



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 3U82 / pdb_00003u82
Title : Binding of herpes simplex virus glycoprotein D to nectin-1 exploits host cell adhesion
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Deposited on : 2011-10-15
Resolution : 3.16 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

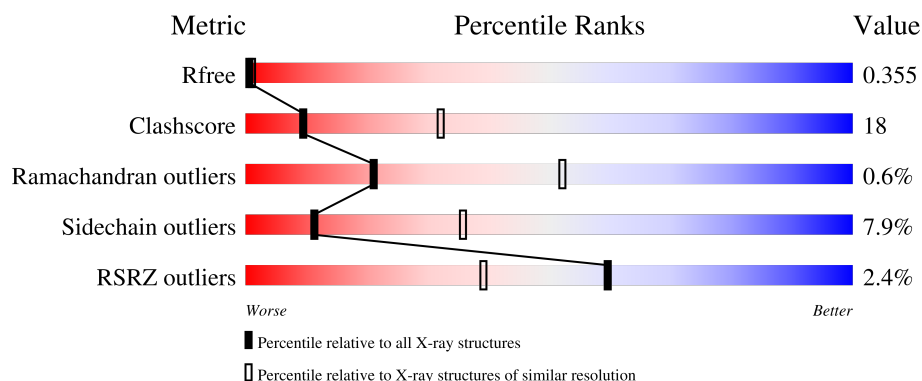
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.16 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}	180053	2361 (3.20-3.12)
Clashscore	190562	2486 (3.20-3.12)
Ramachandran outliers	187476	2405 (3.20-3.12)
Sidechain outliers	187428	2404 (3.20-3.12)
RSRZ outliers	180081	2361 (3.20-3.12)

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 $\leq 5\%$. 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	291	 3% 67% 12% 21%
2	B	317	 2% 68% 20% 6% 5%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4178 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 Envelope glycoprotein D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	231	Total	C	N	O	S	0	1	0
			1818	1167	311	330	10			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	286	HIS	-	expression tag	UNP Q69091
A	287	HIS	-	expression tag	UNP Q69091
A	288	HIS	-	expression tag	UNP Q69091
A	289	HIS	-	expression tag	UNP Q69091
A	290	HIS	-	expression tag	UNP Q69091
A	291	HIS	-	expression tag	UNP Q69091

- Molecule 2 is a protein called Poliovirus receptor-related protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	300	Total	C	N	O	S	0	1	0
			2360	1483	409	457	11			

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	336	ALA	-	expression tag	UNP Q15223
B	337	ALA	-	expression tag	UNP Q15223
B	338	ALA	-	expression tag	UNP Q15223
B	339	LEU	-	expression tag	UNP Q15223
B	340	GLU	-	expression tag	UNP Q15223
B	341	HIS	-	expression tag	UNP Q15223
B	342	HIS	-	expression tag	UNP Q15223
B	343	HIS	-	expression tag	UNP Q15223
B	344	HIS	-	expression tag	UNP Q15223
B	345	HIS	-	expression tag	UNP Q15223

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Chain	Residue	Modelled	Actual	Comment	Reference
B	346	HIS	-	expression tag	UNP Q15223

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	52.53Å 169.04Å 183.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.38 – 3.16 38.38 – 3.16	Depositor EDS
% Data completeness (in resolution range)	81.9 (38.38-3.16) 94.0 (38.38-3.16)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.54 (at 3.18Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, R_{free}	0.321 , 0.344 0.327 , 0.355	Depositor DCC
R_{free} test set	671 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	105.3	Xtriage
Anisotropy	0.843	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 138.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4178	wwPDB-VP
Average B, all atoms (Å ²)	193.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.15% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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	0.73	0/1877	0.87	1/2567 (0.0%)
2	B	0.36	0/2413	0.81	3/3287 (0.1%)
All	All	0.56	0/4290	0.84	4/5854 (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
2	B	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	B	246	GLU	N-CA-C	9.50	130.81	109.81
2	B	246	GLU	N-CA-CB	-8.00	96.13	110.37
2	B	72	ASN	N-CA-C	7.63	127.05	110.80
1	A	110	ILE	CB-CA-C	-5.00	105.90	111.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	71	THR	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	1818	0	1795	76	4
2	B	2360	0	2293	116	5
All	All	4178	0	4088	148	7

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 18.

The worst 5 of 148 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:B:217:ARG:HD3	2:B:245:TYR:CE1	1.40	1.56
2:B:245:TYR:CE2	2:B:274:ASN:HB3	1.66	1.28
1:A:59:TYR:HE1	1:A:253:LEU:CB	1.50	1.23
2:B:217:ARG:CD	2:B:245:TYR:CE1	2.23	1.20
2:B:217:ARG:CD	2:B:245:TYR:HE1	1.55	1.20

The worst 5 of 7 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:50[B]:HIS:NE2	2:B:335:GLU:CG[7_654]	1.76	0.44
1:A:191:TYR:OH	2:B:158:ARG:NH2[5_455]	1.84	0.36
1:A:146:GLU:OE1	1:A:146:GLU:OE2[4_555]	1.99	0.21
2:B:50[B]:HIS:CE1	2:B:335:GLU:OE2[7_654]	2.04	0.16
2:B:50[B]:HIS:NE2	2:B:335:GLU:CD[7_654]	2.09	0.11

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	230/291 (79%)	224 (97%)	6 (3%)	0	100	100
2	B	299/317 (94%)	283 (95%)	13 (4%)	3 (1%)	12	41
All	All	529/608 (87%)	507 (96%)	19 (4%)	3 (1%)	21	52

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	54	ALA
2	B	72	ASN
2	B	246	GLU

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	198/250 (79%)	190 (96%)	8 (4%)	28	56
2	B	261/276 (95%)	233 (89%)	28 (11%)	6	24
All	All	459/526 (87%)	423 (92%)	36 (8%)	11	36

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

Mol	Chain	Res	Type
2	B	285	LEU
2	B	335	GLU
2	B	286	ASN
2	B	291	LYS
2	B	114	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	297	ASN
2	B	332	ASN
2	B	176	ASN

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Mol	Chain	Res	Type
2	B	200	ASN
2	B	220	HIS

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 oligosaccharides 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	231/291 (79%)	0.19	8 (3%)	47 28	98, 169, 268, 369	1 (0%)
2	B	300/317 (94%)	-0.04	5 (1%)	69 48	108, 193, 321, 503	1 (0%)
All	All	531/608 (87%)	0.06	13 (2%)	59 39	98, 179, 291, 503	2 (0%)

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	111	LEU	2.9
2	B	241	LEU	2.7
2	B	93	TYR	2.7
1	A	45	PRO	2.6
2	B	130	PRO	2.5

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 oligosaccharides 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.