



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 27, 2016 – 10:46 PM EDT

PDB ID : 5DTV  
Title : Crystal Structure of the ER-alpha Ligand-binding Domain in complex with a dimethyl-substituted, 3,4-diarylthiophene dioxide core ligand  
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Deposited on : 2015-09-18  
Resolution : 2.29 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](mailto: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.

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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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20027457  
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) : rb-20027457



## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3830 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 Estrogen receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	230	Total	C	N	O	S	0	0	0
			1801	1152	308	322	19			
1	B	238	Total	C	N	O	S	0	0	0
			1815	1159	311	326	19			

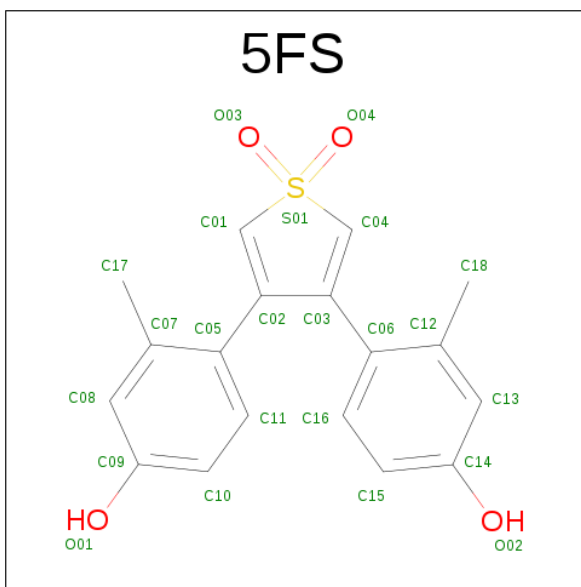
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	537	SER	TYR	engineered mutation	UNP P03372
B	537	SER	TYR	engineered mutation	UNP P03372

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	9	Total	C	N	O	0	0	0
			62	42	11	9			
2	D	9	Total	C	N	O	0	0	0
			73	48	13	12			

- Molecule 3 is 3,4-bis(4-hydroxy-2-methylphenyl)-1H-1lambda 6 -thiophene-1,1-dione (three-letter code: 5FS) (formula: C<sub>18</sub>H<sub>16</sub>O<sub>4</sub>S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	S	0	0
			23	18	4	1		
3	B	1	Total	C	O	S	0	0
			23	18	4	1		

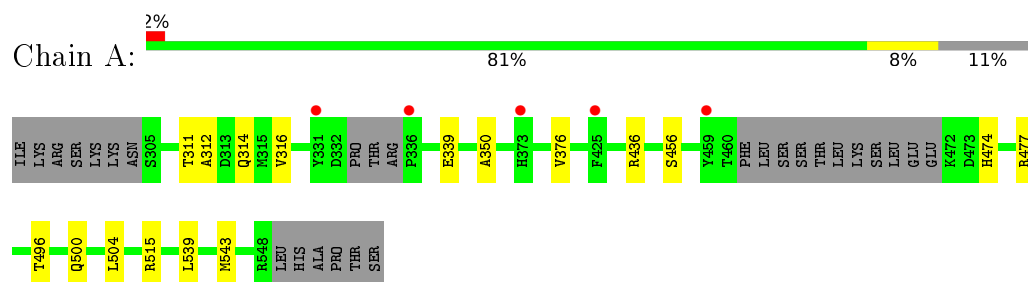
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	15	Total	O	0	0
			15	15		
4	C	1	Total	O	0	0
			1	1		
4	B	16	Total	O	0	0
			16	16		
4	D	1	Total	O	0	0
			1	1		

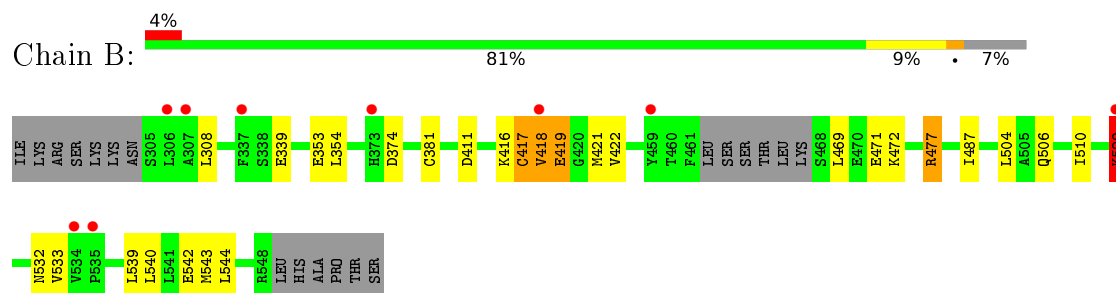
### 3 Residue-property plots [i](#)

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 ( $\text{RSRZ} > 2$ ). 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: Estrogen receptor



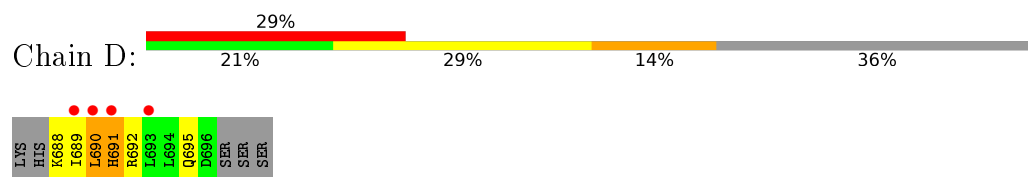
- Molecule 1: Estrogen receptor



- Molecule 2: Nuclear receptor coactivator 2



- Molecule 2: Nuclear receptor coactivator 2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.05Å 82.83Å 58.90Å 90.00° 110.53° 90.00°	Depositor
Resolution (Å)	46.71 – 2.29 46.71 – 2.29	Depositor EDS
% Data completeness (in resolution range)	92.8 (46.71-2.29) 92.8 (46.71-2.29)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.79 (at 2.29Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1690)	Depositor
R, $R_{free}$	0.207 , 0.247 0.207 , 0.246	Depositor DCC
$R_{free}$ test set	1886 reflections (9.16%)	DCC
Wilson B-factor (Å <sup>2</sup> )	46.8	Xtriage
Anisotropy	0.595	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 47.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3830	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.10% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.20	0/1833	0.35	0/2479
1	B	0.22	0/1846	0.41	0/2501
2	C	0.22	0/62	0.45	0/84
2	D	0.31	0/73	0.63	0/97
All	All	0.21	0/3814	0.39	0/5161

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	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	529	LYS	Peptide

### 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	1801	0	1815	13	0
1	B	1815	0	1798	19	0
2	C	62	0	58	1	0
2	D	73	0	77	10	0
3	A	23	0	0	2	0
3	B	23	0	0	1	0
4	A	15	0	0	2	0
4	B	16	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	1	0
All	All	3830	0	3748	41	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 5.

The worst 5 of 41 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:D:688:LYS:HE2	2:D:691:HIS:HB2	1.33	1.10
1:B:417:CYS:O	1:B:419:GLU:N	2.25	0.69
1:B:417:CYS:SG	1:B:418:VAL:N	2.61	0.68
4:A:715:HOH:O	1:B:381:CYS:SG	2.56	0.63
1:B:308:LEU:HD11	1:B:477:ARG:HD3	1.81	0.62

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	224/257 (87%)	219 (98%)	5 (2%)	0	100	100
1	B	234/257 (91%)	218 (93%)	10 (4%)	6 (3%)	7	4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	7/14 (50%)	7 (100%)	0	0	100	100
2	D	7/14 (50%)	4 (57%)	1 (14%)	2 (29%)	0	0
All	All	472/542 (87%)	448 (95%)	16 (3%)	8 (2%)	11	10

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	418	VAL
1	B	533	VAL
2	D	691	HIS
1	B	374	ASP
1	B	417	CYS

### 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	198/232 (85%)	197 (100%)	1 (0%)	92	97
1	B	192/232 (83%)	190 (99%)	2 (1%)	82	91
2	C	5/14 (36%)	5 (100%)	0	100	100
2	D	8/14 (57%)	8 (100%)	0	100	100
All	All	403/492 (82%)	400 (99%)	3 (1%)	88	95

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	339	GLU
1	B	477	ARG
1	B	529	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules 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 ⓘ

2 ligands 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	$\# Z  > 2$
3	5FS	A	601	-	21,25,25	4.95	17 (80%)	25,38,38	2.15	11 (44%)
3	5FS	B	601	-	21,25,25	4.72	16 (76%)	25,38,38	2.26	9 (36%)

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
3	5FS	A	601	-	-	0/8/22/22	0/3/3/3
3	5FS	B	601	-	-	0/8/22/22	0/3/3/3

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	5FS	C06-C03	-12.79	1.33	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	601	5FS	C06-C03	-12.30	1.33	1.49
3	A	601	5FS	C05-C02	-12.16	1.34	1.49
3	B	601	5FS	C05-C02	-11.23	1.35	1.49
3	B	601	5FS	C08-C09	-4.95	1.31	1.39

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	601	5FS	C11-C05-C07	-3.60	114.94	119.99
3	B	601	5FS	C17-C07-C08	-3.57	112.88	119.49
3	B	601	5FS	C10-C09-C08	-3.46	116.20	120.21
3	A	601	5FS	C17-C07-C08	-3.25	113.46	119.49
3	B	601	5FS	C15-C14-C13	-2.93	116.82	120.21

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
3	A	601	5FS	2	0
3	B	601	5FS	1	0

## 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, 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	230/257 (89%)	0.02	5 (2%) 65 73	41, 70, 103, 122	0
1	B	238/257 (92%)	0.21	9 (3%) 44 53	40, 71, 122, 147	0
2	C	9/14 (64%)	0.27	0 100 100	74, 84, 105, 112	0
2	D	9/14 (64%)	1.41	4 (44%) 0 0	108, 117, 136, 136	0
All	All	486/542 (89%)	0.14	18 (3%) 45 54	40, 72, 118, 147	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	373	HIS	5.7
1	B	307	ALA	4.7
1	B	529	LYS	4.6
1	B	535	PRO	4.5
1	B	418	VAL	3.0

### 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 carbohydrates in this entry.

### 6.4 Ligands [i](#)

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	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	5FS	B	601	23/23	0.96	0.15	-0.20	47,57,69,71	0
3	5FS	A	601	23/23	0.95	0.10	-1.74	58,60,62,66	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.