



# Full wwPDB X-ray Structure Validation Report

Mar 1, 2014 – 02:44 AM GMT

PDB ID : 1KDK  
Title : THE STRUCTURE OF THE N-TERMINAL LG DOMAIN OF SHBG IN CRYSTALS SOAKED WITH EDTA  
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Deposited on : 2001-11-13  
Resolution : 1.70 Å(reported)

This is a full wwPDB validation 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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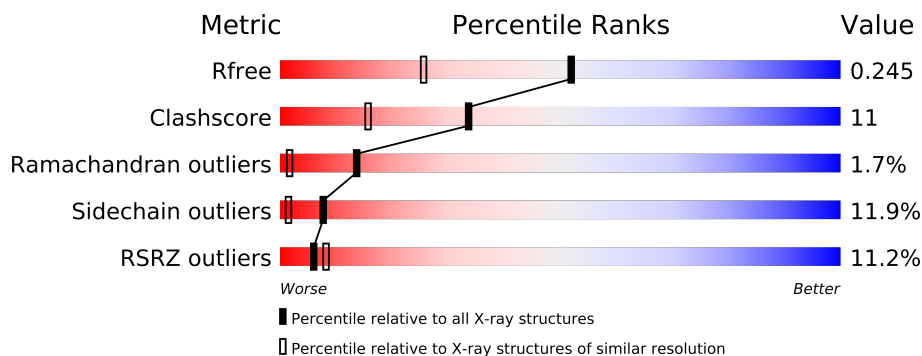
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.70 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))
$R_{free}$	66092	2456 (1.70-1.70)
Clashscore	79885	2929 (1.70-1.70)
Ramachandran outliers	78287	2878 (1.70-1.70)
Sidechain outliers	78261	2878 (1.70-1.70)
RSRZ outliers	66119	2456 (1.70-1.70)

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  $\geq 3$ , 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	177	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1499 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.

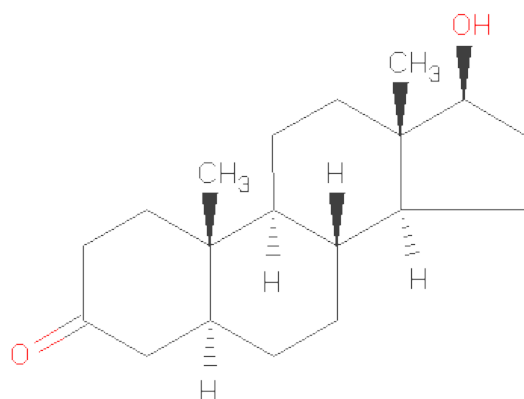
- Molecule 1 is a protein called Sex Hormone-Binding Globulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	177	1389	875	250	258	6	0	2	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	ASP	-	INSERTION	UNP P04278
A	130	PRO	-	INSERTION	UNP P04278
A	131	LEU	-	INSERTION	UNP P04278
A	132	THR	-	INSERTION	UNP P04278
A	133	SER	-	INSERTION	UNP P04278
A	134	LYS	-	INSERTION	UNP P04278
A	135	ARG	-	INSERTION	UNP P04278

- Molecule 2 is 5-ALPHA-DIHYDROTESTOSTERONE (three-letter code: DHT) (formula:  $C_{19}H_{30}O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			21	19	2		

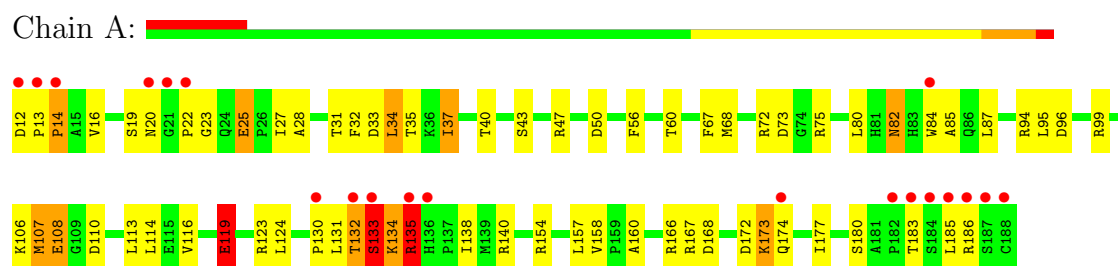
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	89	Total	O	0	0
			89	89		

### 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 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 ( $RSRZ > 2$ ). 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: Sex Hormone-Binding Globulin



## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	103.72Å 103.72Å 85.76Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 1.70 38.70 – 1.70	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-1.70) 98.2 (38.70-1.70)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.02 (at 1.70Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.194 , 0.245 0.202 , 0.245	Depositor DCC
$R_{free}$ test set	1925 reflections (11.10%)	DCC
Wilson B-factor (Å <sup>2</sup> )	24.7	Xtriage
Anisotropy	0.002	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 39.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 19262 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	1499	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.89% 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: DHT

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	0.65	0/1431	1.76	33/1946 (1.7%)

There are no bond length outliers.

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	154	ARG	NE-CZ-NH1	-19.53	110.53	120.30
1	A	75	ARG	NE-CZ-NH1	13.54	127.07	120.30
1	A	135	ARG	CD-NE-CZ	10.08	137.72	123.60
1	A	72	ARG	NE-CZ-NH2	-8.40	116.10	120.30
1	A	167	ARG	CD-NE-CZ	8.35	135.29	123.60
1	A	94	ARG	NE-CZ-NH1	-8.27	116.17	120.30
1	A	123	ARG	NE-CZ-NH2	-7.95	116.32	120.30
1	A	140	ARG	NE-CZ-NH2	7.92	124.26	120.30
1	A	68	MET	CG-SD-CE	7.71	112.54	100.20
1	A	154	ARG	NH1-CZ-NH2	7.66	127.82	119.40
1	A	56	PHE	CB-CG-CD1	7.29	125.90	120.80
1	A	73	ASP	CB-CG-OD1	7.08	124.67	118.30
1	A	110	ASP	CB-CG-OD1	-6.87	112.11	118.30
1	A	75	ARG	NE-CZ-NH2	-6.87	116.86	120.30
1	A	96	ASP	CB-CG-OD2	-6.81	112.17	118.30
1	A	106	LYS	CA-CB-CG	6.78	128.32	113.40
1	A	80	LEU	CA-CB-CG	6.49	130.23	115.30
1	A	108	GLU	CA-CB-CG	6.21	127.07	113.40
1	A	96	ASP	CB-CG-OD1	6.09	123.78	118.30
1	A	56	PHE	CB-CG-CD2	-6.03	116.58	120.80
1	A	32	PHE	CD1-CE1-CZ	5.81	127.07	120.10
1	A	167	ARG	NE-CZ-NH1	5.65	123.12	120.30
1	A	110	ASP	CB-CG-OD2	5.61	123.35	118.30
1	A	114	LEU	CB-CG-CD1	-5.53	101.60	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	47	ARG	NE-CZ-NH2	-5.37	117.62	120.30
1	A	99	ARG	CD-NE-CZ	5.35	131.09	123.60
1	A	119	GLU	CA-CB-CG	5.23	124.90	113.40
1	A	119	GLU	OE1-CD-OE2	-5.22	117.04	123.30
1	A	110	ASP	O-C-N	5.21	131.04	122.70
1	A	28	ALA	N-CA-CB	5.13	117.28	110.10
1	A	33	ASP	CB-CG-OD1	5.11	122.90	118.30
1	A	67	PHE	CB-CG-CD1	-5.05	117.26	120.80
1	A	124	LEU	N-CA-CB	5.04	120.49	110.40

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	1389	0	1372	31	0
2	A	21	0	30	0	0
3	A	89	0	0	4	0
All	All	1499	0	1402	31	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 11.

All (31) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:12:ASP:HA	1:A:166:ARG:HH11	1.37	0.86
1:A:12:ASP:HA	1:A:166:ARG:NH1	1.95	0.81
1:A:23:GLY:HA3	1:A:160:ALA:HB2	1.68	0.73
1:A:34:LEU:HD12	1:A:37:ILE:HD13	1.71	0.72
1:A:60:THR:HG21	1:A:134:LYS:HE2	1.81	0.62
1:A:107:MET:HE1	1:A:131:LEU:HG	1.84	0.59
1:A:40:THR:HG22	1:A:131:LEU:HD12	1.83	0.59
1:A:35:THR:HA	1:A:132:THR:HG23	1.85	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:158:VAL:HG12	3:A:378:HOH:O	2.04	0.57
1:A:23:GLY:HA3	1:A:160:ALA:CB	2.33	0.57
1:A:82:ASN:C	1:A:82:ASN:HD22	2.10	0.54
1:A:172:ASP:OD1	1:A:174:GLN:HG3	2.09	0.52
1:A:130:PRO:HB2	1:A:133:SER:HB2	1.94	0.49
1:A:12:ASP:O	1:A:13:PRO:C	2.51	0.48
1:A:31:THR:HG22	1:A:177:ILE:HD12	1.95	0.48
1:A:13:PRO:O	1:A:14:PRO:C	2.51	0.48
1:A:50:ASP:OD2	3:A:311:HOH:O	2.19	0.47
1:A:20:ASN:O	1:A:22:PRO:HD2	2.15	0.47
1:A:119:GLU:HB2	3:A:389:HOH:O	2.16	0.45
1:A:27:ILE:O	1:A:185:LEU:HD21	2.16	0.45
1:A:82:ASN:ND2	1:A:85:ALA:H	2.15	0.44
1:A:25:GLU:H	1:A:25:GLU:HG2	1.67	0.43
1:A:82:ASN:ND2	1:A:84:TRP:H	2.17	0.42
1:A:43:SER:O	1:A:168:ASP:HA	2.20	0.42
1:A:40:THR:CG2	1:A:131:LEU:HD12	2.50	0.42
1:A:131:LEU:O	1:A:134:LYS:HG2	2.20	0.42
1:A:173:LYS:HG3	3:A:324:HOH:O	2.19	0.41
1:A:31:THR:HG23	1:A:138:ILE:CG2	2.50	0.41
1:A:16:VAL:HG21	1:A:185:LEU:HB3	2.02	0.41
1:A:95:LEU:HD21	1:A:116:VAL:HG11	2.02	0.40
1:A:87:LEU:C	1:A:87:LEU:HD12	2.41	0.40

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	177/177 (100%)	165 (93%)	9 (5%)	3 (2%)	14 2

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	14	PRO
1	A	133	SER
1	A	135	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	153/152 (101%)	135 (88%)	18 (12%)	<b>8</b> <b>1</b>

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	SER
1	A	25	GLU
1	A	34	LEU
1	A	37	ILE
1	A	82	ASN
1	A	107	MET
1	A	108	GLU
1	A	113	LEU
1	A	119	GLU
1	A	132	THR
1	A	133	SER
1	A	134	LYS
1	A	135	ARG
1	A	157	LEU
1	A	173	LYS
1	A	180	SER
1	A	183	THR
1	A	186	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	82	ASN

### 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 ⓘ

1 ligand is 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	$\# Z  > 2$
2	DHT	A	301	-	24,24,24	0.84	0	39,39,39	1.52	4 (10%)

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
2	DHT	A	301	-	-	0/0/58/58	0/0/4/4

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	DHT	C16-C17-C13	4.22	107.92	104.59
2	A	301	DHT	C15-C16-C17	-3.11	102.63	105.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	DHT	O3-C3-C4	-2.41	118.67	121.98
2	A	301	DHT	C14-C13-C17	-2.27	96.81	99.23

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	177/177 (100%)	0.67	20 (11%) 6 8	15, 30, 80, 90	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	13	PRO	7.7
1	A	133	SER	7.5
1	A	12	ASP	6.5
1	A	188	CYS	6.3
1	A	132	THR	6.2
1	A	20	ASN	6.2
1	A	183	THR	5.8
1	A	14	PRO	5.3
1	A	22	PRO	4.4
1	A	182	PRO	4.2
1	A	135	ARG	3.9
1	A	186	ARG	3.7
1	A	185	LEU	3.7
1	A	187	SER	3.5
1	A	184	SER	3.3
1	A	130	PRO	2.8
1	A	21	GLY	2.7
1	A	136	HIS	2.4
1	A	174	GLN	2.4
1	A	84	TRP	2.1

### 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(Å <sup>2</sup> )	Q<0.9
2	DHT	A	301	21/21	0.07	-0.91	16,18,21,24	0

### 6.5 Other polymers

There are no such residues in this entry.