Full wwPDB X-ray Structure Validation Report (i)

Jun 16, 2024 – 11:40 AM EDT

PDB ID	:	4YO2
Title	:	Structure of E2F8, an atypical member of E2F family of transcription factors
Authors	:	Morgunova, E.; Yin, Y.; Jolma, A.; Dave, K.; Schmierer, B.; Popov, A.; Eremina, N.; Nilsson, L.; Taipale, J.
Deposited on	:	2015-03-11
Resolution	:	3.07 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:

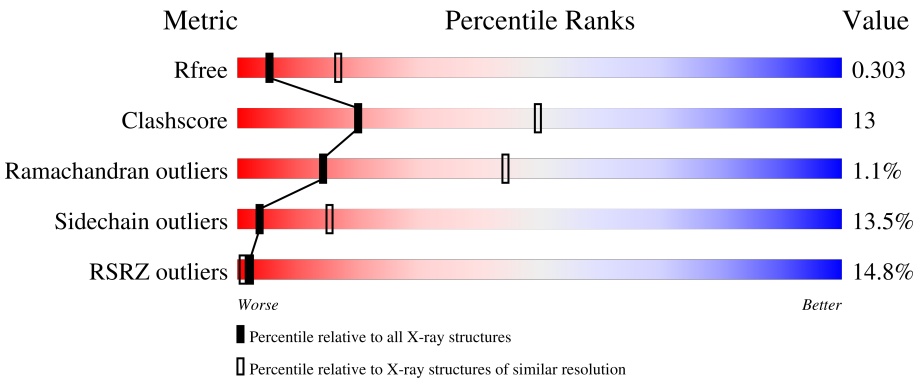
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 3.07 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	1447 (3.10-3.06)
Clashscore	141614	1546 (3.10-3.06)
Ramachandran outliers	138981	1487 (3.10-3.06)
Sidechain outliers	138945	1486 (3.10-3.06)
RSRZ outliers	127900	1416 (3.10-3.06)

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	232	14%; 59%; 18%; •; 20%
2	C	15	33%; 67%
3	D	15	20%; 80%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2130 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 Transcription factor E2F8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	186	1515	959	277	272	7	0	0	0

- Molecule 2 is a DNA chain called DNA (5'-D(P*TP*TP*TP*TP*CP*CP*CP*GP*CP*CP*AP*AP*AP*AP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	C	15	302	145	53	89	15	0	0	0

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

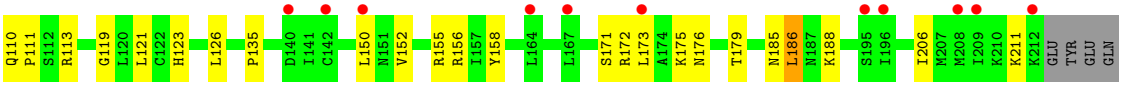
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	D	15	313	149	58	91	15	0	0	0

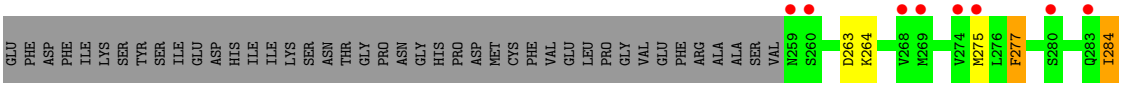
3 Residue-property plots (i)

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: Transcription factor E2F8

Chain A:



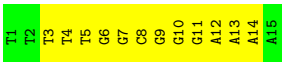


• Molecule 2: DNA (5'-D(P*TP*TP*TP*TP*CP*CP*CP*GP*CP*CP*AP*AP*AP*AP*A)-3')

Chain C:

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

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	98.83Å 98.83Å 121.69Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	14.92 – 3.07 49.59 – 3.07	Depositor EDS
% Data completeness (in resolution range)	96.4 (14.92-3.07) 96.4 (49.59-3.07)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.34 (at 3.07Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.272 , 0.297 0.308 , 0.303	Depositor DCC
R_{free} test set	639 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	86.7	Xtriage
Anisotropy	0.378	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 130.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.43$, $< L^2 > = 0.26$	Xtriage
Estimated twinning fraction	0.135 for -h,-k,l	Xtriage
Reported twinning fraction	0.220 for -h,-k,l	Depositor
Outliers	0 of 12768 reflections	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	2130	wwPDB-VP
Average B, all atoms (Å^2)	153.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.47% 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	A	0.26	0/1537	0.47	0/2061
2	C	0.45	0/337	0.88	0/516
3	D	0.49	0/351	0.91	0/541
All	All	0.34	0/2225	0.65	0/3118

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	A	1515	0	1586	24	0
2	C	302	0	170	15	0
3	D	313	0	171	20	0
All	All	2130	0	1927	49	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 13.

All (49) 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:C:13:DA:H2"	2:C:14:DA:H5"	1.56	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:14:DA:H2"	2:C:15:DA:H5'	1.71	0.72
3:D:6:DG:H2"	3:D:7:DG:C8	2.26	0.70
3:D:7:DG:H2'	3:D:8:DC:C6	2.27	0.69
1:A:172:ARG:NH2	3:D:6:DG:OP1	2.26	0.69
2:C:11:DA:H2"	2:C:12:DA:C8	2.30	0.67
3:D:10:DG:H2"	3:D:11:DG:C8	2.29	0.67
1:A:314:ARG:NH2	3:D:9:DG:N7	2.43	0.66
1:A:185:ASN:O	1:A:188:LYS:N	2.31	0.64
2:C:14:DA:H1'	2:C:15:DA:H5"	1.80	0.61
3:D:3:DT:H2'	3:D:4:DT:C6	2.36	0.60
2:C:6:DC:C6	2:C:6:DC:H5'	2.38	0.58
1:A:158:TYR:CZ	3:D:5:DT:H2'	2.40	0.57
3:D:3:DT:H2"	3:D:4:DT:H5'	1.88	0.55
3:D:3:DT:H2"	3:D:4:DT:C5'	2.37	0.55
2:C:13:DA:C2'	2:C:14:DA:H5"	2.34	0.54
1:A:119:GLY:O	1:A:123:HIS:ND1	2.35	0.54
1:A:284:ILE:N	1:A:284:ILE:HD12	2.23	0.53
1:A:263:ASP:N	1:A:264:LYS:HA	2.22	0.53
1:A:113:ARG:NH2	2:C:6:DC:O4'	2.42	0.52
3:D:4:DT:H2"	3:D:5:DT:C5'	2.40	0.52
1:A:316:TYR:OH	2:C:4:DT:OP2	2.22	0.51
1:A:158:TYR:OH	3:D:5:DT:H5'	2.12	0.50
2:C:8:DG:N2	3:D:8:DC:O2	2.43	0.50
3:D:4:DT:H2"	3:D:5:DT:H5'	1.93	0.49
2:C:14:DA:H2"	2:C:15:DA:C5'	2.42	0.49
3:D:12:DA:H2"	3:D:13:DA:C8	2.47	0.49
2:C:13:DA:H2"	2:C:14:DA:C5'	2.36	0.49
1:A:264:LYS:NZ	3:D:8:DC:OP1	2.46	0.48
2:C:9:DC:H2'	2:C:10:DC:C6	2.48	0.48
3:D:13:DA:H2"	3:D:14:DA:C8	2.48	0.48
3:D:3:DT:H2'	3:D:4:DT:H6	1.76	0.48
1:A:155:ARG:CZ	3:D:6:DG:H2'	2.44	0.48
1:A:301:GLU:HA	1:A:302:ASP:HB3	1.96	0.47
2:C:10:DC:H2"	2:C:11:DA:C8	2.50	0.47
1:A:284:ILE:HG12	1:A:336:GLU:HG2	1.98	0.46
2:C:8:DG:H1'	2:C:9:DC:C6	2.51	0.46
1:A:292:LYS:O	1:A:311:LYS:NZ	2.49	0.46
1:A:284:ILE:HB	1:A:285:VAL:HB	1.98	0.45
1:A:322:LEU:HB3	1:A:328:ILE:HD13	1.97	0.45
1:A:158:TYR:CE1	3:D:5:DT:H2'	2.51	0.45
1:A:326:ASP:N	1:A:326:ASP:OD1	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:12:DA:H2"	3:D:13:DA:N7	2.32	0.43
2:C:12:DA:H2"	2:C:13:DA:C8	2.53	0.43
1:A:277:PHE:CZ	1:A:328:ILE:HD11	2.54	0.42
1:A:110:GLN:N	1:A:111:PRO:HD2	2.35	0.42
1:A:185:ASN:O	1:A:186:LEU:C	2.59	0.41
1:A:332:HIS:HB3	1:A:333:VAL:H	1.70	0.41
1:A:302:ASP:N	1:A:303:LEU:HB3	2.36	0.41

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	A	182/232 (78%)	154 (85%)	26 (14%)	2 (1%)	14 44

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	186	LEU
1	A	135	PRO

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	171/213 (80%)	148 (86%)	23 (14%)	4 15

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	121	LEU
1	A	126	LEU
1	A	150	LEU
1	A	152	VAL
1	A	156	ARG
1	A	171	SER
1	A	173	LEU
1	A	175	LYS
1	A	176	ASN
1	A	179	THR
1	A	206	ILE
1	A	211	LYS
1	A	275	MET
1	A	277	PHE
1	A	284	ILE
1	A	287	LEU
1	A	292	LYS
1	A	299	HIS
1	A	308	PHE
1	A	309	LYS
1	A	312	ILE
1	A	328	ILE
1	A	332	HIS

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	A	186/232 (80%)	0.83	32 (17%)	1	0	72, 148, 333, 537	0
2	C	15/15 (100%)	-0.12	0	100	100	88, 106, 129, 130	0
3	D	15/15 (100%)	-0.08	0	100	100	88, 105, 125, 156	0
All	All	216/262 (82%)	0.70	32 (14%)	2	1	72, 138, 323, 537	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	283	GLN	12.1
1	A	259	ASN	6.3
1	A	287	LEU	5.0
1	A	330	LYS	5.0
1	A	208	MET	4.6
1	A	299	HIS	4.6
1	A	301	GLU	4.5
1	A	209	ILE	4.2
1	A	195	SER	4.0
1	A	142	CYS	4.0
1	A	329	LYS	3.9
1	A	298	ASP	3.6
1	A	300	VAL	3.6
1	A	327	LEU	3.5
1	A	150	LEU	3.5
1	A	260	SER	3.4
1	A	196	ILE	3.2
1	A	280	SER	3.1
1	A	275	MET	3.0
1	A	268	VAL	3.0
1	A	341	PRO	2.9
1	A	288	GLU	2.9
1	A	212	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	173	LEU	2.8
1	A	340	LYS	2.7
1	A	167	LEU	2.5
1	A	164	LEU	2.5
1	A	334	THR	2.4
1	A	269	MET	2.3
1	A	274	VAL	2.3
1	A	140	ASP	2.2
1	A	323	SER	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.