



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 7, 2020 – 01:33 AM BST

PDB ID : 1UZ8
Title : anti-Lewis X Fab fragment in complex with Lewis X
Authors : Van Roon, A.M.M.; Pannu, N.S.; De Vrind, J.P.M.; Hokke, C.H.; Deelder, A.M.; Van Der marel, G.A.; Van Boom, J.H.; Abrahams, J.P.
Deposited on : 2004-03-05
Resolution : 1.80 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

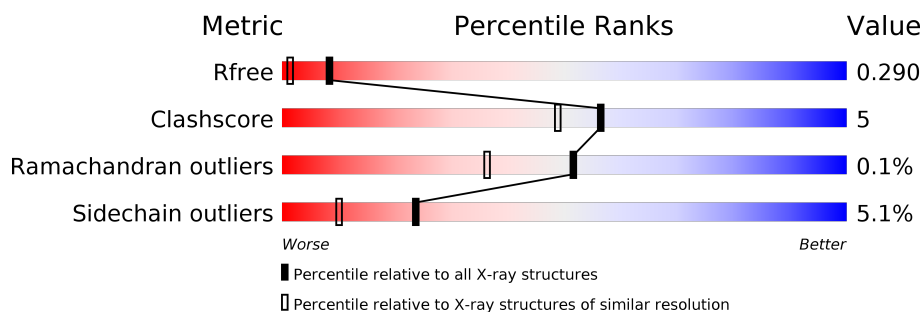
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)

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	218	87% 11% .
1	L	218	83% 14% ..
2	B	212	88% 12%
2	H	212	83% 15% .
3	C	3	67% 33%
3	D	3	67% 33%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7002 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.

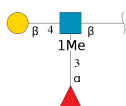
- Molecule 1 is a protein called IGG FAB (IGG3, KAPPA) LIGHT CHAIN 291-2G3-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	218	Total	C	N	O	S	0	3	0
			1704	1065	286	346	7			
1	L	218	Total	C	N	O	S	0	1	0
			1696	1061	282	346	7			

- Molecule 2 is a protein called IGG FAB (IGG3, KAPPA) HEAVY CHAIN 291-2G3-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	212	Total	C	N	O	S	0	2	0
			1619	1029	268	315	7			
2	H	212	Total	C	N	O	S	0	3	0
			1622	1031	268	316	7			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	3	Total	C	N	O	0	0	0
			37	21	1	15			
3	D	3	Total	C	N	O	0	0	0
			37	21	1	15			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	65	Total	O	0	0
			65	65		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	96	Total 96	O 96	0	0
4	H	92	Total 92	O 92	0	0
4	L	34	Total 34	O 34	0	0

3 Residue-property plots


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.

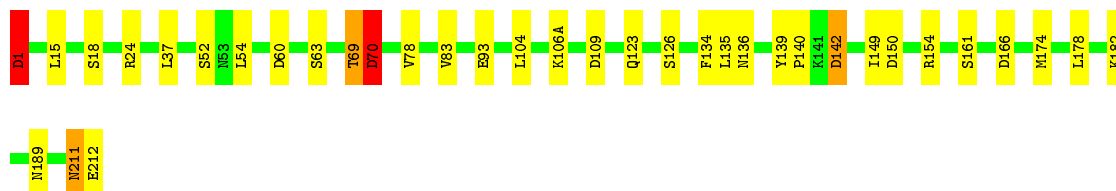
- Molecule 1: IGG FAB (IGG3, KAPPA) LIGHT CHAIN 291-2G3-A

Chain A: 




- Molecule 1: IGG FAB (IGG3, KAPPA) LIGHT CHAIN 291-2G3-A

Chain L: 




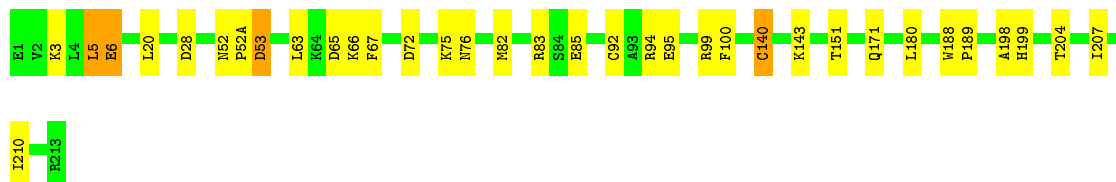
- Molecule 2: IGG FAB (IGG3, KAPPA) HEAVY CHAIN 291-2G3-A

Chain B: 



- Molecule 2: IGG FAB (IGG3, KAPPA) HEAVY CHAIN 291-2G3-A

Chain H: 



- Molecule 3: alpha-L-fucopyranose-(1-3)-[beta-D-galactopyranose-(1-4)]methyl 2-acetamido-2-deoxy-beta-D-glucopyranoside

Chain C: 



- Molecule 3: alpha-L-fucopyranose-(1-3)-[beta-D-galactopyranose-(1-4)]methyl 2-acetamido-2-deoxy-beta-D-glucopyranoside

Chain D:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	45.10Å 60.78Å 91.56Å 95.98° 95.41° 101.71°	Depositor
Resolution (Å)	91.29 – 1.80 45.21 – 1.80	Depositor EDS
% Data completeness (in resolution range)	92.9 (91.29-1.80) 92.9 (45.21-1.80)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.85 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.2.0000	Depositor
R, R_{free}	0.210 , 0.247 0.264 , 0.290	Depositor DCC
R_{free} test set	4064 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	28.2	Xtriage
Anisotropy	0.273	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 51.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7002	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.22% 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: GAL, FUC, MAG

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	0.29	0/1759	0.69	5/2387 (0.2%)
1	L	0.28	0/1739	0.68	6/2362 (0.3%)
2	B	0.36	0/1667	0.75	5/2269 (0.2%)
2	H	0.35	0/1674	0.74	6/2279 (0.3%)
All	All	0.32	0/6839	0.71	22/9297 (0.2%)

There are no bond length outliers.

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	150	ASP	CB-CG-OD2	6.44	124.10	118.30
2	B	65	ASP	CB-CG-OD2	5.96	123.66	118.30
1	L	142	ASP	CB-CG-OD2	5.73	123.46	118.30
2	H	28	ASP	CB-CG-OD2	5.68	123.42	118.30
1	L	70	ASP	CB-CG-OD2	5.67	123.40	118.30

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	1704	0	1636	10	0
1	L	1696	0	1630	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1619	0	1596	16	0
2	H	1622	0	1599	24	0
3	C	37	0	35	0	0
3	D	37	0	35	1	0
4	A	65	0	0	0	0
4	B	96	0	0	1	0
4	H	92	0	0	1	0
4	L	34	0	0	1	0
All	All	7002	0	6531	66	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.

The worst 5 of 66 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:L:189:ASN:HD21	1:L:211:ASN:HB3	1.48	0.78
2:H:94:ARG:HD2	2:H:100:PHE:O	1.83	0.78
2:H:20:LEU:HG	2:H:82:MET:CE	2.13	0.77
2:H:20:LEU:HG	2:H:82:MET:HE2	1.68	0.73
2:B:20:LEU:HD11	2:B:82:MET:CE	2.21	0.71

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	219/218 (100%)	213 (97%)	6 (3%)	0	100	100
1	L	217/218 (100%)	212 (98%)	5 (2%)	0	100	100
2	B	210/212 (99%)	207 (99%)	3 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	H	211/212 (100%)	207 (98%)	3 (1%)	1 (0%)	29	15
All	All	857/860 (100%)	839 (98%)	17 (2%)	1 (0%)	51	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	95	GLU

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	196/193 (102%)	183 (93%)	13 (7%)	16	5
1	L	194/193 (100%)	181 (93%)	13 (7%)	16	5
2	B	183/181 (101%)	180 (98%)	3 (2%)	62	54
2	H	184/181 (102%)	174 (95%)	10 (5%)	22	9
All	All	757/748 (101%)	718 (95%)	39 (5%)	24	10

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	6	GLU
2	H	92	CYS
1	L	142	ASP
2	H	63	LEU
2	H	83	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	189	ASN
2	B	191	GLN
1	L	155	GLN

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Mol	Chain	Res	Type
1	A	160	ASN
1	L	136	ASN

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 ⓘ

6 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	MAG	C	1	3	16,16,16	0.47	0	22,22,22	1.17	1 (4%)
3	FUC	C	2	3	10,10,11	0.64	0	14,14,16	1.00	0
3	GAL	C	3	3	11,11,12	0.74	0	15,15,17	0.92	0
3	MAG	D	1	3	16,16,16	0.48	0	22,22,22	1.42	2 (9%)
3	FUC	D	2	3	10,10,11	0.64	0	14,14,16	0.71	0
3	GAL	D	3	3	11,11,12	0.76	0	15,15,17	0.89	0

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	MAG	C	1	3	-	0/8/28/28	0/1/1/1
3	FUC	C	2	3	-	-	0/1/1/1
3	GAL	C	3	3	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MAG	D	1	3	-	2/8/28/28	0/1/1/1
3	FUC	D	2	3	-	-	0/1/1/1
3	GAL	D	3	3	-	0/2/19/22	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(°)
3	D	1	MAG	CM-O1-C1	4.46	120.16	113.27
3	C	1	MAG	CM-O1-C1	3.74	119.05	113.27
3	D	1	MAG	O5-C5-C4	-2.40	105.34	109.69

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	1	MAG	O5-C5-C6-O6
3	D	1	MAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	1	MAG	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	H	1
2	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	127:GLY	C	133:GLY	N	12.07
1	H	127:GLY	C	133:GLY	N	10.79

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.