



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 31, 2016 – 10:03 PM EDT

PDB ID : 5AAW
Title : Structure of a redesigned cross-reactive antibody to dengue virus with increased in vivo potency
Authors : Wong, Y.; Robinson, L.; Lescar, J.; Sasisekharan, R.
Deposited on : 2015-07-30
Resolution : 3.27 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 : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027107
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) : rb-20027107

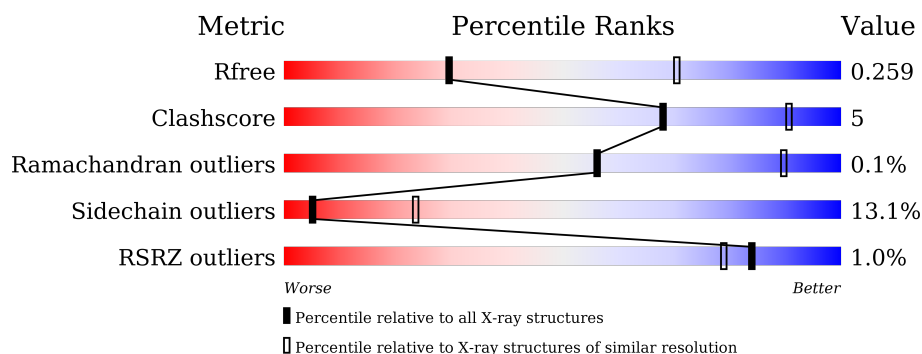
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.27 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	1756 (3.36-3.20)
Clashscore	102246	1941 (3.36-3.20)
Ramachandran outliers	100387	1905 (3.36-3.20)
Sidechain outliers	100360	1903 (3.36-3.20)
RSRZ outliers	91569	1764 (3.36-3.20)

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.

Mol	Chain	Length	Quality of chain
1	A	252	
1	B	252	
1	D	252	
1	F	252	
1	H	252	
1	K	252	

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Mol	Chain	Length	Quality of chain
2	C	115	<div><div><div></div><div></div><div></div></div><div><div>2%</div><div>62%</div><div>19%</div><div>•</div><div>17%</div></div></div>
2	E	115	<div><div><div></div><div></div><div></div></div><div><div>%</div><div>71%</div><div>12%</div><div></div><div>17%</div></div></div>
2	G	115	<div><div><div></div><div></div><div></div></div><div><div>9%</div><div>65%</div><div>15%</div><div>•</div><div>19%</div></div></div>
2	I	115	<div><div><div></div><div></div><div></div></div><div><div>%</div><div>70%</div><div>13%</div><div>•</div><div>17%</div></div></div>
2	J	115	<div><div><div></div><div></div><div></div></div><div><div></div><div>72%</div><div>10%</div><div>•</div><div>17%</div></div></div>
2	L	115	<div><div><div></div><div></div><div></div></div><div><div>%</div><div>71%</div><div>11%</div><div>•</div><div>17%</div></div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 15132 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 SCFV513.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	228	Total	C	N	O	S	0	0	0
			1779	1116	307	346	10			
1	B	229	Total	C	N	O	S	0	0	0
			1788	1121	309	348	10			
1	D	228	Total	C	N	O	S	0	0	0
			1779	1116	307	346	10			
1	F	227	Total	C	N	O	S	0	0	0
			1773	1113	306	344	10			
1	H	228	Total	C	N	O	S	0	1	0
			1787	1122	308	347	10			
1	K	228	Total	C	N	O	S	0	0	0
			1779	1116	307	346	10			

- Molecule 2 is a protein called DENGUE SEROTYPE 4 ENVELOPE PROTEIN DOMAIN 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	96	Total	C	N	O	S	0	1	0
			745	471	126	144	4			
2	E	96	Total	C	N	O	S	0	0	0
			737	467	124	142	4			
2	G	93	Total	C	N	O	S	0	0	0
			706	446	117	139	4			
2	I	96	Total	C	N	O	S	0	0	0
			737	467	124	142	4			
2	J	96	Total	C	N	O	S	0	0	0
			737	467	124	142	4			
2	L	96	Total	C	N	O	S	0	1	0
			745	471	126	144	4			

- Molecule 3 is water.

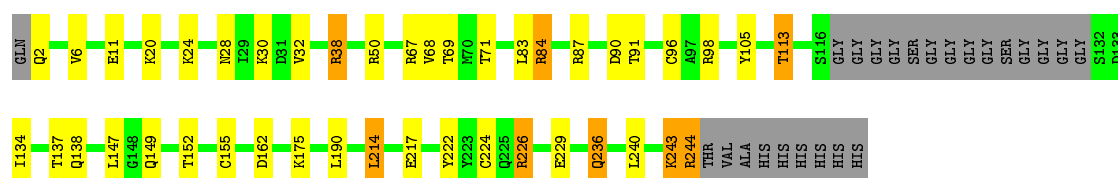
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total 3	O 3	0	0
3	B	6	Total 6	O 6	0	0
3	C	2	Total 2	O 2	0	0
3	D	4	Total 4	O 4	0	0
3	E	5	Total 5	O 5	0	0
3	F	5	Total 5	O 5	0	0
3	G	4	Total 4	O 4	0	0
3	H	3	Total 3	O 3	0	0
3	J	3	Total 3	O 3	0	0
3	K	1	Total 1	O 1	0	0
3	L	4	Total 4	O 4	0	0

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 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.

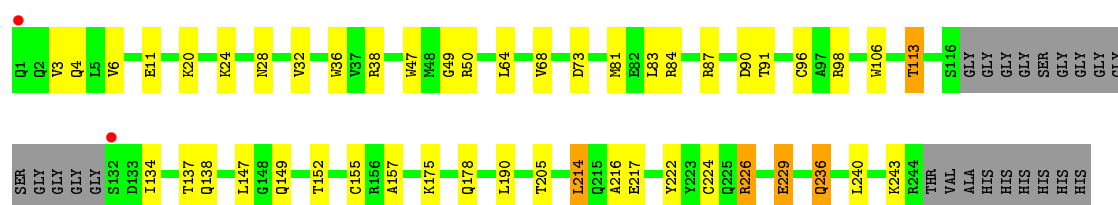
• Molecule 1: SCFV513

Chain A: 



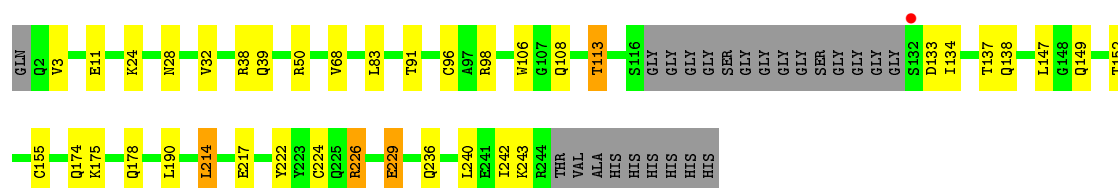
• Molecule 1: SCFV513

Chain B: 



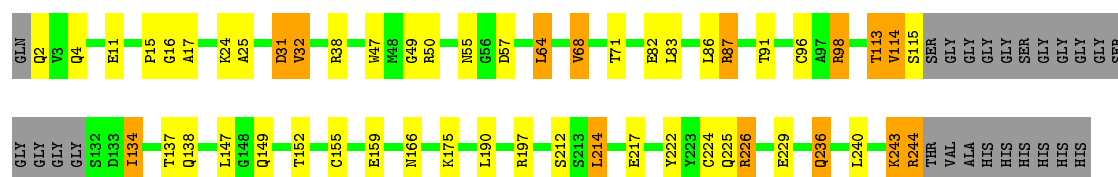
• Molecule 1: SCFV513

Chain D: 



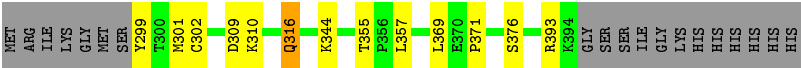
• Molecule 1: SCFV513

Chain F: 





● Molecule 2: DENGUE SEROTYPE 4 ENVELOPE PROTEIN DOMAIN 3



● Molecule 2: DENGUE SEROTYPE 4 ENVELOPE PROTEIN DOMAIN 3



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.11Å 131.67Å 176.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.75 – 3.27 45.71 – 3.27	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.75-3.27) 99.8 (45.71-3.27)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 3.25Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.227 , 0.263 0.225 , 0.259	Depositor DCC
R_{free} test set	1618 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	48.8	Xtriage
Anisotropy	0.057	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 31.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	4 of 31967 reflections (0.013%)	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	15132	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.97% 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, 0.375 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	0.53	0/1819	0.74	1/2465 (0.0%)
1	B	0.49	0/1828	0.71	1/2477 (0.0%)
1	D	0.52	0/1819	0.74	1/2465 (0.0%)
1	F	0.59	0/1813	0.85	3/2457 (0.1%)
1	H	0.52	0/1827	0.74	0/2476
1	K	0.53	0/1819	0.77	2/2465 (0.1%)
2	C	0.54	0/759	0.80	1/1028 (0.1%)
2	E	0.51	0/751	0.74	0/1017
2	G	0.58	0/719	0.81	0/976
2	I	0.52	0/751	0.76	0/1017
2	J	0.51	0/751	0.75	0/1017
2	L	0.51	0/759	0.83	1/1028 (0.1%)
All	All	0.53	0/15415	0.77	10/20888 (0.0%)

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	31	ASP	CB-CG-OD1	9.29	126.66	118.30
2	C	302	CYS	CA-CB-SG	7.82	128.07	114.00
1	K	227	SER	CB-CA-C	-7.60	95.65	110.10
1	F	31	ASP	CB-CG-OD2	-7.29	111.73	118.30
1	D	133	ASP	CB-CG-OD1	5.55	123.29	118.30

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	1779	0	1718	18	0
1	B	1788	0	1729	19	0
1	D	1779	0	1718	12	0
1	F	1773	0	1713	25	0
1	H	1787	0	1728	28	0
1	K	1779	0	1718	13	0
2	C	745	0	746	22	0
2	E	737	0	741	4	0
2	G	706	0	706	5	0
2	I	737	0	741	5	0
2	J	737	0	741	3	0
2	L	745	0	746	11	0
3	A	3	0	0	0	0
3	B	6	0	0	0	0
3	C	2	0	0	0	0
3	D	4	0	0	0	0
3	E	5	0	0	0	0
3	F	5	0	0	0	0
3	G	4	0	0	0	0
3	H	3	0	0	0	0
3	J	3	0	0	1	0
3	K	1	0	0	0	0
3	L	4	0	0	0	0
All	All	15132	0	14745	140	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 140 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:H:182[B]:LEU:HD23	1:H:182[B]:LEU:H	1.14	1.05
1:H:68:VAL:HG12	1:H:81:MET:CE	1.85	1.05
2:C:316:GLN:HB2	2:L:316:GLN:HB3	1.43	0.97
1:H:138:GLN:H	1:H:236:GLN:HE22	1.15	0.93
1:F:138:GLN:H	1:F:236:GLN:HE22	1.16	0.92

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	224/252 (89%)	217 (97%)	7 (3%)	0	100	100
1	B	225/252 (89%)	217 (96%)	8 (4%)	0	100	100
1	D	224/252 (89%)	216 (96%)	8 (4%)	0	100	100
1	F	223/252 (88%)	216 (97%)	7 (3%)	0	100	100
1	H	225/252 (89%)	215 (96%)	10 (4%)	0	100	100
1	K	224/252 (89%)	216 (96%)	8 (4%)	0	100	100
2	C	95/115 (83%)	92 (97%)	3 (3%)	0	100	100
2	E	94/115 (82%)	91 (97%)	3 (3%)	0	100	100
2	G	91/115 (79%)	87 (96%)	4 (4%)	0	100	100
2	I	94/115 (82%)	90 (96%)	4 (4%)	0	100	100
2	J	94/115 (82%)	90 (96%)	3 (3%)	1 (1%)	17	59
2	L	95/115 (83%)	87 (92%)	8 (8%)	0	100	100
All	All	1908/2202 (87%)	1834 (96%)	73 (4%)	1 (0%)	56	90

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	J	316	GLN

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	192/203 (95%)	164 (85%)	28 (15%)	4	19
1	B	193/203 (95%)	169 (88%)	24 (12%)	6	26
1	D	192/203 (95%)	168 (88%)	24 (12%)	6	26
1	F	191/203 (94%)	160 (84%)	31 (16%)	3	14
1	H	193/203 (95%)	168 (87%)	25 (13%)	5	24
1	K	192/203 (95%)	161 (84%)	31 (16%)	3	14
2	C	84/99 (85%)	75 (89%)	9 (11%)	8	33
2	E	83/99 (84%)	76 (92%)	7 (8%)	14	47
2	G	80/99 (81%)	68 (85%)	12 (15%)	3	17
2	I	83/99 (84%)	74 (89%)	9 (11%)	8	33
2	J	83/99 (84%)	74 (89%)	9 (11%)	8	33
2	L	84/99 (85%)	77 (92%)	7 (8%)	14	48
All	All	1650/1812 (91%)	1434 (87%)	216 (13%)	5	23

5 of 216 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	50	ARG
1	F	236	GLN
1	K	155	CYS
1	F	71	THR
1	F	147	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	225	GLN
1	F	236	GLN
2	J	390	HIS
2	E	384	ASN
2	J	384	ASN

5.3.3 RNA ⓘ

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	228/252 (90%)	-0.25	0 100 100	21, 39, 64, 83	1 (0%)
1	B	229/252 (90%)	-0.24	2 (0%) 85 81	22, 39, 74, 105	1 (0%)
1	D	228/252 (90%)	-0.18	1 (0%) 93 91	24, 41, 63, 92	1 (0%)
1	F	227/252 (90%)	-0.06	0 100 100	26, 47, 73, 95	1 (0%)
1	H	228/252 (90%)	-0.25	0 100 100	22, 40, 60, 81	1 (0%)
1	K	228/252 (90%)	-0.24	1 (0%) 93 91	22, 39, 64, 100	1 (0%)
2	C	96/115 (83%)	0.31	2 (2%) 67 58	38, 78, 107, 129	0
2	E	96/115 (83%)	0.03	1 (1%) 84 79	37, 58, 81, 93	0
2	G	93/115 (80%)	0.88	10 (10%) 8 5	63, 91, 124, 141	0
2	I	96/115 (83%)	0.22	1 (1%) 84 79	36, 73, 108, 119	0
2	J	96/115 (83%)	0.05	0 100 100	34, 61, 102, 122	0
2	L	96/115 (83%)	0.09	1 (1%) 84 79	38, 70, 93, 108	0
All	All	1941/2202 (88%)	-0.07	19 (0%) 84 79	21, 46, 95, 141	6 (0%)

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	G	353	SER	5.7
2	G	349	GLY	4.3
2	G	313	ALA	3.7
1	B	132	SER	3.2
2	C	384	ASN	3.0

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.