



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 10, 2025 – 06:03 PM EST

PDB ID : 9OC6 / pdb\_00009oc6  
Title : Crystal structure of receptor FcRn bound to Human Astrovirus 6 spike  
Authors : Agrawal, S.; Wilson, I.A.  
Deposited on : 2025-04-23  
Resolution : 2.97 Å(reported)

This is a Full wwPDB X-ray Structure 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

<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>.

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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	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
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)	:	2.46

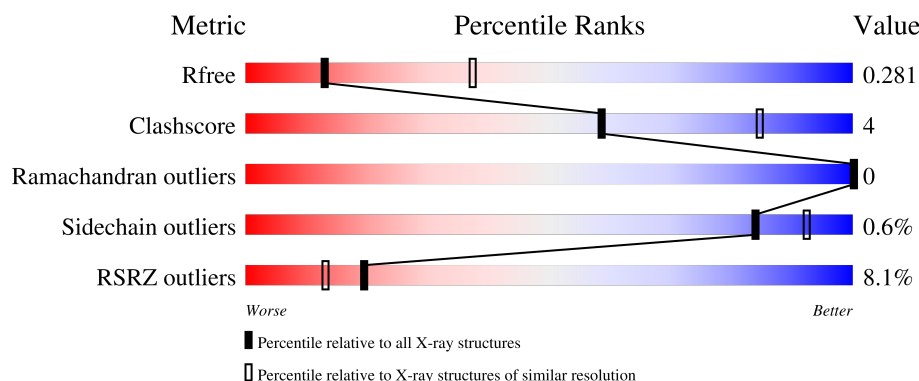
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.97 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))
$R_{free}$	164625	3360 (3.00-2.96)
Clashscore	180529	3751 (3.00-2.96)
Ramachandran outliers	177936	3628 (3.00-2.96)
Sidechain outliers	177891	3631 (3.00-2.96)
RSRZ outliers	164620	3372 (3.00-2.96)

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  $\geq 3$ , 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	C	274	<div> <div>12%</div> <div> <div></div> <div>75%</div> <div>9%</div> <div>15%</div> </div> </div>
2	D	99	<div> <div>4%</div> <div> <div></div> <div>90%</div> <div>10%</div> </div> </div>
3	A	244	<div> <div>2%</div> <div> <div></div> <div>76%</div> <div>10%</div> <div>14%</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4351 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 IgG receptor FcRn large subunit p51.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	232	Total	C	N	O	S	0	0	0
			1828	1181	304	335	8			

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	99	Total	C	N	O	S	0	0	0
			829	528	140	158	3			

- Molecule 3 is a protein called Capsid polypeptide VP90.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	211	Total	C	N	O	S	0	0	0
			1694	1080	287	321	6			

There are 29 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP A0A3G6VE58
A	217	GLY	-	expression tag	UNP A0A3G6VE58
A	218	SER	-	expression tag	UNP A0A3G6VE58
A	219	GLY	-	expression tag	UNP A0A3G6VE58
A	220	LEU	-	expression tag	UNP A0A3G6VE58
A	221	ASN	-	expression tag	UNP A0A3G6VE58
A	222	ASP	-	expression tag	UNP A0A3G6VE58
A	223	ILE	-	expression tag	UNP A0A3G6VE58
A	224	PHE	-	expression tag	UNP A0A3G6VE58
A	225	GLU	-	expression tag	UNP A0A3G6VE58
A	226	ALA	-	expression tag	UNP A0A3G6VE58
A	227	GLN	-	expression tag	UNP A0A3G6VE58
A	228	LYS	-	expression tag	UNP A0A3G6VE58
A	229	ILE	-	expression tag	UNP A0A3G6VE58

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Chain	Residue	Modelled	Actual	Comment	Reference
A	230	GLU	-	expression tag	UNP A0A3G6VE58
A	231	TRP	-	expression tag	UNP A0A3G6VE58
A	232	HIS	-	expression tag	UNP A0A3G6VE58
A	233	GLU	-	expression tag	UNP A0A3G6VE58
A	234	GLY	-	expression tag	UNP A0A3G6VE58
A	235	HIS	-	expression tag	UNP A0A3G6VE58
A	236	HIS	-	expression tag	UNP A0A3G6VE58
A	237	HIS	-	expression tag	UNP A0A3G6VE58
A	238	HIS	-	expression tag	UNP A0A3G6VE58
A	239	HIS	-	expression tag	UNP A0A3G6VE58
A	240	HIS	-	expression tag	UNP A0A3G6VE58
A	241	HIS	-	expression tag	UNP A0A3G6VE58
A	242	HIS	-	expression tag	UNP A0A3G6VE58
A	243	HIS	-	expression tag	UNP A0A3G6VE58
A	244	HIS	-	expression tag	UNP A0A3G6VE58



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	211.93Å 76.68Å 53.81Å 90.00° 98.55° 90.00°	Depositor
Resolution (Å)	29.14 – 2.97 29.14 – 2.97	Depositor EDS
% Data completeness (in resolution range)	99.6 (29.14-2.97) 96.6 (29.14-2.97)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.99 (at 3.00Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, $R_{free}$	0.228 , 0.281 0.229 , 0.281	Depositor DCC
$R_{free}$ test set	1766 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	59.6	Xtriage
Anisotropy	0.492	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 40.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	4351	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.20% 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, 0.333 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	C	0.13	0/1883	0.28	0/2555
2	D	0.10	0/852	0.28	0/1152
3	A	0.11	0/1738	0.30	0/2376
All	All	0.12	0/4473	0.29	0/6083

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	C	1828	0	1750	14	0
2	D	829	0	794	6	0
3	A	1694	0	1659	17	0
All	All	4351	0	4203	37	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 4.

All (37) 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)
1:C:180:PRO:HB3	1:C:203:PHE:HB3	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:8:LEU:HD23	1:C:95:GLY:HA3	1.77	0.66
1:C:47:PRO:HB2	1:C:52:VAL:HG12	1.79	0.63
1:C:154:PHE:HA	1:C:158:SER:HB2	1.82	0.62
3:A:78:MET:HB2	3:A:85:LYS:HG3	1.83	0.60
2:D:16:GLU:HB2	2:D:19:LYS:HG2	1.84	0.59
2:D:33:SER:HB2	2:D:54:LEU:HD21	1.84	0.58
3:A:96:LYS:HG2	3:A:106:VAL:HG13	1.86	0.56
3:A:99:ILE:HG22	3:A:100:THR:HG23	1.91	0.51
1:C:17:PRO:HG3	1:C:23:ALA:HB2	1.92	0.50
1:C:261:GLN:HG3	1:C:262:PRO:HD2	1.94	0.49
3:A:79:VAL:HB	3:A:87:ALA:HB3	1.94	0.49
3:A:190:ILE:O	3:A:190:ILE:HG13	2.11	0.48
2:D:5:PRO:HB3	2:D:30:PHE:HB3	1.96	0.48
1:C:204:TYR:CD1	1:C:205:PRO:HA	2.49	0.47
3:A:49:MET:HE1	3:A:153:PHE:HZ	1.78	0.47
3:A:78:MET:HE2	3:A:85:LYS:HE3	1.95	0.47
3:A:78:MET:HG3	3:A:80:LEU:HD11	1.97	0.47
3:A:8:LEU:HB2	3:A:59:ASP:HB2	1.95	0.47
1:C:5:LEU:O	1:C:97:GLU:HG2	2.15	0.47
2:D:84:HIS:CD2	2:D:86:THR:HG23	2.50	0.47
1:C:252:CYS:HB3	1:C:265:VAL:HB	1.98	0.45
3:A:19:GLU:O	3:A:200:PRO:HG2	2.16	0.45
3:A:99:ILE:HG22	3:A:100:THR:CG2	2.46	0.45
3:A:123:HIS:HB3	3:A:146:THR:HB	1.99	0.44
1:C:98:LEU:HD21	1:C:160:PRO:O	2.17	0.44
2:D:16:GLU:H	2:D:19:LYS:HE2	1.81	0.44
3:A:190:ILE:HA	3:A:194:ILE:HD11	2.00	0.43
3:A:143:ARG:O	3:A:144:SER:HB2	2.19	0.43
1:C:180:PRO:HB2	1:C:200:ALA:HB1	2.01	0.43
3:A:49:MET:HE1	3:A:153:PHE:CZ	2.53	0.43
1:C:11:LEU:HD13	1:C:26:VAL:HG13	2.01	0.42
3:A:6:LYS:HD3	3:A:208:TYR:OH	2.20	0.42
3:A:99:ILE:HD11	3:A:189:ILE:HG12	2.00	0.42
2:D:37:VAL:HB	2:D:66:TYR:CE1	2.54	0.42
1:C:98:LEU:HG	1:C:163:LEU:HB3	2.00	0.41
1:C:210:LEU:CD2	1:C:254:VAL:HG12	2.50	0.41

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	C	218/274 (80%)	208 (95%)	10 (5%)	0	100	100
2	D	97/99 (98%)	97 (100%)	0	0	100	100
3	A	209/244 (86%)	202 (97%)	7 (3%)	0	100	100
All	All	524/617 (85%)	507 (97%)	17 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	C	193/226 (85%)	193 (100%)	0	100	100
2	D	94/94 (100%)	94 (100%)	0	100	100
3	A	192/220 (87%)	189 (98%)	3 (2%)	58	81
All	All	479/540 (89%)	476 (99%)	3 (1%)	84	92

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

Mol	Chain	Res	Type
3	A	7	VAL
3	A	80	LEU
3	A	149	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such

sidechains are listed below:

Mol	Chain	Res	Type
1	C	166	HIS
1	C	229	ASN
3	A	119	GLN

### 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 ⓘ

### 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	C	232/274 (84%)	0.75	34 (14%) 7 5	41, 71, 119, 131	0
2	D	99/99 (100%)	0.37	4 (4%) 43 29	47, 66, 95, 111	0
3	A	211/244 (86%)	-0.15	6 (2%) 55 38	35, 48, 76, 109	0
All	All	542/617 (87%)	0.33	44 (8%) 19 13	35, 60, 113, 131	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	98	LEU	4.3
1	C	51	TRP	4.0
1	C	176	TRP	3.8
3	A	65	PHE	3.8
1	C	59	TRP	3.7
1	C	241	THR	3.6
1	C	60	TYR	3.4
1	C	166	HIS	3.3
1	C	100	PRO	3.3
1	C	253	ILE	3.3
1	C	5	LEU	3.2
1	C	184	LEU	3.1
2	D	99	MET	3.1
1	C	185	LYS	3.0
1	C	242	VAL	3.0
1	C	252	CYS	3.0
1	C	99	GLY	2.9
1	C	192	GLY	2.9
1	C	124	GLN	2.9
1	C	57	VAL	2.9
1	C	265	VAL	2.8
1	C	191	PRO	2.8
1	C	267	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	210	LEU	2.7
1	C	240	LEU	2.6
1	C	84	GLY	2.6
2	D	98	ASP	2.6
1	C	263	LEU	2.5
1	C	238	SER	2.4
1	C	53	TRP	2.4
3	A	67	PRO	2.3
1	C	260	ALA	2.3
3	A	144	SER	2.3
1	C	250	TYR	2.2
3	A	5	LEU	2.2
1	C	177	LYS	2.2
1	C	97	GLU	2.2
2	D	75	LYS	2.2
1	C	254	VAL	2.1
3	A	64	GLU	2.1
2	D	89	GLN	2.0
1	C	258	GLY	2.0
3	A	3	GLU	2.0
1	C	226	PHE	2.0

## 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 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.