



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 06:23 PM GMT

PDB ID : 1AIS
Title : TATA-BINDING PROTEIN/TRANSCRIPTION FACTOR (II)B/TATA-BOX COMPLEX FROM PYROCOCCLUS WOESLI
Authors : Kosa, P.F.; Ghosh, G.; Dedeker, B.S.; Sigler, P.B.
Deposited on : 1997-04-24
Resolution : 2.10 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

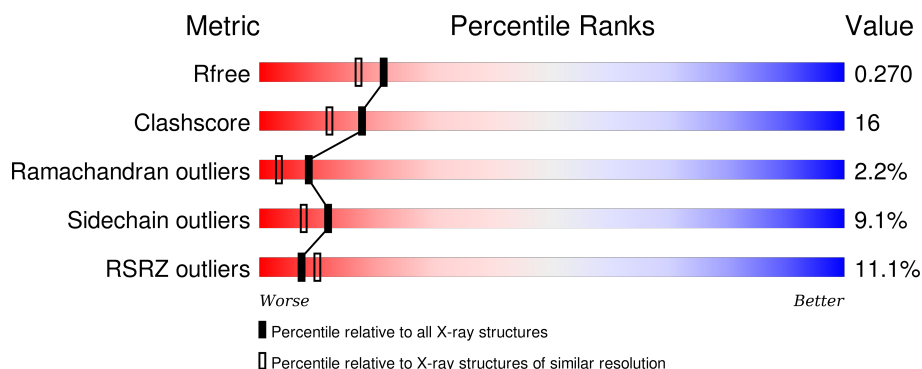
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$. 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	17	<div> <div>35%</div> <div>47%</div> <div>18%</div> </div>
2	E	17	<div> <div>29%</div> <div>65%</div> <div>6%</div> </div>
3	A	182	<div> <div>6%</div> <div>81%</div> <div>12%</div> <div>5% ••</div> </div>
4	B	200	<div> <div>17%</div> <div>60%</div> <div>31%</div> <div>5% ••</div> </div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3929 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*CP*TP*TP*AP*CP*TP*TP*TP*(5IU)P*(5IU)P*AP*AP*AP*GP*C)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	C	17	Total	C	I	N	O	P	0	0	0
			342	165	2	58	101	16			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	17	Total	C	N	O	P	0	0	0
			349	169	65	99	16			

- Molecule 3 is a protein called PROTEIN (TATA-BINDING PROTEIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	181	Total	C	N	O	S	0	0	0
			1414	910	235	262	7			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	182	LEU	-	INSERTION	UNP P62001

- Molecule 4 is a protein called PROTEIN (TRANSCRIPTION INITIATION FACTOR IIB).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	B	193	Total	C	N	O	S	0	0	0
			1536	972	285	276	3			

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	146	Total 146	O 146	0	0
5	B	61	Total 61	O 61	0	0
5	C	36	Total 36	O 36	1	0
5	E	45	Total 45	O 45	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

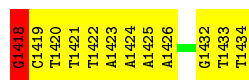
- Molecule 1: DNA (5'-D(*AP*AP*CP*TP*TP*AP*CP*TP*TP*TP*(5IU)P*(5IU)P*AP*AP*AP*GP*C)-3')

Chain C: 




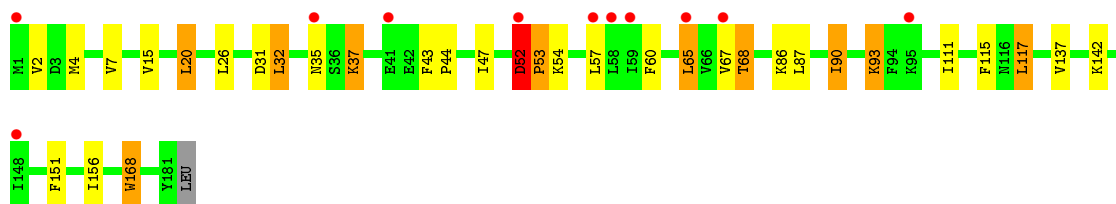
- Molecule 2: DNA (5'-D(*GP*CP*TP*TP*TP*AP*AP*AP*AP*AP*GP*TP*AP*AP*GP*TP*T)-3')

Chain E: 



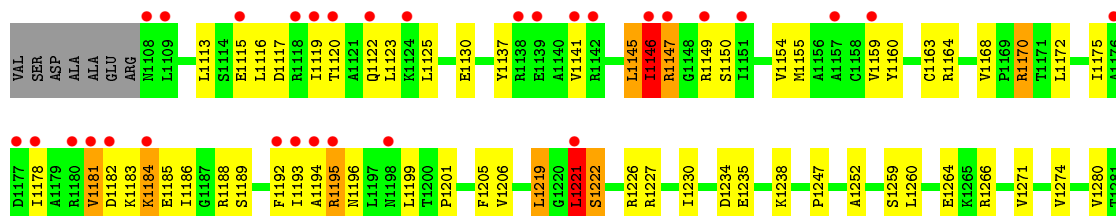
- Molecule 3: PROTEIN (TATA-BINDING PROTEIN)

Chain A: 



- Molecule 4: PROTEIN (TRANSCRIPTION INITIATION FACTOR IIB)

Chain B: 



V1282	
R1285	
Y1286	
K1287	
E1288	
E1291	
K1292	
L1293	
K1294	
I1295	
K1296	
V1297	
F1298	
I1299	
A1300	

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	125.70Å 91.20Å 74.20Å 90.00° 122.70° 90.00°	Depositor
Resolution (Å)	20.00 – 2.10 24.78 – 2.08	Depositor EDS
% Data completeness (in resolution range)	92.0 (20.00-2.10) 96.1 (24.78-2.08)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.10 (at 2.08Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.212 , 0.268 0.219 , 0.270	Depositor DCC
R_{free} test set	1986 reflections (5.23%)	DCC
Wilson B-factor (Å ²)	31.4	Xtriage
Anisotropy	0.286	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 78.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 40467 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3929	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.83% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 5IU

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	0.59	0/337	1.04	1/515 (0.2%)
2	E	0.60	0/392	1.03	1/604 (0.2%)
3	A	0.50	0/1437	0.75	2/1939 (0.1%)
4	B	0.43	0/1553	0.65	1/2086 (0.0%)
All	All	0.50	0/3719	0.79	5/5144 (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	C	0	2
2	E	0	3
All	All	0	5

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	52	ASP	C-N-CD	6.26	141.54	128.40
2	E	1418	DG	N9-C1'-C2'	-5.46	102.23	112.60
4	B	1221	LEU	N-CA-C	5.36	125.47	111.00
1	C	1401	DA	N9-C1'-C2'	-5.22	102.68	112.60
3	A	53	PRO	N-CA-C	-5.15	98.70	112.10

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	1407	DC	Sidechain
1	C	1414	DA	Sidechain
2	E	1418	DG	Sidechain
2	E	1424	DA	Sidechain
2	E	1425	DA	Sidechain

5.2 Too-close contacts

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	342	0	190	22	0
2	E	349	0	195	18	0
3	A	1414	0	1473	22	0
4	B	1536	0	1639	55	0
5	A	146	0	0	0	0
5	B	61	0	0	2	0
5	C	36	0	0	2	0
5	E	45	0	0	0	0
All	All	3929	0	3497	113	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 16.

The worst 5 of 113 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:E:1418:DG:H2''	2:E:1419:DC:C5'	1.72	1.19
2:E:1418:DG:H2''	2:E:1419:DC:H5''	1.29	1.08
1:C:1403:DC:H2''	1:C:1404:DT:H5'	1.14	1.08
2:E:1418:DG:H5'	2:E:1418:DG:H8	1.29	0.97
2:E:1419:DC:H5'	2:E:1419:DC:H6	1.27	0.96

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	A	179/182 (98%)	176 (98%)	2 (1%)	1 (1%)	30	24
4	B	191/200 (96%)	173 (91%)	11 (6%)	7 (4%)	4	1
All	All	370/382 (97%)	349 (94%)	13 (4%)	8 (2%)	8	3

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	52	ASP
4	B	1146	ILE
4	B	1181	VAL
4	B	1221	LEU
4	B	1299	ILE

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	
3	A	159/160 (99%)	144 (91%)	15 (9%)	11	7
4	B	161/166 (97%)	147 (91%)	14 (9%)	13	8
All	All	320/326 (98%)	291 (91%)	29 (9%)	12	7

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	142	LYS

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Mol	Chain	Res	Type
4	B	1145	LEU
4	B	1266	ARG
3	A	168	TRP
4	B	1146	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
4	B	1122	GLN
4	B	1268	GLN
4	B	1198	ASN
3	A	103	GLN
4	B	1213	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	$\# Z > 2$
1	5IU	C	1411	1,2	12,21,22	1.27	2 (16%)	14,30,33	3.76	1 (7%)
1	5IU	C	1412	1,2	12,21,22	1.43	3 (25%)	14,30,33	3.78	1 (7%)

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	5IU	C	1411	1,2	-	0/3/21/22	0/2/2/2
1	5IU	C	1412	1,2	-	0/3/21/22	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1411	5IU	C6-C5	-2.20	1.33	1.38
1	C	1412	5IU	C6-N1	2.28	1.38	1.35
1	C	1412	5IU	C5-I5	2.45	2.16	2.10
1	C	1412	5IU	C4-N3	2.80	1.38	1.33
1	C	1411	5IU	C4-N3	2.96	1.38	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1411	5IU	C4-N3-C2	13.71	127.10	115.25
1	C	1412	5IU	C4-N3-C2	13.87	127.23	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	1411	5IU	2	0
1	C	1412	5IU	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates 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 ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	15/17 (88%)	-0.43	0 100 100	16, 21, 42, 47	0
2	E	17/17 (100%)	-0.64	0 100 100	13, 21, 42, 44	0
3	A	181/182 (99%)	-0.00	11 (6%) 25 33	10, 22, 47, 70	0
4	B	193/200 (96%)	0.81	34 (17%) 2 3	14, 44, 95, 100	0
All	All	406/416 (97%)	0.34	45 (11%) 7 10	10, 29, 91, 100	0

The worst 5 of 45 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	B	1147	ARG	10.9
4	B	1300	ALA	5.8
4	B	1146	ILE	5.7
4	B	1180	ARG	5.4
4	B	1181	VAL	5.0

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

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
1	5IU	C	1411	20/21	0.97	0.07	-	11,17,28,42	1
1	5IU	C	1412	20/21	0.97	0.08	-	15,20,30,55	1

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.