



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 5, 2018 – 11:02 PM EST

PDB ID : 1OP3
Title : Crystal Structure of Fab 2G12 bound to Man1->2Man
Authors : Calarese, D.A.; Scanlan, C.N.; Zwick, M.B.; Deechongkit, S.; Mimura, Y.;
Kunert, R.; Stanfield, R.L.; Kelly, J.W.; Rudd, P.M.; Dwek, R.A.; Katinger,
H.; Burton, D.R.; Wilson, I.A.
Deposited on : 2003-03-04
Resolution : 1.75 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

<http://wwpdb.org/validation/2016/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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20030736

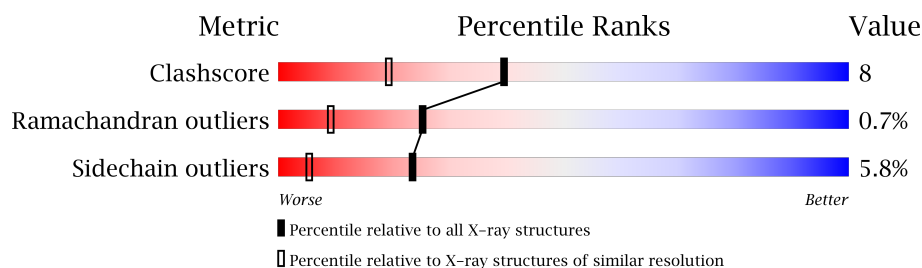
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	112137	1889 (1.76-1.76)
Ramachandran outliers	110173	1868 (1.76-1.76)
Sidechain outliers	110143	1868 (1.76-1.76)

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. 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	K	212	
1	L	212	
2	H	225	
2	M	225	

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
4	MAN	M	503	X	-	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7114 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.

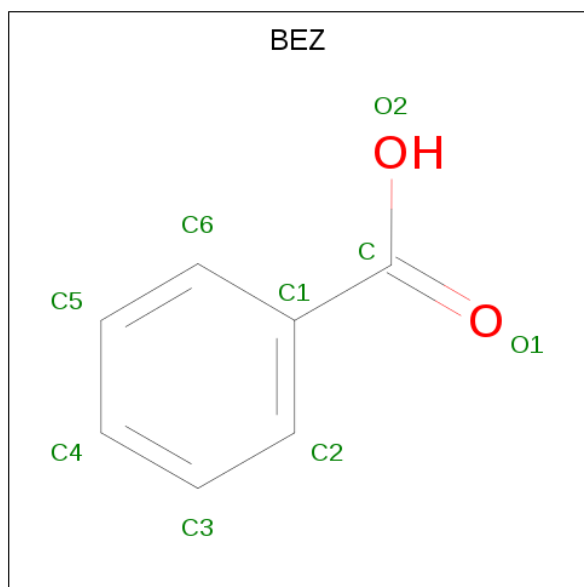
- Molecule 1 is a protein called FAB 2G12, light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	211	Total	C	N	O	S	0	0	0
			1618	1018	272	323	5			
1	K	211	Total	C	N	O	S	0	0	0
			1618	1018	272	323	5			

- Molecule 2 is a protein called FAB 2G12, heavy chain.

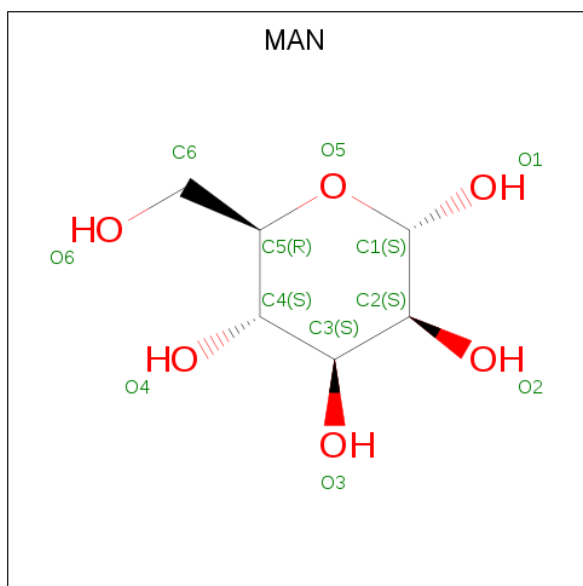
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	224	Total	C	N	O	S	38	0	0
			1675	1053	286	329	7			
2	M	224	Total	C	N	O	S	51	0	0
			1675	1053	286	329	7			

- Molecule 3 is BENZOIC ACID (three-letter code: BEZ) (formula: C₇H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	L	1	Total	C	O	0	0
			9	7	2		

- Molecule 4 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	H	1	Total	C	O	0	0
			12	6	6		
4	H	1	Total	C	O	0	0
			11	6	5		
4	M	1	Total	C	O	0	0
			12	6	6		

- Molecule 5 is water.

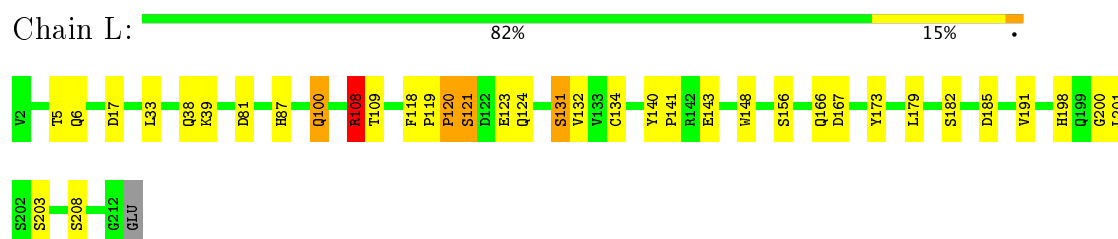
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	L	108	Total	O	0	0
			108	108		
5	H	113	Total	O	0	0
			113	113		
5	K	157	Total	O	0	0
			157	157		
5	M	106	Total	O	0	0
			106	106		

3 Residue-property plots

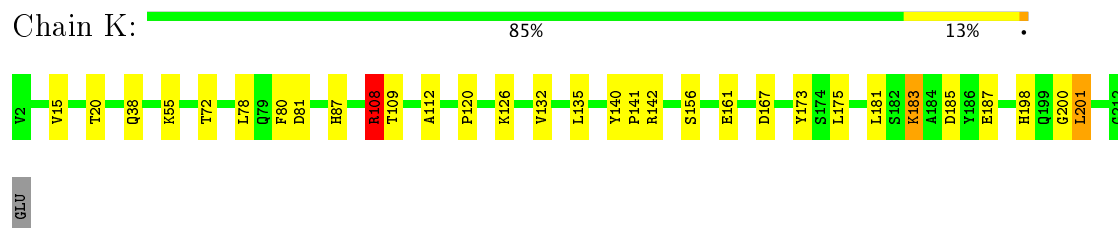
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

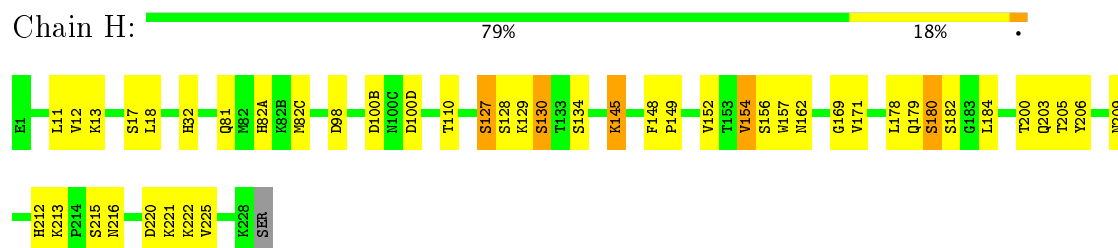
- Molecule 1: FAB 2G12, light chain



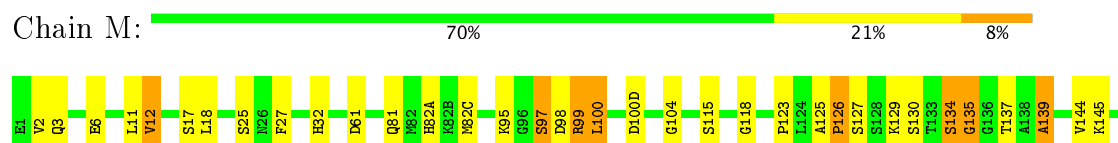
- Molecule 1: FAB 2G12, light chain



- Molecule 2: FAB 2G12, heavy chain



- Molecule 2: FAB 2G12, heavy chain



PL49	VI52	TI53	VI54	S156	HI57	NI62	L166	G169	VI71	LI78	Q179	S180	S182	G183	L184	L187	V191	T192	VI93	T200	Q203	T205	Y206	T207	C208	N209	Y210	N211	H212	S215	D220	K221	K222	Y225	K228	SER
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4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	81.72Å 94.03Å 169.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.75	Depositor
% Data completeness (in resolution range)	95.7 (50.00-1.75)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.230 , 0.251	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7114	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BEZ, 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	K	0.53	1/1654 (0.1%)	0.85	4/2246 (0.2%)
1	L	0.97	6/1654 (0.4%)	0.80	6/2246 (0.3%)
2	H	0.96	4/1708 (0.2%)	0.84	5/2316 (0.2%)
2	M	1.37	11/1709 (0.6%)	1.00	13/2319 (0.6%)
All	All	1.00	22/6725 (0.3%)	0.88	28/9127 (0.3%)

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	H	0	4
2	M	0	3
All	All	0	7

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	M	125	ALA	C-N	-29.64	0.78	1.34
2	M	180	SER	C-N	27.89	1.98	1.34
1	L	121	SER	CB-OG	24.66	1.74	1.42
2	H	180	SER	C-N	23.28	1.87	1.34
2	M	154	VAL	C-N	22.67	1.86	1.34

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M	125	ALA	O-C-N	-14.18	94.16	121.10
1	K	108	ARG	NE-CZ-NH2	-13.51	113.55	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	108	ARG	NE-CZ-NH1	12.05	126.32	120.30
1	L	108	ARG	NE-CZ-NH2	-11.99	114.31	120.30
2	M	135	GLY	C-N-CA	11.22	145.86	122.30

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	127	SER	Mainchain,Peptide
2	H	129	LYS	Peptide
2	H	130	SER	Peptide
2	M	129	LYS	Peptide
2	M	130	SER	Peptide

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	K	1618	0	1580	20	0
1	L	1618	0	1580	24	0
2	H	1675	0	1639	27	0
2	M	1675	0	1640	43	0
3	L	9	0	5	0	0
4	H	23	0	21	0	0
4	M	12	0	12	0	0
5	H	113	0	0	1	0
5	K	157	0	0	2	0
5	L	108	0	0	0	0
5	M	106	0	0	1	0
All	All	7114	0	6477	109	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 8.

The worst 5 of 109 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:H:154:VAL:C	2:H:156:SER:N	1.72	1.43
1:L:121:SER:OG	1:L:121:SER:CB	1.74	1.33
2:M:154:VAL:C	2:M:156:SER:N	1.86	1.27
2:H:180:SER:C	2:H:182:SER:N	1.87	1.26
2:M:180:SER:C	2:M:182:SER:N	1.98	1.16

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	K	209/212 (99%)	202 (97%)	7 (3%)	0	100	100
1	L	209/212 (99%)	199 (95%)	10 (5%)	0	100	100
2	H	211/225 (94%)	205 (97%)	4 (2%)	2 (1%)	20	5
2	M	213/225 (95%)	199 (93%)	10 (5%)	4 (2%)	9	1
All	All	842/874 (96%)	805 (96%)	31 (4%)	6 (1%)	25	9

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	134	SER
2	M	134	SER
2	M	127	SER
2	M	100	LEU
2	H	130	SER

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	K	182/183 (100%)	174 (96%)	8 (4%)	33	10
1	L	182/183 (100%)	172 (94%)	10 (6%)	25	6
2	H	189/190 (100%)	179 (95%)	10 (5%)	26	6
2	M	189/190 (100%)	174 (92%)	15 (8%)	14	2
All	All	742/746 (100%)	699 (94%)	43 (6%)	23	5

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	221	LYS
1	K	156	SER
2	M	200	THR
1	K	78	LEU
1	K	108	ARG

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

Mol	Chain	Res	Type
1	K	87	HIS
1	K	89	GLN
2	M	81	GLN
2	H	82(A)	HIS
2	H	212	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

4 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$
4	MAN	H	501	4	12,12,12	0.53	0	17,17,17	0.88	0
4	MAN	H	502	4	11,11,12	0.39	0	13,15,17	1.04	1 (7%)
3	BEZ	L	504	-	6,9,9	2.17	2 (33%)	8,11,11	0.96	0
4	MAN	M	503	-	12,12,12	0.59	0	17,17,17	1.36	4 (23%)

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
4	MAN	H	501	4	-	0/2/22/22	0/1/1/1
4	MAN	H	502	4	-	0/2/19/22	0/1/1/1
3	BEZ	L	504	-	-	0/0/4/4	0/1/1/1
4	MAN	M	503	-	1/1/5/5	0/2/22/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	504	BEZ	C2-C1	2.50	1.44	1.39
3	L	504	BEZ	C3-C2	3.07	1.44	1.38

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	M	503	MAN	C1-O5-C5	-3.48	107.11	113.39
4	M	503	MAN	C1-C2-C3	-2.00	107.04	110.65
4	M	503	MAN	O4-C4-C5	2.12	114.63	109.28
4	M	503	MAN	O5-C5-C6	2.38	112.10	106.41
4	H	502	MAN	C1-O5-C5	2.72	115.92	112.17

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	M	503	MAN	C1

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	H	9
2	M	9

The worst 5 of 18 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	M	203:GLN	C	205:THR	N	3.67
1	H	203:GLN	C	205:THR	N	3.28
1	M	200:THR	C	203:GLN	N	3.27
1	M	222:LYS	C	225:VAL	N	3.05
1	H	200:THR	C	203:GLN	N	2.93

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.