



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 6WGK  
Title : Fab portion of dupilumab with Crystal Kappa design and intrachain disulfide  
Authors : Druzina, Z.; Atwell, S.; Pustilnik, A.; Antonysamy, S.; Ho, C.; Lieu, R.; Hendle, J.; Benach, J.; Wang, J.  
Deposited on : 2020-04-05  
Resolution : 1.62 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.

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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  
Xtriage (Phenix) : 1.13  
EDS : **FAILED**  
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) : 2.14.4.dev1

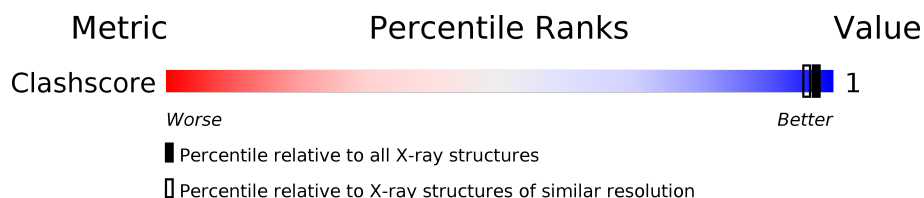
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.62 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	5002 (1.64-1.60)

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  $\geq 3$ , 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 failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	235	 89% • 7%
1	C	235	 91% • 8%
1	E	235	 92% • 7%
1	G	235	 89% • 9%
2	B	217	 96% ••
2	D	217	 97% ••
2	F	217	 96% ••
2	H	217	 96% ••

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 13743 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 Dupilumab Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	218	Total	C	N	O	S	0	4	0
			1636	1027	275	327	7			
1	C	217	Total	C	N	O	S	0	3	0
			1624	1019	274	324	7			
1	E	219	Total	C	N	O	S	0	1	0
			1629	1022	275	324	8			
1	G	214	Total	C	N	O	S	0	2	0
			1535	968	257	303	7			

- Molecule 2 is a protein called Dupilumab Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	215	Total	C	N	O	S	0	10	0
			1681	1058	274	342	7			
2	D	214	Total	C	N	O	S	0	6	0
			1648	1039	266	336	7			
2	F	214	Total	C	N	O	S	0	11	0
			1636	1030	266	333	7			
2	H	212	Total	C	N	O	S	0	2	0
			1563	986	257	313	7			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	140	Total	O	0	0
			140	140		
3	B	113	Total	O	0	0
			113	113		
3	C	114	Total	O	0	0
			114	114		
3	D	72	Total	O	0	0
			72	72		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	89	Total 89	O 89	0	0
3	F	94	Total 94	O 94	0	0
3	G	77	Total 77	O 77	0	0
3	H	92	Total 92	O 92	0	0



Chain D:  97% ..



- Molecule 2: Dupilumab Fab light chain

Chain F:  96% ..



- Molecule 2: Dupilumab Fab light chain

Chain H:  96% ..



## 4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	109.16 Å   79.27 Å   109.56 Å 90.00°   91.87°   90.00°	Depositor
Resolution (Å)	30.00 – 1.62	Depositor
% Data completeness (in resolution range)	95.2 (30.00-1.62)	Depositor
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.42 (at 1.62 Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, $R_{free}$	0.210 , 0.236	Depositor
Wilson B-factor (Å <sup>2</sup> )	24.8	Xtriage
Anisotropy	0.017	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for l,k,-h 0.012 for h,-k,-l 0.007 for l,-k,h	Xtriage
Total number of atoms	13743	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 34.17 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.1219e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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

### 5.1 Standard geometry

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	0.30	0/1684	0.63	0/2293
1	C	0.29	0/1669	0.62	0/2273
1	E	0.29	0/1668	0.61	0/2273
1	G	0.30	0/1575	0.62	0/2152
2	B	0.29	0/1743	0.62	0/2370
2	D	0.28	0/1701	0.61	0/2316
2	F	0.29	0/1698	0.61	0/2316
2	H	0.28	0/1604	0.61	0/2190
All	All	0.29	0/13342	0.62	0/18183

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
2	B	0	3
2	D	0	2
All	All	0	7

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	30	ARG	Sidechain
2	B	147[A]	ARG	Sidechain
2	B	24	ARG	Sidechain
2	B	59	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	C	108	ARG	Sidechain

## 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	1636	0	1589	4	0
1	C	1624	0	1570	1	0
1	E	1629	0	1576	1	0
1	G	1535	0	1435	3	0
2	B	1681	0	1635	5	0
2	D	1648	0	1593	1	0
2	F	1636	0	1545	3	0
2	H	1563	0	1447	2	0
3	A	140	0	0	0	0
3	B	113	0	0	0	0
3	C	114	0	0	0	0
3	D	72	0	0	0	0
3	E	89	0	0	0	0
3	F	94	0	0	0	0
3	G	77	0	0	0	0
3	H	92	0	0	0	0
All	All	13743	0	12390	20	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 1.

The worst 5 of 20 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:147[B]:ARG:HD2	2:B:147[B]:ARG:O	1.66	0.93
2:B:147[B]:ARG:HD2	2:B:147[B]:ARG:C	2.02	0.75
2:D:88:VAL:HG21	2:D:171:GLN:HB3	1.89	0.54
2:H:12:PRO:HB2	2:H:112:LYS:HE3	1.91	0.53
1:G:135:PRO:HD3	1:G:221:LYS:HE2	1.93	0.49

There are no symmetry-related clashes.

### 5.3 Torsion angles [i](#)

#### 5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

#### 5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

#### 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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

### 6.3 Carbohydrates ⓘ

EDS failed to run properly - this section is therefore empty.

### 6.4 Ligands ⓘ

EDS failed to run properly - this section is therefore empty.

### 6.5 Other polymers ⓘ

EDS failed to run properly - this section is therefore empty.