



# wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 10, 2022 – 07:51 PM EST

PDB ID : 1FG9  
Title : 3:1 COMPLEX OF INTERFERON-GAMMA RECEPTOR WITH INTERFERON-GAMMA DIMER  
Authors : Thiel, D.J.; le Du, M.-H.; Walter, R.L.; D'Arcy, A.; Chene, C.; Fountoulakis, M.; Garotta, G.; Winkler, F.K.; Ealick, S.E.  
Deposited on : 2000-07-28  
Resolution : 2.90 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](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 : 4.02b-467  
Xtrriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

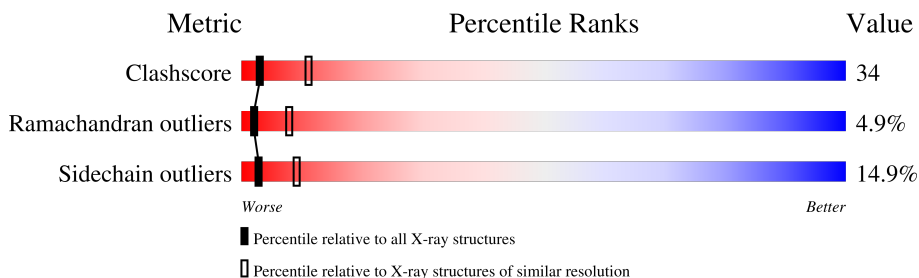
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 Å.




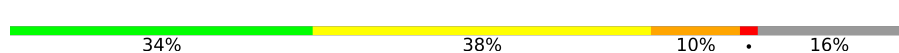
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)

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  $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	134	
1	B	134	
2	C	245	
2	D	245	
2	E	245	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6905 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 INTERFERON GAMMA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	127	1046	666	176	200	4	0	0	0
1	B	127	1044	665	176	199	4	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP P01579
B	0	MET	-	initiating methionine	UNP P01579

- Molecule 2 is a protein called INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	210	1661	1053	276	320	12	0	0	0
2	D	205	1617	1025	269	311	12	0	0	0
2	E	193	1537	972	256	297	12	0	0	0

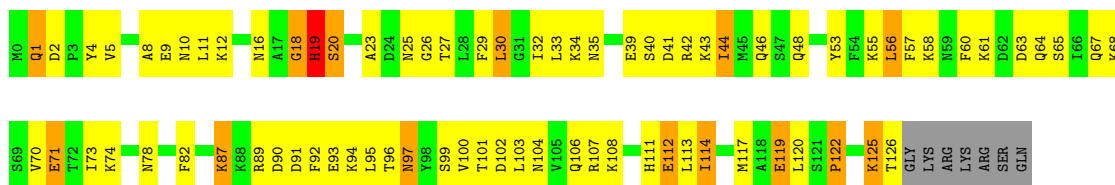
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

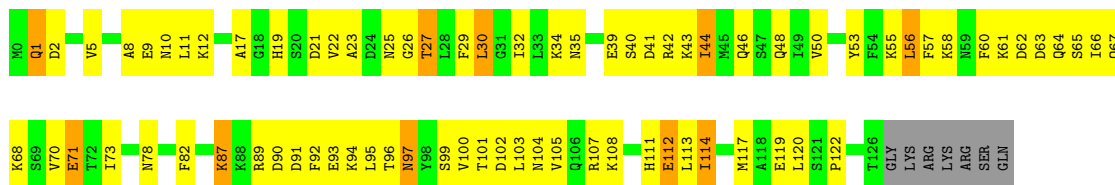
- Molecule 1: INTERFERON GAMMA

Chain A: 



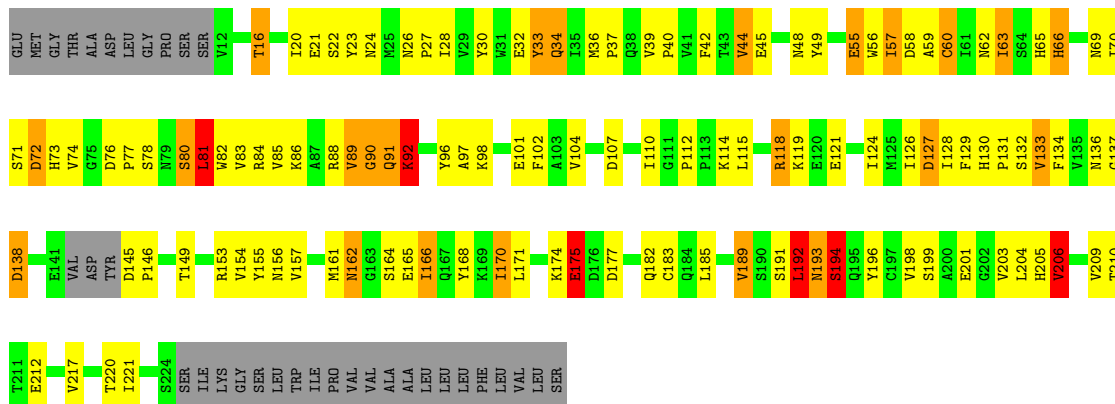
- Molecule 1: INTERFERON GAMMA

Chain B: 



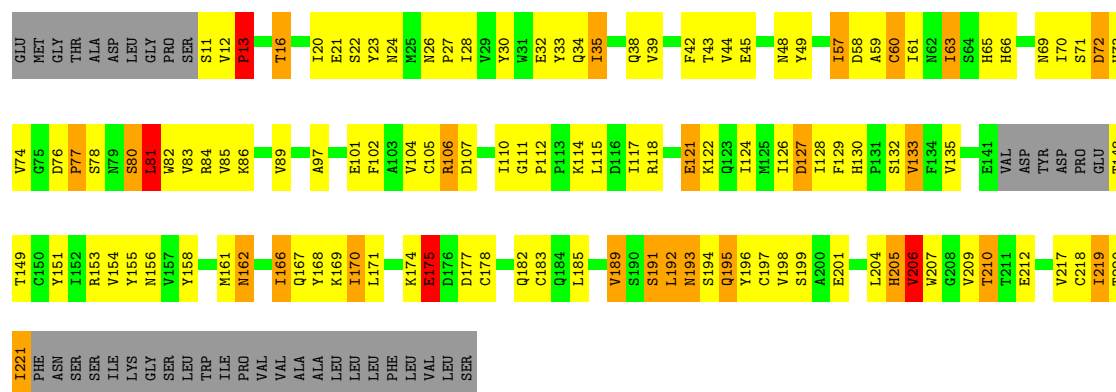
- Molecule 2: INTERFERON-GAMMA RECEPTOR ALPHA CHAIN

Chain C: 



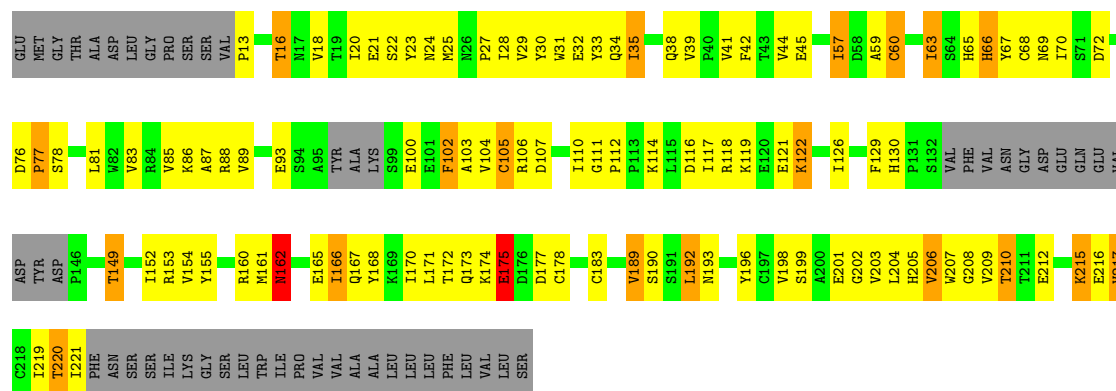
- Molecule 2: INTERFERON-GAMMA RECEPTOR ALPHA CHAIN

Chain D: 34% 38% 10% 16%



• Molecule 2: INTERFERON-GAMMA RECEPTOR ALPHA CHAIN

Chain E: 33% 37% 8% 21%



## 4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	199.30Å 114.65Å 74.34Å 90.00° 116.27° 90.00°	Depositor
Resolution (Å)	6.00 – 2.90	Depositor
% Data completeness (in resolution range)	(Not available) (6.00-2.90)	Depositor
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.237 , 0.302	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	6905	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	60.0	wwPDB-VP

## 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	0.71	0/1064	0.96	5/1424 (0.4%)
1	B	0.70	0/1062	0.88	2/1421 (0.1%)
2	C	0.81	1/1699 (0.1%)	1.02	7/2312 (0.3%)
2	D	0.67	0/1653	0.95	4/2249 (0.2%)
2	E	0.64	0/1571	0.86	1/2134 (0.0%)
All	All	0.71	1/7049 (0.0%)	0.94	19/9540 (0.2%)

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	C	0	1
2	D	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	89	VAL	CB-CG2	-5.65	1.41	1.52

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	56	LEU	CA-CB-CG	9.44	137.02	115.30
1	B	56	LEU	CA-CB-CG	8.53	134.92	115.30
2	C	90	GLY	N-CA-C	-8.13	92.77	113.10
2	D	121	GLU	N-CA-C	7.66	131.69	111.00
2	D	13	PRO	N-CA-C	6.96	130.21	112.10

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	96	TYR	Sidechain
2	D	205	HIS	Mainchain

## 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	1046	0	1048	80	0
1	B	1044	0	1043	89	0
2	C	1661	0	1593	136	0
2	D	1617	0	1557	125	0
2	E	1537	0	1488	90	0
All	All	6905	0	6729	468	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 34.

The worst 5 of 468 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:D:12:VAL:HB	2:D:13:PRO:HD2	1.37	1.07
1:B:1:GLN:HB2	1:B:5:VAL:HG21	1.45	0.98
2:C:205:HIS:HD2	2:C:206:VAL:HG22	1.32	0.92
2:D:149:THR:O	2:D:205:HIS:HB3	1.69	0.91
2:D:169:LYS:O	2:D:170:ILE:HG13	1.73	0.89

There are no symmetry-related clashes.

## 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	125/134 (93%)	99 (79%)	20 (16%)	6 (5%)	2	8
1	B	125/134 (93%)	105 (84%)	18 (14%)	2 (2%)	9	32
2	C	206/245 (84%)	153 (74%)	40 (19%)	13 (6%)	1	4
2	D	201/245 (82%)	154 (77%)	35 (17%)	12 (6%)	1	4
2	E	187/245 (76%)	140 (75%)	39 (21%)	8 (4%)	2	10
All	All	844/1003 (84%)	651 (77%)	152 (18%)	41 (5%)	2	8

5 of 41 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	30	LEU
1	B	30	LEU
2	C	91	GLN
2	C	121	GLU
2	C	162	ASN

### 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	117/123 (95%)	99 (85%)	18 (15%)	2	8
1	B	116/123 (94%)	101 (87%)	15 (13%)	4	13
2	C	188/223 (84%)	160 (85%)	28 (15%)	3	9
2	D	183/223 (82%)	156 (85%)	27 (15%)	3	9
2	E	177/223 (79%)	149 (84%)	28 (16%)	2	8
All	All	781/915 (85%)	665 (85%)	116 (15%)	3	9

5 of 116 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	199	SER

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Mol	Chain	Res	Type
2	E	192	LEU
2	D	72	ASP
2	E	175	GLU
2	E	102	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	205	HIS
2	D	182	GLN
2	E	205	HIS
2	D	173	GLN
2	D	184	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](#)

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](#)

EDS was not executed - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

### 6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.