wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 08:54 AM GMT

PDB ID	:	3GGW
Title	:	Crystal Structure of FAB F22-4 in complex with a Carbohydrate-mimetic peptide
Authors	:	Saul, F.A.; Vulliez-Le Normand, B.; Bentley, G.A.
Deposited on	:	2009-03-02
Resolution	:	1.70 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

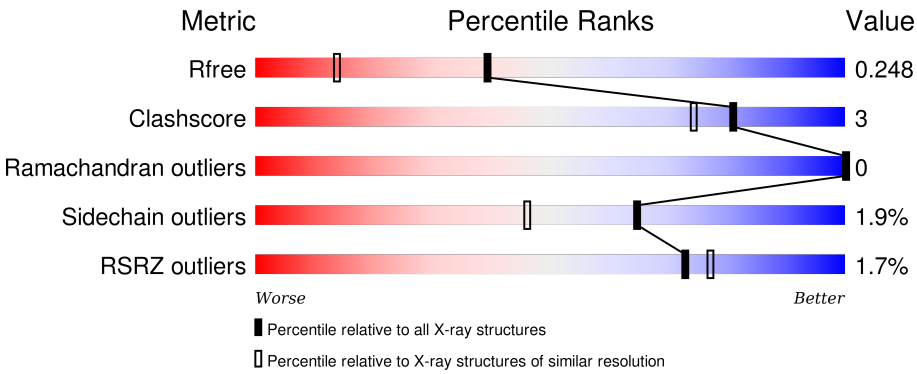
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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}	91344	3190 (1.70-1.70)
Clashscore	102246	3585 (1.70-1.70)
Ramachandran outliers	100387	3527 (1.70-1.70)
Sidechain outliers	100360	3527 (1.70-1.70)
RSRZ outliers	91569	3200 (1.70-1.70)

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 <=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.

Mol	Chain	Length	Quality of chain
1	A	219	2%, 92%, 7%
1	C	219	95%, 5%
2	B	217	4%, 86%, 9%, 5%
2	D	217	83%, 13%, •
3	E	12	8%, 92%, 8%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	F	12	8% 83% 17%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7619 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 F22-4 LIGHT CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	218	1701	1063	289	341	8	0	3	0
1	C	219	1702	1063	289	341	9	0	2	0

- Molecule 2 is a protein called FAB F22-4 HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	207	1601	1022	256	312	11	0	3	0
2	D	209	1606	1023	260	312	11	0	2	0

- Molecule 3 is a protein called PEPTIDE B1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	E	11	105	69	16	20	0	0	0
3	F	12	115	75	18	22	0	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	196	196	196	0	0
4	B	206	206	206	0	0
4	C	215	215	215	0	0
4	D	149	149	149	0	0

Continued on next page...

Continued from previous page...

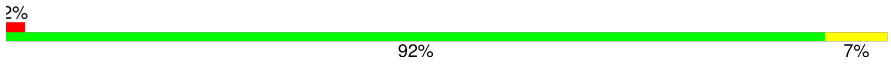
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	E	11	11	11	0	0
			Total	O		
4	F	12	12	12	0	0

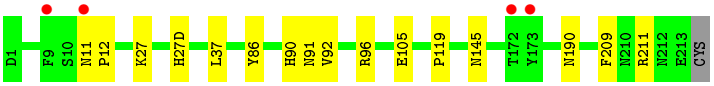
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

- Molecule 1: FAB F22-4 LIGHT CHAIN

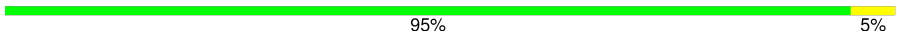
Chain A:

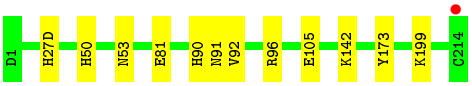




- Molecule 1: FAB F22-4 LIGHT CHAIN

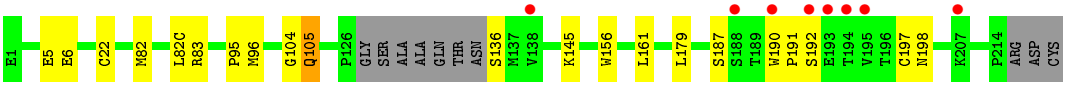
Chain C:





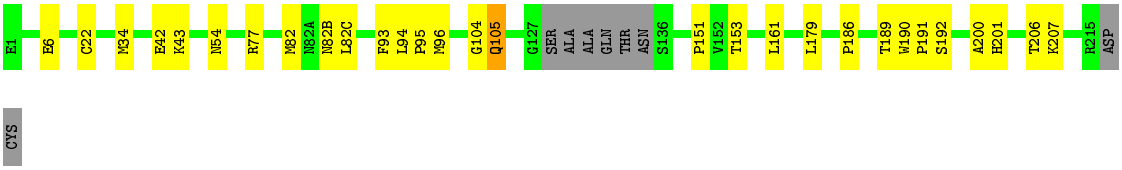
- Molecule 2: FAB F22-4 HEAVY CHAIN

Chain B:



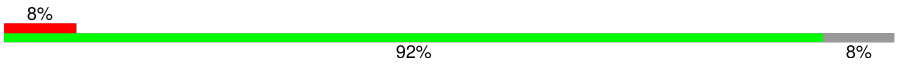
- Molecule 2: FAB F22-4 HEAVY CHAIN

Chain D:



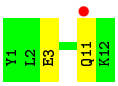
- Molecule 3: PEPTIDE B1

Chain E:



- Molecule 3: PEPTIDE B1

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	66.88Å 69.53Å 110.19Å 90.00° 97.71° 90.00°	Depositor
Resolution (Å)	47.97 – 1.70 47.97 – 1.69	Depositor EDS
% Data completeness (in resolution range)	97.6 (47.97-1.70) 97.6 (47.97-1.69)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	1.77 (at 1.69Å)	Xtriage
Refinement program	REFMAC 5.2.0003	Depositor
R, R_{free}	0.197 , 0.245 0.202 , 0.248	Depositor DCC
R_{free} test set	2146 reflections (2.04%)	DCC
Wilson B-factor (Å^2)	21.3	Xtriage
Anisotropy	0.294	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 48.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	0 of 109436 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7619	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.45% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

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	0.66	0/1749	0.74	0/2376
1	C	0.71	0/1747	0.80	0/2373
2	B	0.80	1/1652 (0.1%)	0.83	2/2253 (0.1%)
2	D	0.68	0/1654	0.78	0/2256
3	E	0.58	0/108	0.65	0/146
3	F	0.55	0/118	0.64	0/157
All	All	0.71	1/7028 (0.0%)	0.78	2/9561 (0.0%)

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	B	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	B	22	CYS	CB-SG	-5.74	1.72	1.81

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	83	ARG	NE-CZ-NH1	6.70	123.65	120.30
2	B	83	ARG	NE-CZ-NH2	-6.63	116.99	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	192	SER	Peptide
2	D	192	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	A	1701	0	1642	12	0
1	C	1702	0	1641	7	0
2	B	1601	0	1579	10	0
2	D	1606	0	1578	15	0
3	E	105	0	95	0	0
3	F	115	0	108	1	0
4	A	196	0	0	3	1
4	B	206	0	0	1	1
4	C	215	0	0	2	1
4	D	149	0	0	1	0
4	E	11	0	0	0	0
4	F	12	0	0	1	0
All	All	7619	0	6643	45	2

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 3.

The worst 5 of 45 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:34:MET:SD	2:D:94:LEU:HG	2.20	0.81
2:B:145:LYS:NZ	4:B:422:HOH:O	2.16	0.72
1:A:190:ASN:HD21	1:A:211:ARG:HH21	1.39	0.70
1:C:105:GLU:OE1	4:C:428:HOH:O	2.11	0.69
1:A:27(D):HIS:HD2	4:A:379:HOH:O	1.84	0.61

All (2) 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)
4:C:311:HOH:O	4:C:421:HOH:O[2_645]	1.84	0.36
4:A:255:HOH:O	4:B:391:HOH:O[2_656]	2.15	0.05

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	219/219 (100%)	215 (98%)	4 (2%)	0	100	100
1	C	219/219 (100%)	216 (99%)	3 (1%)	0	100	100
2	B	206/217 (95%)	204 (99%)	2 (1%)	0	100	100
2	D	207/217 (95%)	205 (99%)	2 (1%)	0	100	100
3	E	9/12 (75%)	9 (100%)	0	0	100	100
3	F	10/12 (83%)	10 (100%)	0	0	100	100
All	All	870/896 (97%)	859 (99%)	11 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	196/194 (101%)	195 (100%)	1 (0%)	92	88
1	C	196/194 (101%)	195 (100%)	1 (0%)	92	88
2	B	187/191 (98%)	184 (98%)	3 (2%)	70	54

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	D	186/191 (97%)	177 (95%)	9 (5%)	31 12
3	E	11/12 (92%)	11 (100%)	0	100 100
3	F	12/12 (100%)	11 (92%)	1 (8%)	14 3
All	All	788/794 (99%)	773 (98%)	15 (2%)	65 46

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	54	ASN
2	D	77	ARG
2	D	179	LEU
2	D	43	LYS
2	D	161	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	31	ASN
2	B	82(B)	ASN
1	C	91	ASN
1	A	190	ASN
1	C	90	HIS

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 carbohydrates 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)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	218/219 (99%)	0.13	4 (1%)	71	76	17, 27, 38, 42	0
1	C	219/219 (100%)	0.03	1 (0%)	91	93	15, 23, 33, 52	0
2	B	207/217 (95%)	0.13	8 (3%)	43	47	14, 21, 43, 51	0
2	D	209/217 (96%)	-0.08	0	100	100	16, 26, 37, 42	0
3	E	11/12 (91%)	0.09	1 (9%)	11	13	21, 25, 45, 48	0
3	F	12/12 (100%)	0.44	1 (8%)	14	16	29, 36, 45, 47	0
All	All	876/896 (97%)	0.06	15 (1%)	73	77	14, 24, 39, 52	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	214	CYS	5.2
2	B	194	THR	4.1
2	B	193	GLU	4.1
1	A	11	ASN	3.4
3	E	11	GLN	3.1

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.