



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 8, 2023 – 09:11 PM EDT

PDB ID : 1QFW
Title : TERNARY COMPLEX OF HUMAN CHORIONIC GONADOTROPIN WITH FV ANTI ALPHA SUBUNIT AND FV ANTI BETA SUBUNIT
Authors : Tegoni, M.; Spinelli, S.; Cambillau, C.
Deposited on : 1999-04-15
Resolution : 3.50 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35
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

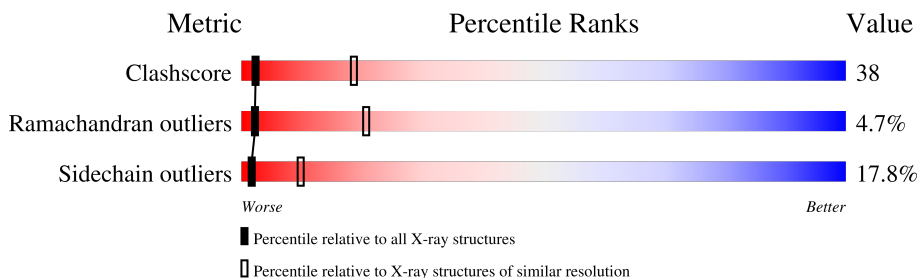
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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))
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)

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	92	51% 30% 13% 5%
2	B	145	38% 24% 8% 6% 23%
3	L	114	35% 48% 14% ..
4	H	117	36% 40% 14% 6% .
5	M	108	50% 42% 6% .
6	I	122	46% 45% 8% .

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 4938 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 GONADOTROPIN ALPHA SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	87	666	412	115	126	13	19	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	4	THR	VAL	conflict	UNP P01215

- Molecule 2 is a protein called GONADOTROPHIN BETA SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	111	810	501	148	148	13	9	0	1

- Molecule 3 is a protein called ANTIBODY (ANTI ALPHA SUBUNIT) (LIGHT CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	L	112	843	531	136	172	4	0	0	1

- Molecule 4 is a protein called ANTIBODY (ANTI ALPHA SUBUNIT) (HEAVY CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	H	112	829	518	139	168	4	0	0	1

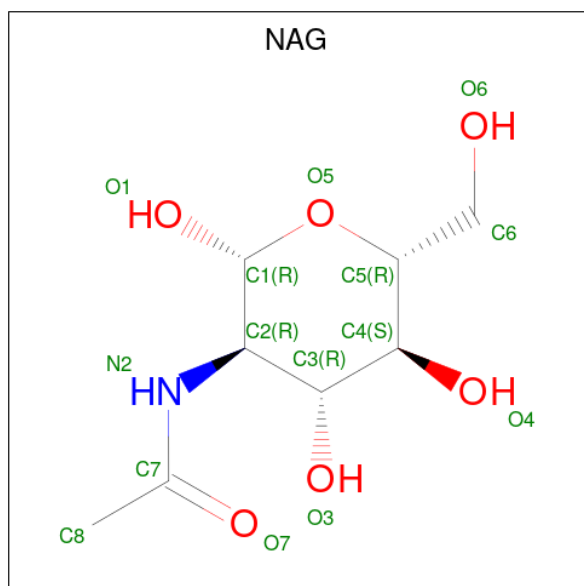
- Molecule 5 is a protein called ANTIBODY (ANTI BETA SUBUNIT) (LIGHT CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	M	108	825	517	136	168	4	19	0	1

- Molecule 6 is a protein called ANTIBODY (ANTI BETA SUBUNIT) (HEAVY CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
6	I	121	937	593	163	177	4	20	0	1

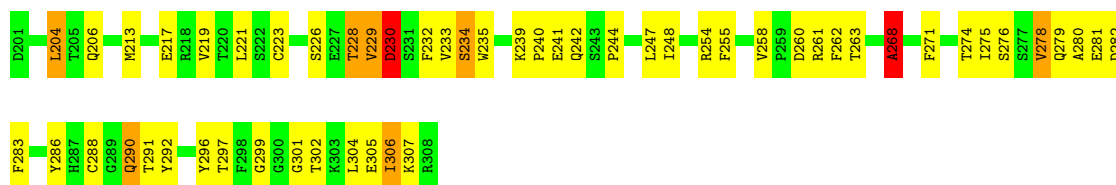
- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 5: ANTIBODY (ANTI BETA SUBUNIT) (LIGHT CHAIN)

Chain M:  50% 42% 6%



- Molecule 6: ANTIBODY (ANTI BETA SUBUNIT) (HEAVY CHAIN)

Chain I:  46% 45% 8%



4 Data and refinement statistics i

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	104.90Å 104.90Å 150.10Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	9.00 – 3.50 21.50 – 3.48	Depositor EDS
% Data completeness (in resolution range)	79.0 (9.00-3.50) 95.9 (21.50-3.48)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.17	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 3.45Å)	Xtrriage
Refinement program	X-PLOR 3.843	Depositor
R, R_{free}	0.260 , 0.310 0.337 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	66.0	Xtrriage
Anisotropy	0.093	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 24.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.015 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.74	EDS
Total number of atoms	4938	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.36% 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](#)

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	0.87	3/682 (0.4%)	0.99	4/922 (0.4%)
2	B	1.55	15/826 (1.8%)	1.96	24/1132 (2.1%)
3	L	0.76	1/862 (0.1%)	1.76	7/1172 (0.6%)
4	H	1.01	3/849 (0.4%)	1.47	19/1160 (1.6%)
5	M	0.80	1/844 (0.1%)	1.24	4/1142 (0.4%)
6	I	1.00	3/961 (0.3%)	0.99	6/1305 (0.5%)
All	All	1.03	26/5024 (0.5%)	1.45	64/6833 (0.9%)

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	3
3	L	0	3
4	H	0	3
5	M	0	3
All	All	0	12

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	6	ARG	C-N	20.18	1.72	1.34
6	I	252	THR	C-O	-16.64	0.91	1.23
5	M	230	ASP	C-N	-16.25	0.96	1.34
6	I	255	GLY	CA-C	-14.89	1.28	1.51
2	B	4	PRO	N-CA	14.37	1.71	1.47

The worst 5 of 64 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	26	SER	O-C-N	-48.59	44.96	122.70
2	B	5	LEU	O-C-N	-37.01	63.48	122.70
5	M	230	ASP	O-C-N	-19.57	91.39	122.70
5	M	230	ASP	C-N-CA	17.96	166.61	121.70
5	M	230	ASP	CA-C-N	14.78	149.72	117.20

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	47	GLY	Mainchain
2	B	5	LEU	Mainchain
2	B	7	PRO	Mainchain
3	L	26	SER	Mainchain
3	L	72	ARG	Sidechain

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	666	0	626	54	1
2	B	810	0	800	66	0
3	L	843	0	782	76	0
4	H	829	0	738	116	0
5	M	825	0	780	41	0
6	I	937	0	898	53	0
7	A	28	0	26	3	0
All	All	4938	0	4650	363	1

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 38.

The worst 5 of 363 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:6:ARG:C	2:B:7:PRO:N	1.72	1.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:4:PRO:CA	2:B:4:PRO:N	1.71	1.26
1:A:92:SER:HB2	2:B:92:LEU:HD23	1.27	1.15
4:H:101:GLY:O	4:H:102:ASN:HB2	1.34	1.15
4:H:51:ILE:O	4:H:52(A):PRO:HD3	1.50	1.10

All (1) 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)
1:A:46:THR:O	1:A:46:THR:O[6_765]	1.97	0.23

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	85/92 (92%)	73 (86%)	8 (9%)	4 (5%)	2	20
2	B	109/145 (75%)	84 (77%)	18 (16%)	7 (6%)	1	14
3	L	108/114 (95%)	81 (75%)	22 (20%)	5 (5%)	2	21
4	H	108/117 (92%)	80 (74%)	22 (20%)	6 (6%)	2	17
5	M	106/108 (98%)	91 (86%)	12 (11%)	3 (3%)	5	32
6	I	119/122 (98%)	90 (76%)	24 (20%)	5 (4%)	3	23
All	All	635/698 (91%)	499 (79%)	106 (17%)	30 (5%)	2	20

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	73	GLY
2	B	4	PRO
4	H	16	ALA
4	H	33	TRP

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Mol	Chain	Res	Type
5	M	268	ALA

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	78/83 (94%)	67 (86%)	11 (14%)	3	19
2	B	93/129 (72%)	70 (75%)	23 (25%)	0	4
3	L	89/98 (91%)	73 (82%)	16 (18%)	1	9
4	H	82/96 (85%)	63 (77%)	19 (23%)	1	4
5	M	93/94 (99%)	80 (86%)	13 (14%)	3	19
6	I	99/101 (98%)	86 (87%)	13 (13%)	4	21
All	All	534/601 (89%)	439 (82%)	95 (18%)	2	10

5 of 95 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	H	28	THR
5	M	228	THR
4	H	45	LEU
4	H	99	ARG
5	M	274	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
5	M	238	GLN
6	I	299	GLN
6	I	253	ASN
3	L	41	GLN
5	M	206	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 [i](#)

2 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
7	NAG	A	94	1	14,14,15	0.40	0	17,19,21	1.04	1 (5%)
7	NAG	A	93	1	14,14,15	0.62	0	17,19,21	1.02	2 (11%)

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
7	NAG	A	94	1	-	2/6/23/26	0/1/1/1
7	NAG	A	93	1	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	94	NAG	C4-C3-C2	-2.85	106.85	111.02
7	A	93	NAG	C4-C3-C2	-2.40	107.50	111.02
7	A	93	NAG	O5-C1-C2	-2.18	107.84	111.29

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	93	NAG	O5-C5-C6-O6
7	A	93	NAG	C4-C5-C6-O6
7	A	93	NAG	C3-C2-N2-C7
7	A	94	NAG	C1-C2-N2-C7
7	A	94	NAG	C3-C2-N2-C7

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	94	NAG	2	0
7	A	93	NAG	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	3
4	H	2
5	M	1

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	6:ARG	C	7:PRO	N	1.72
1	H	26:ASP	C	27:TYR	N	1.17
1	H	100:TYR	C	101:GLY	N	1.17
1	B	5:LEU	C	6:ARG	N	1.10

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	4:PRO	C	5:LEU	N	1.04

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.