS:HB2	4:F:270:HOH:O	2.09	0.52
3:E:179:LEU:HD13	3:E:258:VAL:HG21	1.90	0.52
3:E:249:LYS:HG2	3:E:250:LEU:CD2	2.34	0.52

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		Interatomic	Clash	
Atom-1	Atom-2	distance $(Å)$	overlap (Å)	
3:F:174:LEU:CD1	3:F:234:LEU:HD13	2.38	0.52	
1:C:15:DG:C2'	1:C:16:DG:H5"	2.40	0.52	
3:E:191:ILE:HD11	3:E:201:PHE:HD2	1.75	0.52	
3:E:212:ALA:HB2	4:E:283:HOH:O	2.09	0.52	
3:F:171:LYS:HB3	4:F:263:HOH:O	2.09	0.52	
3:F:248:LYS:HG2	3:F:251:THR:HG21	1.91	0.51	
3:F:177:PHE:O	3:F:181:LEU:HD13	2.11	0.51	
1:A:5:DA:C5'	3:E:249:LYS:HE3	2.40	0.51	
3:F:201:PHE:CZ	3:F:252:TYR:HB2	2.45	0.51	
3:F:195:ASP:HB3	3:F:200:THR:OG1	2.10	0.51	
3:F:226:THR:HB	4:F:268:HOH:O	2.11	0.50	
1:C:6:DG:H2"	1:C:7:DG:C5'	2.41	0.50	
1:C:11:DA:H2"	1:C:12:DG:O5'	2.12	0.49	
3:E:176:GLN:HG3	4:E:288:HOH:O	2.12	0.49	
3:F:191:ILE:HG23	3:F:191:ILE:O	2.12	0.49	
3:F:171:LYS:C	3:F:172:ILE:HG13	2.32	0.49	
1:C:14:DG:H5"	3:F:222:ARG:HH12	1.77	0.48	
3:F:232:ARG:HH21	3:F:236:ASN:HD21	1.61	0.48	
1:A:10:DA:H62	3:E:232:ARG:NH1	2.12	0.48	
3:F:215:TRP:CH2	3:F:219:LYS:HD3	2.49	0.48	
2:D:27:DC:H2"	2:D:28:DC:OP2	2.13	0.48	
3:E:177:PHE:HD2	3:E:178:LEU:HD13	1.79	0.47	
3:E:193:TRP:HH2	3:E:258:VAL:HG11	1.78	0.47	
3:E:247:LYS:H	3:E:247:LYS:CE	2.28	0.47	
1:A:12:DG:C2'	1:A:13:DT:OP2	2.60	0.47	
3:F:171:LYS:HZ2	3:F:173:ARG:HH22	1.63	0.46	
1:C:5:DA:C5'	3:F:249:LYS:HZ2	2.14	0.46	
3:F:190:SER:HB2	3:F:211:LEU:HD23	1.97	0.46	
3:E:174:LEU:HD21	3:E:234:LEU:HD13	1.99	0.45	
1:C:15:DG:H2"	1:C:16:DG:C5'	2.47	0.44	
3:F:171:LYS:HB3	3:F:172:ILE:H	1.63	0.44	
3:F:174:LEU:HD13	3:F:234:LEU:CD1	2.43	0.43	
1:C:15:DG:H1'	1:C:16:DG:H5"	2.00	0.43	
3:F:206:LYS:N	3:F:206:LYS:HD2	2.34	0.43	
1:A:10:DA:N6	3:E:232:ARG:HH11	2.17	0.42	
1:C:14:DG:C5'	3:F:222:ARG:NH1	2.82	0.42	
1:A:9:DG:C6	1:A:10:DA:C6	3.07	0.42	
3:F:194:VAL:HG22	3:F:200:THR:O	2.20	0.42	
4:A:31:HOH:O	3:E:228:GLU:HG3	2.20	0.42	
2:B:25:DC:H2'	4:B:52:HOH:O	2.18	0.42	
3:E:215:TRP:CH2	3:E:219:LYS:HD3	2.54	0.42	

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Atom-1	Atom-2	Interatomic	Clash
		distance (A)	overlap (A)
3:F:202:GLN:HG3	3:F:251:THR:HG22	2.01	0.42
3:F:249:LYS:HB3	3:F:250:LEU:H	1.73	0.42
3:F:188:LYS:HE3	3:F:188:LYS:CA	2.50	0.41
1:C:5:DA:C5'	3:F:249:LYS:HZ1	2.25	0.41
3:E:236:ASN:HD22	3:E:236:ASN:HA	1.62	0.41
3:F:175:TYR:HD2	3:F:237:TYR:CZ	2.39	0.41
3:E:231:ALA:HA	3:E:234:LEU:HB2	2.01	0.41
2:B:28:DC:C2'	2:B:29:DT:H72	2.51	0.40
3:E:180:ASP:O	3:E:184:SER:OG	2.34	0.40
3:F:198:LYS:HE2	3:F:198:LYS:HB3	1.69	0.40
3:F:227:TYR:CZ	3:F:250:LEU:HD12	2.57	0.40

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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
3	Ε	86/89~(97%)	81 (94%)	3~(4%)	2(2%)	6 2
3	F	87/89~(98%)	81 (93%)	2(2%)	4(5%)	2  0
All	All	173/178~(97%)	162 (94%)	5(3%)	6 (4%)	3 1

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	F	195	ASP
3	F	249	LYS
3	Е	256	GLY
3	Е	257	GLU
3	F	247	LYS
3	F	250	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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	Ε	77/78~(99%)	70~(91%)	7~(9%)	9 6
3	F	78/78~(100%)	67~(86%)	11 (14%)	3 1
All	All	155/156~(99%)	137~(88%)	18 (12%)	5 3

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	Е	173	ARG
3	Е	178	LEU
3	Е	211	LEU
3	Е	234	LEU
3	Е	247	LYS
3	Е	251	THR
3	Е	257	GLU
3	F	172	ILE
3	F	174	LEU
3	F	182	LEU
3	F	188	LYS
3	F	200	THR
3	F	211	LEU
3	F	222	ARG
3	F	232	ARG
3	F	234	LEU
3	F	244	LYS
3	F	251	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
3	Е	202	GLN
3	Е	213	HIS
3	Е	221	ASN
3	Е	236	ASN



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$\mathbf{Mol}$	Chain	$\mathbf{Res}$	Type
3	F	236	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 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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

# 6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

# 6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

