wwPDB X-ray Structure Validation Summary Report (i)

Jan 31, 2016 – 07:30 PM GMT

PDB ID	:	1FSK
Title	:	COMPLEX FORMATION BETWEEN A FAB FRAGMENT OF A MONOCLONAL IGG ANTIBODY AND THE MAJOR ALLERGEN FROM BIRCH POLLEN BET V 1
Authors	:	Mirza, O.; Henriksen, A.; Ipsen, H.; Larsen, J.; Wissenbach, M.; Spangfort, M.; Gajhede, M.
Deposited on	:	2000-09-11
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
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:

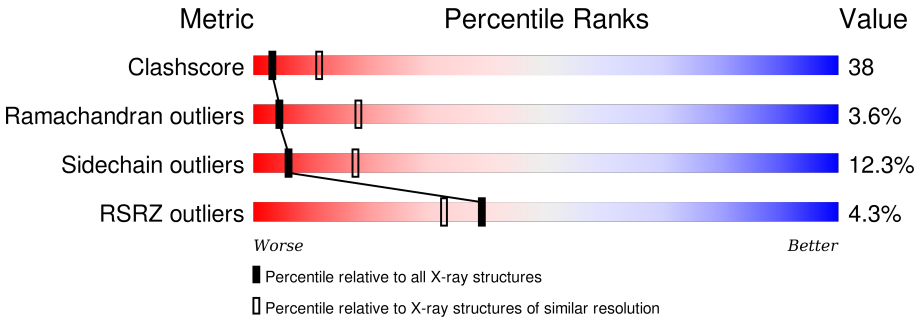
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 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	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (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 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	159	47% 46% 7%
1	D	159	48% 45% 7%
1	G	159	4% 47% 47% 7%
1	J	159	12% 48% 45% 8%
2	B	214	3% 37% 54% 9%
2	E	214	40% 51% 9%
2	H	214	11% 38% 52% 10%

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Mol	Chain	Length	Quality of chain
2	K	214	3% 38% 52% 10%
3	C	220	4% 45% 46% 9%
3	F	220	3% 43% 48% 9%
3	I	220	4% 42% 49% 9%
3	L	220	4% 43% 48% 9%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 18308 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 MAJOR POLLEN ALLERGEN BET V 1-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	159	Total	C	N	O	S	0	0	0
			1230	783	202	244	1			
1	D	159	Total	C	N	O	S	0	0	0
			1230	783	202	244	1			
1	G	159	Total	C	N	O	S	0	0	0
			1230	783	202	244	1			
1	J	159	Total	C	N	O	S	0	0	0
			1230	783	202	244	1			

- Molecule 2 is a protein called IMMUNOGLOBULIN KAPPA LIGHT CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	214	Total	C	N	O	S	0	0	0
			1668	1040	277	344	7			
2	E	214	Total	C	N	O	S	0	0	0
			1668	1040	277	344	7			
2	H	214	Total	C	N	O	S	0	0	0
			1668	1040	277	344	7			
2	K	214	Total	C	N	O	S	0	0	0
			1668	1040	277	344	7			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	4	LEU	MET	CONFLICT	UNP P01837
B	13	VAL	MET	CONFLICT	UNP P01837
B	22	SER	THR	CONFLICT	UNP P01837
B	30	ASP	VAL	CONFLICT	UNP P01837
B	34	PHE	SER	CONFLICT	UNP P01837
B	36	PHE	TYR	CONFLICT	UNP P01837
B	41	ASP	GLU	CONFLICT	UNP P01837
B	48	LEU	ILE	CONFLICT	UNP P01837

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Chain	Residue	Modelled	Actual	Comment	Reference
B	51	PRO	ALA	CONFLICT	UNP P01837
B	68	THR	ALA	CONFLICT	UNP P01837
B	91	SER	GLY	CONFLICT	UNP P01837
B	149	LYS	ASN	CONFLICT	UNP P01837
E	4	LEU	MET	CONFLICT	UNP P01837
E	13	VAL	MET	CONFLICT	UNP P01837
E	22	SER	THR	CONFLICT	UNP P01837
E	30	ASP	VAL	CONFLICT	UNP P01837
E	34	PHE	SER	CONFLICT	UNP P01837
E	36	PHE	TYR	CONFLICT	UNP P01837
E	41	ASP	GLU	CONFLICT	UNP P01837
E	48	LEU	ILE	CONFLICT	UNP P01837
E	51	PRO	ALA	CONFLICT	UNP P01837
E	68	THR	ALA	CONFLICT	UNP P01837
E	91	SER	GLY	CONFLICT	UNP P01837
E	149	LYS	ASN	CONFLICT	UNP P01837
H	4	LEU	MET	CONFLICT	UNP P01837
H	13	VAL	MET	CONFLICT	UNP P01837
H	22	SER	THR	CONFLICT	UNP P01837
H	30	ASP	VAL	CONFLICT	UNP P01837
H	34	PHE	SER	CONFLICT	UNP P01837
H	36	PHE	TYR	CONFLICT	UNP P01837
H	41	ASP	GLU	CONFLICT	UNP P01837
H	48	LEU	ILE	CONFLICT	UNP P01837
H	51	PRO	ALA	CONFLICT	UNP P01837
H	68	THR	ALA	CONFLICT	UNP P01837
H	91	SER	GLY	CONFLICT	UNP P01837
H	149	LYS	ASN	CONFLICT	UNP P01837
K	4	LEU	MET	CONFLICT	UNP P01837
K	13	VAL	MET	CONFLICT	UNP P01837
K	22	SER	THR	CONFLICT	UNP P01837
K	30	ASP	VAL	CONFLICT	UNP P01837
K	34	PHE	SER	CONFLICT	UNP P01837
K	36	PHE	TYR	CONFLICT	UNP P01837
K	41	ASP	GLU	CONFLICT	UNP P01837
K	48	LEU	ILE	CONFLICT	UNP P01837
K	51	PRO	ALA	CONFLICT	UNP P01837
K	68	THR	ALA	CONFLICT	UNP P01837
K	91	SER	GLY	CONFLICT	UNP P01837
K	149	LYS	ASN	CONFLICT	UNP P01837

- Molecule 3 is a protein called ANTIBODY HEAVY CHAIN FAB.

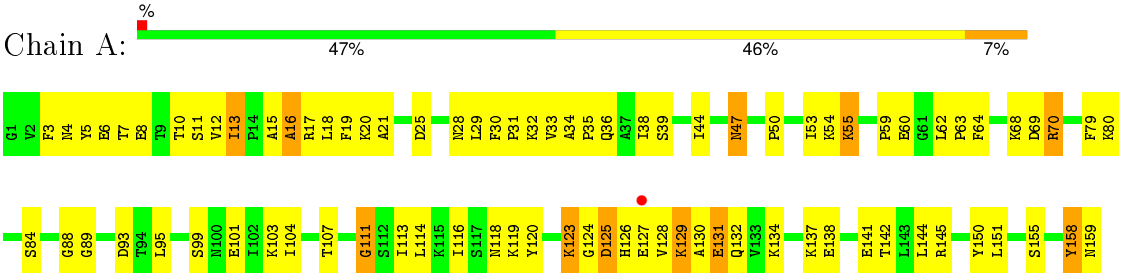
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	220	Total	C	N	O	S	0	0	0
			1679	1066	276	330	7			
3	F	220	Total	C	N	O	S	0	0	0
			1679	1066	276	330	7			
3	I	220	Total	C	N	O	S	0	0	0
			1679	1066	276	330	7			
3	L	220	Total	C	N	O	S	0	0	0
			1679	1066	276	330	7			

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.

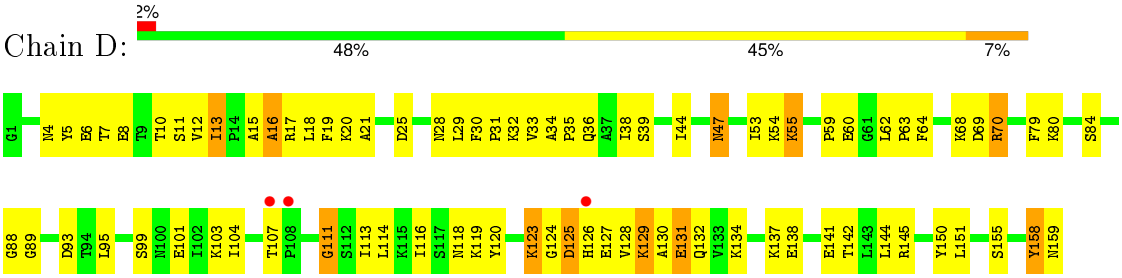
- Molecule 1: MAJOR POLLEN ALLERGEN BET V 1-A

Chain A:



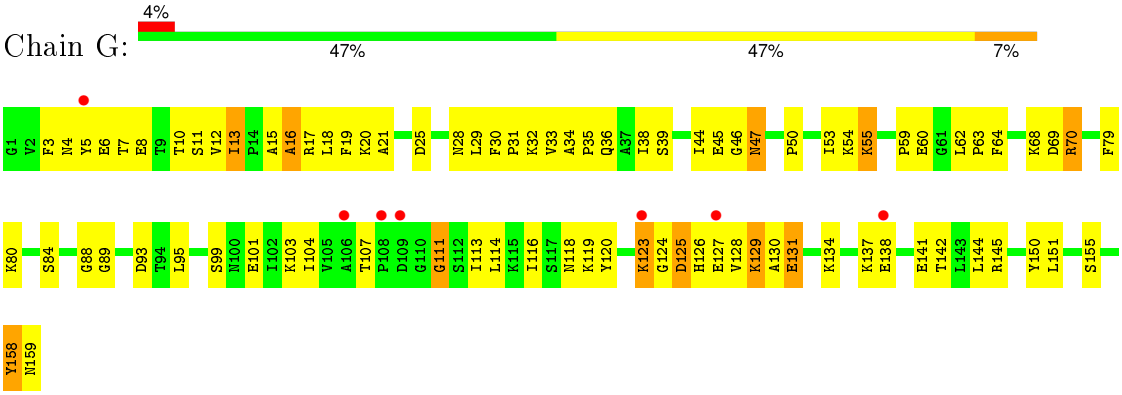
- Molecule 1: MAJOR POLLEN ALLERGEN BET V 1-A

Chain D:



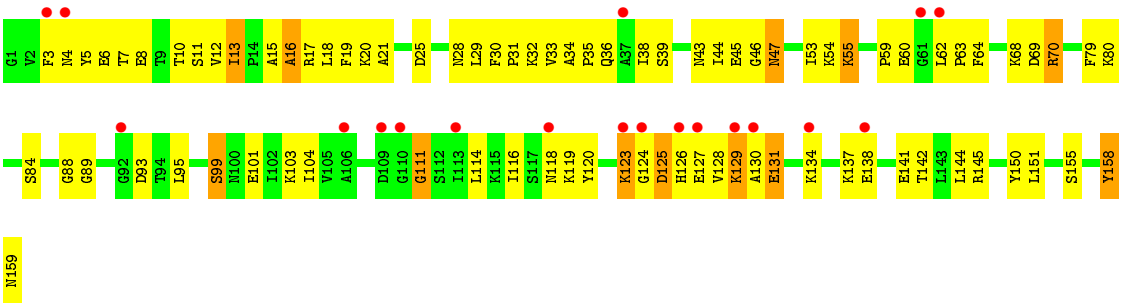
- Molecule 1: MAJOR POLLEN ALLERGEN BET V 1-A

Chain G:



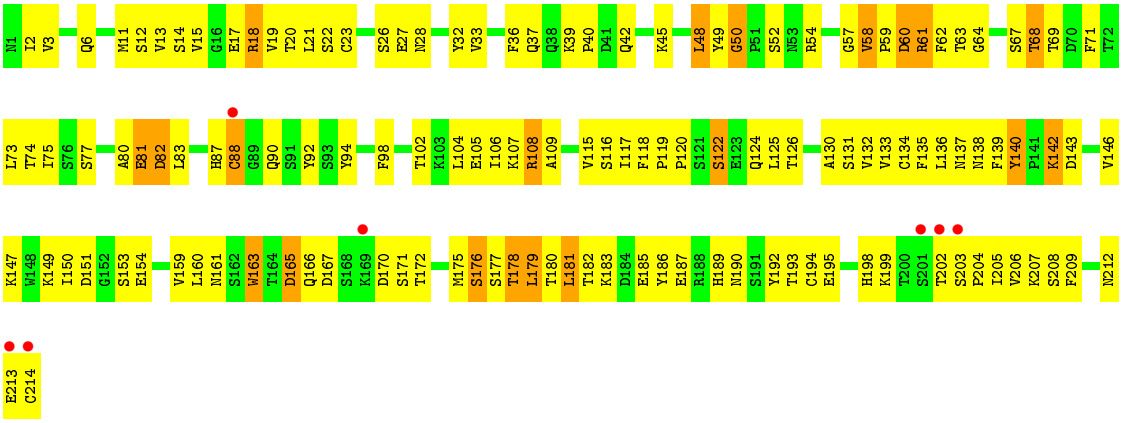
- Molecule 1: MAJOR POLLEN ALLERGEN BET V 1-A

Chain J:



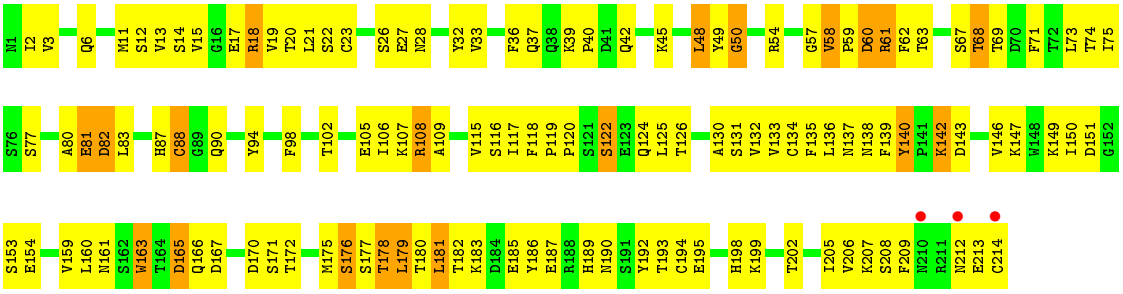
• Molecule 2: IMMUNOGLOBULIN KAPPA LIGHT CHAIN

Chain B:



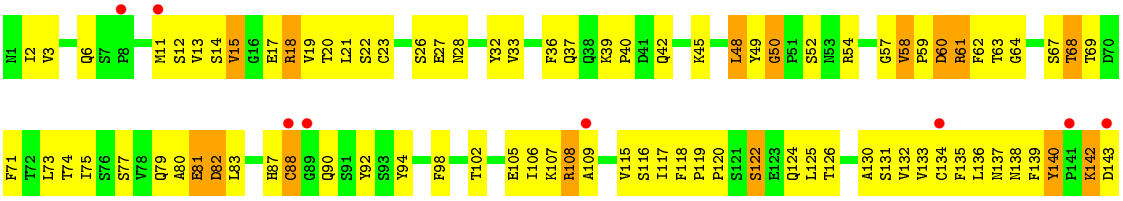
• Molecule 2: IMMUNOGLOBULIN KAPPA LIGHT CHAIN

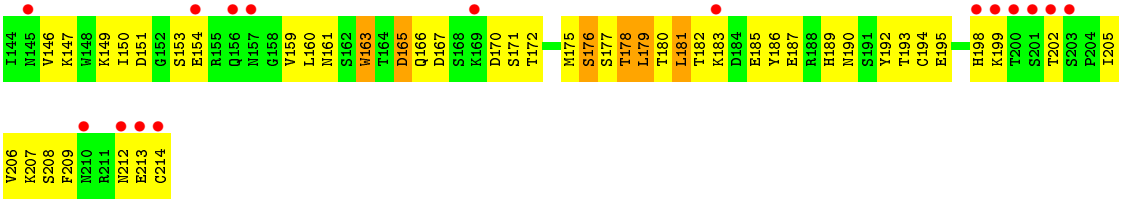
Chain E:



• Molecule 2: IMMUNOGLOBULIN KAPPA LIGHT CHAIN

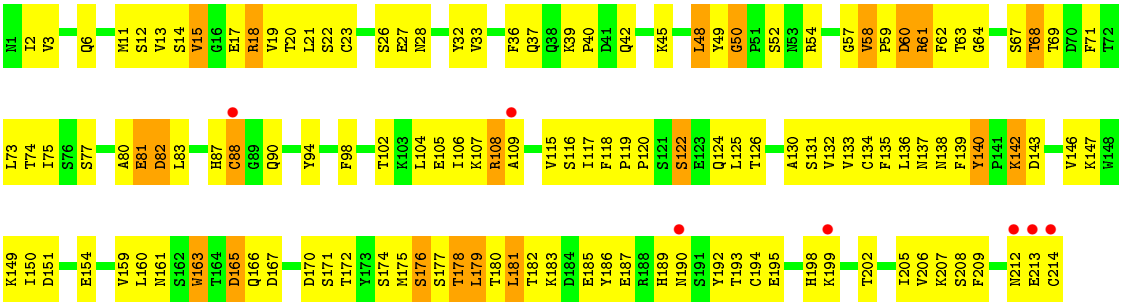
Chain H:





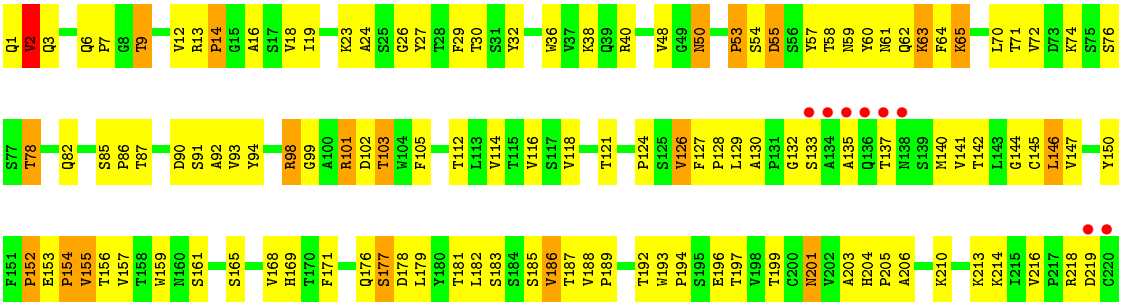
• Molecule 2: IMMUNOGLOBULIN KAPPA LIGHT CHAIN

Chain K:



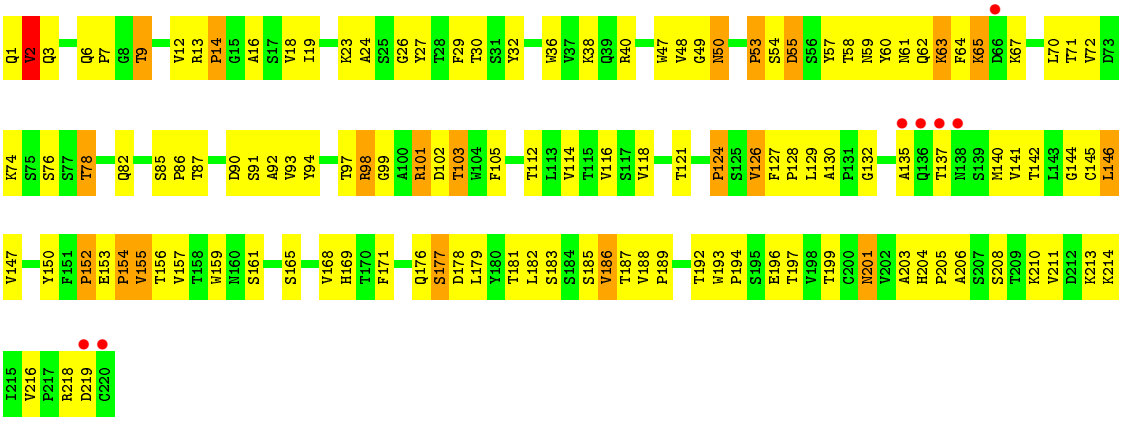
• Molecule 3: ANTIBODY HEAVY CHAIN FAB

Chain C:



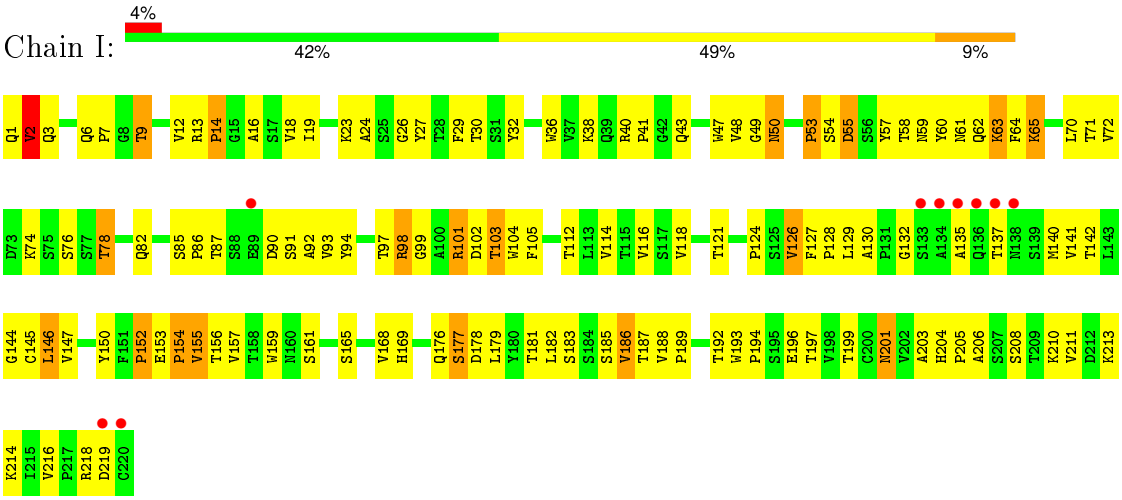
• Molecule 3: ANTIBODY HEAVY CHAIN FAB

Chain F:



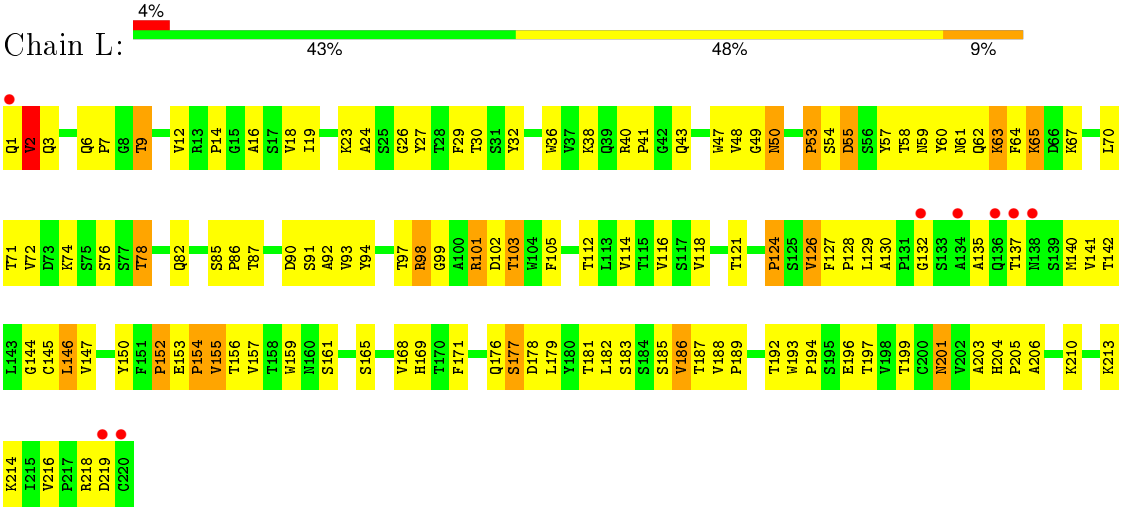
• Molecule 3: ANTIBODY HEAVY CHAIN FAB

Chain I:



• Molecule 3: ANTIBODY HEAVY CHAIN FAB

Chain L:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	91.65Å 99.14Å 108.91Å 105.70° 98.32° 97.62°	Depositor
Resolution (Å)	20.00 – 2.90 20.03 – 2.89	Depositor EDS
% Data completeness (in resolution range)	92.4 (20.00-2.90) 76.3 (20.03-2.89)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.06 (at 2.88Å)	Xtriage
Refinement program	CNS 0.5	Depositor
R, R_{free}	0.253 , 0.285 0.267 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å^2)	54.0	Xtriage
Anisotropy	0.289	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 77.4	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 69230 reflections	Xtriage
F_o,F_c correlation	0.88	EDS
Total number of atoms	18308	wwPDB-VP
Average B, all atoms (Å^2)	63.0	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 31.24 % 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 1.1444e-03.The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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

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	0.51	0/1255	0.71	0/1696
1	D	0.51	0/1255	0.71	0/1696
1	G	0.51	0/1255	0.71	0/1696
1	J	0.51	0/1255	0.71	0/1696
2	B	0.51	0/1707	0.78	1/2319 (0.0%)
2	E	0.51	0/1707	0.78	1/2319 (0.0%)
2	H	0.51	0/1707	0.78	1/2319 (0.0%)
2	K	0.52	0/1707	0.78	1/2319 (0.0%)
3	C	0.54	0/1727	0.77	1/2368 (0.0%)
3	F	0.54	0/1727	0.77	1/2368 (0.0%)
3	I	0.54	0/1727	0.77	1/2368 (0.0%)
3	L	0.54	0/1727	0.77	1/2368 (0.0%)
All	All	0.52	0/18756	0.76	8/25532 (0.0%)

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	K	94	TYR	N-CA-C	-6.08	94.59	111.00
2	E	94	TYR	N-CA-C	-5.92	95.02	111.00
2	H	94	TYR	N-CA-C	-5.85	95.20	111.00
2	B	94	TYR	N-CA-C	-5.84	95.23	111.00
3	I	2	VAL	N-CA-C	-5.11	97.20	111.00

There are no chirality outliers.

There are no planarity outliers.

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	1230	0	1221	74	0
1	D	1230	0	1221	74	0
1	G	1230	0	1221	80	0
1	J	1230	0	1221	81	0
2	B	1668	0	1592	155	0
2	E	1668	0	1592	156	0
2	H	1668	0	1592	154	0
2	K	1668	0	1592	154	0
3	C	1679	0	1635	114	0
3	F	1679	0	1635	114	0
3	I	1679	0	1635	112	0
3	L	1679	0	1635	125	0
All	All	18308	0	17792	1344	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 38.

The worst 5 of 1344 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:49:TYR:HB2	3:C:103:THR:HG21	1.26	1.16
2:E:49:TYR:HB2	3:F:103:THR:HG21	1.28	1.09
2:K:49:TYR:HB2	3:L:103:THR:HG21	1.38	1.05
2:H:49:TYR:HB2	3:I:103:THR:HG21	1.34	1.04
2:B:49:TYR:HB2	3:C:103:THR:CG2	1.92	0.99

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	157/159 (99%)	120 (76%)	28 (18%)	9 (6%)	2	6
1	D	157/159 (99%)	120 (76%)	28 (18%)	9 (6%)	2	6
1	G	157/159 (99%)	120 (76%)	28 (18%)	9 (6%)	2	6
1	J	157/159 (99%)	120 (76%)	28 (18%)	9 (6%)	2	6
2	B	212/214 (99%)	177 (84%)	29 (14%)	6 (3%)	6	24
2	E	212/214 (99%)	177 (84%)	29 (14%)	6 (3%)	6	24
2	H	212/214 (99%)	176 (83%)	30 (14%)	6 (3%)	6	24
2	K	212/214 (99%)	176 (83%)	30 (14%)	6 (3%)	6	24
3	C	218/220 (99%)	192 (88%)	20 (9%)	6 (3%)	6	24
3	F	218/220 (99%)	192 (88%)	20 (9%)	6 (3%)	6	24
3	I	218/220 (99%)	193 (88%)	19 (9%)	6 (3%)	6	24
3	L	218/220 (99%)	192 (88%)	20 (9%)	6 (3%)	6	24
All	All	2348/2372 (99%)	1955 (83%)	309 (13%)	84 (4%)	4	18

5 of 84 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	2	VAL
3	F	2	VAL
3	I	2	VAL
3	L	2	VAL
1	A	130	ALA

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	134/134 (100%)	122 (91%)	12 (9%)	12	34
1	D	134/134 (100%)	122 (91%)	12 (9%)	12	34
1	G	134/134 (100%)	122 (91%)	12 (9%)	12	34
1	J	134/134 (100%)	121 (90%)	13 (10%)	10	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	193/193 (100%)	171 (89%)	22 (11%)	7	21
2	E	193/193 (100%)	171 (89%)	22 (11%)	7	21
2	H	193/193 (100%)	171 (89%)	22 (11%)	7	21
2	K	193/193 (100%)	171 (89%)	22 (11%)	7	21
3	C	192/192 (100%)	163 (85%)	29 (15%)	3	11
3	F	192/192 (100%)	162 (84%)	30 (16%)	3	10
3	I	192/192 (100%)	163 (85%)	29 (15%)	3	11
3	L	192/192 (100%)	162 (84%)	30 (16%)	3	10
All	All	2076/2076 (100%)	1821 (88%)	255 (12%)	6	17

5 of 255 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	146	LEU
2	H	48	LEU
3	L	82	GLN
3	F	155	VAL
1	G	47	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 67 such sidechains are listed below:

Mol	Chain	Res	Type
3	F	169	HIS
1	G	159	ASN
3	L	50	ASN
3	F	201	ASN
1	G	118	ASN

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

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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, 95^{th} 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	159/159 (100%)	-0.19	1 (0%) 90 89	22, 56, 89, 124	0
1	D	159/159 (100%)	-0.13	3 (1%) 70 66	18, 55, 93, 109	0
1	G	159/159 (100%)	0.28	7 (4%) 38 32	27, 76, 108, 128	0
1	J	159/159 (100%)	0.70	19 (11%) 6 3	27, 89, 116, 133	0
2	B	214/214 (100%)	-0.09	7 (3%) 50 42	19, 52, 92, 137	0
2	E	214/214 (100%)	-0.00	3 (1%) 78 76	19, 56, 93, 132	0
2	H	214/214 (100%)	0.78	24 (11%) 7 4	41, 86, 119, 153	0
2	K	214/214 (100%)	0.09	7 (3%) 50 42	32, 62, 91, 132	0
3	C	220/220 (100%)	-0.24	8 (3%) 46 38	18, 44, 84, 123	0
3	F	220/220 (100%)	-0.18	7 (3%) 51 43	14, 49, 86, 121	0
3	I	220/220 (100%)	0.05	9 (4%) 41 34	33, 60, 106, 134	0
3	L	220/220 (100%)	0.01	8 (3%) 46 38	25, 56, 93, 123	0
All	All	2372/2372 (100%)	0.08	103 (4%) 39 32	14, 59, 105, 153	0

The worst 5 of 103 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	214	CYS	8.6
2	H	212	ASN	7.1
2	K	214	CYS	6.1
3	F	220	CYS	5.7
3	L	220	CYS	5.6

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

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.