



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2018 – 09:38 pm GMT

PDB ID : 1A02
Title : STRUCTURE OF THE DNA BINDING DOMAINS OF NFAT, FOS AND JUN BOUND TO DNA
Authors : Chen, L.; Glover, J.N.M.; Hogan, P.G.; Rao, A.; Harrison, S.C.
Deposited on : 1997-12-08
Resolution : 2.70 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 ⓘ symbol.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	trunk30967
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk30967

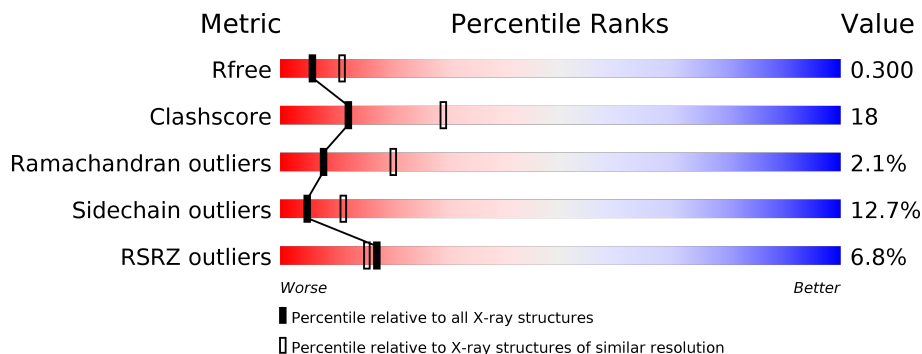
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	111664	2449 (2.70-2.70)
Clashscore	122126	2756 (2.70-2.70)
Ramachandran outliers	120053	2716 (2.70-2.70)
Sidechain outliers	120020	2716 (2.70-2.70)
RSRZ outliers	108989	2376 (2.70-2.70)

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	A	20	<div> <div>40%</div> <div>60%</div> </div>
2	B	20	<div> <div>50%</div> <div>50%</div> </div>
3	N	301	<div> <div>8%</div> <div>47%</div> <div>40%</div> <div>6%</div> <div>7%</div> </div>
4	F	56	<div> <div>2%</div> <div>73%</div> <div>20%</div> <div>5%</div> </div>
5	J	56	<div> <div>7%</div> <div>68%</div> <div>23%</div> <div>7%</div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3974 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(*DTP*DTP*DGP*DGP*DAP*DAP*DAP*DAP*DTP*DTP*DTP*DGP*DTP*DTP*DTP*DCP*DAP*DTP*DAP*DG)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	20	Total	C	N	O	P	0	0	0
			410	199	71	121	19			

- Molecule 2 is a DNA chain called DNA (5'-D(*DAP*DAP*DCP*DTP*DAP*DTP*DGP*DAP*DAP*DAP*DCP*DAP*DAP*DAP*DTP*DTP*DTP*DTP*DCP*DC)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	20	Total	C	N	O	P	0	0	0
			404	196	74	115	19			

- Molecule 3 is a protein called NUCLEAR FACTOR OF ACTIVATED T CELLS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	N	280	Total	C	N	O	S	0	0	0
			2204	1383	404	408	9			

- Molecule 4 is a protein called AP-1 FRAGMENT FOS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	53	Total	C	N	O	S	0	0	0
			442	262	92	87	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	138	MET	GLU	ENGINEERED	UNP P01100
F	154	SER	CYS	ENGINEERED	UNP P01100

- Molecule 5 is a protein called AP-1 FRAGMENT JUN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	J	52	Total 426	C 257	N 92	O 75	S 2	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	263	MET	ILE	ENGINEERED	UNP P05412
J	279	SER	CYS	ENGINEERED	UNP P05412

- Molecule 6 is water.

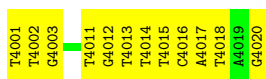
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	20	Total 20	O 20	0	0
6	B	18	Total 18	O 18	0	0
6	N	46	Total 46	O 46	0	0
6	F	3	Total 3	O 3	0	0
6	J	1	Total 1	O 1	0	0

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 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: DNA (5'-D(*DTP*DTP*DGP*DGP*DAP*DAP*DAP*DTP*DTP*DTP*DGP*DTP*DTP*DTP*DCP*DAP*DTP*DAP*DG)-3')

Chain A: 



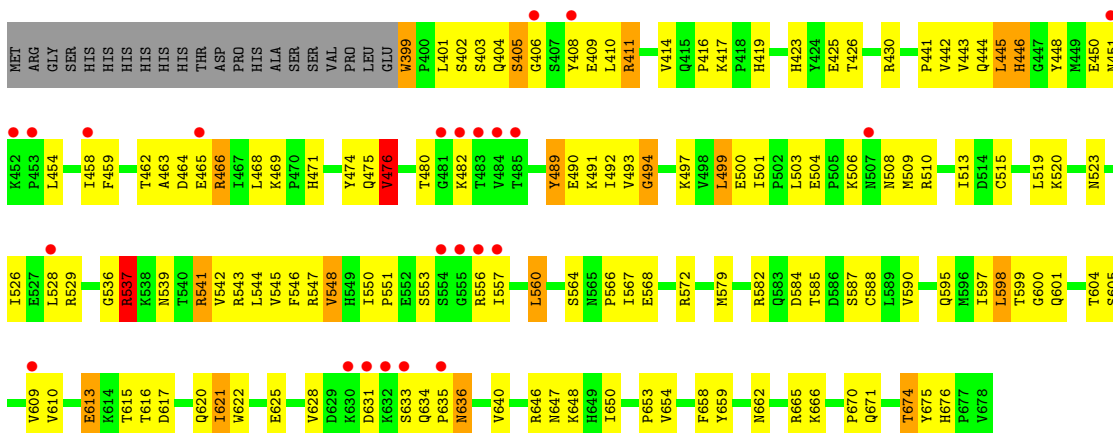
- Molecule 2: DNA (5'-D(*DAP*DAP*DCP*DTP*DAP*DTP*DGP*DAP*DAP*DAP*DCP*DAP*DAP*DAP*DTP*DTP*DTP*DTP*DCP*DC)-3')

Chain B: 



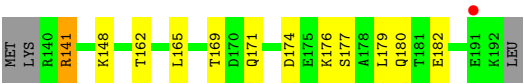
- Molecule 3: NUCLEAR FACTOR OF ACTIVATED T CELLS

Chain N: 

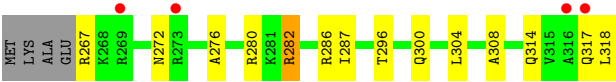


- Molecule 4: AP-1 FRAGMENT FOS

Chain F: 



● Molecule 5: AP-1 FRAGMENT JUN



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	64.66Å 85.46Å 83.37Å 90.00° 112.03° 90.00°	Depositor
Resolution (Å)	10.00 – 2.70 19.49 – 2.69	Depositor EDS
% Data completeness (in resolution range)	90.1 (10.00-2.70) 94.4 (19.49-2.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.12 (at 2.71Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.246 , 0.303 0.254 , 0.300	Depositor DCC
R_{free} test set	1671 reflections (7.57%)	wwPDB-VP
Wilson B-factor (Å ²)	49.2	Xtriage
Anisotropy	0.732	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 63.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.037 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	3974	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.21% 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, 0.333 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	0.86	0/459	1.09	1/708 (0.1%)
2	B	0.80	0/453	1.09	1/696 (0.1%)
3	N	0.52	0/2253	0.82	4/3050 (0.1%)
4	F	0.44	0/441	0.63	0/583
5	J	0.47	0/425	0.69	1/558 (0.2%)
All	All	0.59	0/4031	0.87	7/5595 (0.1%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	J	282	ARG	NE-CZ-NH2	7.23	123.92	120.30
3	N	411	ARG	NE-CZ-NH2	7.11	123.86	120.30
3	N	466	ARG	NE-CZ-NH2	6.53	123.56	120.30
2	B	5011	DC	N1-C1'-C2'	6.00	124.01	112.60
3	N	476	VAL	CB-CA-C	-5.50	100.94	111.40

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	410	0	231	12	0
2	B	404	0	228	14	0
3	N	2204	0	2168	107	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	F	442	0	461	10	0
5	J	426	0	472	8	0
6	A	20	0	0	1	0
6	B	18	0	0	0	0
6	F	3	0	0	0	0
6	J	1	0	0	0	0
6	N	46	0	0	2	0
All	All	3974	0	3560	136	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 18.

The worst 5 of 136 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)
3:N:423:HIS:HB3	3:N:430:ARG:HG3	1.32	1.03
2:B:5003:DC:H2''	2:B:5004:DT:H71	1.42	1.02
1:A:4017:DA:H1'	1:A:4018:DT:H5'	1.40	1.01
3:N:613:GLU:HB2	3:N:622:TRP:HB3	1.42	0.99
3:N:474:TYR:CE1	3:N:520:LYS:HD3	2.09	0.88

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	N	278/301 (92%)	242 (87%)	28 (10%)	8 (3%)	5	12
4	F	51/56 (91%)	51 (100%)	0	0	100	100
5	J	50/56 (89%)	50 (100%)	0	0	100	100
All	All	379/413 (92%)	343 (90%)	28 (7%)	8 (2%)	8	20

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	N	590	VAL
3	N	633	SER
3	N	480	THR
3	N	631	ASP
3	N	405	SER

5.3.2 Protein sidechains ⓘ

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	N	238/269 (88%)	206 (87%)	32 (13%)	4	10
4	F	47/50 (94%)	43 (92%)	4 (8%)	12	27
5	J	45/48 (94%)	39 (87%)	6 (13%)	4	10
All	All	330/367 (90%)	288 (87%)	42 (13%)	5	11

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	N	560	LEU
3	N	616	THR
5	J	282	ARG
3	N	585	THR
3	N	598	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
3	N	523	ASN
3	N	620	GLN
4	F	171	GLN
3	N	477	HIS
3	N	636	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 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 [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	20/20 (100%)	-0.45	0 100 100	28, 36, 61, 64	0
2	B	20/20 (100%)	-0.42	0 100 100	22, 37, 51, 52	0
3	N	280/301 (93%)	0.57	24 (8%) 10 8	23, 53, 90, 99	0
4	F	53/56 (94%)	0.20	1 (1%) 66 68	28, 49, 73, 90	0
5	J	52/56 (92%)	0.30	4 (7%) 13 11	35, 50, 95, 99	0
All	All	425/453 (93%)	0.40	29 (6%) 17 15	22, 50, 89, 99	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	N	483	THR	12.4
3	N	484	VAL	10.2
3	N	481	GLY	9.0
3	N	631	ASP	8.1
3	N	485	THR	6.7

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 carbohydrates 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.