



# wwPDB X-ray Structure Validation Summary Report i

Feb 27, 2014 – 11:46 PM GMT

PDB ID : 2C36  
Title : STRUCTURE OF UNLIGANDED HSV GD REVEALS A MECHANISM FOR RECEPTOR-MEDIATED ACTIVATION OF VIRUS ENTRY  
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Deposited on : 2005-10-04  
Resolution : 2.11 Å(reported)

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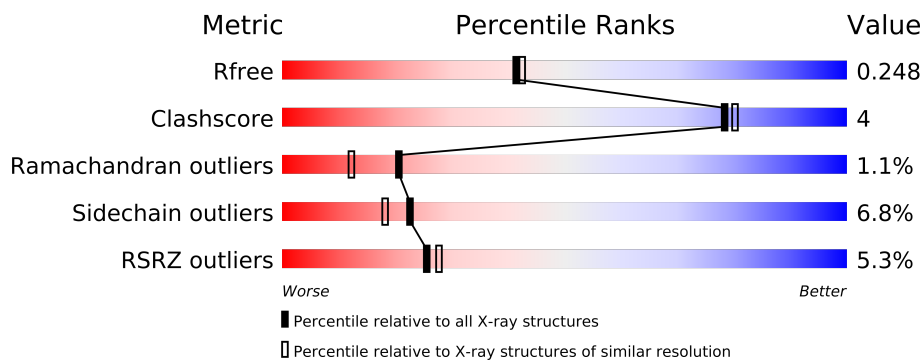
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.11 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	3409 (2.14-2.10)
Clashscore	79885	4090 (2.14-2.10)
Ramachandran outliers	78287	4048 (2.14-2.10)
Sidechain outliers	78261	4049 (2.14-2.10)
RSRZ outliers	66119	3410 (2.14-2.10)

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	285	
1	B	285	

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 4924 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 GLYCOPROTEIN D HSV-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	274	Total	C	N	O	S	0	1	0
			2145	1376	360	398	11			
1	B	274	Total	C	N	O	S	0	2	0
			2149	1378	362	398	11			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	307	CYS	HIS	ENGINEERED MUTATION	UNP P57083
B	307	CYS	HIS	ENGINEERED MUTATION	UNP P57083

- Molecule 2 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	3	Total	C	N	O	0	0
			39	22	2	15		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	307	CYS	HIS	ENGINEERED MUTATION	UNP P57083

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Cl 1 1	0	0
4	A	2	Total Cl 2 2	0	0

- Molecule 5 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	3	Total C N O 39 22 2 15	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	307	CYS	HIS	ENGINEERED MUTATION	UNP P57083

- Molecule 6 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	3	Total C N O 39 22 2 15	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	307	CYS	HIS	ENGINEERED MUTATION	UNP P57083

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	273	Total O 273 273	0	0
7	B	236	Total O 236 236	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	74.25Å 106.19Å 130.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	81.65 – 2.11 29.83 – 2.11	Depositor EDS
% Data completeness (in resolution range)	92.4 (81.65-2.11) 92.5 (29.83-2.11)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.51 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.194 , 0.247 0.201 , 0.248	Depositor DCC
$R_{free}$ test set	2817 reflections (5.33%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.7	Xtriage
Anisotropy	0.761	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 47.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 55706 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4924	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.27% 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: ZN, BMA, NAG, CL, NDG, MAN

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	0.56	0/2217	0.78	1/3041 (0.0%)
1	B	0.61	1/2226 (0.0%)	0.78	5/3054 (0.2%)
All	All	0.58	1/4443 (0.0%)	0.78	6/6095 (0.1%)

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
6	B	1	0
All	All	1	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	91	GLN	CA-CB	10.92	1.77	1.53

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	147	ASP	CB-CG-OD2	7.62	125.16	118.30
1	B	91	GLN	CB-CA-C	5.95	122.30	110.40
1	B	281	ASP	CB-CG-OD2	5.57	123.31	118.30
1	A	87	ASP	CB-CG-OD2	5.55	123.29	118.30
1	B	91	GLN	N-CA-CB	-5.49	100.72	110.60

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	B	1311	NDG	C1

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	281	ASP	Peptide

## 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	2145	0	2100	12	0
1	B	2149	0	2104	19	0
2	A	39	0	34	1	0
3	A	1	0	0	0	0
4	A	2	0	0	0	0
4	B	1	0	0	0	0
5	B	39	0	34	0	0
6	B	39	0	34	0	0
7	A	273	0	0	0	0
7	B	236	0	0	1	0
All	All	4924	0	4306	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 4.

The worst 5 of 31 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:91:GLN:CA	1:B:91:GLN:CB	1.78	1.57
1:B:38:TYR:HA	1:B:132:GLN:HE22	1.51	0.74
1:B:91:GLN:CB	1:B:91:GLN:N	2.50	0.74
1:B:23:PRO:O	1:B:24:VAL:HG12	1.92	0.69
1:B:91:GLN:CG	1:B:91:GLN:CA	2.70	0.67

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	271/285 (95%)	257 (95%)	10 (4%)	4 (2%)	15	7
1	B	272/285 (95%)	259 (95%)	11 (4%)	2 (1%)	30	23
All	All	543/570 (95%)	516 (95%)	21 (4%)	6 (1%)	21	12

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	24	VAL
1	A	282	PRO
1	A	285	THR
1	B	282	PRO
1	A	269	ALA

### 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	236/245 (96%)	220 (93%)	16 (7%)	22	18
1	B	237/245 (97%)	221 (93%)	16 (7%)	22	18
All	All	473/490 (96%)	441 (93%)	32 (7%)	22	18

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	285	THR
1	B	132	GLN
1	B	281	ASP
1	B	53	LEU

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Mol	Chain	Res	Type
1	B	149	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	ASN
1	A	148	ASN
1	B	132	GLN
1	B	148	ASN
1	B	300	GLN

### 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 ⓘ

9 carbohydrates 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	$\# Z  > 2$
2	NAG	A	1308	1,2	12,14,15	0.48	0	15,19,21	1.22	2 (13%)
2	NAG	A	1309	2	12,14,15	0.71	0	15,19,21	1.06	1 (6%)
2	MAN	A	1310	2	10,11,12	0.53	0	11,15,17	3.13	3 (27%)
5	NAG	B	1308	1,5	12,14,15	0.73	1 (8%)	15,19,21	1.20	2 (13%)
5	NAG	B	1309	5	12,14,15	0.56	0	15,19,21	1.52	2 (13%)
5	BMA	B	1310	5	10,11,12	0.56	0	11,15,17	3.09	3 (27%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	NDG	B	1311	1,6	12,14,15	0.60	0	15,19,21	0.97	1 (6%)
6	NDG	B	1312	6	12,14,15	0.39	0	15,19,21	1.81	2 (13%)
6	MAN	B	1313	6	10,11,12	0.54	0	11,15,17	3.12	3 (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
2	NAG	A	1308	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1309	2	-	0/6/23/26	0/1/1/1
2	MAN	A	1310	2	-	0/2/19/22	0/1/1/1
5	NAG	B	1308	1,5	-	0/6/23/26	0/1/1/1
5	NAG	B	1309	5	-	0/6/23/26	0/1/1/1
5	BMA	B	1310	5	-	0/2/19/22	0/1/1/1
6	NDG	B	1311	1,6	1/1/5/7	0/6/23/26	0/1/1/1
6	NDG	B	1312	6	-	0/6/23/26	0/1/1/1
6	MAN	B	1313	6	-	0/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1308	NAG	O5-C5	-2.19	1.41	1.45

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1310	MAN	O5-C5-C4	6.71	119.17	110.65
6	B	1313	MAN	O5-C5-C4	6.25	118.58	110.65
5	B	1310	BMA	C4-C3-C2	6.22	118.86	110.50
6	B	1313	MAN	C4-C3-C2	6.19	118.81	110.50
5	B	1310	BMA	O5-C5-C4	6.03	118.31	110.65

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	B	1311	NDG	C1

There are no torsion outliers.

There are no ring outliers.

## 5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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	274/285 (96%)	0.06	13 (4%) 30 33	34, 42, 68, 78	0
1	B	274/285 (96%)	0.12	15 (5%) 24 26	33, 44, 68, 77	0
All	All	548/570 (96%)	0.09	28 (5%) 25 29	33, 43, 68, 78	0

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	283	VAL	7.6
1	A	283	VAL	6.4
1	A	24	VAL	5.2
1	B	24	VAL	5.1
1	B	256	GLU	5.0

### 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 ⓘ

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
6	NDG	B	1311	14/15	0.46	8.22	88,94,95,99	0
5	NAG	B	1308	14/15	0.09	-0.61	54,57,59,64	0
2	NAG	A	1308	14/15	0.09	-0.61	51,53,58,63	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	A	1309	14/15	0.31	-	67,69,73,76	0
5	NAG	B	1309	14/15	0.28	-	68,72,73,77	0
6	MAN	B	1313	11/12	0.59	-	107,108,108,108	0
6	NDG	B	1312	14/15	0.65	-	102,104,105,106	0
5	BMA	B	1310	11/12	0.46	-	79,81,82,83	0
2	MAN	A	1310	11/12	0.44	-	79,80,81,81	0

## 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	ZN	A	1311	1/1	0.07	-1.53	38,38,38,38	0
4	CL	A	1312	1/1	0.03	-2.58	40,40,40,40	0
4	CL	A	1313	1/1	0.05	-3.24	38,38,38,38	0
4	CL	B	1314	1/1	0.03	-4.88	37,37,37,37	0

## 6.5 Other polymers

There are no such residues in this entry.