



# wwPDB X-ray Structure Validation Summary Report

Feb 26, 2014 – 04:12 PM GMT

PDB ID : 3BEJ  
Title : Structure of human FXR in complex with MFA-1 and co-activator peptide  
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Deposited on : 2007-11-19  
Resolution : 1.90 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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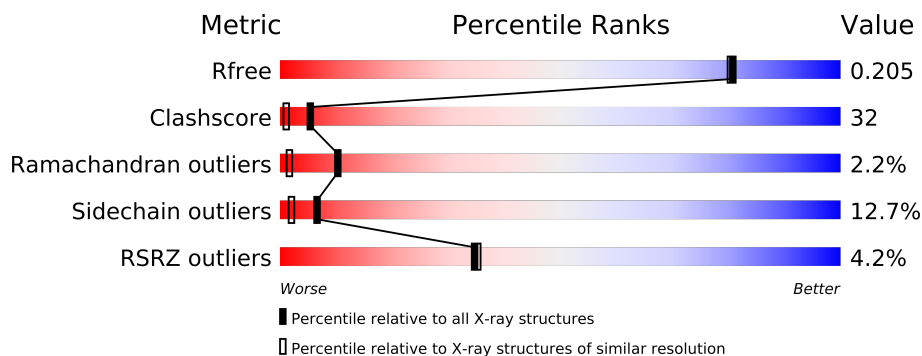
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 1.90 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))
$R_{free}$	66092	3684 (1.90-1.90)
Clashscore	79885	4465 (1.90-1.90)
Ramachandran outliers	78287	4413 (1.90-1.90)
Sidechain outliers	78261	4414 (1.90-1.90)
RSRZ outliers	66119	3686 (1.90-1.90)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	238	
1	B	238	
2	E	25	
2	F	25	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4349 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Bile acid receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	224	Total	C	N	O	S	0	0	0
			1842	1178	310	343	11			
1	B	228	Total	C	N	O	S	0	0	0
			1872	1197	314	350	11			

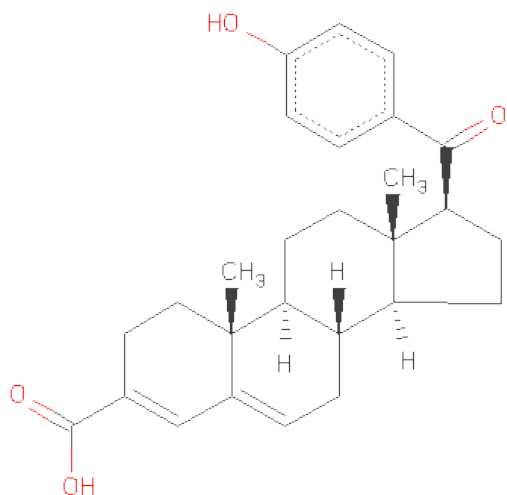
- Molecule 2 is a protein called Nuclear receptor coactivator 1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	11	Total	C	N	O	0	0	0
			101	64	23	14			
2	F	12	Total	C	N	O	0	0	0
			108	68	24	16			

- Molecule 3 is YTTRIUM (III) ION (three-letter code: YT3) (formula: Y).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Y	0	0
			1	1		
3	A	1	Total	Y	0	0
			1	1		

- Molecule 4 is (8ALPHA,10ALPHA,13ALPHA,17BETA)-17-[(4-HYDROXYPHENYL)CARBONYL]ANDROSTA-3,5-DIENE-3-CARBOXYLICACID (three-letter code: MUF) (formula: C<sub>27</sub>H<sub>32</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			31	27	4		
4	B	1	Total	C	O	0	0
			31	27	4		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	141	Total	O	0	0
			141	141		
5	B	213	Total	O	0	0
			213	213		
5	E	4	Total	O	0	0
			4	4		
5	F	4	Total	O	0	0
			4	4		



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	41.64Å 90.89Å 129.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.65 – 1.90 39.65 – 1.89	Depositor EDS
% Data completeness (in resolution range)	99.3 (39.65-1.90) 99.5 (39.65-1.89)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.35 (at 1.89Å)	Xtriage
Refinement program	BUSTER-TNT 2.1.1	Depositor
R, $R_{free}$	0.200 , 0.254 0.207 , 0.205	Depositor DCC
$R_{free}$ test set	3998 reflections (11.17%)	DCC
Wilson B-factor (Å <sup>2</sup> )	25.2	Xtriage
Anisotropy	0.482	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 54.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 39796 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4349	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.48% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MUF, YT3

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	0.55	0/1880	0.73	1/2537 (0.0%)
1	B	0.67	0/1912	0.78	1/2583 (0.0%)
2	E	0.37	0/102	0.89	0/134
2	F	0.47	0/109	1.01	0/144
All	All	0.61	0/4003	0.76	2/5398 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	320	LEU	CA-CB-CG	5.54	128.05	115.30
1	B	422	HIS	N-CA-C	5.25	125.19	111.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1842	0	1838	132	0
1	B	1872	0	1868	96	0
2	E	101	0	110	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	108	0	117	19	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	31	0	30	1	0
4	B	31	0	31	0	0
5	A	141	0	0	17	0
5	B	213	0	0	9	0
5	E	4	0	0	1	0
5	F	4	0	0	2	0
All	All	4349	0	3994	259	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 32.

The worst 5 of 259 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:385:LEU:HD12	1:A:437:LEU:HD21	1.22	1.14
2:E:685:GLU:HB3	2:E:687:HIS:HD1	1.05	1.12
1:A:266:PRO:HB2	1:A:269:ILE:HD13	1.25	1.10
1:B:385:LEU:HD11	1:B:437:LEU:HD21	1.32	1.06
1:B:423:GLN:HB2	1:B:424:PRO:HD3	1.39	1.05

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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	220/238 (92%)	207 (94%)	9 (4%)	4 (2%)	13	3
1	B	226/238 (95%)	216 (96%)	7 (3%)	3 (1%)	18	5
2	E	9/25 (36%)	5 (56%)	1 (11%)	3 (33%)	0	0
2	F	10/25 (40%)	7 (70%)	3 (30%)	0	100	100
All	All	465/526 (88%)	435 (94%)	20 (4%)	10 (2%)	10	2



5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	313	HIS
1	B	423	GLN
1	B	425	GLU
2	E	692	ARG
2	E	686	ARG

### 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	
1	A	207/221 (94%)	182 (88%)	25 (12%)	7	2
1	B	211/221 (96%)	190 (90%)	21 (10%)	11	4
2	E	11/24 (46%)	7 (64%)	4 (36%)	0	0
2	F	12/24 (50%)	6 (50%)	6 (50%)	0	0
All	All	441/490 (90%)	385 (87%)	56 (13%)	6	2

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	262	LYS
1	B	339	LYS
2	F	686	ARG
1	B	264	ARG
1	B	285	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	459	HIS
1	B	250	GLN
1	B	379	GLN
1	A	457	ASN
1	B	344	HIS

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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	$\# Z  > 2$
4	MUF	A	473	-	35,35,35	1.76	12 (34%)	55,55,55	1.97	14 (25%)
4	MUF	B	1	-	35,35,35	1.67	8 (22%)	55,55,55	2.02	15 (27%)

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
4	MUF	A	473	-	-	0/12/70/70	0/1/5/5
4	MUF	B	1	-	-	0/12/70/70	0/1/5/5

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1	MUF	O76-C28	4.21	1.35	1.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	473	MUF	O76-C28	3.99	1.34	1.22
4	B	1	MUF	C1-C10	2.87	1.59	1.54
4	A	473	MUF	C1-C10	2.77	1.59	1.54
4	A	473	MUF	C19-C10	2.60	1.59	1.54

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	473	MUF	C13-C17-C20	-6.78	106.86	115.17
4	B	1	MUF	C13-C17-C20	-6.25	107.51	115.17
4	B	1	MUF	O76-C28-C3	-5.70	111.34	121.28
4	A	473	MUF	O76-C28-C3	-5.61	111.50	121.28
4	A	473	MUF	C16-C17-C13	-4.08	99.92	104.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	224/238 (94%)	0.31	13 (5%) 22 22	16, 35, 61, 75	0
1	B	228/238 (95%)	0.03	4 (1%) 65 67	16, 25, 50, 78	0
2	E	11/25 (44%)	1.22	2 (18%) 2 2	46, 52, 67, 69	0
2	F	12/25 (48%)	0.59	1 (8%) 11 11	30, 39, 62, 70	0
All	All	475/526 (90%)	0.21	20 (4%) 35 35	16, 31, 61, 78	0

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	343	GLY	9.4
1	B	424	PRO	7.2
1	B	423	GLN	6.5
1	A	344	HIS	4.7
1	A	400	ASP	4.3

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates

There are no carbohydrates in this entry.

### 6.4 Ligands

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, 95<sup>th</sup> 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	YT3	B	2	1/1	0.09	0.25	18,18,18,18	0
4	MUF	B	1	31/31	0.09	-0.37	12,20,26,32	0
4	MUF	A	473	31/31	0.10	-0.46	20,28,37,38	0
3	YT3	A	1	1/1	0.08	-2.54	19,19,19,19	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.