wwPDB X-ray Structure Validation Summary Report (i)

Aug 20, 2023 – 06:58 PM EDT

PDB ID	:	2O93
Title	:	Crystal structure of NFAT bound to the HIV-1 LTR tandem kappaB enhancer element
Authors	:	Bates, D.L.; Chen, L.
Deposited on	:	2006-12-13
Resolution	:	3.05 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 (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:

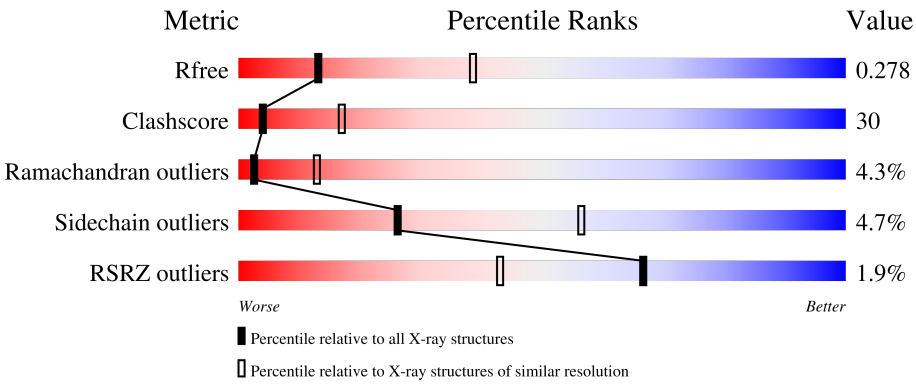
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 3.05 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	1754 (3.10-3.02)
Clashscore	141614	1864 (3.10-3.02)
Ramachandran outliers	138981	1794 (3.10-3.02)
Sidechain outliers	138945	1793 (3.10-3.02)
RSRZ outliers	127900	1713 (3.10-3.02)

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	25	28% 68% •
2	B	25	16% 76% 8%
3	L	301	2% 49% 42% 5% 5%
3	M	301	52% 38% • 6%
3	O	301	4% 41% 49% 6% 5%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 7866 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 kappaB enhancer element, DNA 25-mer.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	A	25	509	243	90	152	24	0	0	0

- Molecule 2 is a DNA chain called kappaB enhancer element, DNA 25-mer.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	B	25	510	242	100	144	24	0	0	0

- Molecule 3 is a protein called actor of activated T-cells, cytoplasmic 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	L	287	2288	1434	417	428	9	0	0	0
3	M	284	2271	1425	414	423	9	0	0	0
3	O	287	2288	1434	417	428	9	0	0	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	378	MET	-	initiating methionine	UNP Q13469
L	379	ARG	-	expression tag	UNP Q13469
L	380	GLY	-	expression tag	UNP Q13469
L	381	SER	-	expression tag	UNP Q13469
L	382	HIS	-	expression tag	UNP Q13469
L	383	HIS	-	expression tag	UNP Q13469
L	384	HIS	-	expression tag	UNP Q13469
L	385	HIS	-	expression tag	UNP Q13469
L	386	HIS	-	expression tag	UNP Q13469
L	387	HIS	-	expression tag	UNP Q13469

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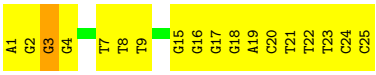
Chain	Residue	Modelled	Actual	Comment	Reference
L	388	THR	-	expression tag	UNP Q13469
L	389	ALA	-	expression tag	UNP Q13469
L	390	PRO	-	expression tag	UNP Q13469
L	391	HIS	-	expression tag	UNP Q13469
L	394	SER	LEU	cloning artifact	UNP Q13469
L	395	VAL	PRO	cloning artifact	UNP Q13469
M	378	MET	-	initiating methionine	UNP Q13469
M	379	ARG	-	expression tag	UNP Q13469
M	380	GLY	-	expression tag	UNP Q13469
M	381	SER	-	expression tag	UNP Q13469
M	382	HIS	-	expression tag	UNP Q13469
M	383	HIS	-	expression tag	UNP Q13469
M	384	HIS	-	expression tag	UNP Q13469
M	385	HIS	-	expression tag	UNP Q13469
M	386	HIS	-	expression tag	UNP Q13469
M	387	HIS	-	expression tag	UNP Q13469
M	388	THR	-	expression tag	UNP Q13469
M	389	ALA	-	expression tag	UNP Q13469
M	390	PRO	-	expression tag	UNP Q13469
M	391	HIS	-	expression tag	UNP Q13469
M	394	SER	LEU	cloning artifact	UNP Q13469
M	395	VAL	PRO	cloning artifact	UNP Q13469
O	378	MET	-	initiating methionine	UNP Q13469
O	379	ARG	-	expression tag	UNP Q13469
O	380	GLY	-	expression tag	UNP Q13469
O	381	SER	-	expression tag	UNP Q13469
O	382	HIS	-	expression tag	UNP Q13469
O	383	HIS	-	expression tag	UNP Q13469
O	384	HIS	-	expression tag	UNP Q13469
O	385	HIS	-	expression tag	UNP Q13469
O	386	HIS	-	expression tag	UNP Q13469
O	387	HIS	-	expression tag	UNP Q13469
O	388	THR	-	expression tag	UNP Q13469
O	389	ALA	-	expression tag	UNP Q13469
O	390	PRO	-	expression tag	UNP Q13469
O	391	HIS	-	expression tag	UNP Q13469
O	394	SER	LEU	cloning artifact	UNP Q13469
O	395	VAL	PRO	cloning artifact	UNP Q13469

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.

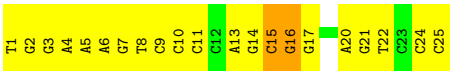
• Molecule 1: kappaB enhancer element, DNA 25-mer

Chain A:



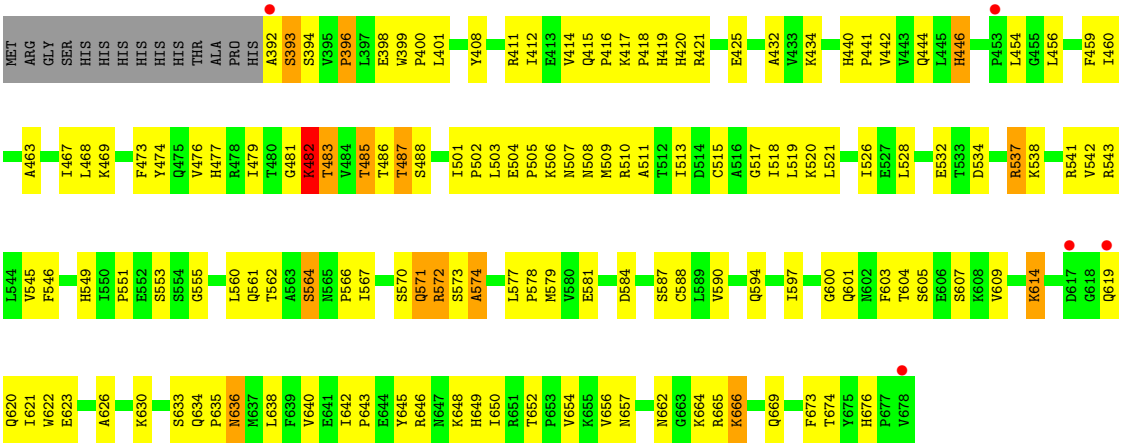
• Molecule 2: kappaB enhancer element, DNA 25-mer

Chain B:



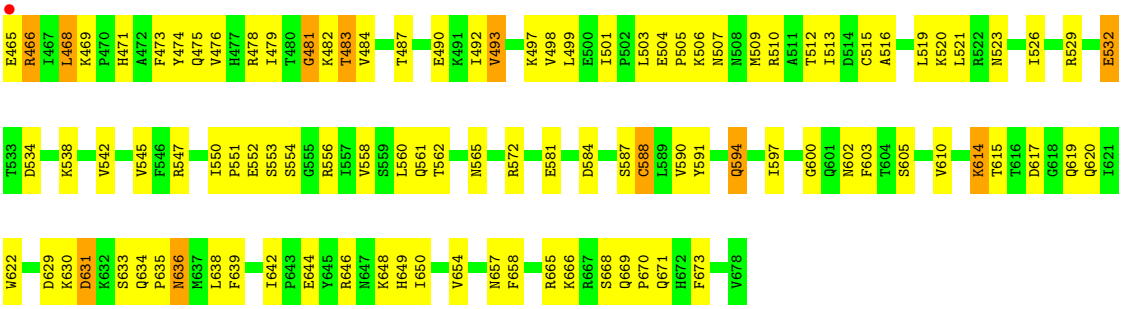
• Molecule 3: actor of activated T-cells, cytoplasmic 2

Chain L:



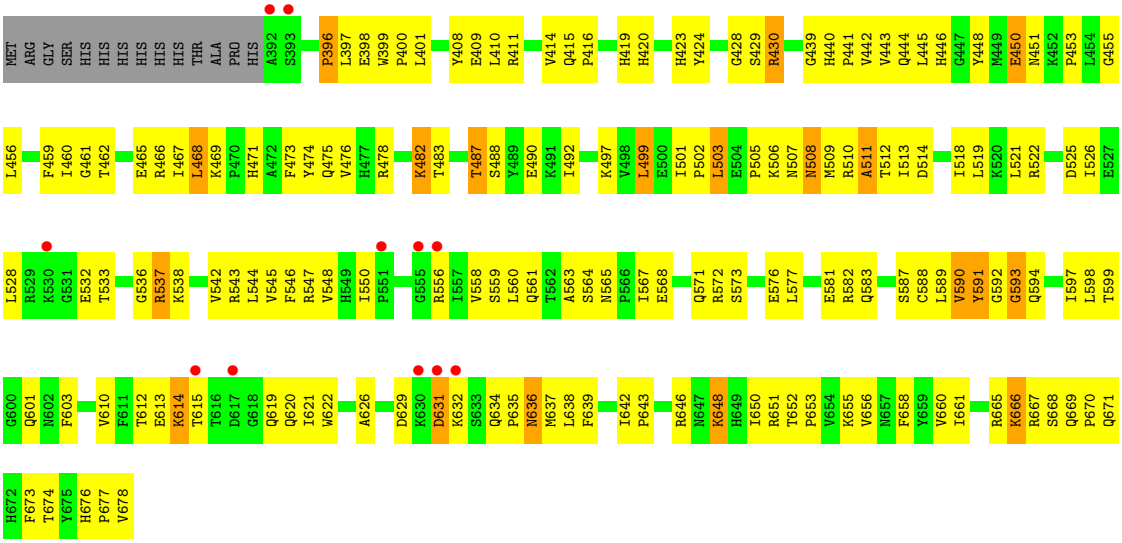
• Molecule 3: actor of activated T-cells, cytoplasmic 2

Chain M:



• Molecule 3: actor of activated T-cells, cytoplasmic 2

Chain O: 4% 41% 49% 6% 5%



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	93.69Å 95.30Å 159.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.05 29.68 – 3.03	Depositor EDS
% Data completeness (in resolution range)	91.8 (30.00-3.05) 90.8 (29.68-3.03)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.41 (at 3.00Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.225 , 0.283 0.224 , 0.278	Depositor DCC
R_{free} test set	2751 reflections (9.98%)	wwPDB-VP
Wilson B-factor (Å^2)	60.1	Xtriage
Anisotropy	0.684	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 60.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.023 for k,h,-l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	7866	wwPDB-VP
Average B, all atoms (Å^2)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.26% 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	0.59	0/569	0.89	0/877
2	B	0.63	0/573	0.87	0/882
3	L	0.37	0/2338	0.62	0/3163
3	M	0.41	0/2321	0.66	0/3140
3	O	0.34	0/2338	0.62	0/3163
All	All	0.42	0/8139	0.68	0/11225

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	A	0	1
2	B	0	2
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	3	DG	Sidechain
2	B	15	DC	Sidechain
2	B	16	DG	Sidechain

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	509	0	284	33	0
2	B	510	0	280	33	0
3	L	2288	0	2293	136	0
3	M	2271	0	2278	112	0
3	O	2288	0	2293	177	0
All	All	7866	0	7428	464	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 30.

The worst 5 of 464 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:O:582:ARG:HB3	3:O:599:THR:HB	1.32	1.10
2:B:14:DG:H2"	2:B:15:DC:H5"	1.09	1.06
1:A:2:DG:H4'	3:L:664:LYS:NZ	1.74	1.01
2:B:14:DG:C2'	2:B:15:DC:H5"	1.89	1.01
3:O:482:LYS:H	3:O:482:LYS:HD3	1.22	1.00

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	L	285/301 (95%)	245 (86%)	28 (10%)	12 (4%)	3 13
3	M	282/301 (94%)	245 (87%)	24 (8%)	13 (5%)	2 12
3	O	285/301 (95%)	232 (81%)	41 (14%)	12 (4%)	3 13
All	All	852/903 (94%)	722 (85%)	93 (11%)	37 (4%)	2 13

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	L	393	SER
3	L	482	LYS
3	L	537	ARG
3	M	450	GLU
3	M	594	GLN

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	L	256/268 (96%)	245 (96%)	11 (4%)	29	59
3	M	254/268 (95%)	245 (96%)	9 (4%)	36	66
3	O	256/268 (96%)	240 (94%)	16 (6%)	18	45
All	All	766/804 (95%)	730 (95%)	36 (5%)	26	56

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	O	508	ASN
3	O	648	LYS
3	O	512	THR
3	O	614	LYS
3	M	429	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
3	O	415	GLN
3	O	595	GLN
3	O	420	HIS
3	O	457	GLN
3	O	634	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)

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	25/25 (100%)	-0.53	0	100	100	32, 48, 62, 71	0
2	B	25/25 (100%)	-0.63	0	100	100	32, 44, 69, 74	0
3	L	287/301 (95%)	-0.08	5 (1%)	70	46	38, 81, 127, 144	0
3	M	284/301 (94%)	-0.33	1 (0%)	92	82	28, 63, 102, 134	0
3	O	287/301 (95%)	0.07	11 (3%)	40	20	36, 91, 148, 196	0
All	All	908/953 (95%)	-0.14	17 (1%)	66	43	28, 74, 134, 196	0

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	O	631	ASP	5.8
3	O	632	LYS	4.8
3	O	392	ALA	4.4
3	O	530	LYS	3.9
3	L	453	PRO	3.7

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 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.