



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 9, 2020 – 06:00 PM BST

PDB ID : 2GJ7
Title : Crystal Structure of a gE-gI/Fc complex
Authors : Sprague, E.R.; Wang, C.; Baker, D.; Bjorkman, P.J.
Deposited on : 2006-03-30
Resolution : 5.00 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 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 : 2.13.1
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) : 2.13.1

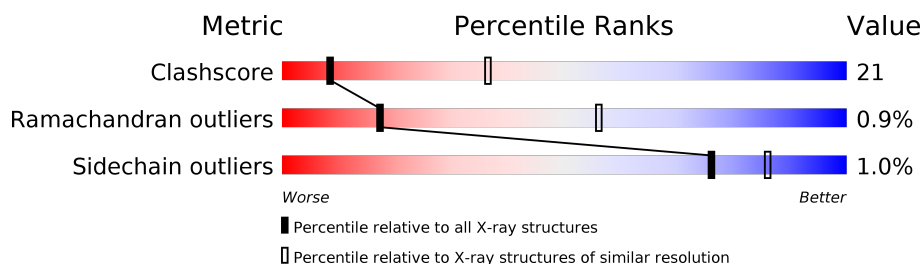
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 5.00 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	1000 (6.16-3.82)
Ramachandran outliers	138981	1146 (6.20-3.80)
Sidechain outliers	138945	1122 (6.20-3.80)

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 ≥ 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	227	
1	B	227	
2	E	401	
2	F	401	
3	C	8	
3	D	8	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	FUC	C	8	X	-	-	-
3	FUC	D	8	X	-	-	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6148 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 Ig gamma-1 chain C region.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	207	Total	C	N	O	S	19	0	0
			1659	1056	279	317	7			
1	B	207	Total	C	N	O	S	11	0	0
			1659	1056	279	317	7			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	221	LEU	-	cloning artifact	UNP P01857
A	222	GLU	-	cloning artifact	UNP P01857
A	356	GLU	ASP	conflict	UNP P01857
A	358	MET	LEU	conflict	UNP P01857
B	221	LEU	-	cloning artifact	UNP P01857
B	222	GLU	-	cloning artifact	UNP P01857
B	356	GLU	ASP	conflict	UNP P01857
B	358	MET	LEU	conflict	UNP P01857

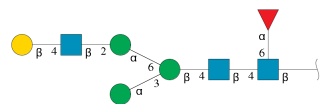
- Molecule 2 is a protein called Glycoprotein E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	171	Total	C	N	O	S	0	0	0
			1319	829	229	250	11			
2	E	171	Total	C	N	O	S	0	0	0
			1319	829	229	250	11			

There are 4 discrepancies between the modelled and reference sequences:

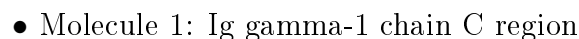
Chain	Residue	Modelled	Actual	Comment	Reference
F	420	ASP	-	cloning artifact	UNP P04488
F	421	ILE	-	cloning artifact	UNP P04488
E	420	ASP	-	cloning artifact	UNP P04488
E	421	ILE	-	cloning artifact	UNP P04488

- Molecule 3 is an oligosaccharide called beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	8	Total	C	N	O	0	0	0
			96	54	3	39			
3	D	8	Total	C	N	O	0	0	0
			96	54	3	39			

- Molecule 1: Ig gamma-1 chain C region



57%

E345	F346	R347	S350	H353	S354	H366	T367	H368	I375	L390	PRO	GLN	ARG	GLY	ASP	LEU	ALA	GLU	PRO	THR	HIS	PRO	HIS	VAL	GLY	ALA	PRO	PRO	HIS	ALA	PRO	THR	HIS	GLY	ALA	LEU	ARG	ASP	THR
------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- 1.3%

38%

NAG1
NAG2
BMA3
MAN4
NAG5
GAL6
MAN7
FUC8

4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	174.73 Å 174.73 Å 316.00 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.00 – 5.00 35.68 – 4.99	Depositor EDS
% Data completeness (in resolution range)	(Not available) (36.00-5.00) 99.5 (35.68-4.99)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.70 (at 5.08 Å)	Xtriage
Refinement program		Depositor
R, R_{free}	(Not available) , (Not available) 0.497 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	210.3	Xtriage
Anisotropy	0.477	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 62.8	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	0.63	EDS
Total number of atoms	6148	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% 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: FUC, GAL, NAG, BMA, 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	0.40	0/1705	0.61	0/2322
1	B	0.40	0/1705	0.61	0/2322
2	E	0.32	0/1359	0.64	0/1866
2	F	0.32	0/1359	0.64	0/1866
All	All	0.37	0/6128	0.62	0/8376

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	A	1659	0	1622	133	0
1	B	1659	0	1623	82	0
2	E	1319	0	1239	76	30
2	F	1319	0	1238	133	30
3	C	96	0	82	1	0
3	D	96	0	82	0	0
All	All	6148	0	5886	249	30

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 21.

The worst 5 of 249 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:A:310:HIS:CD2	2:F:321:PRO:HB3	1.12	1.60
1:A:310:HIS:CG	2:F:321:PRO:CB	1.85	1.60
1:A:310:HIS:CG	2:F:321:PRO:HB3	1.07	1.56
1:A:314:LEU:HB2	2:F:322:ARG:NH1	1.36	1.38
1:A:252:MET:HE3	2:F:247:HIS:CE1	1.61	1.35

The worst 5 of 30 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:F:305:ARG:NH2	2:E:285:GLN:CB[3_444]	0.59	1.61
2:F:285:GLN:CB	2:E:305:ARG:NH2[3_444]	0.81	1.39
2:F:305:ARG:NH1	2:E:285:GLN:O[3_444]	1.28	0.92
2:F:303:THR:CB	2:E:303:THR:CB[3_444]	1.37	0.83
2:F:305:ARG:NH1	2:E:285:GLN:C[3_444]	1.40	0.80

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	205/227 (90%)	203 (99%)	2 (1%)	0	100	100
1	B	205/227 (90%)	199 (97%)	5 (2%)	1 (0%)	29	68
2	E	169/401 (42%)	160 (95%)	6 (4%)	3 (2%)	8	41
2	F	169/401 (42%)	160 (95%)	6 (4%)	3 (2%)	8	41
All	All	748/1256 (60%)	722 (96%)	19 (2%)	7 (1%)	17	56

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	295	ALA
2	F	320	PRO
2	F	339	ALA
2	E	295	ALA
2	E	320	PRO

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	193/210 (92%)	192 (100%)	1 (0%)	88	93
1	B	193/210 (92%)	189 (98%)	4 (2%)	53	72
2	E	144/332 (43%)	143 (99%)	1 (1%)	84	90
2	F	144/332 (43%)	143 (99%)	1 (1%)	84	90
All	All	674/1084 (62%)	667 (99%)	7 (1%)	76	86

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	350	THR
2	E	320	PRO
1	B	439	LYS
2	F	320	PRO
1	B	443	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	310	HIS
1	B	361	ASN
2	E	338	GLN
2	F	368	HIS
2	E	283	HIS

5.3.3 RNA ⓘ

There are no RNA molecules 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 ⓘ

16 monosaccharides 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	$\# Z > 2$
3	NAG	C	1	1,3	14,14,15	0.48	0	17,19,21	0.73	0
3	NAG	C	2	3	14,14,15	0.47	0	17,19,21	0.74	0
3	BMA	C	3	3	11,11,12	0.65	0	15,15,17	0.59	0
3	MAN	C	4	3	11,11,12	0.52	0	15,15,17	0.57	0
3	NAG	C	5	3	14,14,15	0.50	0	17,19,21	0.76	0
3	GAL	C	6	3	11,11,12	0.76	0	15,15,17	0.77	1 (6%)
3	MAN	C	7	3	11,11,12	0.61	0	15,15,17	0.80	0
3	FUC	C	8	3	10,10,11	0.74	0	14,14,16	1.14	2 (14%)
3	NAG	D	1	1,3	14,14,15	0.67	0	17,19,21	0.87	0
3	NAG	D	2	3	14,14,15	0.58	0	17,19,21	0.78	1 (5%)
3	BMA	D	3	3	11,11,12	0.80	0	15,15,17	0.50	0
3	MAN	D	4	3	11,11,12	0.56	0	15,15,17	0.85	1 (6%)
3	NAG	D	5	3	14,14,15	0.48	0	17,19,21	0.79	0
3	GAL	D	6	3	11,11,12	0.56	0	15,15,17	0.51	0
3	MAN	D	7	3	11,11,12	0.54	0	15,15,17	0.59	0
3	FUC	D	8	3	10,10,11	0.76	0	14,14,16	1.04	1 (7%)

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
3	NAG	C	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	2/6/23/26	0/1/1/1
3	BMA	C	3	3	-	0/2/19/22	0/1/1/1
3	MAN	C	4	3	-	2/2/19/22	0/1/1/1
3	NAG	C	5	3	-	0/6/23/26	0/1/1/1
3	GAL	C	6	3	-	1/2/19/22	0/1/1/1
3	MAN	C	7	3	-	2/2/19/22	0/1/1/1
3	FUC	C	8	3	1/1/4/5	-	0/1/1/1
3	NAG	D	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1
3	BMA	D	3	3	-	0/2/19/22	0/1/1/1
3	MAN	D	4	3	-	2/2/19/22	0/1/1/1
3	NAG	D	5	3	-	0/6/23/26	0/1/1/1
3	GAL	D	6	3	-	0/2/19/22	0/1/1/1
3	MAN	D	7	3	-	0/2/19/22	0/1/1/1
3	FUC	D	8	3	1/1/4/5	-	0/1/1/1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	4	MAN	C1-O5-C5	2.59	115.71	112.19
3	D	8	FUC	C1-C2-C3	2.57	112.83	109.67
3	C	8	FUC	C3-C4-C5	2.49	113.65	109.77
3	C	8	FUC	C1-C2-C3	2.43	112.65	109.67
3	C	6	GAL	C1-C2-C3	2.33	112.53	109.67

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	D	8	FUC	C1
3	C	8	FUC	C1

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	4	MAN	O5-C5-C6-O6
3	C	2	NAG	O5-C5-C6-O6
3	C	2	NAG	C4-C5-C6-O6
3	D	2	NAG	C4-C5-C6-O6
3	D	4	MAN	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1	NAG	1	0
3	C	8	FUC	1	0

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 ⓘ

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.