wwPDB X-ray Structure Validation Summary Report (i)

May 15, 2024 – 04:07 PM EDT

PDB ID	:	8G8D
Title	:	Crystal structure of DH1346 Fab in complex with HIV proximal MPER peptide
Authors	:	Niyongabo, A.; Janus, B.M.; Ofek, G.
Deposited on	:	2023-02-17
Resolution	:	2.02 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

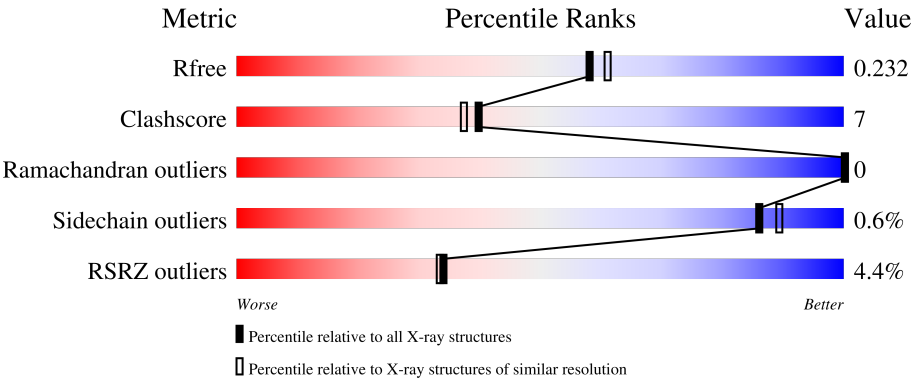
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.02 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	10434 (2.04-2.00)
Clashscore	141614	11643 (2.04-2.00)
Ramachandran outliers	138981	11493 (2.04-2.00)
Sidechain outliers	138945	11492 (2.04-2.00)
RSRZ outliers	127900	10220 (2.04-2.00)

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 of 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 <=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	230	92% 8%
1	H	230	88% 11%
2	B	215	3% 81% 17%
2	L	215	13% 81% 15%
3	C	34	6% 74% 12% 15%

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Mol	Chain	Length	Quality of chain
3	P	34	6% 71% 15% 15%

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	NA	H	303	-	-	-	X

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 14370 atoms, of which 6798 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 DH1346 heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	H	228	Total	C	H	N	O	S	0	0	0
			3386	1092	1672	284	331	7			
1	A	230	Total	C	H	N	O	S	0	0	0
			3401	1098	1677	286	333	7			

- Molecule 2 is a protein called DH1346 light chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	L	208	Total	C	H	N	O	S	0	0	0
			3017	973	1464	261	315	4			
2	B	211	Total	C	H	N	O	S	0	0	0
			3093	995	1503	267	324	4			

- Molecule 3 is a protein called gp41 MPER peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	29	Total	C	H	N	O	0	0	0
			507	180	241	40	46			
3	C	29	Total	C	H	N	O	0	0	0
			507	180	241	40	46			

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	3	Total	Na	0	0
			3	3		
4	L	3	Total	Na	0	0
			3	3		
4	A	2	Total	Na	0	0
			2	2		
4	B	2	Total	Na	0	0
			2	2		

- Molecule 5 is FLUORIDE ION (three-letter code: F) (formula: F).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	L	1	Total F 1 1	0	0

- Molecule 6 is water.

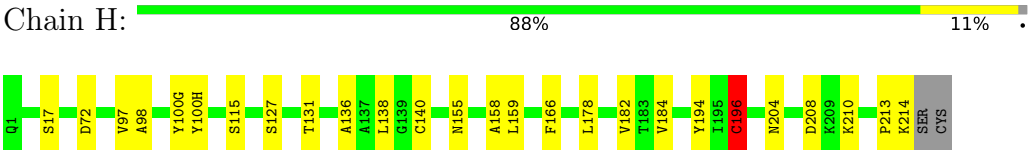
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	H	132	Total O 132 132	0	0
6	L	74	Total O 74 74	0	0
6	P	3	Total O 3 3	0	0
6	A	144	Total O 144 144	0	0
6	B	82	Total O 82 82	0	0
6	C	13	Total O 13 13	0	0

3 Residue-property plots (i)

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 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.

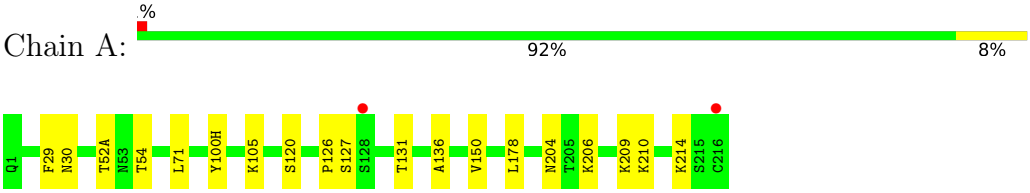
• Molecule 1: DH1346 heavy chain

Chain H:



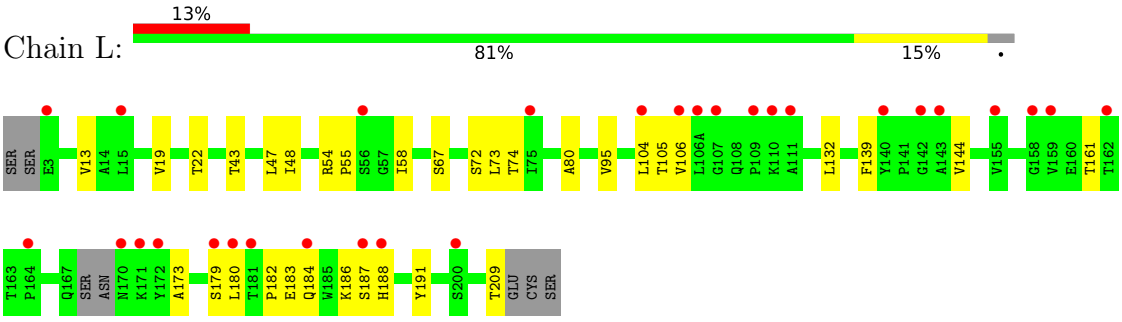
• Molecule 1: DH1346 heavy chain

Chain A:



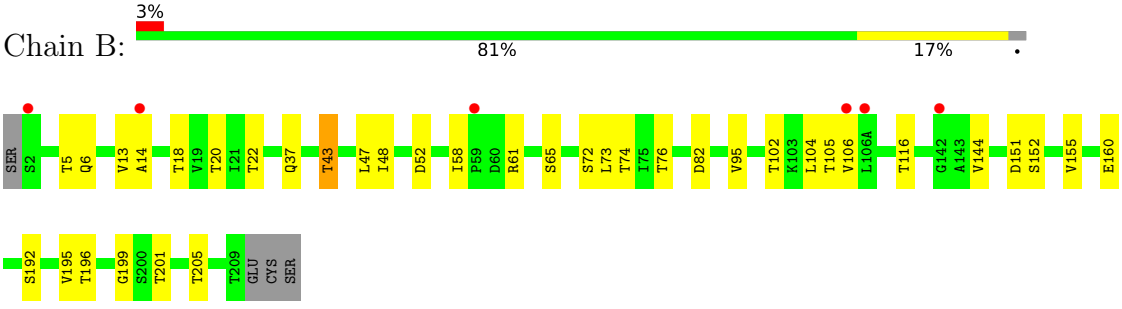
• Molecule 2: DH1346 light chain

Chain L:



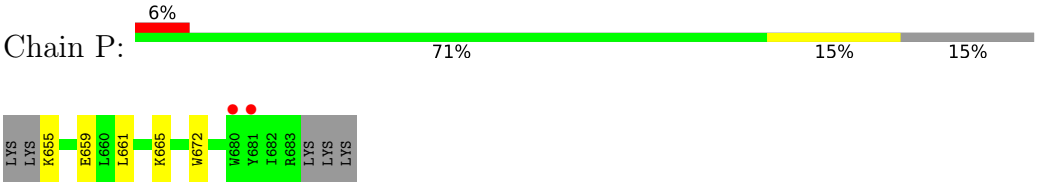
• Molecule 2: DH1346 light chain

Chain B:



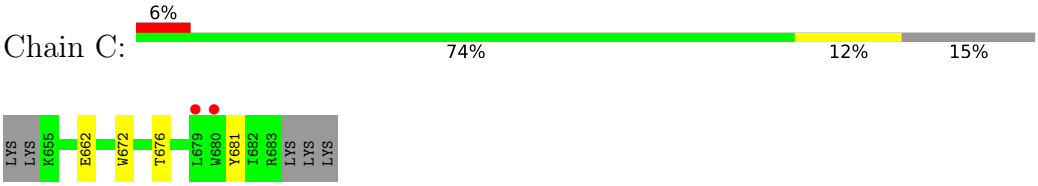
• Molecule 3: gp41 MPER peptide

Chain P:



• Molecule 3: gp41 MPER peptide

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	41.07Å 115.51Å 231.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.98 – 2.02 37.98 – 2.02	Depositor EDS
% Data completeness (in resolution range)	91.7 (37.98-2.02) 91.7 (37.98-2.02)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.49 (at 2.03Å)	Xtriage
Refinement program	PHENIX 1.20	Depositor
R, R_{free}	0.198 , 0.234 0.197 , 0.232	Depositor DCC
R_{free} test set	5094 reflections (7.60%)	wwPDB-VP
Wilson B-factor (Å^2)	30.0	Xtriage
Anisotropy	0.241	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 56.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	14370	wwPDB-VP
Average B, all atoms (Å^2)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.23% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: F, NA

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	0.31	0/1770	0.54	0/2415
1	H	0.41	2/1760 (0.1%)	0.55	0/2401
2	B	0.32	0/1631	0.55	0/2236
2	L	0.31	0/1592	0.55	0/2182
3	C	0.31	0/277	0.42	0/380
3	P	0.56	2/277 (0.7%)	0.57	0/380
All	All	0.35	4/7307 (0.1%)	0.55	0/9994

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	140	CYS	CB-SG	-6.84	1.70	1.82
1	H	196	CYS	CB-SG	-5.88	1.72	1.81
3	P	665	LYS	CE-NZ	5.27	1.62	1.49
3	P	665	LYS	CD-CE	5.18	1.64	1.51

There are no bond angle outliers.

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	1724	1677	1677	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	1714	1672	1672	21	0
2	B	1590	1503	1508	31	0
2	L	1553	1464	1463	30	0
3	C	266	241	241	2	2
3	P	266	241	241	5	2
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	H	3	0	0	0	0
4	L	3	0	0	0	0
5	L	1	0	0	0	0
6	A	144	0	0	9	1
6	B	82	0	0	9	0
6	C	13	0	0	0	0
6	H	132	0	0	4	1
6	L	74	0	0	12	0
6	P	3	0	0	0	0
All	All	7572	6798	6802	101	3

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 7.

The worst 5 of 101 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:97:VAL:HG11	3:P:661:LEU:HD22	1.53	0.89
2:L:67:SER:OG	6:L:401:HOH:O	1.91	0.88
2:B:160:GLU:OE1	6:B:402:HOH:O	1.90	0.87
2:B:199:GLY:O	6:B:401:HOH:O	1.90	0.86
2:L:54:ARG:NH1	6:L:403:HOH:O	2.12	0.83

All (3) 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)
3:P:655:LYS:NZ	3:C:681:TYR:OH[2_455]	2.08	0.12
3:P:655:LYS:HZ3	3:C:681:TYR:OH[2_455]	1.56	0.04
6:H:471:HOH:O	6:A:525:HOH:O[3_554]	2.18	0.02

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	228/230 (99%)	226 (99%)	2 (1%)	0	100	100
1	H	226/230 (98%)	224 (99%)	2 (1%)	0	100	100
2	B	209/215 (97%)	202 (97%)	7 (3%)	0	100	100
2	L	204/215 (95%)	191 (94%)	13 (6%)	0	100	100
3	C	27/34 (79%)	27 (100%)	0	0	100	100
3	P	27/34 (79%)	27 (100%)	0	0	100	100
All	All	921/958 (96%)	897 (97%)	24 (3%)	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	189/193 (98%)	188 (100%)	1 (0%)	88	91
1	H	189/193 (98%)	187 (99%)	2 (1%)	73	77
2	B	177/185 (96%)	176 (99%)	1 (1%)	86	89
2	L	170/185 (92%)	169 (99%)	1 (1%)	86	89
3	C	27/33 (82%)	27 (100%)	0	100	100
3	P	27/33 (82%)	27 (100%)	0	100	100
All	All	779/822 (95%)	774 (99%)	5 (1%)	86	89

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	100(H)	TYR
1	H	196	CYS
2	L	43	THR
1	A	100(H)	TYR
2	B	43	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry

Of 11 ligands modelled in this entry, 11 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

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 (i)

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	230/230 (100%)	-0.19	2 (0%) 84 83	20, 31, 52, 152	0
1	H	228/230 (99%)	-0.19	0 100 100	20, 35, 55, 69	0
2	B	211/215 (98%)	0.17	6 (2%) 53 52	23, 48, 73, 86	0
2	L	208/215 (96%)	0.65	29 (13%) 2 2	24, 58, 94, 104	0
3	C	29/34 (85%)	0.31	2 (6%) 16 16	27, 42, 76, 85	0
3	P	29/34 (85%)	0.37	2 (6%) 16 16	27, 40, 88, 92	0
All	All	935/958 (97%)	0.11	41 (4%) 34 33	20, 39, 80, 152	0

The worst 5 of 41 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	680	TRP	4.8
2	L	140	TYR	4.5
2	L	109	PRO	4.4
3	P	681	TYR	4.0
2	L	3	GLU	3.9

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

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	NA	L	303	1/1	0.25	0.23	104,104,104,104	0
4	NA	H	303	1/1	0.76	0.42	60,60,60,60	0
4	NA	B	301	1/1	0.81	0.41	67,67,67,67	0
4	NA	B	302	1/1	0.90	0.10	49,49,49,49	0
4	NA	A	302	1/1	0.91	0.09	45,45,45,45	0
4	NA	L	301	1/1	0.91	0.22	56,56,56,56	0
4	NA	H	302	1/1	0.91	0.13	40,40,40,40	0
4	NA	L	302	1/1	0.93	0.22	64,64,64,64	0
4	NA	A	301	1/1	0.96	0.16	44,44,44,44	0
4	NA	H	301	1/1	0.97	0.12	35,35,35,35	0
5	F	L	304	1/1	0.98	0.07	31,31,31,31	0

6.5 Other polymers (i)

There are no such residues in this entry.