



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 10, 2023 – 05:25 PM EDT

PDB ID : 4JPJ
Title : Crystal structure of the germline-targeting HIV-1 gp120 engineered outer domain, eOD-GT6
Authors : Julien, J.-P.; Jardine, J.; Schief, W.R.; Wilson, I.A.
Deposited on : 2013-03-19
Resolution : 2.50 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

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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

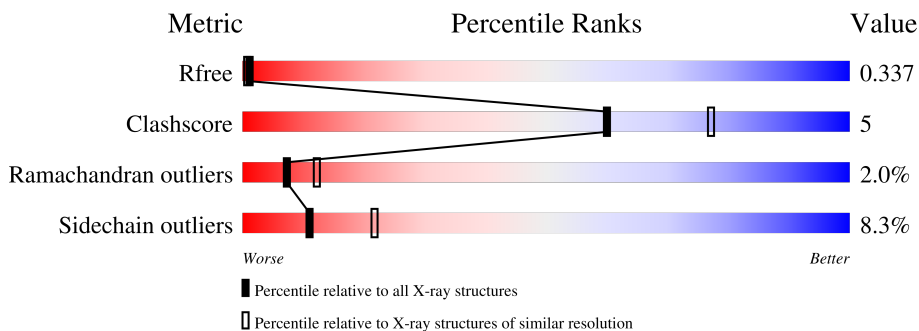
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	181	
1	B	181	
1	C	181	
1	D	181	

2 Entry composition [i](#)

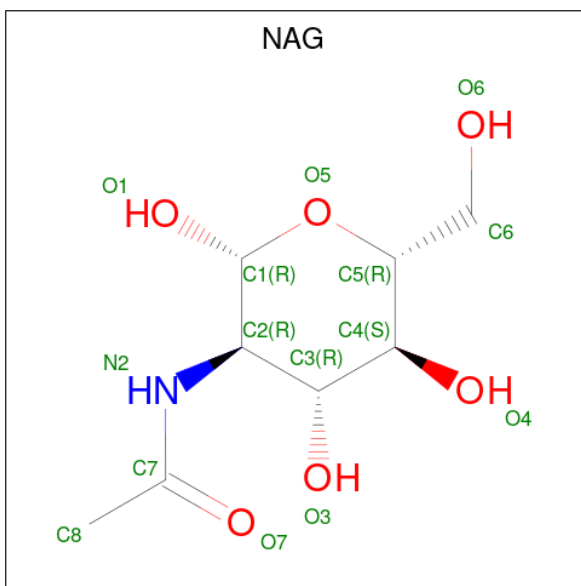
There are 3 unique types of molecules in this entry. The entry contains 5228 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Germline-targeting HIV-1 gp120 engineered outer domain, eOD-GT6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	170	Total 1308	C 809	N 226	O 264	S 9	0	0	0
1	B	169	Total 1301	C 807	N 224	O 261	S 9	0	0	0
1	C	157	Total 1210	C 751	N 207	O 244	S 8	0	0	0
1	D	162	Total 1252	C 777	N 211	O 255	S 9	0	0	0

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	Total 14	C 8	N 1	O 5	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C N O 14 8 1 5	0	0
2	B	1	Total C N O 14 8 1 5	0	0
2	B	1	Total C N O 14 8 1 5	0	0
2	C	1	Total C N O 14 8 1 5	0	0
2	C	1	Total C N O 14 8 1 5	0	0
2	D	1	Total C N O 14 8 1 5	0	0
2	D	1	Total C N O 14 8 1 5	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	9	Total O 9 9	0	0
3	B	23	Total O 23 23	0	0
3	C	9	Total O 9 9	0	0
3	D	4	Total O 4 4	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	44.96Å 217.73Å 44.99Å 90.00° 119.97° 90.00°	Depositor
Resolution (Å)	38.97 – 2.50 38.97 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.7 (38.97-2.50) 99.6 (38.97-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.80 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.210 , 0.262 0.298 , 0.337	Depositor DCC
R_{free} test set	1438 reflections (5.59%)	wwPDB-VP
Wilson B-factor (Å ²)	28.0	Xtriage
Anisotropy	0.156	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 4.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.54$, $\langle L^2 \rangle = 0.38$	Xtriage
Estimated twinning fraction	0.000 for -h-l,k,h 0.000 for l,k,-h-l 0.000 for h,-k,-h-l 0.207 for -h-l,-k,l 0.000 for l,-k,h	Xtriage
Reported twinning fraction	0.489 for H, K, L 0.102 for L, -K, H 0.408 for H+L, -K, -L	Depositor
Outliers	0 of 25744 reflections	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	5228	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.00% 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

5.1 Standard geometry

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

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	0.36	0/1333	0.63	0/1806
1	B	0.34	0/1325	0.58	0/1794
1	C	0.33	0/1231	0.56	0/1668
1	D	0.33	0/1274	0.55	0/1724
All	All	0.34	0/5163	0.58	0/6992

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
1	C	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	29	GLY	Peptide
1	C	169	PHE	Peptide

5.2 Too-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 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	1308	0	1238	12	0
1	B	1301	0	1233	9	0
1	C	1210	0	1151	11	0
1	D	1252	0	1179	14	0
2	A	28	0	26	0	0
2	B	28	0	26	0	0
2	C	28	0	26	0	0
2	D	28	0	26	0	0
3	A	9	0	0	0	0
3	B	23	0	0	0	0
3	C	9	0	0	1	0
3	D	4	0	0	0	0
All	All	5228	0	4905	46	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.

All (46) 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:D:170:ASP:N	1:D:171:SER:HA	1.92	0.82
1:A:27:ASP:N	1:A:28:GLY:HA2	2.03	0.74
1:A:143:GLU:O	1:A:144:PHE:HB2	1.90	0.71
1:A:97:ILE:HG22	1:A:105:CYS:HB3	1.78	0.66
1:A:116:LEU:HA	1:A:119:ILE:HG22	1.79	0.64
1:D:75:ILE:HD11	1:D:119:ILE:HD12	1.82	0.61
1:D:169:PHE:C	1:D:171:SER:HA	2.22	0.60
1:C:83:ASN:HD22	1:C:84:ALA:N	2.02	0.58
1:A:70:GLU:O	1:A:71:GLU:HG3	2.04	0.58
1:B:137:SER:O	1:B:138:SER:HB3	2.04	0.57
1:D:35:THR:HG22	1:D:131:THR:HG23	1.88	0.56
1:A:131:THR:HG23	1:A:170:ASP:HA	1.86	0.56
1:C:27:ASP:HB3	1:C:28:GLY:HA3	1.88	0.55
1:C:27:ASP:HB3	1:C:28:GLY:CA	2.37	0.54
1:D:170:ASP:N	1:D:171:SER:CA	2.70	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:39:ARG:NE	1:D:136:GLN:O	2.41	0.53
1:D:101:GLY:O	1:D:103:GLY:N	2.39	0.52
1:A:48:ILE:O	1:A:48:ILE:HG23	2.09	0.52
1:D:44:ASP:OD2	1:D:45:MET:N	2.44	0.50
1:A:13:PRO:HA	1:A:99:CYS:O	2.12	0.50
1:B:61:GLN:NE2	1:B:145:VAL:O	2.45	0.49
1:C:83:ASN:HD22	1:C:83:ASN:C	2.16	0.49
1:D:116:LEU:HA	1:D:119:ILE:HG22	1.93	0.49
1:B:135:LYS:O	1:B:136:GLN:CB	2.60	0.49
1:A:169:PHE:O	1:A:170:ASP:C	2.50	0.49
1:A:26:ARG:HG3	1:A:38:PHE:CE1	2.48	0.49
1:C:30:VAL:O	1:C:30:VAL:HG23	2.16	0.46
1:B:22:LEU:N	1:B:22:LEU:HD23	2.31	0.46
1:A:116:LEU:HA	1:A:119:ILE:CG2	2.44	0.45
1:C:22:LEU:N	1:C:22:LEU:HD23	2.31	0.45
1:B:135:LYS:O	1:B:136:GLN:HB3	2.17	0.45
1:C:27:ASP:CB	1:C:28:GLY:HA3	2.47	0.44
1:C:170:ASP:O	1:C:171:SER:CB	2.65	0.44
1:D:42:GLY:HA2	1:D:144:PHE:HB3	1.98	0.44
1:B:74:VAL:HG13	1:B:90:GLN:HB3	2.00	0.44
1:C:99:CYS:HA	1:C:105:CYS:HA	2.00	0.44
1:C:29:GLY:HA3	1:C:30:VAL:HA	1.84	0.44
1:D:22:LEU:HD12	1:D:24:LEU:HD21	2.00	0.44
1:D:169:PHE:HA	1:D:171:SER:HA	2.01	0.43
1:B:35:THR:HG22	1:B:36:GLU:N	2.35	0.42
1:A:23:ILE:HG12	1:A:45:MET:HE2	2.02	0.42
1:B:17:SER:CB	1:B:64:LEU:HG	2.50	0.41
1:D:38:PHE:CZ	1:D:123:LEU:HD22	2.55	0.41
1:B:137:SER:O	1:B:145:VAL:HG11	2.20	0.41
1:D:161:THR:O	1:D:162:GLN:HB2	2.20	0.41
1:C:26:ARG:NH1	3:C:304:HOH:O	2.53	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	168/181 (93%)	144 (86%)	18 (11%)	6 (4%)	3	4
1	B	165/181 (91%)	157 (95%)	6 (4%)	2 (1%)	13	24
1	C	151/181 (83%)	136 (90%)	11 (7%)	4 (3%)	5	8
1	D	154/181 (85%)	135 (88%)	18 (12%)	1 (1%)	25	43
All	All	638/724 (88%)	572 (90%)	53 (8%)	13 (2%)	7	12

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	48	ILE
1	A	71	GLU
1	A	144	PHE
1	B	30	VAL
1	B	136	GLN
1	C	170	ASP
1	C	171	SER
1	A	162	GLN
1	D	162	GLN
1	C	169	PHE
1	A	61	GLN
1	A	65	ASN
1	C	129	ASP

5.3.2 Protein sidechains [i](#)

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	148/158 (94%)	134 (90%)	14 (10%)	8	17
1	B	147/158 (93%)	132 (90%)	15 (10%)	7	14
1	C	139/158 (88%)	128 (92%)	11 (8%)	12	24
1	D	144/158 (91%)	136 (94%)	8 (6%)	21	40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	578/632 (92%)	530 (92%)	48 (8%)	11	22

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	ASP
1	A	22	LEU
1	A	44	ASP
1	A	48	ILE
1	A	52	GLN
1	A	56	THR
1	A	64	LEU
1	A	74	VAL
1	A	81	ARG
1	A	114	ASN
1	A	116	LEU
1	A	136	GLN
1	A	141	ASP
1	A	150	ASN
1	B	22	LEU
1	B	36	GLU
1	B	56	THR
1	B	64	LEU
1	B	71	GLU
1	B	74	VAL
1	B	81	ARG
1	B	91	LEU
1	B	116	LEU
1	B	119	ILE
1	B	121	SER
1	B	130	ARG
1	B	135	LYS
1	B	150	ASN
1	B	172	THR
1	C	22	LEU
1	C	52	GLN
1	C	64	LEU
1	C	74	VAL
1	C	75	ILE
1	C	83	ASN
1	C	111	LYS
1	C	122	LYS

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Mol	Chain	Res	Type
1	C	130	ARG
1	C	172	THR
1	C	174	THR
1	D	22	LEU
1	D	33	ASP
1	D	56	THR
1	D	62	LEU
1	D	67	SER
1	D	81	ARG
1	D	131	THR
1	D	172	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	90	GLN
1	A	114	ASN
1	A	150	ASN
1	B	150	ASN
1	C	83	ASN
1	C	90	GLN
1	C	118	GLN
1	D	114	ASN
1	D	118	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 monosaccharides in this entry.

5.6 Ligand geometry

8 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
2	NAG	D	202	1	14,14,15	0.61	0	17,19,21	1.02	1 (5%)
2	NAG	D	201	1	14,14,15	0.44	0	17,19,21	1.52	1 (5%)
2	NAG	B	201	1	14,14,15	0.53	0	17,19,21	1.91	3 (17%)
2	NAG	B	202	1	14,14,15	0.62	0	17,19,21	1.08	1 (5%)
2	NAG	A	202	1	14,14,15	0.57	0	17,19,21	1.52	2 (11%)
2	NAG	C	202	1	14,14,15	0.48	0	17,19,21	1.49	3 (17%)
2	NAG	C	201	1	14,14,15	0.50	0	17,19,21	1.28	2 (11%)
2	NAG	A	201	1	14,14,15	0.34	0	17,19,21	2.30	4 (23%)

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	D	202	1	-	0/6/23/26	0/1/1/1
2	NAG	D	201	1	-	1/6/23/26	0/1/1/1
2	NAG	B	201	1	-	3/6/23/26	0/1/1/1
2	NAG	B	202	1	-	2/6/23/26	0/1/1/1
2	NAG	A	202	1	-	0/6/23/26	0/1/1/1
2	NAG	C	202	1	-	0/6/23/26	0/1/1/1
2	NAG	C	201	1	-	3/6/23/26	0/1/1/1
2	NAG	A	201	1	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	201	NAG	C1-O5-C5	7.98	123.00	112.19
2	D	201	NAG	C1-O5-C5	4.92	118.85	112.19
2	B	201	NAG	C1-O5-C5	4.91	118.85	112.19
2	B	201	NAG	O5-C5-C6	4.87	114.83	107.20
2	A	202	NAG	C1-O5-C5	4.44	118.21	112.19
2	C	202	NAG	C1-O5-C5	3.95	117.55	112.19
2	C	201	NAG	C1-O5-C5	3.64	117.12	112.19
2	A	201	NAG	O5-C1-C2	2.94	115.93	111.29
2	C	201	NAG	O5-C5-C6	2.93	111.80	107.20
2	B	202	NAG	C1-O5-C5	2.44	115.50	112.19
2	B	201	NAG	C4-C3-C2	-2.42	107.48	111.02
2	A	201	NAG	O5-C5-C6	2.30	110.81	107.20
2	D	202	NAG	C4-C3-C2	2.26	114.33	111.02
2	A	202	NAG	C4-C3-C2	-2.22	107.76	111.02
2	C	202	NAG	O5-C5-C6	2.22	110.69	107.20
2	C	202	NAG	C3-C4-C5	-2.19	106.34	110.24
2	A	201	NAG	C4-C3-C2	-2.16	107.85	111.02

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	201	NAG	O5-C5-C6-O6
2	C	201	NAG	O5-C5-C6-O6
2	B	202	NAG	O5-C5-C6-O6
2	B	201	NAG	C4-C5-C6-O6
2	B	202	NAG	C4-C5-C6-O6
2	C	201	NAG	C4-C5-C6-O6
2	A	201	NAG	O5-C5-C6-O6
2	D	201	NAG	C4-C5-C6-O6
2	B	201	NAG	C3-C2-N2-C7
2	C	201	NAG	C3-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.